The Enzyme List
Class 2 — Transferases

Nomenclature Committee
of the
International Union of Biochemistry and Molecular Biology
(NC-IUBMB)

LaTeX version prepared by Andrew McDonald,
School of Biochemistry and Immunology, Trinity College Dublin, Ireland

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Contents

EC 2.1 Transferring one-carbon groups

This subclass contains the methyltransferases (EC 2.1.1), the hydroxymethyl-, formyl- and related transferases (EC 2.1.2), the carboxy- and carbamoyltransferases (EC 2.1.3) and the amidinotransferases (EC 2.1.4).

EC 2.1.1 Methyltransferases

EC 2.1.1.1

Accepted name:	nicotinamide *N*-methyltransferase
Reaction:	*S*-adenosyl-L-methionine + nicotinamide = *S*-adenosyl-L-homocysteine + 1-methylnicotinamide
Other name(s):	nicotinamide methyltransferase
Systematic name:	*S*-adenosyl-L-methionine:nicotinamide *N*-methyltransferase
References:	[469]

[EC 2.1.1.1 created 1961]

EC 2.1.1.2

Accepted name:	guanidinoacetate *N*-methyltransferase
Reaction:	*S*-adenosyl-L-methionine + guanidinoacetate = *S*-adenosyl-L-homocysteine + creatine
Other name(s):	GA methylpherase; guanidinoacetate methyltransferase; guanidinoacetate transmethylase; methionine-guanidinoacetic transmethylase; guanidoacetate methyltransferase
Systematic name:	*S*-adenosyl-L-methionine:*N*-guanidinoacetate methyltransferase
References:	[472, 473]

[EC 2.1.1.2 created 1961]

EC 2.1.1.3

Accepted name: thetin—homocysteine *S*-methyltransferase
Reaction: dimethylsulfonioacetate + L-homocysteine = (methylsulfanyl)acetate + L-methionine
Other name(s): dimethylthetin-homocysteine methyltransferase; thetin-homocysteine methylpherase
Systematic name: dimethylsulfonioacetate:L-homocysteine *S*-methyltransferase
References: [1703, 2177, 2178]

[EC 2.1.1.3 created 1961]

EC 2.1.1.4

Accepted name: acetylserotonin *O*-methyltransferase
Reaction: *S*-adenosyl-L-methionine + *N*-acetylserotonin = *S*-adenosyl-L-homocysteine + melatonin
Other name(s): hydroxyindole methyltransferase; hydroxyindole *O*-methyltransferase; *N*-acetylserotonin *O*-methyltransferase; acetylserotonin methyltransferase
Systematic name: *S*-adenosyl-L-methionine:*N*-acetylserotonin *O*-methyltransferase
Comments: Some other hydroxyindoles also act as acceptor, but more slowly.
References: [140]

[EC 2.1.1.4 created 1961]

EC 2.1.1.5

Accepted name: betaine—homocysteine *S*-methyltransferase
Reaction: betaine + L-homocysteine = dimethylglycine + L-methionine
Other name(s): betaine-homocysteine methyltransferase; betaine-homocysteine transmethylase
Systematic name: trimethylammonioacetate:L-homocysteine *S*-methyltransferase
References: [1703]

[EC 2.1.1.5 created 1961]

EC 2.1.1.6

Accepted name: catechol *O*-methyltransferase
Reaction: *S*-adenosyl-L-methionine + a catechol = *S*-adenosyl-L-homocysteine + a guaiacol
Other name(s): COMT I ; COMT II; *S*-COMT (soluble form of catechol-*O*-methyltransferase); MB-COMT (membrane-bound form of catechol-*O*-methyltransferase); catechol methyltransferase; catecholamine *O*-methyltransferase
Systematic name: *S*-adenosyl-L-methionine:catechol *O*-methyltransferase
Comments: The mammalian enzyme acts more rapidly on catecholamines such as adrenaline or noradrenaline than on catechols.
References: [139, 1175, 1405]

[EC 2.1.1.6 created 1965]

EC 2.1.1.7

Accepted name: nicotinate *N*-methyltransferase
Reaction: *S*-adenosyl-L-methionine + nicotinate = *S*-adenosyl-L-homocysteine + *N*-methylnicotinate
Other name(s): furanocoumarin 8-methyltransferase; furanocoumarin 8-*O*-methyltransferase
Systematic name: *S*-adenosyl-L-methionine:nicotinate *N*-methyltransferase
References: [1540]

[EC 2.1.1.7 created 1965]

EC 2.1.1.8

Accepted name: histamine *N*-methyltransferase
Reaction: *S*-adenosyl-L-methionine + histamine = *S*-adenosyl-L-homocysteine + N^{τ}-methylhistamine
Other name(s): histamine 1-methyltransferase; histamine methyltransferase; histamine-methylating enzyme; imidazolemethyltransferase; *S*-adenosylmethionine-histamine *N*-methyltransferase
Systematic name: *S*-adenosyl-L-methionine:histamine *N-tele*-methyltransferase
References: [404]

[EC 2.1.1.8 created 1965]

EC 2.1.1.9

Accepted name: thiol *S*-methyltransferase
Reaction: *S*-adenosyl-L-methionine + a thiol = *S*-adenosyl-L-homocysteine + a methyl thioether
Other name(s): *S*-methyltransferase; thiol methyltransferase; TMT
Systematic name: *S*-adenosyl-L-methionine:thiol *S*-methyltransferase
Comments: H_2S and a variety of alkyl, aryl and heterocyclic thiols and hydroxy thiols can act as acceptors.
References: [355, 387, 3809]

[EC 2.1.1.9 created 1965]

EC 2.1.1.10

Accepted name: homocysteine *S*-methyltransferase
Reaction: *S*-methyl-L-methionine + L-homocysteine = **2** L-methionine
Other name(s): *S*-adenosylmethionine homocysteine transmethylase; *S*-methylmethionine homocysteine transmethylase; adenosylmethionine transmethylase; methylmethionine:homocysteine methyltransferase; adenosylmethionine:homocysteine methyltransferase; homocysteine methylase; homocysteine methyltransferase; homocysteine transmethylase; L-homocysteine *S*-methyltransferase; *S*-adenosyl-L-methionine:L-homocysteine methyltransferase; *S*-adenosylmethionine-homocysteine transmethylase; *S*-adenosylmethionine:homocysteine methyltransferase
Systematic name: *S*-methyl-L-methionine:L-homocysteine *S*-methyltransferase
Comments: The enzyme uses *S*-adenosyl-L-methionine as methyl donor less actively than *S*-methyl-L-methionine.
References: [172, 3152, 3153, 2339, 2812, 2811, 1156]

[EC 2.1.1.10 created 1965, modified 2010]

EC 2.1.1.11

Accepted name: magnesium protoporphyrin IX methyltransferase
Reaction: *S*-adenosyl-L-methionine + magnesium protoporphyrin IX = *S*-adenosyl-L-homocysteine + magnesium protoporphyrin IX 13-methyl ester
Systematic name: *S*-adenosyl-L-methionine:magnesium-protoporphyrin-IX *O*-methyltransferase
References: [1053, 3173, 345, 1054, 801]

[EC 2.1.1.11 created 1965, modified 2003]

EC 2.1.1.12

Accepted name: methionine *S*-methyltransferase
Reaction: *S*-adenosyl-L-methionine + L-methionine = *S*-adenosyl-L-homocysteine + *S*-methyl-L-methionine
Other name(s): *S*-adenosyl methionine:methionine methyl transferase; methionine methyltransferase; *S*-adenosylmethionine transmethylase; *S*-adenosylmethionine-methionine methyltransferase
Systematic name: *S*-adenosyl-L-methionine:L-methionine *S*-methyltransferase
Comments: Requires Zn^{2+} or Mn^{2+}
References: [1588]

[EC 2.1.1.12 created 1972]

EC 2.1.1.13

Accepted name: methionine synthase

Reaction: 5-methyltetrahydrofolate + L-homocysteine = tetrahydrofolate + L-methionine

Other name(s): 5-methyltetrahydrofolate—homocysteine *S*-methyltransferase; 5-methyltetrahydrofolate—homocysteine transmethylase; *N*-methyltetrahydrofolate:L-homocysteine methyltransferase; N^5-methyltetrahydrofolate methyltransferase; N^5-methyltetrahydrofolate-homocysteine cobalamin methyltransferase; N^5-methyltetrahydrofolic—homocysteine vitamin B_{12} transmethylase; B_{12} N^5-methyltetrahydrofolate homocysteine methyltransferase; methyltetrahydrofolate—homocysteine vitamin B_{12} methyltransferase; tetrahydrofolate methyltransferase; tetrahydropteroylglutamate methyltransferase; tetrahydropteroylglutamic methyltransferase; vitamin B_{12} methyltransferase; cobalamin-dependent methionine synthase; methionine synthase (cobalamin-dependent); MetH

Systematic name: 5-methyltetrahydrofolate:L-homocysteine *S*-methyltransferase

Comments: Contains zinc and cobamide. The enzyme becomes inactivated occasionally during its cycle by oxidation of Co(I) to Co(II). Reactivation by reductive methylation is catalysed by the enzyme itself, with *S*-adenosyl-L-methionine as the methyl donor and a reducing system. For the mammalian enzyme, the reducing system involves NADPH and EC 1.16.1.8, [methionine synthase] reductase. In bacteria, the reducing agent is flavodoxin, and no further catalyst is needed (the flavodoxin is kept in the reduced state by NADPH and EC 1.18.1.2, ferredoxin—NADP$^+$ reductase). Acts on the monoglutamate as well as the triglutamate folate, in contrast with EC 2.1.1.14, 5-methyltetrahydropteroyltriglutamate—homocysteine *S*-methyltransferase, which acts only on the triglutamate.

References: [436, 936, 1172, 2043, 3484, 1502, 2651, 1199, 177]

[EC 2.1.1.13 created 1972, modified 2003]

EC 2.1.1.14

Accepted name: 5-methyltetrahydropteroyltriglutamate—homocysteine *S*-methyltransferase

Reaction: 5-methyltetrahydropteroyltri-L-glutamate + L-homocysteine = tetrahydropteroyltri-L-glutamate + L-methionine

Other name(s): tetrahydropteroyltriglutamate methyltransferase; homocysteine methylase; methyltransferase, tetrahydropteroylglutamate-homocysteine transmethylase; methyltetrahydropteroylpolyglutamate:homocysteine methyltransferase; cobalamin-independent methionine synthase; methionine synthase (cobalamin-independent); MetE

Systematic name: 5-methyltetrahydropteroyltri-L-glutamate:L-homocysteine *S*-methyltransferase

Comments: Requires phosphate and contains zinc. The enzyme from *Escherichia coli* also requires a reducing system. Unlike EC 2.1.1.13, methionine synthase, this enzyme does not contain cobalamin.

References: [1172, 3840, 814, 1101, 2651]

[EC 2.1.1.14 created 1972, modified 2003]

EC 2.1.1.15

Accepted name: fatty-acid *O*-methyltransferase

Reaction: *S*-adenosyl-L-methionine + a fatty acid = *S*-adenosyl-L-homocysteine + a fatty acid methyl ester

Other name(s): fatty acid methyltransferase; fatty acid *O*-methyltransferase

Systematic name: *S*-adenosyl-L-methionine:fatty-acid *O*-methyltransferase

Comments: Oleic acid is the most effective fatty acid acceptor.

References: [32]

[EC 2.1.1.15 created 1972]

EC 2.1.1.16

Accepted name: methylene-fatty-acyl-phospholipid synthase

Reaction: *S*-adenosyl-L-methionine + phospholipid olefinic fatty acid = *S*-adenosyl-L-homocysteine + phospholipid methylene fatty acid

Other name(s): unsaturated-phospholipid methyltransferase

Systematic name: *S*-adenosyl-L-methionine:unsaturated-phospholipid methyltransferase (methenylating)
Comments: The enzyme transfers a methyl group to the 10-position of a Δ-olefinic acyl chain in phosphatidylglycerol or phosphatidylinositol or, more slowly, phosphatidylethanolamine; subsequent proton transfer produces a 10-methylene group (*cf.* EC 2.1.1.79 cyclopropane-fatty-acyl-phospholipid synthase).
References: [31]

[EC 2.1.1.16 created 1972, modified 1986]

EC 2.1.1.17

Accepted name: phosphatidylethanolamine *N*-methyltransferase
Reaction: *S*-adenosyl-L-methionine + phosphatidylethanolamine = *S*-adenosyl-L-homocysteine + phosphatidyl-*N*-methylethanolamine
Other name(s): PEMT; LMTase; lipid methyl transferase; phosphatidylethanolamine methyltransferase; phosphatidylethanolamine-*N*-methylase; phosphatidylethanolamine-*S*-adenosylmethionine methyltransferase
Systematic name: *S*-adenosyl-L-methionine:phosphatidylethanolamine *N*-methyltransferase
References: [1339, 2312, 3096]

[EC 2.1.1.17 created 1972]

EC 2.1.1.18

Accepted name: polysaccharide *O*-methyltransferase
Reaction: *S*-adenosyl-L-methionine + a (1→4)-α-D-glucooligosaccharide = *S*-adenosyl-L-homocysteine + an oligosaccharide containing 6-methyl-D-glucose units
Other name(s): polysaccharide methyltransferase; acylpolysacharide 6-methyltransferase; *S*-adenosyl-L-methionine:1,4-α-D-glucan 6-*O*-methyltransferase
Systematic name: *S*-adenosyl-L-methionine:(1→4)-α-D-glucan 6-*O*-methyltransferase
References: [892]

[EC 2.1.1.18 created 1972]

EC 2.1.1.19

Accepted name: trimethylsulfonium—tetrahydrofolate *N*-methyltransferase
Reaction: trimethylsulfonium + tetrahydrofolate = dimethylsulfide + 5-methyltetrahydrofolate
Other name(s): trimethylsulfonium-tetrahydrofolate methyltransferase
Systematic name: trimethylsulfonium:tetrahydrofolate *N*-methyltransferase
References: [3715]

[EC 2.1.1.19 created 1972]

EC 2.1.1.20

Accepted name: glycine *N*-methyltransferase
Reaction: *S*-adenosyl-L-methionine + glycine = *S*-adenosyl-L-homocysteine + sarcosine
Other name(s): glycine methyltransferase; *S*-adenosyl-L-methionine:glycine methyltransferase; GNMT
Systematic name: *S*-adenosyl-L-methionine:glycine *N*-methyltransferase
Comments: This enzyme is thought to play an important role in the regulation of methyl group metabolism in the liver and pancreas by regulating the ratio between *S*-adenosyl-L-methionine and *S*-adenosyl-L-homocysteine. It is inhibited by 5-methyltetrahydrofolate pentaglutamate [2145]. Sarcosine, which has no physiological role, is converted back into glycine by the action of EC 1.5.8.3, sarcosine dehydrogenase.
References: [334, 2515, 3976, 2145, 3446, 2599]

[EC 2.1.1.20 created 1972, modified 2005]

EC 2.1.1.21

Accepted name: methylamine—glutamate *N*-methyltransferase
Reaction: methylamine + L-glutamate = NH_3 + *N*-methyl-L-glutamate
Other name(s): *N*-methylglutamate synthase; methylamine-glutamate methyltransferase
Systematic name: methylamine:L-glutamate *N*-methyltransferase
References: [3165]

[EC 2.1.1.21 created 1972]

EC 2.1.1.22

Accepted name: carnosine *N*-methyltransferase
Reaction: *S*-adenosyl-L-methionine + carnosine = *S*-adenosyl-L-homocysteine + anserine
Systematic name: *S*-adenosyl-L-methionine:carnosine *N*-methyltransferase
References: [2200]

[EC 2.1.1.22 created 1972]

[2.1.1.23 Deleted entry. protein-arginine N-methyltransferase. Now listed as EC 2.1.1.124 [cytochrome c]-arginine N-methyltransferase, EC 2.1.1.125 histone-arginine N-methyltransferase and EC 2.1.1.126 [myelin basic protein]-arginine N-methyltransferase]

[EC 2.1.1.23 created 1972, modified 1976, modified 1983, deleted 1999]

*[2.1.1.24 Deleted entry. protein-γ-glutamate O-methyltransferase. Now listed as EC 2.1.1.77 protein-*L*-isoaspartate(*D*-aspartate) O-methyltransferase, EC 2.1.1.80 protein-glutamate O-methyltransferase and EC 2.1.1.100 protein-S-isoprenylcysteine O-methyltransferase]*

[EC 2.1.1.24 created 1972, modified 1983, modified 1989, deleted 1992]

EC 2.1.1.25

Accepted name: phenol *O*-methyltransferase
Reaction: *S*-adenosyl-L-methionine + phenol = *S*-adenosyl-L-homocysteine + anisole
Other name(s): PMT
Systematic name: *S*-adenosyl-L-methionine:phenol *O*-methyltransferase
Comments: Acts on a wide variety of simple alkyl-, methoxy- and halo-phenols.
References: [138]

[EC 2.1.1.25 created 1972]

EC 2.1.1.26

Accepted name: iodophenol *O*-methyltransferase
Reaction: *S*-adenosyl-L-methionine + 2-iodophenol = *S*-adenosyl-L-homocysteine + 2-iodophenol methyl ether
Systematic name: *S*-adenosyl-L-methionine:2-iodophenol *O*-methyltransferase
References: [3547]

[EC 2.1.1.26 created 1972]

EC 2.1.1.27

Accepted name: tyramine *N*-methyltransferase
Reaction: *S*-adenosyl-L-methionine + tyramine = *S*-adenosyl-L-homocysteine + *N*-methyltyramine
Other name(s): DIB *O*-methyltransferase (3,5-diiodo-4-hydroxy-benzoic acid); *S*-adenosyl-methionine:tyramine *N*-methyltransferase; tyramine methylpherase
Systematic name: *S*-adenosyl-L-methionine:tyramine *N*-methyltransferase
Comments: Has some activity on phenylethylamine analogues.
References: [2112]

[EC 2.1.1.27 created 1972]

EC 2.1.1.28

Accepted name: phenylethanolamine *N*-methyltransferase

Reaction: *S*-adenosyl-L-methionine + phenylethanolamine = *S*-adenosyl-L-homocysteine + *N*-methylphenylethanolamine

Other name(s): noradrenaline *N*-methyltransferase; noradrenalin *N*-methyltransferase; norepinephrine methyltransferase; norepinephrine *N*-methyltransferase; phenethanolamine methyltransferase; phenethanolamine *N*-methyltransferase

Systematic name: *S*-adenosyl-L-methionine:phenylethanolamine *N*-methyltransferase

Comments: Acts on various phenylethanolamines; converts noradrenaline into adrenaline.

References: [137, 597]

[EC 2.1.1.28 created 1972]

[2.1.1.29 Transferred entry. tRNA (cytosine-5-)-methyltransferase. Now covered by EC 2.1.1.202 [multisite-specific tRNA:(cytosine-C^5)-methyltransferase], EC 2.1.1.203 [tRNA (cytosine^{34}-C^5)-methyltransferase] and EC 2.1.1.204 [RNA (cytosine^{38}-C^5)-methyltransferase]

[EC 2.1.1.29 created 1972, deleted 2011]

[2.1.1.30 Deleted entry. tRNA (purine-2- or -6-)-methyltransferase. Reactions previously described are due to EC 2.1.1.32 tRNA (guanine-N^2-)-methyltransferase]

[EC 2.1.1.30 created 1972, deleted 1981]

[2.1.1.31 Transferred entry. tRNA (guanine-N^1-)-methyltransferase. Now covered by EC 2.1.1.221 (tRNA (guanine^9-N^1)-methyltransferase) and EC 2.1.1.228 (tRNA (guanine^{37}-N^1)-methyltransferase).]

[EC 2.1.1.31 created 1972, deleted 2011]

[2.1.1.32 Transferred entry. tRNA (guanine-N^2-)-methyltransferase. Now covered by EC 2.1.1.213 [tRNA (guanine^{10}-N^2)-dimethyltransferase], EC 2.1.1.214 [tRNA (guanine^{10}-N^2)-monomethyltransferase], EC 2.1.1.215 [tRNA (guanine^{26}-N^2/guanine^{27}-N^2)-dimethyltransferase] and EC 2.1.1.216 [tRNA (guanine^{26}-N^2)-dimethyltransferase]]

[EC 2.1.1.32 created 1972, deleted 2011]

EC 2.1.1.33

Accepted name: tRNA (guanine^{46}-N^7)-methyltransferase

Reaction: *S*-adenosyl-L-methionine + guanine^{46} in tRNA = *S*-adenosyl-L-homocysteine + N^7-methylguanine^{46} in tRNA

Other name(s): Trm8/Trm82; TrmB; tRNA (m^{7}G^{46}) methyltransferase; transfer ribonucleate guanine 7-methyltransferase; 7-methylguanine transfer ribonucleate methylase; tRNA guanine 7-methyltransferase; N^7-methylguanine methylase; *S*-adenosyl-L-methionine:tRNA (guanine-7-*N*-)-methyltransferase

Systematic name: *S*-adenosyl-L-methionine:tRNA (guanine-N^7)-methyltransferase

Comments: The enzyme specifically methylates guanine^{46} at N^7 in tRNA.

References: [119, 4027, 2774, 2010, 55]

[EC 2.1.1.33 created 1972, modified 2011]

EC 2.1.1.34

Accepted name: tRNA (guanosine^{18}-2′-*O*)-methyltransferase

Reaction: *S*-adenosyl-L-methionine + guanosine^{18} in tRNA = *S*-adenosyl-L-homocysteine + 2′-*O*-methylguanosine^{18} in tRNA

Other name(s): tRNA (Gm18) 2′-*O*-methyltransferase; tRNA (Gm18) methyltransferase; TrmH; SpoU

Systematic name: *S*-adenosyl-L-methionine:tRNA (guanosine^{18}-2′-*O*)-methyltransferase

Comments: The enzyme catalyses the methylation of guanosine^{18} in tRNA.

References: [1031, 1812, 1371, 2727, 2506]

[EC 2.1.1.34 created 1972, modified 2005, modified 2011]

EC 2.1.1.35

Accepted name: tRNA (uracil^{54}-C^5)-methyltransferase

Reaction: S-adenosyl-L-methionine + uracil^{54} in tRNA = S-adenosyl-L-homocysteine + 5-methyluracil^{54} in tRNA

Other name(s): transfer RNA uracil^{54} 5-methyltransferase; transfer RNA uracil^{54} methylase; tRNA uracil^{54} 5-methyltransferase; m^{5}U^{54}-methyltransferase; tRNA:m^{5}U^{54}-methyltransferase; RUMT; TrmA; 5-methyluridine^{54} tRNA methyltransferase; tRNA(uracil-54,C^5)-methyltransferase; Trm2; tRNA(m^{5}U^{54})methyltransferase

Systematic name: S-adenosyl-L-methionine:tRNA (uracil^{54}-C^5)-methyltransferase

Comments: Unlike this enzyme, EC 2.1.1.74 (methylenetetrahydrofolate—tRNA-(uracil^{54}-C^5)-methyltransferase (FADH$_2$-oxidizing)), uses 5,10-methylenetetrahydrofolate and FADH$_2$ to supply the atoms for methylation of U^{54} [703].

References: [316, 1134, 1413, 703, 1620, 1166, 247, 3726]

[EC 2.1.1.35 created 1972, modified 2011]

[2.1.1.36 Transferred entry. tRNA (adenine-N^1-)-methyltransferase. Now covered by EC 2.1.1.217 (tRNA (adenine^{22}-N^1)-methyltransferase), EC 2.1.1.218 (tRNA (adenine^9-N^1)-methyltransferase), EC 2.1.1.219 (tRNA (adenine^{57}-N^1/adenine^{58}-N^1)-methyltransferase), EC 2.1.1.220 (tRNA (adenine^{58}-N^1)-methyltransferase).]

[EC 2.1.1.36 created 1972, deleted 2011]

EC 2.1.1.37

Accepted name: DNA (cytosine-5-)-methyltransferase

Reaction: S-adenosyl-L-methionine + DNA containing cytosine = S-adenosyl-L-homocysteine + DNA containing 5-methylcytosine

Other name(s): *Eco*RI methylase; DNA 5-cytosine methylase; DNA cytosine C^5 methylase; DNA cytosine methylase; DNA methylase (ambiguous); DNA methyltransferase (ambiguous); DNA transmethylase (ambiguous); DNA-cytosine 5-methylase; DNA-cytosine methyltransferase; *Hpa*II methylase; *Hpa*II′ methylase; M.*Bsu*RIa; M.*Bsu*RIb; Type II DNA methylase; cytosine 5-methyltransferase; cytosine DNA methylase; cytosine DNA methyltransferase; cytosine-specific DNA methyltransferase; deoxyribonucleate methylase (ambiguous); deoxyribonucleate methyltransferase (ambiguous); deoxyribonucleic (cytosine-5-)-methyltransferase; deoxyribonucleic acid (cytosine-5-)-methyltransferase; deoxyribonucleic acid methylase (ambiguous); deoxyribonucleic acid methyltransferase (ambiguous); deoxyribonucleic acid modification methylase (ambiguous); deoxyribonucleic methylase (ambiguous); methylphosphotriester-DNA methyltransferase (ambiguous); modification methylase (ambiguous); restriction-modification system (ambiguous); site-specific DNA-methyltransferase (cytosine-specific); DNA-(cytosine C$_5$)-methylase

Systematic name: S-adenosyl-L-methionine:DNA (cytosine-5-)-methyltransferase

References: [1087, 1568, 2953, 3235, 3264, 3592, 1648, 2897, 4011]

[EC 2.1.1.37 created 1972, (EC 2.1.1.73 incorporated 2003), modified 2003]

EC 2.1.1.38

Accepted name: O-demethylpuromycin O-methyltransferase

Reaction: S-adenosyl-L-methionine + O-demethylpuromycin = S-adenosyl-L-homocysteine + puromycin

Other name(s): O-demethylpuromycin methyltransferase

Systematic name: S-adenosyl-L-methionine:O-demethylpuromycin O-methyltransferase

Comments: Puromycin is the antibiotic derived from N^6-dimethyladenosine by replacing the 3′-hydroxy group with an amino group and acylating this with 4-O-methyltyrosine.

References: [2816]

[EC 2.1.1.38 created 1972]

EC 2.1.1.39

Accepted name: inositol 3-methyltransferase

Reaction: *S*-adenosyl-L-methionine + *myo*-inositol = *S*-adenosyl-L-homocysteine + 1D-3-*O*-methyl-*myo*-inositol

Other name(s): inositol L-1-methyltransferase; *myo*-inositol 1-methyltransferase; *S*-adenosylmethionine:*myo*-inositol 1-methyltransferase; *myo*-inositol 1-*O*-methyltransferase (name based on 1L-numbering system and not 1D-numbering); *S*-adenosyl-L-methionine:*myo*-inositol 1-*O*-methyltransferase

Systematic name: *S*-adenosyl-L-methionine:1D-*myo*-inositol 3-*O*-methyltransferase

References: [1354]

[EC 2.1.1.39 created 1972, modified 2002]

EC 2.1.1.40

Accepted name: inositol 1-methyltransferase

Reaction: *S*-adenosyl-L-methionine + *myo*-inositol = *S*-adenosyl-L-homocysteine + 1D-1-*O*-methyl-*myo*-inositol

Other name(s): inositol D-1-methyltransferase; *S*-adenosylmethionine:*myo*-inositol 3-methyltransferase; *myo*-inositol 3-*O*-methyltransferase; inositol 3-*O*-methyltransferase (name based on 1L-numbering system and not 1D-numbering); *S*-adenosyl-L-methionine:*myo*-inositol 3-*O*-methyltransferase

Systematic name: *S*-adenosyl-L-methionine:1D-*myo*-inositol 1-*O*-methyltransferase

References: [3716]

[EC 2.1.1.40 created 1972, modified 2002]

EC 2.1.1.41

Accepted name: sterol 24-*C*-methyltransferase

Reaction: *S*-adenosyl-L-methionine + 5α-cholesta-8,24-dien-3β-ol = *S*-adenosyl-L-homocysteine + 24-methylene-5α-cholest-8-en-3β-ol

Other name(s): Δ^{24}-methyltransferase; Δ^{24}-sterol methyltransferase; zymosterol-24-methyltransferase; *S*-adenosyl-4-methionine:sterol Δ^{24}-methyltransferase; SMT1; 24-sterol *C*-methyltransferase; *S*-adenosyl-L-methionine:$\Delta^{24(23)}$-sterol methyltransferase; phytosterol methyltransferase

Systematic name: *S*-adenosyl-L-methionine:zymosterol 24-*C*-methyltransferase

Comments: Requires glutathione. Acts on a range of sterols with a 24(25)-double bond in the sidechain. While zymosterol is the preferred substrate it also acts on desmosterol, 5α-cholesta-7,24-dien-3β-ol, 5α-cholesta-5,7,24-trien-3β-ol, 4α-methylzymosterol and others. S-Adenosyl-L-methionine attacks the *Si*-face of the 24(25) double bond and the C-24 hydrogen is transferred to C-25 on the *Re* face of the double bond.

References: [2300, 3663, 3549, 368, 2434]

[EC 2.1.1.41 created 1972, modified 2001]

EC 2.1.1.42

Accepted name: flavone 3′-*O*-methyltransferase

Reaction: *S*-adenosyl-L-methionine + 3′-hydroxyflavone = *S*-adenosyl-L-homocysteine + 3′-methoxyflavone

Other name(s): *o*-dihydric phenol methyltransferase; luteolin methyltransferase; luteolin 3′-*O*-methyltransferase; *o*-diphenol *m*-*O*-methyltransferase; *o*-dihydric phenol meta-*O*-methyltransferase; *S*-adenosylmethionine:flavone/flavonol 3′-*O*-methyltransferase; quercetin 3′-*O*-methyltransferase

Systematic name: *S*-adenosyl-L-methionine:3′-hydroxyflavone 3′-*O*-methyltransferase

Comments: The enzyme prefers flavones with vicinal 3′,4′-dihydroxyl groups.

References: [802, 2382, 2748, 1674, 1908]

[EC 2.1.1.42 created 1976, modified 2011]

EC 2.1.1.43

Accepted name: histone-lysine *N*-methyltransferase

Reaction: *S*-adenosyl-L-methionine + histone L-lysine = *S*-adenosyl-L-homocysteine + histone N^6-methyl-L-lysine

Other name(s): protein methylase III; protein methylase 3; protein (lysine) methyltransferase; protein methyltransferase II; protein-lysine *N*-methyltransferase; histone H1-specific *S*-adenosylmethionine:protein-lysine *N*-methyltransferase; *S*-adenosyl-L-methionine:histone-L-lysine 6-*N*-methyltransferase

Systematic name: *S*-adenosyl-L-methionine:histone-L-lysine N^6-methyltransferase

Comments: One of a group of enzymes methylating proteins; see also EC 2.1.1.59, [cytochrome-*c*]-lysine *N*-methyltransferase and EC 2.1.1.60, calmodulin-lysine *N*-methyltransferase.

References: [2596, 3662]

[EC 2.1.1.43 created 1976, modified 1982, modified 1983]

EC 2.1.1.44

Accepted name: L-histidine N^{α}-methyltransferase

Reaction: **3** *S*-adenosyl-L-methionine + L-histidine = **3** *S*-adenosyl-L-homocysteine + hercynine (overall reaction)

(1a) *S*-adenosyl-L-methionine + L-histidine = *S*-adenosyl-L-homocysteine + N^{α}-methyl-L-histidine

(1b) *S*-adenosyl-L-methionine + N^{α}-methyl-L-histidine = *S*-adenosyl-L-homocysteine + N^{α},N^{α}-dimethyl-L-histidine

(1c) *S*-adenosyl-L-methionine + N^{α},N^{α}-dimethyl-L-histidine = *S*-adenosyl-L-homocysteine + hercynine

Other name(s): dimethylhistidine *N*-methyltransferase; dimethylhistidine methyltransferase; histidine-α-*N*-methyltransferase; *S*-adenosyl-L-methionine:α-*N*,α-*N*-dimethyl-L-histidine α-*N*-methyltransferase; *S*-adenosyl-L-methionine:N^{α},N^{α}-dimethyl-L-histidine N^{α}-methyltransferase

Systematic name: *S*-adenosyl-L-methionine:L-histidine N^{α}-methyltransferase (hercynine-forming)

Comments: Part of the biosynthetic pathway of ergothioneine.

References: [1457, 3131]

[EC 2.1.1.44 created 1976, modified 2013]

EC 2.1.1.45

Accepted name: thymidylate synthase

Reaction: 5,10-methylenetetrahydrofolate + dUMP = dihydrofolate + dTMP

Other name(s): dTMP synthase; thymidylate synthetase; methylenetetrahydrofolate:dUMP *C*-methyltransferase; TMP synthetase

Systematic name: 5,10-methylenetetrahydrofolate:dUMP *C*-methyltransferase

References: [322, 2024, 3251, 3717]

[EC 2.1.1.45 created 1976]

EC 2.1.1.46

Accepted name: isoflavone 4′-*O*-methyltransferase

Reaction: *S*-adenosyl-L-methionine + a 4′-hydroxyisoflavone = *S*-adenosyl-L-homocysteine + a 4′-methoxyisoflavone

Other name(s): 4′-hydroxyisoflavone methyltransferase; isoflavone methyltransferase; isoflavone *O*-methyltransferase

Systematic name: *S*-adenosyl-L-methionine:4′-hydroxyisoflavone 4′-*O*-methyltransferase

Comments: Requires Mg^{2+} for activity. The enzyme catalyses the methylation of daidzein and genistein. It does not methylate naringenin, apigenin, luteolin or kaempferol.

References: [3819]

[EC 2.1.1.46 created 1976, modified 2011]

EC 2.1.1.47

Accepted name: indolepyruvate *C*-methyltransferase

Reaction: *S*-adenosyl-L-methionine + (indol-3-yl)pyruvate = *S*-adenosyl-L-homocysteine + (*R*)-3-(indol-3-yl)-2-oxobutanoate

Other name(s): ind1 (gene name); indolepyruvate methyltransferase; indolepyruvate 3-methyltransferase; indolepyruvic acid methyltransferase; *S*-adenosyl-L-methionine:indolepyruvate *C*-methyltransferase

Systematic name: *S*-adenosyl-L-methionine:(indol-3-yl)pyruvate C^3-methyltransferase

Comments: The enzyme, characterized from the bacterium *Streptomyces griseus*, is involved in the biosynthesis of the antibacterial drug indolmycin.

References: [1374, 1373, 3295, 780]

[EC 2.1.1.47 created 1976, modified 2016]

[2.1.1.48 Transferred entry. rRNA (adenine-N^6*-)-methyltransferase. Now covered by EC 2.1.1.181 [23S rRNA (adenine*^{1618}*-*N^6*)-methyltransferase], EC 2.1.1.182 [16S rRNA adenine*^{1518}*-*N^6*/adenine*^{1519}*-*N^6*)-dimethyltransferase], EC 2.1.1.183 [18S rRNA (adenine*^{1779}*-*N^6*/adenine*^{1780}*-*N^6*)-dimethyltransferase] and EC 2.1.1.184 [23S rRNA (adenine*^{2085}*-*N^6*)-dimethyltransferase]]*

[EC 2.1.1.48 created 1976, deleted 2010]

EC 2.1.1.49

Accepted name: amine *N*-methyltransferase

Reaction: *S*-adenosyl-L-methionine + an amine = *S*-adenosyl-L-homocysteine + a methylated amine

Other name(s): nicotine *N*-methyltransferase; tryptamine *N*-methyltransferase; arylamine *N*-methyltransferase; tryptamine methyltransferase

Systematic name: *S*-adenosyl-L-methionine:amine *N*-methyltransferase

Comments: An enzyme of very broad specificity; many primary, secondary and tertiary amines can act as acceptors, including tryptamine, aniline, nicotine and a variety of drugs and other xenobiotics.

References: [91, 631]

[EC 2.1.1.49 created 1976, modified 1990 (EC 2.1.1.81 created 1989, incorporated 1990)]

EC 2.1.1.50

Accepted name: loganate *O*-methyltransferase

Reaction: *S*-adenosyl-L-methionine + loganate = *S*-adenosyl-L-homocysteine + loganin

Other name(s): loganate methyltransferase; *S*-adenosyl-L-methionine:loganic acid methyltransferase

Systematic name: *S*-adenosyl-L-methionine:loganate 11-*O*-methyltransferase

Comments: Also acts on secologanate. Methylates the 11-carboxy group of the monoterpenoid loganate.

References: [2095]

[EC 2.1.1.50 created 1976]

[2.1.1.51 Transferred entry. rRNA (guanine-N^1*-)-methyltransferase. Now covered by EC 2.1.1.187 [23S rRNA (guanine*^{745}*-*N^1*)-methyltransferase] and EC 2.1.1.188 [23S rRNA (guanine*^{748}*-*N^1*)-methyltransferase].]*

[EC 2.1.1.51 created 1976, deleted 2010]

[2.1.1.52 Transferred entry. rRNA (guanine-N^2*-)-methyltransferase. Now covered by EC 2.1.1.171 [16S rRNA (guanine*^{966}*-*N^2*)-methyltransferase], EC 2.1.1.172 [16S rRNA (guanine*^{1207}*-*N^2*)-methyltransferase], EC 2.1.1.173 [23S rRNA (guanine*^{2445}*-*N^2*)-methyltransferase] and EC 2.1.1.174 [23S rRNA (guanine*^{1835}*-*N^2*)-methyltransferase]]*

[EC 2.1.1.52 created 1976, deleted 2010]

EC 2.1.1.53

Accepted name: putrescine *N*-methyltransferase

Reaction: *S*-adenosyl-L-methionine + putrescine = *S*-adenosyl-L-homocysteine + *N*-methylputrescine

Other name(s): putrescine methyltransferase

Systematic name: *S*-adenosyl-L-methionine:putrescine *N*-methyltransferase

References: [2282]

[EC 2.1.1.53 created 1976]

EC 2.1.1.54

Accepted name: deoxycytidylate *C*-methyltransferase

Reaction: 5,10-methylenetetrahydrofolate + dCMP = dihydrofolate + deoxy-5-methylcytidylate

Other name(s): deoxycytidylate methyltransferase; dCMP methyltransferase

Systematic name: 5,10-methylenetetrahydrofolate:dCMP *C*-methyltransferase

Comments: dCMP is methylated by formaldehyde in the presence of tetrahydrofolate. CMP, dCTP and CTP can act as acceptors, but more slowly.

References: [1821]

[EC 2.1.1.54 created 1978]

EC 2.1.1.55

Accepted name: tRNA (adenine-N^6-)-methyltransferase

Reaction: *S*-adenosyl-L-methionine + tRNA = *S*-adenosyl-L-homocysteine + tRNA containing N^6-methyladenine

Other name(s): *S*-adenosyl-L-methionine:tRNA (adenine-6-*N*-)-methyltransferase

Systematic name: *S*-adenosyl-L-methionine:tRNA (adenine-N^6-)-methyltransferase

References: [2108, 2274, 3157]

[EC 2.1.1.55 created 1981]

EC 2.1.1.56

Accepted name: mRNA (guanine-N^7)-methyltransferase

Reaction: *S*-adenosyl-L-methionine + a 5′-(5′-triphosphoguanosine)-[mRNA] = *S*-adenosyl-L-homocysteine + a 5′-(N^7-methyl 5′-triphosphoguanosine)-[mRNA]

Other name(s): messenger ribonucleate guanine 7-methyltransferase; guanine-7-methyltransferase; messenger RNA guanine 7-methyltransferase; *S*-adenosyl-L-methionine:mRNA (guanine-7-*N*)-methyltransferase

Systematic name: *S*-adenosyl-L-methionine:mRNA (guanine-N^7)-methyltransferase

Comments: The nucleoside next to the terminal guanosine may be either guanosine or adenosine.

References: [842, 1146, 2141, 2142]

[EC 2.1.1.56 created 1981]

EC 2.1.1.57

Accepted name: methyltransferase cap1

Reaction: *S*-adenosyl-L-methionine + a 5′-(N^7-methyl 5′-triphosphoguanosine)-(purine-ribonucleotide)-[mRNA] = *S*-adenosyl-L-homocysteine + a 5′-(N^7-methyl 5′-triphosphoguanosine)-(2′-*O*-methyl-purine-ribonucleotide)-[mRNA]

Other name(s): messenger ribonucleate nucleoside 2′-methyltransferase; messenger RNA (nucleoside-2′-)-methyltransferase; MTR1; cap1-MTase; mRNA (nucleoside-2′-*O*)-methyltransferase (ambiguous); *S*-adenosyl-L-methionine:mRNA (nucleoside-2′-*O*)-methyltransferase

Systematic name: *S*-adenosyl-L-methionine:5-(N^7-methyl 5-triphosphoguanosine)-(purine-ribonucleotide)-[mRNA] 2-*O*-methyltransferase

Comments: This enzyme catalyses the methylation of the ribose on the first transcribed nucleotide of mRNA or snRNA molecules, which may be either guanosine or adenosine. This methylation event is known as cap1, and occurs in all mRNAs and snRNAs of higher eukaryotes, including insects, vertebrates and their viruses. The human enzyme can also methylate mRNA molecules that lack methylation on the capping 5′-triphosphoguanosine [3823].

References: [189, 188, 353, 842, 1146, 3823]

[EC 2.1.1.57 created 1981 (EC 2.1.1.58 created 1981, incorporated 1984), modified 2014]

[2.1.1.58 Deleted entry. mRNA (adenosine-2′-O-)-methyltransferase. Now included with EC 2.1.1.57, mRNA (nucleoside-2′-O-)-methyltransferase]

[EC 2.1.1.58 created 1981, deleted 1984]

EC 2.1.1.59

Accepted name: [cytochrome *c*]-lysine *N*-methyltransferase
Reaction: *S*-adenosyl-L-methionine + [cytochrome *c*]-L-lysine = *S*-adenosyl-L-homocysteine + [cytochrome *c*]-N^6-methyl-L-lysine
Other name(s): cytochrome *c* (lysine) methyltransferase; cytochrome *c* methyltransferase; cytochrome *c*-specific protein methylase III; cytochrome *c*-specific protein-lysine methyltransferase; *S*-adenosyl-L-methionine:[cytochrome *c*]-L-lysine 6-*N*-methyltransferase
Systematic name: *S*-adenosyl-L-methionine:[cytochrome *c*]-L-lysine N^6-methyltransferase
Comments: One of a group of enzymes methylating proteins; see also EC 2.1.1.43 histone-lysine *N*-methyltransferase and EC 2.1.1.60 calmodulin-lysine *N*-methyltransferase.
References: [796, 2479, 3627]

[EC 2.1.1.59 created 1982, modified 1983]

EC 2.1.1.60

Accepted name: calmodulin-lysine *N*-methyltransferase
Reaction: *S*-adenosyl-L-methionine + calmodulin L-lysine = *S*-adenosyl-L-homocysteine + calmodulin N^6-methyl-L-lysine
Other name(s): *S*-adenosylmethionine:calmodulin (lysine) *N*-methyltransferase; *S*-adenosyl-L-methionine:calmodulin-L-lysine 6-*N*-methyltransferase
Systematic name: *S*-adenosyl-L-methionine:calmodulin-L-lysine N^6-methyltransferase
Comments: One of a group of enzymes methylating proteins; see also EC 2.1.1.43 histone-lysine *N*-methyltransferase and EC 2.1.1.59 [cytochrome-*c*]-lysine *N*-methyltransferase.
References: [3245]

[EC 2.1.1.60 created 1982, modified 1983]

EC 2.1.1.61

Accepted name: tRNA (5-methylaminomethyl-2-thiouridylate)-methyltransferase
Reaction: *S*-adenosyl-L-methionine + tRNA containing 5-aminomethyl-2-thiouridine = *S*-adenosyl-L-homocysteine + tRNA containing 5-methylaminomethyl-2-thiouridylate
Other name(s): transfer ribonucleate 5-methylaminomethyl-2-thiouridylate 5-methyltransferase; tRNA 5-methylaminomethyl-2-thiouridylate 5′-methyltransferase
Systematic name: *S*-adenosyl-L-methionine:tRNA (5-methylaminomethyl-2-thio-uridylate)-methyltransferase
Comments: This enzyme is specific for the terminal methyl group of 5-methylaminomethyl-2-thiouridylate.
References: [3479, 3480]

[EC 2.1.1.61 created 1982, modified 2012]

EC 2.1.1.62

Accepted name: mRNA (2′-*O*-methyladenosine-N^6-)-methyltransferase
Reaction: *S*-adenosyl-L-methionine + a 5-(N^7-methyl 5-triphosphoguanosine)-2′-*O*-methyladenosine-[mRNA] = *S*-adenosyl-L-homocysteine + a 5-(N^7-methyl 5-triphosphoguanosine)-N^6,2′-*O*-dimethyladenosine-[mRNA]
Other name(s): messenger ribonucleate 2′-*O*-methyladenosine N^G-methyltransferase; *S*-adenosyl-L-methionine:mRNA (2′-*O*-methyladenosine-6-*N*-)-methyltransferase
Systematic name: *S*-adenosyl-L-methionine:mRNA (2′-*O*-methyladenosine-N^6-)-methyltransferase
References: [1627, 2171]

[EC 2.1.1.62 created 1982]

EC 2.1.1.63

Accepted name: methylated-DNA—[protein]-cysteine *S*-methyltransferase

Reaction: (1) DNA (containing 6-*O*-methylguanine) + protein L-cysteine = DNA (without 6-*O*-methylguanine) + protein *S*-methyl-L-cysteine
(2) DNA (containing 4-*O*-methylthymine) + protein L-cysteine = DNA (without 4-*O*-methylthymine) + protein *S*-methyl-L-cysteine

Other name(s): *ada* (gene name); *ogt* (gene name); MGT1 (gene name); MGMT (gene name)

Systematic name: DNA-6-*O*-methylguanine/DNA-4-*O*-methylthymine:[protein]-L-cysteine *S*-methyltransferase

Comments: This protein is involved in the repair of methylated DNA. Unlike EC 3.2.2.20, DNA-3-methyladenine glycosidase I and EC 3.2.2.21, DNA-3-methyladenine glycosidase II, which remove the methylated base leaving an apurinic/apyrimidinic site, this enzyme transfers the methyl group from the methylated DNA to an internal cysteine residue, leaving an intact nucleotide. Since the methyl transfer is irreversible, the enzyme can only catalyse a single turnover.

References: [927, 2562, 2186, 2746, 2839, 1739, 3027, 3919]

[EC 2.1.1.63 created 1982, modified 1983, modified 1999, modified 2003, modified 2017]

EC 2.1.1.64

Accepted name: 3-demethylubiquinol 3-*O*-methyltransferase

Reaction: *S*-adenosyl-L-methionine + 3-demethylubiquinol-*n* = *S*-adenosyl-L-homocysteine + ubiquinol-*n*

Other name(s): 5-demethylubiquinone-9 methyltransferase; OMHMB-methyltransferase; 2-octaprenyl-3-methyl-5-hydroxy-6-methoxy-1,4-benzoquinone methyltransferase; *S*-adenosyl-L-methionine:2-octaprenyl-3-methyl-5-hydroxy-6-methoxy-1,4-benzoquinone-*O*-methyltransferase; COQ3 (gene name); Coq3 *O*-methyltransferase; 3-demethylubiquinone-9 3-methyltransferase; *ubiG* (gene name, ambiguous)

Systematic name: *S*-adenosyl-L-methionine:3-hydroxy-2-methoxy-5-methyl-6-(*all-trans*-polyprenyl)-1,4-benzoquinol 3-*O*-methyltransferase

Comments: This enzyme is involved in ubiquinone biosynthesis. Ubiquinones from different organisms have a different number of prenyl units (for example, ubiquinone-6 in *Saccharomyces*, ubiquinone-9 in rat and ubiquinone-10 in human), and thus the natural substrate for the enzymes from different organisms has a different number of prenyl units. However, the enzyme usually shows a low degree of specificity regarding the number of prenyl units. For example, the human COQ3 enzyme can restore biosynthesis of ubiquinone-6 in coq3 deletion mutants of yeast [2740]. The enzymes from yeast, *Escherichia coli* and rat also catalyse the methylation of 3,4-dihydroxy-5-*all-trans*-polyprenylbenzoate [2740] (a reaction that is classified as EC 2.1.1.114, polyprenyldihydroxybenzoate methyltransferase).

References: [1379, 1939, 2740, 1528]

[EC 2.1.1.64 created 1982, modified 2011]

EC 2.1.1.65

Accepted name: licodione 2′-*O*-methyltransferase

Reaction: *S*-adenosyl-L-methionine + licodione = *S*-adenosyl-L-homocysteine + 2′-*O*-methyllicodione

Systematic name: *S*-adenosyl-L-methionine:licodione 2′-*O*-methyltransferase

Comments: As well as licodione [1-(2,4-dihydroxyphenyl)-3-(4-hydroxyphenyl)-1,3-propanedione], the 2″-hydroxy-derivative and isoliquiritigenin can act as acceptors, but more slowly.

References: [143]

[EC 2.1.1.65 created 1983]

[2.1.1.66 Deleted entry. rRNA (adenosine-2′-O-)-methyltransferase. Now covered by EC 2.1.1.230, 23S rRNA (adenosine^{1067}*-2-O)-methyltransferase.]*

[EC 2.1.1.66 created 1984, deleted 2013]

EC 2.1.1.67

Accepted name: thiopurine *S*-methyltransferase

Reaction: *S*-adenosyl-L-methionine + a thiopurine = *S*-adenosyl-L-homocysteine + a thiopurine *S*-methylether

Other name(s): mercaptopurine methyltransferase; thiopurine methyltransferase; 6-thiopurine transmethylase; TPMT

Systematic name: *S*-adenosyl-L-methionine:thiopurine *S*-methyltransferase

Comments: Also acts, more slowly, on thiopyrimidines and aromatic thiols. Not identical with EC 2.1.1.9 thiol *S*-methyltransferase.

References: [2869, 3890, 3891]

[EC 2.1.1.67 created 1984]

EC 2.1.1.68

Accepted name: caffeate *O*-methyltransferase

Reaction: *S*-adenosyl-L-methionine + 3,4-dihydroxy-*trans*-cinnamate = *S*-adenosyl-L-homocysteine + 3-methoxy-4-hydroxy-*trans*-cinnamate

Other name(s): caffeate methyltransferase; caffeate 3-*O*-methyltransferase; *S*-adenosyl-L-methionine:caffeic acid-*O*-methyltransferase

Systematic name: *S*-adenosyl-L-methionine:3,4-dihydroxy-*trans*-cinnamate 3-*O*-methyltransferase

Comments: 3,4-Dihydroxybenzaldehyde and catechol can act as acceptors, but more slowly.

References: [803, 2747, 3190]

[EC 2.1.1.68 created 1984]

EC 2.1.1.69

Accepted name: 5-hydroxyfuranocoumarin 5-*O*-methyltransferase

Reaction: (1) *S*-adenosyl-L-methionine + a 5-hydroxyfurocoumarin = *S*-adenosyl-L-homocysteine + a 5-methoxyfurocoumarin (general reaction)
(2) *S*-adenosyl-L-methionine + bergaptol = *S*-adenosyl-L-homocysteine + bergapten

Other name(s): furanocoumarin 5-methyltransferase; furanocoumarin 5-*O*-methyltransferase; bergaptol 5-*O*-methyltransferase; bergaptol *O*-methyltransferase; bergaptol methyltransferase; *S*-adenosyl-L-methionine:bergaptol *O*-methyltransferase; BMT; *S*-adenosyl-L-methionine:5-hydroxyfuranocoumarin 5-*O*-methyltransferase

Systematic name: *S*-adenosyl-L-methionine:5-hydroxyfurocoumarin 5-*O*-methyltransferase

Comments: Converts bergaptol into bergapten, which has therapeutic potential in the treatment of psoriasis as it has photosensitizing and antiproliferative activities [1270]. The enzyme methylates the 5-hydroxy group of some hydroxy- and methylcoumarins, such as 5-hydroxyxanthotoxin [1249], but has little activity on non-coumarin phenols [3523]. Caffeate, 5-hydroxyferulate and daphnetin are not substrates [1270]. Cu^{2+}, Zn^{2+} and Co^{2+} cause enzyme inhibition [1270]. (see also EC 2.1.1.70, 8-hydroxyfuranocoumarin 8-*O*-methyltransferase)

References: [3523, 3161, 1249, 1270]

[EC 2.1.1.69 created 1984 (EC 2.1.1.92 created 1989, incorporated 2006), modified 2006]

EC 2.1.1.70

Accepted name: 8-hydroxyfuranocoumarin 8-*O*-methyltransferase

Reaction: (1) *S*-adenosyl-L-methionine + an 8-hydroxyfurocoumarin = *S*-adenosyl-L-homocysteine + an 8-methoxyfurocoumarin (general reaction)
(2) *S*-adenosyl-L-methionine + xanthotoxol = *S*-adenosyl-L-homocysteine + xanthotoxin

Other name(s): furanocoumarin 8-methyltransferase; furanocoumarin 8-*O*-methyl-transferase; xanthotoxol 8-*O*-methyltransferase; XMT; 8-hydroxyfuranocoumarin 8-*O*-methyltransferase; SAM:xanthotoxol *O*-methyltransferase; *S*-adenosyl-L-methionine:8-hydroxyfuranocoumarin 8-*O*-methyltransferase; xanthotoxol methyltransferase; xanthotoxol *O*-methyltransferase; *S*-adenosyl-L-methionine:xanthotoxol *O*-methyltransferase; *S*-adenosyl-L-methionine-xanthotoxol *O*-methyltransferase

Systematic name: *S*-adenosyl-L-methionine:8-hydroxyfurocoumarin 8-*O*-methyltransferase

Comments: Converts xanthotoxol into xanthotoxin, which has therapeutic potential in the treatment of psoriasis as it has photosensitizing and antiproliferative activities [1270]. Methylates the 8-hydroxy group of some hydroxy- and methylcoumarins, but has little activity on non-coumarin phenols (see also EC 2.1.1.69, 5-hydroxyfuranocoumarin 5-*O*-methyltransferase).
References: [3523, 1249, 3161, 1270]

[EC 2.1.1.70 created 1984, modified 2006 (EC 2.1.1.93 created 2006, incorporated 2008)]

EC 2.1.1.71

Accepted name: phosphatidyl-*N*-methylethanolamine *N*-methyltransferase
Reaction: *S*-adenosyl-L-methionine + phosphatidyl-*N*-methylethanolamine = *S*-adenosyl-L-homocysteine + phosphatidyl-*N*-dimethylethanolamine
Other name(s): phosphatidylmonomethylethanolamine methyltransferase; methyltransferase II; phospholipid methyltransferase; PLMT; phosphatidyl-*N*-methylethanolamine methyltransferase; phosphatidyl-*N*-monomethylethanolamine methyltransferase; phosphatidylethanolamine methyltransferase I; phosphatidylmonomethylethanolamine methyltransferase
Systematic name: *S*-adenosyl-L-methionine:phosphatidyl-*N*-methylethanolamine *N*-methyltransferase
Comments: The enzyme also catalyses the transfer of a further methyl group, producing phosphatidylcholine.
References: [1339, 3096]

[EC 2.1.1.71 created 1984]

EC 2.1.1.72

Accepted name: site-specific DNA-methyltransferase (adenine-specific)
Reaction: *S*-adenosyl-L-methionine + adenine in DNA = *S*-adenosyl-L-homocysteine + N^6-methyladenine in DNA
Other name(s): modification methylase; restriction-modification system
Systematic name: *S*-adenosyl-L-methionine:adenine in DNA N^6-methyltransferase
Comments: This is a large group of enzymes, most of which form so-called ‘restriction-modification systems’ with nucleases that possess similar site specificity [the nucleases are listed as either EC 3.1.21.3 (type 1 site-specific deoxyribonuclease), EC 3.1.21.4 (type II site-specific deoxyribonuclease) or EC 3.1.21.5 (type III site-specific deoxyribonuclease)]. A complete listing of all of these enzymes has been produced by R.J. Roberts and is available on-line at http://rebase.neb.com/rebase/rebase.html.
References: [1648, 2897, 4011]

[EC 2.1.1.72 created 1984]

[2.1.1.73 Deleted entry. site-specific DNA-methyltransferase (cytosine-specific). Reaction is that of EC 2.1.1.37, DNA (cytosine-5-)-methyltransferase]

[EC 2.1.1.73 created 1984, deleted 2003]

EC 2.1.1.74

Accepted name: methylenetetrahydrofolate—tRNA-(uracil^{54}-C^5)-methyltransferase (FADH$_2$-oxidizing)
Reaction: 5,10-methylenetetrahydrofolate + uracil^{54} in tRNA + FADH$_2$ = tetrahydrofolate + 5-methyluracil^{54} in tRNA + FAD
Other name(s): folate-dependent ribothymidyl synthase; methylenetetrahydrofolate-transfer ribonucleate uracil 5-methyltransferase; 5,10-methylenetetrahydrofolate:tRNA-UΨC (uracil-5-)-methyl-transferase; 5,10-methylenetetrahydrofolate:tRNA (uracil-5-)-methyl-transferase; TrmFO; folate/FAD-dependent tRNA T54 methyltransferase
Systematic name: 5,10-methylenetetrahydrofolate:tRNA (uracil^{54}-C^5)-methyltransferase
Comments: Up to 25% of the bases in mature tRNA are post-translationally modified or hypermodified. One almost universal post-translational modification is the conversion of U^{54} into ribothymidine in the TΨC loop, and this modification is found in most species studied to date [247]. Unlike this enzyme, which uses 5,10-methylenetetrahydrofolate and FADH$_2$ to supply the atoms for methylation of U^{54}, EC 2.1.1.35, tRNA (uracil^{54}-C^5)-methyltransferase, uses *S*-adenosyl-L-methionine.

References: [703, 247, 2465]

[EC 2.1.1.74 created 1983 as EC 2.1.2.12, transferred 1984 to EC 2.1.1.74, modified 2011]

EC 2.1.1.75

Accepted name: apigenin 4′-*O*-methyltransferase
Reaction: *S*-adenosyl-L-methionine + apigenin = *S*-adenosyl-L-homocysteine + acacetin
Other name(s): flavonoid *O*-methyltransferase; flavonoid methyltransferase; *S*-adenosyl-L-methionine:5,7,4′-trihydroxyflavone 4′-*O*-methyltransferase
Systematic name: *S*-adenosyl-L-methionine:apigenin 4′-*O*-methyltransferase
Comments: Converts apigenin into acacetin. Naringenin can also act as an acceptor, but more slowly.
References: [1827]

[EC 2.1.1.75 created 1984]

EC 2.1.1.76

Accepted name: quercetin 3-*O*-methyltransferase
Reaction: *S*-adenosyl-L-methionine + 3,5,7,3′,4′-pentahydroxyflavone = *S*-adenosyl-L-homocysteine + 3-methoxy-5,7,3′,4′-tetrahydroxyflavone
Other name(s): flavonol 3-*O*-methyltransferase; flavonoid 3-methyltransferase
Systematic name: *S*-adenosyl-L-methionine:3,5,7,3′,4′-pentahydroxyflavone 3-*O*-methyltransferase
Comments: Specific for quercetin. Related enzymes bring about the 3-*O*-methylation of other flavonols, such as galangin and kaempferol.
References: [2062, 2064, 2065, 1425]

[EC 2.1.1.76 created 1984]

EC 2.1.1.77

Accepted name: protein-L-isoaspartate(D-aspartate) *O*-methyltransferase
Reaction: *S*-adenosyl-L-methionine + protein L-isoaspartate = *S*-adenosyl-L-homocysteine + protein L-isoaspartate α-methyl ester
Other name(s): protein-L-isoaspartate *O*-methyltransferase; protein-β-aspartate *O*-methyltransferase; D-aspartyl/L-isoaspartyl methyltransferase; L-isoaspartyl/D-aspartyl protein carboxyl methyltransferase; protein (D-aspartate) methyltransferase; protein D-aspartate methyltransferase; protein L-isoaspartate methyltransferase; protein L-isoaspartyl methyltransferase; protein *O*-methyltransferase (L-isoaspartate); L-aspartyl/L-isoaspartyl protein methyltransferase
Systematic name: *S*-adenosyl-L-methionine:protein-L-isoaspartate *O*-methyltransferase
Comments: D-Aspartate (but not L-aspartate) residues in proteins can also act as acceptors. Previously also listed as EC 2.1.1.24.
References: [123, 579, 1683, 2583]

[EC 2.1.1.77 created 1984, modified 1989 (EC 2.1.1.24 created 1972, modified 1983, modified 1989, part incorporated 1992)]

EC 2.1.1.78

Accepted name: isoorientin 3′-*O*-methyltransferase
Reaction: *S*-adenosyl-L-methionine + isoorientin = *S*-adenosyl-L-homocysteine + isoscoparin
Other name(s): isoorientin 3′-methyltransferase
Systematic name: *S*-adenosyl-L-methionine:isoorientin 3′-*O*-methyltransferase
Comments: Also acts on isoorientin 2″-*O*-rhamnoside. Involved in the biosynthesis of flavones.
References: [3632]

[EC 2.1.1.78 created 1986]

EC 2.1.1.79

Accepted name: cyclopropane-fatty-acyl-phospholipid synthase

Reaction: *S*-adenosyl-L-methionine + phospholipid olefinic fatty acid = *S*-adenosyl-L-homocysteine + phospholipid cyclopropane fatty acid

Other name(s): cyclopropane synthetase; unsaturated-phospholipid methyltransferase; cyclopropane synthase; cyclopropane fatty acid synthase; cyclopropane fatty acid synthetase; CFA synthase

Systematic name: *S*-adenosyl-L-methionine:unsaturated-phospholipid methyltransferase (cyclizing)

Comments: The enzyme adds a methylene group across the 9,10 position of a Δ^9-olefinic acyl chain in phosphatidylethanolamine or, more slowly, phosphatidylglycerol or phosphatidylinositol, forming a cyclopropane derivative (*cf.* EC 2.1.1.16 methylene-fatty-acyl-phospholipid synthase).

References: [565, 4025]

[EC 2.1.1.79 created 1986]

EC 2.1.1.80

Accepted name: protein-glutamate *O*-methyltransferase

Reaction: *S*-adenosyl-L-methionine + protein L-glutamate = *S*-adenosyl-L-homocysteine + protein L-glutamate methyl ester

Other name(s): methyl-accepting chemotaxis protein *O*-methyltransferase; *S*-adenosylmethionine-glutamyl methyltransferase; methyl-accepting chemotaxis protein methyltransferase II; *S*-adenosylmethionine:protein-carboxyl *O*-methyltransferase; protein methylase II; MCP methyltransferase I; MCP methyltransferase II; protein *O*-methyltransferase; protein(aspartate)methyltransferase; protein(carboxyl)methyltransferase; protein carboxyl-methylase; protein carboxyl-*O*-methyltransferase; protein carboxylmethyltransferase II; protein carboxymethylase; protein carboxymethyltransferase; protein methyltransferase II

Systematic name: *S*-adenosyl-L-methionine:protein-L-glutamate *O*-methyltransferase

Comments: Forms ester groups with L-glutamate residues in a number of membrane proteins.

References: [425, 1704, 3233, 3896]

[EC 2.1.1.80 created 1989 (EC 2.1.1.24 created 1972, modified 1983, modified 1989, part incorporated 1992)]

[2.1.1.81 Deleted entry. nicotine N-methyltransferase. Now included with EC 2.1.1.49 amine N-methyltransferase]

[EC 2.1.1.81 created 1989, deleted 1990]

EC 2.1.1.82

Accepted name: 3-methylquercetin 7-*O*-methyltransferase

Reaction: *S*-adenosyl-L-methionine + 5,7,3′,4′-tetrahydroxy-3-methoxyflavone = *S*-adenosyl-L-homocysteine + 5,3′,4′-trihydroxy-3,7-dimethoxyflavone

Other name(s): flavonol 7-*O*-methyltransferase; flavonol 7-methyltransferase; 7-OMT; *S*-adenosyl-L-methionine:3′,4′,5,7-tetrahydroxy-3-methoxyflavone 7-*O*-methyltransferase; 3-methylquercitin 7-*O*-methyltransferase [mis-spelt]

Systematic name: *S*-adenosyl-L-methionine:5,7,3′,4′-tetrahydroxy-3-methoxyflavone 7-*O*-methyltransferase

Comments: Involved with EC 2.1.1.76 quercetin 3-*O*-methyltransferase and EC 2.1.1.83 3,7-dimethylquercetin 4′-*O*-methyltransferase in the methylation of quercetin to 3,7,4′-trimethylquercetin in *Chrysosplenium americanum*. Does not act on flavones, dihydroflavonols, or their glucosides.

References: [2064]

[EC 2.1.1.82 created 1989]

EC 2.1.1.83

Accepted name: 3,7-dimethylquercetin 4′-*O*-methyltransferase

Reaction: *S*-adenosyl-L-methionine + 5,3′,4′-trihydroxy-3,7-dimethoxyflavone = *S*-adenosyl-L-homocysteine + 5,3′-dihydroxy-3,7,4′-trimethoxyflavone

Other name(s): flavonol 4′-*O*-methyltransferase; flavonol 4′-methyltransferase; 4′-OMT; *S*-adenosyl-L-methionine:3′,4′,5-trihydroxy-3,7-dimethoxyflavone 4′-*O*-methyltransferase; 3,7-dimethylquercitin 4′-*O*-methyltransferase [mis-spelt]

Systematic name: *S*-adenosyl-L-methionine:5,3′,4′-trihydroxy-3,7-dimethoxyflavone 4′-*O*-methyltransferase

Comments: 3,7-Dimethylquercetagetin can also act as acceptor. Involved with EC 2.1.1.76 quercetin 3-*O*-methyltransferase and EC 2.1.1.82 3-methylquercetin 7-*O*-methyltransferase in the methylation of quercetin to 3,7,4′-trimethylquercetin in *Chrysosplenium americanum*. Does not act on flavones, dihydroflavonols, or their glucosides.

References: [2064, 2065]

[EC 2.1.1.83 created 1989]

EC 2.1.1.84

Accepted name: methylquercetagetin 6-*O*-methyltransferase

Reaction: *S*-adenosyl-L-methionine + 5,6,3′,4′-tetrahydroxy-3,7-dimethoxyflavone = *S*-adenosyl-L-homocysteine + 5,3′,4′-trihydroxy-3,6,7-trimethoxyflavone

Other name(s): flavonol 6-*O*-methyltransferase; flavonol 6-methyltransferase; 6-OMT; *S*-adenosyl-L-methionine:3′,4′,5,6-tetrahydroxy-3,7-dimethoxyflavone 6-*O*-methyltransferase

Systematic name: *S*-adenosyl-L-methionine:5,6,3′,4′-tetrahydroxy-3,7-dimethoxyflavone 6-*O*-methyltransferase

Comments: The enzymes from *Chrysosplenium americanum* also methylates 3,7,3′-trimethylquercetagetin at the 6-position. Does not act on flavones, dihydroflavonols, or their glucosides.

References: [2064, 2065]

[EC 2.1.1.84 created 1989]

EC 2.1.1.85

Accepted name: protein-histidine *N*-methyltransferase

Reaction: *S*-adenosyl-L-methionine + protein L-histidine = *S*-adenosyl-L-homocysteine + protein N^{τ}-methyl-L-histidine

Other name(s): protein methylase IV; protein (histidine) methyltransferase; actin-specific histidine methyltransferase; *S*-adenosyl methionine:protein-histidine *N*-methyltransferase

Systematic name: *S*-adenosyl-L-methionine:protein-L-histidine *N*-*tele*-methyltransferase

Comments: Highly specific for histidine residues, for example, in actin.

References: [3679]

[EC 2.1.1.85 created 1989]

EC 2.1.1.86

Accepted name: tetrahydromethanopterin *S*-methyltransferase

Reaction: 5-methyl-5,6,7,8-tetrahydromethanopterin + CoM + **2** $Na^{+}{}_{in}$ = 5,6,7,8-tetrahydromethanopterin + 2-(methylsulfanyl)ethane-1-sulfonate + **2** $Na^{+}{}_{out}$

Other name(s): tetrahydromethanopterin methyltransferase; *mtrA*-H (gene names); *cmtA* (gene name); N^5-methyltetrahydromethanopterin—coenzyme M methyltransferase; 5-methyl-5,6,7,8-tetrahydromethanopterin:2-mercaptoethanesulfonate 2-methyltransferase

Systematic name: 5-methyl-5,6,7,8-tetrahydromethanopterin:CoM 2-methyltransferase (Na^+-transporting)

Comments: Involved in the formation of methane from CO2 in methanogenic archaea. The reaction involves the export of one or two sodium ions. The enzyme from the archaeon *Methanobacterium thermoautotrophicum* is a membrane-associated multienzyme complex composed of eight different subunits, and contains a 5′-hydroxybenzimidazolyl-cobamide prosthetic group, to which the methyl group is attached during the transfer. A soluble enzyme that is induced by the presence of CO has been reported as well [3664].

References: [3037, 1021, 3811, 1226, 1115, 3664]

[EC 2.1.1.86 created 1989, modified 2000, modified 2017]

EC 2.1.1.87

Accepted name: pyridine *N*-methyltransferase
Reaction: *S*-adenosyl-L-methionine + pyridine = *S*-adenosyl-L-homocysteine + *N*-methylpyridinium
Other name(s): pyridine methyltransferase
Systematic name: *S*-adenosyl-L-methionine:pyridine *N*-methyltransferase
References: [662]

[EC 2.1.1.87 created 1989]

EC 2.1.1.88

Accepted name: 8-hydroxyquercetin 8-*O*-methyltransferase
Reaction: *S*-adenosyl-L-methionine + 3,5,7,8,3′,4′-hexahydroxyflavone = *S*-adenosyl-L-homocysteine + 3,5,7,3′,4′-pentahydroxy-8-methoxyflavone
Other name(s): flavonol 8-*O*-methyltransferase; flavonol 8-methyltransferase; *S*-adenosyl-L-methionine:3,3′,4′,5,7,8-hexahydroxyflavone 8-*O*-methyltransferase; 8-hydroxyquercitin 8-*O*-methyltransferase [mis-spelt]
Systematic name: *S*-adenosyl-L-methionine:3,5,7,8,3′,4′-hexahydroxyflavone 8-*O*-methyltransferase
Comments: Also acts on 8-hydroxykaempferol, but not on the glycosides of 8-hydroxyflavonols. An enzyme from the flower buds of *Lotus corniculatus*.
References: [1503]

[EC 2.1.1.88 created 1989]

EC 2.1.1.89

Accepted name: tetrahydrocolumbamine 2-*O*-methyltransferase
Reaction: *S*-adenosyl-L-methionine + 5,8,13,13a-tetrahydrocolumbamine = *S*-adenosyl-L-homocysteine + tetrahydropalmatine
Other name(s): tetrahydrocolumbamine methyltransferase
Systematic name: *S*-adenosyl-L-methionine:5,8,13,13a-tetrahydrocolumbamine 2-*O*-methyltransferase
Comments: Involved in the biosynthesis of the berberine alkaloids.
References: [249]

[EC 2.1.1.89 created 1989]

EC 2.1.1.90

Accepted name: methanol—corrinoid protein *Co*-methyltransferase
Reaction: methanol + a [Co(I) methanol-specific corrinoid protein] = a [methyl-Co(III) methanol-specific corrinoid protein] + H_2O
Other name(s): methanol cobalamin methyltransferase; methanol:5-hydroxybenzimidazolylcobamide methyltransferase; MT 1 (ambiguous); methanol—5-hydroxybenzimidazolylcobamide *Co*-methyltransferase; *mtaB* (gene name)
Systematic name: methanol:5-hydroxybenzimidazolylcobamide *Co*-methyltransferase
Comments: The enzyme, which catalyses the transfer of methyl groups from methanol to a methanol-specific corrinoid protein (MtaC), is involved in methanogenesis from methanol. Methylation of the corrinoid protein requires the central cobalt to be in the Co(I) state. During methylation the cobalt is oxidized to the Co(III) state. Free cob(I)alamin can substitute for the corrinoid protein *in vitro* [3040]. Inactivated by oxygen and other oxidizing agents, and reactivated by catalytic amounts of ATP and hydrogen.
References: [3637, 3040]

[EC 2.1.1.90 created 1989, modified 2012]

EC 2.1.1.91

Accepted name: isobutyraldoxime *O*-methyltransferase
Reaction: *S*-adenosyl-L-methionine + 2-methylpropanal oxime = *S*-adenosyl-L-homocysteine + 2-methylpropanal *O*-methyloxime

Other name(s): aldoxime methyltransferase; *S*-adenosylmethionine:aldoxime *O*-methyltransferase; aldoxime *O*-methyltransferase
Systematic name: *S*-adenosyl-L-methionine:2-methylpropanal-oxime *O*-methyltransferase
Comments: Oximes of C$_4$ to C$_6$ aldehydes can act as acceptors; the most active substrate is 2-methylbutyroaldoxime.
References: [1228]

[EC 2.1.1.91 created 1989]

[2.1.1.92 Deleted entry. bergaptol O-methyltransferase. Now included with EC 2.1.1.69, 5-hydroxyfuranocoumarin 5-O-methyltransferase. The reaction with bergaptol is a specific example of the general reaction associated with EC 2.1.1.69]

[EC 2.1.1.92 created 1989, deleted 2006]

[2.1.1.93 Deleted entry. xanthotoxol O-methyltransferase. Enzyme is identical to EC 2.1.1.70, 8-hydroxyfuranocoumarin 8-O-methyltransferase]

[EC 2.1.1.93 created 1989, deleted 2008]

EC 2.1.1.94

Accepted name: tabersonine 16-*O*-methyltransferase
Reaction: *S*-adenosyl-L-methionine + 16-hydroxytabersonine = *S*-adenosyl-L-homocysteine + 16-methoxytabersonine
Other name(s): 11-demethyl-17-deacetylvindoline 11-methyltransferase; 11-*O*-demethyl-17-*O*-deacetylvindoline *O*-methyltransferase; *S*-adenosyl-L-methionine:11-*O*-demethyl-17-*O*-deacetylvindoline 11-*O*-methyltransferase
Systematic name: *S*-adenosyl-L-methionine:16-hydroxytabersonine 16-*O*-methyltransferase
Comments: Involved in the biosynthesis of vindoline from tabersonine in the Madagascar periwinkle, *Catharanthus roseus*.
References: [2061, 865]

[EC 2.1.1.94 created 1989, modified 2005]

EC 2.1.1.95

Accepted name: tocopherol *O*-methyltransferase
Reaction: (1) *S*-adenosyl-L-methionine + γ-tocopherol = *S*-adenosyl-L-homocysteine + α-tocopherol
(2) *S*-adenosyl-L-methionine + δ-tocopherol = *S*-adenosyl-L-homocysteine + β-tocopherol
(3) *S*-adenosyl-L-methionine + γ-tocotrienol = *S*-adenosyl-L-homocysteine + α-tocotrienol
(4) *S*-adenosyl-L-methionine + δ-tocotrienol = *S*-adenosyl-L-homocysteine + β-tocotrienol
Other name(s): γ-tocopherol methyltransferase; VTE4 (gene name)
Systematic name: *S*-adenosyl-L-methionine:γ-tocopherol 5-*O*-methyltransferase
Comments: The enzymes from plants and photosynthetic bacteria have similar efficiency with the γ and δ isomers of tocopherols and tocotrienols.
References: [460, 1729, 4040]

[EC 2.1.1.95 created 1989, modified 2013]

EC 2.1.1.96

Accepted name: thioether *S*-methyltransferase
Reaction: *S*-adenosyl-L-methionine + dimethyl sulfide = *S*-adenosyl-L-homocysteine + trimethylsulfonium
Other name(s): *S*-adenosyl-L-methionine:thioether *S*-methyltransferase; thioether methyltransferase
Systematic name: *S*-adenosyl-L-methionine:dimethyl-sulfide *S*-methyltransferase
Comments: Also acts on dimethyl selenide, dimethyl telluride, diethyl sulfide, 1,4-dithiane and many other thioethers.
References: [2334]

[EC 2.1.1.96 created 1990]

EC 2.1.1.97

Accepted name: 3-hydroxyanthranilate 4-*C*-methyltransferase

Reaction: *S*-adenosyl-L-methionine + 3-hydroxyanthranilate = *S*-adenosyl-L-homocysteine + 3-hydroxy-4-methylanthranilate

Other name(s): 3-hydroxyanthranilate 4-methyltransferase

Systematic name: *S*-adenosyl-L-methionine:3-hydroxyanthranilate 4-*C*-methyltransferase

Comments: Involved in the biosynthesis of the antibiotic actinomycin in *Streptomyces antibioticus*.

References: [883]

[EC 2.1.1.97 created 1990]

EC 2.1.1.98

Accepted name: diphthine synthase

Reaction: **3** *S*-adenosyl-L-methionine + 2-[(3*S*)-3-carboxy-3-aminopropyl]-L-histidine-[translation elongation factor 2] = **3** *S*-adenosyl-L-homocysteine + diphthine-[translation elongation factor 2] (overall reaction)

(1a) *S*-adenosyl-L-methionine + 2-[(3*S*)-3-carboxy-3-aminopropyl]-L-histidine-[translation elongation factor 2] = *S*-adenosyl-L-homocysteine + 2-[(3*S*)-3-carboxy-3-(methylamino)propyl]-L-histidine-[translation elongation factor 2]

(1b) *S*-adenosyl-L-methionine + 2-[(3*S*)-3-carboxy-3-(methylamino)propyl]-L-histidine-[translation elongation factor 2] = *S*-adenosyl-L-homocysteine + 2-[(3*S*)-3-carboxy-3-(dimethylamino)propyl]-L-histidine-[translation elongation factor 2]

(1c) *S*-adenosyl-L-methionine + 2-[(3*S*)-3-carboxy-3-(dimethylamino)propyl]-L-histidine-[translation elongation factor 2] = *S*-adenosyl-L-homocysteine + diphthine-[translation elongation factor 2]

Other name(s): *S*-adenosyl-L-methionine:elongation factor 2 methyltransferase (ambiguous); diphthine methyltransferase (ambiguous); *S*-adenosyl-L-methionine:2-(3-carboxy-3-aminopropyl)-L-histidine-[translation elongation factor 2] methyltransferase; Dph5 (ambiguous)

Systematic name: *S*-adenosyl-L-methionine:2-[(3*S*)-3-carboxy-3-aminopropyl]-L-histidine-[translation elongation factor 2] methyltransferase (diphthine-[translation elongation factor 2]-forming)

Comments: This archaeal enzyme produces the trimethylated product diphthine, which is converted into diphthamide by EC 6.3.1.14, diphthine—ammonia ligase. Different from the eukaryotic enzyme, which produces diphthine methyl ester (*cf.* EC 2.1.1.314). In the archaeon *Pyrococcus horikoshii* the enzyme acts on His^{600} of elongation factor 2.

References: [4081]

[EC 2.1.1.98 created 1990, modified 2013, modified 2015]

EC 2.1.1.99

Accepted name: 3-hydroxy-16-methoxy-2,3-dihydrotabersonine *N*-methyltransferase

Reaction: *S*-adenosyl-L-methionine + 3-hydroxy-16-methoxy-2,3-dihydrotabersonine = *S*-adenosyl-L-homocysteine + deacetoxyvindoline

Other name(s): 16-methoxy-2,3-dihydro-3-hydroxytabersonine methyltransferase; NMT; 16-methoxy-2,3-dihydro-3-hydroxytabersonine *N*-methyltransferase; *S*-adenosyl-L-methionine:16-methoxy-2,3-dihydro-3-hydroxytabersonine *N*-methyltransferase

Systematic name: *S*-adenosyl-L-methionine:3-hydroxy-16-methoxy-2,3-dihydrotabersonine *N*-methyltransferase

Comments: Involved in the biosynthesis of vindoline from tabersonine in the Madagascar periwinkle *Catharanthus roseus*.

References: [2061, 2063]

[EC 2.1.1.99 created 1990, modified 2005]

EC 2.1.1.100

Accepted name: protein-*S*-isoprenylcysteine *O*-methyltransferase

Reaction: *S*-adenosyl-L-methionine + protein C-terminal *S*-farnesyl-L-cysteine = *S*-adenosyl-L-homocysteine + protein C-terminal *S*-farnesyl-L-cysteine methyl ester

Other name(s): farnesyl cysteine C-terminal methyltransferase; farnesyl-protein carboxymethyltransferase; protein C-terminal farnesylcysteine *O*-methyltransferase; farnesylated protein C-terminal *O*-methyltransferase; isoprenylated protein methyltransferase; prenylated protein methyltransferase; protein *S*-farnesylcysteine C-terminal methyltransferase; *S*-farnesylcysteine methyltransferase; prenylcysteine carboxylmethyltransferase [misleading]; prenylcysteine carboxymethyltransferase [misleading]; prenylcysteine methyltransferase

Systematic name: *S*-adenosyl-L-methionine:protein-*C*-terminal-*S*-farnesyl-L-cysteine *O*-methyltransferase

Comments: C-terminal *S*-geranylgeranylcysteine and *S*-geranylcysteine residues are also methylated, but more slowly.

References: [580, 2582, 3333]

[EC 2.1.1.100 created 1992 (EC 2.1.1.24 created 1972, modified 1983, modified 1989, part incorporated 1992)]

EC 2.1.1.101

Accepted name: macrocin *O*-methyltransferase

Reaction: *S*-adenosyl-L-methionine + macrocin = *S*-adenosyl-L-homocysteine + tylosin

Other name(s): macrocin methyltransferase; *S*-adenosyl-L-methionine-macrocin *O*-methyltransferase; MOMT (ambiguous); *tylF* (gene name)

Systematic name: *S*-adenosyl-L-methionine:macrocin $3'''$-*O*-methyltransferase

Comments: Requires Mg^{2+}, Mn^{2+} or Co^{2+}. The 3-hydroxy group of the 2-*O*-methyl-6-deoxy-D-allose moiety in the macrolide antibiotic macrosin acts as methyl acceptor, generating tylosin, another macrolide antibiotic. Isolated from the bacterium *Streptomyces fradiae*. Not identical with EC 2.1.1.102, demethylmacrocin *O*-methyltransferase.

References: [236, 1790]

[EC 2.1.1.101 created 1992]

EC 2.1.1.102

Accepted name: demethylmacrocin *O*-methyltransferase

Reaction: *S*-adenosyl-L-methionine + demethylmacrocin = *S*-adenosyl-L-homocysteine + macrocin

Other name(s): demethylmacrocin methyltransferase; DMOMT

Systematic name: *S*-adenosyl-L-methionine:demethylmacrocin $2'''$-*O*-methyltransferase

Comments: Requires Mg^{2+}. The enzyme, isolated from the bacterium *Streptomyces fradiae*, is involved in the biosynthesis of the macrolide antibiotic tylosin. The 2-hydroxy group of a 6-deoxy-D-allose moiety in demethylmacrocin acts as the methyl acceptor. Also acts on demethyllactenocin, giving lactenocin. Not identical with EC 2.1.1.101 macrocin *O*-methyltransferase.

References: [1790]

[EC 2.1.1.102 created 1992]

EC 2.1.1.103

Accepted name: phosphoethanolamine *N*-methyltransferase

Reaction: *S*-adenosyl-L-methionine + ethanolamine phosphate = *S*-adenosyl-L-homocysteine + *N*-methylethanolamine phosphate

Other name(s): phosphoethanolamine methyltransferase

Systematic name: *S*-adenosyl-L-methionine:ethanolamine-phosphate *N*-methyltransferase

Comments: The enzyme may catalyse the transfer of two further methyl groups to the product.

References: [674]

[EC 2.1.1.103 created 1992]

EC 2.1.1.104

Accepted name: caffeoyl-CoA *O*-methyltransferase

Reaction: *S*-adenosyl-L-methionine + caffeoyl-CoA = *S*-adenosyl-L-homocysteine + feruloyl-CoA

Other name(s): caffeoyl coenzyme A methyltransferase; caffeoyl-CoA 3-*O*-methyltransferase; *trans*-caffeoyl-CoA 3-*O*-methyltransferase

Systematic name: *S*-adenosyl-L-methionine:caffeoyl-CoA 3-*O*-methyltransferase

References: [1808]

[EC 2.1.1.104 created 1992]

EC 2.1.1.105

Accepted name: *N*-benzoyl-4-hydroxyanthranilate 4-*O*-methyltransferase

Reaction: *S*-adenosyl-L-methionine + *N*-benzoyl-4-hydroxyanthranilate = *S*-adenosyl-L-homocysteine + *N*-benzoyl-4-methoxyanthranilate

Other name(s): *N*-benzoyl-4-hydroxyanthranilate 4-methyltransferase; benzoyl-CoA:anthranilate *N*-benzoyltransferase

Systematic name: *S*-adenosyl-L-methionine:*N*-benzoyl-4-*O*-hydroxyanthranilate 4-*O*-methyltransferase

Comments: Involved in the biosynthesis of phytoalexins.

References: [2861]

[EC 2.1.1.105 created 1992]

EC 2.1.1.106

Accepted name: tryptophan 2-*C*-methyltransferase

Reaction: *S*-adenosyl-L-methionine + L-tryptophan = *S*-adenosyl-L-homocysteine + L-2-methyltryptophan

Other name(s): *tsrM* (gene name); tryptophan 2-methyltransferase; *S*-adenosylmethionine:tryptophan 2-methyltransferase

Systematic name: *S*-adenosyl-L-methionine:L-tryptophan 2-*C*-methyltransferase

Comments: The enzyme, characterized from the bacterium *Streptomyces laurentii*, is involved in thiostrepton biosynthesis. It is a radical SAM enzyme that contains a [4Fe-4S] center and a cobalamin cofactor. The enzyme first transfers the methyl group from SAM to the bound cobalamin, followed by transfer from methylcobalamin to L-tryptophan, resulting in retention of the original methyl group configuration. The second transfer is likely to involve a CH3 radical species formed from methylcobalamin by the concerted action of a partially ligated radical SAM [4Fe-4S]$^{2+/1+}$ center.

References: [957, 2705, 327, 328]

[EC 2.1.1.106 created 1992]

EC 2.1.1.107

Accepted name: uroporphyrinogen-III *C*-methyltransferase

Reaction: **2** *S*-adenosyl-L-methionine + uroporphyrinogen III = **2** *S*-adenosyl-L-homocysteine + precorrin-2 (overall reaction)
(1a) *S*-adenosyl-L-methionine + uroporphyrinogen III = *S*-adenosyl-L-homocysteine + precorrin-1
(1b) *S*-adenosyl-L-methionine + precorrin-1 = *S*-adenosyl-L-homocysteine + precorrin-2

Other name(s): uroporphyrinogen methyltransferase; uroporphyrinogen-III methyltransferase; adenosylmethionine-uroporphyrinogen III methyltransferase; *S*-adenosyl-L-methionine-dependent uroporphyrinogen III methylase; uroporphyrinogen-III methylase; SirA; CysG; CobA [ambiguous - see EC 2.5.1.17] SUMT; uroporphyrin-III *C*-methyltransferase (incorrect); *S*-adenosyl-L-methionine:uroporphyrin-III *C*-methyltransferase (incorrect)

Systematic name: *S*-adenosyl-L-methionine:uroporphyrinogen-III *C*-methyltransferase

Comments: This enzyme catalyses two sequential methylation reactions, the first forming precorrin-1 and the second leading to the formation of precorrin-2. It is the first of three steps leading to the formation of siroheme from uroporphyrinogen III. The second step involves an NAD$^+$-dependent dehydrogenation to form sirohydrochlorin from precorrin-2 (EC 1.3.1.76, precorrin-2 dehydrogenase) and the third step involves the chelation of Fe^{2+} to sirohydrochlorin to form siroheme (EC 4.99.1.4, sirohydrochlorin ferrochelatase). In *Saccharomyces cerevisiae*, the last two steps are carried out by a single bifunctional enzyme, Met^{8}p. In some bacteria, steps 1-3 are catalysed by a single multifunctional protein called CysG, whereas in *Bacillus megaterium*, three separate enzymes carry out each of the steps, with SirA being responsible for the above reaction. Also involved in the biosynthesis of cobalamin.
References: [3776, 3779, 3108]

[EC 2.1.1.107 created 1992, modified 2004]

EC 2.1.1.108

Accepted name: 6-hydroxymellein *O*-methyltransferase
Reaction: *S*-adenosyl-L-methionine + 6-hydroxymellein = *S*-adenosyl-L-homocysteine + 6-methoxymellein
Other name(s): 6-hydroxymellein methyltransferase
Systematic name: *S*-adenosyl-L-methionine:6-hydroxymellein 6-*O*-methyltransferase
Comments: 3,4-Dehydro-6-hydroxymellein can also act as acceptor. 6-Methoxymellein is a phytoalexin produced by carrot tissue.
References: [1828]

[EC 2.1.1.108 created 1992]

EC 2.1.1.109

Accepted name: demethylsterigmatocystin 6-*O*-methyltransferase
Reaction: *S*-adenosyl-L-methionine + 6-demethylsterigmatocystin = *S*-adenosyl-L-homocysteine + sterigmatocystin
Other name(s): demethylsterigmatocystin methyltransferase; *O*-methyltransferase I
Systematic name: *S*-adenosyl-L-methionine:6-demethylsterigmatocystin 6-*O*-methyltransferase
Comments: Dihydrodemethylsterigmatocystin can also act as acceptor. Involved in the biosynthesis of aflatoxins in fungi.
References: [3932]

[EC 2.1.1.109 created 1992]

EC 2.1.1.110

Accepted name: sterigmatocystin 8-*O*-methyltransferase
Reaction: (1) *S*-adenosyl-L-methionine + sterigmatocystin = *S*-adenosyl-L-homocysteine + 8-*O*-methylsterigmatocystin
(2) *S*-adenosyl-L-methionine + dihydrosterigmatocystin = *S*-adenosyl-L-homocysteine + 8-*O*-methyldihydrosterigmatocystin
Other name(s): sterigmatocystin methyltransferase; *O*-methyltransferase II; sterigmatocystin 7-*O*-methyltransferase (incorrect); *S*-adenosyl-L-methionine:sterigmatocystin 7-*O*-methyltransferase (incorrect); OmtA
Systematic name: *S*-adenosyl-L-methionine:sterigmatocystin 8-*O*-methyltransferase
Comments: Dihydrosterigmatocystin can also act as acceptor. Involved in the biosynthesis of aflatoxins in fungi.
References: [303, 3932, 4007, 1895]

[EC 2.1.1.110 created 1992, modified 2005, modified 2013]

EC 2.1.1.111

Accepted name: anthranilate *N*-methyltransferase
Reaction: *S*-adenosyl-L-methionine + anthranilate = *S*-adenosyl-L-homocysteine + *N*-methylanthranilate

Other name(s): anthranilic acid *N*-methyltransferase
Systematic name: *S*-adenosyl-L-methionine:anthranilate *N*-methyltransferase
Comments: Involved in the biosynthesis of acridine alkaloids in plant tissues.
References: [816]

[EC 2.1.1.111 created 1992]

EC 2.1.1.112

Accepted name: glucuronoxylan 4-*O*-methyltransferase
Reaction: *S*-adenosyl-L-methionine + glucuronoxylan D-glucuronate = *S*-adenosyl-L-homocysteine + glucuronoxylan 4-*O*-methyl-D-glucuronate
Systematic name: *S*-adenosyl-L-methionine:glucuronoxylan-D-glucuronate 4-*O*-methyltransferase
References: [241]

[EC 2.1.1.112 created 1992]

EC 2.1.1.113

Accepted name: site-specific DNA-methyltransferase (cytosine-N^4-specific)
Reaction: *S*-adenosyl-L-methionine + DNA cytosine = *S*-adenosyl-L-homocysteine + DNA N^4-methylcytosine
Other name(s): modification methylase; restriction-modification system; DNA[cytosine-N^4]methyltransferase; m4C-forming MTase; *S*-adenosyl-L-methionine:DNA-cytosine 4-*N*-methyltransferase
Systematic name: *S*-adenosyl-L-methionine:DNA-cytosine N^4-methyltransferase
Comments: This is a large group of enzymes, most of which, with enzymes of similar site specificity listed as EC 3.1.21.3 (type 1 site-specific deoxyribonuclease), EC 3.1.21.4 (type II site-specific deoxyribonuclease) or EC 3.1.21.5 (type III site-specific deoxyribonuclease), form so-called ‘restriction-modification systems’. A complete listing of all of these enzymes has been produced by R.J. Roberts and is available on-line at http://rebase.neb.com/rebase/rebase.html.
References: [1648, 1711, 2897, 4011]

[EC 2.1.1.113 created 1992]

EC 2.1.1.114

Accepted name: polyprenyldihydroxybenzoate methyltransferase
Reaction: *S*-adenosyl-L-methionine + 3,4-dihydroxy-5-*all-trans*-polyprenylbenzoate = *S*-adenosyl-L-homocysteine + 3-methoxy-4-hydroxy-5-*all-trans*-polyprenylbenzoate
Other name(s): 3,4-dihydroxy-5-hexaprenylbenzoate methyltransferase; dihydroxyhexaprenylbenzoate methyltransferase; COQ3 (gene name); Coq3 *O*-methyltransferase; DHHB *O*-methyltransferase
Systematic name: *S*-adenosyl-L-methionine:3,4-dihydroxy-5-*all-trans*-polyprenylbenzoate 3-*O*-methyltransferase
Comments: This enzyme is involved in ubiquinone biosynthesis. Ubiquinones from different organisms have a different number of prenyl units (for example, ubiquinone-6 in *Saccharomyces*, ubiquinone-9 in rat and ubiquinone-10 in human), and thus the natural substrate for the enzymes from different organisms has a different number of prenyl units. However, the enzyme usually shows a low degree of specificity regarding the number of prenyl units. For example, the human COQ3 enzyme can restore biosynthesis of ubiquinone-6 in coq3 deletion mutants of yeast [1528]. The enzymes from yeast and rat also catalyse the methylation of 3-demethylubiquinol-6 and 3-demethylubiquinol-9, respectively [2740] (this activity is classified as EC 2.1.1.64, 3-demethylubiquinol 3-*O*-methyltransferase).
References: [577, 2740, 1528, 3922]

[EC 2.1.1.114 created 1999]

EC 2.1.1.115

Accepted name: (*RS*)-1-benzyl-1,2,3,4-tetrahydroisoquinoline *N*-methyltransferase
Reaction: *S*-adenosyl-L-methionine + (*RS*)-1-benzyl-1,2,3,4-tetrahydroisoquinoline = *S*-adenosyl-L-homocysteine + *N*-methyl-(*RS*)-1-benzyl-1,2,3,4-tetrahydroisoquinoline

Other name(s): norreticuline *N*-methyltransferase
Systematic name: *S*-adenosyl-L-methionine:(*RS*)-1-benzyl-1,2,3,4-tetrahydroisoquinoline *N*-methyltransferase
Comments: Broad substrate specificity for (*RS*)-1-benzyl-1,2,3,4-tetrahydroisoquinolines; including coclaurine, norcoclaurine, isococlaurine, norarmepavine, norreticuline and tetrahydropapaverine. Both *R*- and *S*-enantiomers are methylated. The enzyme participates in the pathway leading to benzylisoquinoline alkaloid synthesis in plants. The physiological substrate is likely to be coclaurine. The enzyme was earlier termed norreticuline *N*-methyltransferase. However, norreticuline has not been found to occur in nature and that name does not reflect the broad specificity of the enzyme for (*RS*)-1-benzyl-1,2,3,4-tetrahydroisoquinolines.
References: [955]

[EC 2.1.1.115 created 1999]

EC 2.1.1.116

Accepted name: 3′-hydroxy-*N*-methyl-(*S*)-coclaurine 4′-*O*-methyltransferase
Reaction: *S*-adenosyl-L-methionine + 3′-hydroxy-*N*-methyl-(*S*)-coclaurine = *S*-adenosyl-L-homocysteine + (*S*)-reticuline
Systematic name: *S*-adenosyl-L-methionine:3′-hydroxy-*N*-methyl-(*S*)-coclaurine 4′-*O*-methyltransferase
Comments: Involved in isoquinoline alkaloid metabolism in plants. The enzyme has also been shown to catalyse the methylation of (*RS*)-laudanosoline, (*S*)-3′-hydroxycoclaurine and (*RS*)-7-*O*-methylnorlaudanosoline.
References: [956]

[EC 2.1.1.116 created 1999]

EC 2.1.1.117

Accepted name: (*S*)-scoulerine 9-*O*-methyltransferase
Reaction: *S*-adenosyl-L-methionine + (*S*)-scoulerine = *S*-adenosyl-L-homocysteine + (*S*)-tetrahydrocolumbamine
Systematic name: *S*-adenosyl-L-methionine:(*S*)-scoulerine 9-*O*-methyltransferase
Comments: The product of this reaction is a precursor for protoberberine alkaloids in plants
References: [2341]

[EC 2.1.1.117 created 1999]

EC 2.1.1.118

Accepted name: columbamine *O*-methyltransferase
Reaction: *S*-adenosyl-L-methionine + columbamine = *S*-adenosyl-L-homocysteine + palmatine
Systematic name: *S*-adenosyl-L-methionine:columbamine *O*-methyltransferase
Comments: The product of this reaction is a protoberberine alkaloid that is widely distributed in the plant kingdom. This enzyme is distinct in specificity from EC 2.1.1.88, 8-hydroxyquercetin 8-*O*-methyltransferase.
References: [2962]

[EC 2.1.1.118 created 1999]

EC 2.1.1.119

Accepted name: 10-hydroxydihydrosanguinarine 10-*O*-methyltransferase
Reaction: *S*-adenosyl-L-methionine + 10-hydroxydihydrosanguinarine = *S*-adenosyl-L-homocysteine + dihydrochelirubine
Systematic name: *S*-adenosyl-L-methionine:10-hydroxydihydrosanguinarine 10-*O*-methyltransferase
Comments: This reaction is part of the pathway for synthesis of benzophenanthridine alkaloids in plants.
References: [687]

[EC 2.1.1.119 created 1999]

EC 2.1.1.120

Accepted name: 12-hydroxydihydrochelirubine 12-*O*-methyltransferase

Reaction: *S*-adenosyl-L-methionine + 12-hydroxydihydrochelirubine = *S*-adenosyl-L-homocysteine + dihydromacarpine

Systematic name: *S*-adenosyl-L-methionine:12-hydroxydihydrochelirubine 12-*O*-methyltransferase

Comments: This reaction is part of the pathway for synthesis of benzophenanthridine alkaloid macarpine in plants.

References: [1575]

[EC 2.1.1.120 created 1999]

EC 2.1.1.121

Accepted name: 6-*O*-methylnorlaudanosoline 5′-*O*-methyltransferase

Reaction: *S*-adenosyl-L-methionine + 6-*O*-methylnorlaudanosoline = *S*-adenosyl-L-homocysteine + nororientaline

Systematic name: *S*-adenosyl-L-methionine:6-*O*-methylnorlaudanosoline 5′-*O*-methyltransferase

Comments: Nororientaline is a precursor of the alkaloid papaverine.

References: [2964]

[EC 2.1.1.121 created 1999]

EC 2.1.1.122

Accepted name: (*S*)-tetrahydroprotoberberine *N*-methyltransferase

Reaction: *S*-adenosyl-L-methionine + (*S*)-7,8,13,14-tetrahydroprotoberberine = *S*-adenosyl-L-homocysteine + *cis*-*N*-methyl-(*S*)-7,8,13,14-tetrahydroprotoberberine

Other name(s): tetrahydroprotoberberine *cis*-*N*-methyltransferase

Systematic name: *S*-adenosyl-L-methionine:(*S*)-7,8,13,14-tetrahydroprotoberberine *cis*-*N*-methyltransferase

Comments: Involved in the biosynthesis of isoquinoline alkaloids in plants.

References: [2966]

[EC 2.1.1.122 created 1999]

EC 2.1.1.123

Accepted name: [cytochrome-*c*]-methionine *S*-methyltransferase

Reaction: *S*-adenosyl-L-methionine + [cytochrome *c*]-methionine = *S*-adenosyl-L-homocysteine + [cytochrome *c*]-*S*-methyl-methionine

Systematic name: *S*-adenosyl-L-methionine:[cytochrome *c*]-methionine *S*-methyltransferase

Comments: The enzyme from *Euglena gracilis* methylates Met-65 of horse heart cytochrome *c*.

References: [878]

[EC 2.1.1.123 created 1999]

[2.1.1.124 Deleted entry. [cytochrome c]-arginine N-methyltransferase. Now covered by EC 2.1.1.319, type I protein arginine methyltransferase, EC 2.1.1.320, type II protein arginine methyltransferase, EC 2.1.1.321, type III protein arginine methyltransferase and EC 2.1.1.322, type IV protein arginine methyltransferase]

[EC 2.1.1.124 created 1999 (EC 2.1.1.23 created 1972, modified 1976, modified 1983, part incorporated 1999), deleted 2015]

[2.1.1.125 Deleted entry. histone-arginine N-methyltransferase. Now covered by EC 2.1.1.319, type I protein arginine methyltransferase, EC 2.1.1.320, type II protein arginine methyltransferase, EC 2.1.1.321, type III protein arginine methyltransferase and EC 2.1.1.322, type IV protein arginine methyltransferase]

[EC 2.1.1.125 created 1999 (EC 2.1.1.23 created 1972, modified 1976, modified 1983, part incorporated 1999), deleted 2015]

[2.1.1.126 Deleted entry. [myelin basic protein]-arginine N-methyltransferase. Now covered by EC 2.1.1.319, type I protein arginine methyltransferase, EC 2.1.1.320, type II protein arginine methyltransferase, EC 2.1.1.321, type III protein arginine methyltransferase and EC 2.1.1.322, type IV protein arginine methyltransferase]

[EC 2.1.1.126 created 1999 (EC 2.1.1.23 created 1972, modified 1976, modified 1983, part incorporated 1999), deleted 2015]

EC 2.1.1.127

Accepted name: [ribulose-bisphosphate carboxylase]-lysine *N*-methyltransferase

Reaction: **3** *S*-adenosyl-L-methionine + [ribulose-1,5-bisphosphate carboxylase]-L-lysine = **3** *S*-adenosyl-L-homocysteine + [ribulose-1,5-bisphosphate carboxylase]-N^6,N^6,N^6-trimethyl-L-lysine

Other name(s): rubisco methyltransferase; ribulose-bisphosphate-carboxylase/oxygenase *N*-methyltransferase; ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit ε*N*-methyltransferase; *S*-adenosyl-L-methionine:[3-phospho-D-glycerate-carboxy-lyase (dimerizing)]-lysine 6-*N*-methyltransferase; RuBisCO methyltransferase; RuBisCO LSMT

Systematic name: *S*-adenosyl-L-methionine:[3-phospho-D-glycerate-carboxy-lyase (dimerizing)]-lysine N^6-methyltransferase

Comments: The enzyme catalyses three successive methylations of Lys-14 in the large subunits of hexadecameric higher plant ribulose-bisphosphate-carboxylase (EC 4.1.1.39). Only the three methylated form is observed [740]. The enzyme from pea (*Pisum sativum*) also three-methylates a specific lysine in the chloroplastic isoforms of fructose-bisphosphate aldolase (EC 4.1.2.13) [2261].

References: [3755, 3982, 740, 2098, 2261]

[EC 2.1.1.127 created 1999, modified 2012]

EC 2.1.1.128

Accepted name: (*RS*)-norcoclaurine 6-*O*-methyltransferase

Reaction: *S*-adenosyl-L-methionine + (*RS*)-norcoclaurine = *S*-adenosyl-L-homocysteine + (*RS*)-coclaurine

Systematic name: *S*-adenosyl-L-methionine:(*RS*)-norcoclaurine 6-*O*-methyltransferase

Comments: The enzyme will also catalyse the 6-*O*-methylation of (*RS*)-norlaudanosoline to form 6-*O*-methylnorlaudanosoline, but this alkaloid has not been found to occur in plants.

References: [2965, 3029, 3312]

[EC 2.1.1.128 created 1999]

EC 2.1.1.129

Accepted name: inositol 4-methyltransferase

Reaction: *S*-adenosyl-L-methionine + *myo*-inositol = *S*-adenosyl-L-homocysteine + 1D-4-*O*-methyl-*myo*-inositol

Other name(s): *myo*-inositol 4-*O*-methyltransferase; *S*-adenosyl-L-methionine:*myo*-inositol 4-*O*-methyltransferase; *myo*-inositol 6-*O*-methyltransferase

Systematic name: *S*-adenosyl-L-methionine:1D-*myo*-inositol 4-methyltransferase

Comments: The enzyme from the rice bean *Vigna umbellata* (Fabaceae) is highly specific for *S*-adenosyl-L-methionine. The enzyme also methylates 1L-1,2,4/3,5-cyclohexanepentol, 2,4,6/3,5-pentahydroxycyclohexanone, D,L-2,3,4,6/5-pentacyclohexanone and 2,2′-anhydro-2-*C*-hydroxymethyl-*myo*-inositol, but at lower rates than that of *myo*-inositol.

References: [3670, 3746]

[EC 2.1.1.129 created 1999 (EC 2.1.1.134 created 1999, incorporated 2002), modified 2002]

EC 2.1.1.130

Accepted name: precorrin-2 C^{20}-methyltransferase

Reaction: *S*-adenosyl-L-methionine + precorrin-2 = *S*-adenosyl-L-homocysteine + precorrin-3A

Systematic name: *S*-adenosyl-L-methionine:precorrin-2 C^{20}-methyltransferase

References: [2915, 2914, 697]

[EC 2.1.1.130 created 1999]

EC 2.1.1.131

Accepted name: precorrin-3B C^{17}-methyltransferase

Reaction: *S*-adenosyl-L-methionine + precorrin-3B = *S*-adenosyl-L-homocysteine + precorrin-4

Other name(s): precorrin-3 methyltransferase; CobJ

Systematic name: *S*-adenosyl-L-methionine:precorrin-3B C^{17}-methyltransferase

Comments: In the aerobic cobalamin biosythesis pathway, four enzymes are involved in the conversion of precorrin-3A to precorrin-6A. The first of the four steps is carried out by EC 1.14.13.83, precorrin-3B synthase (CobG), yielding precorrin-3B as the product. This is followed by three methylation reactions, which introduce a methyl group at C-17 (CobJ; EC 2.1.1.131), C-11 (CobM; EC 2.1.1.133) and C-1 (CobF; EC 2.1.1.152) of the macrocycle, giving rise to precorrin-4, precorrin-5 and precorrin-6A, respectively.

References: [3125, 697]

[EC 2.1.1.131 created 1999]

EC 2.1.1.132

Accepted name: precorrin-6B $C^{5,15}$-methyltransferase (decarboxylating)

Reaction: **2** *S*-adenosyl-L-methionine + precorrin-6B = **2** *S*-adenosyl-L-homocysteine + precorrin-8X + CO_2 (overall reaction)
(1a) *S*-adenosyl-L-methionine + precorrin-6B = *S*-adenosyl-L-homocysteine + precorrin-7 + CO_2
(1b) *S*-adenosyl-L-methionine + precorrin-7 = *S*-adenosyl-L-homocysteine + precorrin-8X

Other name(s): precorrin-6 methyltransferase; precorrin-6Y methylase; precorrin-6Y $C^{5,15}$-methyltransferase (decarboxylating); *cobL* (gene name)

Systematic name: *S*-adenosyl-L-methionine:1-precorrin-6B $C^{5,15}$-methyltransferase (C-12-decarboxylating)

Comments: The enzyme, which participates in the aerobic adenosylcobalamin biosynthesis pathway, has *S*-adenosyl-L-methionine-dependent methyltransferase and decarboxylase activities. The enzyme is a fusion protein with two active sites; one catalyses the methylation at C^{15} and the decarboxylation, while the other catalyses the methylation at C^5.

References: [323, 701]

[EC 2.1.1.132 created 1999, modified 2013]

EC 2.1.1.133

Accepted name: precorrin-4 C^{11}-methyltransferase

Reaction: *S*-adenosyl-L-methionine + precorrin-4 = *S*-adenosyl-L-homocysteine + precorrin-5

Other name(s): precorrin-3 methylase; CobM

Systematic name: *S*-adenosyl-L-methionine:precorrin-4 C^{11} methyltransferase

Comments: In the aerobic cobalamin biosythesis pathway, four enzymes are involved in the conversion of precorrin-3A to precorrin-6A. The first of the four steps is carried out by EC 1.14.13.83, precorrin-3B synthase (CobG), yielding precorrin-3B as the product. This is followed by three methylation reactions, which introduce a methyl group at C-17 (CobJ; EC 2.1.1.131), C-11 (CobM; EC 2.1.1.133) and C-1 (CobF; EC 2.1.1.152) of the macrocycle, giving rise to precorrin-4, precorrin-5 and precorrin-6A, respectively.

References: [633, 2941]

[EC 2.1.1.133 created 1999]

[2.1.1.134 Deleted entry. myo-inositol 6-O-methyltransferase. Now included with EC 2.1.1.129, inositol 4-methyltransferase]

[EC 2.1.1.134 created 1999, deleted 2002]

[2.1.1.135 Transferred entry. [methionine synthase]-cobalamin methyltransferase (cob(II)alamin reducing). Now EC 1.16.1.8, [methionine synthase] reductase]

[EC 2.1.1.135 created 1999, deleted 2003]

EC 2.1.1.136

Accepted name: chlorophenol *O*-methyltransferase
Reaction: *S*-adenosyl-L-methionine + trichlorophenol = *S*-adenosyl-L-homocysteine + trichloroanisole
Other name(s): halogenated phenol *O*-methyltransferase, trichlorophenol *O*-methyltransferase
Systematic name: *S*-adenosyl-L-methionine:trichlorophenol *O*-methyltransferase
Comments: The enzyme from *Trichoderma virgatum,* when cultured in the presence of halogenated phenol, also acts on a range of mono-, di- and trichlorophenols.
References: [1670]

[EC 2.1.1.136 created 2000]

EC 2.1.1.137

Accepted name: arsenite methyltransferase
Reaction: (1) *S*-adenosyl-L-methionine + arsenite = *S*-adenosyl-L-homocysteine + methylarsonate
(2) *S*-adenosyl-L-methionine + methylarsonite = *S*-adenosyl-L-homocysteine + dimethylarsinate
Other name(s): *S*-adenosyl-L-methionine:arsenic(III) methyltransferase; *S*-adenosyl-L-methionine:methylarsonite As-methyltransferase; methylarsonite methyltransferase
Systematic name: *S*-adenosyl-L-methionine:arsenite As-methyltransferase
Comments: An enzyme of the biotransformation pathway that forms dimethylarsinate from inorganic arsenite and arsenate. It methylates arsenite to form methylarsonate, Me-AsO$_3$H$_2$, which is reduced by EC 1.20.4.2, methylarsonate reductase, to methylarsonite, Me-As(OH)$_2$. Methylarsonite is also a substrate for this enzyme (EC 2.1.1.137), which converts it into the much less toxic compound dimethylarsinate (cacodylate), Me$_2$As(O)-OH.
References: [4020, 4021, 4022, 4023, 1972]

[EC 2.1.1.137 created 2000, (EC 2.1.1.138 incorporated 2003), modified 2003]

[2.1.1.138 Deleted entry. methylarsonite methyltransferase. Reaction due to EC 2.1.1.137, arsonite methyltransferase]

[EC 2.1.1.138 created 2000, deleted 2003]

EC 2.1.1.139

Accepted name: 3′-demethylstaurosporine *O*-methyltransferase
Reaction: *S*-adenosyl-L-methionine + 3′-demethylstaurosporine = *S*-adenosyl-L-homocysteine + staurosporine
Other name(s): 3′-demethoxy-3′-hydroxystaurosporine *O*-methyltransferase; staurosporine synthase
Systematic name: *S*-adenosyl-L-methionine:3′-demethylstaurosporine *O*-methyltransferase
Comments: Catalyses the final step in the biosynthesis of staurosporine, an alkaloidal antibiotic that is a potent inhibitor of protein kinases, especially protein kinase C.
References: [3805]

[EC 2.1.1.139 created 2000]

EC 2.1.1.140

Accepted name: (*S*)-coclaurine-*N*-methyltransferase
Reaction: *S*-adenosyl-L-methionine + (*S*)-coclaurine = *S*-adenosyl-L-homocysteine + (*S*)-*N*-methylcoclaurine
Systematic name: *S*-adenosyl-L-methionine:(*S*)-coclaurine-*N*-methyltransferase
Comments: The enzyme is specific for the (*S*)-isomer of coclaurine. Norcoclaurine can also act as an acceptor.
References: [2025]

[EC 2.1.1.140 created 2001]

EC 2.1.1.141

Accepted name: jasmonate *O*-methyltransferase

Reaction: *S*-adenosyl-L-methionine + jasmonate = *S*-adenosyl-L-homocysteine + methyl jasmonate

Other name(s): jasmonic acid carboxyl methyltransferase

Systematic name: *S*-adenosyl-L-methionine:jasmonate *O*-methyltransferase

Comments: 9,10-Dihydrojasmonic acid is a poor substrate for the enzyme. The enzyme does not convert 12-oxo-phytodienoic acid (a precursor of jasmonic acid), salicylic acid, benzoic acid, linolenic acid or cinnamic acid into their corresponding methyl esters. Enzyme activity is inhibited by the presence of divalent cations, e.g., Ca^{2+}, Cu^{2+}, Mg^{2+} and Zn^{2+}.

References: [3143]

[EC 2.1.1.141 created 2001]

EC 2.1.1.142

Accepted name: cycloartenol 24-*C*-methyltransferase

Reaction: *S*-adenosyl-L-methionine + cycloartenol = *S*-adenosyl-L-homocysteine + (24*R*)-24-methylcycloart-25-en-3β-ol

Other name(s): sterol *C*-methyltransferase

Systematic name: *S*-adenosyl-L-methionine:cycloartenol 24-*C*-methyltransferase

Comments: *S*-Adenosyl-L-methionine methylates the *Si* face of the 24(25)-double bond with elimination of a hydrogen atom from the pro-Z methyl group at C-25.

References: [2110]

[EC 2.1.1.142 created 2001]

EC 2.1.1.143

Accepted name: 24-methylenesterol *C*-methyltransferase

Reaction: *S*-adenosyl-L-methionine + 24-methylenelophenol = *S*-adenosyl-L-homocysteine + (*Z*)-24-ethylidenelophenol

Other name(s): SMT$_2$; 24-methylenelophenol *C*-24^1-methyltransferase

Systematic name: *S*-adenosyl-L-methionine:24-methylenelophenol *C*-methyltransferase

Comments: This is the second methylation step of plant sterol biosynthesis (cf EC 2.1.1.142, cycloartenol 24-*C*-methyltransferase).

References: [368]

[EC 2.1.1.143 created 2001]

EC 2.1.1.144

Accepted name: *trans*-aconitate 2-methyltransferase

Reaction: *S*-adenosyl-L-methionine + *trans*-aconitate = *S*-adenosyl-L-homocysteine + (*E*)-3-(methoxycarbonyl)pent-2-enedioate

Systematic name: *S*-adenosyl-L-methionine:(*E*)-prop-1-ene-1,2,3-tricarboxylate $2'$-*O*-methyltransferase

Comments: Also catalyses the formation of the methyl monoester of *cis*-aconitate, isocitrate and citrate, but more slowly. While the enzyme from *Escherichia coli* forms (*E*)-3-(methoxycarbonyl)-pent-2-enedioate as the product, that from *Saccharomyces cerevisiae* forms (*E*)-2-(methoxycarbonylmethyl)butenedioate and is therefore classified as a separate enzyme (*cf.* EC 2.1.1.145, *trans*-aconitate 3-methyltransferase).

References: [455, 457, 456]

[EC 2.1.1.144 created 2002]

EC 2.1.1.145

Accepted name: *trans*-aconitate 3-methyltransferase

Reaction: *S*-adenosyl-L-methionine + *trans*-aconitate = *S*-adenosyl-L-homocysteine + (*E*)-2-(methoxycarbonylmethyl)butenedioate
Systematic name: *S*-adenosyl-L-methionine:(*E*)-prop-1-ene-1,2,3-tricarboxylate $3'$-*O*-methyltransferase
Comments: Also catalyses the formation of the methyl monoester of *cis*-aconitate, isocitrate and citrate, but more slowly. While the enzyme from *Saccharomyces cerevisiae* forms (*E*)-2-(methoxycarbonylmethyl)butenedioate as the product, that from *Escherichia coli* forms (*E*)-3-(methoxycarbonyl)-pent-2-enedioate and is therefore classified as a separate enzyme (*cf*. EC 2.1.1.144, *trans*-aconitate 2-methyltransferase)
References: [455, 457]

[EC 2.1.1.145 created 2002]

EC 2.1.1.146

Accepted name: (iso)eugenol *O*-methyltransferase
Reaction: *S*-adenosyl-L-methionine + isoeugenol = *S*-adenosyl-L-homocysteine + isomethyleugenol
Systematic name: *S*-adenosyl-L-methionine:isoeugenol *O*-methyltransferase
Comments: Acts on eugenol and chavicol as well as isoeugenol.
References: [3752, 1007]

[EC 2.1.1.146 created 2002]

EC 2.1.1.147

Accepted name: corydaline synthase
Reaction: *S*-adenosyl-L-methionine + palmatine + **2** NADPH + H$^+$ = *S*-adenosyl-L-homocysteine + corydaline + **2** NADP$^+$
Systematic name: *S*-adenosyl-L-methionine:protoberberine 13-*C*-methyltransferase
Comments: Also acts on 7,8-dihydropalmatine.
References: [2963]

[EC 2.1.1.147 created 2002]

EC 2.1.1.148

Accepted name: thymidylate synthase (FAD)
Reaction: 5,10-methylenetetrahydrofolate + dUMP + NADPH + H$^+$ = dTMP + tetrahydrofolate + NADP$^+$
Other name(s): Thy1; ThyX
Systematic name: 5,10-methylenetetrahydrofolate,FADH$_2$:dUMP *C*-methyltransferase
Comments: Contains FAD. All thymidylate synthases catalyse a reductive methylation involving the transfer of the methylene group of 5,10-methylenetetrahydrofolate to the C$_5$ position of dUMP and a two electron reduction of the methylene group to a methyl group. Unlike the classical thymidylate synthase, ThyA (EC 2.1.1.45), which uses folate as both a 1-carbon donor and a source of reducing equivalents, this enzyme uses a flavin coenzyme as a source of reducing equivalents, which are derived from NADPH.
References: [2383, 1137, 1128, 1732, 1733, 2270]

[EC 2.1.1.148 created 2003, modified 2010]

[2.1.1.149 Deleted entry. myricetin O-methyltransferase. Now covered by EC 2.1.1.267, flavonoid 3′,5′-methyltransferase.]

[EC 2.1.1.149 created 2003, modified 2011, deleted 2013]

EC 2.1.1.150

Accepted name: isoflavone 7-*O*-methyltransferase
Reaction: *S*-adenosyl-L-methionine + a 7-hydroxyisoflavone = *S*-adenosyl-L-homocysteine + a 7-methoxyisoflavone

Systematic name: *S*-adenosyl-L-methionine:hydroxyisoflavone 7-*O*-methyltransferase
Comments: The enzyme from alfalfa can methylate daidzein, genistein and 6,7,4′-trihydroxyisoflavone but not flavones or flavanones.
References: [810, 1262, 1261, 1263, 1993, 4087]

[EC 2.1.1.150 created 2003]

EC 2.1.1.151

Accepted name: cobalt-factor II C^{20}-methyltransferase
Reaction: *S*-adenosyl-L-methionine + cobalt-factor II = *S*-adenosyl-L-homocysteine + cobalt-factor III
Other name(s): CbiL
Systematic name: *S*-adenosyl-L-methionine:cobalt-factor-II C^{20}-methyltransferase
Comments: Involved in the anaerobic biosynthesis of vitamin B_{12}.
References: [3297]

[EC 2.1.1.151 created 2004]

EC 2.1.1.152

Accepted name: precorrin-6A synthase (deacetylating)
Reaction: *S*-adenosyl-L-methionine + precorrin-5 + H_2O = *S*-adenosyl-L-homocysteine + precorrin-6A + acetate
Other name(s): precorrin-6X synthase (deacetylating); CobF
Systematic name: *S*-adenosyl-L-methionine:precorrin-5 C^1-methyltransferase (deacetylating)
Comments: In the aerobic cobalamin biosythesis pathway, four enzymes are involved in the conversion of precorrin-3A to precorrin-6A. The first of the four steps is carried out by EC 1.14.13.83, precorrin-3B synthase (CobG), yielding precorrin-3B as the product. This is followed by three methylation reactions, which introduce a methyl group at C-17 (CobJ; EC 2.1.1.131), C-11 (CobM; EC 2.1.1.133) and C-1 (CobF; EC 2.1.1.152) of the macrocycle, giving rise to precorrin-4, precorrin-5 and precorrin-6A, respectively.
References: [697, 3778]

[EC 2.1.1.152 created 2004]

EC 2.1.1.153

Accepted name: vitexin 2″-*O*-rhamnoside 7-*O*-methyltransferase
Reaction: *S*-adenosyl-L-methionine + vitexin 2″-*O*-β-L-rhamnoside = *S*-adenosyl-L-homocysteine + 7-*O*-methylvitexin 2″-*O*-β-L-rhamnoside
Systematic name: *S*-adenosyl-L-methionine:vitexin-2″-*O*-β-L-rhamnoside 7-*O*-methyltransferase
Comments: The flavonoids vitexin and isovitexin 2″-*O*-arabinoside do not act as substrates for the enzyme from oats (*Avena sativa*).
References: [1719]

[EC 2.1.1.153 created 2004]

EC 2.1.1.154

Accepted name: isoliquiritigenin 2′-*O*-methyltransferase
Reaction: *S*-adenosyl-L-methionine + isoliquiritigenin = *S*-adenosyl-L-homocysteine + 2′-*O*-methylisoliquiritigenin
Other name(s): chalcone OMT; CHMT
Systematic name: *S*-adenosyl-L-methionine:isoliquiritigenin 2′-*O*-methyltransferase
Comments: Not identical to EC 2.1.1.65, licodione 2′-*O*-methyltransferase [1429]. While EC 2.1.1.154, isoliquiritigenin 2′-*O*-methyltransferase can use licodione as a substrate, EC 2.1.1.65 cannot use isoliquiritigenin as a substrate.
References: [2179, 1429]

[EC 2.1.1.154 created 2004]

EC 2.1.1.155

Accepted name: kaempferol 4′-*O*-methyltransferase

Reaction: *S*-adenosyl-L-methionine + kaempferol = *S*-adenosyl-L-homocysteine + kaempferide

Other name(s): *S*-adenosyl-L-methionine:flavonoid 4′-*O*-methyltransferase; F 4′-OMT

Systematic name: *S*-adenosyl-L-methionine:kaempferol 4′-*O*-methyltransferase

Comments: The enzyme acts on the hydroxy group in the 4′-position of some flavones, flavanones and isoflavones. Kaempferol, apigenin and kaempferol triglucoside are substrates, as is genistein, which reacts more slowly. Compounds with an hydroxy group in the 3′ and 4′ positions, such as quercetin and eriodictyol, do not act as substrates. Similar to EC 2.1.1.75, apigenin 4′-*O*-methyltransferase and EC 2.1.1.83, 3,7-dimethylquercetin 4′-*O*-methyltransferase.

References: [648]

[EC 2.1.1.155 created 2004]

EC 2.1.1.156

Accepted name: glycine/sarcosine *N*-methyltransferase

Reaction: **2** *S*-adenosyl-L-methionine + glycine = **2** *S*-adenosyl-L-homocysteine + *N*,*N*-dimethylglycine (overall reaction)
(1a) *S*-adenosyl-L-methionine + glycine = *S*-adenosyl-L-homocysteine + sarcosine
(1b) *S*-adenosyl-L-methionine + sarcosine = *S*-adenosyl-L-homocysteine + *N*,*N*-dimethylglycine

Other name(s): ApGSMT; glycine-sarcosine methyltransferase; GSMT; GMT; glycine sarcosine *N*-methyltransferase; *S*-adenosyl-L-methionine:sarcosine *N*-methyltransferase

Systematic name: *S*-adenosyl-L-methionine:glycine(or sarcosine) *N*-methyltransferase [sarcosine(or *N*,*N*-dimethylglycine)-forming]

Comments: Cells of the oxygen-evolving halotolerant cyanobacterium *Aphanocthece halophytica* synthesize betaine from glycine by a three-step methylation process. This is the first enzyme and it leads to the formation of either sarcosine or *N*,*N*-dimethylglycine, which is further methylated to yield betaine (*N*,*N*,*N*-trimethylglycine) by the action of EC 2.1.1.157, sarcosine/dimethylglycine *N*-methyltransferase. Differs from EC 2.1.1.20, glycine *N*-methyltransferase, as it can further methylate the product of the first reaction. Acetate, dimethylglycine and *S*-adenosyl-L-homocysteine can inhibit the reaction [3713].

References: [2499, 2500, 3713]

[EC 2.1.1.156 created 2005]

EC 2.1.1.157

Accepted name: sarcosine/dimethylglycine N-methyltransferase

Reaction: **2** *S*-adenosyl-L-methionine + sarcosine = **2** *S*-adenosyl-L-homocysteine + betaine (overall reaction)
(1a) *S*-adenosyl-L-methionine + sarcosine = *S*-adenosyl-L-homocysteine + *N*,*N*-dimethylglycine
(1b) *S*-adenosyl-L-methionine + *N*,*N*-dimethylglycine = *S*-adenosyl-L-homocysteine + betaine

Other name(s): ApDMT; sarcosine-dimethylglycine methyltransferase; SDMT; sarcosine dimethylglycine *N*-methyltransferase; *S*-adenosyl-L-methionine:*N*,*N*-dimethylglycine *N*-methyltransferase

Systematic name: *S*-adenosyl-L-methionine:sarcosine(or *N*,*N*-dimethylglycine) *N*-methyltransferase [*N*,*N*-dimethylglycine(or betaine)-forming]

Comments: Cells of the oxygen-evolving halotolerant cyanobacterium *Aphanocthece halophytica* synthesize betaine from glycine by a three-step methylation process. The first enzyme, EC 2.1.1.156, glycine/sarcosine N-methyltransferase, leads to the formation of either sarcosine or *N*,*N*-dimethylglycine, which is further methylated to yield betaine (*N*,*N*,*N*-trimethylglycine) by the action of this enzyme. Both of these enzymes can catalyse the formation of *N*,*N*-dimethylglycine from sarcosine [3713]. The reactions are strongly inhibited by *S*-adenosyl-L-homocysteine.

References: [2499, 2500, 3713]

[EC 2.1.1.157 created 2005, modified 2010]

EC 2.1.1.158

Accepted name: 7-methylxanthosine synthase

Reaction: *S*-adenosyl-L-methionine + xanthosine = *S*-adenosyl-L-homocysteine + 7-methylxanthosine

Other name(s): xanthosine methyltransferase; XMT; xanthosine:*S*-adenosyl-L-methionine methyltransferase; CtCS1; CmXRS1; CaXMT1; *S*-adenosyl-L-methionine:xanthosine 7-*N*-methyltransferase

Systematic name: *S*-adenosyl-L-methionine:xanthosine N^7-methyltransferase

Comments: The enzyme is specific for xanthosine, as XMP and xanthine cannot act as substrates [2280, 3994]. The enzyme does not have N^1- or N^3- methylation activity [2280]. This is the first methylation step in the production of caffeine.

References: [2427, 2280, 3600, 3994]

[EC 2.1.1.158 created 2007]

EC 2.1.1.159

Accepted name: theobromine synthase

Reaction: *S*-adenosyl-L-methionine + 7-methylxanthine = *S*-adenosyl-L-homocysteine + 3,7-dimethylxanthine

Other name(s): monomethylxanthine methyltransferase; MXMT; CTS1; CTS2; *S*-adenosyl-L-methionine:7-methylxanthine 3-*N*-methyltransferase

Systematic name: *S*-adenosyl-L-methionine:7-methylxanthine N^3-methyltransferase

Comments: This is the third enzyme in the caffeine-biosynthesis pathway. This enzyme can also catalyse the conversion of paraxanthine into caffeine, although the paraxanthine pathway is considered to be a minor pathway for caffeine biosynthesis [3600, 3994].

References: [2516, 3600, 3994]

[EC 2.1.1.159 created 2007]

EC 2.1.1.160

Accepted name: caffeine synthase

Reaction: (1) *S*-adenosyl-L-methionine + 3,7-dimethylxanthine = *S*-adenosyl-L-homocysteine + 1,3,7-trimethylxanthine
(2) *S*-adenosyl-L-methionine + 1,7-dimethylxanthine = *S*-adenosyl-L-homocysteine + 1,3,7-trimethylxanthine
(3) *S*-adenosyl-L-methionine + 7-methylxanthine = *S*-adenosyl-L-homocysteine + 3,7-dimethylxanthine

Other name(s): dimethylxanthine methyltransferase; 3*N*-methyltransferase; DXMT; CCS1; *S*-adenosyl-L-methionine:3,7-dimethylxanthine 1-*N*-methyltransferase

Systematic name: *S*-adenosyl-L-methionine:3,7-dimethylxanthine N^1-methyltransferase

Comments: Paraxanthine is the best substrate for this enzyme but the paraxanthine pathway is considered to be a minor pathway for caffeine biosynthesis [2281, 3600].

References: [1599, 2281, 3600, 1598]

[EC 2.1.1.160 created 2007]

EC 2.1.1.161

Accepted name: dimethylglycine *N*-methyltransferase

Reaction: *S*-adenosyl-L-methionine + *N*,*N*-dimethylglycine = *S*-adenosyl-L-homocysteine + betaine

Other name(s): BsmB; DMT

Systematic name: *S*-adenosyl-L-methionine:*N*,*N*-dimethylglycine *N*-methyltransferase (betaine-forming)

Comments: This enzyme, from the marine cyanobacterium *Synechococcus* sp. WH8102, differs from EC 2.1.1.157, sarcosine/dimethylglycine *N*-methyltransferase in that it cannot use sarcosine as an alternative substrate [2057]. Betaine is a ‘compatible solute’ that enables cyanobacteria to cope with osmotic stress by maintaining a positive cellular turgor.

References: [2057]

[EC 2.1.1.161 created 2007]

EC 2.1.1.162

Accepted name: glycine/sarcosine/dimethylglycine *N*-methyltransferase

Reaction: **3** *S*-adenosyl-L-methionine + glycine = **3** *S*-adenosyl-L-homocysteine + betaine (overall reaction)
(1a) *S*-adenosyl-L-methionine + glycine = *S*-adenosyl-L-homocysteine + sarcosine
(1b) *S*-adenosyl-L-methionine + sarcosine = *S*-adenosyl-L-homocysteine + *N*,*N*-dimethylglycine
(1c) *S*-adenosyl-L-methionine + *N*,*N*-dimethylglycine = *S*-adenosyl-L-homocysteine + betaine

Other name(s): GSDMT; glycine sarcosine dimethylglycine *N*-methyltransferase

Systematic name: *S*-adenosyl-L-methionine:glycine(or sarcosine or *N*,*N*-dimethylglycine) *N*-methyltransferase [sarcosine(or *N*,*N*-dimethylglycine or betaine)-forming]

Comments: Unlike EC 2.1.1.156 (glycine/sarcosine *N*-methyltransferase), EC 2.1.1.157 (sarcosine/dimethylglycine *N*-methyltransferase) and EC 2.1.1.161 (dimethylglycine *N*-methyltransferase), this enzyme, from the halophilic methanoarchaeon *Methanohalophilus portucalensis*, can methylate glycine and all of its intermediates to form the compatible solute betaine [1845].

References: [1845]

[EC 2.1.1.162 created 2007]

EC 2.1.1.163

Accepted name: demethylmenaquinone methyltransferase

Reaction: a demethylmenaquinol + *S*-adenosyl-L-methionine = a menaquinol + *S*-adenosyl-L-homocysteine

Other name(s): *S*-adenosyl-L-methione—DMK methyltransferase; demethylmenaquinone C-methylase; 2-heptaprenyl-1,4-naphthoquinone methyltransferase; 2-demethylmenaquinone methyltransferase; *S*-adenosyl-L-methione:2-demethylmenaquinone methyltransferase

Systematic name: *S*-adenosyl-L-methione:demethylmenaquinone methyltransferase

Comments: The enzyme catalyses the last step in menaquinone biosynthesis. It is able to accept substrates with varying polyprenyl side chain length (the chain length is determined by polyprenyl diphosphate synthase)[1740]. The enzyme from *Escherichia coli* also catalyses the conversion of 2-methoxy-6-octaprenyl-1,4-benzoquinone to 5-methoxy-2-methyl-3-octaprenyl-1,4-benzoquinone during the biosynthesis of ubiquinone [1899]. The enzyme probably acts on menaquinol rather than menaquinone.

References: [1740, 3874, 489, 1899]

[EC 2.1.1.163 created 2009]

EC 2.1.1.164

Accepted name: demethylrebeccamycin-D-glucose *O*-methyltransferase

Reaction: 4′-demethylrebeccamycin + *S*-adenosyl-L-methionine = rebeccamycin + *S*-adenosyl-L-homocysteine

Other name(s): RebM

Systematic name: *S*-adenosyl-L-methionine:demethylrebeccamycin-D-glucose *O*-methyltransferase

Comments: Catalyses the last step in the biosynthesis of rebeccamycin, an indolocarbazole alkaloid produced by the bacterium *Lechevalieria aerocolonigenes*. The enzyme is able to use a wide variety substrates, tolerating variation on the imide heterocycle, deoxygenation of the sugar moiety, and even indolocarbazole glycoside anomers [4035]. The enzyme is a member of the general acid/base-dependent *O*-methyltransferase family [3242].

References: [4035, 3242]

[EC 2.1.1.164 created 2010]

EC 2.1.1.165

Accepted name: methyl halide transferase

Reaction: *S*-adenosyl-L-methionine + iodide = *S*-adenosyl-L-homocysteine + methyl iodide

Other name(s): MCT; methyl chloride transferase; *S*-adenosyl-L-methionine:halide/bisulfide methyltransferase; AtHOL1; AtHOL2; AtHOL3; HARMLESS TO OZONE LAYER protein; HMT; *S*-adenosyl-L-methionine: halide ion methyltransferase; SAM:halide ion methyltransferase

Systematic name: *S*-adenosylmethionine:iodide methyltransferase

Comments: This enzyme contributes to the methyl halide emissions from *Arabidopsis* [2391].

References: [2448, 3049, 125, 1467, 2540, 2391]

[EC 2.1.1.165 created 2010]

EC 2.1.1.166

Accepted name: 23S rRNA (uridine^{2552}-2′-*O*)-methyltransferase

Reaction: *S*-adenosyl-L-methionine + uridine^{2552} in 23S rRNA = *S*-adenosyl-L-homocysteine + 2′-*O*-methyluridine^{2552} in 23S rRNA

Other name(s): Um(2552) 23S ribosomal RNA methyltransferase; heat shock protein RrmJ; RrmJ; FTSJ; Um2552 methyltransferase

Systematic name: *S*-adenosyl-L-methionine:23S rRNA (uridine^{2552}-2′-*O*-)-methyltransferase

Comments: The enzyme catalyses the 2′-*O*-methylation of the universally conserved U^{2552} in the A loop of 23S rRNA [1195].

References: [459, 1194, 1195, 421]

[EC 2.1.1.166 created 2010]

EC 2.1.1.167

Accepted name: 27S pre-rRNA (guanosine^{2922}-2′-*O*)-methyltransferase

Reaction: *S*-adenosyl-L-methionine + guanosine^{2922} in 27S pre-rRNA = *S*-adenosyl-L-homocysteine + 2′-*O*-methylguanosine^{2922} in 27S pre-rRNA

Other name(s): Spb1p (gene name); YCL054W (gene name)

Systematic name: *S*-adenosyl-L-methionine:27S pre-rRNA (guanosine^{2922}-2′-*O*-)-methyltransferase

Comments: Spb1p is a site-specific 2′-*O*-ribose RNA methyltransferase that catalyses the formation of 2′-*O*-methylguanosine^{2922}, a universally conserved position of the catalytic center of the ribosome that is essential for translation. 2′-*O*-Methylguanosine^{2922} is formed at a later stage of the processing, during the maturation of of the 27S pre-rRNA. In absence of snR52, Spb1p can also catalyse the formation of uridine^{2921} [1862].

References: [1862, 351]

[EC 2.1.1.167 created 2010]

EC 2.1.1.168

Accepted name: 21S rRNA (uridine^{2791}-2′-*O*)-methyltransferase

Reaction: *S*-adenosyl-L-methionine + uridine^{2791} in 21S rRNA = *S*-adenosyl-L-homocysteine + 2′-*O*-methyluridine^{2791} in 21S rRNA

Other name(s): MRM2 (gene name); mitochondrial 21S rRNA methyltransferase; mitochondrial rRNA MTase 2

Systematic name: *S*-adenosyl-L-methionine:21S rRNA (uridine^{2791}-2′-*O*-)-methyltransferase

Comments: The enzyme catalyses the methylation of uridine^{2791} of mitochondrial 21S rRNA.

References: [2715]

[EC 2.1.1.168 created 2010]

EC 2.1.1.169

Accepted name: tricetin 3′,4′,5′-*O*-trimethyltransferase

Reaction: **3** *S*-adenosyl-L-methionine + tricetin = **3** *S*-adenosyl-L-homocysteine + 3′,4′,5′-*O*-trimethyltricetin (overall reaction)

(1a) *S*-adenosyl-L-methionine + tricetin = *S*-adenosyl-L-homocysteine + 3′-*O*-methyltricetin

(1b) *S*-adenosyl-L-methionine + 3′-*O*-methyltricetin = *S*-adenosyl-L-homocysteine + 3′,5′-*O*-dimethyltricetin

(1c) *S*-adenosyl-L-methionine + 3′,5′-*O*-dimethyltricetin = *S*-adenosyl-L-homocysteine + 3′,4′,5′-*O*-trimethyltricetin

Other name(s): FOMT; TaOMT1; TaCOMT1; TaOMT2

Systematic name: *S*-adenosyl-L-methionine:tricetin 3′,4′,5′-*O*-trimethyltransferase

Comments: The enzyme from *Triticum aestivum* catalyses the sequential *O*-methylation of tricetin via 3′-*O*-methyltricetin, 3′,5′-*O*-methyltricetin to 3′,4′,5′-*O*-trimethyltricetin [4074].

References: [1763, 4074, 4075]

[EC 2.1.1.169 created 2010]

EC 2.1.1.170

Accepted name: 16S rRNA (guanine^{527}-N^7)-methyltransferase

Reaction: *S*-adenosyl-L-methionine + guanine^{527} in 16S rRNA = *S*-adenosyl-L-homocysteine + N^7-methylguanine^{527} in 16S rRNA

Other name(s): ribosomal RNA small subunit methyltransferase G; 16S rRNA methyltransferase RsmG; GidB; *rsmG* (gene name)

Systematic name: *S*-adenosyl-L-methionine:16S rRNA (guanine^{527}-N^7)-methyltransferase

Comments: The enzyme specifically methylates guanine^{527} at N^7 in 16S rRNA.

References: [2551, 2924]

[EC 2.1.1.170 created 2010]

EC 2.1.1.171

Accepted name: 16S rRNA (guanine^{966}-N^2)-methyltransferase

Reaction: *S*-adenosyl-L-methionine + guanine^{966} in 16S rRNA = *S*-adenosyl-L-homocysteine + N^2-methylguanine^{966} in 16S rRNA

Other name(s): *yhhF* (gene name); *rsmD* (gene name); m^{2}G966 methyltransferase

Systematic name: *S*-adenosyl-L-methionine:16S rRNA (guanine^{966}-N^2)-methyltransferase

Comments: The enzyme efficiently methylates guanine^{966} of the assembled 30S subunits *in vitro*. Protein-free 16S rRNA is not a substrate for RsmD [1940]. The enzyme specifically methylates guanine^{966} at N^2 in 16S rRNA.

References: [1940]

[EC 2.1.1.171 created 1976 as EC 2.1.1.52, part transferred 2010 to EC 2.1.1.171]

EC 2.1.1.172

Accepted name: 16S rRNA (guanine^{1207}-N^2)-methyltransferase

Reaction: *S*-adenosyl-L-methionine + guanine^{1207} in 16S rRNA = *S*-adenosyl-L-homocysteine + N^2-methylguanine^{1207} in 16S rRNA

Other name(s): m^{2}G1207 methyltransferase

Systematic name: *S*-adenosyl-L-methionine:16S rRNA (guanine^{1207}-N^2)-methyltransferase

Comments: The enzyme reacts well with 30S subunits reconstituted from 16S RNA transcripts and 30S proteins but is almost inactive with the corresponding free RNA [3580]. The enzyme specifically methylates guanine^{1207} at N^2 in 16S rRNA.

References: [3580, 3389]

[EC 2.1.1.172 created 1976 as EC 2.1.1.52, part transferred 2010 to EC 2.1.1.172]

EC 2.1.1.173

Accepted name: 23S rRNA (guanine^{2445}-N^2)-methyltransferase

Reaction: *S*-adenosyl-L-methionine + guanine^{2445} in 23S rRNA = *S*-adenosyl-L-homocysteine + N^2-methylguanine^{2445} in 23S rRNA

Other name(s): *ycbY* (gene name); *rlmL* (gene name)

Systematic name: *S*-adenosyl-L-methionine:23S rRNA (guanine^{2445}-N^2)-methyltransferase

Comments: The enzyme methylates 23S rRNA *in vitro*, assembled 50S subunits are not a substrate [1941]. The enzyme specifically methylates guanine^{2445} at N^2 in 23S rRNA.

References: [1941]

[EC 2.1.1.173 created 1976 as EC 2.1.1.52, part transferred 2010 to EC 2.1.1.173]

EC 2.1.1.174

Accepted name: 23S rRNA (guanine^{1835}-N^2)-methyltransferase

Reaction: *S*-adenosyl-L-methionine + guanine^{1835} in 23S rRNA = *S*-adenosyl-L-homocysteine + N^2-methylguanine^{1835} in 23S rRNA

Other name(s): *ygjO* (gene name); *rlmG* (gene name); ribosomal RNA large subunit methyltransferase G

Systematic name: *S*-adenosyl-L-methionine:23S rRNA (guanine^{1835}-N^2)-methyltransferase

Comments: The enzyme methylates 23S rRNA *in vitro*, assembled 50S subunits are not a substrate [3144]. The enzyme specifically methylates guanine^{1835} at N^2 in 23S rRNA.

References: [3144]

[EC 2.1.1.174 created 1976 as EC 2.1.1.52, part transferred 2010 to EC 2.1.1.174]

EC 2.1.1.175

Accepted name: tricin synthase

Reaction: **2** *S*-adenosyl-L-methionine + tricetin = **2** *S*-adenosyl-L-homocysteine + $3',5'$-*O*-dimethyltricetin (overall reaction)
(1a) *S*-adenosyl-L-methionine + tricetin = *S*-adenosyl-L-homocysteine + $3'$-*O*-methyltricetin
(1b) *S*-adenosyl-L-methionine + $3'$-*O*-methyltricetin = *S*-adenosyl-L-homocysteine + $3',5'$-*O*-dimethyltricetin

Other name(s): ROMT-17; ROMT-15; HvOMT1; ZmOMT1

Systematic name: *S*-adenosyl-L-methionine:tricetin $3',5'$-*O*-dimethyltransferase

Comments: The enzymes from *Oryza sativa* (ROMT-15 and ROMT-17) catalyses the stepwise methylation of tricetin to its $3'$-mono- and $3',5'$-dimethyl ethers. In contrast with the wheat enzyme (EC 2.1.1.169, tricetin $3',4',5'$-*O*-trimethyltransferase), tricetin dimethyl ether is not converted to its $3',4',5'$-trimethylated ether derivative [1908]. The enzymes from *Hordeum vulgare* (HvOMT1) and from *Zea mays* (ZmOMT1) form the $3',5'$-dimethyl derivative as the major product [4073].

References: [1908, 4073]

[EC 2.1.1.175 created 2010]

EC 2.1.1.176

Accepted name: 16S rRNA (cytosine^{967}-C^5)-methyltransferase

Reaction: *S*-adenosyl-L-methionine + cytosine^{967} in 16S rRNA = *S*-adenosyl-L-homocysteine + 5-methylcytosine^{967} in 16S rRNA

Other name(s): *rsmB* (gene name); fmu (gene name); 16S rRNA m^{5}C^{967} methyltransferase

Systematic name: *S*-adenosyl-L-methionine:16S rRNA (cytosine^{967}-C^5)-methyltransferase

Comments: The enzyme specifically methylates cytosine^{967} at C^5 in 16S rRNA.

References: [3579, 1167, 937]

[EC 2.1.1.176 created 2010]

EC 2.1.1.177

Accepted name: 23S rRNA (pseudouridine^{1915}-N^3)-methyltransferase

Reaction: *S*-adenosyl-L-methionine + pseudouridine^{1915} in 23S rRNA = *S*-adenosyl-L-homocysteine + N^3-methylpseudouridine^{1915} in 23S rRNA

Other name(s): YbeA; RlmH; pseudouridine methyltransferase; m$^3\Psi$ methyltransferase; Ψ^{1915}-specific methyltransferase; rRNA large subunit methyltransferase H

Systematic name: *S*-adenosyl-L-methionine:23S rRNA (pseudouridine^{1915}-N^3)-methyltransferase

Comments: YbeA does not methylate uridine at position 1915 [854].

References: [854, 2770]

[EC 2.1.1.177 created 2010]

EC 2.1.1.178

Accepted name: 16S rRNA (cytosine^{1407}-C^5)-methyltransferase

Reaction: *S*-adenosyl-L-methionine + cytosine^{1407} in 16S rRNA = *S*-adenosyl-L-homocysteine + 5-methylcytosine^{1407} in 16S rRNA

Other name(s): RNA m^{5}C methyltransferase YebU; RsmF; YebU

Systematic name: *S*-adenosyl-L-methionine:16S rRNA (cytosine^{1407}-C^5)-methyltransferase

Comments: The enzyme specifically methylates cytosine^{1407} at C^5 in 16S rRNA.

References: [74, 1200]

[EC 2.1.1.178 created 2010]

EC 2.1.1.179

Accepted name: 16S rRNA (guanine^{1405}-N^7)-methyltransferase

Reaction: *S*-adenosyl-L-methionine + guanine^{1405} in 16S rRNA = *S*-adenosyl-L-homocysteine + N^7-methylguanine^{1405} in 16S rRNA

Other name(s): methyltransferase Sgm; m^{7}G^{1405} Mtase; Sgm Mtase; Sgm; sisomicin-gentamicin methyltransferase; sisomicin-gentamicin methylase; GrmA; RmtB; RmtC; ArmA

Systematic name: *S*-adenosyl-L-methionine:16S rRNA (guanine^{1405}-N^7)-methyltransferase

Comments: The enzyme from the antibiotic-producing bacterium *Micromonospora zionensis* specifically methylates guanine^{1405} at N^7 in 16S rRNA, thereby rendering the ribosome resistant to 4,6-disubstituted deoxystreptamine aminoglycosides, which include gentamicins and kanamycins [3045].

References: [1415, 3045, 3545, 3044, 3690, 1743, 3089, 3707, 1982]

[EC 2.1.1.179 created 2010]

EC 2.1.1.180

Accepted name: 16S rRNA (adenine^{1408}-N^1)-methyltransferase

Reaction: *S*-adenosyl-L-methionine + adenine^{1408} in 16S rRNA = *S*-adenosyl-L-homocysteine + N^1-methyladenine^{1408} in 16S rRNA

Other name(s): kanamycin-apramycin resistance methylase; 16S rRNA:m^{1}A^{1408} methyltransferase; KamB; NpmA; 16S rRNA m^{1}A^{1408} methyltransferase

Systematic name: *S*-adenosyl-L-methionine:16S rRNA (adenine^{1408}-N^1)-methyltransferase

Comments: The enzyme provides a panaminoglycoside-resistant nature through interference with the binding of aminoglycosides toward the A site of 16S rRNA through N^1-methylation at position adenine^{1408} [3708].

References: [244, 1767, 1358, 3708]

[EC 2.1.1.180 created 2010]

EC 2.1.1.181

Accepted name: 23S rRNA (adenine^{1618}-N^6)-methyltransferase

Reaction: *S*-adenosyl-L-methionine + adenine^{1618} in 23S rRNA = *S*-adenosyl-L-homocysteine + N^6-methyladenine^{1618} in 23S rRNA

Other name(s): rRNA large subunit methyltransferase F; YbiN protein; *rlmF* (gene name); m^{6}A^{1618} methyltransferase

Systematic name: *S*-adenosyl-L-methionine:23S rRNA (adenine^{1618}-N^6)-methyltransferase

Comments: The recombinant YbiN protein is able to methylate partially deproteinized 50 S ribosomal subunit, but neither the completely assembled 50 S subunits nor completely deproteinized 23 S rRNA [3145].

References: [3145]

[EC 2.1.1.181 created 1976 as EC 2.1.1.48, part transferred 2010 to EC 2.1.1.181]

EC 2.1.1.182

Accepted name: 16S rRNA (adenine^{1518}-N^6/adenine^{1519}-N^6)-dimethyltransferase

Reaction: **4** *S*-adenosyl-L-methionine + adenine^{1518}/adenine^{1519} in 16S rRNA = **4** *S*-adenosyl-L-homocysteine + N^6-dimethyladenine^{1518}/N^6-dimethyladenine^{1519} in 16S rRNA

Other name(s): *S*-adenosylmethionine-6-N',N'-adenosyl (rRNA) dimethyltransferase; KsgA; *ksgA* methyltransferase

Systematic name: *S*-adenosyl-L-methionine:16S rRNA (adenine^{1518}-N^6/adenine^{1519}-N^6)-dimethyltransferase

Comments: KsgA introduces the most highly conserved ribosomal RNA modification, the dimethylation of adenine^{1518} and adenine^{1519} in 16S rRNA. Strains lacking the methylase are resistant to kasugamycin [1285].

References: [1285, 1286, 3633, 931, 2513, 2733, 706, 3589]

[EC 2.1.1.182 created 1976 as EC 2.1.1.48, part transferred 2010 to EC 2.1.1.182]

EC 2.1.1.183

Accepted name: 18S rRNA (adenine^{1779}-N^6/adenine^{1780}-N^6)-dimethyltransferase

Reaction: **4** *S*-adenosyl-L-methionine + adenine^{1779}/adenine^{1780} in 18S rRNA = **4** *S*-adenosyl-L-homocysteine + N^6-dimethyladenine^{1779}/N^6-dimethyladenine^{1780} in 18S rRNA

Other name(s): 18S rRNA dimethylase Dim1p; Dim1p; ScDim1; m2(6)A dimethylase; KIDIM1

Systematic name: *S*-adenosyl-L-methionine:18S rRNA (adenine^{1779}-N^6/adenine^{1780}-N^6)-dimethyltransferase

Comments: DIM1 is involved in pre-rRNA processing [1842].

References: [1842, 1843, 2769, 1841, 2512]

[EC 2.1.1.183 created 1976 as EC 2.1.1.48, part transferred 2010 to EC 2.1.1.183]

EC 2.1.1.184

Accepted name: 23S rRNA (adenine^{2085}-N^6)-dimethyltransferase

Reaction: **2** *S*-adenosyl-L-methionine + adenine^{2085} in 23S rRNA = **2** *S*-adenosyl-L-homocysteine + N^6-dimethyladenine^{2085} in 23S rRNA

Other name(s): ErmC$'$ methyltransferase; *ermC* methylase; *ermC* 23S rRNA methyltransferase; rRNA:m^{6}A methyltransferase ErmC$'$; ErmC$'$; rRNA methyltransferase ErmC$'$

Systematic name: *S*-adenosyl-L-methionine:23S rRNA (adenine^{2085}-N^6)-dimethyltransferase

Comments: ErmC is a methyltransferase that confers resistance to the macrolide-lincosamide-streptogramin B group of antibiotics by catalysing the methylation of 23S rRNA at adenine^{2085}.

References: [4072, 713, 714, 441, 3079, 2119]

[EC 2.1.1.184 created 1976 as EC 2.1.1.48, part transferred 2010 to EC 2.1.1.184]

EC 2.1.1.185

Accepted name: 23S rRNA (guanosine^{2251}-$2'$-*O*)-methyltransferase

Reaction: *S*-adenosyl-L-methionine + guanosine^{2251} in 23S rRNA = *S*-adenosyl-L-homocysteine + $2'$-*O*-methylguanosine^{2251} in 23S rRNA

Other name(s): *rlmB* (gene name); *yifH* (gene name)

Systematic name: *S*-adenosyl-L-methionine:23S rRNA (guanosine^{2251}-$2'$-*O*-)-methyltransferase

Comments: The enzyme catalyses the methylation of guanosine^{2251}, a modification conserved in the peptidyltransferase domain of 23S rRNA.

References: [2046, 2239]

[EC 2.1.1.185 created 2010]

EC 2.1.1.186

Accepted name: 23S rRNA (cytidine^{2498}-$2'$-*O*)-methyltransferase

Reaction: *S*-adenosyl-L-methionine + cytidine^{2498} in 23S rRNA = *S*-adenosyl-L-homocysteine + $2'$-*O*-methylcytidine^{2498} in 23S rRNA

Other name(s): YgdE; rRNA large subunit methyltransferase M; RlmM

Systematic name: *S*-adenosyl-L-methionine:23S rRNA (cytidine^{2498}-$2'$-*O*-)-methyltransferase

References: [2772]

[EC 2.1.1.186 created 2010]

EC 2.1.1.187

Accepted name: 23S rRNA (guanine^{745}-N^1)-methyltransferase

Reaction: *S*-adenosyl-L-methionine + guanine^{745} in 23S rRNA = *S*-adenosyl-L-homocysteine + N^1-methylguanine^{745} in 23S rRNA

Other name(s): Rlma(I); Rlma1; 23S rRNA m^{1}G^{745} methyltransferase; YebH; RlmA$^{\mathrm{I}}$ methyltransferase; ribosomal RNA(m^{1}G)-methylase (ambiguous); rRNA(m^{1}G)methylase (ambiguous); RrmA (ambiguous); 23S rRNA:m^{1}G^{745} methyltransferase

Systematic name: *S*-adenosyl-L-methionine:23S rRNA (guanine^{745}-N^1)-methyltransferase

Comments: The enzyme specifically methylates guanine^{745} at N^1 in 23S rRNA.

References: [2008, 1184, 671, 1215, 2006]

[EC 2.1.1.187 created 1976 as EC 2.1.1.51, part transferred 2010 to EC 2.1.1.187]

EC 2.1.1.188

Accepted name: 23S rRNA (guanine^{748}-N^1)-methyltransferase

Reaction: *S*-adenosyl-L-methionine + guanine^{748} in 23S rRNA = *S*-adenosyl-L-homocysteine + N^1-methylguanine^{748} in 23S rRNA

Other name(s): Rlma(II); Rlma2; 23S rRNA m^{1}G^{748} methyltransferase; RlmaII; Rlma II; tylosin-resistance methyltransferase RlmA(II); TlrB; rRNA large subunit methyltransferase II

Systematic name: *S*-adenosyl-L-methionine:23S rRNA (guanine^{748}-N^1)-methyltransferase

Comments: The enzyme specifically methylates guanine^{748} at N^1 in 23S rRNA. The methyltransferase RlmA$^{\mathrm{II}}$ confers resistance to the macrolide antibiotic tylosin in the drug-producing strain *Streptomyces fradiae* [766].

References: [766, 2007, 1883, 1882, 767, 2006]

[EC 2.1.1.188 created 1976 as EC 2.1.1.51, part transferred 2010 to EC 2.1.1.188]

EC 2.1.1.189

Accepted name: 23S rRNA (uracil^{747}-C^5)-methyltransferase

Reaction: *S*-adenosyl-L-methionine + uracil^{747} in 23S rRNA = *S*-adenosyl-L-homocysteine + 5-methyluracil^{747} in 23S rRNA

Other name(s): YbjF; RumB; RNA uridine methyltransferase B

Systematic name: *S*-adenosyl-L-methionine:23S rRNA (uracil^{747}-C^5)-methyltransferase

Comments: The enzyme specifically methylates uracil^{747} at C^5 in 23S rRNA.

References: [2094]

[EC 2.1.1.189 created 2010]

EC 2.1.1.190

Accepted name: 23S rRNA (uracil^{1939}-C^{5})-methyltransferase

Reaction: *S*-adenosyl-L-methionine + uracil^{1939} in 23S rRNA = *S*-adenosyl-L-homocysteine + 5-methyluracil^{1939} in 23S rRNA

Other name(s): RumA; RNA uridine methyltransferase A; YgcA

Systematic name: *S*-adenosyl-L-methionine:23S rRNA (uracil^{1939}-C^{5})-methyltransferase

Comments: The enzyme specifically methylates uracil^{1939} at C^{5} in 23S rRNA [22]. The enzyme contains an [4Fe-4S] cluster coordinated by four conserved cysteine residues [1906].

References: [22, 1906, 2094, 2669, 23, 1907]

[EC 2.1.1.190 created 2010]

EC 2.1.1.191

Accepted name: 23S rRNA (cytosine^{1962}-C^{5})-methyltransferase

Reaction: *S*-adenosyl-L-methionine + cytosine^{1962} in 23S rRNA = *S*-adenosyl-L-homocysteine + 5-methylcytosine^{1962} in 23S rRNA

Other name(s): RlmI; rRNA large subunit methyltransferase I; YccW

Systematic name: *S*-adenosyl-L-methionine:23S rRNA (cytosine^{1962}-C^{5})-methyltransferase

Comments: The enzyme specifically methylates cytosine^{1962} at C^{5} in 23S rRNA.

References: [2771, 3390]

[EC 2.1.1.191 created 2010]

EC 2.1.1.192

Accepted name: 23S rRNA (adenine^{2503}-C^{2})-methyltransferase

Reaction: (1) **2** *S*-adenosyl-L-methionine + adenine^{2503} in 23S rRNA + **2** reduced [2Fe-2S] ferredoxin = *S*-adenosyl-L-homocysteine + L-methionine + 5′-deoxyadenosine + 2-methyladenine^{2503} in 23S rRNA + **2** oxidized [2Fe-2S] ferredoxin

(2) **2** *S*-adenosyl-L-methionine + adenine^{37} in tRNA + **2** reduced [2Fe-2S] ferredoxin = *S*-adenosyl-L-homocysteine + L-methionine + 5′-deoxyadenosine + 2-methyladenine^{37} in tRNA + **2** oxidized [2Fe-2S] ferredoxin

Other name(s): RlmN; YfgB; Cfr

Systematic name: *S*-adenosyl-L-methionine:23S rRNA (adenine^{2503}-C^{2})-methyltransferase

Comments: Contains an [4Fe-4S] cluster [3958]. This enzyme is a member of the ‘AdoMet radical’ (radical SAM) family. *S*-Adenosyl-L-methionine acts as both a radical generator and as the source of the appended methyl group. RlmN first transfers an CH_2 group to a conserved cysteine (Cys^{355} in *Escherichia coli*) [1153], the generated radical from a second *S*-adenosyl-L-methionine then attacks the methyl group, exctracting a hydrogen. The formed radical forms a covalent intermediate with the adenine group of the tRNA [3225]. RlmN is an endogenous enzyme used by the cell to refine functions of the ribosome in protein synthesis [3958]. The enzyme methylates adenosine by a radical mechanism with CH_2 from the *S*-adenosyl-L-methionine and retention of the hydrogen at C-2 of adenosine^{2503} of 23S rRNA. It will also methylate 8-methyladenosine^{2503} of 23S rRNA. *cf.* EC 2.1.1.224 [23S rRNA (adenine^{2503}-C^{8})-methyltransferase].

References: [3542, 3958, 3957, 1151, 335, 1153, 2192, 267, 3225]

[EC 2.1.1.192 created 2010, modified 2011, modified 2014]

EC 2.1.1.193

Accepted name: 16S rRNA (uracil^{1498}-N^{3})-methyltransferase

Reaction: *S*-adenosyl-L-methionine + uracil^{1498} in 16S rRNA = *S*-adenosyl-L-homocysteine + N^{3}-methyluracil^{1498} in 16S rRNA

Other name(s): DUF558 protein; YggJ; RsmE; m^{3}U^{1498} specific methyltransferase
Systematic name: *S*-adenosyl-L-methionine:16S rRNA (uracil^{1498}-N^3)-methyltransferase
Comments: The enzyme specifically methylates uracil^{1498} at N^3 in 16S rRNA.
References: [217, 216]

[EC 2.1.1.193 created 2010]

[2.1.1.194 Deleted entry. 23S rRNA (adenine^{2503}-C^2,C^8)-dimethyltransferase. A mixture of EC 2.1.1.192 (23S rRNA (adenine^{2503}-C^2)-methyltransferase) and EC 2.1.1.224 (23S rRNA (adenine^{2503}-C^8)-methyltransferase)]

[EC 2.1.1.194 created 2010, deleted 2011]

EC 2.1.1.195

Accepted name: cobalt-precorrin-5B (C^1)-methyltransferase
Reaction: cobalt-precorrin-5B + *S*-adenosyl-L-methionine = cobalt-precorrin-6A + *S*-adenosyl-L-homocysteine
Other name(s): cobalt-precorrin-6A synthase; CbiD
Systematic name: *S*-adenosyl-L-methionine:cobalt-precorrin-5B (C^1)-methyltransferase
Comments: This enzyme catalyses the C-1 methylation of cobalt-precorrin-5B in the anaerobic (early cobalt insertion) pathway of adenosylcobalamin biosynthesis.
References: [2931, 2916, 2302]

[EC 2.1.1.195 created 2010]

EC 2.1.1.196

Accepted name: cobalt-precorrin-6B (C^{15})-methyltransferase [decarboxylating]
Reaction: cobalt-precorrin-6B + *S*-adenosyl-L-methionine = cobalt-precorrin-7 + *S*-adenosyl-L-homocysteine + CO_2
Other name(s): *cbiT* (gene name); *S*-adenosyl-L-methionine:precorrin-7 C^{15}-methyltransferase (C-12-decarboxylating); cobalt-precorrin-7 (C^{15})-methyltransferase [decarboxylating]
Systematic name: *S*-adenosyl-L-methionine:precorrin-6B C^{15}-methyltransferase (C-12-decarboxylating)
Comments: This enzyme catalyses both methylation at C-15 and decarboxylation of the C-12 acetate side chain of cobalt-precorrin-6B, a step in the anaerobic (early cobalt insertion) adenosylcobalamin biosynthesis pathway.
References: [1628, 3024, 2302]

[EC 2.1.1.196 created 2010, modified 2013]

EC 2.1.1.197

Accepted name: malonyl-[acyl-carrier protein] *O*-methyltransferase
Reaction: *S*-adenosyl-L-methionine + malonyl-[acyl-carrier protein] = *S*-adenosyl-L-homocysteine + malonyl-[acyl-carrier protein] methyl ester
Other name(s): BioC
Systematic name: *S*-adenosyl-L-methionine:malonyl-[acyl-carrier protein] *O*-methyltransferase
Comments: Involved in an early step of biotin biosynthesis in Gram-negative bacteria. This enzyme catalyses the transfer of a methyl group to the ω-carboxyl group of malonyl-[acyl-carrier protein] forming a methyl ester. The methyl ester is recognized by the fatty acid synthetic enzymes, which process it via the fatty acid elongation cycle to give pimelyl-[acyl-carrier-protein] methyl ester [1971]. While the enzyme can also accept malonyl-CoA, it has a much higher activity with malonyl-[acyl-carrier protein] [1970]
References: [464, 2921, 2585, 583, 1971, 1970]

[EC 2.1.1.197 created 2010, modified 2013]

EC 2.1.1.198

Accepted name: 16S rRNA (cytidine^{1402}-2′-*O*)-methyltransferase
Reaction: *S*-adenosyl-L-methionine + cytidine^{1402} in 16S rRNA = *S*-adenosyl-L-homocysteine + 2′-*O*-methylcytidine^{1402} in 16S rRNA
Other name(s): RsmI; YraL
Systematic name: *S*-adenosyl-L-methionine:16S rRNA (cytidine^{1402}-2′-*O*)-methyltransferase
Comments: RsmI catalyses the 2′-*O*-methylation of cytidine^{1402} and RsmH (EC 2.1.1.199) catalyses the N^4-methylation of cytidine^{1402} in 16S rRNA. Both methylations are necessary for efficient translation initiation at the UUG and GUG codons.
References: [1687]

[EC 2.1.1.198 created 2010]

EC 2.1.1.199

Accepted name: 16S rRNA (cytosine^{1402}-N^4)-methyltransferase
Reaction: *S*-adenosyl-L-methionine + cytosine^{1402} in 16S rRNA = *S*-adenosyl-L-homocysteine + N^4-methylcytosine^{1402} in 16S rRNA
Other name(s): RsmH; MraW
Systematic name: *S*-adenosyl-L-methionine:16S rRNA (cytosine^{1402}-N^4)-methyltransferase
Comments: RsmH catalyses the N^4-methylation of cytosine^{1402} and RsmI (EC 2.1.1.198) catalyses the 2′-*O*-methylation of cytosine^{1402} in 16S rRNA. Both methylations are necessary for efficient translation initiation at the UUG and GUG codons.
References: [1687]

[EC 2.1.1.199 created 2010]

EC 2.1.1.200

Accepted name: tRNA (cytidine^{32}/uridine^{32}-2′-*O*)-methyltransferase
Reaction: (1) *S*-adenosyl-L-methionine + cytidine^{32} in tRNA = *S*-adenosyl-L-homocysteine + 2′-*O*-methylcytidine^{32} in tRNA
(2) *S*-adenosyl-L-methionine + uridine^{32} in tRNA = *S*-adenosyl-L-homocysteine + 2′-*O*-methyluridine^{32} in tRNA
Other name(s): YfhQ; tRNA:Cm32/Um32 methyltransferase; TrMet(Xm32); TrmJ
Systematic name: *S*-adenosyl-L-methionine:tRNA (cytidine^{32}/uridine^{32}-2′-*O*)-methyltransferase
Comments: In *Escherichia coli* YfhQ is the only methyltransferase responsible for the formation of 2′-*O*-methylcytidine^{32} in tRNA. No methylation of cytosine^{34} in tRNA$^{\text{Leu}}$(CAA). *In vitro* the enzyme 2-*O*-methylates cytidine^{32} of tRNA$^{\text{Ser1}}$ and uridine^{32} of tRNA^{Gln2}.
References: [2773]

[EC 2.1.1.200 created 2011]

EC 2.1.1.201

Accepted name: 2-methoxy-6-polyprenyl-1,4-benzoquinol methylase
Reaction: *S*-adenosyl-L-methionine + 2-methoxy-6-*all-trans*-polyprenyl-1,4-benzoquinol = *S*-adenosyl-L-homocysteine + 6-methoxy-3-methyl-2-*all-trans*-polyprenyl-1,4-benzoquinol
Other name(s): *ubiE* (gene name, ambiguous)
Systematic name: *S*-adenosyl-L-methionine:2-methoxy-6-*all-trans*-polyprenyl-1,4-benzoquinol 5-*C*-methyltransferase
Comments: This enzyme is involved in ubiquinone biosynthesis. Ubiquinones from different organisms have a different number of prenyl units (for example, ubiquinone-6 in *Saccharomyces*, ubiquinone-9 in rat and ubiquinone-10 in human), and thus the natural substrate for the enzymes from different organisms has a different number of prenyl units. However, the enzyme usually shows a low degree of specificity regarding the number of prenyl units. For example, when the COQ5 gene from *Saccharomyces cerevisiae* is introduced into *Escherichia coli*, it complements the respiratory deficiency of an *ubiE* mutant [728]. The bifunctional enzyme from *Escherichia coli* also catalyses the methylation of demethylmenaquinol-8 (this activity is classified as EC 2.1.1.163) [1899].

References: [1899, 4006, 728, 197]

[EC 2.1.1.201 created 2011]

EC 2.1.1.202

Accepted name: multisite-specific tRNA:(cytosine-C^{5})-methyltransferase

Reaction: (1) *S*-adenosyl-L-methionine + cytosine^{34} in tRNA precursor = *S*-adenosyl-L-homocysteine + 5-methylcytosine^{34} in tRNA precursor
(2) *S*-adenosyl-L-methionine + cytosine^{40} in tRNA precursor = *S*-adenosyl-L-homocysteine + 5-methylcytosine^{40} in tRNA precursor
(3) *S*-adenosyl-L-methionine + cytosine^{48} in tRNA = *S*-adenosyl-L-homocysteine + 5-methylcytosine^{48} in tRNA
(4) *S*-adenosyl-L-methionine + cytosine^{49} in tRNA = *S*-adenosyl-L-homocysteine + 5-methylcytosine^{49} in tRNA

Other name(s): multisite-specific tRNA:m5*C*-methyltransferase; TRM4 (gene name, gene corresponding to ORF YBL024w)

Systematic name: *S*-adenosyl-L-methionine:tRNA (cytosine-C^{5})-methyltransferase

Comments: The enzyme from *Saccharomyces cerevisiae* is responsible for complete 5-methylcytosine methylations of yeast tRNA. The incidence of modification depends on the cytosine position in tRNA. At positions 34 and 40, 5-methylcytosine is found only in two yeast tRNAs (tRNA$^{\mathrm{Leu}}$(CUA) and tRNA$^{\mathrm{Phe}}$(GAA), respectively), whereas most other elongator yeast tRNAs bear either 5-methylcytosine^{48} or 5-methylcytosine^{49}, but never both in the same tRNA molecule [2331]. The formation of 5-methylcytosine^{34} and 5-methylcytosine^{40} is a strictly intron-dependent process, whereas the formation of 5-methylcytosine^{48} and 5-methylcytosine^{49} is an intron-independent process [1511, 3373].

References: [2331, 1511, 3373, 3725]

[EC 2.1.1.202 created 1976 as EC 2.1.1.29, part transferred 2011 to EC 2.1.1.202]

EC 2.1.1.203

Accepted name: tRNA (cytosine^{34}-C^{5})-methyltransferase

Reaction: *S*-adenosyl-L-methionine + cytosine^{34} in tRNA precursor = *S*-adenosyl-L-homocysteine + 5-methylcytosine^{34} in tRNA precursor

Other name(s): hTrm4 Mtase; hTrm4 methyltransferase; hTrm4 (gene name); tRNA:m5*C*-methyltransferase (ambiguous)

Systematic name: *S*-adenosyl-L-methionine:tRNA (cytosine^{34}-C^{5})-methyltransferase

Comments: The human enzyme is specific for C^{5}-methylation of cytosine^{34} in tRNA precursors. The intron in the human pre-tRNA$^{\mathrm{Leu}}$(CAA) is indispensable for the C^{5}-methylation of cytosine in the first position of the anticodon. It is not able to form 5-methylcytosine at positions 48 and 49 of human and yeast tRNA precursors [413].

References: [413]

[EC 2.1.1.203 created 1976 as EC 2.1.1.29, part transferred 2011 to EC 2.1.1.203]

EC 2.1.1.204

Accepted name: tRNA (cytosine^{38}-C^{5})-methyltransferase

Reaction: *S*-adenosyl-L-methionine + cytosine^{38} in tRNA = *S*-adenosyl-L-homocysteine + 5-methylcytosine^{38} in tRNA

Other name(s): hDNMT2 (gene name); DNMT2 (gene name); TRDMT1 (gene name)

Systematic name: *S*-adenosyl-L-methionine:tRNA (cytosine^{38}-C^{5})-methyltransferase

Comments: The eukaryotic enzyme catalyses methylation of cytosine^{38} in the anti-codon loop of tRNA$^{\mathrm{Asp}}$(GTC), tRNA$^{\mathrm{Val}}$(AAC) and tRNA$^{\mathrm{Gly}}$(GCC). Methylation by Dnmt2 protects tRNAs against stress-induced cleavage by ribonuclease [3061].

References: [1094, 1549, 3061]

[EC 2.1.1.204 created 1976 as EC 2.1.1.29, part transferred 2011 to EC 2.1.1.204]

EC 2.1.1.205

Accepted name: tRNA (cytidine^{32}/guanosine^{34}-2′-*O*)-methyltransferase

Reaction: *S*-adenosyl-L-methionine + cytidine^{32}/guanosine^{34} in tRNA = *S*-adenosyl-L-homocysteine + 2′-*O*-methylcytidine^{32}/2′-*O*-methylguanosine^{34} in tRNA

Other name(s): Trm7p

Systematic name: *S*-adenosyl-L-methionine:tRNA (cytidine^{32}/guanosine^{34}-2′-*O*)-methyltransferase

Comments: The enzyme from *Saccharomyces cerevisiae* catalyses the formation of 2′-*O*-methylnucleotides at positions 32 and 34 of the yeast tRNA$^{\text{Phe}}$, tRNA$^{\text{Trp}}$ and, possibly, tRNA$^{\text{Leu}}$.

References: [2716]

[EC 2.1.1.205 created 2011]

EC 2.1.1.206

Accepted name: tRNA (cytidine^{56}-2′-*O*)-methyltransferase

Reaction: *S*-adenosyl-L-methionine + cytidine^{56} in tRNA = *S*-adenosyl-L-homocysteine + 2′-*O*-methylcytidine^{56} in tRNA

Other name(s): aTrm56; tRNA ribose 2′-*O*-methyltransferase aTrm56; PAB1040 (gene name)

Systematic name: *S*-adenosyl-L-methionine:tRNA (cytidine^{56}-2′-*O*)-methyltransferase

Comments: The archaeal enzyme specifically catalyses the *S*-adenosyl-L-methionine dependent 2′-*O*-ribose methylation of cytidine at position 56 in tRNA transcripts.

References: [2871, 1824]

[EC 2.1.1.206 created 2011]

EC 2.1.1.207

Accepted name: tRNA (cytidine^{34}-2′-*O*)-methyltransferase

Reaction: (1) *S*-adenosyl-L-methionine + cytidine^{34} in tRNA = *S*-adenosyl-L-homocysteine + 2′-*O*-methylcytidine^{34} in tRNA

(2) *S*-adenosyl-L-methionine + 5-carboxymethylaminomethyluridine^{34} in tRNA$^{\text{Leu}}$ = *S*-adenosyl-L-homocysteine + 5-carboxymethylaminomethyl-2′-*O*-methyluridine^{34} in tRNA$^{\text{Leu}}$

Other name(s): *yibK* (gene name); methyltransferase *yibK*; TrmL; tRNA methyltransferase L; tRNA (cytidine^{34}/5-carboxymethylaminomethyluridine^{34}-2′-*O*)-methyltransferase

Systematic name: *S*-adenosyl-L-methionine:tRNA (cytidine^{34}/5-carboxymethylaminomethyluridine^{34}-2′-*O*)-methyltransferase

Comments: The enzyme from *Escherichia coli* catalyses the 2′-*O*-methylation of cytidine or 5-carboxymethylaminomethyluridine at the wobble position at nucleotide 34 in tRNA$^{\text{Leu}}$CmAA and tRNA$^{\text{Leu}}$cmnm^{5}UmAA. The enzyme is selective for the two tRNA$^{\text{Leu}}$ isoacceptors and only methylates these when they present the correct anticodon loop sequence and modification pattern. Specifically, YibK requires a pyrimidine nucleoside at position 34, it has a clear preference for an adenosine at position 35, and it fails to methylate without prior addition of the N^6-(isopentenyl)-2-methylthioadenosine modification at position 37.

References: [268]

[EC 2.1.1.207 created 2011]

EC 2.1.1.208

Accepted name: 23S rRNA (uridine^{2479}-2′-*O*)-methyltransferase

Reaction: *S*-adenosyl-L-methionine + uridine^{2479} in 23S rRNA = *S*-adenosyl-L-homocysteine + 2′-*O*-methyluridine^{2479} in 23S rRNA

Other name(s): AviRb

Systematic name: *S*-adenosyl-L-methionine:23S rRNA (uridine^{2479}-2′-*O*)-methyltransferase

Comments: *Streptomyces viridochromogenes* produces the antibiotic avilamycin A which binds to the 50S ribosomal subunit to inhibit protein synthesis. To protect itself from the antibiotic, *Streptomyces viridochromogenes* utilizes two methyltransferases, 23S rRNA (uridine^{2479}-$2'$-*O*)-methyltransferase and EC 2.1.1.209 [23S rRNA (guanine^{2535}-N^1)-methyltransferase], whose actions confer avilamycin resistance to the RNA.

References: [2327, 3563, 3816]

[EC 2.1.1.208 created 2011]

EC 2.1.1.209

Accepted name: 23S rRNA (guanine^{2535}-N^1)-methyltransferase

Reaction: *S*-adenosyl-L-methionine + guanine^{2535} in 23S rRNA = *S*-adenosyl-L-homocysteine + N^1-methylguanine^{2535} in 23S rRNA

Other name(s): AviRa

Systematic name: *S*-adenosyl-L-methionine:23S rRNA (guanine^{2535}-N^1)-methyltransferase

Comments: *Streptomyces viridochromogenes* produces the antibiotic avilamycin A which binds to the 50S ribosomal subunit to inhibit protein synthesis. To protect itself from the antibiotic, *Streptomyces viridochromogenes* utilizes two methyltransferases, 23S rRNA (guanine^{2535}-N^1)-methyltransferase and EC 2.1.1.208 [23S rRNA (uridine^{2479}-2-*O*)-methyltransferase], whose actions confer avilamycin resistance to the RNA.

References: [3563, 3816, 2326]

[EC 2.1.1.209 created 2011]

EC 2.1.1.210

Accepted name: demethylspheroidene *O*-methyltransferase

Reaction: *S*-adenosyl-L-methionine + demethylspheroidene = *S*-adenosyl-L-homocysteine + spheroidene

Other name(s): 1-hydroxycarotenoid *O*-methylase; 1-hydroxycarotenoid methylase; 1-HO-carotenoid methylase; CrtF

Systematic name: *S*-adenosyl-L-methionine:demethylspheroidene *O*-methyltransferase

Comments: In *Rhodopseudomonas capsulata* and *Rubrivivax gelatinosus* the enzyme is involved in biosynthesis of spheroidene [1,2,3]. In *Rubrivivax gelatinosus* the enzyme also catalyses the methylation of demethylspirilloxanthin to spirilloxanthin and the methylation of 3,4-didehydrorhodopin to anhydrorhodovibrin [2714].

References: [153, 2714, 3124]

[EC 2.1.1.210 created 2011]

EC 2.1.1.211

Accepted name: tRNA$^{\text{Ser}}$ (uridine^{44}-$2'$-*O*)-methyltransferase

Reaction: *S*-adenosyl-L-methionine + uridine^{44} in tRNA$^{\text{Ser}}$ = *S*-adenosyl-L-homocysteine + $2'$-*O*-methyluridine^{44} in tRNA$^{\text{Ser}}$

Other name(s): TRM44

Systematic name: *S*-adenosyl-L-methionine:tRNA$^{\text{Ser}}$ (uridine^{44}-$2'$-*O*)-methyltransferase

Comments: The $2'$-*O*-methylation of uridine^{44} contributes to stability of tRNA$^{\text{Ser}}$(CGA).

References: [1770]

[EC 2.1.1.211 created 2011]

EC 2.1.1.212

Accepted name: 2,7,$4'$-trihydroxyisoflavanone $4'$-*O*-methyltransferase

Reaction: *S*-adenosyl-L-methionine + 2,$4'$,7-trihydroxyisoflavanone = *S*-adenosyl-L-homocysteine + 2,7-dihydroxy-$4'$-methoxyisoflavanone

Other name(s): SAM:2,7,$4'$-trihydroxyisoflavanone $4'$-*O*-methyltransferase; HI$4'$OMT; HMM1; MtIOMT5; *S*-adenosyl-L-methionine:2,7,$4'$-trihydroxyisoflavanone $4'$-*O*-methyltransferase

Systematic name: *S*-adenosyl-L-methionine:2,$4'$,7-trihydroxyisoflavanone $4'$-*O*-methyltransferase

Comments: Specifically methylates 2,$4'$,7-trihydroxyisoflavanone on the $4'$-position. No activity with isoflavones [695]. The enzyme is involved in formononetin biosynthesis in legumes [34]. The protein from pea (*Pisum sativum*) also methylates (+)-6a-hydroxymaackiain at the 3-position (*cf.* EC 2.1.1.270, (+)-6a-hydroxymaackiain 3-*O*-methyltransferase) [35].

References: [34, 695, 1995, 35]

[EC 2.1.1.212 created 2011]

EC 2.1.1.213

Accepted name: tRNA (guanine^{10}-N^2)-dimethyltransferase

Reaction: **2** *S*-adenosyl-L-methionine + guanine^{10} in tRNA = **2** *S*-adenosyl-L-homocysteine + N^2-dimethylguanine^{10} in tRNA (overall reaction)
(1a) *S*-adenosyl-L-methionine + guanine^{10} in tRNA = *S*-adenosyl-L-homocysteine + N^2-methylguanine^{10} in tRNA
(1b) *S*-adenosyl-L-methionine + N^2-methylguanine^{10} in tRNA = *S*-adenosyl-L-homocysteine + N^2-dimethylguanine^{10} in tRNA

Other name(s): PAB1283; N(2),N(2)-dimethylguanosine tRNA methyltransferase; Trm-G10; PabTrm-G10; PabTrm-m2 2G10 enzyme

Systematic name: *S*-adenosyl-L-methionine:tRNA (guanine^{10}-N^2)-dimethyltransferase

References: [109]

[EC 2.1.1.213 created 2011 (EC 2.1.1.32 created 1972, part transferred 2011 to EC 2.1.1.213)]

EC 2.1.1.214

Accepted name: tRNA (guanine^{10}-N^2)-methyltransferase

Reaction: *S*-adenosyl-L-methionine + guanine^{10} in tRNA = *S*-adenosyl-L-homocysteine + N^2-methylguanine^{10} in tRNA

Other name(s): (m^{2}G^{10}) methyltransferase; Trm11-Trm112 complex

Systematic name: *S*-adenosyl-L-methionine:tRNA (guanine^{10}-N^2)-methyltransferase

Comments: In contrast to the archaeal enzyme tRNA (guanine^{10}-N^2)-dimethyltransferase (EC 2.1.1.213), tRNA (guanine^{10}-N^2)-methyltransferase from yeast does not catalyse the methylation from N^2-methylguanine^{10} to N^2-dimethylguanine^{10} in tRNA.

References: [2775]

[EC 2.1.1.214 created 2011 (EC 2.1.1.32 created 1972, part transferred 2011 to EC 2.1.1.214)]

EC 2.1.1.215

Accepted name: tRNA (guanine^{26}-N^2/guanine^{27}-N^2)-dimethyltransferase

Reaction: **4** *S*-adenosyl-L-methionine + guanine^{26}/guanine^{27} in tRNA = **4** *S*-adenosyl-L-homocysteine + N^2-dimethylguanine^{26}/N^2-dimethylguanine^{27} in tRNA

Other name(s): Trm1 (ambiguous); tRNA (N^2,N^2-guanine)-dimethyltransferase; tRNA (m2(2G26) methyltransferase; Trm1[tRNA (m2(2)G26) methyltransferase]

Systematic name: *S*-adenosyl-L-methionine:tRNA (guanine^{26}-N^2/guanine^{27}-N^2)-dimethyltransferase

Comments: The enzyme from *Aquifex aeolicus* is similar to the TRM1 methyltransferases of archaea and eukarya (see EC 2.1.1.216, tRNA (guanine^{26}-N^2)-dimethyltransferase). However, it catalyses the double methylation of guanines at both positions 26 and 27 of tRNA.

References: [134]

[EC 2.1.1.215 created 2011 (EC 2.1.1.32 created 1972, part transferred 2011 to EC 2.1.1.215)]

EC 2.1.1.216

Accepted name: tRNA (guanine^{26}-N^2)-dimethyltransferase

Reaction: **2** *S*-adenosyl-L-methionine + guanine^{26} in tRNA = **2** *S*-adenosyl-L-homocysteine + N^2-dimethylguanine^{26} in tRNA
Other name(s): Trm1p; TRM1; tRNA (m$^2_2$G$_{26}$)dimethyltransferase
Systematic name: *S*-adenosyl-L-methionine:tRNA (guanine^{26}-N^2)-dimethyltransferase
Comments: The enzyme dissociates from its tRNA substrate between the two consecutive methylation reactions. In contrast to EC 2.1.1.215, tRNA (guanine^{26}-N^2/guanine^{27}-N^2)-dimethyltransferase, this enzyme does not catalyse the methylation of guanine^{27} in tRNA.
References: [601, 600, 1998, 2003]

[EC 2.1.1.216 created 2011 (EC 2.1.1.32 created 1972, part transferred 2011 to EC 2.1.1.216)]

EC 2.1.1.217

Accepted name: tRNA (adenine^{22}-N^1)-methyltransferase
Reaction: *S*-adenosyl-L-methionine + adenine^{22} in tRNA = *S*-adenosyl-L-homocysteine + N^1-methyladenine^{22} in tRNA
Other name(s): TrmK; YqfN; Sp1610 (gene name); tRNA: m^{1}A^{22} methyltransferase
Systematic name: *S*-adenosyl-L-methionine:tRNA (adenine^{22}-N^1)-methyltransferase
Comments: The enzyme specifically methylates adenine^{22} in tRNA.
References: [3422, 2929]

[EC 2.1.1.217 created 2011 (EC 2.1.1.36 created 1972, part transferred 2011 to EC 2.1.1.217)]

EC 2.1.1.218

Accepted name: tRNA (adenine^9-N^1)-methyltransferase
Reaction: *S*-adenosyl-L-methionine + adenine^9 in tRNA = *S*-adenosyl-L-homocysteine + N^1-methyladenine^9 in tRNA
Other name(s): Trm10p (ambiguous); tRNA(m^{1}G^9/m^{1}A^9)-methyltransferase; tRNA(m^{1}G^9/m^{1}A^9)MTase; TK0422p (gene name); tRNA m^{1}A^9-methyltransferase; tRNA m^{1}A^9 Mtase
Systematic name: *S*-adenosyl-L-methionine:tRNA (adenine^9-N^1)-methyltransferase
Comments: The enzyme from *Sulfolobus acidocaldarius* specifically methylates adenine^9 in tRNA [1637]. The bifunctional enzyme from *Thermococcus kodakaraensis* also catalyses the methylation of guanine^9 in tRNA (*cf.* EC 2.1.1.221, tRNA (guanine^9-N^1)-methyltransferase).
References: [1637]

[EC 2.1.1.218 created 2011 (EC 2.1.1.36 created 1972, part transferred 2011 to EC 2.1.1.218)]

EC 2.1.1.219

Accepted name: tRNA (adenine^{57}-N^1/adenine^{58}-N^1)-methyltransferase
Reaction: **2** *S*-adenosyl-L-methionine + adenine^{57}/adenine^{58} in tRNA = **2** *S*-adenosyl-L-homocysteine + N^1-methyladenine^{57}/N^1-methyladenine^{58} in tRNA
Other name(s): TrmI; $_{Pab}$TrmI; $_{Aq}$TrmI; $_{Mt}$TrmI
Systematic name: *S*-adenosyl-L-methionine:tRNA (adenine^{57}/adenine^{58}-N^1)-methyltransferase
Comments: The enzyme catalyses the formation of N^1-methyladenine at two adjacent positions (57 and 58) in the T-loop of certain tRNAs (e.g. tRNA$^{\mathrm{Asp}}$). Methyladenosine at position 57 is an obligatory intermediate for the synthesis of methylinosine, which is commonly found at position 57 of archaeal tRNAs.
References: [2930, 1169]

[EC 2.1.1.219 created 2011 (EC 2.1.1.36 created 1972, part transferred 2011 to EC 2.1.1.219)]

EC 2.1.1.220

Accepted name: tRNA (adenine^{58}-N^1)-methyltransferase
Reaction: *S*-adenosyl-L-methionine + adenine^{58} in tRNA = *S*-adenosyl-L-homocysteine + N^1-methyladenine^{58} in tRNA

Other name(s): tRNA m^{1}A^{58} methyltransferase; tRNA (m^{1}A^{58}) methyltransferase; TrmI; tRNA (m^{1}A^{58}) Mtase; Rv2118cp; Gcd10p-Gcd14p; Trm61p-Trm6p

Systematic name: *S*-adenosyl-L-methionine:tRNA (adenine^{58}-N^1)-methyltransferase

Comments: The enzyme specifically methylates adenine^{58} in tRNA. The methylation of A58 is critical for maintaining the stability of initiator tRNA$^{\text{Met}}$ in yeast [75].

References: [778, 3653, 75]

[EC 2.1.1.220 created 2011 (EC 2.1.1.36 created 1972, part transferred 2011 to EC 2.1.1.220)]

EC 2.1.1.221

Accepted name: tRNA (guanine^9-N^1)-methyltransferase

Reaction: *S*-adenosyl-L-methionine + guanine^9 in tRNA = *S*-adenosyl-L-homocysteine + N^1-methylguanine^9 in tRNA

Other name(s): Trm10p (ambiguous); tRNA(m^{1}G^9/m^{1}A^9)-methyltransferase; tRNA(m^{1}G^9/m^{1}A^9)MTase; tRNA (guanine-N(1)-)-methyltransferase; tRNA m^{1}G^9-methyltransferase; tRNA m^{1}G^9 MTase

Systematic name: *S*-adenosyl-L-methionine:tRNA (guanine^9-N^1)-methyltransferase

Comments: The enzyme from *Saccharomyces cerevisiae* specifically methylates guanine^9 [1637, 1480]. The bifunctional enzyme from *Thermococcus kodakaraensis* also catalyses the methylation of adenine^9 in tRNA (*cf.* EC 2.1.1.218, tRNA (adenine^9-N^1)-methyltransferase) [1637].

References: [1637, 1480]

[EC 2.1.1.221 created 2011 (EC 2.1.1.31 created 1971, part transferred 2011 to EC 2.1.1.221)]

EC 2.1.1.222

Accepted name: 2-polyprenyl-6-hydroxyphenol methylase

Reaction: *S*-adenosyl-L-methionine + 3-(*all-trans*-polyprenyl)benzene-1,2-diol = *S*-adenosyl-L-homocysteine + 2-methoxy-6-(*all-trans*-polyprenyl)phenol

Other name(s): *ubiG* (gene name, ambiguous); *ubiG* methyltransferase (ambiguous); 2-octaprenyl-6-hydroxyphenol methylase

Systematic name: *S*-adenosyl-L-methionine:3-(*all-trans*-polyprenyl)benzene-1,2-diol 2-*O*-methyltransferase

Comments: UbiG catalyses both methylation steps in ubiquinone biosynthesis in *Escherichia coli*. The second methylation is classified as EC 2.1.1.64 (3-demethylubiquinol 3-*O*-methyltransferase) [1387]. In eukaryotes Coq3 catalyses the two methylation steps in ubiquinone biosynthesis. However, while the second methylation is common to both enzymes, the first methylation by Coq3 occurs at a different position within the pathway, and thus involves a different substrate and is classified as EC 2.1.1.114 (polyprenyldihydroxybenzoate methyltransferase). The substrate of the eukaryotic enzyme (3,4-dihydroxy-5-*all-trans*-polyprenylbenzoate) differs by an additional carboxylate moiety.

References: [2740, 1387]

[EC 2.1.1.222 created 2011, modified 2013]

EC 2.1.1.223

Accepted name: tRNA$_1^{\text{Val}}$ (adenine^{37}-N^6)-methyltransferase

Reaction: *S*-adenosyl-L-methionine + adenine^{37} in tRNA$_1^{\text{Val}}$ = *S*-adenosyl-L-homocysteine + N^6-methyladenine^{37} in tRNA$_1^{\text{Val}}$

Other name(s): YfiC

Systematic name: *S*-adenosyl-L-methionine:tRNA$_1^{\text{Val}}$ (adenine^{37}-N^6)-methyltransferase

Comments: The enzyme specifically methylates adenine^{37} in tRNA$_1^{\text{Val}}$ (anticodon cmo5UAC).

References: [1096]

[EC 2.1.1.223 created 2011]

EC 2.1.1.224

Accepted name: 23S rRNA (adenine^{2503}-*C*^{8})-methyltransferase

Reaction: **2** *S*-adenosyl-L-methionine + adenine^{2503} in 23S rRNA + **2** reduced [2Fe-2S] ferredoxin = *S*-adenosyl-L-homocysteine + L-methionine + 5′-deoxyadenosine + 8-methyladenine^{2503} in 23S rRNA + **2** oxidized [2Fe-2S] ferredoxin

Other name(s): Cfr (gene name)

Systematic name: *S*-adenosyl-L-methionine:23S rRNA (adenine^{2503}-*C*^{8})-methyltransferase

Comments: This enzyme is a member of the ‘AdoMet radical’ (radical SAM) family. *S*-Adenosyl-L-methionine acts as both a radical generator and as the source of the appended methyl group. It contains an [4Fe-4S] cluster [3,6,7]. Cfr is an plasmid-acquired methyltransferase that protects cells from the action of antibiotics [1057]. The enzyme methylates adenosine at position 2503 of 23S rRNA by a radical mechanism, transferring a CH_2 group from *S*-adenosyl-L-methionine while retaining the hydrogen at the C-8 position of the adenine. Cfr first transfers an CH_2 group to a conserved cysteine (Cys^{338} in *Staphylococcus aureus*) [1153], the generated radical from a second *S*-adenosyl-L-methionine then attacks the methyl group, exctracting a hydrogen. The formed radical forms a covalent intermediate with the adenine group of the tRNA [1152]. The enzyme will also methylate 2-methyladenine produced by the action of EC 2.1.1.192 [23S rRNA (adenine^{2503}-*C*^{2})-methyltransferase].

References: [1057, 1574, 3958, 3957, 1151, 335, 1153, 1152]

[EC 2.1.1.224 created 2011, modified 2014]

EC 2.1.1.225

Accepted name: tRNA:m^{4}X modification enzyme

Reaction: (1) *S*-adenosyl-L-methionine + cytidine^{4} in tRNA$^{\mathrm{Pro}}$ = *S*-adenosyl-L-homocysteine + 2′-*O*-methylcytidine^{4} in tRNA$^{\mathrm{Pro}}$

(2) *S*-adenosyl-L-methionine + cytidine^{4} in tRNA$^{\mathrm{Gly}}$(GCC) = *S*-adenosyl-L-homocysteine + 2′-*O*-methylcytidine^{4} in tRNA$^{\mathrm{Gly}}$(GCC)

(3) *S*-adenosyl-L-methionine + adenosine^{4} in tRNA$^{\mathrm{His}}$ = *S*-adenosyl-L-homocysteine + 2′-*O*-methyladenosine^{4} in tRNA$^{\mathrm{His}}$

Other name(s): TRM13; Trm13p; tRNA:Xm4 modification enzyme

Systematic name: *S*-adenosyl-L-methionine:tRNA$^{Pro/His/Gly}$(GCC) (cytidine/adenosine^{4}-2′-*O*)-methyltransferase

Comments: The enzyme from *Saccharomyces cerevisiae* 2′-*O*-methylates cytidine^{4} in tRNA$^{\mathrm{Pro}}$ and tRNA$^{\mathrm{Gly}}$(GCC), and adenosine^{4} in tRNA$^{\mathrm{His}}$.

References: [3852]

[EC 2.1.1.225 created 2011]

EC 2.1.1.226

Accepted name: 23S rRNA (cytidine^{1920}-2′-*O*)-methyltransferase

Reaction: *S*-adenosyl-L-methionine + cytidine^{1920} in 23S rRNA = *S*-adenosyl-L-homocysteine + 2′-*O*-methylcytidine^{1920} in 23S rRNA

Other name(s): TlyA (ambiguous)

Systematic name: *S*-adenosyl-L-methionine:23S rRNA (cytidine^{1920}-2′-*O*)-methyltransferase

Comments: The bifunctional enzyme from *Mycobacterium tuberculosis* 2′-*O*-methylates cytidine^{1920} in helix 69 of 23S rRNA and cytidine^{1409} in helix 44 of 16S rRNA (*cf.* EC 2.1.1.227, 16S rRNA (cytidine^{1409}-2′-*O*)-methyltransferase). These methylations result in increased susceptibility to the antibiotics capreomycin and viomycin.

References: [1520, 2175]

[EC 2.1.1.226 created 2011]

EC 2.1.1.227

Accepted name: 16S rRNA (cytidine^{1409}-2′-*O*)-methyltransferase

Reaction: *S*-adenosyl-L-methionine + cytidine^{1409} in 16S rRNA = *S*-adenosyl-L-homocysteine + 2′-*O*-methylcytidine^{1409} in 16S rRNA

Other name(s): TlyA (ambiguous)
Systematic name: *S*-adenosyl-L-methionine:16S rRNA (cytidine^{1409}-2$'$-*O*)-methyltransferase
Comments: The bifunctional enzyme from *Mycobacterium tuberculosis* 2$'$-*O*-methylates cytidine^{1409} in helix 44 of 16S rRNA and cytidine^{1920} in helix 69 of 23S rRNA (*cf.* EC 2.1.1.226, 23S rRNA (cytidine^{1920}-2$'$-*O*)-methyltransferase).
References: [1520, 2175]

[EC 2.1.1.227 created 2011]

EC 2.1.1.228

Accepted name: tRNA (guanine^{37}-*N*^{1})-methyltransferase
Reaction: *S*-adenosyl-L-methionine + guanine^{37} in tRNA = *S*-adenosyl-L-homocysteine + *N*^{1}-methylguanine^{37} in tRNA
Other name(s): TrmD; tRNA (m^{1}G^{37}) methyltransferase; transfer RNA (m^{1}G^{37}) methyltransferase; Trm5p; TRMT5; tRNA-(N^{1}G37) methyltransferase; MJ0883 (gene name)
Systematic name: *S*-adenosyl-L-methionine:tRNA (guanine^{37}-*N*^{1})-methyltransferase
Comments: This enzyme is important for the maintenance of the correct reading frame during translation. Unlike TrmD from *Escherichia coli*, which recognizes the G36pG37 motif preferentially, the human enzyme (encoded by TRMT5) also methylates inosine at position 37 [410].
References: [3447, 1887, 2510, 410, 1104, 29]

[EC 2.1.1.228 created 2011 (EC 2.1.1.31 created 1971, part transferred 2011 to EC 2.1.1.228)]

EC 2.1.1.229

Accepted name: tRNA (carboxymethyluridine^{34}-5-*O*)-methyltransferase
Reaction: *S*-adenosyl-L-methionine + carboxymethyluridine^{34} in tRNA = *S*-adenosyl-L-homocysteine + 5-(2-methoxy-2-oxoethyl)uridine^{34} in tRNA
Other name(s): ALKBH8; ABH8; Trm9; tRNA methyltransferase 9
Systematic name: *S*-adenosyl-L-methionine:tRNA (carboxymethyluridine^{34}-5-*O*)-methyltransferase
Comments: The enzyme catalyses the posttranslational modification of uridine residues at the wobble position 34 of the anticodon loop of tRNA.
References: [976, 3288, 1565]

[EC 2.1.1.229 created 2011]

EC 2.1.1.230

Accepted name: 23S rRNA (adenosine^{1067}-2$'$-*O*)-methyltransferase
Reaction: *S*-adenosyl-L-methionine + adenosine^{1067} in 23S rRNA = *S*-adenosyl-L-homocysteine + 2$'$-*O*-methyladenosine^{1067} in 23S rRNA
Other name(s): 23S rRNA A^{1067} 2$'$-methyltransferase; thiostrepton-resistance methylase; nosiheptide-resistance methyltransferase
Systematic name: *S*-adenosyl-L-methionine:23S rRNA (adenosine^{1067}-2$'$-*O*)-methyltransferase
Comments: The methylase that is responsible for autoimmunity in the thiostrepton producer *Streptomyces azureus*, renders ribosomes completely resistant to thiostrepton [3525].
References: [245, 3525, 3524, 3960]

[EC 2.1.1.230 created 2011]

EC 2.1.1.231

Accepted name: flavonoid 4$'$-*O*-methyltransferase
Reaction: *S*-adenosyl-L-methionine + a 4$'$-hydroxyflavanone = *S*-adenosyl-L-homocysteine + a 4$'$-methoxyflavanone
Other name(s): SOMT-2; 4$'$-hydroxyisoflavone methyltransferase

Systematic name: *S*-adenosyl-L-methionine:flavonoid $4'$-*O*-methyltransferase

Comments: The enzyme catalyses the $4'$-methylation of naringenin. *In vitro* it catalyses the $4'$-methylation of apigenin, quercetin, daidzein and genistein.

References: [1678]

[EC 2.1.1.231 created 2011]

EC 2.1.1.232

Accepted name: naringenin 7-*O*-methyltransferase

Reaction: *S*-adenosyl-L-methionine + (2*S*)-naringenin = *S*-adenosyl-L-homocysteine + (2*S*)-sakuranetin

Other name(s): NOMT

Systematic name: *S*-adenosyl-L-methionine:(2*S*)-5,7,$4'$-trihydroxyflavanone 7-*O*-methyltransferase

Comments: The enzyme is involved in the biosynthesis of the sakuranetin, an inducible defense mechanism of the plant *Oryza sativa* (Asian rice) against pathogen attack.

References: [2797]

[EC 2.1.1.232 created 2011]

EC 2.1.1.233

Accepted name: [phosphatase 2A protein]-leucine-carboxy methyltransferase

Reaction: *S*-adenosyl-L-methionine + [phosphatase 2A protein]-leucine = *S*-adenosyl-L-homocysteine + [phosphatase 2A protein]-leucine methyl ester

Other name(s): leucine carboxy methyltransferase-1; LCMT1

Systematic name: *S*-adenosyl-L-methionine:[phosphatase 2A protein]-leucine *O*-methyltransferase

Comments: Methylates the C-terminal leucine of phosphatase 2A. A key regulator of protein phosphatase 2A. The methyl ester is hydrolysed by EC 3.1.1.89 (protein phosphatase methylesterase-1). Occurs mainly in the cytoplasm, Golgi region and late endosomes.

References: [155, 3575]

[EC 2.1.1.233 created 2011]

EC 2.1.1.234

Accepted name: dTDP-3-amino-3,4,6-trideoxy-α-D-glucopyranose *N*,*N*-dimethyltransferase

Reaction: **2** *S*-adenosyl-L-methionine + dTDP-3-amino-3,4,6-trideoxy-α-D-glucopyranose = **2** *S*-adenosyl-L-homocysteine + dTDP-3-dimethylamino-3,4,6-trideoxy-α-D-glucopyranose

Other name(s): DesVI

Systematic name: *S*-adenosyl-L-methionine:dTDP-3-amino-3,4,6-trideoxy-α-D-glucopyranose 3-*N*,*N*-dimethyltransferase

Comments: The enzyme is involved in the biosynthesis of desosamine, a 3-(dimethylamino)-3,4,6-trideoxyhexose found in certain macrolide antibiotics such as erthyromycin, azithromycin, and clarithromycin.

References: [525, 426]

[EC 2.1.1.234 created 2011]

EC 2.1.1.235

Accepted name: dTDP-3-amino-3,6-dideoxy-α-D-glucopyranose *N*,*N*-dimethyltransferase

Reaction: **2** *S*-adenosyl-L-methionine + dTDP-3-amino-3,6-dideoxy-α-D-glucopyranose = **2** *S*-adenosyl-L-homocysteine + dTDP-3-dimethylamino-3,6-dideoxy-α-D-glucopyranose

Other name(s): TylM1

Systematic name: *S*-adenosyl-L-methionine:dTDP-3-amino-3,6-dideoxy-α-D-glucopyranose 3-*N*,*N*-dimethyltransferase

Comments: The enzyme is involved in the biosynthesis of mycaminose, an essential structural component of the macrolide antibiotic tylosin, which is produced by the bacterium *Streptomyces fradiae*.

References: [525, 481]

[EC 2.1.1.235 created 2011]

EC 2.1.1.236

Accepted name: dTDP-3-amino-3,6-dideoxy-α-D-galactopyranose *N*,*N*-dimethyltransferase

Reaction: **2** *S*-adenosyl-L-methionine + dTDP-3-amino-3,6-dideoxy-α-D-galactopyranose = **2** *S*-adenosyl-L-homocysteine + dTDP-3-dimethylamino-3,6-dideoxy-α-D-galactopyranose

Other name(s): RavNMT

Systematic name: *S*-adenosyl-L-methionine:dTDP-3-amino-3,6-dideoxy-α-D-galactopyranose 3-*N*,*N*-dimethyltransferase

Comments: The enzyme is involved in the synthesis of dTDP-D-ravidosamine, the amino sugar moiety of the antibiotic ravidomycin V, which is produced by the bacterium *Streptomyces ravidus*.

References: [1661]

[EC 2.1.1.236 created 2011]

EC 2.1.1.237

Accepted name: mycinamicin III 3$''$-*O*-methyltransferase

Reaction: *S*-adenosyl-L-methionine + mycinamicin III = *S*-adenosyl-L-homocysteine + mycinamicin IV

Other name(s): MycF

Systematic name: *S*-adenosyl-L-methionine:mycinamicin III 3$''$-*O*-methyltransferase

Comments: The enzyme is involved in the biosynthesis of mycinamicin macrolide antibiotics.

References: [1959]

[EC 2.1.1.237 created 2011]

EC 2.1.1.238

Accepted name: mycinamicin VI 2$''$-*O*-methyltransferase

Reaction: *S*-adenosyl-L-methionine + mycinamicin VI = *S*-adenosyl-L-homocysteine + mycinamicin III

Other name(s): MycE

Systematic name: *S*-adenosyl-L-methionine:mycinamicin VI 2$''$-*O*-methyltransferase

Comments: The enzyme is involved in the biosynthesis of mycinamicin macrolide antibiotics. Requires Mg^{2+} for optimal activity.

References: [1959]

[EC 2.1.1.238 created 2011]

EC 2.1.1.239

Accepted name: L-olivosyl-oleandolide 3-*O*-methyltransferase

Reaction: *S*-adenosyl-L-methionine + L-olivosyl-oleandolide = *S*-adenosyl-L-homocysteine + L-oleandrosyl-oleandolide

Other name(s): OleY

Systematic name: *S*-adenosyl-L-methionine:L-olivosyl-oleandolide B 3-*O*-methyltransferase

Comments: The enzyme is involved in the biosynthesis of the macrolide antibiotic oleandomycin in *Streptomyces antibioticus*. It can also act on other monoglycosylated macrolactones, including L-rhamnosyl-erythronolide B and L-mycarosyl-erythronolide B.

References: [2911]

[EC 2.1.1.239 created 2012]

EC 2.1.1.240

Accepted name: *trans*-resveratrol di-*O*-methyltransferase

Reaction: **2** *S*-adenosyl-L-methionine + *trans*-resveratrol = **2** *S*-adenosyl-L-homocysteine + pterostilbene (overall reaction)

(1a) *S*-adenosyl-L-methionine + *trans*-resveratrol = *S*-adenosyl-L-homocysteine + 3-methoxy-4′,5-dihydroxy-*trans*-stilbene
(1b) *S*-adenosyl-L-methionine + 3-methoxy-4′,5-dihydroxy-*trans*-stilbene = *S*-adenosyl-L-homocysteine + pterostilbene

Other name(s): ROMT; resveratrol *O*-methyltransferase; pterostilbene synthase

Systematic name: *S*-adenosyl-L-methionine:*trans*-resveratrol 3,5-*O*-dimethyltransferase

Comments: The enzyme catalyses the biosynthesis of pterostilbene from resveratrol.

References: [3081]

[EC 2.1.1.240 created 2012]

EC 2.1.1.241

Accepted name: 2,4,7-trihydroxy-1,4-benzoxazin-3-one-glucoside 7-*O*-methyltransferase

Reaction: *S*-adenosyl-L-methionine + (2*R*)-4,7-dihydroxy-3-oxo-3,4-dihydro-2*H*-1,4-benzoxazin-2-yl β-D-glucopyranoside = *S*-adenosyl-L-homocysteine + (2*R*)-4-hydroxy-7-methoxy-3-oxo-3,4-dihydro-2*H*-1,4-benzoxazin-2-yl β-D-glucopyranoside

Other name(s): BX7 (gene name); OMT BX7

Systematic name: *S*-adenosyl-L-methionine:(2*R*)-4,7-dihydroxy-3-oxo-3,4-dihydro-2*H*-1,4-benzoxazin-2-yl β-D-glucopyranoside 7-*O*-methyltransferase

Comments: The enzyme is involved in the biosynthesis of the protective and allelophatic benzoxazinoid DIMBOA [(2*R*)-4-hydroxy-7-methoxy-3-oxo-3,4-dihydro-2*H*-1,4-benzoxazin] in some plants, most commonly from the family of Poaceae (grasses).

References: [1529]

[EC 2.1.1.241 created 2012]

EC 2.1.1.242

Accepted name: 16S rRNA (guanine^{1516}-N^2)-methyltransferase

Reaction: *S*-adenosyl-L-methionine + guanine^{1516} in 16S rRNA = *S*-adenosyl-L-homocysteine + N^2-methylguanine^{1516} in 16S rRNA

Other name(s): *yhiQ* (gene name); *rsmJ* (gene name); m^{2}G^{1516} methyltransferase

Systematic name: *S*-adenosyl-L-methionine:16S rRNA (guanine^{1516}-N^2)-methyltransferase

Comments: The enzyme specifically methylates guanine^{1516} at N^2 in 16S rRNA.

References: [215]

[EC 2.1.1.242 created 2012]

EC 2.1.1.243

Accepted name: 2-ketoarginine methyltransferase

Reaction: *S*-adenosyl-L-methionine + 5-guanidino-2-oxopentanoate = *S*-adenosyl-L-homocysteine + 5-guanidino-3-methyl-2-oxopentanoate

Other name(s): *mrsA* (gene name)

Systematic name: *S*-adenosyl-L-methionine:5-carbamimidamido-2-oxopentanoate S-methyltransferase

Comments: The enzyme is involved in production of the rare amino acid 3-methylarginine, which is used by the epiphytic bacterium *Pseudomonas syringae* pv. *syringae* as an antibiotic against the related pathogenic species *Pseudomonas syringae* pv. *glycinea*.

References: [379]

[EC 2.1.1.243 created 2012]

EC 2.1.1.244

Accepted name: protein N-terminal methyltransferase

Reaction: (1) **3** *S*-adenosyl-L-methionine + N-terminal-(A,S)PK-[protein] = **3** *S*-adenosyl-L-homocysteine + N-terminal-*N*,*N*,*N*-trimethyl-*N*-(A,S)PK-[protein] (overall reaction)
(1a) *S*-adenosyl-L-methionine + N-terminal-(A,S)PK-[protein] = *S*-adenosyl-L-homocysteine + N-terminal-*N*-methyl-*N*-(A,S)PK-[protein]
(1b) *S*-adenosyl-L-methionine + N-terminal-*N*-methyl-*N*-(A,S)PK-[protein] = *S*-adenosyl-L-homocysteine + N-terminal-*N*,*N*-dimethyl-*N*-(A,S)PK-[protein]
(1c) *S*-adenosyl-L-methionine + N-terminal-*N*,*N*-dimethyl-*N*-(A,S)PK-serine-[protein] = *S*-adenosyl-L-homocysteine + N-terminal-*N*,*N*,*N*-trimethyl-*N*-(A,S)PK-[protein]
(2) **2** *S*-adenosyl-L-methionine + N-terminal-PPK-[protein] = **2** *S*-adenosyl-L-homocysteine + N-terminal-*N*,*N*-dimethyl-*N*-PPK-[protein] (overall reaction)
(2a) *S*-adenosyl-L-methionine + N-terminal-PPK-[protein] = *S*-adenosyl-L-homocysteine + N-terminal-*N*-methyl-*N*-PPK-[protein]
(2b) *S*-adenosyl-L-methionine + N-terminal-*N*-methyl-*N*-PPK-[protein] = *S*-adenosyl-L-homocysteine + N-terminal-*N*,*N*-dimethyl-*N*-PPK-[protein]

Other name(s): *NMT1* (gene name); METTL11A (gene name)

Systematic name: *S*-adenosyl-L-methionine:N-terminal-(A,P,S)PK-[protein] methyltransferase

Comments: This enzyme methylates the N-terminus of target proteins containing the N-terminal motif [Ala/Pro/Ser]-Pro-Lys after the initiator L-methionine is cleaved. When the terminal amino acid is L-proline, the enzyme catalyses two successive methylations of its α-amino group. When the first amino acid is either L-alanine or L-serine, the enzyme catalyses three successive methylations. The Pro-Lys in positions 2-3 cannot be exchanged for other amino acids [3796, 3551].

References: [3796, 3551]

[EC 2.1.1.244 created 2012]

EC 2.1.1.245

Accepted name: 5-methyltetrahydrosarcinapterin:corrinoid/iron-sulfur protein *Co*-methyltransferase

Reaction: a [methyl-Co(III) corrinoid Fe-S protein] + tetrahydrosarcinapterin = a [Co(I) corrinoid Fe-S protein] + 5-methyltetrahydrosarcinapterin

Other name(s): *cdhD* (gene name); *cdhE* (gene name)

Systematic name: 5-methyltetrahydrosarcinapterin:corrinoid/iron-sulfur protein methyltransferase

Comments: Catalyses the transfer of a methyl group from the cobamide cofactor of a corrinoid/Fe-S protein to the N5 group of tetrahydrosarcinapterin. Forms, together with EC 1.2.7.4, carbon-monoxide dehydrogenase (ferredoxin) and EC 2.3.1.169, CO-methylating acetyl-CoA synthase, the acetyl-CoA decarbonylase/synthase complex that catalyses the demethylation of acetyl-CoA in a reaction that also forms CO$_2$. This reaction is a key step in methanogenesis from acetate.

References: [2172, 1124]

[EC 2.1.1.245 created 2012]

EC 2.1.1.246

Accepted name: [methyl-Co(III) methanol-specific corrinoid protein]:coenzyme M methyltransferase

Reaction: a [methyl-Co(III) methanol-specific corrinoid protein] + CoM = methyl-CoM + a [Co(I) methanol-specific corrinoid protein]

Other name(s): methyltransferase 2 (ambiguous); *mtaA* (gene name)

Systematic name: methylated methanol-specific corrinoid protein:CoM methyltransferase

Comments: The enzyme, which is involved in methanogenesis from methanol, catalyses the transfer of a methyl group from a corrinoid protein (see EC 2.1.1.90, methanol—corrinoid protein *Co*-methyltransferase), where it is bound to the cobalt cofactor, to CoM, forming the substrate for EC 2.8.4.1, coenzyme-B sulfoethylthiotransferase, the enzyme that catalyses the final step in methanogenesis. Free methyl-cob(I)alamin can substitute for the corrinoid protein *in vitro* [3040].

References: [1884, 1225, 3039, 3038, 3040]

[EC 2.1.1.246 created 2012]

EC 2.1.1.247

Accepted name: [methyl-Co(III) methylamine-specific corrinoid protein]:coenzyme M methyltransferase

Reaction: a [methyl-Co(III) methylamine-specific corrinoid protein] + CoM = methyl-CoM + a [Co(I) methylamine-specific corrinoid protein]

Other name(s): methyltransferase 2 (ambiguous); MT2 (ambiguous); MT$_2$-A; *mtbA* (gene name)

Systematic name: methylated monomethylamine-specific corrinoid protein:CoM methyltransferase

Comments: Contains zinc [1884]. The enzyme, which is involved in methanogenesis from mono-, di-, and trimethylamine, catalyses the transfer of a methyl group bound to the cobalt cofactor of several corrinoid proteins (mono-, di-, and trimethylamine-specific corrinoid proteins, *cf.* EC 2.1.1.248, methylamine—corrinoid protein *Co*-methyltransferase, EC 2.1.1.249, dimethylamine—corrinoid protein *Co*-methyltransferase, and EC 2.1.1.250, trimethylamine—corrinoid protein *Co*-methyltransferase) to CoM, forming the substrate for EC 2.8.4.1, coenzyme-B sulfoethylthiotransferase, the enzyme that catalyses the final step in methanogenesis.

References: [428, 1884, 891, 430, 890]

[EC 2.1.1.247 created 2012]

EC 2.1.1.248

Accepted name: methylamine—corrinoid protein *Co*-methyltransferase

Reaction: methylamine + a [Co(I) methylamine-specific corrinoid protein] = a [methyl-Co(III) methylamine-specific corrinoid protein] + NH$_3$

Other name(s): *mtmB* (gene name); monomethylamine methyltransferase

Systematic name: monomethylamine:5-hydroxybenzimidazolylcobamide *Co*-methyltransferase

Comments: The enzyme, which catalyses the transfer of a methyl group from methylamine to a methylamine-specific corrinoid protein (MtmC), is involved in methanogenesis from methylamine. The enzyme contains the unusual amino acid pyrrolysine [1798]. Methylation of the corrinoid protein requires the central cobalt to be in the Co(I) state. During methylation the cobalt is oxidized to the Co(III) state. The methylated corrinoid protein is substrate for EC 2.1.1.247, methylated methylamine-specific corrinoid protein:coenzyme M methyltransferase.

References: [429, 430, 1798]

[EC 2.1.1.248 created 2012]

EC 2.1.1.249

Accepted name: dimethylamine—corrinoid protein *Co*-methyltransferase

Reaction: dimethylamine + a [Co(I) dimethylamine-specific corrinoid protein] = a [methyl-Co(III) dimethylamine-specific corrinoid protein] + methylamine

Other name(s): *mtbB* (gene name); dimethylamine methyltransferase

Systematic name: dimethylamine:5-hydroxybenzimidazolylcobamide *Co*-methyltransferase

Comments: The enzyme, which catalyses the transfer of a methyl group from dimethylamine to a dimethylamine-specific corrinoid protein (MtbC), is involved in methanogenesis from dimethylamine. The enzyme contains the unusual amino acid pyrrolysine [1798]. Methylation of the corrinoid protein requires the central cobalt to be in the Co(I) state. During methylation the cobalt is oxidized to the Co(III) state. The methylated corrinoid protein is substrate for EC 2.1.1.247, methylated methylamine-specific corrinoid protein:coenzyme M methyltransferase.

References: [3782, 890, 1798]

[EC 2.1.1.249 created 2012]

EC 2.1.1.250

Accepted name: trimethylamine—corrinoid protein *Co*-methyltransferase

Reaction: trimethylamine + a [Co(I) trimethylamine-specific corrinoid protein] = a [methyl-Co(III) trimethylamine-specific corrinoid protein] + dimethylamine

Other name(s): *mttB* (gene name); trimethylamine methyltransferase

Systematic name: trimethylamine:5-hydroxybenzimidazolylcobamide *Co*-methyltransferase

Comments: The enzyme, which catalyses the transfer of a methyl group from trimethylamine to a trimethylamine-specific corrinoid protein (MttC), is involved in methanogenesis from trimethylamine. The enzyme contains the unusual amino acid pyrrolysine [1798]. Methylation of the corrinoid protein requires the central cobalt to be in the Co(I) state. During methylation the cobalt is oxidized to the Co(III) state. The methylated corrinoid protein is substrate for EC 2.1.1.247, methylated methylamine-specific corrinoid protein:coenzyme M methyltransferase.

References: [891, 1798]

[EC 2.1.1.250 created 2012]

EC 2.1.1.251

Accepted name: methylated-thiol—coenzyme M methyltransferase

Reaction: methanethiol + CoM = methyl-CoM + hydrogen sulfide (overall reaction)
(1a) methanethiol + a [Co(I) methylated-thiol-specific corrinoid protein] = a [methyl-Co(III) methylated-thiol-specific corrinoid protein] + hydrogen sulfide
(1b) a [methyl-Co(III) methylated-thiol-specific corrinoid protein] + CoM = methyl-CoM + a [Co(I) methylated-thiol-specific corrinoid protein]

Other name(s): *mtsA* (gene name)

Systematic name: methylated-thiol:CoM methyltransferase

Comments: The enzyme, which is involved in methanogenesis from methylated thiols, such as methane thiol, dimethyl sulfide, and 3-*S*-methylmercaptopropionate, catalyses two successive steps - the transfer of a methyl group from the substrate to the cobalt cofactor of a methylated-thiol-specific corrinoid protein (MtsB), and the subsequent transfer of the methyl group from the corrinoid protein to CoM. With most other methanogenesis substrates this process is carried out by two different enzymes (for example, EC 2.1.1.90, methanol—corrinoid protein *Co*-methyltransferase, and EC 2.1.1.246, methylated methanol-specific corrinoid protein:coenzyme M methyltransferase). The cobalt is oxidized during methylation from the Co(I) state to the Co(III) state, and is reduced back to the Co(I) form during demethylation.

References: [2639, 3458, 3459]

[EC 2.1.1.251 created 2012]

EC 2.1.1.252

Accepted name: tetramethylammonium—corrinoid protein *Co*-methyltransferase

Reaction: tetramethylammonium + a [Co(I) tetramethylammonium-specific corrinoid protein] = a [methyl-Co(III) tetramethylammonium-specific corrinoid protein] + trimethylamine

Other name(s): *mtqB* (gene name); tetramethylammonium methyltransferase

Systematic name: tetramethylammonium:5-hydroxybenzimidazolylcobamide *Co*-methyltransferase

Comments: The enzyme, which catalyses the transfer of a methyl group from tetramethylammonium to a tetramethylammonium-specific corrinoid protein (MtqC), is involved in methanogenesis from tetramethylammonium. Methylation of the corrinoid protein requires the central cobalt to be in the Co(I) state. During methylation the cobalt is oxidized to the Co(III) state. The methylated corrinoid protein is substrate for EC 2.1.1.253, methylated tetramethylammonium-specific corrinoid protein:coenzyme M methyltransferase.

References: [117]

[EC 2.1.1.252 created 2012]

EC 2.1.1.253

Accepted name: [methyl-Co(III) tetramethylammonium-specific corrinoid protein]:coenzyme M methyltransferase

Reaction: a [methyl-Co(III) tetramethylammonium-specific corrinoid protein] + CoM = methyl-CoM + a [Co(I) tetramethylammonium-specific corrinoid protein]

Other name(s): methyltransferase 2 (ambiguous); *mtqA* (gene name)

Systematic name: methylated tetramethylammonium-specific corrinoid protein:CoM methyltransferase

Comments: The enzyme, which is involved in methanogenesis from tetramethylammonium, catalyses the transfer of a methyl group from a corrinoid protein (see EC 2.1.1.252, tetramethylammonium—corrinoid protein *Co*-methyltransferase), where it is bound to the cobalt cofactor, to CoM, forming the substrate for EC 2.8.4.1, coenzyme-B sulfoethylthiotransferase, the enzyme that catalyses the final step in methanogenesis.

References: [117]

[EC 2.1.1.253 created 2012]

EC 2.1.1.254

Accepted name: erythromycin $3''$-*O*-methyltransferase

Reaction: (1) *S*-adenosyl-L-methionine + erythromycin C = *S*-adenosyl-L-homocysteine + erythromycin A
(2) *S*-adenosyl-L-methionine + erythromycin D = *S*-adenosyl-L-homocysteine + erythromycin B

Other name(s): EryG

Systematic name: *S*-adenosyl-L-methionine:erythromycin C $3''$-*O*-methyltransferase

Comments: The enzyme methylates the 3 position of the mycarosyl moiety of erythromycin C, forming the most active form of the antibiotic, erythromycin A. It can also methylate the precursor erythromycin D, forming erythromycin B, which is then converted to erythromycin A by EC 1.14.13.154, erythromycin 12 hydroxylase.

References: [2644, 3384]

[EC 2.1.1.254 created 2012]

EC 2.1.1.255

Accepted name: geranyl diphosphate 2-*C*-methyltransferase

Reaction: *S*-adenosyl-L-methionine + geranyl diphosphate = *S*-adenosyl-L-homocysteine + (*E*)-2-methylgeranyl diphosphate

Other name(s): SCO7701; GPP methyltransferase; GPPMT; 2-methyl-GPP synthase; MGPPS; geranyl pyrophosphate methyltransferase

Systematic name: *S*-adenosyl-L-methionine:geranyl-diphosphate 2-*C*-methyltransferase

Comments: This enzyme, along with EC 4.2.3.118, 2-methylisoborneol synthase, produces 2-methylisoborneol, an odiferous compound produced by soil microorganisms with a strong earthy/musty odour.

References: [3747, 108, 1749, 1059]

[EC 2.1.1.255 created 2012]

EC 2.1.1.256

Accepted name: tRNA (guanine^6-N^2)-methyltransferase

Reaction: *S*-adenosyl-L-methionine + guanine^6 in tRNA = *S*-adenosyl-L-homocysteine + N^2-methylguanine^6 in tRNA

Other name(s): methyltransferase Trm14; m^{2}G^6 methyltransferase

Systematic name: *S*-adenosyl-L-methionine:tRNA (guanine^6-N^2)-methyltransferase

Comments: The enzyme specifically methylates guanine^6 at N^2 in tRNA.

References: [2219]

[EC 2.1.1.256 created 2012]

EC 2.1.1.257

Accepted name: tRNA (pseudouridine^{54}-N^1)-methyltransferase

Reaction: *S*-adenosyl-L-methionine + pseudouridine^{54} in tRNA = *S*-adenosyl-L-homocysteine + N^1-methylpseudouridine^{54} in tRNA

Other name(s): TrmY; m$^1\Psi$ methyltransferase

Systematic name: *S*-adenosyl-L-methionine:tRNA (pseudouridine^{54}-N^1)-methyltransferase

Comments: While this archaeal enzyme is specific for the 54 position and does not methylate pseudouridine at position 55, the presence of pseudouridine at position 55 is necessary for the efficient methylation of pseudouridine at position 54 [3910, 512].

References: [527, 3910, 512]

[EC 2.1.1.257 created 2012]

EC 2.1.1.258

Accepted name: 5-methyltetrahydrofolate:corrinoid/iron-sulfur protein *Co*-methyltransferase

Reaction: a [methyl-Co(III) corrinoid Fe-S protein] + tetrahydrofolate = a [Co(I) corrinoid Fe-S protein] + 5-methyltetrahydrofolate

Other name(s): *acsE* (gene name)

Systematic name: 5-methyltetrahydrofolate:corrinoid/iron-sulfur protein methyltransferase

Comments: Catalyses the transfer of a methyl group from the N^5 group of methyltetrahydrofolate to the 5-methoxybenzimidazolylcobamide cofactor of a corrinoid/Fe-S protein. Involved, together with EC 1.2.7.4, carbon-monoxide dehydrogenase (ferredoxin) and EC 2.3.1.169, CO-methylating acetyl-CoA synthase, in the reductive acetyl coenzyme A (Wood-Ljungdahl) pathway of autotrophic carbon fixation in various bacteria and archaea.

References: [2894, 763, 764]

[EC 2.1.1.258 created 2012]

EC 2.1.1.259

Accepted name: [fructose-bisphosphate aldolase]-lysine *N*-methyltransferase

Reaction: **3** *S*-adenosyl-L-methionine + [fructose-bisphosphate aldolase]-L-lysine = **3** *S*-adenosyl-L-homocysteine + [fructose-bisphosphate aldolase]-N^6,N^6,N^6-trimethyl-L-lysine

Other name(s): rubisco methyltransferase; ribulose-bisphosphate-carboxylase/oxygenase *N*-methyltransferase; ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit ε*N*-methyltransferase; *S*-adenosyl-L-methionine:[3-phospho-D-glycerate-carboxy-lyase (dimerizing)]-lysine 6-*N*-methyltransferase

Systematic name: *S*-adenosyl-L-methionine:[fructose-bisphosphate aldolase]-lysine N^6-methyltransferase

Comments: The enzyme methylates a conserved lysine in the C-terminal part of higher plant fructose-bisphosphate aldolase (EC 4.1.2.13). The enzyme from pea (*Pisum sativum*) also methylates Lys-14 in the large subunits of hexadecameric higher plant ribulose-bisphosphate-carboxylase (EC 4.1.1.39) [2261], but that from *Arabidopsis thaliana* does not.

References: [2098, 2261]

[EC 2.1.1.259 created 2012]

EC 2.1.1.260

Accepted name: rRNA small subunit pseudouridine methyltransferase Nep1

Reaction: *S*-adenosyl-L-methionine + pseudouridine^{1191} in yeast 18S rRNA = *S*-adenosyl-L-homocysteine + N^1-methylpseudouridine^{1191} in yeast 18S rRNA

Other name(s): Nep1; nucleolar essential protein 1

Systematic name: *S*-adenosyl-L-methionine:18S rRNA (pseudouridine^{1191}-N^1)-methyltransferase

Comments: This enzyme, which occurs in both prokaryotes and eukaryotes, recognizes specific pseudouridine residues (Ψ) in small subunits of ribosomal RNA based on the local RNA structure. It recognizes Ψ^{914} in 16S rRNA from the archaeon *Methanocaldococcus jannaschii*, Ψ^{1191} in yeast 18S rRNA, and Ψ^{1248} in human 18S rRNA.

References: [3482, 3911, 2232]

[EC 2.1.1.260 created 2012]

EC 2.1.1.261

Accepted name: 4-dimethylallyltryptophan *N*-methyltransferase

Reaction: *S*-adenosyl-L-methionine + 4-dimethylallyl-L-tryptophan = *S*-adenosyl-L-homocysteine + 4-dimethylallyl-L-abrine

Other name(s): *fgaMT* (gene name); *easF* (gene name)

Systematic name: *S*-adenosyl-L-methionine:4-(3-methylbut-2-enyl)-L-tryptophan *N*-methyltransferase

Comments: The enzyme catalyses a step in the pathway leading to biosynthesis of ergot alkaloids in certain fungi.

References: [2886]

[EC 2.1.1.261 created 2012]

EC 2.1.1.262

Accepted name: squalene methyltransferase

Reaction: **2** *S*-adenosyl-L-methionine + squalene = **2** *S*-adenosyl-L-homocysteine + 3,22-dimethyl-1,2,23,24-tetradehydro-2,3,22,23-tetrahydrosqualene (overall reaction)
(1a) *S*-adenosyl-L-methionine + squalene = *S*-adenosyl-L-homocysteine + 3-methyl-1,2-didehydro-2,3-dihydrosqualene
(1b) *S*-adenosyl-L-methionine + 3-methyl-1,2-didehydro-2,3-dihydrosqualene = *S*-adenosyl-L-homocysteine + 3,22-dimethyl-1,2,23,24-tetradehydro-2,3,22,23-tetrahydrosqualene

Other name(s): TMT-1; TMT-2

Systematic name: *S*-adenosyl-L-methionine:squalene *C*-methyltransferase

Comments: Two isoforms differing in their specificity were isolated from the green alga *Botryococcus braunii* BOT22. TMT-1 gave more of the dimethylated form whereas TMT2 gave more of the monomethylated form.

References: [2452]

[EC 2.1.1.262 created 2012]

EC 2.1.1.263

Accepted name: botryococcene *C*-methyltransferase

Reaction: **2** *S*-adenosyl-L-methionine + C_{30} botryococcene = **2** *S*-adenosyl-L-homocysteine + 3,20-dimethyl-1,2,21,22-tetradehydro-2,3,20,21-tetrahydrobotryococcene (overall reaction)
(1a) *S*-adenosyl-L-methionine + C_{30} botryococcene = *S*-adenosyl-L-homocysteine + 3-methyl-1,2-didehydro-2,3-dihydrobotryococcene
(1b) *S*-adenosyl-L-methionine + 3-methyl-1,2-didehydro-2,3-dihydrobotryococcene = *S*-adenosyl-L-homocysteine + 3,20-dimethyl-1,2,21,22-tetradehydro-2,3,20,21-tetrahydrobotryococcene
(2a) *S*-adenosyl-L-methionine + C_{30} botryococcene = *S*-adenosyl-L-homocysteine + 20-methyl-21,22-didehydro-20,21-dihydrobotryococcene
(2b) *S*-adenosyl-L-methionine + 20-methyl-21,22-didehydro-20,21-dihydrobotryococcene = *S*-adenosyl-L-homocysteine + 3,20-dimethyl-1,2,21,22-tetradehydro-2,3,20,21-tetrahydrobotryococcene

Other name(s): TMT-3

Systematic name: *S*-adenosyl-L-methionine:botryococcene *C*-methyltransferase

Comments: Isolated from the green alga *Botryococcus braunii* BOT22. Shows a very weak activity with squalene.

References: [2452]

[EC 2.1.1.263 created 2012]

EC 2.1.1.264

Accepted name: 23S rRNA (guanine^{2069}-N^7)-methyltransferase

Reaction: *S*-adenosyl-L-methionine + guanine^{2069} in 23S rRNA = *S*-adenosyl-L-homocysteine + N^7-methylguanine^{2069} in 23S rRNA

Other name(s): *rlmK* (gene name); 23S rRNA m^{7}G^{2069} methyltransferase

Systematic name: *S*-adenosyl-L-methionine:23S rRNA (guanine^{2069}-N^7)-methyltransferase

Comments: The enzyme specifically methylates guanine^{2069} at position N7 in 23S rRNA. In γ-proteobacteria the enzyme also catalyses EC 2.1.1.173, 23S rRNA (guanine^{2445}-N^2)-methyltransferase, while in β-proteobacteria the activities are carried out by separate proteins [1686]. The enzyme from the γ-proteobacterium *Escherichia coli* has RNA unwinding activity as well [1686].
References: [1686]

[EC 2.1.1.264 created 2012]

EC 2.1.1.265

Accepted name: tellurite methyltransferase
Reaction: *S*-adenosyl-L-methionine + tellurite = *S*-adenosyl-L-homocysteine + methanetelluronate
Other name(s): TehB
Systematic name: *S*-adenosyl-L-methionine:tellurite methyltransferase
Comments: The enzyme is involved in the detoxification of tellurite. It can also methylate selenite and selenium dioxide.
References: [2009, 557]

[EC 2.1.1.265 created 2012]

EC 2.1.1.266

Accepted name: 23S rRNA (adenine^{2030}-N^6)-methyltransferase
Reaction: *S*-adenosyl-L-methionine + adenine^{2030} in 23S rRNA = *S*-adenosyl-L-homocysteine + N^6-methyladenine^{2030} in 23S rRNA
Other name(s): YhiR protein; *rlmJ* (gene name); m^{6}A^{2030} methyltransferase
Systematic name: *S*-adenosyl-L-methionine:23S rRNA (adenine^{2030}-N^6)-methyltransferase
Comments: The recombinant RlmJ protein is most active in methylating deproteinized 23S ribosomal subunit, and does not methylate the completely assembled 50S subunits [1095].
References: [1095]

[EC 2.1.1.266 created 2013]

EC 2.1.1.267

Accepted name: flavonoid 3′,5′-methyltransferase
Reaction: (1) *S*-adenosyl-L-methionine + a 3′-hydroxyflavonoid = *S*-adenosyl-L-homocysteine + a 3′-methoxyflavonoid
(2) *S*-adenosyl-L-methionine + a 5′-hydroxy-3′-methoxyflavonoid = *S*-adenosyl-L-homocysteine + a 3′,5′-dimethoxyflavonoid
Other name(s): AOMT; CrOMT2
Systematic name: *S*-adenosyl-L-methionine:flavonoid 3′-*O*-methyltransferase
Comments: Isolated from *Vitis vinifera* (grape) [1404]. Most active with delphinidin 3-glucoside but also acts on cyanidin 3-glucoside, cyanidin, myricetin, quercetin and quercetin 3-glucoside. The enzyme from *Catharanthus roseus* was most active with myricetin [450].
References: [450, 1404]

[EC 2.1.1.267 created 2013, modified 2014]

EC 2.1.1.268

Accepted name: tRNA$^{\text{Thr}}$ (cytosine^{32}-N^3)-methyltransferase
Reaction: (1) *S*-adenosyl-L-methionine + cytosine^{32} in tRNA$^{\text{Thr}}$ = *S*-adenosyl-L-homocysteine + N^3-methylcytosine^{32} in tRNA$^{\text{Thr}}$
(2) *S*-adenosyl-L-methionine + cytosine^{32} in tRNA$^{\text{Ser}}$ = *S*-adenosyl-L-homocysteine + N^3-methylcytosine^{32} in tRNA$^{\text{Ser}}$
Other name(s): ABP140; Trm140p

Systematic name: *S*-adenosyl-L-methionine:tRNA^{Thr} (cytosine^{32}-N^3)-methyltransferase

Comments: The enzyme from *Saccharomyces cerevisiae* specifically methylates cytosine^{32} in tRNA^{Thr} and in tRNA^{Ser}.

References: [2489, 779]

[EC 2.1.1.268 created 2013]

EC 2.1.1.269

Accepted name: dimethylsulfoniopropionate demethylase

Reaction: *S*,*S*-dimethyl-β-propiothetin + tetrahydrofolate = 3-(methylsulfanyl)propanoate + 5-methyltetrahydrofolate

Other name(s): *dmdA* (gene name); dimethylsulfoniopropionate-dependent demethylase A

Systematic name: *S*,*S*-dimethyl-β-propiothetin:tetrahydrofolate *S*-methyltransferase

Comments: The enzyme from the marine bacteria *Pelagibacter ubique* and *Ruegeria pomeroyi* are specific towards *S*,*S*-dimethyl-β-propiothetin. They do not demethylate glycine-betaine [1499, 2862].

References: [1499, 2862, 3112]

[EC 2.1.1.269 created 2013]

EC 2.1.1.270

Accepted name: (+)-6a-hydroxymaackiain 3-*O*-methyltransferase

Reaction: *S*-adenosyl-L-methionine + (+)-6a-hydroxymaackiain = *S*-adenosyl-L-homocysteine + (+)-pisatin

Other name(s): HM3OMT; HMM2

Systematic name: *S*-adenosyl-L-methionine:(+)-6a-hydroxymaackiain 3-*O*-methyltransferase

Comments: The protein from the plant *Pisum sativum* (garden pea) methylates (+)-6a-hydroxymaackiain at the 3-position. It also methylates 2,7,4′-trihydroxyisoflavanone on the 4′-position (*cf.* EC 2.1.1.212, 2,7,4-trihydroxyisoflavanone 4-*O*-methyltransferase) with lower activity.

References: [2756, 3905, 1995, 35]

[EC 2.1.1.270 created 2013]

EC 2.1.1.271

Accepted name: cobalt-precorrin-4 methyltransferase

Reaction: *S*-adenosyl-L-methionine + cobalt-precorrin-4 = *S*-adenosyl-L-homocysteine + cobalt-precorrin-5A

Other name(s): CbiF

Systematic name: *S*-adenosyl-L-methionine:cobalt-precorrin-4 11-methyltransferase

Comments: Part of the anaerobic route to adenosylcobalamin.

References: [2826, 3109, 1556]

[EC 2.1.1.271 created 2013]

EC 2.1.1.272

Accepted name: cobalt-factor III methyltransferase

Reaction: *S*-adenosyl-L-methionine + cobalt-factor III + reduced acceptor = *S*-adenosyl-L-homocysteine + cobalt-precorrin-4 + acceptor

Other name(s): CbiH$_{60}$ (gene name)

Systematic name: *S*-adenosyl-L-methionine:cobalt-factor III 17-methyltransferase (ring contracting)

Comments: Isolated from *Bacillus megaterium*. The enzyme catalyses both methylation at C-17 and ring contraction. Contains a [4Fe-4S] cluster. It can also convert cobalt-precorrin-3 to cobalt-precorrin-4. The reductant may be thioredoxin.

References: [2301]

[EC 2.1.1.272 created 2013]

EC 2.1.1.273

Accepted name: benzoate *O*-methyltransferase

Reaction: *S*-adenosyl-L-methionine + benzoate = *S*-adenosyl-L-homocysteine + methyl benzoate

Other name(s): BAMT; *S*-adenosyl-L-methionine:benzoic acid carboxyl methyltransferase

Systematic name: *S*-adenosyl-L-methionine:benzoate *O*-methyltransferase

Comments: While the enzyme from the plant *Zea mays* is specific for benzoate [1747], the enzymes from *Arabidopsis* species and *Clarkia breweri* also catalyse the reaction of EC 2.1.1.274, salicylate 1-*O*-methyltransferase [2939, 522]. In snapdragon (*Antirrhinum majus*) two isoforms are found, one specific for benzoate [785, 2375] and one that is also active towards salicylate [2428]. The volatile product is an important scent compound in some flowering species [785].

References: [2939, 785, 2375, 2428, 522, 1747]

[EC 2.1.1.273 created 2013]

EC 2.1.1.274

Accepted name: salicylate 1-*O*-methyltransferase

Reaction: *S*-adenosyl-L-methionine + salicylate = *S*-adenosyl-L-homocysteine + methyl salicylate

Other name(s): SAMT; *S*-adenosyl-L-methionine:salicylic acid carboxyl methyltransferase; salicylate carboxymethyltransferase

Systematic name: *S*-adenosyl-L-methionine:salicylate 1-*O*-methyltransferase

Comments: The enzyme, which is found in flowering plants, also has the activity of EC 2.1.1.273, benzoate *O*-methyltransferase.

References: [2939, 2428, 522, 4088]

[EC 2.1.1.274 created 2013]

EC 2.1.1.275

Accepted name: gibberellin A_9 *O*-methyltransferase

Reaction: *S*-adenosyl-L-methionine + gibberellin A_9 = *S*-adenosyl-L-homocysteine + methyl gibberellin A_9

Other name(s): GAMT1

Systematic name: *S*-adenosyl-L-methionine:gibberellin A_9 *O*-methyltransferase

Comments: The enzyme also methylates gibberellins A_{20} (95%), A_3 (80%), A_4 (69%) and A_{34} (46%) with significant activity.

References: [3650]

[EC 2.1.1.275 created 2013]

EC 2.1.1.276

Accepted name: gibberellin A_4 carboxyl methyltransferase

Reaction: *S*-adenosyl-L-methionine + gibberellin A_4 = *S*-adenosyl-L-homocysteine + methyl gibberellin A_4

Other name(s): GAMT2; gibberellin A_4 *O*-methyltransferase

Systematic name: *S*-adenosyl-L-methionine:gibberellin A_4 *O*-methyltransferase

Comments: The enzyme also methylates gibberellins A_{34} (80%), A_9 (60%), and A_3 (45%) with significant activity.

References: [3650]

[EC 2.1.1.276 created 2013]

EC 2.1.1.277

Accepted name: anthranilate *O*-methyltransferase

Reaction: *S*-adenosyl-L-methionine + anthranilate = *S*-adenosyl-L-homocysteine + *O*-methyl anthranilate

Other name(s): AAMT

Systematic name: *S*-adenosyl-L-methionine:anthranilate *O*-methyltransferase

Comments: In the plant maize (*Zea mays*), the isoforms AAMT1 and AAMT2 are specific for anthranilate while AAMT3 also has the activity of EC 2.1.1.273, benzoate methyltransferase.
References: [1747]

[EC 2.1.1.277 created 2013]

EC 2.1.1.278

Accepted name: indole-3-acetate *O*-methyltransferase
Reaction: *S*-adenosyl-L-methionine + (indol-3-yl)acetate = *S*-adenosyl-L-homocysteine + methyl (indol-3-yl)acetate
Other name(s): IAA carboxylmethyltransferase; IAMT
Systematic name: *S*-adenosyl-L-methionine:(indol-3-yl)acetate *O*-methyltransferase
Comments: Binds Mg^{2+}. The enzyme is found in plants and is important for regulation of the plant hormone (indol-3-yl)acetate. The product, methyl (indol-3-yl)acetate is inactive as hormone [1956].
References: [4088, 1956, 4064]

[EC 2.1.1.278 created 2013]

EC 2.1.1.279

Accepted name: *trans*-anol *O*-methyltransferase
Reaction: (1) *S*-adenosyl-L-methionine + *trans*-anol = *S*-adenosyl-L-homocysteine + *trans*-anethole
(2) *S*-adenosyl-L-methionine + isoeugenol = *S*-adenosyl-L-homocysteine + isomethyleugenol
Other name(s): AIMT1; *S*-adenosyl-L-methionine:*t*-anol/isoeugenol *O*-methyltransferase; *t*-anol *O*-methyltransferase
Systematic name: *S*-adenosyl-L-methionine:*trans*-anol *O*-methyltransferase
Comments: The enzyme from anise (*Pimpinella anisum*) is highly specific for substrates in which the double bond in the propenyl side chain is located between C_7 and C_8, and, in contrast to EC 2.1.1.146, (iso)eugenol *O*-methyltransferase, does not have activity with eugenol or chavicol.
References: [1731]

[EC 2.1.1.279 created 2013]

EC 2.1.1.280

Accepted name: selenocysteine *Se*-methyltransferase
Reaction: *S*-methyl-L-methionine + L-selenocysteine = L-methionine + *Se*-methyl-L-selenocysteine
Other name(s): SMT
Systematic name: *S*-methyl-L-methionine:L-selenocysteine *Se*-methyltransferase
Comments: The enzyme uses *S*-adenosyl-L-methionine as methyl donor less actively than *S*-methyl-L-methionine. The enzyme from broccoli (*Brassica oleracea* var. *italica*) also has the activity of EC 2.1.1.10, homocysteine *S*-methyltransferase [2077].
References: [2440, 2441, 2076, 2077]

[EC 2.1.1.280 created 2013]

EC 2.1.1.281

Accepted name: phenylpyruvate C^3-methyltransferase
Reaction: *S*-adenosyl-L-methionine + 3-phenylpyruvate = *S*-adenosyl-L-homocysteine + (3*S*)-2-oxo-3-phenylbutanoate
Other name(s): phenylpyruvate Cβ-methyltransferase; phenylpyruvate methyltransferase; *mppJ* (gene name)
Systematic name: *S*-adenosyl-L-methionine:2-oxo-3-phenylpropanoate C^3-methyltransferase
Comments: The enzyme from the bacterium *Streptomyces hygroscopicus* NRRL3085 is involved in synthesis of the nonproteinogenic amino acid (2*S*,3*S*)-β-methyl-phenylalanine, a building block of the antibiotic mannopeptimycin.
References: [1397]

[EC 2.1.1.281 created 2013]

EC 2.1.1.282

Accepted name: tRNA$^{\mathrm{Phe}}$ 7-[(3-amino-3-carboxypropyl)-4-demethylwyosine^{37}-N^4]-methyltransferase

Reaction: *S*-adenosyl-L-methionine + 7-[(3*S*)-(3-amino-3-carboxypropyl)]-4-demethylwyosine^{37} in tRNA$^{\mathrm{Phe}}$ = *S*-adenosyl-L-homocysteine + 7-[(3*S*)-(3-amino-3-carboxypropyl)]wyosine^{37} in tRNA$^{\mathrm{Phe}}$

Other name(s): TYW3 (gene name); tRNA-yW synthesizing enzyme-3

Systematic name: *S*-adenosyl-L-methionine:tRNA$^{\mathrm{Phe}}$ 7-[(3*S*)-(3-amino-3-carboxypropyl)-4-demethylwyosine-N^4]-methyltransferase

Comments: The enzyme is involved in the biosynthesis of hypermodified tricyclic bases found at position 37 of certain tRNAs. These modifications are important for translational reading-frame maintenance. The enzyme is found in all eukaryotes and in some archaea, but not in bacteria. The eukaryotic enzyme is involved in the biosynthesis of wybutosine.

References: [2488]

[EC 2.1.1.282 created 2013, modified 2014]

EC 2.1.1.283

Accepted name: emodin *O*-methyltransferase

Reaction: *S*-adenosyl-L-methionine + emodin = *S*-adenosyl-L-homocysteine + questin

Other name(s): EOMT

Systematic name: *S*-adenosyl-L-methionine:emodin 8-*O*-methyltransferase

Comments: The enzyme is involved in biosynthesis of the seco-anthraquinone (+)-geodin.

References: [534]

[EC 2.1.1.283 created 2013]

EC 2.1.1.284

Accepted name: 8-demethylnovobiocic acid C^8-methyltransferase

Reaction: *S*-adenosyl-L-methionine + 8-demethylnovobiocic acid = *S*-adenosyl-L-homocysteine + novobiocic acid

Other name(s): NovO

Systematic name: *S*-adenosyl-L-methionine:8-demethylnovobiocic acid C^8-methyltransferase

Comments: The enzyme is involved in the biosynthesis of the aminocoumarin antibiotic novobiocin.

References: [2591]

[EC 2.1.1.284 created 2013]

EC 2.1.1.285

Accepted name: demethyldecarbamoylnovobiocin *O*-methyltransferase

Reaction: *S*-adenosyl-L-methionine + demethyldecarbamoylnovobiocin = *S*-adenosyl-L-homocysteine + decarbamoylnovobiocin

Other name(s): NovP

Systematic name: *S*-adenosyl-L-methionine:demethyldecarbamoylnovobiocin 4$''$-*O*-methyltransferase

Comments: The enzyme is involved in the biosynthesis of the aminocoumarin antibiotic novobiocin.

References: [2234, 1014]

[EC 2.1.1.285 created 2013]

EC 2.1.1.286

Accepted name: 25S rRNA (adenine^{2142}-N^1)-methyltransferase

Reaction: *S*-adenosyl-L-methionine + adenine^{2142} in 25S rRNA = *S*-adenosyl-L-homocysteine + N^1-methyladenine^{2142} in 25S rRNA

Other name(s): BMT2 (gene name); 25S rRNA m^{1}A^{2142} methyltransferase

Systematic name: *S*-adenosyl-L-methionine:25S rRNA (adenine^{2142}-N^1)-methyltransferase

Comments: In the yeast *Saccharomyces cerevisiae* this methylation is important for resistance towards hydrogen peroxide and the antibiotic anisomycin.

References: [3158]

[EC 2.1.1.286 created 2013]

EC 2.1.1.287

Accepted name: 25S rRNA (adenine^{645}-N^1)-methyltransferase

Reaction: *S*-adenosyl-L-methionine + adenine^{645} in 25S rRNA = *S*-adenosyl-L-homocysteine + N^1-methyladenine^{645} in 25S rRNA

Other name(s): 25S rRNA m^{1}A^{645} methyltransferase; Rrp8

Systematic name: *S*-adenosyl-L-methionine:25S rRNA (adenine^{645}-N^1)-methyltransferase

Comments: The enzyme is found in eukaryotes. The adenine position refers to rRNA in the yeast *Saccharomyces cerevisiae*, in which the enzyme is important for ribosome biogenesis.

References: [2656]

[EC 2.1.1.287 created 2013]

EC 2.1.1.288

Accepted name: aklanonic acid methyltransferase

Reaction: *S*-adenosyl-L-methionine + aklanonate = *S*-adenosyl-L-homocysteine + methyl aklanonate

Other name(s): DauC; AAMT

Systematic name: *S*-adenosyl-L-methionine:aklanonate *O*-methyltransferase

Comments: The enzyme from the Gram-positive bacterium *Streptomyces* sp. C5 is involved in the biosynthesis of the anthracycline daunorubicin.

References: [731]

[EC 2.1.1.288 created 2013]

EC 2.1.1.289

Accepted name: cobalt-precorrin-7 (C^5)-methyltransferase

Reaction: cobalt-precorrin-7 + *S*-adenosyl-L-methionine = cobalt-precorrin-8 + *S*-adenosyl-L-homocysteine

Other name(s): CbiE

Systematic name: *S*-adenosyl-L-methionine:precorrin-7 C^5-methyltransferase

Comments: This enzyme catalyses the methylation at C-5 of cobalt-precorrin-7, a step in the anaerobic (early cobalt insertion) adenosylcobalamin biosynthesis pathway.

References: [3024, 2302]

[EC 2.1.1.289 created 2010]

EC 2.1.1.290

Accepted name: tRNA$^{\text{Phe}}$ [7-(3-amino-3-carboxypropyl)wyosine^{37}-*O*]-methyltransferase

Reaction: *S*-adenosyl-L-methionine + 7-[(3*S*)-3-amino-3-carboxypropyl]wyosine^{37} in tRNA$^{\text{Phe}}$ = *S*-adenosyl-L-homocysteine + 7-[(3*S*)-3-amino-3-(methoxycarbonyl)propyl]wyosine^{37} in tRNA$^{\text{Phe}}$

Other name(s): TYW4 (ambiguous); tRNA-yW synthesizing enzyme-4 (ambiguous)

Systematic name: *S*-adenosyl-L-methionine:tRNA$^{\text{Phe}}$ 7-[(3*S*)-3-amino-3-carboxypropyl]wyosine^{37}-*O*-methyltransferase

Comments: The enzyme is found only in eukaryotes, where it is involved in the biosynthesis of wybutosine, a hypermodified tricyclic base found at position 37 of certain tRNAs. The modification is important for translational reading-frame maintenance. In some species that produce hydroxywybutosine the enzyme uses 7-(2-hydroxy-3-amino-3-carboxypropyl)wyosine^{37} in tRNA$^{\mathrm{Phe}}$ as substrate. The enzyme also has the activity of EC 2.3.1.231, tRNA$^{\mathrm{Phe}}$ 7-[(3*S*)-4-methoxy-(3-amino-3-carboxypropyl)wyosine^{37}-*O*]-carbonyltransferase [3406].

References: [2488, 3406, 1597]

[EC 2.1.1.290 created 2013]

EC 2.1.1.291

Accepted name: (*R*,*S*)-reticuline 7-*O*-methyltransferase

Reaction: (1) *S*-adenosyl-L-methionine + (*S*)-reticuline = *S*-adenosyl-L-homocysteine + (*S*)-laudanine
(2) *S*-adenosyl-L-methionine + (*R*)-reticuline = *S*-adenosyl-L-homocysteine + (*R*)-laudanine

Systematic name: *S*-adenosyl-L-methionine:(*R*,*S*)-reticuline 7-*O*-methyltransferase

Comments: The enzyme from the plant *Papaver somniferum* (opium poppy) methylates (*S*)- and (*R*)-reticuline with equal efficiency and is involved in the biosynthesis of tetrahydrobenzylisoquinoline alkaloids.

References: [2587, 3804]

[EC 2.1.1.291 created 2013]

EC 2.1.1.292

Accepted name: carminomycin 4-*O*-methyltransferase

Reaction: *S*-adenosyl-L-methionine + carminomycin = *S*-adenosyl-L-homocysteine + daunorubicin

Other name(s): DnrK; DauK

Systematic name: *S*-adenosyl-L-methionine:carminomycin 4-*O*-methyltransferase

Comments: The enzymes from the Gram-positive bacteria *Streptomyces* sp. C5 and *Streptomyces peucetius* are involved in the biosynthesis of the anthracycline daunorubicin. *In vitro* the enzyme from *Streptomyces* sp. C5 also catalyses the 4-*O*-methylation of 13-dihydrocarminomycin, rhodomycin D and 10-carboxy-13-deoxycarminomycin [730].

References: [598, 1501, 730]

[EC 2.1.1.292 created 2013]

EC 2.1.1.293

Accepted name: 6-hydroxytryprostatin B *O*-methyltransferase

Reaction: *S*-adenosyl-L-methionine + 6-hydroxytryprostatin B = *S*-adenosyl-L-homocysteine + tryprostatin A

Other name(s): *ftmD* (gene name)

Systematic name: *S*-adenosyl-L-methionine:6-hydroxytryprostatin B *O*-methyltransferase

Comments: Involved in the biosynthetic pathways of several indole alkaloids such as tryprostatins, fumitremorgins and verruculogen.

References: [1601]

[EC 2.1.1.293 created 2013]

EC 2.1.1.294

Accepted name: 3-*O*-phospho-polymannosyl GlcNAc-diphospho-*ditrans*,*octacis*-undecaprenol 3-phosphomethyltransferase

Reaction: *S*-adenosyl-L-methionine + 3-*O*-phospho-α-D-Man-(1→2)-α-D-Man-(1→2)-[α-D-Man-(1→3)-α-D-Man-(1→3)-α-D-Man-(1→2)-α-D-Man-(1→2)]$_n$-α-D-Man-(1→3)-α-D-Man-(1→3)-α-D-Man-(1→3)-α-D-GlcNAc-diphospho-*ditrans*,*octacis*-undecaprenol = *S*-adenosyl-L-homocysteine + 3-*O*-methylphospho-α-D-Man-(1→2)-α-D-Man-(1→2)-[α-D-Man-(1→3)-α-D-Man-(1→3)-α-D-Man-(1→2)-α-D-Man-(1→2)]$_n$-α-D-Man-(1→3)-α-D-Man-(1→3)-α-D-Man-(1→3)-α-D-GlcNAc-diphospho-*ditrans*,*octacis*-undecaprenol

Other name(s): WbdD; *S*-adenosyl-L-methionine:3-*O*-phospho-α-D-Man-(1→2)-α-D-Man-(1→2)-α-D-Man-(1→3)-α-D-Man-(1→3)-[α-D-Man-(1→2)-α-D-Man-(1→2)-α-D-Man-(1→3)-α-D-Man-(1→3)]$_n$-α-D-Man-(1→3)-α-D-Man-(1→3)-α-D-GlcNAc-α-diphospho-*ditrans*,*octacis*-undecaprenol 3-phospho-methyltransferase

Systematic name: *S*-adenosyl-L-methionine:3-*O*-phospho-α-D-Man-(1→2)-α-D-Man-(1→2)-[α-D-Man-(1→3)-α-D-Man-(1→3)-α-D-Man-(1→2)-α-D-Man-(1→2)]$_n$-α-D-Man-(1→3)-α-D-Man-(1→3)-α-D-Man-(1→3)-α-D-GlcNAc-diphospho-*ditrans*,*octacis*-undecaprenol 3-phospho-methyltransferase

Comments: The enzyme is involved in the biosynthesis of the polymannose O-polysaccharide in the outer leaflet of the membrane of *Escherichia coli* serotype O9a. O-Polysaccharide structures vary extensively because of differences in the number and type of sugars in the repeat unit. The dual kinase/methylase WbdD also catalyses the preceding phosphorylation of α-D-Man-(1→2)-α-D-Man-(1→2)-[α-D-Man-(1→3)-α-D-Man-(1→3)-α-D-Man-(1→2)-α-D-Man-(1→2)]$_n$-α-D-Man-(1→3)-α-D-Man-(1→3)-α-D-Man-(1→3)-α-D-GlcNAc-diphospho-*ditrans*,*octacis*-undecaprenol (*cf.* EC 2.7.1.181, polymannosyl GlcNAc-diphospho-*ditrans*,*octacis*-undecaprenol kinase).

References: [574, 575, 576, 1986]

[EC 2.1.1.294 created 2014, modified 2018]

EC 2.1.1.295

Accepted name: 2-methyl-6-phytyl-1,4-hydroquinone methyltransferase

Reaction: (1) *S*-adenosyl-L-methionine + 2-methyl-6-phytylbenzene-1,4-diol = *S*-adenosyl-L-homocysteine + 2,3-dimethyl-6-phytylbenzene-1,4-diol

(2) *S*-adenosyl-L-methionine + 2-methyl-6-*all-trans*-nonaprenylbenzene-1,4-diol = *S*-adenosyl-L-homocysteine + plastoquinol

(3) *S*-adenosyl-L-methionine + 6-geranylgeranyl-2-methylbenzene-1,4-diol = *S*-adenosyl-L-homocysteine + 6-geranylgeranyl-2,3-dimethylbenzene-1,4-diol

Other name(s): VTE3 (gene name); 2-methyl-6-solanyl-1,4-hydroquinone methyltransferase; MPBQ/MSBQ methyltransferase; MPBQ/MSBQ MT

Systematic name: *S*-adenosyl-L-methionine:2-methyl-6-phytyl-1,4-benzoquinol *C*-3-methyltransferase

Comments: Involved in the biosynthesis of plastoquinol, as well as vitamin E (tocopherols and tocotrienols).

References: [3204, 535, 811]

[EC 2.1.1.295 created 2014]

EC 2.1.1.296

Accepted name: methyltransferase cap2

Reaction: *S*-adenosyl-L-methionine + a 5′-(N^7-methyl 5′-triphosphoguanosine)-(2′-*O*-methyl-purine-ribonucleotide)-(ribonucleotide)-[mRNA] = *S*-adenosyl-L-homocysteine + a 5′-(N^7-methyl 5′-triphosphoguanosine)-(2′-*O*-methyl-purine-ribonucleotide)-(2′-*O*-methyl-ribonucleotide)-[mRNA]

Other name(s): MTR2; cap2-MTase; mRNA (nucleoside-2′-*O*)-methyltransferase (ambiguous)

Systematic name: *S*-adenosyl-L-methionine:5′-(N^7-methyl 5′-triphosphoguanosine)-(2′-*O*-methyl-purine-ribonucleotide)-ribonucleotide-[mRNA] 2′-*O*-methyltransferase

Comments: The enzyme, found in higher eukaryotes including insects and vertebrates, and their viruses, methylates the ribose of the ribonucleotide at the second transcribed position of mRNAs and snRNAs. This methylation event is known as cap2. The human enzyme can also methylate mRNA molecules where the upstream purine ribonucleotide is not methylated (see EC 2.1.1.57, methyltransferase cap1), but with lower efficiency [3823].

References: [107, 3823]

[EC 2.1.1.296 created 2014]

EC 2.1.1.297

Accepted name: peptide chain release factor N^5-glutamine methyltransferase

Reaction: *S*-adenosyl-L-methionine + [peptide chain release factor 1 or 2]-L-glutamine = *S*-adenosyl-L-homocysteine + [peptide chain release factor 1 or 2]-N^5-methyl-L-glutamine

Other name(s): N^5-glutamine *S*-adenosyl-L-methionine dependent methyltransferase; N^5-glutamine MTase; HemK; PrmC

Systematic name: *S*-adenosyl-L-methionine:[peptide chain release factor 1 or 2]-L-glutamine (N^5-glutamine)-methyltransferase

Comments: Modifies the glutamine residue in the universally conserved glycylglycylglutamine (GGQ) motif of peptide chain release factor, resulting in almost complete loss of release activity.

References: [2399, 1315, 3107, 3995, 3969, 2613]

[EC 2.1.1.297 created 2014]

EC 2.1.1.298

Accepted name: ribosomal protein L3 N^5-glutamine methyltransferase

Reaction: *S*-adenosyl-L-methionine + [ribosomal protein L3]-L-glutamine = *S*-adenosyl-L-homocysteine + [ribosomal protein L3]-N^5-methyl-L-glutamine

Other name(s): YfcB; PrmB

Systematic name: *S*-adenosyl-L-methionine:[ribosomal protein L3]-L-glutamine (N^5-glutamine)-methyltransferase

Comments: Modifies the glutamine residue in the glycylglycylglutamine (GGQ) motif of ribosomal protein L3 (Gln^{150} in the protein from the bacterium *Escherichia coli*). The enzyme does not act on peptide chain release factor 1 or 2.

References: [1315]

[EC 2.1.1.298 created 2014]

EC 2.1.1.299

Accepted name: protein N-terminal monomethyltransferase

Reaction: *S*-adenosyl-L-methionine + N-terminal-(A,P,S)PK-[protein] = *S*-adenosyl-L-homocysteine + N-terminal-*N*-methyl-*N*-(A,P,S)PK-[protein]

Other name(s): NRMT2 (gene name); METTL11B (gene name); N-terminal monomethylase

Systematic name: *S*-adenosyl-L-methionine:N-terminal-(A,P,S)PK-[protein] monomethyltransferase

Comments: This enzyme methylates the N-terminus of target proteins containing the N-terminal motif [Ala/Pro/Ser]-Pro-Lys after the initiator L-methionine is cleaved. In contrast to EC 2.1.1.244, protein N-terminal methyltransferase, the protein only adds one methyl group to the N-terminal.

References: [2676]

[EC 2.1.1.299 created 2014]

EC 2.1.1.300

Accepted name: pavine *N*-methyltransferase

Reaction: *S*-adenosyl-L-methionine + (±)-pavine = *S*-adenosyl-L-homocysteine + *N*-methylpavine

Other name(s): PavNMT

Systematic name: *S*-adenosyl-L-methionine:(±)-pavine *N*-methyltransferase

Comments: The enzyme, isolated from the plant *Thalictrum flavum*, also methylates (*R*,*S*)-stylopine and (*S*)-scoulerine (11%) with lower activity (14% and 11%, respectively).

References: [1488, 1984]

[EC 2.1.1.300 created 2014]

EC 2.1.1.301

Accepted name: cypemycin N-terminal methyltransferase

Reaction: **2** *S*-adenosyl-L-methionine + N-terminal L-alanine-[cypemycin] = **2** *S*-adenosyl-L-homocysteine + N-terminal *N*,*N*-dimethyl-L-alanine-[cypemycin]

Other name(s): CypM

Systematic name: *S*-adenosyl-L-methionine:N-terminal L-alanine-[cypemycin] N-methyltransferase

Comments: The enzyme, isolated from the bacterium *Streptomyces* sp. OH-4156, can methylate a variety of linear oligopeptides, cyclic peptides such as nisin and haloduracin, and the ε-amino group of lysine [4045]. Cypemycin is a peptide antibiotic, a member of the linaridins, a class of posttranslationally modified ribosomally synthesized peptides.

References: [570, 4045]

[EC 2.1.1.301 created 2014]

EC 2.1.1.302

Accepted name: 3-hydroxy-5-methyl-1-naphthoate 3-*O*-methyltransferase

Reaction: *S*-adenosyl-L-methionine + 3-hydroxy-5-methyl-1-naphthoate = *S*-adenosyl-L-homocysteine + 3-methoxy-5-methyl-1-naphthoate

Other name(s): AziB2

Systematic name: *S*-adenosyl-L-methionine:3-hydroxy-5-methyl-1-naphthoate 3-*O*-methyltransferase

Comments: The enzyme from the bacterium *Streptomyces sahachiroi* is involved in the biosynthesis of 3-methoxy-5-methyl-1-naphthoate, a component of of the the antitumor antibiotic azinomycin B.

References: [738]

[EC 2.1.1.302 created 2014]

EC 2.1.1.303

Accepted name: 2,7-dihydroxy-5-methyl-1-naphthoate 7-*O*-methyltransferase

Reaction: *S*-adenosyl-L-methionine + 2,7-dihydroxy-5-methyl-1-naphthoate = *S*-adenosyl-L-homocysteine + 2-hydroxy-7-methoxy-5-methyl-1-naphthoate

Other name(s): NcsB1; neocarzinostatin *O*-methyltransferase

Systematic name: *S*-adenosyl-L-methionine:2,7-dihydroxy-5-methyl-1-naphthoate 7-*O*-methyltransferase

Comments: The enzyme from the bacterium *Streptomyces carzinostaticus* is involved in the biosynthesis of 2-hydroxy-7-methoxy-5-methyl-1-naphthoate. This compound is part of the enediyne chromophore of the antitumor antibiotic neocarzinostatin. *In vivo* the enzyme catalyses the regiospecific methylation at the 7-hydroxy group of its native substrate 2,7-dihydroxy-5-methyl-1-naphthoate. *In vitro* it also recognizes other dihydroxynaphthoic acids and catalyses their regiospecific *O*-methylation.

References: [2073, 606]

[EC 2.1.1.303 created 2014]

EC 2.1.1.304

Accepted name: L-tyrosine C^3-methyltransferase

Reaction: *S*-adenosyl-L-methionine + L-tyrosine = *S*-adenosyl-L-homocysteine + 3-methyl-L-tyrosine

Other name(s): SfmM2; SacF

Systematic name: *S*-adenosyl-L-methionine:L-tyrosine C^3-methyltransferase

Comments: The enzyme from the bacterium *Streptomyces lavendulae* is involved in biosynthesis of saframycin A, a potent antitumor antibiotic that belongs to the tetrahydroisoquinoline family.

References: [3466]

[EC 2.1.1.304 created 2014]

EC 2.1.1.305

Accepted name: 8-demethyl-8-α-L-rhamnosyltetracenomycin-C $2'$-*O*-methyltransferase

Reaction: *S*-adenosyl-L-methionine + 8-demethyl-8-α-L-rhamnosyltetracenomycin C = *S*-adenosyl-L-homocysteine + 8-demethyl-8-(2-*O*-methyl-α-L-rhamnosyl)tetracenomycin C

Other name(s): ElmMI

Systematic name: *S*-adenosyl-L-methionine:8-demethyl-8-α-L-rhamnosyltetracenomycin-C 2′-*O*-methyltransferase

Comments: The enzyme from the bacterium *Streptomyces olivaceus* is involved in the biosynthesis of the polyketide elloramycin.

References: [2635]

[EC 2.1.1.305 created 2014]

EC 2.1.1.306

Accepted name: 8-demethyl-8-(2-methoxy-α-L-rhamnosyl)tetracenomycin-C 3′-*O*-methyltransferase

Reaction: *S*-adenosyl-L-methionine + 8-demethyl-8-(2-*O*-methyl-α-L-rhamnosyl)tetracenomycin C = *S*-adenosyl-L-homocysteine + 8-demethyl-8-(2,3-di-*O*-methyl-α-L-rhamnosyl)tetracenomycin C

Other name(s): ElmMII

Systematic name: *S*-adenosyl-L-methionine:8-demethyl-8-(2-methoxy-α-L-rhamnosyl)tetracenomycin-C 3′-*O*-methyltransferase

Comments: The enzyme from the bacterium *Streptomyces olivaceus* is involved in the biosynthesis of the polyketide elloramycin.

References: [2635]

[EC 2.1.1.306 created 2014]

EC 2.1.1.307

Accepted name: 8-demethyl-8-(2,3-dimethoxy-α-L-rhamnosyl)tetracenomycin-C 4′-*O*-methyltransferase

Reaction: *S*-adenosyl-L-methionine + 8-demethyl-8-(2,3-di-*O*-methyl-α-L-rhamnosyl)tetracenomycin C = *S*-adenosyl-L-homocysteine + 8-demethyl-8-(2,3,4-tri-*O*-methyl-α-L-rhamnosyl)tetracenomycin C

Other name(s): ElmMIII

Systematic name: *S*-adenosyl-L-methionine:8-demethyl-8-(2,3-di-*O*-methoxy-α-L-rhamnosyl)tetracenomycin-C 4′-*O*-methyltransferase

Comments: The enzyme from the bacterium *Streptomyces olivaceus* is involved in the biosynthesis of the polyketide elloramycin.

References: [2635]

[EC 2.1.1.307 created 2014]

EC 2.1.1.308

Accepted name: 2-hydroxyethylphosphonate methyltransferase

Reaction: *S*-adenosyl-L-methionine + methylcob(III)alamin + 2-hydroxyethylphosphonate = 5′-deoxyadenosine + L-methionine + cob(III)alamin + (2*S*)-2-hydroxypropylphosphonate

Other name(s): Fom3

Systematic name: *S*-adenosyl-L-methionine:methylcob(III)alamin:2-hydroxyethylphosphonate methyltransferase

Comments: Requires cobalamin. The enzyme, isolated from the bacterium *Streptomyces wedmorensis*, is a member of the 'AdoMet radical' (radical SAM) family. Involved in fosfomycin biosynthesis.

References: [3894, 60]

[EC 2.1.1.308 created 2014]

EC 2.1.1.309

Accepted name: 18S rRNA (guanine^{1575}-N^7)-methyltransferase

Reaction: *S*-adenosyl-L-methionine + guanine^{1575} in 18S rRNA = *S*-adenosyl-L-homocysteine + N^7-methylguanine^{1575} in 18S rRNA

Other name(s): 18S rRNA methylase Bud23; BUD23 (gene name)

Systematic name: *S*-adenosyl-L-methionine:18S rRNA (guanine^{1575}-N^7)-methyltransferase

Comments: The enzyme, found in eukaryotes, is involved in pre-rRNA processing. The numbering corresponds to the enzyme from the yeast *Saccharomyces cerevisiae* [3832].

References: [3832]

[EC 2.1.1.309 created 2014]

EC 2.1.1.310

Accepted name: 25S rRNA (cytosine^{2870}-C^{5})-methyltransferase

Reaction: *S*-adenosyl-L-methionine + cytosine^{2870} in 25S rRNA = *S*-adenosyl-L-homocysteine + 5-methylcytosine^{2870} in 25S rRNA

Other name(s): NOP2 (gene name)

Systematic name: *S*-adenosyl-L-methionine:25S rRNA (cytosine^{2870}-C^{5})-methyltransferase

Comments: The enzyme, found in eukaryotes, is specific for cytosine^{2870} of the 25S ribosomal RNA. The numbering corresponds to the enzyme from the yeast *Saccharomyces cerevisiae* [3160].

References: [3160]

[EC 2.1.1.310 created 2014]

EC 2.1.1.311

Accepted name: 25S rRNA (cytosine^{2278}-C^{5})-methyltransferase

Reaction: *S*-adenosyl-L-methionine + cytosine^{2278} in 25S rRNA = *S*-adenosyl-L-homocysteine + 5-methylcytosine^{2278} in 25S rRNA

Other name(s): RCM1 (gene name)

Systematic name: *S*-adenosyl-L-methionine:25S rRNA (cytosine^{2278}-C^{5})-methyltransferase

Comments: The enzyme, found in eukaryotes, is specific for 25*S* cytosine^{2278}. The numbering corresponds to the enzyme from the yeast *Saccharomyces cerevisiae* [3160].

References: [3160]

[EC 2.1.1.311 created 2014]

EC 2.1.1.312

Accepted name: 25S rRNA (uracil^{2843}-N^{3})-methyltransferase

Reaction: *S*-adenosyl-L-methionine + uracil^{2843} in 25S rRNA = *S*-adenosyl-L-homocysteine + N^{3}-methyluracil^{2843} in 25S rRNA

Other name(s): BMT6

Systematic name: *S*-adenosyl-L-methionine:tRNA (uracil^{2843}-N^{3})-methyltransferase

Comments: The enzyme, described from the yeast *Saccharomyces cerevisiae*, is involved in ribosome biogenesis.

References: [3159]

[EC 2.1.1.312 created 2014]

EC 2.1.1.313

Accepted name: 25S rRNA (uracil^{2634}-N^{3})-methyltransferase

Reaction: *S*-adenosyl-L-methionine + uracil^{2634} in 25S rRNA = *S*-adenosyl-L-homocysteine + N^{3}-methyluracil^{2634} in 25S rRNA

Other name(s): BMT5

Systematic name: *S*-adenosyl-L-methionine:tRNA (uracil^{2634}-N^{3})-methyltransferase

Comments: The enzyme, described from the yeast *Saccharomyces cerevisiae*, is involved in ribosome biogenesis.

References: [3159]

[EC 2.1.1.313 created 2014]

EC 2.1.1.314

Accepted name: diphthine methyl ester synthase

Reaction: **4** *S*-adenosyl-L-methionine + 2-[(3*S*)-3-carboxy-3-aminopropyl]-L-histidine-[translation elongation factor 2] = **4** *S*-adenosyl-L-homocysteine + diphthine methyl ester-[translation elongation factor 2]

Other name(s): *S*-adenosyl-L-methionine:elongation factor 2 methyltransferase (ambiguous); diphthine methyltransferase (ambiguous); Dph5 (ambiguous)
Systematic name: *S*-adenosyl-L-methionine:2-[(3*S*)-3-carboxy-3-aminopropyl]-L-histidine-[translation elongation factor 2] methyltransferase (diphthine methyl ester-[translation elongation factor 2]-forming)
Comments: This eukaryotic enzyme is part of the biosynthetic pathway of diphthamide. Different from the archaeal enzyme, which performs only 3 methylations, producing diphthine (*cf.* EC 2.1.1.98). The relevant histidine of elongation factor 2 is His^{715} in mammals and His^{699} in yeast. The order of the 4 methylations is not known.
References: [528, 2285, 1974]

[EC 2.1.1.314 created 2015]

EC 2.1.1.315

Accepted name: 27-*O*-demethylrifamycin SV methyltransferase
Reaction: *S*-adenosyl-L-methionine + 27-*O*-demethylrifamycin SV = *S*-adenosyl-L-homocysteine + rifamycin SV
Other name(s): AdoMet:27-*O*-demethylrifamycin SV methyltransferase
Systematic name: *S*-adenosyl-L-methionine:27-*O*-demethylrifamycin-SV 27-*O*-methyltransferase
Comments: The enzyme, characterized from the bacterium *Amycolatopsis mediterranei*, is involved in biosynthesis of the antitubercular drug rifamycin B.
References: [3928]

[EC 2.1.1.315 created 2015]

EC 2.1.1.316

Accepted name: mitomycin 6-*O*-methyltransferase
Reaction: (1) *S*-adenosyl-L-methionine + 6-demethylmitomycin A = *S*-adenosyl-L-homocysteine + mitomycin A
(2) *S*-adenosyl-L-methionine + 6-demethylmitomycin B = *S*-adenosyl-L-homocysteine + mitomycin B
Other name(s): MmcR; mitomycin 7-*O*-methyltransferase (incorrect); *S*-adenosyl-L-methionine:7-demethylmitomycin-A 7-*O*-methyltransferase (incorrect)
Systematic name: *S*-adenosyl-L-methionine:6-demethylmitomycin-A 6-*O*-methyltransferase
Comments: The enzyme, characterized from the bacterium *Streptomyces lavendulae*, is involved in the biosynthesis of the quinone-containing antibiotics mitomycin A and mitomycin B.
References: [1160, 3241]

[EC 2.1.1.316 created 2015]

EC 2.1.1.317

Accepted name: sphingolipid C^9-methyltransferase
Reaction: *S*-adenosyl-L-methionine + a (4*E*,8*E*)-sphinga-4,8-dienine ceramide = *S*-adenosyl-L-homocysteine + a 9-methyl-(4*E*,8*E*)-sphinga-4,8-dienine ceramide
Systematic name: *S*-adenosyl-L-methionine:(4*E*,8*E*)-sphinga-4,8-dienine ceramide *C*-methyltransferase
Comments: The enzyme, characterized from the fungi *Komagataella pastoris* and *Fusarium graminearum*, acts only on ceramides and has no activity with free sphingoid bases or glucosylceramides.
References: [3503, 2799]

[EC 2.1.1.317 created 2015]

EC 2.1.1.318

Accepted name: [trehalose-6-phosphate synthase]-L-cysteine *S*-methyltransferase
Reaction: *S*-adenosyl-L-methionine + [trehalose-6-phosphate synthase]-L-cysteine = *S*-adenosyl-L-homocysteine + [trehalose-6-phosphate synthase]-*S*-methyl-L-cysteine

Systematic name: *S*-adenosyl-L-methionine:[trehalose-6-phosphate synthase]-L-cysteine *S*-methyltransferase

Comments: The enzyme, characterized from the yeast *Saccharomyces cerevisiae*, enhances the activity of EC 2.4.1.15, trehalose-6-phosphate synthase, resulting in elevating the levels of trehalose in the cell and contributing to stationary phase survival. *In vitro* the enzyme performs *S*-methylation of L-cysteine residues of various protein substrates.

References: [3140]

[EC 2.1.1.318 created 2015]

EC 2.1.1.319

Accepted name: type I protein arginine methyltransferase

Reaction: **2** *S*-adenosyl-L-methionine + [protein]-L-arginine = **2** *S*-adenosyl-L-homocysteine + [protein]-N^{ω},N^{ω}-dimethyl-L-arginine (overall reaction)

(1a) *S*-adenosyl-L-methionine + [protein]-L-arginine = *S*-adenosyl-L-homocysteine + [protein]-N^{ω}-methyl-L-arginine

(1b) *S*-adenosyl-L-methionine + [protein]-N^{ω}-methyl-L-arginine = *S*-adenosyl-L-homocysteine + [protein]-N^{ω},N^{ω}-dimethyl-L-arginine

Other name(s): PRMT1 (gene name); PRMT2 (gene name); PRMT3 (gene name); PRMT4 (gene name); PRMT6 (gene name); PRMT8 (gene name); RMT1 (gene name); CARM1 (gene name)

Systematic name: *S*-adenosyl-L-methionine:[protein]-L-arginine *N*-methyltransferase ([protein]-N^{ω},N^{ω}-dimethyl-L-arginine-forming)

Comments: This eukaryotic enzyme catalyses the sequential dimethylation of one of the terminal guanidino nitrogen atoms in arginine residues, resulting in formation of asymmetric dimethylarginine residues. Some forms (e.g. PRMT1) have a very wide substrate specificity, while others (e.g. PRMT4 and PRMT6) are rather specific. The enzyme has a preference for methylating arginine residues that are flanked by one or more glycine residues [1024]. PRMT1 is responsible for the bulk (about 85%) of total protein arginine methylation activity in mammalian cells [3465]. *cf.* EC 2.1.1.320, type II protein arginine methyltransferase, EC 2.1.1.321, type III protein arginine methyltransferase, and EC 2.1.1.322, type IV protein arginine methyltransferase.

References: [1024, 3465, 3464, 947]

[EC 2.1.1.319 created 2015]

EC 2.1.1.320

Accepted name: type II protein arginine methyltransferase

Reaction: **2** *S*-adenosyl-L-methionine + [protein]-L-arginine = **2** *S*-adenosyl-L-homocysteine + [protein]-N^{ω},$N^{\omega\prime}$-dimethyl-L-arginine (overall reaction)

(1a) *S*-adenosyl-L-methionine + [protein]-L-arginine = *S*-adenosyl-L-homocysteine + [protein]-N^{ω}-methyl-L-arginine

(1b) *S*-adenosyl-L-methionine + [protein]-N^{ω}-methyl-L-arginine = *S*-adenosyl-L-homocysteine + [protein]-N^{ω},$N^{\omega\prime}$-dimethyl-L-arginine

Other name(s): PRMT5 (gene name); PRMT9 (gene name)

Systematic name: *S*-adenosyl-L-methionine:[protein]-L-arginine *N*-methyltransferase ([protein]-N^{ω},$N^{\omega\prime}$-dimethyl-L-arginine-forming)

Comments: The enzyme catalyses the methylation of one of the terminal guanidino nitrogen atoms in arginine residues within proteins, forming monomethylarginine, followed by the methylation of the second terminal nitrogen atom to form a symmetrical dimethylarginine. The mammalian enzyme is active in both the nucleus and the cytoplasm, and plays a role in the assembly of snRNP core particles by methylating certain small nuclear ribonucleoproteins. *cf.* EC 2.1.1.319, type I protein arginine methyltransferase, EC 2.1.1.321, type III protein arginine methyltransferase, and EC 2.1.1.322, type IV protein arginine methyltransferase.

References: [378, 3762, 1839, 504, 94, 1192]

[EC 2.1.1.320 created 2015]

EC 2.1.1.321

Accepted name: type III protein arginine methyltransferase

Reaction: S-adenosyl-L-methionine + [protein]-L-arginine = S-adenosyl-L-homocysteine + [protein]-N^{ω}-methyl-L-arginine

Other name(s): PRMT7 (gene name)

Systematic name: S-adenosyl-L-methionine:[protein]-L-arginine N-methyltransferase ([protein]-N^{ω}-methyl-L-arginine-forming)

Comments: Type III protein arginine methyltransferases catalyse the single methylation of one of the terminal nitrogen atoms of the guanidino group in an L-arginine residue within a protein. Unlike type I and type II protein arginine methyltransferases, which also catalyse this reaction, type III enzymes do not methylate the substrate any further. *cf.* EC 2.1.1.319, type I protein arginine methyltransferase, EC 2.1.1.320, type II protein arginine methyltransferase, and EC 2.1.1.322, type IV protein arginine methyltransferase.

References: [2268, 1100, 888]

[EC 2.1.1.321 created 2015]

EC 2.1.1.322

Accepted name: type IV protein arginine methyltransferase

Reaction: S-adenosyl-L-methionine + [protein]-L-arginine = S-adenosyl-L-homocysteine + [protein]-N^5-methyl-L-arginine

Other name(s): RMT2 (gene name)

Systematic name: S-adenosyl-L-methionine:[protein]-L-arginine N-methyltransferase ([protein]-N^5-methyl-L-arginine-forming)

Comments: This enzyme, characterized from the yeast *Saccharomyces cerevisiae*, methylates the the δ-nitrogen atom of arginine residues within proteins. Among its substrates are Arg^{67} of the ribosomal protein L12. *cf.* EC 2.1.1.319, type I protein arginine methyltransferase, EC 2.1.1.320, type II protein arginine methyltransferase, and EC 2.1.1.321, type III protein arginine methyltransferase.

References: [2454, 538, 2561]

[EC 2.1.1.322 created 2015]

EC 2.1.1.323

Accepted name: (–)-pluviatolide 4-*O*-methyltransferase

Reaction: S-adenosyl-L-methionine + (–)-pluviatolide = S-adenosyl-L-homocysteine + (–)-bursehernin

Other name(s): OMT3 (gene name)

Systematic name: S-adenosyl-L-methionine:(–)-pluviatolide 4-*O*-methyltransferase

Comments: The enzyme, characterized from the plant *Sinopodophyllum hexandrum*, is involved in the biosynthetic pathway of podophyllotoxin, a non-alkaloid toxin lignan whose derivatives are important anticancer drugs.

References: [1872]

[EC 2.1.1.323 created 2016]

EC 2.1.1.324

Accepted name: dTDP-4-amino-2,3,4,6-tetradeoxy-D-glucose *N*,*N*-dimethyltransferase

Reaction: **2** S-adenosyl-L-methionine + dTDP-4-amino-2,3,4,6-tetradeoxy-α-D-*erythro*-hexopyranose = **2** S-adenosyl-L-homocysteine + dTDP-α-D-forosamine (overall reaction)

(1a) S-adenosyl-L-methionine + dTDP-4-amino-2,3,4,6-tetradeoxy-α-D-*erythro*-hexopyranose = S-adenosyl-L-homocysteine + dTDP-4-(methylamino)-2,3,4,6-tetradeoxy-α-D-*erythro*-hexopyranose

(1b) S-adenosyl-L-methionine + dTDP-4-(methylamino)-2,3,4,6-tetradeoxy-α-D-*erythro*-hexopyranose = S-adenosyl-L-homocysteine + dTDP-α-D-forosamine

Other name(s): SpnS; TDP-4-amino-2,3,6-trideoxy-D-glucose *N*,*N*-dimethyltransferase

Systematic name: *S*-adenosyl-L-methionine:dTDP-4-amino-2,3,4,6-tetradeoxy-α-D-*erythro*-hexopyranose *N*,*N*-dimethyltransferase

Comments: The enzyme was isolated from the bacterium *Saccharopolyspora spinosa*, where it is involved in the biosynthesis of spinosyn A, an active ingredient of several commercial insecticides.

References: [1365]

[EC 2.1.1.324 created 2016]

EC 2.1.1.325

Accepted name: juvenile hormone-III synthase

Reaction: (1) *S*-adenosyl-L-methionine + (2*E*,6*E*)-farnesoate = *S*-adenosyl-L-homocysteine + methyl (2*E*,6*E*)-farnesoate

(2) *S*-adenosyl-L-methionine + juvenile hormone III acid = *S*-adenosyl-L-homocysteine + juvenile hormone III

Other name(s): farnesoic acid methyltransferase; juvenile hormone acid methyltransferase; JHAMT

Systematic name: *S*-adenosyl-L-methionine:(2*E*,6*E*)-farnesoate *O*-methyltransferase

Comments: The enzyme, found in insects, is involved in the synthesis of juvenile hormone III, a sesquiterpenoid that regulates several processes including embryonic development, metamorphosis, and reproduction, in many insect species.

References: [3203, 702, 822, 823]

[EC 2.1.1.325 created 2016]

EC 2.1.1.326

Accepted name: *N*-acetyldemethylphosphinothricin *P*-methyltransferase

Reaction: **2** *S*-adenosyl-L-methionine + *N*-acetyldemethylphosphinothricin + reduced acceptor = *S*-adenosyl-L-homocysteine + 5′-deoxyadenosine + L-methionine + *N*-acetylphosphinothricin + oxidized acceptor

Other name(s): *phpK* (gene name); *bcpD* (gene name); *P*-methylase

Systematic name: *S*-adenosyl-L-methionine:*N*-acetyldemethylphosphinothricin *P*-methyltransferase

Comments: The enzyme was originally characterized from bacteria that produce the tripeptides bialaphos and phosalacine, which inhibit plant and bacterial glutamine synthetases. It is a radical *S*-adenosyl-L-methionine (SAM) enzyme that contains a [4Fe-4S] center and a methylcob(III)alamin cofactor. According to the proposed mechanism, the reduced iron-sulfur center donates an electron to SAM, resulting in homolytic cleavage of the carbon-sulfur bond to form a 5′-deoxyadenosyl radical that abstracts the hydrogen atom from the P-H bond of the substrate, forming a phosphinate-centered radical. This radical reacts with methylcob(III)alamin to produce the methylated product and cob(II)alamin, which is reduced by an unknown donor to cob(I)alamin. A potential route for restoring the latter back to methylcob(III)alamin is a nucleophilic attack on a second SAM molecule. The enzyme acts *in vivo* on *N*-acetyldemethylphosphinothricin-L-alanyl-L-alanine or *N*-acetyl-demethylphosphinothricin-L-alanyl-L-leucine, the intermediates in the biosynthesis of bialaphos and phosalacine, respectively. This transformation produces the only example of a carbon-phosphorus-carbon linkage known to occur in nature.

References: [1573, 1321, 3824, 61, 1388]

[EC 2.1.1.326 created 2016]

EC 2.1.1.327

Accepted name: phenazine-1-carboxylate *N*-methyltransferase

Reaction: *S*-adenosyl-L-methionine + phenazine-1-carboxylate = *S*-adenosyl-L-homocysteine + 5-methylphenazine-1-carboxylate

Other name(s): *phzM* (gene name)

Systematic name: *S*-adenosyl-L-methionine:phenazine-1-carboxylate 5-methyltransferase

Comments: The enzyme, characterized from the bacterium *Pseudomonas aeruginosa*, is involved in the biosynthesis of pyocyanin, a toxin produced and secreted by the organism. The enzyme is active *in vitro* only in the presence of EC 1.14.13.218, 5-methylphenazine-1-carboxylate 1-monooxygenase.

References: [2631]

[EC 2.1.1.327 created 2016]

EC 2.1.1.328

Accepted name: *N*-demethylindolmycin *N*-methyltransferase

Reaction: *S*-adenosyl-L-methionine + *N*-demethylindolmycin = *S*-adenosyl-L-homocysteine + indolmycin

Other name(s): ind7 (gene name)

Systematic name: *S*-adenosyl-L-methionine:*N*-demethylindolmycin *N*-methyltransferase

Comments: The enzyme, characterized from the bacterium *Streptomyces griseus*, catalyses the ultimate reaction in the biosynthesis of indolmycin, an antibacterial drug that inhibits the bacterial tryptophan—tRNA ligase (EC 6.1.1.2).

References: [780]

[EC 2.1.1.328 created 2016]

EC 2.1.1.329

Accepted name: demethylphylloquinol methyltransferase

Reaction: *S*-adenosyl-L-methionine + demethylphylloquinol = *S*-adenosyl-L-homocysteine + phylloquinol

Other name(s): *menG* (gene name); 2-phytyl-1,4-naphthoquinol methyltransferase

Systematic name: *S*-adenosyl-L-methionine:2-phytyl-1,4-naphthoquinol *C*-methyltransferase

Comments: The enzyme, found in plants and cyanobacteria, catalyses the final step in the biosynthesis of phylloquinone (vitamin K_1), an electron carrier associated with photosystem I. The enzyme is specific for the quinol form of the substrate, and does not act on the quinone form [881].

References: [3007, 2029, 881]

[EC 2.1.1.329 created 2016]

EC 2.1.1.330

Accepted name: 5′-demethylyatein 5′-*O*-methyltransferase

Reaction: *S*-adenosyl-L-methionine + (–)-5′-demethylyatein = *S*-adenosyl-L-homocysteine + (–)-yatein

Other name(s): OMT1 (gene name)

Systematic name: *S*-adenosyl-L-methionine:(–)-5′-demethylyatein 5′-*O*-methyltransferase

Comments: The enzyme, characterized from the plant *Sinopodophyllum hexandrum*, is involved in the biosynthetic pathway of podophyllotoxin, a non-alkaloid toxin lignan whose derivatives are important anticancer drugs.

References: [1872]

[EC 2.1.1.330 created 2016]

EC 2.1.1.331

Accepted name: bacteriochlorophyllide *d* *C*-12^1-methyltransferase

Reaction: *S*-adenosyl-L-methionine + 8-ethyl-12-methyl-3-vinylbacteriochlorophyllide *d* = *S*-adenosyl-L-homocysteine + 8,12-diethyl-3-vinylbacteriochlorophyllide *d*

Other name(s): *bchR* (gene name)

Systematic name: *S*-adenosyl-L-methionine:8-ethyl-12-methyl-3-vinylbacteriochlorophyllide-*d* *C*-12^1-methyltransferase

Comments: This enzyme, found in green sulfur bacteria (*Chlorobiaceae*) and green flimentous bacteria (*Chloroflexaceae*), is a radical *S*-adenosyl-L-methionine (AdoMet) enzyme and contains a [4Fe-4S] cluster. It adds a methyl group at the C-12^1 position of bacteriochlorophylls of the *c*, *d* and *e* types. This methylation plays a role in fine-tuning the structural arrangement of the bacteriochlorophyll aggregates in chlorosomes and therefore directly influences the chlorosomes absorption properties.

References: [540]

[EC 2.1.1.331 created 2016]

EC 2.1.1.332

Accepted name: bacteriochlorophyllide *d* C-8^2-methyltransferase

Reaction: (1) *S*-adenosyl-L-methionine + 8,12-diethyl-3-vinylbacteriochlorophyllide *d* = *S*-adenosyl-L-homocysteine + 12-ethyl-8-propyl-3-vinylbacteriochlorophyllide *d*
(2) *S*-adenosyl-L-methionine + 12-ethyl-8-propyl-3-vinylbacteriochlorophyllide *d* = *S*-adenosyl-L-homocysteine + 12-ethyl-8-isobutyl-3-vinylbacteriochlorophyllide *d*

Other name(s): *bchQ* (gene name)

Systematic name: *S*-adenosyl-L-methionine:8,12-diethyl-3-vinylbacteriochlorophyllide-*d* C-8^2-methyltransferase

Comments: This enzyme, found in green sulfur bacteria (*Chlorobiaceae*) and green flimentous bacteria (*Chloroflexaceae*), is a radical *S*-adenosyl-L-methionine (AdoMet) enzyme and contains a [4Fe-4S] cluster. It adds one or two methyl groups at the C-8^2 position of bacteriochlorophylls of the *c*, *d* and *e* types. These methylations play a role in fine-tuning the structural arrangement of the bacteriochlorophyll aggregates in chlorosomes and therefore directly influence chlorosomal absorption properties.

References: [540]

[EC 2.1.1.332 created 2016]

EC 2.1.1.333

Accepted name: bacteriochlorophyllide *d* C-20 methyltransferase

Reaction: *S*-adenosyl-L-methionine + a bacteriochlorophyllide *d* = *S*-adenosyl-L-homocysteine + a bacteriochlorophyllide *c*

Other name(s): *bchU* (gene name)

Systematic name: *S*-adenosyl-L-methionine:bacteriochlorophyllide-*d* C-20 methyltransferase

Comments: The enzyme, found in green sulfur bacteria (Chlorobiaceae) and green flimentous bacteria (Chloroflexaceae), catalyses the methylation of the C-20 methine bridge position in bacteriochlorophyllide *d*, forming bacteriochlorophyllide *c*.

References: [2125]

[EC 2.1.1.333 created 2016]

EC 2.1.1.334

Accepted name: methanethiol *S*-methyltransferase

Reaction: *S*-adenosyl-L-methionine + methanethiol = *S*-adenosyl-L-homocysteine + dimethyl sulfide

Other name(s): *mddA* (gene name)

Systematic name: *S*-adenosyl-L-methionine:methanethiol *S*-methyltransferase

Comments: The enzyme, found in many bacterial taxa, is involved in a pathway that converts L-methionine to dimethyl sulfide.

References: [482]

[EC 2.1.1.334 created 2016]

EC 2.1.1.335

Accepted name: 4-amino-anhydrotetracycline N^4-methyltransferase

Reaction: (1) *S*-adenosyl-L-methionine + 4-amino-4-de(dimethylamino)anhydrotetracycline = *S*-adenosyl-L-homocysteine + 4-methylamino-4-de(dimethylamino)anhydrotetracycline
(2) *S*-adenosyl-L-methionine + 4-methylamino-4-de(dimethylamino)anhydrotetracycline = *S*-adenosyl-L-homocysteine + anhydrotetracycline

Other name(s): *oxyT* (gene name); *ctcO* (gene name)

Systematic name: *S*-adenosyl-L-methionine:(4*S*,4a*S*,12a*S*)-4-amino-3,10,11,12a-tetrahydroxy-6-methyl-1,12-dioxo-4a,5-dihydro-4*H*-tetracene-2-carboxamide N^{α}-methyltransferase

Comments: The enzyme, characterized from the bacterium *Streptomyces rimosus*, participates in the biosynthesis of tetracycline antibiotics.

References: [4048]

[EC 2.1.1.335 created 2016]

EC 2.1.1.336

Accepted name: norbelladine *O*-methyltransferase
Reaction: *S*-adenosyl-L-methionine + norbelladine = *S*-adenosyl-L-homocysteine + 4′-*O*-methylnorbelladine
Other name(s): N4OMT1 (gene name)
Systematic name: *S*-adenosyl-L-methionine:norbelladine *O*-methyltransferase
Comments: The enzyme, characterized from the plants *Nerine bowdenii* and *Narcissus pseudonarcissus* (daffodil), participates in the biosynthesis of alkaloids produced by plants that belong to the Amaryllidaceae family.
References: [2111, 1671]

[EC 2.1.1.336 created 2016]

EC 2.1.1.337

Accepted name: reticuline *N*-methyltransferase
Reaction: (1) *S*-adenosyl-L-methionine + (*S*)-reticuline = *S*-adenosyl-L-homocysteine + (*S*)-tembetarine
(2) *S*-adenosyl-L-methionine + (*S*)-corytuberine = *S*-adenosyl-L-homocysteine + (*S*)-magnoflorine
Other name(s): RNMT
Systematic name: *S*-adenosyl-L-methionine:(*S*)-reticuline *N*-methyltransferase
Comments: The enzyme from opium poppy (*Papaver somniferum*) can also methylate (*R*)-reticuline, tetrahydropapaverine, (*S*)-glaucine and (*S*)-bulbocapnine. It is involved in the biosynthesis of the quaternary benzylisoquinoline alkaloid magnoflorine.
References: [2323]

[EC 2.1.1.337 created 2017]

EC 2.1.1.338

Accepted name: desmethylxanthohumol 6′-*O*-methyltransferase
Reaction: *S*-adenosyl-L-methionine + desmethylxanthohumol = *S*-adenosyl-L-homocysteine + xanthohumol
Other name(s): OMT1 (ambiguous)
Systematic name: *S*-adenosyl-L-methionine:desmethylxanthohumol 6′-*O*-methyltransferase
Comments: Found in hops (*Humulus lupulus*). The enzyme can also methylate xanthogalenol.
References: [2395]

[EC 2.1.1.338 created 2017]

EC 2.1.1.339

Accepted name: xanthohumol 4-*O*-methyltransferase
Reaction: *S*-adenosyl-L-methionine + xanthohumol = *S*-adenosyl-L-homocysteine + 4-*O*-methylxanthohumol
Other name(s): OMT2 (ambiguous); *S*-adenosyl-L-methionine:xanthohumol 4′-*O*-methyltransferase (incorrect); xanthohumol 4′-*O*-methyltransferase (incorrect)
Systematic name: *S*-adenosyl-L-methionine:xanthohumol 4-*O*-methyltransferase
Comments: The enzyme from hops (*Humulus lupulus*) has a broad substrate specificity. The best substrates *in vitro* are resveratrol, desmethylxanthohumol, naringenin chalcone and isoliquiritigenin.
References: [2395]

[EC 2.1.1.339 created 2017, modified 2018]

EC 2.1.1.340

Accepted name: 3-aminomethylindole *N*-methyltransferase

Reaction: **2** *S*-adenosyl-L-methionine + 3-(aminomethyl)indole = **2** *S*-adenosyl-L-homocysteine + gramine (overall reaction)
(1a) *S*-adenosyl-L-methionine + 3-(aminomethyl)indole = *S*-adenosyl-L-homocysteine + (1*H*-indol-3-yl)-*N*-methylmethanamine
(1b) *S*-adenosyl-L-methionine + (1*H*-indol-3-yl)-*N*-methylmethanamine = *S*-adenosyl-L-homocysteine + gramine

Other name(s): NMT (gene name)

Systematic name: *S*-adenosyl-L-methionine:3-(aminomethyl)indole *N*-methyltransferase (gramine-forming)

Comments: The enzyme, characterized from *Hordeum vulgare* (barley), catalyses two successive *N*-methylation reactions during the biosynthesis of gramine, a toxic indole alkaloid.

References: [1925, 1869]

[EC 2.1.1.340 created 2017]

EC 2.1.1.341

Accepted name: vanillate/3-*O*-methylgallate *O*-demethylase

Reaction: (1) vanillate + tetrahydrofolate = protocatechuate + 5-methyltetrahydrofolate
(2) 3-*O*-methylgallate + tetrahydrofolate = gallate + 5-methyltetrahydrofolate

Other name(s): *ligM* (gene name)

Systematic name: vanillate:tetrahydrofolate *O*-methyltransferase

Comments: The enzyme, characterized from the bacterium *Sphingomonas* sp. SYK6, is involved in the degradation of lignin. The enzyme has similar activities with vanillate and 3-*O*-methylgallate.

References: [2464, 2148, 5]

[EC 2.1.1.341 created 2017]

EC 2.1.1.342

Accepted name: anaerobilin synthase

Reaction: **2** *S*-adenosyl-L-methionine + protoheme + **2** reduced flavodoxin = *S*-adenosyl-L-homocysteine + L-methionine + 5′-deoxyadenosine + anaerobilin + Fe^{2+} + **2** oxidized flavodoxin

Other name(s): *chuW* (gene name)

Systematic name: *S*-adenosyl-L-methionine:protoheme *C*-methyltransferase (anaerobilin-producing)

Comments: The enzyme, studied from the bacterium *Escherichia coli* O157:H7, is a radical SAM (AdoMet) enzyme that is involved in heme degradation and iron utilization under anaerobic conditions. The enzyme uses two SAM molecules for the reaction. The first molecule is used to generate a 5′-deoxyadenosyl radical, which abstracts a hydrogen atom from the methyl group of the second SAM molecule. The newly formed methylene radical attacks the substrate, causing a rearrangement of the porphyrin ring that results in the liberation of iron.

References: [1851, 1850]

[EC 2.1.1.342 created 2017]

EC 2.1.1.343

Accepted name: 8-amino-8-demethylriboflavin *N*,*N*-dimethyltransferase

Reaction: **2** *S*-adenosyl-L-methionine + 8-amino-8-demethylriboflavin = **2** *S*-adenosyl-L-homocysteine + roseoflavin (overall reaction)
(1a) *S*-adenosyl-L-methionine + 8-amino-8-demethylriboflavin = *S*-adenosyl-L-homocysteine + 8-demethyl-8-(methylamino)riboflavin
(1b) *S*-adenosyl-L-methionine + 8-demethyl-8-(methylamino)riboflavin = *S*-adenosyl-L-homocysteine + roseoflavin

Other name(s): *rosA* (gene name)

Systematic name: *S*-adenosyl-L-methionine:8-amino-8-demethylriboflavin *N*,*N*-dimethyltransferase

Comments: The enzyme, characterized from the soil bacterium *Streptomyces davawensis*, catalyses the last two steps in the biosynthesis of the antibiotic roseoflavin.

References: [1497, 3550]

[EC 2.1.1.343 created 2017]

EC 2.1.1.344

Accepted name: ornithine lipid *N*-methyltransferase

Reaction: **3** *S*-adenosyl-L-methionine + an ornithine lipid = **3** *S*-adenosyl-L-homocysteine + an *N*,*N*,*N*-trimethylornithine lipid (overall reaction)
(1a) *S*-adenosyl-L-methionine + an ornithine lipid = *S*-adenosyl-L-homocysteine + an *N*-methylornithine lipid
(1b) *S*-adenosyl-L-methionine + an *N*-methylornithine lipid = *S*-adenosyl-L-homocysteine + an *N*,*N*-dimethylornithine lipid
(1c) *S*-adenosyl-L-methionine + an *N*,*N*-dimethylornithine lipid = *S*-adenosyl-L-homocysteine + an *N*,*N*,*N*-trimethylornithine lipid

Other name(s): *olsG* (gene name)

Systematic name: *S*-adenosyl-L-methionine:ornithine lipid *N*-methyltransferase

Comments: The enzyme, characterized from the bacterium *Singulisphaera acidiphila*, catalyses three successive methylations of the terminal δ-nitrogen in ornithine lipids.

References: [856]

[EC 2.1.1.344 created 2017]

EC 2.1.1.345

Accepted name: psilocybin synthase

Reaction: **2** *S*-adenosyl-L-methionine + 4-hydroxytryptamine 4-phosphate = **2** *S*-adenosyl-L-homocysteine + psilocybin (overall reaction)
(1a) *S*-adenosyl-L-methionine + 4-hydroxytryptamine 4-phosphate = *S*-adenosyl-L-homocysteine + 4-hydroxy-*N*-methyltryptamine 4-phosphate
(1b) *S*-adenosyl-L-methionine + 4-hydroxy-*N*-methyltryptamine 4-phosphate = *S*-adenosyl-L-homocysteine + psilocybin

Other name(s): PsiM

Systematic name: *S*-adenosyl-L-methionine:4-hydroxytryptamine-4-phosphate *N*,*N*-dimethyltransferase

Comments: Isolated from the fungus *Psilocybe cubensis*. The product, psilocybin, is a psychoactive compound.

References: [961]

[EC 2.1.1.345 created 2017]

EC 2.1.1.346

Accepted name: U6 snRNA m^{6}A methyltransferase

Reaction: *S*-adenosyl-L-methionine + adenine in U6 snRNA = *S*-adenosyl-L-homocysteine + N^6-methyladenine in U6 snRNA

Other name(s): METTL16 (gene name)

Systematic name: *S*-adenosyl-L-methionine:adenine in U6 snRNA methyltransferase

Comments: This enzyme, found in vertebrates, methylates a specific adenine in a hairpin structure of snRNA. The effects of the binding of the methyltransferase to its substrate is important for the regulation of the activity of an isoform of EC 2.5.1.6, methionine adenosyltransferase, that produces *S*-adenosyl-L-methionine [2658, 3772]. The enzyme also binds (and maybe methylates) the lncRNAs XIST and MALAT1 as well as a number of pre-mRNAs at specific positions often found in the intronic regions [3772].

References: [2658, 3772]

[EC 2.1.1.346 created 2018]

EC 2.1.1.347

Accepted name: (+)-*O*-methylkolavelool synthase

Reaction: *S*-adenosyl-L-methionine + (+)-kolavelool = *S*-adenosyl-L-homocysteine + (+)-*O*-methylkolavelool

Other name(s): Haur_2147 (locus name)

Systematic name: *S*-adenosyl-L-methionine:(+)-kolavelool *O*-methyltransferase

Comments: Isolated from the bacterium *Herpetosiphon aurantiacus*.

References: [2410]

[EC 2.1.1.347 created 2018]

EC 2.1.1.348

Accepted name: mRNA m^{6}A methyltransferase

Reaction: *S*-adenosyl-L-methionine + adenine in mRNA = *S*-adenosyl-L-homocysteine + N^6-methyladenine in mRNA

Other name(s): METTL3 (gene name); METTL14 (gene name)

Systematic name: *S*-adenosyl-L-methionine:adenine in mRNA methyltransferase

Comments: This enzyme, found in eukaryotes, methylates adenines in mRNA with the consensus sequence RRACH.

References: [2002, 3760]

[EC 2.1.1.348 created 2018]

EC 2.1.1.349

Accepted name: toxoflavin synthase

Reaction: (1) *S*-adenosyl-L-methionine + 1,6-didemethyltoxoflavin = *S*-adenosyl-L-homocysteine + reumycin
(2) *S*-adenosyl-L-methionine + reumycin = *S*-adenosyl-L-homocysteine + toxoflavin

Other name(s): *toxA* (gene name)

Systematic name: *S*-adenosyl-L-methionine:1,6-didemethyltoxoflavin N^1,N^6-dimethyltransferase (toxoflavin-forming)

Comments: The enzyme is a dual-specificity methyltransferase that catalyses the last two steps of toxoflavin biosynthesis. Toxoflavin is a major virulence factor of several bacterial crop pathogens.

References: [889]

[EC 2.1.1.349 created 2018]

EC 2.1.1.350

Accepted name: menaquinone C^8-methyltransferase

Reaction: (1) **2** *S*-adenosyl-L-methionine + a menaquinone + reduced flavodoxin = *S*-adenosyl-L-homocysteine + L-methionine + 5′-deoxyadenosine + an 8-methylmenaquinone + oxidized flavodoxin
(2) **2** *S*-adenosyl-L-methionine + a 2-demethylmenaquinone + reduced flavodoxin = *S*-adenosyl-L-homocysteine + L-methionine + 5′-deoxyadenosine + a 2-demethyl-8-methylmenaquinone + oxidized flavodoxin

Other name(s): *mqnK* (gene name); *menK* (gene name)

Systematic name: *S*-adenosyl-L-methionine:menaquinone C^8-methyltransferase

Comments: The enzyme, found in a wide range of bacteria and archaea, is a radical SAM (AdoMet) enzyme that utilizes two molecules of *S*-adenosyl-L-methionine, one as the methyl group donor, and one for the creation of a 5′-deoxyadenosine radical that drives the reaction forward.

References: [1279]

[EC 2.1.1.350 created 2018]

EC 2.1.1.351

Accepted name: nocamycin *O*-methyltransferase

Reaction: *S*-adenosyl-L-methionine + nocamycin E = *S*-adenosyl-L-homocysteine + nocamycin I

Other name(s): *ncmP* (gene name)

Systematic name: *S*-adenosyl-L-methionine:nocamycin E *O*-methyltransferase

Comments: The enzyme, isolated from the bacterium *Saccharothrix syringae*, is involved in the biosynthesis of nocamycin I and nocamycin II.

References: [2283]

[EC 2.1.1.351 created 2018]

EC 2.1.1.352

Accepted name: 3-*O*-acetyl-4′-*O*-demethylpapaveroxine 4′-*O*-methyltransferase

Reaction: *S*-adenosyl-L-methionine + 3-*O*-acetyl-4′-*O*-demethylpapaveroxine = *S*-adenosyl-L-homocysteine + 3-*O*-acetylpapaveroxine

Systematic name: *S*-adenosyl-L-methionine:3-*O*-acetyl-4′-*O*-demethylpapaveroxine 4′-*O*-methyltransferase

Comments: This activity is part of the noscapine biosynthesis pathway, as characterized in the plant *Papaver somniferum* (opium poppy). It is catalysed by heterodimeric complexes of the OMT2 gene product and the product of either OMT3 or 6OMT. OMT2 is the catalytic subunit in both complexes.

References: [1963, 2624]

[EC 2.1.1.352 created 2018]

EC 2.1.2 Hydroxymethyl-, formyl- and related transferases

EC 2.1.2.1

Accepted name: glycine hydroxymethyltransferase

Reaction: 5,10-methylenetetrahydrofolate + glycine + H_2O = tetrahydrofolate + L-serine

Other name(s): serine aldolase; threonine aldolase; serine hydroxymethylase; serine hydroxymethyltransferase; allothreonine aldolase; L-serine hydroxymethyltransferase; L-threonine aldolase; serine hydroxymethyltransferase; serine transhydroxymethylase

Systematic name: 5,10-methylenetetrahydrofolate:glycine hydroxymethyltransferase

Comments: A pyridoxal-phosphate protein. Also catalyses the reaction of glycine with acetaldehyde to form L-threonine, and with 4-trimethylammoniobutanal to form 3-hydroxy-N^6,N^6,N^6-trimethyl-L-lysine.

References: [36, 321, 985, 1811, 3074]

[EC 2.1.2.1 created 1961, modified 1983]

EC 2.1.2.2

Accepted name: phosphoribosylglycinamide formyltransferase

Reaction: 10-formyltetrahydrofolate + N^1-(5-phospho-D-ribosyl)glycinamide = tetrahydrofolate + N^2-formyl-N^1-(5-phospho-D-ribosyl)glycinamide

Other name(s): 2-amino-*N*-ribosylacetamide 5′-phosphate transformylase; GAR formyltransferase; GAR transformylase; glycinamide ribonucleotide transformylase; GAR TFase; 5,10-methenyltetrahydrofolate:2-amino-*N*-ribosylacetamide ribonucleotide transformylase

Systematic name: 10-formyltetrahydrofolate:5′-phosphoribosylglycinamide *N*-formyltransferase

References: [1234, 3259, 3775]

[EC 2.1.2.2 created 1961, modified 2000]

EC 2.1.2.3

Accepted name: phosphoribosylaminoimidazolecarboxamide formyltransferase

Reaction: 10-formyltetrahydrofolate + 5-amino-1-(5-phospho-D-ribosyl)imidazole-4-carboxamide = tetrahydrofolate + 5-formamido-1-(5-phospho-D-ribosyl)imidazole-4-carboxamide
Other name(s): 5-amino-4-imidazolecarboxamide ribonucleotide transformylase; AICAR transformylase; 10-formyltetrahydrofolate:5′-phosphoribosyl-5-amino-4-imidazolecarboxamide formyltransferase; 5′-phosphoribosyl-5-amino-4-imidazolecarboxamide formyltransferase; 5-amino-1-ribosyl-4-imidazolecarboxamide 5′-phosphate transformylase; 5-amino-4-imidazolecarboxamide ribotide transformylase; AICAR formyltransferase; aminoimidazolecarboxamide ribonucleotide transformylase
Systematic name: 10-formyltetrahydrofolate:5′-phosphoribosyl-5-amino-4-imidazole-carboxamide *N*-formyltransferase
References: [1234]

[EC 2.1.2.3 created 1961, modified 2000]

EC 2.1.2.4
Accepted name: glycine formimidoyltransferase
Reaction: 5-formimidoyltetrahydrofolate + glycine = tetrahydrofolate + *N*-formimidoylglycine
Other name(s): formiminoglycine formiminotransferase; FIG formiminotransferase; glycine formiminotransferase
Systematic name: 5-formimidoyltetrahydrofolate:glycine *N*-formimidoyltransferase
References: [2782, 2783, 2995]

[EC 2.1.2.4 created 1961, modified 2000]

EC 2.1.2.5
Accepted name: glutamate formimidoyltransferase
Reaction: 5-formimidoyltetrahydrofolate + L-glutamate = tetrahydrofolate + *N*-formimidoyl-L-glutamate
Other name(s): glutamate formyltransferase; formiminoglutamic acid transferase; formiminoglutamic formiminotransferase; glutamate formiminotransferase
Systematic name: 5-formimidoyltetrahydrofolate:L-glutamate *N*-formimidoyltransferase
Comments: A pyridoxal-phosphate protein. Also catalyses formyl transfer from 5-formyltetrahydrofolate to L-glutamate (a reaction formerly listed as EC 2.1.2.6). In eukaryotes, it occurs as a bifunctional enzyme that also has formimidoyltetrahydrofolate cyclodeaminase (EC 4.3.1.4) activity.
References: [2248, 3227, 3426]

[EC 2.1.2.5 created 1961, modified 2000 (EC 2.1.2.6 created 1965, incorporated 1984)]

[2.1.2.6 Deleted entry. glutamate formyltransferase. Now included with EC 2.1.2.5, glutamate formimidoyltransferase]

[EC 2.1.2.6 created 1965, deleted 1984]

EC 2.1.2.7
Accepted name: D-alanine 2-hydroxymethyltransferase
Reaction: 5,10-methylenetetrahydrofolate + D-alanine + H_2O = tetrahydrofolate + 2-methylserine
Other name(s): 2-methylserine hydroxymethyltransferase
Systematic name: 5,10-methylenetetrahydrofolate:D-alanine 2-hydroxymethyltransferase
Comments: Also acts on 2-hydroxymethylserine.
References: [3868]

[EC 2.1.2.7 created 1972]

EC 2.1.2.8
Accepted name: deoxycytidylate 5-hydroxymethyltransferase
Reaction: 5,10-methylenetetrahydrofolate + H_2O + deoxycytidylate = tetrahydrofolate + 5-hydroxymethyldeoxycytidylate
Other name(s): dCMP hydroxymethylase; *d*-cytidine 5′-monophosphate hydroxymethylase; deoxyCMP hydroxymethylase; deoxycytidylate hydroxymethylase; deoxycytidylic hydroxymethylase

Systematic name: 5,10-methylenetetrahydrofolate:deoxycytidylate 5-hydroxymethyltransferase
References: [2159]

[EC 2.1.2.8 created 1972]

EC 2.1.2.9
Accepted name: methionyl-tRNA formyltransferase
Reaction: 10-formyltetrahydrofolate + L-methionyl-$tRNA^{fMet}$ = tetrahydrofolate + N-formylmethionyl-$tRNA^{fMet}$
Other name(s): N^{10}-formyltetrahydrofolic-methionyl-transfer ribonucleic transformylase; formylmethionyl-transfer ribonucleic synthetase; methionyl ribonucleic formyltransferase; methionyl-tRNA Met formyltransferase; methionyl-tRNA transformylase; methionyl-transfer RNA transformylase; methionyl-transfer ribonucleate methyltransferase; methionyl-transfer ribonucleic transformylase
Systematic name: 10-formyltetrahydrofolate:L-methionyl-tRNA *N*-formyltransferase
References: [732]

[EC 2.1.2.9 created 1972, modified 2002, modified 2012]

EC 2.1.2.10
Accepted name: aminomethyltransferase
Reaction: [protein]-S^8-aminomethyldihydrolipoyllysine + tetrahydrofolate = [protein]-dihydrolipoyllysine + 5,10-methylenetetrahydrofolate + NH_3
Other name(s): *S*-aminomethyldihydrolipoylprotein:(6*S*)-tetrahydrofolate aminomethyltransferase (ammonia-forming); T-protein; glycine synthase; tetrahydrofolate aminomethyltransferase; [protein]-8-*S*-aminomethyldihydrolipoyllysine:tetrahydrofolate aminomethyltransferase (ammonia-forming)
Systematic name: [protein]-S^8-aminomethyldihydrolipoyllysine:tetrahydrofolate aminomethyltransferase (ammonia-forming)
Comments: A component, with EC 1.4.4.2 glycine dehydrogenase (decarboxylating) and EC 1.8.1.4, dihydrolipoyl dehydrogenanse, of the glycine cleavage system, formerly known as glycine synthase. The glycine cleavage system is composed of four components that only loosely associate: the P protein (EC 1.4.4.2), the T protein (EC 2.1.2.10), the L protein (EC 1.8.1.4) and the lipoyl-bearing H protein [2435].
References: [2553, 2665, 2435]

[EC 2.1.2.10 created 1972, modified 2003, modified 2006]

EC 2.1.2.11
Accepted name: 3-methyl-2-oxobutanoate hydroxymethyltransferase
Reaction: 5,10-methylenetetrahydrofolate + 3-methyl-2-oxobutanoate + H_2O = tetrahydrofolate + 2-dehydropantoate
Other name(s): α-ketoisovalerate hydroxymethyltransferase; dehydropantoate hydroxymethyltransferase; ketopantoate hydroxymethyltransferase; oxopantoate hydroxymethyltransferase; 5,10-methylene tetrahydrofolate:α-ketoisovalerate hydroxymethyltransferase
Systematic name: 5,10-methylenetetrahydrofolate:3-methyl-2-oxobutanoate hydroxymethyltransferase
References: [2751, 3495]

[EC 2.1.2.11 created 1982]

[2.1.2.12 Deleted entry. now EC 2.1.1.74 methylenetetrahydrofolate-tRNA-(uracil-5-)-methyltransferase (FADH$_2$-oxidizing)]

[EC 2.1.2.12 created 1983, deleted 1984]

EC 2.1.2.13
Accepted name: UDP-4-amino-4-deoxy-L-arabinose formyltransferase

Reaction: 10-formyltetrahydrofolate + UDP-4-amino-4-deoxy-β-L-arabinopyranose = 5,6,7,8-tetrahydrofolate + UDP-4-deoxy-4-formamido-β-L-arabinopyranose
Other name(s): UDP-L-Ara4N formyltransferase; ArnAFT
Systematic name: 10-formyltetrahydrofolate:UDP-4-amino-4-deoxy-β-L-arabinose *N*-formyltransferase
Comments: The activity is part of a bifunctional enzyme also performing the reaction of EC 1.1.1.305 [UDP-glucuronic acid dehydrogenase (UDP-4-keto-hexauronic acid decarboxylating)].
References: [381, 1026, 3856, 1027, 3956]

[EC 2.1.2.13 created 2010]

EC 2.1.3 Carboxy- and carbamoyltransferases

EC 2.1.3.1

Accepted name: methylmalonyl-CoA carboxytransferase
Reaction: (*S*)-methylmalonyl-CoA + pyruvate = propanoyl-CoA + oxaloacetate
Other name(s): transcarboxylase; methylmalonyl coenzyme A carboxyltransferase; methylmalonyl-CoA transcarboxylase; oxalacetic transcarboxylase; methylmalonyl-CoA carboxyltransferase; methylmalonyl-CoA carboxyltransferase; (*S*)-2-methyl-3-oxopropanoyl-CoA:pyruvate carboxyltransferase; (*S*)-2-methyl-3-oxopropanoyl-CoA:pyruvate carboxytransferase carboxytransferase [incorrect]
Systematic name: (*S*)-methylmalonyl-CoA:pyruvate carboxytransferase
Comments: A biotinyl-protein, containing cobalt and zinc.
References: [1352, 3410]

[EC 2.1.3.1 created 1961]

EC 2.1.3.2

Accepted name: aspartate carbamoyltransferase
Reaction: carbamoyl phosphate + L-aspartate = phosphate + *N*-carbamoyl-L-aspartate
Other name(s): carbamylaspartotranskinase; aspartate transcarbamylase; aspartate carbamyltransferase; aspartic acid transcarbamoylase; aspartic carbamyltransferase; aspartic transcarbamylase; carbamylaspartotranskinase; L-aspartate transcarbamoylase; L-aspartate transcarbamylase; carbamoylaspartotranskinase; aspartate transcarbamylase; aspartate transcarbamoylase; ATCase
Systematic name: carbamoyl-phosphate:L-aspartate carbamoyltransferase
References: [2050, 2859, 3174]

[EC 2.1.3.2 created 1961]

EC 2.1.3.3

Accepted name: ornithine carbamoyltransferase
Reaction: carbamoyl phosphate + L-ornithine = phosphate + L-citrulline
Other name(s): citrulline phosphorylase; ornithine transcarbamylase; OTC; carbamylphosphate-ornithine transcarbamylase; L-ornithine carbamoyltransferase; L-ornithine carbamyltransferase; L-ornithine transcarbamylase; ornithine carbamyltransferase
Systematic name: carbamoyl-phosphate:L-ornithine carbamoyltransferase
Comments: The plant enzyme also catalyses the reactions of EC 2.1.3.6 putrescine carbamoyltransferase, EC 2.7.2.2 carbamate kinase and EC 3.5.3.12 agmatine deiminase, thus acting as putrescine synthase, converting agmatine [(4-aminobutyl)guanidine] and ornithine into putrescine and citrulline, respectively.
References: [313, 2131, 2132, 2130]

[EC 2.1.3.3 created 1961]

[2.1.3.4 Deleted entry. malonyl-CoA carboxyltransferase]

[EC 2.1.3.4 created 1965, deleted 1972]

EC 2.1.3.5

Accepted name: oxamate carbamoyltransferase

Reaction: carbamoyl phosphate + oxamate = phosphate + *N*-carbamoyl-2-oxoglycine

Other name(s): oxamic transcarbamylase

Systematic name: carbamoyl-phosphate:oxamate carbamoyltransferase

References: [343]

[EC 2.1.3.5 created 1976]

EC 2.1.3.6

Accepted name: putrescine carbamoyltransferase

Reaction: carbamoyl phosphate + putrescine = phosphate + *N*-carbamoylputrescine

Other name(s): PTCase; putrescine synthase; putrescine transcarbamylase

Systematic name: carbamoyl-phosphate:putrescine carbamoyltransferase

Comments: The plant enzyme also catalyses the reactions of EC 2.1.3.3 ornithine carbamoyltransferase, EC 2.7.2.2 carbamate kinase and EC 3.5.3.12 agmatine deiminase, thus acting as putrescine synthase, converting agmatine [(4-aminobutyl)guanidine] and ornithine into putrescine and citrulline, respectively.

References: [2928, 3311]

[EC 2.1.3.6 created 1976]

EC 2.1.3.7

Accepted name: 3-hydroxymethylcephem carbamoyltransferase

Reaction: carbamoyl phosphate + a 3-hydroxymethylceph-3-em-4-carboxylate = phosphate + a 3-carbamoyloxymethylcephem

Systematic name: carbamoyl-phosphate:3-hydroxymethylceph-3-em-4-carboxylate carbamoyltransferase

Comments: Acts on a wide range of 3-hydroxymethylcephems (a subclass of the cephalosporin antibiotics). Activated by ATP.

References: [391]

[EC 2.1.3.7 created 1983]

EC 2.1.3.8

Accepted name: lysine carbamoyltransferase

Reaction: carbamoyl phosphate + L-lysine = phosphate + L-homocitrulline

Other name(s): lysine transcarbamylase

Systematic name: carbamoyl-phosphate:L-lysine carbamoyltransferase

Comments: Not identical with EC 2.1.3.3 ornithine carbamoyltransferase.

References: [1362]

[EC 2.1.3.8 created 1986]

EC 2.1.3.9

Accepted name: *N*-acetylornithine carbamoyltransferase

Reaction: carbamoyl phosphate + N^2-acetyl-L-ornithine = phosphate + *N*-acetyl-L-citrulline

Other name(s): acetylornithine transcarbamylase; *N*-acetylornithine transcarbamylase; AOTC; carbamoyl-phosphate:2-*N*-acetyl-L-ornithine carbamoyltransferase; AOTCase

Systematic name: carbamoyl-phosphate:N^2-acetyl-L-ornithine carbamoyltransferase

Comments: Differs from EC 2.1.3.3, ornithine carbamoyltransferase. This enzyme replaces EC 2.1.3.3 in the canonic arginine biosynthetic pathway of several Eubacteria and has no catalytic activity with L-ornithine as substrate.

References: [3179, 2322]

[EC 2.1.3.9 created 2005]

EC 2.1.3.10

Accepted name: malonyl-*S*-ACP:biotin-protein carboxyltransferase

Reaction: a malonyl-[acyl-carrier protein] + a biotinyl-[protein] = an acetyl-[acyl-carrier protein] + a carboxybiotinyl-[protein]

Other name(s): malonyl-*S*-acyl-carrier protein:biotin-protein carboxyltransferase; MadC/MadD; Mad*C*,D; malonyl-[acyl-carrier protein]:biotinyl-[protein] carboxyltransferase

Systematic name: malonyl-[acyl-carrier protein]:biotinyl-[protein] carboxytransferase

Comments: Derived from the components MadC and MadD of the anaerobic bacterium *Malonomonas rubra*, this enzyme is a component of EC 7.2.4.4, biotin-dependent malonate decarboxylase. The carboxy group is transferred from malonate to the prosthetic group of the biotin protein (MadF) with retention of configuration [2240]. Similar to EC 4.1.1.87, malonyl-*S*-ACP decarboxylase, which forms part of the biotin-independent malonate decarboxylase (EC 4.1.1.88), this enzyme also follows on from EC 2.3.1.187, acetyl-*S*-ACP:malonate ACP transferase, and results in the regeneration of the acetyl-[acyl-carrier protein] [736].

References: [277, 2240, 736]

[EC 2.1.3.10 created 2008, modified 2018]

EC 2.1.3.11

Accepted name: *N*-succinylornithine carbamoyltransferase

Reaction: carbamoyl phosphate + N^2-succinyl-L-ornithine = phosphate + *N*-succinyl-L-citrulline

Other name(s): succinylornithine transcarbamylase; *N*-succinyl-L-ornithine transcarbamylase; SOTCase

Systematic name: carbamoyl phosphate:N^2-succinyl-L-ornithine carbamoyltransferase

Comments: This enzyme is specific for *N*-succinyl-L-ornithine and cannot use either L-ornithine (see EC 2.1.3.3, ornithine carbamoyltransferase) or *N*-acetyl-L-ornithine (see EC 2.1.3.9, *N*-acetylornithine carbamoyltransferase) as substrate. However, a single amino-acid substitution (Pro^{90} → Glu^{90}) is sufficient to switch the enzyme to one that uses *N*-acetyl-L-ornithine as substrate. It is essential for *de novo* arginine biosynthesis in the obligate anaerobe *Bacteroides fragilis*, suggesting that this organism uses an alternative pathway for synthesizing arginine.

References: [3178, 3180]

[EC 2.1.3.11 created 2008]

EC 2.1.3.12

Accepted name: decarbamoylnovobiocin carbamoyltransferase

Reaction: carbamoyl phosphate + decarbamoylnovobiocin = phosphate + novobiocin

Other name(s): *novN* (gene name)

Systematic name: carbamoyl phosphate:decarbamoylnovobiocin 3$''$-*O*-carbamoyltransferase

Comments: The enzyme catalyses the last step in the biosynthesis of the aminocoumarin antibiotic novobiocin. The reaction is activated by ATP [2234].

References: [2234, 1013]

[EC 2.1.3.12 created 2013]

[2.1.3.13 Deleted entry. ATP carbamoyltransferase. The enzyme has been replaced by EC 6.1.2.2, nebramycin 5$'$ synthase.]

[EC 2.1.3.13 created 2013, deleted 2014]

[2.1.3.14 Deleted entry. tobramycin carbamoyltransferase. The enzyme has been replaced by EC 6.1.2.2, nebramycin 5′ synthase]

[EC 2.1.3.14 created 2013, deleted 2014]

EC 2.1.3.15

Accepted name: acetyl-CoA carboxytransferase

Reaction: [biotin carboxyl-carrier protein]-N^6-carboxybiotinyl-L-lysine + acetyl-CoA = [biotin carboxyl-carrier protein]-N^6-biotinyl-L-lysine + malonyl-CoA

Other name(s): *accAD* (gene names)

Systematic name: [biotin carboxyl-carrier protein]-N^6-carboxybiotinyl-L-lysine:acetyl-CoA:carboxytransferase

Comments: The enzyme catalyses the transfer of a carboxyl group carried on a biotinylated biotin carboxyl carrier protein (BCCP) to acetyl-CoA, forming malonyl-CoA. In some organisms this activity is part of a multi-domain polypeptide that includes the carrier protein and EC 6.3.4.14, biotin carboxylase (see EC 6.4.1.2, acetyl-CoA carboxylase). Some enzymes can also carboxylate propanonyl-CoA and butanoyl-CoA (*cf.* EC 6.4.1.3, propionyl-CoA carboxylase).

References: [307, 561]

[EC 2.1.3.15 created 2017]

EC 2.1.4 Amidinotransferases

EC 2.1.4.1

Accepted name: glycine amidinotransferase

Reaction: L-arginine + glycine = L-ornithine + guanidinoacetate

Other name(s): arginine-glycine amidinotransferase; arginine-glycine transamidinase; glycine transamidinase

Systematic name: L-arginine:glycine amidinotransferase

Comments: Canavanine can act instead of arginine.

References: [360, 596, 2195, 2822, 2823, 2824, 3729, 3730]

[EC 2.1.4.1 created 1961 as EC 2.6.2.1, transferred 1965 to EC 2.1.4.1]

EC 2.1.4.2

Accepted name: *scyllo*-inosamine-4-phosphate amidinotransferase

Reaction: L-arginine + 1-amino-1-deoxy-*scyllo*-inositol 4-phosphate = L-ornithine + 1-guanidino-1-deoxy-*scyllo*-inositol 4-phosphate

Other name(s): L-arginine:inosamine-*P*-amidinotransferase; inosamine-*P* amidinotransferase; L-arginine:inosamine phosphate amidinotransferase; inosamine-phosphate amidinotransferase

Systematic name: L-arginine:1-amino-1-deoxy-*scyllo*-inositol-4-phosphate amidinotransferase

Comments: 1D-1-Guanidino-3-amino-1,3-dideoxy-*scyllo*-inositol 6-phosphate, streptamine phosphate and 2-deoxystreptamine phosphate can also act as acceptors; canavanine can act as donor.

References: [3740]

[EC 2.1.4.2 created 1976, modified 2001]

EC 2.1.5 Methylenetransferases

EC 2.1.5.1

Accepted name: sesamin methylene transferase

Reaction: (1) (+)-sesamin + tetrahydrofolate = (+)-demethylpiperitol + 5,10-methylenetetrahydrofolate
(2) (+)-demethylpiperitol + tetrahydrofolate = (+)-didemethylpinoresinol + 5,10-methylenetetrahydrofolate

Other name(s): *sesA* (gene name)
Systematic name: (+)-sesamin:tetrahydrofolate *N*-methylenetransferase
Comments: This enzyme was characterized from the bacterium *Sinomonas* sp. No.22. It catalyses a cleavage of a methylene bridge, followed by the transfer of the methylene group to tetrahydrofolate. The enzyme is also active with (+)-episesamin, (–)-asarinin, (+)-sesaminol, (+)-sesamolin, and piperine.
References: [1814]

[EC 2.1.5.1 created 2018]

EC 2.2 Transferring aldehyde or ketonic groups

This single sub-subclass (EC 2.2.1) contains transketolases and transaldolases.

EC 2.2.1 Transketolases and transaldolases

EC 2.2.1.1
Accepted name: transketolase
Reaction: sedoheptulose 7-phosphate + D-glyceraldehyde 3-phosphate = D-ribose 5-phosphate + D-xylulose 5-phosphate
Other name(s): glycolaldehydetransferase
Systematic name: sedoheptulose-7-phosphate:D-glyceraldehyde-3-phosphate glycolaldehydetransferase
Comments: A thiamine-diphosphate protein. Wide specificity for both reactants, e.g. converts hydroxypyruvate and R-CHO into CO_2 and R-CHOH-CO-CH_2OH. The enzyme from the bacterium *Alcaligenes faecalis* shows high activity with D-erythrose 4-phosphate as acceptor.
References: [1189, 750, 1370, 2788]

[EC 2.2.1.1 created 1961]

EC 2.2.1.2
Accepted name: transaldolase
Reaction: sedoheptulose 7-phosphate + D-glyceraldehyde 3-phosphate = D-erythrose 4-phosphate + D-fructose 6-phosphate
Other name(s): dihydroxyacetonetransferase; dihydroxyacetone synthase; formaldehyde transketolase
Systematic name: sedoheptulose-7-phosphate:D-glyceraldehyde-3-phosphate glyceronetransferase
References: [1369, 2787, 3582]

[EC 2.2.1.2 created 1961]

EC 2.2.1.3
Accepted name: formaldehyde transketolase
Reaction: D-xylulose 5-phosphate + formaldehyde = D-glyceraldehyde 3-phosphate + glycerone
Other name(s): dihydroxyacetone synthase
Systematic name: D-xylulose-5-phosphate:formaldehyde glycolaldehydetransferase
Comments: A thiamine-diphosphate protein. Not identical with EC 2.2.1.1 transketolase. Also converts hydroxypyruvate and formaldehyde into glycerone and CO_2.
References: [445, 1600, 3720]

[EC 2.2.1.3 created 1984]

EC 2.2.1.4
Accepted name: acetoin—ribose-5-phosphate transaldolase

Reaction: 3-hydroxybutan-2-one + D-ribose 5-phosphate = acetaldehyde + 1-deoxy-D-altro-heptulose 7-phosphate

Other name(s): 1-deoxy-D-altro-heptulose-7-phosphate synthetase; 1-deoxy-D-altro-heptulose-7-phosphate synthase; 3-hydroxybutan-2-one:D-ribose-5-phosphate aldehydetransferase [wrong substrate name]

Systematic name: 3-hydroxybutan-2-one:D-ribose-5-phosphate aldehydetransferase

Comments: A thiamine-diphosphate protein.

References: [3988]

[EC 2.2.1.4 created 1989]

EC 2.2.1.5

Accepted name: 2-hydroxy-3-oxoadipate synthase

Reaction: 2-oxoglutarate + glyoxylate = 2-hydroxy-3-oxoadipate + CO_2

Other name(s): 2-hydroxy-3-oxoadipate glyoxylate-lyase (carboxylating); α-ketoglutaric-glyoxylic carboligase; oxoglutarate: glyoxylate carboligase

Systematic name: 2-oxoglutarate:glyoxylate succinaldehydetransferase (decarboxylating)

Comments: The bacterial enzyme requires thiamine diphosphate. The product decarboxylates to 5-hydroxy-4-oxopentanoate. The enzyme can decarboxylate 2-oxoglutarate. Acetaldehyde can replace glyoxylate.

References: [3077, 3078, 3341]

[EC 2.2.1.5 created 1972 as EC 4.1.3.15, transferred 2002 to EC 2.2.1.5]

EC 2.2.1.6

Accepted name: acetolactate synthase

Reaction: **2** pyruvate = 2-acetolactate + CO_2

Other name(s): α-acetohydroxy acid synthetase; α-acetohydroxyacid synthase; α-acetolactate synthase; α-acetolactate synthetase; acetohydroxy acid synthetase; acetohydroxyacid synthase; acetolactate pyruvate-lyase (carboxylating); acetolactic synthetase

Systematic name: pyruvate:pyruvate acetaldehydetransferase (decarboxylating)

Comments: This enzyme requires thiamine diphosphate. The reaction shown is in the pathway of biosynthesis of valine; the enzyme can also transfer the acetaldehyde from pyruvate to 2-oxobutanoate, forming 2-ethyl-2-hydroxy-3-oxobutanoate, also known as 2-aceto-2-hydroxybutanoate, a reaction in the biosynthesis of isoleucine.

References: [237, 1416, 3357, 186]

[EC 2.2.1.6 created 1972 as EC 4.1.3.18, transferred 2002 to EC 2.2.1.6]

EC 2.2.1.7

Accepted name: 1-deoxy-D-xylulose-5-phosphate synthase

Reaction: pyruvate + D-glyceraldehyde 3-phosphate = 1-deoxy-D-xylulose 5-phosphate + CO_2

Other name(s): 1-deoxy-D-xylulose-5-phosphate pyruvate-lyase (carboxylating); DXP-synthase

Systematic name: pyruvate:D-glyceraldehyde-3-phosphate acetaldehydetransferase (decarboxylating)

Comments: Requires thiamine diphosphate. The enzyme forms part of an alternative nonmevalonate pathway for terpenoid biosynthesis (for diagram, click here).

References: [3303, 1835]

[EC 2.2.1.7 created 2001 as EC 4.1.3.37 transferred 2002 to EC 2.2.1.7]

EC 2.2.1.8

Accepted name: fluorothreonine transaldolase

Reaction: L-threonine + fluoroacetaldehyde = acetaldehyde + 4-fluoro-L-threonine

Systematic name: fluoroacetaldehyde:L-threonine aldehydetransferase

Comments: A pyridoxal phosphate protein. Can also convert chloroacetaldehyde into4-chloro-L-threonine. Unlike EC 2.1.2.1, glycine hydroxymethyltransferase, does not use glycine as a substrate.

References: [2376, 2377]

[EC 2.2.1.8 created 2003]

EC 2.2.1.9

Accepted name: 2-succinyl-5-enolpyruvyl-6-hydroxy-3-cyclohexene-1-carboxylic-acid synthase

Reaction: isochorismate + 2-oxoglutarate = 5-enolpyruvoyl-6-hydroxy-2-succinyl-cyclohex-3-ene-1-carboxylate + CO_2

Other name(s): SEPHCHC synthase; MenD

Systematic name: isochorismate:2-oxoglutarate 4-oxopentanoatetransferase (decarboxylating)

Comments: Requires Mg^{2+} for maximal activity. This enzyme is involved in the biosynthesis of vitamin K_2 (menaquinone). In most anaerobes and all Gram-positive aerobes, menaquinone is the sole electron transporter in the respiratory chain and is essential for their survival. It had previously been thought that the products of the reaction were (1*R*,6*R*)-6-hydroxy-2-succinylcyclohexa-2,4-diene-1-carboxylate (SHCHC), pyruvate and CO_2 but it is now known that two separate enzymes are involved: this enzyme and EC 4.2.99.20, 2-succinyl-6-hydroxy-2,4-cyclohexadiene-1-carboxylate synthase. Under basic conditions, the product can spontaneously lose pyruvate to form SHCHC.

References: [1513]

[EC 2.2.1.9 created 2008 (EC 2.5.1.64 created 2003, part-incorporated 2008)]

EC 2.2.1.10

Accepted name: 2-amino-3,7-dideoxy-D-*threo*-hept-6-ulosonate synthase

Reaction: L-aspartate 4-semialdehyde + 1-deoxy-D-*threo*-hexo-2,5-diulose 6-phosphate = 2-amino-3,7-dideoxy-D-*threo*-hept-6-ulosonate + 2,3-dioxopropyl phosphate

Other name(s): ADH synthase; ADHS; MJ0400 (gene name)

Systematic name: L-aspartate 4-semialdehyde:1-deoxy-D-*threo*-hexo-2,5-diulose 6-phosphate methylglyoxaltransferase

Comments: The enzyme plays a key role in an alternative pathway of the biosynthesis of 3-dehydroquinate (DHQ), which is involved in the canonical pathway for the biosynthesis of aromatic amino acids. The enzyme can also catalyse the reaction of EC 4.1.2.13, fructose-bisphosphate aldolase.

References: [3836, 3012, 2305]

[EC 2.2.1.10 created 2012]

EC 2.2.1.11

Accepted name: 6-deoxy-5-ketofructose 1-phosphate synthase

Reaction: (1) 2-oxopropanal + D-fructose 1,6-bisphosphate = D-glyceraldehyde 3-phosphate + 1-deoxy-D-*threo*-hexo-2,5-diulose 6-phosphate
(2) 2-oxopropanal + D-fructose 1-phosphate = D-glyceraldehyde + 1-deoxy-D-*threo*-hexo-2,5-diulose 6-phosphate

Other name(s): DKFP synthase

Systematic name: 2-oxopropanal:D-fructose 1,6-bisphosphate glycerone-phosphotransferase

Comments: The enzyme plays a key role in an alternative pathway of the biosynthesis of 3-dehydroquinate (DHQ), which is involved in the canonical pathway for the biosynthesis of aromatic amino acids. The enzyme can also catalyse the reaction of EC 4.1.2.13, fructose-bisphosphate aldolase.

References: [3838, 3012]

[EC 2.2.1.11 created 2012]

EC 2.2.1.12

Accepted name: 3-acetyloctanal synthase

Reaction: pyruvate + (*E*)-oct-2-enal = (*S*)-3-acetyloctanal + CO_2

Other name(s): *pigD* (gene name)

Systematic name: pyruvate:(*E*)-oct-2-enal acetaldehydetransferase (decarboxylating)
Comments: Requires thiamine diphosphate. The enzyme, characterized from the bacterium *Serratia marcescens*, participates in the biosynthesis of the antibiotic prodigiosin. The enzyme decarboxylates pyruvate, followed by attack of the resulting two-carbon fragment on (*E*)-oct-2-enal, resulting in a Stetter reaction. *In vitro* the enzyme can act on a number of α,β-unsaturated carbonyl compounds, including aldehydes and ketones, and can catalyse both 1-2 and 1-4 carboligations depending on the substrate.
References: [3863, 775, 1592]

[EC 2.2.1.12 created 2014]

EC 2.3 Acyltransferases

This subclass contains enzymes that transfer acyl groups, forming either esters or amides. In most cases, the donor is the corresponding acyl-CoA derivative. Sub-subclasses are based on the acyl group that is transferred: acyl groups other than aminoacyl groups (EC 2.3.1), aminoacyltransferases (EC 2.3.2) and acyl groups that are converted into alkyl groups on transfer (EC 2.3.3).

EC 2.3.1 Transferring groups other than aminoacyl groups

EC 2.3.1.1
Accepted name: amino-acid *N*-acetyltransferase
Reaction: acetyl-CoA + L-glutamate = CoA + *N*-acetyl-L-glutamate
Other name(s): *N*-acetylglutamate synthase; AGAS; acetylglutamate acetylglutamate synthetase; acetylglutamic synthetase; amino acid acetyltransferase; *N*-acetyl-L-glutamate synthetase; *N*-acetylglutamate synthetase
Systematic name: acetyl-CoA:L-glutamate *N*-acetyltransferase
Comments: Also acts with L-aspartate and, more slowly, with some other amino acids.
References: [2089]

[EC 2.3.1.1 created 1961]

EC 2.3.1.2
Accepted name: imidazole *N*-acetyltransferase
Reaction: acetyl-CoA + imidazole = CoA + *N*-acetylimidazole
Other name(s): imidazole acetylase; imidazole acetyltransferase
Systematic name: acetyl-CoA:imidazole *N*-acetyltransferase
Comments: Also acts with propanoyl-CoA.
References: [1690]

[EC 2.3.1.2 created 1961]

EC 2.3.1.3
Accepted name: glucosamine *N*-acetyltransferase
Reaction: acetyl-CoA + D-glucosamine = CoA + *N*-acetyl-D-glucosamine
Other name(s): glucosamine acetylase; glucosamine acetyltransferase
Systematic name: acetyl-CoA:D-glucosamine *N*-acetyltransferase
References: [555]

[EC 2.3.1.3 created 1961]

EC 2.3.1.4
Accepted name: glucosamine-phosphate *N*-acetyltransferase

Reaction: acetyl-CoA + D-glucosamine 6-phosphate = CoA + *N*-acetyl-D-glucosamine 6-phosphate

Other name(s): phosphoglucosamine transacetylase; phosphoglucosamine acetylase; glucosamine-6-phosphate acetylase; D-glucosamine-6-*P* *N*-acetyltransferase; aminodeoxyglucosephosphate acetyltransferase; glucosamine 6-phosphate acetylase; glucosamine 6-phosphate *N*-acetyltransferase; *N*-acetylglucosamine-6-phosphate synthase; phosphoglucosamine *N*-acetylase; glucosamine-6-phosphate *N*-acetyltransferase

Systematic name: acetyl-CoA:D-glucosamine-6-phosphate *N*-acetyltransferase

References: [679, 680, 2636, 341]

[EC 2.3.1.4 created 1961, modified 2002]

EC 2.3.1.5

Accepted name: arylamine *N*-acetyltransferase

Reaction: acetyl-CoA + an arylamine = CoA + an *N*-acetylarylamine

Other name(s): arylamine acetylase; β-naphthylamine *N*-acetyltransferase; 4-aminobiphenyl *N*-acetyltransferase; acetyl CoA-arylamine *N*-acetyltransferase; 2-naphthylamine *N*-acetyltransferase; arylamine acetyltransferase; indoleamine *N*-acetyltransferase; *N*-acetyltransferase (ambiguous); *p*-aminosalicylate *N*-acetyltransferase; serotonin acetyltransferase; serotonin *N*-acetyltransferase

Systematic name: acetyl-CoA:arylamine *N*-acetyltransferase

Comments: Wide specificity for aromatic amines, including serotonin; also catalyses acetyl-transfer between arylamines without CoA.

References: [554, 2641, 3424, 3813]

[EC 2.3.1.5 created 1961]

EC 2.3.1.6

Accepted name: choline *O*-acetyltransferase

Reaction: acetyl-CoA + choline = CoA + *O*-acetylcholine

Other name(s): choline acetylase; choline acetyltransferase

Systematic name: acetyl-CoA:choline *O*-acetyltransferase

Comments: Propanoyl-CoA can act, more slowly, in place of acetyl-CoA.

References: [288, 291, 971, 3110]

[EC 2.3.1.6 created 1961]

EC 2.3.1.7

Accepted name: carnitine *O*-acetyltransferase

Reaction: acetyl-CoA + carnitine = CoA + *O*-acetylcarnitine

Other name(s): acetyl-CoA-carnitine *O*-acetyltransferase; acetylcarnitine transferase; carnitine acetyl coenzyme A transferase; carnitine acetylase; carnitine acetyltransferase; carnitine-acetyl-CoA transferase; CATC

Systematic name: acetyl-CoA:carnitine *O*-acetyltransferase

Comments: Also acts on propanoyl-CoA and butanoyl-CoA (*cf.* EC 2.3.1.21 carnitine *O*-palmitoyltransferase and EC 2.3.1.137 carnitine *O*-octanoyltransferase).

References: [505, 965, 2277]

[EC 2.3.1.7 created 1961]

EC 2.3.1.8

Accepted name: phosphate acetyltransferase

Reaction: acetyl-CoA + phosphate = CoA + acetyl phosphate

Other name(s): phosphotransacetylase; phosphoacylase; PTA

Systematic name: acetyl-CoA:phosphate acetyltransferase

Comments: Also acts with other short-chain acyl-CoAs.

References: [284, 3314, 3315]

[EC 2.3.1.8 created 1961, modified 1976]

EC 2.3.1.9

Accepted name: acetyl-CoA *C*-acetyltransferase
Reaction: **2** acetyl-CoA = CoA + acetoacetyl-CoA
Other name(s): acetoacetyl-CoA thiolase; β-acetoacetyl coenzyme A thiolase; 2-methylacetoacetyl-CoA thiolase [misleading]; 3-oxothiolase; acetyl coenzyme A thiolase; acetyl-CoA acetyltransferase; acetyl-CoA:*N*-acetyltransferase; thiolase II
Systematic name: acetyl-CoA:acetyl-CoA *C*-acetyltransferase
References: [2079, 3337]

[EC 2.3.1.9 created 1961]

EC 2.3.1.10

Accepted name: hydrogen-sulfide *S*-acetyltransferase
Reaction: acetyl-CoA + hydrogen sulfide = CoA + thioacetate
Other name(s): hydrogen-sulfide acetyltransferase
Systematic name: acetyl-CoA:hydrogen-sulfide *S*-acetyltransferase
References: [375]

[EC 2.3.1.10 created 1961]

EC 2.3.1.11

Accepted name: thioethanolamine *S*-acetyltransferase
Reaction: acetyl-CoA + 2-aminoethanethiol = CoA + *S*-(2-aminoethyl)thioacetate
Other name(s): thioltransacetylase B; thioethanolamine acetyltransferase; acetyl-CoA:thioethanolamine *S*-acetyltransferase
Systematic name: acetyl-CoA:2-aminoethanethiol *S*-acetyltransferase
Comments: 2-Sulfanylethanol (2-mercaptoethanol) can act as a substrate [375].
References: [375, 1177]

[EC 2.3.1.11 created 1961, modified 2006]

EC 2.3.1.12

Accepted name: dihydrolipoyllysine-residue acetyltransferase
Reaction: acetyl-CoA + enzyme N^6-(dihydrolipoyl)lysine = CoA + enzyme N^6-(*S*-acetyldihydrolipoyl)lysine
Other name(s): acetyl-CoA:dihydrolipoamide *S*-acetyltransferase; dihydrolipoamide *S*-acetyltransferase; dihydrolipoate acetyltransferase; dihydrolipoic transacetylase; dihydrolipoyl acetyltransferase; lipoate acetyltransferase; lipoate transacetylase; lipoic acetyltransferase; lipoic acid acetyltransferase; lipoic transacetylase; lipoylacetyltransferase; thioltransacetylase A; transacetylase X; enzyme-dihydrolipoyllysine:acetyl-CoA *S*-acetyltransferase; acetyl-CoA:enzyme 6-*N*-(dihydrolipoyl)lysine *S*-acetyltransferase
Systematic name: acetyl-CoA:enzyme N^6-(dihydrolipoyl)lysine *S*-acetyltransferase
Comments: A multimer (24-mer or 60-mer, depending on the source) of this enzyme forms the core of the pyruvate dehydrogenase multienzyme complex, and binds tightly both EC 1.2.4.1, pyruvate dehydrogenase (acetyl-transferring) and EC 1.8.1.4, dihydrolipoyl dehydrogenase. The lipoyl group of this enzyme is reductively acetylated by EC 1.2.4.1, and the only observed direction catalysed by EC 2.3.1.12 is that where the acetyl group is passed to coenzyme A.
References: [375, 1177, 1178, 2665]

[EC 2.3.1.12 created 1961, modified 2003]

EC 2.3.1.13

Accepted name: glycine *N*-acyltransferase

Reaction: acyl-CoA + glycine = CoA + *N*-acylglycine

Other name(s): glycine acyltransferase; glycine-*N*-acylase

Systematic name: acyl-CoA:glycine *N*-acyltransferase

Comments: The CoA derivatives of a number of aliphatic and aromatic acids, but not phenylacetyl-CoA or (indol-3-yl)acetyl-CoA, can act as donor. Not identical with EC 2.3.1.68 glutamine *N*-acyltransferase or EC 2.3.1.71 glycine *N*-benzoyltransferase.

References: [2417, 3056, 3797]

[EC 2.3.1.13 created 1961]

EC 2.3.1.14

Accepted name: glutamine *N*-phenylacetyltransferase

Reaction: phenylacetyl-CoA + L-glutamine = CoA + α-*N*-phenylacetyl-L-glutamine

Other name(s): glutamine phenylacetyltransferase; phenylacetyl-CoA:L-glutamine *N*-acetyltransferase

Systematic name: phenylacetyl-CoA:L-glutamine α-*N*-phenylacetyltransferase

References: [2290]

[EC 2.3.1.14 created 1961]

EC 2.3.1.15

Accepted name: glycerol-3-phosphate 1-*O*-acyltransferase

Reaction: acyl-CoA + *sn*-glycerol 3-phosphate = CoA + 1-acyl-*sn*-glycerol 3-phosphate

Other name(s): α-glycerophosphate acyltransferase; 3-glycerophosphate acyltransferase; ACP:*sn*-glycerol-3-phosphate acyltransferase; glycerol 3-phosphate acyltransferase; glycerol phosphate acyltransferase; glycerol phosphate transacylase; glycerophosphate acyltransferase; glycerophosphate transacylase; *sn*-glycerol 3-phosphate acyltransferase; *sn*-glycerol-3-phosphate acyltransferase; glycerol-3-phosphate *O*-acyltransferase (ambiguous)

Systematic name: acyl-CoA:*sn*-glycerol-3-phosphate 1-*O*-acyltransferase

Comments: Acyl-[acyl-carrier protein] can also act as acyl donor. The enzyme acts only on derivatives of fatty acids of chain length larger than C_{10}.

References: [293, 954, 1132, 3953]

[EC 2.3.1.15 created 1961, modified 1976, modified 1990]

EC 2.3.1.16

Accepted name: acetyl-CoA *C*-acyltransferase

Reaction: acyl-CoA + acetyl-CoA = CoA + 3-oxoacyl-CoA

Other name(s): β-ketothiolase; 3-ketoacyl-CoA thiolase; KAT; β-ketoacyl coenzyme A thiolase; β-ketoacyl-CoA thiolase; β-ketoadipyl coenzyme A thiolase; β-ketoadipyl-CoA thiolase; 3-ketoacyl CoA thiolase; 3-ketoacyl coenzyme A thiolase; 3-ketoacyl thiolase; 3-ketothiolase; 3-oxoacyl-CoA thiolase; 3-oxoacyl-coenzyme A thiolase; 6-oxoacyl-CoA thiolase; acetoacetyl-CoA β-ketothiolase; acetyl-CoA acyltransferase; ketoacyl-CoA acyltransferase; ketoacyl-coenzyme A thiolase; long-chain 3-oxoacyl-CoA thiolase; oxoacyl-coenzyme A thiolase; pro-3-ketoacyl-CoA thiolase; thiolase I; 2-methylacetoacetyl-CoA thiolase [misleading]

Systematic name: acyl-CoA:acetyl-CoA *C*-acyltransferase

References: [256, 1091, 3335]

[EC 2.3.1.16 created 1961]

EC 2.3.1.17

Accepted name: aspartate *N*-acetyltransferase

Reaction: acetyl-CoA + L-aspartate = CoA + *N*-acetyl-L-aspartate

Other name(s): aspartate acetyltransferase; L-aspartate *N*-acetyltransferase

Systematic name: acetyl-CoA:L-aspartate *N*-acetyltransferase

References: [1092, 1718]

[EC 2.3.1.17 created 1965]

EC 2.3.1.18

Accepted name: galactoside *O*-acetyltransferase

Reaction: acetyl-CoA + a β-D-galactoside = CoA + a 6-acetyl-β-D-galactoside

Other name(s): thiogalactoside acetyltransferase; galactoside acetyltransferase; thiogalactoside transacetylase

Systematic name: acetyl-CoA:β-D-galactoside 6-acetyltransferase

Comments: Acts on thiogalactosides and phenylgalactoside.

References: [4017, 4018]

[EC 2.3.1.18 created 1965]

EC 2.3.1.19

Accepted name: phosphate butyryltransferase

Reaction: butanoyl-CoA + phosphate = CoA + butanoyl phosphate

Other name(s): phosphotransbutyrylase

Systematic name: butanoyl-CoA:phosphate butanoyltransferase

References: [3628]

[EC 2.3.1.19 created 1965]

EC 2.3.1.20

Accepted name: diacylglycerol *O*-acyltransferase

Reaction: acyl-CoA + 1,2-diacyl-*sn*-glycerol = CoA + triacylglycerol

Other name(s): diglyceride acyltransferase; 1,2-diacylglycerol acyltransferase; diacylglycerol acyltransferase; diglyceride *O*-acyltransferase; palmitoyl-CoA-*sn*-1,2-diacylglycerol acyltransferase; acyl-CoA:1,2-diacylglycerol *O*-acyltransferase

Systematic name: acyl-CoA:1,2-diacyl-*sn*-glycerol *O*-acyltransferase

Comments: Palmitoyl-CoA and other long-chain acyl-CoAs can act as donors.

References: [590, 1140, 1616, 3812]

[EC 2.3.1.20 created 1965]

EC 2.3.1.21

Accepted name: carnitine *O*-palmitoyltransferase

Reaction: palmitoyl-CoA + L-carnitine = CoA + L-palmitoylcarnitine

Other name(s): CPT; CPTo; outer malonyl-CoA inhibitable carnitine palmitoyltransferase; CPTi; CPT I (outer membrane carnitine palmitoyl transferase); carnitine palmitoyltransferase I; carnitine palmitoyltransferase II; CPT-A; CPT-B; acylcarnitine transferase; carnitine palmitoyltransferase; carnitine palmitoyltransferase-A; L-carnitine palmitoyltransferase; palmitoylcarnitine transferase

Systematic name: palmitoyl-CoA:L-carnitine *O*-palmitoyltransferase

Comments: Broad specificity to acyl group, over the range C_8 to C_{18}; optimal activity with palmitoyl-CoA. *cf.* EC 2.3.1.7 carnitine *O*-acetyltransferase and EC 2.3.1.137 carnitine *O*-octanoyltransferase.

References: [719, 1264, 2278]

[EC 2.3.1.21 created 1972]

EC 2.3.1.22

Accepted name: 2-acylglycerol *O*-acyltransferase
Reaction: acyl-CoA + 2-acylglycerol = CoA + diacylglycerol
Other name(s): acylglycerol palmitoyltransferase; monoglyceride acyltransferase; acyl coenzyme A-monoglyceride acyltransferase; monoacylglycerol acyltransferase
Systematic name: acyl-CoA:2-acylglycerol *O*-acyltransferase
Comments: Various 2-acylglycerols can act as acceptor; palmitoyl-CoA and other long-chain acyl-CoAs can act as donors. The *sn*-1 position and the *sn*-3 position are both acylated, at about the same rate.
References: [2109]

[EC 2.3.1.22 created 1972, modified 1986, modified 1989]

EC 2.3.1.23

Accepted name: 1-acylglycerophosphocholine *O*-acyltransferase
Reaction: acyl-CoA + 1-acyl-*sn*-glycero-3-phosphocholine = CoA + 1,2-diacyl-*sn*-glycero-3-phosphocholine
Other name(s): lysolecithin acyltransferase; 1-acyl-*sn*-glycero-3-phosphocholine acyltransferase; acyl coenzyme A-monoacylphosphatidylcholine acyltransferase; acyl-CoA:1-acyl-glycero-3-phosphocholine transacylase; lysophosphatide acyltransferase; lysophosphatidylcholine acyltransferase
Systematic name: acyl-CoA:1-acyl-*sn*-glycero-3-phosphocholine *O*-acyltransferase
Comments: Acts preferentially with unsaturated acyl-CoA derivatives. 1-Acyl-*sn*-glycero-3-phosphoinositol can also act as acceptor.
References: [258, 1329, 2245, 3634]

[EC 2.3.1.23 created 1972]

EC 2.3.1.24

Accepted name: sphingosine *N*-acyltransferase
Reaction: acyl-CoA + sphingosine = CoA + a ceramide
Other name(s): ceramide synthetase; sphingosine acyltransferase
Systematic name: acyl-CoA:sphingosine *N*-acyltransferase
Comments: Acts on sphingosine or its 2-epimer.
References: [3306]

[EC 2.3.1.24 created 1972]

EC 2.3.1.25

Accepted name: plasmalogen synthase
Reaction: acyl-CoA + 1-*O*-(alk-1-enyl)glycero-3-phosphocholine = CoA + plasmenylcholine
Other name(s): lysoplasmenylcholine acyltransferase; *O*-1-alkenylglycero-3-phosphorylcholine acyltransferase; 1-alkenyl-glycero-3-phosphorylcholine:acyl-CoA acyltransferase; 1-alkenylglycerophosphocholine *O*-acyltransferase
Systematic name: acyl-CoA:1-*O*-(alk-1-enyl)-glycero-3-phosphocholine 2-*O*-acyltransferase
References: [3722, 113]

[EC 2.3.1.25 created 1972, modified 2013]

EC 2.3.1.26

Accepted name: sterol *O*-acyltransferase
Reaction: acyl-CoA + cholesterol = CoA + cholesterol ester
Other name(s): cholesterol acyltransferase; sterol-ester synthase; sterol-ester synthetase; sterol-ester synthase; acyl coenzyme A-cholesterol-*O*-acyltransferase; acyl-CoA:cholesterol acyltransferase; ACAT; acyl-coenzyme A:cholesterol *O*-acyltransferase; cholesterol ester synthase; cholesterol ester synthetase; cholesteryl ester synthetase
Systematic name: acyl-CoA:cholesterol *O*-acyltransferase

Comments: The animal enzyme is highly specific for transfer of acyl groups with a single *cis* double bond that is nine carbon atoms distant from the carboxy group.

References: [3150, 3294, 3450]

[EC 2.3.1.26 created 1972]

EC 2.3.1.27

Accepted name: cortisol *O*-acetyltransferase

Reaction: acetyl-CoA + cortisol = CoA + cortisol 21-acetate

Other name(s): cortisol acetyltransferase; corticosteroid acetyltransferase; corticosteroid-21-*O*-acetyltransferase

Systematic name: acetyl-CoA:cortisol *O*-acetyltransferase

References: [3521]

[EC 2.3.1.27 created 1972]

EC 2.3.1.28

Accepted name: chloramphenicol *O*-acetyltransferase

Reaction: acetyl-CoA + chloramphenicol = CoA + chloramphenicol 3-acetate

Other name(s): chloramphenicol acetyltransferase; chloramphenicol acetylase; chloramphenicol transacetylase; CAT I; CAT II; CAT III

Systematic name: acetyl-CoA:chloramphenicol 3-*O*-acetyltransferase

References: [3163, 3164]

[EC 2.3.1.28 created 1972]

EC 2.3.1.29

Accepted name: glycine *C*-acetyltransferase

Reaction: acetyl-CoA + glycine = CoA + L-2-amino-3-oxobutanoate

Other name(s): 2-amino-3-ketobutyrate CoA ligase; 2-amino-3-ketobutyrate coenzyme A ligase; 2-amino-3-ketobutyrate-CoA ligase; glycine acetyltransferase; aminoacetone synthase; aminoacetone synthetase; KBL; AKB ligase

Systematic name: acetyl-CoA:glycine *C*-acetyltransferase

Comments: This is a pyridoxal-phosphate-dependent enzyme that acts in concert with EC 1.1.1.103, L-threonine 3-dehydrogenase, in the degradation of threonine to form glycine [807]. This threonine degradation pathway is common to prokaryotic and eukaryotic cells and the two enzymes involved form a complex [3085].

References: [2194, 2345, 807, 3085]

[EC 2.3.1.29 created 1972]

EC 2.3.1.30

Accepted name: serine *O*-acetyltransferase

Reaction: acetyl-CoA + L-serine = CoA + *O*-acetyl-L-serine

Other name(s): SATase; L-serine acetyltransferase; serine acetyltransferase; serine transacetylase

Systematic name: acetyl-CoA:L-serine *O*-acetyltransferase

References: [1782, 3262]

[EC 2.3.1.30 created 1972]

EC 2.3.1.31

Accepted name: homoserine *O*-acetyltransferase

Reaction: acetyl-CoA + L-homoserine = CoA + *O*-acetyl-L-homoserine

Other name(s): homoserine acetyltransferase; homoserine transacetylase; homoserine-*O*-transacetylase; L-homoserine *O*-acetyltransferase
Systematic name: acetyl-CoA:L-homoserine *O*-acetyltransferase
References: [2386]

[EC 2.3.1.31 created 1972]

EC 2.3.1.32

Accepted name: lysine *N*-acetyltransferase
Reaction: acetyl phosphate + L-lysine = phosphate + N^6-acetyl-L-lysine
Other name(s): lysine acetyltransferase; acetyl-phosphate:L-lysine 6-*N*-acetyltransferase
Systematic name: acetyl-phosphate:L-lysine N^6-acetyltransferase
References: [2595]

[EC 2.3.1.32 created 1972]

EC 2.3.1.33

Accepted name: histidine *N*-acetyltransferase
Reaction: acetyl-CoA + L-histidine = CoA + *N*-acetyl-L-histidine
Other name(s): acetylhistidine synthetase; histidine acetyltransferase
Systematic name: acetyl-CoA:L-histidine *N*-acetyltransferase
References: [214]

[EC 2.3.1.33 created 1972]

EC 2.3.1.34

Accepted name: D-tryptophan *N*-acetyltransferase
Reaction: acetyl-CoA + D-tryptophan = CoA + *N*-acetyl-D-tryptophan
Other name(s): D-tryptophan acetyltransferase; acetyl-CoA-D-tryptophan-α-*N*-acetyltransferase
Systematic name: acetyl-CoA:D-tryptophan *N*-acetyltransferase
References: [4032]

[EC 2.3.1.34 created 1972]

EC 2.3.1.35

Accepted name: glutamate *N*-acetyltransferase
Reaction: N^2-acetyl-L-ornithine + L-glutamate = L-ornithine + *N*-acetyl-L-glutamate
Other name(s): ornithine transacetylase; α-*N*-acetyl-L-ornithine:L-glutamate *N*-acetyltransferase; acetylglutamate synthetase; acetylglutamate-acetylornithine transacetylase; acetylglutamic synthetase; acetylglutamic-acetylornithine transacetylase; acetylornithinase; acetylornithine glutamate acetyltransferase; glutamate acetyltransferase; *N*-acetyl-L-glutamate synthetase; *N*-acetylglutamate synthase; *N*-acetylglutamate synthetase; ornithine acetyltransferase; 2-*N*-acetyl-L-ornithine:L-glutamate *N*-acetyltransferase
Systematic name: N^2-acetyl-L-ornithine:L-glutamate *N*-acetyltransferase
Comments: Also has some hydrolytic activity on acetyl-L-ornithine, but the rate is 1% of that of transferase activity.
References: [3321]

[EC 2.3.1.35 created 1972]

EC 2.3.1.36

Accepted name: D-amino-acid *N*-acetyltransferase

Reaction: acetyl-CoA + a D-amino acid = CoA + an *N*-acetyl-D-amino acid
Other name(s): D-amino acid acetyltransferase; D-amino acid-α-*N*-acetyltransferase
Systematic name: acetyl-CoA:D-amino-acid *N*-acetyltransferase
References: [4033]

[EC 2.3.1.36 created 1972]

EC 2.3.1.37
Accepted name: 5-aminolevulinate synthase
Reaction: succinyl-CoA + glycine = 5-aminolevulinate + CoA + CO_2
Other name(s): ALAS; ALA synthase; α-aminolevulinic acid synthase; δ-aminolevulinate synthase; δ-aminolevulinate synthetase; δ-aminolevulinic acid synthase; δ-aminolevulinic acid synthetase; δ-aminolevulinic synthetase; 5-aminolevulinate synthetase; 5-aminolevulinic acid synthetase; ALA synthetase; aminolevulinate synthase; aminolevulinate synthetase; aminolevulinic acid synthase; aminolevulinic acid synthetase; aminolevulinic synthetase
Systematic name: succinyl-CoA:glycine *C*-succinyltransferase (decarboxylating)
Comments: A pyridoxal-phosphate protein. The enzyme in erythrocytes is genetically distinct from that in other tissues.
References: [310, 1668, 2802, 3102, 3103, 3434, 3774]

[EC 2.3.1.37 created 1972]

EC 2.3.1.38
Accepted name: [acyl-carrier-protein] *S*-acetyltransferase
Reaction: acetyl-CoA + an [acyl-carrier protein] = CoA + an acetyl-[acyl-carrier protein]
Other name(s): acetyl coenzyme A-acyl-carrier-protein transacylase; [acyl-carrier-protein]-acetyltransferase; [ACP]-acetyltransferase; ACAT; acetyl-CoA:[acyl-carrier-protein] *S*-acetyltransferase
Systematic name: acetyl-CoA:[acyl-carrier protein] *S*-acetyltransferase
Comments: This enzyme, along with EC 2.3.1.39, [acyl-carrier-protein] *S*-malonyltransferase, is essential for the initiation of fatty-acid biosynthesis in bacteria. The substrate acetyl-CoA protects the enzyme against inhibition by *N*-ethylmaleimide or iodoacetamide [2048]. This is one of the activities associated with β-ketoacyl-ACP synthase III (EC 2.3.1.180) [3578].
References: [2761, 3647, 3862, 2048, 3578, 2806]

[EC 2.3.1.38 created 1972, modified 2006]

EC 2.3.1.39
Accepted name: [acyl-carrier-protein] *S*-malonyltransferase
Reaction: malonyl-CoA + an [acyl-carrier protein] = CoA + a malonyl-[acyl-carrier protein]
Other name(s): [acyl carrier protein]malonyltransferase; FabD; malonyl coenzyme A-acyl carrier protein transacylase; malonyl transacylase; malonyl transferase; malonyl-CoA-acyl carrier protein transacylase; malonyl-CoA:[acyl-carrier-protein] *S*-malonyltransferase; malonyl-CoA:ACP transacylase; malonyl-CoA:ACP-SH transacylase; malonyl-CoA:AcpM transacylase; malonyl-CoA:acyl carrier protein transacylase; malonyl-CoA:acyl-carrier-protein transacylase; malonyl-CoA/dephospho-CoA acyltransferase; MAT; MCAT; MdcH
Systematic name: malonyl-CoA:[acyl-carrier protein] *S*-malonyltransferase

Comments: This enzyme, along with EC 2.3.1.38, [acyl-carrier-protein] *S*-acetyltransferase, is essential for the initiation of fatty-acid biosynthesis in bacteria. This enzyme also provides the malonyl groups for polyketide biosynthesis [3414]. The product of the reaction, malonyl-ACP, is an elongation substrate in fatty-acid biosynthesis. In *Mycobacterium tuberculosis*, holo-ACP (the product of EC 2.7.8.7, holo-[acyl-carrier-protein] synthase) is the preferred substrate [1787]. This enzyme also forms part of the multienzyme complexes EC 4.1.1.88 (biotin-independent malonate decarboxylase) and EC 4.1.1.89 (biotin-dependent malonate decarboxylase). Malonylation of ACP is immediately followed by decarboxylation within the malonate-decarboxylase complex to yield acetyl-ACP, the catalytically active species of the decarboxylase [736]. In the enzyme from *Klebsiella pneumoniae*, methylmalonyl-CoA can also act as a substrate but acetyl-CoA cannot [1348] whereas the enzyme from *Pseudomonas putida* can use both as substrates [551]. The ACP subunit found in fatty-acid biosynthesis contains a pantetheine-4′-phosphate prosthetic group; that from malonate decarboxylase also contains pantetheine-4′-phosphate but in the form of a 2′-(5-triphosphoribosyl)-3′-dephospho-CoA prosthetic group.

References: [47, 2761, 3862, 1541, 1787, 1623, 3414, 1349, 1752, 1348, 551, 736]

[EC 2.3.1.39 created 1972, modified 2006, modified 2008]

EC 2.3.1.40

Accepted name: acyl-[acyl-carrier-protein]—phospholipid *O*-acyltransferase

Reaction: an acyl-[acyl-carrier protein] + *O*-(2-acyl-*sn*-glycero-3-phospho)ethanolamine = an [acyl-carrier protein] + *O*-(1,2-diacyl-*sn*-glycero-3-phospho)ethanolamine

Other name(s): acyl-[acyl-carrier protein]:*O*-(2-acyl-*sn*-glycero-3-phospho)-ethanolamine *O*-acyltransferase

Systematic name: acyl-[acyl-carrier protein]:*O*-(2-acyl-*sn*-glycero-3-phospho)ethanolamine *O*-acyltransferase

References: [3486]

[EC 2.3.1.40 created 1972]

EC 2.3.1.41

Accepted name: β-ketoacyl-[acyl-carrier-protein] synthase I

Reaction: an acyl-[acyl-carrier protein] + a malonyl-[acyl-carrier protein] = a 3-oxoacyl-[acyl-carrier protein] + CO_2 + an [acyl-carrier protein]

Other name(s): β-ketoacyl-ACP synthase I; β-ketoacyl synthetase; β-ketoacyl-ACP synthetase; β-ketoacyl-acyl carrier protein synthetase; β-ketoacyl-[acyl carrier protein] synthase; β-ketoacylsynthase; condensing enzyme (ambiguous); 3-ketoacyl-acyl carrier protein synthase; fatty acid condensing enzyme; acyl-malonyl(acyl-carrier-protein)-condensing enzyme; acyl-malonyl acyl carrier protein-condensing enzyme; β-ketoacyl acyl carrier protein synthase; 3-oxoacyl-[acyl-carrier-protein] synthase; 3-oxoacyl:ACP synthase I; KASI; KAS I; FabF1; FabB; acyl-[acyl-carrier-protein]:malonyl-[acyl-carrier-protein] *C*-acyltransferase (decarboxylating)

Systematic name: acyl-[acyl-carrier protein]:malonyl-[acyl-carrier protein] *C*-acyltransferase (decarboxylating)

Comments: This enzyme is responsible for the chain-elongation step of dissociated (type II) fatty-acid biosynthesis, i.e. the addition of two C atoms to the fatty-acid chain. *Escherichia coli* mutants that lack this enzyme are deficient in unsaturated fatty acids. The enzyme can use fatty acyl thioesters of ACP (C_2 to C_{16}) as substrates, as well as fatty acyl thioesters of Co-A (C_4 to C_{16}) [653]. The substrate specificity is very similar to that of EC 2.3.1.179, β-ketoacyl-ACP synthase II, with the exception that the latter enzyme is far more active with palmitoleoyl-ACP ($C16\Delta^9$) as substrate, allowing the organism to regulate its fatty-acid composition with changes in temperature [653, 1023].

References: [47, 2761, 3552, 653, 1023, 3749, 630]

[EC 2.3.1.41 created 1972, modified 2006]

EC 2.3.1.42

Accepted name: glycerone-phosphate *O*-acyltransferase

Reaction: acyl-CoA + glycerone phosphate = CoA + acylglycerone phosphate

Other name(s): dihydroxyacetone phosphate acyltransferase
Systematic name: acyl-CoA:glycerone-phosphate *O*-acyltransferase
Comments: A membrane protein. Uses CoA derivatives of palmitate, stearate and oleate, with highest activity on palmitoyl-CoA.
References: [174, 699, 1197]

[EC 2.3.1.42 created 1972]

EC 2.3.1.43
Accepted name: phosphatidylcholine—sterol *O*-acyltransferase
Reaction: phosphatidylcholine + a sterol = 1-acylglycerophosphocholine + a sterol ester
Other name(s): lecithin—cholesterol acyltransferase; phospholipid—cholesterol acyltransferase; LCAT (lecithin-cholesterol acyltransferase); lecithin:cholesterol acyltransferase; lysolecithin acyltransferase
Systematic name: phosphatidylcholine:sterol *O*-acyltransferase
Comments: Palmitoyl, oleoyl and linoleoyl residues can be transferred; a number of sterols, including cholesterol, can act as acceptors. The bacterial enzyme also catalyses the reactions of EC 3.1.1.4 phospholipase A_2 and EC 3.1.1.5 lysophospholipase.
References: [208, 418, 1077, 3624]

[EC 2.3.1.43 created 1972, modified 1976]

EC 2.3.1.44
Accepted name: *N*-acetylneuraminate 4-*O*-acetyltransferase
Reaction: acetyl-CoA + *N*-acetylneuraminate = CoA + *N*-acetyl-4-*O*-acetylneuraminate
Other name(s): sialate *O*-acetyltransferase
Systematic name: acetyl-CoA:*N*-acetylneuraminate 4-*O*-acetyltransferase
Comments: Both free and glycosidically bound *N*-acetyl- and *N*-glycolyl- neuraminates can act as *O*-acetyl acceptors.
References: [3063, 3064]

[EC 2.3.1.44 created 1972]

EC 2.3.1.45
Accepted name: *N*-acetylneuraminate 7-*O*(or 9-*O*)-acetyltransferase
Reaction: acetyl-CoA + *N*-acetylneuraminate = CoA + *N*-acetyl-7-*O*(or 9-*O*)-acetylneuraminate
Other name(s): *N*-acetylneuraminate 7(8)-*O*-acetyltransferase; sialate *O*-acetyltransferase; *N*-acetylneuraminate 7,8-*O*-acetyltransferase; acetyl-CoA:*N*-acetylneuraminate-7- or 8-*O*-acetyltransferase; acetyl-CoA:*N*-acetylneuraminate-7- and/or 8-*O*-acetyltransferase; glycoprotein 7(9)-*O*-acetyltransferase; acetyl-CoA:*N*-acetylneuraminate-9(7)-*O*-acetyltransferase; *N*-acetylneuraminate O^7-(or O^9-)acetyltransferase; acetyl-CoA:*N*-acetylneuraminate-9(or 7)-*O*-acetyltransferase
Systematic name: acetyl-CoA:*N*-acetylneuraminate 7-*O*(or 9-*O*)-acetyltransferase
Comments: Both free and glycosidically bound *N*-acetyl- and *N*-glycolylneuraminates can act as *O*-acetyl acceptors.
References: [3063, 3064]

[EC 2.3.1.45 created 1972]

EC 2.3.1.46
Accepted name: homoserine *O*-succinyltransferase
Reaction: succinyl-CoA + L-homoserine = CoA + *O*-succinyl-L-homoserine
Other name(s): homoserine *O*-transsuccinylase; homoserine succinyltransferase
Systematic name: succinyl-CoA:L-homoserine *O*-succinyltransferase
References: [2947]

[EC 2.3.1.46 created 1976]

EC 2.3.1.47

Accepted name: 8-amino-7-oxononanoate synthase
Reaction: pimeloyl-[acyl-carrier protein] + L-alanine = 8-amino-7-oxononanoate + CO_2 + holo-[acyl-carrier protein]
Other name(s): 7-keto-8-aminopelargonic acid synthetase; 7-keto-8-aminopelargonic synthetase; 8-amino-7-oxopelargonate synthase; *bioF* (gene name)
Systematic name: 6-carboxyhexanoyl-[acyl-carrier protein]:L-alanine *C*-carboxyhexanoyltransferase (decarboxylating)
Comments: A pyridoxal-phosphate protein. The enzyme catalyses the decarboxylative condensation of L-alanine and pimeloyl-[acyl-carrier protein], a key step in the pathway for biotin biosynthesis. Pimeloyl-CoA can be used with lower efficiency [1971].
References: [820, 56, 2728, 3799, 1971]

[EC 2.3.1.47 created 1976, modified 2013]

EC 2.3.1.48

Accepted name: histone acetyltransferase
Reaction: acetyl-CoA + [protein]-L-lysine = CoA + [protein]-N^6-acetyl-L-lysine
Other name(s): nucleosome-histone acetyltransferase; histone acetokinase; histone acetylase; histone transacetylase; lysine acetyltransferase; protein lysine acetyltransferase; acetyl-CoA:histone acetyltransferase
Systematic name: acetyl-CoA:[protein]-L-lysine acetyltransferase
Comments: A group of enzymes acetylating histones. Several of the enzymes can also acetylate lysines in other proteins [1893, 3510].
References: [1004, 2103, 1893, 3510, 3900, 670]

[EC 2.3.1.48 created 1976, modified 2017]

EC 2.3.1.49

Accepted name: deacetyl-[citrate-(*pro*-3*S*)-lyase] *S*-acetyltransferase
Reaction: *S*-acetylphosphopantetheine + holo-[citrate (*pro*-3*S*)-lyase] = phosphopantetheine + acetyl-[citrate (*pro*-3*S*)-lyase]
Other name(s): *S*-acetyl phosphopantetheine:deacetyl citrate lyase *S*-acetyltransferase; deacetyl-[citrate-(*pro*-3*S*)-lyase] acetyltransferase; *S*-acetylphosphopantetheine:deacetyl-[citrate-oxaloacetate-lyase((*pro*-3*S*)-CH_2COO-→acetate)] *S*-acetyltransferase
Systematic name: *S*-acetylphosphopantetheine:holo-[citrate (*pro*-3*S*)-lyase] *S*-acetyltransferase
Comments: Both this enzyme and EC 6.2.1.22, [citrate (*pro*-3*S*)-lyase] ligase, acetylate and activate EC 4.1.3.6, citrate (*pro*-3*S*)-lyase.
References: [3240]

[EC 2.3.1.49 created 1976]

EC 2.3.1.50

Accepted name: serine *C*-palmitoyltransferase
Reaction: palmitoyl-CoA + L-serine = CoA + 3-dehydro-D-sphinganine + CO_2
Other name(s): serine palmitoyltransferase; SPT; 3-oxosphinganine synthetase; acyl-CoA:serine C-2 acyltransferase decarboxylating
Systematic name: palmitoyl-CoA:L-serine *C*-palmitoyltransferase (decarboxylating)
Comments: A pyridoxal-phosphate protein.
References: [374, 3349]

[EC 2.3.1.50 created 1976, modified 1982]

EC 2.3.1.51

Accepted name: 1-acylglycerol-3-phosphate *O*-acyltransferase
Reaction: acyl-CoA + 1-acyl-*sn*-glycerol 3-phosphate = CoA + 1,2-diacyl-*sn*-glycerol 3-phosphate
Other name(s): 1-acyl-*sn*-glycero-3-phosphate acyltransferase; 1-acyl-*sn*-glycerol 3-phosphate acyltransferase; 1-acylglycero-3-phosphate acyltransferase; 1-acylglycerolphosphate acyltransferase; 1-acylglycerophosphate acyltransferase; lysophosphatidic acid-acyltransferase
Systematic name: acyl-CoA:1-acyl-*sn*-glycerol-3-phosphate 2-*O*-acyltransferase
Comments: Acyl-[acyl-carrier protein] can also act as an acyl donor. The animal enzyme is specific for the transfer of unsaturated fatty acyl groups.
References: [954, 1329, 3952]

[EC 2.3.1.51 created 1976, modified 1990]

EC 2.3.1.52

Accepted name: 2-acylglycerol-3-phosphate *O*-acyltransferase
Reaction: acyl-CoA + 2-acyl-*sn*-glycerol 3-phosphate = CoA + 1,2-diacyl-*sn*-glycerol 3-phosphate
Other name(s): 2-acylglycerophosphate acyltransferase
Systematic name: acyl-CoA:2-acyl-*sn*-glycerol 3-phosphate *O*-acyltransferase
Comments: Saturated acyl-CoA thioesters are the most effective acyl donors.
References: [3952]

[EC 2.3.1.52 created 1976]

EC 2.3.1.53

Accepted name: phenylalanine *N*-acetyltransferase
Reaction: acetyl-CoA + L-phenylalanine = CoA + *N*-acetyl-L-phenylalanine
Other name(s): acetyl-CoA-L-phenylalanine α-*N*-acetyltransferase
Systematic name: acetyl-CoA:L-phenylalanine *N*-acetyltransferase
Comments: Also acts, more slowly, on L-histidine and L-alanine.
References: [1948]

[EC 2.3.1.53 created 1976]

EC 2.3.1.54

Accepted name: formate *C*-acetyltransferase
Reaction: acetyl-CoA + formate = CoA + pyruvate
Other name(s): pyruvate formate-lyase; pyruvic formate-lyase; formate acetyltransferase
Systematic name: acetyl-CoA:formate *C*-acetyltransferase
References: [1713]

[EC 2.3.1.54 created 1976]

[2.3.1.55 Deleted entry. kanamycin $6'$-N-acetyltransferase identical to EC 2.3.1.82 aminoglycoside $N^{6'}$-acetyltransferase]

[EC 2.3.1.55 created 1976, deleted 1999]

EC 2.3.1.56

Accepted name: aromatic-hydroxylamine *O*-acetyltransferase
Reaction: *N*-hydroxy-4-acetylaminobiphenyl + *N*-hydroxy-4-aminobiphenyl = *N*-hydroxy-4-aminobiphenyl + *N*-acetoxy-4-aminobiphenyl
Other name(s): aromatic hydroxylamine acetyltransferase; arylhydroxamate acyltransferase; arylhydroxamate N,*O*-acetyltransferase; arylhydroxamic acid N,*O*-acetyltransferase; arylhydroxamic acyltransferase; N,*O*-acetyltransferase; *N*-hydroxy-2-acetylaminofluorene *N*-O acyltransferase
Systematic name: *N*-hydroxy-4-acetylaminobiphenyl:*N*-hydroxy-4-aminobiphenyl *O*-acetyltransferase

Comments: Transfers the *N*-acetyl group of some aromatic acethydroxamates to the *O*-position of some aromatic hydroxylamines.
References: [211]

[EC 2.3.1.56 created 1976]

EC 2.3.1.57

Accepted name: diamine *N*-acetyltransferase
Reaction: acetyl-CoA + an alkane-α,ω-diamine = CoA + an *N*-acetyldiamine
Other name(s): spermidine acetyltransferase; putrescine acetyltransferase; putrescine (diamine)-acetylating enzyme; diamine acetyltransferase; spermidine/spermine N^1-acetyltransferase; spermidine N^1-acetyltransferase; acetyl-coenzyme A-1,4-diaminobutane *N*-acetyltransferase; putrescine acetylase; putrescine *N*-acetyltransferase
Systematic name: acetyl-CoA:alkane-α,ω-diamine *N*-acetyltransferase
Comments: Acts on propane-1,3-diamine, pentane-1,5-diamine, putrescine, spermidine (forming N^1- and N^8-acetylspermidine), spermine, N^1-acetylspermidine and N^8-acetylspermidine.
References: [2792]

[EC 2.3.1.57 created 1976, modified 1989]

EC 2.3.1.58

Accepted name: 2,3-diaminopropionate *N*-oxalyltransferase
Reaction: oxalyl-CoA + L-2,3-diaminopropanoate = CoA + N^3-oxalyl-L-2,3-diaminopropanoate
Other name(s): oxalyldiaminopropionate synthase; ODAP synthase; oxalyl-CoA:L-α,β-diaminopropionic acid oxalyltransferase; oxalyldiaminopropionic synthase; oxalyl-CoA:L-2,3-diaminopropanoate 3-*N*-oxalyltransferase
Systematic name: oxalyl-CoA:L-2,3-diaminopropanoate N^3-oxalyltransferase
References: [2105]

[EC 2.3.1.58 created 1976]

EC 2.3.1.59

Accepted name: gentamicin 2′-*N*-acetyltransferase
Reaction: acetyl-CoA + gentamicin C_{1a} = CoA + $N^{2\prime}$-acetylgentamicin C_{1a}
Other name(s): gentamycin acetyltransferase II; gentamycin 2′-*N*-acetyltransferase; acetyl-CoA:gentamycin-C_{1a} $N^{2\prime}$-acetyltransferase
Systematic name: acetyl-CoA:gentamicin-C_{1a} $N^{2\prime}$-acetyltransferase
Comments: The antibiotics gentamicin A, sisomicin, tobramycin, paromomycin, neomycin B, kanamycin B and kanamycin C can also act as acceptors.
References: [274]

[EC 2.3.1.59 created 1976]

EC 2.3.1.60

Accepted name: gentamicin 3-*N*-acetyltransferase
Reaction: acetyl-CoA + gentamicin C = CoA + N^3-acetylgentamicin C
Other name(s): gentamycin acetyltransferase I; aminoglycoside acetyltransferase AAC(3)-1; gentamycin 3-*N*-acetyltransferase; acetyl-CoA:gentamycin-C N^3-acetyltransferase; acetyl-CoA:gentamicin-C $N^{3\prime}$-acetyltransferase (incorrect); gentamicin 3′-*N*-acetyltransferase (incorrect)
Systematic name: acetyl-CoA:gentamicin-C N^3-acetyltransferase
Comments: Also acetylates sisomicin.
References: [88, 305, 3857]

[EC 2.3.1.60 created 1976, modified 2015]

EC 2.3.1.61

Accepted name: dihydrolipoyllysine-residue succinyltransferase

Reaction: succinyl-CoA + enzyme N^6-(dihydrolipoyl)lysine = CoA + enzyme N^6-(*S*-succinyldihydrolipoyl)lysine

Other name(s): dihydrolipoamide *S*-succinyltransferase; dihydrolipoamide succinyltransferase; dihydrolipoic transsuccinylase; dihydrolipolyl transsuccinylase; dihydrolipoyl transsuccinylase; lipoate succinyltransferase (*Escherichia coli*); lipoic transsuccinylase; lipoyl transsuccinylase; succinyl-CoA:dihydrolipoamide *S*-succinyltransferase; succinyl-CoA:dihydrolipoate *S*-succinyltransferase; enzyme-dihydrolipoyllysine:succinyl-CoA *S*-succinyltransferase

Systematic name: succinyl-CoA:enzyme-N^6-(dihydrolipoyl)lysine *S*-succinyltransferase

Comments: A multimer (24-mer) of this enzyme forms the core of the multienzyme complex, and binds tightly both EC 1.2.4.2, oxoglutarate dehydrogenase (succinyl-transferring) and EC 1.8.1.4, dihydrolipoyl dehydrogenase. The lipoyl group of this enzyme is reductively succinylated by EC 1.2.4.2, and the only observed direction catalysed by EC 2.3.1.61 is that where this succinyl group is passed to coenzyme A.

References: [718, 2842, 1712, 2665]

[EC 2.3.1.61 created 1978, modified 2003]

EC 2.3.1.62

Accepted name: 2-acylglycerophosphocholine *O*-acyltransferase

Reaction: acyl-CoA + 2-acyl-*sn*-glycero-3-phosphocholine = CoA + phosphatidylcholine

Other name(s): 2-acylglycerol-3-phosphorylcholine acyltransferase; 2-acylglycerophosphocholine acyltransferase

Systematic name: acyl-CoA:2-acyl-*sn*-glycero-3-phosphocholine *O*-acyltransferase

References: [1856, 3635]

[EC 2.3.1.62 created 1978]

EC 2.3.1.63

Accepted name: 1-alkylglycerophosphocholine *O*-acyltransferase

Reaction: acyl-CoA + 1-alkyl-*sn*-glycero-3-phosphocholine = CoA + 2-acyl-1-alkyl-*sn*-glycero-3-phosphocholine

Systematic name: acyl-CoA:1-alkyl-*sn*-glycero-3-phosphocholine *O*-acyltransferase

Comments: May be identical with EC 2.3.1.23 1-acylglycerophosphocholine *O*-acyltransferase.

References: [3723, 3724]

[EC 2.3.1.63 created 1978]

EC 2.3.1.64

Accepted name: agmatine N^4-coumaroyltransferase

Reaction: 4-coumaroyl-CoA + agmatine = CoA + *N*-(4-guanidinobutyl)-4-hydroxycinnamamide

Other name(s): *p*-coumaroyl-CoA-agmatine *N*-*p*-coumaroyltransferase; agmatine coumaroyltransferase; 4-coumaroyl-CoA:agmatine 4-*N*-coumaroyltransferase

Systematic name: 4-coumaroyl-CoA:agmatine N^4-coumaroyltransferase

References: [309]

[EC 2.3.1.64 created 1983]

EC 2.3.1.65

Accepted name: bile acid-CoA:amino acid *N*-acyltransferase

Reaction: choloyl-CoA + glycine = CoA + glycocholate

Other name(s): glycine—taurine *N*-acyltransferase; amino acid *N*-choloyltransferase; BAT; glycine *N*-choloyltransferase; BACAT; cholyl-CoA glycine-taurine *N*-acyltransferase; cholyl-CoA:taurine *N*-acyltransferase

Systematic name: choloyl-CoA:glycine *N*-choloyltransferase

Comments: Also acts on CoA derivatives of other bile acids. Taurine and 2-fluoro-β-alanine can act as substrates, but more slowly [1524]. The enzyme can also conjugate fatty acids to glycine and can act as a very-long-chain acyl-CoA thioesterase [2505]. Bile-acid—amino-acid conjugates serve as detergents in the gastrointestinal tract, solubilizing long chain fatty acids, mono- and diglycerides, fat-soluble vitamins and cholesterol [1524]. This is the second enzyme in a two-step process leading to the conjugation of bile acids with amino acids; the first step is the conversion of bile acids into their acyl-CoA thioesters, which is catalysed by EC 6.2.1.7, cholate—CoA ligase.

References: [651, 1538, 3672, 1524, 868, 1260, 2505]

[EC 2.3.1.65 created 1983, modified 2005]

EC 2.3.1.66

Accepted name: leucine *N*-acetyltransferase

Reaction: acetyl-CoA + L-leucine = CoA + *N*-acetyl-L-leucine

Other name(s): leucine acetyltransferase

Systematic name: acetyl-CoA:L-leucine *N*-acetyltransferase

Comments: Propanoyl-CoA can act as a donor, but more slowly. L-Arginine, L-valine, L-phenylalanine and peptides containing L-leucine can act as acceptors.

References: [3395]

[EC 2.3.1.66 created 1983]

EC 2.3.1.67

Accepted name: 1-alkylglycerophosphocholine *O*-acetyltransferase

Reaction: acetyl-CoA + 1-alkyl-*sn*-glycero-3-phosphocholine = CoA + 2-acetyl-1-alkyl-*sn*-glycero-3-phosphocholine

Other name(s): acetyl-CoA:1-alkyl-2-lyso-*sn*-glycero-3-phosphocholine 2-*O*-acetyltransferase; acetyl-CoA:lyso-PAF acetyltransferase; 1-alkyl-2-lysolecithin acetyltransferase; acyl-CoA:1-alkyl-*sn*-glycero-3-phosphocholine acyltransferase; blood platelet-activating factor acetyltransferase; lyso-GPC:acetyl CoA acetyltransferase; lyso-platelet activating factor:acetyl-CoA acetyltransferase; lysoPAF:acetyl CoA acetyltransferase; PAF acetyltransferase; platelet-activating factor acylhydrolase; platelet-activating factor-synthesizing enzyme; 1-alkyl-2-lyso-*sn*-glycero-3-phosphocholine acetyltransferase; lyso-platelet-activating factor:acetyl-CoA acetyltransferase

Systematic name: acetyl-CoA:1-alkyl-*sn*-glycero-3-phosphocholine 2-*O*-acetyltransferase

References: [3912]

[EC 2.3.1.67 created 1984]

EC 2.3.1.68

Accepted name: glutamine *N*-acyltransferase

Reaction: acyl-CoA + L-glutamine = CoA + *N*-acyl-L-glutamine

Systematic name: acyl-CoA:L-glutamine *N*-acyltransferase

Comments: Phenylacetyl-CoA and (indol-3-yl)acetyl-CoA, but not benzoyl-CoA, can act as acyl donors. Not identical with EC 2.3.1.13 glycine *N*-acyltransferase or EC 2.3.1.71 glycine *N*-benzoyltransferase.

References: [3797]

[EC 2.3.1.68 created 1984]

EC 2.3.1.69

Accepted name: monoterpenol *O*-acetyltransferase
Reaction: acetyl-CoA + a monoterpenol = CoA + a monoterpenol acetate ester
Other name(s): menthol transacetylase
Systematic name: acetyl-CoA:monoterpenol *O*-acetyltransferase
Comments: (-)-Menthol, (+)-neomenthol, borneol, and also cyclohexanol and decan-1-ol can be acetylated.
References: [632, 2144]

[EC 2.3.1.69 created 1984]

[2.3.1.70 Deleted entry. CDP-acylglycerol O-arachidonoyltransferase. This enzyme was deleted following a retraction of the evidence upon which the entry had been drafted (Thompson, W. and Zuk, R.T. Acylation of CDP-monoacylglycerol cannot be confirmed. J. Biol. Chem. 258 (1983) 9623. [PMID: 6885763]).]

[EC 2.3.1.70 created 1984, deleted 2009]

EC 2.3.1.71

Accepted name: glycine *N*-benzoyltransferase
Reaction: benzoyl-CoA + glycine = CoA + hippurate
Other name(s): benzoyl CoA-amino acid *N*-acyltransferase; benzoyl-CoA:glycine *N*-acyltransferase
Systematic name: benzoyl-CoA:glycine *N*-benzoyltransferase
Comments: Not identical with EC 2.3.1.13, glycine *N*-acyltransferase or EC 2.3.1.68, glutamine *N*-acyltransferase
References: [2417]

[EC 2.3.1.71 created 1984]

EC 2.3.1.72

Accepted name: indoleacetylglucose—inositol *O*-acyltransferase
Reaction: 1-*O*-(indol-3-yl)acetyl-β-D-glucose + *myo*-inositol = D-glucose + *O*-(indol-3-yl)acetyl-*myo*-inositol
Other name(s): indole-3-acetyl-β-1-D-glucoside:*myo*-inositol indoleacetyltransferase; 1-*O*-(indol-3-ylacetyl)-β-D-glucose:*myo*-inositol indole-3-ylacetyltransferase
Systematic name: 1-*O*-(indol-3-yl)acetyl-β-D-glucose:*myo*-inositol (indol-3-yl)acetyltransferase
Comments: The position of acylation is indeterminate because of the ease of acyl transfer between hydroxy groups.
References: [2237, 2236]

[EC 2.3.1.72 created 1984, modified 2003]

EC 2.3.1.73

Accepted name: diacylglycerol—sterol *O*-acyltransferase
Reaction: a 1,2-diacyl-*sn*-glycerol + sterol = a 1-acyl-*sn*-glycerol + sterol ester
Other name(s): 1,2-diacyl-*sn*-glycerol:sterol acyl transferase
Systematic name: 1,2-diacyl-*sn*-glycerol:sterol *O*-acyltransferase
Comments: Cholesterol, sitosterol, campesterol and diacylglycerol can act as acceptors. Transfers a number of long-chain fatty acyl groups.
References: [208, 1015, 1016]

[EC 2.3.1.73 created 1984]

EC 2.3.1.74

Accepted name: chalcone synthase
Reaction: **3** malonyl-CoA + 4-coumaroyl-CoA = **4** CoA + naringenin chalcone + **3** CO_2
Other name(s): naringenin-chalcone synthase; flavanone synthase; $6'$-deoxychalcone synthase; chalcone synthetase; DOCS; CHS

Systematic name: malonyl-CoA:4-coumaroyl-CoA malonyltransferase (cyclizing)

Comments: The enzyme catalyses the first committed step in the biosynthesis of flavonoids. It can also act on dihydro-4-coumaroyl-CoA, forming phloretin.

References: [142, 1283, 3936]

[EC 2.3.1.74 created 1984, modified 2018]

EC 2.3.1.75

Accepted name: long-chain-alcohol *O*-fatty-acyltransferase

Reaction: acyl-CoA + a long-chain alcohol = CoA + a long-chain ester

Other name(s): wax synthase; wax-ester synthase

Systematic name: acyl-CoA:long-chain-alcohol *O*-acyltransferase

Comments: Transfers saturated or unsaturated acyl residues of chain-length C_{18} to C_{20} to long-chain alcohols, forming waxes. The best acceptor is *cis*-icos-11-en-1-ol.

References: [3906]

[EC 2.3.1.75 created 1984]

EC 2.3.1.76

Accepted name: retinol *O*-fatty-acyltransferase

Reaction: acyl-CoA + retinol = CoA + retinyl ester

Other name(s): retinol acyltransferase; retinol fatty-acyltransferase

Systematic name: acyl-CoA:retinol *O*-acyltransferase

Comments: Acts on palmitoyl-CoA and other long-chain fatty-acyl derivatives of CoA.

References: [1282, 2937]

[EC 2.3.1.76 created 1984]

EC 2.3.1.77

Accepted name: triacylglycerol—sterol *O*-acyltransferase

Reaction: triacylglycerol + a 3β-hydroxysteroid = diacylglycerol + a 3β-hydroxysteroid ester

Other name(s): triacylglycerol:sterol acyltransferase

Systematic name: triacylglycerol:3β-hydroxysteroid *O*-acyltransferase

Comments: Tripalmitoylglycerol and, more slowly, other triacylglycerols containing C_6 to C_{22} fatty acids, can act as donors. The best acceptors are 3β-hydroxysteroids with a planar ring system.

References: [4085]

[EC 2.3.1.77 created 1984]

EC 2.3.1.78

Accepted name: heparan-α-glucosaminide *N*-acetyltransferase

Reaction: acetyl-CoA + heparan sulfate α-D-glucosaminide = CoA + heparan sulfate *N*-acetyl-α-D-glucosaminide

Other name(s): acetyl-CoA:α-glucosaminide *N*-acetyltransferase

Systematic name: acetyl-CoA:heparan-α-D-glucosaminide *N*-acetyltransferase

Comments: Brings about the acetylation of glucosamine groups of heparan sulfate and heparin from which the sulfate has been removed. Also acts on heparin. Not identical with EC 2.3.1.3 glucosamine *N*-acetyltransferase or EC 2.3.1.4 glucosamine-phosphate *N*-acetyltransferase.

References: [1707, 2731]

[EC 2.3.1.78 created 1984]

EC 2.3.1.79

Accepted name: maltose *O*-acetyltransferase

Reaction: acetyl-CoA + maltose = CoA + 6-*O*-acetyl-α-D-glucopyranosyl-(1→4)-D-glucose

Other name(s): maltose transacetylase; maltose *O*-acetyltransferase; MAT

Systematic name: acetyl-CoA:maltose *O*-acetyltransferase

Comments: Not identical with EC 2.3.1.18, galactoside *O*-acetyltransferase. The acetyl group is added exclusively to the C6 position of glucose and to the C6 position of the non-reducing glucose residue of maltose [1911]. Other substrates of this enzyme are glucose, which is a better substrate than maltose [376], and mannose and frucose, which are poorer substrates than maltose [376]. Isopropyl-β-thio-galactose, which is a good substrate for EC 2.3.1.118 is a poor substrate for this enzyme [1911].

References: [958, 376, 1911]

[EC 2.3.1.79 created 1984]

EC 2.3.1.80

Accepted name: cysteine-*S*-conjugate *N*-acetyltransferase

Reaction: acetyl-CoA + an L-cysteine-*S*-conjugate = CoA + an *N*-acetyl-L-cysteine-*S*-conjugate

Systematic name: acetyl-CoA:S-substituted L-cysteine *N*-acetyltransferase

Comments: *S*-Benzyl-L-cysteine and, in decreasing order of activity, *S*-butyl-L-cysteine, *S*-propyl-L-cysteine, *O*-benzyl-L-serine and *S*-ethyl-L-cysteine, can act as acceptors.

References: [787]

[EC 2.3.1.80 created 1984]

EC 2.3.1.81

Accepted name: aminoglycoside 3-*N*-acetyltransferase

Reaction: acetyl-CoA + a 2-deoxystreptamine antibiotic = CoA + N^3-acetyl-2-deoxystreptamine antibiotic

Other name(s): 3-aminoglycoside acetyltransferase; 3-*N*-aminoglycoside acetyltransferase; aminoglycoside N^3-acetyltransferase; acetyl-CoA:2-deoxystreptamine-antibiotic $N^{3'}$-acetyltransferase (incorrect); aminoglycoside $N^{3'}$-acetyltransferase (incorrect)

Systematic name: acetyl-CoA:2-deoxystreptamine-antibiotic N^3-acetyltransferase

Comments: Different from EC 2.3.1.60 gentamicin 3-*N*-acetyltransferase. A wide range of antibiotics containing the 2-deoxystreptamine ring can act as acceptors, including gentamicin, kanamycin, tobramycin, neomycin and apramycin.

References: [681]

[EC 2.3.1.81 created 1984, modified 2015]

EC 2.3.1.82

Accepted name: aminoglycoside 6′-*N*-acetyltransferase

Reaction: acetyl-CoA + kanamycin-B = CoA + $N^{6'}$-acetylkanamycin-B

Other name(s): aminoglycoside $N^{6'}$-acetyltransferase; aminoglycoside-6′-acetyltransferase; aminoglycoside-6-*N*-acetyltransferase; kanamycin acetyltransferase

Systematic name: acetyl-CoA:kanamycin-B $N^{6'}$-acetyltransferase

Comments: The antibiotics kanamycin A, kanamycin B, neomycin, gentamicin C_{1a}, gentamicin C_2 and sisomicin are substrates. The antibiotic tobramycin, but not paromomycin, can also act as acceptor. The 6-amino group of the purpurosamine ring is acetylated.

References: [1881, 275, 768]

[EC 2.3.1.82 created 1976 as EC 2.3.1.55, transferred 1999 to EC 2.3.1.82, modified 1999, modified 2015]

EC 2.3.1.83

Accepted name: phosphatidylcholine—dolichol *O*-acyltransferase

Reaction: 3-*sn*-phosphatidylcholine + dolichol = 1-acyl-*sn*-glycero-3-phosphocholine + acyldolichol
Systematic name: 3-*sn*-phosphatidylcholine:dolichol *O*-acyltransferase
References: [1625, 2790]

[EC 2.3.1.83 created 1984]

EC 2.3.1.84

Accepted name: alcohol *O*-acetyltransferase
Reaction: acetyl-CoA + an alcohol = CoA + an acetyl ester
Other name(s): alcohol acetyltransferase
Systematic name: acetyl-CoA:alcohol *O*-acetyltransferase
Comments: Acts on a range of short-chain aliphatic alcohols, including methanol and ethanol
References: [4005]

[EC 2.3.1.84 created 1984]

EC 2.3.1.85

Accepted name: fatty-acid synthase
Reaction: acetyl-CoA + ***n*** malonyl-CoA + **2*n*** NADPH + **2*n*** H^+ = a long-chain fatty acid + (***n*+1**) CoA + ***n*** CO_2 + **2*n*** $NADP^+$
Other name(s): FASN (gene name)
Systematic name: acyl-CoA:malonyl-CoA *C*-acyltransferase (decarboxylating, oxoacyl- and enoyl-reducing and thioester-hydrolysing)
Comments: The animal enzyme is a multi-functional protein catalysing the reactions of EC 2.3.1.38 [acyl-carrier-protein] *S*-acetyltransferase, EC 2.3.1.39 [acyl-carrier-protein] *S*-malonyltransferase, EC 2.3.1.41 3-oxoacyl-[acyl-carrier-protein] synthase, EC 1.1.1.100 3-oxoacyl-[acyl-carrier-protein] reductase, EC 4.2.1.59 3-hydroxyacyl-[acyl-carrier-protein] dehydratase, EC 1.3.1.39 enoyl-[acyl-carrier-protein] reductase (NADPH, *Re*-specific) and EC 3.1.2.14 oleoyl-[acyl-carrier-protein] hydrolase. *cf.* EC 2.3.1.86, fatty-acyl-CoA synthase.
References: [3356, 3721]

[EC 2.3.1.85 created 1984]

EC 2.3.1.86

Accepted name: fatty-acyl-CoA synthase
Reaction: acetyl-CoA + ***n*** malonyl-CoA + **2*n*** NADPH + **4*n*** H^+ = long-chain-acyl-CoA + ***n*** CoA + ***n*** CO_2 + **2*n*** $NADP^+$
Other name(s): yeast fatty acid synthase; FAS1 (gene name); FAS2 (gene name)
Systematic name: acyl-CoA:malonyl-CoA *C*-acyltransferase (decarboxylating, oxoacyl- and enoyl- reducing)
Comments: The enzyme from yeasts (Ascomycota and Basidiomycota) is a multi-functional protein complex composed of two subunits. One subunit catalyses the reactions EC 1.1.1.100, 3-oxoacyl-[acyl-carrier-protein] reductase and EC 2.3.1.41, 3-oxoacyl-[acyl-carrier-protein] synthase, while the other subunit catalyses the reactions of EC 2.3.1.38, [acyl-carrier-protein] *S*-acetyltransferase, EC 2.3.1.39, [acyl-carrier-protein] *S*-malonyltransferase, EC 4.2.1.59, 3-hydroxypalmitoyl-[acyl-carrier-protein] dehydratase, EC 1.3.1.10, enoyl-[acyl-carrier-protein] reductase (NADPH, *Si*-specific) and EC 1.1.1.279, (*R*)-3-hydroxyacid ester dehydrogenase. The enzyme differs from the animal enzyme (EC 2.3.1.85) in that the enoyl reductase domain requires FMN as a cofactor, and the ultimate product is an acyl-CoA (usually palmitoyl-CoA) instead of a free fatty acid.
References: [3120, 3721, 3494]

[EC 2.3.1.86 created 1984, modified 2003, modified 2013]

EC 2.3.1.87

Accepted name: aralkylamine *N*-acetyltransferase
Reaction: acetyl-CoA + a 2-arylethylamine = CoA + an *N*-acetyl-2-arylethylamine
Other name(s): serotonin acetyltransferase; serotonin acetylase; arylalkylamine *N*-acetyltransferase; serotonin *N*-acetyltransferase; AANAT; melatonin rhythm enzyme
Systematic name: acetyl-CoA:2-arylethylamine *N*-acetyltransferase
Comments: Narrow specificity towards 2-arylethylamines, including serotonin (5-hydroxytryptamine), tryptamine, 5-methoxytryptamine and phenylethylamine. This is the penultimate enzyme in the production of melatonin (5-methoxy-*N*-acetyltryptamine) and controls its synthesis (*cf.* EC 2.1.1.4, acetylserotonin *O*-methyltransferase). Differs from EC 2.3.1.5 arylamine *N*-acetyltransferase.
References: [3696, 901, 1654]

[EC 2.3.1.87 created 1986, modified 2005]

[2.3.1.88 Transferred entry. peptide α-N-acetyltransferase. Now covered by EC 2.3.1.254, N-terminal methionine N^{α}*-acetyltransferase NatB, EC 2.3.1.255, N-terminal amino-acid* N^{α}*-acetyltransferase NatA, EC 2.3.1.256, N-terminal methionine* N^{α}*-acetyltransferase NatC, EC 2.3.1.257, N-terminal* L*-serine* N^{α}*-acetyltransferase NatD, EC 2.3.1.258, N-terminal methionine* N^{α}*-acetyltransferase NatE and EC 2.3.1.259, N-terminal methionine* N^{α}*-acetyltransferase NatF]*

[EC 2.3.1.88 created 1986, modified 1989, deleted 2016]

EC 2.3.1.89

Accepted name: tetrahydrodipicolinate *N*-acetyltransferase
Reaction: acetyl-CoA + (*S*)-2,3,4,5-tetrahydropyridine-2,6-dicarboxylate + H_2O = CoA + L-2-acetamido-6-oxoheptanedioate
Other name(s): tetrahydrodipicolinate acetylase; tetrahydrodipicolinate:acetyl-CoA acetyltransferase; acetyl-CoA:L-2,3,4,5-tetrahydrodipicolinate N^2-acetyltransferase; acetyl-CoA:(*S*)-2,3,4,5-tetrahydropyridine-2,6-dicarboxylate 2-*N*-acetyltransferase
Systematic name: acetyl-CoA:(*S*)-2,3,4,5-tetrahydropyridine-2,6-dicarboxylate N^2-acetyltransferase
References: [515]

[EC 2.3.1.89 created 1986]

EC 2.3.1.90

Accepted name: β-glucogallin *O*-galloyltransferase
Reaction: **2** 1-*O*-galloyl-β-D-glucose = D-glucose + 1-*O*,6-*O*-digalloyl-β-D-glucose
Systematic name: 1-*O*-galloyl-β-D-glucose:1-*O*-galloyl-β-D-glucose *O*-galloyltransferase
Comments: β-Glucogallin can act as donor and as acceptor. Digalloylglucose can also act as acceptor, with the formation of 1-*O*,2-*O*,6-*O*-trigalloylglucose
References: [715, 1149]

[EC 2.3.1.90 created 1986]

EC 2.3.1.91

Accepted name: sinapoylglucose—choline *O*-sinapoyltransferase
Reaction: 1-*O*-sinapoyl-β-D-glucose + choline = D-glucose + sinapoylcholine
Other name(s): sinapine synthase
Systematic name: 1-*O*-sinapoyl-β-D-glucose:choline 1-*O*-sinapoyltransferase
References: [1126]

[EC 2.3.1.91 created 1986]

EC 2.3.1.92

Accepted name: sinapoylglucose—malate *O*-sinapoyltransferase
Reaction: 1-*O*-sinapoyl-β-D-glucose + (*S*)-malate = D-glucose + sinapoyl-(*S*)-malate

Other name(s): 1-sinapoylglucose-L-malate sinapoyltransferase; sinapoylglucose:malate sinapoyltransferase
Systematic name: 1-*O*-sinapoyl-β-D-glucose:(*S*)-malate *O*-sinapoyltransferase
References: [3361]

[EC 2.3.1.92 created 1986]

EC 2.3.1.93

Accepted name: 13-hydroxylupanine *O*-tigloyltransferase
Reaction: (*E*)-2-methylcrotonoyl-CoA + 13-hydroxylupanine = CoA + 13-[(*E*)-2-methylcrotonoyl]oxylupanine
Other name(s): tigloyl-CoA:13-hydroxylupanine *O*-tigloyltransferase; 13-hydroxylupanine acyltransferase
Systematic name: (*E*)-2-methylcrotonoyl-CoA:13-hydroxylupanine *O*-2-methylcrotonoyltransferase
Comments: Benzoyl-CoA and, more slowly, pentanoyl-CoA, 3-methylbutanoyl-CoA and butanoyl-CoA can act as acyl donors. Involved in the synthesis of lupanine alkaloids.
References: [3873, 2548, 3397]

[EC 2.3.1.93 created 1986, modified 2011]

EC 2.3.1.94

Accepted name: 6-deoxyerythronolide-B synthase
Reaction: propanoyl-CoA + **6** (2*S*)-methylmalonyl-CoA + **6** NADPH + **6** H^+ = 6-deoxyerythronolide B + **7** CoA + **6** CO_2 + H_2O + **6** $NADP^+$
Other name(s): erythronolide condensing enzyme; malonyl-CoA:propionyl-CoA malonyltransferase (cyclizing); erythronolide synthase; malonyl-CoA:propanoyl-CoA malonyltransferase (cyclizing); deoxyerythronolide B synthase; 6-deoxyerythronolide B synthase; DEBS
Systematic name: propanoyl-CoA:(2*S*)-methylmalonyl-CoA malonyltransferase (cyclizing)
Comments: The product, 6-deoxyerythronolide B, contains a 14-membered lactone ring and is an intermediate in the biosynthesis of erythromycin antibiotics. Biosynthesis of 6-deoxyerythronolide B requires 28 active sites that are precisely arranged along three large polypeptides, denoted DEBS1, -2 and -3 []. The polyketide product is synthesized by the processive action of a loading didomain, six extension modules and a terminal thioesterase domain [1664]. Each extension module contains a minimum of a ketosynthase (KS), an acyltransferase (AT) and an acyl-carrier protein (ACP). The KS domain both accepts the growing polyketide chain from the previous module and catalyses the subsequent decarboxylative condensation between this substrate and an ACP-bound methylmalonyl extender unit, introduce by the AT domain. This combined effort gives rise to a new polyketide intermediate that has been extended by two carbon atoms [1664].
References: [2564, 2896, 2682, 3576, 1664]

[EC 2.3.1.94 created 1989, modified 2008]

EC 2.3.1.95

Accepted name: trihydroxystilbene synthase
Reaction: **3** malonyl-CoA + 4-coumaroyl-CoA = **4** CoA + *trans*-resveratrol + **4** CO_2
Other name(s): resveratrol synthase; stilbene synthase (ambiguous)
Systematic name: malonyl-CoA:4-coumaroyl-CoA malonyltransferase (cyclizing)
Comments: Not identical with EC 2.3.1.74 naringenin-chalcone synthase or EC 2.3.1.146 pinosylvin synthase.
References: [3104]

[EC 2.3.1.95 created 1989]

[2.3.1.96 Deleted entry. glycoprotein N-palmitoyltransferase]

[EC 2.3.1.96 created 1989, deleted 2018]

EC 2.3.1.97

Accepted name: glycylpeptide *N*-tetradecanoyltransferase
Reaction: tetradecanoyl-CoA + an N-terminal-glycyl-[protein] = CoA + an N-terminal-*N*-tetradecanoylglycyl-[protein]
Other name(s): NMT (gene name); peptide *N*-myristoyltransferase; myristoyl-CoA-protein *N*-myristoyltransferase; myristoyl-coenzyme A:protein *N*-myristoyl transferase; myristoylating enzymes; protein *N*-myristoyltransferase; tetradecanoyl-CoA:glycylpeptide *N*-tetradecanoyltransferase
Systematic name: tetradecanoyl-CoA:N-terminal-glycine-[protein] N-tetradecanoyltransferase
Comments: The enzyme catalyses the transfer of myristic acid from myristoyl-CoA to the amino group of the N-terminal glycine residue in a variety of eukaryotic proteins. It uses an ordered Bi Bi reaction in which myristoyl-CoA binds to the enzyme prior to the binding of the peptide substrate, and CoA release precedes the release of the myristoylated peptide. The enzyme from yeast is profoundly affected by amino acids further from the N-terminus, and is particularly stimulated by a serine residue at position 5.
References: [1171, 1314, 3557, 2196, 877]

[EC 2.3.1.97 created 1989, modified 1990, modified 2018]

EC 2.3.1.98
Accepted name: chlorogenate—glucarate *O*-hydroxycinnamoyltransferase
Reaction: chlorogenate + glucarate = quinate + 2-*O*-caffeoylglucarate
Other name(s): chlorogenate:glucarate caffeoyltransferase; chlorogenic acid:glucaric acid *O*-caffeoyltransferase; chlorogenate:glucarate caffeoyltransferase
Systematic name: chlorogenate:glucarate *O*-(hydroxycinnamoyl)transferase
Comments: Galactarate can act as acceptor, more slowly. Involved with EC 2.3.1.99 quinate *O*-hydroxycinnamoyltransferase in the formation of caffeoylglucarate in tomato.
References: [3362, 3363]

[EC 2.3.1.98 created 1989, modified 1990]

EC 2.3.1.99
Accepted name: quinate *O*-hydroxycinnamoyltransferase
Reaction: feruloyl-CoA + quinate = CoA + *O*-feruloylquinate
Other name(s): hydroxycinnamoyl coenzyme A-quinate transferase
Systematic name: feruloyl-CoA:quinate *O*-(hydroxycinnamoyl)transferase
Comments: Caffeoyl-CoA and 4-coumaroyl-CoA can also act as donors, but more slowly. Involved in the biosynthesis of chlorogenic acid in sweet potato and, with EC 2.3.1.98 chlorogenate—glucarate *O*-hydroxycinnamoyltransferase, in the formation of caffeoyl-CoA in tomato.
References: [3363, 3364, 3681]

[EC 2.3.1.99 created 1989, modified 1990]

EC 2.3.1.100
Accepted name: [myelin-proteolipid] *O*-palmitoyltransferase
Reaction: palmitoyl-CoA + [myelin proteolipid] = CoA + *O*-palmitoyl-[myelin proteolipid]
Other name(s): myelin PLP acyltransferase; acyl-protein synthetase; myelin-proteolipid *O*-palmitoyltransferase
Systematic name: palmitoyl-CoA:[myelin-proteolipid] *O*-palmitoyltransferase
Comments: The enzyme in brain transfers long-chain acyl residues to the endogenous myelin proteolipid
References: [315]

[EC 2.3.1.100 created 1989]

EC 2.3.1.101
Accepted name: formylmethanofuran—tetrahydromethanopterin *N*-formyltransferase

Reaction: formylmethanofuran + 5,6,7,8-tetrahydromethanopterin = methanofuran + 5-formyl-5,6,7,8-tetrahydromethanopterin

Other name(s): formylmethanofuran-tetrahydromethanopterin formyltransferase; formylmethanofuran:tetrahydromethanopterin formyltransferase; *N*-formylmethanofuran(CHO-MFR):tetrahydromethanopterin(H_4MPT) formyltransferase; FTR; formylmethanofuran:5,6,7,8-tetrahydromethanopterin N^5-formyltransferase

Systematic name: formylmethanofuran:5,6,7,8-tetrahydromethanopterin 5-formyltransferase

Comments: Methanofuran is a complex 4-substituted furfurylamine and is involved in the formation of methane from CO_2 in *Methanobacterium thermoautotrophicum*.

References: [754, 1920]

[EC 2.3.1.101 created 1989]

EC 2.3.1.102

Accepted name: N^6-hydroxylysine *N*-acetyltransferase

Reaction: acetyl-CoA + N^6-hydroxy-L-lysine = CoA + N^6-acetyl-N^6-hydroxy-L-lysine

Other name(s): N^6-hydroxylysine:acetyl CoA N^6-transacetylase; N^6-hydroxylysine acetylase; acetyl-CoA:6-*N*-hydroxy-L-lysine 6-acetyltransferase; N^6-hydroxylysine *O*-acetyltransferase (incorrect)

Systematic name: acetyl-CoA:N^6-hydroxy-L-lysine 6-acetyltransferase

Comments: Involved in the synthesis of aerobactin from lysine in a strain of *Escherichia coli*.

References: [624, 688]

[EC 2.3.1.102 created 1989]

EC 2.3.1.103

Accepted name: sinapoylglucose—sinapoylglucose *O*-sinapoyltransferase

Reaction: **2** 1-*O*-sinapoyl-β-D-glucose = D-glucose + 1,2-bis-*O*-sinapoyl-β-D-glucose

Other name(s): hydroxycinnamoylglucose-hydroxycinnamoylglucose hydroxycinnamoyltransferase; 1-(hydroxycinnamoyl)-glucose:1-(hydroxycinnamoyl)-glucose hydroxycinnamoyltransferase; 1-*O*-(4-hydroxy-3,5-dimethoxycinnamoyl)-β-D-glucoside:1-*O*-(4-hydroxy-3,5-dimethoxycinnamoyl)-β-D-glucoside 1-*O*-sinapoyltransferase

Systematic name: 1-*O*-sinapoyl-β-D-glucose:1-*O*-sinnapoyl-β-D-glucose 1-*O*-sinapoyltransferase

Comments: The plant enzyme, characterized from Brassicaceae, is involved in secondary metabolism.

References: [656, 950]

[EC 2.3.1.103 created 1989]

[2.3.1.104 Deleted entry. 1-alkenylglycerophosphocholine O-acyltransferase. The activity is covered by EC 2.3.1.25, plasmalogen synthase]

[EC 2.3.1.104 created 1989, deleted 2013]

EC 2.3.1.105

Accepted name: alkylglycerophosphate 2-*O*-acetyltransferase

Reaction: acetyl-CoA + 1-alkyl-*sn*-glycero-3-phosphate = CoA + 1-alkyl-2-acetyl-*sn*-glycero-3-phosphate

Other name(s): alkyllyso-GP:acetyl-CoA acetyltransferase

Systematic name: acetyl-CoA:1-alkyl-*sn*-glycero-3-phosphate 2-*O*-acetyltransferase

Comments: Involved in the biosynthesis of thrombocyte activating factor in animal tissues.

References: [1904]

[EC 2.3.1.105 created 1989]

EC 2.3.1.106

Accepted name: tartronate *O*-hydroxycinnamoyltransferase

Reaction: sinapoyl-CoA + 2-hydroxymalonate = CoA + sinapoyltartronate

Other name(s): tartronate sinapoyltransferase; hydroxycinnamoyl-coenzyme-A:tartronate hydroxycinnamoyltransferase

Systematic name: sinapoyl-CoA:2-hydroxymalonate *O*-(hydroxycinnamoyl)transferase

Comments: 4-Coumaroyl-CoA (4-hydroxycinnamoyl-CoA), caffeoyl-CoA (3,4-dihydroxycinnamoyl-CoA) and feruloyl-CoA (4-hydroxy-3-methoxycinnamoyl-CoA) can also act as donors for the enzyme from the mung bean (*Vigna radiata*).

References: [3366]

[EC 2.3.1.106 created 1989, modified 1990, modified 2002]

EC 2.3.1.107

Accepted name: deacetylvindoline *O*-acetyltransferase

Reaction: acetyl-CoA + deacetylvindoline = CoA + vindoline

Other name(s): deacetylvindoline acetyltransferase; DAT; 17-*O*-deacetylvindoline-17-*O*-acetyltransferase; acetyl-coenzyme A-deacetylvindoline 4-*O*-acetyltransferase; acetyl-CoA-17-*O*-deacetylvindoline 17-*O*-acetyltransferase; acetylcoenzyme A:deacetylvindoline 4-*O*-acetyltransferase; acetylcoenzyme A:deacetylvindoline *O*-acetyltransferase; 17-*O*-deacetylvindoline *O*-acetyltransferase; acetyl-CoA:17-*O*-deacetylvindoline 17-*O*-acetyltransferase

Systematic name: acetyl-CoA:deacetylvindoline 4-*O*-acetyltransferase

Comments: Catalyses the final step in the biosynthesis of vindoline from tabersonine in the Madagascar periwinkle, *Catharanthus roseus*.

References: [864]

[EC 2.3.1.107 created 1989, modified 2005]

EC 2.3.1.108

Accepted name: α-tubulin *N*-acetyltransferase

Reaction: acetyl-CoA + [α-tubulin]-L-lysine = CoA + [α-tubulin]-N^6-acetyl-L-lysine

Other name(s): α-tubulin acetylase; TAT; α-tubulin acetyltransferase; tubulin *N*-acetyltransferase; acetyl-CoA:α-tubulin-L-lysine *N*-acetyltransferase; acetyl-CoA:[α-tubulin]-L-lysine 6-*N*-acetyltransferase

Systematic name: acetyl-CoA:[α-tubulin]-L-lysine N^6-acetyltransferase

Comments: The enzyme from *Chlamydomonas* flagella also acetylates mammalian brain α-tubulin.

References: [1136]

[EC 2.3.1.108 created 1989]

EC 2.3.1.109

Accepted name: arginine *N*-succinyltransferase

Reaction: succinyl-CoA + L-arginine = CoA + N^2-succinyl-L-arginine

Other name(s): arginine succinyltransferase; AstA; arginine and ornithine N^2-succinyltransferase; AOST; AST; succinyl-CoA:L-arginine 2-*N*-succinyltransferase

Systematic name: succinyl-CoA:L-arginine N^2-succinyltransferase

Comments: Also acts on L-ornithine. This is the first enzyme in the arginine succinyltransferase (AST) pathway for the catabolism of arginine [3791]. This pathway converts the carbon skeleton of arginine into glutamate, with the concomitant production of ammonia and conversion of succinyl-CoA into succinate and CoA. The five enzymes involved in this pathway are EC 2.3.1.109 (arginine *N*-succinyltransferase), EC 3.5.3.23 (*N*-succinylarginine dihydrolase), EC 2.6.1.81 (succinylornithine transaminase), EC 1.2.1.71 (succinylglutamate-semialdehyde dehydrogenase) and EC 3.5.1.96 (succinylglutamate desuccinylase) [3792, 644].

References: [3791, 3792, 3567, 1469, 3090, 644, 645]

[EC 2.3.1.109 created 1989, modified 2006]

EC 2.3.1.110

Accepted name: tyramine *N*-feruloyltransferase

Reaction: feruloyl-CoA + tyramine = CoA + *N*-feruloyltyramine

Other name(s): tyramine *N*-feruloyl-CoA transferase; feruloyltyramine synthase; feruloyl-CoA tyramine *N*-feruloyl-CoA transferase; tyramine feruloyltransferase

Systematic name: feruloyl-CoA:tyramine *N*-(hydroxycinnamoyl)transferase

Comments: Cinnamoyl-CoA, 4-coumaroyl-CoA and sinapoyl-CoA can also act as donors, and some aromatic amines can act as acceptors.

References: [2430]

[EC 2.3.1.110 created 1989]

EC 2.3.1.111

Accepted name: mycocerosate synthase

Reaction: (1) a long-chain acyl-[mycocerosic acid synthase] + **3** methylmalonyl-CoA + **6** NADPH + **6** H^+ = a trimethylated-mycocerosoyl-[mycocerosate synthase] + **3** CoA + **3** CO_2 + **6** $NADP^+$ + **3** H_2O
(2) a long-chain acyl-[mycocerosic acid synthase] + **4** methylmalonyl-CoA + **8** NADPH + **8** H^+ = a tetramethylated-mycocerosoyl-[mycocerosate synthase] + **4** CoA + **4** CO_2 + **8** $NADP^+$ + **4** H_2O

Other name(s): *mas* (gene name); mycocerosic acid synthase; acyl-CoA:methylmalonyl-CoA *C*-acyltransferase (decarboxylating, oxoacyl- and enoyl-reducing); long-chain acyl-CoA:methylmalonyl-CoA *C*-acyltransferase (mycocerosate-forming)

Systematic name: long-chain acyl-[mycocerosic acid synthase]:methylmalonyl-CoA *C*-acyltransferase (mycocerosate-forming)

Comments: The enzyme, characterized from mycobacteria, is loaded with a long-chain acyl moiety by EC 6.2.1.49, long-chain fatty acid adenylyltransferase FadD28, and elongates it by incorporation of three or four methylmalonyl (but not malonyl) residues, to form tri- or tetramethyl-branched fatty-acids, respectively, such as 2,4,6,8-tetramethyloctacosanoate (C_{32}-mycocerosate). Since the enzyme lacks a thioesterase domain, the product remains bound and requires additional enzyme(s) for removal. Even though the enzyme can accept C_6 to C_{20} substrates *in vitro*, it prefers to act on C_{14}-C_{20} substrates *in vivo*.

References: [2795, 2161, 3569, 2218]

[EC 2.3.1.111 created 1989, modified 2016, modified 2017]

EC 2.3.1.112

Accepted name: D-tryptophan *N*-malonyltransferase

Reaction: malonyl-CoA + D-tryptophan = CoA + N^2-malonyl-D-tryptophan

Systematic name: malonyl-CoA:D-tryptophan *N*-malonyltransferase

Comments: 1-Aminocyclopropane-1-carboxylate can act instead of malonyl-CoA.

References: [2158]

[EC 2.3.1.112 created 1989]

EC 2.3.1.113

Accepted name: anthranilate *N*-malonyltransferase

Reaction: malonyl-CoA + anthranilate = CoA + *N*-malonylanthranilate

Systematic name: malonyl-CoA:anthranilate *N*-malonyltransferase

References: [2158]

[EC 2.3.1.113 created 1989]

EC 2.3.1.114

Accepted name: 3,4-dichloroaniline *N*-malonyltransferase

Reaction: malonyl-CoA + 3,4-dichloroaniline = CoA + *N*-(3,4-dichlorophenyl)-malonamate
Systematic name: malonyl-CoA:3,4-dichloroaniline *N*-malonyltransferase
References: [2158]

[EC 2.3.1.114 created 1989]

EC 2.3.1.115

Accepted name: isoflavone-7-*O*-β-glucoside 6″-*O*-malonyltransferase
Reaction: malonyl-CoA + biochanin A 7-*O*-β-D-glucoside = CoA + biochanin A 7-*O*-(6-*O*-malonyl-β-D-glucoside)
Other name(s): flavone/flavonol 7-*O*-β-D-glucoside malonyltransferase; flavone (flavonol) 7-*O*-glycoside malonyltransferase; malonyl-CoA:flavone/flavonol 7-*O*-glucoside malonyltransferase; MAT-7; malonyl-coenzyme A:isoflavone 7-*O*-glucoside-6″-malonyltransferase; malonyl-coenzyme A:flavone/flavonol-7-*O*-glycoside malonyltransferase
Systematic name: malonyl-CoA:isoflavone-7-*O*-β-D-glucoside 6″-*O*-malonyltransferase
Comments: The 6-position of the glucose residue of formononetin can also act as acceptor; some other 7-*O*-glucosides of isoflavones, flavones and flavonols can also act, but more slowly.
References: [1734, 2157]

[EC 2.3.1.115 created 1989]

EC 2.3.1.116

Accepted name: flavonol-3-*O*-β-glucoside *O*-malonyltransferase
Reaction: malonyl-CoA + flavonol 3-*O*-β-D-glucoside = CoA + flavonol 3-*O*-(6-*O*-malonyl-β-D-glucoside)
Other name(s): flavonol 3-*O*-glucoside malonyltransferase; MAT-3; malonyl-coenzyme A:flavonol-3-*O*-glucoside malonyltransferase
Systematic name: malonyl-CoA:flavonol-3-*O*-β-D-glucoside 6″-*O*-malonyltransferase
References: [2157]

[EC 2.3.1.116 created 1989]

EC 2.3.1.117

Accepted name: 2,3,4,5-tetrahydropyridine-2,6-dicarboxylate *N*-succinyltransferase
Reaction: succinyl-CoA + (*S*)-2,3,4,5-tetrahydropyridine-2,6-dicarboxylate + H_2O = CoA + *N*-succinyl-L-2-amino-6-oxoheptanedioate
Other name(s): tetrahydropicolinate succinylase; tetrahydrodipicolinate *N*-succinyltransferase; tetrahydrodipicolinate succinyltransferase; succinyl-CoA:tetrahydrodipicolinate *N*-succinyltransferase; succinyl-CoA:2,3,4,5-tetrahydropyridine-2,6-dicarboxylate *N*-succinyltransferase
Systematic name: succinyl-CoA:(*S*)-2,3,4,5-tetrahydropyridine-2,6-dicarboxylate *N*-succinyltransferase
Comments: Involved in the biosynthesis of lysine in bacteria (including cyanobacteria) and higher plants. The 1992 edition of the Enzyme List erroneously gave the name 2,3,4,5-tetrahydropyridine-2-carboxylate *N*-succinyltransferase to this enzyme.
References: [3234]

[EC 2.3.1.117 created 1989, modified 2001]

EC 2.3.1.118

Accepted name: *N*-hydroxyarylamine *O*-acetyltransferase
Reaction: acetyl-CoA + an *N*-hydroxyarylamine = CoA + an *N*-acetoxyarylamine
Other name(s): arylhydroxamate N,*O*-acetyltransferase; arylamine *N*-acetyltransferase; *N*-hydroxy-2-aminofluorene-*O*-acetyltransferase
Systematic name: acetyl-CoA:*N*-hydroxyarylamine *O*-acetyltransferase
Comments: The enzyme from liver, but not that from bacteria, can also catalyse *N*-acetylation of arylamines and *N,O*-acetylation of arylhydroxamates.

References: [2999]

[EC 2.3.1.118 created 1989]

[2.3.1.119 Deleted entry. icosanoyl-CoA synthase. Now covered by EC 2.3.1.199, very-long-chain 3-oxoacyl-CoA synthase, EC 1.1.1.330, very-long-chain 3-oxoacyl-CoA reductase, EC 4.2.1.134, very-long-chain (3R)-3-hydroxyacyl-CoA dehydratase, and EC 1.3.1.93, very-long-chain enoyl-CoA reductase.]

[EC 2.3.1.119 created 1990, deleted 2015]

[2.3.1.120 Deleted entry. 6′-deoxychalcone synthase. The reaction listed is due to EC 2.3.1.74 naringenin-chalcone synthase]

[EC 2.3.1.120 created 1990, deleted 1992]

EC 2.3.1.121

Accepted name: 1-alkenylglycerophosphoethanolamine *O*-acyltransferase

Reaction: acyl-CoA + 1-alkenylglycerophosphoethanolamine = CoA + 1-alkenyl-2-acylglycerophosphoethanolamine

Systematic name: acyl-CoA:1-alkenylglycerophosphoethanolamine *O*-acyltransferase

Comments: Long-chain unsaturated acyl-CoAs are the best substrates.

References: [114]

[EC 2.3.1.121 created 1990]

EC 2.3.1.122

Accepted name: trehalose *O*-mycolyltransferase

Reaction: **2** α,α-trehalose 6-mycolate = α,α-trehalose + α,α-trehalose 6,6′-bismycolate

Other name(s): α,α’-trehalose 6-monomycolate:α,α’-trehalose mycolyltransferase; α,α’-trehalose-6-mycolate:α,α’-trehalose-6-mycolate 6′-mycolyltransferase

Systematic name: α,α-trehalose-6-mycolate:α,α-trehalose-6-mycolate 6′-mycolyltransferase

Comments: Catalyses the exchange of mycolic acid between trehalose, trehalose mycolate and trehalose bismycolate. Trehalose 6-palmitate can also act as donor.

References: [3028]

[EC 2.3.1.122 created 1990]

EC 2.3.1.123

Accepted name: dolichol *O*-acyltransferase

Reaction: palmitoyl-CoA + dolichol = CoA + dolichyl palmitate

Other name(s): acyl-CoA:dolichol acyltransferase

Systematic name: palmitoyl-CoA:dolichol *O*-palmitoyltransferase

Comments: Other acyl-CoAs can also act, but more slowly. α-Saturated dolichols are acylated more rapidly than the α-unsaturated analogues.

References: [3544]

[EC 2.3.1.123 created 1990]

[2.3.1.124 Deleted entry. diacylglycerol acyltransferase. Already listed as EC 2.3.1.20, diacylglycerol O-acyltransferase]

[EC 2.3.1.124 created 1990, deleted 1992]

EC 2.3.1.125

Accepted name: 1-alkyl-2-acetylglycerol *O*-acyltransferase

Reaction: acyl-CoA + 1-*O*-alkyl-2-acetyl-*sn*-glycerol = CoA + 1-*O*-alkyl-2-acetyl-3-acyl-*sn*-glycerol

Other name(s): 1-hexadecyl-2-acetylglycerol acyltransferase
Systematic name: acyl-CoA:1-*O*-alkyl-2-acetyl-*sn*-glycerol *O*-acyltransferase
Comments: A number of acyl-CoAs can act as acyl donor; maximum activity is obtained with linoleoyl-CoA. Not identical with EC 2.3.1.20 diacylglycerol *O*-acyltransferase.
References: [1616]

[EC 2.3.1.125 created 1990]

EC 2.3.1.126
Accepted name: isocitrate *O*-dihydroxycinnamoyltransferase
Reaction: caffeoyl-CoA + isocitrate = CoA + 2-*O*-caffeoylisocitrate
Systematic name: caffeoyl-CoA:isocitrate 2-*O*-(3,4-dihydroxycinnamoyl)transferase
Comments: Feruloyl-CoA and 4-coumaroyl-CoA can also act as donors.
References: [3365]

[EC 2.3.1.126 created 1990]

EC 2.3.1.127
Accepted name: ornithine *N*-benzoyltransferase
Reaction: **2** benzoyl-CoA + L-ornithine = **2** CoA + N^2,N^5-dibenzoyl-L-ornithine
Other name(s): ornithine *N*-acyltransferase
Systematic name: benzoyl-CoA:L-ornithine *N*-benzoyltransferase
References: [3149]

[EC 2.3.1.127 created 1990]

[2.3.1.128 Transferred entry. ribosomal-protein-alanine N-acetyltransferase, now classified as EC 2.3.1.266, [ribosomal protein S18]-alanine N-acetyltransferase, and EC 2.3.1.267, [ribosomal protein S5]-alanine N-acetyltransferase.]

[EC 2.3.1.128 created 1990, deleted 2018]

EC 2.3.1.129
Accepted name: acyl-[acyl-carrier-protein]—UDP-*N*-acetylglucosamine *O*-acyltransferase
Reaction: (*R*)-3-hydroxytetradecanoyl-[acyl-carrier protein] + UDP-*N*-acetyl-α-D-glucosamine = an [acyl-carrier protein] + UDP-3-*O*-[(3*R*)-3-hydroxytetradecanoyl]-*N*-acetyl-α-D-glucosamine
Other name(s): UDP-*N*-acetylglucosamine acyltransferase; uridine diphosphoacetylglucosamine acyltransferase; acyl-[acyl-carrier-protein]-UDP-*N*-acetylglucosamine *O*-acyltransferase; (*R*)-3-hydroxytetradecanoyl-[acyl-carrier-protein]:UDP-*N*-acetylglucosamine 3-*O*-(3-hydroxytetradecanoyl)transferase
Systematic name: (*R*)-3-hydroxytetradecanoyl-[acyl-carrier protein]:UDP-*N*-acetyl-α-D-glucosamine 3-*O*-(3-hydroxytetradecanoyl)transferase
Comments: Involved with EC 2.4.1.182 (lipid-A-disaccharide synthase) and EC 2.7.1.130 (tetraacyldisaccharide 4′-kinase) in the biosynthesis of the phosphorylated glycolipid, Lipid A, in the outer membrane of *Escherichia coli*.
References: [77]

[EC 2.3.1.129 created 1990]

EC 2.3.1.130
Accepted name: galactarate *O*-hydroxycinnamoyltransferase
Reaction: feruloyl-CoA + galactarate = CoA + *O*-feruloylgalactarate
Other name(s): galacturate hydroxycinnamoyltransferase
Systematic name: feruloyl-CoA:galactarate *O*-(hydroxycinnamoyl)transferase
Comments: Sinapoyl-CoA and 4-coumaroyl-CoA can also act as donors.
References: [3364]

[EC 2.3.1.130 created 1990]

EC 2.3.1.131

Accepted name: glucarate *O*-hydroxycinnamoyltransferase

Reaction: sinapoyl-CoA + glucarate = CoA + *O*-sinapoylglucarate

Systematic name: sinapoyl-CoA:glucarate *O*-(hydroxycinnamoyl)transferase

Comments: 4-Coumaroyl-CoA, feruloyl-CoA and caffeoyl-CoA can also act as donors, but more slowly.

References: [3364]

[EC 2.3.1.131 created 1990]

EC 2.3.1.132

Accepted name: glucarolactone *O*-hydroxycinnamoyltransferase

Reaction: sinapoyl-CoA + glucarolactone = CoA + *O*-sinapoylglucarolactone

Systematic name: sinapoyl-CoA:glucarolactone *O*-(hydroxycinnamoyl)transferase

Comments: 4-Coumaroyl-CoA, feruloyl-CoA and caffeoyl-CoA can also act as donors, but more slowly.

References: [3364]

[EC 2.3.1.132 created 1990]

EC 2.3.1.133

Accepted name: shikimate *O*-hydroxycinnamoyltransferase

Reaction: 4-coumaroyl-CoA + shikimate = CoA + 4-coumaroylshikimate

Other name(s): shikimate hydroxycinnamoyltransferase

Systematic name: 4-coumaroyl-CoA:shikimate *O*-(hydroxycinnamoyl)transferase

Comments: Caffeoyl-CoA, feruloyl-CoA and sinapoyl-CoA can also act as donors, but more slowly.

References: [3364, 3608]

[EC 2.3.1.133 created 1990]

EC 2.3.1.134

Accepted name: galactolipid *O*-acyltransferase

Reaction: **2** mono-β-D-galactosyldiacylglycerol = acylmono-β-D-galactosyldiacylglycerol + mono-β-D-galactosylacylglycerol

Other name(s): galactolipid:galactolipid acyltransferase

Systematic name: mono-β-D-galactosyldiacylglycerol:mono-β-D-galactosyldiacylglycerol acyltransferase

Comments: Di-D-galactosyldiacylglycerol can also act as acceptor.

References: [1267, 1281]

[EC 2.3.1.134 created 1990]

EC 2.3.1.135

Accepted name: phosphatidylcholine—retinol *O*-acyltransferase

Reaction: phosphatidylcholine + retinol—[cellular-retinol-binding-protein] = 2-acylglycerophosphocholine + retinyl-ester—[cellular-retinol-binding-protein]

Other name(s): lecithin—retinol acyltransferase; phosphatidylcholine:retinol-(cellular-retinol-binding-protein) *O*-acyltransferase; lecithin:retinol acyltransferase; lecithin-retinol acyltransferase; retinyl ester synthase; LRAT; lecithin retinol acyl transferase

Systematic name: phosphatidylcholine:retinol—[cellular-retinol-binding-protein] *O*-acyltransferase

Comments: A key enzyme in retinoid metabolism, catalysing the transfer of an acyl group from the *sn*-1 position of phosphatidylcholine to retinol, forming retinyl esters which are then stored. Recognizes the substrate both in free form and when bound to cellular-retinol-binding-protein, but has higher affinity for the bound form. Can also esterify 11-*cis*-retinol.

References: [2091, 2984, 2985, 2155, 2969]

[EC 2.3.1.135 created 1992, modified 2011]

EC 2.3.1.136

Accepted name: polysialic-acid *O*-acetyltransferase

Reaction: acetyl-CoA + an α-2,8-linked polymer of sialic acid = CoA + polysialic acid acetylated at O-7 or O-9

Systematic name: acetyl-CoA:polysialic-acid *O*-acetyltransferase

Comments: Acts only on substrates containing more than 14 sialosyl residues. Catalyses the modification of capsular polysaccharides in some strains of *Escherichia coli*.

References: [1322]

[EC 2.3.1.136 created 1992]

EC 2.3.1.137

Accepted name: carnitine *O*-octanoyltransferase

Reaction: octanoyl-CoA + L-carnitine = CoA + L-octanoylcarnitine

Other name(s): medium-chain/long-chain carnitine acyltransferase; carnitine medium-chain acyltransferase; easily solubilized mitochondrial carnitine palmitoyltransferase; overt mitochondrial carnitine palmitoyltransferase

Systematic name: octanoyl-CoA:L-carnitine *O*-octanoyltransferase

Comments: Acts on a range of acyl-CoAs, with optimal activity with C6 or C8 acyl groups. *cf.* EC 2.3.1.7 (carnitine *O*-acetyltransferase) and EC 2.3.1.21 (carnitine *O*-palmitoyltransferase).

References: [880, 1264, 2278]

[EC 2.3.1.137 created 1992]

EC 2.3.1.138

Accepted name: putrescine *N*-hydroxycinnamoyltransferase

Reaction: caffeoyl-CoA + putrescine = CoA + *N*-caffeoylputrescine

Other name(s): caffeoyl-CoA putrescine *N*-caffeoyl transferase; PHT; putrescine hydroxycinnamoyl transferase; hydroxycinnamoyl-CoA:putrescine hydroxycinnamoyltransferase; putrescine hydroxycinnamoyltransferase

Systematic name: caffeoyl-CoA:putrescine *N*-(3,4-dihydroxycinnamoyl)transferase

Comments: Feruloyl-CoA, cinnamoyl-CoA and sinapoyl-CoA can also act as donors, but more slowly.

References: [2429]

[EC 2.3.1.138 created 1992]

EC 2.3.1.139

Accepted name: ecdysone *O*-acyltransferase

Reaction: palmitoyl-CoA + ecdysone = CoA + ecdysone palmitate

Other name(s): acyl-CoA:ecdysone acyltransferase; fatty acyl-CoA:ecdysone acyltransferase

Systematic name: palmitoyl-CoA:ecdysone palmitoyltransferase

References: [3255]

[EC 2.3.1.139 created 1992]

EC 2.3.1.140

Accepted name: rosmarinate synthase

Reaction: caffeoyl-CoA + (*R*)-3-(3,4-dihydroxyphenyl)lactate = CoA + rosmarinate

Other name(s): rosmarinic acid synthase; caffeoyl-coenzyme A:3,4-dihydroxyphenyllactic acid caffeoyltransferase; 4-coumaroyl-CoA:4-hydroxyphenyllactic acid 4-coumaroyl transferase; RAS (gene name)

Systematic name: caffeoyl-CoA:(*R*)-3-(3,4-dihydroxyphenyl)lactate 2′-*O*-caffeoyl-transferase

Comments: Involved, with EC 1.1.1.237 (hydroxyphenylpyruvate reductase) in the biosynthesis of rosmarinic acid. Characterized from the plant *Melissa officinalis* L. (lemon balm).

References: [2674, 2675, 3817]

[EC 2.3.1.140 created 1992, modified 2013]

EC 2.3.1.141

Accepted name: galactosylacylglycerol *O*-acyltransferase

Reaction: an acyl-[acyl-carrier protein] + a 2-acyl-3-*O*-(β-D-galactosyl)-*sn*-glycerol = an [acyl-carrier protein] + a 1,2-diacyl-3-*O*-(β-D-galactosyl)-*sn*-glycerol

Other name(s): acyl-acyl-carrier protein: lysomonogalactosyldiacylglycerol acyltransferase; acyl-ACP:lyso-MGDG acyltransferase; acyl-[acyl-carrier-protein]:D-galactosylacylglycerol *O*-acyltransferase

Systematic name: acyl-[acyl-carrier protein]:2-acyl-3-*O*-(β-D-galactosyl)-*sn*-glycerol *O*-acyltransferase

Comments: Transfers long-chain acyl groups to the *sn*-1 position of the glycerol residue.

References: [526]

[EC 2.3.1.141 created 1992]

EC 2.3.1.142

Accepted name: glycoprotein *O*-fatty-acyltransferase

Reaction: palmitoyl-CoA + mucus glycoprotein = CoA + *O*-palmitoylglycoprotein

Other name(s): protein acyltransferase

Systematic name: fatty-acyl-CoA:mucus-glycoprotein fatty-acyltransferase

References: [1591]

[EC 2.3.1.142 created 1992]

EC 2.3.1.143

Accepted name: β-glucogallin—tetrakisgalloylglucose *O*-galloyltransferase

Reaction: 1-*O*-galloyl-β-D-glucose + 1,2,3,6-tetrakis-*O*-galloyl-β-D-glucose = D-glucose + 1,2,3,4,6-pentakis-*O*-galloyl-β-D-glucose

Other name(s): β-glucogallin-tetragalloylglucose 4-galloyltransferase; β-glucogallin:1,2,3,6-tetra-*O*-galloylglucose 4-*O*-galloyltransferase; β-glucogallin:1,2,3,6-tetra-*O*-galloyl-β-D-glucose 4-*O*-galloyltransferase

Systematic name: 1-*O*-galloyl-β-D-glucose:1,2,3,6-tetrakis-*O*-galloyl-β-D-glucose 4-*O*-galloyltransferase

References: [463]

[EC 2.3.1.143 created 1992]

EC 2.3.1.144

Accepted name: anthranilate *N*-benzoyltransferase

Reaction: benzoyl-CoA + anthranilate = CoA + *N*-benzoylanthranilate

Systematic name: benzoyl-CoA:anthranilate *N*-benzoyltransferase

Comments: Cinnamoyl-CoA, 4-coumaroyl-CoA and salicyloyl-CoA can act as donors, but more slowly. Involved in the biosynthesis of phytoalexins.

References: [2861]

[EC 2.3.1.144 created 1992]

EC 2.3.1.145

Accepted name: piperidine *N*-piperoyltransferase

Reaction: (*E*,*E*)-piperoyl-CoA + piperidine = CoA + *N*-[(*E*,*E*)-piperoyl]-piperidine

Other name(s): piperidine piperoyltransferase; piperoyl-CoA:piperidine *N*-piperoyltransferase
Systematic name: (*E*,*E*)-piperoyl-CoA:piperidine *N*-piperoyltransferase
Comments: Pyrrolidine and 3-pyrroline can also act as acceptors, but more slowly.
References: [1034]

[EC 2.3.1.145 created 1992]

EC 2.3.1.146

Accepted name: pinosylvin synthase
Reaction: **3** malonyl-CoA + cinnamoyl-CoA = **4** CoA + pinosylvin + **4** CO$_2$
Other name(s): stilbene synthase (ambiguous); pine stilbene synthase (ambiguous)
Systematic name: malonyl-CoA:cinnamoyl-CoA malonyltransferase (cyclizing)
Comments: Not identical with EC 2.3.1.74 (naringenin-chalcone synthase) or EC 2.3.1.95 (trihydroxystilbene synthase).
References: [1032]

[EC 2.3.1.146 created 1992]

EC 2.3.1.147

Accepted name: glycerophospholipid arachidonoyl-transferase (CoA-independent)
Reaction: 1-organyl-2-arachidonoyl-*sn*-glycero-3-phosphocholine + 1-organyl-2-lyso-*sn*-glycero-3-phosphoethanolamine = 1-organyl-2-arachidonoyl-*sn*-glycero-3-phosphoethanolamine + 1-organyl-2-lyso-*sn*-glycero-3-phosphocholine
Systematic name: 1-organyl-2-arachidonoyl-*sn*-glycero-3-phosphocholine:1-organyl-2-lyso-*sn*-glycero-3-phosphoethanolamine arachidonoyltransferase (CoA-independent)
Comments: Catalyses the transfer of arachidonate and other polyenoic fatty acids from intact choline or ethanolamine-containing glycerophospholipids to the *sn*-2 position of a *lyso*-glycerophospholipid. The organyl group on *sn*-1 of the donor or acceptor molecule can be alkyl, acyl or alk-1-enyl. The term ‘radyl’ has sometimes been used to refer to such substituting groups. Differs from EC 2.3.1.148 glycerophospholipid acyltransferase (CoA-dependent) in not requiring CoA and in its specificity for poly-unsaturated acyl groups.
References: [2904, 3265]

[EC 2.3.1.147 created 1999]

EC 2.3.1.148

Accepted name: glycerophospholipid acyltransferase (CoA-dependent)
Reaction: 1-organyl-2-acyl-*sn*-glycero-3-phosphocholine + 1-organyl-2-lyso-*sn*-glycero-3-phosphoethanolamine = 1-organyl-2-acyl-*sn*-glycero-3-phosphoethanolamine + 1-organyl-2-lyso-*sn*-glycero-3-phosphocholine
Systematic name: 1-organyl-2-acyl-*sn*-glycero-3-phosphocholine:1-organyl-2-lyso-*sn*-glycero-3-phosphoethanolamine acyltransferase (CoA-dependent)
Comments: Catalyses the transfer of fatty acids from intact choline- or ethanolamine-containing glycerophospholipids to the *sn*-2 position of a *lyso*-glycerophospholipid. The organyl group on *sn*-1 of the donor or acceptor molecule can be alkyl, acyl or alk-1-enyl. The term ‘radyl’ has sometimes been used to refer to such substituting groups. Differs from EC 2.3.1.147 glycerophospholipid arachidonoyl-transferase (CoA-independent) in requiring CoA and not favouring the transfer of polyunsaturated acyl groups.
References: [1449, 2904, 3265]

[EC 2.3.1.148 created 1999]

EC 2.3.1.149

Accepted name: platelet-activating factor acetyltransferase

Reaction: 1-alkyl-2-acetyl-*sn*-glycero-3-phosphocholine + 1-organyl-2-lyso-*sn*-glycero-3-phospholipid = 1-alkyl-2-lyso-*sn*-glycero-3-phosphocholine + 1-organyl-2-acetyl-*sn*-glycero-3-phospholipid
Other name(s): PAF acetyltransferase
Systematic name: 1-alkyl-2-acetyl-*sn*-glycero-3-phosphocholine:1-organyl-2-lyso-*sn*-glycero-3-phospholipid acetyltransferase
Comments: Catalyses the transfer of the acetyl group from 1-alkyl-2-acetyl-*sn*-glycero-3-phosphocholine (platelet-activating factor) to the *sn*-2 position of lyso-glycerophospholipids containing ethanolamine, choline, serine, inositol or phosphate groups at the *sn*-3 position as well as to sphingosine and long-chain fatty alcohols. The organyl group can be alkyl, acyl or alk-1-enyl (sometimes also collectively referred to as ‘radyl’).
References: [1905]

[EC 2.3.1.149 created 1999]

EC 2.3.1.150

Accepted name: salutaridinol 7-*O*-acetyltransferase
Reaction: acetyl-CoA + salutaridinol = CoA + 7-*O*-acetylsalutaridinol
Systematic name: acetyl-CoA:salutaridinol 7-*O*-acetyltransferase
Comments: The enzyme is present in the poppy, *Papaver somniferum*. At pH 8-9 the product, 7-*O*-acetylsalutaridinol, spontaneously closes the 4→5 oxide bridge by allylic elimination to form the morphine precursor thebaine
References: [1937, 1938]

[EC 2.3.1.150 created 1999]

EC 2.3.1.151

Accepted name: 2,3′,4,6-tetrahydroxybenzophenone synthase
Reaction: **3** malonyl-CoA + 3-hydroxybenzoyl-CoA = **4** CoA + 2,3′,4,6-tetrahydroxybenzophenone + **3** CO_2
Other name(s): benzophenone synthase (ambiguous); BPS (ambiguous)
Systematic name: malonyl-CoA:3-hydroxybenzoyl-CoA malonyltransferase (decarboxylating, 2,3′,4,6-tetrahydroxybenzophenone-forming)
Comments: Involved in the biosynthesis of plant xanthones. Benzoyl-CoA can replace 3-hydroxybenzoyl-CoA (*cf.* EC 2.3.1.220, 2,4,6-trihydroxybenzophenone synthase).
References: [250]

[EC 2.3.1.151 created 1999, modified 2013]

EC 2.3.1.152

Accepted name: alcohol *O*-cinnamoyltransferase
Reaction: 1-*O*-*trans*-cinnamoyl-β-D-glucopyranose + ROH = alkyl cinnamate + glucose
Systematic name: 1-*O*-*trans*-cinnamoyl-β-D-glucopyranose:alcohol *O*-cinnamoyltransferase
Comments: Acceptor alcohols (ROH) include methanol, ethanol and propanol. No cofactors are required as 1-*O*-*trans*-cinnamoyl-β-D-glucopyranose itself is an ”energy-rich” (activated) acyl-donor, comparable to CoA-thioesters. 1-*O*-*trans*-Cinnamoyl-β-D-gentobiose can also act as the acyl donor, but with much less affinity.
References: [2284, 1871]

[EC 2.3.1.152 created 1999]

EC 2.3.1.153

Accepted name: anthocyanin 5-(6‴-hydroxycinnamoyltransferase)
Reaction: 4-hydroxycinnamoyl-CoA + anthocyanidin 3,5-diglucoside = CoA + anthocyanidin 3-glucoside 5-(6-*O*-4-hydroxycinnamoylglucoside)

Systematic name: 4-hydroxycinnamoyl-CoA:anthocyanidin 3,5-diglucoside 5-*O*-glucoside-$6'''$-*O*-4-hydroxycinnamoyltransferase

Comments: Isolated from the plant *Gentiana triflora*. Transfers the hydroxycinnamoyl group only to the C-5 glucoside of anthocyanin. Caffeoyl-CoA, but not malonyl-CoA, can substitute as an acyl donor.

References: [992, 993]

[EC 2.3.1.153 created 1999, modified 2013]

[2.3.1.154 Transferred entry. Propionyl-CoA C^2*-trimethyltridecanoyltransferase. Now EC 2.3.1.176, propanoyl-CoA C-acyltransferase.]*

[EC 2.3.1.154 created 2000, deleted 2015]

EC 2.3.1.155

Accepted name: acetyl-CoA *C*-myristoyltransferase

Reaction: myristoyl-CoA + acetyl-CoA = CoA + 3-oxopalmitoyl-CoA

Systematic name: myristoyl-CoA:acetyl-CoA *C*-myristoyltransferase

Comments: A peroxisomal enzyme involved in branched chain fatty acid β-oxidation in peroxisomes. It differs from EC 2.3.1.154 (propionyl-CoA C^2-trimethyldecanoyltransferase) in not being active towards 3-oxopristanoyl-CoA.

References: [2276]

[EC 2.3.1.155 created 2000]

EC 2.3.1.156

Accepted name: phloroisovalerophenone synthase

Reaction: (1) isovaleryl-CoA + **3** malonyl-CoA = **4** CoA + **3** CO_2 + phlorisovalerophenone
(2) isobutyryl-CoA^{+} 3 malonyl-CoA = **4** CoA + **3** CO_2 + phlorisobutyrophenone

Other name(s): valerophenone synthase; 3-methyl-1-(trihydroxyphenyl)butan-1-one synthase; acylphloroglucinol synthase; isovaleryl-CoA:malonyl-CoA acyltransferase

Systematic name: acyl-CoA:malonyl-CoA acyltransferase

Comments: Closely related to EC 2.3.1.74, naringenin-chalcone synthase. Also acts on isobutyryl-CoA as substrate to give phlorisobutyrophenone. The products are intermediates in the biosynthesis of the bitter acids in hops (*Humulus lupulus*) and glucosides in strawberry (Fragaria X ananassa). It is also able to generate naringenin chalcone from 4-coumaroyl-CoA.

References: [997, 4091, 3284]

[EC 2.3.1.156 created 2000]

EC 2.3.1.157

Accepted name: glucosamine-1-phosphate *N*-acetyltransferase

Reaction: acetyl-CoA + α-D-glucosamine 1-phosphate = CoA + *N*-acetyl-α-D-glucosamine 1-phosphate

Systematic name: acetyl-CoA:α-D-glucosamine-1-phosphate *N*-acetyltransferase

Comments: The enzyme from several bacteria (e.g., *Escherichia coli*, *Bacillus subtilis* and *Haemophilus influenzae*) has been shown to be bifunctional and also to possess the activity of EC 2.7.7.23, UDP-*N*-acetylglucosamine diphosphorylase.

References: [2221, 1033, 2560]

[EC 2.3.1.157 created 2001]

EC 2.3.1.158

Accepted name: phospholipid:diacylglycerol acyltransferase

Reaction: phospholipid + 1,2-diacyl-*sn*-glycerol = lysophospholipid + triacylglycerol

Other name(s): PDAT

Systematic name: phospholipid:1,2-diacyl-*sn*-glycerol *O*-acyltransferase

Comments: This enzyme differs from EC 2.3.1.20, diacylglycerol *O*-acyltransferase, by synthesising triacylglycerol using an acyl-CoA-independent mechanism. The specificity of the enzyme for the acyl group in the phospholipid varies with species, e.g., the enzyme from castor bean (*Ricinus communis*) preferentially incorporates vernoloyl (12,13-epoxyoctadec-9-enoyl) groups into triacylglycerol, whereas that from the hawk's beard (*Crepis palaestina*) incorporates both ricinoleoyl (12-hydroxyoctadec-9-enoyl) and vernoloyl groups. The enzyme from the yeast *Saccharomyces cerevisiae* specifically transfers acyl groups from the *sn*-2 position of the phospholipid to diacylglycerol, thus forming an *sn*-1-lysophospholipid.

References: [657]

[EC 2.3.1.158 created 2001]

EC 2.3.1.159

Accepted name: acridone synthase

Reaction: **3** malonyl-CoA + *N*-methylanthraniloyl-CoA = **4** CoA + 1,3-dihydroxy-*N*-methylacridone + **3** CO$_2$

Systematic name: malonyl-CoA:*N*-methylanthraniloyl-CoA malonyltransferase (cyclizing)

Comments: Belongs to a superfamily of plant polyketide synthases. Has many similarities to chalcone and stilbene synthases (see reaction synthesis)

References: [240, 2101, 2066, 1547]

[EC 2.3.1.159 created 2002]

EC 2.3.1.160

Accepted name: vinorine synthase

Reaction: acetyl-CoA + 16-epivellosimine = CoA + vinorine

Systematic name: acyl-CoA:16-epivellosimine *O*-acetyltransferase (cyclizing)

Comments: The reaction proceeds in two stages. The indole nitrogen of 16-epivellosimine interacts with its aldehyde group giving an hydroxy-substituted new ring. This alcohol is then acetylated. Also acts on gardneral (11-methoxy-16-epivellosimine). Generates the ajmalan skeleton, which forms part of the route to ajmaline.

References: [2685, 242, 2084, 2085]

[EC 2.3.1.160 created 2002]

EC 2.3.1.161

Accepted name: lovastatin nonaketide synthase

Reaction: **9** malonyl-CoA + **11** NADPH + **10** H$^+$ + *S*-adenosyl-L-methionine + holo-[lovastatin nonaketide synthase] = dihydromonacolin L-[lovastatin nonaketide synthase] + **9** CoA + **9** CO$_2$ + **11** NADP$^+$ + *S*-adenosyl-L-homocysteine + **6** H$_2$O

Other name(s): LNKS; LovB; LovC; acyl-CoA:malonyl-CoA *C*-acyltransferase (decarboxylating, oxoacyl- and enoyl-reducing, thioester-hydrolysing)

Systematic name: acyl-CoA:malonyl-CoA *C*-acyltransferase (dihydromonacolin L acid-forming)

Comments: This fungal enzyme system comprises a multi-functional polyketide synthase (PKS) and an enoyl reductase. The PKS catalyses many of the chain building reactions of EC 2.3.1.85, fatty-acid synthase, as well as a reductive methylation and a Diels-Alder reaction, while the reductase is responsible for three enoyl reductions that are necessary for dihydromonacolin L acid production.

References: [2083, 1641, 126]

[EC 2.3.1.161 created 2002, modified 2015, modified 2016]

EC 2.3.1.162

Accepted name: taxadien-5α-ol *O*-acetyltransferase

Reaction: acetyl-CoA + taxa-4(20),11-dien-5α-ol = CoA + taxa-4(20),11-dien-5α-yl acetate
Other name(s): acetyl coenzyme A:taxa-4(20),11(12)-dien-5α-ol *O*-acetyl transferase
Systematic name: acetyl-CoA:taxa-4(20),11-dien-5α-ol *O*-acetyltransferase
Comments: This is the third enzyme in the biosynthesis of the diterpenoid antineoplastic drug taxol (paclitaxel), which is widely used in the treatment of carcinomas, sarcomas and melanomas.
References: [3738, 3739]

[EC 2.3.1.162 created 2002]

EC 2.3.1.163

Accepted name: 10-hydroxytaxane *O*-acetyltransferase
Reaction: acetyl-CoA + 10-desacetyltaxuyunnanin C = CoA + taxuyunnanin C
Other name(s): acetyl coenzyme A: 10-hydroxytaxane *O*-acetyltransferase
Systematic name: acetyl-CoA:taxan-10β-ol *O*-acetyltransferase
Comments: Acts on a number of related taxane diterpenoids with a free 10β-hydroxy group. May be identical to EC 2.3.1.167, 10-deacetylbaccatin III 10-*O*-acetyltransferase.
References: [2222]

[EC 2.3.1.163 created 2002]

EC 2.3.1.164

Accepted name: isopenicillin-N *N*-acyltransferase
Reaction: phenylacetyl-CoA + isopenicillin N + H_2O = CoA + penicillin G + L-2-aminohexanedioate
Other name(s): acyl-coenzyme A:isopenicillin N acyltransferase; isopenicillin N:acyl-CoA: acyltransferase
Systematic name: acyl-CoA:isopenicillin N *N*-acyltransferase
Comments: Proceeds by a two stage mechanism via 6-aminopenicillanic acid. Different from EC 3.5.1.11, penicillin amidase.
References: [3540, 99]

[EC 2.3.1.164 created 2002]

EC 2.3.1.165

Accepted name: 6-methylsalicylic-acid synthase
Reaction: acetyl-CoA + **3** malonyl-CoA + NADPH + H^+ = 6-methylsalicylate + **4** CoA + **3** CO_2 + $NADP^+$ + H_2O
Other name(s): MSAS; 6-methylsalicylic acid synthase
Systematic name: acyl-CoA:malonyl-CoA *C*-acyltransferase (decarboxylating, oxoacyl-reducing, thioester-hydrolysing and cyclizing)
Comments: A multienzyme complex with a 4′-phosphopantetheine prosthetic group on the acyl carrier protein. It has a similar sequence to vertebrate type I fatty acid synthase. Acetoacetyl-CoA can also act as a starter molecule.
References: [3296, 545, 2880]

[EC 2.3.1.165 created 2002]

EC 2.3.1.166

Accepted name: 2α-hydroxytaxane 2-*O*-benzoyltransferase
Reaction: benzoyl-CoA + 10-deacetyl-2-debenzoylbaccatin III = CoA + 10-deacetylbaccatin III
Other name(s): benzoyl-CoA:taxane 2α-*O*-benzoyltransferase
Systematic name: benzoyl-CoA:taxan-2α-ol *O*-benzoyltransferase
Comments: The enzyme was studied using the semisynthetic substrate 2-debenzoyl-7,13-diacetylbaccatin III. It will not acylate the hydroxy group at 1β, 7β, 10β or 13α of 10-deacetyl baccatin III, or at 2α or 5α of taxa-4(20),11-diene-2α,5α-diol.
References: [3737]

[EC 2.3.1.166 created 2002]

EC 2.3.1.167

Accepted name: 10-deacetylbaccatin III 10-*O*-acetyltransferase

Reaction: acetyl-CoA + 10-deacetylbaccatin III = CoA + baccatin III

Systematic name: acetyl-CoA:taxan-10β-ol *O*-acetyltransferase

Comments: The enzyme will not acylate the hydroxy group at 1β, 7β or 13α of 10-deacetyl baccatin III, or at 5α of taxa-4(20),11-dien-5α-ol. May be identical to EC 2.3.1.163, 10-hydroxytaxane *O*-acetyltransferase.

References: [3736]

[EC 2.3.1.167 created 2002]

EC 2.3.1.168

Accepted name: dihydrolipoyllysine-residue (2-methylpropanoyl)transferase

Reaction: 2-methylpropanoyl-CoA + enzyme N^6-(dihydrolipoyl)lysine = CoA + enzyme N^6-(*S*-[2-methylpropanoyl]dihydrolipoyl)lysine

Other name(s): dihydrolipoyl transacylase; enzyme-dihydrolipoyllysine:2-methylpropanoyl-CoA *S*-(2-methylpropanoyl)transferase; 2-methylpropanoyl-CoA:enzyme-6-*N*-(dihydrolipoyl)lysine *S*-(2-methylpropanoyl)transferase

Systematic name: 2-methylpropanoyl-CoA:enzyme-N^6-(dihydrolipoyl)lysine *S*-(2-methylpropanoyl)transferase

Comments: A multimer (24-mer) of this enzyme forms the core of the multienzyme 3-methyl-2-oxobutanoate dehydrogenase complex, and binds tightly both EC 1.2.4.4, 3-methyl-2-oxobutanoate dehydrogenase (2-methylpropanoyl-transferring) and EC 1.8.1.4, dihydrolipoyl dehydrogenase. The lipoyl group of this enzyme is reductively 2-methylpropanoylated by EC 1.2.4.4, and the only observed direction catalysed by EC 2.3.1.168 is that where this 2-methylpropanoyl is passed to coenzyme A. In addition to the 2-methylpropanoyl group, formed when EC 1.2.4.4 acts on the oxoacid that corresponds with valine, this enzyme also transfers the 3-methylbutanoyl and *S*-2-methylbutanoyl groups, donated to it when EC 1.2.4.4 acts on the oxo acids corresponding with leucine and isoleucine.

References: [2154, 562, 3915, 2665]

[EC 2.3.1.168 created 2003]

EC 2.3.1.169

Accepted name: CO-methylating acetyl-CoA synthase

Reaction: acetyl-CoA + a [Co(I) corrinoid Fe-S protein] = CO + CoA + a [methyl-Co(III) corrinoid Fe-S protein]

Systematic name: acetyl-CoA:corrinoid protein *O*-acetyltransferase

Comments: Contains nickel, copper and iron-sulfur clusters. Involved, together with EC 1.2.7.4, carbon-monoxide dehydrogenase (ferredoxin), in the synthesis of acetyl-CoA from CO_2 and H_2.

References: [2793, 765]

[EC 2.3.1.169 created 2003, modified 2015]

EC 2.3.1.170

Accepted name: 6′-deoxychalcone synthase

Reaction: **3** malonyl-CoA + 4-coumaroyl-CoA + NADPH + H^+ = **4** CoA + isoliquiritigenin + **3** CO_2 + $NADP^+$ + H_2O

Systematic name: malonyl-CoA:4-coumaroyl-CoA malonyltransferase (cyclizing, reducing)

Comments: Isoliquiritigenin is the precursor of liquiritigenin, a 5-deoxyflavanone.

References: [141]

[EC 2.3.1.170 created 2004]

EC 2.3.1.171

Accepted name: anthocyanin $6''$-*O*-malonyltransferase
Reaction: malonyl-CoA + an anthocyanidin 3-*O*-β-D-glucoside = CoA + an anthocyanidin 3-*O*-(6-*O*-malonyl-β-D-glucoside)
Systematic name: malonyl-CoA:anthocyanidin-3-*O*-β-D-glucoside $6''$-*O*-malonyltransferase
Comments: Acts on pelargonidin 3-*O*-glucoside in dahlia (*Dahlia variabilis*), delphinidin 3-*O*-glucoside, and on cyanidin 3-*O*-glucoside in transgenic petunia (*Petunia hybrida*).
References: [3399]

[EC 2.3.1.171 created 2004]

EC 2.3.1.172

Accepted name: anthocyanin 5-*O*-glucoside $6'''$-*O*-malonyltransferase
Reaction: malonyl-CoA + pelargonidin 3-*O*-(6-caffeoyl-β-D-glucoside) 5-*O*-β-D-glucoside = CoA + $4'''$-demalonylsalvianin
Systematic name: malonyl-CoA:pelargonidin-3-*O*-(6-caffeoyl-β-D-glucoside)-5-*O*-β-D-glucoside $6'''$-*O*-malonyltransferase
Comments: Specific for the penultimate step in salvianin biosynthesis. The enzyme also catalyses the malonylation of shisonin to malonylshisonin [cyanidin 3-*O*-($6''$-*O*-*p*-coumaryl-β-D-glucoside)-5-($6'''$-*O*-malonyl-β-D-glucoside)]. The compounds $4'''$-demalonylsalvianin, salvianin, pelargonidin 3,5-diglucoside and delphinidin 3,5-diglucoside cannot act as substrates.
References: [3398]

[EC 2.3.1.172 created 2004]

EC 2.3.1.173

Accepted name: flavonol-3-*O*-triglucoside *O*-coumaroyltransferase
Reaction: 4-coumaroyl-CoA + a flavonol 3-*O*-[β-D-glucosyl-(1→2)-β-D-glucosyl-(1→2)-β-D-glucoside] = CoA + a flavonol 3-*O*-[6-(4-coumaroyl)-β-D-glucosyl-(1→2)-β-D-glucosyl-(1→2)-β-D-glucoside]
Other name(s): 4-coumaroyl-CoA:flavonol-3-*O*-[β-D-glucosyl-(1→2)-β-D-glucoside] $6'''$-*O*-4-coumaroyltransferase (incorrect)
Systematic name: 4-coumaroyl-CoA:flavonol 3-*O*-[β-D-glucosyl-(1→2)-β-D-glucosyl-(1→2)-β-D-glucoside] $6'''$-*O*-4-coumaroyltransferase
Comments: Acylates kaempferol 3-*O*-triglucoside on the terminal glucosyl unit, almost certainly at C-6.
References: [3050]

[EC 2.3.1.173 created 2004]

EC 2.3.1.174

Accepted name: 3-oxoadipyl-CoA thiolase
Reaction: succinyl-CoA + acetyl-CoA = CoA + 3-oxoadipyl-CoA
Systematic name: succinyl-CoA:acetyl-CoA *C*-succinyltransferase
Comments: The enzyme from the bacterium *Escherichia coli* also has the activity of EC 2.3.1.223 (3-oxo-5,6-dehydrosuberyl-CoA thiolase).
References: [1589, 1081, 3504]

[EC 2.3.1.174 created 2005, modified 2013]

EC 2.3.1.175

Accepted name: deacetylcephalosporin-C acetyltransferase
Reaction: acetyl-CoA + deacetylcephalosporin C = CoA + cephalosporin C
Other name(s): acetyl-CoA:deacetylcephalosporin-C acetyltransferase; DAC acetyltransferase; *cefG*; deacetylcephalosporin C acetyltransferase; acetyl coenzyme A:DAC acetyltransferase; acetyl-CoA:DAC acetyltransferase; CPC acetylhydrolase; acetyl-CoA:DAC *O*-acetyltransferase; DAC-AT

Systematic name: acetyl-CoA:deacetylcephalosporin-C *O*-acetyltransferase
Comments: This enzyme catalyses the final step in the biosynthesis of cephalosporin C.
References: [2168, 1185, 2164, 1186, 3657, 2136]

[EC 2.3.1.175 created 2005]

EC 2.3.1.176

Accepted name: propanoyl-CoA *C*-acyltransferase
Reaction: 3α,7α,12α-trihydroxy-5β-cholanoyl-CoA + propanoyl-CoA = CoA + 3α,7α,12α-trihydroxy-24-oxo-5β-cholestanoyl-CoA
Other name(s): SCP2 (gene name); peroxisomal thiolase 2; sterol carrier protein-χ; SCP$_{\chi}$; PTE-2 (ambiguous); propionyl-CoA C^2-trimethyltridecanoyltransferase; 3-oxopristanoyl-CoA hydrolase; 3-oxopristanoyl-CoA thiolase; peroxisome sterol carrier protein thiolase; sterol carrier protein; oxopristanoyl-CoA thiolase; peroxisomal 3-oxoacyl coenzyme A thiolase; SCPx; 4,8,12-trimethyltridecanoyl-CoA:propanoyl-CoA 2-*C*-4,8,12-trimethyltridecanoyltransferase
Systematic name: 3α,7α,12α-trihydroxy-5β-cholanoyl-CoA:propanoyl-CoA *C*-acyltransferase
Comments: Also acts on dihydroxy-5β-cholestanoyl-CoA and other branched chain acyl-CoA derivatives. The enzyme catalyses the penultimate step in the formation of bile acids. The bile acid moiety is transferred from the acyl-CoA thioester (RCO-SCoA) to either glycine or taurine (NH$_2$R$'$) by EC 2.3.1.65, bile acid-CoA:amino acid *N*-acyltransferase [867].
References: [2653, 1590, 867, 3132, 3745, 2976]

[EC 2.3.1.176 created 2005 (EC 2.3.1.154 created 2000, incorporated 2015)]

EC 2.3.1.177

Accepted name: 3,5-dihydroxybiphenyl synthase
Reaction: **3** malonyl-CoA + benzoyl-CoA = **4** CoA + 3,5-dihydroxybiphenyl + **4** CO$_2$
Other name(s): BIS1; biphenyl synthase (ambiguous)
Systematic name: malonyl-CoA:benzoyl-CoA malonyltransferase
Comments: A polyketide synthase that is involved in the production of the phytoalexin aucuparin. 2-Hydroxybenzoyl-CoA can also act as substrate but it leads to the derailment product 4-hydroxycoumarin (*cf.* EC 2.3.1.208, 4-hydroxycoumarin synthase) [1990]. This enzyme uses the same starter substrate as EC 2.3.1.151, benzophenone synthase.
References: [1988, 1990]

[EC 2.3.1.177 created 2006, modified 2012]

EC 2.3.1.178

Accepted name: diaminobutyrate acetyltransferase
Reaction: acetyl-CoA + L-2,4-diaminobutanoate = CoA + (2*S*)-4-acetamido-2-aminobutanoate
Other name(s): L-2,4-diaminobutyrate acetyltransferase; L-2,4-diaminobutanoate acetyltransferase; EctA; diaminobutyric acid acetyltransferase; DABA acetyltransferase; 2,4-diaminobutanoate acetyltransferase; DAB acetyltransferase; DABAcT; acetyl-CoA:L-2,4-diaminobutanoate 4-*N*-acetyltransferase
Systematic name: acetyl-CoA:L-2,4-diaminobutanoate N^4-acetyltransferase
Comments: Requires Na$^+$ or K$^+$ for maximal activity [2874]. Ornithine, lysine, aspartate, and α-, β- and γ-aminobutanoate cannot act as substrates [2874]. However, acetyl-CoA can be replaced by propanoyl-CoA, although the reaction proceeds more slowly [2874]. Forms part of the ectoine-biosynthesis pathway.
References: [2673, 2568, 2874, 1807, 2044]

[EC 2.3.1.178 created 2006]

EC 2.3.1.179

Accepted name: β-ketoacyl-[acyl-carrier-protein] synthase II

Reaction: a (*Z*)-hexadec-11-enoyl-[acyl-carrier protein] + a malonyl-[acyl-carrier protein] = a (*Z*)-3-oxooctadec-13-enoyl-[acyl-carrier protein] + CO_2 + an [acyl-carrier protein]

Other name(s): KASII; KAS II; FabF; 3-oxoacyl-acyl carrier protein synthase I; β-ketoacyl-ACP synthase II; (*Z*)-hexadec-11-enoyl-[acyl-carrier-protein]:malonyl-[acyl-carrier-protein] *C*-acyltransferase (decarboxylating)

Systematic name: (*Z*)-hexadec-11-enoyl-[acyl-carrier protein]:malonyl-[acyl-carrier protein] *C*-acyltransferase (decarboxylating)

Comments: Involved in the dissociated (or type II) fatty acid biosynthesis system that occurs in plants and bacteria. While the substrate specificity of this enzyme is very similar to that of EC 2.3.1.41, β-ketoacyl-ACP synthase I, it differs in that palmitoleoyl-ACP is not a good substrate of EC 2.3.1.41 but is an excellent substrate of this enzyme [653, 1023]. The fatty-acid composition of *Escherichia coli* changes as a function of growth temperature, with the proportion of unsaturated fatty acids increasing with lower growth temperature. This enzyme controls the temperature-dependent regulation of fatty-acid composition, with mutants lacking this acivity being deficient in the elongation of palmitoleate to *cis*-vaccenate at low temperatures [2762, 1022].

References: [653, 1023, 2762, 1022, 2099, 630]

[EC 2.3.1.179 created 2006]

EC 2.3.1.180

Accepted name: β-ketoacyl-[acyl-carrier-protein] synthase III

Reaction: acetyl-CoA + a malonyl-[acyl-carrier protein] = an acetoacetyl-[acyl-carrier protein] + CoA + CO_2

Other name(s): 3-oxoacyl:ACP synthase III; 3-ketoacyl-acyl carrier protein synthase III; KASIII; KAS III; FabH; β-ketoacyl-acyl carrier protein synthase III; β-ketoacyl-ACP synthase III; β-ketoacyl (acyl carrier protein) synthase III; acetyl-CoA:malonyl-[acyl-carrier-protein] *C*-acyltransferase

Systematic name: acetyl-CoA:malonyl-[acyl-carrier protein] *C*-acyltransferase

Comments: Involved in the dissociated (or type II) fatty-acid biosynthesis system that occurs in plants and bacteria. In contrast to EC 2.3.1.41 (β-ketoacyl-ACP synthase I) and EC 2.3.1.179 (β-ketoacyl-ACP synthase II), this enzyme specifically uses CoA thioesters rather than acyl-ACP as the primer [3578]. In addition to the above reaction, the enzyme can also catalyse the reaction of EC 2.3.1.38, [acyl-carrier-protein] *S*-acetyltransferase, but to a much lesser extent [3578]. The enzyme is responsible for initiating both straight- and branched-chain fatty-acid biosynthesis [1209], with the substrate specificity in an organism reflecting the fatty-acid composition found in that organism [1209, 2778]. For example, *Streptococcus pneumoniae*, a Gram-positive bacterium, is able to use both straight- and branched-chain (C_4-C_6) acyl-CoA primers [1658] whereas *Escherichia coli*, a Gram-negative organism, uses primarily short straight-chain acyl CoAs, with a preference for acetyl-CoA [553, 2778].

References: [3578, 1209, 1658, 553, 2778, 1962, 630]

[EC 2.3.1.180 created 2006]

EC 2.3.1.181

Accepted name: lipoyl(octanoyl) transferase

Reaction: an octanoyl-[acyl-carrier protein] + a protein = a protein N^6-(octanoyl)lysine + an [acyl-carrier protein]

Other name(s): LipB; lipoyl (octanoyl)-[acyl-carrier-protein]-protein *N*-lipoyltransferase; lipoyl (octanoyl)-acyl carrier protein:protein transferase; lipoate/octanoate transferase; lipoyltransferase; octanoyl-[acyl carrier protein]-protein *N*-octanoyltransferase; lipoyl(octanoyl)transferase; octanoyl-[acyl-carrier-protein]:protein *N*-octanoyltransferase

Systematic name: octanoyl-[acyl-carrier protein]:protein *N*-octanoyltransferase

Comments: This is the first committed step in the biosynthesis of lipoyl cofactor. Lipoylation is essential for the function of several key enzymes involved in oxidative metabolism, as it converts apoprotein into the biologically active holoprotein. Examples of such lipoylated proteins include pyruvate dehydrogenase (E_2 domain), 2-oxoglutarate dehydrogenase (E_2 domain), the branched-chain 2-oxoacid dehydrogenases and the glycine cleavage system (H protein) [352, 3409]. Lipoyl-ACP can also act as a substrate [4067] although octanoyl-ACP is likely to be the true substrate [2665]. The other enzyme involved in the biosynthesis of lipoyl cofactor is EC 2.8.1.8, lipoyl synthase. An alternative lipoylation pathway involves EC 6.3.1.20, lipoate—protein ligase, which can lipoylate apoproteins using exogenous lipoic acid (or its analogues).

References: [2435, 352, 3409, 4067, 3712, 2665]

[EC 2.3.1.181 created 2006, modified 2016]

EC 2.3.1.182

Accepted name: (*R*)-citramalate synthase

Reaction: acetyl-CoA + pyruvate + H_2O = CoA + (2*R*)-2-hydroxy-2-methylbutanedioate

Other name(s): CimA

Comments: One of the enzymes involved in a novel pyruvate pathway for isoleucine biosynthesis that is found in some, mainly archaeal, bacteria [1384, 3927]. The enzyme can be inhibited by isoleucine, the end-product of the pathway, but not by leucine [3927]. The enzyme is highly specific for pyruvate as substrate, as the 2-oxo acids 3-methyl-2-oxobutanoate, 2-oxobutanoate, 4-methyl-2-oxopentanoate, 2-oxohexanoate and 2-oxoglutarate cannot act as substrate [1384, 3927].

References: [1384, 3927]

[EC 2.3.1.182 created 2007]

EC 2.3.1.183

Accepted name: phosphinothricin acetyltransferase

Reaction: acetyl-CoA + phosphinothricin = CoA + *N*-acetylphosphinothricin

Other name(s): PAT; PPT acetyltransferase; Pt-*N*-acetyltransferase; ac-Pt

Systematic name: acetyl-CoA:phosphinothricin *N*-acetyltransferase

Comments: The substrate phosphinothricin is used as a nonselective herbicide and is a potent inhibitor of EC 6.3.1.2, glutamate—ammonia ligase, a key enzyme of nitrogen metabolism in plants [777].

References: [367, 777]

[EC 2.3.1.183 created 2007]

EC 2.3.1.184

Accepted name: acyl-homoserine-lactone synthase

Reaction: an acyl-[acyl-carrier protein] + *S*-adenosyl-L-methionine = an [acyl-carrier protein] + *S*-methyl-5′-thioadenosine + an *N*-acyl-L-homoserine lactone

Other name(s): acyl-homoserine lactone synthase; acyl homoserine lactone synthase; acyl-homoserinelactone synthase; acylhomoserine lactone synthase; AHL synthase; AHS; AHSL synthase; AhyI; AinS; AinS protein; autoinducer synthase; autoinducer synthesis protein *rhlI*; EsaI; ExpISCC$_{1;}$ ExpISCC3065; LasI; LasR; LuxI; LuxI protein; LuxM; *N*-acyl homoserine lactone synthase; RhlI; YspI ; acyl-[acyl carrier protein]:*S*-adenosyl-L-methionine acyltranserase (lactone-forming, methylthioadenosine-releasing)

Systematic name: acyl-[acyl-carrier protein]:*S*-adenosyl-L-methionine acyltranserase (lactone-forming, methylthioadenosine-releasing)

Comments: Acyl-homoserine lactones (AHLs) are produced by a number of bacterial species and are used by them to regulate the expression of virulence genes in a process known as quorum-sensing. Each bacterial cell has a basal level of AHL and, once the population density reaches a critical level, it triggers AHL-signalling which, in turn, initiates the expression of particular virulence genes [2630]. *N*-(3-Oxohexanoyl)-[acyl-carrier protein] and hexanoyl-[acyl-carrier protein] are the best substrates [3060]. The fatty-acyl substrate is derived from fatty-acid biosynthesis through acyl-[acyl-carrier protein] rather than from fatty-acid degradation through acyl-CoA [3060]. *S*-Adenosyl-L-methionine cannot be replaced by methionine, *S*-adenosylhomocysteine, homoserine or homoserine lactone [3060].

References: [3060, 3790, 498, 1217, 2630, 3610, 1119, 2835, 1118]

[EC 2.3.1.184 created 2007]

EC 2.3.1.185

Accepted name: tropine acyltransferase

Reaction: an acyl-CoA + tropine = CoA + an *O*-acyltropine

Other name(s): tropine:acyl-CoA transferase; acetyl-CoA:tropan-3-ol acyltransferase; tropine acetyltransferase; tropine tigloyltransferase; TAT

Systematic name: acyl-CoA:tropine *O*-acyltransferase

Comments: This enzyme exhibits absolute specificity for the endo/3α configuration found in tropine as pseudotropine (tropan-3β-ol; see EC 2.3.1.186, pseudotropine acyltransferase) is not a substrate [365]. Acts on a wide range of aliphatic acyl-CoA derivatives, with tigloyl-CoA and acetyl-CoA being the best substrates. It is probably involved in the formation of the tropane alkaloid littorine, which is a precursor of hyoscyamine [1958].

References: [2900, 2901, 365, 1958]

[EC 2.3.1.185 created 2008]

EC 2.3.1.186

Accepted name: pseudotropine acyltransferase

Reaction: an acyl-CoA + pseudotropine = CoA + an *O*-acylpseudotropine

Other name(s): pseudotropine:acyl-CoA transferase; tigloyl-CoA:pseudotropine acyltransferase; acetyl-CoA:pseudotropine acyltransferase; pseudotropine acetyltransferase; pseudotropine tigloyltransferase; PAT

Systematic name: acyl-CoA:pseudotropine *O*-acyltransferase

Comments: This enzyme exhibits absolute specificity for the exo/3β configuration found in pseudotropine as tropine (tropan-3α-ol; see EC 2.3.1.185, tropine acyltransferase) and nortropine are not substrates [2784]. Acts on a wide range of aliphatic acyl-CoA derivatives, including acetyl-CoA, β-methylcrotonyl-CoA and tigloyl-CoA [2784].

References: [2784, 2900, 2901, 365]

[EC 2.3.1.186 created 2008]

EC 2.3.1.187

Accepted name: acetyl-*S*-ACP:malonate ACP transferase

Reaction: an acetyl-[acyl-carrier protein] + malonate = a malonyl-[acyl-carrier protein] + acetate

Other name(s): acetyl-*S*-ACP:malonate ACP-SH transferase; acetyl-*S*-acyl-carrier protein:malonate acyl-carrier-protein-transferase; MdcA; MadA; ACP transferase; malonate/acetyl-CoA transferase; malonate:ACP transferase; acetyl-*S*-acyl carrier protein:malonate acyl carrier protein-SH transferase

Systematic name: acetyl-[acyl-carrier-protein]:malonate *S*-[acyl-carrier-protein]transferase

Comments: This is the first step in the catalysis of malonate decarboxylation and involves the exchange of an acetyl thioester residue bound to the activated acyl-carrier protein (ACP) subunit of the malonate decarboxylase complex for a malonyl thioester residue [1349]. This enzyme forms the α subunit of the multienzyme complexes biotin-independent malonate decarboxylase (EC 4.1.1.88) and biotin-dependent malonate decarboxylase (EC 7.2.4.4). The enzyme can also use acetyl-CoA as a substrate but more slowly [550].

References: [1327, 1349, 1752, 550, 736]

[EC 2.3.1.187 created 2008, modified 2018]

EC 2.3.1.188

Accepted name: ω-hydroxypalmitate *O*-feruloyl transferase

Reaction: feruloyl-CoA + 16-hydroxypalmitate = CoA + 16-feruloyloxypalmitate

Other name(s): hydroxycinnamoyl-CoA ω-hydroxypalmitic acid *O*-hydroxycinnamoyltransferase; HHT

Systematic name: feruloyl-CoA:16-hydroxypalmitate feruloyltransferase

Comments: *p*-Coumaroyl-CoA and sinapoyl-CoA also act as substrates. The enzyme is widely distributed in roots of higher plants.

References: [2039, 2040, 2041]

[EC 2.3.1.188 created 2009]

EC 2.3.1.189

Accepted name: mycothiol synthase

Reaction: desacetylmycothiol + acetyl-CoA = CoA + mycothiol

Other name(s): MshD

Systematic name: acetyl-CoA:desacetylmycothiol *O*-acetyltransferase

Comments: This enzyme catalyses the last step in the biosynthesis of mycothiol, the major thiol in most actinomycetes, including *Mycobacterium* [3299]. The enzyme is a member of a large family of GCN5-related *N*-acetyltransferases (GNATs) [1745]. The enzyme has been purified from *Mycobacterium tuberculosis* H37Rv. Acetyl-CoA is the preferred CoA thioester but propionyl-CoA is also a substrate [3677].

References: [3299, 1745, 3677]

[EC 2.3.1.189 created 2010]

EC 2.3.1.190

Accepted name: acetoin dehydrogenase

Reaction: acetoin + CoA + NAD$^+$ = acetaldehyde + acetyl-CoA + NADH + H$^+$

Other name(s): acetoin dehydrogenase complex; acetoin dehydrogenase enzyme system; AoDH ES

Systematic name: acetyl-CoA:acetoin *O*-acetyltransferase

Comments: Requires thiamine diphosphate. This enzyme, which belongs to the family of 2-oxo acid dehydrogenase complexes, catalyses the oxidative-hydrolytic cleavage of acetoin to acetaldehyde and acetyl-CoA in many bacterial strains, both aerobic and anaerobic. The enzyme is composed of multiple copies of three enzymic components: acetoin oxidoreductase (E1), dihydrolipoamide acetyltransferase (E2) and dihydrolipoyl dehydrogenase (E3).

References: [2764, 2571, 1795, 1395, 1396]

[EC 2.3.1.190 created 2010]

EC 2.3.1.191

Accepted name: UDP-3-*O*-(3-hydroxymyristoyl)glucosamine *N*-acyltransferase

Reaction: (3*R*)-3-hydroxytetradecanoyl-[acyl-carrier protein] + UDP-3-*O*-[(3*R*)-3-hydroxytetradecanoyl]-α-D-glucosamine = UDP-2-*N*,3-*O*-bis[(3*R*)-3-hydroxytetradecanoyl]-α-D-glucosamine + a holo-[acyl-carrier protein]

Other name(s): UDP-3-*O*-acyl-glucosamine *N*-acyltransferase; UDP-3-*O*-(R-3-hydroxymyristoyl)-glucosamine *N*-acyltransferase; acyltransferase LpxD; acyl-ACP:UDP-3-*O*-(3-hydroxyacyl)-GlcN *N*-acyltransferase; *firA* (gene name); *lpxD* (gene name); (3*R*)-3-hydroxymyristoyl-[acyl-carrier protein]:UDP-3-*O*-[(3*R*)-3-hydroxymyristoyl]-α-D-glucosamine *N*-acetyltransferase

Systematic name: (3*R*)-3-hydroxytetradecanoyl-[acyl-carrier protein]:UDP-3-*O*-[(3*R*)-3-hydroxytetradecanoyl]-α-D-glucosamine *N*-acetyltransferase

Comments: The enzyme catalyses a step of lipid A biosynthesis. LpxD from *Escherichia* prefers (*R*,*S*)-3-hydroxytetradecanoyl-[acyl-carrier protein] over (*R*,*S*)-3-hydroxyhexadecanoyl-[acyl-carrier protein] [210]. *Escherichia coli* lipid A acyltransferases do not have an absolute specificity for 14-carbon hydroxy fatty acids but can transfer fatty acids differing by one carbon unit if the fatty acid substrates are available. When grown on 1% propionic acid, lipid A also contains the odd-chain fatty acids tridecanoic acid, pentadecanoic acid, hydroxytridecanoic acid, and hydroxypentadecanoic acid [170].
References: [210, 420, 209, 1634, 170]

[EC 2.3.1.191 created 2010]

EC 2.3.1.192
Accepted name: glycine *N*-phenylacetyltransferase
Reaction: phenylacetyl-CoA + glycine = CoA + phenylacetylglycine
Other name(s): arylacetyl-CoA *N*-acyltransferase; arylacetyltransferase; GAT (gene name)
Systematic name: phenylacetyl-CoA:glycine *N*-phenylacetyltransferase
Comments: Not identical with EC 2.3.1.13 (glycine *N*-acyltransferase). This enzyme was purified from bovine liver mitochondria. L-asparagine, L-glutamine and L-arginine are alternative substrates to glycine, but have higher K_m values.
References: [2417, 1630, 3673]

[EC 2.3.1.192 created 2010]

EC 2.3.1.193
Accepted name: tRNA^{Met} cytidine acetyltransferase
Reaction: [elongator tRNA^{Met}]-cytidine^{34} + ATP + acetyl-CoA + H_2O = CoA + [elongator tRNA^{Met}]-N^4-acetylcytidine^{34} + ADP + phosphate
Other name(s): YpfI; TmcA
Systematic name: acetyl-CoA:[elongator tRNA^{Met}]-cytidine^{34} N^4-acetyltransferase (ATP-hydrolysing)
Comments: The enzyme acetylates the wobble base cytidine^{34} of the CAU anticodon of elongation-specific tRNA^{Met}. *Escherichia coli* TmcA strictly discriminates elongator tRNA^{Met} from tRNA^{Ile}, which is structurally similar and has the same anticodon loop, mainly by recognizing the C^{27}-G^{43} pair in the anticodon stem. The enzyme can use GTP in place of ATP for formation of N^4-acetylcytidine [1438].
References: [1438, 546]

[EC 2.3.1.193 created 2011]

EC 2.3.1.194
Accepted name: acetoacetyl-CoA synthase
Reaction: acetyl-CoA + malonyl-CoA = acetoacetyl-CoA + CoA + CO_2
Other name(s): NphT7
Systematic name: acetyl-CoA:malonyl-CoA *C*-acetyltransferase (decarboxylating)
Comments: The enzyme from the soil bacterium *Streptomyces* sp. CL190 produces acetoacetyl-CoA to be used for mevalonate production via the mevalonate pathway. Unlike the homologous EC 2.3.1.180 (β-ketoacyl-[acyl-carrier-protein] synthase III), this enzyme does not accept malonyl-[acyl-carrier-protein] as a substrate.
References: [2552]

[EC 2.3.1.194 created 2011]

EC 2.3.1.195
Accepted name: (*Z*)-3-hexen-1-ol acetyltransferase
Reaction: acetyl-CoA + (3*Z*)-hex-3-en-1-ol = CoA + (3*Z*)-hex-3-en-1-yl acetate
Other name(s): CHAT; At3g03480

Systematic name: acetyl-CoA:(3*Z*)-hex-3-en-1-ol acetyltransferase

Comments: The enzyme is resonsible for the production of (3*Z*)-hex-3-en-1-yl acetate, the major volatile compound released upon mechanical wounding of the leaves of *Arabidopsis thaliana* [677].

References: [677, 676]

[EC 2.3.1.195 created 2011]

EC 2.3.1.196

Accepted name: benzyl alcohol *O*-benzoyltransferase

Reaction: benzoyl-CoA + benzyl alcohol = CoA + benzyl benzoate

Other name(s): benzoyl-CoA:benzyl alcohol benzoyltransferase; benzoyl-CoA:benzyl alcohol/phenylethanol benzoyltransferase; benzoyl-coenzyme A:benzyl alcohol benzoyltransferase; benzoyl-coenzyme A:phenylethanol benzoyltransferase

Systematic name: benzoyl-CoA:benzyl alcohol *O*-benzoyltransferase

Comments: The enzyme is involved in volatile benzenoid and benzoic acid biosynthesis. The enzyme from *Petunia hybrida* also catalyses the formation of 2-phenylethyl benzoate from benzoyl-CoA and 2-phenylethanol. The apparent catalytic efficiency of the enzyme from *Petunia hybrida* with benzoyl-CoA is almost 6-fold higher than with acetyl-CoA [337].

References: [337, 676]

[EC 2.3.1.196 created 2011]

EC 2.3.1.197

Accepted name: dTDP-3-amino-3,6-dideoxy-α-D-galactopyranose 3-*N*-acetyltransferase

Reaction: acetyl-CoA + dTDP-3-amino-3,6-dideoxy-α-D-galactopyranose = CoA + dTDP-3-acetamido-3,6-dideoxy-α-D-galactopyranose

Other name(s): FdtC; dTDP-D-Fucp3N acetylase

Systematic name: acetyl-CoA:dTDP-3-amino-3,6-dideoxy-α-D-galactopyranose 3-*N*-acetyltransferase

Comments: The product, dTDP-3-acetamido-3,6-dideoxy-α-D-galactose, is a component of the glycan chain of the crystalline bacterial cell surface layer protein (S-layer glycoprotein) of *Aneurinibacillus thermoaerophilus*.

References: [2688]

[EC 2.3.1.197 created 2012]

EC 2.3.1.198

Accepted name: glycerol-3-phosphate 2-*O*-acyltransferase

Reaction: an acyl-CoA + *sn*-glycerol 3-phosphate = CoA + a 2-acyl-*sn*-glycerol 3-phosphate

Other name(s): *sn*-2-glycerol-3-phosphate *O*-acyltransferase; glycerol-3-phosphate *O*-acyltransferase (ambiguous)

Systematic name: acyl-CoA:*sn*-glycerol 3-phosphate 2-*O*-acyltransferase

Comments: A membrane-associated enzyme required for suberin or cutin synthesis in plants. Active with a wide range of acyl-CoA substrates (C16:0-C24:0). The enzyme from some sources has much higher activity with ω-oxidized acyl-CoAs. Some enzymes are bifunctional and have an additional phosphatase activity producing *sn*-2-monoacylglycerols.

References: [3964]

[EC 2.3.1.198 created 2012]

EC 2.3.1.199

Accepted name: very-long-chain 3-oxoacyl-CoA synthase

Reaction: a very-long-chain acyl-CoA + malonyl-CoA = a very-long-chain 3-oxoacyl-CoA + CO_2 + CoA

Other name(s): very-long-chain 3-ketoacyl-CoA synthase; very-long-chain β-ketoacyl-CoA synthase; condensing enzyme (ambiguous); CUT1 (gene name); CER6 (gene name); FAE1 (gene name); KCS (gene name); ELO (gene name)

Systematic name: malonyl-CoA:very-long-chain acyl-CoA malonyltransferase (decarboxylating and thioester-hydrolysing)

Comments: This is the first component of the elongase, a microsomal protein complex responsible for extending palmitoyl-CoA and stearoyl-CoA (and modified forms thereof) to very-long-chain acyl CoAs. Multiple forms exist with differing preferences for the substrate, and thus the specific form expressed determines the local composition of very-long-chain fatty acids [318, 712]. For example, the FAE1 form from the plant *Arabidopsis thaliana* accepts only 16 and 18 carbon substrates, with oleoyl-CoA (18:1) being the preferred substrate [1040], while CER6 from the same plant prefers substrates with chain length of C_{22} to C_{32} [2247, 3566]. *cf.* EC 1.1.1.330, very-long-chain 3-oxoacyl-CoA reductase, EC 4.2.1.134, very-long-chain (3*R*)-3-hydroxyacyl-[acyl-carrier protein] dehydratase, and EC 1.3.1.93, very-long-chain enoyl-CoA reductase

References: [3543, 2528, 743, 2247, 1040, 318, 712, 3566]

[EC 2.3.1.199 created 2012]

EC 2.3.1.200

Accepted name: lipoyl amidotransferase

Reaction: [glycine cleavage system H]-N^6-lipoyl-L-lysine + a [lipoyl-carrier protein] = glycine cleavage system H + a [lipoyl-carrier protein]-N^6-lipoyl-L-lysine

Other name(s): LipL (gene name, ambiguous)

Systematic name: [glycine cleavage system H]-N^6-lipoyl-L-lysine:[lipoyl-carrier protein]-N^6-L-lysine lipoyltransferase

Comments: In the bacterium *Listeria monocytogenes* the enzyme takes part in a pathway for scavenging of lipoic acid. The enzyme is bound to 2-oxo-acid dehydrogenases such as the pyruvate dehydrogenase complex, where it transfers the lipoyl moiety from lipoyl-[glycine cleavage system H] to the E2 subunits of the complexes.

References: [558]

[EC 2.3.1.200 created 2012]

EC 2.3.1.201

Accepted name: UDP-2-acetamido-3-amino-2,3-dideoxy-glucuronate *N*-acetyltransferase

Reaction: acetyl-CoA + UDP-2-acetamido-3-amino-2,3-dideoxy-α-D-glucuronate = CoA + UDP-2,3-diacetamido-2,3-dideoxy-α-D-glucuronate

Other name(s): WbpD; WlbB

Systematic name: acetyl-CoA:UDP-2-acetamido-3-amino-2,3-dideoxy-α-D-glucuronate *N*-acetyltransferase

Comments: This enzyme participates in the biosynthetic pathway for UDP-α-D-ManNAc3NAcA (UDP-2,3-diacetamido-2,3-dideoxy-α-D-mannuronic acid), an important precursor of B-band lipopolysaccharide.

References: [3827, 1864]

[EC 2.3.1.201 created 2012]

EC 2.3.1.202

Accepted name: UDP-4-amino-4,6-dideoxy-*N*-acetyl-β-L-altrosamine *N*-acetyltransferase

Reaction: acetyl-CoA + UDP-4-amino-4,6-dideoxy-*N*-acetyl-β-L-altrosamine = CoA + UDP-2,4-diacetamido-2,4,6-trideoxy-β-L-altropyranose

Other name(s): PseH

Systematic name: acetyl-CoA:UDP-4-amino-4,6-dideoxy-*N*-acetyl-β-L-altrosamine *N*-acetyltransferase

Comments: Isolated from *Helicobacter pylori*. The enzyme is involved in the biosynthesis of pseudaminic acid.

References: [3098]

[EC 2.3.1.202 created 2012]

EC 2.3.1.203

Accepted name: UDP-*N*-acetylbacillosamine *N*-acetyltransferase

Reaction: acetyl-CoA + UDP-*N*-acetylbacillosamine = CoA + UDP-N,N'-diacetylbacillosamine

Other name(s): UDP-4-amino-4,6-dideoxy-*N*-acetyl-α-D-glucosamine *N*-acetyltransferase; *pglD* (gene name)

Systematic name: acetyl-CoA:UDP-4-amino-4,6-dideoxy-*N*-acetyl-α-D-glucosamine *N*-acetyltransferase

Comments: The product, UDP-N,N'-diacetylbacillosamine, is an intermediate in protein glycosylation pathways in several bacterial species, including N-linked glycosylation of certain L-asparagine residues in *Campylobacter* species [2559, 2809] and O-linked glycosylation of certain L-serine residues in *Neisseria* species [1232].

References: [2559, 2809, 1232]

[EC 2.3.1.203 created 2012, modified 2013]

EC 2.3.1.204

Accepted name: octanoyl-[GcvH]:protein *N*-octanoyltransferase

Reaction: [glycine cleavage system H]-N^6-octanoyl-L-lysine + a [lipoyl-carrier protein] = glycine cleavage system H + a [lipoyl-carrier protein]-N^6-octanoyl-L-lysine

Other name(s): LipL; octanoyl-[GcvH]:E2 amidotransferase; *ywfL* (gene name)

Systematic name: [glycine cleavage system H]-N^6-octanoyl-L-lysine:[lipoyl-carrier protein]-N^6-L-lysine octanoyltransferase

Comments: In the bacterium *Bacillus subtilis* it has been shown that the enzyme catalyses the amidotransfer of the octanoyl moiety from [glycine cleavage system H]-N^6-octanoyl-L-lysine (i.e. octanoyl-GcvH) to the E2 subunit (dihydrolipoamide acetyltransferase) of pyruvate dehydrogenase.

References: [559, 2137]

[EC 2.3.1.204 created 2012]

EC 2.3.1.205

Accepted name: fumigaclavine B *O*-acetyltransferase

Reaction: acetyl-CoA + fumigaclavine B = CoA + fumigaclavine A

Other name(s): FgaAT

Systematic name: acetyl-CoA:fumigaclavine B *O*-acetyltransferase

Comments: The enzyme participates in the biosynthesis of fumigaclavine C, an ergot alkaloid produced by some fungi of the *Trichocomaceae* family.

References: [2012]

[EC 2.3.1.205 created 2012]

EC 2.3.1.206

Accepted name: 3,5,7-trioxododecanoyl-CoA synthase

Reaction: **3** malonyl-CoA + hexanoyl-CoA = **3** CoA + 3,5,7-trioxododecanoyl-CoA + **3** CO_2

Other name(s): TKS (ambiguous); olivetol synthase (incorrect)

Systematic name: malonyl-CoA:hexanoyl-CoA malonyltransferase (3,5,7-trioxododecanoyl-CoA-forming)

Comments: A polyketide synthase catalysing the first committed step in the cannabinoids biosynthetic pathway of the plant *Cannabis sativa*. The enzyme was previously thought to also function as a cyclase, but the cyclization is now known to be catalysed by EC 4.4.1.26, olivetolic acid cyclase.

References: [3478, 1003]

[EC 2.3.1.206 created 2012]

EC 2.3.1.207

Accepted name: β-ketodecanoyl-[acyl-carrier-protein] synthase

Reaction: octanoyl-CoA + a malonyl-[acyl-carrier protein] = a 3-oxodecanoyl-[acyl-carrier protein] + CoA + CO_2

Systematic name: octanoyl-CoA:malonyl-[acyl-carrier protein] *C*-heptanoylltransferase (decarboxylating, CoA-forming)
Comments: This enzyme, which has been characterized from the bacterium *Pseudomonas aeruginosa* PAO1, catalyses the condensation of octanoyl-CoA, obtained from exogenously supplied fatty acids via β-oxidation, with malonyl-[acp], forming 3-oxodecanoyl-[acp], an intermediate of the fatty acid elongation cycle. The enzyme provides a shunt for β-oxidation degradation intermediates into *de novo* fatty acid biosynthesis.
References: [4013]

[EC 2.3.1.207 created 2012]

EC 2.3.1.208
Accepted name: 4-hydroxycoumarin synthase
Reaction: malonyl-CoA + 2-hydroxybenzoyl-CoA = **2** CoA + 4-hydroxycoumarin + CO_2
Other name(s): BIS2; BIS3
Systematic name: malonyl-CoA:2-hydroxybenzoyl-CoA malonyltransferase
Comments: The enzyme, a polyketide synthase, can also accept benzoyl-CoA as substrate, which it condenses with 3 malonyl-CoA molecules to form 3,5-dihydroxybiphenyl (*cf.* EC 2.3.1.177, biphenyl synthase) [1991].
References: [1991]

[EC 2.3.1.208 created 2012]

EC 2.3.1.209
Accepted name: dTDP-4-amino-4,6-dideoxy-D-glucose acyltransferase
Reaction: acetyl-CoA + dTDP-4-amino-4,6-dideoxy-α-D-glucose = CoA + dTDP-4-acetamido-4,6-dideoxy-α-D-glucose
Other name(s): VioB
Systematic name: acetyl-CoA:dTDP-4-amino-4,6-dideoxy-α-D-glucose *N*-acetyltransferase
Comments: The non-activated product, 4-acetamido-4,6-dideoxy-α-D-glucose, is part of the O antigens of *Shigella dysenteriae* type 7 and *Escherichia coli* O7.
References: [3769]

[EC 2.3.1.209 created 2012]

EC 2.3.1.210
Accepted name: dTDP-4-amino-4,6-dideoxy-D-galactose acyltransferase
Reaction: acetyl-CoA + dTDP-4-amino-4,6-dideoxy-α-D-galactose = CoA + dTDP-4-acetamido-4,6-dideoxy-α-D-galactose
Other name(s): TDP-fucosamine acetyltransferase; WecD; RffC
Systematic name: acetyl-CoA:dTDP-4-amino-4,6-dideoxy-α-D-galactose *N*-acetyltransferase
Comments: The product, TDP-4-acetamido-4,6-dideoxy-D-galactose, is utilized in the biosynthesis of enterobacterial common antigen (ECA).
References: [1410]

[EC 2.3.1.210 created 2012]

EC 2.3.1.211
Accepted name: bisdemethoxycurcumin synthase
Reaction: **2** 4-coumaroyl-CoA + malonyl-CoA + H_2O = **3** CoA + bisdemethoxycurcumin + **2** CO_2
Other name(s): CUS; curcuminoid synthase (ambiguous)
Systematic name: 4-coumaroyl-CoA:malonyl-CoA 4-coumaryltransferase (bisdemethoxycurcumin-forming)

Comments: A polyketide synthase characterized from the plant *Oryza sativa* (rice) that catalyses the formation of the C_6-C_7-C_6 diarylheptanoid scaffold of bisdemethoxycurcumin. Unlike the process in the plant *Curcuma longa* (turmeric), where the conversion is carried out via a diketide intermediate by two different enzymes (EC 2.3.1.218, phenylpropanoylacetyl-CoA synthase and EC 2.3.1.217, curcumin synthase), the diketide intermediate formed by this enzyme remains within the enzyme's cavity and is not released to the environment.
References: [2320]

[EC 2.3.1.211 created 2013]

EC 2.3.1.212

Accepted name: benzalacetone synthase
Reaction: 4-coumaroyl-CoA + malonyl-CoA + H_2O = **2** CoA + 4-hydroxybenzalacetone + **2** CO_2
Other name(s): BAS
Systematic name: 4-coumaroyl-CoA:malonyl-CoA 4-coumaryltransferase (4-hydroxybenzalacetone-forming)
Comments: A polyketide synthase that catalyses the C_6-C_4 skeleton of phenylbutanoids in higher plants.
References: [356, 3, 4069, 2319]

[EC 2.3.1.212 created 2013]

EC 2.3.1.213

Accepted name: cyanidin 3-*O*-(6-*O*-glucosyl-2-*O*-xylosylgalactoside) $6'''$-*O*-hydroxycinnamoyltransferase
Reaction: 1-*O*-(4-hydroxycinnamoyl)-β-D-glucose + cyanidin 3-*O*-(6-*O*-β-D-glucosyl-2-*O*-β-D-xylosyl-β-D-galactoside) = β-D-glucose + cyanidin 3-*O*-[6-*O*-(6-*O*-4-hydroxycinnamoyl-β-D-glucosyl)-2-*O*-β-D-xylosyl-β-D-galactoside]
Other name(s): 1-*O*-(4-hydroxycinnamoyl)-β-D-glucose:cyanidin 3-*O*-(2”-*O*-xylosyl-6”-*O*-glucosylgalactoside) $6'''$-*O*-(4-hydroxycinnamoyl)transferase
Systematic name: 1-*O*-(4-hydroxycinnamoyl)-β-D-glucose:cyanidin 3-*O*-(6-*O*-β-D-glucosyl-2-*O*-β-D-xylosyl-β-D-galactoside) $6'''$-*O*-(4-hydroxycinnamoyl)transferase
Comments: Isolated from the plant *Daucus carota* (Afghan cultivar carrot). In addition to 1-*O*-(4-hydroxycinnamoyl)-β-D-glucose, the enzyme can use the 1-*O*-sinapoyl- and 1-*O*-feruloyl- derivatives of β-D-glucose.
References: [1072]

[EC 2.3.1.213 created 2013]

EC 2.3.1.214

Accepted name: pelargonidin 3-*O*-(6-caffeoylglucoside) 5-*O*-(6-*O*-malonylglucoside) $4'''$-malonyltransferase
Reaction: malonyl-CoA + $4'''$-demalonylsalvianin = CoA + salvianin
Other name(s): malonyl-CoA:anthocyanin 5-glucoside $4'''$-*O*-malonyltransferase; Ss5MaT2
Systematic name: malonyl-CoA:$4'''$-demalonylsalvianin $4'''$-*O*-malonyltransferase
Comments: Isolated from the plant *Salvia splendens* (scarlet sage).
References: [3400]

[EC 2.3.1.214 created 2013]

EC 2.3.1.215

Accepted name: anthocyanidin 3-*O*-glucoside $6''$-*O*-acyltransferase
Reaction: 4-hydroxycinnamoyl-CoA + an anthocyanidin 3-*O*-β-D-glucoside = CoA + an anthocyanidin 3-*O*-[6-*O*-(4-hydroxycinnamoyl)-β-D-glucoside]
Systematic name: 4-hydroxycinnamoyl-CoA:anthocyanin-3-*O*-glucoside $6''$-*O*-acyltransferase

Comments: Isolated from the plants *Perilla frutescens* and *Gentiana triflora* (clustered gentian). Acts on a range of anthocyanidin 3-*O*-glucosides, 3,5-di-*O*-glucosides and cyanidin 3-rutinoside. It did not act on delphinidin 3,3′,7-tri-*O*-glucoside. Recombinant *Perilla frutescens* enzyme could utilize caffeoyl-CoA but not malonyl-CoA as alternative acyl donor.
References: [991, 3993]

[EC 2.3.1.215 created 2013]

EC 2.3.1.216

Accepted name: 5,7-dihydroxy-2-methylchromone synthase
Reaction: **5** malonyl-CoA = **5** CoA + 5,7-dihydroxy-2-methyl-4*H*-chromen-4-one + **5** CO_2 + H_2O
Other name(s): pentaketide chromone synthase
Systematic name: malonyl-CoA:malonyl-CoA malonyltransferase (5,7-dihydroxy-2-methyl-4*H*-chromen-4-one-forming)
Comments: A polyketide synthase from the plant *Aloe arborescens* (aloe).
References: [4]

[EC 2.3.1.216 created 2013]

EC 2.3.1.217

Accepted name: curcumin synthase
Reaction: feruloyl-CoA + feruloylacetyl-CoA + H_2O = **2** CoA + curcumin + CO_2
Other name(s): CURS; CURS1 (gene name); CURS2 (gene name); CURS3 (gene name)
Systematic name: feruloyl-CoA:feruloylacetyl-CoA feruloyltransferase (curcumin-forming)
Comments: A polyketide synthase from the plant *Curcuma longa* (turmeric). Three isoforms exist, CURS1, CURS2 and CURS3. While CURS1 and CURS2 prefer feruloyl-CoA as a starter substrate, CURS3 can accept 4-coumaroyl-CoA equally well [1606] (see EC 2.3.1.219, demethoxycurcumin synthase).
References: [1605, 1606, 1607]

[EC 2.3.1.217 created 2013]

EC 2.3.1.218

Accepted name: phenylpropanoylacetyl-CoA synthase
Reaction: (1) feruloyl-CoA + malonyl-CoA = feruloylacetyl-CoA + CO_2 + CoA
(2) 4-coumaroyl-CoA + malonyl-CoA = (4-coumaroyl)acetyl-CoA + CO_2 + CoA
Other name(s): phenylpropanoyl-diketide-CoA synthase; DCS
Systematic name: phenylpropanoyl-CoA:malonyl-CoA phenylpropanoyl-transferase (decarboxylating)
Comments: The enzyme has been characterized from the plant *Curcuma longa* (turmeric). It prefers feruloyl-CoA, and has no activity with cinnamoyl-CoA.
References: [1605]

[EC 2.3.1.218 created 2013]

EC 2.3.1.219

Accepted name: demethoxycurcumin synthase
Reaction: (1) 4-coumaroyl-CoA + feruloylacetyl-CoA + H_2O = **2** CoA + demethoxycurcumin + CO_2
(2) 4-coumaroyl-CoA + (4-coumaroyl)acetyl-CoA + H_2O = **2** CoA + bisdemethoxycurcumin + CO_2
Other name(s): CURS3
Systematic name: 4-coumaroyl-CoA:feruloylacetyl-CoA feruloyltransferase (demethoxycurcumin-forming)
Comments: A polyketide synthase from the plant *Curcuma longa* (turmeric). Three isoforms exist, CURS1, CURS2 and CURS3. While CURS1 and CURS2 prefer feruloyl-CoA as a starter substrate (*cf.* EC 2.3.1.217, curcumin synthase), CURS3 can accept 4-coumaroyl-CoA equally well [1606].
References: [1606]

[EC 2.3.1.219 created 2013]

EC 2.3.1.220

Accepted name: 2,4,6-trihydroxybenzophenone synthase

Reaction: **3** malonyl-CoA + benzoyl-CoA = **4** CoA + 2,4,6-trihydroxybenzophenone + **3** CO_2

Other name(s): benzophenone synthase (ambiguous); BPS (ambiguous)

Systematic name: malonyl-CoA:benzoyl-CoA malonyltransferase (2,4,6-trihydroxybenzophenone-forming)

Comments: Involved in the biosynthesis of plant xanthones. The enzyme from the plant *Hypericum androsaemum* L can use 3-hydroxybenzoyl-CoA instead of benzoyl-CoA, but with lower activity (*cf.* EC 2.3.1.151, 2,3′,4,6-tetrahydroxybenzophenone synthase).

References: [3088, 2496]

[EC 2.3.1.220 created 2013]

EC 2.3.1.221

Accepted name: noranthrone synthase

Reaction: **7** malonyl-CoA + hexanoyl-[acyl-carrier protein] = **7** CoA + norsolorinic acid anthrone + [acyl-carrier protein] + **7** CO_2 + **2** H_2O

Other name(s): polyketide synthase A (ambiguous); PksA (ambiguous); norsolorinic acid anthrone synthase

Systematic name: malonyl-CoA:hexanoate malonyltransferase (norsolorinic acid anthrone-forming)

Comments: A multi-domain polyketide synthase involved in the synthesis of aflatoxins in the fungus *Aspergillus parasiticus*. The hexanoyl starter unit is provided to the acyl-carrier protein (ACP) domain by a dedicated fungal fatty acid synthase [627].

References: [627, 626, 1754]

[EC 2.3.1.221 created 2013]

EC 2.3.1.222

Accepted name: phosphate propanoyltransferase

Reaction: propanoyl-CoA + phosphate = CoA + propanoyl phosphate

Other name(s): PduL

Systematic name: propanoyl-CoA:phosphate propanoyltransferase

Comments: Part of the degradation pathway for propane-1,2-diol .

References: [2013]

[EC 2.3.1.222 created 2013]

EC 2.3.1.223

Accepted name: 3-oxo-5,6-didehydrosuberyl-CoA thiolase

Reaction: 2,3-didehydroadipoyl-CoA + acetyl-CoA = CoA + 3-oxo-5,6-didehydrosuberoyl-CoA

Other name(s): *paaJ* (gene name)

Systematic name: 2,3-didehydroadipoyl-CoA:acetyl-CoA *C*-didehydroadipoyltransferase (double bond migration)

Comments: The enzyme acts in the opposite direction. The enzymes from the bacteria *Escherichia coli* and *Pseudomonas* sp. Y2 also have the activity of EC 2.3.1.174 (3-oxoadipyl-CoA thiolase).

References: [3504]

[EC 2.3.1.223 created 2013]

EC 2.3.1.224

Accepted name: acetyl-CoA-benzylalcohol acetyltransferase

Reaction: (1) acetyl-CoA + benzyl alcohol = CoA + benzyl acetate
(2) acetyl-CoA + cinnamyl alcohol = CoA + cinnamyl acetate

Other name(s): BEAT
Systematic name: acetyl-CoA:benzylalcohol *O*-acetyltransferase
Comments: The enzyme is found in flowers like *Clarkia breweri*, where it is important for floral scent production. Unlike EC 2.3.1.84, alcohol *O*-acetyltransferase, this enzyme is active with alcohols that contain a benzyl ring.
References: [784]

[EC 2.3.1.224 created 2013]

EC 2.3.1.225

Accepted name: protein *S*-acyltransferase
Reaction: palmitoyl-CoA + [protein]-L-cysteine = [protein]-*S*-palmitoyl-L-cysteine + CoA
Other name(s): DHHC palmitoyl transferase; *S*-protein acyltransferase; G-protein palmitoyltransferase
Systematic name: palmitoyl-CoA:[protein]-L-cysteine *S*-palmitoyltransferase
Comments: The enzyme catalyses the posttranslational protein palmitoylation that plays a role in protein-membrane interactions, protein trafficking, and enzyme activity. Palmitoylation increases the hydrophobicity of proteins or protein domains and contributes to their membrane association.
References: [794, 3656, 230, 1507, 4077]

[EC 2.3.1.225 created 2013]

EC 2.3.1.226

Accepted name: carboxymethylproline synthase
Reaction: malonyl-CoA + (*S*)-1-pyrroline-5-carboxylate + H_2O = CoA + (2*S*,5*S*)-5-carboxymethylproline + CO_2
Other name(s): CarB (ambiguous)
Systematic name: malonyl-CoA:(*S*)-1-pyrroline-5-carboxylate malonyltransferase (cyclizing)
Comments: The enzyme is involved in the biosynthesis of the carbapenem β-lactam antibiotic (5*R*)-carbapen-2-em-3-carboxylate in the bacterium *Pectobacterium carotovorum*.
References: [3252, 1037, 3292, 3253, 228, 1203]

[EC 2.3.1.226 created 2013]

EC 2.3.1.227

Accepted name: GDP-perosamine *N*-acetyltransferase
Reaction: acetyl-CoA + GDP-4-amino-4,6-dideoxy-α-D-mannose = CoA + GDP-4-acetamido-4,6-dideoxy-α-D-mannose
Other name(s): *perB* (gene name); GDP-α-D-perosamine *N*-acetyltransferase
Systematic name: acetyl-CoA:GDP-4-amino-4,6-dideoxy-α-D-mannose *N*-acetyltransferase
Comments: D-Perosamine is one of several dideoxy sugars found in the O-antigen component of the outer membrane lipopolysaccharides of Gram-negative bacteria.
References: [43]

[EC 2.3.1.227 created 2013]

EC 2.3.1.228

Accepted name: isovaleryl-homoserine lactone synthase
Reaction: isovaleryl-CoA + *S*-adenosyl-L-methionine = CoA + *S*-methyl-5′-thioadenosine + *N*-isovaleryl-L-homoserine lactone
Other name(s): IV-HSL synthase; BjaI
Systematic name: isovaleryl-CoA:*S*-adenosyl-L-methionine isovaleryltranserase (lactone-forming, methylthioadenosine-releasing)
Comments: The enzyme, found in the bacterium *Bradyrhizobium japonicum*, does not accept isovaleryl-[acyl-carrier protein] as acyl donor (*cf.* EC 2.3.1.184, acyl-homoserine-lactone synthase).

References: [1977]

[EC 2.3.1.228 created 2013]

EC 2.3.1.229

Accepted name: 4-coumaroyl-homoserine lactone synthase

Reaction: 4-coumaroyl-CoA + *S*-adenosyl-L-methionine = CoA + *S*-methyl-$5'$-thioadenosine + *N*-(4-coumaroyl)-L-homoserine lactone

Other name(s): *p*-coumaryl-homoserine lactone synthase; RpaI

Systematic name: 4-coumaroyl-CoA:*S*-adenosyl-L-methionine *trans*-4-coumaroyltranserase (lactone-forming, methylthioadenosine-releasing)

Comments: The enzyme is found in the bacterium *Rhodopseudomonas palustris*, which produces *N*-(4-coumaroyl)-L-homoserine lactone as a quorum-sensing signal.

References: [3059]

[EC 2.3.1.229 created 2013]

EC 2.3.1.230

Accepted name: 2-heptyl-4(1*H*)-quinolone synthase

Reaction: octanoyl-CoA + (2-aminobenzoyl)acetate = 2-heptyl-4-quinolone + CoA + CO_2 + H_2O (overall reaction)
(1a) octanoyl-CoA + L-cysteinyl-[PqsC protein] = *S*-octanoyl-L-cysteinyl-[PqsC protein] + CoA
(1b) *S*-octanoyl-L-cysteinyl-[PqsC protein] + (2-aminobenzoyl)acetate = 1-(2-aminophenyl)decane-1,3-dione + CO_2 + L-cysteinyl-[PqsC protein]
(1c) 1-(2-aminophenyl)decane-1,3-dione = 2-heptyl-4-quinolone + H_2O

Other name(s): *pqsBC* (gene names); malonyl-CoA:anthraniloyl-CoA *C*-acetyltransferase (decarboxylating)

Systematic name: octanoyl-CoA:(2-aminobenzoyl)acetate octanoyltransferase

Comments: The enzyme, characterized from the bacterium *Pseudomonas aeruginosa*, is a heterodimeric complex. The PqsC subunit acquires an octanoyl group from octanoyl-CoA and attaches it to an internal cysteine residue. Together with the PqsB subunit, the proteins catalyse the coupling of the octanoyl group with (2-aminobenzoyl)acetate, leading to decarboxylation and dehydration events that result in closure of the quinoline ring.

References: [788, 773]

[EC 2.3.1.230 created 2013, modified 2017]

EC 2.3.1.231

Accepted name: tRNA^{Phe} 7-[3-amino-3-(methoxycarbonyl)propyl]wyosine^{37}-*N*-methoxycarbonyltransferase

Reaction: *S*-adenosyl-L-methionine + 7-[(3*S*)-3-amino-3-(methoxycarbonyl)propyl]wyosine^{37} in tRNA^{Phe} + CO_2 = *S*-adenosyl-L-homocysteine + wybutosine^{37} in tRNA^{Phe}

Other name(s): TYW4 (ambiguous); tRNA-yW synthesizing enzyme-4 (ambiguous)

Systematic name: *S*-adenosyl-L-methionine:tRNA^{Phe} 7-[(3*S*)-3-amino-3-(methoxycarbonyl)propyl]wyosine^{37}-*N*-methyltransferase (carbon dioxide-adding)

Comments: The enzyme is found only in eukaryotes, where it is involved in the biosynthesis of wybutosine, a hypermodified tricyclic base found at position 37 of certain tRNAs. The modification is important for translational reading-frame maintenance. In some species that produce hydroxywybutosine the enzyme uses 7-[2-hydroxy-3-amino-3-(methoxycarbonyl)propyl]wyosine^{37} in tRNA^{Phe} as substrate. The enzyme also has the activity of EC 2.1.1.290, tRNA^{Phe} [7-(3-amino-3-carboxypropyl)wyosine^{37}-*O*]-methyltransferase [3406].

References: [2488, 3406, 1597]

[EC 2.3.1.231 created 2013]

EC 2.3.1.232

Accepted name: methanol *O*-anthraniloyltransferase

Reaction: anthraniloyl-CoA + methanol = CoA + *O*-methyl anthranilate

Other name(s): AMAT; anthraniloyl-coenzyme A (CoA):methanol acyltransferase

Systematic name: anthraniloyl-CoA:methanol *O*-anthraniloyltransferase

Comments: The enzyme from Concord grape (*Vitis labrusca*) is solely responsible for the production of *O*-methyl anthranilate, an important aroma and flavor compound in the grape. The enzyme has a broad substrate specificity, and can use a range of alcohols with substantial activity, the best being butanol, benzyl alcohol, iso-pentanol, octanol and 2-propanol. It can use benzoyl-CoA and acetyl-CoA as acyl donors with lower efficiency. In addition to *O*-methyl anthranilate, the enzyme might be responsible for the production of ethyl butanoate, methyl-3-hydroxy butanoate and ethyl-3-hydroxy butanoate, which are present in large quantities in the grapes. Also catalyses EC 2.3.1.196, benzyl alcohol *O*-benzoyltransferase.

References: [3751]

[EC 2.3.1.232 created 2014]

EC 2.3.1.233

Accepted name: 1,3,6,8-tetrahydroxynaphthalene synthase

Reaction: **5** malonyl-CoA = 1,3,6,8-tetrahydroxynaphthalene + **5** CoA + **5** CO_2 + H_2O

Other name(s): PKS1; THNS; SCO1206; RppA

Systematic name: malonyl-CoA C-acyl transferase (1,3,6,8-tetrahydroxynaphthalene forming)

Comments: Isolated from the fungus *Colletotrichum lagenarium* [981], and the bacteria *Streptomyces coelicolor* [1479, 131] and *Streptomyces peucetius* [1041]. It only uses malonyl-CoA, without invovement of acetyl-CoA.

References: [981, 1479, 131, 1041]

[EC 2.3.1.233 created 2014]

EC 2.3.1.234

Accepted name: N^6-L-threonylcarbamoyladenine synthase

Reaction: L-threonylcarbamoyladenylate + adenine^{37} in tRNA = AMP + N^6-L-threonylcarbamoyladenine^{37} in tRNA

Other name(s): t6A synthase; Kae1; *ygjD* (gene name); Qri7

Systematic name: L-threonylcarbamoyladenylate:adenine^{37} in tRNA N^6-L-threonylcarbamoyltransferase

Comments: The enzyme is involved in the synthesis of N^6-threonylcarbamoyladenosine^{37} in tRNAs, which is found in tRNAs with the anticodon NNU, i.e. tRNA^{Ile}, tRNA^{Thr}, tRNA^{Asn}, tRNA^{Lys}, tRNA^{Ser} and tRNA^{Arg} [2668].

References: [1875, 723, 2668, 3744]

[EC 2.3.1.234 created 2014 as EC 2.6.99.4, transferred 2014 to EC 2.3.1.234]

EC 2.3.1.235

Accepted name: tetracenomycin F2 synthase

Reaction: **10** malonyl-CoA = tetracenomycin F2 + **10** CoA + **10** CO_2 + **2** H_2O

Other name(s): TCM PKS

Systematic name: malonyl-CoA:acetate malonyltransferase (tetracenomycin F2 forming)

Comments: A multi-domain polyketide synthase involved in the synthesis of tetracenomycin in the bacterium *Streptomyces glaucescens*. It involves a ketosynthase complex (TcmKL), an acyl carrier protein (TcmM), a malonyl CoA:ACP acyltransferase (MAT), and a cyclase (TcmN). A malonyl-CoA molecule is initially bound to the acyl carrier protein and decarboxylated to form an acetyl starter unit. Additional two-carbon units are added from nine more malonyl-CoA molecules.

References: [184]

[EC 2.3.1.235 created 2014]

EC 2.3.1.236

Accepted name: 5-methylnaphthoic acid synthase

Reaction: acetyl-CoA + **5** malonyl-CoA + **3** NADPH + **3** H^+ = 5-methyl-1-naphthoate + **6** CoA + **5** CO_2 + **4** H_2O + **3** $NADP^+$

Other name(s): AziB

Systematic name: malonyl-CoA:acetyl-CoA malonyltransferase (5-methyl-1-naphthoic acid forming)

Comments: A multi-domain polyketide synthase involved in the synthesis of azinomycin B in the bacterium *Streptomyces griseofuscus*.

References: [4066]

[EC 2.3.1.236 created 2014]

EC 2.3.1.237

Accepted name: neocarzinostatin naphthoate synthase

Reaction: acetyl-CoA + **5** malonyl-CoA + **2** NADPH + **2** H^+ = 2-hydroxy-5-methyl-1-naphthoate + **6** CoA + **5** CO_2 + **3** H_2O + **2** $NADP^+$

Other name(s): naphthoic acid synthase; NNS; *ncsB* (gene name)

Systematic name: malonyl-CoA:acetyl-CoA malonyltransferase (2-hydroxy-5-methyl-1-naphthoic acid forming)

Comments: A multi-domain polyketide synthase involved in the synthesis of neocarzinostatin in the bacterium *Streptomyces carzinostaticus*.

References: [3343]

[EC 2.3.1.237 created 2014]

EC 2.3.1.238

Accepted name: monacolin J acid methylbutanoate transferase

Reaction: monacolin J acid + (*S*)-2-methylbutanoyl-[2-methylbutanoate polyketide synthase] = lovastatin acid + [2-methylbutanoate polyketide synthase]

Other name(s): LovD

Systematic name: monacolin J acid:(*S*)-2-methylbutanoyl-[2-methylbutanoate polyketide synthase] (*S*)-2-methylbutanoate transferase

Comments: The enzyme catalyses the ultimate reaction in the lovastatin biosynthesis pathway of the filamentous fungus *Aspergillus terreus*.

References: [1641, 3921, 3920]

[EC 2.3.1.238 created 2014]

EC 2.3.1.239

Accepted name: 10-deoxymethynolide synthase

Reaction: malonyl-CoA + **5** (2*S*)-methylmalonyl-CoA + **5** NADPH + **5** H^+ = 10-deoxymethynolide + **6** CoA + **6** CO_2 + **5** $NADP^+$ + **2** H_2O

Other name(s): pikromycin PKS

Systematic name: (2*S*)-methylmalonyl-CoA:malonyl-CoA malonyltransferase (10-deoxymethynolide forming)

Comments: The product, 10-deoxymethynolide, contains a 12-membered ring and is an intermediate in the biosynthesis of methymycin in the bacterium *Streptomyces venezuelae*. The enzyme also produces narbonolide (see EC 2.3.1.240, narbonolide synthase). The enzyme has 29 active sites arranged in four polypeptides (pikAI - pikAIV) with a loading domain, six extension modules and a terminal thioesterase domain. Each extension module contains a ketosynthase (KS), keto reductase (KR), an acyltransferase (AT) and an acyl-carrier protein (ACP). Not all active sites are used in the biosynthesis.

References: [2053, 1700, 3959, 3831]

[EC 2.3.1.239 created 2014]

EC 2.3.1.240

Accepted name: narbonolide synthase

Reaction: malonyl-CoA + **6** (2*S*)-methylmalonyl-CoA + **5** NADPH + **5** H^+ = narbonolide + **7** CoA + **7** CO_2 + **5** $NADP^+$ + **2** H_2O

Other name(s): pikromycin PKS

Systematic name: (2*S*)-methylmalonyl-CoA:malonyl-CoA malonyltransferase (narbonolide forming)

Comments: The product, narbonolide, contains a 14-membered ring and is an intermediate in the biosynthesis of narbonomycin and pikromycin in the bacterium *Streptomyces venezuelae*. The enzyme also produces 10-deoxymethynolide (see EC 2.3.1.239, 10-deoxymethynolide synthase). The enzyme has 29 active sites arranged in four polypeptides (pikAI - pikAIV) with a loading domain, six extension modules and a terminal thioesterase domain. Each extension module contains a ketosynthase (KS), keto reductase (KR), an acyltransferase (AT) and an acyl-carrier protein (ACP). Not all active sites are used in the biosynthesis.

References: [2053, 1700, 3959, 3831]

[EC 2.3.1.240 created 2014]

EC 2.3.1.241

Accepted name: Kdo$_2$-lipid IV$_A$ lauroyltransferase

Reaction: a dodecanoyl-[acyl-carrier protein] + Kdo$_2$-lipid IV$_A$ = dodecanoyl-Kdo$_2$-lipid IV$_A$ + an [acyl-carrier protein]

Other name(s): LpxL; *htrB* (gene name); dodecanoyl-[acyl-carrier protein]:α-Kdo-(2→4)-α-Kdo-(2→6)-lipid IV$_A$ *O*-dodecanoyltransferase; lauroyl-[acyl-carrier protein]:Kdo$_2$-lipid IV$_A$ *O*-lauroyltransferase; (Kdo)$_2$-lipid IV$_A$ lauroyltransferase; α-Kdo-(2→4)-α-(2→6)-lipid IV$_A$ lauroyltransferase

Systematic name: dodecanoyl-[acyl-carrier protein]:Kdo$_2$-lipid IV$_A$ *O*-dodecanoyltransferase

Comments: The enzyme, characterized from the bacterium *Escherichia coli*, is involved in the biosynthesis of the phosphorylated outer membrane glycolipid lipid A.

References: [585, 3246]

[EC 2.3.1.241 created 2014]

EC 2.3.1.242

Accepted name: Kdo$_2$-lipid IV$_A$ palmitoleoyltransferase

Reaction: a (9*Z*)-hexadec-9-enoyl-[acyl-carrier protein] + Kdo$_2$-lipid IV$_A$ = (9*Z*)-hexadec-9-enoyl-Kdo$_2$-lipid IV$_A$ + an [acyl-carrier protein]

Other name(s): LpxP; palmitoleoyl-acyl carrier protein-dependent acyltransferase; cold-induced palmitoleoyl transferase; palmitoleoyl-[acyl-carrier protein]:Kdo$_2$-lipid IV$_A$ *O*-palmitoleoyltransferase; (Kdo)$_2$-lipid IV$_A$ palmitoleoyltransferase; α-Kdo-(2→4)-α-(2→6)-lipid IV$_A$ palmitoleoyltransferase

Systematic name: (9*Z*)-hexadec-9-enoyl-[acyl-carrier protein]:Kdo$_2$-lipid IV$_A$ *O*-palmitoleoyltransferase

Comments: The enzyme, characterized from the bacterium *Escherichia coli*, is induced upon cold shock and is involved in the formation of a cold-adapted variant of the outer membrane glycolipid lipid A.

References: [485, 3703]

[EC 2.3.1.242 created 2014]

EC 2.3.1.243

Accepted name: lauroyl-Kdo$_2$-lipid IV$_A$ myristoyltransferase

Reaction: a tetradecanoyl-[acyl-carrier protein] + dodecanoyl-Kdo$_2$-lipid IV$_A$ = dodecanoyl-(tetradecanoyl)-Kdo$_2$-lipid IV$_A$ + an [acyl-carrier protein]

Other name(s): MsbB acyltransferase; *lpxM* (gene name); myristoyl-[acyl-carrier protein]:α-Kdo-(2→4)-α-Kdo-(2→6)-(dodecanoyl)-lipid IV$_A$ *O*-myristoyltransferase

Systematic name: tetradecanoyl-[acyl-carrier protein]:dodecanoyl-Kdo$_2$-lipid IV$_A$ *O*-tetradecanoyltransferase
Comments: The enzyme, characterized from the bacterium *Escherichia coli*, is involved in the biosynthesis of the phosphorylated outer membrane glycolipid lipid A.
References: [586]

[EC 2.3.1.243 created 2014]

EC 2.3.1.244

Accepted name: 2-methylbutanoate polyketide synthase
Reaction: **2** malonyl-CoA + [2-methylbutanoate polyketide synthase] + **2** NADPH + **3** H$^+$ + *S*-adenosyl-L-methionine = (*S*)-2-methylbutanoyl-[2-methylbutanoate polyketide synthase] + **2** CoA + **2** CO$_2$ + **2** NADP$^+$ + *S*-adenosyl-L-homocysteine + H$_2$O
Other name(s): LovF
Systematic name: acyl-CoA:malonyl-CoA *C*-acyltransferase (2-methylbutanoate-forming)
Comments: This polyketide synthase enzyme forms the (*S*)-2-methylbutanoate side chain during lovastatin biosynthesis by the filamentous fungus *Aspergillus terreus*. The overall reaction comprises a single condensation reaction followed by α-methylation, β-ketoreduction, dehydration, and α,β-enoyl reduction.
References: [1641, 2205]

[EC 2.3.1.244 created 2015, modified 2016]

EC 2.3.1.245

Accepted name: 3-hydroxy-5-phosphonooxypentane-2,4-dione thiolase
Reaction: glycerone phosphate + acetyl-CoA = 3-hydroxy-5-phosphooxypentane-2,4-dione + CoA
Other name(s): *lsrF* (gene name)
Systematic name: acetyl-CoA:glycerone phosphate *C*-acetyltransferase
Comments: The enzyme participates in a degradation pathway of the bacterial quorum-sensing autoinducer molecule AI-2.
References: [727, 2129]

[EC 2.3.1.245 created 2015]

EC 2.3.1.246

Accepted name: 3,5-dihydroxyphenylacetyl-CoA synthase
Reaction: **4** malonyl-CoA = (3,5-dihydroxyphenylacetyl)-CoA + **3** CoA + **4** CO$_2$ + H$_2$O
Other name(s): DpgA
Systematic name: malonyl-CoA:malonyl-CoA malonyltransferase (3,5-dihydroxyphenylacetyl-CoA-forming)
Comments: The enzyme, characterized from the bacterium *Amycolatopsis mediterranei*, is involved in biosynthesis of the nonproteinogenic amino acid (*S*)-3,5-dihydroxyphenylglycine, a component of the vancomycin-type antibiotic balhimycin.
References: [2683, 524, 3581, 3901]

[EC 2.3.1.246 created 2015]

EC 2.3.1.247

Accepted name: 3-keto-5-aminohexanoate cleavage enzyme
Reaction: (5*S*)-5-amino-3-oxohexanoate + acetyl-CoA = L-3-aminobutanoyl-CoA + acetoacetate
Other name(s): *kce* (gene name)
Systematic name: (5*S*)-5-amino-3-oxohexanoate:acetyl-CoA ethylamine transferase
Comments: Requires Zn^{2+}. The enzyme, isolated from the bacteria *Fusobacterium nucleatum* and *Cloacimonas acidaminovorans*, is involved in the anaerobic fermentation of lysine.
References: [193, 1783, 259]

[EC 2.3.1.247 created 2015]

EC 2.3.1.248

Accepted name: spermidine disinapoyl transferase

Reaction: **2** sinapoyl-CoA + spermidine = **2** CoA + N^1,N^8-bis(sinapoyl)-spermidine

Other name(s): SDT

Systematic name: sinapoyl-CoA:spermidine *N*-(hydroxycinnamoyl)transferase

Comments: The enzyme from the plant *Arabidopsis thaliana* has no activity with 4-coumaroyl-CoA (*cf.* EC 2.3.1.249, spermidine dicoumaroyl transferase).

References: [2071]

[EC 2.3.1.248 created 2015]

EC 2.3.1.249

Accepted name: spermidine dicoumaroyl transferase

Reaction: **2** 4-coumaroyl-CoA + spermidine = **2** CoA + N^1,N^8-bis(4-coumaroyl)-spermidine

Other name(s): SCT

Systematic name: 4-coumaroyl-CoA:spermidine *N*-(hydroxycinnamoyl)transferase

Comments: The enzyme from the plant *Arabidopsis thaliana* has no activity with sinapoyl-CoA (*cf.* EC 2.3.1.248, spermidine disinapoyl transferase).

References: [2071]

[EC 2.3.1.249 created 2015]

EC 2.3.1.250

Accepted name: [Wnt protein] *O*-palmitoleoyl transferase

Reaction: (9*Z*)-hexadec-9-enoyl-CoA + [Wnt]-L-serine = CoA + [Wnt]-*O*-(9*Z*)-hexadec-9-enoyl-L-serine

Other name(s): porcupine; PORCN (gene name)

Systematic name: (9*Z*)-hexadec-9-enoyl-CoA:[Wnt]-L-serine *O*-hexadecenoyltransferase

Comments: The enzyme, found in animals, modifies a specific serine residue in Wnt proteins, e.g. Ser^{209} in human Wnt3a and Ser^{224} in chicken WNT1 [1009, 2267]. The enzyme can accept C_{13} to C_{16} fatty acids *in vitro*, but only (9*Z*)-hexadecenoate modification is observed *in vivo* [3436]. *cf.* EC 3.1.1.98, [Wnt protein]-*O*-palmitoleoyl-L-serine hydrolase.

References: [3436, 1009, 2267]

[EC 2.3.1.250 created 2015]

EC 2.3.1.251

Accepted name: lipid IV_A palmitoyltransferase

Reaction: (1) 1-palmitoyl-2-acyl-*sn*-glycero-3-phosphocholine + hexa-acyl lipid A = 2-acyl-*sn*-glycero-3-phosphocholine + hepta-acyl lipid A
(2) 1-palmitoyl-2-acyl-*sn*-glycero-3-phosphocholine + lipid II_A = 2-acyl-*sn*-glycero-3-phosphocholine + lipid II_B
(3) 1-palmitoyl-2-acyl-*sn*-glycero-3-phosphocholine + lipid IV_A = 2-acyl-*sn*-glycero-3-phosphocholine + lipid IV_B

Other name(s): PagP; *crcA* (gene name)

Systematic name: 1-palmitoyl-2-acyl-*sn*-glycero-3-phosphocholine:lipid-IV_A palmitoyltransferase

Comments: Isolated from the bacteria *Escherichia coli* and *Salmonella typhimurium*. The enzyme prefers phosphatidylcholine with a palmitoyl group at the *sn*-1 position and palmitoyl or stearoyl groups at the *sn*-2 position. There is some activity with corresponding phosphatidylserines but only weak activity with other diacylphosphatidyl compounds. The enzyme also acts on Kdo-(2→4)-Kdo-(2→6)-lipid IV_A.

References: [311, 637]

[EC 2.3.1.251 created 2015]

EC 2.3.1.252

Accepted name: mycolipanoate synthase

Reaction: a long-chain acyl-CoA + **3** (*R*)-methylmalonyl-CoA + **6** NADPH + **6** H^+ + holo-[mycolipanoate synthase] = mycolipanoyl-[mycolipanoate synthase] + **4** CoA + **3** CO_2 + **6** $NADP^+$ + **3** H_2O

Other name(s): msl3 (gene name); Pks3/4; mycolipanoic acid synthase

Systematic name: long-chain acyl-CoA:methylmalonyl-CoA *C*-acyltransferase (mycolipanoate-forming)

Comments: This mycobacterial enzyme accepts long-chain fatty acyl groups from their CoA esters and extends them by incorporation of three methylmalonyl (but not malonyl) residues, forming trimethyl-branched fatty-acids such as (2*S*,4*S*,6*S*)-2,4,6-trimethyltetracosanoate (C_{27}-mycolipanoate). Since the enzyme lacks a thioesterase domain, the product remains bound to the enzyme and requires additional enzyme(s) for removal.

References: [3244, 781]

[EC 2.3.1.252 created 2016]

EC 2.3.1.253

Accepted name: phloroglucinol synthase

Reaction: **3** malonyl-CoA = phloroglucinol + **3** CO_2 + **3** CoA

Other name(s): *phlD* (gene name)

Systematic name: malonyl-CoA:malonyl-CoA malonyltransferase (decarboxylating, phloroglucinol-forming)

Comments: The enzyme, characterized from the bacterium *Pseudomonas protegens* Pf-5, is a type III polyketide synthase. The mechanism involves the cyclization of an activated 3,5-dioxoheptanedioate intermediate. The enzyme exhibits broad substrate specificity, and can accept C_4-C_{12} aliphatic acyl-CoAs and phenylacetyl-CoA as the starter molecules, forming 6-(polyoxoalkyl)-α-pyrones by sequential condensation with malonyl-CoA.

References: [12, 4034]

[EC 2.3.1.253 created 2016]

EC 2.3.1.254

Accepted name: N-terminal methionine N^{α}-acetyltransferase NatB

Reaction: (1) acetyl-CoA + an N-terminal L-methionyl-L-asparaginyl-[protein] = an N-terminal N^{α}-acetyl-L-methionyl-L-asparaginyl-[protein] + CoA

(2) acetyl-CoA + an N-terminal L-methionyl-L-glutaminyl-[protein] = an N-terminal N^{α}-acetyl-L-methionyl-L-glutaminyl-[protein] + CoA

(3) acetyl-CoA + an N-terminal L-methionyl-L-aspartyl-[protein] = an N-terminal N^{α}-acetyl-L-methionyl-L-aspartyl-[protein] + CoA

(4) acetyl-CoA + an N-terminal L-methionyl-L-glutamyl-[protein] = an N-terminal N^{α}-acetyl-L-methionyl-L-glutamyl-[protein] + CoA

Other name(s): NAA20 (gene name); NAA25 (gene name)

Systematic name: acetyl-CoA:N-terminal Met-Asn/Gln/Asp/Glu-[protein] Met-N^{α}-acetyltransferase

Comments: N-terminal acetylases (NATs) catalyse the covalent attachment of an acetyl moiety from acetyl-CoA to the free α-amino group at the N-terminus of a protein. This irreversible modification neutralizes the positive charge at the N-terminus and makes the N-terminal residue larger and more hydrophobic, and may also play a role in membrane targeting and gene silencing. The NatB complex is found in all eukaryotic organisms, and specifically targets N-terminal L-methionine residues attached to Asn, Asp, Gln, or Glu residues at the second position.

References: [3318, 896, 1891]

[EC 2.3.1.254 created 1989 as EC 2.3.1.88, part transferred 2016 to EC 2.3.1.254]

EC 2.3.1.255

Accepted name: N-terminal amino-acid N^{α}-acetyltransferase NatA

Reaction: (1) acetyl-CoA + an N-terminal-glycyl-[protein] = an N-terminal-N^{α}-acetyl-glycyl-[protein] + CoA
(2) acetyl-CoA + an N-terminal-L-alanyl-[protein] = an N-terminal-N^{α}-acetyl-L-alanyl-[protein] + CoA
(3) acetyl-CoA + an N-terminal-L-seryl-[protein] = an N-terminal-N^{α}-acetyl-L-seryl-[protein] + CoA
(4) acetyl-CoA + an N-terminal-L-valyl-[protein] = an N-terminal-N^{α}-acetyl-L-valyl-[protein] + CoA
(5) acetyl-CoA + an N-terminal-L-cysteinyl-[protein] = an N-terminal-N^{α}-acetyl-L-cysteinyl-[protein] + CoA
(6) acetyl-CoA + an N-terminal-L-threonyl-[protein] = an N-terminal-N^{α}-acetyl-L-threonyl-[protein] + CoA

Other name(s): NAA10 (gene name); NAA15 (gene name); ARD1 (gene name)

Systematic name: acetyl-CoA:N-terminal-Gly/Ala/Ser/Val/Cys/Thr-[protein] N^{α}-acetyltransferase

Comments: N-terminal-acetylases (NATs) catalyse the covalent attachment of an acetyl moiety from acetyl-CoA to the free α-amino group at the N-terminus of a protein. This irreversible modification neutralizes the positive charge at the N-terminus and makes the N-terminal residue larger and more hydrophobic. The NatA complex is found in all eukaryotic organisms, and specifically targets N-terminal Ala, Gly, Cys, Ser, Thr, and Val residues, that became available after removal of the initiator methionine.

References: [2349, 2619, 3380, 1028, 3924, 755]

[EC 2.3.1.255 created 1989 as EC 2.3.1.88, part transferred 2016 to EC 2.3.1.255]

EC 2.3.1.256

Accepted name: N-terminal methionine N^{α}-acetyltransferase NatC

Reaction: (1) acetyl-CoA + an N-terminal-L-methionyl-L-leucyl-[protein] = an N-terminal-N^{α}-acetyl-L-methionyl-L-leucyl-[protein] + CoA
(2) acetyl-CoA + an N-terminal-L-methionyl-L-isoleucyl-[protein] = an N-terminal-N^{α}-acetyl-L-methionyl-L-isoleucyl-[protein] + CoA
(3) acetyl-CoA + an N-terminal-L-methionyl-L-phenylalanyl-[protein] = an N-terminal-N^{α}-acetyl-L-methionyl-L-phenylalanyl-[protein] + CoA
(4) acetyl-CoA + an N-terminal-L-methionyl-L-tryptophyl-[protein] = an N-terminal-N^{α}-acetyl-L-methionyl-L-tryptophyl-[protein] + CoA
(5) acetyl-CoA + an N-terminal-L-methionyl-L-tyrosyl-[protein] = an N-terminal-N^{α}-acetyl-L-methionyl-L-tyrosyl-[protein] + CoA

Other name(s): NAA30 (gene name); NAA35 (gene name); NAA38 (gene name); MAK3 (gene name); MAK10 (gene name); MAK31 (gene name)

Systematic name: acetyl-CoA:N-terminal-Met-Leu/Ile/Phe/Trp/Tyr-[protein] Met N^{α}-acetyltransferase

Comments: N-terminal-acetylases (NATs) catalyse the covalent attachment of an acetyl moiety from acetyl-CoA to the free α-amino group at the N-terminus of a protein. This irreversible modification neutralizes the positive charge at the N-terminus and makes the N-terminal residue larger and more hydrophobic, and may also play a role in membrane targeting and gene silencing. The NatC complex is found in all eukaryotic organisms, and specifically targets N-terminal L-methionine residues attached to bulky hydrophobic residues at the second position, including Leu, Ile, Phe, Trp, and Tyr residues.

References: [2735, 2736, 2670, 3822, 3319]

[EC 2.3.1.256 created 1989 as EC 2.3.1.88, part transferred 2016 to EC 2.3.1.256]

EC 2.3.1.257

Accepted name: N-terminal L-serine N^{α}-acetyltransferase NatD

Reaction: (1) acetyl-CoA + an N-terminal-L-seryl-[histone H4] = an N-terminal-N^{α}-acetyl-L-seryl-[histone H4] + CoA
(2) acetyl-CoA + an N-terminal-L-seryl-[histone H2A] = an N-terminal-N^{α}-acetyl-L-seryl-[histone H2A] + CoA

Other name(s): NAA40 (gene name)

Systematic name: acetyl-CoA:N-terminal-L-seryl-[histone 4/2A] L-serine N^{α}-acetyltransferase

Comments: N-terminal-acetylases (NATs) catalyse the covalent attachment of an acetyl moiety from acetyl-CoA to the free α-amino group at the N-terminus of a protein. This irreversible modification neutralizes the positive charge at the N-terminus and makes the N-terminal residue larger and more hydrophobic. NatD is found in all eukaryotic organisms, and acetylates solely the serine residue at the N-terminus of histones H2A or H4. Efficient recognition and acetylation by NatD requires at least the first 30 to 50 highly conserved amino acid residues of the histone N terminus.

References: [3286, 2734, 2097]

[EC 2.3.1.257 created 1989 as EC 2.3.1.88, part transferred 2016 to EC 2.3.1.257]

EC 2.3.1.258

Accepted name: N-terminal methionine N^{α}-acetyltransferase NatE

Reaction: (1) acetyl-CoA + an N-terminal-L-methionyl-L-alanyl-[protein] = an N-terminal-N^{α}-acetyl-L-methionyl-L-alanyl-[protein] + CoA
(2) acetyl-CoA + an N-terminal-L-methionyl-L-seryl-[protein] = an N-terminal-N^{α}-acetyl-L-methionyl-L-seryl-[protein] + CoA
(3) acetyl-CoA + an N-terminal-L-methionyl-L-valyl-[protein] = an N-terminal-N^{α}-acetyl-L-methionyl-L-valyl-[protein] + CoA
(4) acetyl-CoA + an N-terminal-L-methionyl-L-threonyl-[protein] = an N-terminal-N^{α}-acetyl-L-methionyl-L-threonyl-[protein] + CoA
(5) acetyl-CoA + an N-terminal-L-methionyl-L-lysyl-[protein] = an N-terminal-N^{α}-acetyl-L-methionyl-L-lysyl-[protein] + CoA
(6) acetyl-CoA + an N-terminal-L-methionyl-L-leucyl-[protein] = an N-terminal-N^{α}-acetyl-L-methionyl-L-leucyl-[protein] + CoA
(7) acetyl-CoA + an N-terminal-L-methionyl-L-phenylalanyl-[protein] = an N-terminal-N^{α}-acetyl-L-methionyl-L-phenylalanyl-[protein] + CoA
(8) acetyl-CoA + an N-terminal-L-methionyl-L-tyrosyl-[protein] = an N-terminal-N^{α}-acetyl-L-methionyl-L-tyrosyl-[protein] + CoA

Other name(s): NAA50 (gene name); NAT5; SAN

Systematic name: acetyl-CoA:N-terminal-Met-Ala/Ser/Val/Thr/Lys/Leu/Phe/Tyr-[protein] Met-N^{α}-acetyltransferase

Comments: N-terminal-acetylases (NATs) catalyse the covalent attachment of an acetyl moiety from acetyl-CoA to the free α-amino group at the N-terminus of a protein. This irreversible modification neutralizes the positive charge at the N-terminus, makes the N-terminal residue larger and more hydrophobic, and prevents its removal by hydrolysis. It may also play a role in membrane targeting and gene silencing. NatE is found in all eukaryotic organisms and plays an important role in chromosome resolution and segregation. It specifically targets N-terminal L-methionine residues attached to Lys, Val, Ala, Tyr, Phe, Leu, Ser, and Thr. There is some substrate overlap with EC 2.3.1.256, N-terminal methionine N^{α}-acetyltransferase NatC. In addition, the acetylation of Met followed by small residues such as Ser, Thr, Ala, or Val suggests a kinetic competition between NatE and EC 3.4.11.18, methionyl aminopeptidase. The enzyme also has the activity of EC 2.3.1.48, histone acetyltransferase, and autoacetylates several of its own lysine residues.

References: [1377, 2713, 861, 664]

[EC 2.3.1.258 created 1989 as EC 2.3.1.88, part transferred 2016 to EC 2.3.1.258]

EC 2.3.1.259

Accepted name: N-terminal methionine N^{α}-acetyltransferase NatF

Reaction: acetyl-CoA + an N-terminal-L-methionyl-[transmembrane protein] = an N-terminal-N^{α}-acetyl-L-methionyl-[transmembrane protein] + CoA

Other name(s): NAA60 (gene name)

Systematic name: acetyl-CoA:N-terminal-Met-Lys/Ser/Val/Leu/Gln/Ile/Tyr/Thr-[transmembrane protein] Met-N^{α}-acetyltransferase

Comments: N-terminal-acetylases (NATs) catalyse the covalent attachment of an acetyl moiety from acetyl-CoA to the free α-amino group at the N-terminus of a protein. This irreversible modification neutralizes the positive charge at the N-terminus, makes the N-terminal residue larger and more hydrophobic, and prevents its removal by hydrolysis. NatF is found only in higher eukaryotes, and is absent from yeast. Unlike other Nat systems the enzyme is located in the Golgi apparatus. It faces the cytosolic side of intracellular membranes, and specifically acetylates transmembrane proteins whose N termini face the cytosol. NatF targets N-terminal L-methionine residues attached to Lys, Ser, Val, Leu, Gln, Ile, Tyr and Thr residues.

References: [665, 40]

[EC 2.3.1.259 created 1989 as EC 2.3.1.88, part transferred 2016 to EC 2.3.1.259]

EC 2.3.1.260

Accepted name: tetracycline polyketide synthase

Reaction: malonamoyl-[OxyC acyl-carrier protein] + **8** malonyl-CoA = 18-carbamoyl-3,5,7,9,11,13,15,17-octaoxooctadecanoyl-[OxyC acyl-carrier protein] + **8** CO_2 + **8** CoA

Systematic name: malonyl-CoA:malonamoyl-[OxyC acyl-carrier protein] malonyltransferase

Comments: The synthesis, in the bacterium *Streptomyces rimosus*, of the tetracycline antibiotics core skeleton requires a minimal polyketide synthase (PKS) consisting of a ketosynthase (KS), a chain length factor (CLF), and an acyl-carrier protein (ACP). Initiation involves an amide-containing starter unit that becomes the C-2 amide that is present in the tetracycline compounds. Following the initiation, the PKS catalyses the iterative condensation of 8 malonyl-CoA molecules to yield the polyketide backbone of tetracycline. Throughout the proccess, the nascent chain is attached to the OxyC acyl-carrier protein.

References: [3522, 4047, 4008]

[EC 2.3.1.260 created 2016]

EC 2.3.1.261

Accepted name: (4-hydroxyphenyl)alkanoate synthase

Reaction: (1) 4-hydroxybenzoyl-[(4-hydroxyphenyl)alkanoate synthase] + **8** malonyl-CoA + **16** NADPH + **16** H^+ = 17-(4-hydroxyphenyl)heptadecanoyl-[(4-hydroxyphenyl)alkanoate synthase] + **8** CO_2 + **8** CoA + **16** $NADP^+$ + **8** H_2O

(2) 4-hydroxybenzoyl-[(4-hydroxyphenyl)alkanoate synthase] + **9** malonyl-CoA + **18** NADPH + **18** H^+ + holo-[(4-hydroxyphenyl)alkanoate synthase] = 19-(4-hydroxyphenyl)nonadecanoyl-[(4-hydroxyphenyl)alkanoate synthase] + **9** CO_2 + **9** CoA + **18** $NADP^+$ + **9** H_2O

Other name(s): msl7 (gene name); Pks15/1

Systematic name: malonyl-CoA:4-hydroxybenzoyl-[(4-hydroxyphenyl)alkanoate synthase] malonyltransferase [(4-hydroxyphenyl)alkanoate-forming]

Comments: The enzyme is part of the biosynthetic pathway of phenolphthiocerol, a lipid that serves as a virulence factor of pathogenic mycobacteria. It catalyses the elongation of 4-hydroxybenzoate that is loaded on its acyl-carrier domain to form (4-hydroxyphenyl)alkanoate intermediates. The enzyme adds either 8 or 9 malonyl-CoA units, resulting in formation of 17-(4-hydroxyphenyl)heptadecanoate or 19-(4-hydroxyphenyl)nonadecanoate, respectively. As the enzyme lacks a thioesterase domain [3244], the product remains loaded on the acyl-carrier domain at the end of catalysis, and has to be hydrolysed by an as-yet unknown mechanism.

References: [3244, 599, 3232]

[EC 2.3.1.261 created 2017]

EC 2.3.1.262

Accepted name: anthraniloyl-CoA anthraniloyltransferase

Reaction: anthraniloyl-CoA + malonyl-CoA = 2-aminobenzoylacetyl-CoA + CoA + CO_2 (overall reaction)

(1a) anthraniloyl-CoA + L-cysteinyl-[PqsD protein] = *S*-anthraniloyl-L-cysteinyl-[PqsD protein] + CoA

(1b) *S*-anthraniloyl-L-cysteinyl-[PqsD protein] + malonyl-CoA = 2-aminobenzoylacetyl-CoA + CO$_2$ + L-cysteinyl-[PqsD protein]

Other name(s): *pqsD* (gene name)

Systematic name: anthraniloyl-CoA:malonyl-CoA anthraniloyltransferase

Comments: The enzyme, characterized from the bacterium *Pseudomonas aeruginosa*, participates in the synthesis of the secondary metabolites 2-heptyl-3-hydroxy-4(1*H*)-quinolone and 4-hydroxy-2(1*H*)-quinolone. The enzyme transfers an anthraniloyl group from anthraniloyl-CoA to an internal L-cysteine residue, followed by its transfer to malonyl-CoA to produce a short-lived product that can cyclize spontaneously to form 4-hydroxy-2(1*H*)-quinolone. However, when EC 3.1.2.32, 2-aminobenzoylacetyl-CoA thioesterase, is present, it removes the CoA moiety from the product, forming the stable 2-aminobenzoylacetate.

References: [276, 788, 772]

[EC 2.3.1.262 created 2017]

EC 2.3.1.263

Accepted name: 2-amino-4-oxopentanoate thiolase

Reaction: acetyl-CoA + D-alanine = CoA + (2*R*)-2-amino-4-oxopentanoate

Other name(s): AKPT; AKP thiolase; 2-amino-4-ketopentanoate thiolase

Systematic name: acetyl-CoA:D-alanine acetyltransferase

Comments: A pyridoxal $5'$-phosphate enzyme. The enzyme, characterized from the bacterium *Clostridium sticklandii*, is part of a degradation pathway of ornithine. It is specific for acetyl-CoA and D-alanine.

References: [1505, 923]

[EC 2.3.1.263 created 2017]

EC 2.3.1.264

Accepted name: β-lysine N^6-acetyltransferase

Reaction: acetyl-CoA + (3*S*)-3,6-diaminohexanoate = CoA + (3*S*)-6-acetamido-3-aminohexanoate

Other name(s): *ablB* (gene name)

Systematic name: acetyl-CoA:(3*S*)-3,6-diaminohexanoate N^6-acetyltransferase

Comments: The enzyme is found in some methanogenic archaea and bacteria. In archaea it is induced under salt stress. The product, N^6-acetyl-β-L-lysine, serves as a compatible solute, conferring high salt resistance on the producing organisms.

References: [2687, 2352]

[EC 2.3.1.264 created 2017]

EC 2.3.1.265

Accepted name: phosphatidylinositol dimannoside acyltransferase

Reaction: (1) an acyl-CoA + 2,6-di-*O*-α-D-mannosyl-1-phosphatidyl-1D-*myo*-inositol = CoA + 2-*O*-(6-*O*-acyl-α-D-mannosyl)-6-*O*-α-D-mannosyl-1-phosphatidyl-1D-*myo*-inositol
(2) an acyl-CoA + 2-*O*-α-D-mannosyl-1-phosphatidyl-1D-*myo*-inositol = CoA + 2-*O*-(6-*O*-acyl-α-D-mannosyl)-1-phosphatidyl-1D-*myo*-inositol

Other name(s): PIM2 acyltransferase; *ptfP*1 (gene name)

Systematic name: acyl-CoA:2,6-di-*O*-α-D-mannosyl-1-phosphatidyl-1D-*myo*-inositol acyltransferase

Comments: The enzyme, found in Corynebacteriales, is involved in the biosynthesis of phosphatidyl-*myo*-inositol mannosides (PIMs).

References: [3408]

[EC 2.3.1.265 created 2017]

EC 2.3.1.266

Accepted name: [ribosomal protein S18]-alanine *N*-acetyltransferase

Reaction: acetyl-CoA + an N-terminal L-alanyl-[S18 protein of 30S ribosome] = CoA + an N-terminal *N*-acetyl-L-alanyl-[S18 protein of 30S ribosome]

Other name(s): *rimI* (gene name)

Systematic name: acetyl-CoA:N-terminal L-alanyl-[S18 protein of 30S ribosome] *N*-acetyltransferase

Comments: The enzyme, characterized from bacteria, is specific for protein S18, a component of the 30S ribosomal subunit. *cf.* EC 2.3.1.267, [ribosomal protein S5]-alanine *N*-acetyltransferase.

References: [1461, 4002]

[EC 2.3.1.266 created 1990 as EC 2.3.1.128, part transferred 2018 to EC 2.3.1.266]

EC 2.3.1.267

Accepted name: [ribosomal protein S5]-alanine *N*-acetyltransferase

Reaction: acetyl-CoA + an N-terminal L-alanyl-[S5 protein of 30S ribosome] = CoA + an N-terminal *N*-acetyl-L-alanyl-[S5 protein of 30S ribosome]

Other name(s): *rimJ* (gene name)

Systematic name: acetyl-CoA:N-terminal L-alanyl-[S5 protein of 30S ribosome] *N*-acetyltransferase

Comments: The enzyme, characterized from bacteria, is specific for protein S5, a component of the 30S ribosomal subunit. It also plays a role in maturation of the 30S ribosomal subunit. *cf.* EC 2.3.1.266, [ribosomal protein S18]-alanine *N*-acetyltransferase.

References: [4002, 2956, 2955]

[EC 2.3.1.267 created 1990 as EC 2.3.1.128, part transferred 2018 to EC 2.3.1.267]

EC 2.3.1.268

Accepted name: ethanol *O*-acetyltransferase

Reaction: ethanol + acetyl-CoA = ethyl acetate + CoA

Other name(s): eat1 (gene name); ethanol acetyltransferase

Systematic name: acetyl-CoA:ethanol *O*-acetyltransferase

Comments: The enzyme, characterized from the yeast *Wickerhamomyces anomalus*, is responsible for most ethyl acetate synthesis in known ethyl acetate-producing yeasts. It is only distantly related to enzymes classified as EC 2.3.1.84, alcohol *O*-acetyltransferase. The enzyme also possesses thioesterase and esterase activities, which are inhibited by high ethanol concentrations.

References: [1796]

[EC 2.3.1.268 created 2018]

EC 2.3.1.269

Accepted name: apolipoprotein *N*-acyltransferase

Reaction: a phosphoglycerolipid + an [apolipoprotein]-*S*-1,2-diacyl-*sn*-glyceryl-L-cysteine = a 1-lysophosphoglycerolipid + a [lipoprotein]-*N*-acyl-*S*-1,2-diacyl-*sn*-glyceryl-L-cysteine

Other name(s): *lnt* (gene name); Lnt

Systematic name: phosphoglyceride:[apolipoprotein]-*S*-1,2-diacyl-*sn*-glyceryl-L-cysteine *N*-acyltransferase

Comments: This bacterial enzyme transfers a fatty acid from a membrane phospholipid to form an amide linkage with the N-terminal cysteine residue of apolipoproteins, generating a triacylated molecule.

References: [1180, 2899, 1331]

[EC 2.3.1.269 created 2018]

EC 2.3.1.270

Accepted name: lyso-ornithine lipid *O*-acyltransferase

Reaction: a lyso-ornithine lipid + an acyl-[acyl-carrier protein] = an ornithine lipid + a holo-[acyl-carrier protein]

Other name(s): *olsA* (gene name)
Systematic name: N^{α}-[(3*R*)-hydroxy-acyl]-L-ornithine *O*-acyltransferase
Comments: This bacterial enzyme catalyses the second step in the formation of ornithine lipids.
References: [3815, 145, 1952]

[EC 2.3.1.270 created 2018]

EC 2.3.1.271

Accepted name: L-glutamate-5-semialdehyde *N*-acetyltransferase
Reaction: acetyl-CoA + L-glutamate-5-semialdehyde = CoA + *N*-acetyl-L-glutamate 5-semialdehyde
Other name(s): MPR1 (gene name); MPR2 (gene name)
Systematic name: acetyl-CoA:L-glutamate-5-semialdehyde *N*-acetyltransferase
Comments: The enzyme, characterized from the yeast *Saccharomyces cerevisiae* Σ1278b, *N*-acetylates L-glutamate-5-semialdehyde, an L-proline biosynthesis/utilization intermediate, into *N*-acetyl-L-glutamate 5-semialdehyde, an intermediate of L-arginine biosynthesis, under oxidative stress conditions. Its activity results in conversion of L-proline to L-arginine, and reduction in the concentration of L-glutamate 5-semialdehyde and its equilibrium partner, (*S*)-1-pyrroline-5-carboxylate, which has been linked to production of reactive oxygen species stress. The enzyme also acts on (*S*)-1-acetylazetidine-2-carboxylate, a toxic L-proline analog produced by some plants, resulting in its detoxification and conferring resistance on the yeast.
References: [3186, 2490, 2467, 2468, 2420]

[EC 2.3.1.271 created 2018]

EC 2.3.1.272

Accepted name: 2-acetylphloroglucinol acetyltransferase
Reaction: **2** 2-acetylphloroglucinol = 2,4-diacetylphloroglucinol + phloroglucinol
Other name(s): MAPG ATase
Systematic name: 2-acetylphloroglucinol *C*-acetyltransferase
Comments: The enzyme from the bacterium *Pseudomonas* sp. YGJ3 is composed of three subunits named PhlA, PhlB and PhlC. Production of 2,4-diacetylphloroglucinol, which has antibiotic activity, is strongly inhibited by chloride ions.
References: [1252]

[EC 2.3.1.272 created 2018]

EC 2.3.1.273

Accepted name: diglucosylglycerate octanoyltransferase
Reaction: octanoyl-CoA + 2-*O*-[α-D-glucopyranosyl-(1→6)-α-D-glucopyranosyl]-D-glycerate. = 2-*O*-[6-*O*-octanoyl-α-D-glucopyranosyl-(1→6)-α-D-glucopyranosyl]-D-glycerate. + CoA
Other name(s): *octT* (gene name); DGG octanoyltransferase
Systematic name: octanoyl-CoA:2-*O*-[α-D-glucopyranosyl-(1→6)-α-D-glucopyranosyl]-D-glycerate octanoyltransferase
Comments: The enzyme, characterized from mycobacteria, is involved in the biosynthesis of methylglucose lipopolysaccharide (MGLP). The enzyme can also act on 2-*O*-(α-D-glucopyranosyl)-D-glycerate, but with lower activity.
References: [2118]

[EC 2.3.1.273 created 2018]

EC 2.3.1.274

Accepted name: phosphate acyltransferase
Reaction: an acyl-[acyl-carrier protein] + phosphate = an acyl phosphate + an [acyl-carrier protein]
Other name(s): *plsX* (gene name); acyl-ACP phosphotransacylase; acyl-[acyl-carrier-protein]—phosphate acyltransferase; phosphate-acyl-ACP acyltransferase

Systematic name: an acyl-[acyl-carrier protein]:phosphate acyltransferase

Comments: The enzyme, found in bacteria, catalyses the synthesis of fatty acyl-phosphate from acyl-[acyl-carrier protein], a step in the most widely distributed bacterial pathway for the initiation of phospholipid formation. While the activity is modestly enhanced by Mg^{2+}, the enzyme does not require a divalent cation.

References: [2059, 4004, 1685, 1551]

[EC 2.3.1.274 created 2018]

EC 2.3.1.275

Accepted name: acyl phosphate:glycerol-3-phosphate acyltransferase

Reaction: an acyl phosphate + *sn*-glycerol 3-phosphate = a 1-acyl-*sn*-glycerol 3-phosphate + phosphate

Other name(s): *plsY* (gene name); G3P acyltransferase; GPAT; lysophosphatidic acid synthase; LPA synthase

Systematic name: acyl phosphoate:*sn*-glycerol 3-phosphate acyltransferase

Comments: The enzyme, found in bacteria, catalyses a step in the most widely distributed bacterial pathway for the initiation of phospholipid formation. The enzyme is membrane-bound.

References: [2059, 4004, 2058, 1221]

[EC 2.3.1.275 created 2018]

EC 2.3.1.276

Accepted name: galactosamine-1-phosphate *N*-acetyltransferase

Reaction: acetyl-CoA + α-D-galactosamine 1-phosphate = CoA + *N*-acetyl-α-D-galactosamine 1-phosphate

Other name(s): ST0452 (locus name)

Systematic name: acetyl-CoA:α-D-galactosamine-1-phosphate *N*-acetyltransferase

Comments: The enzyme, characterized from the archaeon *Sulfolobus tokodaii*, is also active toward α-D-glucosamine 1-phosphate (*cf.* EC 2.3.1.157, glucosamine-1-phosphate *N*-acetyltransferase). In addition, that enzyme contains a second domain that catalyses the activities of EC 2.7.7.23, UDP-*N*-acetylglucosamine diphosphorylase, EC 2.7.7.24, glucose-1-phosphate thymidylyltransferase, and EC 2.7.7.83, UDP-*N*-acetylgalactosamine diphosphorylase.

References: [4059, 4058, 652]

[EC 2.3.1.276 created 2018]

EC 2.3.1.277

Accepted name: 2-oxo-3-(phosphooxy)propyl 3-oxoalkanoate synthase

Reaction: a medium-chain 3-oxoacyl-[acyl-carrier protein] + glycerone phosphate = 2-oxo-3-(phosphooxy)propyl 3-oxoalkanoate + a holo-[acyl-carrier protein]

Other name(s): *afsA* (gene name); *scbA* (gene name); *barX* (gene name)

Systematic name: 3-oxoacyl-[acyl-carrier protein]:glycerone phosphate 3-oxonacylltransferase

Comments: The enzyme catalyses the first committed step in the biosynthesis of γ-butyrolactone autoregulators that control secondary metabolism and morphological development in *Streptomyces* bacteria.

References: [1372, 1596, 1386, 1909]

[EC 2.3.1.277 created 2018]

EC 2.3.1.278

Accepted name: mycolipenoyl-CoA—2-(long-chain-fatty acyl)-trehalose mycolipenoyltransferase

Reaction: a mycolipenoyl-CoA + a 2-(long-chain-fatty acyl)-trehalose = a 2-(long-chain-fatty acyl)-3-mycolipenoyl-trehalose + CoA

Other name(s): *papA3* (gene name)

Systematic name: mycolipenoyl-CoA:2-(long-chain-fatty acyl)-trehalose 3-mycolipenoyltransferase

Comments: The enzyme, characterized from the bacterium *Mycobacterium tuberculosis*, participates in the biosynthesis of polyacyltrehalose (PAT), a pentaacylated, trehalose-based glycolipid found in the cell wall of pathogenic strains. The enzyme catalyses two successive activities - it first transfers an acyl (often palmitoyl) group to position 2 (see EC 2.3.1.279, long-chain-acyl-CoA—trehalose acyltransferase), followed by the transfer of a mycolipenyl group to position 3.
References: [1247]

[EC 2.3.1.278 created 2018]

EC 2.3.1.279

Accepted name: long-chain-acyl-CoA—trehalose acyltransferase
Reaction: a long-chain-fatty acyl-CoA + α,α-trehalose = a 2-(long-chain-fatty acyl)-trehalose + CoA
Other name(s): *papA3* (gene name)
Systematic name: long-chain-fatty acyl-CoA:α,α-trehalose 2-acyltransferase
Comments: The enzyme, characterized from the bacterium *Mycobacterium tuberculosis*, participates in the biosynthesis of polyacyltrehalose (PAT), a pentaacylated, trehalose-based glycolipid found in the cell wall of pathogenic strains. The enzyme catalyses two successive activities - it first transfers an acyl (often palmitoyl) group to position 2, followed by the transfer of a mycolipenyl group to position 3 (see EC 2.3.1.278, mycolipenoyl-CoA—2-(long-chain-fatty acyl)-trehalose mycolipenoyltransferase).
References: [1247]

[EC 2.3.1.279 created 2018]

EC 2.3.1.280

Accepted name: (aminoalkyl)phosphonate *N*-acetyltransferase
Reaction: acetyl-CoA + (aminomethyl)phosphonate = CoA + (acetamidomethyl)phosphonate
Other name(s): *phnO* (gene name)
Systematic name: acetyl-CoA:(aminomethyl)phosphonate *N*-acetyltransferase
Comments: The enzyme, characterized from the bacterium *Escherichia coli*, is able to acetylate a range of (aminoalkyl)phosphonic acids. Requires a divalent metal ion for activity.
References: [855, 1382]

[EC 2.3.1.280 created 2018]

EC 2.3.2 Aminoacyltransferases

EC 2.3.2.1

Accepted name: D-glutamyltransferase
Reaction: (1) D-glutamine + D-glutamate = NH_3 + γ-D-glutamyl-D-glutamate
(2) L(or D)-glutamine + (γ-D-glutamyl)$_n$-[peptide] = NH_3 + (γ-D-glutamyl)$_{n+1}$-[peptide]
Other name(s): D-glutamyl transpeptidase; D-γ-glutamyl transpeptidase
Systematic name: glutamine:D-glutamyl-peptide 5-glutamyltransferase
Comments: The enzyme catalyses two reactions. The first is the transfer of a glutamyl residue from L- or D-glutamine to D-glutamate via a γ linkage, forming γ-glutamyl-D-glutamate, and the second is the transfer of additional glutamyl residues to the peptide, extending the polypeptide chain.
References: [3860, 3859]

[EC 2.3.2.1 created 1961, modified 1976, modified 2013]

EC 2.3.2.2

Accepted name: γ-glutamyltransferase
Reaction: a (5-L-glutamyl)-peptide + an amino acid = a peptide + a 5-L-glutamyl amino acid

Other name(s): glutamyl transpeptidase; α-glutamyl transpeptidase; γ-glutamyl peptidyltransferase; γ-glutamyl transpeptidase (ambiguous); γ-GPT; γ-GT; γ-GTP; L-γ-glutamyl transpeptidase; L-γ-glutamyltransferase; L-glutamyltransferase; GGT (ambiguous); γ-glutamyltranspeptidase (ambiguous)
Systematic name: (5-L-glutamyl)-peptide:amino-acid 5-glutamyltransferase
Comments: The mammlian enzyme is part of the cell antioxidant defense mechanism. It initiates extracellular glutathione (GSH) breakdown, provides cells with a local cysteine supply and contributes to maintain intracelular GSH levels. The protein also has EC 3.4.19.13 (glutathione hydrolase) activity [2547, 336]. The enzyme consists of two chains that are created by the proteolytic cleavage of a single precursor polypeptide. The N-terminal L-threonine of the C-terminal subunit functions as the active site for both the cleavage and the hydrolysis reactions [2547, 336].
References: [1102, 1917, 2547, 336, 3845]

[EC 2.3.2.2 created 1972, modified 1976, modified 2011]

EC 2.3.2.3

Accepted name: lysyltransferase
Reaction: L-lysyl-tRNA^{Lys} + phosphatidylglycerol = tRNA^{Lys} + 3-*O*-L-lysyl-1-*O*-phosphatidylglycerol
Other name(s): L-lysyl-tRNA:phosphatidylglycerol 3-*O*-lysyltransferase
Systematic name: L-lysyl-tRNA^{Lys}:phosphatidylglycerol 3-*O*-lysyltransferase
References: [1934]

[EC 2.3.2.3 created 1972, modified 2013]

[2.3.2.4 Transferred entry. γ-glutamylcyclotransferase. Now classified as EC 4.3.2.9, γ-glutamylcyclotransferase]

[EC 2.3.2.4 created 1972, deleted 2017]

EC 2.3.2.5

Accepted name: glutaminyl-peptide cyclotransferase
Reaction: L-glutaminyl-peptide = 5-oxoprolyl-peptide + NH$_3$
Other name(s): glutaminyl-tRNA cyclotransferase; glutaminyl cyclase; glutaminyl-transfer ribonucleate cyclotransferase
Systematic name: L-glutaminyl-peptide γ-glutamyltransferase (cyclizing)
Comments: Involved in the formation of thyrotropin-releasing hormone and other biologically active peptides containing N-terminal pyroglutamyl residues. The enzyme from papaya also acts on glutaminyl-tRNA.
References: [438, 907, 2228]

[EC 2.3.2.5 created 1972, modified 1990]

EC 2.3.2.6

Accepted name: lysine/arginine leucyltransferase
Reaction: (1) L-leucyl-tRNA^{Leu} + N-terminal L-lysyl-[protein] = tRNA^{Leu} + N-terminal L-leucyl-L-lysyl-[protein]
(2) L-leucyl-tRNA^{Leu} + N-terminal L-arginyl-[protein] = tRNA^{Leu} + N-terminal L-leucyl-L-arginyl-[protein]
Other name(s): leucyl, phenylalanine-tRNA-protein transferase; leucyl-phenylalanine-transfer ribonucleate-protein aminoacyltransferase; leucyl-phenylalanine-transfer ribonucleate-protein transferase; L-leucyl-tRNA:protein leucyltransferase; leucyltransferase (misleading); L/FK,R-transferase; *aat* (gene name); L-leucyl-tRNA^{Leu}:protein leucyltransferase
Systematic name: L-leucyl-tRNA^{Leu}:[protein] N-terminal L-lysine/L-arginine leucyltransferase

Comments: Requires a univalent cation. The enzyme participates in the N-end rule protein degradation pathway in certain bacteria, by attaching the primary destabilizing residue L-leucine to the N-termini of proteins that have an N-terminal L-arginine or L-lysine residue. Once modified, the proteins are recognized by EC 3.4.21.92, the ClpAP/ClpS endopeptidase system. The enzyme also transfers L-phenylalanine *in vitro*, but this has not been observed *in vivo* [3212]. *cf.* EC 2.3.2.29, aspartate/glutamate leucyltransferase, and EC 2.3.2.8, arginyltransferase.
References: [1918, 1919, 3275, 3539, 3212, 9]

[EC 2.3.2.6 created 1972, modified 1976, modified 2013, modified 2016]

EC 2.3.2.7

Accepted name: aspartyltransferase
Reaction: L-asparagine + hydroxylamine = NH$_3$ + β-L-aspartylhydroxamate
Other name(s): β-aspartyl transferase; aspartotransferase
Systematic name: L-asparagine:hydroxylamine γ-aspartyltransferase
References: [1504]

[EC 2.3.2.7 created 1972]

EC 2.3.2.8

Accepted name: arginyltransferase
Reaction: L-arginyl-tRNA^{Arg} + protein = tRNA^{Arg} + L-arginyl-[protein]
Other name(s): arginine transferase; arginyl-transfer ribonucleate-protein aminoacyltransferase; arginyl-transfer ribonucleate-protein transferase; arginyl-tRNA protein transferase; L-arginyl-tRNA:protein arginyltransferase
Systematic name: L-arginyl-tRNA^{Arg}:protein arginyltransferase
Comments: Requires mercaptoethanol and a univalent cation. Peptides and proteins containing an N-terminal glutamate, aspartate or cystine residue can act as acceptors.
References: [3273, 3274, 3277]

[EC 2.3.2.8 created 1972, modified 1976, modified 2013]

EC 2.3.2.9

Accepted name: agaritine γ-glutamyltransferase
Reaction: agaritine + acceptor = 4-hydroxymethylphenylhydrazine + γ-L-glutamyl-acceptor
Other name(s): (γ-L-glutamyl)-N^1-(4-hydroxymethylphenyl)hydrazine:(acceptor) γ-glutamyltransferase; (γ-L-glutamyl)-1-*N*-(4-hydroxymethylphenyl)hydrazine:(acceptor) γ-glutamyltransferase; (γ-L-glutamyl)-1-*N*-(4-hydroxymethylphenyl)hydrazine:acceptor γ-glutamyltransferase
Systematic name: (γ-L-glutamyl)-N^1-(4-hydroxymethylphenyl)hydrazine:acceptor γ-glutamyltransferase
Comments: 4-Hydroxyaniline, cyclohexylamine, 1-naphthylhydrazine and similar compounds can act as acceptors; the enzyme also catalyses the hydrolysis of agaritine.
References: [1060]

[EC 2.3.2.9 created 1972]

EC 2.3.2.10

Accepted name: UDP-*N*-acetylmuramoylpentapeptide-lysine N^6-alanyltransferase
Reaction: L-alanyl-tRNA^{Ala} + UDP-*N*-acetyl-α-D-muramoyl-L-alanyl-D-glutamyl-L-lysyl-D-alanyl-D-alanine = tRNA^{Ala} + UDP-*N*-acetyl-α-D-muramoyl-L-alanyl-D-glutamyl-N^6-(L-alanyl)-L-lysyl-D-alanyl-D-alanine

Other name(s): alanyl-transfer ribonucleate-uridine diphosphoacetylmuramoylpentapeptide transferase; UDP-*N*-acetylmuramoylpentapeptide lysine N^6-alanyltransferase; uridine diphosphoacetylmuramoylpentapeptide lysine N^6-alanyltransferase; L-alanyl-tRNA:UDP-*N*-acetylmuramoyl-L-alanyl-D-glutamyl-L-lysyl-D-alanyl-D-alanine 6-*N*-alanyltransferase; L-alanyl-tRNA:UDP-*N*-acetylmuramoyl-L-alanyl-D-glutamyl-L-lysyl-D-alanyl-D-alanine N^6-alanyltransferase
Systematic name: L-alanyl-tRNA^{Ala}:UDP-*N*-acetyl-α-D-muramoyl-L-alanyl-D-glutamyl-L-lysyl-D-alanyl-D-alanine N^6-alanyltransferase
Comments: Also acts on L-seryl-tRNA^{Ser}.
References: [2723]

[EC 2.3.2.10 created 1972, modified 2013]

EC 2.3.2.11

Accepted name: alanylphosphatidylglycerol synthase
Reaction: L-alanyl-tRNA^{Ala} + phosphatidylglycerol = tRNA^{Ala} + 3-*O*-L-alanyl-1-*O*-phosphatidylglycerol
Other name(s): *O*-alanylphosphatidylglycerol synthase; alanyl phosphatidylglycerol synthetase
Systematic name: L-alanyl-tRNA^{Ala}:phosphatidylglycerol alanyltransferase
References: [1117]

[EC 2.3.2.11 created 1972, modified 2013]

EC 2.3.2.12

Accepted name: peptidyltransferase
Reaction: peptidyl-tRNA$_1$ + aminoacyl-tRNA$_2$ = tRNA$_1$ + peptidyl(aminoacyl-tRNA$_2$)
Other name(s): transpeptidase; ribosomal peptidyltransferase
Systematic name: peptidyl-tRNA:aminoacyl-tRNA *N*-peptidyltransferase
Comments: The enzyme is a ribozyme. Two non-equivlant ribonucleoprotein subunits operate in non-concerted fashion in peptide elongation. The small subunit forms the mRNA-binding machinery and decoding center, the large subunit performs the main ribosomal catalytic function in the peptidyl-transferase center.
References: [2980, 2981, 3562, 3702]

[EC 2.3.2.12 created 1976]

EC 2.3.2.13

Accepted name: protein-glutamine γ-glutamyltransferase
Reaction: protein glutamine + alkylamine = protein N^5-alkylglutamine + NH$_3$
Other name(s): transglutaminase; Factor XIIIa; fibrinoligase; fibrin stabilizing factor; glutaminylpeptide γ-glutamyltransferase; polyamine transglutaminase; tissue transglutaminase; *R*-glutaminyl-peptide:amine γ-glutamyl transferase
Systematic name: protein-glutamine:amine γ-glutamyltransferase
Comments: Requires Ca^{2+}. The γ-carboxamide groups of peptide-bound glutamine residues act as acyl donors, and the 6-amino-groups of protein- and peptide-bound lysine residues act as acceptors, to give intra- and inter-molecular N^6-(5-glutamyl)-lysine crosslinks. Formed by proteolytic cleavage from plasma Factor XIII
References: [920, 921, 922, 3442]

[EC 2.3.2.13 created 1978, modified 1981, modified 1983]

EC 2.3.2.14

Accepted name: D-alanine γ-glutamyltransferase
Reaction: L-glutamine + D-alanine = NH$_3$ + γ-L-glutamyl-D-alanine
Systematic name: L-glutamine:D-alanine γ-glutamyltransferase

Comments: D-Phenylalanine and D-2-aminobutyrate can also act as acceptors, but more slowly. The enzyme also catalyses some of the reactions of EC 2.3.2.2 (γ-glutamyltransferase).

References: [1618]

[EC 2.3.2.14 created 1989]

EC 2.3.2.15

Accepted name: glutathione γ-glutamylcysteinyltransferase

Reaction: glutathione + $[\text{Glu(-Cys)}]_n$-Gly = Gly + $[\text{Glu(-Cys)}]_{n+1}$-Gly

Other name(s): phytochelatin synthase; γ-glutamylcysteine dipeptidyl transpeptidase

Systematic name: glutathione:poly(4-glutamyl-cysteinyl)glycine 4-glutamylcysteinyltransferase

References: [1141]

[EC 2.3.2.15 created 1992]

EC 2.3.2.16

Accepted name: lipid II:glycine glycyltransferase

Reaction: MurNAc-L-Ala-D-isoglutaminyl-L-Lys-D-Ala-D-Ala-diphospho-*ditrans*,*octacis*-undecaprenyl-GlcNAc + glycyl-tRNA^{Gly} = MurNAc-L-Ala-D-isoglutaminyl-L-Lys-(N^6-Gly)-D-Ala-D-Ala-diphospho-*ditrans*,*octacis*-undecaprenyl-GlcNAc + tRNA^{Gly}

Other name(s): *N*-acetylmuramoyl-L-alanyl-D-glutamyl-L-lysyl-D-alanyl-D-alanine-diphosphoundecaprenyl-*N*-acetylglucosamine:N^6-glycine transferase; *femX* (gene name); alanyl-D-alanine-diphospho-*ditrans*,*octacis*-undecaprenyl-*N*-acetylglucosamine:glycine N^6-glycyltransferase

Systematic name: MurNAc-L-Ala-D-isoglutaminyl-L-Lys-D-Ala-D-Ala-diphospho-*ditrans*,*octacis*-undecaprenyl-GlcNAc:glycine N^6-glycyltransferase

Comments: The enzyme from *Staphylococcus aureus* catalyses the transfer of glycine from a charged tRNA to MurNAc-L-Ala-D-isoglutaminyl-L-Lys-D-Ala-D-Ala-diphosphoundecaprenyl-GlcNAc (lipid II), attaching it to the N^6 of the L-Lys at position 3 of the pentapeptide. This is the first step in the synthesis of the pentaglycine interpeptide bridge that is used in *S. aureus* for the crosslinking of different glycan strands to each other. Four additional Gly residues are subsequently attached by EC 2.3.2.17 (*N*-acetylmuramoyl-L-alanyl-D-glutamyl-L-lysyl-(N^6-glycyl)-D-alanyl-D-alanine-diphosphoundecaprenyl-*N*-acetylglucosamine:glycine glycyltransferase) and EC 2.3.2.18 (*N*-acetylmuramoyl-L-alanyl-D-glutamyl-L-lysyl-(N^6-triglycine)-D-alanyl-D-alanine-diphosphoundecaprenyl-*N*-acetylglucosamine:glycine glycyltransferase).

References: [3094]

[EC 2.3.2.16 created 2010]

EC 2.3.2.17

Accepted name: *N*-acetylmuramoyl-L-alanyl-D-glutamyl-L-lysyl-(N^6-glycyl)-D-alanyl-D-alanine-diphosphoundecaprenyl-*N*-acetylglucosamine:glycine glycyltransferase

Reaction: MurNAc-L-Ala-D-isoglutaminyl-L-Lys-(N^6-Gly)-D-Ala-D-Ala-diphospho-*ditrans*,*octacis*-undecaprenyl-GlcNAc + **2** glycyl-tRNA^{Gly} = MurNAc-L-Ala-D-isoglutaminyl-L-Lys-(N^6-tri-Gly)-D-Ala-D-Ala-diphospho-*ditrans*,*octacis*-undecaprenyl-GlcNAc + **2** tRNA^{Gly}

Other name(s): *femA* (gene name); *N*-acetylmuramoyl-L-alanyl-D-glutamyl-L-lysyl-(N^6-glycyl)-D-alanyl-D-alanine-*ditrans*,*octacis*-diphosphoundecaprenyl-*N*-acetylglucosamine:glycine glycyltransferase

Systematic name: MurNAc-L-Ala-D-isoglutaminyl-L-Lys-(N^6-Gly)-D-Ala-D-Ala-diphospho-*ditrans*,*octacis*-undecaprenyl-GlcNAc:glycine glycyltransferase

Comments: This enzyme catalyses the successive transfer of two Gly moieties from charged tRNAs to MurNAc-L-Ala-D-isoglutaminyl-L-Lys-(N^6-Gly)-D-Ala-D-Ala-diphospho-*ditrans*,*octacis*-undecaprenyl-GlcNAc, attaching them to a Gly residue previously attached by EC 2.3.2.16 (lipid II:glycine glycyltransferase) to the N^6 of the L-Lys at position 3 of the pentapeptide. This is the second step in the synthesis of the pentaglycine interpeptide bridge that is used by *Staphylococcus aureus* for the crosslinking of different glycan strands to each other. The next step is catalysed by EC 2.3.2.18 (*N*-acetylmuramoyl-L-alanyl-D-glutamyl-L-lysyl-(N^6-triglycine)-D-alanyl-D-alanine-diphosphoundecaprenyl-*N*-acetylglucosamine:glycine glycyltransferase). This enzyme is essential for methicillin resistance [281].

References: [281, 1526, 272, 3094]

[EC 2.3.2.17 created 2010]

EC 2.3.2.18

Accepted name: *N*-acetylmuramoyl-L-alanyl-D-glutamyl-L-lysyl-(N^6-triglycine)-D-alanyl-D-alanine-diphosphoundecaprenyl-*N*-acetylglucosamine:glycine glycyltransferase

Reaction: MurNAc-L-Ala-D-isoglutaminyl-L-Lys-(N^6-tri-Gly)-D-Ala-D-Ala-diphospho-*ditrans*,*octacis*-undecaprenyl-GlcNAc + **2** glycyl-tRNA^{Gly} = MurNAc-L-Ala-D-isoglutaminyl-L-Lys-(N^6-penta-Gly)-D-Ala-D-Ala-diphospho-*ditrans*,*octacis*-undecaprenyl-GlcNAc + **2** tRNA^{Gly}

Other name(s): *femB* (gene name); *N*-acetylmuramoyl-L-alanyl-D-glutamyl-L-lysyl-(N^6-triglycine)-D-alanyl-D-alanine-*ditrans*,*octacis*-diphosphoundecaprenyl-*N*-acetylglucosamine:glycine glycyltransferase

Systematic name: MurNAc-L-Ala-D-isoglutaminyl-L-Lys-(N^6-tri-Gly)-D-Ala-D-Ala-diphospho-*ditrans*,*octacis*-undecaprenyl-GlcNAc:glycine glycyltransferase

Comments: This *Staphylococcus aureus* enzyme catalyses the successive transfer of two Gly moieties from charged tRNAs to MurNAc-L-Ala-D-isoglutaminyl-L-Lys-(N^6-tri-Gly)-D-Ala-D-Ala-diphosphoundecaprenyl-GlcNAc, attaching them to the three Gly molecules that were previously attached to the N^6 of the L-Lys at position 3 of the pentapeptide by EC 2.3.2.16 (lipid II:glycine glycyltransferase) and EC 2.3.2.17 (*N*-acetylmuramoyl-L-alanyl-D-glutamyl-L-lysyl-(N^6-glycyl)-D-alanyl-D-alanine-diphosphoundecaprenyl-*N*-acetylglucosamine:glycine glycyltransferase). This is the last step in the synthesis of the pentaglycine interpeptide bridge that is used in this organism for the crosslinking of different glycan strands to each other.

References: [813, 2919, 3094]

[EC 2.3.2.18 created 2010]

EC 2.3.2.19

Accepted name: ribostamycin:4-(γ-L-glutamylamino)-(*S*)-2-hydroxybutanoyl-[BtrI acyl-carrier protein] 4-(γ-L-glutamylamino)-(*S*)-2-hydroxybutanoate transferase

Reaction: 4-(γ-L-glutamylamino)-(*S*)-2-hydroxybutanoyl-[BtrI acyl-carrier protein] + ribostamycin = γ-L-glutamyl-butirosin B + BtrI acyl-carrier protein

Other name(s): *btrH* (gene name)

Systematic name: ribostamycin:4-(γ-L-glutamylamino)-(*S*)-2-hydroxybutanoyl-[BtrI acyl-carrier protein] 4-(γ-L-glutamylamino)-(*S*)-2-hydroxybutanoate transferase

Comments: The enzyme attaches the side chain of the aminoglycoside antibiotics of the butirosin family. The side chain confers resistance against several aminoglycoside-modifying enzymes.

References: [2020]

[EC 2.3.2.19 created 2012]

EC 2.3.2.20

Accepted name: cyclo(L-leucyl-L-phenylalanyl) synthase

Reaction: L-leucyl-tRNA^{Leu} + L-phenylalanyl-tRNA^{Phe} = tRNA^{Leu} + tRNA^{Phe} + cyclo(L-leucyl-L-phenylalanyl)

Other name(s): AlbC; cFL synthase

Systematic name: L-leucyl-tRNA^{Leu}:L-phenylalanyl-tRNA^{Phe} leucyltransferase (cyclizing)

Comments: The reaction proceeds following a ping-pong mechanism forming a covalent intermediate between an active site serine and the L-phenylalanine residue [3041]. The protein, found in the bacterium *Streptomyces noursei*, also forms cyclo(L-phenylalanyl-L-phenylalanyl), cyclo(L-methionyl-L-phenylalanyl), cyclo(L-phenylalanyl-L-tyrosyl) and cyclo(L-methionyl-L-tyrosyl) [1099].
References: [1099, 3041]

[EC 2.3.2.20 created 2013]

EC 2.3.2.21

Accepted name: cyclo(L-tyrosyl-L-tyrosyl) synthase
Reaction: **2** L-tyrosyl-tRNA$^{\text{Tyr}}$ = **2** tRNA$^{\text{Tyr}}$ + cyclo(L-tyrosyl-L-tyrosyl)
Other name(s): Rv2275 (gene name); cYY synthase; cyclodityrosine synthase
Systematic name: L-tyrosyl-tRNA$^{\text{Tyr}}$:L-tyrosyl-tRNA$^{\text{Tyr}}$ tyrosyltransferase (cyclizing)
Comments: The reaction proceeds following a ping-pong mechanism forming a covalent intermediate between an active site serine and the first L-tyrosine residue [3676]. The protein, from the bacterium *Mycobacterium tuberculosis*, also forms small amounts of cyclo(L-tyrosyl-L-phenylalanyl) [1099].
References: [1099, 3676]

[EC 2.3.2.21 created 2013]

EC 2.3.2.22

Accepted name: cyclo(L-leucyl-L-leucyl) synthase
Reaction: **2** L-leucyl-tRNA$^{\text{Leu}}$ = **2** tRNA$^{\text{Leu}}$ + cyclo(L-leucyl-L-leucyl)
Other name(s): YvmC; cLL synthase; cyclodileucine synthase
Systematic name: L-leucyl-tRNA$^{\text{Leu}}$:L-leucyl-tRNA$^{\text{Leu}}$ leucyltransferase (cyclizing)
Comments: The reaction proceeds following a ping-pong mechanism forming a covalent intermediate between an active site serine and the first L-leucine residue [348]. The proteins from bacteria of the genus *Bacillus* also form small amounts of cyclo(L-phenylalanyl-L-leucyl) and cyclo(L-leucyl-L-methionyl) [1099].
References: [1099, 348]

[EC 2.3.2.22 created 2013]

EC 2.3.2.23

Accepted name: E2 ubiquitin-conjugating enzyme
Reaction: *S*-ubiquitinyl-[E1 ubiquitin-activating enzyme]-L-cysteine + [E2 ubiquitin-conjugating enzyme]-L-cysteine = [E1 ubiquitin-activating enzyme]-L-cysteine + *S*-ubiquitinyl-[E2 ubiquitin-conjugating enzyme]-L-cysteine
Other name(s): ubiquitin-carrier-protein E2; UBC (ambiguous); ubiquitin-conjugating enzyme E2
Systematic name: *S*-ubiquitinyl-[E1 ubiquitin-activating enzyme]-L-cysteine:[E2 ubiquitin-conjugating enzyme] ubiquitinyl transferase
Comments: The E2 ubiquitin-conjugating enzyme acquires the activated ubquitin from the E1 ubiquitin-activating enzyme (EC 6.2.1.45) and binds it via a transthioesterification reaction to itself. In the human enzyme the catalytic center is located at Cys-87 where ubiquitin is bound via its C-terminal glycine in a thioester linkage.
References: [3646, 678, 2616, 603, 1954]

[EC 2.3.2.23 created 2015]

EC 2.3.2.24

Accepted name: (E3-independent) E2 ubiquitin-conjugating enzyme
Reaction: [E1 ubiquitin-activating enzyme]-*S*-ubiquitinyl-L-cysteine + [acceptor protein]-L-lysine = [E1 ubiquitin-activating enzyme]-L-cysteine + [acceptor protein]-N^6-monoubiquitinyl-L-lysine (overall reaction)

(1a) [E1 ubiquitin-activating enzyme]-*S*-ubiquitinyl-L-cysteine + [(E3-independent) E2 ubiquitin-conjugating enzyme]-L-cysteine = [E1 ubiquitin-activating enzyme]-L-cysteine + [(E3-independent) ubiquitin-conjugating enzyme]-*S*-monoubiquitinyl-L-cysteine
(1b) [(E3-independent) E2 ubiquitin-conjugating E2 enzyme]-*S*-monoubiquitinyl-L-cysteine + [acceptor protein]-L-lysine = [(E3-independent) E2 ubiquitin-conjugating enzyme]-L-cysteine + [acceptor protein]-N^6-monoubiquitinyl-L-lysine

Other name(s): E2-230K; UBE2O; E3-independent ubiquitin-conjugating enzyme E2

Systematic name: [E1 ubiquitin-activating enzyme]-*S*-ubiquitinyl-L-cysteine:L-lysine ubiquitinyl transferase ([E3 ubiquitin transferase]-independent)

Comments: The enzyme transfers a single ubiquitin directly from an ubiquitinated E1 ubiquitin-activating enzyme to itself, and on to a lysine residue of the acceptor protein without involvement of E3 ubiquitin transferases (*cf.* EC 2.3.2.26, EC 2.3.2.27). It forms a labile ubiquitin adduct in the presence of E1, ubiquitin, and Mg^{2+}-ATP and catalyses the conjugation of ubiquitin to protein substrates, independently of E3. This transfer has only been observed with small proteins. *In vitro* a transfer to small acceptors (e.g. L-lysine, *N*-acetyl-L-lysine methyl ester) has been observed [2699].

References: [2699, 1347, 2800]

[EC 2.3.2.24 created 2015]

EC 2.3.2.25

Accepted name: N-terminal E2 ubiquitin-conjugating enzyme

Reaction: *S*-ubiquitinyl-[E1 ubiquitin-activating enzyme]-L-cysteine + [acceptor protein]-*N*-terminal-amino acid = [E1 ubiquitin-activating enzyme]-L-cysteine + N-terminal-ubiquitinyl-[acceptor protein] (overall reaction)
(1a) *S*-ubiquitinyl-[E1 ubiquitin-activating enzyme]-L-cysteine + [N-terminal E2 ubiquitin-conjugating enzyme]-L-cysteine = [E1 ubiquitin-activating enzyme]-L-cysteine + *S*-ubiquitinyl-[N-terminal ubiquitin-conjugating enzyme]-L-cysteine
(1b) *S*-ubiquitinyl-[N-terminal E2 ubiquitin-conjugating E2 enzyme]-L-cysteine + [acceptor protein]-*N*-terminal-amino acid = [N-terminal E2 ubiquitin-conjugating enzyme]-L-cysteine + N-ubiquitinyl-[acceptor protein]-*N*-terminal amino acid

Other name(s): Ube2w; N-terminal ubiquitin-conjugating enzyme E2

Systematic name: *S*-ubiquitinyl-[E1 ubiquitin-activating enzyme]-L-cysteine:acceptor protein ubiquitin ligase (peptide bond-forming)

Comments: The enzyme ubiquitinylates the N-terminus of the acceptor protein. It is not reactive towards free lysine.

References: [386, 3477, 3052]

[EC 2.3.2.25 created 2015]

EC 2.3.2.26

Accepted name: HECT-type E3 ubiquitin transferase

Reaction: [E2 ubiquitin-conjugating enzyme]-*S*-ubiquitinyl-L-cysteine + [acceptor protein]-L-lysine = [E2 ubiquitin-conjugating enzyme]-L-cysteine + [acceptor protein]-N^6-ubiquitinyl-L-lysine (overall reaction)
(1a) [E2 ubiquitin-conjugating enzyme]-*S*-ubiquitinyl-L-cysteine + [HECT-type E3 ubiquitin transferase]-L-cysteine = [E2 ubiquitin-conjugating enzyme]-L-cysteine + [HECT-type E3 ubiquitin transferase]-*S*-ubiquitinyl-L-cysteine
(1b) [HECT-type E3 ubiquitin transferase]-*S*-ubiquitinyl-L-cysteine + [acceptor protein]-L-lysine = [HECT-type E3 ubiquitin transferase]-L-cysteine + [acceptor protein]-N^6-ubiquitinyl-L-lysine

Other name(s): HECT E3 ligase (misleading); ubiquitin transferase HECT-E3; *S*-ubiquitinyl-[HECT-type E3-ubiquitin transferase]-L-cysteine:acceptor protein ubiquitin transferase (isopeptide bond-forming)

Systematic name: [E2 ubiquitin-conjugating enzyme]-*S*-ubiquitinyl-L-cysteine:[acceptor protein] ubiquitin transferase (isopeptide bond-forming)

Comments: In the first step the enzyme transfers ubiquitin from the E2 ubiquitin-conjugating enzyme (EC 2.3.2.23) to a cysteine residue in its HECT domain (which is located in the C-terminal region), forming a thioester bond. In a subsequent step the enzyme transfers the ubiquitin to an acceptor protein, resulting in the formation of an isopeptide bond between the C-terminal glycine residue of ubiquitin and the ε-amino group of an L-lysine residue of the acceptor protein. *cf.* EC 2.3.2.27, RING-type E3 ubiquitin transferase and EC 2.3.2.31, RBR-type E3 ubiquitin transferase.

References: [2152, 2229]

[EC 2.3.2.26 created 2015, modified 2017]

EC 2.3.2.27

Accepted name: RING-type E3 ubiquitin transferase

Reaction: [E2 ubiquitin-conjugating enzyme]-*S*-ubiquitinyl-L-cysteine + [acceptor protein]-L-lysine = [E2 ubiquitin-conjugating enzyme]-L-cysteine + [acceptor protein]-N^6-ubiquitinyl-L-lysine

Other name(s): RING E3 ligase (misleading); ubiquitin transferase RING E3; *S*-ubiquitinyl-[ubiquitin-conjugating E2 enzyme]-L-cysteine:acceptor protein ubiquitin transferase (isopeptide bond-forming, RING-type)

Systematic name: [E2 ubiquitin-conjugating enzyme]-*S*-ubiquitinyl-L-cysteine:[acceptor protein] ubiquitin transferase (isopeptide bond-forming; RING-type)

Comments: RING E3 ubiquitin transferases serve as mediators bringing the ubiquitin-charged E2 ubiquitin-conjugating enzyme (EC 2.3.2.23) and an acceptor protein together to enable the direct transfer of ubiquitin through the formation of an isopeptide bond between the C-terminal glycine residue of ubiquitin and the ε-amino group of an L-lysine residue of the acceptor protein. Unlike EC 2.3.2.26, HECT-type E3 ubiquitin transferase, the RING-E3 domain does not form a catalytic thioester intermediate with ubiquitin. Many members of the RING-type E3 ubiquitin transferase family are not able to bind a substrate directly, and form a complex with a cullin scaffold protein and a substrate recognition module (the complexes are named CRL for Cullin-RING-Ligase). In these complexes, the RING-type E3 ubiquitin transferase provides an additional function, mediating the transfer of a NEDD8 protein from a dedicated E2 carrier to the cullin protein (see EC 2.3.2.32, cullin-RING-type E3 NEDD8 transferase). *cf.* EC 2.3.2.31, RBR-type E3 ubiquitin transferase.

References: [819, 2229, 2726, 2767, 2230]

[EC 2.3.2.27 created 2015, modified 2017]

EC 2.3.2.28

Accepted name: L-*allo*-isoleucyltransferase

Reaction: L-*allo*-isoleucyl-[CmaA peptidyl-carrier protein] + holo-[CmaD peptidyl-carrier protein] = L-*allo*-isoleucyl-[CmaD peptidyl-carrier protein] + holo-[CmaA peptidyl-carrier protein]

Other name(s): CmaE

Systematic name: L-*allo*-isoleucyl-[CmaA peptidyl-carrier protein]:holo-[CmaD peptidyl-carrier protein] L-*allo*-isoleucyltransferase

Comments: The enzyme, characterized from the bacterium *Pseudomonas syringae*, is involved in the biosynthesis of the toxin coronatine.

References: [3625, 3372]

[EC 2.3.2.28 created 2015]

EC 2.3.2.29

Accepted name: aspartate/glutamate leucyltransferase

Reaction: (1) L-leucyl-$tRNA^{Leu}$ + N-terminal L-glutamyl-[protein] = $tRNA^{Leu}$ + N-terminal L-leucyl-L-glutamyl-[protein]
(2) L-leucyl-$tRNA^{Leu}$ + N-terminal L-aspartyl-[protein] = $tRNA^{Leu}$ + N-terminal L-leucyl-L-aspartyl-[protein]

Other name(s): leucylD,E-transferase; *bpt* (gene name)

Systematic name: L-leucyl-tRNA^{Leu}:[protein] N-terminal L-glutamate/L-aspartate leucyltransferase

Comments: The enzyme participates in the N-end rule protein degradation pathway in certain bacteria, by attaching the primary destabilizing residue L-leucine to the N-termini of proteins that have an N-terminal L-aspartate or L-glutamate residue. Once modified, the proteins are recognized by EC 3.4.21.92, the ClpAP/ClpS endopeptidase system. *cf.* EC 2.3.2.6, lysine/arginine leucyltransferase, and EC 2.3.2.8, arginyltransferase.

References: [1122]

[EC 2.3.2.29 created 2016]

EC 2.3.2.30

Accepted name: L-ornithine N^{α}-acyltransferase

Reaction: L-ornithine + a (3*R*)-3-hydroxyacyl-[acyl-carrier protein] = a lyso-ornithine lipid + a holo-[acyl-carrier protein]

Other name(s): *olsB* (gene name)

Systematic name: L-ornithine N^{α}-(3*R*)-3-hydroxy-acyltransferase

Comments: The enzyme, found in bacteria, catalyses the first step in the biosynthesis of ornithine lipids.

References: [1008, 3659]

[EC 2.3.2.30 created 2017]

EC 2.3.2.31

Accepted name: RBR-type E3 ubiquitin transferase

Reaction: [E2 ubiquitin-conjugating enzyme]-*S*-ubiquitinyl-L-cysteine + [acceptor protein]-L-lysine = [E2 ubiquitin-conjugating enzyme]-L-cysteine + [acceptor protein]-N^6-ubiquitinyl-L-lysine (overall reaction)

(1a) [E2 ubiquitin-conjugating enzyme]-*S*-ubiquitinyl-L-cysteine + [RBR-type E3 ubiquitin transferase]-L-cysteine = [E2 ubiquitin-conjugating enzyme]-L-cysteine + [RBR-type E3 ubiquitin transferase]-*S*-ubiquitinyl-L-cysteine

(1b) [RBR-type E3 ubiquitin transferase]-*S*-ubiquitinyl-L-cysteine + [acceptor protein]-L-lysine = [RBR-type E3 ubiquitin transferase]-L-cysteine + [acceptor protein]-N^6-ubiquitinyl-L-lysine

Systematic name: [E2 ubiquitin-conjugating enzyme]-*S*-ubiquitinyl-L-cysteine:acceptor protein ubiquitin transferase (isopeptide bond-forming; RBR-type)

Comments: RBR-type E3 ubiquitin transferases have two RING fingers separated by an internal motif (IBR, for In Between RING). The enzyme interacts with the CRL (Cullin-RING ubiquitin Ligase) complexes formed by certain RING-type E3 ubiquitin transferase (see EC 2.3.2.27), which include a neddylated cullin scaffold protein and a substrate recognition module. The RING1 domain binds an EC 2.3.2.23, E2 ubiquitin-conjugating enzyme, and transfers the ubiquitin that is bound to it to an internal cysteine residue in the RING2 domain, followed by the transfer of the ubiquitin from RING2 to the substrate [3127]. Once the substrate has been ubiquitylated by the RBR-type ligase, it can be ubiqutylated further using ubiquitin carried directly on E2 enzymes, in a reaction catalysed by EC 2.3.2.27. Activity of the RBR-type enzyme is dependent on neddylation of the cullin protein in the CRL complex [1636, 3127]. *cf.* EC 2.3.2.26, HECT-type E3 ubiquitin transferase, EC 2.3.2.27, RING-type E3 ubiquitin transferase, and EC 2.3.2.32, cullin-RING-type E3 NEDD8 transferase.

References: [3821, 1636, 782, 3127]

[EC 2.3.2.31 created 2017]

EC 2.3.2.32

Accepted name: cullin-RING-type E3 NEDD8 transferase

Reaction: [E2 NEDD8-conjugating enzyme]-*S*-[NEDD8-protein]-yl-L-cysteine + [cullin]-L-lysine = [E2 NEDD8-conjugating enzyme]-L-cysteine + [cullin]-N^6-[NEDD8-protein]-yl-L-lysine

Other name(s): RBX1 (gene name)

Systematic name: [E2 NEDD8-conjugating enzyme]-*S*-[NEDD8-protein]-yl-L-cysteine:[cullin] [NEDD8-protein] transferase (isopeptide bond-forming; RING-type)

Comments: Some RING-type E3 ubiquitin transferase (EC 2.3.2.27) are not able to bind a substrate protein directly. Instead, they form a complex with a cullin scaffold protein and a substrate recognition module, which is named CRL for Cullin-RING-Ligase. The cullin protein needs to be activated by the ubiquitin-like protein NEDD8 in a process known as neddylation. The transfer of NEDD8 from a NEDD8-specific E2 enzyme onto the cullin protein is a secondary function of the RING-type E3 ubiquitin transferase in the CRL complex. The process requires auxiliary factors that belong to the DCN1 (defective in cullin neddylation 1) family.

References: [1672, 1830, 3126, 3128, 2296]

[EC 2.3.2.32 created 2017]

EC 2.3.3 Acyl groups converted into alkyl groups on transfer

EC 2.3.3.1

Accepted name: citrate (*Si*)-synthase

Reaction: acetyl-CoA + H_2O + oxaloacetate = citrate + CoA

Other name(s): (*R*)-citric synthase; citrate oxaloacetate-lyase [(*pro*-3*S*)-$CH_2COO^-\rightarrow$acetyl-CoA]

Systematic name: acetyl-CoA:oxaloacetate *C*-acetyltransferase [thioester-hydrolysing, (*pro*-*S*)-carboxymethyl forming]

Comments: The stereospecificity of this enzyme is opposite to that of EC 2.3.3.3, citrate (*Re*)-synthase, which is found in some anaerobes. Citrate synthase for which the stereospecificity with respect to C_2 of oxaloacetate has not been established are included in EC 2.3.3.16, citrate synthase.

References: [1936, 1587, 3642]

[EC 2.3.3.1 created 1961 as EC 4.1.3.7, transferred 2002 to EC 2.3.3.1, modified 2014]

EC 2.3.3.2

Accepted name: decylcitrate synthase

Reaction: lauroyl-CoA + H_2O + oxaloacetate = (2*S*,3*S*)-2-hydroxytridecane-1,2,3-tricarboxylate + CoA

Other name(s): 2-decylcitrate synthase; (2*S*,3*S*)-2-hydroxytridecane-1,2,3-tricarboxylate oxaloacetate-lyase (CoA-acylating)

Systematic name: dodecanoyl-CoA:oxaloacetate *C*-dodecanoyltransferase (thioester-hydrolysing, 1-carboxyundecyl-forming)

References: [2088, 2086]

[EC 2.3.3.2 created 1972 as EC 4.1.3.23, transferred 2002 to EC 2.3.3.2]

EC 2.3.3.3

Accepted name: citrate (*Re*)-synthase

Reaction: acetyl-CoA + H_2O + oxaloacetate = citrate + CoA

Other name(s): (*R*)-citrate synthase; *Re*-citrate-synthase; citrate oxaloacetate-lyase [(*pro*-3*R*)-$CH_2COO^-\rightarrow$acetyl-CoA]

Systematic name: acetyl-CoA:oxaloacetate *C*-acetyltransferase [thioester-hydrolysing, (*pro*-*R*)-carboxymethyl-forming]

Comments: This enzyme is inactivated by oxygen and is found in some anaerobes. Its stereospecificity is opposite to that of EC 2.3.3.1, citrate (*Si*)-synthase.

References: [742, 1113, 1114]

[EC 2.3.3.3 created 1972 as EC 4.1.3.28, transferred 2002 to EC 2.3.3.3]

EC 2.3.3.4

Accepted name: decylhomocitrate synthase

Reaction: dodecanoyl-CoA + H_2O + 2-oxoglutarate = (3*S*,4*S*)-3-hydroxytetradecane-1,3,4-tricarboxylate + CoA
Other name(s): 2-decylhomocitrate synthase; 3-hydroxytetradecane-1,3,4-tricarboxylate 2-oxoglutarate-lyase (CoA-acylating)
Systematic name: dodecanoyl-CoA:2-oxoglutarate *C*-dodecanoyltransferase (thioester-hydrolysing, 1-carboxyundecyl-forming)
Comments: Decanoyl-CoA can act instead of dodecanoyl-CoA, but 2-oxoglutarate cannot be replaced by oxaloacetate or pyruvate.
References: [2087, 377]

[EC 2.3.3.4 created 1976 as EC 4.1.3.29, transferred 2002 to EC 2.3.3.4]

EC 2.3.3.5

Accepted name: 2-methylcitrate synthase
Reaction: propanoyl-CoA + H_2O + oxaloacetate = (2*S*,3*S*)-2-hydroxybutane-1,2,3-tricarboxylate + CoA
Other name(s): 2-methylcitrate oxaloacetate-lyase; MCS; methylcitrate synthase; methylcitrate synthetase
Systematic name: propanoyl-CoA:oxaloacetate *C*-propanoyltransferase (thioester-hydrolysing, 1-carboxyethyl-forming)
Comments: The enzyme acts on acetyl-CoA, propanoyl-CoA, butanoyl-CoA and pentanoyl-CoA. The relative rate of condensation of acetyl-CoA and oxaloacetate is 140% of that of propanoyl-CoA and oxaloacetate, but the enzyme is distinct from EC 2.3.3.1, citrate (*Si*)-synthase. Oxaloacetate cannot be replaced by glyoxylate, pyruvate or 2-oxoglutarate.
References: [3596, 3509, 1375, 393, 751]

[EC 2.3.3.5 created 1978 as EC 4.1.3.31, transferred 2002 to EC 2.3.3.5, modified 2015]

EC 2.3.3.6

Accepted name: 2-ethylmalate synthase
Reaction: acetyl-CoA + H_2O + 2-oxobutanoate = (*R*)-2-ethylmalate + CoA
Other name(s): (*R*)-2-ethylmalate 2-oxobutanoyl-lyase (CoA-acetylating); 2-ethylmalate-3-hydroxybutanedioate synthase; propylmalate synthase; propylmalic synthase
Systematic name: acetyl-CoA:2-oxobutanoate *C*-acetyltransferase (thioester-hydrolysing, carboxymethyl-forming)
Comments: Also acts on (*R*)-2-(n-propyl)-malate. Formerly wrongly included with EC 2.3.3.7 3-ethylmalate synthase.
References: [3370]

[EC 2.3.3.6 created 1983 as EC 4.1.3.33, transferred 2002 to EC 2.3.3.6]

EC 2.3.3.7

Accepted name: 3-ethylmalate synthase
Reaction: butanoyl-CoA + H_2O + glyoxylate = 3-ethylmalate + CoA
Other name(s): 2-ethyl-3-hydroxybutanedioate synthase; 3-ethylmalate glyoxylate-lyase (CoA-butanoylating)
Systematic name: butanoyl-CoA:glyoxylate *C*-butanoyltransferase (thioester-hydrolysing, 1-carboxypropyl-forming)
References: [2801]

[EC 2.3.3.7 created 1965 as EC 4.1.3.10, modified 1983, transferred 2002 to EC 2.3.3.10]

EC 2.3.3.8

Accepted name: ATP citrate synthase
Reaction: ADP + phosphate + acetyl-CoA + oxaloacetate = ATP + citrate + CoA
Other name(s): ATP-citric lyase; ATP:citrate oxaloacetate-lyase [(*pro-S*)-$CH_2COO^- \rightarrow$acetyl-CoA] (ATP-dephosphorylating); acetyl-CoA:oxaloacetate acetyltransferase (isomerizing; ADP-phosphorylating); adenosine triphosphate citrate lyase; citrate cleavage enzyme; citrate-ATP lyase; citric cleavage enzyme; ATP citrate (*pro-S*)-lyase
Systematic name: acetyl-CoA:oxaloacetate *C*-acetyltransferase [(*pro-S*)-carboxymethyl-forming, ADP-phosphorylating]

Comments: The enzyme can be dissociated into components, two of which are identical with EC 4.1.3.34 (citryl-CoA lyase) and EC 6.2.1.18 (citrate—CoA ligase).
References: [1967, 3305]

[EC 2.3.3.8 created 1965 as EC 4.1.3.8, modified 1986, transferred 2002 to EC 2.3.3.8]

EC 2.3.3.9

Accepted name: malate synthase
Reaction: acetyl-CoA + glyoxylate + H_2O = (*S*)-malate + CoA
Other name(s): L-malate glyoxylate-lyase (CoA-acetylating); glyoxylate transacetylase; glyoxylate transacetase; glyoxylic transacetase; malate condensing enzyme; malate synthetase; malic synthetase; malic-condensing enzyme; acetyl-CoA:glyoxylate *C*-acetyltransferase (thioester-hydrolysing, carboxymethyl-forming)
Systematic name: acetyl-CoA:glyoxylate *C*-acetyltransferase [(*S*)-malate-forming]
Comments: The enzyme catalyses the irreversible condensation of acetyl-CoA with glyoxylate to form (*S*)-malate. Among other functions, the enzyme participates in the glyoxylate cycle, a modified version of the TCA cycle that bypasses steps that lead to a loss of CO_2.
References: [744, 2291, 92, 3257]

[EC 2.3.3.9 created 1961 as EC 4.1.3.2, transferred 2002 to EC 2.3.3.9]

EC 2.3.3.10

Accepted name: hydroxymethylglutaryl-CoA synthase
Reaction: acetyl-CoA + H_2O + acetoacetyl-CoA = (*S*)-3-hydroxy-3-methylglutaryl-CoA + CoA
Other name(s): (*S*)-3-hydroxy-3-methylglutaryl-CoA acetoacetyl-CoA-lyase (CoA-acetylating); 3-hydroxy-3-methylglutaryl CoA synthetase; 3-hydroxy-3-methylglutaryl coenzyme A synthase; 3-hydroxy-3-methylglutaryl coenzyme A synthetase; 3-hydroxy-3-methylglutaryl-CoA synthase; 3-hydroxy-3-methylglutaryl-coenzyme A synthase; β-hydroxy-β-methylglutaryl-CoA synthase; HMG-CoA synthase; acetoacetyl coenzyme A transacetase; hydroxymethylglutaryl coenzyme A synthase; hydroxymethylglutaryl coenzyme A-condensing enzyme
Systematic name: acetyl-CoA:acetoacetyl-CoA *C*-acetyltransferase (thioester-hydrolysing, carboxymethyl-forming)
References: [2961]

[EC 2.3.3.10 created 1961 as EC 4.1.3.5, transferred 2002 to EC 2.3.3.10]

EC 2.3.3.11

Accepted name: 2-hydroxyglutarate synthase
Reaction: propanoyl-CoA + H_2O + glyoxylate = 2-hydroxyglutarate + CoA
Other name(s): 2-hydroxyglutaratic synthetase; 2-hydroxyglutaric synthetase; α-hydroxyglutarate synthase; hydroxyglutarate synthase; 2-hydroxyglutarate glyoxylate-lyase (CoA-propanoylating)
Systematic name: propanoyl-CoA:glyoxylate *C*-propanoyltransferase (thioester-hydrolysing, 2-carboxyethyl-forming)
References: [2848]

[EC 2.3.3.11 created 1965 as EC 4.1.3.9, transferred 2002 to EC 2.3.3.11]

EC 2.3.3.12

Accepted name: 3-propylmalate synthase
Reaction: pentanoyl-CoA + H_2O + glyoxylate = 3-propylmalate + CoA
Other name(s): 3-(n-propyl)-malate synthase; 3-propylmalate glyoxylate-lyase (CoA-pentanoylating); β-n-propylmalate synthase; n-propylmalate synthase
Systematic name: pentanoyl-CoA:glyoxylate *C*-pentanoyltransferase (thioester-hydrolysing, 1-carboxybutyl-forming)
References: [1441]

[EC 2.3.3.12 created 1972 as EC 4.1.3.11, transferred 2002 to EC 2.3.3.12]

EC 2.3.3.13

Accepted name: 2-isopropylmalate synthase

Reaction: acetyl-CoA + 3-methyl-2-oxobutanoate + H_2O = (2*S*)-2-isopropylmalate + CoA

Other name(s): 3-carboxy-3-hydroxy-4-methylpentanoate 3-methyl-2-oxobutanoate-lyase (CoA-acetylating); α-isopropylmalate synthetase; α-isopropylmalate synthase; α-isopropylmalic synthetase; isopropylmalate synthase; isopropylmalate synthetase

Systematic name: acetyl-CoA:3-methyl-2-oxobutanoate *C*-acetyltransferase (thioester-hydrolysing, carboxymethyl-forming)

Comments: Requires K^+.

References: [1737, 3798, 589]

[EC 2.3.3.13 created 1972 as EC 4.1.3.12, transferred 2002 to EC 2.3.3.13]

EC 2.3.3.14

Accepted name: homocitrate synthase

Reaction: acetyl-CoA + H_2O + 2-oxoglutarate = (2*R*)-2-hydroxybutane-1,2,4-tricarboxylate + CoA

Other name(s): 2-hydroxybutane-1,2,4-tricarboxylate 2-oxoglutarate-lyase (CoA-acetylating); acetyl-coenzyme A:2-ketoglutarate C-acetyl transferase; homocitrate synthetase; HCS

Systematic name: acetyl-CoA:2-oxoglutarate *C*-acetyltransferase (thioester-hydrolysing, carboxymethyl forming)

Comments: Belongs in the α-aminoadipate pathway of lysine synthesis, along with EC 4.2.1.36, homoaconitate hydratase. The enzyme also acts with oxaloacetate as substrate, but more slowly [3909, 84].

References: [3369, 3909, 84]

[EC 2.3.3.14 created 1972 as EC 4.1.3.21, transferred 2002 to EC 2.3.3.14]

EC 2.3.3.15

Accepted name: sulfoacetaldehyde acetyltransferase

Reaction: acetyl phosphate + sulfite = 2-sulfoacetaldehyde + phosphate

Other name(s): Xsc

Systematic name: acetyl-phosphate:sulfite *S*-acetyltransferase (acyl-phosphate hydrolysing, 2-oxoethyl-forming)

Comments: The reaction occurs in the reverse direction to that shown above. Requires Mg^{2+}.

References: [2967]

[EC 2.3.3.15 created 2003]

EC 2.3.3.16

Accepted name: citrate synthase (unknown stereospecificity)

Reaction: acetyl-CoA + H_2O + oxaloacetate = citrate + CoA

Other name(s): citrate condensing enzyme; CoA-acetylating citrate oxaloacetate-lyase; citrate synthetase; citric synthase; citric-condensing enzyme; citrogenase; condensing enzyme (ambiguous); oxaloacetate transacetase; oxalacetic transacetase

Systematic name: acetyl-CoA:oxaloacetate *C*-acetyltransferase (thioester-hydrolysing)

Comments: This entry has been included to accommodate those citrate synthases for which the stereospecificity with respect to C_2 of oxaloacetate has not been established [*cf.* EC 2.3.3.1, citrate (*Si*)-synthase and EC 2.3.3.3, citrate (*Re*)-synthase].

References: [2028, 3223, 262, 1901, 2174]

[EC 2.3.3.16 created 2014]

EC 2.3.3.17

Accepted name: methylthioalkylmalate synthase
Reaction: an ω-(methylsulfanyl)-2-oxoalkanoate + acetyl-CoA + H_2O = a 2-[ω-(methylsulfanyl)alkyl]malate + CoA
Other name(s): MAM1 (gene name); MAM3 (gene name); acetyl-CoA:ω-(methylthio)-2-oxoalkanoate *C*-acetyltransferase
Systematic name: acetyl-CoA:ω-(methylsulfanyl)-2-oxoalkanoate *C*-acetyltransferase
Comments: The enzyme, characterized from the plant *Arabidopsis thaliana*, is involved in the L-methionine side-chain elongation pathway, forming substrates for the biosynthesis of aliphatic glucosinolates. Two forms are known - MAM1 catalyses only only the first two rounds of methionine chain elongation, while MAM3 catalyses all six cycles, up to formation of L-hexahomomethionine.
References: [3507, 3508]

[EC 2.3.3.17 created 2016]

EC 2.3.3.18
Accepted name: 2-phosphinomethylmalate synthase
Reaction: acetyl-CoA + H_2O + 3-(hydroxyphosphinoyl)pyruvate = phosphinomethylmalate + CoA
Other name(s): *pmmS* (gene name)
Systematic name: acetyl-CoA:phosphinopyruvate C-acetyltransferase (thioester-hydrolysing, phosphinomethylmalate-forming)
Comments: The enzyme, characterized from the bacterium *Streptomyces hygroscopicus*, participates in the pathway for bialaphos biosynthesis. It requires a divalent metal ion and can also act on oxaloacetate.
References: [3199, 3198]

[EC 2.3.3.18 created 2017]

EC 2.3.3.19
Accepted name: 2-phosphonomethylmalate synthase
Reaction: acetyl-CoA + H_2O + 3-phosphonopyruvate = (*R*)-2-(phosphonomethyl)malate + CoA
Other name(s): 2-phosphinomethylmalic acid synthase; PMM synthase
Systematic name: acetyl-CoA:3-phosphonopyruvate *C*-acetyltransferase
Comments: The enzyme, isolated from several *Streptomyces* species, participate in the biosynthesis of certain phosphonate antibiotics. The enzyme is analogous to EC 2.3.3.1 (*Si*)-citrate synthase.
References: [3197, 3199, 829]

[EC 2.3.3.19 created 2017]

EC 2.3.3.20
Accepted name: acyl-CoA:acyl-CoA alkyltransferase
Reaction: **2** an acyl-CoA + H_2O = a (2*R*)-2-alkyl-3-oxoalkanoate + **2** CoA
Other name(s): *oleA* (gene name)
Systematic name: acyl-CoA:acyl-CoA alkyltransferase [(2*R*)-2-alkyl-3-oxoalkanoate-forming]
Comments: The enzyme, found in certain bacterial species, catalyses a head-to-head non-decarboxylative Claisen condensation of two acyl-CoA molecules, resulting in formation of a 2-alkyl-3-oxoalkanoic acid. It is part of a pathway for the production of olefins.
References: [3383, 959, 1082, 1083]

[EC 2.3.3.20 created 2018]

EC 2.4 Glycosyltransferases

This subclass contains enzymes that transfer glycosyl groups. Some of these enzymes also catalyse hydrolysis, which can be regarded as transfer of a glycosyl group from the donor to water. Also, inorganic phosphate can act as acceptor in the case of phosphorylases; phosphorolysis of glycogen is regarded as transfer of one sugar residue from glycogen to phosphate. However, the more general case is the transfer of a sugar from an oligosaccharide or a high-energy compound to another carbohydrate molecule that acts as the acceptor. Sub-subclasses are based on the type of sugar residue being transferred: hexosyltransferases (EC 2.4.1), pentosyltransferases (EC 2.4.2) and other glycosyl groups (EC 2.4.99).

EC 2.4.1 Hexosyltransferases

EC 2.4.1.1

Accepted name: glycogen phosphorylase

Reaction: [(1→4)-α-D-glucosyl]$_n$ + phosphate = [(1→4)-α-D-glucosyl]$_{n-1}$ + α-D-glucose 1-phosphate

Other name(s): muscle phosphorylase *a* and *b*; amylophosphorylase; polyphosphorylase; amylopectin phosphorylase; glucan phosphorylase; α-glucan phosphorylase; 1,4-α-glucan phosphorylase; glucosan phosphorylase; granulose phosphorylase; maltodextrin phosphorylase; muscle phosphorylase; myophosphorylase; potato phosphorylase; starch phosphorylase; 1,4-α-D-glucan:phosphate α-D-glucosyltransferase; phosphorylase (ambiguous)

Systematic name: (1→4)-α-D-glucan:phosphate α-D-glucosyltransferase

Comments: This entry covers several enzymes from different sources that act *in vivo* on different forms of (1→4)-α-D-glucans. Some of these enzymes catalyse the first step in the degradation of large branched glycan polymers - the phosphorolytic cleavage of α-1,4-glucosidic bonds from the non-reducing ends of linear poly(1→4)-α-D-glucosyl chains within the polymers. The enzyme stops when it reaches the fourth residue away from an α-1,6 branching point, leaving a highly branched core known as a limit dextrin. The accepted name of the enzyme should be modified for each specific instance by substituting ”glycogen” with the name of the natural substrate, e.g. maltodextrin phosphorylase, starch phosphorylase, etc.

References: [1210, 1129, 238, 623, 523, 905]

[EC 2.4.1.1 created 1961, modified 2013]

EC 2.4.1.2

Accepted name: dextrin dextranase

Reaction: [(1→4)-α-D-glucosyl]$_n$ + [(1→6)-α-D-glucosyl]$_m$ = [(1→4)-α-D-glucosyl]$_{n-1}$ + [(1→6)-α-D-glucosyl]$_{m+1}$

Other name(s): dextrin 6-glucosyltransferase; dextran dextrinase; 1,4-α-D-glucan:1,6-α-D-glucan 6-α-D-glucosyltransferase

Systematic name: (1→4)-α-D-glucan:(1→6)-α-D-glucan 6-α-D-glucosyltransferase

References: [1271, 1272, 1273]

[EC 2.4.1.2 created 1961]

[2.4.1.3 Deleted entry. amylomaltase. Now included with EC 2.4.1.25, 4-α-glucanotransferase]

[EC 2.4.1.3 created 1961, deleted 1972]

EC 2.4.1.4

Accepted name: amylosucrase

Reaction: sucrose + [(1→4)-α-D-glucosyl]$_n$ = D-fructose + [(1→4)-α-D-glucosyl]$_{n+1}$

Other name(s): sucrose—glucan glucosyltransferase; sucrose-1,4-α-glucan glucosyltransferase; sucrose:1,4-α-D-glucan 4-α-D-glucosyltransferase

Systematic name: sucrose:(1→4)-α-D-glucan 4-α-D-glucosyltransferase

References: [885, 1271, 1274]

[EC 2.4.1.4 created 1961]

EC 2.4.1.5

Accepted name: dextransucrase
Reaction: sucrose + [(1→6)-α-D-glucosyl]$_{n}$ = D-fructose + [(1→6)-α-D-glucosyl]$_{n+1}$
Other name(s): sucrose 6-glucosyltransferase; SGE; CEP; sucrose-1,6-α-glucan glucosyltransferase; sucrose:1,6-α-D-glucan 6-α-D-glucosyltransferase
Systematic name: sucrose:(1→6)-α-D-glucan 6-α-D-glucosyltransferase
References: [165, 166, 1271]

[EC 2.4.1.5 created 1961]

[2.4.1.6 Deleted entry. maltose 3-glycosyltransferase]

[EC 2.4.1.6 created 1961, deleted 1972]

EC 2.4.1.7

Accepted name: sucrose phosphorylase
Reaction: sucrose + phosphate = D-fructose + α-D-glucose 1-phosphate
Other name(s): sucrose glucosyltransferase; disaccharide glucosyltransferase
Systematic name: sucrose:phosphate α-D-glucosyltransferase
Comments: In the forward reaction, arsenate may replace phosphate. In the reverse reaction, various ketoses and L-arabinose may replace D-fructose.
References: [759, 1243, 3228]

[EC 2.4.1.7 created 1961]

EC 2.4.1.8

Accepted name: maltose phosphorylase
Reaction: maltose + phosphate = D-glucose + β-D-glucose 1-phosphate
Systematic name: maltose:phosphate 1-β-D-glucosyltransferase
References: [759, 909, 2776, 3889]

[EC 2.4.1.8 created 1961]

EC 2.4.1.9

Accepted name: inulosucrase
Reaction: sucrose + [(2→1)-β-D-fructosyl]$_{n}$ = glucose + [(2→1)-β-D-fructosyl]$_{n+1}$
Other name(s): sucrose 1-fructosyltransferase; sucrose:2,1-β-D-fructan 1-β-D-fructosyltransferase
Systematic name: sucrose:(2→1)-β-D-fructan 1-β-D-fructosyltransferase
Comments: Converts sucrose into inulin and D-glucose. Some other sugars can act as D-fructosyl acceptors.
References: [302, 700, 806]

[EC 2.4.1.9 created 1961]

EC 2.4.1.10

Accepted name: levansucrase
Reaction: sucrose + [6)-β-D-fructofuranosyl-(2→]$_{n}$ α-D-glucopyranoside = D-glucose + [6)-β-D-fructofuranosyl-(2→]$_{n+1}$ α-D-glucopyranoside
Other name(s): sucrose 6-fructosyltransferase; β-2,6-fructosyltransferase; β-2,6-fructan:D-glucose 1-fructosyltransferase; sucrose:2,6-β-D-fructan 6-β-D-fructosyltransferase; sucrose:(2→6)-β-D-fructan 6-β-D-fructosyltransferase
Systematic name: sucrose:[6)-β-D-fructofuranosyl-(2→]$_{n}$ α-D-glucopyranoside 6-β-D-fructosyltransferase
Comments: Some other sugars can act as D-fructosyl acceptors.
References: [1271, 1313, 2846, 2220]

[EC 2.4.1.10 created 1961, modified 2011]

EC 2.4.1.11

Accepted name: glycogen(starch) synthase

Reaction: UDP-α-D-glucose + [(1→4)-α-D-glucosyl]$_n$ = UDP + [(1→4)-α-D-glucosyl]$_{n+1}$

Other name(s): UDP-glucose—glycogen glucosyltransferase; glycogen (starch) synthetase; UDP-glucose-glycogen glucosyltransferase; UDP-glycogen synthase; UDPG-glycogen synthetase; UDPG-glycogen transglucosylase; uridine diphosphoglucose-glycogen glucosyltransferase; UDP-glucose:glycogen 4-α-D-glucosyltransferase

Systematic name: UDP-α-D-glucose:glycogen 4-α-D-glucosyltransferase (configuration-retaining)

Comments: The accepted name varies according to the source of the enzyme and the nature of its synthetic product (*cf.* EC 2.4.1.1, phosphorylase). Glycogen synthase from animal tissues is a complex of a catalytic subunit and the protein glycogenin. The enzyme requires glucosylated glycogenin as a primer; this is the reaction product of EC 2.4.1.186 (glycogenin glucosyltransferase). A similar enzyme utilizes ADP-glucose (EC 2.4.1.21, starch synthase).

References: [57, 218, 1928, 1930, 2720]

[EC 2.4.1.11 created 1961]

EC 2.4.1.12

Accepted name: cellulose synthase (UDP-forming)

Reaction: UDP-α-D-glucose + [(1→4)-β-D-glucosyl]$_n$ = UDP + [(1→4)-β-D-glucosyl]$_{n+1}$

Other name(s): UDP-glucose—β-glucan glucosyltransferase; UDP-glucose-cellulose glucosyltransferase; GS-I; β-1,4-glucosyltransferase; uridine diphosphoglucose-1,4-β-glucan glucosyltransferase; β-1,4-glucan synthase; β-1,4-glucan synthetase; β-glucan synthase; 1,4-β-D-glucan synthase; 1,4-β-glucan synthase; glucan synthase; UDP-glucose-1,4-β-glucan glucosyltransferase; uridine diphosphoglucose-cellulose glucosyltransferase; UDP-glucose:1,4-β-D-glucan 4-β-D-glucosyltransferase; UDP-glucose:(1→4)-β-D-glucan 4-β-D-glucosyltransferase

Systematic name: UDP-α-D-glucose:(1→4)-β-D-glucan 4-β-D-glucosyltransferase (configuration-inverting)

Comments: Involved in the synthesis of cellulose. A similar enzyme utilizes GDP-glucose [EC 2.4.1.29 cellulose synthase (GDP-forming)].

References: [1069]

[EC 2.4.1.12 created 1961]

EC 2.4.1.13

Accepted name: sucrose synthase

Reaction: NDP-α-D-glucose + D-fructose = NDP + sucrose

Other name(s): UDPglucose-fructose glucosyltransferase; sucrose synthetase; sucrose-UDP glucosyltransferase; sucrose-uridine diphosphate glucosyltransferase; uridine diphosphoglucose-fructose glucosyltransferase; NDP-glucose:D-fructose 2-α-D-glucosyltransferase

Systematic name: NDP-α-D-glucose:D-fructose 2-α-D-glucosyltransferase (configuration-retaining)

Comments: Although UDP is generally considered to be the preferred nucleoside diphosphate for sucrose synthase, numerous studies have shown that ADP serves as an effective acceptor molecule to produce ADP-glucose [704, 2373, 2400, 2742, 2938, 3229, 3463]. Sucrose synthase has a dual role in producing both UDP-glucose (necessary for cell wall and glycoprotein biosynthesis) and ADP-glucose (necessary for starch biosynthesis) [202].

References: [132, 477, 704, 2373, 2400, 2742, 2938, 3229, 3463, 202]

[EC 2.4.1.13 created 1961, modified 2003]

EC 2.4.1.14

Accepted name: sucrose-phosphate synthase

Reaction: UDP-α-D-glucose + D-fructose 6-phosphate = UDP + sucrose 6^{F}-phosphate

Other name(s): UDP-glucose—fructose-phosphate glucosyltransferase; sucrosephosphate—UDP glucosyltransferase; UDP-glucose-fructose-phosphate glucosyltransferase; SPS; uridine diphosphoglucose-fructose phosphate glucosyltransferase; sucrose 6-phosphate synthase; sucrose phosphate synthetase; sucrose phosphate-uridine diphosphate glucosyltransferase; sucrose phosphate synthase; UDP-glucose:D-fructose-6-phosphate 2-α-D-glucosyltransferase

Systematic name: UDP-α-D-glucose:D-fructose-6-phosphate 2-α-D-glucosyltransferase (configuration-retaining)

Comments: Requires Mg^{2+} or Mn^{2+} for maximal activity [646]. The enzyme from *Synechocystis* sp. strain PCC 6803 is not specific for UDP-glucose as it can use ADP-glucose and, to a lesser extent, GDP-glucose as substrates [646]. The enzyme from rice leaves is activated by glucose 6-phosphate but that from cyanobacterial species is not [646]. While the reaction catalysed by this enzyme is reversible, the enzyme usually works in concert with EC 3.1.3.24, sucrose-phosphate phosphatase, to form sucrose, making the above reaction essentially irreversible [1400]. The F in sucrose 6^{F}-phosphate is used to indicate that the fructose residue of sucrose carries the substituent.

References: [2214, 646, 1400, 641, 560]

[EC 2.4.1.14 created 1961, modified 2008]

EC 2.4.1.15

Accepted name: α,α-trehalose-phosphate synthase (UDP-forming)

Reaction: UDP-α-D-glucose + D-glucose 6-phosphate = UDP + α,α-trehalose 6-phosphate

Other name(s): UDP-glucose—glucose-phosphate glucosyltransferase; trehalosephosphate-UDP glucosyltransferase; UDP-glucose-glucose-phosphate glucosyltransferase; α,α-trehalose phosphate synthase (UDP-forming); phosphotrehalose-uridine diphosphate transglucosylase; trehalose 6-phosphate synthase; trehalose 6-phosphate synthetase; trehalose phosphate synthase; trehalose phosphate synthetase; trehalose phosphate-uridine diphosphate glucosyltransferase; trehalose-*P* synthetase; transglucosylase; uridine diphosphoglucose phosphate glucosyltransferase; UDP-glucose:D-glucose-6-phosphate 1-α-D-glucosyltransferase

Systematic name: UDP-α-D-glucose:D-glucose-6-phosphate 1-α-D-glucosyltransferase (configuration-retaining)

Comments: See also EC 2.4.1.36 [α,α-trehalose-phosphate synthase (GDP-forming)].

References: [449, 465, 2037, 2378]

[EC 2.4.1.15 created 1961]

EC 2.4.1.16

Accepted name: chitin synthase

Reaction: UDP-*N*-acetyl-α-D-glucosamine + [(1→4)-*N*-acetyl-β-D-glucosaminyl]$_{n}$ = UDP + [(1→4)-*N*-acetyl-β-D-glucosaminyl]$_{n+1}$

Other name(s): chitin-UDP *N*-acetylglucosaminyltransferase; chitin-uridine diphosphate acetylglucosaminyltransferase; chitin synthetase; *trans*-*N*-acetylglucosaminosylase; UDP-*N*-acetyl-D-glucosamine:chitin 4-β-*N*-acetylglucosaminyl-transferase; UDP-*N*-acetyl-α-D-glucosamine:chitin 4-β-*N*-acetylglucosaminyltransferase

Systematic name: UDP-*N*-acetyl-α-D-glucosamine:chitin 4-β-*N*-acetylglucosaminyltransferase (configuration-inverting)

Comments: Converts UDP-*N*-acetyl-α-D-glucosamine into chitin and UDP.

References: [1070, 3051]

[EC 2.4.1.16 created 1961]

EC 2.4.1.17

Accepted name: glucuronosyltransferase

Reaction: UDP-α-D-glucuronate + acceptor = UDP + acceptor β-D-glucuronoside

Other name(s): 1-naphthol glucuronyltransferase; 1-naphthol-UDP-glucuronosyltransferase; 17β-hydroxysteroid UDP-glucuronosyltransferase; 3α-hydroxysteroid UDP-glucuronosyltransferase; 4-hydroxybiphenyl UDP-glucuronosyltransferase; 4-methylumbelliferone UDP-glucuronosyltransferase; 4-nitrophenol UDP-glucuronyltransferase; 4-nitrophenol UDPGT; 17-OH steroid UDPGT; 3-OH androgenic UDPGT; bilirubin uridine diphosphoglucuronyltransferase; bilirubin UDP-glucuronosyltransferase; bilirubin monoglucuronide glucuronyltransferase; bilirubin UDPGT; bilirubin glucuronyltransferase; ciramadol UDP-glucuronyltransferase; estriol UDP-glucuronosyltransferase; estrone UDP-glucuronosyltransferase; uridine diphosphoglucuronosyltransferase; uridine diphosphoglucuronate-bilirubin glucuronoside glucuronosyltransferase; uridine diphosphoglucuronate-bilirubin glucuronosyltransferase; uridine diphosphoglucuronate-estriol glucuronosyltransferase; uridine diphosphoglucuronate-estradiol glucuronosyltransferase; uridine diphosphoglucuronate-4-hydroxybiphenyl glucuronosyltransferase; uridine diphosphoglucuronate-1,2-diacylglycerol glucuronosyltransferase; uridine diphosphoglucuronate-estriol 16α-glucuronosyltransferase; GT; morphine glucuronyltransferase; *p*-hydroxybiphenyl UDP glucuronyltransferase; *p*-nitrophenol UDP-glucuronosyltransferase; *p*-nitrophenol UDP-glucuronyltransferase; *p*-nitrophenylglucuronosyltransferase; *p*-phenylphenol glucuronyltransferase; phenyl-UDP-glucuronosyltransferase; PNP-UDPGT; UDP glucuronate-estradiol-glucuronosyltransferase; UDP glucuronosyltransferase; UDP glucuronate-estriol glucuronosyltransferase; UDP glucuronic acid transferase; UDP glucuronyltransferase; UDP-glucuronate-4-hydroxybiphenyl glucuronosyltransferase; UDP-glucuronate-bilirubin glucuronyltransferase; UDP-glucuronosyltransferase; UDP-glucuronyltransferase; UDPGA transferase; UDPGA-glucuronyltransferase; UDPGT; uridine diphosphoglucuronyltransferase; uridine diphosphate glucuronyltransferase; uridine 5′-diphosphoglucuronyltransferase; UDP-glucuronate β-D-glucuronosyltransferase (acceptor-unspecific)

Systematic name: UDP-α-D-glucuronate β-D-glucuronosyltransferase (acceptor-unspecific; configuration-inverting)

Comments: This entry denotes a family of enzymes accepting a wide range of substrates, including phenols, alcohols, amines and fatty acids. Some of the activities catalysed were previously listed separately as EC 2.4.1.42, EC 2.4.1.59, EC 2.4.1.61, EC 2.4.1.76, EC 2.4.1.77, EC 2.4.1.84, EC 2.4.1.107 and EC 2.4.1.108. A temporary nomenclature for the various forms, whose delineation is in a state of flux, is suggested in Ref. 1.

References: [339, 340, 422, 799, 1131, 1500]

[EC 2.4.1.17 created 1961 (EC 2.4.1.42, EC 2.4.1.59 and EC 2.4.1.61 all created 1972, EC 2.4.1.76, EC 2.4.1.77 and EC 2.4.1.84 all created 1976, EC 2.4.1.107 and EC 2.4.1.108 both created 1983, all incorporated 1984)]

EC 2.4.1.18

Accepted name: 1,4-α-glucan branching enzyme

Reaction: Transfers a segment of a (1→4)-α-D-glucan chain to a primary hydroxy group in a similar glucan chain

Other name(s): branching enzyme; amylo-(1,4→1,6)-transglycosylase; Q-enzyme; α-glucan-branching glycosyltransferase; amylose isomerase; enzymatic branching factor; branching glycosyltransferase; enzyme Q; glucosan transglycosylase; glycogen branching enzyme; plant branching enzyme; α-1,4-glucan:α-1,4-glucan-6-glycosyltransferase; starch branching enzyme; 1,4-α-D-glucan:1,4-α-D-glucan 6-α-D-(1,4-α-D-glucano)-transferase

Systematic name: (1→4)-α-D-glucan:(1→4)-α-D-glucan 6-α-D-[(1→4)-α-D-glucano]-transferase

Comments: Converts amylose into amylopectin. The accepted name requires a qualification depending on the product, glycogen or amylopectin, e.g. glycogen branching enzyme, amylopectin branching enzyme. The latter has frequently been termed Q-enzyme.

References: [195, 238, 1271, 402]

[EC 2.4.1.18 created 1961]

EC 2.4.1.19

Accepted name: cyclomaltodextrin glucanotransferase

Reaction: Cyclizes part of a (1→4)-α-D-glucan chain by formation of a (1→4)-α-D-glucosidic bond

Other name(s): *Bacillus macerans* amylase; cyclodextrin glucanotransferase; α-cyclodextrin glucanotransferase; α-cyclodextrin glycosyltransferase; β-cyclodextrin glucanotransferase; β-cyclodextrin glycosyltransferase; γ-cyclodextrin glycosyltransferase; cyclodextrin glycosyltransferase; cyclomaltodextrin glucotransferase; cyclomaltodextrin glycosyltransferase; konchizaimu; α-1,4-glucan 4-glycosyltransferase, cyclizing; BMA; CGTase; neutral-cyclodextrin glycosyltransferase; 1,4-α-D-glucan 4-α-D-(1,4-α-D-glucano)-transferase (cyclizing)
Systematic name: (1→4)-α-D-glucan:(1→4)-α-D-glucan 4-α-D-[(1→4)-α-D-glucano]-transferase (cyclizing)
Comments: Cyclomaltodextrins (*Schardinger dextrins*) of various sizes (6,7,8, etc. glucose units) are formed reversibly from starch and similar substrates. Will also disproportionate linear maltodextrins without cyclizing (*cf.* EC 2.4.1.25, 4-α-glucanotransferase).
References: [716, 953, 1271, 3122]

[EC 2.4.1.19 created 1961]

EC 2.4.1.20

Accepted name: cellobiose phosphorylase
Reaction: cellobiose + phosphate = α-D-glucose 1-phosphate + D-glucose
Systematic name: cellobiose:phosphate α-D-glucosyltransferase
References: [54, 144]

[EC 2.4.1.20 created 1965]

EC 2.4.1.21

Accepted name: starch synthase (glycosyl-transferring)
Reaction: ADP-α-D-glucose + [(1→4)-α-D-glucosyl]$_n$ = ADP + [(1→4)-α-D-glucosyl]$_{n+1}$
Other name(s): ADP-glucose—starch glucosyltransferase; adenosine diphosphate glucose-starch glucosyltransferase; adenosine diphosphoglucose-starch glucosyltransferase; ADP-glucose starch synthase; ADP-glucose synthase; ADP-glucose transglucosylase; ADP-glucose-starch glucosyltransferase; ADPG starch synthetase; ADPG-starch glucosyltransferase; starch synthetase; ADP-glucose:1,4-α-D-glucan 4-α-D-glucosyltransferase
Systematic name: ADP-α-D-glucose:(1→4)-α-D-glucan 4-α-D-glucosyltransferase
Comments: The accepted name varies according to the source of the enzyme and the nature of its synthetic product, e.g. starch synthase, bacterial glycogen synthase. Similar to EC 2.4.1.11 [glycogen(starch) synthase] but the preferred or mandatory nucleoside diphosphate sugar substrate is ADP-α-D-glucose. The entry covers starch and glycogen synthases utilizing ADP-α-D-glucose.
References: [499, 974, 1133, 1929, 2757]

[EC 2.4.1.21 created 1965]

EC 2.4.1.22

Accepted name: lactose synthase
Reaction: UDP-α-D-galactose + D-glucose = UDP + lactose
Other name(s): UDP-galactose—glucose galactosyltransferase; *N*-acetyllactosamine synthase; uridine diphosphogalactose-glucose galactosyltransferase; lactose synthetase; UDP-galactose:D-glucose 4-β-D-galactotransferase; UDP-galactose:D-glucose 4-β-D-galactosyltransferase
Systematic name: UDP-α-D-galactose:D-glucose 4-β-D-galactosyltransferase
Comments: The enzyme is a complex of two proteins, A and B. In the absence of the B protein (α-lactalbumin), the enzyme catalyses the transfer of galactose from UDP-α-D-galactose to *N*-acetylglucosamine (EC 2.4.1.90 *N*-acetyllactosamine synthase).
References: [910, 1330, 3787]

[EC 2.4.1.22 created 1965]

EC 2.4.1.23

Accepted name: sphingosine β-galactosyltransferase

Reaction: UDP-α-D-galactose + sphingosine = UDP + psychosine

Other name(s): psychosine—UDP galactosyltransferase; galactosyl-sphingosine transferase; psychosine-uridine diphosphate galactosyltransferase; UDP-galactose:sphingosine *O*-galactosyl transferase; uridine diphosphogalactose-sphingosine β-galactosyltransferase; UDP-galactose:sphingosine 1-β-galactotransferase; UDP-galactose:sphingosine 1-β-galactosyltransferase

Systematic name: UDP-α-D-galactose:sphingosine 1-β-galactosyltransferase

References: [584]

[EC 2.4.1.23 created 1965]

EC 2.4.1.24

Accepted name: 1,4-α-glucan 6-α-glucosyltransferase

Reaction: Transfers an α-D-glucosyl residue in a (1→4)-α-D-glucan to the primary hydroxy group of glucose, free or combined in a (1→4)-α-D-glucan

Other name(s): oligoglucan-branching glycosyltransferase; 1,4-α-D-glucan 6-α-D-glucosyltransferase; T-enzyme; D-glucosyltransferase; 1,4-α-D-glucan:1,4-α-D-glucan(D-glucose) 6-α-D-glucosyltransferase

Systematic name: (1→4)-α-D-glucan:(1→4)-α-D-glucan(D-glucose) 6-α-D-glucosyltransferase

References: [2, 196, 3026]

[EC 2.4.1.24 created 1965]

EC 2.4.1.25

Accepted name: 4-α-glucanotransferase

Reaction: Transfers a segment of a (1→4)-α-D-glucan to a new position in an acceptor, which may be glucose or a (1→4)-α-D-glucan

Other name(s): disproportionating enzyme; dextrin glycosyltransferase; D-enzyme; debranching enzyme maltodextrin glycosyltransferase; amylomaltase; dextrin transglycosylase; 1,4-α-D-glucan:1,4-α-D-glucan 4-α-D-glycosyltransferase

Systematic name: (1→4)-α-D-glucan:(1→4)-α-D-glucan 4-α-D-glycosyltransferase

Comments: This entry covers the former separate entry for EC 2.4.1.3 (amylomaltase). The plant enzyme has been termed D-enzyme. An enzymic activity of this nature forms part of the mammalian and yeast glycogen debranching system (see EC 3.2.1.33 amylo-α-1,6-glucosidase).

References: [1271, 2068, 2649, 3728, 3830]

[EC 2.4.1.25 created 1965 (EC 2.4.1.3 created 1961, incorporated 1972)]

EC 2.4.1.26

Accepted name: DNA α-glucosyltransferase

Reaction: Transfers an α-D-glucosyl residue from UDP-glucose to an hydroxymethylcytosine residue in DNA

Other name(s): uridine diphosphoglucose-deoxyribonucleate α-glucosyltransferase; UDP-glucose-DNA α-glucosyltransferase; uridine diphosphoglucose-deoxyribonucleate α-glucosyltransferase; T_2-HMC-α-glucosyl transferase; T_4-HMC-α-glucosyl transferase; T_6-HMC-α-glucosyl transferase

Systematic name: UDP-glucose:DNA α-D-glucosyltransferase

References: [1762]

[EC 2.4.1.26 created 1965]

EC 2.4.1.27

Accepted name: DNA β-glucosyltransferase

Reaction: Transfers a β-D-glucosyl residue from UDP-α-D-glucose to an hydroxymethylcytosine residue in DNA

Other name(s): T_4-HMC-β-glucosyl transferase; T_4-β-glucosyl transferase; T4 phage β-glucosyltransferase; UDP glucose-DNA β-glucosyltransferase; uridine diphosphoglucose-deoxyribonucleate β-glucosyltransferase; UDP-glucose:DNA β-D-glucosyltransferase
Systematic name: UDP-α-D-glucose:DNA β-D-glucosyltransferase (configuration-inverting)
References: [1762]

[EC 2.4.1.27 created 1965]

EC 2.4.1.28

Accepted name: glucosyl-DNA β-glucosyltransferase
Reaction: Transfers a β-D-glucosyl residue from UDP-α-D-glucose to a glucosylhydroxymethylcytosine residue in DNA
Other name(s): T_6-glucosyl-HMC-β-glucosyl transferase; T_6-β-glucosyl transferase; uridine diphosphoglucose-glucosyldeoxyribonucleate β-glucosyltransferase
Systematic name: UDP-α-D-glucose:D-glucosyl-DNA β-D-glucosyltransferase (configuration-inverting)
References: [1762]

[EC 2.4.1.28 created 1965]

EC 2.4.1.29

Accepted name: cellulose synthase (GDP-forming)
Reaction: GDP-α-D-glucose + [(1→4)-β-D-glucosyl]$_n$ = GDP + [(1→4)-β-D-glucosyl]$_{n+1}$
Other name(s): cellulose synthase (guanosine diphosphate-forming); cellulose synthetase; guanosine diphosphoglucose-1,4-β-glucan glucosyltransferase; guanosine diphosphoglucose-cellulose glucosyltransferase; GDP-glucose:1,4-β-D-glucan 4-β-D-glucosyltransferase
Systematic name: GDP-α-D-glucose:(1→4)-β-D-glucan 4-β-D-glucosyltransferase (configuration-inverting)
Comments: Involved in the synthesis of cellulose. A similar enzyme [EC 2.4.1.12, cellulose synthase (UDP-forming)] utilizes UDP-α-D-glucose.
References: [499, 919]

[EC 2.4.1.29 created 1965]

EC 2.4.1.30

Accepted name: 1,3-β-oligoglucan phosphorylase
Reaction: [(1→3)-β-D-glucosyl]$_n$ + phosphate = [(1→3)-β-D-glucosyl]$_{n-1}$ + α-D-glucose 1-phosphate
Other name(s): β-1,3-oligoglucan:orthophosphate glucosyltransferase II; β-1,3-oligoglucan phosphorylase; 1,3-β-D-oligoglucan:phosphate α-D-glucosyltransferase
Systematic name: (1→3)-β-D-glucan:phosphate α-D-glucosyltransferase
Comments: Does not act on laminarin. Differs in specificity from EC 2.4.1.31 (laminaribiose phosphorylase) and EC 2.4.1.97 (1,3-β-D-glucan phosphorylase).
References: [2123, 2122]

[EC 2.4.1.30 created 1972]

EC 2.4.1.31

Accepted name: laminaribiose phosphorylase
Reaction: 3-β-D-glucosyl-D-glucose + phosphate = D-glucose + α-D-glucose 1-phosphate
Systematic name: 3-β-D-glucosyl-D-glucose:phosphate α-D-glucosyltransferase
Comments: Also acts on 1,3-β-D-oligoglucans. Differs in specificity from EC 2.4.1.30 (1,3-β-oligoglucan phosphorylase) and EC 2.4.1.97 (1,3-β-D-glucan phosphorylase).
References: [1090, 2113]

[EC 2.4.1.31 created 1972]

EC 2.4.1.32

Accepted name: glucomannan 4-β-mannosyltransferase

Reaction: GDP-mannose + (glucomannan)$_n$ = GDP + (glucomannan)$_{n+1}$

Other name(s): GDP-man-β-mannan manosyltransferase; glucomannan-synthase; GDPmannose:glucomannan 1,4-β-D-mannosyltransferase; GDP-mannose:glucomannan 1,4-β-D-mannosyltransferase

Systematic name: GDP-mannose:glucomannan 4-β-D-mannosyltransferase

References: [825]

[EC 2.4.1.32 created 1972]

EC 2.4.1.33

Accepted name: mannuronan synthase

Reaction: GDP-α-D-mannuronate + [(1→4)-β-D-mannuronosyl]$_n$ = GDP + [(1→4)-β-D-mannuronosyl]$_{n+1}$

Other name(s): mannuronosyl transferase; alginate synthase (incorrect); alg8 (gene name); alg44 (gene name); GDP-D-mannuronate:alginate D-mannuronyltransferase

Systematic name: GDP-α-D-mannuronate:mannuronan D-mannuronatetransferase

Comments: The enzyme catalyses the polymerization of β-D-mannuronate residues into a mannuronan polymer, an intermediate in the biosynthesis of alginate. It is found in brown algae and in alginate-producing bacterial species from the *Pseudomonas* and *Azotobacter* genera.

References: [1973, 2868, 2524]

[EC 2.4.1.33 created 1972, modified 2015]

EC 2.4.1.34

Accepted name: 1,3-β-glucan synthase

Reaction: UDP-glucose + [(1→3)-β-D-glucosyl]$_n$ = UDP + [(1→3)-β-D-glucosyl]$_{n+1}$

Other name(s): 1,3-β-D-glucan—UDP glucosyltransferase; UDP-glucose—1,3-β-D-glucan glucosyltransferase; callose synthetase; 1,3-β-D-glucan-UDP glucosyltransferase; UDP-glucose-1,3-β-D-glucan glucosyltransferase; paramylon synthetase; UDP-glucose-β-glucan glucosyltransferase; GS-II; (1,3)-β-glucan (callose) synthase; β-1,3-glucan synthase; β-1,3-glucan synthetase; 1,3-β-D-glucan synthetase; 1,3-β-D-glucan synthase; 1,3-β-glucan-uridine diphosphoglucosyltransferase; callose synthase; UDP-glucose-1,3-β-glucan glucosyltransferase; UDP-glucose:(1,3)β-glucan synthase; uridine diphosphoglucose-1,3-β-glucan glucosyltransferase; UDP-glucose:1,3-β-D-glucan 3-β-D-glucosyltransferase

Systematic name: UDP-glucose:(1→3)-β-D-glucan 3-β-D-glucosyltransferase

References: [2124]

[EC 2.4.1.34 created 1972]

EC 2.4.1.35

Accepted name: phenol β-glucosyltransferase

Reaction: UDP-glucose + a phenol = UDP + an aryl β-D-glucoside

Other name(s): UDPglucosyltransferase (ambiguous); phenol-β-D-glucosyltransferase; UDP glucosyltransferase (ambiguous); UDP-glucose glucosyltransferase (ambiguous); uridine diphosphoglucosyltransferase

Systematic name: UDP-glucose:phenol β-D-glucosyltransferase

Comments: Acts on a wide range of phenols.

References: [798]

[EC 2.4.1.35 created 1972]

EC 2.4.1.36

Accepted name: α,α-trehalose-phosphate synthase (GDP-forming)

Reaction: GDP-glucose + glucose 6-phosphate = GDP + α,α-trehalose 6-phosphate

Other name(s): GDP-glucose—glucose-phosphate glucosyltransferase; guanosine diphosphoglucose-glucose phosphate glucosyltransferase; trehalose phosphate synthase (GDP-forming)
Systematic name: GDP-glucose:D-glucose-6-phosphate 1-α-D-glucosyltransferase
Comments: See also EC 2.4.1.15 [α,α-trehalose-phosphate synthase (UDP-forming)].
References: [824]

[EC 2.4.1.36 created 1972]

EC 2.4.1.37

Accepted name: fucosylgalactoside 3-α-galactosyltransferase
Reaction: UDP-α-D-galactose + α-L-fucosyl-(1→2)-D-galactosyl-R = UDP + α-D-galactosyl-(1→3)-[α-L-fucosyl(1→2)]-D-galactosyl-R (where R can be OH, an oligosaccharide or a glycoconjugate)
Other name(s): UDP-galactose:*O*-α-L-fucosyl(1→2)D-galactose α-D-galactosyltransferase; UDPgalactose:glycoprotein-α-L-fucosyl-(1,2)-D-galactose 3-α-D-galactosyltransferase; [blood group substance] α-galactosyltransferase; blood-group substance B-dependent galactosyltransferase; glycoprotein-fucosylgalactoside α-galactosyltransferase; histo-blood group B transferase; histo-blood substance B-dependent galactosyltransferase; UDP-galactose:α-L-fucosyl-1,2-D-galactoside 3-α-D-galactosyltransferase; UDP-galactose:α-L-fucosyl-(1→2)-D-galactoside 3-α-D-galactosyltransferase
Systematic name: UDP-α-D-galactose:α-L-fucosyl-(1→2)-D-galactoside 3-α-D-galactosyltransferase
Comments: Acts on blood group substance, and can use a number of 2-fucosyl-galactosides as acceptors.
References: [2785]

[EC 2.4.1.37 created 1972, modified 1999, modified 2002]

EC 2.4.1.38

Accepted name: β-*N*-acetylglucosaminylglycopeptide β-1,4-galactosyltransferase
Reaction: UDP-α-D-galactose + *N*-acetyl-β-D-glucosaminylglycopeptide = UDP + β-D-galactosyl-(1→4)-*N*-acetyl-β-D-glucosaminylglycopeptide
Other name(s): UDP-galactose—glycoprotein galactosyltransferase; glycoprotein 4-β-galactosyl-transferase; β-*N*-acetyl-β1-4-galactosyltransferase; thyroid glycoprotein β-galactosyltransferase; glycoprotein β-galactosyltransferase; thyroid galactosyltransferase; uridine diphosphogalactose-glycoprotein galactosyltransferase; β-*N*-acetylglucosaminyl-glycopeptide β-1,4-galactosyltransferase; GalT; UDP-galactose:*N*-acetyl-β-D-glucosaminylglycopeptide β-1,4-galactosyltransferase; UDP-galactose:*N*-acetyl-β-D-glucosaminylglycopeptide 4-β-galactosyltransferase
Systematic name: UDP-α-D-galactose:*N*-acetyl-β-D-glucosaminylglycopeptide 4-β-galactosyltransferase
Comments: Terminal *N*-acetyl-β-D-glucosaminyl residues in polysaccharides, glycoproteins and glycopeptides can act as acceptor. High activity is shown towards such residues in branched-chain polysaccharides when these are linked by β-1,6-links to galactose residues; lower activity towards residues linked to galactose by β-1,3-links. A component of EC 2.4.1.22 (lactose synthase).
References: [300, 325, 326, 3301]

[EC 2.4.1.38 created 1972, modified 1976, modified 1980, modified 1986]

EC 2.4.1.39

Accepted name: steroid *N*-acetylglucosaminyltransferase
Reaction: UDP-*N*-acetyl-α-D-glucosamine + estradiol-17α 3-D-glucuronoside = UDP + 17α-(*N*-acetyl-D-glucosaminyl)-estradiol 3-D-glucuronoside
Other name(s): hydroxy steroid acetylglucosaminyltransferase; steroid acetylglucosaminyltransferase; uridine diphosphoacetylglucosamine-steroid acetylglucosaminyltransferase
Systematic name: UDP-*N*-acetyl-α-D-glucosamine:estradiol-17α-3-D-glucuronoside 17α-*N*-acetylglucosaminyltransferase
References: [594]

[EC 2.4.1.39 created 1972]

EC 2.4.1.40

Accepted name: glycoprotein-fucosylgalactoside α-*N*-acetylgalactosaminyltransferase

Reaction: UDP-*N*-acetyl-α-D-galactosamine + glycoprotein-α-L-fucosyl-(1→2)-D-galactose = UDP + glycoprotein-*N*-acetyl-α-D-galactosaminyl-(1→3)-[α-L-fucosyl-(1→2)]-D-galactose

Other name(s): A-transferase; histo-blood group A glycosyltransferase (Fucα1→2Galα1→3-*N*-acetylgalactosaminyltransferase); UDP-GalNAc:Fucα1→2Galα1→3-*N*-acetylgalactosaminyltransferase; α-3-*N*-acetylgalactosaminyltransferase; blood-group substance α-acetyltransferase; blood-group substance A-dependent acetylgalactosaminyltransferase; fucosyl-galactose acetylgalactosaminyltransferase; histo-blood group A acetylgalactosaminyltransferase; histo-blood group A transferase; UDP-*N*-acetyl-D-galactosamine:α-L-fucosyl-1,2-D-galactose 3-*N*-acetyl-D-galactosaminyltransferase; UDP-*N*-acetyl-D-galactosamine:glycoprotein-α-L-fucosyl-(1,2)-D-galactose 3-*N*-acetyl-D-galactosaminyltransferase

Systematic name: UDP-*N*-acetyl-α-D-galactosamine:glycoprotein-α-L-fucosyl-(1→2)-D-galactose 3-*N*-acetyl-D-galactosaminyltransferase

Comments: Acts on blood group substance, and can use a number of 2-fucosyl-galactosides as acceptors.

References: [1725, 3453, 3970]

[EC 2.4.1.40 created 1972, modified 1999]

EC 2.4.1.41

Accepted name: polypeptide *N*-acetylgalactosaminyltransferase

Reaction: (1) UDP-*N*-acetyl-α-D-galactosamine + [protein]-L-serine = UDP + [protein]-3-*O*-(*N*-acetyl-α-D-galactosaminyl)-L-serine

(2) UDP-*N*-acetyl-α-D-galactosamine + [protein]-L-threonine = UDP + [protein]-3-*O*-(*N*-acetyl-α-D-galactosaminyl)-L-threonine

Other name(s): protein-UDP acetylgalactosaminyltransferase; UDP-GalNAc:polypeptide *N*-acetylgalactosaminyl transferase; UDP-*N*-acetylgalactosamine:κ-casein polypeptide *N*-acetylgalactosaminyltransferase; uridine diphosphoacetylgalactosamine-glycoprotein acetylgalactosaminyltransferase; glycoprotein acetylgalactosaminyltransferase; polypeptide-*N*-acetylgalactosamine transferase; UDP-acetylgalactosamine-glycoprotein acetylgalactosaminyltransferase; UDP-acetylgalactosamine:peptide-*N*-galactosaminyltransferase; UDP-GalNAc:polypeptide *N*-acetylgalactosaminyltransferase; UDP-*N*-acetyl-α-D-galactosamine:polypeptide *N*-acetylgalactosaminyltransferase; UDP-*N*-acetylgalactosamine-glycoprotein *N*-acetylgalactosaminyltransferase; UDP-*N*-acetylgalactosamine-protein *N*-acetylgalactosaminyltransferase; UDP-*N*-acetylgalactosamine:polypeptide *N*-acetylgalactosaminyltransferase; UDP-*N*-acetylgalactosamine:protein *N*-acetylgalactosaminyl transferase; ppGalNAc-T; UDP-*N*-acetyl-α-D-galactosamine:polypeptide *N*-acetylgalactosaminyltransferase

Systematic name: UDP-*N*-α-acetyl-D-galactosamine:[protein]-3-*O*-*N*-acetyl-α-D-galactosaminyl transferase (configuration-retaining)

Comments: Requires both Mn^{2+} and Ca^{2+}. The glycosyl residue is transferred to threonine or serine hydroxy groups on the polypeptide core of submaxillary mucin, κ-casein, apofetuin and some other acceptors of high molecular mass.

References: [3379, 3452]

[EC 2.4.1.41 created 1972, modified 1989]

[2.4.1.42 Deleted entry. UDP-glucuronate—estriol 17β-D-glucuronosyltransferase. Now included with EC 2.4.1.17, glucuronosyltransferase]

[EC 2.4.1.42 created 1972, deleted 1984]

EC 2.4.1.43

Accepted name: polygalacturonate 4-α-galacturonosyltransferase

Reaction: UDP-α-D-galacturonate + $[(1\rightarrow4)\text{-}\alpha\text{-D-galacturonosyl}]_n$ = UDP + $[(1\rightarrow4)\text{-}\alpha\text{-D-galacturonosyl}]_{n+1}$

Other name(s): UDP galacturonate-polygalacturonate α-galacturonosyltransferase; uridine diphosphogalacturonate-polygalacturonate α-galacturonosyltransferase; UDP-D-galacturonate:1,4-α-poly-D-galacturonate 4-α-D-galacturonosyltransferase; UDP-D-galacturonate:(1→4)-α-poly-D-galacturonate 4-α-D-galacturonosyltransferase
Systematic name: UDP-α-D-galacturonate:(1→4)-α-poly-D-galacturonate 4-α-D-galacturonosyltransferase (configuration-retaining)
References: [3684]

[EC 2.4.1.43 created 1972]

EC 2.4.1.44

Accepted name: lipopolysaccharide 3-α-galactosyltransferase
Reaction: UDP-α-D-galactose + lipopolysaccharide = UDP + 3-α-D-galactosyl-[lipopolysaccharide glucose]
Other name(s): UDP-galactose:lipopolysaccharide α,3-galactosyltransferase; UDP-galactose:polysaccharide galactosyltransferase; uridine diphosphate galactose:lipopolysaccharide α-3-galactosyltransferase; uridine diphosphogalactose-lipopolysaccharide α,3-galactosyltransferase; UDP-galactose:lipopolysaccharide 3-α-D-galactosyltransferase
Systematic name: UDP-α-D-galactose:lipopolysaccharide 3-α-D-galactosyltransferase
Comments: Transfers α-D-galactosyl residues to D-glucose in the partially completed core of lipopolysaccharide [*cf.* EC 2.4.1.56 (lipopolysaccharide *N*-acetylglucosaminyltransferase), EC 2.4.1.58 (lipopolysaccharide glucosyltransferase I) and EC 2.4.1.73 (lipopolysaccharide glucosyltransferase II)].
References: [837, 3886]

[EC 2.4.1.44 created 1972, modified 2002]

[2.4.1.45 Deleted entry. 2-hydroxyacylsphingosine 1-β-galactosyltransferase, now included with EC 2.4.1.47, N-acylsphingosine galactosyltransferase]

[EC 2.4.1.45 created 1972, deleted 2016]

EC 2.4.1.46

Accepted name: monogalactosyldiacylglycerol synthase
Reaction: UDP-α-D-galactose + a 1,2-diacyl-*sn*-glycerol = UDP + a 1,2-diacyl-3-*O*-(β-D-galactosyl)-*sn*-glycerol
Other name(s): uridine diphosphogalactose-1,2-diacylglycerol galactosyltransferase; UDP-galactose:diacylglycerol galactosyltransferase; MGDG synthase; UDP galactose-1,2-diacylglycerol galactosyltransferase; UDP-galactose-diacylglyceride galactosyltransferase; UDP-galactose:1,2-diacylglycerol 3-β-D-galactosyltransferase; 1β-MGDG; 1,2-diacylglycerol 3-β-galactosyltransferase; UDP-galactose:1,2-diacyl-*sn*-glycerol 3-β-D-galactosyltransferase
Systematic name: UDP-α-D-galactose:1,2-diacyl-*sn*-glycerol 3-β-D-galactosyltransferase
Comments: This enzyme adds only one galactosyl group to the diacylglycerol; EC 2.4.1.241, digalactosyldiacylglycerol synthase, adds a galactosyl group to the product of the above reaction. There are three isoforms in *Arabidopsis* that can be divided into two types, A-type (MGD1) and B-type (MGD2 and MGD3). MGD1 is the isoform responsible for the bulk of monogalactosyldiacylglycerol (MGDG) synthesis in *Arabidopsis* [269].
References: [3655, 3820, 2241, 269]

[EC 2.4.1.46 created 1972, modified 2003, modified 2005]

EC 2.4.1.47

Accepted name: *N*-acylsphingosine galactosyltransferase
Reaction: UDP-α-D-galactose + a ceramide = UDP + a β-D-galactosylceramide

Other name(s): UGT8 (gene name); CGT (gene name); UDP galactose-*N*-acylsphingosine galactosyltransferase; uridine diphosphogalactose-acylsphingosine galactosyltransferase; UDP-galactose:*N*-acylsphingosine D-galactosyltransferase; UDP-α-D-galactose:*N*-acylsphingosine D-galactosyltransferase; 2-hydroxyacylsphingosine 1-β-galactosyltransferase

Systematic name: UDP-α-D-galactose:*N*-acylsphingosine β-D-galactosyltransferase (configuration-inverting)

Comments: This membrane-bound, endoplasmic reticulum-located enzyme catalyses the last step in the synthesis of galactocerebrosides, which are abundant sphingolipids of the myelin membrane of the central nervous system and peripheral nervous system. It has a strong preference for ceramides that contain hydroxylated fatty acids.

References: [983, 2310, 2309, 227, 33, 1772, 3114, 3304, 902]

[EC 2.4.1.47 created 1972]

EC 2.4.1.48

Accepted name: heteroglycan α-mannosyltransferase

Reaction: GDP-mannose + heteroglycan = GDP + 2(or 3)-α-D-mannosyl-heteroglycan

Other name(s): GDP mannose α-mannosyltransferase; guanosine diphosphomannose-heteroglycan α-mannosyltransferase

Systematic name: GDP-mannose:heteroglycan 2-(or 3-)-α-D-mannosyltransferase

Comments: The acceptor is a heteroglycan primer containing mannose, galactose and xylose. 1,2- and 1,3-mannosyl bonds are formed.

References: [90]

[EC 2.4.1.48 created 1972]

EC 2.4.1.49

Accepted name: cellodextrin phosphorylase

Reaction: [(1→4)-β-D-glucosyl]$_{n}$ + phosphate = [(1→4)-β-D-glucosyl]$_{n-1}$ + α-D-glucose 1-phosphate

Other name(s): β-1,4-oligoglucan:orthophosphate glucosyltransferase; 1,4-β-D-oligo-D-glucan:phosphate α-D-glucosyltransferase

Systematic name: (1→4)-β-D-glucan:phosphate α-D-glucosyltransferase

References: [3176]

[EC 2.4.1.49 created 1972]

EC 2.4.1.50

Accepted name: procollagen galactosyltransferase

Reaction: UDP-α-D-galactose + [procollagen]-(5*R*)-5-hydroxy-L-lysine = UDP + [procollagen]-(5*R*)-5-*O*-(β-D-galactosyl)-5-hydroxy-L-lysine

Other name(s): hydroxylysine galactosyltransferase; collagen galactosyltransferase; collagen hydroxylysyl galactosyltransferase; UDP galactose-collagen galactosyltransferase; uridine diphosphogalactose-collagen galactosyltransferase; UDPgalactose:5-hydroxylysine-collagen galactosyltransferase; UDP-galactose:procollagen-5-hydroxy-L-lysine D-galactosyltransferase; UDP-α-D-galactose:procollagen-5-hydroxy-L-lysine D-galactosyltransferase

Systematic name: UDP-α-D-galactose:[procollagen]-(5*R*)-5-hydroxy-L-lysine 5-β-D-galactosyltransferase (configuration-inverting)

Comments: Involved in the synthesis of carbohydrate units in the complement system (*cf.* EC 2.4.1.66 procollagen glucosyltransferase).

References: [364, 1701, 3068]

[EC 2.4.1.50 created 1972, modified 1983]

[2.4.1.51 Deleted entry. UDP-N-acetylglucosamine—glycoprotein N-acetylglucosaminyltransferase. Now listed as EC 2.4.1.101 (α-1,3-mannosyl-glycoprotein 2-β-N-acetylglucosaminyltransferase), EC 2.4.1.143 (α-1,6-mannosyl-glycoprotein 2-

β-N-acetylglucosaminyltransferase), EC 2.4.1.144 (β-1,4-mannosyl-glycoprotein 4-β-N-acetylglucosaminyltransferase) and EC 2.4.1.145 (α-1,3-mannosyl-glycoprotein 4-β-N-acetylglucosaminyltransferase)]

[EC 2.4.1.51 created 1972, deleted 1984]

EC 2.4.1.52

Accepted name: poly(glycerol-phosphate) α-glucosyltransferase

Reaction: ***n*** UDP-α-D-glucose + 4-*O*-poly[(2*R*)-glycerophospho]-(2*R*)-glycerophospho-*N*-acetyl-β-D-mannosaminyl-(1→4)-*N*-acetyl-α-D-glucosaminyl-diphospho-*ditrans*,*octacis*-undecaprenol = ***n*** UDP + 4-*O*-poly[(2*R*)-2-α-D-glucosyl-1-glycerophospho]-(2*R*)-glycerophospho-*N*-acetyl-β-D-mannosaminyl-(1→4)-*N*-acetyl-α-D-glucosaminyl-diphospho-*ditrans*,*octacis*-undecaprenol

Other name(s): UDP glucose-poly(glycerol-phosphate) α-glucosyltransferase; uridine diphosphoglucose-poly(glycerol-phosphate) α-glucosyltransferase; *tagE* (gene name); UDP-glucose:poly(glycerol-phosphate) α-D-glucosyltransferase

Systematic name: UDP-α-D-glucose:4-*O*-poly[(2*R*)-glycerophospho]-(2*R*)-glycerophospho-*N*-acetyl-β-D-mannosaminyl-(1→4)-*N*-acetyl-α-D-glucosaminyl-diphospho-*ditrans*,*octacis*-undecaprenol α-D-glucosyltransferase (configuration-retaining)

Comments: Involved in the biosynthesis of poly glycerol phosphate teichoic acids in bacterial cell walls. This enzyme, isolated from *Bacillus subtilis* 168, adds an α-D-glucose to the free OH groups of the glycerol units. The enzyme has a strong preference for UDP-α-glucose as the sugar donor. It has no activity with poly(ribitol phosphate).

References: [1071, 62]

[EC 2.4.1.52 created 1972, modified 2017]

EC 2.4.1.53

Accepted name: poly(ribitol-phosphate) β-glucosyltransferase

Reaction: ***n*** UDP-α-D-glucose + 4-*O*-[(1-D-ribitylphospho)$_n$-(1-D-ribitylphospho)-(2*R*)-1-glycerophospho]-*N*-acetyl-β-D-mannosaminyl-(1→4)-*N*-acetyl-α-D-glucosaminyl-diphospho-*ditrans*,*octacis*-undecaprenol = ***n*** UDP + 4-*O*-[(2-β-D-glucosyl-1-D-ribitylphospho)$_n$-(1-D-ribitylphospho)-(2*R*)-1-glycerophospho]-*N*-acetyl-β-D-mannosaminyl-(1→4)-*N*-acetyl-α-D-glucosaminyl-diphospho-*ditrans*,*octacis*-undecaprenol

Other name(s): TarQ; UDP glucose-poly(ribitol-phosphate) β-glucosyltransferase; uridine diphosphoglucose-poly(ribitol-phosphate) β-glucosyltransferase; UDP-D-glucose polyribitol phosphate glucosyl transferase; UDP-D-glucose:polyribitol phosphate glucosyl transferase; UDP-glucose:poly(ribitol-phosphate) β-D-glucosyltransferase

Systematic name: UDP-α-D-glucose:4-*O*-[(1-D-ribitylphospho)$_n$-(1-D-ribitylphospho)-(2*R*)-1-glycerophospho]-*N*-acetyl-β-D-mannosaminyl-(1→4)-*N*-acetyl-α-D-glucosaminyl-diphospho-*ditrans*,*octacis*-undecaprenol β-D-glucosyltransferase (configuration-inverting)

Comments: Involved in the biosynthesis of poly ribitol phosphate teichoic acids in the cell wall of the bacterium *Bacillus subtilis* W23. This enzyme adds a β-D-glucose to the hydroxyl group at the 2 position of the ribitol phosphate units.

References: [547, 407]

[EC 2.4.1.53 created 1972, modified 2018]

EC 2.4.1.54

Accepted name: undecaprenyl-phosphate mannosyltransferase

Reaction: GDP-α-D-mannose + undecaprenyl phosphate = GDP + D-mannosyl-1-phosphoundecaprenol

Other name(s): guanosine diphosphomannose-undecaprenyl phosphate mannosyltransferase; GDP mannose-undecaprenyl phosphate mannosyltransferase; GDP-D-mannose:lipid phosphate transmannosylase; GDP-mannose:undecaprenyl-phosphate D-mannosyltransferase

Systematic name: GDP-α-D-mannose:undecaprenyl-phosphate D-mannosyltransferase

Comments: Requires phosphatidylglycerol.

References: [1844, 2973]

[EC 2.4.1.54 created 1972]

[2.4.1.55 Transferred entry. teichoic-acid synthase. Now EC 2.7.8.14, CDP-ribitol ribitolphosphotransferase]

[EC 2.4.1.55 created 1972, deleted 1982]

EC 2.4.1.56

Accepted name: lipopolysaccharide *N*-acetylglucosaminyltransferase

Reaction: UDP-*N*-acetyl-α-D-glucosamine + lipopolysaccharide = UDP + *N*-acetyl-α-D-glucosaminyllipopolysaccharide

Other name(s): UDP-*N*-acetylglucosamine-lipopolysaccharide *N*-acetylglucosaminyltransferase; uridine diphosphoacetylglucosamine-lipopolysaccharide acetylglucosaminyltransferase; UDP-*N*-acetyl-D-glucosamine:lipopolysaccharide *N*-acetyl-D-glucosaminyltransferase

Systematic name: UDP-*N*-acetyl-α-D-glucosamine:lipopolysaccharide *N*-acetyl-D-glucosaminyltransferase

Comments: Transfers *N*-acetylglucosaminyl residues to a D-galactose residue in the partially completed lipopolysaccharide core [*cf.* EC 2.4.1.44 (lipopolysaccharide 3-α-galactosyltransferase), EC 2.4.1.58 (lipopolysaccharide glucosyltransferase I) and EC 2.4.1.73 (lipopolysaccharide glucosyltransferase II)].

References: [2577]

[EC 2.4.1.56 created 1972]

[2.4.1.57 Deleted entry. phosphatidylinositol α-mannosyltransferase. Newer studies have shown that this is catalysed by two independent activities now covered by EC 2.4.1.345, phosphatidyl-myo-inositol α-mannosyl transferase and EC 2.4.1.346, phosphatidyl-myo-inositol dimannoside synthase]

[EC 2.4.1.57 created 1972, modified 2003, deleted 2017]

EC 2.4.1.58

Accepted name: lipopolysaccharide glucosyltransferase I

Reaction: UDP-glucose + lipopolysaccharide = UDP + D-glucosyl-lipopolysaccharide

Other name(s): UDP-glucose:lipopolysaccharide glucosyltransferase I; lipopolysaccharide glucosyltransferase; uridine diphosphate glucose:lipopolysaccharide glucosyltransferase I; uridine diphosphoglucose-lipopolysaccharide glucosyltransferase

Systematic name: UDP-glucose:lipopolysaccharide glucosyltransferase

Comments: Transfers glucosyl residues to the backbone portion of lipopolysaccharide [*cf.* EC 2.4.1.44 (lipopolysaccharide 3-α-galactosyltransferase, EC 2.4.1.56 (lipopolysaccharide *N*-acetylglucosaminyltransferase) and EC 2.4.1.73 (lipopolysaccharide glucosyltransferase II)].

References: [2350, 2943]

[EC 2.4.1.58 created 1972]

[2.4.1.59 Deleted entry. UDP-glucuronate—estradiol glucuronosyltransferase. Now included with EC 2.4.1.17, glucuronosyltransferase]

[EC 2.4.1.59 created 1972, deleted 1984]

EC 2.4.1.60

Accepted name: abequosyltransferase

Reaction: CDP-α-D-abequose + α-D-mannopyranosyl-(1→4)-α-L-rhamnopyranosyl-(1→3)-β-D-galactopyranosyl-diphosphodecaprenol = CDP + α-D-abequopyranosyl-(1→3)-α-D-mannopyranosyl-(1→4)-α-L-rhamnopyranosyl-(1→3)-β-D-galactopyranosyl-diphosphodecaprenol

Other name(s): trihexose diphospholipid abequosyltransferase

Systematic name: CDP-α-D-abequose:Man(α1→4)Rha(α1→3)Gal(β-1)-diphospholipid D-abequosyltransferase

References: [2579, 1996]

[EC 2.4.1.60 created 1972, modified 2012]

[2.4.1.61 Deleted entry. UDP-glucuronate—estriol 16α-glucuronosyltransferase. Now included with EC 2.4.1.17, glucuronosyltransferase]

[EC 2.4.1.61 created 1972, deleted 1984]

EC 2.4.1.62

Accepted name: ganglioside galactosyltransferase

Reaction: UDP-α-D-galactose + an *N*-acetyl-β-D-galactosaminyl-(1→4)-[α-*N*-acetylneuraminyl-(2→3)]-β-D-galactosyl-(1→4)-β-D-glucosyl-(1↔1)-ceramide = UDP + a β-D-galactosyl-(1→3)-*N*-acetyl-β-D-galactosaminyl-(1→4)-[α-*N*-acetylneuraminyl-(2→3)]-β-D-galactosyl-(1→4)-β-D-glucosyl-(1↔1)-ceramide

Other name(s): UDP-galactose—ceramide galactosyltransferase; uridine diphosphogalactose-ceramide galactosyltransferase; UDP galactose-LAC Tet-ceramide α-galactosyltransferase; UDP-galactose-GM2 galactosyltransferase; uridine diphosphogalactose-GM2 galactosyltransferase; uridine diphosphate D-galactose:glycolipid galactosyltransferase; UDP-galactose:*N*-acetylgalactosaminyl-(*N*-acetylneuraminyl) galactosyl-glucosyl-ceramide galactosyltransferase; UDP-galactose-GM2 ganglioside galactosyltransferase; GM1-synthase; UDP-galactose:*N*-acetyl-D-galactosaminyl-(*N*-acetylneuraminyl)-D-galactosyl-D-glucosyl-*N*-acylsphingosine β-1,3-D-galactosyltransferase; UDP-galactose:*N*-acetyl-D-galactosaminyl-(*N*-acetylneuraminyl)-D-galactosyl-(1→4)-β-D-glucosyl-*N*-acylsphingosine 3-β-D-galactosyltransferase

Systematic name: UDP-α-D-galactose:*N*-acetyl-β-D-galactosaminyl-(1→4)-[α-*N*-acetylneuraminyl-(2→3)]-β-D-galactosyl-(1→4)-β-D-glucosyl-(1↔1)-ceramide 3-β-D-galactosyltransferase

Comments: The substrate is also known as ganglioside GM2, the product as gangloside GM1a

References: [225, 3984, 3986]

[EC 2.4.1.62 created 1972, modified 2013]

EC 2.4.1.63

Accepted name: linamarin synthase

Reaction: UDP-glucose + 2-hydroxy-2-methylpropanenitrile = UDP + linamarin

Other name(s): uridine diphosphoglucose-ketone glucosyltransferase; uridine diphosphate-glucose-ketone cyanohydrin β-glucosyltransferase; UDP glucose ketone cyanohydrin glucosyltransferase; UDP-glucose:ketone cyanohydrin β-glucosyltransferase; uridine diphosphoglucose-ketone cyanohydrin glucosyltransferase

Systematic name: UDP-glucose:2-hydroxy-2-methylpropanenitrile β-D-glucosyltransferase

Comments: The enzyme glucosylates the cyanohydrins of butanone and pentan-3-one as well as that of acetone.

References: [1196]

[EC 2.4.1.63 created 1972]

EC 2.4.1.64

Accepted name: α,α-trehalose phosphorylase

Reaction: α,α-trehalose + phosphate = D-glucose + β-D-glucose 1-phosphate

Other name(s): trehalose phosphorylase

Systematic name: α,α-trehalose:phosphate β-D-glucosyltransferase

References: [261]

[EC 2.4.1.64 created 1972]

EC 2.4.1.65

Accepted name: 3-galactosyl-*N*-acetylglucosaminide 4-α-L-fucosyltransferase

Reaction: GDP-β-L-fucose + β-D-galactosyl-(1→3)-*N*-acetyl-β-D-glucosaminyl-R = GDP + β-D-galactosyl-(1→3)-[α-L-fucosyl-(1→4)]-*N*-acetyl-β-D-glucosaminyl-R

Other name(s): (Lea)-dependent (α-3/4)-fucosyltransferase; α(1,3/1,4) fucosyltransferase III; α-(1→4)-L-fucosyltransferase; α-4-L-fucosyltransferase; β-acetylglucosaminylsaccharide fucosyltransferase; FucT-II; Lewis α-(1→3/4)-fucosyltransferase; Lewis blood group α-(1→3/4)-fucosyltransferase; Lewis(Le) blood group gene-dependent α-(1→3/4)-L-fucosyltransferase; blood group Lewis α-4-fucosyltransferase; blood-group substance Lea-dependent fucosyltransferase; guanosine diphosphofucose-β-acetylglucosaminylsaccharide 4-α-L-fucosyltransferase; guanosine diphosphofucose-glycoprotein 4-α-L-fucosyltransferase; guanosine diphosphofucose-glycoprotein 4-α-fucosyltransferase; 3-α-galactosyl-*N*-acetylglucosaminide 4-α-L-fucosyltransferase; GDP-β-L-fucose:3-β-D-galactosyl-*N*-acetyl-D-glucosaminyl-R 4^{I}-α-L-fucosyltransferase; GDP-L-fucose:3-β-D-galactosyl-*N*-acetyl-D-glucosaminyl-R 4^{I}-α-L-fucosyltransferase

Systematic name: GDP-β-L-fucose:β-D-galactosyl-(1→3)-*N*-acetyl-β-D-glucosaminyl-R 4^{I}-α-L-fucosyltransferase (configuration-inverting)

Comments: This enzyme is the product of the Lewis blood group gene. Normally acts on a glycoconjugate where R (see reaction) is a glycoprotein or glycolipid. Although it is a 4-fucosyltransferase, it has a persistent 3-fucosyltransferase activity towards the glucose residue in free lactose. This enzyme fucosylates on O-4 of an *N*-acetylglucosamine that carries a galactosyl group on O-3, unlike EC 2.4.1.152, 4-galactosyl-*N*-acetylglucosaminide 3-α-L-fucosyltransferase, which fucosylates on O-3 of an *N*-acetylglucosamine that carries a galactosyl group on O-4. Enzymes catalysing the 4-α-fucosylation of the GlcNAc in β-D-Gal-(1→3)-β-GlcNAc sequences (with some activity also as 3-α-fucosyltransferases) are present in plants, where the function *in vivo* is the modification of *N*-glycans. In addition, the *fucTa* gene of *Helicobacter* strain UA948 encodes a fucosyltransferase with both 3-α- and 4-α-fucosyltransferase activities.

References: [2763, 2819, 3869, 2082]

[EC 2.4.1.65 created 1972, modified 2001, modified twice 2002]

EC 2.4.1.66

Accepted name: procollagen glucosyltransferase

Reaction: UDP-α-D-glucose + [procollagen]-(5*R*)-5-*O*-(β-D-galactosyl)-5-hydroxy-L-lysine = UDP + [procollagen]-(5*R*)-5-*O*-[α-D-glucosyl-(1→2)-β-D-galactosyl]-5-hydroxy-L-lysine

Other name(s): galactosylhydroxylysine glucosyltransferase; collagen glucosyltransferase; collagen hydroxylysyl glucosyltransferase; galactosylhydroxylysyl glucosyltransferase; UDP-glucose-collagenglucosyltransferase; uridine diphosphoglucose-collagen glucosyltransferase; UDP-glucose:5-(D-galactosyloxy)-L-lysine-procollagen D-glucosyltransferase; UDP-glucose:(2*S*,5*R*)-5-*O*-(β-D-galactosyl)-5-hydroxy-L-lysine-[procollagen] D-glucosyltransferase

Systematic name: UDP-α-D-glucose:[procollagen]-(5*R*)-5-*O*-(β-D-galactosyl)-5-hydroxy-L-lysine 2-α-D-glucosyltransferase (configuration-retaining)

Comments: Involved in the synthesis of carbohydrate units in the complement system (*cf.* EC 2.4.1.50 procollagen galactosyltransferase).

References: [362, 363, 444, 1701, 3308]

[EC 2.4.1.66 created 1972]

EC 2.4.1.67

Accepted name: galactinol—raffinose galactosyltransferase

Reaction: α-D-galactosyl-(1→3)-1D-*myo*-inositol + raffinose = *myo*-inositol + stachyose

Other name(s): galactinol-raffinose galactosyltransferase; stachyose synthetase; α-D-galactosyl-(1→3)-*myo*-inositol:raffinose galactosyltransferase

Systematic name: α-D-galactosyl-(1→3)-1D-*myo*-inositol:raffinose galactosyltransferase

Comments: This enzyme also catalyses galactosyl transfer from stachyose to raffinose (shown by labelling) [1581]. For synthesis of the substrate, see EC 2.4.1.123, inositol 3-α-galactosyltransferase. See also EC 2.4.1.82, galactinol—sucrose galactosyltransferase.

References: [3471, 3472, 1912, 1581]

[EC 2.4.1.67 created 1972, modified 2003]

EC 2.4.1.68

Accepted name: glycoprotein 6-α-L-fucosyltransferase

Reaction: GDP-β-L-fucose + *N*^{4}-β-D-GlcNAc-(1→2)-α-D-Man-(1→3)-[β-D-GlcNAc-(1→2)-α-D-Man-(1→6)]-β-D-Man-(1→4)-β-D-GlcNAc-(1→4)-β-D-GlcNAc-L-asparaginyl-[protein] = GDP + *N*^{4}-β-D-GlcNAc-(1→2)-α-D-Man-(1→3)-[β-D-GlcNAc-(1→2)-α-D-Man-(1→6)]-β-D-Man-(1→4)-β-D-GlcNAc-(1→4)-[α-L-Fuc-(1→6)]-β-D-GlcNAc-L-asparaginyl-[protein]

Other name(s): GDP-fucose—glycoprotein fucosyltransferase; GDP-L-Fuc:*N*-acetyl-β-D-glucosaminide α1→6fucosyltransferase; GDP-L-fucose-glycoprotein fucosyltransferase; glycoprotein fucosyltransferase; guanosine diphosphofucose-glycoprotein fucosyltransferase; GDP-L-fucose:glycoprotein (L-fucose to asparagine-linked *N*-acetylglucosamine of 4-*N*-*N*-acetyl-β-D-glucosaminyl-(1→2)-α-D-mannosyl-(1→3)-[*N*-acetyl-β-D-glucosaminyl-(1→2)-α-D-mannosyl-(1→6)]-β-D-mannosyl-(1→4)-*N*-acetyl-β-D-glucosaminyl-(1→4)-*N*-acetyl-β-D-glucosaminylasparagine) 6-α-L-fucosyltransferase; FucT; GDP-L-fucose:glycoprotein (L-fucose to asparagine-linked *N*-acetylglucosamine of *N*^{4}-*N*-acetyl-β-D-glucosaminyl-(1→2)-α-D-mannosyl-(1→3)-[*N*-acetyl-β-D-glucosaminyl-(1→2)-α-D-mannosyl-(1→6)]-β-D-mannosyl-(1→4)-*N*-acetyl-β-D-glucosaminyl-(1→4)-*N*-acetyl-β-D-glucosaminylasparagine) 6-α-L-fucosyltransferase; GDP-β-L-fucose:glycoprotein (L-fucose to asparagine-linked *N*-acetylglucosamine of *N*^{4}-*N*-acetyl-β-D-glucosaminyl-(1→2)-α-D-mannosyl-(1→3)-[*N*-acetyl-β-D-glucosaminyl-(1→2)-α-D-mannosyl-(1→6)]-β-D-mannosyl-(1→4)-*N*-acetyl-β-D-glucosaminyl-(1→4)-*N*-acetyl-β-D-glucosaminylasparagine) 6-α-L-fucosyltransferase

Systematic name: GDP-β-L-fucose:*N*^{4}-β-D-GlcNAc-(1→2)-α-D-Man-(1→3)-[β-D-GlcNAc-(1→2)-α-D-Man-(1→6)]-β-D-Man-(1→4)-β-D-GlcNAc-(1→4)-β-D-GlcNAc-L-asparaginyl-[protein] 6-α-L-fucosyltransferase (configuration-inverting)

Comments: This enzyme catalyses a reaction similar to that of EC 2.4.1.214, glycoprotein 3-α-L-fucosyltransferase, but transfers the L-fucosyl group from GDP-β-L-fucose to form an α1,6-linkage rather than an α1,3-linkage.

References: [2033, 3705, 3616]

[EC 2.4.1.68 created 1972, modified 2002]

EC 2.4.1.69

Accepted name: type 1 galactoside α-(1,2)-fucosyltransferase

Reaction: GDP-β-L-fucose + β-D-galactosyl-(1→3)-*N*-acetyl-β-D-glucosaminyl-R = GDP + α-L-fucosyl-(1→2)-β-D-galactosyl-(1→3)-*N*-acetyl-β-D-glucosaminyl-R

Other name(s): galactoside 2-α-L-fucosyltransferase (ambiguous); blood group H α-2-fucosyltransferase (ambiguous); guanosine diphosphofucose-galactoside 2-L-fucosyltransferase; α-(1→2)-L-fucosyltransferase (ambiguous); α-2-fucosyltransferase (ambiguous); α-2-L-fucosyltransferase (ambiguous); blood-group substance H-dependent fucosyltransferase (ambiguous); guanosine diphosphofucose-glycoprotein 2-α-fucosyltransferase (ambiguous); guanosine diphosphofucose-β-D-galactosyl-α-2-L-fucosyltransferase (ambiguous); guanosine diphosphofucose-galactosylacetylglucosaminylgalactosylglucosylceramide α-L-fucosyltransferase (ambiguous); guanosine diphosphofucose-glycoprotein 2-α-L-fucosyltransferase (ambiguous); secretor-type β-galactoside α1→2fucosyltransferase; β-galactoside α1→2fucosyltransferase (ambiguous); GDP-β-L-fucose:β-D-galactosyl-R 2-α-L-fucosyltransferase (ambiguous); FUT2 (gene name); GDP-β-L-fucose:β-D-galactosyl-(1→3)-*N*-acetyl-β-D-glucosaminyl-(1→3)-β-D-galactosyl-(1→4)-β-D-glucosyl-(1↔1)-ceramide 2-α-L-fucosyltransferase

Systematic name: GDP-β-L-fucose:β-D-galactosyl-(1→3)-*N*-acetyl-β-D-glucosaminyl-R α-(1,2)-L-fucosyltransferase (configuration-inverting)

Comments: The enzyme acts on a glycoconjugates where R (see reaction) is a glycoprotein or glycosphingolipid. The recognized moiety of the substrate is known as a type 1 histo-blood group antigen precursor disaccharide, and the action of the enzyme produces an H type 1 antigen. In humans the main enzyme performing this reaction is encoded by the FUT2 gene (also known as the Secretor gene), which is also able to act on type 2 substrates (see EC 2.4.1.344). The enzyme from the bacterium *Helicobacter pylori* cannot act on type 2 substrates.

References: [298, 299, 1816, 1730, 3748]

[EC 2.4.1.69 created 1972 (EC 2.4.1.89 created 1976, incorporated 1984), modified 2002, modified 2017]

EC 2.4.1.70

Accepted name: poly(ribitol-phosphate) α-*N*-acetylglucosaminyltransferase

Reaction: ***n*** UDP-*N*-acetyl-α-D-glucosamine + 4-*O*-(D-ribitylphospho)$_n$-di[(2*R*)-1-glycerophospho]-*N*-acetyl-β-D-mannosaminyl-(1→4)-*N*-acetyl-α-D-glucosaminyl-diphospho-*ditrans*,*octacis*-undecaprenol = ***n*** UDP + 4-*O*-(2-*N*-acetyl-α-D-glucosaminyl-D-ribitylphospho)$_n$-di[(2*R*)-1-glycerophospho]-*N*-acetyl-β-D-mannosaminyl-(1→4)-*N*-acetyl-α-D-glucosaminyl-diphospho-*ditrans*,*octacis*-undecaprenol

Other name(s): TarM; UDP acetylglucosamine-poly(ribitol phosphate) acetylglucosaminyltransferase (ambiguous); uridine diphosphoacetylglucosamine-poly(ribitol phosphate) acetylglucosaminyltransferase (ambiguous); UDP-*N*-acetyl-D-glucosamine:poly(ribitol-phosphate) *N*-acetyl-D-glucosaminyltransferase (ambiguous); UDP-*N*-acetyl-α-D-glucosamine:poly(ribitol-phosphate) *N*-acetyl-α-D-glucosaminyltransferase (ambiguous); poly(ribitol-phosphate) *N*-acetylglucosaminyltransferase (ambiguous)

Systematic name: UDP-*N*-acetyl-α-D-glucosamine:4-*O*-(D-ribitylphospho)$_n$-di[(2*R*)-1-glycerophospho]-*N*-acetyl-β-D-mannosaminyl-(1→4)-*N*-acetyl-α-D-glucosaminyl-diphospho-*ditrans*,*octacis*-undecaprenol α-*N*-acetyl-D-glucosaminyltransferase (configuration-retaining)

Comments: Involved in the biosynthesis of poly(ribitol phosphate) teichoic acids in the cell wall of the bacterium *Staphylococcus aureus*. This enzyme adds an *N*-acetyl-α-D-glucosamine to the hydroxyl group at the 2 position of the ribitol phosphate units. *cf.* EC 2.4.1.355 [poly(ribitol-phosphate) β-*N*-acetylglucosaminyltransferase].

References: [2422, 3918, 3266, 1727]

[EC 2.4.1.70 created 1972, modified 2018]

EC 2.4.1.71

Accepted name: arylamine glucosyltransferase

Reaction: UDP-glucose + an arylamine = UDP + an *N*-D-glucosylarylamine

Other name(s): UDP glucose-arylamine glucosyltransferase; uridine diphosphoglucose-arylamine glucosyltransferase

Systematic name: UDP-glucose:arylamine *N*-D-glucosyltransferase

References: [952]

[EC 2.4.1.71 created 1972]

[2.4.1.72 Transferred entry. 1,4-β-xylan synthase. Now EC 2.4.2.24, 1,4-β-D-xylan synthase]

[EC 2.4.1.72 created 1972, deleted 1976]

EC 2.4.1.73

Accepted name: lipopolysaccharide glucosyltransferase II

Reaction: UDP-glucose + lipopolysaccharide = UDP + α-D-glucosyl-lipopolysaccharide

Other name(s): uridine diphosphoglucose-galactosylpolysaccharide glucosyltransferase

Systematic name: UDP-glucose:galactosyl-lipopolysaccharide α-D-glucosyltransferase

Comments: Transfers glucosyl residues to the D-galactosyl-D-glucosyl side-chains in the partially completed core of lipopolysaccharides. *cf.* EC 2.4.1.44 (lipopolysaccharide 3-α-galactosyltransferase), EC 2.4.1.56 (lipopolysaccharide *N*-acetylglucosaminyltransferase) and EC 2.4.1.58 (lipopolysaccharide glucosyltransferase I).

References: [809]

[EC 2.4.1.73 created 1972]

EC 2.4.1.74

Accepted name: glycosaminoglycan galactosyltransferase

Reaction: UDP-α-D-galactose + glycosaminoglycan = UDP + D-galactosylglycosaminoglycan

Other name(s): uridine diphosphogalactose-mucopolysaccharide galactosyltransferase; UDP-galactose:glycosaminoglycan D-galactosyltransferase

Systematic name: UDP-α-D-galactose:glycosaminoglycan D-galactosyltransferase

Comments: Involved in the biosynthesis of galactose-containing glycosaminoglycan of the ameboid protozoan *Dictyostelium discoideum*.

References: [3391]

[EC 2.4.1.74 created 1972, modified 1980]

[2.4.1.75 Deleted entry. UDP-galacturonosyltransferase. Insufficient evidence to conclude that this is a different enzyme from EC 2.4.1.43, polygalacturonate 4-α-galacturonosyltransferase]

[EC 2.4.1.75 created 1976, deleted 2005]

[2.4.1.76 Deleted entry. UDP-glucuronate—bilirubin glucuronosyltransferase. Now included with EC 2.4.1.17, glucuronosyltransferase]

[EC 2.4.1.76 created 1976, deleted 1984]

[2.4.1.77 Deleted entry. UDP-glucuronate—bilirubin-glucuronoside glucuronosyltransferase. Now included with EC 2.4.1.17, glucuronosyltransferase]

[EC 2.4.1.77 created 1976, deleted 1984]

EC 2.4.1.78

Accepted name: phosphopolyprenol glucosyltransferase

Reaction: UDP-glucose + polyprenyl phosphate = UDP + polyprenylphosphate-glucose

Other name(s): uridine diphosphoglucose-polyprenol monophosphate glucosyltransferase; UDP-glucose:polyprenol monophosphate glucosyltransferase

Systematic name: UDP-glucose:phosphopolyprenol D-glucosyltransferase

Comments: Ficaprenyl phosphate is the best substrate; other polyprenols can also act as substrates, but more slowly.

References: [1498]

[EC 2.4.1.78 created 1976]

EC 2.4.1.79

Accepted name: globotriaosylceramide 3-β-*N*-acetylgalactosaminyltransferase

Reaction: UDP-*N*-acetyl-α-D-galactosamine + α-D-galactosyl-(1→4)-β-D-galactosyl-(1→4)-β-D-glucosyl-(1↔1)-ceramide = UDP + *N*-acetyl-β-D-galactosaminyl-(1→3)-α-D-galactosyl-(1→4)-β-D-galactosyl-(1→4)-β-D-glucosyl-(1↔1)-ceramide

Other name(s): uridine diphosphoacetylgalactosamine-galactosylgalactosylglucosylceramide acetylgalactosaminyltransferase; globoside synthetase; UDP-*N*-acetylgalactosamine:globotriaosylceramide β-3-*N*-acetylgalactosaminyltransferase; galactosylgalactosylglucosylceramide β-D-acetylgalactosaminyltransferase; UDP-*N*-acetylgalactosamine:globotriaosylceramide β1,3-*N*-acetylgalactosaminyltransferase; globoside synthase; gUDP-*N*-acetyl-D-galactosamine:D-galactosyl-1,4-D-galactosyl-1,4-D-glucosylceramide β-*N*-acetyl-D-galactosaminyltransferase; β3GalNAc-T1; UDP-*N*-acetyl-D-galactosamine:α-D-galactosyl-(1→4)-β-D-galactosyl-(1→4)-β-D-glucosylceramide 3^{III}-β-*N*-acetyl-D-galactosaminyltransferase; UDP-*N*-acetyl-D-galactosamine:α-D-galactosyl-(1→4)-β-D-galactosyl-(1→4)-β-D-glucosyl-(1↔1)-ceramide 3^{III}-β-*N*-acetyl-D-galactosaminyltransferase; UDP-*N*-acetyl-D-galactosamine:α-D-galactosyl-(1→4)-β-D-galactosyl-(1→4)-β-D-glucosyl-(1↔1)-ceramide III^3-β-*N*-acetyl-D-galactosaminyltransferase

Systematic name: UDP-*N*-acetyl-α-D-galactosamine:α-D-galactosyl-(1→4)-β-D-galactosyl-(1→4)-β-D-glucosyl-(1↔1)-ceramide III^3-β-*N*-acetyl-D-galactosaminyltransferase

Comments: Globoside is a neutral glycosphingolipid in human erythrocytes and has blood-group-*P*-antigen activity [2549]. The enzyme requires a divalent cation for activity, with Mn^{2+} required for maximal activity [3469]. UDP-GalNAc is the only sugar donor that is used efficiently by the enzyme: UDP-Gal and UDP-GlcNAc result in very low enzyme activity [3469]. Lactosylceramide, globoside and gangliosides GM3 and GD3 are not substrates [2549]. For explanation of the superscripted ‘3′ in the systematic name, see GL-5.3.4.
References: [541, 1453, 3469, 2549]

[EC 2.4.1.79 created 1976, modified 2006]

EC 2.4.1.80

Accepted name: ceramide glucosyltransferase
Reaction: UDP-α-D-glucose + an *N*-acylsphingosine = UDP + a β-D-glucosyl-*N*-acylsphingosine
Other name(s): UDP-glucose:ceramide glucosyltransferase; ceramide:UDP-Glc glucosyltransferase; uridine diphosphoglucose-ceramide glucosyltransferase; ceramide:UDP-glucose glucosyltransferase; glucosylceramide synthase; UDP-glucose:*N*-acylsphingosine D-glucosyltransferase
Systematic name: UDP-α-D-glucose:*N*-acylsphingosine β-D-glucosyltransferase (configuration-inverting)
Comments: Sphingosine and dihydrosphingosine can also act as acceptors; CDP-glucose can act as donor.
References: [226]

[EC 2.4.1.80 created 1976]

EC 2.4.1.81

Accepted name: flavone 7-*O*-β-glucosyltransferase
Reaction: UDP-glucose + 5,7,3′,4′-tetrahydroxyflavone = UDP + 7-*O*-β-D-glucosyl-5,7,3′,4′-tetrahydroxyflavone
Other name(s): UDP-glucose-apigenin β-glucosyltransferase; UDP-glucose-luteolin β-D-glucosyltransferase; uridine diphosphoglucose-luteolin glucosyltransferase; uridine diphosphoglucose-apigenin 7-*O*-glucosyltransferase; UDP-glucosyltransferase (ambiguous)
Systematic name: UDP-glucose:5,7,3′,4′-tetrahydroxyflavone 7-*O*-β-D-glucosyltransferase
Comments: A number of flavones, flavanones and flavonols can function as acceptors. Different from EC 2.4.1.91 (flavonol 3-*O*-glucosyltransferase).
References: [3393]

[EC 2.4.1.81 created 1976]

EC 2.4.1.82

Accepted name: galactinol—sucrose galactosyltransferase
Reaction: α-D-galactosyl-(1→3)-1D-*myo*-inositol + sucrose = *myo*-inositol + raffinose
Other name(s): 1-α-D-galactosyl-*myo*-inositol:sucrose 6-α-D-galactosyltransferase; α-D-galactosyl-(1→3)-*myo*-inositol:sucrose 6-α-D-galactosyltransferase; raffinose synthase; RafS
Systematic name: α-D-galactosyl-(1→3)-1D-*myo*-inositol:sucrose 6-α-D-galactosyltransferase
Comments: 4-Nitrophenyl α-D-galactopyranoside can also act as donor. The enzyme also catalyses an exchange reaction between raffinose and sucrose (*cf.* EC 2.4.1.123, inositol 3-α-galactosyltransferase).
References: [1912, 1913]

[EC 2.4.1.82 created 1976, modified 2003]

EC 2.4.1.83

Accepted name: dolichyl-phosphate β-D-mannosyltransferase
Reaction: GDP-α-D-mannose + dolichyl phosphate = GDP + dolichyl β-D-mannosyl phosphate

Other name(s): GDP-Man:DolP mannosyltransferase; dolichyl mannosyl phosphate synthase; dolichyl-phospho-mannose synthase; GDP-mannose:dolichyl-phosphate mannosyltransferase; guanosine diphosphomannose-dolichol phosphate mannosyltransferase; dolichol phosphate mannose synthase; dolichyl phosphate mannosyltransferase; dolichyl-phosphate mannose synthase; GDP-mannose-dolichol phosphate mannosyltransferase; GDP-mannose-dolichylmonophosphate mannosyltransferase; mannosylphosphodolichol synthase; mannosylphosphoryldolichol synthase

Systematic name: GDP-mannose:dolichyl-phosphate β-D-mannosyltransferase

Comments: Acts only on long-chain polyprenyl phosphates and α-dihydropolyprenyl phosphates that are larger than C_{35}.

References: [147, 390, 1240, 2602, 2878]

[EC 2.4.1.83 created 1976, modified 1983]

[2.4.1.84 Deleted entry. UDP-glucuronate—1,2-diacylglycerol glucuronosyltransferase. Now included with EC 2.4.1.17, glucuronosyltransferase]

[EC 2.4.1.84 created 1976, deleted 1984]

EC 2.4.1.85

Accepted name: cyanohydrin β-glucosyltransferase

Reaction: UDP-α-D-glucose + (*S*)-4-hydroxymandelonitrile = UDP + (*S*)-4-hydroxymandelonitrile β-D-glucoside

Other name(s): uridine diphosphoglucose-*p*-hydroxymandelonitrile glucosyltransferase; UDP-glucose-*p*-hydroxymandelonitrile glucosyltransferase; uridine diphosphoglucose-cyanohydrin glucosyltransferase; uridine diphosphoglucose:aldehyde cyanohydrin β-glucosyltransferase; UDP-glucose:(*S*)-4-hydroxymandelonitrile β-D-glucosyltransferase; UGT85B1; UDP-glucose:*p*-hydroxymandelonitrile-*O*-glucosyltransferase; UDP-D-glucose:(*S*)-4-hydroxymandelonitrile β-D-glucosyltransferase

Systematic name: UDP-α-D-glucose:(*S*)-4-hydroxymandelonitrile β-D-glucosyltransferase (configuration-inverting)

Comments: Acts on a wide range of substrates *in vitro*, including cyanohydrins, terpenoids, phenolics, hexanol derivatives and plant hormones, in a regiospecific manner [1214]. This enzyme is involved in the biosynthesis of the cyanogenic glucoside dhurrin in sorghum, along with EC 1.14.14.36, tyrosine *N*-monooxygenase and EC 1.14.14.37, 4-hydroxyphenylacetaldehyde oxime monooxygenase. This reaction prevents the disocciation and release of toxic hydrogen cyanide [1214].

References: [2838, 1533, 1214, 439, 1792]

[EC 2.4.1.85 created 1976, modified 2005]

EC 2.4.1.86

Accepted name: *N*-acetyl-β-D-glucosaminide β-(1,3)-galactosyltransferase

Reaction: UDP-α-D-galactose + *N*-acetyl-β-D-glucosaminyl-R = UDP + β-D-galactosyl-(1→3)-*N*-acetyl-β-D-glucosaminyl-R

Other name(s): B3GALT1 (gene name); uridine diphosphogalactose-acetyl-glucosaminylgalactosylglucosylceramide galactosyltransferase; GalT-4; UDP-galactose:*N*-acetyl-D-glucosaminyl-1,3-D-galactosyl-1,4-D-glucosylceramide β-D-galactosyltransferase; UDP-galactose:*N*-acetyl-D-glucosaminyl-(1→3)-D-galactosyl-(1→4)-D-glucosylceramide 3-β-D-galactosyltransferase; UDP-galactose:*N*-acetyl-β-D-glucosaminyl-(1→3)-β-D-galactosyl-(1→4)-β-D-glucosylceramide 3-β-D-galactosyltransferase; UDP-galactose:*N*-acetyl-β-D-glucosaminyl-(1→3)-β-D-galactosyl-(1→4)-β-D-glucosyl(1↔1)ceramide 3-β-D-galactosyltransferase; UDP-galactose:*N*-acetyl-β-D-glucosaminyl-(1→3)-β-D-galactosyl-(1→4)-β-D-glucosyl-(1↔1)-ceramide 3-β-D-galactosyltransferase; glucosaminylgalactosylglucosylceramide β-galactosyltransferase; UDP-α-D-galactose:*N*-acetyl-β-D-glucosaminyl-(1→3)-β-D-galactosyl-(1→4)-β-D-glucosyl-(1↔1)-ceramide 3-β-D-galactosyltransferase

Systematic name: UDP-α-D-galactose:*N*-acetyl-β-D-glucosaminyl-R 3-β-D-galactosyltransferase

Comments: The enzyme transfers galactose from UDP-α-D-galactose to the 3-position of substrates with a non-reducing terminal *N*-acetyl-β-D-glucosamine (β-GlcNAc) residue. It can act on both glycolipids and glycoproteins, generating a structure known as the type 1 histo-blood group antigen precursor.

References: [219, 223, 66, 67, 190]

[EC 2.4.1.86 created 1976, modified 2017]

EC 2.4.1.87

Accepted name: *N*-acetyllactosaminide 3-α-galactosyltransferase

Reaction: UDP-α-D-galactose + β-D-galactosyl-(1→4)-β-*N*-acetyl-D-glucosaminyl-R = UDP + α-D-galactosyl-(1→3)-β-D-galactosyl-(1→4)-β-*N*-acetylglucosaminyl-R (where R can be OH, an oligosaccharide or a glycoconjugate)

Other name(s): α-galactosyltransferase; UDP-Gal:β-D-Gal(1,4)-D-GlcNAc α(1,3)-galactosyltransferase; UDP-Gal:*N*-acetyllactosaminide α(1,3)-galactosyltransferase; UDP-Gal:*N*-acetyllactosaminide α-1,3-D-galactosyltransferase; UDP-Gal:Galβ1→4GlcNAc-R α1→3-galactosyltransferase; UDP-galactose-acetyllactosamine α-D-galactosyltransferase; UDPgalactose:β-D-galactosyl-β-1,4-*N*-acetyl-D-glucosaminyl-glycopeptide α-1,3-D-galactosyltransferase; glucosaminylglycopeptide α-1,3-galactosyltransferase; uridine diphosphogalactose-acetyllactosamine α1→3-galactosyltransferase; uridine diphosphogalactose-acetyllactosamine galactosyltransferase; uridine diphosphogalactose-galactosylacetylglucosaminylgalactosylglucosylceramide galactosyltransferase; β-D-galactosyl-*N*-acetylglucosaminylglycopeptide α-1,3-galactosyltransferase; UDP-galactose:*N*-acetyllactosaminide 3-α-D-galactosyltransferase; UDP-galactose:β-D-galactosyl-1,4-β-*N*-acetyl-D-glucosaminyl-R 3-α-D-galactosyltransferase; UDP-galactose:β-D-galactosyl-(1→4)-β-*N*-acetyl-D-glucosaminyl-R 3-α-D-galactosyltransferase

Systematic name: UDP-α-D-galactose:β-D-galactosyl-(1→4)-β-*N*-acetyl-D-glucosaminyl-R 3-α-D-galactosyltransferase

Comments: Acts on β-galactosyl-1,4-*N*-acetylglucosaminyl termini on asialo-α_1-acid glycoprotein and *N*-acetyllactosamine (β-D-galactosyl-1,4-*N*-acetyl-β-D-glucosamine), but not on 2′-fucosylated-*N*-acetyllactosamine. The non-reducing terminal *N*-acetyllactosamine residues of glycoproteins can also act as acceptor. Now includes EC 2.4.1.124 and EC 2.4.1.151.

References: [220, 326, 320]

[EC 2.4.1.87 created 1976, modified 1989, modified 2002 (EC 2.4.1.124 created 1984, incorporated 2002, EC 2.4.1.151 created 1984, incorporated 2002)]

EC 2.4.1.88

Accepted name: globoside α-*N*-acetylgalactosaminyltransferase

Reaction: UDP-*N*-acetyl-α-D-galactosamine + *N*-acetyl-β-D-galactosaminyl-(1→3)-α-D-galactosyl-(1→4)-β-D-galactosyl-(1→4)-β-D-glucosyl-(1↔1)-ceramide = UDP + *N*-acetyl-α-D-galactosaminyl-(1→3)-*N*-acetyl-β-D-galactosaminyl-(1→3)-α-D-galactosyl-(1→4)-β-D-galactosyl-(1→4)-β-D-glucosyl-(1↔1)-ceramide

Other name(s): uridine diphosphoacetylgalactosamine-globoside α-acetylgalactosaminyltransferase; Forssman synthase; globoside acetylgalactosaminyltransferase; UDP-*N*-acetyl-D-galactosamine:*N*-acetyl-D-galactosaminyl-1,3-D-galactosyl-1,4-D-galactosyl-1,4-D-glucosylceramide α-*N*-acetyl-D-galactosaminyltransferase; UDP-*N*-acetyl-D-galactosamine:*N*-acetyl-D-galactosaminyl-(1→3)-D-galactosyl-(1→4)-D-galactosyl-(1→4)-D-glucosyl-(1↔1)-ceramide α-*N*-acetyl-D-galactosaminyltransferase

Systematic name: UDP-*N*-acetyl-α-D-galactosamine:*N*-acetyl-β-D-galactosaminyl-(1→3)-α-D-galactosyl-(1→4)-β-D-galactosyl-(1→4)-β-D-glucosyl-(1↔1)-ceramide α-*N*-acetyl-D-galactosaminyltransferase

References: [1667]

[EC 2.4.1.88 created 1976]

[2.4.1.89 Deleted entry. Galactosylglucosaminylgalactosylglucosylceramide α-L-fucosyltransferase - now included with EC 2.4.1.69 galactoside 2-α-L-fucosyltransferase]

[EC 2.4.1.89 created 1976, deleted 1984]

EC 2.4.1.90

Accepted name: *N*-acetyllactosamine synthase

Reaction: UDP-α-D-galactose + *N*-acetyl-D-glucosamine = UDP + *N*-acetyllactosamine

Other name(s): UDP-galactose—*N*-acetylglucosamine β-D-galactosyltransferase; uridine diphosphogalactose-acetylglucosamine galactosyltransferase; β-1,4-galactosyltransferase; acetyllactosamine synthetase; lactosamine synthase; lactosamine synthetase; lactose synthetase A protein; *N*-acetyllactosamine synthetase; UDP-galactose *N*-acetylglucosamine β-4-galactosyltransferase; UDP-galactose-acetylglucosamine galactosyltransferase; UDP-galactose-*N*-acetylglucosamine β-1,4-galactosyltransferase; UDP-galactose-*N*-acetylglucosamine galactosyltransferase; β1-4-galactosyltransferase; UDP-Gal:*N*-acetylglucosamine β1-4-galactosyltransferase; β1-4GalT; NAL synthetase; UDP-β-1,4-galactosyltransferase; Gal-T; UDP-galactose:*N*-acetylglucosaminide β1-4-galactosyltransferase; UDPgalactose:*N*-acetylglucosaminyl(β1-4)galactosyltransferase; β-*N*-acetylglucosaminide β1-4-galactosyltransferase; UDP-galactose:*N*-acetyl-D-glucosamine 4-β-D-galactosyltransferase

Systematic name: UDP-α-D-galactose:*N*-acetyl-D-glucosamine 4-β-D-galactosyltransferase

Comments: The reaction is catalysed by a component of EC 2.4.1.22 (lactose synthase), which is identical with EC 2.4.1.38 (β-*N*-acetylglucosaminyl-glycopeptide β-1,4-galactosyltransferase), and by an enzyme from the Golgi apparatus of animal tissues. Formerly listed also as EC 2.4.1.98.

References: [721, 1289, 1330, 1408, 3057]

[EC 2.4.1.90 created 1976 (EC 2.4.1.98 created 1980, incorporated 1984)]

EC 2.4.1.91

Accepted name: flavonol 3-*O*-glucosyltransferase

Reaction: UDP-glucose + a flavonol = UDP + a flavonol 3-*O*-β-D-glucoside

Other name(s): GTI; uridine diphosphoglucose-flavonol 3-*O*-glucosyltransferase; UDP-glucose:flavonol 3-*O*-glucosyltransferase; UDPG:flavonoid-3-*O*-glucosyltransferase

Systematic name: UDP-glucose:flavonol 3-*O*-D-glucosyltransferase

Comments: Acts on a variety of flavonols, including quercetin and quercetin 7-*O*-glucoside. Different from EC 2.4.1.81 (flavone 7-*O*-β-glucosyltransferase).

References: [1709, 3392]

[EC 2.4.1.91 created 1976]

EC 2.4.1.92

Accepted name: (*N*-acetylneuraminyl)-galactosylglucosylceramide *N*-acetylgalactosaminyltransferase

Reaction: UDP-*N*-acetyl-α-D-galactosamine + *O*-(*N*-acetyl-α-neuraminyl)-(2→3)-*O*-β-D-galactopyranosyl-(1→4)-β-D-glucopyranosyl-(1↔1)-ceramide = UDP + *O*-2-(acetylamino)-2-deoxy-β-D-galactopyranosyl-(1→4)-*O*-[*N*-acetyl-α-neuraminyl-(2→3)]-*O*-β-D-galactopyranosyl-(1→4)-β-D-glucopyranosyl-(1↔1)-ceramide

Other name(s): uridine diphosphoacetylgalactosamine-ganglioside GM3 acetylgalactosaminyltransferase; ganglioside GM2 synthase; ganglioside GM3 acetylgalactosaminyltransferase; GM2 synthase; UDP acetylgalactosamine-(*N*-acetylneuraminyl)-D-galactosyl-D-glucosylceramide acetylgalactosaminyltransferase; UDP-*N*-acetyl-D-galactosamine:1-*O*-[*O*-(*N*-acetyl-α-neuraminyl)-(2→3)-*O*-β-D-galactopyranosyl-(1→4)-β-D-glucopyranosyl]-ceramide 1,4-β-*N*-acetyl-D-galactosaminyltransferase acetylgalactosaminyltransferase; UDP-*N*-acetylgalactosamine GM3 *N*-acetylgalactosaminyltransferase; uridine diphosphoacetylgalactosamine-acetylneuraminylgalactosylglucosylceramide acetylgalactosaminyltransferase; uridine diphosphoacetylgalactosamine-hematoside acetylgalactosaminyltransferase; GM2/GD2-synthase; β-1,4*N*-acetylgalactosaminyltransferase; asialo-GM2 synthase; GalNAc-T; UDP-*N*-acetyl-D-galactosamine:(*N*-acetylneuraminyl)-D-galactosyl-D-glucosylceramide *N*-acetyl-D-galactosaminyltransferase; UDP-*N*-acetyl-D-galactosamine:1-*O*-[*O*-(*N*-acetyl-α-neuraminyl)-(2→3)-*O*-β-D-galactopyranosyl-(1→4)-β-D-glucopyranosyl]-ceramide 4-β-*N*-acetyl-D-galactosaminyltransferase

Systematic name: UDP-*N*-acetyl-α-D-galactosamine:*O*-(*N*-acetyl-α-neuraminyl)-(2→3)-*O*-β-D-galactopyranosyl-(1→4)-β-D-glucopyranosyl-(1↔1)-ceramide 4-β-*N*-acetyl-D-galactosaminyltransferase

Comments: This enzyme catalyses the formation of the gangliosides (i.e. sialic-acid-containing glycosphingolipids) GM2, GD2 and SM2 from GM3, GD3 and SM3, respectively. Asialo-GM3 [1619] and lactosylceramide [2730] are also substrates, but glycoproteins and oligosaccharides are not substrates.
References: [729, 2730, 1619, 1242, 2385, 999, 3954]

[EC 2.4.1.92 created 1976, modified 2006]

[2.4.1.93 Transferred entry. inulin fructotransferase (depolymerizing, difructofuranose-1,2′:2,3′-dianhydride-forming). Now EC 4.2.2.18, inulin fructotransferase (DFA-III-forming). The enzyme was wrongly classified as a transferase rather than a lyase]

[EC 2.4.1.93 created 1976, deleted 2004]

EC 2.4.1.94

Accepted name: protein *N*-acetylglucosaminyltransferase
Reaction: UDP-*N*-acetyl-D-glucosamine + [protein]-L-asparagine = UDP + [protein]-N^4-(*N*-acetyl-D-glucosaminyl)-L-asparagine
Other name(s): uridine diphosphoacetylglucosamine-protein acetylglucosaminyltransferase; uridine diphospho-*N*-acetylglucosamine:polypeptide β-*N*-acetylglucosaminyltransferase; *N*-acetylglucosaminyltransferase I
Systematic name: UDP-*N*-acetyl-D-glucosamine:[protein]-L-asparagine β-*N*-acetyl-D-glucosaminyl-transferase
Comments: The acceptor is the asparagine residue in a sequence of the form Asn-Xaa-Thr or Asn-Xaa-Ser.
References: [1655, 1656, 1657]

[EC 2.4.1.94 created 1978, modified 2010]

[2.4.1.95 Deleted entry. bilirubin-glucuronoside glucuronosyltransferase]

[EC 2.4.1.95 created 1978, deleted 2018]

EC 2.4.1.96

Accepted name: *sn*-glycerol-3-phosphate 1-galactosyltransferase
Reaction: UDP-α-D-galactose + *sn*-glycerol 3-phosphate = UDP + 1-*O*-α-D-galactosyl-*sn*-glycerol 3-phosphate
Other name(s): isofloridoside-phosphate synthase; UDP-Gal:*sn-glycero*-3-phosphoric acid 1-α-galactosyl-transferase; UDPgalactose:*sn*-glycerol-3-phosphate α-D-galactosyltransferase; uridine diphosphogalactose-glycerol phosphate galactosyltransferase; glycerol 3-phosphate 1α-galactosyltransferase; UDP-galactose:*sn*-glycerol-3-phosphate 1-α-D-galactosyltransferase
Systematic name: UDP-α-D-galactose:*sn*-glycerol-3-phosphate 1-α-D-galactosyltransferase
Comments: The product is hydrolysed by a phosphatase to isofloridoside, which is involved in osmoregulation (*cf.* EC 2.4.1.137 *sn*-glycerol-3-phosphate 2-α-galactosyltransferase).
References: [1612, 1613]

[EC 2.4.1.96 created 1978]

EC 2.4.1.97

Accepted name: 1,3-β-D-glucan phosphorylase
Reaction: $[(1\to3)\text{-}\beta\text{-D-glucosyl}]_n$ + phosphate = $[(1\to3)\text{-}\beta\text{-D-glucosyl}]_{n-1}$ + α-D-glucose 1-phosphate
Other name(s): laminarin phosphoryltransferase; 1,3-β-D-glucan:orthophosphate glucosyltransferase; 1,3-β-D-glucan:phosphate α-D-glucosyltransferase
Systematic name: (1→3)-β-D-glucan:phosphate α-D-glucosyltransferase
Comments: Acts on a range of β-1,3-oligoglucans, and on glucans of laminarin type. Different from EC 2.4.1.30 (1,3-β-oligoglucan phosphorylase) and EC 2.4.1.31 (laminaribiose phosphorylase).
References: [50]

[EC 2.4.1.97 created 1978]

[2.4.1.98 Deleted entry. UDP-galactose—N-acetylglucosamine β-D-*galactosyl-transferase. Now included with EC 2.4.1.90, N-acetyllactosamine synthase]*

[EC 2.4.1.98 created 1980, deleted 1984]

EC 2.4.1.99

Accepted name: sucrose:sucrose fructosyltransferase

Reaction: **2** sucrose = D-glucose + β-D-fructofuranosyl-(2→1)-β-D-fructofuranosyl α-D-glucopyranoside

Other name(s): SST; sucrose:sucrose 1-fructosyltransferase; sucrose-sucrose 1-fructosyltransferase; sucrose 1^F-fructosyltransferase; sucrose:sucrose 1^F-β-D-fructosyltransferase

Systematic name: sucrose:sucrose 1′-β-D-fructosyltransferase

Comments: For definition of the prime in the systematic name, see 2-Carb-36.2.

References: [1297, 2074]

[EC 2.4.1.99 created 1981, modified 2004]

EC 2.4.1.100

Accepted name: 2,1-fructan:2,1-fructan 1-fructosyltransferase

Reaction: $[\beta\text{-D-fructosyl-}(2\to1)\text{-}]_m$ + $[\beta\text{-D-fructosyl-}(2\to1)\text{-}]_n$ = $[\beta\text{-D-fructosyl-}(2\to1)\text{-}]_{m-1}$ + $[\beta\text{-D-fructosyl-}(2\to1)\text{-}]_{n+1}$

Other name(s): 1,2-β-D-fructan 1^F-fructosyltransferase; fructan:fructan fructosyl transferase; FFT; 1,2-β-fructan 1^F-fructosyltransferase; 1,2-β-D-fructan:1,2-β-D-fructan 1^F-β-D-fructosyltransferase; fructan:fructan 1-fructosyl transferase; 2,1-β-D-fructan:2,1-β-D-fructan 1-β-D-fructosyltransferase

Systematic name: (2→1)-β-D-fructan:(2→1)-β-D-fructan 1-β-D-fructosyltransferase

References: [1297, 3668]

[EC 2.4.1.100 created 1981, modified 2004]

EC 2.4.1.101

Accepted name: α-1,3-mannosyl-glycoprotein 2-β-*N*-acetylglucosaminyltransferase

Reaction: UDP-*N*-acetyl-α-D-glucosamine + $Man_5GlcNAc_2$-[protein] = UDP + $Man_5GlcNAc_3$-[protein]

Other name(s): MGAT1 (gene name); *N*-acetylglucosaminyltransferase I; *N*-glycosyl-oligosaccharide-glycoprotein *N*-acetylglucosaminyltransferase I; uridine diphosphoacetylglucosamine-α-1,3-mannosylglycoprotein β-1,2-*N*-acetylglucosaminyltransferase; UDP-*N*-acetylglucosaminyl:α-1,3-D-mannoside-β-1,2-*N*-acetylglucosaminyltransferase I; UDP-*N*-acetylglucosaminyl:α-3-D-mannoside β-1,2-*N*-acetylglucosaminyltransferase I; α-1,3-mannosyl-glycoprotein β-1,2-*N*-acetylglucosaminyltransferase; GnTI; GlcNAc-T I; UDP-*N*-acetyl-D-glucosamine:3-(α-D-mannosyl)-β-D-mannosyl-glycoprotein 2-β-*N*-acetyl-D-glucosaminyltransferase

Systematic name: UDP-*N*-acetyl-α-D-glucosamine:α-D-mannosyl-(1→3)-β-D-mannosyl-glycoprotein 2-β-*N*-acetyl-D-glucosaminyltransferase (configuration-inverting)

Comments: The enzyme, found in plants and animals, participates in the processing of *N*-glycans in the Golgi apparatus. Its action is required before the other *N*-acetylglucosaminyltransferases involved in the process (GlcNAcT-II through VI) can act. While the natural substrate (produced by EC 3.2.1.113, mannosyl-oligosaccharide 1,2-α-mannosidase) is described here, the minimal substrate recognized by the enzyme is α-D-Man-(1→3)-β-D-Man-R.

References: [1227, 2215, 2570, 2569, 2275, 3058, 3658, 3614]

[EC 2.4.1.101 created 1983, modified 2001 (EC 2.4.1.51 created 1972, part incorporated 1984), modified 2018]

EC 2.4.1.102

Accepted name: β-1,3-galactosyl-*O*-glycosyl-glycoprotein β-1,6-*N*-acetylglucosaminyltransferase

Reaction: UDP-*N*-acetyl-α-D-glucosamine + O^3-[β-D-galactosyl-(1→3)-*N*-acetyl-α-D-galactosaminyl]-L-seryl/threonyl-[protein] = UDP + O^3-β-D-galactosyl-(1→3)-[*N*-acetyl-β-D-glucosaminyl-(1→6)]-*N*-acetyl-α-D-galactosaminyl-L-seryl/threonyl-[protein]

Other name(s): *O*-glycosyl-oligosaccharide-glycoprotein *N*-acetylglucosaminyltransferase I; β6-*N*-acetylglucosaminyltransferase; uridine diphosphoacetylglucosamine-mucin β-(1→6)-acetylglucosaminyltransferase; core 2 acetylglucosaminyltransferase; core 6-β-GlcNAc-transferase A; UDP-*N*-acetyl-D-glucosamine:*O*-glycosyl-glycoprotein (*N*-acetyl-D-glucosamine to *N*-acetyl-D-galactosamine of β-D-galactosyl-1,3-*N*-acetyl-D-galactosaminyl-R) β-1,6-*N*-acetyl-D-glucosaminyltransferase; GCNT1; GCNT3; UDP-*N*-acetyl-D-glucosamine:*O*-glycosyl-glycoprotein (*N*-acetyl-D-glucosamine to *N*-acetyl-D-galactosamine of β-D-galactosyl-(1→3)-*N*-acetyl-D-galactosaminyl-R) 6-β-*N*-acetyl-D-glucosaminyltransferase

Systematic name: UDP-*N*-acetyl-α-D-glucosamine:O^3-[β-D-galactosyl-(1→3)-*N*-acetyl-α-D-galactosaminyl]-glycoprotein 6-β-*N*-acetyl-D-glucosaminyltransferase (configuration-inverting)

Comments: The enzyme catalyses the addition of *N*-acetyl-α-D-glucosamine to the core 1 structure of *O*-glycans forming core 2.

References: [398, 3854, 3855]

[EC 2.4.1.102 created 1983, modified 2018]

EC 2.4.1.103

Accepted name: alizarin 2-β-glucosyltransferase

Reaction: UDP-glucose + 1,2-dihydroxy-9,10-anthraquinone = UDP + 1-hydroxy-2-(β-D-glucosyloxy)-9,10-anthraquinone

Other name(s): uridine diphosphoglucose-alizarin glucosyltransferase

Systematic name: UDP-glucose:1,2-dihydroxy-9,10-anthraquinone 2-*O*-β-D-glucosyltransferase

Comments: Acts on other hydroxy- and dihydroxy-derivatives of 9,10-anthraquinone.

References: [2156]

[EC 2.4.1.103 created 1983]

EC 2.4.1.104

Accepted name: *o*-dihydroxycoumarin 7-*O*-glucosyltransferase

Reaction: UDP-glucose + 7,8-dihydroxycoumarin = UDP + daphnin

Other name(s): uridine diphosphoglucose-*o*-dihydroxycoumarin 7-*O*-glucosyltransferase; UDP-glucose:*o*-dihydroxycoumarin glucosyltransferase

Systematic name: UDP-glucose:7,8-dihydroxycoumarin 7-*O*-β-D-glucosyltransferase

Comments: Converts the aglycone daphetin into daphnin and, more slowly, esculetin into cichoriin, umbelliferone into skimmin, hydrangetin into hydrangin and scopoletin into scopolin.

References: [1423]

[EC 2.4.1.104 created 1983]

EC 2.4.1.105

Accepted name: vitexin β-glucosyltransferase

Reaction: UDP-glucose + vitexin = UDP + vitexin $2''$-*O*-β-D-glucoside

Other name(s): uridine diphosphoglucose-vitexin $2''$-glucosyltransferase

Systematic name: UDP-glucose:vitexin $2''$-*O*-β-D-glucosyltransferase

Comments: Vitexin is a flavonoid from *Cannabis sativa* (hemp) and some populations of *Silene alba*.

References: [1280]

[EC 2.4.1.105 created 1983]

EC 2.4.1.106

Accepted name: isovitexin β-glucosyltransferase

Reaction: UDP-glucose + isovitexin = UDP + isovitexin $2''$-*O*-β-D-glucoside

Other name(s): uridine diphosphoglucose-isovitexin $2''$-glucosyltransferase

Systematic name: UDP-glucose:isovitexin 2″-*O*-β-D-glucosyltransferase
Comments: Isovitexin is a flavonoid from petals of *Silene alba*.
References: [1280]

[EC 2.4.1.106 created 1983]

[2.4.1.107 Deleted entry. UDP-glucuronate—testosterone glucuronosyltransferase. Now included with EC 2.4.1.17, glucuronosyltransferase]

[EC 2.4.1.107 created 1983, deleted 1984]

[2.4.1.108 Deleted entry. UDP-glucuronate—phenol glucuronosyltransferase. Now included with EC 2.4.1.17, glucuronosyltransferase]

[EC 2.4.1.108 created 1983, deleted 1984]

EC 2.4.1.109

Accepted name: dolichyl-phosphate-mannose—protein mannosyltransferase
Reaction: (1) dolichyl β-D-mannosyl phosphate + L-threonyl-[protein] = dolichyl phosphate + 3-*O*-(α-D-mannosyl)-L-threonyl-[protein]
(2) dolichyl β-D-mannosyl phosphate + L-seryl-[protein] = dolichyl phosphate + 3-*O*-(α-D-mannosyl)-L-seryl-[protein]
Other name(s): dolichol phosphomannose-protein mannosyltransferase; protein *O*-D-mannosyltransferase; dolichyl-phosphate-D-mannose:protein *O*-D-mannosyltransferase; dolichyl-phosphate-mannose-protein mannosyltransferase; dolichyl-D-mannosyl-phosphate:protein *O*-D-mannosyltransferase
Systematic name: dolichyl β-D-mannosyl-phosphate:L-threonyl/L-seryl-[protein] *O*-D-mannosyltransferase (configuration-inverting)
Comments: The enzyme transfers mannosyl residues to the hydroxy group of serine or threonine residues, producing cell-wall mannoproteins. It acts only on long-chain α-dihydropolyprenyl derivatives, larger than C_{35}.
References: [147, 2602]

[EC 2.4.1.109 created 1983, modified 2014]

EC 2.4.1.110

Accepted name: tRNA-queuosine β-mannosyltransferase
Reaction: GDP-mannose + tRNA^{Asp}-queuosine = GDP + tRNA^{Asp}-*O*-5″-β-D-mannosylqueuosine
Systematic name: GDP-mannose:tRNA^{Asp}-queuosine *O*-5″-β-D-mannosyltransferase
References: [2545]

[EC 2.4.1.110 created 1984]

EC 2.4.1.111

Accepted name: coniferyl-alcohol glucosyltransferase
Reaction: UDP-glucose + coniferyl alcohol = UDP + coniferin
Other name(s): uridine diphosphoglucose-coniferyl alcohol glucosyltransferase; UDP-glucose coniferyl alcohol glucosyltransferase
Systematic name: UDP-glucose:coniferyl-alcohol 4′-β-D-glucosyltransferase
Comments: Sinapyl alcohol can also act as acceptor.
References: [1424]

[EC 2.4.1.111 created 1984]

[2.4.1.112 Deleted entry. α-1,4-glucan-protein synthase (UDP-forming). The protein referred to in this entry is now known to be glycogenin so the entry has been incorporated into EC 2.4.1.186, glycogenin glucosyltransferase]

[EC 2.4.1.112 created 1984, deleted 2007]

EC 2.4.1.113

Accepted name: α-1,4-glucan-protein synthase (ADP-forming)

Reaction: ADP-glucose + protein = ADP + α-D-glucosyl-protein

Other name(s): ADP-glucose:protein glucosyltransferase; adenosine diphosphoglucose-protein glucosyltransferase

Systematic name: ADP-glucose:protein 4-α-D-glucosyltransferase

Comments: The enzyme builds up α-1,4-glucan chains covalently bound to protein, thus acting as an initiator of glycogen synthesis.

References: [191]

[EC 2.4.1.113 created 1984]

EC 2.4.1.114

Accepted name: 2-coumarate *O*-β-glucosyltransferase

Reaction: UDP-glucose + *trans*-2-hydroxycinnamate = UDP + *trans*-β-D-glucosyl-2-hydroxycinnamate

Other name(s): uridine diphosphoglucose-*o*-coumarate glucosyltransferase; UDPG:*o*-coumaric acid *O*-glucosyltransferase

Systematic name: UDP-glucose:*trans*-2-hydroxycinnamate *O*-β-D-glucosyltransferase

Comments: Coumarinate (*cis*-2-hydroxycinnamate) does not act as acceptor.

References: [1710, 2749]

[EC 2.4.1.114 created 1984]

EC 2.4.1.115

Accepted name: anthocyanidin 3-*O*-glucosyltransferase

Reaction: UDP-D-glucose + an anthocyanidin = UDP + an anthocyanidin-3-*O*-β-D-glucoside

Other name(s): uridine diphosphoglucose-anthocyanidin 3-*O*-glucosyltransferase; UDP-glucose:anthocyanidin/flavonol 3-*O*-glucosyltransferase; UDP-glucose:cyanidin-3-*O*-glucosyltransferase; UDP-glucose:anthocyanidin 3-*O*-D-glucosyltransferase; 3-GT

Systematic name: UDP-D-glucose:anthocyanidin 3-*O*-β-D-glucosyltransferase

Comments: The anthocyanidin compounds cyanidin, delphinidin, peonidin and to a lesser extent pelargonidin can act as substrates. The enzyme does not catalyse glucosylation of the 5-position of cyanidin and does not act on flavanols such as quercetin and kaempferol (*cf.* EC 2.4.1.91 flavonol 3-*O*-glucosyltransferase). In conjunction with EC 1.14.20.4, anthocyanidin oxygenase, it is involved in the conversion of leucoanthocyanidin into anthocyanidin 3-glucoside. It may act on the pseudobase precursor of the anthocyanidin rather than on the anthocyanidin itself [2401].

References: [1578, 929, 2401]

[EC 2.4.1.115 created 1984 (EC 2.4.1.233 created 2004, incorporated 2005), modified 2005]

EC 2.4.1.116

Accepted name: cyanidin 3-*O*-rutinoside 5-*O*-glucosyltransferase

Reaction: UDP-α-D-glucose + cyanidin-3-*O*-rutinoside = UDP + cyanidin 3-*O*-rutinoside 5-*O*-β-D-glucoside

Other name(s): uridine diphosphoglucose-cyanidin 3-rhamnosylglucoside 5-*O*-glucosyltransferase; cyanidin-3-rhamnosylglucoside 5-*O*-glucosyltransferase; UDP-glucose:cyanidin-3-*O*-D-rhamnosyl-1,6-D-glucoside 5-*O*-D-glucosyltransferase

Systematic name: UDP-α-D-glucose:cyanidin-3-*O*-α-L-rhamnosyl-(1→6)-β-D-glucoside 5-*O*-β-D-glucosyltransferase

Comments: Isolated from the plants *Silene dioica* (red campion) [1579], *Iris ensata* (Japanese iris) [3933] and *Iris hollandica* (Dutch iris) [1442]. Also acts on the 3-*O*-rutinosides of pelargonidin, delphinidin and malvidin, but not the corresponding glucosides or 6-acylglucosides. The enzyme does not catalyse the glucosylation of the 5-hydroxy group of cyanidin 3-glucoside.

References: [1579, 3933, 1442]

[EC 2.4.1.116 created 1984 (EC 2.4.1.235 created 2004, incorporated 2006), modified 2006, modified 2013]

EC 2.4.1.117

Accepted name: dolichyl-phosphate β-glucosyltransferase

Reaction: UDP-α-D-glucose + dolichyl phosphate = UDP + dolichyl β-D-glucosyl phosphate

Other name(s): polyprenyl phosphate:UDP-D-glucose glucosyltransferase; UDP-glucose dolichyl-phosphate glucosyltransferase; uridine diphosphoglucose-dolichol glucosyltransferase; UDP-glucose:dolichol phosphate glucosyltransferase; UDP-glucose:dolicholphosphoryl glucosyltransferase; UDP-glucose:dolichyl monophosphate glucosyltransferase; UDP-glucose:dolichyl phosphate glucosyltransferase; UDP-glucose:dolichyl-phosphate β-D-glucosyltransferase

Systematic name: UDP-α-D-glucose:dolichyl-phosphate β-D-glucosyltransferase (configuration-inverting)

Comments: Solanesyl phosphate and ficaprenyl phosphate can act as acceptors, but more slowly.

References: [254, 1308, 3682]

[EC 2.4.1.117 created 1984]

EC 2.4.1.118

Accepted name: cytokinin 7-β-glucosyltransferase

Reaction: UDP-glucose + an N^6-alkylaminopurine = UDP + an N^6-alkylaminopurine-7-β-D-glucoside

Other name(s): uridine diphosphoglucose-zeatin 7-glucosyltransferase; cytokinin 7-glucosyltransferase; UDP-glucose:zeatin 7-glucosyltransferase

Systematic name: UDP-glucose:N^6-alkylaminopurine 7-glucosyltransferase

Comments: Acts on a range of N^6-substituted adenines, including zeatin and N^6-benzylaminopurine, but not N^6-benzyladenine. With some acceptors, 9-β-D-glucosides are also formed.

References: [843, 845]

[EC 2.4.1.118 created 1984]

[2.4.1.119 Transferred entry. dolichyl-diphosphooligosaccharideprotein glycotransferase. As the enzyme transfers more than one hexosyl group, it has been transferred to EC 2.4.99.18, dolichyl-diphosphooligosaccharideprotein glycotransferase]

[EC 2.4.1.119 created 1984, deleted 2012]

EC 2.4.1.120

Accepted name: sinapate 1-glucosyltransferase

Reaction: UDP-α-D-glucose + sinapate = UDP + 1-*O*-sinapoyl-β-D-glucose

Other name(s): uridine diphosphoglucose-sinapate glucosyltransferase; UDP-glucose:sinapic acid glucosyltransferase; uridine $5'$-diphosphoglucose-hydroxycinnamic acid acylglucosyltransferase; UDP-glucose:sinapate D-glucosyltransferase

Systematic name: UDP-α-D-glucose:sinapate D-glucosyltransferase

Comments: Some other hydroxycinnamates, including 4-coumarate, ferulate and caffeate, can act as acceptors, but more slowly. Only glucose esters, not glucosides, are formed (*cf.* EC 2.4.1.126 hydroxycinnamate 4-β-glucosyltransferase).

References: [3360]

[EC 2.4.1.120 created 1984]

EC 2.4.1.121

Accepted name: indole-3-acetate β-glucosyltransferase

Reaction: UDP-glucose + (indol-3-yl)acetate = UDP + 1-*O*-(indol-3-yl)acetyl-β-D-glucose

Other name(s): uridine diphosphoglucose-indoleacetate glucosyltransferase; UDPG-indol-3-ylacetyl glucosyl transferase; UDP-glucose:indol-3-ylacetate glucosyltransferase; indol-3-ylacetylglucose synthase; UDP-glucose:indol-3-ylacetate glucosyl-transferase; IAGlu synthase; IAA-glucose synthase; UDP-glucose:indole-3-acetate β-D-glucosyltransferase

Systematic name: UDP-glucose:(indol-3-yl)acetate β-D-glucosyltransferase
References: [2237]

[EC 2.4.1.121 created 1984]

EC 2.4.1.122

Accepted name: *N*-acetylgalactosaminide β-1,3-galactosyltransferase
Reaction: UDP-α-D-galactose + *N*-acetyl-α-D-galactosaminyl-R = UDP + β-D-galactosyl-(1→3)-*N*-acetyl-α-D-galactosaminyl-R
Other name(s): glycoprotein-*N*-acetylgalactosamine 3-β-galactosyltransferase; uridine diphosphogalactose-mucin β-(1→3)-galactosyltransferase; UDP-galactose:glycoprotein-*N*-acetyl-D-galactosamine 3-β-D-galactosyltransferase; UDP-Gal:α-D-GalNAc-1,3-α-D-GalNAc-diphosphoundecaprenol β-1,3-galactosyltransferase; *wbnJ* (gene name); *wbiP* (gene name); C1GALT1 (gene name); UDP-α-D-galactose:glycoprotein-*N*-acetyl-D-galactosamine 3-β-D-galactosyltransferase
Systematic name: UDP-α-D-galactose:*N*-acetyl-α-D-galactosaminyl-R β-1,3-galactosyltransferase (configuration-inverting)
Comments: The eukaryotic enzyme can act on non-reducing O-serine-linked *N*-acetylgalactosamine residues in mucin glycoproteins, forming the T-antigen. The bacterial enzyme, found in some pathogenic strains, is involved in biosynthesis of the O-antigen repeating unit.
References: [1310, 2216, 3058, 1544, 3977, 3893]

[EC 2.4.1.122 created 1984 (EC 2.4.1.307 created 2013, incorporated 2016), modified 2016]

EC 2.4.1.123

Accepted name: inositol 3-α-galactosyltransferase
Reaction: UDP-α-D-galactose + *myo*-inositol = UDP + *O*-α-D-galactosyl-(1→3)-1D-*myo*-inositol
Other name(s): UDP-D-galactose:inositol galactosyltransferase; UDP-galactose:*myo*-inositol 1-α-D-galactosyltransferase; UDPgalactose:*myo*-inositol 1-α-D-galactosyltransferase; galactinol synthase; inositol 1-α-galactosyltransferase; uridine diphosphogalactose-inositol galactosyltransferase; GolS; UDP-galactose:*myo*-inositol 3-α-D-galactosyltransferase
Systematic name: UDP-α-D-galactose:*myo*-inositol 3-α-D-galactosyltransferase
Comments: An enzyme from plants involved in the formation of raffinose and stachyose [*cf.* EC 2.4.1.67 (galactinol—raffinose galactosyltransferase) and EC 2.4.1.82 (galactinol—sucrose galactosyltransferase)].
References: [2690]

[EC 2.4.1.123 created 1984, modified 2003]

[2.4.1.124 Transferred entry. N-acetyllactosamine 3-α-galactosyltransferase. Now EC 2.4.1.87, N-acetyllactosaminide 3-α-galactosyltransferase]

[EC 2.4.1.124 created 1984, deleted 2002]

EC 2.4.1.125

Accepted name: sucrose—1,6-α-glucan 3(6)-α-glucosyltransferase
Reaction: (1) sucrose + [(1→6)-α-D-glucosyl]$_n$ = D-fructose + [(1→6)-α-D-glucosyl]$_{n+1}$
(2) sucrose + [(1→6)-α-D-glucosyl]$_n$ = D-fructose + (1→3)-α-D-glucosyl-[(1→6)-α-D-glucosyl]$_n$
Other name(s): water-soluble-glucan synthase (misleading); GTF-I; GTF-S; GTF-SI; sucrose-1,6-α-glucan 3(6)-α-glucosyltransferase; sucrose:1,6-α-D-glucan 3-α- and 6-α-glucosyltransferase; sucrose:1,6-, 1,3-α-D-glucan 3-α- and 6-α-D-glucosyltransferase; sucrose:1,6-α-D-glucan 3(6)-α-D-glucosyltransferase; *gtfB* (gene name); *gtfC* (gene name); *gtfD* (gene name)
Systematic name: sucrose:(1→6)-α-D-glucan 3(6)-α-D-glucosyltransferase

Comments: The enzyme was characterized from the dental caries bacterium *Streptococcus mutans*. It transfers glucosyl residues from sucrose to either the 6- or the 3-positions of glucose residues in glucans, producing a highly-branched extracellular D-glucan polymers that promote attachment of the bacteria to teeth. Three types of the enzyme have been described; the insoluble polymers produced by GTF-I and GTF-SI contain 85% α(1→3) bonds and 15% α(1→6) bonds, while the soluble polymers produced by GTF-S contain only 30% of α(1→3) bonds and 70% α(1→6) bonds. *cf.* EC 2.4.1.5, dextransucrase [2294].

References: [2344, 3191, 3586, 994, 2294, 1464]

[EC 2.4.1.125 created 1984]

EC 2.4.1.126

Accepted name: hydroxycinnamate 4-β-glucosyltransferase

Reaction: UDP-glucose + *trans*-4-hydroxycinnamate = UDP + 4-*O*-β-D-glucosyl-4-hydroxycinnamate

Other name(s): uridine diphosphoglucose-hydroxycinnamate glucosyltransferase; UDP-glucose-hydroxycinnamate glucosyltransferase; hydroxycinnamoyl glucosyltransferase

Systematic name: UDP-glucose:*trans*-4-hydroxycinnamate 4-*O*-β-D-glucosyltransferase

Comments: Acts on 4-coumarate, ferulate, caffeate and sinapate, forming a mixture of 4-glucosides and glucose esters (*cf.* EC 2.4.1.120 sinapate 1-glucosyltransferase).

References: [917]

[EC 2.4.1.126 created 1984]

EC 2.4.1.127

Accepted name: monoterpenol β-glucosyltransferase

Reaction: UDP-glucose + (-)-menthol = UDP + (-)-menthyl *O*-β-D-glucoside

Other name(s): uridine diphosphoglucose-monoterpenol glucosyltransferase; UDPglucose:monoterpenol glucosyltransferase

Systematic name: UDP-glucose:(-)-menthol *O*-β-D-glucosyltransferase

Comments: (+)-Neomenthol can also act as acceptor.

References: [917]

[EC 2.4.1.127 created 1984]

EC 2.4.1.128

Accepted name: scopoletin glucosyltransferase

Reaction: UDP-glucose + scopoletin = UDP + scopolin

Other name(s): uridine diphosphoglucose-scopoletin glucosyltransferase; UDP-glucose:scopoletin glucosyltransferase; SGTase

Systematic name: UDP-glucose:scopoletin *O*-β-D-glucosyltransferase

References: [1335]

[EC 2.4.1.128 created 1984]

EC 2.4.1.129

Accepted name: peptidoglycan glycosyltransferase

Reaction: [GlcNAc-(1→4)-Mur2Ac(oyl-L-Ala-γ-D-Glu-L-Lys-D-Ala-D-Ala)]$_{n}$-diphosphoundecaprenol + GlcNAc-(1→4)-Mur2Ac(oyl-L-Ala-γ-D-Glu-L-Lys-D-Ala-D-Ala)-diphosphoundecaprenol = [GlcNAc-(1→4)-Mur2Ac(oyl-L-Ala-γ-D-Glu-L-Lys-D-Ala-D-Ala)]$_{n+1}$-diphosphoundecaprenol + undecaprenyl diphosphate

Other name(s): PG-II; bactoprenyldiphospho-*N*-acetylmuramoyl-(*N*-acetyl-D-glucosaminyl)-pentapeptide:peptidoglycan *N*-acetylmuramoyl-*N*-acetyl-D-glucosaminyltransferase; penicillin binding protein (3 or 1B); peptidoglycan transglycosylase; undecaprenyldiphospho-(*N*-acetyl-D-glucosaminyl-(1→4)-*N*-acetyl-D-muramoylpentapeptide):undecaprenyldiphospho-(*N*-acetyl-D-glucosaminyl-(1→4)-*N*-acetyl-D-muramoylpentapeptide) disaccharidetransferase

Systematic name: [poly-*N*-acetyl-D-glucosaminyl-(1→4)-(*N*-acetyl-D-muramoylpentapeptide)]-diphosphoundecaprenol:[*N*-acetyl-D-glucosaminyl-(1→4)-*N*-acetyl-D-muramoylpentapeptide]-diphosphoundecaprenol disaccharidetransferase

Comments: The enzyme also works when the lysine residue is replaced by *meso*-2,6-diaminoheptanedioate (*meso*-2,6-diaminopimelate, A2pm) combined with adjacent residues through its L-centre, as it is in Gram-negative and some Gram-positive organisms. The undecaprenol involved is *ditrans*,*octacis*-undecaprenol (for definitions, click here). Involved in the synthesis of cell-wall peptidoglycan.

References: [3457, 1086, 3639]

[EC 2.4.1.129 created 1984, modified 2002]

[2.4.1.130 Transferred entry. dolichyl-phosphate-mannose—glycolipid α-mannosyltransferase. Now covered by EC 2.4.1.258 (Dol-P-Man:Man$_5$GlcNAc$_2$-PP-Dol α-1,3-mannosyltransferase), EC 2.4.1.259 (Dol-P-Man:Man$_6$GlcNAc$_2$-PP-Dol α-1,2-mannosyltransfe EC 2.4.1.260 (Dol-P-Man:Man$_7$GlcNAc$_2$-PP-Dol α-1,6-mannosyltransferase) and EC 2.4.1.261 (Dol-P-Man:Man$_8$GlcNAc$_2$-PP-Dol α-1,2-mannosyltransferase).]

[EC 2.4.1.130 created 1984, deleted 2011]

EC 2.4.1.131

Accepted name: GDP-Man:Man$_3$GlcNAc$_2$-*PP*-dolichol α-1,2-mannosyltransferase

Reaction: **2** GDP-α-D-mannose + α-D-Man-(1→3)-[α-D-Man-(1→6)]-β-D-Man-(1→4)-β-D-GlcNAc-(1→4)-α-D-GlcNAc-diphosphodolichol = **2** GDP + α-D-Man-(1→2)-α-D-Man-(1→2)-α-D-Man-(1→3)-[α-D-Man-(1→6)]-β-D-Man-(1→4)-β-D-GlcNAc-(1→4)-α-D-GlcNAc-diphosphodolichol

Other name(s): ALG11; ALG11 mannosyltransferase; LEW3 (gene name); At2G40190 (gene name); gmd3 (gene name); galactomannan deficiency protein 3; GDP-mannose:glycolipid 1,2-α-D-mannosyltransferase; glycolipid 2-α-mannosyltransferase; GDP-mannose:glycolipid 2-α-D-mannosyltransferase; GDP-Man:Man$_3$GlcNAc$_2$-*PP*-Dol α-1,2-mannosyltransferase; GDP-α-D-mannose:D-Man-α-(1→3)-[D-Man-α-(1→6)]-D-Man-β-(1→4)-D-GlcNAc-β-(1→4)-D-GlcNAc-diphosphodolichol 2-α-D-mannosyltransferase

Systematic name: GDP-α-D-mannose:α-D-Man-(1→3)-[α-D-Man-(1→6)]-β-D-Man-(1→4)-β-D-GlcNAc-(1→4)-α-D-GlcNAc-diphosphodolichol 2-α-D-mannosyltransferase (configuration-retaining)

Comments: The biosynthesis of asparagine-linked glycoproteins (N-linked protein glycosylation) utilizes a dolichyl diphosphate-linked glycosyl donor, which is assembled by the series of membrane-bound glycosyltransferases that comprise the dolichol pathway. ALG11 mannosyltransferase from *Saccharomyces cerevisiae* carries out two sequential steps in the formation of the lipid-linked core oligosaccharide, adding two mannose residues in α(1→2) linkages to the nascent oligosaccharide.

References: [2573, 11, 3117]

[EC 2.4.1.131 created 1984, modified 2011, modified 2012]

EC 2.4.1.132

Accepted name: GDP-Man:Man$_1$GlcNAc$_2$-*PP*-dolichol α-1,3-mannosyltransferase

Reaction: GDP-α-D-mannose + β-D-Man-(1→4)-β-D-GlcNAc-(1→4)-α-D-GlcNAc-diphosphodolichol = GDP + α-D-Man-(1→3)-β-D-Man-(1→4)-β-D-GlcNAc-(1→4)-α-D-GlcNAc-diphosphodolichol

Other name(s): Alg2 mannosyltransferase (ambiguous); ALG2 (gene name, ambiguous); glycolipid 3-α-mannosyltransferase; GDP-mannose:glycolipid 3-α-D-mannosyltransferase; GDP-Man:Man$_1$GlcNAc$_2$-*PP*-Dol α-1,3-mannosyltransferase; GDP-D-mannose:D-Man-β-(1→4)-D-GlcNAc-β-(1→4)-D-GlcNAc-diphosphodolichol 3-α-mannosyltransferase

Systematic name: GDP-α-D-mannose:β-D-Man-(1→4)-β-D-GlcNAc-(1→4)-α-D-GlcNAc-diphosphodolichol 3-α-D-mannosyltransferase (configuration-retaining)

Comments: The biosynthesis of asparagine-linked glycoproteins utilizes a dolichyl diphosphate-linked glycosyl donor, which is assembled by the series of membrane-bound glycosyltransferases that comprise the dolichol pathway. Alg2 mannosyltransferase from *Saccharomyces cerevisiae* carries out an α1,3-mannosylation of D-Man-β-(1→4)-D-GlcNAc-β-(1→4)-D-GlcNAc-diphosphodolichol, followed by an α1,6-mannosylation (*cf.* EC 2.4.1.257), to form the first branched pentasaccharide intermediate of the dolichol pathway [1577, 2573].

References: [1577, 2573]

[EC 2.4.1.132 created 1984, modified 2011, modified 2012]

EC 2.4.1.133

Accepted name: xylosylprotein 4-β-galactosyltransferase

Reaction: UDP-α-D-galactose + [protein]-3-*O*-(β-D-xylosyl)-L-serine = UDP + [protein]-3-*O*-(β-D-galactosyl-(1→4)-β-D-xylosyl)-L-serine

Other name(s): UDP-D-galactose:D-xylose galactosyltransferase; UDP-D-galactose:xylose galactosyltransferase; galactosyltransferase I; uridine diphosphogalactose-xylose galactosyltransferase; UDP-galactose:*O*-β-D-xylosylprotein 4-β-D-galactosyltransferase; UDP-α-D-galactose:*O*-β-D-xylosylprotein 4-β-D-galactosyltransferase; UDP-α-D-galactose:*O*-β-D-xylosyl-[protein] 4-β-D-galactosyltransferase

Systematic name: UDP-α-D-galactose:[protein]-3-*O*-(β-D-xylosyl)-L-serine 4-β-D-galactosyltransferase (configuration-inverting)

Comments: Involved in the biosynthesis of the linkage region of glycosaminoglycan chains as part of proteoglycan biosynthesis (chondroitin, dermatan and heparan sulfates). Requires Mn^{2+}.

References: [3118, 2550]

[EC 2.4.1.133 created 1984, modified 2002]

EC 2.4.1.134

Accepted name: galactosylxylosylprotein 3-β-galactosyltransferase

Reaction: UDP-α-D-galactose + [protein]-3-*O*-(β-D-galactosyl-(1→4)-β-D-xylosyl)-L-serine = UDP + [protein]-3-*O*-(β-D-galactosyl-(1→3)-β-D-galactosyl-(1→4)-β-D-xylosyl)-L-serine

Other name(s): galactosyltransferase II; uridine diphosphogalactose-galactosylxylose galactosyltransferase; UDP-galactose:4-β-D-galactosyl-*O*-β-D-xylosylprotein 3-β-D-galactosyltransferase; UDP-α-D-galactose:4-β-D-galactosyl-*O*-β-D-xylosylprotein 3-β-D-galactosyltransferase

Systematic name: UDP-α-D-galactose:[protein]-3-*O*-(β-D-galactosyl-(1→4)-β-D-xylosyl)-L-serine (configuration-inverting)

Comments: Involved in the biosynthesis of the linkage region of glycosaminoglycan chains as part of proteoglycan biosynthesis (chondroitin, dermatan and heparan sulfates). Requires Mn^{2+}.

References: [2903, 3118, 159]

[EC 2.4.1.134 created 1984, modified 2002]

EC 2.4.1.135

Accepted name: galactosylgalactosylxylosylprotein 3-β-glucuronosyltransferase

Reaction: UDP-α-D-glucuronate + [protein]-3-*O*-(β-D-galactosyl-(1→3)-β-D-galactosyl-(1→4)-β-D-xylosyl)-L-serine = UDP + [protein]-3-*O*-(β-D-GlcA-(1→3)-β-D-Gal-(1→3)-β-D-Gal-(1→4)-β-D-Xyl)-L-serine

Other name(s): glucuronosyltransferase I; uridine diphosphate glucuronic acid:acceptor glucuronosyltransferase; UDP-glucuronate:3-β-D-galactosyl-4-β-D-galactosyl-*O*-β-D-xylosyl-protein D-glucuronosyltransferase; UDP-glucuronate:3-β-D-galactosyl-4-β-D-galactosyl-*O*-β-D-xylosylprotein D-glucuronosyltransferase

Systematic name: UDP-α-D-glucuronate:[protein]-3-*O*-(β-D-galactosyl-(1→3)-β-D-galactosyl-(1→4)-β-D-xylosyl)-L-serine D-glucuronosyltransferase (configuration-inverting)

Comments: Involved in the biosynthesis of the linkage region of glycosaminoglycan chains as part of proteoglycan biosynthesis (chondroitin, dermatan and heparan sulfates). Requires Mn^{2+}.

References: [1287, 1288, 1698]

[EC 2.4.1.135 created 1984, modified 2002, modified 2016]

EC 2.4.1.136

Accepted name: gallate 1-β-glucosyltransferase
Reaction: UDP-glucose + gallate = UDP + 1-galloyl-β-D-glucose
Other name(s): UDP-glucose—vanillate 1-glucosyltransferase; UDPglucose:vanillate 1-*O*-glucosyltransferase; UDPglucose:gallate glucosyltransferase
Systematic name: UDP-glucose:gallate β-D-glucosyltransferase
Comments: A number of substituted benzoic acids and, more slowly, cinnamic acids, can act as acceptors. Vanillin is the best acceptor investigated.
References: [1147, 1148]

[EC 2.4.1.136 created 1984]

EC 2.4.1.137

Accepted name: *sn*-glycerol-3-phosphate 2-α-galactosyltransferase
Reaction: UDP-α-D-galactose + *sn*-glycerol 3-phosphate = UDP + 2-(α-D-galactosyl)-*sn*-glycerol 3-phosphate
Other name(s): floridoside-phosphate synthase; UDP-galactose:*sn*-glycerol-3-phosphate-2-D-galactosyl transferase; FPS; UDP-galactose,*sn*-3-glycerol phosphate:1→2′ galactosyltransferase; floridoside phosphate synthetase; floridoside phosphate synthase; UDP-galactose:*sn*-glycerol-3-phosphate 2-α-D-galactosyltransferase
Systematic name: UDP-α-D-galactose:*sn*-glycerol-3-phosphate 2-α-D-galactosyltransferase
Comments: The product is hydrolysed by a phosphatase to floridoside (*cf.* EC 2.4.1.96 *sn*-glycerol-3-phosphate 1-galactosyltransferase).
References: [1127]

[EC 2.4.1.137 created 1984]

EC 2.4.1.138

Accepted name: mannotetraose 2-α-*N*-acetylglucosaminyltransferase
Reaction: UDP-*N*-acetyl-α-D-glucosamine + α-D-Man-(1→3)-α-D-Man-(1→2)-α-D-Man-(1→2)-D-Man = UDP + α-D-Man-(1→3)-[α-D-GlcNAc-(1→2)]-α-D-Man-(1→2)-α-D-Man-(1→2)-D-Man
Other name(s): α-*N*-acetylglucosaminyltransferase; uridine diphosphoacetylglucosamine mannoside α1→2-αcetylglucosaminyltransferase; UDP-*N*-acetyl-D-glucosamine:mannotetraose α-*N*-acetyl-D-glucosaminyltransferase
Systematic name: UDP-*N*-acetyl-α-D-glucosamine:α-D-mannosyl-(1→3)-α-D-mannosyl-(1→2)-α-D-mannosyl-(1→2)-D-mannose α-*N*-acetyl-D-glucosaminyltransferase (configuration-retaining)
References: [762]

[EC 2.4.1.138 created 1984]

EC 2.4.1.139

Accepted name: maltose synthase
Reaction: **2** α-D-glucose 1-phosphate + H_2O = maltose + **2** phosphate
Systematic name: α-D-glucose-1-phosphate:α-D-glucose-1-phosphate 4-α-D-glucosyltransferase (dephosphorylating)
Comments: Neither free phosphate nor maltose 1-phosphate is an intermediate in the reaction.
References: [3073]

[EC 2.4.1.139 created 1984]

EC 2.4.1.140

Accepted name: alternansucrase

Reaction: Transfers alternately an α-D-glucosyl residue from sucrose to the 6-position and the 3-position of the non-reducing terminal residue of an α-D-glucan, thus producing a glucan having alternating α-(1→6)- and α-(1→3)-linkages

Other name(s): sucrose-1,6(3)-α-glucan 6(3)-α-glucosyltransferase; sucrose:1,6-, 1,3-α-D-glucan 3-α- and 6-α-D-glucosyltransferase; sucrose:1,6(1,3)-α-D-glucan 6(3)-α-D-glucosyltransferase

Systematic name: sucrose:(1→6)[(1→3)]-α-D-glucan 6(3)-α-D-glucosyltransferase

Comments: The product, which has quite different properties from other dextrans, has been called alternan.

References: [621]

[EC 2.4.1.140 created 1984, modified 2003]

EC 2.4.1.141

Accepted name: *N*-acetylglucosaminyldiphosphodolichol *N*-acetylglucosaminyltransferase

Reaction: UDP-*N*-acetyl-α-D-glucosamine + *N*-acetyl-α-D-glucosaminyl-diphosphodolichol = UDP + *N*-acetyl-β-D-glucosaminyl-(1→4)-*N*-acetyl-α-D-glucosaminyl-diphosphodolichol

Other name(s): UDP-GlcNAc:dolichyl-pyrophosphoryl-GlcNAc GlcNAc transferase; uridine diphosphoacetylglucosamine-dolichylacetylglucosamine pyrophosphate acetylglucosaminyltransferase; *N*,*N*′-diacetylchitobiosylpyrophosphoryldolichol synthase; UDP-*N*-acetyl-D-glucosamine:*N*-acetyl-D-glucosaminyl-diphosphodolichol *N*-acetyl-D-glucosaminyltransferase

Systematic name: UDP-*N*-acetyl-α-D-glucosamine:*N*-acetyl-α-D-glucosaminyl-diphosphodolichol 4-β-*N*-acetyl-D-glucosaminyltransferase (configuration-inverting)

References: [3156, 3591]

[EC 2.4.1.141 created 1984]

EC 2.4.1.142

Accepted name: chitobiosyldiphosphodolichol β-mannosyltransferase

Reaction: GDP-α-D-mannose + *N*-acetyl-β-D-glucosaminyl-(1→4)-*N*-acetyl-α-D-glucosaminyl-diphosphodolichol = GDP + β-D-mannosyl-(1→4)-*N*-acetyl-β-D-glucosaminyl-(1→4)-*N*-acetyl-α-D-glucosaminyl-diphosphodolichol

Other name(s): guanosine diphosphomannose-dolichol diphosphochitobiose mannosyltransferase; GDP-mannose-dolichol diphosphochitobiose mannosyltransferase; GDP-mannose:chitobiosyldiphosphodolichol β-D-mannosyltransferase

Systematic name: GDP-α-D-mannose:*N*-acetyl-β-D-glucosaminyl-(1→4)-*N*-acetyl-α-D-glucosaminyl-diphosphodolichol 4-β-D-mannosyltransferase (configuration-inverting)

References: [3156, 3443]

[EC 2.4.1.142 created 1984, modified 2001]

EC 2.4.1.143

Accepted name: α-1,6-mannosyl-glycoprotein 2-β-*N*-acetylglucosaminyltransferase

Reaction: UDP-*N*-acetyl-α-D-glucosamine + β-D-GlcNAc-(1→2)-α-D-Man-(1→3)-[α-D-Man-(1→6)]-β-D-Man-(1→4)-β-D-GlcNAc-(1→4)-β-D-GlcNAc-*N*-Asn-[protein] = UDP + β-D-GlcNAc-(1→2)-α-D-Man-(1→3)-[β-D-GlcNAc-(1→2)-α-D-Man-(1→6)]-β-D-Man-(1→4)-β-D-GlcNAc-(1→4)-β-D-GlcNAc-*N*-Asn-[protein]

Other name(s): MGAT2 (gene name); *N*-acetylglucosaminyltransferase II; *N*-glycosyl-oligosaccharide-glycoprotein *N*-acetylglucosaminyltransferase II; acetylglucosaminyltransferase II; uridine diphosphoacetylglucosamine-mannoside α1→6-acetylglucosaminyltransferase; uridine diphosphoacetylglucosamine-α-1,6-mannosylglycoprotein β-1-2-*N*-acetylglucosaminyltransferase; uridine diphosphoacetylglucosamine-α-D-mannoside β1-2-acetylglucosaminyltransferase; UDP-GlcNAc:mannoside α1-6 acetylglucosaminyltransferase; α-1,6-mannosyl-glycoprotein β-1,2-*N*-acetylglucosaminyltransferase; GnTII; GlcNAc-T II; UDP-*N*-acetyl-D-glucosamine:6-(α-D-mannosyl)-β-D-mannosyl-glycoprotein 2-β-*N*-acetyl-D-glucosaminyltransferase

Systematic name: UDP-*N*-acetyl-α-D-glucosamine:α-D-mannosyl-(1→6)-β-D-mannosyl-glycoprotein 2-β-*N*-acetyl-D-glucosaminyltransferase (configuration-inverting)

Comments: The enzyme, found in plants and animals, participates in the processing of *N*-glycans in the Golgi apparatus. Its activity initiates the synthesis of the second antenna of di-antennary complex *N*-glycans. While the natural substrate (produced by EC 3.2.1.114, mannosyl-oligosaccharide 1,3-1,6-α-mannosidase) is described here, the minimal substrate recognized by the enzyme is α-D-Man-(1→6)-[β-D-GlcNAc-(1→2)-α-D-Man-(1→3)]-β-D-Man-R.

References: [1227, 2215, 2569, 3058, 265, 266, 3462]

[EC 2.4.1.143 created 1984, modified 2001 (EC 2.4.1.51 created 1972, part incorporated 1984), modified 2018]

EC 2.4.1.144

Accepted name: β-1,4-mannosyl-glycoprotein 4-β-*N*-acetylglucosaminyltransferase

Reaction: UDP-*N*-acetyl-α-D-glucosamine + β-D-GlcNAc-(1→2)-α-D-Man-(1→3)-[β-D-GlcNAc-(1→2)-α-D-Man-(1→6)]-β-D-Man-(1→4)-β-D-GlcNAc-(1→4)-β-D-GlcNAc-*N*-Asn-[protein] = UDP + β-D-GlcNAc-(1→2)-α-D-Man-(1→3)-[β-D-GlcNAc-(1→2)-α-D-Man-(1→6)]-[β-D-GlcNAc-(1→4)]-β-D-Man-(1→4)-β-D-GlcNAc-(1→4)-β-D-GlcNAc-*N*-Asn-[protein]

Other name(s): *N*-acetylglucosaminyltransferase III; *N*-glycosyl-oligosaccharide-glycoprotein *N*-acetylglucosaminyltransferase III; uridine diphosphoacetylglucosamine-glycopeptide β4-acetylglucosaminyltransferase III; β-1,4-mannosyl-glycoprotein β-1,4-*N*-acetylglucosaminyltransferase; GnTIII; GlcNAc-T III; MGAT3 (gene name); UDP-*N*-acetyl-D-glucosamine:β-D-mannosyl-glycoprotein 4-β-*N*-acetyl-D-glucosaminyltransferase

Systematic name: UDP-*N*-acetyl-α-D-glucosamine:β-D-mannosyl-glycoprotein 4-β-*N*-acetyl-D-glucosaminyltransferase (configuration-inverting)

Comments: The enzyme, found in vertebrates, participates in the processing of *N*-glycans in the Golgi apparatus. The residue added by the enzyme at position 4 of the β-linked mannose of the trimannosyl core of *N*-glycans is known as a bisecting GlcNAc. Unlike GlcNAc residues added to other positions, it is not extended or modified. In addition, its presence prevents the action of other branching enzymes involved in the process such as GlcNAc-T IV (EC 2.4.1.145) and GlcNAc-T V (EC 2.4.1.155), and thus increased activity of GlcNAc-T III leads to a decrease in highly branched *N*-glycan structures.

References: [2418, 3058, 394, 2463, 1431]

[EC 2.4.1.144 created 1984, modified 2001 (EC 2.4.1.51 created 1972, part incorporated 1984), modified 2018]

EC 2.4.1.145

Accepted name: α-1,3-mannosyl-glycoprotein 4-β-*N*-acetylglucosaminyltransferase

Reaction: UDP-*N*-acetyl-α-D-glucosamine + β-D-GlcNAc-(1→2)-α-D-Man-(1→3)-[β-D-GlcNAc-(1→2)-α-D-Man-(1→6)]-β-D-Man-(1→4)-β-D-GlcNAc-(1→4)-β-D-GlcNAc-*N*-Asn-[protein] = UDP + β-D-GlcNAc-(1→2)-[β-D-GlcNAc-(1→4)]-α-D-Man-(1→3)-[β-D-GlcNAc-(1→2)-α-D-Man-(1→6)]-β-D-Man-(1→4)-β-D-GlcNAc-(1→4)-β-D-GlcNAc-*N*-Asn-[protein]

Other name(s): *N*-acetylglucosaminyltransferase IV; *N*-glycosyl-oligosaccharide-glycoprotein *N*-acetylglucosaminyltransferase IV; β-acetylglucosaminyltransferase IV; uridine diphosphoacetylglucosamine-glycopeptide β4-acetylglucosaminyltransferase IV; α-1,3-mannosylglycoprotein β-1,4-*N*-acetylglucosaminyltransferase; GnTIV; UDP-*N*-acetyl-D-glucosamine:3-[2-(*N*-acetyl-β-D-glucosaminyl)-α-D-mannosyl]-glycoprotein 4-β-*N*-acetyl-D-glucosaminyltransferase

Systematic name: UDP-*N*-acetyl-α-D-glucosamine:*N*-acetyl-β-D-glucosaminyl-(1→2)-α-D-mannosyl-(1→3)-β-D-mannosyl-glycoprotein 4-β-*N*-acetyl-D-glucosaminyltransferase (configuration-inverting)

Comments: Requires Mn^{2+}. The enzyme, found in vertebrates, participates in the processing of *N*-glycans in the Golgi apparatus. By adding a glucosaminyl residue to biantennary N-linked glycans, it enables the synthesis of tri- and tetra-antennary complexes.

References: [1075, 2527, 2265, 3999, 3998, 3444]

[EC 2.4.1.145 created 1984, modified 2001 (EC 2.4.1.51 created 1972, part incorporated 1984), modified 2018]

EC 2.4.1.146

Accepted name: β-1,3-galactosyl-*O*-glycosyl-glycoprotein β-1,3-*N*-acetylglucosaminyltransferase

Reaction: UDP-*N*-acetyl-α-D-glucosamine + 3-*O*-β-D-galactosyl-(1→3)-[*N*-acetyl-β-D-glucosaminyl-(1→6)]-*N*-acetyl-α-D-galactosaminyl-L-seryl/threonyl-[protein] = UDP + 3-*O*-*N*-acetyl-β-D-glucosaminyl-(1→3)-β-D-galactosyl-(1→3)-[*N*-acetyl-β-D-glucosaminyl-(1→6)]-*N*-acetyl-α-D-galactosaminyl-L-seryl/threonyl-[protein]

Other name(s): *O*-glycosyl-oligosaccharide-glycoprotein *N*-acetylglucosaminyltransferase II; uridine diphosphoacetylglucosamine-mucin β(1→3)-acetylglucosaminyltransferase (elongating); elongation 3β-GalNAc-transferase; UDP-*N*-acetyl-D-glucosamine:*O*-glycosyl-glycoprotein (*N*-acetyl-D-glucosamine to β-D-galactose of β-D-galactosyl-1,3-(*N*-acetyl-D-glucosaminyl-1,6)-*N*-acetyl-D-galactosaminyl-R) β-1,3-*N*-acetyl-D-glucosaminyltransferase; UDP-*N*-acetyl-D-glucosamine:β-D-galactosyl-(1→3)-[*N*-acetyl-D-glucosaminyl-(1→6)]-*N*-acetyl-D-galactosaminyl-R 3-β-*N*-acetyl-D-glucosaminyltransferase; B3GNT3 (gene name)

Systematic name: UDP-*N*-acetyl-α-D-glucosamine:3-*O*-β-D-galactosyl-(1→3)-[*N*-acetyl-β-D-glucosaminyl-(1→6)]-*N*-acetyl-α-D-galactosaminyl-L-seryl/threonyl-[protein] 3-β-*N*-acetyl-D-glucosaminyltransferase (configuration-inverting)

Comments: The enzyme catalyses the addition of *N*-acetyl-α-D-glucosamine to the core 2 structure of *O*-glycans.

References: [398, 3209]

[EC 2.4.1.146 created 1984, modified 2018]

EC 2.4.1.147

Accepted name: acetylgalactosaminyl-*O*-glycosyl-glycoprotein β-1,3-*N*-acetylglucosaminyltransferase

Reaction: UDP-*N*-acetyl-α-D-glucosamine + O^3-[*N*-acetyl-α-D-galactosaminyl]-L-threonyl/L-seryl-[protein] = UDP + O^3-[*N*-acetyl-β-D-glucosaminyl-(1→3)-*N*-acetyl-α-D-galactosaminyl]-L-threonyl/L-seryl-[protein]

Other name(s): *O*-glycosyl-oligosaccharide-glycoprotein *N*-acetylglucosaminyltransferase III; uridine diphosphoacetylglucosamine-mucin β(1→3)-acetylglucosaminyltransferase; mucin core 3 β3-GlcNAc-transferase; Core 3β-GlcNAc-transferase; UDP-*N*-acetyl-D-glucosamine:*O*-glycosyl-glycoprotein (*N*-acetyl-D-glucosamine to *N*-acetyl-D-galactosaminyl-R) β-1,3-*N*-acetyl-D-glucosaminyltransferase; UDP-*N*-acetyl-D-glucosamine:*N*-acetyl-β-D-galactosaminyl-R 3-β-*N*-acetyl-D-glucosaminyltransferase (incorrect)

Systematic name: UDP-*N*-acetyl-α-D-glucosamine:O^3-[*N*-acetyl-α-D-galactosaminyl]-L-threonyl/L-seryl-[protein] 3-β-*N*-acetyl-D-glucosaminyltransferase

Comments: The product of the enzyme is known as core 3, one of the eight core structures of mucin-type *O*-glycans. O-Linked glycans are polysaccharides or oligosaccharides that are linked to a protein via the oxygen atom in the side chain of an L-serine or L-threonine residue.

References: [398, 397, 3654]

[EC 2.4.1.147 created 1984, modified 2015]

EC 2.4.1.148

Accepted name: acetylgalactosaminyl-*O*-glycosyl-glycoprotein β-1,6-*N*-acetylglucosaminyltransferase

Reaction: UDP-*N*-acetyl-D-glucosamine + *N*-acetyl-β-D-glucosaminyl-(1→3)-*N*-acetyl-D-galactosaminyl-R = UDP + *N*-acetyl-β-D-glucosaminyl-(1→6)-[*N*-acetyl-β-D-glucosaminyl-(1→3)]-*N*-acetyl-D-galactosaminyl-R

Other name(s): *O*-glycosyl-oligosaccharide-glycoprotein *N*-acetylglucosaminyltransferase IV; uridine diphosphoacetylglucosamine-mucin β(1→6)-acetylglucosaminyltransferase B; core 4 β6-GalNAc-transferase; core 6β-GalNAc-transferase B; UDP-*N*-acetyl-D-glucosamine:*O*-oligosaccharide-glycoprotein (*N*-acetyl-D-glucosamine to *N*-acetyl-D-galactosamine of *N*-acetyl-β-D-glucosaminyl-1,3-*N*-acetyl-D-galactosaminyl-R) β-1,6-*N*-acetyl-D-glucosaminyltransferase

Systematic name: UDP-*N*-acetyl-D-glucosamine:*N*-acetyl-β-D-glucosaminyl-(1→3)-*N*-acetyl-D-galactosaminyl-R 6-β-*N*-acetyl-D-glucosaminyltransferase

Comments: *cf.* EC 2.4.1.102 (β-1,3-galactosyl-*O*-glycosyl-glycoprotein β-1,6-*N*-acetylglucosaminyltransferase), EC 2.4.1.146 (β-1,3-galactosyl-*O*-glycosyl-glycoprotein β-1,3-*N*-acetylglucosaminyltransferase) and EC 2.4.1.147 (acetylgalactosaminyl-*O*-glycosyl-glycoprotein β-1,3-*N*-acetylglucosaminyltransferase).

References: [398]

[EC 2.4.1.148 created 1984]

EC 2.4.1.149

Accepted name: *N*-acetyllactosaminide β-1,3-*N*-acetylglucosaminyltransferase

Reaction: UDP-*N*-acetyl-α-D-glucosamine + β-D-galactosyl-(1→4)-*N*-acetyl-β-D-glucosaminyl-R = UDP + *N*-acetyl-β-D-glucosaminyl-(1→3)-β-D-galactosyl-(1→4)-*N*-acetyl-β-D-glucosaminyl-R

Other name(s): uridine diphosphoacetylglucosamine-acetyllactosaminide β1→3-acetylglucosaminyltransferase; poly-*N*-acetyllactosamine extension enzyme; Galβ1→4GlcNAc-R β1→3 *N*-acetylglucosaminyltransferase; UDP-GlcNAc:GalR β-D-3-*N*-acetylglucosaminyltransferase; *N*-acetyllactosamine β(1-3)*N*-acetylglucosaminyltransferase; UDP-GlcNAc:Galβ1→4GlcNAcβ-Rβ1→3-*N*-acetylglucosaminyltransferase; GnTE; UDP-*N*-acetyl-D-glucosamine:β-D-galactosyl-1,4-*N*-acetyl-D-glucosamine β-1,3-acetyl-D-glucosaminyltransferase; β-galactosyl-*N*-acetylglucosaminylgalactosylglucosyl-ceramide β-1,3-acetylglucosaminyltransferase; UDP-*N*-acetyl-D-glucosamine:β-D-galactosyl-(1→4)-*N*-acetyl-D-glucosamine 3-β-*N*-acetyl-D-glucosaminyltransferase

Systematic name: UDP-*N*-acetyl-α-D-glucosamine:β-D-galactosyl-(1→4)-*N*-acetyl-β-D-glucosaminyl-R 3-β *N*-acetylglucosaminyltransferase (configuration-inverting)

Comments: Acts on β-galactosyl-1,4-*N*-acetylglucosaminyl termini on glycoproteins, glycolipids, and oligosaccharides.

References: [708, 221, 3454]

[EC 2.4.1.149 created 1984 (EC 2.4.1.163 created 1989, incorporated 2016), modified 2016]

EC 2.4.1.150

Accepted name: *N*-acetyllactosaminide β-1,6-*N*-acetylglucosaminyltransferase

Reaction: UDP-*N*-acetyl-α-D-glucosamine + β-D-Gal-(1→4)-β-D-GlcNAc-(1→3)-β-D-Gal-(1→4)-β-D-GlcNAc-R = UDP + β-D-Gal-(1→4)-β-D-GlcNAc-(1→3)-[β-D-GlcNAc-(1→6)]-β-D-Gal-(1→4)-β-D-GlcNAc-R

Other name(s): GCNT2 (gene name); GCNT3 (gene name); IGnT; I-branching β1,6-*N*-acetylglucosaminyltransferase; *N*-acetylglucosaminyltransferase; uridine diphosphoacetylglucosamine-acetyllactosaminide β1→6-acetylglucosaminyltransferase; Galβ1→4GlcNAc-R β1→6 *N*-acetylglucosaminyltransferase; UDP-*N*-acetyl-D-glucosamine:β-D-galactosyl-1,4-*N*-acetyl-D-glucosaminide β-1,6-*N*-acetyl-D-glucosaminyltransferase

Systematic name: UDP-*N*-acetyl-α-D-glucosamine:β-D-galactosyl-(1→4)-*N*-acetyl-β-D-glucosaminyl-(1→3)-β-D-galactosyl-(1→4)-*N*-acetyl-β-D-glucosaminide 6-β-*N*-acetylglucosaminyltransferase (configuration-inverting)

Comments: The enzyme acts on poly-*N*-acetyllactosamine [glycan chains of β-D-galactosyl-(1→4)-*N*-acetyl-D-glucosamine units connected by β(1,3) linkages] attached to proteins or lipids. It transfers a GlcNAc residue by β(1,6)-linkage to galactosyl residues close to non-reducing terminals, introducing a branching pattern known as I branching.

References: [708, 221, 2712, 306, 3607, 3975]

[EC 2.4.1.150 created 1984 (EC 2.4.1.164 created 1989, incorporated 2016), modified 2017]

[2.4.1.151 Transferred entry. N-acetyllactosaminide α-1,3-galactosyltransferase. Now EC 2.4.1.87, N-acetyllactosaminide 3-α-galactosyltransferase]

[EC 2.4.1.151 created 1984, deleted 2002]

EC 2.4.1.152

Accepted name: 4-galactosyl-*N*-acetylglucosaminide 3-α-L-fucosyltransferase

Reaction: GDP-β-L-fucose + (1→4)-β-D-galactosyl-*N*-acetyl-D-glucosaminyl-R = GDP + (1→4)-β-D-galactosyl-[α-(1→3)-L-fucosyl]-*N*-acetyl-D-glucosaminyl-R

Other name(s): Lewis-negative α-3-fucosyltransferase; plasma α-3-fucosyltransferase; guanosine diphosphofucose-glucoside α1→3-fucosyltransferase; galactoside 3-fucosyltransferase; GDP-L-fucose:1,4-β-D-galactosyl-*N*-acetyl-D-glucosaminyl-R 3-L-fucosyltransferase; GDP-β-L-fucose:1,4-β-D-galactosyl-*N*-acetyl-D-glucosaminyl-R 3-L-fucosyltransferase; GDP-β-L-fucose:1,4-β-D-galactosyl-*N*-acetyl-D-glucosaminyl-R 3-α-L-fucosyltransferase

Systematic name: GDP-β-L-fucose:(1→4)-β-D-galactosyl-*N*-acetyl-D-glucosaminyl-R 3-α-L-fucosyltransferase

Comments: Normally acts on a glycoconjugate where R (see reaction) is a glycoprotein or glycolipid. This enzyme fucosylates on O-3 of an *N*-acetylglucosamine that carries a galactosyl group on O-4, unlike EC 2.4.1.65, 3-galactosyl-*N*-acetylglucosaminide 4-α-L-fucosyltransferase, which fucosylates on O-4 of an *N*-acetylglucosamine that carries a galactosyl group on O-3.

References: [1525, 3058, 2082]

[EC 2.4.1.152 created 1984, modified 2002]

EC 2.4.1.153

Accepted name: UDP-*N*-acetylglucosamine—dolichyl-phosphate *N*-acetylglucosaminyltransferase

Reaction: UDP-*N*-acetyl-α-D-glucosamine + dolichyl phosphate = UDP + dolichyl *N*-acetyl-α-D-glucosaminyl phosphate

Other name(s): *aglK* (gene name); dolichyl-phosphate α-*N*-acetylglucosaminyltransferase; UDP-*N*-acetyl-D-glucosamine:dolichyl-phosphate α-*N*-acetyl-D-glucosaminyltransferase

Systematic name: UDP-*N*-acetyl-α-D-glucosamine:dolichyl-phosphate α-*N*-acetyl-D-glucosaminyltransferase

Comments: The enzyme, characterized from the methanogenic archaeon *Methanococcus voltae*, initiates N-linked glycosylation in that organism. The enzyme differs from the eukaryotic enzyme, which leaves one additional phosphate group on the dolichyl product (*cf.* EC 2.7.8.15, UDP-*N*-acetylglucosamine—dolichyl-phosphate *N*-acetylglucosaminephosphotransferase).

References: [1863]

[EC 2.4.1.153 created 1984, modified 2015]

[2.4.1.154 Deleted entry. globotriosylceramide β*-1,6-N-acetylgalactosaminyl-transferase. The enzyme is identical to EC 2.4.1.79, globotriaosylceramide 3-*β*-N-acetylgalactosaminyltransferase. The reference cited referred to a 1→3 linkage and not to a 1→6 linkage, as indicated in the enzyme entry]*

[EC 2.4.1.154 created 1986, deleted 2006]

EC 2.4.1.155

Accepted name: α-1,6-mannosyl-glycoprotein 6-β-*N*-acetylglucosaminyltransferase

Reaction: UDP-*N*-acetyl-α-D-glucosamine + β-D-GlcNAc-(1→2)-[β-D-GlcNAc-(1→4)]-α-D-Man-(1→3)-[β-D-GlcNAc-(1→2)-α-D-Man-(1→6)]-β-D-Man-(1→4)-β-D-GlcNAc-(1→4)-β-D-GlcNAc-*N*-Asn-[protein] = UDP + β-D-GlcNAc-(1→2)-[β-D-GlcNAc-(1→4)]-α-D-Man-(1→3)-[β-D-GlcNAc-(1→2)-[β-D-GlcNAc-(1→6)]-α-D-Man-(1→6)]-β-D-Man-(1→4)-β-D-GlcNAc-(1→4)-β-D-GlcNAc-*N*-Asn-[protein]

Other name(s): MGAT5 (gene name); *N*-acetylglucosaminyltransferase V; α-mannoside β-1,6-*N*-acetylglucosaminyltransferase; uridine diphosphoacetylglucosamine-α-mannoside β1→6-acetylglucosaminyltransferase; UDP-*N*-acetylglucosamine:α-mannoside-β1,6 *N*-acetylglucosaminyltransferase; α-1,3(6)-mannosylglycoprotein β-1,6-*N*-acetylglucosaminyltransferase; GnTV; GlcNAc-T V; UDP-*N*-acetyl-D-glucosamine:6-[2-(*N*-acetyl-β-D-glucosaminyl)-α-D-mannosyl]-glycoprotein 6-β-*N*-acetyl-D-glucosaminyltransferase

Systematic name: UDP-*N*-acetyl-α-D-glucosamine:*N*-acetyl-β-D-glucosaminyl-(1→2)-α-D-mannosyl-(1→6)-β-D-mannosyl-glycoprotein 6-β-*N*-acetyl-D-glucosaminyltransferase (configuration-inverting)

Comments: Requires Mg^{2+}. The enzyme, found in vertebrates, participates in the processing of *N*-glycans in the Golgi apparatus. It catalyses the addition of *N*-acetylglucosamine in β 1-6 linkage to the α-linked mannose of biantennary N-linked oligosaccharides, and thus enables the synthesis of tri- and tetra-antennary complexes.

References: [642, 1334, 3211, 1163, 2618, 3001]

[EC 2.4.1.155 created 1986, modified 2001, modified 2018]

EC 2.4.1.156

Accepted name: indolylacetyl-*myo*-inositol galactosyltransferase

Reaction: UDP-α-D-galactose + (indol-3-yl)acetyl-*myo*-inositol = UDP + 5-*O*-(indol-3-yl)acetyl-*myo*-inositol D-galactoside

Other name(s): uridine diphosphogalactose-indolylacetylinositol galactosyltransferase; indol-3-ylacetyl-*myo*-inositol galactoside synthase; UDP-galactose:indol-3-ylacetyl-*myo*-inositol 5-*O*-D-galactosyltransferase; UDP-galactose:(indol-3-yl)acetyl-*myo*-inositol 5-*O*-D-galactosyltransferase

Systematic name: UDP-α-D-galactose:(indol-3-yl)acetyl-*myo*-inositol 5-*O*-D-galactosyltransferase

References: [614]

[EC 2.4.1.156 created 1986]

[2.4.1.157 Transferred entry. 1,2-diacylglycerol 3-glucosyltransferase. Now classified as EC 2.4.1.336, monoglucosyldiacylglycerol synthase, and EC 2.4.1.337, 1,2-diacylglycerol 3-α-glucosyltransferase]

[EC 2.4.1.157 created 1986, deleted 2015]

EC 2.4.1.158

Accepted name: 13-hydroxydocosanoate 13-β-glucosyltransferase

Reaction: UDP-glucose + 13-hydroxydocosanoate = UDP + 13-β-D-glucosyloxydocosanoate

Other name(s): 13-glucosyloxydocosanoate 2′-β-glucosyltransferase; UDP-glucose:13-hydroxydocosanoic acid glucosyltransferase; uridine diphosphoglucose-hydroxydocosanoate glucosyltransferase; UDP-glucose-13-hydroxydocosanoate glucosyltransferase

Systematic name: UDP-glucose:13-hydroxydocosanoate 13-β-D-glucosyltransferase

Comments: 13-β-D-Glucosyloxydocosanoate can also act as acceptor, leading to the formation by *Candida bogoriensis* of the extracellular glycolipid, hydroxydocosanoate sophoroside diacetate.

References: [385]

[EC 2.4.1.158 created 1986]

EC 2.4.1.159

Accepted name: flavonol-3-*O*-glucoside L-rhamnosyltransferase

Reaction: UDP-β-L-rhamnose + a flavonol 3-*O*-β-D-glucoside = UDP + a flavonol 3-*O*-[α-L-rhamnosyl-(1→6)-β-D-glucoside]

Other name(s): uridine diphosphorhamnose-flavonol 3-*O*-glucoside rhamnosyltransferase; UDP-rhamnose:flavonol 3-*O*-glucoside rhamnosyltransferase; UDP-L-rhamnose:flavonol-3-*O*-D-glucoside 6′′-*O*-L-rhamnosyltransferase

Systematic name: UDP-β-L-rhamnose:flavonol-3-*O*-β-D-glucoside 6′′-*O*-L-rhamnosyltransferase (configuration-inverting)

Comments: A configuration-inverting rhamnosyltransferase that converts flavonol 3-*O*-glucosides to 3-*O*-rutinosides. Also acts, more slowly, on rutin, quercetin 3-*O*-galactoside and flavonol 3-*O*-rhamnosides.

References: [1709, 1532]

[EC 2.4.1.159 created 1986, modified 2015]

EC 2.4.1.160

Accepted name: pyridoxine 5′-*O*-β-D-glucosyltransferase

Reaction: UDP-glucose + pyridoxine = UDP + 5′-*O*-β-D-glucosylpyridoxine

Other name(s): UDP-glucose:pyridoxine 5′-*O*-β-glucosyltransferase; uridine diphosphoglucose-pyridoxine 5′-β-glucosyltransferase; UDP-glucose-pyridoxine glucosyltransferase

Systematic name: UDP-glucose:pyridoxine 5′-*O*-β-D-glucosyltransferase

Comments: 4′-Deoxypyridoxine and pyridoxamine can also act as acceptors, but more slowly.

References: [3429]

[EC 2.4.1.160 created 1986]

EC 2.4.1.161

Accepted name: oligosaccharide 4-α-D-glucosyltransferase

Reaction: Transfers the non-reducing terminal α-D-glucose residue from a (1→4)-α-D-glucan to the 4-position of a free glucose or of a glucosyl residue at the non-reducing terminus of a (1→4)-α-D-glucan, thus bringing about the rearrangement of oligosaccharides

Other name(s): amylase III; 1,4-α-glucan:1,4-α-glucan 4-α-glucosyltransferase; 1,4-α-D-glucan:1,4-α-D-glucan 4-α-D-glucosyltransferase; α-1,4-transglucosylase

Systematic name: (1→4)-α-D-glucan:(1→4)-α-D-glucan 4-α-D-glucosyltransferase

Comments: The enzyme acts on amylose, amylopectin, glycogen and maltooligosaccharides. No detectable free glucose is formed, indicating the enzyme does not act as a hydrolase. The enzyme from the bacterium *Cellvibrio japonicus* has the highest activity with maltotriose as a donor, and also accepts maltose [1866], while the enzyme from amoeba does not accept maltose [2425, 2426]. Oligosaccharides with 1→6 linkages cannot function as donors, but can act as acceptors [1866]. Unlike EC 2.4.1.25, 4-α-glucanotransferase, this enzyme can transfer only a single glucosyl residue.

References: [2425, 2426, 1866]

[EC 2.4.1.161 created 1989, modified 2013]

EC 2.4.1.162

Accepted name: aldose β-D-fructosyltransferase

Reaction: α-D-aldosyl^{1} β-D-fructoside + D-aldose^{2} = D-aldose^{1} + α-D-aldosyl^{2} β-D-fructoside

Systematic name: α-D-aldosyl-β-D-fructoside:aldose 1-β-D-fructosyltransferase

References: [517]

[EC 2.4.1.162 created 1989, modified 1999]

[2.4.1.163 Transferred entry. β-galactosyl-N-acetylglucosaminylgalactosylglucosyl-ceramide β-1,3-acetylglucosaminyltransferase, now included in EC 2.4.1.149, N-acetyllactosaminide β-1,3-N-acetylglucosaminyltransferase]

[EC 2.4.1.163 created 1989, deleted 2016]

[2.4.1.164 Transferred entry. galactosyl-N-acetylglucosaminylgalactosylglucosyl-ceramide β-1,6-N-acetylglucosaminyltransferase, now included with EC 2.4.1.150, N-acetyllactosaminide β-1,6-N-acetylglucosaminyltransferase]

[EC 2.4.1.164 created 1989, deleted 2016]

EC 2.4.1.165

Accepted name: *N*-acetylneuraminylgalactosylglucosylceramide β-1,4-*N*-acetylgalactosaminyltransferase

Reaction: UDP-*N*-acetyl-α-D-galactosamine + α-*N*-acetylneuraminyl-(2→3)-β-D-galactosyl-(1→4)-β-D-glucosyl-(1↔1)-ceramide = UDP + *N*-acetyl-β-D-galactosaminyl-(1→4)-[α-*N*-acetylneuraminyl-(2→3)]-β-D-galactosyl-(1→4)-β-D-glucosyl-(1↔1)-ceramide

Other name(s): uridine diphosphoacetylgalactosamine-acetylneuraminyl(α2→3)galactosyl(β1→4)glucosyl β1→4-acetylgalactosaminyltransferase; UDP-*N*-acetyl-D-galactosamine:*N*-acetylneuraminyl-2,3-α-D-galactosyl-1,4-β-D-glucosylceramide β-1,4-*N*-acetylgalactosaminyltransferase; UDP-*N*-acetyl-D-galactosamine:*N*-acetylneuraminyl-(2→3)-α-D-galactosyl-(1→4)-β-D-glucosyl(1↔1)ceramide 4-β-*N*-acetylgalactosaminyltransferase; UDP-*N*-acetyl-D-galactosamine:*N*-acetylneuraminyl-(2→3)-α-D-galactosyl-(1→4)-β-D-glucosyl-(1↔1)-ceramide 4-β-*N*-acetylgalactosaminyltransferase

Systematic name: UDP-*N*-acetyl-α-D-galactosamine:α-*N*-acetylneuraminyl-(2→3)-β-D-galactosyl-(1→4)-β-D-glucosyl-(1↔1)-ceramide 4-β-*N*-acetylgalactosaminyltransferase
Comments: Requires Mn^{2+}. Only substances containing sialic acid residues can act as acceptors; bovine fetuin is the best acceptor tested.
References: [541, 2711, 3455]

[EC 2.4.1.165 created 1989]

EC 2.4.1.166

Accepted name: raffinose—raffinose α-galactosyltransferase
Reaction: **2** raffinose = 1^F-α-D-galactosylraffinose + sucrose
Other name(s): raffinose (raffinose donor) galactosyltransferase; raffinose:raffinose α-galactosyltransferase; raffinose—raffinose α-galactotransferase
Systematic name: raffinose:raffinose α-D-galactosyltransferase
Comments: The 3^F position of raffinose can also act as galactosyl acceptor; the enzyme is involved in the accumulation of the tetrasaccharides lychnose and isolychnose in the leaves of *Cerastium arvense* and other plants of the family Caryophyllaceae during late autumn.
References: [1367]

[EC 2.4.1.166 created 1989]

EC 2.4.1.167

Accepted name: sucrose 6^F-α-galactosyltransferase
Reaction: UDP-α-D-galactose + sucrose = UDP + 6^F-α-D-galactosylsucrose
Other name(s): uridine diphosphogalactose-sucrose 6^F-α-galactosyltransferase; UDPgalactose:sucrose 6fru-α-galactosyltransferase; sucrose 6^F-α-galactotransferase; UDP-galactose:sucrose 6^F-α-D-galactosyltransferase
Systematic name: UDP-α-D-galactose:sucrose 6^F-α-D-galactosyltransferase
Comments: The enzyme is involved in the synthesis of the trisaccharide planteose and higher analogues in the seeds of *Plantago* and *Sesamum* species.
References: [1368]

[EC 2.4.1.167 created 1989]

EC 2.4.1.168

Accepted name: xyloglucan 4-glucosyltransferase
Reaction: Transfers a β-D-glucosyl residue from UDP-glucose on to a glucose residue in xyloglucan, forming a β-(1→4)-D-glucosyl-D-glucose linkage
Other name(s): uridine diphosphoglucose-xyloglucan 4β-glucosyltransferase; xyloglucan 4β-D-glucosyltransferase; xyloglucan glucosyltransferase; UDP-glucose:xyloglucan 1,4-β-D-glucosyltransferase
Systematic name: UDP-glucose:xyloglucan 4-β-D-glucosyltransferase
Comments: In association with EC 2.4.2.39 (xyloglucan 6-xylosyltransferase), this enzyme brings about the synthesis of xyloglucan; concurrent transfers of glucose and xylose are essential for this synthesis. Not identical with EC 2.4.1.12 cellulose synthase (UDP-forming).
References: [1255, 1254]

[EC 2.4.1.168 created 1989]

[2.4.1.169 Transferred entry. xyloglucan 6-xylosyltransferase. Now EC 2.4.2.39, xyloglucan 6-xylosyltransferase]

[EC 2.4.1.169 created 1989, deleted 2003]

EC 2.4.1.170

Accepted name: isoflavone 7-*O*-glucosyltransferase

Reaction: UDP-glucose + an isoflavone = UDP + an isoflavone 7-*O*-β-D-glucoside

Other name(s): uridine diphosphoglucose-isoflavone 7-*O*-glucosyltransferase; UDPglucose-favonoid 7-*O*-glucosyltransferase; UDPglucose:isoflavone 7-*O*-glucosyltransferase

Systematic name: UDP-glucose:isoflavone 7-*O*-β-D-glucosyltransferase

Comments: The $4'$-methoxy isoflavones biochanin A and formononetin and, more slowly, the $4'$-hydroxyisoflavones genistein and daidzein, can act as acceptors. The enzyme does not act on isoflavanones, flavones, flavanones, flavanols or coumarins.

References: [1768]

[EC 2.4.1.170 created 1989]

EC 2.4.1.171

Accepted name: methyl-*ONN*-azoxymethanol β-D-glucosyltransferase

Reaction: UDP-glucose + methyl-*ONN*-azoxymethanol = UDP + cycasin

Other name(s): cycasin synthase; uridine diphosphoglucose-methylazoxymethanol glucosyltransferase; UDP-glucose-methylazoxymethanol glucosyltransferase

Systematic name: UDP-glucose:methyl-*ONN*-azoxymethanol β-D-glucosyltransferase

Comments: Brings about the biosynthesis of the toxic substance cycasin in the leaves of Japanese cycad, *Cycas revoluta*.

References: [3430]

[EC 2.4.1.171 created 1989]

EC 2.4.1.172

Accepted name: salicyl-alcohol β-D-glucosyltransferase

Reaction: UDP-glucose + salicyl alcohol = UDP + salicin

Other name(s): uridine diphosphoglucose-salicyl alcohol 2-glucosyltransferase; UDPglucose:salicyl alcohol phenyl-glucosyltransferase

Systematic name: UDP-glucose:salicyl-alcohol β-D-glucosyltransferase

References: [2279]

[EC 2.4.1.172 created 1989]

EC 2.4.1.173

Accepted name: sterol 3β-glucosyltransferase

Reaction: UDP-glucose + a sterol = UDP + a sterol 3-β-D-glucoside

Other name(s): UDPG:sterol glucosyltransferase; UDP-glucose-sterol β-glucosyltransferase; sterol:UDPG glucosyltransferase; UDPG-SGTase; uridine diphosphoglucose-poriferasterol glucosyltransferase; uridine diphosphoglucose-sterol glucosyltransferase; sterol glucosyltransferase; sterol-β-D-glucosyltransferase; UDP-glucose-sterol glucosyltransferase

Systematic name: UDP-glucose:sterol 3-*O*-β-D-glucosyltransferase

Comments: Not identical with EC 2.4.1.192 (nuatigenin 3β-glucosyltransferase) or EC 2.4.1.193 (sarsapogenin 3β-glucosyltransferase).

References: [795, 1566, 1567, 2366, 3879]

[EC 2.4.1.173 created 1989]

EC 2.4.1.174

Accepted name: glucuronylgalactosylproteoglycan 4-β-*N*-acetylgalactosaminyltransferase

Reaction: UDP-*N*-acetyl-α-D-galactosamine + [protein]-3-*O*-(β-D-GlcA-(1→3)-β-D-Gal-(1→3)-β-D-Gal-(1→4)-β-D-Xyl)-L-serine = UDP + [protein]-3-*O*-(β-D-GalNAc-(1→4)-β-D-GlcA-(1→3)-β-D-Gal-(1→3)-β-D-Gal-(1→4)-β-D-Xyl)-L-serine

Other name(s): *N*-acetylgalactosaminyltransferase I; glucuronylgalactosylproteoglycan β-1,4-*N*-acetylgalactosaminyltransferase; uridine diphosphoacetylgalactosamine-chondroitin acetylgalactosaminyltransferase I; UDP-*N*-acetyl-D-galactosamine:D-glucuronyl-1,3-β-D-galactosylproteoglycan β-1,4-*N*-acetylgalactosaminyltransferase; UDP-*N*-acetyl-D-galactosamine:D-glucuronyl-(1→3)-β-D-galactosyl-proteoglycan 4-β-*N*-acetylgalactosaminyltransferase

Systematic name: UDP-*N*-acetyl-D-galactosamine:[protein]-3-*O*-(β-D-GlcA-(1→3)-β-D-Gal-(1→3)-β-D-Gal-(1→4)-β-D-Xyl)-L-serine 4-β-*N*-acetylgalactosaminyltransferase (configuration-inverting)

Comments: Requires Mn^{2+}. Involved in the biosynthesis of chondroitin sulfate. Key enzyme activity for the initiation of chondroitin and dermatan sulfates, transferring GalNAc to the GlcA-Gal-Gal-Xyl-Ser core.

References: [2920, 3620]

[EC 2.4.1.174 created 1989, modified 2002]

EC 2.4.1.175

Accepted name: glucuronosyl-*N*-acetylgalactosaminyl-proteoglycan 4-β-*N*-acetylgalactosaminyltransferase

Reaction: (1) UDP-*N*-acetyl-α-D-galactosamine + [protein]-3-*O*-(β-D-GlcA-(1→3)-β-D-GalNAc-(1→4)-β-D-GlcA-(1→3)-β-D-Gal-(1→3)-β-D-Gal-(1→4)-β-D-Xyl)-L-serine = UDP + [protein]-3-*O*-(β-D-GalNAc-(1→4)-β-D-GlcA-(1→3)-β-D-GalNAc-(1→4)-β-D-GlcA-(1→3)-β-D-Gal-(1→3)-β-D-Gal-(1→4)-β-D-Xyl)-L-serine

(2) UDP-*N*-acetyl-α-D-galactosamine + [protein]-3-*O*-(β-D-GlcA-(1→3)-[β-D-GalNAc-(1→4)-β-D-GlcA-(1→3)]$_n$-β-D-GalNAc-(1→4)-β-D-GlcA-(1→3)-β-D-Gal-(1→3)-β-D-Gal-(1→4)-β-D-Xyl)-L-serine = UDP + [protein]-3-*O*-([β-D-GalNAc-(1→4)-β-D-GlcA-(1→3)]$_{n+1}$-β-D-GalNAc-(1→4)-β-D-GlcA-(1→3)-β-D-Gal-(1→3)-β-D-Gal-(1→4)-β-D-Xyl)-L-serine

Other name(s): *N*-acetylgalactosaminyltransferase II; UDP-*N*-acetyl-D-galactosamine:D-glucuronyl-*N*-acetyl-1,3-β-D-galactosaminylproteoglycan β-1,4-*N*-acetylgalactosaminyltransferase; chondroitin synthase; glucuronyl-*N*-acetylgalactosaminylproteoglycan β-1,4-*N*-acetylgalactosaminyltransferase; uridine diphosphoacetylgalactosamine-chondroitin acetylgalactosaminyltransferase II; UDP-*N*-acetyl-D-galactosamine:β-D-glucuronosyl-(1→3)-*N*-acetyl-β-D-galactosaminyl-proteoglycan 4-β-*N*-acetylgalactosaminyltransferase; UDP-*N*-acetyl-α-D-galactosamine:β-D-glucuronosyl-(1→3)-*N*-acetyl-β-D-galactosaminyl-proteoglycan 4-β-*N*-acetylgalactosaminyltransferase

Systematic name: UDP-*N*-acetyl-α-D-galactosamine:[protein]-3-*O*-(β-D-GlcA-(1→3)-β-D-GalNAc-(1→4)-β-D-GlcA-(1→3)-β-D-Gal-(1→3)-β-D-Gal-(1→4)-β-D-Xyl)-L-serine 4-β-*N*-acetylgalactosaminyltransferase (configuration-inverting)

Comments: Involved in the biosynthesis of chondroitin sulfate. The human form of this enzyme is a bifunctional glycosyltransferase, which also has the 3-β-glucuronosyltransferase (EC 2.4.1.226, *N*-acetylgalactosaminyl-proteoglycan 3-β-glucuronosyltransferase) activity required for the synthesis of the chondroitin sulfate disaccharide repeats. Similar chondroitin synthase 'co-polymerases' can be found in *Pasteurella multocida* and *Escherichia coli*.

References: [2920, 1699, 693, 2462]

[EC 2.4.1.175 created 1989, modified 2002]

EC 2.4.1.176

Accepted name: gibberellin β-D-glucosyltransferase

Reaction: UDP-glucose + gibberellin = UDP + gibberellin 2-*O*-β-D-glucoside

Other name(s): uridine diphosphoglucose-gibberellate 7-glucosyltransferase; uridine diphosphoglucose-gibberellate 3-*O*-glucosyltransferase

Systematic name: UDP-glucose:gibberellin 2-*O*-β-D-glucosyltransferase

Comments: Acts on the plant hormone gibberellin GA_3 and related compounds.

References: [3137]

[EC 2.4.1.176 created 1989]

EC 2.4.1.177

Accepted name: cinnamate β-D-glucosyltransferase
Reaction: UDP-glucose + *trans*-cinnamate = UDP + *trans*-cinnamoyl β-D-glucoside
Other name(s): uridine diphosphoglucose-cinnamate glucosyltransferase; UDPG:*t*-cinnamate glucosyltransferase
Systematic name: UDP-glucose:*trans*-cinnamate β-D-glucosyltransferase
Comments: 4-Coumarate, 2-coumarate, benzoate, feruloate and caffeate can also act as acceptors, but more slowly. Involved in the biosynthesis of chlorogenic acid in the root of the sweet potato, *Ipomoea batatas*.
References: [3195]

[EC 2.4.1.177 created 1989]

EC 2.4.1.178

Accepted name: hydroxymandelonitrile glucosyltransferase
Reaction: UDP-glucose + 4-hydroxymandelonitrile = UDP + taxiphyllin
Other name(s): cyanohydrin glucosyltransferase; uridine diphosphoglucose-cyanohydrin glucosyltransferase
Systematic name: UDP-glucose:4-hydroxymandelonitrile glucosyltransferase
Comments: 3,4-Dihydroxymandelonitrile can also act as acceptor.
References: [1376, 2750]

[EC 2.4.1.178 created 1989]

EC 2.4.1.179

Accepted name: lactosylceramide β-1,3-galactosyltransferase
Reaction: UDP-α-D-galactose + β-D-galactosyl-(1→4)-β-D-glucosyl-R = UDP + β-D-galactosyl-(1→3)-β-D-galactosyl-(1→4)-β-D-glucosyl-R
Other name(s): uridine diphosphogalactose-lactosylceramide β1→3-galactosyltransferase; UDP-galactose:D-galactosyl-1,4-β-D-glucosyl-R β-1,3-galactosyltransferase; UDP-galactose:D-galactosyl-(1→4)-β-D-glucosyl-R 3-β-galactosyltransferase; UDP-α-D-galactose:D-galactosyl-(1→4)-β-D-glucosyl-R 3-β-galactosyltransferase
Systematic name: UDP-α-D-galactose:β-D-galactosyl-(1→4)-β-D-glucosyl-R 3-β-galactosyltransferase
Comments: R may be an oligosaccharide or a glycolipid; lactose can also act as acceptor, but more slowly. Involved in the elongation of oligosaccharide chains, especially in glycolipids.
References: [168]

[EC 2.4.1.179 created 1989]

EC 2.4.1.180

Accepted name: lipopolysaccharide *N*-acetylmannosaminouronosyltransferase
Reaction: UDP-*N*-acetyl-α-D-mannosaminouronate + *N*-acetyl-α-D-glucosaminyl-diphospho-*ditrans*,*octacis*-undecaprenol = UDP + *N*-acetyl-β-D-mannosaminouronyl-(1→4)-*N*-acetyl-α-D-glucosaminyl-diphospho-*ditrans*,*octacis*-undecaprenol
Other name(s): ManNAcA transferase; uridine diphosphoacetylmannosaminuronate-acetylglucosaminylpyrophosphorylundecaprenol acetylmannosaminuronosyltransferase; UDP-*N*-acetyl-β-D-mannosaminouronate:lipid I *N*-acetyl-β-D-mannosaminouronosyltransferase (incorrect)
Systematic name: UDP-*N*-acetyl-α-D-mannosaminouronate:lipid I *N*-acetyl-α-D-mannosaminouronosyltransferase
Comments: Involved in the biosynthesis of common antigen in *Enterobacteriaceae*.
References: [203]

[EC 2.4.1.180 created 1990, modified 2011]

EC 2.4.1.181

Accepted name: hydroxyanthraquinone glucosyltransferase
Reaction: UDP-glucose + an hydroxyanthraquinone = UDP + a glucosyloxyanthraquinone

Other name(s): uridine diphosphoglucose-anthraquinone glucosyltransferase; anthraquinone-specific glucosyltransferase

Systematic name: UDP-glucose:hydroxyanthraquinone *O*-glucosyltransferase

Comments: A range of anthraquinones and some flavones can act as acceptors; best substrates are emodin, anthrapurpurin, quinizarin, 2,6-dihydroanthraquinone and 1,8-dihydroxyanthraquinone.

References: [1665]

[EC 2.4.1.181 created 1990]

EC 2.4.1.182

Accepted name: lipid-A-disaccharide synthase

Reaction: UDP-2-*N*,3-*O*-bis[(3*R*)-3-hydroxytetradecanoyl]-α-D-glucosamine + 2-*N*,3-*O*-bis[(3*R*)-3-hydroxytetradecanoyl]-α-D-glucosaminyl 1-phosphate = UDP + 2-*N*,3-*O*-bis[(3*R*)-3-hydroxytetradecanoyl]-β-D-glucosaminyl-(1→6)-2-*N*,3-*O*-bis[(3*R*)-3-hydroxytetradecanoyl]-α-D-glucosaminyl 1-phosphate

Other name(s): UDP-2,3-bis(3-hydroxytetradecanoyl)glucosamine:2,3-bis-(3-hydroxytetradecanoyl)-β-D-glucosaminyl-1-phosphate 2,3-bis(3-hydroxytetradecanoyl)-glucosaminyltransferase (incorrect)

Systematic name: UDP-2-*N*,3-*O*-bis[(3*R*)-3-hydroxytetradecanoyl]-α-D-glucosamine:2-*N*,3-*O*-bis[(3*R*)-3-hydroxytetradecanoyl]-α-D-glucosaminyl-1-phosphate 2-*N*,3-*O*-bis[(3*R*)-3-hydroxytetradecanoyl]-D-glucosaminyltransferase

Comments: Involved with EC 2.3.1.129 (acyl-[acyl-carrier-protein]—UDP-*N*-acetylglucosamine *O*-acyltransferase) and EC 2.7.1.130 (tetraacyldisaccharide 4′-kinase) in the biosynthesis of the phosphorylated glycolipid, lipid A, in the outer membrane of *Escherichia coli*.

References: [2830, 634]

[EC 2.4.1.182 created 1990]

EC 2.4.1.183

Accepted name: α-1,3-glucan synthase

Reaction: UDP-glucose + [α-D-glucosyl-(1→3)]$_n$ = UDP + [α-D-glucosyl-(1→3)]$_{n+1}$

Other name(s): uridine diphosphoglucose-1,3-α-glucan glucosyltransferase; 1,3-α-D-glucan synthase; UDP-glucose:α-D-(1-3)-glucan 3-α-D-glucosyltransferase

Systematic name: UDP-glucose:α-D-(1→3)-glucan 3-α-D-glucosyltransferase

Comments: A glucan primer is needed to begin the reaction, which brings about elongation of the glucan chains.

References: [85]

[EC 2.4.1.183 created 1990]

EC 2.4.1.184

Accepted name: galactolipid galactosyltransferase

Reaction: **2** a 1,2-diacyl-3-*O*-(β-D-galactosyl)-*sn*-glycerol = a 1,2-diacyl-3-*O*-[β-D-galactosyl-(1→6)-β-D-galactosyl]-*sn*-glycerol + a 1,2-diacyl-*sn*-glycerol

Other name(s): galactolipid-galactolipid galactosyltransferase; galactolipid:galactolipid galactosyltransferase; interlipid galactosyltransferase; GGGT; DGDG synthase (ambiguous); digalactosyldiacylglycerol synthase (ambiguous); 3-(β-D-galactosyl)-1,2-diacyl-*sn*-glycerol:mono-3-(β-D-galactosyl)-1,2-diacyl-*sn*-glycerol β-D-galactosyltransferase; 3-(β-D-galactosyl)-1,2-diacyl-*sn*-glycerol:3-(β-D-galactosyl)-1,2-diacyl-*sn*-glycerol β-D-galactosyltransferase; SFR2 (gene name)

Systematic name: 1,2-diacyl-3-*O*-(β-D-galactosyl)-*sn*-glycerol:1,2-diacyl-3-*O*-(β-D-galactosyl)-*sn*-glycerol β-D-galactosyltransferase

Comments: The enzyme converts monogalactosyldiacylglycerol to digalactosyldiacylglycerol, trigalactosyldiacylglycerol and tetragalactosyldiacylglycerol. All residues are connected by β linkages. The activity is localized to chloroplast envelope membranes, but it does not contribute to net galactolipid synthesis in plants, which is performed by EC 2.4.1.46, monogalactosyldiacylglycerol synthase, and EC 2.4.1.241, digalactosyldiacylglycerol synthase. Note that the β,β-digalactosyldiacylglycerol formed by this enzyme is different from the more common α,β-digalactosyldiacylglycerol formed by EC 2.4.1.241. The enzyme provides an important mechanism for the stabilization of the chloroplast membranes during freezing and drought stress.

References: [756, 1267, 1266, 1632, 269, 940, 2286]

[EC 2.4.1.184 created 1990, modified 2005, modified 2015]

EC 2.4.1.185

Accepted name: flavanone 7-*O*-β-glucosyltransferase

Reaction: UDP-glucose + a flavanone = UDP + a flavanone 7-*O*-β-D-glucoside

Other name(s): uridine diphosphoglucose-flavanone 7-*O*-glucosyltransferase; naringenin 7-*O*-glucosyltransferase; hesperetin 7-*O*-glucosyl-transferase

Systematic name: UDP-glucose:flavanone 7-*O*-β-D-glucosyltransferase

Comments: Naringenin and hesperetin can act as acceptors. No action on flavones or flavonols.

References: [2197, 2198]

[EC 2.4.1.185 created 1992]

EC 2.4.1.186

Accepted name: glycogenin glucosyltransferase

Reaction: UDP-α-D-glucose + glycogenin = UDP + α-D-glucosylglycogenin

Other name(s): glycogenin; priming glucosyltransferase; UDP-glucose:glycogenin glucosyltransferase

Systematic name: UDP-α-D-glucose:glycogenin α-D-glucosyltransferase

Comments: The first reaction of this enzyme is to catalyse its own glucosylation, normally at Tyr-194 of the protein if this group is free. When Tyr-194 is replaced by Thr or Phe, the enzyme's Mn^{2+}-dependent self-glucosylation activity is lost but its intermolecular transglucosylation ability remains [64]. It continues to glucosylate an existing glucosyl group until a length of about 5–13 residues has been formed. Further lengthening of the glycogen chain is then carried out by EC 2.4.1.11, glycogen (starch) synthase. The enzyme is not highly specific for the donor, using UDP-xylose in addition to UDP-glucose (although not glucosylating or xylosylating a xylosyl group so added). It can also use CDP-glucose and TDP-glucose, but not ADP-glucose or GDP-glucose. Similarly it is not highly specific for the acceptor, using water (i.e. hydrolysing UDP-glucose) among others. Various forms of the enzyme exist, and different forms predominate in different organs. Thus primate liver contains glycogenin-2, of molecular mass 66 kDa, whereas the more widespread form is glycogenin-1, with a molecular mass of 38 kDa.

References: [1791, 2719, 2720, 1642, 2910, 2030, 64, 63, 2335, 1047]

[EC 2.4.1.186 created 1992 (EC 2.4.1.112 created 1984, incorporated 2007)]

EC 2.4.1.187

Accepted name: *N*-acetylglucosaminyldiphosphoundecaprenol *N*-acetyl-β-D-mannosaminyltransferase

Reaction: UDP-*N*-acetyl-α-D-mannosamine + *N*-acetyl-α-D-glucosaminyl-diphospho-*ditrans*,*octacis*-undecaprenol = UDP + *N*-acetyl-β-D-mannosaminyl-(1→4)-*N*-acetyl-α-D-glucosaminyl-diphospho-*ditrans*,*octacis*-undecaprenol

Other name(s): uridine diphosphoacetyl-mannosamineacetylglucosaminylpyrophosphorylundecaprenol acetylmannosaminyltransferase; *N*-acetylmannosaminyltransferase; UDP-*N*-acetylmannosamine:*N*-acetylglucosaminyl diphosphorylundecaprenol *N*-acetylmannosaminyltransferase; UDP-*N*-acetyl-D-mannosamine:*N*-acetyl-β-D-glucosaminyldiphosphoundecaprenol β-1,4-*N*-acetylmannosaminyltransferase; UDP-*N*-acetyl-D-mannosamine:*N*-acetyl-β-D-glucosaminyldiphosphoundecaprenol 4-β-*N*-acetylmannosaminyltransferase; *tagA* (gene name); *tarA* (gene name); UDP-*N*-acetyl-α-D-mannosamine:*N*-acetyl-β-D-glucosaminyl-diphospho-*ditrans*,*octacis*-undecaprenol 4-β-*N*-acetylmannosaminyltransferase

Systematic name: UDP-*N*-acetyl-α-D-mannosamine:*N*-acetyl-α-D-glucosaminyldiphospho-*ditrans*,*octacis*-undecaprenol 4-β-*N*-acetylmannosaminyltransferase (configuration-inverting)

Comments: Involved in the biosynthesis of teichoic acid linkage units in bacterial cell walls.

References: [2374, 1062, 4054]

[EC 2.4.1.187 created 1992, modified 2016]

EC 2.4.1.188

Accepted name: *N*-acetylglucosaminyldiphosphoundecaprenol glucosyltransferase

Reaction: UDP-α-D-glucose + *N*-acetyl-D-glucosaminyl-diphospho-*ditrans*,*octacis*-undecaprenol = UDP + β-D-glucosyl-(1→4)-*N*-acetyl-D-glucosaminyl-diphospho-*ditrans*,*octacis*-undecaprenol

Other name(s): UDP-D-glucose:*N*-acetylglucosaminyl pyrophosphorylundecaprenol glucosyltransferase; uridine diphosphoglucose-acetylglucosaminylpyrophosphorylundecaprenol glucosyltransferase; UDP-glucose:*N*-acetyl-D-glucosaminyldiphosphoundecaprenol 4-β-D-glucosyltransferase

Systematic name: UDP-α-D-glucose:*N*-acetyl-D-glucosaminyl-diphospho-*ditrans*,*octacis*-undecaprenol 4-β-D-glucosyltransferase

References: [1817]

[EC 2.4.1.188 created 1992]

EC 2.4.1.189

Accepted name: luteolin 7-*O*-glucuronosyltransferase

Reaction: UDP-α-D-glucuronate + luteolin = UDP + luteolin 7-*O*-β-D-glucuronide

Other name(s): uridine diphosphoglucuronate-luteolin 7-*O*-glucuronosyltransferase; LGT; UDP-glucuronate:luteolin 7-*O*-glucuronosyltransferase

Systematic name: UDP-α-D-glucuronate:luteolin 7-*O*-glucuronosyltransferase (configuration-inverting)

Comments: The enzyme participates in the biosynthesis of luteolin triglucuronide, the major flavone found in the photosynthetically-active mesophyll of the primary leaves of *Secale cereale* (rye).

References: [3115]

[EC 2.4.1.189 created 1992]

EC 2.4.1.190

Accepted name: luteolin-7-*O*-glucuronide $2''$-*O*-glucuronosyltransferase

Reaction: UDP-α-D-glucuronate + luteolin 7-*O*-β-D-glucuronide = UDP + luteolin 7-*O*-[β-D-glucuronosyl-(1→2)-β-D-glucuronide]

Other name(s): uridine diphosphoglucuronate-luteolin 7-*O*-glucuronide glucuronosyltransferase; LMT; UDP-glucuronate:luteolin 7-*O*-glucuronide-glucuronosyltransferase; UDP-glucuronate:luteolin-7-*O*-β-D-glucuronide $2''$-*O*-glucuronosyltransferase

Systematic name: UDP-α-D-glucuronate:luteolin-7-*O*-β-D-glucuronide $2''$-*O*-glucuronosyltransferase (configuration-inverting)

Comments: The enzyme participates in the biosynthesis of luteolin triglucuronide, the major flavone found in the photosynthetically-active mesophyll of the primary leaves of *Secale cereale* (rye).

References: [3115, 89]

[EC 2.4.1.190 created 1992]

EC 2.4.1.191

Accepted name: luteolin-7-*O*-diglucuronide 4′-*O*-glucuronosyltransferase

Reaction: UDP-α-D-glucuronate + luteolin 7-*O*-[β-D-glucuronosyl-(1→2)-β-D-glucuronide] = UDP + luteolin 7-*O*-[β-D-glucuronosyl-(1→2)-β-D-glucuronide]-4′-*O*-β-D-glucuronide

Other name(s): uridine diphosphoglucuronate-luteolin 7-*O*-diglucuronide glucuronosyltransferase; UDP-glucuronate:luteolin 7-*O*-diglucuronide-glucuronosyltransferase; UDPglucuronate:luteolin 7-*O*-diglucuronide-4′-*O*-glucuronosyl-transferase; LDT; UDP-glucuronate:luteolin-7-*O*-β-D-diglucuronide 4′-*O*-glucuronosyltransferase

Systematic name: UDP-α-D-glucuronate:luteolin-7-*O*-β-D-diglucuronide 4′-*O*-glucuronosyltransferase (configuration-inverting)

Comments: The enzyme participates in the biosynthesis of luteolin triglucuronide, the major flavone found in the photosynthetically-active mesophyll of the primary leaves of *Secale cereale* (rye).

References: [3115]

[EC 2.4.1.191 created 1992, modified 2011]

EC 2.4.1.192

Accepted name: nuatigenin 3β-glucosyltransferase

Reaction: UDP-glucose + (20*S*,22*S*,25*S*)-22,25-epoxyfurost-5-ene-3β,26-diol = UDP + (20*S*,22*S*,25*S*)-22,25-epoxyfurost-5-ene-3β,26-diol 3-*O*-β-D-glucoside

Other name(s): uridine diphosphoglucose-nuatigenin glucosyltransferase

Systematic name: UDP-glucose:(20*S*,22*S*,25*S*)-22,25-epoxyfurost-5-ene-3β,26-diol 3-*O*-β-D-glucosyltransferase

Comments: Some other sapogenins can act as glucosyl acceptors. Involved in the biosynthesis of plant saponins. Not identical with EC 2.4.1.173 (sterol 3β-glucosyltransferase) or EC 2.4.1.193 (sarsapogenin 3β-glucosyltransferase).

References: [1566, 1567]

[EC 2.4.1.192 created 1992]

EC 2.4.1.193

Accepted name: sarsapogenin 3β-glucosyltransferase

Reaction: UDP-glucose + (25*S*)-5β-spirostan-3β-ol = UDP + (25*S*)-5β-spirostan-3β-ol 3-*O*-β-D-glucoside

Other name(s): uridine diphosphoglucose-sarsapogenin glucosyltransferase

Systematic name: UDP-glucose:(25*S*)-5β-spirostan-3β-ol 3-*O*-β-D-glucosyltransferase

Comments: Specific to 5β-spirostanols. Involved in the biosynthesis of plant saponins. Not identical with EC 2.4.1.173 (sterol 3β-glucosyltransferase) or EC 2.4.1.192 (nuatigenin 3β-glucosyltransferase).

References: [2593]

[EC 2.4.1.193 created 1992]

EC 2.4.1.194

Accepted name: 4-hydroxybenzoate 4-*O*-β-D-glucosyltransferase

Reaction: UDP-glucose + 4-hydroxybenzoate = UDP + 4-(β-D-glucosyloxy)benzoate

Other name(s): uridine diphosphoglucose-4-hydroxybenzoate glucosyltransferase; UDP-glucose:4-(β-D-glucopyranosyloxy)benzoic acid glucosyltransferase; HBA glucosyltransferase; *p*-hydroxybenzoate glucosyltransferase; PHB glucosyltransferase; PHB-*O*-glucosyltransferase

Systematic name: UDP-glucose:4-hydroxybenzoate 4-*O*-β-D-glucosyltransferase

References: [1604]

[EC 2.4.1.194 created 1992]

EC 2.4.1.195

Accepted name: *N*-hydroxythioamide *S*-β-glucosyltransferase

Reaction: (1) UDP-α-D-glucose + (*Z*)-2-phenyl-1-thioacetohydroximate = UDP + desulfoglucotropeolin
(2) UDP-α-D-glucose + an (*E*)-ω-(methylsulfanyl)alkyl-thiohydroximate = UDP + an aliphatic desulfoglucosinolate
(3) UDP-α-D-glucose + (*E*)-2-(1*H*-indol-3-yl)-1-thioacetohydroximate = UDP + desulfoglucobrassicin

Other name(s): UGT74B1 (gene name); desulfoglucosinolate-uridine diphosphate glucosyltransferase; uridine diphosphoglucose-thiohydroximate glucosyltransferase; thiohydroximate β-D-glucosyltransferase; UDPG:thiohydroximate glucosyltransferase; thiohydroximate *S*-glucosyltransferase; thiohydroximate glucosyltransferase; UDP-glucose:thiohydroximate *S*-β-D-glucosyltransferase; UDP-glucose:*N*-hydroxy-2-phenylethanethioamide *S*-β-D-glucosyltransferase

Systematic name: UDP-α-D-glucose:*N*-hydroxy-2-phenylethanethioamide *S*-β-D-glucosyltransferase

Comments: The enzyme specifically glucosylates the thiohydroximate functional group. It is involved in the biosynthesis of glucosinolates in cruciferous plants, and acts on aliphatic, aromatic, and indolic substrates.

References: [1489, 2841, 2126, 863, 1154]

[EC 2.4.1.195 created 1992, modified 2006, modified 2018]

EC 2.4.1.196

Accepted name: nicotinate glucosyltransferase

Reaction: UDP-glucose + nicotinate = UDP + *N*-glucosylnicotinate

Other name(s): uridine diphosphoglucose-nicotinate *N*-glucosyltransferase; UDP-glucose:nicotinic acid-*N*-glucosyltransferase

Systematic name: UDP-glucose:nicotinate *N*-glucosyltransferase

References: [3617]

[EC 2.4.1.196 created 1992]

EC 2.4.1.197

Accepted name: high-mannose-oligosaccharide β-1,4-*N*-acetylglucosaminyltransferase

Reaction: Transfers an *N*-acetyl-D-glucosamine residue from UDP-*N*-acetyl-D-glucosamine to the 4-position of a mannose linked α-(1→6) to the core mannose of high-mannose oligosaccharides produced by *Dictyostelium discoideum*

Other name(s): uridine diphosphoacetylglucosamine-oligosaccharide acetylglucosaminyltransferase; acetylglucosamine-oligosaccharide acetylglucosaminyltransferase; UDP-GlcNAc:oligosaccharide β-*N*-acetylglucosaminyltransferase; UDP-*N*-acetyl-D-glucosamine:high-mannose-oligosaccharide β-1,4-*N*-acetylglucosaminyltransferase

Systematic name: UDP-*N*-acetyl-D-glucosamine:high-mannose-oligosaccharide 4-β-*N*-acetylglucosaminyltransferase

Comments: The activity of the intersecting mannose residue as acceptor is dependent on two other mannose residues attached by α-1,3 and α-1,6 links.

References: [3154]

[EC 2.4.1.197 created 1992]

EC 2.4.1.198

Accepted name: phosphatidylinositol *N*-acetylglucosaminyltransferase

Reaction: UDP-*N*-acetyl-α-D-glucosamine + 1-phosphatidyl-1D-*myo*-inositol = UDP + 6-(*N*-acetyl-α-D-glucosaminyl)-1-phosphatidyl-1D-*myo*-inositol

Other name(s): UDP-*N*-acetyl-D-glucosamine:phosphatidylinositol *N*-acetyl-D-glucosaminyltransferase; uridine diphosphoacetylglucosamine α1,6-acetyl-D-glucosaminyltransferase; UDP-*N*-acetyl-D-glucosamine:1-phosphatidyl-1D-*myo*-inositol 6-(*N*-acetyl-α-D-glucosaminyl)transferase

Systematic name: UDP-*N*-acetyl-α-D-glucosamine:1-phosphatidyl-1D-*myo*-inositol 6-(*N*-acetyl-α-D-glucosaminyl)transferase (configuration-retaining)

Comments: Involved in the first step of glycosylphosphatidylinositol (GPI) anchor formation in all eukaryotes. In mammalian cells, the enzyme is composed of at least five subunits (PIG-A, PIG-H, PIG-C, GPI1 and PIG-*P*). PIG-A subunit is the catalytic subunit. In some species, the long-chain acyl groups of the phosphatidyl group are partly replaced by long-chain alkyl or alk-1-enyl groups.

References: [746, 3783, 3784]

[EC 2.4.1.198 created 1992, modified 2002]

EC 2.4.1.199

Accepted name: β-mannosylphosphodecaprenol—mannooligosaccharide 6-mannosyltransferase

Reaction: β-D-mannosylphosphodecaprenol + (1→6)-α-D-mannosyloligosaccharide = decaprenol phosphate + (1→6)-α-D-mannosyl-(1→6)-α-D-mannosyl-oligosaccharide

Other name(s): mannosylphospholipid-methylmannoside α-1,6-mannosyltransferase; β-D-mannosylphosphodecaprenol:1,6-α-D-mannosyloligosaccharide 1,6-α-D-mannosyltransferase

Systematic name: β-D-mannosylphosphodecaprenol:(1→6)-α-D-mannosyloligosaccharide 6-α-D-mannosyltransferase

Comments: Involved in the formation of mannooligosaccharides in the membrane of *Mycobacterium smegmatis*.

References: [3989]

[EC 2.4.1.199 created 1992]

[2.4.1.200 Transferred entry. inulin fructotransferase (depolymerizing, difructofuranose-1,2′:2′,1-dianhydride-forming). Now EC 4.2.2.17, inulin fructotransferase (DFA-I-forming). The enzyme was wrongly classified as a transferase rather than a lyase]

[EC 2.4.1.200 created 1992, deleted 2004]

EC 2.4.1.201

Accepted name: α-1,6-mannosyl-glycoprotein 4-β-*N*-acetylglucosaminyltransferase

Reaction: UDP-*N*-acetyl-α-D-glucosamine + β-D-GlcNAc-(1→2)-[β-D-GlcNAc-(1→4)]-α-D-Man-(1→3)-[β-D-GlcNAc-(1→2)-[β-D-GlcNAc-(1→6)]-α-D-Man-(1→6)]-β-D-Man-(1→4)-β-D-GlcNAc-(1→4)-β-D-GlcNAc-*N*-Asn-[protein] = UDP + β-D-GlcNAc-(1→2)-[β-D-GlcNAc-(1→4)]-α-D-Man-(1→3)-[β-D-GlcNAc-(1→2)-[β-D-GlcNAc-(1→4)]-[β-D-GlcNAc-(1→6)]-α-D-Man-(1→6)]-β-D-Man-(1→4)-β-D-GlcNAc-(1→4)-β-D-GlcNAc-*N*-Asn-[protein]

Other name(s): MGAT4C (gene name); *N*-acetylglucosaminyltransferase VI; *N*-glycosyl-oligosaccharide-glycoprotein *N*-acetylglucosaminyltransferase VI; uridine diphosphoacetylglucosamine-glycopeptide β-1→4-acetylglucosaminyltransferase VI; mannosyl-glycoprotein β-1,4-*N*-acetylglucosaminyltransferase; GnTVI; GlcNAc-T VI; UDP-*N*-acetyl-D-glucosamine:2,6-bis(*N*-acetyl-β-D-glucosaminyl)-α-D-mannosyl-glycoprotein 4-β-*N*-acetyl-D-glucosaminyltransferase

Systematic name: UDP-*N*-acetyl-α-D-glucosamine:*N*-acetyl-β-D-glucosaminyl-(1→6)-[*N*-acetyl-β-D-glucosaminyl-(1→2)]-α-D-mannosyl-glycoprotein 4-β-*N*-acetyl-D-glucosaminyltransferase (configuration-inverting)

Comments: Requires a high concentration of Mn^{2+} for maximal activity. The enzyme, characterized from hen oviduct membranes, participates in the processing of *N*-glycans in the Golgi apparatus. It transfers GlcNAc in β1-4 linkage to a D-mannose residue that already has GlcNAc residues attached at positions 2 and 6 by β linkages. No homologous enzyme appears to exist in mammals.

References: [396, 3432, 3004]

[EC 2.4.1.201 created 1992, modified 2001, modified 2018]

EC 2.4.1.202

Accepted name: 2,4-dihydroxy-7-methoxy-2*H*-1,4-benzoxazin-3(4*H*)-one 2-D-glucosyltransferase

Reaction: (1) UDP-α-D-glucose + 2,4-dihydroxy-7-methoxy-2*H*-1,4-benzoxazin-3(4*H*)-one = UDP + (2*R*)-4-hydroxy-7-methoxy-3-oxo-3,4-dihydro-2*H*-1,4-benzoxazin-2-yl β-D-glucopyranoside
(2) UDP-α-D-glucose + 2,4-dihydroxy-2*H*-1,4-benzoxazin-3(4*H*)-one = UDP + (2*R*)-4-hydroxy-3-oxo-3,4-dihydro-2*H*-1,4-benzoxazin-2-yl β-D-glucopyranoside

Other name(s): uridine diphosphoglucose-2,4-dihydroxy-7-methoxy-2*H*-1,4-benzoxazin-3(4*H*)-one 2-glucosyltransferase; BX8; BX9; benzoxazinoid glucosyltransferase; DIMBOA glucosyltransferase
Systematic name: UDP-α-D-glucose:2,4-dihydroxy-7-methoxy-2*H*-1,4-benzoxazin-3(4*H*)-one 2-β-D-glucosyltransferase
Comments: The enzyme is involved in the detoxification of the benzoxazinoids DIBOA (2,4-dihydroxy-2*H*-1,4-benzoxazin-3(4*H*)-one) and DIMBOA (2,4-dihydroxy-7-methoxy-2*H*-1,4-benzoxazin-3(4*H*)-one) which are stored as the respective non-toxic glucosides in the vacuoles in some plants, most commonly from the family of Poaceae (grasses). Benzoxazinoids are known to exhibit antimicrobial, antifeedant, and antiinsecticidal effects and are involved in the interaction of plants with other plants, insects, or microorganisms.
References: [163, 3701]

[EC 2.4.1.202 created 1992, modified 2012]

EC 2.4.1.203

Accepted name: *trans*-zeatin *O*-β-D-glucosyltransferase
Reaction: UDP-glucose + *trans*-zeatin = UDP + *O*-β-D-glucosyl-*trans*-zeatin
Other name(s): zeatin *O*-β-D-glucosyltransferase; uridine diphosphoglucose-zeatin *O*-glucosyltransferase; zeatin *O*-glucosyltransferase
Systematic name: UDP-glucose:*trans*-zeatin *O*-β-D-glucosyltransferase
Comments: Unlike EC 2.4.1.215, *cis*-zeatin *O*-β-D-glucosyltransferase, UDP-D-xylose can also act as donor (*cf.* EC 2.4.2.40, zeatin *O*-β-D-xylosyltransferase).
References: [745]

[EC 2.4.1.203 created 1992, modified 2001]

[2.4.1.204 Transferred entry. zeatin O-β-D-xylosyltransferase. Now EC 2.4.2.40, zeatin O-β-D-xylosyltransferase]

[EC 2.4.1.204 created 1992, deleted 2003]

EC 2.4.1.205

Accepted name: galactogen 6β-galactosyltransferase
Reaction: UDP-α-D-galactose + galactogen = UDP + (1→6)-β-D-galactosylgalactogen
Other name(s): uridine diphosphogalactose-galactogen galactosyltransferase; 1,6-D-galactosyltransferase; β-(1-6)-D-galactosyltransferase; UDP-galactose:galactogen β-1,6-D-galactosyltransferase
Systematic name: UDP-α-D-galactose:galactogen 6-β-D-galactosyltransferase
Comments: Galactogen from *Helix pomatia* is the most effective acceptor.
References: [1116]

[EC 2.4.1.205 created 1992]

EC 2.4.1.206

Accepted name: lactosylceramide 1,3-*N*-acetyl-β-D-glucosaminyltransferase
Reaction: UDP-*N*-acetyl-α-D-glucosamine + β-D-galactosyl-(1→4)-β-D-glucosyl-(1↔1)-ceramide = UDP + *N*-acetyl-β-D-glucosaminyl-(1→3)-β-D-galactosyl-(1→4)-β-D-glucosyl-(1↔1)-ceramide
Other name(s): LA2 synthase; β1→3-*N*-acetylglucosaminyltransferase; uridine diphosphoacetylglucosamine-lactosylceramide β-acetylglucosaminyltransferase; lactosylceramide β-acetylglucosaminyltransferase; UDP-*N*-acetyl-D-glucosamine:D-galactosyl-1,4-β-D-glucosylceramide β-1,3-acetylglucosaminyltransferase; UDP-*N*-acetyl-D-glucosamine:β-D-galactosyl-(1→4)-β-D-glucosyl(1↔1)ceramide 3-β-*N*-acetylglucosaminyltransferase; UDP-*N*-acetyl-D-glucosamine:β-D-galactosyl-(1→4)-β-D-glucosyl-(1↔1)-ceramide 3-β-*N*-acetylglucosaminyltransferase
Systematic name: UDP-*N*-acetyl-α-D-glucosamine:β-D-galactosyl-(1→4)-β-D-glucosyl-(1↔1)-ceramide 3-β-*N*-acetylglucosaminyltransferase (configuration-inverting)
References: [1111, 1359, 2661]

[EC 2.4.1.206 created 1992]

EC 2.4.1.207

Accepted name: xyloglucan:xyloglucosyl transferase

Reaction: breaks a β-(1→4) bond in the backbone of a xyloglucan and transfers the xyloglucanyl segment on to O-4 of the non-reducing terminal glucose residue of an acceptor, which can be a xyloglucan or an oligosaccharide of xyloglucan

Other name(s): endo-xyloglucan transferase; xyloglucan endotransglycosylase

Systematic name: xyloglucan:xyloglucan xyloglucanotransferase

Comments: Does not use cello-oligosaccharides as either donor or acceptor.

References: [973, 2473, 690, 2036]

[EC 2.4.1.207 created 1999]

EC 2.4.1.208

Accepted name: diglucosyl diacylglycerol synthase (1,2-linking)

Reaction: UDP-α-D-glucose + 1,2-diacyl-3-*O*-(α-D-glucopyranosyl)-*sn*-glycerol = 1,2-diacyl-3-*O*-[α-D-glucopyranosyl-(1→2)-*O*-α-D-glucopyranosyl]-*sn*-glycerol + UDP

Other name(s): monoglucosyl diacylglycerol (1→2) glucosyltransferase; MGlcDAG (1→2) glucosyltransferase; DGlcDAG synthase (ambiguous); UDP-glucose:1,2-diacyl-3-*O*-(α-D-glucopyranosyl)-*sn*-glycerol (1→2) glucosyltransferase; diglucosyl diacylglycerol synthase

Systematic name: UDP-α-D-glucose:1,2-diacyl-3-*O*-(α-D-glucopyranosyl)-*sn*-glycerol 2-glucosyltransferase

Comments: The enzyme from *Acholeplasma laidlawii* requires Mg^{2+}.

References: [1586]

[EC 2.4.1.208 created 1999, modified 2014]

EC 2.4.1.209

Accepted name: *cis*-*p*-coumarate glucosyltransferase

Reaction: UDP-glucose + *cis*-*p*-coumarate = 4′-*O*-β-D-glucosyl-*cis*-*p*-coumarate + UDP

Systematic name: UDP-glucose:*cis*-*p*-coumarate β-D-glucosyltransferase

Comments: *cis*-Caffeic acid also serves as a glucosyl acceptor with the enzyme from *Sphagnum fallax kinggr*. The corresponding *trans*-isomers are not substrates.

References: [2820]

[EC 2.4.1.209 created 2000]

EC 2.4.1.210

Accepted name: limonoid glucosyltransferase

Reaction: UDP-glucose + limonin = glucosyl-limonin + UDP

Other name(s): uridine diphosphoglucose-limonoid glucosyltransferase

Systematic name: UDP-glucose:limonin glucosyltransferase

Comments: The enzyme purified from navel orange *albedo* tissue also acts on the related tetranortriterpenoid nomilin.

References: [3200]

[EC 2.4.1.210 created 2000]

EC 2.4.1.211

Accepted name: 1,3-β-galactosyl-*N*-acetylhexosamine phosphorylase

Reaction: β-D-galactopyranosyl-(1→3)-*N*-acetyl-D-glucosamine + phosphate = α-D-galactopyranose 1-phosphate + *N*-acetyl-D-glucosamine

Other name(s): lacto-*N*-biose phosphorylase; LNBP; galacto-*N*-biose phosphorylase
Systematic name: β-D-galactopyranosyl-(1→3)-*N*-acetyl-D-hexosamine:phosphate galactosyltransferase
Comments: Reaction also occurs with β-D-galactopyranosyl-(1→3)-*N*-acetyl-D-galactosamine as the substrate, giving *N*-acetyl-D-galactosamine as the product.
References: [717]

[EC 2.4.1.211 created 2001]

EC 2.4.1.212

Accepted name: hyaluronan synthase
Reaction: (1) UDP-*N*-acetyl-α-D-glucosamine + β-D-glucuronosyl-(1→3)-*N*-acetyl-β-D-glucosaminyl-(1→4)-[nascent hyaluronan] = UDP + *N*-acetyl-β-D-glucosaminyl-(1→4)-β-D-glucuronosyl-(1→3)-*N*-acetyl-β-D-glucosaminyl-(1→4)-[nascent hyaluronan]
(2) UDP-α-D-glucuronate + *N*-acetyl-β-D-glucosaminyl-(1→4)-β-D-glucuronosyl-(1→3)-[nascent hyaluronan] = UDP + β-D-glucuronosyl-(1→3)-*N*-acetyl-β-D-glucosaminyl-(1→4)-β-D-glucuronosyl-(1→3)-[nascent hyaluronan]
Other name(s): spHAS; seHAS; Alternating UDP-α-*N*-acetyl-D-glucosamine:β-D-glucuronosyl-(1→3)-[nascent hyaluronan] 4-*N*-acetyl-β-D-glucosaminyltransferase and UDP-α-D-glucuronate:*N*-acetyl-β-D-glucosaminyl-(1→4)-[nascent hyaluronan] 3-β-D-glucuronosyltransferase
Systematic name: Alternating UDP-*N*-acetyl-α-D-glucosamine:β-D-glucuronosyl-(1→3)-[nascent hyaluronan] 4-*N*-acetyl-β-D-glucosaminyltransferase and UDP-α-D-glucuronate:*N*-acetyl-β-D-glucosaminyl-(1→4)-[nascent hyaluronan] 3-β-D-glucuronosyltransferase (configuration-inverting)
Comments: The enzyme from *Streptococcus* Group A and Group C requires Mg^{2+}. The enzyme adds GlcNAc to nascent hyaluronan when the non-reducing end is GlcA, but it adds GlcA when the non-reducing end is GlcNAc [692]. The enzyme is highly specific for UDP-GlcNAc and UDP-GlcA; no copolymerization is observed if either is replaced by UDP-Glc, UDP-Gal, UDP-GalNAc or UDP-GalA. Similar enzymes have been found in a variety of organisms.
References: [694, 1517, 692, 3538]

[EC 2.4.1.212 created 2001, modified 2007]

EC 2.4.1.213

Accepted name: glucosylglycerol-phosphate synthase
Reaction: ADP-α-D-glucose + *sn*-glycerol 3-phosphate = 2-(α-D-glucopyranosyl)-*sn*-glycerol 3-phosphate + ADP
Other name(s): ADP-glucose:*sn*-glycerol-3-phosphate 2-β-D-glucosyltransferase (incorrect)
Systematic name: ADP-α-D-glucose:*sn*-glycerol-3-phosphate 2-α-D-glucopyranosyltransferase
Comments: Acts with EC 3.1.3.69 (glucosylglycerol phosphatase) to form glucosylglycerol, an osmolyte that endows cyanobacteria with resistance to salt.
References: [1193, 2127]

[EC 2.4.1.213 created 2001, modified 2015]

EC 2.4.1.214

Accepted name: glycoprotein 3-α-L-fucosyltransferase
Reaction: GDP-β-L-fucose + N^4-β-D-GlcNAc-(1→2)-α-D-Man-(1→3)-[β-D-GlcNAc-(1→2)-α-D-Man-(1→6)]-β-D-Man-(1→4)-β-D-GlcNAc-(1→4)-β-D-GlcNAc-L-asparaginyl-[protein] = GDP + N^4-β-D-GlcNAc-(1→2)-α-D-Man-(1→3)-[β-D-GlcNAc-(1→2)-α-D-Man-(1→6)]-β-D-Man-(1→4)-β-D-GlcNAc-(1→4)-[α-L-Fuc-(1→3)]-β-D-GlcNAc-L-asparaginyl-[protein]

Other name(s): GDP-L-Fuc:*N*-acetyl-β-D-glucosaminide α1,3-fucosyltransferase; GDP-L-Fuc:Asn-linked GlcNAc α1,3-fucosyltransferase; GDP-fucose:β-*N*-acetylglucosamine (Fuc to (Fucα1→6GlcNAc)-Asn-peptide) α1→3-fucosyltransferase; GDP-L-fucose:glycoprotein (L-fucose to asparagine-linked *N*-acetylglucosamine of 4-*N*-*N*-acetyl-β-D-glucosaminyl-(1→2)-α-D-mannosyl-(1→3)-[*N*-acetyl-β-D-glucosaminyl-(1→2)-α-D-mannosyl-(1→6)]-β-D-mannosyl-(1→4)-*N*-acetyl-β-D-glucosaminyl-(1→4)-*N*-acetyl-β-D-glucosaminylasparagine) 3-α-L-fucosyl-transferase; GDP-L-fucose:glycoprotein (L-fucose to asparagine-linked *N*-acetylglucosamine of N^4-*N*-acetyl-β-D-glucosaminyl-(1→2)-α-D-mannosyl-(1→3)-[*N*-acetyl-β-D-glucosaminyl-(1→2)-α-D-mannosyl-(1→6)]-β-D-mannosyl-(1→4)-*N*-acetyl-β-D-glucosaminyl-(1→4)-*N*-acetyl-β-D-glucosaminylasparagine) 3-α-L-fucosyl-transferase; GDP-β-L-fucose:glycoprotein (L-fucose to asparagine-linked *N*-acetylglucosamine of N^4-*N*-acetyl-β-D-glucosaminyl-(1→2)-α-D-mannosyl-(1→3)-[*N*-acetyl-β-D-glucosaminyl-(1→2)-α-D-mannosyl-(1→6)]-β-D-mannosyl-(1→4)-*N*-acetyl-β-D-glucosaminyl-(1→4)-*N*-acetyl-β-D-glucosaminylasparagine) 3-α-L-fucosyl-transferase

Systematic name: GDP-β-L-fucose:N^4-β-D-GlcNAc-(1→2)-α-D-Man-(1→3)-[β-D-GlcNAc-(1→2)-α-D-Man-(1→6)]-β-D-Man-(1→4)-β-D-GlcNAc-(1→4)-β-D-GlcNAc-L-asparaginyl-[protein] 3-α-L-fucosyltransferase (configuration-retaining)

Comments: Requires Mn^{2+}. The enzyme transfers to N-linked oligosaccharide structures (*N*-glycans), generally with a specificity for *N*-glycans with one unsubstituted non-reducing terminal GlcNAc residue. This enzyme catalyses a reaction similar to that of EC 2.4.1.68, glycoprotein 6-α-L-fucosyltransferase, but transferring the L-fucosyl group from GDP-β-L-fucose to form an α1,3-linkage rather than an α1,6-linkage. The *N*-glycan products of this enzyme are present in plants, insects and some other invertebrates (e.g., *Schistosoma*, *Haemonchus*, *Lymnaea*).

References: [3870, 862, 1924, 3644, 3322]

[EC 2.4.1.214 created 2001]

EC 2.4.1.215

Accepted name: *cis*-zeatin *O*-β-D-glucosyltransferase

Reaction: UDP-glucose + *cis*-zeatin = UDP + *O*-β-D-glucosyl-*cis*-zeatin

Systematic name: UDP-glucose:*cis*-zeatin *O*-β-D-glucosyltransferase

Comments: The enzyme from maize can use *cis*-zeatin and UDP-glucose as substrates, but not *cis*-ribosylzeatin, *trans*-zeatin or *trans*-ribosylzeatin. Unlike EC 2.4.1.203, *trans*-zeatin *O*-β-D-glucosyltransferase, UDP-D-xylose cannot act as a donor.

References: [2138]

[EC 2.4.1.215 created 2001]

EC 2.4.1.216

Accepted name: trehalose 6-phosphate phosphorylase

Reaction: α,α-trehalose 6-phosphate + phosphate = glucose 6-phosphate + β-D-glucose 1-phosphate

Other name(s): trehalose 6-phosphate:phosphate β-D-glucosyltransferase

Systematic name: α,α-trehalose 6-phosphate:phosphate β-D-glucosyltransferase

Comments: The enzyme from *Lactococcus lactis* is specific for trehalose 6-phosphate. Differs from EC 2.4.1.64, α,α-trehalose phosphorylase, in that trehalose is not a substrate.

References: [83]

[EC 2.4.1.216 created 2001]

EC 2.4.1.217

Accepted name: mannosyl-3-phosphoglycerate synthase

Reaction: GDP-mannose + 3-phospho-D-glycerate = GDP + 2-(α-D-mannosyl)-3-phosphoglycerate

Other name(s): MPG synthase; GDP-mannose:3-phosphoglycerate 3-α-D-mannosyltransferase

Systematic name: GDP-mannose:3-phospho-D-glycerate 3-α-D-mannosyltransferase

Comments: Requires Mg^{2+}. The enzyme is absolutely specific for GDPmannose and 3-phosphoglycerate, and transfers the mannosyl group with retention of configuration. In the hyperthermophilic archaeon *Pyrococcus horikoshii*, the mannosyl-3-phosphoglycerate formed is subsequently dephosphorylated by a specific phosphatase, EC 3.1.3.70 (mannosyl-3-phosphoglycerate phosphatase), producing mannosylglycerate.
References: [836]

[EC 2.4.1.217 created 2002]

EC 2.4.1.218

Accepted name: hydroquinone glucosyltransferase
Reaction: UDP-glucose + hydroquinone = UDP + hydroquinone-*O*-β-D-glucopyranoside
Other name(s): arbutin synthase; hydroquinone:*O*-glucosyltransferase
Systematic name: UDP-glucose:hydroquinone-*O*-β-D-glucosyltransferase
Comments: Hydroquinone is the most effective acceptor, but over 40 phenolic compounds are also glucosylated, but at lower rates.
References: [104, 103]

[EC 2.4.1.218 created 2002]

EC 2.4.1.219

Accepted name: vomilenine glucosyltransferase
Reaction: UDP-glucose + vomilenine = UDP + raucaffricine
Other name(s): UDPG:vomilenine 21-β-D-glucosyltransferase
Systematic name: UDP-glucose:vomilenine 21-*O*-β-D-glucosyltransferase
Comments: The indole alkaloid raucaffricine accumulates during the culture of *Rauvolfia* cell suspensions.
References: [3781, 3780, 2978]

[EC 2.4.1.219 created 2002]

EC 2.4.1.220

Accepted name: indoxyl-UDPG glucosyltransferase
Reaction: UDP-glucose + indoxyl = UDP + indican
Other name(s): indoxyl-UDPG-glucosyltransferase
Systematic name: UDP-glucose:indoxyl 3-*O*-β-D-glucosyltransferase
Comments: Also acts to a limited extent on 4-, 5-, 6- and 7-hydroxyindole. After enzymic or chemical hydrolysis, indican forms indoxyl, which, in turn, is converted in the presence of oxygen to the dye indigo.
References: [2120]

[EC 2.4.1.220 created 2002]

EC 2.4.1.221

Accepted name: peptide-*O*-fucosyltransferase
Reaction: transfers an α-L-fucosyl residue from GDP-β-L-fucose to the serine hydroxy group of a protein acceptor
Other name(s): GDP-L-fucose:polypeptide fucosyltransferase; GDP-fucose protein *O*-fucosyltransferase; GDP-fucose:polypeptide fucosyltransferase
Systematic name: GDP-β-L-fucose:polypeptide *O*-α-L-fucosyltransferase
Comments: Involved in the biosynthesis of *O*-fucosylated epidermal growth factor (EGF) and thrombospondin type 1 repeats. The attachment of *O*-linked fucose to serine or threonine occurs on EGF domains within the sequence Cys-Xaa-Xaa-Gly-Gly-Ser/Thr-Cys.
References: [3767, 3766, 3765, 1355]

[EC 2.4.1.221 created 2002]

EC 2.4.1.222

Accepted name:	*O*-fucosylpeptide 3-β-*N*-acetylglucosaminyltransferase
Reaction:	transfers a β-D-GlcNAc residue from UDP-D-GlcNAc to the fucose residue of a fucosylated protein acceptor
Other name(s):	*O*-fucosylpeptide β-1,3-*N*-acetylglucosaminyltransferase; fringe (ambiguous)
Systematic name:	UDP-D-GlcNAc:*O*-L-fucosylpeptide 3-β-*N*-acetyl-D-glucosaminyltransferase
Comments:	O-Fucosylpeptide 3-β-*N*-acetylglucosaminyltransferases are the products of fringe genes. O-linked fucose is an unusual form of glycosylation where the fucose is attached directly to proteins through the hydroxy groups of Ser or Thr residues.
References:	[2292]

[EC 2.4.1.222 created 2002]

EC 2.4.1.223

Accepted name:	glucuronosyl-galactosyl-proteoglycan 4-α-*N*-acetylglucosaminyltransferase
Reaction:	UDP-*N*-acetyl-α-D-glucosamine + [protein]-3-*O*-(β-D-GlcA-(1→3)-β-D-Gal-(1→3)-β-D-Gal-(1→4)-β-D-Xyl)-L-serine = UDP + [protein]-3-*O*-(α-D-GlcNAc-(1→4)-β-D-GlcA-(1→3)-β-D-Gal-(1→3)-β-D-Gal-(1→4)-β-D-Xyl)-L-serine
Other name(s):	α-*N*-acetylglucosaminyltransferase I; α1,4-*N*-acetylglucosaminyltransferase; glucuronosylgalactosyl-proteoglycan 4-α-*N*-acetylglucosaminyltransferase; UDP-*N*-acetyl-D-glucosamine:β-D-glucuronosyl-(1→3)-β-D-galactosyl-(1→3)-β-D-galactosyl-(1→4)-β-D-xylosyl-proteoglycan 4^{IV}-α-*N*-acetyl-D-glucosaminyltransferase; glucuronyl-galactosyl-proteoglycan 4-α-*N*-acetylglucosaminyltransferase
Systematic name:	UDP-*N*-acetyl-α-D-glucosamine:[protein]-3-*O*-(β-D-GlcA-(1→3)-β-D-Gal-(1→3)-β-D-Gal-(1→4)-β-D-Xyl)-L-serine 4^{IV}-α-*N*-acetyl-D-glucosaminyltransferase (configuration-retaining)
Comments:	Enzyme involved in the initiation of heparin and heparan sulfate synthesis, transferring GlcNAc to the (GlcA-Gal-Gal-Xyl-)Ser core. Apparently products of both the human EXTL2 and EXTL3 genes can catalyse this reaction. In *Caenorhabditis elegans*, the product of the *rib-2* gene displays this activity as well as that of EC 2.4.1.224, glucuronosyl-*N*-acetylglucosaminyl-proteoglycan 4-α-*N*-acetylglucosaminyltransferase. For explanation of the use of a superscript in the systematic name, see 2-Carb-37.2.
References:	[1697, 1696]

[EC 2.4.1.223 created 2002, modified 2016]

EC 2.4.1.224

Accepted name:	glucuronosyl-*N*-acetylglucosaminyl-proteoglycan 4-α-*N*-acetylglucosaminyltransferase
Reaction:	UDP-*N*-acetyl-D-glucosamine + β-D-glucuronosyl-(1→4)-*N*-acetyl-α-D-glucosaminyl-proteoglycan = UDP + *N*-acetyl-α-D-glucosaminyl-(1→4)-β-D-glucuronosyl-(1→4)-*N*-acetyl-α-D-glucosaminyl-proteoglycan
Other name(s):	α-*N*-acetylglucosaminyltransferase II glucuronyl-*N*-acetylglucosaminylproteoglycan α-1,4-*N*-acetylglucosaminyltransferase
Systematic name:	UDP-*N*-acetyl-D-glucosamine:β-D-glucuronosyl-(1→4)-*N*-acetyl-α-D-glucosaminyl-proteoglycan 4-α-*N*-acetylglucosaminyltransferase
Comments:	Involved in the biosynthesis of heparin and heparan sulfate. Some forms of the enzyme from human (particularly the enzyme complex encoded by the EXT1 and EXT2 genes) act as bifunctional glycosyltransferases, which also have the 4-β-glucuronosyltransferase (EC 2.4.1.225, *N*-acetylglucosaminyl-proteoglycan 4-β-glucuronosyltransferase) activity required for the synthesis of the heparan sulfate disaccharide repeats. Other human forms of this enzyme (e.g. the product of the EXTL1 gene) have only the 4-α-*N*-acetylglucosaminyltransferase activity. In *Caenorhabditis elegans*, the product of the rib-2 gene displays the activities of this enzyme as well as EC 2.4.1.223, glucuronosyl-galactosyl-proteoglycan 4-α-*N*-acetylglucosaminyltransferase.
References:	[1675, 1696, 3139, 1975]

[EC 2.4.1.224 created 2002]

EC 2.4.1.225

Accepted name: *N*-acetylglucosaminyl-proteoglycan 4-β-glucuronosyltransferase

Reaction: UDP-α-D-glucuronate + *N*-acetyl-α-D-glucosaminyl-(1→4)-β-D-glucuronosyl-proteoglycan = UDP + β-D-glucuronosyl-(1→4)-*N*-acetyl-α-D-glucosaminyl-(1→4)-β-D-glucuronosyl-proteoglycan

Other name(s): *N*-acetylglucosaminylproteoglycan β-1,4-glucuronyltransferase; heparan glucuronyltransferase II

Systematic name: UDP-α-D-glucuronate:*N*-acetyl-α-D-glucosaminyl-(1→4)-β-D-glucuronosyl-proteoglycan 4-β-glucuronosyltransferase

Comments: Involved in the biosynthesis of heparin and heparan sulfate. Some forms of the human enzyme (particularly the enzyme complex encoded by the *EXT1* and *EXT2* genes) act as bifunctional glycosyltransferases, which also have the glucuronosyl-*N*-acetylglucosaminyl-proteoglycan 4-α-*N*-acetylglucosaminyltransferase (EC 2.4.1.224) activity required for the synthesis of the heparan sulfate disaccharide repeats.

References: [3139, 1975]

[EC 2.4.1.225 created 2002]

EC 2.4.1.226

Accepted name: *N*-acetylgalactosaminyl-proteoglycan 3-β-glucuronosyltransferase

Reaction: (1) UDP-α-D-glucuronate + [protein]-3-*O*-(β-D-GalNAc-(1→4)-β-D-GlcA-(1→3)-β-D-Gal-(1→3)-β-D-Gal-(1→4)-β-D-Xyl)-L-serine = UDP + [protein]-3-*O*-(β-D-GlcA-(1→3)-β-D-GalNAc-(1→4)-β-D-GlcA-(1→3)-β-D-Gal-(1→3)-β-D-Gal-(1→4)-β-D-Xyl)-L-serine
(2) UDP-α-D-glucuronate + [protein]-3-*O*-([β-D-GalNAc-(1→4)-β-D-GlcA-(1→3)]$_n$-β-D-GalNAc-(1→4)-β-D-GlcA-(1→3)-β-D-Gal-(1→3)-β-D-Gal-(1→4)-β-D-Xyl)-L-serine = UDP + [protein]-3-*O*-(β-D-GlcA-(1→3)-[β-D-GalNAc-(1→4)-β-D-GlcA-(1→3)]$_n$-β-D-GalNAc-(1→4)-β-D-GlcA-(1→3)-β-D-Gal-(1→3)-β-D-Gal-(1→4)-β-D-Xyl)-L-serine

Other name(s): chondroitin glucuronyltransferase II; α-D-glucuronate:*N*-acetyl-β-D-galactosaminyl-(1→4)-β-D-glucuronosyl-proteoglycan 3-β-glucuronosyltransferase; UDP-α-D-glucuronate:*N*-acetyl-β-D-galactosaminyl-(1→4)-β-D-glucuronosyl-proteoglycan 3-β-glucuronosyltransferase

Systematic name: UDP-α-D-glucuronate:[protein]-3-*O*-(β-D-GalNAc-(1→4)-β-D-GlcA-(1→3)-β-D-Gal-(1→3)-β-D-Gal-(1→4)-β-D-Xyl)-L-serine = UDP + [protein]-3-*O*-(β-D-GlcA-(1→3)-β-D-GalNAc-(1→4)-β-D-GlcA-(1→3)-β-D-Gal-(1→3)-β-D-Gal-(1→4)-β-D-Xyl)-L-serine 3-β-glucuronosyltransferase (configuration-inverting)

Comments: Involved in the biosynthesis of chondroitin and dermatan sulfate. The human chondroitin synthetase is a bifunctional glycosyltransferase, which has the 3-β-glucuronosyltransferase and 4-β-*N*-acetylgalactosaminyltransferase (EC 2.4.1.175) activities required for the synthesis of the chondroitin sulfate disaccharide repeats. Similar chondroitin synthase 'co-polymerases' can be found in *Pasteurella multocida* and *Escherichia coli*. There is also another human protein with apparently only the 3-β-glucuronosyltransferase activity.

References: [1699, 693, 2462, 1107]

[EC 2.4.1.226 created 2002, modified 2018]

EC 2.4.1.227

Accepted name: undecaprenyldiphospho-muramoylpentapeptide β-*N*-acetylglucosaminyltransferase

Reaction: UDP-*N*-acetyl-α-D-glucosamine + Mur2Ac(oyl-L-Ala-γ-D-Glu-L-Lys-D-Ala-D-Ala)-diphosphoundecaprenol = UDP + β-D-GlcNAc-(1→4)-Mur2Ac(oyl-L-Ala-γ-D-Glu-L-Lys-D-Ala-D-Ala)-diphosphoundecaprenol

Other name(s): MurG transferase; UDP-*N*-D-glucosamine:*N*-acetyl-α-D-muramyl(oyl-L-Ala-γ-D-Glu-L-Lys-D-Ala-D-Ala)-diphosphoundecaprenol β-1,4-*N*-acetylglucosaminlytransferase; UDP-*N*-acetyl-D-glucosamine:*N*-acetyl-α-D-muramyl(oyl-L-Ala-γ-D-Glu-L-Lys-D-Ala-D-Ala)-diphosphoundecaprenol 4-β-*N*-acetylglucosaminlytransferase

Systematic name: UDP-*N*-acetyl-α-D-glucosamine:*N*-acetyl-α-D-muramyl(oyl-L-Ala-γ-D-Glu-L-Lys-D-Ala-D-Ala)-diphosphoundecaprenol 4-β-*N*-acetylglucosaminlytransferase (configuration-inverting)

Comments: The enzyme also works when the lysine residue is replaced by *meso*-2,6-diaminoheptanedioate (*meso*-2,6-diaminopimelate, A2pm) combined with adjacent residues through its L-centre, as it is in Gram-negative and some Gram-positive organisms. The undecaprenol involved is *ditrans*,*octacis*-undecaprenol (for definitions, click here).

References: [3640]

[EC 2.4.1.227 created 2002]

EC 2.4.1.228

Accepted name: lactosylceramide 4-α-galactosyltransferase

Reaction: UDP-α-D-galactose + β-D-galactosyl-(1→4)-β-D-glucosyl-(1↔1)-ceramide = UDP + α-D-galactosyl-(1→4)-β-D-galactosyl-(1→4)-β-D-glucosyl-(1↔1)-ceramide

Other name(s): Galβ1-4Glcβ1-Cer α1,4-galactosyltransferase; globotriaosylceramide/CD77 synthase; histo-blood group Pk UDP-galactose; UDP-galactose:lactosylceramide 4^{II}-α-D-galactosyltransferase; UDP-galactose:β-D-galactosyl-(1→4)-D-glucosyl(1↔1)ceramide 4^{II}-α-D-galactosyltransferase; UDP-galactose:β-D-galactosyl-(1→4)-D-glucosyl-(1↔1)-ceramide 4^{II}-α-D-galactosyltransferase

Systematic name: UDP-α-D-galactose:β-D-galactosyl-(1→4)-D-glucosyl-(1↔1)-ceramide 4^{II}-α-D-galactosyltransferase

Comments: For explanation of superscript II in systematic name, see 2-carb.37.

References: [169, 3323, 1744]

[EC 2.4.1.228 created 2002]

EC 2.4.1.229

Accepted name: [Skp1-protein]-hydroxyproline *N*-acetylglucosaminyltransferase

Reaction: UDP-*N*-acetyl-α-D-glucosamine + [Skp1-protein]-*trans*-4-hydroxy-L-proline = UDP + [Skp1-protein]-*O*-(*N*-acetyl-α-D-glucosaminyl)-*trans*-4-hydroxy-L-proline

Other name(s): Skp1-HyPro GlcNAc-transferase; UDP-*N*-acetylglucosamine (GlcNAc):hydroxyproline polypeptide GlcNAc-transferase; UDP-GlcNAc:Skp1-hydroxyproline GlcNAc-transferase; UDP-GlcNAc:hydroxyproline polypeptide GlcNAc-transferase; UDP-*N*-acetyl-D-glucosamine:[Skp1-protein]-hydroxyproline *N*-acetyl-D-glucosaminyl-transferase

Systematic name: UDP-*N*-acetyl-α-D-glucosamine:[Skp1-protein]-*trans*-4-hydroxy-L-proline *N*-acetyl-α-D-glucosaminyl-transferase

Comments: Skp1 is a cytoplasmic and nuclear protein required for the ubiquitination of cell cycle regulatory proteins and transcriptional factors. In *Dictyostelium* Skp1 is modified by the linear pentasaccharide Galα1-6Galα1-L-Fucα1-2Galβ1-3GlcNAc, which is attached to a hydroxyproline residue at position 143. This enzyme catalyses the first step in the building up of the pentasaccharide by attaching an *N*-acetylglucosaminyl group to the hydroxyproline residue. It requires dithiothreitol and a divalent cation for activity.

References: [3638, 3499, 3825]

[EC 2.4.1.229 created 2003, modified 2013]

EC 2.4.1.230

Accepted name: kojibiose phosphorylase

Reaction: 2-α-D-glucosyl-D-glucose + phosphate = D-glucose + β-D-glucose 1-phosphate

Systematic name: 2-α-D-glucosyl-D-glucose:phosphate β-D-glucosyltransferase

Comments: The enzyme from *Thermoanaerobacter brockii* can act with α-1,2-oligoglucans, such as selaginose, as substrate, but more slowly. The enzyme is inactive when dissaccharides with linkages other than α-1,2 linkages, such as sophorose, trehalose, neotrehalose, nigerose, laminaribiose, maltose, cellobiose, isomaltose, gentiobiose, sucrose and lactose, are used as substrates.

References: [497, 496]

[EC 2.4.1.230 created 2003]

EC 2.4.1.231

Accepted name: α,α-trehalose phosphorylase (configuration-retaining)

Reaction: α,α-trehalose + phosphate = α-D-glucose + α-D-glucose 1-phosphate

Other name(s): trehalose phosphorylase[ambiguous]

Systematic name: α,α-trehalose:phosphate α-D-glucosyltransferase

Comments: Unlike EC 2.4.1.64, α,α-trehalose phosphorylase, this enzyme retains its anomeric configuration. Vanadate is a strong competitive inhibitor of this reversible reaction.

References: [817, 818, 2451]

[EC 2.4.1.231 created 2003]

EC 2.4.1.232

Accepted name: initiation-specific α-1,6-mannosyltransferase

Reaction: Transfers an α-D-mannosyl residue from GDP-mannose into lipid-linked oligosaccharide, forming an α-(1→6)-D-mannosyl-D-mannose linkage

Other name(s): α-1,6-mannosyltransferase; GDP-mannose:oligosaccharide 1,6-α-D-mannosyltransferase; GDP-mannose:glycolipid 1,6-α-D-mannosyltransferase; glycolipid 6-α-mannosyltransferase; GDP-mannose:oligosaccharide 1,6-α-D-mannosyltransferase

Systematic name: GDP-mannose:oligosaccharide 6-α-D-mannosyltransferase

Comments: Requires Mn^{2+}. In *Saccharomyces cerevisiae*, this enzyme catalyses an essential step in the outer chain elongation of N-linked oligosaccharides. Man$_8$GlcNAc and Man$_9$GlcNAc are equally good substrates.

References: [2926, 2837, 2409, 3948, 638, 3585, 2416, 3396, 3983]

[EC 2.4.1.232 created 2004]

[2.4.1.233 Deleted entry. anthocyanidin 3-O-glucosyltransferase. The enzyme is identical to EC 2.4.1.115, anthocyanidin 3-O-glucosyltransferase]

[EC 2.4.1.233 created 2004, deleted 2005]

EC 2.4.1.234

Accepted name: kaempferol 3-*O*-galactosyltransferase

Reaction: UDP-α-D-galactose + kaempferol = UDP + kaempferol 3-*O*-β-D-galactoside

Other name(s): F$_3$GalTase; UDP-galactose:kaempferol 3-*O*-β-D-galactosyltransferase

Systematic name: UDP-α-D-galactose:kaempferol 3-*O*-β-D-galactosyltransferase

Comments: Acts on the endogenous flavonols kaempferol and quercetin, to a lesser extent on myricetin and fisetin, and weakly on galangin and isorhamnetin. The reaction can occur equally well in both directions.

References: [2256]

[EC 2.4.1.234 created 2004]

[2.4.1.235 Deleted entry. cyanidin 3-O-rutinoside 5-O-glucosyltransferase. Enzyme is identical to EC 2.4.1.116, cyanidin 3-O-rutinoside 5-O-glucosyltransferase]

[EC 2.4.1.235 created 2004, deleted 2006]

EC 2.4.1.236

Accepted name: flavanone 7-*O*-glucoside 2″-*O*-β-L-rhamnosyltransferase

Reaction: UDP-β-L-rhamnose + a flavanone 7-*O*-β-D-glucoside = UDP + a flavanone 7-*O*-[α-L-rhamnosyl-(1→2)-β-D-glucoside]

Other name(s): UDP-rhamnose:flavanone-7-*O*-glucoside-2″-*O*-rhamnosyltransferase; 1→2 UDP-rhamnosyltransferase; UDP-L-rhamnose:flavanone-7-*O*-glucoside 2″-*O*-β-L-rhamnosyltransferase

Systematic name: UDP-β-L-rhamnose:flavanone-7-*O*-glucoside 2″-*O*-α-L-rhamnosyltransferase

Comments: Acts on the 7-*O*-glucoside of naringenin and hesperetin, also the flavone 7-*O*-glucosides of luteolin and apigenin.
References: [185]

[EC 2.4.1.236 created 2004]

EC 2.4.1.237

Accepted name: flavonol 7-*O*-β-glucosyltransferase
Reaction: UDP-glucose + a flavonol = UDP + a flavonol 7-*O*-β-D-glucoside
Other name(s): UDP-glucose:flavonol 7-*O*-glucosyltransferase
Systematic name: UDP-glucose:flavonol 7-*O*-β-D-glucosyltransferase
Comments: Acts on the flavonols gossypetin (8-hydroxyquercetin) and to a lesser extent on quercetin, kaempferol and myricetin.
References: [3344]

[EC 2.4.1.237 created 2004]

EC 2.4.1.238

Accepted name: delphinidin 3,5-di-*O*-glucoside 3′-*O*-glucosyltransferase
Reaction: UDP-α-D-glucose + delphinidin 3,5-di-*O*-β-D-glucoside = UDP + delphinidin 3,3′,5-tri-*O*-β-D-glucoside
Other name(s): UDP-glucose:anthocyanin 3′-*O*-glucosyltransferase; 3’GT
Systematic name: UDP-α-D-glucose:delphinidin-3,5-di-*O*-β-D-glucoside 3′-*O*-glucosyltransferase
Comments: Isolated from the plant *Gentiana triflora* (clustered gentian).
References: [995]

[EC 2.4.1.238 created 2004, modified 2013]

EC 2.4.1.239

Accepted name: flavonol-3-*O*-glucoside glucosyltransferase
Reaction: UDP-glucose + a flavonol 3-*O*-β-D-glucoside = UDP + a flavonol 3-*O*-β-D-glucosyl-(1→2)-β-D-glucoside
Other name(s): UDP-glucose:flavonol-3-*O*-glucoside 2″-*O*-β-D-glucosyltransferase
Systematic name: UDP-glucose:flavonol-3-*O*-β-D-glucoside 2″-*O*-β-D-glucosyltransferase
Comments: One of three specific glucosyltransferases in pea (*Pisum sativum*) that successively add a β-D-glucosyl group first to O-3 of kaempferol, and then to O-2 of the previously added glucosyl group giving the 3-*O*-sophoroside and then the 3-*O*-sophorotrioside (see also EC 2.4.1.91, flavonol 3-*O*-glucosyltransferase and EC 2.4.1.240, flavonol-3-*O*-glycoside glucosyltransferase). TDP-glucose can replace UDP-glucose as the glucose donor but the reaction proceeds more slowly.
References: [1543]

[EC 2.4.1.239 created 2004]

EC 2.4.1.240

Accepted name: flavonol-3-*O*-glycoside glucosyltransferase
Reaction: UDP-glucose + a flavonol 3-*O*-β-D-glucosyl-(1→2)-β-D-glucoside = UDP + a flavonol 3-*O*-β-D-glucosyl-(1→2)-β-D-glucosyl-(1→2)-β-D-glucoside
Systematic name: UDP-glucose:flavonol-3-*O*-β-D-glucosyl-(1→2)-β-D-glucoside 2‴-*O*-β-D-glucosyltransferase
Comments: One of three specific glucosyltransferases in pea (*Pisum sativum*) thatsuccessively add a β-D-glucosyl group first to O-3 of kaempferol, and then to O-2 of the previously added glucosyl group giving the 3-*O*-sophoroside and then the 3-*O*-sophorotrioside (see also EC 2.4.1.91 flavonol 3-*O*-glucosyltransferase, and EC 2.4.1.239 flavonol-3-*O*-glucoside glucosyltransferase).
References: [1543]

[EC 2.4.1.240 created 2004]

EC 2.4.1.241

Accepted name: digalactosyldiacylglycerol synthase

Reaction: UDP-α-D-galactose + 1,2-diacyl-3-*O*-(β-D-galactosyl)-*sn*-glycerol = UDP + 1,2-diacyl-3-*O*-[α-D-galactosyl-(1→6)-β-D-galactosyl]-*sn*-glycerol

Other name(s): DGD1; DGD2; DGDG synthase (ambiguous); UDP-galactose-dependent DGDG synthase; UDP-galactose-dependent digalactosyldiacylglycerol synthase; UDP-galactose:MGDG galactosyltransferase; UDP-galactose:3-(β-D-galactosyl)-1,2-diacyl-*sn*-glycerol 6-α-galactosyltransferase

Systematic name: UDP-α-D-galactose:1,2-diacyl-3-*O*-(β-D-galactosyl)-*sn*-glycerol 6-α-galactosyltransferase

Comments: Requires Mg^{2+}. Diacylglycerol cannot serve as an acceptor molecule for galactosylation as in the reaction catalysed by EC 2.4.1.46, monogalactosyldiacylglyerol synthase. When phosphate is limiting, phospholipids in plant membranes are reduced but these are replaced, at least in part, by the glycolipids digalactosyldiacylglycerol (DGDG) and sulfoquinovosyldiacylglycerol [1632]. While both DGD1 and DGD2 are increased under phosphate-limiting conditions, DGD2 does not contribute significantly under optimal growth conditions. DGD2 is responsible for the synthesis of DGDG molecular species that are rich in C_{16} fatty acids at *sn*-1 of diacylglycerol whereas DGD1 leads to molecular species rich in C_{18} fatty acids [1632]. The enzyme has been localized to the outer side of chloroplast envelope membranes.

References: [1631, 1231, 1632, 269]

[EC 2.4.1.241 created 2005]

EC 2.4.1.242

Accepted name: NDP-glucose—starch glucosyltransferase

Reaction: NDP-glucose + $[(1\rightarrow4)\text{-}\alpha\text{-D-glucosyl}]_n$ = NDP + $[(1\rightarrow4)\text{-}\alpha\text{-D-glucosyl}]_{n+1}$

Other name(s): granule-bound starch synthase; starch synthase II (ambiguous); waxy protein; starch granule-bound nucleoside diphosphate glucose-starch glucosyltransferase; granule-bound starch synthase I; GBSSI; granule-bound starch synthase II; GBSSII; GBSS; NDPglucose-starch glucosyltransferase

Systematic name: NDP-glucose:(1→4)-α-D-glucan 4-α-D-glucosyltransferase

Comments: Unlike EC 2.4.1.11, glycogen(starch) synthase and EC 2.4.1.21, starch synthase, which use UDP-glucose and ADP-glucose, respectively, this enzyme can use either UDP- or ADP-glucose. Mutants that lack the Wx (waxy) allele cannot produce this enzyme, which plays an important role in the normal synthesis of amylose. In such mutants, only amylopectin is produced in the endosperm [989] or pollen [2432].

References: [3574, 2406, 989, 2365, 2432]

[EC 2.4.1.242 created 2005]

EC 2.4.1.243

Accepted name: 6^G-fructosyltransferase

Reaction: $[1\text{-}\beta\text{-D-fructofuranosyl-}(2\rightarrow1)\text{-}]_{m+1}$-α-D-glucopyranoside + $[1\text{-}\beta\text{-D-fructofuranosyl-}(2\rightarrow1)\text{-}]_n$-α-D-glucopyranoside = $[1\text{-}\beta\text{-D-fructofuranosyl-}(2\rightarrow1)\text{-}]_m$-α-D-glucopyranoside + $[1\text{-}\beta\text{-D-fructofuranosyl-}(2\rightarrow1)\text{-}]_n$-β-D-fructofuranosyl-(2→6)-α-D-glucopyranoside ($m > 0$; $n \geq 0$)

Other name(s): fructan:fructan 6^G-fructosyltransferase; 1^F(1-β-D-fructofuranosyl)m sucrose:1F(1-β-D-fructofuranosyl)nsucrose 6^G-fructosyltransferase; 6^G-FFT; 6^G-FT; 6^G-fructotransferase

Systematic name: 1^F-oligo[β-D-fructofuranosyl-(2→1)-]sucrose 6^G-β-D-fructotransferase

Comments: Inulins are polysaccharides consisting of linear or branched D-fructofuranosyl chains attached to the fructosyl residue of sucrose by a β(2→1) linkage. This enzyme catalyses the transfer of the terminal (2→1)-linked -D-fructosyl group of an inulin chain onto O-6 position of the glucose residue of another inulin molecule [3205]. For example, if 1-kestose [1F-(β-D-fructofuranosyl)sucrose] is both the donor and recipient in the reaction shown above, i.e., if $m = 1$ and $n = 1$, then the products will be sucrose and 6^G-di-β-D-fructofuranosylsucrose. In this notation, the superscripts F and G are used to specify whether the fructose or glucose residue of the sucrose carries the substituent. Alternatively, this may be indicated by the presence and/or absence of primes (see http://www.chem.qmul.ac.uk/iupac/2carb/36.html#362). Sucrose cannot be a donor substrate in the reaction (i.e. m cannot be zero) and inulin cannot act as an acceptor. Side reactions catalysed are transfer of a β-D-fructosyl group between compounds of the structure 1^F-(1-β-D-fructofuranosyl)*m*-6^G-(1-β-D-fructofuranosyl)n sucrose, where $m \geq 0$ and $n = 1$ for the donor, and $m \geq 0$ and $n \geq 0$ for the acceptor.

References: [3205, 3206, 3207, 3604]

[EC 2.4.1.243 created 2006]

EC 2.4.1.244

Accepted name: *N*-acetyl-β-glucosaminyl-glycoprotein 4-β-*N*-acetylgalactosaminyltransferase

Reaction: UDP-*N*-acetyl-α-D-galactosamine + *N*-acetyl-β-D-glucosaminyl group = UDP + *N*-acetyl-β-D-galactosaminyl-(1→4)-*N*-acetyl-β-D-glucosaminyl group

Other name(s): β1,4-*N*-acetylgalactosaminyltransferase III; β4GalNAc-T3; β1,4-*N*-acetylgalactosaminyltransferase IV; β4GalNAc-T4; UDP-*N*-acetyl-D-galactosamine:*N*-acetyl-D-glucosaminyl-group β-1,4-*N*-acetylgalactosaminyltransferase; UDP-*N*-acetyl-D-galactosamine:*N*-acetyl-β-D-glucosaminyl-group 4-β-*N*-acetylgalactosaminyltransferase

Systematic name: UDP-*N*-acetyl-α-D-galactosamine:*N*-acetyl-β-D-glucosaminyl-group 4-β-*N*-acetylgalactosaminyltransferase

Comments: The enzyme from human can transfer *N*-acetyl-D-galactosamine (GalNAc) to *N*-glycan and *O*-glycan substrates that have *N*-acetyl-D-glucosamine (GlcNAc) but not D-glucuronic acid (GlcUA) at their non-reducing end. The *N*-acetyl-β-D-glucosaminyl group is normally on a core oligosaccharide although benzyl glycosides have been used in enzyme-characterization experiments. Some glycohormones, e.g. lutropin and thyrotropin contain the *N*-glycan structure containing the *N*-acetyl-β-D-galactosaminyl-(1→4)-*N*-acetyl-β-D-glucosaminyl group.

References: [3035, 1106]

[EC 2.4.1.244 created 2006]

EC 2.4.1.245

Accepted name: α,α-trehalose synthase

Reaction: NDP-α-D-glucose + D-glucose = α,α-trehalose + NDP

Other name(s): trehalose synthase; trehalose synthetase; UDP-glucose:glucose 1-glucosyltransferase; TreT; PhGT; ADP-glucose:D-glucose 1-α-D-glucosyltransferase

Systematic name: NDP-α-D-glucose:D-glucose 1-α-D-glucosyltransferase

Comments: Requires Mg^{2+} for maximal activity [2779]. The enzyme-catalysed reaction is reversible [2779]. In the reverse direction to that shown above, the enzyme is specific for α,α-trehalose as substrate, as it cannot use α- or β-paranitrophenyl glucosides, maltose, sucrose, lactose or cellobiose [2779]. While the enzymes from the thermophilic bacterium *Rubrobacter xylanophilus* and the hyperthermophilic archaeon *Pyrococcus horikoshii* can use ADP-, UDP- and GDP-α-D-glucose to the same extent [2983, 2478], that from the hyperthermophilic archaeon *Thermococcus litoralis* has a marked preference for ADP-α-D-glucose [2779] and that from the hyperthermophilic archaeon *Thermoproteus tenax* has a marked preference for UDP-α-D-glucose [1773].

References: [2779, 2983, 2478, 1773]

[EC 2.4.1.245 created 2008, modified 2013]

EC 2.4.1.246

Accepted name: mannosylfructose-phosphate synthase

Reaction: GDP-mannose + D-fructose 6-phosphate = GDP + β-D-fructofuranosyl-α-D-mannopyranoside 6^F-phosphate

Other name(s): mannosylfructose-6-phosphate synthase; MFPS

Systematic name: GDP-mannose:D-fructose-6-phosphate 2-α-D-mannosyltransferase

Comments: This enzyme, from the soil proteobacterium and plant pathogen *Agrobacterium tumefaciens* strain C^{58}, requires Mg^{2+} or Mn^{2+} for activity. GDP-mannose can be replaced by ADP-mannose but with a concomitant decrease in activity. The product of this reaction is dephosphorylated by EC 3.1.3.79 (mannosylfructose-phosphate phosphatase) to form the non-reducing disaccharide mannosylfructose, which is the major endogenous osmolyte produced by several α-proteobacteria in response to osmotic stress. The F in the product name is used to indicate that the fructose residue of sucrose carries the substituent.

References: [3553]

[EC 2.4.1.246 created 2008]

EC 2.4.1.247

Accepted name: β-D-galactosyl-(1→4)-L-rhamnose phosphorylase

Reaction: β-D-galactosyl-(1→4)-L-rhamnose + phosphate = L-rhamnose + α-D-galactose 1-phosphate

Other name(s): D-galactosyl-β1→4-L-rhamnose phosphorylase; GalRhaP

Systematic name: β-D-galactosyl-(1→4)-L-rhamnose:phosphate 1-α-D-galactosyltransferase

Comments: The enzyme from *Clostridium phytofermentans* is also active towards towards β-D-galactosyl derivatives of L-mannose, L-lyxose, D-glucose, 2-deoxy-D-glucose, and D-galactose in this order. Differs from 1,3-β-galactosyl-*N*-acetylhexosamine phosphorylase (EC 2.4.1.211) in being active towards L-rhamnose and inactive towards *N*-acetyl hexosamine derivatives.

References: [2402]

[EC 2.4.1.247 created 2009]

EC 2.4.1.248

Accepted name: cycloisomaltooligosaccharide glucanotransferase

Reaction: cyclizes part of a (1→6)-α-D-glucan chain by formation of a (1→6)-α-D-glucosidic bond

Systematic name: (1→6)-α-D-glucan:(1→6)-α-D-glucan 6-α-D-[1→6α-D-glucano]-transferase (cyclizing)

Comments: Specific for (1→6)-α-D-glucans (dextrans) and, unlike cyclomaltodextrin glucanotransferase (EC 2.4.1.19), without activity towards (1→4)-α-D-glucans, such as amylose. It also has no activity on oligosaccharides, such as amylopectin and pullulan, containing (1→6)-α-D-glucosidic linkages at branch points. The enzyme from *Bacillus circulans* T-3040 has been shown to form cycloisomalto-oligosaccharides of three sizes (7, 8 and 9 glucose units). It will also catalyse the disproportionation of two isomalto-oligosaccharides molecules to yield a series of isomalto-oligosachharides and the addition of D-glucose to cycloisomalto-oligosaccharides with ring opening to form isomalto-oligosaccharides.

References: [3421, 2525, 3950]

[EC 2.4.1.248 created 2009]

EC 2.4.1.249

Accepted name: delphinidin 3′,5′-*O*-glucosyltransferase

Reaction: **2** UDP-glucose + delphinidin 3-*O*-(6″-*O*-malonyl)-β-D-glucoside = **2** UDP + delphinidin 3-*O*-(6″-*O*-malonyl)-β-D-glucoside-3′,5′-di-*O*-β-D-glucoside (overall reaction)
(1a) UDP-glucose + delphinidin 3-*O*-(6″-*O*-malonyl)-β-D-glucoside = UDP + delphinidin 3-*O*-(6″-*O*-malonyl)-β-D-glucoside-3′-*O*-β-D-glucoside
(1b) UDP-glucose + delphinidin 3-*O*-(6″-*O*-malonyl)-β-D-glucoside-3′-*O*-β-D-glucoside = UDP + delphinidin 3-*O*-(6″-*O*-malonyl)-β-D-glucoside-3′,5′-di-*O*-β-D-glucoside

Other name(s): UDP-glucose:anthocyanin 3′,5′-*O*-glucosyltransferase; UA3′5’GZ
Systematic name: UDP-glucose:delphinidin 3-*O*-(6″-*O*-malonyl)-β-D-glucoside 3′-*O*-glucosyltransferase
Comments: Ternatins are a group of polyacetylated delphinidin glucosides that confer blue color to the petals of *Clitoria ternatea* (butterfly pea). This enzyme catalyses two reactions in the biosynthesis of ternatin C5: the conversion of delphinidin 3-*O*-(6″-*O*-malonyl)-β-D-glucoside to delphinidin 3-*O*-(6″-*O*-malonyl)-β-D-glucoside-3′-*O*-β-D-glucoside, followed by the conversion of the later to ternatin C5, by transferring two glucosyl groups in a stepwise manner [1735].
References: [1735]

[EC 2.4.1.249 created 2009]

EC 2.4.1.250

Accepted name: D-inositol-3-phosphate glycosyltransferase
Reaction: UDP-*N*-acetyl-α-D-glucosamine + 1D-*myo*-inositol 3-phosphate = 1-*O*-(2-acetamido-2-deoxy-α-D-glucopyranosyl)-1D-*myo*-inositol 3-phosphate + UDP
Other name(s): mycothiol glycosyltransferases; MshA; UDP-*N*-acetyl-D-glucosamine:1D-*myo*-inositol 3-phosphate α-D-glycosyltransferase
Systematic name: UDP-*N*-acetyl-α-D-glucosamine:1D-*myo*-inositol 3-phosphate α-D-glycosyltransferase (configuration-retaining)
Comments: The enzyme, which belongs to the GT-B fold superfamily, catalyses the first dedicated reaction in the biosynthesis of mycothiol [2445]. The substrate was initially believed to be inositol, but eventually shown to be D-*myo*-inositol 3-phosphate [2446]. A substantial conformational change occurs upon UDP binding, which generates the binding site for D-*myo*-inositol 3-phosphate [3675].
References: [2445, 2446, 3675]

[EC 2.4.1.250 created 2010]

EC 2.4.1.251

Accepted name: GlcA-β-(1→2)-D-Man-α-(1→3)-D-Glc-β-(1→4)-D-Glc-α-1-diphospho-*ditrans*,*octacis*-undecaprenol 4-β-mannosyltransferase
Reaction: GDP-mannose + GlcA-β-(1→2)-D-Man-α-(1→3)-D-Glc-β-(1→4)-D-Glc-α-1-diphospho-*ditrans*,*octacis*-undecaprenol = GDP + D-Man-β-(1→4)- GlcA-β-(1→2)-D-Man-α-(1→3)-D-Glc-β-(1→4)-D-Glc-α-1-diphospho-*ditrans*,*octacis*-undecaprenol
Other name(s): GumI
Systematic name: GDP-mannose:GlcA-β-(1→2)-D-Man-α-(1→3)-D-Glc-β-(1→4)-D-Glc-α-1-diphospho-*ditrans*,*octacis*-undecaprenol 4-β-mannosyltransferase
Comments: The enzyme is involved in the biosynthesis of the exopolysaccharide xanthan.
References: [1609, 1430, 1684]

[EC 2.4.1.251 created 2011]

EC 2.4.1.252

Accepted name: GDP-mannose:cellobiosyl-diphosphopolyprenol α-mannosyltransferase
Reaction: GDP-mannose + D-Glc-β-(1→4)-Glc-α-1-diphospho-*ditrans*,*octacis*-undecaprenol = GDP + D-Man-α-(1→3)-D-Glc-β-(1→4)-D-Glc-α-1-diphospho-*ditrans*,*octacis*-undecaprenol
Other name(s): GumH; AceA; α1,3-mannosyltransferase AceA
Systematic name: GDP-mannose:D-Glc-β-(1→4)-Glc-α-1-diphospho-*ditrans*,*octacis*-undecaprenol 3-α-mannosyltransferase
Comments: In the bacterium *Gluconacetobacter xylinus* (previously known as *Acetobacter xylinum*) the enzyme is involved in the biosynthesis of the exopolysaccharide acetan [1036]. In *Xanthomonas campestris* the enzyme is involved in the biosynthesis of the exopolysaccharide xanthan [1609].
References: [1036, 1, 2677, 1926, 1609]

[EC 2.4.1.252 created 2011]

EC 2.4.1.253

Accepted name: baicalein 7-*O*-glucuronosyltransferase
Reaction: UDP-D-glucuronate + baicalein = UDP + baicalin
Other name(s): UBGAT
Systematic name: UDP-D-glucuronate:5,6,7-trihydroxyflavone 7-*O*-glucuronosyltransferase
Comments: The enzyme is specific for UDP-D-glucuronate as a sugar donor and flavones with substitution *ortho*-to the 7-OH group such as baicalein (6-OH), scutellarein (6-OH) and wogonin (8-OMe).
References: [2389]

[EC 2.4.1.253 created 2011]

EC 2.4.1.254

Accepted name: cyanidin-3-*O*-glucoside $2''$-*O*-glucuronosyltransferase
Reaction: UDP-α-D-glucuronate + cyanidin 3-*O*-β-D-glucoside = UDP + cyanidin 3-*O*-(2-*O*-β-D-glucuronosyl)-β-D-glucoside
Other name(s): BpUGT94B1; UDP-glucuronic acid:anthocyanin glucuronosyltransferase; UDP-glucuronic acid:anthocyanidin 3-glucoside $2'$-*O*-β-glucuronosyltransferase; BpUGAT; UDP-D-glucuronate:cyanidin-3-*O*-β-glucoside 2-*O*-β-glucuronosyltransferase
Systematic name: UDP-α-D-glucuronate:cyanidin-3-*O*-β-D-glucoside 2-*O*-β-D-glucuronosyltransferase
Comments: The enzyme is highly specific for cyanidin 3-*O*-glucosides and UDP-α-D-glucuronate. Involved in the production of glucuronosylated anthocyanins that are the origin of the red coloration of flowers of *Bellis perennis* [3047].
References: [3047, 2580]

[EC 2.4.1.254 created 2011]

EC 2.4.1.255

Accepted name: protein *O*-GlcNAc transferase
Reaction: (1) UDP-*N*-acetyl-α-D-glucosamine + [protein]-L-serine = UDP + [protein]-3-*O*-(*N*-acetyl-β-D-glucosaminyl)-L-serine
(2) UDP-*N*-acetyl-α-D-glucosamine + [protein]-L-threonine = UDP + [protein]-3-*O*-(*N*-acetyl-β-D-glucosaminyl)-L-threonine
Other name(s): O-GlcNAc transferase; OGTase; O-linked *N*-acetylglucosaminyltransferase; uridine diphospho-*N*-acetylglucosamine:polypeptide β-*N*-acetylglucosaminyltransferase; protein O-linked β-*N*-acetylglucosamine transferase
Systematic name: UDP-*N*-α-acetyl-D-glucosamine:[protein]-3-*O*-*N*-acetyl-β-D-glucosaminyl transferase
Comments: Within higher eukaryotes post-translational modification of protein serines/threonines with *N*-acetylglucosamine (*O*-GlcNAc) is dynamic, inducible and abundant, regulating many cellular processes by interfering with protein phosphorylation. EC 2.4.1.255 (protein *O*-GlcNAc transferase) transfers GlcNAc onto substrate proteins and EC 3.2.1.169 (protein *O*-GlcNAcase) cleaves GlcNAc from the modified proteins.
References: [180, 573, 2815, 1201, 2060, 1880]

[EC 2.4.1.255 created 2011]

EC 2.4.1.256

Accepted name: dolichyl-*P*-Glc:Glc$_2$Man$_9$GlcNAc$_2$-*PP*-dolichol α-1,2-glucosyltransferase
Reaction: dolichyl β-D-glucosyl phosphate + D-Glc-α-(1→3)-D-Glc-α-(1→3)-D-Man-α-(1→2)-D-Man-α-(1→2)-D-Man-α-(1→3)-[D-Man-α-(1→2)-D-Man-α-(1→3)-[D-Man-α-(1→2)-D-Man-α-(1→6)]-D-Man-α-(1→6)]-D-Man-β-(1→4)-D-GlcNAc-β-(1→4)-D-GlcNAc-diphosphodolichol = D-Glc-α-(1→2)-D-Glc-α-(1→3)-D-Glc-α-(1→3)-D-Man-α-(1→2)-D-Man-α-(1→2)-D-Man-α-(1→3)-[D-Man-α-(1→2)-D-Man-α-(1→3)-[D-Man-α-(1→2)-D-Man-α-(1→6)]-D-Man-α-(1→6)]-D-Man-β-(1→4)-D-GlcNAc-β-(1→4)-D-GlcNAc-diphosphodolichol + dolichyl phosphate
Other name(s): ALG10; Dol-*P*-Glc:Glc$_2$Man$_9$GlcNAc$_2$-*PP*-Dol α-1,2-glucosyltransferase

Systematic name: dolichyl β-D-glucosyl phosphate:D-Glc-α-(1→3)-D-Glc-α-(1→3)-D-Man-α-(1→2)-D-Man-α-(1→2)-D-Man-α-(1→3)-[D-Man-α-(1→2)-D-Man-α-(1→3)-[D-Man-α-(1→2)-D-Man-α-(1→6)]-D-Man-α-(1→6)]-D-Man-β-(1→4)-D-GlcNAc-β-(1→4)-D-GlcNAc-diphosphodolichol 2-α-D-glucosyltransferase

Comments: This eukaryotic enzyme performs the final step in the synthesis of the lipid-linked oligosaccharide, attaching D-glucose in an α-1,2-linkage to the outermost D-glucose in the long branch. The lipid-linked oligosaccharide is involved in N-linked protein glycosylation of selected asparagine residues of nascent polypeptide chains in eukaryotic cells.

References: [423]

[EC 2.4.1.256 created 2011, modified 2012]

EC 2.4.1.257

Accepted name: GDP-Man:Man$_2$GlcNAc$_2$-*PP*-dolichol α-1,6-mannosyltransferase

Reaction: GDP-α-D-mannose + α-D-Man-(1→3)-β-D-Man-(1→4)-β-D-GlcNAc-(1→4)-α-D-GlcNAc-diphosphodolichol = GDP + α-D-Man-(1→3)-[α-D-Man-(1→6)]-β-D-Man-(1→4)-β-D-GlcNAc-(1→4)-α-D-GlcNAc-diphosphodolichol

Other name(s): GDP-Man:Man$_2$GlcNAc$_2$-*PP*-Dol α-1,6-mannosyltransferase; Alg2 mannosyltransferase (ambiguous); ALG2 (gene name, ambiguous); GDP-Man:Man$_1$GlcNAc$_2$-*PP*-dolichol mannosyltransferase (ambiguous); GDP-D-mannose:D-Man-α-(1→3)-D-Man-β-(1→4)-D-GlcNAc-β-(1→4)-D-GlcNAc-diphosphodolichol α-6-mannosyltransferase

Systematic name: GDP-α-D-mannose:α-D-Man-(1→3)-β-D-Man-(1→4)-β-D-GlcNAc-(1→4)-α-D-GlcNAc-diphosphodolichol 6-α-D-mannosyltransferase (configuration-retaining)

Comments: The biosynthesis of asparagine-linked glycoproteins utilizes a dolichyl diphosphate-linked glycosyl donor, which is assembled by the series of membrane-bound glycosyltransferases that comprise the dolichol pathway. Alg2 mannosyltransferase from *Saccharomyces cerevisiae* carries out an α1,3-mannosylation (*cf.* EC 2.4.1.132) of β-D-Man-(1→4)-β-D-GlcNAc-(1→4)-α-D-GlcNAc-diphosphodolichol, followed by an α1,6-mannosylation, to form the first branched pentasaccharide intermediate of the dolichol pathway [1577, 2573].

References: [1577, 2573]

[EC 2.4.1.257 created 2011, modified 2012]

EC 2.4.1.258

Accepted name: dolichyl-*P*-Man:Man$_5$GlcNAc$_2$-*PP*-dolichol α-1,3-mannosyltransferase

Reaction: dolichyl β-D-mannosyl phosphate + α-D-Man-(1→2)-α-D-Man-(1→2)-α-D-Man-(1→3)-[α-D-Man-(1→6)]-β-D-Man-(1→4)-β-D-GlcNAc-(1→4)-α-D-GlcNAc-diphosphodolichol = α-D-Man-(1→2)-α-D-Man-(1→2)-α-D-Man-(1→3)-[α-D-Man-(1→3)-α-D-Man-(1→6)]-β-D-Man-(1→4)-β-D-GlcNAc-(1→4)-α-D-GlcNAc-diphosphodolichol + dolichyl phosphate

Other name(s): Man$_5$GlcNAc$_2$-*PP*-Dol mannosyltransferase; ALG3; dolichyl-*P*-Man:Man(5)GlcNAc(2)-*PP*-dolichyl mannosyltransferase; Not56-like protein; Alg3 α-1,3-mannosyl transferase; Dol-*P*-Man:Man$_5$GlcNAc$_2$-*PP*-Dol α-1,3-mannosyltransferase; dolichyl β-D-mannosyl phosphate:D-Man-α-(1→2)-D-Man-α-(1→2)-D-Man-α-(1→3)-[D-Man-α-(1→6)]-D-Man-β-(1→4)-D-GlcNAc-β-(1→4)-D-GlcNAc-diphosphodolichol α-1,3-mannosyltransferase

Systematic name: dolichyl β-D-mannosyl phosphate:α-D-Man-(1→2)-α-D-Man-(1→2)-α-D-Man-(1→3)-[α-D-Man-(1→6)]-β-D-Man-(1→4)-β-D-GlcNAc-(1→4)-α-D-GlcNAc-diphosphodolichol 3-α-D-mannosyltransferase (configuration-inverting)

Comments: The formation of *N*-glycosidic linkages of glycoproteins involves the ordered assembly of the common Glc$_3$Man$_9$GlcNAc$_2$ core-oligosaccharide on the lipid carrier dolichyl diphosphate. Early mannosylation steps occur on the cytoplasmic side of the endoplasmic reticulum with GDP-Man as donor, the final reactions from Man$_5$GlcNAc$_2$-*PP*-dolichol to Man$_9$Glc-NAc$_2$-*PP*-dolichol on the lumenal side use dolichyl β-D-mannosyl phosphate. The first step of this assembly pathway on the luminal side of the endoplasmic reticulum is catalysed by ALG3.

References: [3155, 568]

[EC 2.4.1.258 created 1976 as EC 2.4.1.130, part transferred 2011 to EC 2.4.1.258, modified 2012]

EC 2.4.1.259

Accepted name: dolichyl-*P*-Man:Man$_6$GlcNAc$_2$-*PP*-dolichol α-1,2-mannosyltransferase

Reaction: dolichyl β-D-mannosyl phosphate + α-D-Man-(1→2)-α-D-Man-(1→2)-α-D-Man-(1→3)-[α-D-Man-(1→3)-α-D-Man-(1→6)]-β-D-Man-(1→4)-β-D-GlcNAc-(1→4)-α-D-GlcNAc-diphosphodolichol = α-D-Man-(1→2)-α-D-Man-(1→2)-α-D-Man-(1→3)-[α-D-Man-(1→2)-α-D-Man-(1→3)-α-D-Man-(1→6)]-β-D-Man-(1→4)-β-D-GlcNAc-(1→4)-α-D-GlcNAc-diphosphodolichol + dolichyl phosphate

Other name(s): ALG9; ALG9 α1,2 mannosyltransferase; dolichylphosphomannose-dependent ALG9 mannosyltransferase; ALG9 mannosyltransferase; Dol-*P*-Man:Man$_6$GlcNAc$_2$-*PP*-Dol α-1,2-mannosyltransferase; dolichyl β-D-mannosyl phosphate:D-Man-α-(1→2)-D-Man-α-(1→2)-D-Man-α-(1→3)-[D-Man-α-(1→3)-D-Man-α-(1→6)]-D-Man-β-(1→4)-D-GlcNAc-β-(1→4)-D-GlcNAc-diphosphodolichol α-1,2-mannosyltransferase

Systematic name: dolichyl β-D-mannosyl phosphate:α-D-Man-(1→2)-α-D-Man-(1→2)-α-D-Man-(1→3)-[α-D-Man-(1→3)-α-D-Man-(1→6)]-β-D-Man-(1→4)-β-D-GlcNAc-(1→4)-α-D-GlcNAc-diphosphodolichol 2-α-D-mannosyltransferase (configuration-inverting)

Comments: The formation of *N*-glycosidic linkages of glycoproteins involves the ordered assembly of the common Glc$_3$Man$_9$GlcNAc$_2$ core-oligosaccharide on the lipid carrier dolichyl diphosphate. Early mannosylation steps occur on the cytoplasmic side of the endoplasmic reticulum with GDP-Man as donor, the final reactions from Man$_5$GlcNAc$_2$-*PP*-Dol to Man$_9$Glc-NAc$_2$-*PP*-Dol on the lumenal side use dolichyl β-D-mannosyl phosphate. ALG9 mannosyltransferase catalyses the addition of two different α-1,2-mannose residues - the addition of α-1,2-mannose to Man$_6$GlcNAc$_2$-*PP*-Dol (EC 2.4.1.259) and the addition of α-1,2-mannose to Man$_8$GlcNAc$_2$-*PP*-Dol (EC 2.4.1.261).

References: [3691, 568, 946]

[EC 2.4.1.259 created 1976 as EC 2.4.1.130, part transferred 2011 to EC 2.4.1.259, modified 2012]

EC 2.4.1.260

Accepted name: dolichyl-*P*-Man:Man$_7$GlcNAc$_2$-*PP*-dolichol α-1,6-mannosyltransferase

Reaction: dolichyl β-D-mannosyl phosphate + α-D-Man-(1→2)-α-D-Man-(1→2)-α-D-Man-(1→3)-[α-D-Man-(1→2)-α-D-Man-(1→3)-α-D-Man-(1→6)]-β-D-Man-β-(1→4)-β-D-GlcNAc-(1→4)-α-D-GlcNAc-diphosphodolichol = α-D-Man-α-(1→2)-α-D-Man-(1→2)-α-D-Man-(1→3)-[α-D-Man-(1→2)-α-D-Man-(1→3)-[α-D-Man-(1→6)]-α-D-Man-(1→6)]-β-D-Man-(1→4)-β-D-GlcNAc-(1→4)-α-D-GlcNAc-diphosphodolichol + dolichyl phosphate

Other name(s): ALG12; ALG12 mannosyltransferase; ALG12 α1,6mannosyltransferase; dolichyl-*P*-mannose:Man$_7$GlcNAc$_2$-*PP*-dolichyl mannosyltransferase; dolichyl-*P*-Man:Man$_7$GlcNAc$_2$-*PP*-dolichyl α6-mannosyltransferase; EBS4; Dol-*P*-Man:Man$_7$GlcNAc$_2$-*PP*-Dol α-1,6-mannosyltransferase; dolichyl β-D-mannosyl phosphate:D-Man-α-(1→2)-D-Man-α-(1→2)-D-Man-α-(1→3)-[D-Man-α-(1→2)-D-Man-α-(1→3)-D-Man-α-(1→6)]-D-Man-β-(1→4)-D-GlcNAc-β-(1→4)-D-GlcNAc-diphosphodolichol α-1,6-mannosyltransferase

Systematic name: dolichyl β-D-mannosyl phosphate:α-D-Man-(1→2)-α-D-Man-(1→2)-α-D-Man-(1→3)-[α-D-Man-(1→2)-α-D-Man-(1→3)-α-D-Man-(1→6)]-β-D-Man-β-(1→4)-β-D-GlcNAc-(1→4)-α-D-GlcNAc-diphosphodolichol 6-α-D-mannosyltransferase (configuration-inverting)

Comments: The formation of *N*-glycosidic linkages of glycoproteins involves the ordered assembly of the common Glc$_3$Man$_9$GlcNAc$_2$ core-oligosaccharide on the lipid carrier dolichyl diphosphate. Early mannosylation steps occur on the cytoplasmic side of the endoplasmic reticulum with GDP-Man as donor, the final reactions from Man$_5$GlcNAc$_2$-*PP*-Dol to Man$_9$Glc-NAc$_2$-*PP*-Dol on the lumenal side use dolichyl β-D-mannosyl phosphate.

References: [946, 1366, 569, 1155]

[EC 2.4.1.260 created 1976 as EC 2.4.1.130, part transferred 2011 to EC 2.4.1.160, modified 2012]

EC 2.4.1.261

Accepted name: dolichyl-*P*-Man:Man$_8$GlcNAc$_2$-*PP*-dolichol α-1,2-mannosyltransferase

Reaction: dolichyl β-D-mannosyl phosphate + α-D-Man-(1→2)-α-D-Man-(1→2)-α-D-Man-(1→3)-[α-D-Man-(1→2)-α-D-Man-(1→3)-[α-D-Man-(1→6)]-α-D-Man-(1→6)]-β-D-Man-(1→4)-β-D-GlcNAc-(1→4)-α-D-GlcNAc-diphosphodolichol = α-D-Man-(1→2)-α-D-Man-(1→2)-α-D-Man-(1→3)-[α-D-Man-(1→2)-α-D-Man-(1→3)-[α-D-Man-(1→2)-α-D-Man-(1→6)]-α-D-Man-(1→6)]-β-D-Man-(1→4)-β-D-GlcNAc-(1→4)-α-D-GlcNAc-diphosphodolichol + dolichyl phosphate

Other name(s): ALG9; ALG9 α1,2 mannosyltransferase; dolichylphosphomannose-dependent ALG9 mannosyltransferase; ALG9 mannosyltransferase; Dol-*P*-Man:Man$_8$GlcNAc$_2$-*PP*-Dol α-1,2-mannosyltransferase; dolichyl β-D-mannosyl phosphate:D-Man-α-(1→2)-D-Man-α-(1→2)-D-Man-α-(1→3)-[D-Man-α-(1→2)-D-Man-α-(1→3)-[D-Man-α-(1→6)]-D-Man-α-(1→6)]-D-Man-β-(1→4)-D-GlcNAc-β-(1→4)-D-GlcNAc-diphosphodolichol 2-α-D-mannosyltransferase

Systematic name: dolichyl β-D-mannosyl phosphate:α-D-Man-(1→2)-α-D-Man-(1→2)-α-D-Man-(1→3)-[α-D-Man-(1→2)-α-D-Man-(1→3)-[α-D-Man-(1→6)]-α-D-Man-(1→6)]-β-D-Man-(1→4)-β-D-GlcNAc-(1→4)-α-D-GlcNAc-diphosphodolichol 2-α-D-mannosyltransferase (configuration-inverting)

Comments: The formation of *N*-glycosidic linkages of glycoproteins involves the ordered assembly of the common Glc$_3$Man$_9$GlcNAc$_2$ core-oligosaccharide on the lipid carrier dolichyl diphosphate. Early mannosylation steps occur on the cytoplasmic side of the endoplasmic reticulum with GDP-Man as donor, the final reactions from Man$_5$GlcNAc$_2$-*PP*-Dol to Man$_9$Glc-NAc$_2$-*PP*-Dol on the lumenal side use dolichyl β-D-mannosyl phosphate. ALG9 mannosyltransferase catalyses the addition of two different α-1,2-mannose residues: the addition of α-1,2-mannose to Man$_6$GlcNAc$_2$-*PP*-Dol (EC 2.4.1.259) and the addition of α-1,2-mannose to Man$_8$GlcNAc$_2$-*PP*-Dol (EC 2.4.1.261).

References: [3691, 946]

[EC 2.4.1.261 created 1976 as EC 2.4.1.130, part transferred 2011 to EC 2.4.1.261, modified 2012]

EC 2.4.1.262

Accepted name: soyasapogenol glucuronosyltransferase

Reaction: UDP-α-D-glucuronate + soyasapogenol B = UDP + soyasapogenol B 3-*O*-β-D-glucuronide

Other name(s): UGASGT; UDP-D-glucuronate:soyasapogenol 3-*O*-D-glucuronosyltransferase

Systematic name: UDP-α-D-glucuronate:soyasapogenol 3-*O*-D-glucuronosyltransferase (configuration-inverting)

Comments: Requires a divalent ion, Mg^{2+} better than Mn^{2+}, better than Ca^{2+}. Also acts on soysapogenol A and E.

References: [1829]

[EC 2.4.1.262 created 2011]

EC 2.4.1.263

Accepted name: abscisate β-glucosyltransferase

Reaction: UDP-α-D-glucose + abscisate = UDP + β-D-glucopyranosyl abscisate

Other name(s): ABA-glucosyltransferase; ABA-GTase; AOG; UDP-D-glucose:abscisate β-D-glucosyltransferase

Systematic name: UDP-α-D-glucose:abscisate β-D-glucosyltransferase (configuration-inverting)

Comments: The enzyme acts better on (*S*)-2-*trans*-abscisate than the natural (*S*)-2-*cis* isomer, abscisate, or its enantiomer, the (*R*)-2-*cis* isomer.

References: [3931]

[EC 2.4.1.263 created 2011]

EC 2.4.1.264

Accepted name: D-Man-α-(1→3)-D-Glc-β-(1→4)-D-Glc-α-1-diphosphoundecaprenol 2-β-glucuronosyltransferase

Reaction: UDP-α-D-glucuronate + α-D-Man-(1→3)-β-D-Glc-(1→4)-α-D-Glc-1-diphospho-*ditrans*,*octacis*-undecaprenol = UDP + β-D-GlcA-(1→2)-α-D-Man-(1→3)-β-D-Glc-(1→4)-α-D-Glc-1-diphospho-*ditrans*,*octacis*-undecaprenol

Other name(s): GumK; UDP-glucuronate:D-Man-α-(1→3)-D-Glc-β-(1→4)-D-Glc-α-1-diphospho-*ditrans*,*octacis*-undecaprenol β-1,2-glucuronyltransferase; D-Man-α-(1→3)-D-Glc-β-(1→4)-D-Glc-α-1-diphosphoundecaprenol 2-β-glucuronyltransferase

Systematic name: UDP-α-D-glucuronate:α-D-Man-(1→3)-β-D-Glc-(1→4)-α-D-Glc-1-diphospho-*ditrans*,*octacis*-undecaprenol β-1,2-glucuronosyltransferase (configuration-inverting)

Comments: The enzyme is involved in the biosynthesis of the exopolysaccharides xanthan (in the bacterium *Xanthomonas campestris*) and acetan (in the bacterium *Gluconacetobacter xylinus*).

References: [1609, 1430, 1684, 205, 206, 3697, 204]

[EC 2.4.1.264 created 2011, modified 2016]

EC 2.4.1.265

Accepted name: dolichyl-*P*-Glc:Glc$_1$Man$_9$GlcNAc$_2$-*PP*-dolichol α-1,3-glucosyltransferase

Reaction: dolichyl β-D-glucosyl phosphate + α-D-Glc-(1→3)-α-D-Man-(1→2)-α-D-Man-(1→2)-α-D-Man-(1→3)-[α-D-Man-(1→2)-α-D-Man-(1→3)-[α-D-Man-(1→2)-α-D-Man-(1→6)]-α-D-Man-(1→6)]-β-D-Man-(1→4)-β-D-GlcNAc-(1→4)-α-D-GlcNAc-diphosphodolichol = α-D-Glc-(1→3)-α-D-Glc-(1→3)-α-D-Man-(1→2)-α-D-Man-(1→2)-α-D-Man-(1→3)-[α-D-Man-(1→2)-α-D-Man-(1→3)-[α-D-Man-(1→2)-α-D-Man-(1→6)]-α-D-Man-(1→6)]-β-D-Man-(1→4)-β-D-GlcNAc-(1→4)-α-D-GlcNAc-diphosphodolichol + dolichyl phosphate

Other name(s): ALG8; Dol-*P*-Glc:Glc$_1$Man$_9$GlcNAc$_2$-*PP*-Dol α-1,3-glucosyltransferase; dolichyl β-D-glucosyl phosphate:D-Glc-α-(1→3)-D-Man-α-(1→2)-D-Man-α-(1→2)-D-Man-α-(1→3)-[D-Man-α-(1→2)-D-Man-α-(1→3)-[D-Man-α-(1→2)-D-Man-α-(1→6)]-D-Man-α-(1→6)]-D-Man-β-(1→4)-D-GlcNAc-β-(1→4)-D-GlcNAc-diphosphodolichol α-1,3-glucosyltransferase

Systematic name: dolichyl β-D-glucosyl phosphate:α-D-Glc-(1→3)-α-D-Man-(1→2)-α-D-Man-(1→2)-α-D-Man-(1→3)-[α-D-Man-(1→2)-α-D-Man-(1→3)-[α-D-Man-(1→2)-α-D-Man-(1→6)]-α-D-Man-(1→6)]-β-D-Man-(1→4)-β-D-GlcNAc-(1→4)-α-D-GlcNAc-diphosphodolichol 3-α-D-glucosyltransferase (configuration-inverting)

Comments: The successive addition of three glucose residues by EC 2.4.1.267 (dolichyl-*P*-Glc:Man$_9$GlcNAc$_2$-*PP*-dolichol α-1,3-glucosyltransferase), EC 2.4.1.265 and EC 2.4.1.256 (dolichyl-*P*-Glc:Glc$_2$Man$_9$GlcNAc$_2$-*PP*-dolichol α-1,2-glucosyltransferase) represents the final stage of the lipid-linked oligosaccharide assembly.

References: [3316, 2971, 503]

[EC 2.4.1.265 created 2011, modified 2012]

EC 2.4.1.266

Accepted name: glucosyl-3-phosphoglycerate synthase

Reaction: NDP-glucose + 3-phospho-D-glycerate = NDP + 2-*O*-(α-D-glucopyranosyl)-3-phospho-D-glycerate

Other name(s): GpgS protein; GPG synthase; glucosylphosphoglycerate synthase

Systematic name: NDP-glucose:3-phospho-D-glycerate 2-α-D-glucosyltransferase

Comments: The enzyme is involved in biosynthesis of 2-*O*-(α-D-glucopyranosyl)-D-glycerate via the two-step pathway in which glucosyl-3-phosphoglycerate synthase catalyses the conversion of GDP-glucose and 3-phospho-D-glycerate into 2-*O*-(α-D-glucopyranosyl)-3-phospho-D-glycerate, which is then converted to 2-*O*-(α-D-glucopyranosyl)-D-glycerate by EC 3.1.3.85 glucosyl-3-phosphoglycerate phosphatase. The activity is dependent on divalent cations (Mn^{2+}, Co^{2+}, or Mg^{2+}). The enzyme from *Persephonella marina* shows moderate flexibility on the sugar donor concerning the nucleotide moiety (UDP-glucose, ADP-glucose, GDP-glucose) but is strictly specific for glucose. The enzyme is also strictly specific for 3-phospho-D-glycerate as acceptor [618]. The enzyme from *Methanococcoides burtonii* is strictly specific for GDP-glucose and 3-phospho-D-glycerate [619]. This enzyme catalyses the first glucosylation step in methylglucose lipopolysaccharide biosynthesis in mycobacteria [2664, 1038].

References: [618, 619, 835, 2664, 1038, 1611]

[EC 2.4.1.266 created 2011]

EC 2.4.1.267

Accepted name: dolichyl-*P*-Glc:Man$_9$GlcNAc$_2$-*PP*-dolichol α-1,3-glucosyltransferase

Reaction: dolichyl β-D-glucosyl phosphate + α-D-Man-(1→2)-α-D-Man-(1→2)-α-D-Man-(1→3)-[α-D-Man-(1→2)-α-D-Man-(1→3)-[α-D-Man-(1→2)-α-D-Man-(1→6)]-α-D-Man-(1→6)]-β-D-Man-(1→4)-β-D-GlcNAc-(1→4)-α-D-GlcNAc-diphosphodolichol = α-D-Glc-(1→3)-α-D-Man-(1→2)-α-D-Man-(1→2)-α-D-Man-(1→3)-[α-D-Man-(1→2)-α-D-Man-(1→3)-[α-D-Man-(1→2)-α-D-Man-(1→6)]-α-D-Man-(1→6)]-β-D-Man-(1→4)-β-D-GlcNAc-(1→4)-α-D-GlcNAc-diphosphodolichol + dolichyl phosphate

Other name(s): ALG6; Dol-*P*-Glc:Man$_9$GlcNAc$_2$-*PP*-Dol α-1,3-glucosyltransferase; dolichyl β-D-glucosyl phosphate:D-Man-α-(1→2)-D-Man-α-(1→2)-D-Man-α-(1→3)-[D-Man-α-(1→2)-D-Man-α-(1→3)-[D-Man-α-(1→2)-D-Man-α-(1→6)]-D-Man-α-(1→6)]-D-Man-β-(1→4)-D-GlcNAc-β-(1→4)-D-GlcNAc-diphosphodolichol α-1,3-glucosyltransferase

Systematic name: dolichyl β-D-glucosyl phosphate:α-D-Man-(1→2)-α-D-Man-(1→2)-α-D-Man-(1→3)-[α-D-Man-(1→2)-α-D-Man-(1→3)-[α-D-Man-(1→2)-α-D-Man-(1→6)]-α-D-Man-(1→6)]-β-D-Man-(1→4)-β-D-GlcNAc-(1→4)-α-D-GlcNAc-diphosphodolichol 3-α-D-glucosyltransferase (configuration-inverting)

Comments: The successive addition of three glucose residues by EC 2.4.1.267, EC 2.4.1.265 (Dol-*P*-Glc:Glc$_1$Man$_9$GlcNAc$_2$-*PP*-Dol α-1,3-glucosyltransferase) and EC 2.4.1.256 (Dol-*P*-Glc:Glc$_2$Man$_9$GlcNAc$_2$-*PP*-Dol α-1,2-glucosyltransferase) represents the final stage of the lipid-linked oligosaccharide assembly.

References: [2863, 2970, 3828]

[EC 2.4.1.267 created 2011, modified 2012]

EC 2.4.1.268

Accepted name: glucosylglycerate synthase

Reaction: ADP-glucose + D-glycerate = 2-*O*-(α-D-glucopyranosyl)-D-glycerate + ADP

Other name(s): Ggs (gene name)

Systematic name: ADP-glucose:D-glycerate 2-α-D-glucosyltransferase

Comments: *Persephonella marina* possesses two enzymic systems for the synthesis of glucosylglycerate. The first one is a single-step pathway in which glucosylglycerate synthase catalyses the synthesis of 2-*O*-(α-D-glucopyranosyl)-D-glycerate in one-step from ADP-glucose and D-glycerate. The second system is a two-step pathway in which EC 2.4.1.266 (glucosyl-3-phosphoglycerate synthase) catalyses the conversion of NDP-glucose and 3-phospho-D-glycerate into 2-*O*-(α-D-glucopyranosyl)-3-phospho-D-glycerate, which is then converted to 2-*O*-(α-D-glucopyranosyl)-D-glycerate by EC 3.1.3.85 (glucosyl-3-phosphoglycerate phosphatase).

References: [894, 895]

[EC 2.4.1.268 created 2011]

EC 2.4.1.269

Accepted name: mannosylglycerate synthase

Reaction: GDP-α-D-mannose + D-glycerate = GDP + 2-*O*-(α-D-mannopyranosyl)-D-glycerate

Systematic name: GDP-α-D-mannose:D-glycerate 2-α-D-mannosyltransferase

Comments: *Rhodothermus marinus* can also form mannosylglycerate via a two-step pathway catalysed by EC 2.4.1.217 (mannosyl-3-phosphoglycerate synthase) and EC 3.1.3.70 (mannosyl-3-phosphoglycerate phosphatase) [2146]. Depending on experimental conditions mannosylglycerate synthase is more or less specific for the GDP-mannose and D-glycerate [2146, 918].

References: [2146, 918]

[EC 2.4.1.269 created 2011]

EC 2.4.1.270

Accepted name: mannosylglucosyl-3-phosphoglycerate synthase

Reaction: GDP-mannose + 2-*O*-(α-D-glucopyranosyl)-3-phospho-D-glycerate = GDP + 2-*O*-[2-*O*-(α-D-mannopyranosyl)-α-D-glucopyranosyl]-3-phospho-D-glycerate

Other name(s): MggA
Systematic name: GDP-mannose:2-*O*-(α-D-glucosyl)-3-phospho-D-glycerate 2-*O*-α-D-mannosyltransferase
Comments: The enzyme is involved in synthesis of 2-[2-*O*-(α-D-mannopranosyl)-α-D-glucopyranosyl]-D-glycerate. *Petrotoga miotherma* and *Petrotoga mobilis* accumulate this compound in response to water stress imposed by salt.
References: [895]

[EC 2.4.1.270 created 2011]

EC 2.4.1.271

Accepted name: crocetin glucosyltransferase
Reaction: (1) UDP-α-D-glucose + crocetin = UDP + β-D-glucosyl crocetin
(2) UDP-α-D-glucose + β-D-glucosyl crocetin = UDP + bis(β-D-glucosyl) crocetin
(3) UDP-α-D-glucose + β-D-gentiobiosyl crocetin = UDP + β-D-gentiobiosyl β-D-glucosyl crocetin
Other name(s): crocetin GTase; UGTCs2; UGT75L6; UDP-glucose:crocetin glucosyltransferase; UDP-glucose:crocetin 8-*O*-D-glucosyltransferase
Systematic name: UDP-α-D-glucose:crocetin 8-*O*-D-glucosyltransferase
Comments: In the plants *Crocus sativus* and *Gardenia jasminoides* this enzyme esterifies a free carboxyl group of crocetin and some crocetin glycosyl esters. The enzyme from *Gardenia* can also form glucosyl esters with 4-coumarate, caffeate and ferulate [2393].
References: [620, 2304, 2393]

[EC 2.4.1.271 created 2011]

EC 2.4.1.272

Accepted name: soyasapogenol B glucuronide galactosyltransferase
Reaction: UDP-α-D-galactose + soyasapogenol B 3-*O*-β-D-glucuronide = UDP + soyasaponin III
Other name(s): UDP-galactose:SBMG-galactosyltransferase; UGT73P2; GmSGT2 (gene name); UDP-galactose:soyasapogenol B 3-*O*-glucuronide β-D-galactosyltransferase
Systematic name: UDP-α-D-galactose:soyasapogenol B 3-*O*-glucuronide β-D-galactosyltransferase
Comments: Part of the biosynthetic pathway for soyasaponins.
References: [3183]

[EC 2.4.1.272 created 2011]

EC 2.4.1.273

Accepted name: soyasaponin III rhamnosyltransferase
Reaction: UDP-β-L-rhamnose + soyasaponin III = UDP + soyasaponin I
Other name(s): UGT91H4; GmSGT3 (gene name); UDP-rhamnose:soyasaponin III rhamnosyltransferase
Systematic name: UDP-β-L-rhamnose:soyasaponin III rhamnosyltransferase
Comments: Part of the biosynthetic pathway for soyasaponins.
References: [3183]

[EC 2.4.1.273 created 2011]

EC 2.4.1.274

Accepted name: glucosylceramide β-1,4-galactosyltransferase
Reaction: UDP-α-D-galactose + β-D-glucosyl-(1↔1)-ceramide = UDP + β-D-galactosyl-(1→4)-β-D-glucosyl-(1↔1)-ceramide
Other name(s): lactosylceramide synthase; uridine diphosphate-galactose:glucosyl ceramide β 1-4 galactosyltransferase; UDP-Gal:glucosylceramide β1→4galactosyltransferase; GalT-2 (misleading); UDP-galactose:β-D-glucosyl-(1↔1)-ceramide β-1,4-galactosyltransferase
Systematic name: UDP-α-D-galactose:β-D-glucosyl-(1↔1)-ceramide 4-β-D-galactosyltransferase

Comments: Involved in the synthesis of several different major classes of glycosphingolipids.
References: [513, 3568, 514, 2491, 3456]

[EC 2.4.1.274 created 2011]

EC 2.4.1.275
Accepted name: neolactotriaosylceramide β-1,4-galactosyltransferase
Reaction: UDP-α-D-galactose + *N*-acetyl-β-D-glucosaminyl-(1→3)-β-D-galactosyl-(1→4)-β-D-glucosyl-(1↔1)-ceramide = UDP + β-D-galactosyl-(1→4)-*N*-acetyl-β-D-glucosaminyl-(1→3)-β-D-galactosyl-(1→4)-β-D-glucosyl-(1↔1)-ceramide
Other name(s): β4Gal-T4; UDP-galactose:*N*-acetyl-β-D-glucosaminyl-(1→3)-β-D-galactosyl-(1→4)-β-D-glucosyl-(1↔1)-ceramide β-1,4-galactosyltransferase; lactotriaosylceramide β-1,4-galactosyltransferase (incorrect)
Systematic name: UDP-α-D-galactose:*N*-acetyl-β-D-glucosaminyl-(1→3)-β-D-galactosyl-(1→4)-β-D-glucosyl-(1↔1)-ceramide 4-β-D-galactosyltransferase
References: [3121]

[EC 2.4.1.275 created 2011, modified 2013]

EC 2.4.1.276
Accepted name: zeaxanthin glucosyltransferase
Reaction: **2** UDP-glucose + zeaxanthin = **2** UDP + zeaxanthin bis(β-D-glucoside)
Other name(s): *crtX* (gene name)
Systematic name: UDP-glucose:zeaxanthin β-D-glucosyltransferase
Comments: The reaction proceeds in two steps with the monoglucoside as an intermediate.
References: [1409]

[EC 2.4.1.276 created 2011]

EC 2.4.1.277
Accepted name: 10-deoxymethynolide desosaminyltransferase
Reaction: dTDP-3-dimethylamino-3,4,6-trideoxy-α-D-glucopyranose + 10-deoxymethynolide = dTDP + 10-deoxymethymycin
Other name(s): glycosyltransferase DesVII; DesVII
Systematic name: dTDP-3-dimethylamino-3,4,6-trideoxy-α-D-glucopyranose:10-deoxymethynolide 3-dimethylamino-4,6-dideoxy-α-D-glucosyltransferase
Comments: DesVII is the glycosyltransferase responsible for the attachment of dTDP-D-desosamine to 10-deoxymethynolide or narbonolide during the biosynthesis of methymycin, neomethymycin, narbomycin, and pikromycin in the bacterium *Streptomyces venezuelae*. Activity requires an additional protein partner, DesVIII.
References: [358, 357, 1364]

[EC 2.4.1.277 created 2011, modified 2014]

EC 2.4.1.278
Accepted name: 3-α-mycarosylerythronolide B desosaminyl transferase
Reaction: dTDP-D-desosamine + 3-α-L-mycarosylerythronolide B = dTDP + erythromycin D
Other name(s): EryCIII; dTDP-3-dimethylamino-4,6-dideoxy-α-D-glucopyranose:3-α-mycarosylerythronolide B 3-dimethylamino-4,6-dideoxy-α-D-glucosyltransferase
Systematic name: dTDP-3-dimethylamino-3,4,6-trideoxy-α-D-glucopyranose:3-α-mycarosylerythronolide B 3-dimethylamino-3,4,6-trideoxy-β-D-glucosyltransferase
Comments: The enzyme is involved in erythromycin biosynthesis.
References: [4012, 1889, 2295]

[EC 2.4.1.278 created 2012, modified 2014]

EC 2.4.1.279

Accepted name: nigerose phosphorylase

Reaction: 3-*O*-α-D-glucopyranosyl-D-glucopyranose + phosphate = D-glucose + β-D-glucose 1-phosphate

Other name(s): cphy1874 (gene name)

Systematic name: 3-*O*-α-D-glucopyranosyl-D-glucopyranose:phosphate β-D-glucosyltransferase

Comments: The enzymes from *Clostridium phytofermentans* is specific for nigerose, and shows only 0.5% relative activity with kojibiose (*cf.* EC 2.4.1.230, kojibiose phosphorylase).

References: [2455]

[EC 2.4.1.279 created 2012]

EC 2.4.1.280

Accepted name: *N*,*N*′-diacetylchitobiose phosphorylase

Reaction: *N*,*N*′-diacetylchitobiose + phosphate = *N*-acetyl-D-glucosamine + *N*-acetyl-α-D-glucosamine 1-phosphate

Other name(s): *chbP* (gene name)

Systematic name: *N*,*N*′-diacetylchitobiose:phosphate *N*-acetyl-D-glucosaminyltransferase

Comments: The enzyme is specific for *N*,*N*′-diacetylchitobiose and does not phosphorylate other *N*-acetylchitooligosaccharides, cellobiose, trehalose, lactose, maltose or sucrose.

References: [2621, 1363, 1320]

[EC 2.4.1.280 created 2012]

EC 2.4.1.281

Accepted name: 4-*O*-β-D-mannosyl-D-glucose phosphorylase

Reaction: 4-*O*-β-D-mannopyranosyl-D-glucopyranose + phosphate = D-glucose + α-D-mannose 1-phosphate

Other name(s): mannosylglucose phosphorylase

Systematic name: 4-*O*-β-D-mannopyranosyl-D-glucopyranose:phosphate α-D-mannosyltransferase

Comments: This enzyme forms part of a mannan catabolic pathway in the anaerobic bacterium *Bacteroides fragilis* NCTC 9343.

References: [3141]

[EC 2.4.1.281 created 2012]

EC 2.4.1.282

Accepted name: 3-*O*-α-D-glucosyl-L-rhamnose phosphorylase

Reaction: 3-*O*-α-D-glucopyranosyl-L-rhamnopyranose + phosphate = L-rhamnopyranose + β-D-glucose 1-phosphate

Other name(s): cphy1019 (gene name)

Systematic name: 3-*O*-α-D-glucopyranosyl-L-rhamnopyranose:phosphate β-D-glucosyltransferase

Comments: The enzyme does not phosphorylate α,α-trehalose, kojibiose, nigerose, or maltose. In the reverse phosphorolysis reaction the enzyme is specific for L-rhamnose as acceptor and β-D-glucose 1-phosphate as donor.

References: [2456]

[EC 2.4.1.282 created 2012]

EC 2.4.1.283

Accepted name: 2-deoxystreptamine *N*-acetyl-D-glucosaminyltransferase

Reaction: UDP-*N*-acetyl-α-D-glucosamine + 2-deoxystreptamine = UDP + 2′-*N*-acetylparomamine

Other name(s): *btrM* (gene name); *neoD* (gene name); *kanF* (gene name)
Systematic name: UDP-*N*-acetyl-α-D-glucosamine:2-deoxystreptamine *N*-acetyl-D-glucosaminyltransferase
Comments: Involved in the biosynthetic pathways of several clinically important aminocyclitol antibiotics, including kanamycin, butirosin, neomycin and ribostamycin. Unlike the enzyme from the bacterium *Streptomyces kanamyceticus*, which can also accept UDP-D-glucose [2623] (*cf.* EC 2.4.1.284, 2-deoxystreptamine glucosyltransferase), the enzyme from *Bacillus circulans* can only accept UDP-*N*-acetyl-α-D-glucosamine [3990].
References: [3990, 2623]

[EC 2.4.1.283 created 2012]

EC 2.4.1.284

Accepted name: 2-deoxystreptamine glucosyltransferase
Reaction: UDP-α-D-glucose + 2-deoxystreptamine = UDP + 2′-deamino-2′-hydroxyparomamine
Other name(s): *kanF* (gene name)
Systematic name: UDP-α-D-glucose:2-deoxystreptamine 6-α-D-glucosyltransferase
Comments: Involved in the biosynthesis of kanamycin B and kanamycin C. Also catalyses EC 2.4.1.283, 2-deoxystreptamine *N*-acetyl-D-glucosaminyltransferase, but activity is only one fifth of that with UDP-α-D-glucose.
References: [2623]

[EC 2.4.1.284 created 2012]

EC 2.4.1.285

Accepted name: UDP-GlcNAc:ribostamycin *N*-acetylglucosaminyltransferase
Reaction: UDP-*N*-acetyl-α-D-glucosamine + ribostamycin = UDP + 2‴-acetyl-6‴-hydroxyneomycin C
Other name(s): *neoK* (gene name)
Systematic name: UDP-*N*-acetyl-α-D-glucosamine:ribostamycin *N*-acetylglucosaminyltransferase
Comments: Involved in biosynthesis of the aminoglycoside antibiotic neomycin. Requires a divalent metal ion, optimally Mg^{2+}, Mn^{2+} or Co^{2+}.
References: [3990]

[EC 2.4.1.285 created 2012]

EC 2.4.1.286

Accepted name: chalcone 4′-*O*-glucosyltransferase
Reaction: (1) UDP-α-D-glucose + naringenin chalcone = UDP + 2′,4,4′,6′-tetrahydroxychalcone 4′-*O*-β-D-glucoside
(2) UDP-α-D-glucose + 2′,3,4,4′,6′-pentahydroxychalcone = UDP + 2′,3,4,4′,6′-pentahydroxychalcone 4′-*O*-β-D-glucoside
Other name(s): 4′CGT
Systematic name: UDP-α-D-glucose:2′,4,4′,6′-tetrahydroxychalcone 4′-*O*-β-D-glucosyltransferase
Comments: Isolated from the plant *Antirrhinum majus* (snapdragon). Involved in the biosynthesis of aurones, plant flavonoids that provide yellow color to the flowers.
References: [2567]

[EC 2.4.1.286 created 2012]

EC 2.4.1.287

Accepted name: rhamnopyranosyl-*N*-acetylglucosaminyl-diphospho-decaprenol β-1,4/1,5-galactofuranosyltransferase
Reaction: **2** UDP-α-D-galactofuranose + α-L-rhamnopyranosyl-(1→3)-*N*-acetyl-α-D-glucosaminyl-diphospho-*trans*,*octacis*-decaprenol = **2** UDP + β-D-galactofuranosyl-(1→5)-β-D-galactofuranosyl-(1→4)-α-L-rhamnopyranosyl-(1→3)-*N*-acetyl-α-D-glucosaminyl-diphospho-*trans*,*octacis*-decaprenol (overall reaction)

(1a) UDP-α-D-galactofuranose + α-L-rhamnopyranosyl-(1→3)-*N*-acetyl-α-D-glucosaminyl-diphospho-*trans-octacis*-decaprenol = UDP + β-D-galactofuranosyl-(1→4)-α-L-rhamnopyranosyl-(1→3)-*N*-acetyl-α-D-glucosaminyl-diphospho-*trans-octacis*-decaprenol
(1b) UDP-α-D-galactofuranose + β-D-galactofuranosyl-(1→4)-α-L-rhamnopyranosyl-(1→3)-*N*-acetyl-α-D-glucosaminyl-diphospho-*trans-octacis*-decaprenol = UDP + β-D-galactofuranosyl-(1→5)-β-D-galactofuranosyl-(1→4)-α-L-rhamnopyranosyl-(1→3)-*N*-acetyl-α-D-glucosaminyl-diphospho-*trans-octacis*-decaprenol

Other name(s): arabinogalactan galactofuranosyl transferase 1; GlfT1

Systematic name: UDP-α-D-galactofuranose:α-L-rhamnopyranosyl-(1→3)-*N*-acetyl-α-D-glucosaminyl-diphospho-*trans*,*octacis*-decaprenol 4-β/4-β-galactofuranosyltransferase (configuration-inverting)

Comments: Isolated from the bacteria *Mycobacterium tuberculosis* and *M. smegmatis*, the enzyme has dual β-(1→4) and β-(1→5) transferase action. Involved in the formation of the cell wall in mycobacteria.

References: [2246, 257]

[EC 2.4.1.287 created 2012, modified 2017]

EC 2.4.1.288

Accepted name: galactofuranosylgalactofuranosylrhamnosyl-*N*-acetylglucosaminyl-diphospho-decaprenol β-1,5/1,6-galactofuranosyltransferase

Reaction: **28** UDP-α-D-galactofuranose + β-D-galactofuranosyl-(1→5)-β-D-galactofuranosyl-(1→4)-α-L-rhamnopyranosyl-(1→3)-*N*-acetyl-α-D-glucosaminyl-diphospho-*trans*,*octacis*-decaprenol = **28** UDP + [β-D-galactofuranosyl-(1→5)-β-D-galactofuranosyl-(1→6)]$_{14}$-β-D-galactofuranosyl-(1→5)-β-D-galactofuranosyl-(1→4)-α-L-rhamnopyranosyl-(1→3)-*N*-acetyl-α-D-glucosaminyl-diphospho-*trans*,*octacis*-decaprenol

Other name(s): GlfT2

Systematic name: UDP-α-D-galactofuranose:β-D-galactofuranosyl-(1→5)-β-D-galactofuranosyl-(1→4)-α-L-rhamnopyranosyl-(1→3)-*N*-acetyl-α-D-glucosaminyl-diphospho-*trans*,*octacis*-decaprenol 4-β/5-β-D-galactofuranosyltransferase

Comments: Isolated from *Mycobacterium tuberculosis*. The enzyme adds approximately twenty-eight galactofuranosyl residues with alternating 1→5 and 1→6 links forming a galactan domain with approximately thirty galactofuranosyl residues. Involved in the formation of the cell wall in mycobacteria.

References: [2934, 2180, 3829]

[EC 2.4.1.288 created 2012]

EC 2.4.1.289

Accepted name: *N*-acetylglucosaminyl-diphospho-decaprenol L-rhamnosyltransferase

Reaction: dTDP-6-deoxy-β-L-mannose + *N*-acetyl-α-D-glucosaminyl-diphospho-*trans*,*octacis*-decaprenol = dTDP + α-L-rhamnopyranosyl-(1→3)-*N*-acetyl-α-D-glucosaminyl-diphospho-*trans*,*octacis*-decaprenol

Other name(s): WbbL

Systematic name: dTDP-6-deoxy-β-L-mannose:*N*-acetyl-α-D-glucosaminyl-diphospho-*trans*,*octacis*-decaprenol 3-α-L-rhamnosyltransferase

Comments: Requires Mn^{2+} or Mg^{2+}. Isolated from *Mycobacterium smegmatis* [2258] and *Mycobacterium tuberculosis* [1162]. The enzyme catalyses the addition of a rhamnosyl unit to *N*-acetyl-α-D-glucosaminyl-diphospho-*trans*,*octacis*-decaprenol, completing the synthesis of the linkage unit that attaches the arabinogalactan moiety to the peptidoglycan moiety in Mycobacterial cell wall.

References: [2258, 1162]

[EC 2.4.1.289 created 2012]

EC 2.4.1.290

Accepted name: *N*,*N*′-diacetylbacillosaminyl-diphospho-undecaprenol α-1,3-*N*-acetylgalactosaminyltransferase

Reaction: UDP-*N*-acetyl-α-D-galactosamine + *N*,*N*′-diacetyl-α-D-bacillosaminyl-diphospho-*tritrans*,*heptacis*-undecaprenol = UDP + *N*-acetyl-D-galactosaminyl-α-(1→3)-*N*,*N*′-diacetyl-α-D-bacillosaminyl-diphospho-*tritrans*,*heptacis*-undecaprenol

Other name(s): PglA

Systematic name: UDP-*N*-acetyl-α-D-galactosamine:*N*,*N*′-diacetyl-α-D-bacillosaminyl-diphospho-*tritrans*,*heptacis*-undecaprenol 3-α-*N*-acetyl-D-galactosaminyltransferase

Comments: Isolated from *Campylobacter jejuni*. Part of a bacterial N-linked glycosylation pathway.

References: [1080]

[EC 2.4.1.290 created 2012]

EC 2.4.1.291

Accepted name: *N*-acetylgalactosamine-*N*,*N*′-diacetylbacillosaminyl-diphospho-undecaprenol 4-α-*N*-acetylgalactosaminyltransferase

Reaction: UDP-*N*-acetyl-α-D-galactosamine + *N*-acetyl-D-galactosaminyl-α-(1→3)-*N*,*N*′-diacetyl-α-D-bacillosaminyl-diphospho-*tritrans*,*heptacis*-undecaprenol = UDP + *N*-acetyl-D-galactosaminyl-α-(1→4)-*N*-acetyl-D-galactosaminyl-α-(1→3)-*N*,*N*′-diacetyl-α-D-bacillosaminyl-diphospho-*tritrans*,*heptacis*-undecaprenol

Other name(s): PglJ

Systematic name: UDP-*N*-acetyl-α-D-galactosamine:*N*-acetylgalactosaminyl-α-(1→3)-*N*,*N*′-diacetyl-α-D-bacillosaminyl-diphospho-*tritrans*,*heptacis*-undecaprenol 3-α-*N*-acetyl-D-galactosaminyltransferase

Comments: Isolated from *Campylobacter jejuni*. Part of a bacterial N-linked glycosylation pathway.

References: [1080, 533]

[EC 2.4.1.291 created 2012]

EC 2.4.1.292

Accepted name: GalNAc-α-(1→4)-GalNAc-α-(1→3)-diNAcBac-*PP*-undecaprenol α-1,4-*N*-acetyl-D-galactosaminyltransferase

Reaction: **3** UDP-*N*-acetyl-α-D-galactosamine + GalNAc-α-(1→4)-GalNAc-α-(1→3)-diNAcBac-*PP*-*tritrans*,*heptacis*-undecaprenol = **3** UDP + [GalNAc-α-(1→4)]$_4$-GalNAc-α-(1→3)-diNAcBac-*PP*-*tritrans*,*heptacis*-undecaprenol

Other name(s): PglH

Systematic name: UDP-*N*-acetyl-α-D-galactosamine:GalNAc-α-(1→4)-GalNAc-α-(1→3)-diNAcBac-*PP*-*tritrans*,*heptacis*-undecaprenol 4-α-*N*-acetyl-D-galactosaminyltransferase

Comments: Isolated from *Campylobacter jejuni*. Part of a bacterial N-linked glycosylation pathway.

References: [1080, 3570, 361]

[EC 2.4.1.292 created 2012]

EC 2.4.1.293

Accepted name: GalNAc$_5$-diNAcBac-*PP*-undecaprenol β-1,3-glucosyltransferase

Reaction: UDP-α-D-glucose + [GalNAc-α-(1→4)]$_4$-GalNAc-α-(1→3)-diNAcBac-diphospho-*tritrans*,*heptacis*-undecaprenol = UDP + [GalNAc-α-(1→4)]$_2$-[Glc-β-(1→3)]-[GalNAc-α-(1→4)]$_2$-GalNAc-α-(1→3)-diNAcBac-diphospho-*tritrans*,*heptacis*-undecaprenol

Other name(s): PglI

Systematic name: UDP-α-D-glucose:[GalNAc-α-(1→4)]4-GalNAc-α-(1→3)-diNAcBac-diphospho-*tritrans*,*heptacis*-undecaprenol 3-β-D-glucosyltransferase

Comments: Isolated from the bacterium *Campylobacter jejuni*. Part of a bacterial N-linked glycosylation pathway.

References: [1080, 1633]

[EC 2.4.1.293 created 2012]

EC 2.4.1.294

Accepted name: cyanidin 3-*O*-galactosyltransferase
Reaction: UDP-α-D-galactose + cyanidin = UDP + cyanidin 3-*O*-β-D-galactoside
Other name(s): UDP-galactose:cyanidin galactosyltransferase
Systematic name: UDP-α-D-galactose:cyanidin 3-*O*-galactosyltransferase
Comments: Isolated from the plant *Daucus carota* (Afghan cultivar carrot).
References: [2932]

[EC 2.4.1.294 created 2013]

EC 2.4.1.295

Accepted name: anthocyanin 3-*O*-sambubioside 5-*O*-glucosyltransferase
Reaction: UDP-α-D-glucose + an anthocyanidin 3-*O*-β-D-sambubioside = UDP + an anthocyanidin 5-*O*-β-D-glucoside 3-*O*-β-D-sambubioside
Systematic name: UDP-α-D-glucose:anthocyanidin-3-*O*-β-D-sambubioside 5-*O*-glucosyltransferase
Comments: Isolated from the plant *Matthiola incana* (stock). No activity with anthocyanidin 3-*O*-glucosides.
References: [3506]

[EC 2.4.1.295 created 2013]

EC 2.4.1.296

Accepted name: anthocyanidin 3-*O*-coumaroylrutinoside 5-*O*-glucosyltransferase
Reaction: UDP-α-D-glucose + an anthocyanidin 3-*O*-[2-*O*-(4-coumaroyl)-α-L-rhamnosyl-(1→6)-β-D-glucoside] = UDP + an anthocyanidin 3-*O*-[2-*O*-(4-coumaroyl)-α-L-rhamnosyl-(1→6)-β-D-glucoside] 5-*O*-β-D-glucoside
Systematic name: UDP-α-D-glucose:anthocyanidin-3-*O*-[3-*O*-(4-coumaroyl)-α-L-rhamnosyl-(1→6)-β-D-glucoside] 5-*O*-β-D-glucosyltransferase
Comments: Isolated from the plant *Petunia hybrida*. It does not act on an anthocyanidin 3-*O*-rutinoside
References: [1534]

[EC 2.4.1.296 created 2013]

EC 2.4.1.297

Accepted name: anthocyanidin 3-*O*-glucoside 2″-*O*-glucosyltransferase
Reaction: UDP-α-D-glucose + an anthocyanidin 3-*O*-β-D-glucoside = UDP + an anthocyanidin 3-*O*-sophoroside
Other name(s): 3GGT
Systematic name: UDP-α-D-glucose:anthocyanidin-3-*O*-glucoside 2″-*O*-glucosyltransferase
Comments: Isolated from *Ipomoea nil* (Japanese morning glory).
References: [2321]

[EC 2.4.1.297 created 2013]

EC 2.4.1.298

Accepted name: anthocyanidin 3-*O*-glucoside 5-*O*-glucosyltransferase
Reaction: UDP-α-D-glucose + an anthocyanidin 3-*O*-β-D-glucoside = UDP + an anthocyanidin 3,5-di-*O*-β-D-glucoside
Other name(s): UDP-glucose:anthocyanin 5-*O*-glucosyltransferase
Systematic name: UDP-α-D-glucose:anthocyanidin-3-*O*-β-D-glucoside 5-*O*-glucosyltransferase
Comments: Isolated from the plants *Perilla frutescens* var. crispa, *Verbena hybrida* [3955], *Dahlia variabilis* [2514] and *Gentiana triflora* (clustered gentian) [2415]. It will also act on anthocyanidin 3-*O*-(6-*O*-malonylglucoside) [2514] and is much less active with hydroxycinnamoylglucose derivatives [2415]. There is no activity in the absence of the 3-*O*-glucoside group.
References: [3955, 2514, 2415]

[EC 2.4.1.298 created 2013]

EC 2.4.1.299

Accepted name: cyanidin 3-*O*-glucoside 5-*O*-glucosyltransferase (acyl-glucose)

Reaction: 1-*O*-sinapoyl-β-D-glucose + cyanidin 3-*O*-β-D-glucoside = sinapate + cyanidin 3,5-di-*O*-β-D-glucoside

Other name(s): AA5GT

Systematic name: 1-*O*-sinapoyl-β-D-glucose:cyanidin-3-*O*-β-D-glucoside 5-*O*-β-D-glucosyltransferase

Comments: Isolated from the plant *Dianthus caryophyllus* (carnation). Also acts on other anthocyanidins and with other acyl-glucose donors. *cf.* EC 2.4.1.298, anthocyanidin 3-*O*-glucoside 5-*O*-glucosyltransferase.

References: [2162, 2475]

[EC 2.4.1.299 created 2013]

EC 2.4.1.300

Accepted name: cyanidin 3-*O*-glucoside 7-*O*-glucosyltransferase (acyl-glucose)

Reaction: 1-*O*-vanilloyl-β-D-glucose + cyanidin 3-*O*-β-D-glucoside = vanillate + cyanidin 3,7-di-*O*-β-D-glucoside

Other name(s): AA7GT

Systematic name: 1-*O*-vanilloyl-β-D-glucose:cyanidin-3-*O*-β-D-glucoside 7-*O*-β-D-glucosyltransferase

Comments: Isolated from the plant *Delphinium grandiflorum* (delphinium). Also acts on other anthocyanidins and with other acyl-glucose derivatives.

References: [2162]

[EC 2.4.1.300 created 2013]

EC 2.4.1.301

Accepted name: 2′-deamino-2′-hydroxyneamine 1-α-D-kanosaminyltransferase

Reaction: (1) UDP-α-D-kanosamine + 2′-deamino-2′-hydroxyneamine = UDP + kanamycin A
(2) UDP-α-D-kanosamine + neamine = UDP + kanamycin B
(3) UDP-α-D-kanosamine + paromamine = UDP + kanamycin C
(4) UDP-α-D-kanosamine + 2′-deamino-2′-hydroxyparomamine = UDP + kanamycin X

Other name(s): *kanE* (gene name); *kanM*2 (gene name)

Systematic name: UDP-α-D-kanosamine:2′-deamino-2′-hydroxyneamine 1-α-D-kanosaminyltransferase

Comments: Involved in the biosynthetic pathway of kanamycins. The enzyme characterized from the bacterium *Streptomyces kanamyceticus* can also accept UDP-α-D-glucose with lower efficiency [2623].

References: [1805, 2623]

[EC 2.4.1.301 created 2013]

EC 2.4.1.302

Accepted name: L-demethylnoviosyl transferase

Reaction: dTDP-4-*O*-demethyl-β-L-noviose + novobiocic acid = dTDP + demethyldecarbamoyl novobiocin

Other name(s): *novM* (gene name); dTDP-β-L-noviose:novobiocic acid 7-*O*-noviosyltransferase; L-noviosyl transferase

Systematic name: dTDP-4-*O*-demethyl-β-L-noviose:novobiocic acid 7-*O*-[4-*O*-demethyl-L-noviosyl]transferase

Comments: The enzyme is involved in the biosynthesis of the aminocoumarin antibiotic, novobiocin.

References: [2233, 45]

[EC 2.4.1.302 created 2013, modified 2016]

EC 2.4.1.303

Accepted name: UDP-Gal:α-D-GlcNAc-diphosphoundecaprenol β-1,3-galactosyltransferase

Reaction: UDP-α-D-galactose + *N*-acetyl-α-D-glucosaminyl-diphospho-*ditrans*,*octacis*-undecaprenol = UDP + β-D-Gal-(1→3)-α-D-GlcNAc-diphospho-*ditrans*,*octacis*-undecaprenol

Other name(s): WbbD; WbbD β3Gal-transferase; UDP-Gal:GlcNAc-R β1,3-galactosyltransferase; UDP-Gal:GlcNAcα-pyrophosphate-R β1,3-galactosyltransferase; UDP-Gal:GlcNAc-R galactosyltransferase

Systematic name: UDP-α-D-galactose:*N*-acetyl-α-D-glucosaminyl-diphospho-*ditrans*,*octacis*-undecaprenol 3-β-galactosyltransferase (configuration-inverting)

Comments: The enzyme is involved in the the biosynthesis of the O-antigen repeating unit of *Escherichia coli* O7:K1 (VW187). Requires Mn^{2+}. *cf.* EC 2.4.1.343, UDP-Gal:α-D-GlcNAc-diphosphoundecaprenol α-1,3-galactosyltransferase.

References: [2887, 399]

[EC 2.4.1.303 created 2013, modified 2017]

EC 2.4.1.304

Accepted name: UDP-Gal:α-D-GlcNAc-diphosphoundecaprenol β-1,4-galactosyltransferase

Reaction: UDP-α-D-galactose + *N*-acetyl-α-D-glucosaminyl-diphospho-*ditrans*,*octacis*-undecaprenol = UDP + β-D-Gal-(1→4)-α-D-GlcNAc-diphospho-*ditrans*,*octacis*-undecaprenol

Other name(s): WfeD; UDP-Gal:GlcNAc-R 1,4-Gal-transferase; UDP-Gal:GlcNAc-pyrophosphate-lipid β-1,4-galactosyltransferase

Systematic name: UDP-α-D-galactose:*N*-acetyl-α-D-glucosaminyl-diphospho-*ditrans*,*octacis*-undecaprenol β-1,4-galactosyltransferase

Comments: The enzyme is involved in the the biosynthesis of the O-polysaccharide repeating unit of the bacterium *Shigella boydii* B14. The activity is stimulated by Mn^{2+} or to a lesser extent by Mg^{2+}, Ca^{2+}, Ni^{2+} or Pb^{2+}.

References: [3923]

[EC 2.4.1.304 created 2013]

EC 2.4.1.305

Accepted name: UDP-Glc:α-D-GlcNAc-glucosaminyl-diphosphoundecaprenol β-1,3-glucosyltransferase

Reaction: UDP-α-D-glucose + *N*-acetyl-α-D-glucosaminyl-diphospho-*ditrans*,*octacis*-undecaprenol = UDP + β-D-Glc-(1→3)-α-D-GlcNAc-diphospho-*ditrans*,*octacis*-undecaprenol

Other name(s): WfaP; WfgD; UDP-Glc:GlcNAc-pyrophosphate-lipid β-1,3-glucosyltransferase; UDP-Glc:GlcNAc-diphosphate-lipid β-1,3-glucosyltransferase

Systematic name: UDP-α-D-glucose:*N*-acetyl-α-D-glucosaminyl-diphospho-*ditrans*,*octacis*-undecaprenol β-1,3-glucosyltransferase

Comments: The enzyme is involved in the the biosynthesis of the O-polysaccharide repeating unit of the bacterium *Escherichia coli* serotype O56 and serotype O152.

References: [395]

[EC 2.4.1.305 created 2013]

EC 2.4.1.306

Accepted name: UDP-GalNAc:α-D-GalNAc-diphosphoundecaprenol α-1,3-*N*-acetylgalactosaminyltransferase

Reaction: UDP-*N*-acetyl-α-D-galactosamine + *N*-acetyl-α-D-galactosaminyl-diphospho-*ditrans*,*octacis*-undecaprenol = UDP + α-D-GalNAc-(1→3)-α-D-GalNAc-diphospho-*ditrans*,*octacis*-undecaprenol

Other name(s): WbnH

Systematic name: UDP-*N*-acetyl-α-D-galactosamine:*N*-acetyl-α-D-galactosaminyl-diphospho-*ditrans*,*octacis*-undecaprenol α-1,3-*N*-acetyl-D-galactosyltransferase

Comments: The enzyme is involved in the the biosynthesis of the O-polysaccharide repeating unit of *Escherichia coli* serotype O86.

References: [3979]

[EC 2.4.1.306 created 2013]

[2.4.1.307 Deleted entry. UDP-Gal:α-D-GalNAc-1,3-α-D-GalNAc-diphosphoundecaprenol β-1,3-galactosyltransferase. Now included in EC 2.4.1.122, glycoprotein-N-acetylgalactosamine β-1,3-galactosyltransferase]

[EC 2.4.1.307 created 2013, deleted 2016]

EC 2.4.1.308

Accepted name: GDP-Fuc:β-D-Gal-1,3-α-D-GalNAc-1,3-α-GalNAc-diphosphoundecaprenol α-1,2-fucosyltransferase

Reaction: GDP-β-L-fucose + β-D-Gal-(1→3)-α-D-GalNAc-(1→3)-α-D-GalNAc-diphospho-*ditrans*,*octacis*-undecaprenol = GDP + α-L-Fuc-(1→2)-β-D-Gal-(1→3)-α-D-GalNAc-(1→3)-α-D-GalNAc-diphospho-*ditrans*,*octacis*-undecaprenol

Other name(s): WbnK

Systematic name: GDP-β-L-fucose:β-D-Gal-(1→3)-α-D-GalNAc-(1→3)-α-D-GalNAc-diphospho-*ditrans*,*octacis*-undecaprenol α-1,2-fucosyltransferase

Comments: The enzyme is involved in the biosynthesis of the O-polysaccharide repeating unit of the bacterium *Escherichia coli* serotype O86.

References: [3978, 3893]

[EC 2.4.1.308 created 2013]

EC 2.4.1.309

Accepted name: UDP-Gal:α-L-Fuc-1,2-β-Gal-1,3-α-GalNAc-1,3-α-GalNAc-diphosphoundecaprenol α-1,3-galactosyltransferase

Reaction: UDP-α-D-galactose + α-L-Fuc-(1→2)-β-D-Gal-(1→3)-α-D-GalNAc-(1→3)-α-D-GalNAc-diphospho-*ditrans*,*octacis*-undecaprenol = UDP + α-D-Gal-(1→3)-(α-L-Fuc-(1→2))-β-D-Gal-(1→3)-α-D-GalNAc-(1→3)-α-D-GalNAc-diphospho-*ditrans*,*octacis*-undecaprenol

Other name(s): WbnI

Systematic name: UDP-α-D-galactose:α-L-Fuc-(1→2)-β-D-Gal-(1→3)-α-D-GalNAc-(1→3)-α-D-GalNAc-diphospho-*ditrans*,*octacis*-undecaprenol α-1,3-galactosyltransferase

Comments: The enzyme is involved in the the biosynthesis of the O-polysaccharide repeating unit of the bacterium *Escherichia coli* serotype O86.

References: [3978, 3980, 3893]

[EC 2.4.1.309 created 2013]

EC 2.4.1.310

Accepted name: vancomycin aglycone glucosyltransferase

Reaction: UDP-α-D-glucose + vancomycin aglycone = UDP + devancosaminyl-vancomycin

Other name(s): GtfB (ambiguous)

Systematic name: UDP-α-D-glucose:vancomycin aglycone 48-*O*-β-glucosyltransferase

Comments: The enzyme from the bacterium *Amycolatopsis orientalis* is involved in the biosynthesis of the glycopeptide antibiotic chloroeremomycin.

References: [2038, 2347]

[EC 2.4.1.310 created 2013]

EC 2.4.1.311

Accepted name: chloroorienticin B synthase

Reaction: dTDP-β-L-4-*epi*-vancosamine + desvancosaminyl-vancomycin = dTDP + chloroorienticin B

Other name(s): GtfA

Systematic name: dTDP-L-4-*epi*-vancosamine:desvancosaminyl-vancomycin vancosaminyltransferase

Comments: The enzyme from the bacterium *Amycolatopsis orientalis* is involved in the biosynthesis of the glycopeptide antibiotic chloroeremomycin.

References: [2346, 2056]

[EC 2.4.1.311 created 2013]

EC 2.4.1.312

Accepted name: protein *O*-mannose β-1,4-*N*-acetylglucosaminyltransferase

Reaction: UDP-*N*-acetyl-α-D-glucosamine + 3-*O*-(α-D-mannosyl)-L-threonyl-[protein] = UDP + 3-*O*-[*N*-acetyl-β-D-glucosaminyl-(1→4)-α-D-mannosyl]-L-threonyl-[protein]

Other name(s): GTDC2 (gene name); POMGNT2

Systematic name: UDP-*N*-acetyl-α-D-glucosamine:α-D-mannosyl-threonyl-[protein] 4-β-*N*-acetyl-D-glucosaminyltransferase

Comments: The human protein is involved in the formation of a phosphorylated trisaccharide on a threonine residue of α-dystroglycan, an extracellular peripheral glycoprotein that acts as a receptor for extracellular matrix proteins containing laminin-G domains.

References: [4001]

[EC 2.4.1.312 created 2013]

EC 2.4.1.313

Accepted name: protein *O*-mannose β-1,3-*N*-acetylgalactosaminyltransferase

Reaction: UDP-*N*-acetyl-α-D-galactosamine + 3-*O*-[*N*-acetyl-β-D-glucosaminyl-(1→4)-α-D-mannosyl]-L-threonyl-[protein] = UDP + 3-*O*-[*N*-acetyl-β-D-galactosaminyl-(1→3)-*N*-acetyl-β-D-glucosaminyl-(1→4)-α-D-mannosyl]-L-threonyl-[protein]

Other name(s): B3GALNT2

Systematic name: UDP-*N*-acetyl-α-D-galactosamine:*N*-acetyl-β-D-glucosaminyl-(1→4)-α-D-mannosyl-threonyl-[protein] 3-β-*N*-acetyl-D-galactosaminyltransferase

Comments: The human protein is specific for UDP-*N*-acetyl-α-D-galactosamine as donor [1343]. The enzyme is involved in the formation of a phosphorylated trisaccharide on a threonine residue of α-dystroglycan, an extracellular peripheral glycoprotein that acts as a receptor for extracellular matrix proteins containing laminin-G domains.

References: [1343, 4001]

[EC 2.4.1.313 created 2013]

EC 2.4.1.314

Accepted name: ginsenoside Rd glucosyltransferase

Reaction: UDP-α-D-glucose + ginsenoside Rd = UDP + ginsenoside Rb1

Other name(s): UDPG:ginsenoside Rd glucosyltransferase; UDP-glucose:ginsenoside Rd glucosyltransferase; UGRdGT

Systematic name: UDP-glucose:ginsenoside-Rd β-1,6-glucosyltransferase

Comments: The glucosyl group forms a 1→6 bond to the glucosyloxy moiety at C-20 of ginsenoside Rd. Isolated from sanchi ginseng (*Panax notoginseng*).

References: [446]

[EC 2.4.1.314 created 2013]

EC 2.4.1.315

Accepted name: diglucosyl diacylglycerol synthase (1,6-linking)

Reaction: (1) UDP-α-D-glucose + 1,2-diacyl-3-*O*-(β-D-glucopyranosyl)-*sn*-glycerol = 1,2-diacyl-3-*O*-[β-D-glucopyranosyl-(1→6)-*O*-β-D-glucopyranosyl]-*sn*-glycerol + UDP
(2) UDP-α-D-glucose + 1,2-diacyl-3-*O*-[β-D-glucopyranosyl-(1→6)-*O*-β-D-glucopyranosyl]-*sn*-glycerol = 1,2-diacyl-3-*O*-[β-D-glucopyranosyl-(1→6)-β-D-glucopyranosyl-(1→6)-*O*-β-D-glucopyranosyl]-*sn*-glycerol + UDP

Other name(s): monoglucosyl diacylglycerol (1→6) glucosyltransferase; MGlcDAG (1→6) glucosyltransferase; DGlcDAG synthase (ambiguous); UGT106B1; *ypfP* (gene name)
Systematic name: UDP-α-D-glucose:1,2-diacyl-3-*O*-(β-D-glucopyranosyl)-*sn*-glycerol 6-glucosyltransferase
Comments: The enzyme is found in several bacterial species. The enzyme from *Bacillus subtilis* is specific for glucose [1536]. The enzyme from *Mycoplasma genitalium* can incoporate galactose with similar efficiency, but forms mainly 1,2-diacyl-diglucopyranosyl-*sn*-glycerol *in vivo* [86]. The enzyme from *Staphylococcus aureus* can also form glucosyl-glycero-3-phospho-(1′-*sn*-glycerol) [1535].
References: [1536, 1535, 86]

[EC 2.4.1.315 created 2014]

EC 2.4.1.316
Accepted name: tylactone mycaminosyltransferase
Reaction: tylactone + dTDP-α-D-mycaminose = dTDP + 5-*O*-β-D-mycaminosyltylactone
Other name(s): *tylM*2 (gene name)
Systematic name: dTDP-α-D-mycaminose:tylactone 5-*O*-β-D-mycaminosyltransferase
Comments: The enzyme participates in the biosynthetic pathway of the macrolide antibiotic tylosin, which is produced by several species of *Streptomyces* bacteria. Activity is significantly enhanced by the presence of an accessory protein encoded by the *tylM*3 gene.
References: [1006, 2210]

[EC 2.4.1.316 created 2014]

EC 2.4.1.317
Accepted name: *O*-mycaminosyltylonolide 6-deoxyallosyltransferase
Reaction: 5-*O*-β-D-mycaminosyltylonolide + dTDP-6-deoxy-α-D-allose = dTDP + demethyllactenocin
Other name(s): *tylN* (gene name)
Systematic name: dTDP-6-deoxy-α-D-allose:5-*O*-β-D-mycaminosyltylonolide 23-*O*-6-deoxy-α-D-allosyltransferase
Comments: The enzyme participates in the biosynthetic pathway of the macrolide antibiotic tylosin, which is produced by several species of *Streptomyces* bacteria.
References: [3872]

[EC 2.4.1.317 created 2014]

EC 2.4.1.318
Accepted name: demethyllactenocin mycarosyltransferase
Reaction: dTDP-β-L-mycarose + demethyllactenocin = dTDP + demethylmacrocin
Other name(s): *tylCV* (gene name); *tylC*5 (gene name)
Systematic name: dTDP-β-L-mycarose:demethyllactenocin 4′-*O*-α-L-mycarosyltransferase
Comments: The enzyme participates in the biosynthetic pathway of the macrolide antibiotic tylosin, which is produced by several species of *Streptomyces* bacteria.
References: [229]

[EC 2.4.1.318 created 2014]

EC 2.4.1.319
Accepted name: β-1,4-mannooligosaccharide phosphorylase
Reaction: $[(1\to4)\text{-}\beta\text{-D-mannosyl}]_n$ + phosphate = $[(1\to4)\text{-}\beta\text{-D-mannosyl}]_{n-1}$ + α-D-mannose 1-phosphate
Other name(s): RaMP2
Systematic name: 1,4-β-D-mannooligosaccharide:phosphate α-D-mannosyltransferase
Comments: The enzyme, isolated from the ruminal bacterium *Ruminococcus albus*, catalyses the reversible phosphorolysis of β-1,4-mannooligosaccharide with a minimum size of three monomers.
References: [1614]

[EC 2.4.1.319 created 2014]

EC 2.4.1.320

Accepted name: 1,4-β-mannosyl-*N*-acetylglucosamine phosphorylase
Reaction: 4-*O*-β-D-mannopyranosyl-*N*-acetyl-D-glucosamine + phosphate = *N*-acetyl-D-glucosamine + α-D-mannose 1-phosphate
Other name(s): BT1033
Systematic name: 4-*O*-β-D-mannopyranosyl-*N*-acetyl-D-glucosamine:phosphate α-D-mannosyltransferase
Comments: The enzyme isolated from the anaerobic bacterium *Bacteroides thetaiotaomicron* is involved in the degradation of host-derived *N*-glycans.
References: [2460]

[EC 2.4.1.320 created 2014]

EC 2.4.1.321

Accepted name: cellobionic acid phosphorylase
Reaction: 4-*O*-β-D-glucopyranosyl-D-gluconate + phosphate = α-D-glucose 1-phosphate + D-gluconate
Systematic name: 4-*O*-β-D-glucopyranosyl-D-gluconate:phosphate α-D-glucosyltransferase
Comments: The enzyme occurs in cellulolytic bacteria and fungi. It catalyses the reversible phosphorolysis of cellobionic acid. In the synthetic direction it produces 4-*O*-β-D-glucopyranosyl-D-glucuronate from α-D-glucose 1-phosphate and D-glucuronate with low activity
References: [2458]

[EC 2.4.1.321 created 2014]

EC 2.4.1.322

Accepted name: devancosaminyl-vancomycin vancosaminetransferase
Reaction: dTDP-β-L-vancosamine + devancosaminyl-vancomycin = dTDP + vancomycin
Other name(s): devancosaminyl-vancomycin TDP-vancosaminyltransferase; GtfD; dTDP-β-L-vancomycin:desvancosaminyl-vancomycin β-L-vancosaminetransferase; desvancosaminyl-vancomycin vancosaminetransferase
Systematic name: dTDP-β-L-vancomycin:devancosaminyl-vancomycin β-L-vancosaminetransferase
Comments: The enzyme, isolated from the bacterium *Amycolatopsis orientalis*, catalyses the ultimate step in the biosynthesis of the antibiotic vancomycin.
References: [2038, 2348]

[EC 2.4.1.322 created 2014]

EC 2.4.1.323

Accepted name: 7-deoxyloganetic acid glucosyltransferase
Reaction: UDP-α-D-glucose + 7-deoxyloganetate = UDP + 7-deoxyloganate
Other name(s): UGT8
Systematic name: UDP-α-D-glucose:7-deoxyloganetate *O*-D-glucosyltransferase
Comments: Isolated from the plant *Catharanthus roseus* (Madagascar periwinkle). Involved in loganin and secologanin biosynthesis. Does not react with 7-deoxyloganetin. *cf.* EC 2.4.1.324 7-deoxyloganetin glucosyltransferase.
References: [115]

[EC 2.4.1.323 created 2014]

EC 2.4.1.324

Accepted name: 7-deoxyloganetin glucosyltransferase

Reaction: UDP-α-D-glucose + 7-deoxyloganetin = UDP + 7-deoxyloganin

Other name(s): UDPglucose:iridoid glucosyltransferase; UGT6; UGT85A24

Systematic name: UDP-α-D-glucose:7-deoxyloganetin *O*-D-glucosyltransferase

Comments: Isolated from the plants *Catharanthus roseus* (Madagascar periwinkle) and *Gardenia jasminoides* (cape jasmine). With *Gardenia* it also acts on genipin. Involved in loganin and secologanin biosynthesis. Does not react with 7-deoxyloganetate. *cf.* EC 2.4.1.323 7-deoxyloganetic acid glucosyltransferase.

References: [2392, 115]

[EC 2.4.1.324 created 2014]

EC 2.4.1.325

Accepted name: TDP-*N*-acetylfucosamine:lipid II *N*-acetylfucosaminyltransferase

Reaction: dTDP-4-acetamido-4,6-dideoxy-α-D-galactose + *N*-acetyl-β-D-mannosaminouronyl-(1→4)-*N*-acetyl-α-D-glucosaminyl-diphospho-*ditrans*,*octacis*-undecaprenol = dTDP + 4-acetamido-4,6-dideoxy-α-D-galactosyl-(1→4)-*N*-acetyl-β-D-mannosaminouronyl-(1→4)-*N*-acetyl-α-D-glucosaminyl-diphospho-*ditrans*,*octacis*-undecaprenol

Other name(s): TDP-Fuc4NAc:lipid II Fuc4NAc-transferase; TDP-Fuc4NAc:lipid II Fuc4NAc transferase; *wecF* (gene name)

Systematic name: dTDP-*N*-acetyl-α-D-fucose:*N*-acetyl-β-D-mannosaminouronyl-(1→4)-*N*-acetyl-α-D-glucosaminyl-diphospho-*ditrans*,*octacis*-undecaprenol *N*-acetylfucosaminyltransferase

Comments: Involved in the enterobacterial common antigen (ECA) biosynthesis in the bacterium *Escherichia coli*. The trisaccharide of the product (lipid III) is the repeat unit of ECA.

References: [2794]

[EC 2.4.1.325 created 2014]

EC 2.4.1.326

Accepted name: aklavinone 7-L-rhodosaminyltransferase

Reaction: dTDP-β-L-rhodosamine + aklavinone = dTDP + aclacinomycin T

Other name(s): AknS/AknT; aklavinone 7-β-L-rhodosaminyltransferase; dTDP-β-L-rhodosamine:aklavinone 7-α-L-rhodosaminyltransferase

Systematic name: dTDP-β-L-rhodosamine:aklavinone 7-α-L-rhodosaminyltransferase (configuration-inverting)

Comments: Isolated from the bacterium *Streptomyces galilaeus*. Forms a complex with its accessory protein AknT, and has very low activity in its absence. The enzyme can also use dTDP-2-deoxy-β-L-fucose. Involved in the biosynthesis of other aclacinomycins.

References: [2054, 1921]

[EC 2.4.1.326 created 2014, modified 2015]

EC 2.4.1.327

Accepted name: aclacinomycin-T 2-deoxy-L-fucose transferase

Reaction: dTDP-2-deoxy-β-L-fucose + aclacinomycin T = dTDP + aclacinomycin S

Other name(s): AknK

Systematic name: dTDP-2-deoxy-β-L-fucose:7-(α-L-rhodosaminyl)aklavinone 2-deoxy-α-L-fucosyltransferase

Comments: The enzyme, isolated from the bacterium *Streptomyces galilaeus*, is involved in the biosynthesis of other aclacinomycins. Also acts on idarubicin. It will slowly add a second 2-deoxy-L-fucose unit to aclacinomycin S *in vitro*.

References: [2055]

[EC 2.4.1.327 created 2014]

EC 2.4.1.328

Accepted name: erythronolide mycarosyltransferase
Reaction: dTDP-β-L-mycarose + erythronolide B = dTDP + 3-α-L-mycarosylerythronolide B
Other name(s): EryBV
Systematic name: dTDP-β-L-mycarose:erythronolide B L-mycarosyltransferase
Comments: Isolated from the bacterium *Saccharopolyspora erythraea*. The enzyme is involved in the biosynthesis of the antibiotic erythromycin.
References: [4036]

[EC 2.4.1.328 created 2014]

EC 2.4.1.329

Accepted name: sucrose 6^{F}-phosphate phosphorylase
Reaction: sucrose 6^{F}-phosphate + phosphate = α-D-glucopyranose 1-phosphate + β-D-fructofuranose 6-phosphate
Other name(s): sucrose 6′-phosphate phosphorylase
Systematic name: sucrose 6^{F}-phosphate:phosphate 1-α-D-glucosyltransferase
Comments: The enzyme, isolated from the thermophilic bacterium *Thermoanaerobacterium thermosaccharolyticum*, catalyses the reversible phosphorolysis of sucrose 6^{F}-phosphate. It also acts on sucrose with lower activity.
References: [3669]

[EC 2.4.1.329 created 2014]

EC 2.4.1.330

Accepted name: β-D-glucosyl crocetin β-1,6-glucosyltransferase
Reaction: (1) UDP-α-D-glucose + β-D-glucosyl crocetin = UDP + β-D-gentiobiosyl crocetin
(2) UDP-α-D-glucose + bis(β-D-glucosyl) crocetin = UDP + β-D-gentiobiosyl β-D-glucosyl crocetin
(3) UDP-α-D-glucose + β-D-gentiobiosyl β-D-glucosyl crocetin = UDP + crocin
Other name(s): UGT94E5; UDP-glucose:crocetin glucosyl ester glucosyltransferasee
Systematic name: UDP-α-D-glucose:β-D-glucosyl crocetin β-1,6-glucosyltransferase
Comments: The enzyme, characterized from the plant *Gardenia jasminoides*, adds a glucose to several crocetin glycosyl esters, but not to crocetin (*cf.* EC 2.4.1.271, crocetin glucosyltransferase).
References: [2393]

[EC 2.4.1.330 created 2014]

EC 2.4.1.331

Accepted name: 8-demethyltetracenomycin C L-rhamnosyltransferase
Reaction: dTDP-β-L-rhamnose + 8-demethyltetracenomycin C = dTDP + 8-demethyl-8-α-L-rhamnosyltetracenomycin C
Other name(s): *elmGT*
Systematic name: dTDP-β-L-rhamnose:8-demethyltetracenomycin C 3-α-L-rhamnosyltransferase
Comments: Isolated from *Streptomyces olivaceus* Tü2353. Involved in elloramycin biosynthesis. *In vitro* it can also utilize other 6-deoxy D- or L-hexoses.
References: [324]

[EC 2.4.1.331 created 2014]

EC 2.4.1.332

Accepted name: 1,2-α-glucosylglycerol phosphorylase
Reaction: 2-*O*-α-D-glucopyranosyl-glycerol + phosphate = β-D-glucose 1-phosphate + glycerol
Other name(s): 2-*O*-α-D-glucopyranosylglycerol phosphorylase
Systematic name: 2-*O*-α-D-glucopyranosyl-glycerol:phosphate β-D-glucosyltransferase

Comments: The enzyme has been isolated from the bacterium *Bacillus selenitireducens*. In the absence of glycerol the enzyme produces α-D-glucopyranose and phosphate from β-D-glucopyranose 1-phosphate. In this reaction the glucosyl residue is transferred to a water molecule with an inversion of the anomeric conformation.

References: [2459, 3554]

[EC 2.4.1.332 created 2014]

EC 2.4.1.333

Accepted name: 1,2-β-oligoglucan phosphorylase

Reaction: [(1→2)-β-D-glucosyl]$_n$ + phosphate = [(1→2)-β-D-glucosyl]$_{n-1}$ + α-D-glucose 1-phosphate

Systematic name: 1,2-β-D-glucan:phosphate α-D-glucosyltransferase

Comments: The enzyme has been isolated from the bacterium *Listeria innocua*. It catalyses the reversible phosphorolysis of β-(1→2)-D-glucans. The minimum length of the substrate for the phosphorolytic reaction is 3 D-glucose units. In the synthetic reaction starting from sophorose and α-D-glucose 1-phosphate the average polymerisation degree is 39.

References: [2403]

[EC 2.4.1.333 created 2014]

EC 2.4.1.334

Accepted name: 1,3-α-oligoglucan phosphorylase

Reaction: [(1→3)-α-D-glucosyl]$_n$ + phosphate = [(1→3)-α-D-glucosyl]$_{n-1}$ + β-D-glucose 1-phosphate

Systematic name: 1,3-α-D-glucan:phosphate β-D-glucosyltransferase

Comments: The enzyme, isolated from the bacterium *Clostridium phytofermentans*, catalyses a reversible reaction. Substrates for the phosphorolytic reaction are α-1,3-linked oligoglucans with a polymerisation degree of 3 or more. Nigerose (i.e. 3-*O*-α-D-glucopyranosyl-D-glucopyranose) is not phosphorylyzed but can serve as substrate in the reverse direction (*cf.* EC 2.4.1.279, nigerose phosphorylase).

References: [2457]

[EC 2.4.1.334 created 2014]

EC 2.4.1.335

Accepted name: dolichyl *N*-acetyl-α-D-glucosaminyl phosphate 3-β-D-2,3-diacetamido-2,3-dideoxy-β-D-glucuronosyltransferase

Reaction: UDP-2,3-diacetamido-2,3-dideoxy-α-D-glucuronate + an archaeal dolichyl *N*-acetyl-α-D-glucosaminyl phosphate = UDP + an archaeal dolichyl 3-*O*-(2,3-diacetamido-2,3-dideoxy-β-D-glucuronsyl)-*N*-acetyl-α-D-glucosaminyl phosphate

Other name(s): AglC; UDP-Glc-2,3-diNAcA glycosyltransferase

Systematic name: UDP-2,3-diacetamido-2,3-dideoxy-α-D-glucuronate:dolichyl *N*-acetyl-α-D-glucosaminyl-phosphate 3-β-D-2,3-diacetamido-2,3-dideoxy-β-D-glucuronosyltransferase

Comments: The enzyme, characterized from the methanogenic archaeon *Methanococcus voltae*, participates in the *N*-glycosylation of proteins. Dolichol used by archaea is different from that used by eukaryotes. It is much shorter (C_{55}-C_{60}), it is α,ω-saturated and it may have additional unsaturated positions in the chain.

References: [1863]

[EC 2.4.1.335 created 2015]

EC 2.4.1.336

Accepted name: monoglucosyldiacylglycerol synthase

Reaction: UDP-α-D-glucose + a 1,2-diacyl-*sn*-glycerol = UDP + a 1,2-diacyl-3-*O*-(β-D-glucopyranosyl)-*sn*-glycerol

Other name(s): *mgdA* (gene name)
Systematic name: UDP-α-D-glucose:1,2-diacyl-*sn*-glycerol 3-β-D-glucosyltransferase
Comments: The enzymes from cyanobacteria are involved in the biosynthesis of galactolipids found in their photosynthetic membranes. The enzyme belongs to the GT2 family of configuration-inverting glycosyltranferases [133]. *cf.* EC 2.4.1.337, 1,2-diacylglycerol 3-α-glucosyltransferase.
References: [3032, 133, 4015]

[EC 2.4.1.336 created 2015]

EC 2.4.1.337

Accepted name: 1,2-diacylglycerol 3-α-glucosyltransferase
Reaction: UDP-α-D-glucose + a 1,2-diacyl-*sn*-glycerol = UDP + a 1,2-diacyl-3-*O*-(α-D-glucopyranosyl)-*sn*-glycerol
Other name(s): *mgs* (gene name); UDP-glucose:diacylglycerol glucosyltransferase; UDP-glucose:1,2-diacylglycerol glucosyltransferase; uridine diphosphoglucose-diacylglycerol glucosyltransferase; UDP-glucose-diacylglycerol glucosyltransferase; UDP-glucose:1,2-diacylglycerol 3-D-glucosyltransferase; UDP-glucose:1,2-diacyl-*sn*-glycerol 3-D-glucosyltransferase; 1,2-diacylglycerol 3-glucosyltransferase (ambiguous)
Systematic name: UDP-α-D-glucose:1,2-diacyl-*sn*-glycerol 3-α-D-glucosyltransferase
Comments: The enzyme from the bacterium *Acholeplasma laidlawii*, which lacks a cell wall, produces the major non-bilayer lipid in the organism. The enzyme from the bacterium *Agrobacterium tumefaciens* acts under phosphate deprivation, generating glycolipids as surrogates for phospholipids. The enzyme belongs to the GT4 family of configuration-retaining glycosyltransferases. Many diacylglycerols with long-chain acyl groups can act as acceptors. *cf.* EC 2.4.1.336, monoglucosyldiacylglycerol synthase.
References: [1585, 1957, 279, 3138]

[EC 2.4.1.337 created 2015]

EC 2.4.1.338

Accepted name: validoxylamine A glucosyltransferase
Reaction: UDP-α-D-glucose + validoxylamine A = UDP + validamycin A
Other name(s): *vldK* (gene name); *valG* (gene name)
Systematic name: UDP-α-D-glucose:validoxylamine-A 4′-*O*-glucosyltransferase
Comments: The enzyme, characterized from the bacterium *Streptomyces hygroscopicus* subsp. *limoneus*, catalyses the ultimate step in the biosynthesis of the antifungal agent validamycin A.
References: [158, 3926]

[EC 2.4.1.338 created 2016]

EC 2.4.1.339

Accepted name: β-1,2-mannobiose phosphorylase
Reaction: β-D-mannopyranosyl-(1→2)-D-mannopyranose + phosphate = D-mannopyranose + α-D-mannose 1-phosphate
Systematic name: β-D-mannopyranosyl-(1→2)-D-mannopyranose:phosphate α-D-mannosyltransferase
Comments: The enzyme, originally characterized from the thermophilic anaerobic bacterium *Thermoanaerobacter* sp. X514, catalyses a reversible reaction. *cf.* EC 2.4.1.340, 1,2-β-oligomannan phosphorylase.
References: [544, 3584]

[EC 2.4.1.339 created 2016]

EC 2.4.1.340

Accepted name: 1,2-β-oligomannan phosphorylase
Reaction: [(1→2)-β-D-mannosyl]$_n$ + phosphate = [(1→2)-β-D-mannosyl]$_{n-1}$ + α-D-mannose 1-phosphate

Systematic name: (1→2)-β-D-mannan:phosphate β-D-mannosyl transferase (configuration-inverting)

Comments: The enzyme, originally characterized from the thermophilic anaerobic bacterium *Thermoanaerobacter* sp. X514, catalyses a reversible reaction. In the synthetic direction it produces oligosaccharides with a degree of polymerization (DP) of 3, 4 and 5. The phosphorolysis reaction proceeds to completion, although activity is highest when the substrate has at least three residues. *cf.* EC 2.4.1.339, β-1,2-mannobiose phosphorylase.

References: [544]

[EC 2.4.1.340 created 2016]

EC 2.4.1.341

Accepted name: α-1,2-colitosyltransferase

Reaction: GDP-β-L-colitose + β-D-galactopyranosyl-(1→3)-*N*-acetyl-D-glucosamine = GDP + α-L-colitosyl-(1→2)-β-D-galactosyl-(1→3)-*N*-acetyl-D-glucosamine

Other name(s): *wbgN* (gene name)

Systematic name: GDP-β-L-colitose:β-D-galactopyranosyl-(1→3)-*N*-acetyl-D-glucosamine L-colitosyltransferase (configuration-inverting)

Comments: The enzyme, characterized from the bacterium *Escherichia coli* O55:H7, participates in the biosynthesis of an O-antigen. The reaction involves anomeric inversion, and does not require any metal ions. The enzyme is highly specific towards the acceptor, exclusively recognizing lacto-*N*-biose, but can accept GDP-L-fucose as the donor with almost the same activity as with GDP-β-L-colitose.

References: [3907]

[EC 2.4.1.341 created 2016]

EC 2.4.1.342

Accepted name: α-maltose-1-phosphate synthase

Reaction: ADP-α-D-glucose + α-D-glucose-1-phosphate = ADP + α-maltose-1-phosphate

Other name(s): *glgM* (gene name)

Systematic name: ADP-α-D-glucose:α-D-glucose-1-phosphate 4-α-D-glucosyltransferase (configuration-retaining)

Comments: The enzyme, found in *Mycobacteria*, can also use UDP-α-D-glucose with much lower catalytic efficiency.

References: [1746]

[EC 2.4.1.342 created 2016]

EC 2.4.1.343

Accepted name: UDP-Gal:α-D-GlcNAc-diphosphoundecaprenol α-1,3-galactosyltransferase

Reaction: UDP-α-D-galactose + *N*-acetyl-α-D-glucosaminyl-diphospho-*ditrans*,*octacis*-undecaprenol = UDP + α-D-Gal-(1→3)-α-D-GlcNAc-diphospho-*ditrans*,*octacis*-undecaprenol

Other name(s): *wclR* (gene name)

Systematic name: UDP-α-D-galactose:*N*-acetyl-α-D-glucosaminyl-diphospho-*ditrans*,*octacis*-undecaprenol 3-α-galactosyltransferase (configuration-retaining)

Comments: The enzyme is involved in the the biosynthesis of the O-antigen repeating unit of *Escherichia coli* O3. Requires a divalent metal ion (Mn^{2+}, Mg^{2+} or Fe^{2+}). *cf.* EC 2.4.1.303, UDP-Gal:α-D-GlcNAc-diphosphoundecaprenol β-1,3-galactosyltransferase.

References: [519]

[EC 2.4.1.343 created 2017]

EC 2.4.1.344

Accepted name: type 2 galactoside α-(1,2)-fucosyltransferase

Reaction: GDP-β-L-fucose + β-D-galactosyl-(1→4)-*N*-acetyl-β-D-glucosaminyl-R = GDP + α-L-fucosyl-(1→2)-β-D-galactosyl-(1→4)-*N*-acetyl-β-D-glucosaminyl-R

Other name(s): blood group H α-2-fucosyltransferase (ambiguous); guanosine diphosphofucose-galactoside 2-L-fucosyltransferase (ambiguous); α-(1→2)-L-fucosyltransferase (ambiguous); α-2-fucosyltransferase (ambiguous); α-2-L-fucosyltransferase (ambiguous); blood-group substance H-dependent fucosyltransferase (ambiguous); guanosine diphosphofucose-glycoprotein 2-α-fucosyltransferase (ambiguous); guanosine diphosphofucose-lactose fucosyltransferase; GDP fucose-lactose fucosyltransferase; guanosine diphospho-L-fucose-lactose fucosyltransferase; guanosine diphosphofucose-β-D-galactosyl-α-2-L-fucosyltransferase (ambiguous); guanosine diphosphofucose-galactosylacetylglucosaminylgalactosylglucosylceramide α-L-fucosyltransferase (ambiguous); guanosine diphosphofucose-glycoprotein 2-α-L-fucosyltransferase (ambiguous); H-gene-encoded β-galactoside α(1→2)fucosyltransferase; β-galactoside α(1→2)fucosyltransferase (ambiguous); GDP-L-fucose:lactose fucosyltransferase; GDP-β-L-fucose:β-D-galactosyl-R 2-α-L-fucosyltransferase (ambiguous); FUT1 (gene name); FUT2 (gene name)

Systematic name: GDP-β-L-fucose:β-D-galactosyl-(1→4)-*N*-acetyl-β-D-glucosaminyl-R α-(1,2)-L-fucosyltransferase (configuration-inverting)

Comments: The enzyme acts on a glycoconjugates where R (see reaction) is a glycoprotein or glycosphingolipid. The recognized moiety of the substrate is known as a type 2 histo-blood group antigen precursor disaccharide, and the action of the enzyme produces an H type 2 antigen. Humans possess two enzymes able to catalyse this reaction, encoded by the FUT1 and FUT2 genes (also known as the H and Secretor genes, respectively), but only FUT1 is expressed in red blood cells. *cf.* EC 2.4.1.69, type 1 galactoside α-(1,2)-fucosyltransferase.

References: [224, 1145, 853, 1867]

[EC 2.4.1.344 created 2017]

EC 2.4.1.345

Accepted name: phosphatidyl-*myo*-inositol α-mannosyltransferase

Reaction: GDP-α-D-mannose + 1-phosphatidyl-1D-*myo*-inositol = GDP + 2-*O*-(α-D-mannosyl)-1-phosphatidyl-1D-*myo*-inositol

Other name(s): mannosyltransferase PimA; PimA; guanosine diphosphomannose-phosphatidyl-inositol α-mannosyltransferase (ambiguous)

Systematic name: GDP-α-D-mannose:1-phosphatidyl-1D-*myo*-inositol 2-α-D-mannosyltransferase (configuration-retaining)

Comments: Requires Mg^{2+}. The enzyme, found in Corynebacteriales, is involved in the biosynthesis of phosphatidyl-*myo*-inositol mannosides (PIMs).

References: [1753, 1165, 1058, 2908]

[EC 2.4.1.345 created 2017]

EC 2.4.1.346

Accepted name: phosphatidyl-*myo*-inositol dimannoside synthase

Reaction: (1) GDP-α-D-mannose + 2-*O*-α-D-mannosyl-1-phosphatidyl-1D-*myo*-inositol = GDP + 2,6-di-*O*-α-D-mannosyl-1-phosphatidyl-1D-*myo*-inositol
(2) GDP-α-D-mannose + 2-*O*-(6-*O*-acyl-α-D-mannosyl)-1-phosphatidyl-1D-*myo*-inositol = GDP + 2-*O*-(6-*O*-acyl-α-D-mannosyl)-6-*O*-α-D-mannosyl-1-phosphatidyl-1D-*myo*-inositol

Other name(s): mannosyltransferase PimB; PimB; guanosine diphosphomannose-phosphatidyl-inositol α-mannosyltransferase (ambiguous)

Systematic name: GDP-α-D-mannose:2-*O*-α-D-mannosyl-1-phosphatidyl-1D-*myo*-inositol 6-α-D-mannosyltransferase (configuration-retaining)

Comments: Requires Mg^{2+}. The enzyme, found in Corynebacteriales, is involved in the biosynthesis of phosphatidyl-*myo*-inositol mannosides (PIMs).

References: [1170, 2271, 231]

[EC 2.4.1.346 created 2017]

EC 2.4.1.347

Accepted name: α,α-trehalose-phosphate synthase (ADP-forming)

Reaction: ADP-α-D-glucose + D-glucose 6-phosphate = ADP + α,α-trehalose 6-phosphate

Other name(s): *otsA* (gene name); ADP-glucose—glucose-phosphate glucosyltransferase

Systematic name: ADP-α-D-glucose:D-glucose-6-phosphate 1-α-D-glucosyltransferase (configuration-retaining)

Comments: The enzyme has been reported from the yeast *Saccharomyces cerevisiae* and from mycobacteria. The enzyme from *Mycobacterium tuberculosis* can also use UDP-α-D-glucose, but the activity with ADP-α-D-glucose, which is considered the main substrate *in vivo*, is higher.

References: [897, 2609, 734]

[EC 2.4.1.347 created 2017]

EC 2.4.1.348

Accepted name: *N*-acetyl-α-D-glucosaminyl-diphospho-*ditrans*,*octacis*-undecaprenol 3-α-mannosyltransferase

Reaction: GDP-α-D-mannose + *N*-acetyl-α-D-glucosaminyl-diphospho-*ditrans*,*octacis*-undecaprenol = GDP + α-D-mannosyl-(1→3)-*N*-acetyl-α-D-glucosaminyl-diphospho-*ditrans*,*octacis*-undecaprenol

Other name(s): WbdC

Systematic name: GDP-α-D-mannose:*N*-acetyl-α-D-glucosaminyl-diphospho-*ditrans*,*octacis*-undecaprenol 3-α-mannosyltransferase (configuration-retaining)

Comments: The enzyme is involved in the biosynthesis of the linker region of the polymannose O-polysaccharide in the outer leaflet of the membrane of *Escherichia coli* serotypes O8, O9 and O9a.

References: [1135]

[EC 2.4.1.348 created 2017]

EC 2.4.1.349

Accepted name: mannosyl-*N*-acetyl-α-D-glucosaminyl-diphospho-*ditrans*,*octacis*-undecaprenol 3-α-mannosyltransferase

Reaction: **2** GDP-α-D-mannose + α-D-mannosyl-(1→3)-*N*-acetyl-α-D-glucosaminyl-diphospho-*ditrans*,*octacis*-undecaprenol = **2** GDP + α-D-mannosyl-(1→3)-α-D-mannosyl-(1→3)-α-D-mannosyl-(1→3)-*N*-acetyl-α-D-glucosaminyl-diphospho-*ditrans*,*octacis*-undecaprenol

Other name(s): WbdB

Systematic name: GDP-α-D-mannose:α-D-mannosyl-(1→3)-*N*-acetyl-α-D-glucosaminyl-diphospho-*ditrans*,*octacis*-undecaprenol 3-α-mannosyltransferase (configuration-retaining)

Comments: The enzyme is involved in the biosynthesis of the linker region of the polymannose O-polysaccharide in the outer leaflet of the membrane of *Escherichia coli* serotypes O8, O9 and O9a. It has no activity with *N*-acetyl-α-D-glucosaminyl-diphospho-*ditrans*,*octacis*-undecaprenol (*cf*. EC 2.4.1.348, *N*-acetyl-α-D-glucosaminyl-diphospho-*ditrans*,*octacis*-undecaprenol 3-α-mannosyltransferase).

References: [1135]

[EC 2.4.1.349 created 2017]

EC 2.4.1.350

Accepted name: mogroside IE synthase

Reaction: UDP-α-D-glucose + mogrol = mogroside IE + UDP

Other name(s): UGT74AC1; mogrol *C*-3 hydroxyl glycosyltransferase

Systematic name: UDP-α-D-glucose:mogrol 3-*O*-glucosyltransferase

Comments: Isolated from the plant *Siraitia grosvenorii* (monk fruit).

References: [659]

[EC 2.4.1.350 created 2017]

EC 2.4.1.351

Accepted name: rhamnogalacturonan I rhamnosyltransferase
Reaction: UDP-β-L-rhamnose + α-D-galacturonosyl-[(1→2)-α-L-rhamnosyl-(1→4)-α-D-galacturonosyl]$_n$ = UDP + [(1→2)-α-L-rhamnosyl-(1→4)-α-D-galacturonosyl]$_{n+1}$
Other name(s): RRT; RG I rhamnosyltransferase
Systematic name: UDP-β-L-rhamnose:rhamnogalacturonan I 4-rhamnosyltransferase (configuration-inverting)
Comments: The enzyme, characterized from *Vigna angularis* (azuki beans), participates in the biosynthesis of rhamnogalacturonan type I. It does not require any metal ions, and prefers substrates with a degree of polymerization larger than 7.
References: [3603]

[EC 2.4.1.351 created 2018]

EC 2.4.1.352

Accepted name: glucosylglycerate phosphorylase
Reaction: 2-*O*-(α-D-glucopyranosyl)-D-glycerate + phosphate = α-D-glucopyranose 1-phosphate + D-glycerate
Systematic name: 2-*O*-(α-D-glucopyranosyl)-D-glycerate:phosphate α-D-glucosyltransferase (configuration-retaining)
Comments: The enzyme has been characterized from the bacterium *Meiothermus silvanus*.
References: [944]

[EC 2.4.1.352 created 2018]

EC 2.4.1.353

Accepted name: sordaricin 6-deoxyaltrosyltransferase
Reaction: GDP-6-deoxy-α-D-altrose + sordaricin = $4'$-*O*-demethylsordarin + GDP
Other name(s): SdnJ
Systematic name: GDP-6-deoxy-α-D-altrose:sordaricin 6-deoxy-D-altrosyltransferase
Comments: The enzyme, isolated from the fungus *Sordaria araneosa*, is involved in the biosynthesis of the glycoside antibiotic sordarin.
References: [1804]

[EC 2.4.1.353 created 2018]

EC 2.4.1.354

Accepted name: (*R*)-mandelonitrile β-glucosyltransferase
Reaction: UDP-α-D-glucose + (*R*)-mandelonitrile = UDP + (*R*)-prunasin
Other name(s): UGT85A19 (gene name)
Systematic name: UDP-α-D-glucose:(*R*)-mandelonitrile β-D-glucosyltransferase (configuration-inverting)
Comments: The enzyme, characterized from *Prunus dulcis* (almond), is involved in the biosynthesis of the cyanogenic glycosides (*R*)-prunasin and (*R*)-amygdalin.
References: [948]

[EC 2.4.1.354 created 2018]

EC 2.4.1.355

Accepted name: poly(ribitol-phosphate) β-*N*-acetylglucosaminyltransferase
Reaction: ***n*** UDP-*N*-acetyl-α-D-glucosamine + 4-*O*-(D-ribitylphospho)$_n$-di[(2*R*)-1-glycerophospho]-*N*-acetyl-β-D-mannosaminyl-(1→4)-*N*-acetyl-α-D-glucosaminyl-diphospho-*ditrans*,*octacis*-undecaprenol = ***n*** UDP + 4-*O*-(2-*N*-acetyl-β-D-glucosaminyl-D-ribitylphospho)$_n$-di[(2*R*)-1-glycerophospho]-*N*-acetyl-β-D-mannosaminyl-(1→4)-*N*-acetyl-α-D-glucosaminyl-diphospho-*ditrans*,*octacis*-undecaprenol
Other name(s): TarS
Systematic name: UDP-*N*-acetyl-α-D-glucosamine:4-*O*-(D-ribitylphospho)$_n$-di[(2*R*)-1-glycerophospho]-*N*-acetyl-β-D-mannosaminyl-(1→4)-*N*-acetyl-α-D-glucosaminyl-diphospho-*ditrans*,*octacis*-undecaprenol β-*N*-acetyl-D-glucosaminyltransferase (configuration-inverting)

Comments: Involved in the biosynthesis of poly(ribitol-phosphate) teichoic acids in the cell wall of the bacterium *Staphylococcus aureus*. This enzyme adds an *N*-acetyl-β-D-glucosamine to the OH group at the 2 position of the ribitol phosphate units. *cf.* EC 2.4.1.70 [poly(ribitol-phosphate) α-*N*-acetylglucosaminyltransferase].
References: [2421, 407, 3267]

[EC 2.4.1.355 created 2018]

EC 2.4.1.356

Accepted name: glucosyl-dolichyl phosphate glucuronosyltransferase
Reaction: UDP-α-D-glucuronate + an archaeal dolichyl β-D-glucosyl phosphate = UDP + an archaeal dolichyl β-D-glucuronosyl-(1→3)-β-D-glucosyl phosphate
Other name(s): *aglG* (gene name)
Systematic name: UDP-α-D-glucuronate:dolichyl phosphate glucuronosyltransferase (configuration-inverting)
Comments: The enzyme, characterized from the halophilic archaeon *Haloferax volcanii*, participates in the protein *N*-glycosylation pathway. Dolichol used by archaea is different from that used by eukaryotes. It is much shorter (C_{55}-C_{60}) and is α,ω-saturated. However, *in vitro* the enzyme was also able to act on a substrate with an unsaturated end.
References: [4014, 828]

[EC 2.4.1.356 created 2018]

EC 2.4.1.357

Accepted name: phlorizin synthase
Reaction: UDP-α-D-glucose + phloretin = UDP + phlorizin
Other name(s): MdPGT$_1$: P2’GT
Systematic name: UDP-α-D-glucose:phloretin 2′-*O*-D-glucosyltransferase
Comments: Isolated from *Malus* X *domestica* (apple). Phlorizin inhibits sodium-linked glucose transporters. It gives the characteristic flavour of apples and cider.
References: [1545, 3937]

[EC 2.4.1.357 created 2018]

EC 2.4.1.358

Accepted name: acylphloroglucinol glucosyltransferase
Reaction: UDP-α-D-glucose + 2-acylphloroglucinol = UDP + 2-acylphloroglucinol 1-*O*-β-D-glucoside
Other name(s): UGT71K3
Systematic name: UDP-α-D-glucose:2-acylphloroglucinol 1-*O*-β-glucosyltransferase
Comments: Isolated from strawberries (*Fragaria* X *ananassa*). Acts best on phloroisovalerophenone and phlorobutyrophenone but will also glycosylate many other phenolic compounds. A minor product of the reaction is the 5-*O*-β-D-glucoside.
References: [3285]

[EC 2.4.1.358 created 2018]

EC 2.4.1.359

Accepted name: glucosylglycerol phosphorylase (configuration-retaining)
Reaction: 2-*O*-α-D-glucopyranosyl-glycerol + phosphate = α-D-glucose 1-phosphate + glycerol
Other name(s): 2-*O*-α-D-glucosylglycerol phosphorylase (retaining)
Systematic name: 2-*O*-α-D-glucopyranosyl-glycerol:phosphate α-D-glucosyltransferase (configuration-retaining)
Comments: The enzyme, characterized from the halotolerant bacterium *Marinobacter adhaerens*, is likely responsible for degradation of the compatible solute 2-*O*-α-D-glucopyranosyl-glycerol when the environmental salt concentration decreases. *cf.* EC 2.4.1.332, 1,2-α-glucosylglycerol phosphorylase.
References: [943]

[EC 2.4.1.359 created 2018]

EC 2.4.1.360

Accepted name: 2-hydroxyflavanone *C*-glucosyltransferase

Reaction: UDP-α-D-glucose + a 2′-hydroxy-β-oxodihydrochalcone = UDP + a 3′-(β-D-glucopyranosyl)-2′-hydroxy-β-oxodihydrochalcone

Other name(s): *OsCGT*

Systematic name: UDP-α-D-glucose:2′-hydroxy-β-oxodihydrochalcone *C*6/8-β-D-glucosyltransferase

Comments: The enzyme has been characterized in *Oryza sativa* (rice), various *Citrus* spp., *Glycine max* (soybean), and *Fagopyrum esculentum* (buckwheat). Flavanone substrates require a 2-hydroxy group. The *meta*-stable flavanone substrates such as 2-hydroxynaringenin exist in an equilibrium with open forms such as 1-(4-hydroxyphenyl)-3-(2,4,6-trihydroxyphenyl)propane-1,3-dione, which are the actual substrates for the glucosyl-transfer reaction (see EC 1.14.14.162, flavanone 2-hydroxylase). The enzyme can also act on dihydrochalcones. The enzymes from citrus plants can catalyse a second C-glycosylation reaction at position 5.

References: [380, 2390, 1337, 1465]

[EC 2.4.1.360 created 2018]

EC 2.4.2 Pentosyltransferases

EC 2.4.2.1

Accepted name: purine-nucleoside phosphorylase

Reaction: (1) purine ribonucleoside + phosphate = purine + α-D-ribose 1-phosphate
(2) purine 2′-deoxyribonucleoside + phosphate = purine + 2-deoxy-α-D-ribose 1-phosphate

Other name(s): inosine phosphorylase; PNPase; PUNPI; PUNPII; inosine-guanosine phosphorylase; nucleotide phosphatase; purine deoxynucleoside phosphorylase; purine deoxyribonucleoside phosphorylase; purine nucleoside phosphorylase; purine ribonucleoside phosphorylase

Systematic name: purine-nucleoside:phosphate ribosyltransferase

Comments: Specificity not completely determined. Can also catalyse ribosyltransferase reactions of the type catalysed by EC 2.4.2.5, nucleoside ribosyltransferase.

References: [21, 963, 1302, 1560, 3043, 3583]

[EC 2.4.2.1 created 1961]

EC 2.4.2.2

Accepted name: pyrimidine-nucleoside phosphorylase

Reaction: (1) uridine + phosphate = uracil + α-D-ribose 1-phosphate
(2) thymidine + phosphate = thymine + 2-deoxy-α-D-ribose 1-phosphate
(3) 2′-deoxyuridine + phosphate = uracil + 2-deoxy-α-D-ribose 1-phosphate

Other name(s): Py-NPase; *pdp* (gene name)

Systematic name: pyrimidine-nucleoside:phosphate (2′-deoxy)-α-D-ribosyltransferase

Comments: Unlike EC 2.4.2.3, uridine phosphorylase, and EC 2.4.2.4, thymidine phosphorylase, this enzyme can accept both the ribonucleoside uridine and the 2′-deoxyribonucleosides 2′-deoxyuridine and thymidine [1202]. The reaction is reversible, and the enzyme does not distinguish between α-D-ribose 1-phosphate and 2-deoxy-α-D-ribose 1-phosphate in the synthetic direction.

References: [963, 3043, 1202, 2556, 2768]

[EC 2.4.2.2 created 1961]

EC 2.4.2.3

Accepted name: uridine phosphorylase

Reaction: uridine + phosphate = uracil + α-D-ribose 1-phosphate
Other name(s): pyrimidine phosphorylase; UrdPase; UPH; UPase
Systematic name: uridine:phosphate α-D-ribosyltransferase
Comments: The enzyme participates the the pathways of pyrimidine ribonucleosides degradation and salvage. The mammalian enzyme also accepts 2′-deoxyuridine.
References: [466, 2594, 1910, 2739, 3785, 2005]

[EC 2.4.2.3 created 1961]

EC 2.4.2.4

Accepted name: thymidine phosphorylase
Reaction: thymidine + phosphate = thymine + 2-deoxy-α-D-ribose 1-phosphate
Other name(s): pyrimidine phosphorylase; thymidine-orthophosphate deoxyribosyltransferase; animal growth regulators, blood platelet-derived endothelial cell growth factors; blood platelet-derived endothelial cell growth factor; deoxythymidine phosphorylase; gliostatins; pyrimidine deoxynucleoside phosphorylase; thymidine:phosphate deoxy-D-ribosyltransferase
Systematic name: thymidine:phosphate deoxy-α-D-ribosyltransferase
Comments: The enzyme in some tissues also catalyses deoxyribosyltransferase reactions of the type catalysed by EC 2.4.2.6, nucleoside deoxyribosyltransferase.
References: [964, 4084, 4083]

[EC 2.4.2.4 created 1961]

EC 2.4.2.5

Accepted name: nucleoside ribosyltransferase
Reaction: D-ribosyl-base^1 + base^2 = D-ribosyl-base^2 + base^1
Other name(s): nucleoside *N*-ribosyltransferase
Systematic name: nucleoside:purine(pyrimidine) D-ribosyltransferase
Comments: Base^1 and base^2 represent various purines and pyrimidines.
References: [1728]

[EC 2.4.2.5 created 1961]

EC 2.4.2.6

Accepted name: nucleoside deoxyribosyltransferase
Reaction: 2-deoxy-D-ribosyl-base^1 + base^2 = 2-deoxy-D-ribosyl-base^2 + base^1
Other name(s): purine(pyrimidine) nucleoside:purine(pyrimidine) deoxyribosyl transferase; deoxyribose transferase; nucleoside *trans*-*N*-deoxyribosylase; *trans*-deoxyribosylase; *trans*-*N*-deoxyribosylase; *trans*-*N*-glycosidase; nucleoside deoxyribosyltransferase I (purine nucleoside:purine deoxyribosyltransferase: strictly specific for transfer between purine bases); nucleoside deoxyribosyltransferase II [purine(pyrimidine) nucleoside:purine(pyrimidine) deoxyribosyltransferase]
Systematic name: nucleoside:purine(pyrimidine) deoxy-D-ribosyltransferase
Comments: Base^1 and base^2 represent various purines and pyrimidines.
References: [1563, 2092, 2944]

[EC 2.4.2.6 created 1961]

EC 2.4.2.7

Accepted name: adenine phosphoribosyltransferase
Reaction: AMP + diphosphate = adenine + 5-phospho-α-D-ribose 1-diphosphate
Other name(s): AMP pyrophosphorylase; transphosphoribosidase; APRT; AMP-pyrophosphate phosphoribosyltransferase; adenine phosphoribosylpyrophosphate transferase; adenosine phosphoribosyltransferase; adenylate pyrophosphorylase; adenylic pyrophosphorylase

Systematic name: AMP:diphosphate phospho-D-ribosyltransferase
Comments: 5-Amino-4-imidazolecarboxamide can replace adenine.
References: [914, 1757, 2067]

[EC 2.4.2.7 created 1961]

EC 2.4.2.8
Accepted name: hypoxanthine phosphoribosyltransferase
Reaction: IMP + diphosphate = hypoxanthine + 5-phospho-α-D-ribose 1-diphosphate
Other name(s): IMP pyrophosphorylase; transphosphoribosidase; hypoxanthine—guanine phosphoribosyltransferase; guanine phosphoribosyltransferase; GPRT; HPRT; guanosine 5′-phosphate pyrophosphorylase; IMP-GMP pyrophosphorylase; HGPRTase; 6-hydroxypurine phosphoribosyltransferase; 6-mercaptopurine phosphoribosyltransferase; GMP pyrophosphorylase; guanine-hypoxanthine phosphoribosyltransferase; guanosine phosphoribosyltransferase; guanylate pyrophosphorylase; guanylic pyrophosphorylase; inosinate pyrophosphorylase; inosine 5′-phosphate pyrophosphorylase; inosinic acid pyrophosphorylase; inosinic pyrophosphorylase; 6-mercaptopurine phosphoribosyltransferase; purine-6-thiol phosphoribosyltransferase
Systematic name: IMP:diphosphate phospho-D-ribosyltransferase
Comments: Guanine and 6-mercaptopurine can replace hypoxanthine.
References: [913, 1757, 2067, 2870]

[EC 2.4.2.8 created 1961, modified 1982]

EC 2.4.2.9
Accepted name: uracil phosphoribosyltransferase
Reaction: UMP + diphosphate = uracil + 5-phospho-α-D-ribose 1-diphosphate
Other name(s): UMP pyrophosphorylase; UPRTase; UMP:pyrophosphate phosphoribosyltransferase; uridine 5′-phosphate pyrophosphorylase; uridine monophosphate pyrophosphorylase; uridylate pyrophosphorylase; uridylic pyrophosphorylase
Systematic name: UMP:diphosphate phospho-α-D-ribosyltransferase
References: [625, 913]

[EC 2.4.2.9 created 1961]

EC 2.4.2.10
Accepted name: orotate phosphoribosyltransferase
Reaction: orotidine 5′-phosphate + diphosphate = orotate + 5-phospho-α-D-ribose 1-diphosphate
Other name(s): orotidylic acid phosphorylase; orotidine-5′-phosphate pyrophosphorylase; OPRTase; orotate phosphoribosyl pyrophosphate transferase; orotic acid phosphoribosyltransferase; orotidine 5′-monophosphate pyrophosphorylase; orotidine monophosphate pyrophosphorylase; orotidine phosphoribosyltransferase; orotidylate phosphoribosyltransferase; orotidylate pyrophosphorylase; orotidylic acid pyrophosphorylase; orotidylic phosphorylase; orotidylic pyrophosphorylase
Systematic name: orotidine-5′-phosphate:diphosphate phospho-α-D-ribosyl-transferase
Comments: The enzyme from higher eukaryotes also catalyses the reaction listed as EC 4.1.1.23, orotidine-5′-phosphate decarboxylase.
References: [1530, 1966, 2187]

[EC 2.4.2.10 created 1961, modified 1986]

[2.4.2.11 Transferred entry. nicotinate phosphoribosyltransferase. Now EC 6.3.4.21, nicotinate phosphoribosyltransferase.]

[EC 2.4.2.11 created 1961, deleted 2013]

EC 2.4.2.12

Accepted name: nicotinamide phosphoribosyltransferase
Reaction: nicotinamide D-ribonucleotide + diphosphate = nicotinamide + 5-phospho-α-D-ribose 1-diphosphate
Other name(s): NMN pyrophosphorylase; nicotinamide mononucleotide pyrophosphorylase; nicotinamide mononucleotide synthetase; NMN synthetase; nicotinamide-nucleotide:diphosphate phospho-α-D-ribosyltransferase
Systematic name: nicotinamide-D-ribonucleotide:diphosphate phospho-α-D-ribosyltransferase
References: [2758]

[EC 2.4.2.12 created 1961]

[2.4.2.13 Transferred entry. now EC 2.5.1.6 methionine adenosyltransferase]

[EC 2.4.2.13 created 1961, deleted 1965]

EC 2.4.2.14

Accepted name: amidophosphoribosyltransferase
Reaction: 5-phospho-β-D-ribosylamine + diphosphate + L-glutamate = L-glutamine + 5-phospho-α-D-ribose 1-diphosphate + H_2O
Other name(s): phosphoribosyldiphosphate 5-amidotransferase; glutamine phosphoribosyldiphosphate amidotransferase; α-5-phosphoribosyl-1-pyrophosphate amidotransferase; 5′-phosphoribosylpyrophosphate amidotransferase; 5-phosphoribosyl-1-pyrophosphate amidotransferase; 5-phosphororibosyl-1-pyrophosphate amidotransferase; glutamine 5-phosphoribosylpyrophosphate amidotransferase; glutamine ribosylpyrophosphate 5-phosphate amidotransferase; phosphoribose pyrophosphate amidotransferase; phosphoribosyl pyrophosphate amidotransferase; phosphoribosylpyrophosphate glutamyl amidotransferase; 5-phosphoribosylamine:diphosphate phospho-α-D-ribosyltransferase (glutamate-amidating)
Systematic name: 5-phospho-β-D-ribosylamine:diphosphate phospho-α-D-ribosyltransferase (glutamate-amidating)
References: [488, 1233]

[EC 2.4.2.14 created 1961]

EC 2.4.2.15

Accepted name: guanosine phosphorylase
Reaction: guanosine + phosphate = guanine + α-D-ribose 1-phosphate
Systematic name: guanosine:phosphate α-D-ribosyltransferase
Comments: Also acts on deoxyguanosine.
References: [3939]

[EC 2.4.2.15 created 1965]

EC 2.4.2.16

Accepted name: urate-ribonucleotide phosphorylase
Reaction: urate D-ribonucleotide + phosphate = urate + α-D-ribose 1-phosphate
Other name(s): UAR phosphorylase; urate-ribonucleotide:phosphate D-ribosyltransferase; urate-ribonucleotide:phosphate α-D-ribosyltransferase
Systematic name: urate-D-ribonucleotide:phosphate α-D-ribosyltransferase
References: [1870]

[EC 2.4.2.16 created 1965]

EC 2.4.2.17

Accepted name: ATP phosphoribosyltransferase
Reaction: 1-(5-phospho-β-D-ribosyl)-ATP + diphosphate = ATP + 5-phospho-α-D-ribose 1-diphosphate

Other name(s): phosphoribosyl-ATP pyrophosphorylase; adenosine triphosphate phosphoribosyltransferase; phosphoribosyladenosine triphosphate:pyrophosphate phosphoribosyltransferase; phosphoribosyl ATP synthetase; phosphoribosyl ATP:pyrophosphate phosphoribosyltransferase; phosphoribosyl-ATP:pyrophosphate-phosphoribosyl phosphotransferase; phosphoribosyladenosine triphosphate pyrophosphorylase; phosphoribosyladenosine triphosphate synthetase; 1-(5-phospho-D-ribosyl)-ATP:diphosphate phospho-α-D-ribosyl-transferase

Systematic name: 1-(5-phospho-β-D-ribosyl)-ATP:diphosphate phospho-α-D-ribosyl-transferase

Comments: Involved in histidine biosynthesis.

References: [70, 2139, 3700]

[EC 2.4.2.17 created 1972]

EC 2.4.2.18

Accepted name: anthranilate phosphoribosyltransferase

Reaction: *N*-(5-phospho-D-ribosyl)-anthranilate + diphosphate = anthranilate + 5-phospho-α-D-ribose 1-diphosphate

Other name(s): phosphoribosyl-anthranilate pyrophosphorylase; PRT; anthranilate 5-phosphoribosylpyrophosphate phosphoribosyltransferase; anthranilate phosphoribosylpyrophosphate phosphoribosyltransferase; phosphoribosylanthranilate pyrophosphorylase; phosphoribosylanthranilate transferase; anthranilate-PP-ribose-*P* phosphoribosyltransferase

Systematic name: *N*-(5-phospho-D-ribosyl)-anthranilate:diphosphate phospho-α-D-ribosyltransferase

Comments: In some organisms, this enzyme is part of a multifunctional protein together with one or more other components of the system for biosynthesis of tryptophan [EC 4.1.1.48 (indole-3-glycerol-phosphate synthase), EC 4.1.3.27 (anthranilate synthase), EC 4.2.1.20 (tryptophan synthase) and EC 5.3.1.24 (phosphoribosylanthranilate isomerase)].

References: [628, 1417, 1463, 3801]

[EC 2.4.2.18 created 1972]

EC 2.4.2.19

Accepted name: nicotinate-nucleotide diphosphorylase (carboxylating)

Reaction: β-nicotinate D-ribonucleotide + diphosphate + CO_2 = pyridine-2,3-dicarboxylate + 5-phospho-α-D-ribose 1-diphosphate

Other name(s): quinolinate phosphoribosyltransferase (decarboxylating); quinolinic acid phosphoribosyltransferase; QAPRTase; NAD^+ pyrophosphorylase; nicotinate mononucleotide pyrophosphorylase (carboxylating); quinolinic phosphoribosyltransferase

Systematic name: β-nicotinate-D-ribonucleotide:diphosphate phospho-α-D-ribosyltransferase (carboxylating)

Comments: The reaction is catalysed in the opposite direction. Since quinolinate is synthesized from L-tryptophan in eukaryotes, but from L-aspartate in some prokaryotes, this is the first NAD^+ biosynthesis enzyme shared by both eukaryotes and prokaryotes [1603].

References: [1042, 2592, 1603]

[EC 2.4.2.19 created 1972]

EC 2.4.2.20

Accepted name: dioxotetrahydropyrimidine phosphoribosyltransferase

Reaction: a 2,4-dioxotetrahydropyrimidine D-ribonucleotide + diphosphate = a 2,4-dioxotetrahydropyrimidine + 5-phospho-α-D-ribose 1-diphosphate

Other name(s): dioxotetrahydropyrimidine-ribonucleotide pyrophosphorylase; dioxotetrahydropyrimidine phosphoribosyl transferase; dioxotetrahydropyrimidine ribonucleotide pyrophosphorylase; 2,4-dioxotetrahydropyrimidine-nucleotide:diphosphate phospho-α-D-ribosyltransferase

Systematic name: 2,4-dioxotetrahydropyrimidine-D-ribonucleotide:diphosphate phospho-α-D-ribosyltransferase

Comments: Acts (in the reverse direction) on uracil and other pyrimidines and pteridines containing a 2,4-diketo structure.

References: [1245]

[EC 2.4.2.20 created 1972]

EC 2.4.2.21

Accepted name: nicotinate-nucleotide—dimethylbenzimidazole phosphoribosyltransferase

Reaction: β-nicotinate D-ribonucleotide + 5,6-dimethylbenzimidazole = nicotinate + α-ribazole 5′-phosphate

Other name(s): nicotinate mononucleotide-dimethylbenzimidazole phosphoribosyltransferase; nicotinate ribonucleotide:benzimidazole (adenine) phosphoribosyltransferase; nicotinate-nucleotide:dimethylbenzimidazole phospho-D-ribosyltransferase; CobT; nicotinate mononucleotide (NaMN):5,6-dimethylbenzimidazole phosphoribosyltransferase

Systematic name: nicotinate-nucleotide:5,6-dimethylbenzimidazole phospho-D-ribosyltransferase

Comments: Also acts on benzimidazole, and the clostridial enzyme acts on adenine to form 7-α-D-ribosyladenine 5′-phosphate. The product of the reaction, α-ribazole 5′-phosphate, forms part of the corrin-biosynthesis pathway and is a substrate for EC 2.7.8.26, adenosylcobinamide-GDP ribazoletransferase [461]. It can also be dephosphorylated to form α-ribazole by the action of EC 3.1.3.73, α-ribazole phosphatase.

References: [966, 967, 1001, 461, 536, 537]

[EC 2.4.2.21 created 1972]

EC 2.4.2.22

Accepted name: xanthine phosphoribosyltransferase

Reaction: XMP + diphosphate = 5-phospho-α-D-ribose 1-diphosphate + xanthine

Other name(s): Xan phosphoribosyltransferase; xanthosine 5′-phosphate pyrophosphorylase; xanthylate pyrophosphorylase; xanthylic pyrophosphorylase; XMP pyrophosphorylase; 5-phospho-α-D-ribose-1-diphosphate:xanthine phospho-D-ribosyltransferase; 9-(5-phospho-β-D-ribosyl)xanthine:diphosphate 5-phospho-α-D-ribosyltransferase

Systematic name: XMP:diphosphate 5-phospho-α-D-ribosyltransferase

References: [1788]

[EC 2.4.2.22 created 1972]

[2.4.2.23 Transferred entry. deoxyuridine phosphorylase. This activity has been shown to be catalysed by EC 2.4.2.2, pyrimidine-nucleoside phosphorylase, EC 2.4.2.3, uridine phosphorylase, and EC 2.4.2.4, thymidine phosphorylase.]

[EC 2.4.2.23 created 1972, deleted 2013]

EC 2.4.2.24

Accepted name: 1,4-β-D-xylan synthase

Reaction: UDP-D-xylose + [(1→4)-β-D-xylan]$_n$ = UDP + [(1→4)-β-D-xylan]$_{n+1}$

Other name(s): uridine diphosphoxylose-1,4-β-xylan xylosyltransferase; 1,4-β-xylan synthase; xylan synthase; xylan synthetase; UDP-D-xylose:1,4-β-D-xylan 4-β-D-xylosyltransferase

Systematic name: UDP-D-xylose:(1→4)-β-D-xylan 4-β-D-xylosyltransferase

References: [167]

[EC 2.4.2.24 created 1972 as EC 2.4.1.72, transferred 1976 to EC 2.4.2.24]

EC 2.4.2.25

Accepted name: flavone apiosyltransferase

Reaction: UDP-α-D-apiose + apigenin 7-*O*-β-D-glucoside = UDP + apigenin 7-*O*-[β-D-apiosyl-(1→2)-β-D-glucoside]

Other name(s): uridine diphosphoapiose-flavone apiosyltransferase; UDP-apiose:7-*O*-(β-D-glucosyl)-flavone apiosyltransferase

Systematic name: UDP-apiose:5,4′-dihydroxyflavone 7-*O*-β-D-glucoside 2″-*O*-β-D-apiofuranosyltransferase
Comments: 7-*O*-β-D-Glucosides of a number of flavonoids and of 4-substituted phenols can act as acceptors.
References: [2576]

[EC 2.4.2.25 created 1976]

EC 2.4.2.26

Accepted name: protein xylosyltransferase
Reaction: UDP-α-D-xylose + [protein]-L-serine = UDP + [protein]-3-*O*-(β-D-xylosyl)-L-serine
Other name(s): UDP-D-xylose:core protein β-D-xylosyltransferase; UDP-D-xylose:core protein xylosyltransferase; UDP-D-xylose:proteoglycan core protein β-D-xylosyltransferase; UDP-xylose-core protein β-D-xylosyltransferase; uridine diphosphoxylose-core protein β-xylosyltransferase; uridine diphosphoxylose-protein xylosyltransferase; UDP-D-xylose:protein β-D-xylosyltransferase
Systematic name: UDP-α-D-xylose:protein β-D-xylosyltransferase (configuration-inverting)
Comments: Involved in the biosynthesis of the linkage region of glycosaminoglycan chains as part of proteoglycan biosynthesis (chondroitin, dermatan and heparan sulfates).
References: [3355, 1112]

[EC 2.4.2.26 created 1976, modified 2002, modified 2016]

EC 2.4.2.27

Accepted name: dTDP-dihydrostreptose—streptidine-6-phosphate dihydrostreptosyltransferase
Reaction: dTDP-L-dihydrostreptose + streptidine 6-phosphate = dTDP + *O*-(1→4)-α-L-dihydrostreptosyl-streptidine 6-phosphate
Other name(s): thymidine diphosphodihydrostreptose-streptidine 6-phosphate dihydrostreptosyltransferase
Systematic name: dTDP-L-dihydrostreptose:streptidine-6-phosphate dihydrostreptosyltransferase
References: [1717]

[EC 2.4.2.27 created 1982]

EC 2.4.2.28

Accepted name: *S*-methyl-5′-thioadenosine phosphorylase
Reaction: *S*-methyl-5′-thioadenosine + phosphate = adenine + *S*-methyl-5-thio-α-D-ribose 1-phosphate
Other name(s): 5′-deoxy-5′-methylthioadenosine phosphorylase; MTA phosphorylase; MeSAdo phosphorylase; MeSAdo/Ado phosphorylase; methylthioadenosine phosphorylase; methylthioadenosine nucleoside phosphorylase; 5′-methylthioadenosine:phosphate methylthio-D-ribosyl-transferase; *S*-methyl-5-thioadenosine phosphorylase; *S*-methyl-5-thioadenosine:phosphate *S*-methyl-5-thio-α-D-ribosyl-transferase
Systematic name: *S*-methyl-5′-thioadenosine:phosphate *S*-methyl-5-thio-α-D-ribosyl-transferase
Comments: Also acts on 5′-deoxyadenosine and other analogues having 5′-deoxy groups.
References: [483, 1011, 2655]

[EC 2.4.2.28 created 1983]

EC 2.4.2.29

Accepted name: tRNA-guanosine^{34} transglycosylase
Reaction: (1) guanine^{34} in tRNA + queuine = queuine^{34} in tRNA + guanine
(2) guanine^{34} in tRNA + 7-aminomethyl-7-carbaguanine = 7-aminomethyl-7-carbaguanine^{34} in tRNA + guanine
Other name(s): guanine insertion enzyme (ambiguous); tRNA transglycosylase (ambiguous); Q-insertase (ambiguous); queuine^{34} transfer ribonucleate ribosyltransferase; transfer ribonucleate glycosyltransferase (ambiguous); tRNA guanine^{34} transglycosidase; queuine tRNA-ribosyltransferase (ambiguous); TGT; [tRNA]-guanine^{34}:queuine tRNA-D-ribosyltransferase; transfer ribonucleic acid guanine^{34} transglycosylase

Systematic name: tRNA-guanosine^{34}:queuine tRNA-D-ribosyltransferase

Comments: Certain prokaryotic and eukaryotic tRNAs contain the modified base queuine at position 34. In eukaryotes queuine is salvaged from food and incorporated into tRNA directly via a base-exchange reaction, replacing guanine. In eubacteria, which produce queuine *de novo*, the enzyme catalyses the exchange of guanine with the queuine precursor $preQ_1$, which is ultimately modified to queuosine [3541, 344]. The eubacterial enzyme can also use an earlier intermediate, $preQ_0$, to replace guanine in unmodified tRNA$^{\text{Tyr}}$ and tRNA$^{\text{Asn}}$ [2546]. This enzyme acts after EC 1.7.1.13, $preQ_1$ synthase, in the queuine-biosynthesis pathway.

References: [1385, 2546, 3201, 3541, 344]

[EC 2.4.2.29 created 1984, modified 2007, modified 2012]

EC 2.4.2.30

Accepted name: NAD$^+$ ADP-ribosyltransferase

Reaction: NAD$^+$ + (ADP-D-ribosyl)$_n$-acceptor = nicotinamide + (ADP-D-ribosyl)$_{n+1}$-acceptor + H$^+$

Other name(s): poly(ADP-ribose) synthase; ADP-ribosyltransferase (polymerizing); NAD ADP-ribosyltransferase; PARP; PARP-1; NAD$^+$:poly(adenine-diphosphate-D-ribosyl)-acceptor ADP-D-ribosyl-transferase (incorrect); NAD$^+$:poly(adenosine-diphosphate-D-ribosyl)-acceptor ADP-D-ribosyl-transferase

Systematic name: NAD$^+$:poly(ADP-D-ribosyl)-acceptor ADP-D-ribosyl-transferase

Comments: The ADP-D-ribosyl group of NAD$^+$ is transferred to an acceptor carboxy group on a histone or the enzyme itself, and further ADP-ribosyl groups are transferred to the 2′-position of the terminal adenosine moiety, building up a polymer with an average chain length of 20–30 units.

References: [3598, 3599, 3619]

[EC 2.4.2.30 created 1984, modified 1990]

EC 2.4.2.31

Accepted name: NAD$^+$—protein-arginine ADP-ribosyltransferase

Reaction: NAD$^+$ + protein L-arginine = nicotinamide + N^{ω}-(ADP-D-ribosyl)-protein-L-arginine

Other name(s): ADP-ribosyltransferase; mono(ADP-ribosyl)transferase; NAD$^+$:L-arginine ADP-D-ribosyltransferase; NAD(P)$^+$-arginine ADP-ribosyltransferase; NAD(P)$^+$:L-arginine ADP-D-ribosyltransferase; mono-ADP-ribosyltransferase; ART; ART1; ART2; ART3; ART4; ART5; ART6; ART7; NAD(P)$^+$—protein-arginine ADP-ribosyltransferase; NAD(P)$^+$:protein-L-arginine ADP-D-ribosyltransferase

Systematic name: NAD$^+$:protein-L-arginine ADP-D-ribosyltransferase

Comments: Protein mono-ADP-ribosylation is a reversible post-translational modification that plays a role in the regulation of cellular activities [615]. Arginine residues in proteins act as acceptors. Free arginine, agmatine [(4-aminobutyl)guanidine], arginine methyl ester and guanidine can also do so. The enzyme from some, but not all, species can also use NADP$^+$ as acceptor (giving rise to N^{ω}-[(2′-phospho-ADP)-D-ribosyl]-protein-L-arginine as the product), but more slowly [2328, 2615]. The enzyme catalyses the NAD$^+$-dependent activation of EC 4.6.1.1, adenylate cyclase. Some bacterial enterotoxins possess similar enzymic activities. (*cf.* EC 2.4.2.36 NAD$^+$—diphthamide ADP-ribosyltransferase).

References: [2328, 2329, 3598, 615, 2615]

[EC 2.4.2.31 created 1984, modified 1990, modified 2006]

EC 2.4.2.32

Accepted name: dolichyl-phosphate D-xylosyltransferase

Reaction: UDP-D-xylose + dolichyl phosphate = UDP + dolichyl D-xylosyl phosphate

Systematic name: UDP-D-xylose:dolichyl-phosphate D-xylosyltransferase

References: [3714]

[EC 2.4.2.32 created 1984, modified 2003]

EC 2.4.2.33

Accepted name: dolichyl-xylosyl-phosphate—protein xylosyltransferase
Reaction: dolichyl D-xylosyl phosphate + protein = dolichyl phosphate + D-xylosylprotein
Systematic name: dolichyl-D-xylosyl-phosphate:protein D-xylosyltransferase
References: [3714]

[EC 2.4.2.33 created 1984]

EC 2.4.2.34

Accepted name: indolylacetylinositol arabinosyltransferase
Reaction: UDP-L-arabinose + (indol-3-yl)acetyl-1D-*myo*-inositol = UDP + (indol-3-yl)acetyl-*myo*-inositol 3-L-arabinoside
Other name(s): arabinosylindolylacetylinositol synthase; UDP-L-arabinose:indol-3-ylacetyl-*myo*-inositol L-arabinosyltransferase; UDP-L-arabinose:(indol-3-yl)acetyl-*myo*-inositol L-arabinosyltransferase
Systematic name: UDP-L-arabinose:(indol-3-yl)acetyl-1D-*myo*-inositol L-arabinosyltransferase
Comments: The position of acylation is indeterminate because of the ease of acyl transfer between hydroxy groups. For a diagram showing the biosynthesis of UDP-L-arabinose, click here.
References: [613]

[EC 2.4.2.34 created 1986, modified 2003]

EC 2.4.2.35

Accepted name: flavonol-3-*O*-glycoside xylosyltransferase
Reaction: UDP-α-D-xylose + a flavonol 3-*O*-glycoside = UDP + a flavonol 3-[β-D-xylosyl-(1→2)-β-D-glycoside]
Other name(s): UDP-D-xylose:flavonol-3-*O*-glycoside 2$''$-*O*-β-D-xylosyltransferase
Systematic name: UDP-α-D-xylose:flavonol-3-*O*-glycoside 2$''$-*O*-β-D-xylosyltransferase
Comments: Flavonol 3-*O*-glucoside, flavonol 3-*O*-galactoside and, more slowly, rutin, can act as acceptors.
References: [1709]

[EC 2.4.2.35 created 1986, modified 2014]

EC 2.4.2.36

Accepted name: NAD$^+$—diphthamide ADP-ribosyltransferase
Reaction: NAD$^+$ + diphthamide-[translation elongation factor 2] = nicotinamide + *N*-(ADP-D-ribosyl)diphthamide-[translation elongation factor 2]
Other name(s): ADP-ribosyltransferase; mono(ADPribosyl)transferase; NAD—diphthamide ADP-ribosyltransferase; NAD$^+$:peptide-diphthamide *N*-(ADP-D-ribosyl)transferase
Systematic name: NAD$^+$:diphthamide-[translation elongation factor 2] *N*-(ADP-D-ribosyl)transferase
Comments: Diphtheria toxin and some other bacterial toxins catalyse this reaction, which inactivates translation elongation factor 2 (EF2). The acceptor is diphthamide, a unique modification of a histidine residue in the elongation factor found in archaebacteria and all eukaryotes, but not in eubacteria. *cf.* EC 2.4.2.31 NAD(P)$^+$—protein-arginine ADP-ribosyltransferase. The relevant histidine of EF2 is His^{715} in mammals, His^{699} in yeast and His^{600} in *Pyrococcus horikoshii*.
References: [1888, 3598]

[EC 2.4.2.36 created 1990, modified 2013]

EC 2.4.2.37

Accepted name: NAD$^+$—dinitrogen-reductase ADP-D-ribosyltransferase
Reaction: NAD$^+$ + [dinitrogen reductase]-L-arginine = nicotinamide + [dinitrogen reductase]-N^{ω}-α-(ADP-D-ribosyl)-L-arginine
Other name(s): NAD-azoferredoxin (ADPribose)transferase; NAD-dinitrogen-reductase ADP-D-ribosyltransferase; *draT* (gene name)

Systematic name: NAD$^+$:[dinitrogen reductase] (ADP-D-ribosyl)transferase

Comments: The combined action of this enzyme and EC 3.2.2.24, ADP-ribosyl-[dinitrogen reductase] hydrolase, controls the activity level of nitrogenase (EC 1.18.6.1). In the presence of ammonium, the product of nitrogenase, this enzyme covalently links an ADP-ribose moiety to a specific arginine residue of the dinitrogenase reductase component of nitrogenase, blocking its activity.

References: [2051, 911, 2333]

[EC 2.4.2.37 created 1992, modified 2015]

EC 2.4.2.38

Accepted name: glycoprotein 2-β-D-xylosyltransferase

Reaction: UDP-α-D-xylose + N^4-β-D-GlcNAc-(1→2)-α-D-Man-(1→3)-[β-D-GlcNAc-(1→2)-α-D-Man-(1→6)]-β-D-Man-(1→4)-β-D-GlcNAc-(1→4)-β-D-GlcNAc-L-asparaginyl-[protein] = UDP + N^4-β-D-GlcNAc-(1→2)-α-D-Man-(1→3)-[β-D-GlcNAc-(1→2)-α-D-Man-(1→6)]-[β-D-Xyl-(1→2)]-β-D-Man-(1→4)-β-D-GlcNAc-(1→4)-β-D-GlcNAc-L-asparaginyl-[protein]

Other name(s): β1,2-xylosyltransferase; UDP-D-xylose:glycoprotein (D-xylose to the 3,6-disubstituted mannose of 4-*N*-*N*-acetyl-β-D-glucosaminyl-(1→2)-α-D-mannosyl-(1→3)-[*N*-acetyl-β-D-glucosaminyl-(1→2)-α-D-mannosyl-(1→6)]-β-D-mannosyl-(1→4)-*N*-acetyl-β-D-glucosaminyl-(1→4)-*N*-acetyl-β-D-glucosaminylasparagine) 2-β-D-xylosyltransferase; UDP-D-xylose:glycoprotein (D-xylose to the 3,6-disubstituted mannose of N^4-*N*-acetyl-β-D-glucosaminyl-(1→2)-α-D-mannosyl-(1→3)-[*N*-acetyl-β-D-glucosaminyl-(1→2)-α-D-mannosyl-(1→6)]-β-D-mannosyl-(1→4)-*N*-acetyl-β-D-glucosaminyl-(1→4)-*N*-acetyl-β-D-glucosaminylasparagine) 2-β-D-xylosyltransferase

Systematic name: UDP-α-D-xylose:N^4-β-D-GlcNAc-(1→2)-α-D-mannosyl-(1→3)-[β-D-GlcNAc-(1→2)-α-D-mannosyl-(1→6)]-β-D-mannosyl-(1→4)-β-D-GlcNAc-(1→4)-β-D-GlcNAc-L-asparaginyl-[protein] 2-β-D-xylosyltransferase (configuration-inverting)

Comments: Specific for N-linked oligosaccharides (*N*-glycans).

References: [4031, 3368]

[EC 2.4.2.38 created 2001]

EC 2.4.2.39

Accepted name: xyloglucan 6-xylosyltransferase

Reaction: Transfers an α-D-xylosyl residue from UDP-D-xylose to a glucose residue in xyloglucan, forming an α-(1→6)-D-xylosyl-D-glucose linkage

Other name(s): uridine diphosphoxylose-xyloglucan 6α-xylosyltransferase; xyloglucan 6-α-D-xylosyltransferase; UDP-D-xylose:xyloglucan 1,6-α-D-xylosyltransferase

Systematic name: UDP-D-xylose:xyloglucan 6-α-D-xylosyltransferase

Comments: In association with EC 2.4.1.168 (xyloglucan 4-glucosyltransferase), this enzyme brings about the synthesis of xyloglucan; concurrent transfers of glucose and xylose are necessary for this synthesis.

References: [1255, 1254]

[EC 2.4.2.39 created 1989 as EC 2.4.1.169, transferred 2003 to EC 2.4.2.39]

EC 2.4.2.40

Accepted name: zeatin *O*-β-D-xylosyltransferase

Reaction: UDP-D-xylose + zeatin = UDP + *O*-β-D-xylosylzeatin

Other name(s): uridine diphosphoxylose-zeatin xylosyltransferase; zeatin *O*-xylosyltransferase

Systematic name: UDP-D-xylose:zeatin *O*-β-D-xylosyltransferase

Comments: Does not act on UDP-glucose (*cf.* EC 2.4.1.103 alizarin 2-β-glucosyltransferase).

References: [3593]

[EC 2.4.2.40 created 1992 as EC 2.4.1.204, transferred 2003 to EC 2.4.2.40]

EC 2.4.2.41

Accepted name: xylogalacturonan β-1,3-xylosyltransferase

Reaction: Transfers a xylosyl residue from UDP-D-xylose to a D-galactose residue in xylogalacturonan, forming a β-1,3-D-xylosyl-D-galactose linkage.

Other name(s): xylogalacturonan xylosyltransferase; XGA xylosyltransferase

Systematic name: UDP-D-xylose:xylogalacturonan 3-β-D-xylosyltransferase

Comments: Involved in plant cell wall synthesis. The enzyme from *Arabidopsis thaliana* also transfers D-xylose from UDP-D-xylose onto oligogalacturonide acceptors. The enzyme did not show significant activity with UDP-glucose, UDP-galactose, or UDP-*N*-acetyl-D-glucosamine as sugar donors.

References: [1508]

[EC 2.4.2.41 created 2009]

EC 2.4.2.42

Accepted name: UDP-D-xylose:β-D-glucoside α-1,3-D-xylosyltransferase

Reaction: UDP-α-D-xylose + Glcβ-Ser^{53}-EGF-like domain of bovine factor IX(45-87) = UDP + Xylα(1-3)Glcβ-Ser^{53}-EGF-like domain of bovine factor IX(45-87)

Other name(s): β-glucoside α-1,3-xylosyltransferase

Systematic name: UDP-α-D-xylose:β-D-glucoside 3-α-D-xylosyltransferase

Comments: The enzyme is involved in the biosynthesis of the Xylα(1-3)Xylα(1-3)Glcβ-1-*O*-Ser on epidermal growth factor-like domains [1459].

References: [1459, 2563]

[EC 2.4.2.42 created 2010]

EC 2.4.2.43

Accepted name: lipid IV_A 4-amino-4-deoxy-L-arabinosyltransferase

Reaction: (1) 4-amino-4-deoxy-α-L-arabinopyranosyl *ditrans*,*octacis*-undecaprenyl phosphate + α-Kdo-(2→4)-α-Kdo-(2→6)-lipid A = α-Kdo-(2→4)-α-Kdo-(2→6)-[4-*P*-L-Ara4N]-lipid A + *ditrans*,*octacis*-undecaprenyl phosphate
(2) 4-amino-4-deoxy-α-L-arabinopyranosyl *ditrans*,*octacis*-undecaprenyl phosphate + lipid IV_A = lipid II_A + *ditrans*,*octacis*-undecaprenyl phosphate
(3) 4-amino-4-deoxy-α-L-arabinopyranosyl *ditrans*,*octacis*-undecaprenyl phosphate + α-Kdo-(2→4)-α-Kdo-(2→6)-lipid IV_A = 4′-α-L-Ara4N-α-Kdo-(2→4)-α-Kdo-(2→6)-lipid IV_A + *ditrans*,*octacis*-undecaprenyl phosphate

Other name(s): undecaprenyl phosphate-α-L-Ara4N transferase; 4-amino-4-deoxy-L-arabinose lipid A transferase; polymyxin resistance protein PmrK; *arnT* (gene name)

Systematic name: 4-amino-4-deoxy-α-L-arabinopyranosyl *ditrans*,*octacis*-undecaprenyl phosphate:lipid IV_A 4-amino-4-deoxy-L-arabinopyranosyltransferase

Comments: Integral membrane protein present in the inner membrane of certain Gram negative endobacteria. In strains that do not produce 3-deoxy-D-*manno*-octulosonic acid (Kdo), the enzyme adds a single arabinose unit to the 1-phosphate moiety of the tetra-acylated lipid A precursor, lipid IV_A. In the presence of a Kdo disaccharide, the enzyme primarily adds an arabinose unit to the 4-phosphate of lipid A molecules. The *Salmonella typhimurium* enzyme can add arabinose units to both positions.

References: [3565, 3564, 4078, 388, 1443]

[EC 2.4.2.43 created 2010, modified 2011]

EC 2.4.2.44

Accepted name: *S*-methyl-5′-thioinosine phosphorylase

Reaction: *S*-methyl-5′-thioinosine + phosphate = hypoxanthine + *S*-methyl-5-thio-α-D-ribose 1-phosphate

Other name(s): MTIP; MTI phosphorylase; methylthioinosine phosphorylase

Systematic name: *S*-methyl-5′-thioinosine:phosphate *S*-methyl-5-thio-α-D-ribosyl-transferase

Comments: No activity with *S*-methyl-5′-thioadenosine. The catabolism of of 5′-methylthioadenosine in *Pseudomonas aeruginosa* involves deamination to *S*-methyl-5′-thioinosine (EC 3.5.4.31, *S*-methyl-5′-thioadenosine deaminase) and phosphorolysis to hypoxanthine [1168].

References: [1168]

[EC 2.4.2.44 created 2011]

EC 2.4.2.45

Accepted name: decaprenyl-phosphate phosphoribosyltransferase

Reaction: *trans*,*octacis*-decaprenyl phosphate + 5-phospho-α-D-ribose 1-diphosphate = *trans*,*octacis*-decaprenylphospho-β-D-ribofuranose 5-phosphate + diphosphate

Other name(s): 5-phospho-α-D-ribose-1-diphosphate:decaprenyl-phosphate 5-phosphoribosyltransferase; 5-phospho-α-D-ribose 1-pyrophosphate:decaprenyl phosphate 5-phosphoribosyltransferase; DPPR synthase; Rv3806

Systematic name: *trans*,*octacis*-decaprenylphospho-β-D-ribofuranose 5-phosphate:diphosphate phospho-α-D-ribosyltransferase

Comments: Requires Mg^{2+}. Isolated from *Mycobacterium tuberculosis*. Has some activity with other polyprenyl phosphates.

References: [1394]

[EC 2.4.2.45 created 2012]

EC 2.4.2.46

Accepted name: galactan 5-*O*-arabinofuranosyltransferase

Reaction: Adds an α-D-arabinofuranosyl group from *trans*,*octacis*-decaprenylphospho-β-D-arabinofuranose at the 5-*O*-position of the eighth, tenth and twelfth galactofuranose unit of the galactofuranan chain of [β-D-galactofuranosyl-(1→5)-β-D-galactofuranosyl-(1→6)]$_{14}$-β-D-galactofuranosyl-(1→5)-β-D-galactofuranosyl-(1→4)-α-L-rhamnopyranosyl-(1→3)-*N*-acetyl-α-D-glucosaminyl-diphospho-*trans*,*octacis*-decaprenol

Other name(s): AftA; Rv3792

Systematic name: galactofuranan:*trans*,*octacis*-decaprenylphospho-β-D-arabinofuranose 5-*O*-α-D-arabinofuranosyltransferase

Comments: Isolated from *Mycobacterium tuberculosis* and *Corynebacterium glutamicum*. These arabinofuranosyl groups form the start of an arabinofuranan chain as part of the of the cell wall in mycobacteria.

References: [51]

[EC 2.4.2.46 created 2012]

EC 2.4.2.47

Accepted name: arabinofuranan 3-*O*-arabinosyltransferase

Reaction: Adds an α-D-arabinofuranosyl group from *trans*,*octacis*-decaprenylphospho-β-D-arabinofuranose at the 3-*O*-position of an α-(1→5)-arabinofuranan chain attached to a β-(1→5)-galactofuranan chain

Other name(s): AftC

Systematic name: α-(1→5)-arabinofuranan:*trans*,*octacis*-decaprenylphospho-β-D-arabinofuranose 3-*O*-α-D-arabinofuranosyltransferase

Comments: Isolated from *Mycobacterium smegmatis*. Involved in the formation of the cell wall in mycobacteria.

References: [308, 4042]

[EC 2.4.2.47 created 2012]

EC 2.4.2.48

Accepted name: tRNA-guanine^{15} transglycosylase

Reaction: guanine^{15} in tRNA + 7-cyano-7-carbaguanine = 7-cyano-7-carbaguanine^{15} in tRNA + guanine

Other name(s): tRNA transglycosylase (ambiguous); transfer ribonucleate glycosyltransferase (ambiguous); tRNA guanine^{15} transglycosidase; TGT (ambiguous); transfer ribonucleic acid guanine^{15} transglycosylase
Systematic name: tRNA-guanine^{15}:7-cyano-7-carbaguanine tRNA-D-ribosyltransferase
Comments: Archaeal tRNAs contain the modified nucleoside archaeosine at position 15. This archaeal enzyme catalyses the exchange of guanine at position 15 of tRNA with the base $preQ_0$, which is ultimately modified to form the nucleoside archaeosine (*cf.* EC 2.6.1.97) [160].
References: [160]

[EC 2.4.2.48 created 2012]

EC 2.4.2.49

Accepted name: neamine phosphoribosyltransferase
Reaction: neamine + 5-phospho-α-D-ribose 1-diphosphate = 5″-phosphoribostamycin + diphosphate
Other name(s): *btrL* (gene name); *neoM* (gene name)
Systematic name: neamine:5-phospho-α-D-ribose 1-diphosphate phosphoribosyltransferase
Comments: Involved in the biosynthetic pathways of several clinically important aminocyclitol antibiotics, including ribostamycin, neomycin and butirosin. The enzyme requires a divalent metal ion, optimally Mg^{2+}, Ni^{2+} or Co^{2+}.
References: [1803]

[EC 2.4.2.49 created 2013]

EC 2.4.2.50

Accepted name: cyanidin 3-*O*-galactoside 2″-*O*-xylosyltransferase
Reaction: UDP-α-D-xylose + cyanidin 3-*O*-β-D-galactoside = UDP + cyanidin 3-*O*-(β-D-xylosyl-(1→2)-β-D-galactoside)
Other name(s): CGXT
Systematic name: UDP-α-D-xylose:cyanidin-3-*O*-β-D-galactoside 2″-*O*-xylosyltransferase
Comments: Isolated from the plant *Daucus carota* (Afghan cultivar carrot).
References: [2932]

[EC 2.4.2.50 created 2013]

EC 2.4.2.51

Accepted name: anthocyanidin 3-*O*-glucoside 2‴-*O*-xylosyltransferase
Reaction: UDP-α-D-xylose + an anthocyanidin 3-*O*-β-D-glucoside = UDP + an anthocyanidin 3-*O*-β-D-sambubioside
Other name(s): uridine 5′-diphosphate-xylose:anthocyanidin 3-*O*-glucose-xylosyltransferase; UGT79B1
Systematic name: UDP-α-D-xylose:anthocyanidin-3-*O*-β-D-glucoside 2‴-*O*-xylosyltransferase
Comments: Isolated from the plants *Matthiola incana* (stock) [3505] and *Arabidopsis thaliana* (mouse-eared cress) [3992]. The enzyme has similar activity with the 3-glucosides of pelargonidin, cyanidin, delphinidin, quercetin and kaempferol as well as with cyanidin 3-*O*-rhamnosyl-(1→6)-glucoside and cyanidin 3-*O*-(6-acylglucoside). There is no activity with other UDP-sugars or with cyanidin 3,5-diglucoside.
References: [3505, 3992]

[EC 2.4.2.51 created 2013]

EC 2.4.2.52

Accepted name: triphosphoribosyl-dephospho-CoA synthase
Reaction: ATP + 3′-dephospho-CoA = 2′-(5-triphospho-α-D-ribosyl)-3′-dephospho-CoA + adenine
Other name(s): 2′-(5″-triphosphoribosyl)-3-dephospho-CoA synthase; ATP:dephospho-CoA 5-triphosphoribosyl transferase; CitG; ATP:dephospho-CoA 5′-triphosphoribosyl transferase; MdcB; ATP:3-dephospho-CoA 5″-triphosphoribosyltransferase; MadG

Systematic name: ATP:3′-dephospho-CoA 5-triphospho-α-D-ribosyltransferase

Comments: ATP cannot be replaced by GTP, CTP, UTP, ADP or AMP. The reaction involves the formation of a new α (1″→2′) glycosidic bond between the two ribosyl moieties, with concomitant displacement of the adenine moiety of ATP [3091, 1351]. The 2′-(5-triphosphoribosyl)-3′-dephospho-CoA produced can be transferred by EC 2.7.7.61, citrate lyase holo-[acyl-carrier protein] synthase, to the apo-acyl-carrier protein subunit (γ-subunit) of EC 4.1.3.6, citrate (*pro*-3*S*) lyase, thus converting it from an apo-enzyme into a holo-enzyme [3091, 3093]. Alternatively, it can be transferred to the apo-ACP subunit of malonate decarboxylase by the action of EC 2.7.7.66, malonate decarboxylase holo-[acyl-carrier protein] synthase [1351].

References: [3091, 3092, 3093, 1351]

[EC 2.4.2.52 created 2002 as EC 2.7.8.25, modified 2008, transferred 2013 to EC 2.4.2.52]

EC 2.4.2.53

Accepted name: undecaprenyl-phosphate 4-deoxy-4-formamido-L-arabinose transferase

Reaction: UDP-4-deoxy-4-formamido-β-L-arabinopyranose + *ditrans*,*octacis*-undecaprenyl phosphate = UDP + 4-deoxy-4-formamido-α-L-arabinopyranosyl *ditrans*,*octacis*-undecaprenyl phosphate

Other name(s): undecaprenyl-phosphate Ara4FN transferase; Ara4FN transferase; polymyxin resistance protein PmrF; UDP-4-amino-4-deoxy-α-L-arabinose:*ditrans*,*polycis*-undecaprenyl phosphate 4-amino-4-deoxy-α-L-arabinosyltransferase

Systematic name: UDP-4-amino-4-deoxy-α-L-arabinose:*ditrans*,*octacis*-undecaprenyl phosphate 4-amino-4-deoxy-α-L-arabinosyltransferase

Comments: The enzyme shows no activity with UDP-4-amino-4-deoxy-β-L-arabinose.

References: [382, 381]

[EC 2.4.2.53 created 2010 as EC 2.7.8.30, modified 2011, transferred 2013 to EC 2.4.2.53]

EC 2.4.2.54

Accepted name: β-ribofuranosylphenol 5′-phosphate synthase

Reaction: 5-phospho-α-D-ribose 1-diphosphate + 4-hydroxybenzoate = 4-(β-D-ribofuranosyl)phenol 5′-phosphate + CO_2 + diphosphate

Other name(s): β-RFAP synthase (incorrect); β-RFA-*P* synthase (incorrect); AF2089 (gene name); MJ1427 (gene name); β-ribofuranosylhydroxybenzene 5′-phosphate synthase; 4-(β-D-ribofuranosyl)aminobenzene 5′-phosphate synthase (incorrect); β-ribofuranosylaminobenzene 5′-phosphate synthase (incorrect); 5-phospho-α-D-ribose 1-diphosphate:4-aminobenzoate 5-phospho-β-D-ribofuranosyltransferase (decarboxylating) (incorrect)

Systematic name: 5-phospho-α-D-ribose-1-diphosphate:4-hydroxybenzoate 5-phospho-β-D-ribofuranosyltransferase (decarboxylating)

Comments: The enzyme is involved in biosynthesis of tetrahydromethanopterin in archaea. It was initially thought to use 4-aminobenzoate as a substrate, but was later shown to utilize 4-hydroxybenzoate [3837]. The activity is dependent on Mg^{2+} or Mn^{2+} [2818].

References: [2818, 3130, 791, 3837]

[EC 2.4.2.54 created 2013, modified 2014, modified 2015]

EC 2.4.2.55

Accepted name: nicotinate D-ribonucleotide:phenol phospho-D-ribosyltransferase

Reaction: nicotinate D-ribonucleotide + phenol = nicotinate + phenyl 5-phospho-α-D-ribofuranoside

Other name(s): ArsAB

Systematic name: nicotinate D-ribonucleotide:phenol phospho-D-ribosyltransferase

Comments: The enzyme is involved in the biosynthesis of phenolic cobamides in the Gram-positive bacterium *Sporomusa ovata*. It can also transfer the phospho-D-ribosyl group to 4-methylphenol and 5,6-dimethylbenzimidazole. The related EC 2.4.2.21, nicotinate-nucleotide dimethylbenzimidazole phosphoribosyltransferase, also transfers the phospho-D-ribosyl group from nicotinate D-ribonucleotide to 5,6-dimethylbenzimidazole, but shows no activity with 4-methylphenol or phenol.

References: [501]

[EC 2.4.2.55 created 2013]

EC 2.4.2.56

Accepted name: kaempferol 3-*O*-xylosyltransferase

Reaction: UDP-α-D-xylose + kaempferol = UDP + kaempferol 3-*O*-β-D-xyloside

Other name(s): F3XT; UDP-D-xylose:flavonol 3-*O*-xylosyltransferase; flavonol 3-*O*-xylosyltransferase

Systematic name: UDP-α-D-xylose:kaempferol 3-*O*-D-xylosyltransferase

Comments: The enzyme from the plant *Euonymus alatus* also catalyses the 3-*O*-D-xylosylation of other flavonols (e.g. quercetin, isorhamnetin, rhamnetin, myricetin, fisetin) with lower activity.

References: [1458]

[EC 2.4.2.56 created 2013]

EC 2.4.2.57

Accepted name: AMP phosphorylase

Reaction: (1) AMP + phosphate = adenine + α-D-ribose 1,5-bisphosphate
(2) CMP + phosphate = cytosine + α-D-ribose 1,5-bisphosphate
(3) UMP + phosphate = uracil + α-D-ribose 1,5-bisphosphate

Other name(s): AMPpase; nucleoside monophosphate phosphorylase; *deoA* (gene name)

Systematic name: AMP:phosphate α-D-ribosyl 5′-phosphate-transferase

Comments: The enzyme from archaea is involved in AMP metabolism and CO_2 fixation through type III RubisCO enzymes. The activity with CMP and UMP requires activation by cAMP [98].

References: [3034, 98, 2474]

[EC 2.4.2.57 created 2014]

EC 2.4.2.58

Accepted name: hydroxyproline *O*-arabinosyltransferase

Reaction: UDP-β-L-arabinofuranose + [protein]-*trans*-4-hydroxy-L-proline = UDP + [protein]-*trans*-4-(β-L-arabinofuranosyl)oxy-L-proline

Other name(s): HPAT

Systematic name: UDP-β-L-arabinofuranose:[protein]-*trans*-4-hydroxy-L-proline L-arabinofuranosyl transferase (configuration-retaining)

Comments: The enzyme, found in plants and mosses, catalyses the *O*-arabinosylation of hydroxyprolines in hydroxyproline-rich glycoproteins. The enzyme acts on the first hydroxyproline in the motif Val-hydroxyPro-hydroxyPro-Ser.

References: [2518]

[EC 2.4.2.58 created 2016]

EC 2.4.2.59

Accepted name: sulfide-dependent adenosine diphosphate thiazole synthase

Reaction: NAD^+ + glycine + sulfide = nicotinamide + ADP-5-ethyl-4-methylthiazole-2-carboxylate + **3** H_2O

Other name(s): Thi4 (ambiguous)

Systematic name: NAD^+:glycine ADP-D-ribosyltransferase (sulfide-adding)

Comments: This iron dependent enzyme, found in archaea, is involved in the biosynthesis of thiamine phosphate. The homologous enzyme from plants and fungi (EC 2.4.2.60, cysteine-dependent adenosine diphosphate thiazole synthase) uses an intrinsic cysteine as sulfur donor and, unlike the archaeal enzyme, is a single turn-over enzyme.

References: [4050, 857]

[EC 2.4.2.59 created 2018]

EC 2.4.2.60

Accepted name: cysteine-dependent adenosine diphosphate thiazole synthase

Reaction: NAD^+ + glycine + [ADP-thiazole synthase]-L-cysteine = nicotinamide + ADP-5-ethyl-4-methylthiazole-2-carboxylate + [ADP-thiazole synthase]-dehydroalanine + **3** H_2O

Other name(s): THI4 (gene name) (ambiguous); THI1 (gene name); ADP-thiazole synthase

Systematic name: NAD^+:glycine ADP-D-ribosyltransferase (dehydroalanine-producing)

Comments: This iron dependent enzyme, found in fungi and plants, is involved in the thiamine phosphate biosynthesis pathway. It is a single turn-over enzyme since the cysteine residue is not regenerated *in vivo* [4050]. The homologous enzyme in archaea (EC 2.4.2.59, sulfide-dependent adenosine diphosphate thiazole synthase) uses sulfide as sulfur donor.

References: [1084, 511, 4050]

[EC 2.4.2.60 created 2018]

EC 2.4.2.61

Accepted name: α-dystroglycan β1,4-xylosyltransferase

Reaction: UDP-α-D-xylose + 3-*O*-[Rib-ol-*P*-Rib-ol-*P*-3-β-D-GalNAc-(1→3)-β-D-GlcNAc-(1→4)-*O*-6-*P*-α-D-Man]-Ser/Thr-[protein] = UDP + 3-*O*-[β-D-Xyl-(1→4)-Rib-ol-*P*-Rib-ol-*P*-3-β-D-GalNAc-(1→3)-β-D-GlcNAc-(1→4)-*O*-6-*P*-α-D-Man]-Ser/Thr-[protein]

Other name(s): TMEM5 (gene name)

Systematic name: UDP-α-D-xylose:3-*O*-[Rib-ol-*P*-Rib-ol-*P*-3-β-D-GalNAc-(1→3)-β-D-GlcNAc-(1→4)-*O*-6-*P*-α-D-Man]-Ser/Thr-[protein] xylosyltransferase

Comments: This eukaryotic enzyme catalyses a step in the biosynthesis of the glycan moiety of the membrane protein α-dystroglycan. It is specific for the second ribitol 5-phosphate in the nascent glycan chain as acceptor.

References: [3706, 2116]

[EC 2.4.2.61 created 2018]

EC 2.4.99 Transferring other glycosyl groups

EC 2.4.99.1

Accepted name: β-galactoside α-(2,6)-sialyltransferase

Reaction: CMP-*N*-acetyl-β-neuraminate + β-D-galactosyl-R = CMP + *N*-acetyl-α-neuraminyl-(2→6)-β-D-galactosyl-R

Other name(s): ST6Gal-I; CMP-*N*-acetylneuraminate:β-D-galactosyl-1,4-*N*-acetyl-β-D-glucosamine α-2,6-*N*-acetylneuraminyltransferase; lactosylceramide α-2,6-*N*-sialyltransferase; CMP-*N*-acetylneuraminate:β-D-galactosyl-(1→4)-*N*-acetyl-β-D-glucosamine α-(2→6)-*N*-acetylneuraminyltransferase; β-galactoside α-2,6-sialyltransferase

Systematic name: CMP-*N*-acetyl-β-neuraminate:β-D-galactoside α-(2→6)-*N*-acetylneuraminyltransferase (configuration-inverting)

Comments: The enzyme acts on the terminal non-reducing β-D-galactosyl residue of the oligosaccharide moiety of glycoproteins and glycolipids.

References: [3302, 1319, 207, 2642, 3058, 42]

[EC 2.4.99.1 created 1972, modified 1976, modified 1986, modified 2016 (EC 2.4.99.11 created 1992, incorporated 2016), modified 2017]

EC 2.4.99.2

Accepted name: β-D-galactosyl-(1→3)-*N*-acetyl-β-D-galactosaminide α-2,3-sialyltransferase

Reaction: CMP-*N*-acetyl-β-neuraminate + a β-D-galactosyl-(1→3)-*N*-acetyl-β-D-galactosaminyl-R = CMP + an *N*-acetyl-α-neuraminyl-(2→3)-β-D-galactosyl-(1→3)-*N*-acetyl-β-D-galactosaminyl-R

Other name(s): CMP-*N*-acetylneuraminate:D-galactosyl-*N*-acetyl-D-galactosaminyl-(*N*-acetylneuraminyl)-D-galactosyl-D-glucosyl-(1↔1)-ceramide *N*-acetylneuraminyltransferase (ambiguous); monosialoganglioside sialyltransferase; CMP-*N*-acetylneuraminate:a β-D-galactosyl-(1→3)-*N*-acetyl-β-D-galactosaminyl-(1→4)-[α-*N*-acetylneuraminyl-(2→3)]-β-D-galactosyl-(1→4)-β-D-glucosyl-(1↔1)-ceramide *N*-acetyl-β-neuraminyltransferase

Systematic name: CMP-*N*-acetyl-β-neuraminate:a β-D-galactosyl-(1→3)-*N*-acetyl-β-D-galactosaminyl-R α-(2→3)-*N*-acetylneuraminyltransferase (configuration-inverting)

Comments: The enzyme recognizes the sequence β-D-galactosyl-(1→3)-*N*-acetyl-D-galactosaminyl (known as type 1 histo-blood group precursor disaccharide) in non-reducing termini of glycan moieties in glycoproteins and glycolipids [2836]. When acting on ganglioside GM1a, it forms ganglioside GD1a [3985].

References: [2836, 3985]

[EC 2.4.99.2 created 1976, modified 1986, modified 2017]

EC 2.4.99.3

Accepted name: α-*N*-acetylgalactosaminide α-2,6-sialyltransferase

Reaction: CMP-*N*-acetylneuraminate + glycano-(1→3)-(*N*-acetyl-α-D-galactosaminyl)-glycoprotein = CMP + glycano-[(2→6)-α-*N*-acetylneuraminyl]-(*N*-acetyl-D-galactosaminyl)-glycoprotein

Systematic name: CMP-*N*-acetylneuraminate:glycano-1,3-(*N*-acetyl-α-D-galactosaminyl)-glycoprotein α-2,6-*N*-acetylneuraminyltransferase

Comments: α-*N*-Acetylgalactosamine linked to threonine or serine is also an acceptor, when substituted at the 3-position.

References: [2987]

[EC 2.4.99.3 created 1984, modified 1986]

EC 2.4.99.4

Accepted name: β-galactoside α-2,3-sialyltransferase

Reaction: CMP-*N*-acetylneuraminate + β-D-galactosyl-(1→3)-*N*-acetyl-α-D-galactosaminyl-R = CMP + α-*N*-acetylneuraminyl-(2→3)-β-D-galactosyl-(1→3)-*N*-acetyl-α-D-galactosaminyl-R

Other name(s): CMP-*N*-acetylneuraminate:β-D-galactoside α-2,3-*N*-acetylneuraminyl-transferase

Systematic name: CMP-*N*-acetylneuraminate:β-D-galactoside α-(2→3)-*N*-acetylneuraminyl-transferase

Comments: The acceptor is Galβ1,3GalNAc-R, where R is H, a threonine or serine residue in a glycoprotein, or a glycolipid. Lactose can also act as acceptor. May be identical with EC 2.4.99.2 monosialoganglioside sialyltransferase.

References: [2836, 2988]

[EC 2.4.99.4 created 1984, modified 1986]

EC 2.4.99.5

Accepted name: galactosyldiacylglycerol α-2,3-sialyltransferase

Reaction: CMP-*N*-acetyl-β-neuraminate + 1,2-diacyl-3-β-D-galactosyl-*sn*-glycerol = CMP + 1,2-diacyl-3-[3-(*N*-acetyl-α-D-neuraminyl)-β-D-galactosyl]-*sn*-glycerol

Systematic name: CMP-*N*-acetyl-β-neuraminate:1,2-diacyl-3-β-D-galactosyl-*sn*-glycerol *N*-acetylneuraminyltransferase

Comments: The β-D-galactosyl residue of the oligosaccharide of glycoproteins may also act as acceptor.

References: [2700, 3807, 3808]

[EC 2.4.99.5 created 1984, modified 1986]

EC 2.4.99.6

Accepted name: *N*-acetyllactosaminide α-2,3-sialyltransferase

Reaction: CMP-*N*-acetyl-β-neuraminate + β-D-galactosyl-(1→4)-*N*-acetyl-β-D-glucosaminyl-R = CMP + *N*-acetyl-α-neuraminyl-(2→3)-β-D-galactosyl-(1→4)-*N*-acetyl-β-D-glucosaminyl-R

Other name(s): cytidine monophosphoacetylneuraminate-β-galactosyl(1→4)acetylglucosaminide α2→3-sialyltransferase; α2→3 sialyltransferase (ambiguous); SiaT (ambiguous); CMP-*N*-acetylneuraminate:β-D-galactosyl-1,4-*N*-acetyl-D-glucosaminyl-glycoprotein α-2,3-*N*-acetylneuraminyltransferase; neolactotetraosylceramide α-2,3-sialyltransferase; CMP-*N*-acetylneuraminate:β-D-galactosyl-(1→4)-*N*-acetyl-D-glucosaminyl-glycoprotein α-(2→3)-*N*-acetylneuraminyltransferase

Systematic name: CMP-*N*-acetyl-β-neuraminate:β-D-galactosyl-(1→4)-*N*-acetyl-β-D-glucosaminyl-R (2→3)-*N*-acetyl-α-neuraminyltransferase (configuration-inverting)

Comments: The enzyme recognizes the sequence β-D-galactosyl-(1→4)-*N*-acetyl-D-glucosaminyl (known as type 2 histo-blood group precursor disaccharide) in non-reducing termini of glycan moieties in glycoproteins and glycolipids. The enzyme from chicken brain was shown to act on neolactotetraosylceramide, producing ganglioside LM1 [222].

References: [707, 222]

[EC 2.4.99.6 created 1984, modified 1986 (EC 2.4.99.10 created 1986, incorporated 2017)]

EC 2.4.99.7

Accepted name: α-*N*-acetylneuraminyl-2,3-β-galactosyl-1,3-*N*-acetylgalactosaminide 6-α-sialyltransferase

Reaction: CMP-*N*-acetylneuraminate + *N*-acetyl-α-neuraminyl-(2→3)-β-D-galactosyl-(1→3)-*N*-acetyl-D-galactosaminyl-R = CMP + *N*-acetyl-α-neuraminyl-(2→3)-β-D-galactosyl-(1→3)-[*N*-acetyl-α-neuraminyl-(2→6)]-*N*-acetyl-D-galactosaminyl-R

Other name(s): sialyltransferase; cytidine monophosphoacetylneuraminate-(α-*N*-acetylneuraminyl-2,3-β-galactosyl-1,3)-*N*-acetylgalactosaminide-α-2,6-sialyltransferase; α-*N*-acetylneuraminyl-2,3-β-galactosyl-1,3-*N*-acetyl-galactosaminide α-2,6-sialyltransferase; SIAT7; ST6GALNAC; (α-*N*-acetylneuraminyl-2,3-β-galactosyl-1,3)-*N*-acetyl-galactosaminide 6-α-sialyltransferase; CMP-*N*-acetylneuraminate:(α-*N*-acetylneuraminyl-2,3-β-D-galactosyl-1,3)-*N*-acetyl-D-galactosaminide α-2,6-*N*-acetylneuraminyltransferase

Systematic name: CMP-*N*-acetylneuraminate:*N*-acetyl-α-neuraminyl-(2→3)-β-D-galactosyl-(1→3)- *N*-acetyl-D-galactosaminide galactosamine-6-α-*N*-acetylneuraminyltransferase

Comments: Attaches *N*-acetylneuraminic acid in α-2,6-linkage to *N*-acetyl-galactosamine only when present in the structure of α-*N*-acetyl-neuraminyl-(2→3)-β-galactosyl-(1→3)-*N*-acetylgalactosaminyl-R, where R may be protein or *p*-nitrophenol. Not identical with EC 2.4.99.3 α-*N*-acetylgalactosaminide α-2,6-sialyltransferase.

References: [282]

[EC 2.4.99.7 created 1984, modified 1986, modified 2004]

EC 2.4.99.8

Accepted name: α-*N*-acetylneuraminate α-2,8-sialyltransferase

Reaction: CMP-*N*-acetylneuraminate + α-*N*-acetylneuraminyl-(2→3)-β-D-galactosyl-R = CMP + α-*N*-acetylneuraminyl-(2→8)-α-*N*-acetylneuraminyl-(2→3)-β-D-galactosyl-R

Other name(s): cytidine monophosphoacetylneuraminate-ganglioside GM3; α-2,8-sialyltransferase; ganglioside GD3 synthase; ganglioside GD3 synthetase sialyltransferase; CMP-NeuAc:LM1(α2-8) sialyltranferase; GD3 synthase; SAT-2

Systematic name: CMP-*N*-acetylneuraminate:α-*N*-acetylneuraminyl-(2→3)-β-D-galactoside α-(2→8)-*N*-acetylneuraminyltransferase

Comments: Gangliosides act as acceptors.

References: [846, 1323, 2190, 1259]

[EC 2.4.99.8 created 1984, modified 1986]

EC 2.4.99.9

Accepted name: lactosylceramide α-2,3-sialyltransferase

Reaction: CMP-*N*-acetylneuraminate + β-D-galactosyl-(1→4)-β-D-glucosyl-(1↔1)-ceramide = CMP + α-*N*-acetylneuraminyl-(2→3)-β-D-galactosyl-(1→4)-β-D-glucosyl-(1↔1)-ceramide
Other name(s): cytidine monophosphoacetylneuraminate-lactosylceramide α2,3- sialyltransferase; CMP-acetylneuraminate-lactosylceramide-sialyltransferase; CMP-acetylneuraminic acid:lactosylceramide sialyltransferase; CMP-sialic acid:lactosylceramide-sialyltransferase; cytidine monophosphoacetylneuraminate-lactosylceramide sialyltransferase; ganglioside GM3 synthetase; GM3 synthase; GM3 synthetase; SAT 1; CMP-*N*-acetylneuraminate:lactosylceramide α-2,3-*N*-acetylneuraminyltransferase; CMP-*N*-acetylneuraminate:β-D-galactosyl-(1→4)-β-D-glucosyl(1↔1)ceramide α-(2→3)-*N*-acetylneuraminyltransferase
Systematic name: CMP-*N*-acetylneuraminate:β-D-galactosyl-(1→4)-β-D-glucosyl-(1↔1)-ceramide α-(2→3)-*N*-acetylneuraminyltransferase
Comments: Lactose cannot act as acceptor.
References: [226, 908, 1323]

[EC 2.4.99.9 created 1984, modified 1986]

[2.4.99.10 Transferred entry. neolactotetraosylceramide α-2,3-sialyltransferase. Now included in EC 2.4.99.6, N-acetyllactosaminide α-2,3-sialyltransferase]

[EC 2.4.99.10 created 1986, deleted 2017]

[2.4.99.11 Deleted entry. lactosylceramide α-2,6-N-sialyltransferase. Now included with EC 2.4.99.1, β-galactoside α-2,6-sialyltransferase]

[EC 2.4.99.11 created 1992, deleted 2016]

EC 2.4.99.12

Accepted name: lipid IV$_A$ 3-deoxy-D-*manno*-octulosonic acid transferase
Reaction: lipid IV$_A$ + CMP-β-Kdo = α-Kdo-(2→6)-lipid IV$_A$ + CMP
Other name(s): KDO transferase; *waaA* (gene name); *kdtA* (gene name); 3-deoxy-D-*manno*-oct-2-ulosonic acid transferase; 3-deoxy-*manno*-octulosonic acid transferase; lipid IV$_A$ KDO transferase
Systematic name: CMP-3-deoxy-D-*manno*-oct-2-ulosonate:lipid IV$_A$ 3-deoxy-D-*manno*-oct-2-ulosonate transferase
Comments: The bifunctional enzyme from *Escherichia coli* transfers two 3-deoxy-D-*manno*-oct-2-ulosonate residues to lipid IV$_A$ (*cf.* EC 2.4.99.13 [(Kdo)-lipid IV$_A$ 3-deoxy-D-*manno*-octulosonic acid transferase]) [264]. The monofunctional enzymes from *Aquifex aeolicus* and *Haemophilus influenzae* catalyse the transfer of a single 3-deoxy-D-*manno*-oct-2-ulosonate residue from CMP-3-deoxy-D-*manno*-oct-2-ulosonate to lipid IV$_A$ [2107, 3833]. The enzymes from *Chlamydia* transfer three or more 3-deoxy-D-*manno*-oct-2-ulosonate residues and generate genus-specific epitopes [2021].
References: [264, 2107, 3833, 2021]

[EC 2.4.99.12 created 2010, modified 2011]

EC 2.4.99.13

Accepted name: (Kdo)-lipid IV$_A$ 3-deoxy-D-*manno*-octulosonic acid transferase
Reaction: α-Kdo-(2→6)-lipid IV$_A$ + CMP-β-Kdo = α-Kdo-(2→4)-α-Kdo-(2→6)-lipid IV$_A$ + CMP
Other name(s): Kdo transferase; *waaA* (gene name); *kdtA* (gene name); 3-deoxy-D-*manno*-oct-2-ulosonic acid transferase; 3-deoxy-*manno*-octulosonic acid transferase; (KDO)-lipid IV$_A$ 3-deoxy-D-*manno*-octulosonic acid transferase
Systematic name: CMP-3-deoxy-D-*manno*-oct-2-ulosonate:(Kdo)-lipid IV$_A$ 3-deoxy-D-*manno*-oct-2-ulosonate transferase
Comments: The bifunctional enzyme from *Escherichia coli* transfers two 3-deoxy-D-*manno*-oct-2-ulosonate residues to lipid IV$_A$ (*cf.* EC 2.4.99.12 [lipid IV$_A$ 3-deoxy-D-*manno*-octulosonic acid transferase]) [264]. The enzymes from *Chlamydia* transfer three or more 3-deoxy-D-*manno*-oct-2-ulosonate residues and generate genus-specific epitopes [].
References: [264, 2021]

[EC 2.4.99.13 created 2010, modified 2011]

EC 2.4.99.14

Accepted name: (Kdo)$_2$-lipid IV$_A$ (2-8) 3-deoxy-D-*manno*-octulosonic acid transferase

Reaction: α-Kdo-(2→4)-α-Kdo-(2→6)-lipid IV$_A$ + CMP-β-Kdo = α-Kdo-(2→8)-α-Kdo-(2→4)-α-Kdo-(2→6)-lipid IV$_A$ + CMP

Other name(s): Kdo transferase; *waaA* (gene name); *kdtA* (gene name); 3-deoxy-D-*manno*-oct-2-ulosonic acid transferase; 3-deoxy-*manno*-octulosonic acid transferase; (KDO)$_2$-lipid IV$_A$ (2-8) 3-deoxy-D-*manno*-octulosonic acid transferase

Systematic name: CMP-3-deoxy-D-*manno*-oct-2-ulosonate:(Kdo)$_2$-lipid IV$_A$ 3-deoxy-D-*manno*-oct-2-ulosonate transferase [(2→8) glycosidic bond-forming]

Comments: The enzymes from *Chlamydia* transfer three or more 3-deoxy-D-*manno*-oct-2-ulosonate residues and generate genus-specific epitopes.

References: [2021, 2106, 263]

[EC 2.4.99.14 created 2010, modified 2011]

EC 2.4.99.15

Accepted name: (Kdo)$_3$-lipid IV$_A$ (2-4) 3-deoxy-D-*manno*-octulosonic acid transferase

Reaction: α-Kdo-(2→8)-α-Kdo-(2→4)-α-Kdo-(2→6)-lipid IV$_A$ + CMP-β-Kdo = α-Kdo-(2→8)-[α-Kdo-(2→4)]-α-Kdo-(2→4)-α-Kdo-(2→6)-lipid IV$_A$ + CMP

Other name(s): Kdo transferase; *waaA* (gene name); *kdtA* (gene name); 3-deoxy-D-*manno*-oct-2-ulosonic acid transferase; 3-deoxy-*manno*-octulosonic acid transferase; (KDO)$_3$-lipid IV$_A$ (2-4) 3-deoxy-D-*manno*-octulosonic acid transferase

Systematic name: CMP-3-deoxy-D-*manno*-oct-2-ulosonate:(Kdo)$_3$-lipid IV$_A$ 3-deoxy-D-*manno*-oct-2-ulosonate transferase [(2→4) glycosidic bond-forming]

Comments: The enzyme from *Chlamydia psittaci* transfers four Kdo residues to lipid A, forming a branched tetrasaccharide with the structure α-Kdo-(2,8)-[α-Kdo-(2,4)]-α-Kdo-(2,4)-α-Kdo (*cf.* EC 2.4.99.12 [lipid IV$_A$ 3-deoxy-D-*manno*-octulosonic acid transferase], EC 2.4.99.13 [(Kdo)-lipid IV$_A$ 3-deoxy-D-*manno*-octulosonic acid transferase], and EC 2.4.99.14 [(Kdo)$_2$-lipid IV$_A$ (2-8) 3-deoxy-D-*manno*-octulosonic acid transferase]).

References: [372, 1360]

[EC 2.4.99.15 created 2010, modified 2011]

EC 2.4.99.16

Accepted name: starch synthase (maltosyl-transferring)

Reaction: α-maltose 1-phosphate + [(1→4)-α-D-glucosyl]$_n$ = phosphate + [(1→4)-α-D-glucosyl]$_{n+2}$

Other name(s): α1,4-glucan:maltose-1-*P* maltosyltransferase; GMPMT

Systematic name: α-maltose 1-phosphate:(1→4)-α-D-glucan 4-α-D-maltosyltransferase

Comments: The enzyme from the bacterium *Mycobacterium smegmatis* is specific for maltose. It has no activity with α-D-glucose.

References: [826, 3413]

[EC 2.4.99.16 created 2012]

EC 2.4.99.17

Accepted name: *S*-adenosylmethionine:tRNA ribosyltransferase-isomerase

Reaction: *S*-adenosyl-L-methionine + 7-aminomethyl-7-carbaguanosine^{34} in tRNA = L-methionine + adenine + epoxyqueuosine^{34} in tRNA

Other name(s): QueA enzyme; queuosine biosynthesis protein QueA

Systematic name: *S*-adenosyl-L-methionine:7-aminomethyl-7-deazaguanosine ribosyltransferase (ribosyl isomerizing; L-methionine, adenine releasing)

Comments: The reaction is a combined transfer and isomerization of the ribose moiety of *S*-adenosyl-L-methionine to the modified guanosine base in the wobble position in tRNAs specific for Tyr, His, Asp or Asn. It is part of the queuosine biosynthesis pathway.

References: [3249, 3250, 1691, 1857, 2160, 1142]

[EC 2.4.99.17 created 2012]

EC 2.4.99.18

Accepted name: dolichyl-diphosphooligosaccharide—protein glycotransferase

Reaction: dolichyl diphosphooligosaccharide + [protein]-L-asparagine = dolichyl diphosphate + a glycoprotein with the oligosaccharide chain attached by *N*-β-D-glycosyl linkage to a protein L-asparagine

Other name(s): dolichyldiphosphooligosaccharide-protein glycosyltransferase; asparagine *N*-glycosyltransferase; dolichyldiphosphooligosaccharide-protein oligosaccharyltransferase; dolichylpyrophosphodiacetylchitobiose-protein glycosyltransferase; oligomannosyltransferase; oligosaccharide transferase; dolichyldiphosphoryloligosaccharide-protein oligosaccharyltransferase; dolichyl-diphosphooligosaccharide:protein-L-asparagine oligopolysaccharidotransferase; STT3

Systematic name: dolichyl-diphosphooligosaccharide:protein-L-asparagine *N*-β-D-oligopolysaccharidotransferase

Comments: Occurs in eukaryotes that form a glycoprotein by the transfer of a glucosyl-mannosyl-glucosamine polysaccharide to the side-chain of an L-asparagine residue in the sequence -Asn-Xaa-Ser- or -Asn-Xaa-Thr- (Xaa not Pro) in nascent polypeptide chains. The basic oligosaccharide is the tetradecasaccharide $Glc_3Man_9GlcNAc_2$ (for diagram click here). However, smaller oligosaccharides derived from it and oligosaccharides with additional monosaccharide units attached may be involved. See ref [3287] for a review of *N*-glycoproteins in eukaryotes. $Man_3GlcNAc_2$ seems to be common for all of the oligosaccharides involved with the terminal *N*-acetylglucosamine linked to the protein L-asparagine. Occurs on the cytosolic face of the endoplasmic reticulum. The dolichol involved normally has 14-21 isoprenoid units with two *trans* double-bonds at the ω end, and the rest of the double-bonds in *cis* form.

References: [672, 3287]

[EC 2.4.99.18 created 1984 as EC 2.4.1.119, transferred 2012 to EC 2.4.99.18]

EC 2.4.99.19

Accepted name: undecaprenyl-diphosphooligosaccharide—protein glycotransferase

Reaction: *tritrans*,*heptacis*-undecaprenyl diphosphooligosaccharide + [protein]-L-asparagine = *tritrans*,*heptacis*-undecaprenyl diphosphate + a glycoprotein with the oligosaccharide chain attached by *N*-β-D-glycosyl linkage to protein L-asparagine

Other name(s): PglB

Systematic name: *tritrans*,*heptacis*-undecaprenyl-diphosphooligosaccharide:protein-L-asparagine *N*-β-D-oligosaccharidotransferase

Comments: A bacterial enzyme that has been isolated from *Campylobacter jejuni* [2102] and *Campylobacter lari* [2016]. It forms a glycoprotein by the transfer of a glucosyl-*N*-acetylgalactosaminyl-*N*,*N*′-diacetylbacillosamine ($GalNAc_2(Glc)GalNAc_3diNAcBac$) polysaccharide and related oligosaccharides to the side-chain of an L-asparagine residue in the sequence -Asp/Glu-Xaa-Asn-Xaa’-Ser/Thr- (Xaa and Xaa’ not Pro) in nascent polypeptide chains. Requires Mn^{2+} or Mg^{2+}. Occurs on the external face of the plasma membrane. The polyprenol involved is normally *tritrans*,*heptacis*-undecaprenol but a decaprenol is used by some species.

References: [2102, 2016]

[EC 2.4.99.19 created 2012]

EC 2.4.99.20

Accepted name: 2′-phospho-ADP-ribosyl cyclase/2′-phospho-cyclic-ADP-ribose transferase

Reaction: $NADP^+$ + nicotinate = nicotinate-adenine dinucleotide phosphate + nicotinamide (overall reaction)
(1a) $NADP^+$ = 2′-phospho-cyclic ADP-ribose + nicotinamide

(1b) 2′-phospho-cyclic ADP-ribose + nicotinate = nicotinate-adenine dinucleotide phosphate
Other name(s): diphosphopyridine nucleosidase (ambiguous); CD38 (gene name); BST1 (gene name)
Systematic name: $NADP^+$:nicotinate ADP-ribosyltransferase
Comments: This multiunctional enzyme catalyses both the removal of nicotinamide from $NADP^+$, forming 2′-phospho-cyclic ADP-ribose, and the addition of nicotinate to the cyclic product, forming $NAADP^+$, a calcium messenger that can mobilize intracellular Ca^{2+} stores and activate Ca^{2+} influx to regulate a wide range of physiological processes. In addition, the enzyme also catalyses EC 3.2.2.6, ADP-ribosyl cyclase/cyclic ADP-ribose hydrolase.
References: [548, 2311]

[EC 2.4.99.20 created 2014]

EC 2.4.99.21
Accepted name: dolichyl-phosphooligosaccharide-protein glycotransferase
Reaction: an archaeal dolichyl phosphooligosaccharide + [protein]-L-asparagine = an archaeal dolichyl phosphate + a glycoprotein with the oligosaccharide chain attached by *N*-β-D-glycosyl linkage to a protein L-asparagine
Other name(s): AglB; archaeal oligosaccharyl transferase; dolichyl-monophosphooligosaccharide-protein glycotransferase
Systematic name: dolichyl-phosphooligosaccharide:protein-L-asparagine *N*-β-D-oligosaccharidotransferase
Comments: The enzyme, characterized from the archaea *Methanococcus voltae* and *Haloferax volcanii*, transfers a glycan component from dolichyl phosphooligosaccharide to external proteins. It is different from EC 2.4.99.18, dolichyl-diphosphooligosaccharide-protein glycotransferase, which uses dolichyl diphosphate as carrier compound in bacteria and eukaryotes. The enzyme participates in the *N*-glycosylation of proteins in some archaea. It requires Mn^{2+}. Dolichol used by archaea is different from that used by eukaryotes. It is much shorter (C_{55}-C_{60}), it is α,ω-saturated and it may have additional unsaturated positions in the chain.
References: [494, 1863, 588]

[EC 2.4.99.21 created 2015]

EC 2.5 Transferring alkyl or aryl groups, other than methyl groups

This subclass contains only one sub-subclass at present. It is somewhat heterogeneous, containing enzymes that transfer alkyl or related groups that are either substituted or unsubstituted.

EC 2.5.1 Transferring alkyl or aryl groups, other than methyl groups (only sub-subclass identified to date)

EC 2.5.1.1
Accepted name: dimethylallyl*trans*transferase
Reaction: dimethylallyl diphosphate + isopentenyl diphosphate = diphosphate + geranyl diphosphate
Other name(s): geranyl-diphosphate synthase; prenyltransferase; dimethylallyltransferase; DMAPP:IPP-dimethylallyltransferase; (2*E*,6*E*)-farnesyl diphosphate synthetase; diprenyltransferase; geranyl pyrophosphate synthase; geranyl pyrophosphate synthetase; *trans*-farnesyl pyrophosphate synthetase
Systematic name: dimethylallyl-diphosphate:isopentenyl-diphosphate dimethylallyl*trans*transferase
Comments: This enzyme will not accept larger prenyl diphosphates as efficient donors.
References: [182, 2994]

[EC 2.5.1.1 created 1961]

EC 2.5.1.2

Accepted name: thiamine pyridinylase

Reaction: thiamine + pyridine = 1-[(4-amino-2-methylpyrimidin-5-yl)methyl]pyridinium + 4-methyl-5-(2-hydroxyethyl)thiazole

Other name(s): pyrimidine transferase; thiaminase I; thiamin hydrolase; thiamin pyridinolase; thiaminase; thiamine pyridinolase; thiamin pyridinylase; thiamin:base 2-methyl-4-aminopyrimidine-5-methenyltransferase

Systematic name: thiamine:base 2-methyl-4-aminopyrimidine-5-methenyltransferase

Comments: Various bases and thiol compounds can act instead of pyridine.

References: [987, 1644, 3878]

[EC 2.5.1.2 created 1961, modified 1976, modified 2001]

EC 2.5.1.3

Accepted name: thiamine phosphate synthase

Reaction: (1) 4-amino-2-methyl-5-(diphosphooxymethyl)pyrimidine + 2-[(2*R*,5*Z*)-2-carboxy-4-methylthiazol-5(2*H*)-ylidene]ethyl phosphate = diphosphate + thiamine phosphate + CO_2
(2) 4-amino-2-methyl-5-(diphosphooxymethyl)pyrimidine + 2-(2-carboxy-4-methylthiazol-5-yl)ethyl phosphate = diphosphate + thiamine phosphate + CO_2
(3) 4-amino-2-methyl-5-(diphosphooxymethyl)pyrimidine + 4-methyl-5-(2-phosphooxyethyl)thiazole = diphosphate + thiamine phosphate

Other name(s): thiamine phosphate pyrophosphorylase; thiamine monophosphate pyrophosphorylase; TMP-PPase; thiamine-phosphate diphosphorylase; *thiE* (gene name); TH1 (gene name); THI6 (gene name); 2-methyl-4-amino-5-hydroxymethylpyrimidine-diphosphate:4-methyl-5-(2-phosphoethyl)thiazole 2-methyl-4-aminopyrimidine-5-methenyltransferase; 4-amino-2-methyl-5-diphosphomethylpyrimidine:2-[(2*R*,5*Z*)-2-carboxy-4-methylthiazol-5(2*H*)-ylidene]ethyl phosphate 4-amino-2-methylpyrimidine-5-methenyltransferase (decarboxylating)

Systematic name: 4-amino-2-methyl-5-(diphosphooxymethyl)pyrimidine:2-[(2*R*,5*Z*)-2-carboxy-4-methylthiazol-5(2*H*)-ylidene]ethyl phosphate 4-amino-2-methylpyrimidine-5-methenyltransferase (decarboxylating)

Comments: The enzyme catalyses the penultimate reaction in thiamine *de novo* biosynthesis, condensing the pyrimidine and thiazole components. The enzyme is thought to accept the product of EC 2.8.1.10, thiazole synthase, as its substrate. However, it has been shown that in some bacteria, such as *Bacillus subtilis*, an additional enzyme, thiazole tautomerase (EC 5.3.99.10) converts that compound into its tautomer 2-(2-carboxy-4-methylthiazol-5-yl)ethyl phosphate, and that it is the latter that serves as the substrate for the synthase. In addition to this activity, the enzyme participates in a salvage pathway, acting on 4-methyl-5-(2-phosphooxyethyl)thiazole, which is produced from thiamine degradation products. In yeast this activity is found in a bifunctional enzyme (THI6) and in the plant *Arabidopsis thaliana* the activity is part of a trifunctional enzyme (TH1).

References: [462, 1886, 1617, 152, 549, 30]

[EC 2.5.1.3 created 1965, modified 2015]

EC 2.5.1.4

Accepted name: adenosylmethionine cyclotransferase

Reaction: *S*-adenosyl-L-methionine = *S*-methyl-5′-thioadenosine + 2-aminobutan-4-olide

Other name(s): adenosylmethioninase

Systematic name: *S*-adenosyl-L-methionine alkyltransferase (cyclizing)

References: [2336, 2337]

[EC 2.5.1.4 created 1965]

EC 2.5.1.5

Accepted name: galactose-6-sulfurylase

Reaction: Eliminates sulfate from the D-galactose 6-sulfate residues of porphyran, producing 3,6-anhydrogalactose residues

Other name(s): porphyran sulfatase; galactose-6-sulfatase; galactose 6-sulfatase

Systematic name: D-galactose-6-sulfate:alkyltransferase (cyclizing)

References: [2844, 2845]

[EC 2.5.1.5 created 1965]

EC 2.5.1.6

Accepted name: methionine adenosyltransferase

Reaction: ATP + L-methionine + H_2O = phosphate + diphosphate + *S*-adenosyl-L-methionine

Other name(s): adenosylmethionine synthetase; ATP-methionine adenosyltransferase; methionine *S*-adenosyltransferase; methionine-activating enzyme; *S*-adenosyl-L-methionine synthetase; *S*-adenosylmethionine synthase; *S*-adenosylmethionine synthetase; AdoMet synthetase

Systematic name: ATP:L-methionine *S*-adenosyltransferase

References: [470, 471, 2338]

[EC 2.5.1.6 created 1961 as EC 2.4.2.13, transferred 1965 to EC 2.5.1.6]

EC 2.5.1.7

Accepted name: UDP-*N*-acetylglucosamine 1-carboxyvinyltransferase

Reaction: phospho*enol*pyruvate + UDP-*N*-acetyl-α-D-glucosamine = phosphate + UDP-*N*-acetyl-3-*O*-(1-carboxyvinyl)-α-D-glucosamine

Other name(s): MurA transferase; UDP-*N*-acetylglucosamine 1-carboxyvinyl-transferase; UDP-*N*-acetylglucosamine enoylpyruvyltransferase; enoylpyruvate transferase; phospho*enol*pyruvate-UDP-acetylglucosamine-3-enolpyruvyltransferase; phospho*enol*pyruvate:UDP-2-acetamido-2-deoxy-D-glucose 2-enoyl-1-carboxyethyltransferase; phospho*enol*pyruvate:uridine diphosphate *N*-acetylglucosamine enolpyruvyltransferase; phospho*enol*pyruvate:uridine-5′-diphospho-*N*-acetyl-2-amino-2-deoxyglucose 3-enolpyruvyltransferase; phosphopyruvate-uridine diphosphoacetylglucosamine pyruvatetransferase; pyruvate-UDP-acetylglucosamine transferase; pyruvate-uridine diphospho-*N*-acetylglucosamine transferase; pyruvate-uridine diphospho-*N*-acetyl-glucosamine transferase; pyruvic-uridine diphospho-*N*-acetylglucosaminyltransferase; phospho*enol*pyruvate:UDP-*N*-acetyl-D-glucosamine 1-carboxyvinyltransferase

Systematic name: phospho*enol*pyruvate:UDP-*N*-acetyl-α-D-glucosamine 1-carboxyvinyltransferase

References: [1176, 4028, 3640]

[EC 2.5.1.7 created 1972, modified 1983, modified 2002]

[2.5.1.8 Transferred entry. tRNA isopentenyltransferase. As it is now known that the substrate is dimethylallyl diphosphate, the enzyme has been transferred to EC 2.5.1.75, tRNA dimethylallyltransferase]

[EC 2.5.1.8 created 1972, deleted 2009]

EC 2.5.1.9

Accepted name: riboflavin synthase

Reaction: **2** 6,7-dimethyl-8-(1-D-ribityl)lumazine = riboflavin + 4-(1-D-ribitylamino)-5-amino-2,6-dihydroxypyrimidine

Other name(s): heavy riboflavin synthase; light riboflavin synthase; riboflavin synthetase; riboflavine synthase; riboflavine synthetase

Systematic name: 6,7-dimethyl-8-(1-D-ribityl)lumazine:6,7-dimethyl-8-(1-D-ribityl)lumazine 2,3-butanediyltransferase

Comments: A flavoprotein (riboflavin).

References: [2724, 2725, 3709]

[EC 2.5.1.9 created 1972]

EC 2.5.1.10

Accepted name: (2*E*,6*E*)-farnesyl diphosphate synthase
Reaction: geranyl diphosphate + isopentenyl diphosphate = diphosphate + (2*E*,6*E*)-farnesyl diphosphate
Other name(s): farnesyl-diphosphate synthase; geranyl transferase I; prenyltransferase; farnesyl pyrophosphate synthetase; farnesylpyrophosphate synthetase; geranyl*trans*transferase
Systematic name: geranyl-diphosphate:isopentenyl-diphosphate geranyl*trans*transferase
Comments: Some forms of this enzyme will also use dimethylallyl diphosphate as a substrate. The enzyme will not accept larger prenyl diphosphates as efficient donors.
References: [2078, 2526, 2840, 3437, 3438]

[EC 2.5.1.10 created 1972, modified 2010]

[2.5.1.11 Transferred entry. trans-octaprenyltranstransferase. Now covered by EC 2.5.1.84 (all-trans-nonaprenyl-diphosphate synthase [geranyl-diphosphate specific]) and EC 2.5.1.85 (all-trans-nonaprenyl diphosphate synthase [geranylgeranyl-diphosphate specific])]

[EC 2.5.1.11 created 1972, deleted 2010]

[2.5.1.12 Deleted entry. glutathione S-alkyltransferase. Now included with EC 2.5.1.18 glutathione transferase]

[EC 2.5.1.12 created 1972, deleted 1976]

[2.5.1.13 Deleted entry. glutathione S-aryltransferase. Now included with EC 2.5.1.18 glutathione transferase]

[EC 2.5.1.13 created 1972, deleted 1976]

[2.5.1.14 Deleted entry. glutathione S-aralkyltransferase. Now included with EC 2.5.1.18 glutathione transferase]

[EC 2.5.1.14 created 1972, deleted 1976]

EC 2.5.1.15

Accepted name: dihydropteroate synthase
Reaction: (7,8-dihydropterin-6-yl)methyl diphosphate + 4-aminobenzoate = diphosphate + 7,8-dihydropteroate
Other name(s): dihydropteroate pyrophosphorylase; DHPS; 7,8-dihydropteroate synthase; 7,8-dihydropteroate synthetase; 7,8-dihydropteroic acid synthetase; dihydropteroate synthetase; dihydropteroic synthetase; 2-amino-4-hydroxy-6-hydroxymethyl-7,8-dihydropteridine-diphosphate:4-aminobenzoate 2-amino-4-hydroxydihydropteridine-6-methenyltransferase; (2-amino-4-hydroxy-7,8-dihydropteridin-6-yl)methyl-diphosphate:4-aminobenzoate 2-amino-4-hydroxydihydropteridine-6-methenyltransferase
Systematic name: (7,8-dihydropterin-6-yl)methyl diphosphate:4-aminobenzoate 2-amino-4-hydroxy-7,8-dihydropteridine-6-methenyltransferase
Comments: The enzyme participates in the biosynthetic pathways for folate (in bacteria, plants and fungi) and methanopterin (in archaea). The enzyme exists in varying types of multifunctional proteins in different organisms. The enzyme from the plant *Arabidopsis thaliana* also harbors the activity of EC 2.7.6.3, 2-amino-4-hydroxy-6-hydroxymethyldihydropteridine diphosphokinase [3358], while the enzyme from yeast *Saccharomyces cerevisiae* is trifunctional with the two above mentioned activities as well as EC 4.1.2.25, dihydroneopterin aldolase [1174].
References: [2881, 3208, 1174, 3358]

[EC 2.5.1.15 created 1972, modified 2015]

EC 2.5.1.16

Accepted name: spermidine synthase
Reaction: *S*-adenosyl 3-(methylsulfanyl)propylamine + putrescine = *S*-methyl-5′-thioadenosine + spermidine
Other name(s): aminopropyltransferase; putrescine aminopropyltransferase; spermidine synthetase; SpeE; *S*-adenosylmethioninamine:putrescine 3-aminopropyltransferase; *S*-adenosyl 3-(methylthio)propylamine:putrescine 3-aminopropyltransferase
Systematic name: *S*-adenosyl 3-(methylsulfanyl)propylamine:putrescine 3-aminopropyltransferase

Comments: The enzymes from the plant *Glycine max* and from mammalia are highly specific for putrescine as the amine acceptor [2654, 3996]. The enzymes from the bacteria *Escherichia coli* and *Thermotoga maritima* prefer putrescine but are more tolerant towards other amine acceptors, such as spermidine and cadaverine [369, 1766]. *cf.* EC 2.5.1.22 (spermine synthase) and EC 2.5.1.23 (*sym*-norspermidine synthase).

References: [1212, 2654, 3423, 3425, 369, 1766, 3996]

[EC 2.5.1.16 created 1972, modified 1982, modified 2013]

EC 2.5.1.17

Accepted name: corrinoid adenosyltransferase

Reaction: (1) **2** ATP + **2** cob(II)alamin + a reduced flavoprotein = **2** triphosphate + **2** adenosylcob(III)alamin + an oxidized flavoprotein (overall reaction)
(1a) **2** cob(II)alamin + **2** [corrinoid adenosyltransferase] = **2** [corrinoid adenosyltransferase]-cob(II)alamin
(1b) a reduced flavoprotein + **2** [corrinoid adenosyltransferase]-cob(II)alamin = an oxidized flavoprotein + **2** [corrinoid adenosyltransferase]-cob(I)alamin (spontaneous)
(1c) **2** ATP + **2** [corrinoid adenosyltransferase]-cob(I)alamin = **2** triphosphate + **2** adenosylcob(III)alamin + **2** [corrinoid adenosyltransferase]
(2) **2** ATP + **2** cob(II)yrinic acid *a*,*c*-diamide + a reduced flavoprotein = **2** triphosphate + **2** adenosylcob(III)yrinic acid *a*,*c*-diamide + an oxidized flavoprotein (overall reaction)
(2a) **2** cob(II)yrinic acid *a*,*c*-diamide + **2** [corrinoid adenosyltransferase] = **2** [corrinoid adenosyltransferase]-cob(II)yrinic acid *a*,*c*-diamide
(2b) a reduced flavoprotein + **2** [corrinoid adenosyltransferase]-cob(II)yrinic acid *a*,*c*-diamide = an oxidized flavoprotein + **2** [corrinoid adenosyltransferase]-cob(I)yrinic acid *a*,*c*-diamide (spontaneous)
(2c) **2** ATP + **2** [corrinoid adenosyltransferase]-cob(I)yrinic acid *a*,*c*-diamide = **2** triphosphate + **2** adenosylcob(III)yrinic acid *a*,*c*-diamide + **2** [corrinoid adenosyltransferase]

Other name(s): MMAB (gene name); *cobA* (gene name); *cobO* (gene name); *pduO* (gene name); ATP:corrinoid adenosyltransferase; cob(I)alamin adenosyltransferase; aquacob(I)alamin adenosyltransferase; aquocob(I)alamin vitamin B_{12s} adenosyltransferase; ATP:cob(I)alamin *Co*β-adenosyltransferase; ATP:cob(I)yrinic acid-*a*,*c*-diamide *Co*β-adenosyltransferase; cob(I)yrinic acid *a*,*c*-diamide adenosyltransferase

Systematic name: ATP:cob(II)alamin *Co*β-adenosyltransferase

Comments: The corrinoid adenosylation pathway comprises three steps: (i) reduction of Co(III) within the corrinoid to Co(II) by a one-electron transfer. This can occur non-enzymically in the presence of dihydroflavin nucleotides or reduced flavoproteins [925]. (ii) Co(II) is bound by corrinoid adenosyltransferase, resulting in displacement of the lower axial ligand by an aromatic residue. The reduction potential of the 4-coordinate Co(II) intermediate is raised by 250 mV compared with the free compound, bringing it to within physiological range. This is followed by a second single-electron transfer from either free dihydroflavins or the reduced flavin cofactor of flavoproteins, resulting in reduction to Co(I) [2224]. (iii) the Co(I) conducts a nucleophilic attack on the adenosyl moiety of ATP, resulting in transfer of the deoxyadenosyl group and oxidation of the cobalt atom to Co(III) state. Three types of corrinoid adenosyltransferases, not related by sequence, have been described. In the anaerobic bacterium *Salmonella enterica* they are encoded by the *cobA* gene (a housekeeping enzyme involved in both the *de novo* biosynthesis and the salvage of adenosylcobalamin), the *pduO* gene (involved in (*S*)-propane-1,2-diol utilization), and the *eutT* gene (involved in ethanolamine utilization). Since EutT hydrolyses triphosphate to diphosphate and phosphate during catalysis, it is classified as a separate enzyme. The mammalian enzyme belongs to the PduO type. The enzyme can act on other corrinoids, such as cob(II)inamide.

References: [3689, 235, 925, 926, 3381, 2225, 2224]

[EC 2.5.1.17 created 1972, modified 2004, modified 2018]

EC 2.5.1.18

Accepted name: glutathione transferase

Reaction: RX + glutathione = HX + R-S-glutathione

Other name(s): glutathione *S*-transferase; glutathione *S*-alkyltransferase; glutathione *S*-aryltransferase; *S*-(hydroxyalkyl)glutathione lyase; glutathione *S*-aralkyltransferase; glutathione *S*-alkyl transferase; GST

Systematic name: RX:glutathione R-transferase

Comments: A group of enzymes of broad specificity. R may be an aliphatic, aromatic or heterocyclic group; X may be a sulfate, nitrile or halide group. Also catalyses the addition of aliphatic epoxides and arene oxides to glutathione, the reduction of polyol nitrate by glutathione to polyol and nitrile, certain isomerization reactions and disulfide interchange.

References: [1190, 1492, 1493, 1624, 3170]

[EC 2.5.1.18 created 1976 (EC 2.5.1.12, EC 2.5.1.13, EC 2.5.1.14 and EC 4.4.1.7 created 1972, incorporated 1976)]

EC 2.5.1.19

Accepted name: 3-phosphoshikimate 1-carboxyvinyltransferase

Reaction: phospho*enol*pyruvate + 3-phosphoshikimate = phosphate + 5-*O*-(1-carboxyvinyl)-3-phosphoshikimate

Other name(s): 5-enolpyruvylshikimate-3-phosphate synthase; 3-enolpyruvylshikimate 5-phosphate synthase; 3-enolpyruvylshikimic acid-5-phosphate synthetase; 5′-enolpyruvylshikimate-3-phosphate synthase; 5-enolpyruvyl-3-phosphoshikimate synthase; 5-enolpyruvylshikimate-3-phosphate synthetase; 5-enolpyruvylshikimate-3-phosphoric acid synthase; enolpyruvylshikimate phosphate synthase; EPSP synthase

Systematic name: phospho*enol*pyruvate:3-phosphoshikimate 5-*O*-(1-carboxyvinyl)-transferase

References: [2307]

[EC 2.5.1.19 created 1976, modified 1983, modified 1989]

EC 2.5.1.20

Accepted name: rubber *cis*-polyprenyl*cis*transferase

Reaction: *polycis*-polyprenyl diphosphate + isopentenyl diphosphate = diphosphate + a *polycis*-polyprenyl diphosphate longer by one C_5 unit

Other name(s): rubber allyltransferase; rubber transferase; isopentenyl pyrophosphate *cis*-1,4-polyisoprenyl transferase; *cis*-prenyl transferase; rubber polymerase; rubber prenyltransferase

Systematic name: *polycis*-polyprenyl-diphosphate:isopentenyl-diphosphate polyprenyl*cis*transferase

Comments: Rubber particles act as acceptor.

References: [102, 2201]

[EC 2.5.1.20 created 1976]

EC 2.5.1.21

Accepted name: squalene synthase

Reaction: **2** (2*E*,6*E*)-farnesyl diphosphate + NAD(P)H + H^+ = squalene + **2** diphosphate + NAD(P)$^+$ (overall reaction)
(1a) **2** (2*E*,6*E*)-farnesyl diphosphate = diphosphate + presqualene diphosphate
(1b) presqualene diphosphate + NAD(P)H + H^+ = squalene + diphosphate + NAD(P)$^+$

Other name(s): farnesyltransferase; presqualene-diphosphate synthase; presqualene synthase; squalene synthetase; farnesyl-diphosphate farnesyltransferase; SQS

Systematic name: (2*E*,6*E*)-farnesyl-diphosphate:(2*E*,6*E*)-farnesyl-diphosphate farnesyltransferase

Comments: This microsomal enzyme catalyses the first committed step in the biosynthesis of sterols. The enzyme from yeast requires either Mg^{2+} or Mn^{2+} for activity. In the absence of NAD(P)H, presqualene diphosphate (PSPP) is accumulated. When NAD(P)H is present, presqualene diphosphate does not dissociate from the enzyme during the synthesis of squalene from farnesyl diphosphate (FPP) [2789]. High concentrations of FPP inhibit the production of squalene but not of PSPP [2789].

References: [1832, 848, 3473, 2027, 3169, 24, 2612, 2789]

[EC 2.5.1.21 created 1976, modified 2005, modified 2012]

EC 2.5.1.22

Accepted name: spermine synthase

Reaction: *S*-adenosyl 3-(methylsulfanyl)propylamine + spermidine = *S*-methyl-5′-thioadenosine + spermine

Other name(s): spermidine aminopropyltransferase; spermine synthetase; *S*-adenosylmethioninamine:spermidine 3-aminopropyltransferase; *S*-adenosyl 3-(methylthio)propylamine:spermidine 3-aminopropyltransferase

Systematic name: *S*-adenosyl 3-(methylsulfanyl)propylamine:spermidine 3-aminopropyltransferase

Comments: The enzyme from mammalia is highly specific for spermidine [2598, 2654]. *cf.* EC 2.5.1.16 (spermidine synthase) and EC 2.5.1.23 (*sym*-norspermidine synthase).

References: [1317, 2598, 2654]

[EC 2.5.1.22 created 1982, modified 2013]

EC 2.5.1.23

Accepted name: *sym*-norspermidine synthase

Reaction: *S*-adenosyl 3-(methylsulfanyl)propylamine + propane-1,3-diamine = *S*-methyl-5′-thioadenosine + bis(3-aminopropyl)amine

Other name(s): *S*-adenosylmethioninamine:propane-1,3-diamine 3-aminopropyltransferase; *S*-adenosyl 3-(methylthio)propylamine:propane-1,3-diamine 3-aminopropyltransferase

Systematic name: *S*-adenosyl 3-(methylsulfanyl)propylamine:propane-1,3-diamine 3-aminopropyltransferase

Comments: The enzyme has been originally characterized from the protist *Euglena gracilis* [52, 3680]. The enzyme from the archaeon *Sulfolobus solfataricus* can transfer the propylamine moiety from *S*-adenosyl 3-(methylsulfanyl)propylamine to putrescine, *sym*-norspermidine and spermidine with lower efficiency [451]. *cf.* EC 2.5.1.16 (spermidine synthase) and EC 2.5.1.22 (spermine synthase).

References: [52, 3680, 451]

[EC 2.5.1.23 created 1983, modified 2013]

EC 2.5.1.24

Accepted name: discadenine synthase

Reaction: *S*-adenosyl-L-methionine + N^6-(Δ^2-isopentenyl)-adenine = *S*-methyl-5′-thioadenosine + discadenine

Other name(s): discadenine synthetase; *S*-adenosyl-L-methionine:6-*N*-(Δ^2-isopentenyl)-adenine 3-(3-amino-3-carboxypropyl)-transferase

Systematic name: *S*-adenosyl-L-methionine:N^6-(Δ^2-isopentenyl)-adenine 3-(3-amino-3-carboxypropyl)-transferase

References: [3481]

[EC 2.5.1.24 created 1984]

EC 2.5.1.25

Accepted name: tRNA-uridine aminocarboxypropyltransferase

Reaction: *S*-adenosyl-L-methionine + uridine^{47} tRNA$^{\text{Phe}}$ = *S*-methyl-5′-thioadenosine + 3-[(3*S*)-3-amino-3-carboxypropyl]-uridine^{47} in tRNA$^{\text{Phe}}$

Other name(s): *S*-adenosyl-L-methionine:tRNA-uridine 3-(3-amino-3-carboxypropyl)transferase

Systematic name: *S*-adenosyl-L-methionine:uridine^{47} in tRNA$^{\text{Phe}}$ 3-[(3*S*)-3-amino-3-carboxypropyl]transferase

Comments: The enzyme was studied in the bacterium *Escherichia coli*. The modification is found in the variable loop of the tRNA.

References: [2469]

[EC 2.5.1.25 created 1984, modified 2014]

EC 2.5.1.26

Accepted name: alkylglycerone-phosphate synthase
Reaction: 1-acyl-glycerone 3-phosphate + a long-chain alcohol = an alkyl-glycerone 3-phosphate + a long-chain acid anion
Other name(s): alkyldihydroxyacetonephosphate synthase; alkyldihydroxyacetone phosphate synthetase; alkyl DHAP synthetase; alkyl-DHAP; dihydroxyacetone-phosphate acyltransferase; DHAP-AT
Systematic name: 1-acyl-glycerone-3-phosphate:long-chain-alcohol *O*-3-phospho-2-oxopropanyltransferase
Comments: The ester-linked fatty acid of the substrate is cleaved and replaced by a long-chain alcohol in an ether linkage.
References: [401, 3913]

[EC 2.5.1.26 created 1984]

EC 2.5.1.27

Accepted name: adenylate dimethylallyltransferase
Reaction: dimethylallyl diphosphate + AMP = diphosphate + N^6-(dimethylallyl)adenosine $5'$-phosphate
Other name(s): cytokinin synthase (ambiguous); isopentenyltransferase (ambiguous); 2-isopentenyl-diphosphate:AMP Δ^2-isopentenyltransferase; adenylate isopentenyltransferase (ambiguous); IPT
Systematic name: dimethylallyl-diphosphate:AMP dimethylallyltransferase
Comments: Involved in the biosynthesis of cytokinins in plants. Some isoforms from the plant *Arabidopsis thaliana* are specific for AMP while others also have the activity of EC 2.5.1.112, adenylate dimethylallyltransferase (ADP/ATP-dependent).
References: [520, 3448, 3005]

[EC 2.5.1.27 created 1984, modified 2002, modified 2013]

EC 2.5.1.28

Accepted name: dimethylallyl*cis*transferase
Reaction: dimethylallyl diphosphate + isopentenyl diphosphate = diphosphate + neryl diphosphate
Other name(s): neryl-diphosphate synthase
Systematic name: dimethylallyl-diphosphate:isopentenyl-diphosphate dimethylallyl*cis*transferase
Comments: This enzyme will not use larger prenyl diphosphates as efficient donors.
References: [182, 301]

[EC 2.5.1.28 created 1984]

EC 2.5.1.29

Accepted name: geranylgeranyl diphosphate synthase
Reaction: (2*E*,6*E*)-farnesyl diphosphate + isopentenyl diphosphate = diphosphate + geranylgeranyl diphosphate
Other name(s): geranylgeranyl-diphosphate synthase; geranylgeranyl pyrophosphate synthetase; geranylgeranyl-*PP* synthetase; farnesyltransferase; geranylgeranyl pyrophosphate synthase; farnesyl*trans*transferase (obsolete)
Systematic name: (2*E*,6*E*)-farnesyl-diphosphate:isopentenyl-diphosphate farnesyl*trans*transferase
Comments: Some forms of this enzyme will also use geranyl diphosphate and dimethylallyl diphosphate as donors; it will not use larger prenyl diphosphates as efficient donors.
References: [2992]

[EC 2.5.1.29 created 1984, modified 2011]

EC 2.5.1.30

Accepted name: heptaprenyl diphosphate synthase
Reaction: (2*E*,6*E*)-farnesyl diphosphate + **4** isopentenyl diphosphate = **4** diphosphate + *all-trans*-heptaprenyl diphosphate
Other name(s): *all-trans*-heptaprenyl-diphosphate synthase; heptaprenyl pyrophosphate synthase; heptaprenyl pyrophosphate synthetase; HepPP synthase; HepPS; heptaprenylpyrophosphate synthetase

Systematic name: (2*E*,6*E*)-farnesyl-diphosphate:isopentenyl-diphosphate farnesyl*trans*transferase (adding 4 isopentenyl units)

Comments: This enzyme catalyses the condensation reactions resulting in the formation of *all-trans*-heptaprenyl diphosphate, the isoprenoid side chain of ubiquinone-7 and menaquinone-7. The enzyme adds four isopentenyl diphosphate molecules sequentially to farnesyl diphosphate with *trans* stereochemistry.

References: [3439, 4055, 4056, 3405]

[EC 2.5.1.30 created 1984, modified 2010]

EC 2.5.1.31

Accepted name: *ditrans*,*polycis*-undecaprenyl-diphosphate synthase [(2*E*,6*E*)-farnesyl-diphosphate specific]

Reaction: (2*E*,6*E*)-farnesyl diphosphate + **8** isopentenyl diphosphate = **8** diphosphate + *ditrans*,*octacis*-undecaprenyl diphosphate

Other name(s): *di-trans*,*poly-cis*-undecaprenyl-diphosphate synthase; undecaprenyl-diphosphate synthase; bactoprenyl-diphosphate synthase; UPP synthetase; undecaprenyl diphosphate synthetase; undecaprenyl pyrophosphate synthetase; *di-trans*,*poly-cis*-decaprenylcistransferase

Systematic name: (2*E*,6*E*)-farnesyl-diphosphate:isopentenyl-diphosphate cistransferase (adding 8 isopentenyl units)

Comments: Undecaprenyl pyrophosphate synthase catalyses the consecutive condensation reactions of a farnesyl diphosphate with eight isopentenyl diphosphates, in which new *cis*-double bonds are formed, to generate undecaprenyl diphosphate that serves as a lipid carrier for peptidoglycan synthesis of bacterial cell wall [1179].

References: [2380, 3438, 1179, 1723, 982, 978, 2607, 1662]

[EC 2.5.1.31 created 1984, modified 2011]

EC 2.5.1.32

Accepted name: 15-*cis*-phytoene synthase

Reaction: **2** geranylgeranyl diphosphate = 15-*cis*-phytoene + **2** diphosphate (overall reaction)
(1a) **2** geranylgeranyl diphosphate = diphosphate + prephytoene diphosphate
(1b) prephytoene diphosphate = 15-*cis*-phytoene + diphosphate

Other name(s): PSY (gene name); *crtB* (gene name); prephytoene-diphosphate synthase; phytoene synthetase; PSase; geranylgeranyl-diphosphate geranylgeranyltransferase

Systematic name: geranylgeranyl-diphosphate:geranylgeranyl-diphosphate geranylgeranyltransferase (15-*cis*-phytoene forming)

Comments: Requires Mn^{2+} for activity. The enzyme condenses two molecules of geranylgeranyl diphosphate to give prephytoene diphosphate, followed by rearrangement of the cyclopropylcarbinyl intermediate to 15-*cis*-phytoene.

References: [500, 3017, 3123, 2269, 3076]

[EC 2.5.1.32 created 1984, modified 2005, modified 2012]

[2.5.1.33 Transferred entry. trans-pentaprenyltranstransferase. Now covered by EC 2.5.1.82 (hexaprenyl diphosphate synthase [geranylgeranyl-diphosphate specific]) and EC 2.5.1.83 (hexaprenyl-diphosphate synthase [(2E,6E)-farnesyl-diphosphate specific])]

[EC 2.5.1.33 created 1984, deleted 2010]

EC 2.5.1.34

Accepted name: 4-dimethylallyltryptophan synthase

Reaction: dimethylallyl diphosphate + L-tryptophan = diphosphate + 4-(3-methylbut-2-enyl)-L-tryptophan

Other name(s): dimethylallylpyrophosphate:L-tryptophan dimethylallyltransferase; dimethylallyltryptophan synthetase; dimethylallylpyrophosphate:tryptophan dimethylallyl transferase; DMAT synthetase; 4-(γ,γ-dimethylallyl)tryptophan synthase; tryptophan dimethylallyltransferase

Systematic name: dimethylallyl-diphosphate:L-tryptophan 4-dimethylallyltransferase

References: [1902]

[EC 2.5.1.34 created 1984, modified 2010]

EC 2.5.1.35

Accepted name: aspulvinone dimethylallyltransferase
Reaction: **2** dimethylallyl diphosphate + aspulvinone E = **2** diphosphate + aspulvinone H
Other name(s): dimethylallyl pyrophosphate:aspulvinone dimethylallyltransferase
Systematic name: dimethylallyl-diphosphate:aspulvinone-E dimethylallyltransferase
Comments: This enzyme will also use as acceptor aspulvinone G, a hydroxylated derivative of the complex phenolic pigment aspulvinone E.
References: [3440]

[EC 2.5.1.35 created 1984]

EC 2.5.1.36

Accepted name: trihydroxypterocarpan dimethylallyltransferase
Reaction: (1) dimethylallyl diphosphate + (6a*S*,11a*S*)-3,6a,9-trihydroxypterocarpan = diphosphate + 2-dimethylallyl-(6a*S*,11a*S*)-3,6a,9-trihydroxypterocarpan
(2) dimethylallyl diphosphate + (6a*S*,11a*S*)-3,6a,9-trihydroxypterocarpan = diphosphate + 4-dimethylallyl-(6a*S*,11a*S*)-3,6a,9-trihydroxypterocarpan
Other name(s): glyceollin synthase; dimethylallylpyrophosphate:3,6a,9-trihydroxypterocarpan dimethylallyltransferase; dimethylallylpyrophosphate:trihydroxypterocarpan dimethylallyl transferase; dimethylallyl-diphosphate:(6a*S*,11a*S*)-3,6a,9-trihydroxypterocarpan dimethyltransferase
Systematic name: dimethylallyl-diphosphate:(6a*S*,11a*S*)-3,6a,9-trihydroxypterocarpan dimethylallyltransferase
Comments: Part of the glyceollin biosynthesis system in soy bean.
References: [1942, 4019]

[EC 2.5.1.36 created 1989]

[2.5.1.37 Transferred entry. leukotriene-C_4 synthase. Now EC 4.4.1.20, leukotriene-C_4 synthase. The enzyme was incorrectly classified as a transferase]

[EC 2.5.1.37 created 1989, deleted 2004]

EC 2.5.1.38

Accepted name: isonocardicin synthase
Reaction: *S*-adenosyl-L-methionine + nocardicin G = *S*-methyl-5′-thioadenosine + isonocardicin C
Other name(s): nocardicin aminocarboxypropyltransferase; *S*-adenosyl-L-methionine:nocardicin-E 3-amino-3-carboxypropyltransferase
Systematic name: *S*-adenosyl-L-methionine:nocardicin-G 3-amino-3-carboxypropyltransferase
Comments: The enzyme, characterized from the bacterium *Nocardia uniformis*, is involved in the biosynthesis of the β-lactam antibiotic nocardicin A. The enzyme can act on nocardicin E, F, and G, producing isonocardicin A, B, and C, respectively. However, the *in vivo* substrate is believed to be nocardicin G [1635].
References: [3865, 2847, 1635]

[EC 2.5.1.38 created 1992, modified 2016]

EC 2.5.1.39

Accepted name: 4-hydroxybenzoate polyprenyltransferase
Reaction: a polyprenyl diphosphate + 4-hydroxybenzoate = diphosphate + a 4-hydroxy-3-polyprenylbenzoate
Other name(s): nonaprenyl-4-hydroxybenzoate transferase; 4-hydroxybenzoate transferase; *p*-hydroxybenzoate dimethylallyltransferase; *p*-hydroxybenzoate polyprenyltransferase; *p*-hydroxybenzoic acid-polyprenyl transferase; *p*-hydroxybenzoic-polyprenyl transferase; 4-hydroxybenzoate nonaprenyltransferase

Systematic name: polyprenyl-diphosphate:4-hydroxybenzoate polyprenyltransferase

Comments: This enzyme, involved in the biosynthesis of ubiquinone, attaches a polyprenyl side chain to a 4-hydroxybenzoate ring, producing the first ubiquinone intermediate that is membrane bound. The number of isoprenoid subunits in the side chain varies in different species. The enzyme does not have any specificity concerning the length of the polyprenyl tail, and accepts tails of various lengths with similar efficiency [2,4,5].

References: [1564, 2211, 2544, 934, 3561]

[EC 2.5.1.39 created 1992, modified 2010]

[2.5.1.40 Transferred entry. aristolochene synthase. Now EC 4.2.3.9, aristolochene synthase]

[EC 2.5.1.40 created 1992, deleted 1999]

EC 2.5.1.41

Accepted name: phosphoglycerol geranylgeranyltransferase

Reaction: geranylgeranyl diphosphate + *sn*-glycerol 1-phosphate = diphosphate + 3-(*O*-geranylgeranyl)-*sn*-glycerol 1-phosphate

Other name(s): glycerol phosphate geranylgeranyltransferase; geranylgeranyl-transferase (ambiguous); prenyltransferase (ambiguous); (*S*)-3-*O*-geranylgeranylglyceryl phosphate synthase; (*S*)-geranylgeranylglyceryl phosphate synthase; GGGP synthase; (*S*)-GGGP synthase; GGGPS; geranylgeranyl diphosphate:*sn*-glyceryl phosphate geranylgeranyltransferase; geranylgeranyl diphosphate:*sn*-glycerol-1-phosphate geranylgeranyltransferase

Systematic name: geranylgeranyl-diphosphate:*sn*-glycerol-1-phosphate geranylgeranyltransferase

Comments: This cytosolic enzyme catalyses the first pathway-specific step in the biosynthesis of the core membrane diether lipids in archaebacteria [518]. Requires Mg^{2+} for maximal activity [518]. It catalyses the alkylation of the primary hydroxy group in *sn*-glycerol 1-phosphate by geranylgeranyl diphosphate (GGPP) in a prenyltransfer reaction where a hydroxy group is the nucleophile in the acceptor substrate [518]. The other enzymes involved in the biosynthesis of polar lipids in Archaea are EC 1.1.1.261 (*sn*-glycerol-1-phosphate dehydrogenase), EC 2.5.1.42 (geranylgeranylglycerol-phosphate geranylgeranyltransferase) and EC 2.7.7.67 (CDP-archaeol synthase), which lead to the formation of CDP-unsaturated archaeol. The final step in the pathway involves the addition of L-serine, with concomitant removal of CMP, leading to the production of unsaturated archaetidylserine [2317].

References: [4038, 518, 2433, 2646, 2317]

[EC 2.5.1.41 created 1992, modified 2009]

EC 2.5.1.42

Accepted name: geranylgeranylglycerol-phosphate geranylgeranyltransferase

Reaction: geranylgeranyl diphosphate + 3-(*O*-geranylgeranyl)-*sn*-glycerol 1-phosphate = diphosphate + 2,3-bis-(*O*-geranylgeranyl)-*sn*-glycerol 1-phosphate

Other name(s): geranylgeranyloxyglycerol phosphate geranylgeranyltransferase; geranylgeranyltransferase II; (*S*)-2,3-di-*O*-geranylgeranylglyceryl phosphate synthase; DGGGP synthase; DGGGPS; geranylgeranyl diphosphate:*sn*-3-*O*-(geranylgeranyl)glycerol 1-phosphate geranylgeranyltransferase

Systematic name: geranylgeranyl diphosphate:3-(*O*-geranylgeranyl)-*sn*-glycerol 1-phosphate geranylgeranyltransferase

Comments: This enzyme is an integral-membrane protein that carries out the second prenyltransfer reaction involved in the formation of polar membrane lipids in Archaea. Requires a divalent metal cation, such as Mg^{2+} or Mn^{2+}, for activity [1293]. 4-Hydroxybenzoate, 1,4-dihydroxy 2-naphthoate, homogentisate and α-glycerophosphate cannot act as prenyl-acceptor substrates [1293]. The other enzymes involved in the biosynthesis of polar lipids in Archaea are EC 1.1.1.261 (*sn*-glycerol-1-phosphate dehydrogenase), EC 2.5.1.41 (phosphoglycerol geranylgeranyltransferase), which, together with this enzyme, alkylates the hydroxy groups of glycerol 1-phosphate to yield unsaturated archaetidic acid, which is acted upon by EC 2.7.7.67 (CDP-archaeol synthase) to form CDP-unsaturated archaeol. The final step in the pathway involves the addition of L-serine, with concomitant removal of CMP, leading to the production of unsaturated archaetidylserine [2317]. Belongs in the UbiA prenyltransferase family [1293].

References: [4038, 1293, 2317]

[EC 2.5.1.42 created 1992, modified 2009]

EC 2.5.1.43

Accepted name: nicotianamine synthase

Reaction: **3** *S*-adenosyl-L-methionine = **3** *S*-methyl-$5'$-thioadenosine + nicotianamine

Systematic name: *S*-adenosyl-L-methionine:*S*-adenosyl-L-methionine:*S*-adenosyl-L-methionine 3-amino-3-carboxypropyltransferase

References: [1326]

[EC 2.5.1.43 created 1999]

EC 2.5.1.44

Accepted name: homospermidine synthase

Reaction: (1) **2** putrescine = *sym*-homospermidine + NH$_3$ + H$^+$

(2) putrescine + spermidine = *sym*-homospermidine + propane-1,3-diamine

Systematic name: putrescine:putrescine 4-aminobutyltransferase (ammonia-forming)

Comments: The reaction of this enzyme occurs in three steps, with some of the intermediates presumably remaining enzyme-bound: NAD$^+$-dependent dehydrogenation of putrescine, transfer of the 4-aminobutylidene group from dehydroputrescine to a second molecule of putrescine and reduction of the imine intermediate to form homospermidine. Hence the overall reaction is transfer of a 4-aminobutyl group. Differs from EC 2.5.1.45, homospermidine synthase (spermidine-specific), which cannot use putrescine as donor of the aminobutyl group.

References: [3435, 366, 3949, 3310, 2504, 2503]

[EC 2.5.1.44 created 1999, modified 2001]

EC 2.5.1.45

Accepted name: homospermidine synthase (spermidine-specific)

Reaction: spermidine + putrescine = *sym*-homospermidine + propane-1,3-diamine

Systematic name: spermidine:putrescine 4-aminobutyltransferase (propane-1,3-diamine-forming)

Comments: The reaction of this enzyme occurs in three steps, with some of the intermediates presumably remaining enzyme-bound: (a) NAD$^+$-dependent dehydrogenation of spermidine, (b) transfer of the 4-aminobutylidene group from dehydrospermidine to putrescine and (c) reduction of the imine intermediate to form homospermidine. This enzyme is more specific than EC 2.5.1.44, homospermidine synthase, which is found in bacteria, as it cannot use putrescine as donor of the 4-aminobutyl group. Forms part of the biosynthetic pathway of the poisonous pyrrolizidine alkaloids of the ragworts (*Senecio*).

References: [366, 2503, 2501]

[EC 2.5.1.45 created 2001]

EC 2.5.1.46

Accepted name: deoxyhypusine synthase

Reaction: [eIF5A-precursor]-lysine + spermidine = [eIF5A-precursor]-deoxyhypusine + propane-1,3-diamine (overall reaction)

(1a) spermidine + NAD$^+$ = dehydrospermidine + NADH

(1b) dehydrospermidine + [enzyme]-lysine = *N*-(4-aminobutylidene)-[enzyme]-lysine + propane-1,3-diamine

(1c) *N*-(4-aminobutylidene)-[enzyme]-lysine + [eIF5A-precursor]-lysine = *N*-(4-aminobutylidene)-[eIF5A-precursor]-lysine + [enzyme]-lysine

(1d) *N*-(4-aminobutylidene)-[eIF5A-precursor]-lysine + NADH + H$^+$ = [eIF5A-precursor]-deoxyhypusine + NAD$^+$

Other name(s): spermidine:eIF5A-lysine 4-aminobutyltransferase (propane-1,3-diamine-forming)

Systematic name: [eIF5A-precursor]-lysine:spermidine 4-aminobutyltransferase (propane-1,3-diamine-forming)

Comments: The eukaryotic initiation factor eIF5A contains a hypusine residue that is essential for activity. This enzyme catalyses the first reaction of hypusine formation from one specific lysine residue of the eIF5A precursor. The reaction occurs in four steps: NAD$^+$-dependent dehydrogenation of spermidine (1a), formation of an enzyme-imine intermediate by transfer of the 4-aminobutylidene group from dehydrospermidine to the active site lysine residue (Lys^{329} for the human enzyme; 1b), transfer of the same 4-aminobutylidene group from the enzyme intermediate to the e1F5A precursor (1c), reduction of the e1F5A-imine intermediate to form a deoxyhypusine residue (1d). Hence the overall reaction is transfer of a 4-aminobutyl group. For the plant enzyme, homospermidine can substitute for spermidine and putrescine can substitute for the lysine residue of the eIF5A precursor. Hypusine is formed from deoxyhypusine by the action of EC 1.14.99.29, deoxyhypusine monooxygenase.

References: [3883, 3881, 529, 2502, 2503, 3882, 3884, 1519, 3475]

[EC 2.5.1.46 provisional version created 1999 as EC 1.1.1.249 deleted 1999, revised and reinstated 2001 as EC 2.5.1.46]

EC 2.5.1.47

Accepted name: cysteine synthase

Reaction: *O*-acetyl-L-serine + hydrogen sulfide = L-cysteine + acetate

Other name(s): *O*-acetyl-L-serine sulfhydrylase; *O*-acetyl-L-serine sulfohydrolase; *O*-acetylserine (thiol)-lyase; *O*-acetylserine (thiol)-lyase A; *O*-acetylserine sulfhydrylase; O^3-acetyl-L-serine acetate-lyase (adding hydrogen-sulfide); acetylserine sulfhydrylase; cysteine synthetase; *S*-sulfocysteine synthase; 3-*O*-acetyl-L-serine:hydrogen-sulfide 2-amino-2-carboxyethyltransferase; O^3-acetyl-L-serine:hydrogen-sulfide 2-amino-2-carboxyethyltransferase

Systematic name: *O*-acetyl-L-serine:hydrogen-sulfide 2-amino-2-carboxyethyltransferase

Comments: A pyridoxal-phosphate protein. Some alkyl thiols, cyanide, pyrazole and some other heterocyclic compounds can act as acceptors. Not identical with EC 2.5.1.51 (β-pyrazolylalanine synthase), EC 2.5.1.52 (L-mimosine synthase) and EC 2.5.1.53 (uracilylalanine synthase).

References: [248, 1220, 1437, 2370, 3433, 297]

[EC 2.5.1.47 created 1972 as EC 4.2.99.8, modified 1976, modified 1990, transferred 2002 to EC 2.5.1.47]

EC 2.5.1.48

Accepted name: cystathionine γ-synthase

Reaction: O^4-succinyl-L-homoserine + L-cysteine = L-cystathionine + succinate

Other name(s): *O*-succinyl-L-homoserine succinate-lyase (adding cysteine); *O*-succinylhomoserine (thiol)-lyase; homoserine *O*-transsuccinylase; *O*-succinylhomoserine synthase; *O*-succinylhomoserine synthetase; cystathionine synthase; cystathionine synthetase; homoserine transsuccinylase; 4-*O*-succinyl-L-homoserine:L-cysteine *S*-(3-amino-3-carboxypropyl)transferase

Systematic name: O^4-succinyl-L-homoserine:L-cysteine *S*-(3-amino-3-carboxypropyl)transferase

Comments: A pyridoxal-phosphate protein. Also reacts with hydrogen sulfide and methanethiol as replacing agents, producing homocysteine and methionine, respectively. In the absence of thiol, can also catalyse β,γ-elimination to form 2-oxobutanoate, succinate and ammonia.

References: [916, 1583, 3848, 3847, 581, 2827]

[EC 2.5.1.48 created 1972 as EC 4.2.99.9, transferred 2002 to EC 2.5.1.48]

EC 2.5.1.49

Accepted name: *O*-acetylhomoserine aminocarboxypropyltransferase

Reaction: *O*-acetyl-L-homoserine + methanethiol = L-methionine + acetate

Other name(s): *O*-acetyl-L-homoserine acetate-lyase (adding methanethiol); *O*-acetyl-L-homoserine sulfhydrolase; *O*-acetylhomoserine (thiol)-lyase; *O*-acetylhomoserine sulfhydrolase; methionine synthase (misleading)

Systematic name: *O*-acetyl-L-homoserine:methanethiol 3-amino-3-carboxypropyltransferase

Comments: Also reacts with other thiols and H_2S, producing homocysteine or thioethers. The name methionine synthase is more commonly applied to EC 2.1.1.13, methionine synthase. The enzyme from baker's yeast also catalyses the reaction of EC 2.5.1.47 cysteine synthase, but more slowly.

References: [1645, 3261, 3945, 3943, 3946, 3944, 3193]

[EC 2.5.1.49 created 1972 as EC 4.2.99.10, transferred 2002 to EC 2.5.1.49]

EC 2.5.1.50

Accepted name: zeatin 9-aminocarboxyethyltransferase

Reaction: *O*-acetyl-L-serine + zeatin = lupinate + acetate

Other name(s): β-(9-cytokinin)-alanine synthase; β-(9-cytokinin)alanine synthase; *O*-acetyl-L-serine acetate-lyase (adding N^6-substituted adenine); lupinate synthetase; lupinic acid synthase; lupinic acid synthetase; 3-*O*-acetyl-L-serine:zeatin 2-amino-2-carboxyethyltransferase

Systematic name: *O*-acetyl-L-serine:zeatin 2-amino-2-carboxyethyltransferase

Comments: The enzyme acts not only on zeatin but also on other N^6-substituted adenines. The reaction destroys their cytokinin activity and forms the corresponding 3-(adenin-9-yl)-L-alanine.

References: [844, 2289]

[EC 2.5.1.50 created 1984 as EC 4.2.99.13, transferred 2002 to EC 2.5.1.50]

EC 2.5.1.51

Accepted name: β-pyrazolylalanine synthase

Reaction: *O*-acetyl-L-serine + pyrazole = 3-(pyrazol-1-yl)-L-alanine + acetate

Other name(s): β-(1-pyrazolyl)alanine synthase; β-pyrazolealanine synthase; β-pyrazolylalanine synthase (acetylserine); O^3-acetyl-L-serine acetate-lyase (adding pyrazole); BPA-synthase; pyrazolealanine synthase; pyrazolylalaninase; 3-*O*-acetyl-L-serine:pyrazole 1-(2-amino-2-carboxyethyl)transferase; O^3-acetyl-L-serine:pyrazole 1-(2-amino-2-carboxyethyl)transferase

Systematic name: *O*-acetyl-L-serine:pyrazole 1-(2-amino-2-carboxyethyl)transferase

Comments: The enzyme is highly specific for acetylserine and pyrazole. Not identical with EC 2.5.1.52 L-mimosine synthase.

References: [2367, 2368, 2371, 2486]

[EC 2.5.1.51 created 1989 as EC 4.2.99.14 (EC 4.2.99.17 incorporated 1992), transferred 2002 to EC 2.5.1.51]

EC 2.5.1.52

Accepted name: L-mimosine synthase

Reaction: *O*-acetyl-L-serine + 3,4-dihydroxypyridine = 3-(3,4-dihydroxypyridin-1-yl)-L-alanine + acetate

Other name(s): O^3-acetyl-L-serine acetate-lyase (adding 3,4-dihydroxypyridin-1-yl); 3-*O*-acetyl-L-serine:3,4-dihydroxypyridine 1-(2-amino-2-carboxyethyl)transferase; O^3-acetyl-L-serine:3,4-dihydroxypyridine 1-(2-amino-2-carboxyethyl)transferase

Systematic name: *O*-acetyl-L-serine:3,4-dihydroxypyridine 1-(2-amino-2-carboxyethyl)transferase

Comments: Brings about the biosynthesis of L-mimosine in plants of the *Mimosa* and *Leucaena* genera. Not identical with EC 2.5.1.51, β-pyrazolylalanine synthase.

References: [2367, 2368, 2371, 2486]

[EC 2.5.1.52 created 1989 as EC 4.2.99.15, transferred 2002 to EC 2.5.1.52]

EC 2.5.1.53

Accepted name: uracilylalanine synthase

Reaction: *O*-acetyl-L-serine + uracil = 3-(uracil-1-yl)-L-alanine + acetate

Other name(s): O^3-acetyl-L-serine acetate-lyase (adding uracil); isowillardiine synthase; willardiine synthase; 3-*O*-acetyl-L-serine:uracil 1-(2-amino-2-carboxyethyl)transferase; O^3-acetyl-L-serine:uracil 1-(2-amino-2-carboxyethyl)transferase

Systematic name: *O*-acetyl-L-serine:uracil 1-(2-amino-2-carboxyethyl)transferase

Comments: The enzyme produces the non-proteinogenic amino acid L-willardiine, which is naturally found in the plants *Acacia willardiana*, *Mimosa pigra*, and *Pisum sativum* (pea). The enzyme from *Pisum* species also produces L-isowillardiine. Not identical with EC 2.5.1.47 cysteine synthase.

References: [28, 1437, 2369]

[EC 2.5.1.53 created 1990 as EC 4.2.99.16, transferred 2002 to EC 2.5.1.53]

EC 2.5.1.54

Accepted name: 3-deoxy-7-phosphoheptulonate synthase

Reaction: phospho*enol*pyruvate + D-erythrose 4-phosphate + H_2O = 3-deoxy-D-*arabino*-hept-2-ulosonate 7-phosphate + phosphate

Other name(s): 2-dehydro-3-deoxy-phosphoheptonate aldolase; 2-keto-3-deoxy-D-*arabino*-heptonic acid 7-phosphate synthetase; 3-deoxy-D-*arabino*-2-heptulosonic acid 7-phosphate synthetase; 3-deoxy-D-*arabino*-heptolosonate-7-phosphate synthetase; 3-deoxy-D-*arabino*-heptulosonate 7-phosphate synthetase; 7-phospho-2-keto-3-deoxy-D-*arabino*-heptonate D-erythrose-4-phosphate lyase (pyruvate-phosphorylating); 7-phospho-2-dehydro-3-deoxy-D-*arabino*-heptonate D-erythrose-4-phosphate lyase (pyruvate-phosphorylating); D-erythrose-4-phosphate-lyase; D-erythrose-4-phosphate-lyase (pyruvate-phosphorylating); DAH7-*P* synthase; DAHP synthase; DS-Co; DS-Mn; KDPH synthase; KDPH synthetase; deoxy-D-*arabino*-heptulosonate-7-phosphate synthetase; phospho-2-dehydro-3-deoxyheptonate aldolase; phospho-2-keto-3-deoxyheptanoate aldolase; phospho-2-keto-3-deoxyheptonate aldolase; phospho-2-keto-3-deoxyheptonic aldolase; phospho-2-oxo-3-deoxyheptonate aldolase

Systematic name: phospho*enol*pyruvate:D-erythrose-4-phosphate *C*-(1-carboxyvinyl)transferase (phosphate-hydrolysing, 2-carboxy-2-oxoethyl-forming)

References: [3309, 1542, 3095]

[EC 2.5.1.54 created 1965 as EC 4.1.2.15, modified 1976, transferred 2002 to EC 2.5.1.54]

EC 2.5.1.55

Accepted name: 3-deoxy-8-phosphooctulonate synthase

Reaction: phospho*enol*pyruvate + D-arabinose 5-phosphate + H_2O = 3-deoxy-D-*manno*-octulosonate 8-phosphate + phosphate

Other name(s): 2-dehydro-3-deoxy-D-octonate-8-phosphate D-arabinose-5-phosphate-lyase (pyruvate-phosphorylating); 2-dehydro-3-deoxy-phosphooctonate aldolase; 2-keto-3-deoxy-8-phosphooctonic synthetase; 3-deoxy-D-*manno*-octulosonate-8-phosphate synthase; 3-deoxy-D-mannooctulosonate-8-phosphate synthetase; 3-deoxyoctulosonic 8-phosphate synthetase; KDOP synthase; phospho-2-keto-3-deoxyoctonate aldolase

Systematic name: phospho*enol*pyruvate:D-arabinose-5-phosphate *C*-(1-carboxyvinyl)transferase (phosphate-hydrolysing, 2-carboxy-2-oxoethyl-forming)

References: [1949, 1793, 121]

[EC 2.5.1.55 created 1965 as EC 4.1.2.16, transferred 2002 to EC 2.5.1.55]

EC 2.5.1.56

Accepted name: *N*-acetylneuraminate synthase

Reaction: phospho*enol*pyruvate + *N*-acetyl-D-mannosamine + H_2O = phosphate + *N*-acetylneuraminate

Other name(s): (NANA)condensing enzyme; *N*-acetylneuraminate pyruvate-lyase (pyruvate-phosphorylating); NeuAc synthase

Systematic name: phospho*enol*pyruvate:*N*-acetyl-D-mannosamine *C*-(1-carboxyvinyl)transferase (phosphate-hydrolysing, 2-carboxy-2-oxoethyl-forming)

References: [319, 1748]

[EC 2.5.1.56 created 1972 as EC 4.1.3.19, transferred 2002 to EC 2.5.1.56]

EC 2.5.1.57

Accepted name: *N*-acylneuraminate-9-phosphate synthase

Reaction: phospho*enol*pyruvate + *N*-acyl-D-mannosamine 6-phosphate + H_2O = *N*-acylneuraminate 9-phosphate + phosphate

Other name(s): *N*-acetylneuraminate 9-phosphate lyase; *N*-acetylneuraminate 9-phosphate sialic acid 9-phosphate synthase; *N*-acetylneuraminate 9-phosphate synthetase; *N*-acylneuraminate-9-phosphate pyruvate-lyase (pyruvate-phosphorylating); sialic acid 9-phosphate synthetase

Systematic name: phospho*enol*pyruvate:*N*-acyl-D-mannosamine-6-phosphate 1-(2-carboxy-2-oxoethyl)transferase

Comments: Acts on *N*-glycoloyl and *N*-acetyl-derivatives.

References: [2935, 3788, 2413]

[EC 2.5.1.57 created 1972 as EC 4.1.3.20, transferred 2002 to EC 2.5.1.57]

EC 2.5.1.58

Accepted name: protein farnesyltransferase

Reaction: farnesyl diphosphate + protein-cysteine = *S*-farnesyl protein + diphosphate

Other name(s): FTase

Systematic name: farnesyl-diphosphate:protein-cysteine farnesyltransferase

Comments: This enzyme, along with protein geranylgeranyltransferase types I (EC 2.5.1.59) and II (EC 2.5.1.60), constitutes the protein prenyltransferase family of enzymes. Catalyses the formation of a thioether linkage between the C-1 of an isoprenyl group and a cysteine residue fourth from the C-terminus of the protein. These protein acceptors have the C-terminal sequence CA1A2X, where the terminal residue, X, is preferably serine, methionine, alanine or glutamine; leucine makes the protein a substrate for EC 2.5.1.59. The enzymes are relaxed in specificity for A1, but cannot act if A2 is aromatic. Substrates of the prenyltransferases include Ras, Rho, Rab, other Ras-related small GTP-binding proteins, γ-subunits of heterotrimeric G-proteins, nuclear lamins, centromeric proteins and many proteins involved in visual signal transduction. A zinc metalloenzyme that requires Mg^{2+} for activity.

References: [998, 487, 2031, 2235, 2032, 1048]

[EC 2.5.1.58 created 2003]

EC 2.5.1.59

Accepted name: protein geranylgeranyltransferase type I

Reaction: geranylgeranyl diphosphate + protein-cysteine = *S*-geranylgeranyl-protein + diphosphate

Other name(s): GGTase-I; GGTaseI

Systematic name: geranylgeranyl-diphosphate:protein-cysteine geranyltransferase

Comments: This enzyme, along with protein farnesyltransferase (EC 2.5.1.58) and protein geranylgeranyltransferase type II (EC 2.5.1.60), constitutes the protein prenyltransferase family of enzymes. Catalyses the formation of a thioether linkage between the C-1 atom of the geranylgeranyl group and a cysteine residue fourth from the C-terminus of the protein. These protein acceptors have the C-terminal sequence CA1A2X, where the terminal residue, X, is preferably leucine; serine, methionine, alanine or glutamine makes the protein a substrate for EC 2.5.1.58. The enzymes are relaxed in specificity for A1, but cannot act if A2 is aromatic. Known targets of this enzyme include most γ-subunits of heterotrimeric G proteins and Ras-related GTPases such as members of the Ras and Rac/Rho families. A zinc metalloenzyme. The Zn^{2+} is required for peptide, but not for isoprenoid, substrate binding.

References: [487, 4039, 1048]

[EC 2.5.1.59 created 2003]

EC 2.5.1.60

Accepted name: protein geranylgeranyltransferase type II

Reaction: geranylgeranyl diphosphate + protein-cysteine = *S*-geranylgeranyl-protein + diphosphate

Other name(s): GGTaseII; Rab geranylgeranyltransferase; RabGGTase; geranylgeranyl-diphosphate,geranylgeranyl-diphosphate:protein-cysteine geranyltransferase

Systematic name: geranylgeranyl-diphosphate:protein-cysteine geranyltransferase

Comments: This enzyme, along with protein farnesyltransferase (EC 2.5.1.58) and protein geranylgeranyltransferase type I (EC 2.5.1.59), constitutes the protein prenyltransferase family of enzymes. Attaches geranylgeranyl groups to two C-terminal cysteines in Ras-related GTPases of a single family, the Rab family (Ypt/Sec4 in lower eukaryotes) that terminate in XXCC, XCXC and CCXX motifs. Reaction is entirely dependent on the Rab substrate being bound to Rab escort protein (REP). Post-translational modification with the geranylgeranyl moiety is essential for Rab GTPases to be able to control the processes of membrane docking and fusion [2796].

References: [487, 3864, 4041, 3519, 2796, 1048]

[EC 2.5.1.60 created 2003]

EC 2.5.1.61

Accepted name: hydroxymethylbilane synthase

Reaction: **4** porphobilinogen + H_2O = hydroxymethylbilane + **4** NH_3

Other name(s): HMB-synthase; porphobilinogen deaminase; pre-uroporphyrinogen synthase; uroporphyrinogen I synthase; uroporphyrinogen I synthetase; uroporphyrinogen synthase; uroporphyrinogen synthetase; porphobilinogen ammonia-lyase (polymerizing); (4-[2-carboxyethyl]-3-[carboxymethyl]pyrrol-2-yl)methyltransferase (hydrolysing)

Systematic name: porphobilinogen:(4-[2-carboxyethyl]-3-[carboxymethyl]pyrrol-2-yl)methyltransferase (hydrolysing)

Comments: The enzyme works by stepwise addition of pyrrolylmethyl groups until a hexapyrrole is present at the active centre. The terminal tetrapyrrole is then hydrolysed to yield the product, leaving a cysteine-bound dipyrrole on which assembly continues. In the presence of a second enzyme, EC 4.2.1.75 uroporphyrinogen-III synthase, which is often called cosynthase, the product is cyclized to form uroporphyrinogen-III. If EC 4.2.1.75 is absent, the hydroxymethylbilane cyclizes spontaneously to form uroporphyrinogen I.

References: [233, 975, 1950, 3777, 2249, 232]

[EC 2.5.1.61 created 1972 as EC 4.3.1.8, transferred 2003 to EC 2.6.1.61]

EC 2.5.1.62

Accepted name: chlorophyll synthase

Reaction: chlorophyllide *a* + phytyl diphosphate = chlorophyll *a* + diphosphate

Systematic name: chlorophyllide-*a*:phytyl-diphosphate phytyltransferase

Comments: Requires Mg^{2+}. The enzyme is modified by binding of the first substrate, phytyl diphosphate, before reaction of the modified enzyme with the second substrate, chlorophyllide *a*, can occur. The reaction also occurs when phytyl diphosphate is replaced by geranylgeranyl diphosphate.

References: [3080, 2581, 2959]

[EC 2.5.1.62 created 2003]

EC 2.5.1.63

Accepted name: adenosyl-fluoride synthase

Reaction: *S*-adenosyl-L-methionine + fluoride = $5'$-deoxy-$5'$-fluoroadenosine + L-methionine

Other name(s): fluorinase

Systematic name: *S*-adenosyl-L-methionine:fluoride adenosyltransferase

References: [2530, 752]

[EC 2.5.1.63 created 2003]

[2.5.1.64 Transferred entry. 2-succinyl-6-hydroxy-2,4-cyclohexadiene-1-carboxylate synthase. The reaction that was attributed to this enzyme is now known to be catalysed by two separate enzymes: EC 2.2.1.9 (2-succinyl-5-enolpyruvyl-6-hydroxy-3-cyclohexene-1-carboxylic-acid synthase) and EC 4.2.99.20 (2-succinyl-6-hydroxy-2,4-cyclohexadiene-1-carboxylate synthase)]

[EC 2.5.1.64 created 2003, deleted 2008]

EC 2.5.1.65

Accepted name: *O*-phosphoserine sulfhydrylase

Reaction: *O*-phospho-L-serine + hydrogen sulfide = L-cysteine + phosphate

Other name(s): *O*-phosphoserine(thiol)-lyase

Systematic name: *O*-phospho-L-serine:hydrogen-sulfide 2-amino-2-carboxyethyltransferase

Comments: A pyridoxal-phosphate protein. The enzyme from *Aeropyrum pernix* acts on both *O*-phospho-L-serine and O^3-acetyl-L-serine, in contrast with EC 2.5.1.47, cysteine synthase, which acts only on O^3-acetyl-L-serine.

References: [2262, 2263, 2264]

[EC 2.5.1.65 created 2004]

EC 2.5.1.66

Accepted name: N^2-(2-carboxyethyl)arginine synthase

Reaction: D-glyceraldehyde 3-phosphate + L-arginine = N^2-(2-carboxyethyl)-L-arginine + phosphate

Other name(s): CEAS; N^2-(2-carboxyethyl)arginine synthetase; CEA synthetase; glyceraldehyde-3-phosphate:L-arginine 2-*N*-(2-hydroxy-3-oxopropyl) transferase (2-carboxyethyl-forming)

Systematic name: glyceraldehyde-3-phosphate:L-arginine N^2-(2-hydroxy-3-oxopropyl) transferase (2-carboxyethyl-forming)

Comments: The enzyme requires thiamine diphosphate and catalyses the first step in the clavulanic-acid-biosynthesis pathway. The 2-hydroxy-3-oxo group transferred from glyceraldehyde 3-phosphate is isomerized during transfer to form the 2-carboxyethyl group.

References: [458, 1653]

[EC 2.5.1.66 created 2004]

EC 2.5.1.67

Accepted name: chrysanthemyl diphosphate synthase

Reaction: **2** dimethylallyl diphosphate = diphosphate + chrysanthemyl diphosphate

Other name(s): CPPase

Systematic name: dimethylallyl-diphosphate:dimethylallyl-diphosphate dimethylallyltransferase (chrysanthemyl-diphosphate-forming)

Comments: Requires a divalent metal ion for activity, with Mg^{2+} being better than Mn^{2+} [2891]. Chrysanthemyl diphosphate is a monoterpene with a non-head-to-tail linkage. It is unlike most monoterpenoids, which are derived from geranyl diphosphate and have isoprene units that are linked head-to-tail. The mechanism of its formation is similar to that of the early steps of squalene and phytoene biosynthesis. Chrysanthemyl diphosphate is the precursor of chrysanthemic acid, the acid half of the pyrethroid insecticides found in chrysanthemums.

References: [2891, 847]

[EC 2.5.1.67 created 2007]

EC 2.5.1.68

Accepted name: (2*Z*,6*E*)-farnesyl diphosphate synthase

Reaction: geranyl diphosphate + isopentenyl diphosphate = diphosphate + (2*Z*,6*E*)-farnesyl diphosphate

Other name(s): (*Z*)-farnesyl diphosphate synthase; *Z*-farnesyl diphosphate synthase

Systematic name: geranyl-diphosphate:isopentenyl-diphosphate geranyl*cis*transferase

Comments: Requires Mg^{2+} or Mn^{2+} for activity. The product of this reaction is an intermediate in the synthesis of decaprenyl phosphate, which plays a central role in the biosynthesis of most features of the mycobacterial cell wall, including peptidoglycan, linker unit galactan and arabinan. Neryl diphosphate can also act as substrate.

References: [3111]

[EC 2.5.1.68 created 2007, modified 2010]

EC 2.5.1.69

Accepted name: lavandulyl diphosphate synthase
Reaction: **2** dimethylallyl diphosphate = diphosphate + lavandulyl diphosphate
Other name(s): FDS-5
Systematic name: dimethylallyl-diphosphate:dimethylallyl-diphosphate dimethylallyltransferase (lavandulyl-diphosphate-forming)
Comments: Lavandulyl diphosphate is a monoterpene with a non-head-to-tail linkage. It is unlike most monoterpenoids, which are derived from geranyl diphosphate and have isoprene units that are linked head-to-tail. When this enzyme is incubated with dimethylallyl diphosphate and isopentenyl diphosphate, it also forms the regular monoterpene geranyl diphosphate [1290]. The enzyme from *Artemisia tridentata* (big sagebrush) forms both lavandulyl diphosphate and chrysanthemyl diphosphate (see EC 2.5.1.67, chrysanthemyl diphosphate synthase) when dimethylally diphosphate is the sole substrate.
References: [847, 1290]

[EC 2.5.1.69 created 2007]

EC 2.5.1.70

Accepted name: naringenin 8-dimethylallyltransferase
Reaction: dimethylallyl diphosphate + (-)-(2*S*)-naringenin = diphosphate + sophoraflavanone B
Other name(s): N8DT
Systematic name: dimethylallyl-diphosphate:naringenin 8-dimethylallyltransferase
Comments: Requires Mg^{2+}. This membrane-bound protein is located in the plastids [4065]. In addition to naringenin, the enzyme can prenylate several other flavanones at the C-8 position, but more slowly. Along with EC 1.14.13.103 (8-dimethylallylnaringenin 2′-hydroxylase) and EC 2.5.1.71 (leachianone G 2″-dimethylallyltransferase), this enzyme forms part of the sophoraflavanone-G-biosynthesis pathway.
References: [3947, 4065]

[EC 2.5.1.70 created 2007]

EC 2.5.1.71

Accepted name: leachianone-G 2″-dimethylallyltransferase
Reaction: dimethylallyl diphosphate + leachianone G = diphosphate + sophoraflavanone G
Other name(s): LG 2″-dimethylallyltransferase; leachianone G 2″-dimethylallyltransferase; LGDT
Systematic name: dimethylallyl-diphosphate:leachianone-G 2″-dimethylallyltransferase
Comments: This membrane-bound enzyme is located in the plastids and requires Mg^{2+} for activity. The reaction forms the lavandulyl sidechain of sophoraflavanone G by transferring a dimethylallyl group to the 2″ position of another dimethylallyl group attached at postiion 8 of leachianone G. The enzyme is specific for dimethylallyl diphosphate as the prenyl donor, as it cannot be replaced by isopentenyl diphosphate or geranyl diphosphate. Euchrenone a$_7$ (a 5-deoxy derivative of leachianone G) and kenusanone I (a 7-methoxy derivative of leachianone G) can also act as substrates, but more slowly. Along with EC 1.14.13.103 (8-dimethylallylnaringenin 2′-hydroxylase) and EC 2.5.1.70 (naringenin 8-dimethylallyltransferase), this enzyme forms part of the sophoraflavanone-G-biosynthesis pathway.
References: [4065]

[EC 2.5.1.71 created 2007]

EC 2.5.1.72

Accepted name: quinolinate synthase
Reaction: glycerone phosphate + iminosuccinate = pyridine-2,3-dicarboxylate + **2** H$_2$O + phosphate
Other name(s): NadA; QS; quinolinate synthetase
Systematic name: glycerone phosphate:iminosuccinate alkyltransferase (cyclizing)

Comments: An iron-sulfur protein that requires a [4Fe-4S] cluster for activity [684]. Quinolinate synthase catalyses the second step in the *de novo* biosynthesis of NAD$^+$ from aspartate in some bacteria, with EC 1.4.3.16 (L-aspartate oxidase) catalysing the first step and EC 2.4.2.19 [nicotinate-nucleotide diphosphorylase (carboxylating)] the third step. In *Escherichia coli*, two of the residues that are involved in the [4Fe-4S] cluster binding appear to undergo reversible disulfide-bond formation that regulates the activity of the enzyme [3042].

References: [684, 1603, 3006, 2945, 3042]

[EC 2.5.1.72 created 2008]

EC 2.5.1.73

Accepted name: *O*-phospho-L-seryl-tRNA:Cys-tRNA synthase

Reaction: *O*-phospho-L-seryl-tRNA$^{\text{Cys}}$ + sulfide = L-cysteinyl-tRNA$^{\text{Cys}}$ + phosphate

Other name(s): SepCysS; Sep-tRNA:Cys-tRNA synthase

Systematic name: *O*-phospho-L-seryl-tRNA$^{\text{Cys}}$:hydrogen sulfide 2-aminopropanoate transferase

Comments: In organisms like *Archaeoglobus fulgidus* lacking EC 6.1.1.16 (cysteine—tRNA ligase) for the direct Cys-tRNA$^{\text{Cys}}$ formation, Cys-tRNA$^{\text{Cys}}$ is produced by an indirect pathway, in which EC 6.1.1.27 (*O*-phosphoseryl-tRNA ligase) ligates *O*-phosphoserine to tRNA$^{\text{Cys}}$, and EC 2.5.1.73 converts the produced *O*-phospho-L-seryl-tRNA$^{\text{Cys}}$ to Cys-tRNA$^{\text{Cys}}$. The SepRS/SepCysS pathway is the sole route for cysteine biosynthesis in the organism [996]. *Methanosarcina mazei* can use both pathways, the direct route using EC 6.1.1.16 (cysteine—tRNA ligase) and the indirect pathway with EC 6.1.1.27 (*O*-phosphoseryl-tRNA ligase) and EC 2.5.1.73 [1248].

References: [996, 1248, 4010]

[EC 2.5.1.73 created 2009]

EC 2.5.1.74

Accepted name: 1,4-dihydroxy-2-naphthoate polyprenyltransferase

Reaction: an *all-trans*-polyprenyl diphosphate + 1,4-dihydroxy-2-naphthoate = a demethylmenaquinol + diphosphate + CO$_2$

Systematic name: *all-trans*-polyprenyl diphosphate:1,4-dihydroxy-2-naphthoate polyprenyltransferase

Comments: This enzyme catalyses a step in the synthesis of menaquinone, in which the prenyl chain synthesized by polyprenyl diphosphate synthase is transferred to 1,4-dihydroxy-2-naphthoate (DHNA). The bacterial enzyme is an inner membrane protein [3202], with the C-terminus located in the periplasm [3394]. It is highly specific for DHNA but not for a specific length of the prenyl chain [3002].

References: [3202, 3002, 3394, 661]

[EC 2.5.1.74 created 2009]

EC 2.5.1.75

Accepted name: tRNA dimethylallyltransferase

Reaction: dimethylallyl diphosphate + adenine^{37} in tRNA = diphosphate + N^6-dimethylallyladenine^{37} in tRNA

Other name(s): tRNA prenyltransferase; MiaA; transfer ribonucleate isopentenyltransferase (incorrect); Δ^2-isopentenyl pyrophosphate:tRNA-Δ^2-isopentenyl transferase (incorrect); Δ^2-isopentenyl pyrophosphate:transfer ribonucleic acid Δ^2-isopentenyltransferase (incorrect); dimethylallyl-diphosphate: tRNA dimethylallyltransferase

Systematic name: dimethylallyl-diphosphate:adenine^{37} in tRNA dimethylallyltransferase

Comments: Formerly known as tRNA isopentenyltransferase (EC 2.5.1.8), but it is now known that dimethylallyl diphosphate, rather than isopentenyl diphosphate, is the substrate.

References: [1943, 3272, 2299]

[EC 2.5.1.75 created 1972 as EC 2.5.1.8, transferred 2009 to EC 2.5.1.75]

EC 2.5.1.76

Accepted name: cysteate synthase

Reaction: *O*-phospho-L-serine + sulfite = L-cysteate + phosphate

Other name(s): sulfite:*O*-phospho-L-serine sulfotransferase (phosphate-hydrolysing, L-cysteate-forming)

Systematic name: sulfite:*O*-phospho-L-serine sulfonotransferase (phosphate-hydrolysing, L-cysteate-forming)

Comments: A pyridoxal-phosphate protein. It is highly specific for *O*-phospho-L-serine and sulfite. The reaction proceeds through a dehydroalanine (2-aminoacrylic acid) intermediate. The enzyme from *Methanosarcina acetivorans* is evolutionarily related to threonine synthase (EC 4.2.3.1), but the reaction is more similar to that of *O*-phosphoserine sulfhydrylase (EC 2.5.1.65).

References: [1123]

[EC 2.5.1.76 created 2009]

*[2.5.1.77 Transferred entry. 7,8-didemethyl-8-hydroxy-5-deazariboflavin synthase. Now EC 2.5.1.147, 5-amino-6-(*D*-ribitylamino)urac* L*-tyrosine 4-methylphenol transferase and EC 4.3.1.32, 7,8-didemethyl-8-hydroxy-5-deazariboflavin synthase.]*

[EC 2.5.1.77 created 2010, deleted 2018]

EC 2.5.1.78

Accepted name: 6,7-dimethyl-8-ribityllumazine synthase

Reaction: 1-deoxy-L-*glycero*-tetrulose 4-phosphate + 5-amino-6-(D-ribitylamino)uracil = 6,7-dimethyl-8-(D-ribityl)lumazine + **2** H_2O + phosphate

Other name(s): lumazine synthase; 6,7-dimethyl-8-ribityllumazine synthase 2; 6,7-dimethyl-8-ribityllumazine synthase 1; lumazine synthase 2; lumazine synthase 1; type I lumazine synthase; type II lumazine synthase; RIB4; MJ0303; RibH; Pbls; MbtLS; RibH1 protein; RibH2 protein; RibH1; RibH2

Systematic name: 5-amino-6-(D-ribitylamino)uracil butanedionetransferase

Comments: Involved in riboflavin biosynthesis.

References: [1693, 1018, 150, 2325, 149, 1088, 1537, 4051, 906, 649, 1188, 2313, 2314]

[EC 2.5.1.78 created 2010]

EC 2.5.1.79

Accepted name: thermospermine synthase

Reaction: *S*-adenosyl 3-(methylsulfanyl)propylamine + spermidine = *S*-methyl-5′-thioadenosine + thermospermine + H^+

Other name(s): TSPMS; ACL5; SAC51; *S*-adenosyl 3-(methylthio)propylamine:spermidine 3-aminopropyltransferase (thermospermine synthesizing)

Systematic name: *S*-adenosyl 3-(methylsulfanyl)propylamine:spermidine 3-aminopropyltransferase (thermospermine forming)

Comments: This plant enzyme is crucial for the proper functioning of xylem vessel elements in the vascular tissues of plants [2364].

References: [2925, 1722, 2364]

[EC 2.5.1.79 created 2010, modified 2013]

EC 2.5.1.80

Accepted name: 7-dimethylallyltryptophan synthase

Reaction: dimethylallyl diphosphate + L-tryptophan = diphosphate + 7-(3-methylbut-2-enyl)-L-tryptophan

Other name(s): 7-DMATS

Systematic name: dimethylallyl-diphosphate:L-tryptophan 7-dimethylallyltransferase

Comments: This enzyme is more flexible towards the aromatic substrate than EC 2.5.1.34 (4-dimethylallyltryptophan synthase), but similar to that enzyme, accepts only dimethylallyl diphosphate as the prenyl donor.

References: [1784, 1786]

[EC 2.5.1.80 created 2010]

EC 2.5.1.81

Accepted name: geranylfarnesyl diphosphate synthase

Reaction: geranylgeranyl diphosphate + isopentenyl diphosphate = (2*E*,6*E*,10*E*,14*E*)-geranylfarnesyl diphosphate + diphosphate

Other name(s): FGPP synthase; (all-E) geranylfarnesyl diphosphate synthase; GFPS; Fgs

Systematic name: geranylgeranyl-diphosphate:isopentenyl-diphosphate *trans*transferase (adding 1 isopentenyl unit)

Comments: The enzyme from *Methanosarcina mazei* is involved in biosynthesis of the polyprenyl side-chain of methanophenazine, an electron carrier utilized for methanogenesis. It prefers geranylgeranyl diphosphate and farnesyl diphosphate as allylic substrate [2517]. The enzyme from *Aeropyrum pernix* prefers farnesyl diphosphate as allylic substrate. The enzyme is involved in the biosynthesis of C_{25}-C_{25} membrane lipids [3428].

References: [2517, 3428, 3427, 1898]

[EC 2.5.1.81 created 2010]

EC 2.5.1.82

Accepted name: hexaprenyl diphosphate synthase [geranylgeranyl-diphosphate specific]

Reaction: geranylgeranyl diphosphate + **2** isopentenyl diphosphate = **2** diphosphate + *all-trans*-hexaprenyl diphosphate

Other name(s): HexPS(ambiguous); (all-E) hexaprenyl diphosphate synthase; (all-trans) hexaprenyl diphosphate synthase; hexaprenyl pyrophosphate synthase (ambiguous); HexPPs (ambiguous); hexaprenyl diphosphate synthase (ambiguous)

Systematic name: geranylgeranyl-diphosphate:isopentenyl-diphosphate transferase (adding 2 isopentenyl units)

Comments: The enzyme prefers geranylgeranyl diphosphate to farnesyl diphosphate as an allylic substrate and does not show activity for geranyl diphosphate and dimethylallyl diphosphate. Requires Mg^{2+} [1291].

References: [1291, 1292, 3385]

[EC 2.5.1.82 created 1984 as EC 2.5.1.33, part transferred 2010 to EC 2.5.1.82]

EC 2.5.1.83

Accepted name: hexaprenyl diphosphate synthase [(2*E*,6*E*)-farnesyl-diphosphate specific]

Reaction: (2*E*,6*E*)-farnesyl diphosphate + **3** isopentenyl diphosphate = **3** diphosphate + *all-trans*-hexaprenyl diphosphate

Other name(s): HexPS (ambiguous); hexaprenyl pyrophosphate synthetase (ambiguous); hexaprenyl diphosphate synthase (ambiguous)

Systematic name: (2*E*,6*E*)-farnesyl-diphosphate:isopentenyl-diphosphate farnesyl*trans*transferase (adding 3 isopentenyl units)

Comments: The enzyme prefers farnesyl diphosphate to geranylgeranyl diphosphate as an allylic substrate and does not show activity for geranyl diphosphate and dimethylallyl diphosphate [979].

References: [979, 3194, 2387]

[EC 2.5.1.83 created 1984 as EC 2.5.1.33, part transferred 2010 to EC 2.5.1.83]

EC 2.5.1.84

Accepted name: *all-trans*-nonaprenyl diphosphate synthase [geranyl-diphosphate specific]

Reaction: geranyl diphosphate + **7** isopentenyl diphosphate = **7** diphosphate + *all-trans*-nonaprenyl diphosphate

Other name(s): nonaprenyl diphosphate synthase (ambiguous); solanesyl diphosphate synthase (ambiguous); SolPP synthase (ambiguous); SPP-synthase (ambiguous); SPP synthase (ambiguous); solanesyl-diphosphate synthase (ambiguous); OsSPS2

Systematic name: geranyl-diphosphate:isopentenyl-diphosphate *trans*transferase (adding 7 isopentenyl units)

Comments: (2*E*,6*E*)-Farnesyl diphosphate and geranylgeranyl diphosphate are less effective as substrates than geranyl diphosphate. The enzyme is involved in the synthesis of the side chain of menaquinone-9 [2993]. In *Oryza sativa* the enzyme SPS2 is involved in providing solanesyl diphosphate for plastoquinone-9 formation [2533].

References: [2993, 980, 2533, 2539, 1108, 3493]

[EC 2.5.1.84 created 1972 as EC 2.5.1.11, part transferred 2010 to EC 2.5.1.84]

EC 2.5.1.85

Accepted name: *all-trans*-nonaprenyl diphosphate synthase [geranylgeranyl-diphosphate specific]

Reaction: geranylgeranyl diphosphate + **5** isopentenyl diphosphate = **5** diphosphate + *all-trans*-nonaprenyl diphosphate

Other name(s): nonaprenyl diphosphate synthase (ambiguous); solanesyl diphosphate synthase (ambiguous); At-SPS2; At-SPS1; SPS1; SPS2

Systematic name: geranylgeranyl-diphosphate:isopentenyl-diphosphate *trans*transferase (adding 5 isopentenyl units)

Comments: Geranylgeranyl diphosphate is preferred over farnesyl diphosphate as allylic substrate [1340]. The plant *Arabidopsis thaliana* has two different enzymes that catalyse this reaction. SPS1 contributes to the biosynthesis of the ubiquinone side-chain while SPS2 supplies the precursor of the plastoquinone side-chains [1341].

References: [1340, 1341, 1546]

[EC 2.5.1.85 created 1972 as EC 2.5.1.11, part transferred 2010 to EC 2.5.1.85]

EC 2.5.1.86

Accepted name: *trans*,*polycis*-decaprenyl diphosphate synthase

Reaction: (2*Z*,6*E*)-farnesyl diphosphate + **7** isopentenyl diphosphate = **7** diphosphate + *trans*,*octacis*-decaprenyl diphosphate

Other name(s): Rv2361c; (2*Z*,6*Z*,10*Z*,14*Z*,18*Z*,22*Z*,26*Z*,30*Z*,34*E*)-decaprenyl diphosphate synthase

Systematic name: (2*Z*,6*E*)-farnesyl-diphosphate:isopentenyl-diphosphate farnesyl*cis*transferase (adding 7 isopentenyl units)

Comments: The enzyme is involved in the biosynthesis of decaprenyl phosphate, which plays a central role in the biosynthesis of essential mycobacterial cell wall components, such as the mycolyl-arabinogalactan-peptidoglycan complex and lipoarabinomannan [3758].

References: [1610, 3758, 629]

[EC 2.5.1.86 created 2010]

EC 2.5.1.87

Accepted name: *ditrans*,*polycis*-polyprenyl diphosphate synthase [(2*E*,6*E*)-farnesyl diphosphate specific]

Reaction: (2*E*,6*E*)-farnesyl diphosphate + ***n*** isopentenyl diphosphate = ***n*** diphosphate + *ditrans*,*polycis*-polyprenyl diphosphate (***n*** = 10–55)

Other name(s): RER2; Rer2p; Rer2p *Z*-prenyltransferase; Srt1p; Srt2p *Z*-prenyltransferase; ACPT; dehydrodolichyl diphosphate synthase 1

Systematic name: (2*E*,6*E*)-farnesyl-diphosphate:isopentenyl-diphosphate *cis*transferase (adding 10–55 isopentenyl units)

Comments: The enzyme is involved in biosynthesis of dolichol (a long-chain polyprenol) with a saturated α-isoprene unit, which serves as a glycosyl carrier in protein glycosylation [3030]. The yeast *Saccharomyces cerevisiae* has two different enzymes that catalyse this reaction. Rer2p synthesizes a well-defined family of polyprenols of 13–18 isoprene residues with dominating C_{80} (16 isoprene residues) extending to C_{120}, while Srt1p synthesizes mainly polyprenol with 22 isoprene subunits. Largest Srt1p products reach C_{290} [2752]. The enzyme from *Arabidopsis thaliana* catalyses the formation of polyprenyl diphosphates with predominant carbon number C_{120} [2529].

References: [3030, 2752, 3031, 2529, 643]

[EC 2.5.1.87 created 2010]

EC 2.5.1.88

Accepted name: *trans*,*polycis*-polyprenyl diphosphate synthase [(2*Z*,6*E*)-farnesyl diphosphate specific]

Reaction: (2*Z*,6*E*)-farnesyl diphosphate + ***n*** isopentenyl diphosphate = ***n*** diphosphate + *trans*,*polycis*-polyprenyl diphosphate (***n*** = 9–11)

Systematic name: (2*Z*,6*E*)-farnesyl-diphosphate:isopentenyl-diphosphate *cis*transferase (adding 9–11 isopentenyl units)

Comments: Highest activity with (2*Z*,6*E*)-farnesyl diphosphate as allylic substrate. Broad product specificity with the major product being dodecaprenyl diphosphate. Synthesizes even C_{70} prenyl diphosphate as the maximum chain-length product [68].

References: [68]

[EC 2.5.1.88 created 2010]

EC 2.5.1.89

Accepted name: *tritrans*,*polycis*-undecaprenyl diphosphate synthase [geranylgeranyl-diphosphate specific]

Reaction: geranylgeranyl diphosphate + **7** isopentenyl diphosphate = **7** diphosphate + *tritrans*,*heptacis*-undecaprenyl diphosphate

Systematic name: geranylgeranyl-diphosphate:isopentenyl-diphosphate cistransferase (adding 7 isopentenyl units)

Comments: This enzyme is involved in the biosynthesis of the glycosyl carrier lipid in some archaebacteria. Unlike EC 2.5.1.31, its counterpart in most bacteria, it prefers geranylgeranyl diphosphate to farnesyl diphosphate as the allylic substrate, resulting in production of a *tritrans*,*polycis* variant of undecaprenyl diphosphate [1294].

References: [1294]

[EC 2.5.1.89 created 2010, modified 2011]

EC 2.5.1.90

Accepted name: *all*-*trans*-octaprenyl-diphosphate synthase

Reaction: (2*E*,6*E*)-farnesyl diphosphate + **5** isopentenyl diphosphate = **5** diphosphate + *all*-*trans*-octaprenyl diphosphate

Other name(s): octaprenyl-diphosphate synthase; octaprenyl pyrophosphate synthetase; polyprenylpyrophosphate synthetase; terpenoidallyltransferase; terpenyl pyrophosphate synthetase; *trans*-heptaprenyl*trans*transferase; *trans*-prenyltransferase

Systematic name: (2*E*,6*E*)-farnesyl-diphosphate:isopentenyl-diphosphate farnesyl*trans*transferase (adding 5 isopentenyl units)

Comments: This enzyme catalyses the condensation reactions resulting in the formation of *all*-*trans*-octaprenyl diphosphate, the isoprenoid side chain of ubiquinone-8 and menaquinone-8. The enzyme adds five isopentenyl diphosphate molecules sequentially to farnesyl diphosphate with *trans* stereochemistry

References: [986, 116]

[EC 2.5.1.90 created 2010]

EC 2.5.1.91

Accepted name: *all*-*trans*-decaprenyl-diphosphate synthase

Reaction: (2*E*,6*E*)-farnesyl diphosphate + **7** isopentenyl diphosphate = **7** diphosphate + *all*-*trans*-decaprenyl diphosphate

Other name(s): decaprenyl-diphosphate synthase; decaprenyl pyrophosphate synthetase; polyprenylpyrophosphate synthetase; terpenoidallyltransferase; terpenyl pyrophosphate synthetase; *trans*-prenyltransferase

Systematic name: (2*E*,6*E*)-farnesyl-diphosphate:isopentenyl-diphosphate farnesyl*trans*transferase (adding 7 isopentenyl units)

Comments: This enzyme catalyses the condensation reactions resulting in the formation of *all-trans*-decaprenyl diphosphate, the isoprenoid side chain of ubiquinone-10 and menaquinone-10. The enzyme adds seven isopentenyl diphosphate molecules sequentially to farnesyl diphosphate with *trans* stereochemistry.

References: [2998]

[EC 2.5.1.91 created 2010]

EC 2.5.1.92

Accepted name: (2*Z*,6*Z*)-farnesyl diphosphate synthase

Reaction: dimethylallyl diphosphate + **2** isopentenyl diphosphate = **2** diphosphate + (2*Z*,6*Z*)-farnesyl diphosphate

Other name(s): *cis*,*cis*-farnesyl diphosphate synthase; *Z*,*Z*-FPP synthase; zFPS; *Z*,*Z*-farnesyl pyrophosphate synthase

Systematic name: dimethylallyl-diphosphate:isopentenyl-diphosphate *cis*transferase (adding 2 isopentenyl units)

Comments: This enzyme, originally characterized from wild tomato, specifically forms (2*Z*,6*Z*)-farnesyl diphosphate via neryl diphosphate and isopentenyl diphosphate. In wild tomato it is involved in the biosynthesis of several sesquiterpenes. See also EC 2.5.1.68 [(2*Z*,6*E*)-farnesyl diphosphate synthase] and EC 2.5.1.10 [(2*E*,6*E*)-farnesyl diphosphate synthase].

References: [3010]

[EC 2.5.1.92 created 2010, modified 2011]

EC 2.5.1.93

Accepted name: 4-hydroxybenzoate geranyltransferase

Reaction: geranyl diphosphate + 4-hydroxybenzoate = 3-geranyl-4-hydroxybenzoate + diphosphate

Other name(s): PGT$_1$; PGT$_2$; 4HB geranyltransferase; 4HB:geranyltransferase; *p*-hydroxybenzoate geranyltransferase; PHB geranyltransferase; geranyl diphosphate:4-hydroxybenzoate geranyltransferase

Systematic name: geranyl-diphosphate:4-hydroxybenzoate 3-geranyltransferase

Comments: The enzyme is involved in shikonin biosynthesis. It has a strict substrate specificity for geranyl diphosphate and an absolute requirement for Mg^{2+} [2343].

References: [2532, 2343, 3971]

[EC 2.5.1.93 created 2010]

EC 2.5.1.94

Accepted name: adenosyl-chloride synthase

Reaction: *S*-adenosyl-L-methionine + chloride = 5-deoxy-5-chloroadenosine + L-methionine

Other name(s): chlorinase; 5′-chloro-5′-deoxyadenosine synthase

Systematic name: *S*-adenosyl-L-methionine:chloride adenosyltransferase

Comments: This enzyme, isolated from the marine bacterium *Salinispora tropica*, catalyses an early step in the pathway leading to biosynthesis of the proteosome inhibitor salinosporamide A. The enzyme is very similar to EC 2.5.1.63, adenosyl-fluoride synthase, but does not accept fluoride.

References: [858]

[EC 2.5.1.94 created 2011]

EC 2.5.1.95

Accepted name: xanthan ketal pyruvate transferase

Reaction: phospho*enol*pyruvate + D-Man-β-(1→4)-D-GlcA-β-(1→2)-D-Man-α-(1→3)-D-Glc-β-(1→4)-D-Glc-α-1-diphospho-*ditrans*,*octacis*-undecaprenol = 4,6-CH$_3$(COO$^-$)C-D-Man-β-(1→4)-D-GlcA-β-(1→2)-D-Man-α-(1→3)-D-Glc-β-(1→4)-D-Glc-α-1-diphospho-*ditrans*,*octacis*-undecaprenol + phosphate

Other name(s): KPT

Systematic name: phospho*enol*pyruvate:D-Man-β-(1→4)-GlcA-β-(1→2)-D-Man-α-(1→3)-D-Glc-β-(1→4)-D-Glc-α-1-diphospho-*ditrans*,*octacis*-undecaprenol 4,6-*O*-(1-carboxyethan-1,1-diyl)transferase

Comments: Involved in the biosynthesis of the polysaccharide xanthan. 30-40% of the terminal mannose residues of xanthan have a 4,6-*O*-(1-carboxyethan-1,1-diyl) ketal group. It also acts on the 6-*O*-acetyl derivative of the inner mannose unit.

References: [2147]

[EC 2.5.1.95 created 2011, modified 2012]

EC 2.5.1.96

Accepted name: 4,4′-diapophytoene synthase

Reaction: **2** (2*E*,6*E*)-farnesyl diphosphate = 15-*cis*-4,4′-diapophytoene + **2** diphosphate (overall reaction)
(1a) **2** (2*E*,6*E*)-farnesyl diphosphate = diphosphate + presqualene diphosphate
(1b) presqualene diphosphate = 15-*cis*-4,4′-diapophytoene + diphosphate

Other name(s): dehydrosqualene synthase; DAP synthase; C_{30} carotene synthase; CrtM

Systematic name: farnesyl-diphosphate:farnesyl-diphosphate farnesyltransferase (15-*cis*-4,4′-diapophytoene forming)

Comments: Requires Mn^{2+}. Typical of *Staphylococcus aureus* and some other bacteria such as *Heliobacillus* sp.

References: [3612, 2657, 1799, 1994]

[EC 2.5.1.96 created 2011]

EC 2.5.1.97

Accepted name: pseudaminic acid synthase

Reaction: phospho*enol*pyruvate + 2,4-bis(acetylamino)-2,4,6-trideoxy-β-L-altropyranose + H_2O = 5,7-bis(acetylamino)-3,5,7,9-tetradeoxy-L-*glycero*-α-L-*manno*-2-nonulopyranosonic acid + phosphate

Other name(s): PseI; NeuB3

Systematic name: phospho*enol*pyruvate:2,4-bis(acetylamino)-2,4,6-trideoxy-β-L-altropyranose transferase (phosphate-hydrolysing, 2,7-acetylamino-transfering, 2-carboxy-2-oxoethyl-forming)

Comments: The enzyme requires a divalent metal ion, the highest activity values are observed in the presence of Mn^{2+} and Co^{2+} (10 mM).

References: [556]

[EC 2.5.1.97 created 2011]

EC 2.5.1.98

Accepted name: *Rhizobium leguminosarum* exopolysaccharide glucosyl ketal-pyruvate-transferase

Reaction: phospho*enol*pyruvate + [β-D-GlcA-(1→4)-2-*O*-Ac-β-D-GlcA-(1→4)-β-D-Glc-(1→4)-[3-*O*-(CH$_3$CH(OH)CH$_2$C(O))-4,6-CH$_3$(COO$^-$)C-β-D-Gal-(1→4)-β-D-Glc-(1→4)-β-D-Glc-(1→4)-β-D-Glc-(1→6)]-2(or 3)-*O*-Ac-α-D-Glc-(1→6)]$_n$ = [β-D-GlcA-(1→4)-2-*O*-Ac-β-D-GlcA-(1→4)-β-D-Glc-(1→4)-[3-*O*-(CH$_3$CH(OH)CH$_2$C(O))-4,6-CH$_3$(COO$^-$)C-β-D-Gal-(1→3)-4,6-CH$_3$(COO$^-$)C-β-D-Glc-(1→4)-β-D-Glc-(1→4)-β-D-Glc-(1→6)]-2(or 3)-*O*-Ac-α-D-Glc-(1→6)]$_n$ + phosphate

Other name(s): PssM; phospho*enol*pyruvate:[D-GlcA-β-(1→4)-2-*O*-Ac-D-GlcA-β-(1→4)-D-Glc-β-(1→4)-[3-*O*-CH$_3$-CH$_2$CH(OH)C(O)-D-Gal-β-(1→4)-D-Glc-β-(1→4)-D-Glc-β-(1→4)-D-Glc-β-(1→6)]-2(or 3)-*O*-Ac-D-Glc-α-(1→6)]$_n$ 4,6-*O*-(1-carboxyethan-1,1-diyl)transferase

Systematic name: phospho*enol*pyruvate:[β-D-GlcA-(1→4)-2-*O*-Ac-β-D-GlcA-(1→4)-β-D-Glc-(1→4)-[3-*O*-CH$_3$-CH$_2$CH(OH)C(O)-4,6-CH$_3$(COO$^-$)C-β-D-Gal-(1→4)-β-D-Glc-(1→4)-β-D-Glc-(1→4)-β-D-Glc-(1→6)]-2(or 3)-*O*-Ac-α-D-Glc-(1→6)]$_n$ 4,6-*O*-(1-carboxyethan-1,1-diyl)transferase

Comments: The enzyme is responsible for pyruvylation of the subterminal glucose in the acidic octasaccharide repeating unit of the exopolysaccharide of *Rhizobium leguminosarum* (bv. *viciae* strain VF39) which is necessary to establish nitrogen-fixing symbiosis with *Pisum sativum*, *Vicia faba*, and *Vicia sativa*.

References: [1471]

[EC 2.5.1.98 created 2012, modified 2018]

[2.5.1.99 Deleted entry. all-trans-phytoene synthase. The activity was an artifact caused by photoisomerization of the product of EC 2.5.1.32, 15-cis-phytoene synthase.]

[EC 2.5.1.99 created 2012, deleted 2018]

EC 2.5.1.100

Accepted name: fumigaclavine A dimethylallyltransferase
Reaction: fumigaclavine A + dimethylallyl diphosphate = fumigaclavine C + diphosphate
Other name(s): FgaPT1
Systematic name: dimethylallyl-diphosphate:fumigaclavine A dimethylallyltransferase
Comments: Fumigaclavine C is an ergot alkaloid produced by some fungi of the *Trichocomaceae* family. Activity does not require any metal ions.
References: [3615]

[EC 2.5.1.100 created 2012]

EC 2.5.1.101

Accepted name: *N*,*N*′-diacetyllegionaminate synthase
Reaction: 2,4-diacetamido-2,4,6-trideoxy-α-D-mannopyranose + phospho*enol*pyruvate + H_2O = *N*,*N*′-diacetyllegionaminate + phosphate
Other name(s): *neuB* (gene name); *legI* (gene name)
Systematic name: phospho*enol*pyruvate:2,4-diacetamido-2,4,6-trideoxy-α-D-mannopyranose 1-(2-carboxy-2-oxoethyl)transferase
Comments: Requires a divalent metal such as Mn^{2+}. Isolated from the bacteria *Legionella pneumophila* and *Campylobacter jejuni*, where it is involved in the biosynthesis of legionaminic acid, a virulence-associated, cell surface sialic acid-like derivative.
References: [1074, 3100]

[EC 2.5.1.101 created 2012]

EC 2.5.1.102

Accepted name: geranyl-pyrophosphate—olivetolic acid geranyltransferase
Reaction: geranyl diphosphate + 2,4-dihydroxy-6-pentylbenzoate = diphosphate + cannabigerolate
Other name(s): GOT (ambiguous)
Systematic name: geranyl-diphosphate:olivetolate geranyltransferase
Comments: Part of the cannabinoids biosynthetic pathway of the plant *Cannabis sativa*. The enzyme can also use neryl diphosphate as substrate, forming cannabinerolate.
References: [886]

[EC 2.5.1.102 created 2012]

EC 2.5.1.103

Accepted name: presqualene diphosphate synthase
Reaction: **2** (2*E*,6*E*)-farnesyl diphosphate = presqualene diphosphate + diphosphate
Other name(s): SSL-1 (gene name); *hpnD* (gene name)
Systematic name: (2*E*,6*E*)-farnesyl-diphosphate:(2*E*,6*E*)-farnesyl-diphosphate farnesyltransferase (presqualene diphosphate-forming)
Comments: Isolated from the green alga *Botryococcus braunii* BOT22. Unlike EC 2.5.1.21, squalene synthase, where squalene is formed in one step from farnesyl diphosphate, in this alga the intermediate presqualene diphosphate is generated and released by this enzyme. This compound is then converted into either squalene (by EC 1.3.1.96, *Botryococcus* squalene synthase) or botryococcene (EC 1.3.1.97, botryococcene synthase).
References: [2453, 2608]

[EC 2.5.1.103 created 2012]

EC 2.5.1.104

Accepted name: N^1-aminopropylagmatine synthase

Reaction: *S*-adenosyl 3-(methylsulfanyl)propylamine + agmatine = *S*-methyl-$5'$-thioadenosine + N^1-(3-aminopropyl)agmatine

Other name(s): agmatine/cadaverine aminopropyl transferase; ACAPT; PF0127 (gene name); triamine/agmatine aminopropyltransferase; SpeE; agmatine aminopropyltransferase; *S*-adenosyl 3-(methylthio)propylamine:agmatine 3-aminopropyltransferase

Systematic name: *S*-adenosyl 3-(methylsulfanyl)propylamine:agmatine 3-aminopropyltransferase

Comments: The enzyme is involved in the biosynthesis of spermidine from agmatine in some archaea and bacteria. The enzyme from the Gram-negative bacterium *Thermus thermophilus* accepts agmatine, spermidine and norspermidine with similar catalytic efficiency. The enzymes from the archaea *Pyrococcus furiosus* and *Thermococcus kodakarensis* prefer agmatine, but can utilize cadaverine, putrescine and propane-1,3-diamine with much lower catalytic efficiency. *cf.* EC 2.5.1.16, spermidine synthase, and EC 2.5.1.23, *sym*-norspermidine synthase.

References: [2538, 452, 2318, 2537]

[EC 2.5.1.104 created 2013]

EC 2.5.1.105

Accepted name: 7,8-dihydropterin-6-yl-methyl-4-(β-D-ribofuranosyl)aminobenzene $5'$-phosphate synthase

Reaction: (7,8-dihydropterin-6-yl)methyl diphosphate + 4-(β-D-ribofuranosyl)aniline $5'$-phosphate = *N*-[(7,8-dihydropterin-6-yl)methyl]-4-(β-D-ribofuranosyl)aniline $5'$-phosphate + diphosphate

Other name(s): MJ0301 (gene name); dihydropteroate synthase (ambiguous)

Systematic name: (7,8-dihydropterin-6-yl)methyl diphosphate:4-(β-D-ribofuranosyl)aniline $5'$-phosphate 6-hydroxymethyl-7,8-dihydropterintransferase

Comments: The enzyme, which has been studied in the archaeon *Methanocaldococcus jannaschii*, is involved in the biosynthesis of tetrahydromethanopterin.

References: [3925]

[EC 2.5.1.105 created 2013]

EC 2.5.1.106

Accepted name: tryprostatin B synthase

Reaction: dimethylallyl diphosphate + brevianamide F = diphosphate + tryprostatin B

Other name(s): *ftmPT*1 (gene name); brevianamide F prenyltransferase (ambiguous)

Systematic name: dimethylallyl-diphosphate:brevianamide-F dimethylallyl-*C*-2-transferase

Comments: The enzyme from the fungus *Aspergillus fumigatus* can also prenylate other tryptophan-containing cyclic dipeptides. Prenylation occurs mainly at C-2 [1159], but also at C-3 [3887]. Involved in the biosynthetic pathways of several indole alkaloids such as tryprostatins, cyclotryprostatins, spirotryprostatins, fumitremorgins and verruculogen.

References: [1159, 3887]

[EC 2.5.1.106 created 2013]

EC 2.5.1.107

Accepted name: verruculogen prenyltransferase

Reaction: dimethylallyl diphosphate + verruculogen = diphosphate + fumitremorgin A

Other name(s): FtmPT3

Systematic name: dimethylallyl-diphosphate:verruculogen dimethylallyl-*O*-transferase

Comments: Found in a number of fungi. Catalyses the last step in the biosynthetic pathway of the indole alkaloid fumitremorgin A. The enzyme from the fungus *Neosartorya fischeri* is also active with fumitremorgin B and 12α,13α-dihydroxyfumitremorgin C.

References: [2363]

[EC 2.5.1.107 created 2013]

EC 2.5.1.108

Accepted name: 2-(3-amino-3-carboxypropyl)histidine synthase

Reaction: *S*-adenosyl-L-methionine + L-histidine-[translation elongation factor 2] = *S*-methyl-5′-thioadenosine + 2-[(3*S*)-3-amino-3-carboxypropyl]-L-histidine-[translation elongation factor 2]

Other name(s): Dph2

Systematic name: *S*-adenosyl-L-methionine:L-histidine-[translation elongation factor 2] 2-[(3*S*)-3-amino-3-carboxypropyl]transferase

Comments: A [4Fe-4S] enzyme that modifies a histidine residue of the translation elongation factor 2 (EF2) via a 3-amino-3-carboxypropyl radical. The enzyme is present in archae and eukaryotes but not in eubacteria. The enzyme is a member of the ‘AdoMet radical’ (radical SAM) family and generates the 3-amino-3-carboxypropyl radical by an uncanonical clevage of *S*-adenosyl-L-methionine. The relevant histidine of EF2 is His^{715} in mammals, His^{699} in yeast and His^{600} in *Pyrococcus horikoshii*. Part of diphthamide biosynthesis.

References: [2011, 4053, 4080, 753]

[EC 2.5.1.108 created 2013]

EC 2.5.1.109

Accepted name: brevianamide F prenyltransferase (deoxybrevianamide E-forming)

Reaction: dimethylallyl diphosphate + brevianamide F = diphosphate + deoxybrevianamide E

Other name(s): NotF; BrePT; brevianamide F reverse prenyltransferase

Systematic name: dimethylallyl-diphosphate:brevianamide-F *tert*-dimethylallyl-*C*-2-transferase

Comments: The enzyme from the fungus *Aspergilus* sp. MF297-2 is specific for brevianamide F [739], while the enzyme from *Aspergillus versicolor* accepts a broad range of trytophan-containing cyclic dipeptides [3981]. Involved in the biosynthetic pathways of several indole alkaloids such as paraherquamides and malbrancheamides.

References: [739, 3981]

[EC 2.5.1.109 created 2013]

EC 2.5.1.110

Accepted name: 12α,13α-dihydroxyfumitremorgin C prenyltransferase

Reaction: dimethylallyl diphosphate + 12α,13α-dihydroxyfumitremorgin C = diphosphate + fumitremorgin B

Other name(s): *ftmH* (gene name); FtmPT2

Systematic name: dimethylallyl-diphosphate:12α,13α-dihydroxyfumitremorgin C dimethylallyl-*N*-1-transferase

Comments: The enzyme from the fungus *Aspergillus fumigatus* also shows some activity with fumitremorgin C. Involved in the biosynthetic pathways of several indole alkaloids such as fumitremorgins and verruculogen.

References: [1158]

[EC 2.5.1.110 created 2013]

EC 2.5.1.111

Accepted name: 4-hydroxyphenylpyruvate 3-dimethylallyltransferase

Reaction: dimethylallyl diphosphate + 4-hydroxyphenylpyruvate = diphosphate + 3-dimethylallyl-4-hydroxyphenylpyruvate

Other name(s): CloQ; 4HPP dimethylallyltransferase; NovQ

Systematic name: dimethylallyl diphosphate:4-hydroxyphenylpyruvate 3-dimethylallyltransferase

Comments: The enzyme is involved in the biosynthesis of the 3-dimethylallyl-4-hydroxyphenylpyruvate moiety of the aminocoumarin antibiotics clorobiocin and novobiocin [2732].

References: [2732, 1629, 2231, 2588]

[EC 2.5.1.111 created 2013]

EC 2.5.1.112

Accepted name: adenylate dimethylallyltransferase (ADP/ATP-dependent)

Reaction: (1) dimethylallyl diphosphate + ADP = diphosphate + N^6-(dimethylallyl)adenosine 5′-diphosphate
(2) dimethylallyl diphosphate + ATP = diphosphate + N^6-(dimethylallyl)adenosine 5′-triphosphate

Other name(s): cytokinin synthase (ambiguous); isopentenyltransferase (ambiguous); 2-isopentenyl-diphosphate:ADP/ATP Δ^2-isopentenyltransferase; adenylate isopentenyltransferase (ambiguous); dimethylallyl diphosphate:ATP/ADP isopentenyltransferase: IPT

Systematic name: dimethylallyl-diphosphate:ADP/ATP dimethylallyltransferase

Comments: Involved in the biosynthesis of cytokinins in plants. The IPT4 isoform from the plant *Arabidopsis thaliana* is specific for ADP and ATP [1557]. Other isoforms, such as IPT1 from *Arabidopsis thaliana* [1557, 3448] and the enzyme from the common hop, *Humulus lupulus* [3005], also have a lower activity with AMP (*cf.* EC 2.5.1.27, adenylate dimethylallyltransferase).

References: [1557, 3448, 3005]

[EC 2.5.1.112 created 2013]

EC 2.5.1.113

Accepted name: [CysO sulfur-carrier protein]-thiocarboxylate-dependent cysteine synthase

Reaction: *O*-phospho-L-serine + [CysO sulfur-carrier protein]-Gly-NH-CH_2-C(O)SH = [CysO sulfur-carrier protein]-Gly-NH-CH_2-C(O)-*S*-L-cysteine + phosphate

Other name(s): CysM

Systematic name: *O*-phospho-L-serine:thiocarboxylated [CysO sulfur-carrier protein] 2-amino-2-carboxyethyltransferase

Comments: A pyridoxal-phosphate protein. The enzyme participates in an alternative pathway for L-cysteine biosynthesis that involves a protein-bound thiocarboxylate as the sulfide donor. The enzyme from the bacterium *Mycobacterium tuberculosis* also has very low activity with O^3-acetyl-L-serine (*cf.* EC 2.5.1.65, *O*-phosphoserine sulfhydrylase).

References: [2557, 1548, 26, 27]

[EC 2.5.1.113 created 2013]

EC 2.5.1.114

Accepted name: tRNA^{Phe} (4-demethylwyosine^{37}-C7) aminocarboxypropyltransferase

Reaction: *S*-adenosyl-L-methionine + 4-demethylwyosine^{37} in tRNA^{Phe} = *S*-methyl-5′-thioadenosine + 7-[(3*S*)-3-amino-3-carboxypropyl]-4-demethylwyosine^{37} in tRNA^{Phe}

Other name(s): TYW2; tRNA-yW synthesizing enzyme-2; TRM12 (gene name); taw2 (gene name)

Systematic name: *S*-adenosyl-L-methionine:tRNA^{Phe} (4-demethylwyosine^{37}-C7)-[(3*S*)-3-amino-3-carboxypropyl]transferase

Comments: The enzyme, which is found in all eukaryotes and in the majority of Euryarchaeota (but not in the Crenarchaeota), is involved in the hypermodification of the guanine nucleoside at position 37 of tRNA leading to formation of assorted wye bases. This modification is essential for translational reading-frame maintenance. The eukaryotic enzyme is involved in biosynthesis of the tricyclic base wybutosine, which is found only in tRNA^{Phe}.

References: [3613, 2912, 685]

[EC 2.5.1.114 created 2013]

EC 2.5.1.115

Accepted name: homogentisate phytyltransferase

Reaction: phytyl diphosphate + homogentisate = diphosphate + 2-methyl-6-phytylbenzene-1,4-diol + CO_2

Other name(s): HPT; VTE2 (gene name)

Systematic name: phytyl diphosphate:homogentisate phytyltransferase

Comments: Requires Mg^{2+} for activity [2990]. Involved in the biosynthesis of the vitamin E tocopherols. While the enzyme from the cyanobacterium *Synechocystis* PCC 6803 has an appreciable activity with geranylgeranyl diphosphate (EC 2.5.1.116, homogentisate geranylgeranyltransferase), the enzyme from the plant *Arabidopsis thaliana* has only a low activity with that substrate [1,3,4].

References: [592, 3046, 2990, 3963]

[EC 2.5.1.115 created 2014]

EC 2.5.1.116

Accepted name: homogentisate geranylgeranyltransferase

Reaction: geranylgeranyl diphosphate + homogentisate = diphosphate + 6-geranylgeranyl-2-methylbenzene-1,4-diol + CO_2

Other name(s): HGGT; slr1736 (gene name)

Systematic name: geranylgeranyl diphosphate:homogentisate geranylgeranyltransferase

Comments: Requires Mg^{2+} for activity. Involved in the biosynthesis of the vitamin E, tocotrienols. While the enzyme from the bacterium *Synechocystis* PCC 6803 has higher activity with phytyl diphosphate (EC 2.5.1.115, homogentisate phytyltransferase), the enzymes from barley, rice and wheat have only a low activity with that substrate [454].

References: [592, 454, 3963]

[EC 2.5.1.116 created 2014]

EC 2.5.1.117

Accepted name: homogentisate solanesyltransferase

Reaction: *all-trans*-nonaprenyl diphosphate + homogentisate = diphosphate + 2-methyl-6-*all-trans*-nonaprenylbenzene-1,4-diol + CO_2

Other name(s): HST; PDS2 (gene name)

Systematic name: *all-trans*-nonaprenyl diphosphate:homogentisate nonaprenyltransferase

Comments: Requires Mg^{2+} for activity. Part of the biosynthesis pathway of plastoquinol-9. The enzymes purified from the plant *Arabidopsis thaliana* and the alga *Chlamydomonas reinhardtii* are also active *in vitro* with unsaturated C_{10}-C_{20} prenyl diphosphates, producing main products that are not decarboxylated [2989].

References: [2990, 2989]

[EC 2.5.1.117 created 2014]

EC 2.5.1.118

Accepted name: β-(isoxazolin-5-on-2-yl)-L-alanine synthase

Reaction: *O*-acetyl-L-serine + isoxazolin-5-one = 3-(5-oxoisoxazolin-2-yl)-L-alanine + acetate

Systematic name: *O*-acetyl-L-serine:isoxazolin-5-one 2-(2-amino-2-carboxyethyl)transferase

Comments: The enzyme from the plants *Lathyrus odoratus* (sweet pea) and *L. sativus* (grass pea) also forms 3-(5-oxoisoxazolin-4-yl)-L-alanine *in vitro* (*cf.* EC 2.5.1.119). However, only 3-(5-oxoisoxazolin-2-yl)-L-alanine is formed *in vivo*. 3-(5-oxoisoxazolin-2-yl)-L-alanine is the biosynthetic precursor of the neurotoxin N^3-oxalyl-L-2,3-diaminopropanoic acid, the cause of lathyrism. Closely related and possibly identical to EC 2.5.1.47, cysteine synthase, and EC 2.5.1.51, β-pyrazolylalanine synthase.

References: [1436]

[EC 2.5.1.118 created 2014]

EC 2.5.1.119

Accepted name: β-(isoxazolin-5-on-4-yl)-L-alanine synthase

Reaction: *O*-acetyl-L-serine + isoxazolin-5-one = 3-(5-oxoisoxazolin-4-yl)-L-alanine + acetate

Systematic name: *O*-acetyl-L-serine:isoxazolin-5-one 4-(2-amino-2-carboxyethyl)transferase

Comments: 3-(5-Oxoisoxazolin-4-yl)-L-alanine is an antifungal antibiotic produced by the bacterium *Streptomyces platensis*. The enzymes from the plants *Lathyrus odoratus* (sweet pea), *L. sativus* (grass pea) and *Citrullus vulgaris* (watermelon) that catalyse EC 2.5.1.118 (β-(isoxazolin-5-on-2-yl)-L-alanine synthase) also catalyse this reaction *in vitro*, but not *in vivo*. Closely related and possibly identical to EC 2.5.1.47, cysteine synthase, and EC 2.5.1.51, β-pyrazolylalanine synthase.

References: [1436]

[EC 2.5.1.119 created 2014]

EC 2.5.1.120

Accepted name: aminodeoxyfutalosine synthase

Reaction: *S*-adenosyl-L-methionine + 3-[(1-carboxyvinyl)oxy]benzoate + H_2O = 6-amino-6-deoxyfutalosine + L-methionine + HCO_3^-

Other name(s): MqnE; AFL synthase; aminofutalosine synthase; *S*-adenosyl-L-methionine:3-[(1-carboxyvinyl)-oxy]benzoate adenosyltransferase (bicarbonate-hydrolysing, 6-amino-6-deoxyfutalosine-forming)

Systematic name: *S*-adenosyl-L-methionine:3-[(1-carboxyvinyl)-oxy]benzoate adenosyltransferase (HCO_3^--hydrolysing, 6-amino-6-deoxyfutalosine-forming)

Comments: This enzyme is a member of the 'AdoMet radical' (radical SAM) family. *S*-Adenosyl-L-methionine acts as both a radical generator and as the source of the transferred adenosyl group. The enzyme, found in several bacterial species, is part of the futalosine pathway for menaquinone biosynthesis.

References: [2100]

[EC 2.5.1.120 created 2014]

EC 2.5.1.121

Accepted name: 5,10-dihydrophenazine-1-carboxylate 9-dimethylallyltransferase

Reaction: dimethylallyl diphosphate + 5,10-dihydrophenazine-1-carboxylate = diphosphate + 9-(dimethylallyl)-5,10-dihydrophenazine-1-carboxylate

Other name(s): PpzP; dihydrophenazine-1-carboxylate dimethylallyltransferase; 5,10-dihydrophenazine 1-carboxylate dimethylallyltransferase

Systematic name: dimethylallyl diphosphate:5,10-dihydrophenazine-1-carboxylate 9-dimethylallyltransferase

Comments: The enzyme is involved in the biosynthesis of prenylated phenazines by the bacterium *Streptomyces anulatus*. It is specific for both dimethylallyl diphosphate and 5,10-dihydrophenazine-1-carboxylate.

References: [3008]

[EC 2.5.1.121 created 2014]

EC 2.5.1.122

Accepted name: 4-*O*-dimethylallyl-L-tyrosine synthase

Reaction: dimethylallyl diphosphate + L-tyrosine = diphosphate + 4-*O*-dimethylallyl-L-tyrosine

Other name(s): SirD

Systematic name: dimethylallyl diphosphate:L-tyrosine 4-*O*-dimethylallyltransferase

Comments: The enzyme is involved in biosynthesis of the phytotoxin sirodesmin PL by the phytopathogenic ascomycete *Leptosphaeria maculans*.

References: [1785, 4086]

[EC 2.5.1.122 created 2014]

EC 2.5.1.123

Accepted name: flaviolin linalyltransferase

Reaction: geranyl diphosphate + flaviolin = 3-linalylflaviolin + diphosphate
Other name(s): Fnq26
Systematic name: geranyl-diphosphate:flaviolin 3-linalyltransferase
Comments: Does not require Mg^{2+} or any other metal ions. Isolated from the bacterium *Streptomyces cinnamonensis*. *In vitro* the enzyme also forms traces of 3-geranylflaviolin.
References: [1187]

[EC 2.5.1.123 created 2014]

EC 2.5.1.124

Accepted name: 6-linalyl-2-*O*,3-dimethylflaviolin synthase
Reaction: geranyl diphosphate + 2-*O*,3-dimethylflaviolin = diphosphate + 6-linalyl-2-*O*,3-dimethylflaviolin
Other name(s): Fur7; 6-(3,7-dimethylocta-1,6-dien-3-yl)-5,7-dihydroxy-2-methoxy-3-methylnaphthalene-1,4-dione synthase
Systematic name: geranyl diphosphate:2-*O*-methyl-3-methylflaviolin geranyltransferase (6-linalyl-2-*O*,3-dimethylflaviolin-forming)
Comments: The enzyme is involved in biosynthesis of the polyketide-isoprenoid furaquinocin D in the bacterium *Streptomyces* sp. KO-3988. It catalyses the transfer of a geranyl group to 2-*O*,3-dimethylflaviolin to yield 6-linalyl-2-*O*,3-dimethylflaviolin and 7-*O*-geranyl-2-*O*,3-dimethylflaviolin (*cf.* EC 2.5.1.125, 7-geranyloxy-5-hydroxy-2-methoxy-3-methylnaphthalene-1,4-dione synthase) in a 10:1 ratio.
References: [1815]

[EC 2.5.1.124 created 2014]

EC 2.5.1.125

Accepted name: 7-geranyloxy-5-hydroxy-2-methoxy-3-methylnaphthalene-1,4-dione synthase
Reaction: geranyl diphosphate + 2-*O*,3-dimethylflaviolin = diphosphate + 7-*O*-geranyl-2-*O*,3-dimethylflaviolin
Other name(s): Fur7
Systematic name: geranyl diphosphate:2-*O*,3-dimethylflaviolin geranyltransferase (7-*O*-geranyl-2-*O*,3-dimethylflaviolin-forming)
Comments: The enzyme is involved in furaquinocin biosynthesis in the bacterium *Streptomyces* sp. KO-3988. It catalyses the transfer of a geranyl group to 2-*O*,3-dimethylflaviolin to yield 7-*O*-geranyl-2-*O*,3-dimethylflaviolin and 6-linalyl-2-*O*,3-dimethylflaviolin (*cf.* EC 2.5.1.124, 6-linalyl-2-*O*,3-dimethylflaviolin synthase) in a 1:10 ratio.
References: [1815]

[EC 2.5.1.125 created 2014]

EC 2.5.1.126

Accepted name: norspermine synthase
Reaction: *S*-adenosyl 3-(methylsulfanyl)propylamine + norspermidine = *S*-methyl-$5'$-thioadenosine + norspermine
Other name(s): long-chain polyamine synthase (ambiguous)
Systematic name: *S*-adenosyl 3-(methylsulfanyl)propylamine:norspermidine 3-aminopropyltransferase
Comments: The enzyme, characterized from the thermophilic archaeon *Pyrobaculum aerophilum*, can also synthesize norspermidine from propane-1,3-diamine and thermospermine from spermidine (with lower activity). The long-chain polyamines stabilize double-stranded DNA at high temperatures. In contrast to EC 2.5.1.127, caldopentamine synthase, this enzyme does not accept norspermine as a substrate.
References: [1721]

[EC 2.5.1.126 created 2014]

EC 2.5.1.127

Accepted name: caldopentamine synthase

Reaction: *S*-adenosyl 3-(methylsulfanyl)propylamine + norspermine = *S*-methyl-5′-thioadenosine + caldopentamine

Other name(s): long-chain polyamine synthase (ambiguous)

Systematic name: *S*-adenosyl 3-(methylsulfanyl)propylamine:norspermine 3-aminopropyltransferase

Comments: The enzyme, characterized from the thermophilic archaeon *Hyperthermus butylicus*, can also synthesize norspermine from norspermidine and thermospermine from spermidine (with lower activity). The long-chain polyamines stabilize double-stranded DNA at high temperatures. In contrast to EC 2.5.1.23, *sym*-norspermidine synthase and EC 2.5.1.126, norspermine synthase, this enzyme shows no activity with propane-1,3-diamine.

References: [1721]

[EC 2.5.1.127 created 2014]

EC 2.5.1.128

Accepted name: N^4-bis(aminopropyl)spermidine synthase

Reaction: **2** *S*-adenosyl 3-(methylsulfanyl)propylamine + spermidine = **2** *S*-methyl-5′-thioadenosine + N^4-bis(aminopropyl)spermidine (overall reaction)

(1a) *S*-adenosyl 3-(methylsulfanyl)propylamine + spermidine = *S*-methyl-5′-thioadenosine + N^4-aminopropylspermidine

(1b) *S*-adenosyl 3-(methylsulfanyl)propylamine + N^4-aminopropylspermidine = *S*-methyl-5′-thioadenosine + N^4-bis(aminopropyl)spermidine

Systematic name: *S*-adenosyl 3-(methylsulfanyl)propylamine:spermidine 3-aminopropyltransferase [N^4-bis(aminopropyl)spermidine synthesizing]

Comments: The enzyme, characterized from the thermophilic archaeon *Thermococcus kodakarensis*, synthesizes the branched-chain polyamine N^4-bis(aminopropyl)spermidine, which is required for cell growth at high-temperature. When spermine is used as substrate, the enzyme forms N^4-aminopropylspermine.

References: [2543]

[EC 2.5.1.128 created 2014]

EC 2.5.1.129

Accepted name: flavin prenyltransferase

Reaction: dimethylallyl phosphate + $FMNH_2$ = prenylated $FMNH_2$ + phosphate

Other name(s): *ubiX* (gene name); PAD1 (gene name)

Systematic name: dimethylallyl-phosphate:$FMNH_2$ prenyltransferase

Comments: The enzyme produces the modified flavin cofactor prenylated $FMNH_2$, which is required by EC 4.1.1.98, 4-hydroxy-3-polyprenylbenzoate decarboxylase, and EC 4.1.1.102, phenacrylate decarboxylase. The enzyme acts as a flavin prenyltransferase, linking a dimethylallyl moiety to the flavin N-5 and C-6 atoms and thus adding a fourth non-aromatic ring to the flavin isoalloxazine group.

References: [3835]

[EC 2.5.1.129 created 2015]

EC 2.5.1.130

Accepted name: 2-carboxy-1,4-naphthoquinone phytyltransferase

Reaction: phytyl diphosphate + 2-carboxy-1,4-naphthoquinone = demethylphylloquinone + diphosphate + CO_2

Other name(s): *menA* (gene name); ABC4 (gene name); 1,4-dioxo-2-naphthoate phytyltransferase; 1,4-diketo-2-naphthoate phytyltransferase

Systematic name: phytyl-diphosphate:2-carboxy-1,4-naphthoquinone phytyltransferase

Comments: This enzyme, found in plants and cyanobacteria, catalyses a step in the synthesis of phylloquinone (vitamin K_1), an electron carrier associated with photosystem I. The enzyme catalyses the transfer of the phytyl chain synthesized by EC 1.3.1.83, geranylgeranyl diphosphate reductase, to 2-carboxy-1,4-naphthoquinone.

References: [1527, 3189]

[EC 2.5.1.130 created 2015]

EC 2.5.1.131

Accepted name: (4-4-[2-(γ-L-glutamylamino)ethyl]phenoxymethylfuran-2-yl)methanamine synthase

Reaction: [5-(aminomethyl)furan-3-yl]methyl diphosphate + γ-L-glutamyltyramine = (4-4-[2-(γ-L-glutamylamino)ethyl]phenoxymethylfuran-2-yl)methanamine + diphosphate

Other name(s): MfnF

Systematic name: [5-(aminomethyl)furan-3-yl]methyl-diphosphate:γ-L-glutamyltyramine [5-(aminomethyl)furan-3-yl]methyltransferase

Comments: The enzyme, isolated from the archaeon *Methanocaldococcus jannaschii*, participates in the biosynthesis of the methanofuran cofactor.

References: [3768]

[EC 2.5.1.131 created 2015]

EC 2.5.1.132

Accepted name: 3-deoxy-D-*glycero*-D-*galacto*-nonulopyranosonate 9-phosphate synthase

Reaction: phospho*enol*pyruvate + D-mannose 6-phosphate + H_2O = 3-deoxy-D-*glycero*-D-*galacto*-non-2-ulopyranosonate 9-phosphate + phosphate

Other name(s): 3-deoxy-D-*glycero*-D-*galacto*-nononate 9-phosphate synthase; 2-keto-3-deoxy-D-*glycero*-D-*galacto*-9-phosphonononic acid synthase; Kdn 9-*P* synthase

Systematic name: phospho*enol*pyruvate:D-mannose-6-phosphate 1-(2-carboxy-2-oxoethyl)transferase

Comments: The enzyme participates in the biosynthesis of the sialic acid 3-deoxy-D-*glycero*-D-*galacto*-non-2-ulopyranosonate (Kdn). The human sialic acid synthase (EC 2.5.1.57) is also able to catalyse the reaction. Kdn is abundant in extracellular glycoconjugates of lower vertebrates such as fish and amphibians, but is also found in the capsular polysaccharides of bacteria that belong to the *Bacteroides* genus.

References: [87, 1879, 3754]

[EC 2.5.1.132 created 2016]

EC 2.5.1.133

Accepted name: bacteriochlorophyll *a* synthase

Reaction: geranylgeranyl diphosphate + bacteriochlorophyllide *a* = geranylgeranyl-bacteriochlorophyllide *a* + diphosphate

Other name(s): *bchG* (gene name)

Systematic name: geranylgeranyl-diphosphate:bacteriochlorophyllide-*a* geranylgeranytransferase

Comments: The enzyme catalyses the addition of a geranylgeranyl hydrophobic chain to bacteriochlorophyllide *a* via an ester bond with the 17-propionate residue. The side chain is later modified to a phytyl chain, resulting in bacteriochlorophyll *a*.

References: [2581, 16, 1017, 2991]

[EC 2.5.1.133 created 2016]

EC 2.5.1.134

Accepted name: cystathionine β-synthase (*O*-acetyl-L-serine)

Reaction: *O*-acetyl-L-serine + L-homocysteine = L-cystathionine + acetate

Other name(s): MccB; *O*-acetylserine dependent cystathionine β-synthase

Systematic name: *O*-acetyl-L-serine:L-homocysteine 2-amino-2-carboxyethyltransferase

Comments: A pyridoxal 5′-phosphate protein. The enzyme, purified from the bacterium *Bacillus subtilis*, also has a low activity with L-serine (*cf.* EC 4.2.1.22, cystathionine β-synthase).

References: [1407]

[EC 2.5.1.134 created 2016]

EC 2.5.1.135

Accepted name: validamine 7-phosphate valienyltransferase
Reaction: GDP-valienol + validamine 7-phosphate = validoxylamine A $7'$-phosphate + GDP
Other name(s): *vldE* (gene name); *valL* (gene name)
Systematic name: GDP-valienol:validamine 7-phosphate valienyltransferase
Comments: The enzyme, characterized from several *Streptomyces* strains, is involved in the biosynthesis of the antifungal agent validamycin A.
References: [118, 4070, 491]

[EC 2.5.1.135 created 2016]

EC 2.5.1.136

Accepted name: 2-acylphloroglucinol 4-prenyltransferase
Reaction: dimethylallyl diphosphate + a 2-acylphloroglucinol = diphosphate + a 2-acyl-4-prenylphloroglucinol
Other name(s): PT-1 (gene name); PT1L (gene name); aromatic prenyltransferase (ambiguous)
Systematic name: dimethylallyl diphosphate:2-acylphloroglucinol 4-dimethylallyltransferase
Comments: The enzyme, characterized from hop (*Humulus lupulus*), acts on phlorisovalerophenone, phlormethylbutanophenone, and phlorisobutanophenone during the synthesis of bitter acids. It also acts with much lower activity on naringenin chalcone. Forms a complex with EC 2.5.1.137, 2-acyl-4-prenylphloroglucinol 6-prenyltransferase, which catalyses additional prenylation reactions. Requires Mg^{2+}.
References: [3587, 1955]

[EC 2.5.1.136 created 2017]

EC 2.5.1.137

Accepted name: 2-acyl-4-prenylphloroglucinol 6-prenyltransferase
Reaction: (1) dimethylallyl diphosphate + a 2-acyl-4-prenylphloroglucinol = diphosphate + a 2-acyl-4,6-bisprenylphloroglucinol
(2) dimethylallyl diphosphate + a 2-acyl-4,6-bisprenylphloroglucinol = diphosphate + a 2-acyl-4,6,6-trisprenylcyclohexa-2,4-dien-1-one
Other name(s): PT2 (gene name); aromatic prenyltransferase (ambiguous)
Systematic name: dimethylallyl diphosphate:2-acyl-4-prenylphloroglucinol 6-dimethylallyltransferase
Comments: The enzyme, characterized from hop (*Humulus lupulus*), catalyses two successive prenylations of a 2-acyl-4-prenylphloroglucinol during the synthesis of bitter acids. Forms a complex with EC 2.5.1.136, 2-acylphloroglucinol 4-prenyltransferase, which catalyses the initial prenylation of the substrates. Requires Mg^{2+}.
References: [1955]

[EC 2.5.1.137 created 2017]

EC 2.5.1.138

Accepted name: coumarin 8-geranyltransferase
Reaction: (1) geranyl diphosphate + umbelliferone = diphosphate + 8-geranylumbelliferone
(2) geranyl diphosphate + esculetin = diphosphate + 8-geranylesculetin
Other name(s): ClPT1
Systematic name: geranyl diphosphate:umbelliferone 8-geranyltransferase
Comments: The enzyme, characterized from the plant *Citrus limon*, is specific for geranyl diphosphate as a prenyl donor. It also has low activity with the coumarins 5,7-dihydroxycoumarin and 5-methoxy-7-hydroxycoumarin.
References: [2358]

[EC 2.5.1.138 created 2017]

EC 2.5.1.139

Accepted name: umbelliferone 6-dimethylallyltransferase
Reaction: dimethylallyl diphosphate + umbelliferone = diphosphate + demethylsuberosin
Other name(s): PcPT
Systematic name: dimethylallyl diphosphate:umbelliferone 6-dimethylallyltransferase
Comments: The enzyme from parsley (*Petroselinum crispum*) is specific for umbelliferone and dimethylallyl diphosphate. A minor product is osthenol, which is produced by transfer of the dimethylallyl group to C-8 of umbelliferone.
References: [1204, 1584]

[EC 2.5.1.139 created 2017]

EC 2.5.1.140

Accepted name: *N*-(2-amino-2-carboxyethyl)-L-glutamate synthase
Reaction: *O*-phospho-L-serine + L-glutamate = *N*-[(2*S*)-2-amino-2-carboxyethyl]-L-glutamate + phosphate
Other name(s): SbnA; ACEGA synthase
Systematic name: *O*-phospho-L-serine:L-glutamate *N*-(2*S*)-2-amino-2-carboxyethyltransferase
Comments: The enzyme, characterized from the bacterium *Staphylococcus aureus*, is involved in the biosynthesis of the siderophore staphyloferrin B.
References: [243, 1726]

[EC 2.5.1.140 created 2017]

EC 2.5.1.141

Accepted name: heme *o* synthase
Reaction: (2*E*,6*E*)-farnesyl diphosphate + protoheme IX + H_2O = diphosphate + ferroheme *o*
Other name(s): *ctaB* (gene name); COX10 (gene name)
Systematic name: (2*E*,6*E*)-farnesyl-diphosphate:protoheme IX farnesyl*trans*transferase
Comments: The enzyme, found in many archaea, bacteria, and eukaryotes, produces heme *o*, which in many cases is further modified into heme *a*. In organisms that produce heme *a*, the enzyme forms a complex with heme *a* synthase.
References: [2997, 3407, 1076, 403, 2287]

[EC 2.5.1.141 created 2017]

EC 2.5.1.142

Accepted name: nerylneryl diphosphate synthase
Reaction: dimethylallyl diphosphate + **3** isopentenyl diphosphate = **3** diphosphate + nerylneryl diphosphate
Other name(s): CPT2
Systematic name: dimethylallyl-diphosphate:isopentenyl-diphosphate *cis*transferase (adding 3 isopentenyl units)
Comments: Isolated from the plant *Solanum lycopersicum* (tomato).
References: [37, 2163]

[EC 2.5.1.142 created 2017]

EC 2.5.1.143

Accepted name: pyridinium-3,5-biscarboxylic acid mononucleotide synthase
Reaction: deamido-NAD$^+$ + hydrogencarbonate = AMP + pyridinium-3,5-biscarboxylate mononucleotide
Other name(s): LarB; P2CMN synthase; nicotinic acid adenine dinucleotide carboxylase/hydrolase; NaAD carboxylase/hydrolase

Systematic name: deamido-NAD$^+$:hydrogencarbonate nicotinate-β-D-ribonucleotidyltransferase

Comments: This enzyme, found in the bacterium *Lactobacillus plantarum*, is involved in the biosynthesis of a nickel-pincer cofactor. It carboxylates the pyridinium ring of deamido-NAD$^+$ and cleaves the phosphoanhydride bond to release AMP and generate pyridinium-3,5-biscarboxylic acid mononucleotide (P2CMN).

References: [720]

[EC 2.5.1.143 created 2018]

EC 2.5.1.144

Accepted name: *S*-sulfo-L-cysteine synthase (*O*-acetyl-L-serine-dependent)

Reaction: *O*-acetyl-L-serine + thiosulfate = *S*-sulfo-L-cysteine + acetate

Other name(s): cysteine synthase B; *cysM* (gene name); CS26 (gene name)

Systematic name: *O*-acetyl-L-serine:thiosulfate 2-amino-2-carboxyethyltransferase

Comments: In plants, the activity is catalysed by a chloroplastic enzyme that plays an important role in chloroplast function and is essential for light-dependent redox regulation within the chloroplast. The bacterial enzyme also catalyses the activity of EC 2.5.1.47, cysteine synthase. *cf.* EC 2.8.5.1, *S*-sulfo-L-cysteine synthase (3-phospho-L-serine-dependent).

References: [1298, 2405, 290, 289, 1109]

[EC 2.5.1.144 created 2018]

EC 2.5.1.145

Accepted name: phosphatidylglycerol—prolipoprotein diacylglyceryl transferase

Reaction: L-1-phosphatidyl-*sn*-glycerol + a [prolipoprotein]-L-cysteine = *sn*-glycerol 1-phosphate + an [prolipoprotein]-*S*-1,2-diacyl-*sn*-glyceryl-L-cysteine

Other name(s): *lgt* (gene name)

Systematic name: L-1-phosphatidyl-*sn*-glycerol:[prolipoprotein]-L-cysteine diacyl-*sn*-glyceryltransferase

Comments: This bacterial enzyme, which is associated with the membrane, catalyses the transfer of an *sn*-1,2-diacylglyceryl group from phosphatidylglycerol to the sulfhydryl group of the prospective N-terminal cysteine of a prolipoprotein, the first step in the formation of mature triacylated lipoproteins.

References: [3021, 2777, 1005, 3020, 2597]

[EC 2.5.1.145 created 2018]

EC 2.5.1.146

Accepted name: 3-geranyl-3-[(*Z*)-2-isocyanoethenyl]indole synthase

Reaction: geranyl diphosphate + 3-[(*Z*)-2-isocyanoethenyl]-1*H*-indole = 3-geranyl-3-[(*Z*)-2-isocyanoethenyl]-1*H*-indole + diphosphate

Other name(s): *famD*2 (gene name)

Systematic name: geranyl-diphosphate:3-[(*Z*)-2-isocyanoethenyl]-1*H*-indole geranyltransferase

Comments: The enzyme, characterized from the cyanobacterium *Fischerella ambigua* UTEX 1903, participates in the biosynthesis of hapalindole-type alkaloids.

References: [1960]

[EC 2.5.1.146 created 2018]

EC 2.5.1.147

Accepted name: 5-amino-6-(D-ribitylamino)uracil—L-tyrosine 4-hydroxyphenyl transferase

Reaction: 5-amino-6-(D-ribitylamino)uracil + L-tyrosine + *S*-adenosyl-L-methionine = 5-amino-5-(4-hydroxybenzyl)-6-(D-ribitylimino)-5,6-dihydrouracil + 2-iminoacetate + L-methionine + $5'$-deoxyadenosine

Other name(s): *cofH* (gene name); *cbiF* (gene name) (ambiguous)

Systematic name: 5-amino-6-(D-ribitylamino)uracil:L-tyrosine, 4-hydroxyphenyl transferase

Comments: The enzyme is involved in the production of 7,8-didemethyl-8-hydroxy-5-deazariboflavin (FO), the precursor of the redox cofactor coenzyme F_{420}, which is found in methanogens and in various actinobacteria. FO is also produced by some cyanobacteria and eukaryotes. The enzyme, which forms a complex with EC 4.3.1.32, 7,8-didemethyl-8-hydroxy-5-deazariboflavin synthase, is a radical SAM enzyme that uses the 5′-deoxyadenosyl radical to initiate the reaction.

References: [698, 2696]

[EC 2.5.1.147 created 2010 as EC 2.5.1.77, part transferred 2018 to EC 2.5.1.147]

EC 2.5.1.148

Accepted name: lycopaoctaene synthase

Reaction: **2** geranylgeranyl diphosphate + NADPH + H^+ = lycopaoctaene + **2** diphosphate + $NADP^+$ (overall reaction)

(1a) **2** geranylgeranyl diphosphate = diphosphate + prephytoene diphosphate

(1b) prephytoene diphosphate + NADPH + H^+ = lycopaoctaene + diphosphate + $NADP^+$

Other name(s): LOS (gene name)

Systematic name: geranylgeranyl diphosphate:geranylgeranyl diphosphate geranylgeranyltransferase

Comments: The enzyme, characterized from the green microalga *Botryococcus braunii* race L, in involved in biosynthesis of (14*E*,18*E*)-lycopadiene. *In vitro*, the enzyme can accept (2*E*,6*E*)-farnesyl diphosphate and phytyl diphosphate as substrates, and is also able to catalyse the condensation of two different substrate molecules, forming chimeric products. However, the use of these alternative substrates is not significant *in vivo*.

References: [3511, 3512]

[EC 2.5.1.148 created 2018]

EC 2.5.1.149

Accepted name: lycopene elongase/hydratase (flavuxanthin-forming)

Reaction: (1) dimethylallyl diphosphate + *all-trans*-lycopene + acceptor + H_2O = nonaflavuxanthin + reduced electron acceptor + diphosphate

(2) dimethylallyl diphosphate + nonaflavuxanthin + acceptor + H_2O = flavuxanthin + reduced electron acceptor + diphosphate

Other name(s): *crtEb* (gene name)

Systematic name: dimethylallyl-diphosphate:*all-trans*-lycopene dimethylallyltransferase (hydrating, flavuxanthin-forming)

Comments: The enzyme, characterized from the bacterium *Corynebacterium glutamicum*, is bifunctional. It catalyses the elongation of the C_{40} carotenoid *all-trans*-lycopene by attaching an isoprene unit at C-2, as well as the hydroxylation of the new isoprene unit. The enzyme acts at both ends of the substrate, forming the C_{50} carotenoid flavuxanthin via the C_{45} intermediate nonaflavuxanthin. *cf.* EC 2.5.1.150, lycopene elongase/hydratase (dihydrobisanhydrobacterioruberin-forming).

References: [1794, 1277]

[EC 2.5.1.149 created 2018]

EC 2.5.1.150

Accepted name: lycopene elongase/hydratase (dihydrobisanhydrobacterioruberin-forming)

Reaction: (1) dimethylallyl diphosphate + *all-trans*-lycopene + H_2O = dihydroisopentenyldehydrorhodopin + diphosphate

(2) dimethylallyl diphosphate + isopentenyldehydrorhodopin + H_2O = dihydrobisanhydrobacterioruberin + diphosphate

Other name(s): *lbtA* (gene name); *lyeJ* (gene name)

Systematic name: dimethylallyl-diphosphate:*all-trans*-lycopene dimethylallyltransferase (hydrating, dihydrobisanhydrobacterioruberin-forming)

Comments: The enzyme, characterized from the bacterium *Dietzia* sp. CQ4 and the halophilic archaea *Halobacterium salinarum* and *Haloarcula japonica*, is bifunctional. It catalyses the elongation of the C_{40} carotenoid *all-trans*-lycopene by attaching an isoprene unit at C-2 as well as the hydroxylation of the previous end of the molecule. The enzyme acts at both ends of the substrate, and combined with the action of EC 1.3.99.37, 1-hydroxy-2-isopentenylcarotenoid 3,4-desaturase, it forms the C_{50} carotenoid dihydrobisanhydrobacterioruberin. *cf.* EC 2.5.1.149, lycopene elongase/hydratase (flavuxanthin-forming).

References: [3474, 792, 3966]

[EC 2.5.1.150 created 2018]

EC 2.5.1.151

Accepted name: alkylcobalamin dealkylase

Reaction: an alkylcobalamin + [alkylcobalamin reductase] + glutathione = cob(I)alamin-[alkylcobalamin reductase] + an *S*-alkylglutathione

Other name(s): MMACHC (gene name)

Systematic name: alkylcobalamin:glutathione *S*-alkyltransferase

Comments: This mammalian enzyme, which is cytosolic, can bind internalized alkylcobalamins and process them to cob(I)alamin using the thiolate of glutathione for nucleophilic displacement. The product remains bound to the protein, and, following its oxidation to cob(II)alamin, is transferred by the enzyme, together with its interacting partner MMADHC, directly to downstream enzymes involved in adenosylcobalamin and methylcobalamin biosynthesis. In addition to its dealkylase function, the enzyme also catalyse an entirely different decyanase reaction with cyanocobalamin [*cf.* EC 1.16.1.6, cyanocobalamin reductase (cyanide-eliminating)].

References: [1211, 1680, 1774]

[EC 2.5.1.151 created 2018]

EC 2.6 Transferring nitrogenous groups

This subclass contains enzymes that transfer a nitrogenous group from a donor to an acceptor. Most enzymes in this subclass belong in EC 2.6.1, which is for enzymes that transfer amino groups from a donor, generally an amino acid, to an acceptor, generally a 2-oxo acid. It should be kept in mind that transamination by this reaction also involves an oxidoreduction; the donor is oxidized to a ketone, while the acceptor is reduced. Nevertheless, since the transfer of the amino group is the most prominent feature of this reaction, these enzymes have been classified as aminotransferases rather than oxidoreductases (transaminating). Most of these enzymes are pyridoxal-phosphate proteins. Sub-subclasses are based on the type of nitrogenous group that is transferred: transaminase (EC 2.6.1), oximinotransferase (EC 2.6.3) and other nitrogenous groups (EC 2.6.99).

EC 2.6.1 Transaminases

‘Transaminase’ may be replaced by ‘aminotransferase’

EC 2.6.1.1

Accepted name: aspartate transaminase

Reaction: L-aspartate + 2-oxoglutarate = oxaloacetate + L-glutamate

Other name(s): glutamic-oxaloacetic transaminase; glutamic-aspartic transaminase; transaminase A; AAT; AspT; 2-oxoglutarate-glutamate aminotransferase; aspartate α-ketoglutarate transaminase; aspartate aminotransferase; aspartate-2-oxoglutarate transaminase; aspartic acid aminotransferase; aspartic aminotransferase; aspartyl aminotransferase; AST; glutamate-oxalacetate aminotransferase; glutamate-oxalate transaminase; glutamic-aspartic aminotransferase; glutamic-oxalacetic transaminase; glutamic oxalic transaminase; GOT (enzyme) [ambiguous]; L-aspartate transaminase; L-aspartate-α-ketoglutarate transaminase; L-aspartate-2-ketoglutarate aminotransferase; L-aspartate-2-oxoglutarate aminotransferase; L-aspartate-2-oxoglutarate-transaminase; L-aspartic aminotransferase; oxaloacetate-aspartate aminotransferase; oxaloacetate transferase; aspartate:2-oxoglutarate aminotransferase; glutamate oxaloacetate transaminase

Systematic name: L-aspartate:2-oxoglutarate aminotransferase

Comments: A pyridoxal-phosphate protein. Also acts on L-tyrosine, L-phenylalanine and L-tryptophan. Aspartate transaminase activity can be formed from the aromatic-amino-acid transaminase (EC 2.6.1.57) of *Escherichia coli* by controlled proteolysis [2176], some EC 2.6.1.57 activity can be found in this enzyme from other sources [3106]; indeed the enzymes are identical in *Trichomonas vaginalis* [2049].

References: [181, 292, 930, 1300, 1506, 2049, 2176, 3106, 3213]

[EC 2.6.1.1 created 1961, modified 1976]

EC 2.6.1.2

Accepted name: alanine transaminase

Reaction: L-alanine + 2-oxoglutarate = pyruvate + L-glutamate

Other name(s): glutamic-pyruvic transaminase; glutamic-alanine transaminase; GPT (ambiguous); β-alanine aminotransferase; alanine aminotransferase; alanine-α-ketoglutarate aminotransferase; alanine-pyruvate aminotransferase; ALT; glutamic acid-pyruvic acid transaminase; glutamic-pyruvic aminotransferase; L-alanine aminotransferase; L-alanine transaminase; L-alanine-α-ketoglutarate aminotransferase; pyruvate transaminase; pyruvate-alanine aminotransferase; pyruvate-glutamate transaminase

Systematic name: L-alanine:2-oxoglutarate aminotransferase

Comments: A pyridoxal-phosphate protein. 2-Aminobutanoate can act slowly instead of alanine.

References: [789, 790, 1130, 1447, 3866]

[EC 2.6.1.2 created 1961]

EC 2.6.1.3

Accepted name: cysteine transaminase

Reaction: L-cysteine + 2-oxoglutarate = mercaptopyruvate + L-glutamate

Other name(s): cysteine aminotransferase; L-cysteine aminotransferase; CGT

Systematic name: L-cysteine:2-oxoglutarate aminotransferase

Comments: A pyridoxal-phosphate protein.

References: [510]

[EC 2.6.1.3 created 1961]

EC 2.6.1.4

Accepted name: glycine transaminase

Reaction: glycine + 2-oxoglutarate = glyoxylate + L-glutamate

Other name(s): glutamic-glyoxylic transaminase; glycine aminotransferase; glyoxylate-glutamic transaminase; L-glutamate:glyoxylate aminotransferase; glyoxylate-glutamate aminotransferase

Systematic name: glycine:2-oxoglutarate aminotransferase

Comments: A pyridoxal-phosphate protein.

References: [2397, 3526]

[EC 2.6.1.4 created 1961, modified 1982]

EC 2.6.1.5

Accepted name: tyrosine transaminase
Reaction: L-tyrosine + 2-oxoglutarate = 4-hydroxyphenylpyruvate + L-glutamate
Other name(s): tyrosine aminotransferase; glutamic-hydroxyphenylpyruvic transaminase; glutamic phenylpyruvic aminotransferase; L-phenylalanine 2-oxoglutarate aminotransferase; L-tyrosine aminotransferase; phenylalanine aminotransferase; phenylalanine transaminase; phenylalanine-α-ketoglutarate transaminase; phenylpyruvate transaminase; phenylpyruvic acid transaminase; tyrosine-α-ketoglutarate aminotransferase; tyrosine-α-ketoglutarate transaminase; tyrosine-2-ketoglutarate aminotransferase; TyrAT
Systematic name: L-tyrosine:2-oxoglutarate aminotransferase
Comments: A pyridoxal-phosphate protein. L-Phenylalanine can act instead of L-tyrosine. The mitochondrial enzyme may be identical with EC 2.6.1.1 (aspartate transaminase). The three isoenzymic forms are interconverted by EC 3.4.22.32 (stem bromelain) and EC 3.4.22.33 (fruit bromelain). The enzyme can also catalyse the final step in the methionine-salvage pathway of *Klebsiella pneumoniae* [1278].
References: [468, 467, 1485, 1643, 2253, 2951, 3142, 1278]

[EC 2.6.1.5 created 1961]

EC 2.6.1.6

Accepted name: leucine transaminase
Reaction: L-leucine + 2-oxoglutarate = 4-methyl-2-oxopentanoate + L-glutamate
Other name(s): L-leucine aminotransferase; leucine 2-oxoglutarate transaminase; leucine aminotransferase; leucine-α-ketoglutarate transaminase
Systematic name: L-leucine:2-oxoglutarate aminotransferase
Comments: A pyridoxal-phosphate protein. This enzyme differs from EC 2.6.1.42, branched-chain-amino-acid transaminase, in that it does not act on L-valine or L-isoleucine, although it does act on L-methionine. The mitochondrial form from rat liver differs in physical characteristics from the cytoplasmic form.
References: [38, 1435]

[EC 2.6.1.6 created 1961, modified 1982]

EC 2.6.1.7

Accepted name: kynurenine—oxoglutarate transaminase
Reaction: L-kynurenine + 2-oxoglutarate = 4-(2-aminophenyl)-2,4-dioxobutanoate + L-glutamate
Other name(s): kynurenine transaminase (cyclizing); kynurenine 2-oxoglutarate transaminase; kynurenine aminotransferase; L-kynurenine aminotransferase
Systematic name: L-kynurenine:2-oxoglutarate aminotransferase
Comments: A pyridoxal-phosphate protein. Also acts on 3-hydroxykynurenine. The product 4-(2-aminophenyl)-2,4-dioxobutanoate is converted into kynurenate by a spontaneous reaction.
References: [1494, 2151]

[EC 2.6.1.7 created 1961, modified 1983]

EC 2.6.1.8

Accepted name: 2,5-diaminovalerate transaminase
Reaction: 2,5-diaminopentanoate + 2-oxoglutarate = 5-amino-2-oxopentanoate + L-glutamate
Other name(s): diamino-acid transaminase; diamino acid aminotransferase
Systematic name: 2,5-diaminopentanoate:2-oxoglutarate aminotransferase
Comments: A pyridoxal-phosphate protein. 2,5-Diaminoglutarate can act instead of diaminopentanoate.
References: [2895]

[EC 2.6.1.8 created 1961, modified 1982]

EC 2.6.1.9

Accepted name: histidinol-phosphate transaminase
Reaction: L-histidinol phosphate + 2-oxoglutarate = 3-(imidazol-4-yl)-2-oxopropyl phosphate + L-glutamate
Other name(s): imidazolylacetolphosphate transaminase; glutamic-imidazoleacetol phosphate transaminase; histidinol phosphate aminotransferase; imidazoleacetol phosphate transaminase; L-histidinol phosphate aminotransferase; histidine:imidazoleacetol phosphate transaminase; IAP transaminase; imidazolylacetolphosphate aminotransferase
Systematic name: L-histidinol-phosphate:2-oxoglutarate aminotransferase
Comments: A pyridoxal-phosphate protein.
References: [69, 2140]

[EC 2.6.1.9 created 1961]

[2.6.1.10 Deleted entry. D*-aspartate transaminase. Now included with EC 2.6.1.21,* D*-amino-acid transaminase]*

[EC 2.6.1.10 created 1961, deleted 1972]

EC 2.6.1.11

Accepted name: acetylornithine transaminase
Reaction: N^2-acetyl-L-ornithine + 2-oxoglutarate = *N*-acetyl-L-glutamate 5-semialdehyde + L-glutamate
Other name(s): acetylornithine δ-transaminase; ACOAT; acetylornithine 5-aminotransferase; acetylornithine aminotransferase; *N*-acetylornithine aminotransferase; *N*-acetylornithine-δ-transaminase; N^2-acetylornithine 5-transaminase; N^2-acetyl-L-ornithine:2-oxoglutarate aminotransferase; succinylornithine aminotransferase; 2-*N*-acetyl-L-ornithine:2-oxoglutarate 5-aminotransferase
Systematic name: N^2-acetyl-L-ornithine:2-oxoglutarate 5-aminotransferase
Comments: A pyridoxal-phosphate protein. Also acts on L-ornithine and N^2-succinyl-L-ornithine.
References: [48, 3694, 3792, 3693]

[EC 2.6.1.11 created 1961, modified 2004 (EC 2.6.1.69 created 1989, incorporated 2004)]

EC 2.6.1.12

Accepted name: alanine—oxo-acid transaminase
Reaction: L-alanine + a 2-oxo carboxylate = pyruvate + an L-amino acid
Other name(s): L-alanine-α-keto acid aminotransferase; leucine-alanine transaminase; alanine-keto acid aminotransferase; alanine-oxo acid aminotransferase
Systematic name: L-alanine:2-oxo-acid aminotransferase
Comments: A pyridoxal-phosphate protein.
References: [65, 2950, 3009, 3866]

[EC 2.6.1.12 created 1961]

EC 2.6.1.13

Accepted name: ornithine aminotransferase
Reaction: L-ornithine + a 2-oxo carboxylate = L-glutamate 5-semialdehyde + an L-amino acid
Other name(s): ornithine δ-transaminase; L-ornithine:α-ketoglutarate δ-aminotransferase; OAT; L-ornithine 5-aminotransferase; L-ornithine aminotransferase; ornithine 5-aminotransferase; ornithine transaminase; ornithine-α-ketoglutarate aminotransferase; ornithine-2-oxoacid aminotransferase; ornithine-keto acid aminotransferase; ornithine-keto acid transaminase; ornithine-ketoglutarate aminotransferase; ornithine-oxo acid aminotransferase; ornithine:α-oxoglutarate transaminase; ornithine—oxo-acid transaminase
Systematic name: L-ornithine:2-oxo-acid aminotransferase
Comments: A pyridoxal-phosphate protein.
References: [904, 1608, 2206, 2660, 2780, 3371]

[EC 2.6.1.13 created 1961]

EC 2.6.1.14

Accepted name: asparagine—oxo-acid transaminase

Reaction: L-asparagine + a 2-oxo carboxylate = 2-oxosuccinamate + an amino acid

Other name(s): asparagine-keto acid aminotransferase

Systematic name: L-asparagine:2-oxo-acid aminotransferase

Comments: A pyridoxal-phosphate protein.

References: [2208]

[EC 2.6.1.14 created 1961]

EC 2.6.1.15

Accepted name: glutamine—pyruvate transaminase

Reaction: L-glutamine + pyruvate = 2-oxoglutaramate + L-alanine

Other name(s): glutaminase II; L-glutamine transaminase L; glutamine-oxo-acid transaminase

Systematic name: L-glutamine:pyruvate aminotransferase

Comments: A pyridoxal-phosphate protein. L-Methionine can act as donor; glyoxylate can act as acceptor.

References: [608, 2207]

[EC 2.6.1.15 created 1961]

EC 2.6.1.16

Accepted name: glutamine—fructose-6-phosphate transaminase (isomerizing)

Reaction: L-glutamine + D-fructose 6-phosphate = L-glutamate + D-glucosamine 6-phosphate

Other name(s): hexosephosphate aminotransferase; glucosamine-6-phosphate isomerase (glutamine-forming); glutamine-fructose-6-phosphate transaminase (isomerizing); D-fructose-6-phosphate amidotransferase; glucosaminephosphate isomerase; glucosamine 6-phosphate synthase; GlcN6P synthase

Systematic name: L-glutamine:D-fructose-6-phosphate isomerase (deaminating)

Comments: Although the overall reaction is that of a transferase, the mechanism involves the formation of ketimine between fructose 6-phosphate and a 6-amino group from a lysine residue at the active site, which is subsequently displaced by ammonia (transamidination).

References: [1044, 1161, 1927, 3500]

[EC 2.6.1.16 created 1961, deleted 1972, reinstated 1984, modified 2000 (EC 5.3.1.19 created 1972, incorporated 1984)]

EC 2.6.1.17

Accepted name: succinyldiaminopimelate transaminase

Reaction: *N*-succinyl-L-2,6-diaminoheptanedioate + 2-oxoglutarate = *N*-succinyl-L-2-amino-6-oxoheptanedioate + L-glutamate

Other name(s): succinyldiaminopimelate aminotransferase; *N*-succinyl-L-diaminopimelic glutamic transaminase

Systematic name: *N*-succinyl-L-2,6-diaminoheptanedioate:2-oxoglutarate aminotransferase

Comments: A pyridoxal-phosphate protein.

References: [2671]

[EC 2.6.1.17 created 1965]

EC 2.6.1.18

Accepted name: β-alanine—pyruvate transaminase

Reaction: L-alanine + 3-oxopropanoate = pyruvate + β-alanine

Other name(s): β-alanine-pyruvate aminotransferase; β-alanine-α-alanine transaminase

Systematic name: L-alanine:3-oxopropanoate aminotransferase

Comments: A pyridoxal-phosphate protein.

References: [1251, 3345]

[EC 2.6.1.18 created 1965]

EC 2.6.1.19

Accepted name: 4-aminobutyrate—2-oxoglutarate transaminase

Reaction: 4-aminobutanoate + 2-oxoglutarate = succinate semialdehyde + L-glutamate

Other name(s): β-alanine-oxoglutarate transaminase; aminobutyrate aminotransferase (ambiguous); β-alanine aminotransferase; β-alanine-oxoglutarate aminotransferase; γ-aminobutyrate aminotransaminase (ambiguous); γ-aminobutyrate transaminase (ambiguous); γ-aminobutyrate-α-ketoglutarate aminotransferase; γ-aminobutyrate-α-ketoglutarate transaminase; γ-aminobutyrate:α-oxoglutarate aminotransferase; γ-aminobutyric acid aminotransferase (ambiguous); γ-aminobutyric acid transaminase (ambiguous); γ-aminobutyric acid-α-ketoglutarate transaminase; γ-aminobutyric acid-α-ketoglutaric acid aminotransferase; γ-aminobutyric acid-2-oxoglutarate transaminase; γ-aminobutyric transaminase (ambiguous); 4-aminobutyrate aminotransferase (ambiguous); 4-aminobutyrate-2-ketoglutarate aminotransferase; 4-aminobutyrate-2-oxoglutarate aminotransferase; 4-aminobutyrate-2-oxoglutarate transaminase; 4-aminobutyric acid 2-ketoglutaric acid aminotransferase; 4-aminobutyric acid aminotransferase (ambiguous); aminobutyrate transaminase (ambiguous); GABA aminotransferase (ambiguous); GABA transaminase (ambiguous); GABA transferase; GABA-α-ketoglutarate aminotransferase; GABA-α-ketoglutarate transaminase; GABA-α-ketoglutaric acid transaminase; GABA-α-oxoglutarate aminotransferase; GABA-2-oxoglutarate aminotransferase; GABA-2-oxoglutarate transaminase; GABA-oxoglutarate aminotransferase; GABA-oxoglutarate transaminase; glutamate-succinic semialdehyde transaminase; GabT

Systematic name: 4-aminobutanoate:2-oxoglutarate aminotransferase

Comments: Requires pyridoxal phosphate. Some preparations also act on β-alanine, 5-aminopentanoate and (*R*,*S*)-3-amino-2-methylpropanoate.

References: [3129, 130, 3065, 212]

[EC 2.6.1.19 created 1965, modified 1982, modified 2012]

[2.6.1.20 Deleted entry. tyrosine—pyruvate transaminase]

[EC 2.6.1.20 created 1965, deleted 1972]

EC 2.6.1.21

Accepted name: D-amino-acid transaminase

Reaction: D-alanine + 2-oxoglutarate = pyruvate + D-glutamate

Other name(s): D-aspartate transaminase; D-alanine aminotransferase; D-aspartic aminotransferase; D-alanine-D-glutamate transaminase; D-alanine transaminase; D-amino acid aminotransferase

Systematic name: D-alanine:2-oxoglutarate aminotransferase

Comments: A pyridoxal-phosphate protein. The enzyme from thermophilic *Bacillus* species acts on many D-amino acids with D-alanine and D-2-aminobutyrate as the best amino donors. It can similarly use any of several 2-oxo acids as amino acceptor, with 2-oxoglutarate and 2-oxobutyrate among the best. The enzyme from some other sources has a broader specificity [3470].

References: [3530, 3531, 2143, 2589, 3991, 3470, 938, 3641, 3378]

[EC 2.6.1.21 created 1972 (EC 2.6.1.10 created 1961, incorporated 1972), modified 2005]

EC 2.6.1.22

Accepted name: (*S*)-3-amino-2-methylpropionate transaminase

Reaction: (*S*)-3-amino-2-methylpropanoate + 2-oxoglutarate = 2-methyl-3-oxopropanoate + L-glutamate

Other name(s): L-3-aminoisobutyrate transaminase; β-aminobutyric transaminase; L-3-aminoisobutyric aminotransferase; β-aminoisobutyrate-α-ketoglutarate transaminase

Systematic name: (*S*)-3-amino-2-methylpropanoate:2-oxoglutarate aminotransferase

Comments: Also acts on β-alanine and other ω-amino acids having carbon chains between 2 and 5. The two enantiomers of the 2-methyl-3-oxopropanoate formed by the enzyme interconvert by enolization, so that this enzyme, together with EC 2.6.1.40, (*R*)-3-amino-2-methylpropionate—pyruvate transaminase, provide a route for interconversion of the enantiomers of 3-amino-2-methylpropanoate.
References: [1558, 3460]

[EC 2.6.1.22 created 1972, modified 1982, modified 2004]

EC 2.6.1.23

Accepted name: 4-hydroxyglutamate transaminase
Reaction: 4-hydroxy-L-glutamate + 2-oxoglutarate = 4-hydroxy-2-oxoglutarate + L-glutamate
Other name(s): 4-hydroxyglutamate aminotransferase
Systematic name: 4-hydroxy-L-glutamate:2-oxoglutarate aminotransferase
Comments: Oxaloacetate can replace 2-oxoglutarate. This enzyme may be identical with EC 2.6.1.1 aspartate transaminase.
References: [1093, 1826]

[EC 2.6.1.23 created 1972, modified 1982]

EC 2.6.1.24

Accepted name: diiodotyrosine transaminase
Reaction: 3,5-diiodo-L-tyrosine + 2-oxoglutarate = 4-hydroxy-3,5-diiodophenylpyruvate + L-glutamate
Other name(s): diiodotyrosine aminotransferase; halogenated tyrosine aminotransferase; halogenated tyrosine transaminase
Systematic name: 3,5-diiodo-L-tyrosine:2-oxoglutarate aminotransferase
Comments: A pyridoxal-phosphate protein. Also acts on 3,5-dichloro-, 3,5-dibromo- and 3-iodo-L-tyrosine, thyroxine and triiodothyronine.
References: [2411, 2412]

[EC 2.6.1.24 created 1972 (EC 2.6.1.25 created 1972, incorporated 1972)]

[2.6.1.25 Deleted entry. thyroxine transaminase. Now included with EC 2.6.1.24 diiodotyrosine transaminase]

[EC 2.6.1.25 created 1972, deleted 1984]

EC 2.6.1.26

Accepted name: thyroid-hormone transaminase
Reaction: L-3,5,3′-triiodothyronine + 2-oxoglutarate = 3-[4-(4-hydroxy-3-iodophenoxy)-3,5-diiodophenyl]-2-oxopropanoate + L-glutamate
Other name(s): 3,5-dinitrotyrosine transaminase; thyroid hormone aminotransferase
Systematic name: L-3,5,3′-triiodothyronine:2-oxoglutarate aminotransferase
Comments: A pyridoxal-phosphate protein. Acts on monoiodotyrosine, diiodotyrosine, triiodothyronine, thyroxine and dinitrotyrosine (unlike EC 2.6.1.24 diiodotyrosine transaminase, which does not act on dinitrotyrosine). Pyruvate or oxaloacetate can act as acceptors.
References: [3276]

[EC 2.6.1.26 created 1972]

EC 2.6.1.27

Accepted name: tryptophan transaminase
Reaction: L-tryptophan + 2-oxoglutarate = (indol-3-yl)pyruvate + L-glutamate
Other name(s): L-phenylalanine-2-oxoglutarate aminotransferase; tryptophan aminotransferase; 5-hydroxytryptophan-ketoglutaric transaminase; hydroxytryptophan aminotransferase; L-tryptophan aminotransferase; L-tryptophan transaminase

Systematic name: L-tryptophan:2-oxoglutarate aminotransferase
Comments: A pyridoxal-phosphate protein. Also acts on 5-hydroxytryptophan and, to a lesser extent, on the phenyl amino acids.
References: [1035, 2565, 3467]

[EC 2.6.1.27 created 1972]

EC 2.6.1.28

Accepted name: tryptophan—phenylpyruvate transaminase
Reaction: L-tryptophan + phenylpyruvate = (indol-3-yl)pyruvate + L-phenylalanine
Other name(s): L-tryptophan-α-ketoisocaproate aminotransferase
Systematic name: L-tryptophan:phenylpyruvate aminotransferase
Comments: Valine, leucine and isoleucine can replace tryptophan as amino donor.
References: [1738, 3382]

[EC 2.6.1.28 created 1972]

EC 2.6.1.29

Accepted name: diamine transaminase
Reaction: an α,ω-diamine + 2-oxoglutarate = an ω-aminoaldehyde + L-glutamate
Other name(s): amine transaminase; amine-ketoacid transaminase; diamine aminotransferase; diamine-ketoglutaric transaminase
Systematic name: diamine:2-oxoglutarate aminotransferase
References: [1681]

[EC 2.6.1.29 created 1972]

EC 2.6.1.30

Accepted name: pyridoxamine—pyruvate transaminase
Reaction: pyridoxamine + pyruvate = pyridoxal + L-alanine
Other name(s): pyridoxamine-pyruvic transaminase
Systematic name: pyridoxamine:pyruvate aminotransferase
References: [3711]

[EC 2.6.1.30 created 1972]

EC 2.6.1.31

Accepted name: pyridoxamine—oxaloacetate transaminase
Reaction: pyridoxamine + oxaloacetate = pyridoxal + L-aspartate
Systematic name: pyridoxamine:oxaloacetate aminotransferase
References: [3710, 3902]

[EC 2.6.1.31 created 1972]

EC 2.6.1.32

Accepted name: valine—3-methyl-2-oxovalerate transaminase
Reaction: L-valine + (*S*)-3-methyl-2-oxopentanoate = 3-methyl-2-oxobutanoate + L-isoleucine
Other name(s): valine—isoleucine transaminase; valine-3-methyl-2-oxovalerate aminotransferase; alanine-valine transaminase; valine-2-keto-methylvalerate aminotransferase; valine-isoleucine aminotransferase
Systematic name: L-valine:(*S*)-3-methyl-2-oxopentanoate aminotransferase
References: [1552]

[EC 2.6.1.32 created 1972, modified 1976]

EC 2.6.1.33

Accepted name: dTDP-4-amino-4,6-dideoxy-D-glucose transaminase

Reaction: dTDP-4-amino-4,6-dideoxy-α-D-glucose + 2-oxoglutarate = dTDP-4-dehydro-6-deoxy-α-D-glucose + L-glutamate

Other name(s): thymidine diphospho-4-amino-4,6-dideoxyglucose aminotransferase; thymidine diphospho-4-amino-6-deoxyglucose aminotransferase; thymidine diphospho-4-keto-6-deoxy-D-glucose transaminase; thymidine diphospho-4-keto-6-deoxy-D-glucose-glutamic transaminase; TDP-4-keto-6-deoxy-D-glucose transaminase; VioA; dTDP-4-amino-4,6-dideoxy-D-glucose:2-oxoglutarate aminotransferase

Systematic name: dTDP-4-amino-4,6-dideoxy-α-D-glucose:2-oxoglutarate aminotransferase

Comments: A pyridoxal-phosphate protein.

References: [2166, 3769]

[EC 2.6.1.33 created 1972]

EC 2.6.1.34

Accepted name: UDP-*N*-acetylbacillosamine transaminase

Reaction: UDP-*N*-acetylbacillosamine + 2-oxoglutarate = UDP-2-acetamido-2,6-dideoxy-α-D-*xylo*-hex-4-ulose + L-glutamate

Other name(s): uridine diphospho-4-amino-2-acetamido-2,4,6-trideoxyglucose aminotransferase; UDP-4-amino-4,6-dideoxy-*N*-acetyl-α-D-glucosamine transaminase; UDP-2-acetamido-4-amino-2,4,6-trideoxyglucose transaminase; *pglE* (gene name); UDP-2-acetamido-4-amino-2,4,6-trideoxyglucose:2-oxoglutarate aminotransferase

Systematic name: UDP-4-amino-4,6-dideoxy-*N*-acetyl-α-D-glucosamine:2-oxoglutarate aminotransferase

Comments: A pyridoxal-phosphate protein. The enzyme is involved in biosynthesis of UDP-*N*,*N*′-diacetylbacillosamine, an intermediate in protein glycosylation pathways in several bacterial species, including N-linked glycosylation of certain L-asparagine residues in *Campylobacter* species [2559, 3099, 2809] and O-linked glycosylation of certain L-serine residues in *Neisseria* species [1232].

References: [741, 2559, 3099, 2809, 1232]

[EC 2.6.1.34 created 1972, modified 2013]

EC 2.6.1.35

Accepted name: glycine—oxaloacetate transaminase

Reaction: glycine + oxaloacetate = glyoxylate + L-aspartate

Other name(s): glycine-oxalacetate aminotransferase

Systematic name: glycine:oxaloacetate aminotransferase

Comments: A pyridoxal-phosphate protein.

References: [1049]

[EC 2.6.1.35 created 1972]

EC 2.6.1.36

Accepted name: L-lysine 6-transaminase

Reaction: L-lysine + 2-oxoglutarate = (*S*)-2-amino-6-oxohexanoate + L-glutamate

Other name(s): lysine 6-aminotransferase; lysine ε-aminotransferase; lysine ε-transaminase; lysine:2-ketoglutarate 6-aminotransferase; L-lysine-α-ketoglutarate aminotransferase; L-lysine-α-ketoglutarate 6-aminotransferase

Systematic name: L-lysine:2-oxoglutarate 6-aminotransferase

Comments: A pyridoxal-phosphate protein. The product (L-allysine) is converted into the intramolecularly dehydrated form, (*S*)-2,3,4,5-tetrahydropyridine-2-carboxylate.

References: [3271, 3270]

[EC 2.6.1.36 created 1972, modified 2011]

EC 2.6.1.37

Accepted name: 2-aminoethylphosphonate—pyruvate transaminase

Reaction: (2-aminoethyl)phosphonate + pyruvate = 2-phosphonoacetaldehyde + L-alanine

Other name(s): (2-aminoethyl)phosphonate transaminase; (2-aminoethyl)phosphonate aminotransferase; (2-aminoethyl)phosphonic acid aminotransferase; 2-aminoethylphosphonate-pyruvate aminotransferase; 2-aminoethylphosphonate aminotransferase; 2-aminoethylphosphonate transaminase; AEP transaminase; AEPT

Systematic name: (2-aminoethyl)phosphonate:pyruvate aminotransferase

Comments: A pyridoxal-phosphate protein. 2-Aminoethylarsonate can replace 2-aminoethylphosphonate as a substrate.

References: [2424, 793, 1838, 1837]

[EC 2.6.1.37 created 1972, modified 1982, modified 2001]

EC 2.6.1.38

Accepted name: histidine transaminase

Reaction: L-histidine + 2-oxoglutarate = (imidazol-5-yl)pyruvate + L-glutamate

Other name(s): histidine aminotransferase; histidine-2-oxoglutarate aminotransferase

Systematic name: L-histidine:2-oxoglutarate aminotransferase

References: [612, 3846]

[EC 2.6.1.38 created 1972]

EC 2.6.1.39

Accepted name: 2-aminoadipate transaminase

Reaction: L-2-aminoadipate + 2-oxoglutarate = 2-oxoadipate + L-glutamate

Other name(s): α-aminoadipate aminotransferase; 2-aminoadipate aminotransferase; 2-aminoadipic aminotransferase; glutamic-ketoadipic transaminase; glutamate-α-ketoadipate transaminase

Systematic name: L-2-aminoadipate:2-oxoglutarate aminotransferase

Comments: A pyridoxal-phosphate protein.

References: [2165]

[EC 2.6.1.39 created 1972]

EC 2.6.1.40

Accepted name: (*R*)-3-amino-2-methylpropionate—pyruvate transaminase

Reaction: (*R*)-3-amino-2-methylpropanoate + pyruvate = 2-methyl-3-oxopropanoate + L-alanine

Other name(s): D-3-aminoisobutyrate—pyruvate transaminase; β-aminoisobutyrate-pyruvate aminotransferase; D-3-aminoisobutyrate-pyruvate aminotransferase; D-3-aminoisobutyrate-pyruvate transaminase; (*R*)-3-amino-2-methylpropionate transaminase; D-β-aminoisobutyrate:pyruvate aminotransferase

Systematic name: (*R*)-3-amino-2-methylpropanoate:pyruvate aminotransferase

Comments: The two enantiomers of the 2-methyl-3-oxopropanoate formed by the enzyme interconvert by enolization, so that this enzyme, together with EC 2.6.1.22, (*S*)-3-amino-2-methylpropionate transaminase, provide a route for interconversion of the enantiomers of 3-amino-2-methylpropanoate.

References: [1559, 3460]

[EC 2.6.1.40 created 1972 (EC 2.6.1.61 created 1982, incorporated 2004) modified 2004]

EC 2.6.1.41

Accepted name: D-methionine—pyruvate transaminase

Reaction: D-methionine + pyruvate = 4-(methylsulfanyl)-2-oxobutanoate + L-alanine

Other name(s): D-methionine transaminase; D-methionine aminotransferase

Systematic name: D-methionine:pyruvate aminotransferase

Comments: Oxaloacetate can replace pyruvate.

References: [2117]

[EC 2.6.1.41 created 1972, modified 1982]

EC 2.6.1.42

Accepted name: branched-chain-amino-acid transaminase

Reaction: L-leucine + 2-oxoglutarate = 4-methyl-2-oxopentanoate + L-glutamate

Other name(s): transaminase B; branched-chain amino acid aminotransferase; branched-chain amino acid-glutamate transaminase; branched-chain aminotransferase; L-branched chain amino acid aminotransferase; glutamate-branched-chain amino acid transaminase

Systematic name: branched-chain-amino-acid:2-oxoglutarate aminotransferase

Comments: Also acts on L-isoleucine and L-valine, and thereby differs from EC 2.6.1.6, leucine transaminase, which does not. It also differs from EC 2.6.1.66, valine—pyruvate transaminase.

References: [38, 39, 1428, 3485, 2960]

[EC 2.6.1.42 created 1972]

EC 2.6.1.43

Accepted name: aminolevulinate transaminase

Reaction: 5-aminolevulinate + pyruvate = 4,5-dioxopentanoate + L-alanine

Other name(s): aminolevulinate aminotransferase, γ,δ-dioxovalerate aminotransferase; γ,δ-dioxovaleric acid transaminase; 4,5-dioxovalerate aminotransferase; 4,5-dioxovaleric acid transaminase; 4,5-dioxovaleric transaminase; 5-aminolevulinic acid transaminase; alanine-γ,δ-dioxovalerate aminotransferase; alanine-dioxovalerate aminotransferase; alanine:4,5-dioxovalerate aminotransferase; aminolevulinic acid transaminase; dioxovalerate transaminase; L-alanine-4,5-dioxovalerate aminotransferase; L-alanine:4,5-dioxovaleric acid transaminase; L-alanine:dioxovalerate transaminase; DOVA transaminase; 4,5-dioxovaleric acid aminotransferase

Systematic name: 5-aminolevulinate:pyruvate aminotransferase

Comments: A pyridoxal-phosphate protein.

References: [1052, 2436]

[EC 2.6.1.43 created 1972]

EC 2.6.1.44

Accepted name: alanine—glyoxylate transaminase

Reaction: L-alanine + glyoxylate = pyruvate + glycine

Other name(s): AGT; alanine-glyoxylate aminotransferase; alanine-glyoxylic aminotransferase; L-alanine-glycine transaminase

Systematic name: L-alanine:glyoxylate aminotransferase

Comments: A pyridoxal-phosphate protein. With one component of the animal enzyme, 2-oxobutanoate can replace glyoxylate. A second component also catalyses the reaction of EC 2.6.1.51 serine—pyruvate transaminase.

References: [2484, 2555, 3527]

[EC 2.6.1.44 created 1972, modified 1982]

EC 2.6.1.45

Accepted name: serine—glyoxylate transaminase

Reaction: L-serine + glyoxylate = 3-hydroxypyruvate + glycine

Systematic name: L-serine:glyoxylate aminotransferase
Comments: A pyridoxal-phosphate protein.
References: [1448, 1688, 3260]

[EC 2.6.1.45 created 1972]

EC 2.6.1.46

Accepted name: diaminobutyrate—pyruvate transaminase
Reaction: L-2,4-diaminobutanoate + pyruvate = L-aspartate 4-semialdehyde + L-alanine
Other name(s): diaminobutyrate-pyruvate aminotransferase; L-diaminobutyric acid transaminase
Systematic name: L-2,4-diaminobutanoate:pyruvate aminotransferase
Comments: A pyridoxal-phosphate protein.
References: [2813]

[EC 2.6.1.46 created 1972]

EC 2.6.1.47

Accepted name: alanine—oxomalonate transaminase
Reaction: L-alanine + oxomalonate = pyruvate + aminomalonate
Other name(s): alanine-oxomalonate aminotransferase; L-alanine-ketomalonate transaminase; alanine-ketomalonate (mesoxalate) transaminase
Systematic name: L-alanine:oxomalonate aminotransferase
Comments: A pyridoxal-phosphate protein.
References: [2394]

[EC 2.6.1.47 created 1972]

EC 2.6.1.48

Accepted name: 5-aminovalerate transaminase
Reaction: 5-aminopentanoate + 2-oxoglutarate = 5-oxopentanoate + L-glutamate
Other name(s): 5-aminovalerate aminotransferase; δ-aminovalerate aminotransferase; δ-aminovalerate transaminase
Systematic name: 5-aminopentanoate:2-oxoglutarate aminotransferase
Comments: A pyridoxal-phosphate protein.
References: [1427]

[EC 2.6.1.48 created 1972]

EC 2.6.1.49

Accepted name: dihydroxyphenylalanine transaminase
Reaction: L-dopa + 2-oxoglutarate = 3,4-dihydroxyphenylpyruvate + L-glutamate
Other name(s): dopa transaminase; dihydroxyphenylalanine aminotransferase; aspartate-DOPP transaminase (ADT); L-dopa transaminase; dopa aminotransferase; glutamate-DOPP transaminase (GDT); phenylalanine-DOPP transaminase (PDT); DOPA 2-oxoglutarate aminotransferase; DOPAATS
Systematic name: 3,4-dihydroxy-L-phenylalanine:2-oxoglutarate aminotransferase
Comments: A pyridoxal-phosphate protein.
References: [924, 2810]

[EC 2.6.1.49 created 1972]

EC 2.6.1.50

Accepted name: glutamine—*scyllo*-inositol transaminase
Reaction: L-glutamine + 2,4,6/3,5-pentahydroxycyclohexanone = 2-oxoglutaramate + 1-amino-1-deoxy-*scyllo*-inositol

Other name(s): glutamine *scyllo*-inosose aminotransferase; L-glutamine-keto-*scyllo*-inositol aminotransferase; glutamine-*scyllo*-inosose transaminase; L-glutamine-*scyllo*-inosose transaminase
Systematic name: L-glutamine:2,4,6/3,5-pentahydroxycyclohexanone aminotransferase
Comments: A pyridoxal-phosphate protein.
References: [3735]

[EC 2.6.1.50 created 1972]

EC 2.6.1.51

Accepted name: serine—pyruvate transaminase
Reaction: L-serine + pyruvate = 3-hydroxypyruvate + L-alanine
Other name(s): SPT; hydroxypyruvate:L-alanine transaminase
Systematic name: L-serine:pyruvate aminotransferase
Comments: A pyridoxal-phosphate protein. The liver enzyme may be identical with EC 2.6.1.44 alanine-glyoxylate transaminase.
References: [539, 1789, 3009]

[EC 2.6.1.51 created 1972]

EC 2.6.1.52

Accepted name: phosphoserine transaminase
Reaction: (1) *O*-phospho-L-serine + 2-oxoglutarate = 3-phosphooxypyruvate + L-glutamate
(2) 4-phosphooxy-L-threonine + 2-oxoglutarate = (3*R*)-3-hydroxy-2-oxo-4-phosphooxybutanoate + L-glutamate
Other name(s): PSAT; phosphoserine aminotransferase; 3-phosphoserine aminotransferase; hydroxypyruvic phosphate-glutamic transaminase; L-phosphoserine aminotransferase; phosphohydroxypyruvate transaminase; phosphohydroxypyruvic-glutamic transaminase; 3-*O*-phospho-L-serine:2-oxoglutarate aminotransferase; SerC; PdxC; 3PHP transaminase
Systematic name: *O*-phospho-L-serine:2-oxoglutarate aminotransferase
Comments: A pyridoxal-phosphate protein. This enzyme catalyses the second step in the phosphorylated pathway of serine biosynthesis in *Escherichia coli* [2721, 4062]. It also catalyses the third step in the biosynthesis of the coenzyme pyridoxal 5′-phosphate in *Escherichia coli* (using Reaction 2 above) [4062]. In *Escherichia coli*, pyridoxal 5′-phosphate is synthesized *de novo* by a pathway that involves EC 1.2.1.72 (erythrose-4-phosphate dehydrogenase), EC 1.1.1.290 (4-phosphoerythronate dehydrogenase), EC 2.6.1.52 (phosphoserine transaminase), EC 1.1.1.262 (4-hydroxythreonine-4-phosphate dehydrogenase), EC 2.6.99.2 (pyridoxine 5′-phosphate synthase) and EC 1.4.3.5 (with pyridoxine 5′-phosphate as substrate). Pyridoxal phosphate is the cofactor for both activities and therefore seems to be involved in its own biosynthesis [776]. Non-phosphorylated forms of serine and threonine are not substrates [776].
References: [1342, 2721, 4062, 776, 4061]

[EC 2.6.1.52 created 1972, modified 2006]

[2.6.1.53 Transferred entry. glutamate synthase. Now EC 1.4.1.13, glutamate synthase (NADPH)]

[EC 2.6.1.53 created 1972, deleted 1976]

EC 2.6.1.54

Accepted name: pyridoxamine-phosphate transaminase
Reaction: pyridoxamine 5′-phosphate + 2-oxoglutarate = pyridoxal 5′-phosphate + D-glutamate
Other name(s): pyridoxamine phosphate aminotransferase; pyridoxamine 5′-phosphate-α-ketoglutarate transaminase; pyridoxamine 5′-phosphate transaminase
Systematic name: pyridoxamine-5′-phosphate:2-oxoglutarate aminotransferase (D-glutamate-forming)
Comments: Also acts, more slowly, on pyridoxamine.
References: [3468]

[EC 2.6.1.54 created 1976]

EC 2.6.1.55

Accepted name: taurine—2-oxoglutarate transaminase

Reaction: taurine + 2-oxoglutarate = 2-sulfoacetaldehyde + L-glutamate

Other name(s): taurine aminotransferase; taurine transaminase; taurine—α-ketoglutarate aminotransferase; taurine—glutamate transaminase

Systematic name: taurine:2-oxoglutarate aminotransferase

Comments: A pyridoxal-phosphate protein. Also acts on D,L-3-amino-isobutanoate, β-alanine and 3-aminopropanesulfonate. Involved in the microbial utilization of β-alanine.

References: [3558, 602]

[EC 2.6.1.55 created 1976, modified 2003]

EC 2.6.1.56

Accepted name: 1D-1-guanidino-3-amino-1,3-dideoxy-*scyllo*-inositol transaminase

Reaction: 1D-1-guanidino-3-amino-1,3-dideoxy-*scyllo*-inositol + pyruvate = 1D-1-guanidino-1-deoxy-3-dehydro-*scyllo*-inositol + L-alanine

Other name(s): guanidinoaminodideoxy-*scyllo*-inositol-pyruvate aminotransferase; L-alanine-*N*-amidino-3-(or 5-)keto-*scyllo*-inosamine transaminase

Systematic name: 1D-1-guanidino-3-amino-1,3-dideoxy-*scyllo*-inositol:pyruvate aminotransferase

Comments: L-Glutamate and L-glutamine can also act as amino donors.

References: [3731, 3735]

[EC 2.6.1.56 created 1976]

EC 2.6.1.57

Accepted name: aromatic-amino-acid transaminase

Reaction: an aromatic amino acid + 2-oxoglutarate = an aromatic oxo acid + L-glutamate

Other name(s): aromatic amino acid aminotransferase; aromatic aminotransferase; ArAT

Systematic name: aromatic-amino-acid:2-oxoglutarate aminotransferase

Comments: A pyridoxal-phosphate protein. L-Methionine can also act as donor, but more slowly; oxaloacetate can act as acceptor. Controlled proteolysis converts the enzyme into EC 2.6.1.1 aspartate transaminase.

References: [2176]

[EC 2.6.1.57 created 1976]

EC 2.6.1.58

Accepted name: phenylalanine(histidine) transaminase

Reaction: L-phenylalanine + pyruvate = phenylpyruvate + L-alanine

Other name(s): phenylalanine (histidine) aminotransferase; phenylalanine(histidine):pyruvate aminotransferase; histidine:pyruvate aminotransferase; L-phenylalanine(L-histidine):pyruvate aminotransferase

Systematic name: L-phenylalanine:pyruvate aminotransferase

Comments: L-Histidine and L-tyrosine can act instead of L-phenylalanine; in the reverse reaction, L-methionine, L-serine and L-glutamine can replace L-alanine.

References: [2260]

[EC 2.6.1.58 created 1978]

EC 2.6.1.59

Accepted name: dTDP-4-amino-4,6-dideoxygalactose transaminase

Reaction: dTDP-4-amino-4,6-dideoxy-α-D-galactose + 2-oxoglutarate = dTDP-4-dehydro-6-deoxy-α-D-galactose + L-glutamate

Other name(s): thymidine diphosphoaminodideoxygalactose aminotransferase; thymidine diphosphate 4-keto-6-deoxy-D-glucose transaminase; WecE; dTDP-4,6-dideoxy-D-galactose:2-oxoglutarate aminotransferase; dTDP-4,6-dideoxy-α-D-galactose:2-oxoglutarate aminotransferase
Systematic name: dTDP-4-amino-4,6-dideoxy-α-D-galactose:2-oxoglutarate aminotransferase
Comments: A pyridoxal-phosphate protein.
References: [2534, 1419]

[EC 2.6.1.59 created 1978]

EC 2.6.1.60

Accepted name: aromatic-amino-acid—glyoxylate transaminase
Reaction: an aromatic amino acid + glyoxylate = an aromatic oxo acid + glycine
Systematic name: aromatic-amino-acid:glyoxylate aminotransferase
Comments: Phenylalanine, kynurenine, tyrosine and histidine can act as amino donors; glyoxylate, pyruvate and hydroxypyruvate can act as amino acceptors.
References: [1223]

[EC 2.6.1.60 created 1978]

[2.6.1.61 Deleted entry. (R)-3-amino-2-methylpropionate transaminase. Enzyme is identical to EC 2.6.1.40, (R)-3-amino-2-methylpropionate—pyruvate transaminase]

[EC 2.6.1.61 created 1982, deleted 2004]

EC 2.6.1.62

Accepted name: adenosylmethionine—8-amino-7-oxononanoate transaminase
Reaction: *S*-adenosyl-L-methionine + 8-amino-7-oxononanoate = *S*-adenosyl-4-(methylsulfanyl)-2-oxobutanoate + 7,8-diaminononanoate
Other name(s): 7,8-diaminonanoate transaminase; 7,8-diaminononanoate transaminase; DAPA transaminase (ambiguous); 7,8-diaminopelargonic acid aminotransferase; DAPA aminotransferase (ambiguous); 7-keto-8-aminopelargonic acid; diaminopelargonate synthase; 7-keto-8-aminopelargonic acid aminotransferase
Systematic name: *S*-adenosyl-L-methionine:8-amino-7-oxononanoate aminotransferase
Comments: A pyridoxal 5′-phosphate enzyme. *S*-adenosylhomocysteine can also act as donor.
References: [1477, 1478, 3354]

[EC 2.6.1.62 created 1983]

EC 2.6.1.63

Accepted name: kynurenine—glyoxylate transaminase
Reaction: L-kynurenine + glyoxylate = 4-(2-aminophenyl)-2,4-dioxobutanoate + glycine
Other name(s): kynurenine-glyoxylate aminotransferase
Systematic name: L-kynurenine:glyoxylate aminotransferase (cyclizing)
Comments: Acts, more slowly, on L-phenylalanine, L-histidine and L-tyrosine.
References: [1222]

[EC 2.6.1.63 created 1983]

EC 2.6.1.64

Accepted name: glutamine—phenylpyruvate transaminase
Reaction: L-glutamine + phenylpyruvate = 2-oxoglutaramate + L-phenylalanine
Other name(s): glutamine transaminase K; glutamine-phenylpyruvate aminotransferase
Systematic name: L-glutamine:phenylpyruvate aminotransferase

Comments: A pyridoxal-phosphate protein. L-Methionine, L-histidine and L-tyrosine can act as donors. The enzyme has little activity on pyruvate and glyoxylate (*cf.* EC 2.6.1.15 glutamine—pyruvate transaminase).
References: [607, 609]

[EC 2.6.1.64 created 1984]

EC 2.6.1.65

Accepted name: N^6-acetyl-β-lysine transaminase
Reaction: 6-acetamido-3-aminohexanoate + 2-oxoglutarate = 6-acetamido-3-oxohexanoate + L-glutamate
Other name(s): ε-acetyl-β-lysine aminotransferase
Systematic name: 6-acetamido-3-aminohexanoate:2-oxoglutarate aminotransferase
Comments: A pyridoxal-phosphate protein.
References: [371]

[EC 2.6.1.65 created 1984]

EC 2.6.1.66

Accepted name: valine—pyruvate transaminase
Reaction: L-valine + pyruvate = 3-methyl-2-oxobutanoate + L-alanine
Other name(s): transaminase C; valine-pyruvate aminotransferase; alanine-oxoisovalerate aminotransferase
Systematic name: L-valine:pyruvate aminotransferase
Comments: Different from EC 2.6.1.42, branched-chain-amino-acid-transaminase.
References: [872, 2960]

[EC 2.6.1.66 created 1984]

EC 2.6.1.67

Accepted name: 2-aminohexanoate transaminase
Reaction: L-2-aminohexanoate + 2-oxoglutarate = 2-oxohexanoate + L-glutamate
Other name(s): norleucine transaminase; norleucine (leucine) aminotransferase; leucine L-norleucine: 2-oxoglutarate aminotransferase
Systematic name: L-2-aminohexanoate:2-oxoglutarate aminotransferase
Comments: A pyridoxal-phosphate protein. Also acts on L-leucine and, more slowly, on L-isoleucine, L-2-aminopentanoate and L-aspartate.
References: [1010]

[EC 2.6.1.67 created 1989]

[2.6.1.68 Deleted entry. ornithine(lysine) transaminase. Now classified as EC 2.6.1.13, ornithine aminotransferase and EC 2.6.1.36, L-lysine 6-transaminase]

[EC 2.6.1.68 created 1989, deleted 2016]

[2.6.1.69 Deleted entry. N^2*-acetylornithine 5-transaminase. Enzyme is identical to EC 2.6.1.11, acetylornithine transaminase]*

[EC 2.6.1.69 created 1989, deleted 2004]

EC 2.6.1.70

Accepted name: aspartate—phenylpyruvate transaminase
Reaction: L-aspartate + phenylpyruvate = oxaloacetate + L-phenylalanine
Other name(s): aspartate-phenylpyruvate aminotransferase
Systematic name: L-aspartate:phenylpyruvate aminotransferase

Comments: The enzyme from *Pseudomonas putida* also acts on 4-hydroxy-phenylpyruvate and, more slowly, on L-glutamate and L-histidine.
References: [1357]

[EC 2.6.1.70 created 1989]

EC 2.6.1.71

Accepted name: lysine—pyruvate 6-transaminase
Reaction: L-lysine + pyruvate = (*S*)-2-amino-6-oxohexanoate + L-alanine
Other name(s): lysine-pyruvate aminotransferase; Lys-AT
Systematic name: L-lysine:pyruvate aminotransferase
References: [3087]

[EC 2.6.1.71 created 1990, modified 2011]

EC 2.6.1.72

Accepted name: D-4-hydroxyphenylglycine transaminase
Reaction: D-4-hydroxyphenylglycine + 2-oxoglutarate = 4-hydroxyphenylglyoxylate + L-glutamate
Other name(s): D-hydroxyphenylglycine aminotransferase
Systematic name: D-4-hydroxyphenylglycine:2-oxoglutarate aminotransferase
Comments: A pyridoxal-phosphate protein.
References: [709, 710]

[EC 2.6.1.72 created 1990]

EC 2.6.1.73

Accepted name: methionine—glyoxylate transaminase
Reaction: L-methionine + glyoxylate = 4-(methylsulfanyl)-2-oxobutanoate + glycine
Other name(s): methionine-glyoxylate aminotransferase; MGAT
Systematic name: L-methionine:glyoxylate aminotransferase
Comments: L-Glutamate can also act as donor.
References: [1078]

[EC 2.6.1.73 created 1992]

EC 2.6.1.74

Accepted name: cephalosporin-C transaminase
Reaction: (7*R*)-7-(5-carboxy-5-oxopentanoyl)aminocephalosporinate + D-glutamate = cephalosporin C + 2-oxoglutarate
Other name(s): cephalosporin C aminotransferase; L-alanine:cephalosporin-C aminotransferase
Systematic name: cephalosporin-C:2-oxoglutarate aminotransferase
Comments: A number of D-amino acids, including D-alanine, D-aspartate and D-methionine can also act as amino-group donors. Although this enzyme acts on several free D-amino acids, it differs from EC 2.6.1.21, D-alanine transaminase, in that it can use cephalosporin C as an amino donor.
References: [105]

[EC 2.6.1.74 created 1992, modified 2005]

EC 2.6.1.75

Accepted name: cysteine-conjugate transaminase
Reaction: *S*-(4-bromophenyl)-L-cysteine + 2-oxoglutarate = *S*-(4-bromophenyl)mercaptopyruvate + L-glutamate
Other name(s): cysteine conjugate aminotransferase; cysteine-conjugate α-ketoglutarate transaminase (CAT-1)

Systematic name: *S*-(4-bromophenyl)-L-cysteine:2-oxoglutarate aminotransferase
Comments: A number of cysteine conjugates can also act.
References: [3546]

[EC 2.6.1.75 created 1992]

EC 2.6.1.76

Accepted name: diaminobutyrate—2-oxoglutarate transaminase
Reaction: L-2,4-diaminobutanoate + 2-oxoglutarate = L-aspartate 4-semialdehyde + L-glutamate
Other name(s): L-2,4-diaminobutyrate:2-ketoglutarate 4-aminotransferase; 2,4-diaminobutyrate 4-aminotransferase; diaminobutyrate aminotransferase; DABA aminotransferase; DAB aminotransferase; EctB; diaminibutyric acid aminotransferase; L-2,4-diaminobutyrate:2-oxoglutarate 4-aminotransferase
Systematic name: L-2,4-diaminobutanoate:2-oxoglutarate 4-aminotransferase
Comments: A pyridoxal-phosphate protein that requires potassium for activity [2568]. In the proteobacterium *Acinetobacter baumannii*, this enzyme is cotranscribed with the neighbouring *ddc* gene that also encodes EC 4.1.1.86, diaminobutyrate decarboxylase. Differs from EC 2.6.1.46, diaminobutyrate—pyruvate transaminase, which has pyruvate as the amino-group acceptor. This is the first enzyme in the ectoine-biosynthesis pathway, the other enzymes involved being EC 2.3.1.178, diaminobutyrate acetyltransferase and EC 4.2.1.108, ectoine synthase [2673, 2568].
References: [1432, 1433, 2673, 2568, 1807, 2044]

[EC 2.6.1.76 created 2000, modified 2006]

EC 2.6.1.77

Accepted name: taurine—pyruvate aminotransferase
Reaction: taurine + pyruvate = L-alanine + 2-sulfoacetaldehyde
Other name(s): Tpa
Systematic name: taurine:pyruvate aminotransferase
Comments: The enzyme from the bacterium *Bilophila wadsworthia* requires pyridoxal $5'$-phosphate as a cofactor, and catalyses a reversible reaction that starts an anaerobic taurine degradation pathway. β-Alanine is also a significant amino group donor. The enzyme from the bacterium *Pseudomonas denitrificans* PD1222 can also use hypotaurine, producing 2-sulfinoacetaldehyde, which spontaneously hydrolyses to sulfite and acetaldehyde. Unlike, EC 2.6.1.55, taurine—2-oxoglutarate transaminase, 2-oxoglutarate cannot serve as an acceptor for the amino group.
References: [1873, 602, 2149, 887]

[EC 2.6.1.77 created 2003]

EC 2.6.1.78

Accepted name: aspartate—prephenate aminotransferase
Reaction: L-arogenate + oxaloacetate = prephenate + L-aspartate
Other name(s): prephenate transaminase (ambiguous); PAT (ambiguous); prephenate aspartate aminotransferase; L-aspartate:prephenate aminotransferase
Systematic name: L-arogenate:oxaloacetate aminotransferase
Comments: A pyridoxal-phosphate protein. Glutamate can also act as the amino donor, but more slowly (*cf.* EC 2.6.1.79, glutamate—prephenate aminotransferase).
References: [686]

[EC 2.6.1.78 created 2005]

EC 2.6.1.79

Accepted name: glutamate—prephenate aminotransferase
Reaction: L-arogenate + 2-oxoglutarate = prephenate + L-glutamate

Other name(s): prephenate transaminase (ambiguous); PAT (ambiguous); L-glutamate:prephenate aminotransferase
Systematic name: L-arogenate:2-oxoglutarate aminotransferase
Comments: A pyridoxal-phosphate protein. Aspartate can also act as the amino donor, but more slowly (*cf.* EC 2.6.1.78, aspartate—prephenate aminotransferase). The enzyme from higher plants shows a marked preference for prephenate as substrate compared to pyruvate, phenylpyruvate or 4-hydroxyphenylpyruvate [350].
References: [350, 3222, 349]

[EC 2.6.1.79 created 2005]

EC 2.6.1.80

Accepted name: nicotianamine aminotransferase
Reaction: nicotianamine + 2-oxoglutarate = $3''$-deamino-$3''$-oxonicotianamine + L-glutamate
Other name(s): NAAT; NAAT-I; NAAT-II; NAAT-III; nicotianamine transaminase
Systematic name: nicotianamine:2-oxoglutarate aminotransferase
Comments: A pyridoxal-phosphate protein. This enzyme is produced by grasses. They secrete both the nicotianamine and the transaminated product into the soil around them. Both compounds chelate iron(II) and iron(III); these chelators, called mugineic acid family phytosiderophores, are taken up by the grass, which is thereby supplied with iron.
References: [1580, 3441, 3054]

[EC 2.6.1.80 created 2005]

EC 2.6.1.81

Accepted name: succinylornithine transaminase
Reaction: N^2-succinyl-L-ornithine + 2-oxoglutarate = *N*-succinyl-L-glutamate 5-semialdehyde + L-glutamate
Other name(s): succinylornithine aminotransferase; N^2-succinylornithine 5-aminotransferase; AstC; SOAT; 2-*N*-succinyl-L-ornithine:2-oxoglutarate 5-aminotransferase
Systematic name: N^2-succinyl-L-ornithine:2-oxoglutarate 5-aminotransferase
Comments: A pyridoxal-phosphate protein. Also acts on N^2-acetyl-L-ornithine and L-ornithine, but more slowly [644]. In *Pseudomonas aeruginosa*, the arginine-inducible succinylornithine transaminase, acetylornithine transaminase (EC 2.6.1.11) and ornithine aminotransferase (EC 2.6.1.13) activities are catalysed by the same enzyme, but this is not the case in all species [3317]. This is the third enzyme in the arginine succinyltransferase (AST) pathway for the catabolism of arginine [3792]. This pathway converts the carbon skeleton of arginine into glutamate, with the concomitant production of ammonia and conversion of succinyl-CoA into succinate and CoA. The five enzymes involved in this pathway are EC 2.3.1.109 (arginine *N*-succinyltransferase), EC 3.5.3.23 (*N*-succinylarginine dihydrolase), EC 2.6.1.81 (succinylornithine transaminase), EC 1.2.1.71 (succinylglutamate-semialdehyde dehydrogenase) and EC 3.5.1.96 (succinylglutamate desuccinylase) [644, **?**].
References: [3792, 3090, 644, 1469, 3317]

[EC 2.6.1.81 created 2006]

EC 2.6.1.82

Accepted name: putrescine—2-oxoglutarate transaminase
Reaction: putrescine + 2-oxoglutarate = 1-pyrroline + L-glutamate + H_2O (overall reaction)
(1a) putrescine + 2-oxoglutarate = 4-aminobutanal + L-glutamate
(1b) 4-aminobutanal = 1-pyrroline + H_2O (spontaneous)
Other name(s): putrescine-α-ketoglutarate transaminase; YgjG; putrescine:α-ketoglutarate aminotransferase; PAT; putrescine transaminase (ambiguous); putrescine aminotransferase (ambiguous); butane-1,4-diamine:2-oxoglutarate aminotransferase
Systematic name: putrescine:2-oxoglutarate aminotransferase

Comments: A pyridoxal $5'$-phosphate protein [3014]. The product, 4-aminobutanal, spontaneously cyclizes to form 1-pyrroline, which is a substrate for EC 1.2.1.19, aminobutyraldehyde dehydrogenase. Cadaverine and spermidine can also act as substrates [3014]. Forms part of the arginine-catabolism pathway [3015]. *cf.* EC 2.6.1.113, putrescine—pyruvate transaminase.

References: [2765, 3015, 3014]

[EC 2.6.1.82 created 2006, modified 2017]

EC 2.6.1.83

Accepted name: LL-diaminopimelate aminotransferase

Reaction: LL-2,6-diaminoheptanedioate + 2-oxoglutarate = (*S*)-2,3,4,5-tetrahydropyridine-2,6-dicarboxylate + L-glutamate + H_2O

Other name(s): LL-diaminopimelate transaminase; LL-DAP aminotransferase; LL-DAP-AT

Systematic name: LL-2,6-diaminoheptanedioate:2-oxoglutarate aminotransferase

Comments: A pyridoxal-phosphate enzyme. In vivo, the reaction occurs in the opposite direction to that shown above. This is one of the final steps in the lysine-biosynthesis pathway of plants (ranging from mosses to flowering plants). *meso*-Diaminoheptanedioate, an isomer of LL-2,6-diaminoheptanedioate, and the structurally related compounds lysine and ornithine are not substrates. 2-Oxoglutarate cannot be replaced by oxaloacetate or pyruvate. It is not yet known if the substrate of the biosynthetic reaction is the cyclic or acyclic form of tetrahydropyridine-2,6-dicarboxylate.

References: [1401]

[EC 2.6.1.83 created 2006]

EC 2.6.1.84

Accepted name: arginine—pyruvate transaminase

Reaction: L-arginine + pyruvate = 5-guanidino-2-oxopentanoate + L-alanine

Other name(s): arginine:pyruvate transaminase; AruH; ATase

Systematic name: L-arginine:pyruvate aminotransferase

Comments: A pyridoxal-phosphate protein. While L-arginine is the best substrate, the enzyme exhibits broad substrate specificity, with L-lysine, L-methionine, L-leucine, L-ornithine and L-glutamine also able to act as substrates, but more slowly. Pyruvate cannot be replaced by 2-oxoglutarate as amino-group acceptor. This is the first catalytic enzyme of the arginine transaminase pathway for L-arginine utilization in *Pseudomonas aeruginosa*. This pathway is only used when the major route of arginine catabolism, i.e. the arginine succinyltransferase pathway, is blocked.

References: [3967, 3968]

[EC 2.6.1.84 created 2007]

EC 2.6.1.85

Accepted name: aminodeoxychorismate synthase

Reaction: chorismate + L-glutamine = 4-amino-4-deoxychorismate + L-glutamate

Other name(s): ADC synthase; 4-amino-4-deoxychorismate synthase; PabB; chorismate:L-glutamine amido-ligase (incorrect)

Systematic name: chorismate:L-glutamine aminotransferase

Comments: The enzyme is composed of two parts, PabA and PabB. In the absence of PabA and glutamine, PabB converts ammonia and chorismate into 4-amino-4-deoxychorismate (in the presence of Mg^{2+}). PabA converts glutamine into glutamate only in the presence of stoichiometric amounts of PabB. This enzyme is coupled with EC 4.1.3.38, aminodeoxychorismate lyase, to form 4-aminobenzoate.

References: [3972, 3688]

[EC 2.6.1.85 created 2003 as EC 6.3.5.8, transferred 2007 to EC 2.6.1.85]

EC 2.6.1.86

Accepted name: 2-amino-4-deoxychorismate synthase

Reaction: (2*S*)-2-amino-4-deoxychorismate + L-glutamate = chorismate + L-glutamine

Other name(s): ADIC synthase; 2-amino-2-deoxyisochorismate synthase; SgcD

Systematic name: (2*S*)-2-amino-4-deoxychorismate:2-oxoglutarate aminotransferase

Comments: Requires Mg^{2+}. The reaction occurs in the reverse direction to that shown above. In contrast to most anthranilate-synthase I (ASI) homologues, this enzyme is not inhibited by tryptophan. In *Streptomyces globisporus*, the sequential action of this enzyme and EC 1.3.99.24, 2-amino-4-deoxychorismate dehydrogenase, leads to the formation of the benzoxazolinate moiety of the enediyne antitumour antibiotic C-1027 [1858, 4009]. In certain Pseudomonads the enzyme participates in the biosynthesis of phenazine, a precursor for several compounds with antibiotic activity [2193, 1877].

References: [1858, 4009, 2193, 1877]

[EC 2.6.1.86 created 2008]

EC 2.6.1.87

Accepted name: UDP-4-amino-4-deoxy-L-arabinose aminotransferase

Reaction: UDP-4-amino-4-deoxy-β-L-arabinopyranose + 2-oxoglutarate = UDP-β-L-*threo*-pentapyranos-4-ulose + L-glutamate

Other name(s): UDP-(β-L-*threo*-pentapyranosyl-4$''$-ulose diphosphate) aminotransferase; UDP-4-amino-4-deoxy-L-arabinose—oxoglutarate aminotransferase; UDP-Ara4O aminotransferase; UDP-L-Ara4N transaminase

Systematic name: UDP-4-amino-4-deoxy-β-L-arabinose:2-oxoglutarate aminotransferase

Comments: A pyridoxal 5$'$-phosphate enzyme.

References: [383, 2487]

[EC 2.6.1.87 created 2010]

EC 2.6.1.88

Accepted name: methionine transaminase

Reaction: L-methionine + a 2-oxo carboxylate = 4-(methylsulfanyl)-2-oxobutanoate + an L-amino acid

Other name(s): methionine-oxo-acid transaminase

Systematic name: L-methionine:2-oxo-acid aminotransferase

Comments: The enzyme is most active with L-methionine. It participates in the L-methionine salvage pathway from *S*-methyl-5$'$-thioadenosine, a by-product of polyamine biosynthesis. The enzyme from the bacterium *Klebsiella pneumoniae* can use several different amino acids as amino donor, with aromatic amino acids being the most effective [1278]. The enzyme from the plant *Arabidopsis thaliana* is also a part of the chain elongation pathway in the biosynthesis of methionine-derived glucosinolates [3116].

References: [1278, 749, 3116]

[EC 2.6.1.88 created 2011]

EC 2.6.1.89

Accepted name: dTDP-3-amino-3,6-dideoxy-α-D-glucopyranose transaminase

Reaction: dTDP-3-amino-3,6-dideoxy-α-D-glucopyranose + 2-oxoglutarate = dTDP-3-dehydro-6-deoxy-α-D-glucopyranose + L-glutamate

Other name(s): TylB; TDP-3-keto-6-deoxy-D-glucose 3-aminotransferase; TDP-3-dehydro-6-deoxy-D-glucose 3-aminotransferase; dTDP-3-keto-6-deoxy-D-glucose 3-aminotransferase; dTDP-3-dehydro-6-deoxy-D-glucose 3-aminotransferase

Systematic name: dTDP-3-amino-3,6-dideoxy-α-D-glucopyranose:2-oxoglutarate aminotransferase

Comments: A pyridoxal-phosphate protein. The reaction occurs in the reverse direction. The enzyme is involved in biosynthesis of D-mycaminose.

References: [2209]

[EC 2.6.1.89 created 2011]

EC 2.6.1.90

Accepted name: dTDP-3-amino-3,6-dideoxy-α-D-galactopyranose transaminase

Reaction: dTDP-3-amino-3,6-dideoxy-α-D-galactopyranose + 2-oxoglutarate = dTDP-3-dehydro-6-deoxy-α-D-galactopyranose + L-glutamate

Other name(s): dTDP-6-deoxy-D-xylohex-3-uloseaminase; FdtB; TDP-3-keto-6-deoxy-D-galactose-3-aminotransferase; RavAMT; TDP-3-keto-6-deoxy-D-galactose 3-aminotransferase; TDP-3-dehydro-6-deoxy-D-galactose 3-aminotransferase

Systematic name: dTDP-3-amino-3,6-dideoxy-α-D-galactopyranose:2-oxoglutarate aminotransferase

Comments: A pyridoxal-phosphate protein. The enzyme is involved in the biosynthesis of dTDP-3-acetamido-3,6-dideoxy-α-D-galactose. The reaction occurs in the reverse direction.

References: [2688]

[EC 2.6.1.90 created 2011]

*[2.6.1.91 Deleted entry. UDP-4-amino-4,6-dideoxy-N-acetyl-*α*-*D*-glucosamine transaminase. Identical to EC 2.6.1.34, UDP-N-acetylbacillosamine transaminase.]*

[EC 2.6.1.91 created 2011, deleted 2013]

EC 2.6.1.92

Accepted name: UDP-4-amino-4,6-dideoxy-*N*-acetyl-β-L-altrosamine transaminase

Reaction: UDP-4-amino-4,6-dideoxy-*N*-acetyl-β-L-altrosamine + 2-oxoglutarate = UDP-2-acetamido-2,6-dideoxy-β-L-*arabino*-hex-4-ulose + L-glutamate

Other name(s): PseC; UDP-4-amino-4,6-dideoxy-*N*-acetyl-β-L-altrosamine:2-oxoglutarate aminotransferase; UDP-β-L-*threo*-pentapyranos-4-ulose transaminase; UDP-4-dehydro-6-deoxy-D-glucose transaminase

Systematic name: UDP-4-amino-4,6-dideoxy-*N*-acetyl-β-L-altrosamine:2-oxoglutarate transaminase

Comments: A pyridoxal 5′-phosphate protein. The enzyme transfers the primary amino group of L-glutamate to C-4″ of UDP-4-dehydro sugars, forming a C-N bond in a stereo configuration opposite to that of UDP. The enzyme from the bacterium *Bacillus cereus* has been shown to act on UDP-2-acetamido-2,6-dideoxy-β-L-*arabino*-hex-4-ulose, UDP-β-L-*threo*-pentapyranos-4-ulose, UDP-4-dehydro-6-deoxy-D-glucose, and UDP-2-acetamido-2,6-dideoxy-α-D-*xylo*-hex-4-ulose. *cf.* EC 2.6.1.34, UDP-*N*-acetylbacillosamine transaminase, which catalyses a similar reaction, but forms the C-N bond in the same stereo configuration as that of UDP.

References: [3099, 3097, 2330, 1420]

[EC 2.6.1.92 created 2011, modified 2018]

EC 2.6.1.93

Accepted name: neamine transaminase

Reaction: neamine + 2-oxoglutarate = 6′-dehydroparomamine + L-glutamate

Other name(s): glutamate—6′-dehydroparomamine aminotransferase; *btrB* (gene name); *neoN* (gene name); *kacL* (gene name)

Systematic name: neamine:2-oxoglutarate aminotransferase

Comments: The reaction occurs *in vivo* in the opposite direction. Involved in the biosynthetic pathways of several clinically important aminocyclitol antibiotics, including kanamycin B, butirosin, neomycin and ribostamycin. Works in combination with EC 1.1.3.43, paromamine 6-oxidase, to replace the 6′-hydroxy group of paromamine with an amino group. The enzyme from the bacterium *Streptomyces kanamyceticus* can also catalyse EC 2.6.1.94, 2′-deamino-2′-hydroxyneamine transaminase, which leads to production of kanamycin A [2623]. The enzyme from the bacterium *Streptomyces fradiae* can also catalyse EC 2.6.1.95, leading to production of neomycin C [582].

References: [1391, 582, 2623]

[EC 2.6.1.93 created 2012]

EC 2.6.1.94

Accepted name: 2′-deamino-2′-hydroxyneamine transaminase

Reaction: 2′-deamino-2′-hydroxyneamine + 2-oxoglutarate = 2′-deamino-2′-hydroxy-6′-dehydroparomamine + L-glutamate

Other name(s): *kacL* (gene name)

Systematic name: 2′-deamino-2′-hydroxyneamine:2-oxoglutarate aminotransferase

Comments: The reaction occurs *in vivo* in the opposite direction. Involved in the biosynthetic pathway of kanamycin A and kanamycin D. The enzyme, characterized from the bacterium *Streptomyces kanamyceticus*, can also catalyse EC 2.6.1.93, neamine transaminase.

References: [2623]

[EC 2.6.1.94 created 2012]

EC 2.6.1.95

Accepted name: neomycin C transaminase

Reaction: neomycin C + 2-oxoglutarate = 6‴-deamino-6‴-oxoneomycin C + L-glutamate

Other name(s): *neoN* (gene name)

Systematic name: 2-oxoglutarate:neomycin C aminotransferase

Comments: The reaction occurs *in vivo* in the opposite direction. Involved in the biosynthetic pathway of aminoglycoside antibiotics of the neomycin family. Works in combination with EC 1.1.3.44, 6‴-hydroxyneomycin C oxidase, to replace the 6‴-hydroxy group of 6‴-deamino-6‴-hydroxyneomycin C with an amino group. The enzyme, characterized from the bacterium *Streptomyces fradiae*, can also catalyse EC 2.6.1.93, neamine transaminase.

References: [1391, 582]

[EC 2.6.1.95 created 2012]

EC 2.6.1.96

Accepted name: 4-aminobutyrate—pyruvate transaminase

Reaction: (1) 4-aminobutanoate + pyruvate = succinate semialdehyde + L-alanine
(2) 4-aminobutanoate + glyoxylate = succinate semialdehyde + glycine

Other name(s): aminobutyrate aminotransferase (ambiguous); γ-aminobutyrate aminotransaminase (ambiguous); γ-aminobutyrate transaminase (ambiguous); γ-aminobutyric acid aminotransferase (ambiguous); γ-aminobutyric acid pyruvate transaminase; γ-aminobutyric acid transaminase (ambiguous); γ-aminobutyric transaminase (ambiguous); 4-aminobutyrate aminotransferase (ambiguous); 4-aminobutyric acid aminotransferase (ambiguous); aminobutyrate transaminase (ambiguous); GABA aminotransferase (ambiguous); GABA transaminase (ambiguous); GABA transferase; POP2 (gene name)

Systematic name: 4-aminobutanoate:pyruvate aminotransferase

Comments: Requires pyridoxal 5′-phosphate. The enzyme is found in plants that do not have the 2-oxoglutarate dependent enzyme (*cf.* EC 2.6.1.19). The reaction with pyruvate is reversible while the reaction with glyoxylate only takes place in the forward direction.

References: [490, 2603, 572, 571]

[EC 2.6.1.96 created 2012]

EC 2.6.1.97

Accepted name: archaeosine synthase

Reaction: L-glutamine + 7-cyano-7-carbaguanine^{15} in tRNA + H_2O = L-glutamate + archaeine^{15} in tRNA

Other name(s): ArcS; TgtA2; MJ1022 (gene name); glutamine:preQ$_0$-tRNA amidinotransferase (incorrect)

Systematic name: L-glutamine:7-cyano-7-carbaguanine aminotransferase

Comments: In Euryarchaeota the reaction is catalysed by ArcS [2693, 2694]. In Crenarchaeota, which do not have an ArcS homologue, the reaction is catalysed either by a homologue of EC 6.3.4.20, 7-cyano-7-deazaguanine synthase that includes a glutaminase domain (*cf.* EC 3.5.1.2), or by a homologue of EC 1.7.1.13, $preQ_1$ synthase [2694]. The enzyme from the Euryarchaeon *Methanocaldococcus jannaschii* can also use arginine and ammonium as amino donors.

References: [2693, 2694]

[EC 2.6.1.97 created 2012]

EC 2.6.1.98

Accepted name: UDP-2-acetamido-2-deoxy-*ribo*-hexuluronate aminotransferase

Reaction: UDP-2-acetamido-3-amino-2,3-dideoxy-α-D-glucuronate + 2-oxoglutarate = UDP-2-acetamido-2-deoxy-α-D-*ribo*-hex-3-uluronate + L-glutamate

Other name(s): WbpE; WlbC

Systematic name: UDP-2-acetamido-3-amino-2,3-dideoxy-α-D-glucuronate:2-oxoglutarate aminotransferase

Comments: A pyridoxal 5′-phosphate protein. This enzyme participates in the biosynthetic pathway for UDP-α-D-ManNAc3NAcA (UDP-2,3-diacetamido-2,3-dideoxy-α-D-mannuronic acid), an important precursor of B-band lipopolysaccharide. The enzymes from *Pseudomonas aeruginosa* serotype O5 and *Thermus thermophilus* form a complex with the previous enzyme in the pathway, EC 1.1.1.335 (UDP-*N*-acetyl-2-amino-2-deoxyglucuronate oxidase).

References: [3827, 1864, 1865]

[EC 2.6.1.98 created 2012]

EC 2.6.1.99

Accepted name: L-tryptophan—pyruvate aminotransferase

Reaction: L-tryptophan + pyruvate = indole-3-pyruvate + L-alanine

Other name(s): TAA1 (gene name); vt2 (gene name)

Systematic name: L-tryptophan:pyruvate aminotransferase

Comments: This plant enzyme, along with EC 1.14.13.168, indole-3-pyruvate monooxygenase, is responsible for the biosynthesis of the plant hormone indole-3-acetate from L-tryptophan.

References: [3476, 2150, 2695, 4068]

[EC 2.6.1.99 created 2012]

EC 2.6.1.100

Accepted name: L-glutamine:2-deoxy-*scyllo*-inosose aminotransferase

Reaction: L-glutamine + 2-deoxy-*scyllo*-inosose = 2-oxoglutaramate + 2-deoxy-*scyllo*-inosamine

Other name(s): *btrR* (gene name); *neoB* (gene name); *kanB* (gene name)

Systematic name: L-glutamine:2-deoxy-*scyllo*-inosose aminotransferase

Comments: Involved in the biosynthetic pathways of several clinically important aminocyclitol antibiotics, including kanamycin, butirosin, neomycin and ribostamycin. Also catalyses EC 2.6.1.101, L-glutamine:5-amino-2,3,4-trihydroxycyclohexanone aminotransferase [1390].

References: [3461, 1390, 1806, 1518]

[EC 2.6.1.100 created 2013]

EC 2.6.1.101

Accepted name: L-glutamine:3-amino-2,3-dideoxy-*scyllo*-inosose aminotransferase

Reaction: L-glutamine + 3-amino-2,3-dideoxy-*scyllo*-inosose = 2-oxoglutaramate + 2-deoxystreptamine

Systematic name: L-glutamine:5-amino-2,3,4-trihydroxycyclohexanone aminotransferase

Comments: Involved in the biosynthetic pathways of several clinically important aminocyclitol antibiotics, including kanamycin, butirosin, neomycin and ribostamycin. Also catalyses EC 2.6.1.100, L-glutamine:2-deoxy-*scyllo*-inosose aminotransferase.

References: [1390, 1806]

[EC 2.6.1.101 created 2013]

EC 2.6.1.102

Accepted name: GDP-perosamine synthase

Reaction: GDP-α-D-perosamine + 2-oxoglutarate = GDP-4-dehydro-α-D-rhamnose + L-glutamate

Other name(s): RfbE; GDP-4-keto-6-deoxy-D-mannose-4-aminotransferase; GDP-perosamine synthetase; PerA; GDP-4-amino-4,6-dideoxy-α-D-mannose:2-oxoglutarate aminotransferase

Systematic name: GDP-α-D-perosamine:2-oxoglutarate aminotransferase

Comments: A pyridoxal 5′-phosphate enzyme. D-Perosamine is one of several dideoxy sugars found in the O-specific polysaccharide of the lipopolysaccharide component of the outer membrane of Gram-negative bacteria. The enzyme catalyses the final step in GDP-α-D-perosamine synthesis.

References: [44, 4060, 43, 604]

[EC 2.6.1.102 created 2013]

EC 2.6.1.103

Accepted name: (*S*)-3,5-dihydroxyphenylglycine transaminase

Reaction: (*S*)-3,5-dihydroxyphenylglycine + 2-oxoglutarate = 2-(3,5-dihydroxyphenyl)-2-oxoacetate + L-glutamate

Other name(s): HpgT

Systematic name: (*S*)-3,5-dihydroxyphenylglycine:2-oxoglutarate aminotransferase

Comments: A pyridoxal-5′-phosphate protein. The enzyme from the bacterium *Amycolatopsis orientalis* catalyses the reaction in the reverse direction as part of the biosynthesis of the (*S*)-3,5-dihydroxyphenylglycine constituent of the glycopeptide antibiotic chloroeremomycin.

References: [3016]

[EC 2.6.1.103 created 2013]

EC 2.6.1.104

Accepted name: 3-dehydro-glucose-6-phosphate—glutamate transaminase

Reaction: kanosamine 6-phosphate + 2-oxoglutarate = 3-dehydro-D-glucose 6-phosphate + L-glutamate

Other name(s): 3-oxo-glucose-6-phosphate:glutamate aminotransferase; *ntdA* (gene name)

Systematic name: kanosamine 6-phosphate:2-oxoglutarate aminotransferase

Comments: A pyridoxal-phosphate protein. The enzyme, found in the bacterium *Bacillus subtilis*, is involved in a kanosamine biosynthesis pathway.

References: [3643, 3674]

[EC 2.6.1.104 created 2014]

EC 2.6.1.105

Accepted name: lysine—8-amino-7-oxononanoate transaminase

Reaction: L-lysine + 8-amino-7-oxononanoate = (*S*)-2-amino-6-oxohexanoate + 7,8-diaminononanoate

Other name(s): DAPA aminotransferase (ambiguous); *bioA* (gene name) (ambiguous); *bioK* (gene name)

Systematic name: L-lysine:8-amino-7-oxononanoate aminotransferase

Comments: A pyridoxal 5′-phosphate enzyme [726]. Participates in the pathway for biotin biosynthesis.
The enzyme from the bacterium *Bacillus subtilis* cannot use *S*-adenosyl-L-methionine as amino donor and catalyses an alternative reaction for the conversion of 8-amino-7-oxononanoate to 7,8-diaminononanoate (*cf.* EC 2.6.1.62, adenosylmethionine—8-amino-7-oxononanoate transaminase).

References: [112, 726]

[EC 2.6.1.105 created 2014]

EC 2.6.1.106

Accepted name: dTDP-3-amino-3,4,6-trideoxy-α-D-glucose transaminase
Reaction: dTDP-3-amino-3,4,6-trideoxy-α-D-glucose + 2-oxoglutarate = dTDP-3-dehydro-4,6-deoxy-α-D-glucose + L-glutamate
Other name(s): *desV* (gene name); megDII (gene name); *eryCI* (gene name)
Systematic name: dTDP-3-amino-3,4,6-trideoxy-α-D-glucose:2-oxoglutarate aminotransferase
Comments: A pyridoxal-phosphate protein. The enzyme is involved in the biosynthesis of dTDP-α-D-desosamine, a sugar found in several bacterial macrolide antibiotics including erythromycin, megalomicin A, mycinamicin II, and oleandomycin. The reaction occurs in the reverse direction.
References: [427]

[EC 2.6.1.106 created 2014]

EC 2.6.1.107

Accepted name: β-methylphenylalanine transaminase
Reaction: (2*S*,3*S*)-3-methylphenylalanine + 2-oxoglutarate = (3*S*)-2-oxo-3-phenylbutanoate + L-glutamate
Other name(s): TyrB
Systematic name: (2*S*,3*S*)-3-methylphenylalanine:2-oxoglutarate aminotransferase
Comments: Requires pyridoxal phosphate. Isolated from the bacterium *Streptomyces hygroscopicus* NRRL3085. It is involved in the biosynthesis of the glycopeptide antibiotic mannopeptimycin.
References: [1397]

[EC 2.6.1.107 created 2014]

EC 2.6.1.108

Accepted name: (5-formylfuran-3-yl)methyl phosphate transaminase
Reaction: L-alanine + (5-formylfuran-3-yl)methyl phosphate = pyruvate + [5-(aminomethyl)furan-3-yl]methyl phosphate
Other name(s): *mfnC* (gene name); [5-(hydroxymethyl)furan-3-yl]methyl phosphate transaminase
Systematic name: L-alanine:(5-formylfuran-3-yl)methyl phosphate aminotransferase
Comments: A pyridoxal 5′-phosphate protein. The enzyme, characterized from the archaebacterium *Methanocaldococcus jannaschii*, participates in the biosynthesis of the cofactor methanofuran. Requires pyridoxal 5′-phosphate.
References: [2251]

[EC 2.6.1.108 created 2015]

EC 2.6.1.109

Accepted name: 8-amino-3,8-dideoxy-α-D-*manno*-octulosonate transaminase
Reaction: 8-amino-3,8-dideoxy-α-D-*manno*-octulosonate + 2-oxoglutarate = 8-dehydro-3-deoxy-α-D-*manno*-octulosonate + L-glutamate
Other name(s): *kdnA* (gene name)
Systematic name: 8-amino-3,8-dideoxy-α-D-*manno*-octulosonate:2-oxoglutarate aminotransferase
Comments: The enzyme, characterized from the bacterium *Shewanella oneidensis*, forms 8-amino-3,8-dideoxy-α-D-*manno*-octulosonate, an aminated form of Kdo found in lipopolysaccharides of members of the *Shewanella* genus. *cf.* EC 1.1.3.48, 3-deoxy-α-D-*manno*-octulosonate 8-oxidase.
References: [1025]

[EC 2.6.1.109 created 2015]

EC 2.6.1.110

Accepted name: dTDP-4-dehydro-2,3,6-trideoxy-D-glucose 4-aminotransferase
Reaction: dTDP-4-amino-2,3,4,6-tetradeoxy-α-D-*erythro*-hexopyranose + 2-oxoglutarate = dTDP-4-dehydro-2,3,6-trideoxy-α-D-hexopyranose + L-glutamate

Other name(s): SpnR; TDP-4-keto-2,3,6-trideoxy-D-glucose 4-aminotransferase
Systematic name: dTDP-4-amino-2,3,4,6-tetradeoxy-α-D-*erythro*-hexopyranose:2-oxoglutarate aminotransferase
Comments: A pyridoxal-phosphate protein. The enzyme, isolated from the bacterium *Saccharopolyspora spinosa*, participates in the biosynthesis of forosamine.
References: [1365]

[EC 2.6.1.110 created 2016]

EC 2.6.1.111

Accepted name: 3-aminobutanoyl-CoA transaminase
Reaction: 3-aminobutanoyl-CoA + 2-oxoglutarate = acetoacetyl-CoA + L-glutamate
Other name(s): *kat* (gene name); acyl-CoA β-transaminase
Systematic name: 3-aminobutanoyl-CoA:2-oxoglutarate aminotransferase
Comments: The enzyme, found in bacteria, is part of a L-lysine degradation pathway. The enzyme is also active with other β-amino compounds such as 3-amino-5-methylhexanoyl-CoA and 3-amino-3-phenylpropanoyl-CoA.
References: [2667]

[EC 2.6.1.111 created 2017]

EC 2.6.1.112

Accepted name: (*S*)-ureidoglycine—glyoxylate transaminase
Reaction: (*S*)-ureidoglycine + glyoxylate = *N*-carbamoyl-2-oxoglycine + glycine
Other name(s): (*S*)-ureidoglycine—glyoxylate aminotransferase; UGXT; PucG
Systematic name: (*S*)-ureidoglycine:glyoxylate aminotransferase
Comments: A pyridoxal 5′-phosphate protein. The protein, found in bacteria, can use other amino-group acceptors, but is specific for (*S*)-ureidoglycine.
References: [2804]

[EC 2.6.1.112 created 2017]

EC 2.6.1.113

Accepted name: putrescine—pyruvate transaminase
Reaction: putrescine + pyruvate = 4-aminobutanal + alanine
Other name(s): *spuC* (gene name)
Systematic name: putrescine:pyruvate aminotransferase
Comments: A pyridoxal 5′-phosphate protein. The enzyme, studied in the bacterium *Pseudomonas aeruginosa*, participates in a putrescine degradation pathway. *cf.* EC 2.6.1.82, putrescine—2-oxoglutarate aminotransferase.
References: [2052]

[EC 2.6.1.113 created 2017]

EC 2.6.1.114

Accepted name: 8-demethyl-8-aminoriboflavin-5′-phosphate synthase
Reaction: L-glutamate + FMN + O_2 + H_2O + **3** acceptor = 2-oxoglutarate + 8-amino-8-demethylriboflavin 5′-phosphate + CO_2 + **3** reduced acceptor (overall reaction)
(1a) FMN + O_2 = 8-demethyl-8-formylriboflavin 5′-phosphate + H_2O
(1b) 8-demethyl-8-formylriboflavin 5′-phosphate + H_2O + acceptor = 8-carboxy-8-demethylriboflavin 5′-phosphate + reduced acceptor
(1c) L-glutamate + 8-carboxy-8-demethylriboflavin 5′-phosphate + H_2O + **2** acceptor = 2-oxoglutarate + 8-amino-8-demethylriboflavin 5′-phosphate + CO_2 + **2** reduced acceptor
Other name(s): *rosB* (gene name)

Systematic name: L-glutamate:FMN aminotransferase (oxidizing, decarboxylating)
Comments: The enzyme, characterized from the bacterium *Streptomyces davawensis*, has the activities of an oxidoreductase, a decarboxylase, and an aminotransferase. Its combined actions result in the replacement of a methyl substituent of one of the aromatic rings of FMN by an amino group, a step in the biosynthetic pathway of roseoflavin. The reaction requires thiamine for completion.
References: [3119, 1510, 1751]

[EC 2.6.1.114 created 2018]

EC 2.6.2 Amidinotransferases (deleted sub-subclass)

[2.6.2.1 Transferred entry. now EC 2.1.4.1 glycine amidinotransferase]

[EC 2.6.2.1 created 1961, deleted 1965]

EC 2.6.3 Oximinotransferases

EC 2.6.3.1
Accepted name: oximinotransferase
Reaction: pyruvate oxime + acetone = pyruvate + acetone oxime
Other name(s): transoximinase; oximase; pyruvate-acetone oximinotransferase; transoximase
Systematic name: pyruvate-oxime:acetone oximinotransferase
Comments: Acetaldehyde can act instead of acetone; D-glucose oxime can act instead of pyruvate oxime.
References: [3940, 3941, 3942]

[EC 2.6.3.1 created 1961]

EC 2.6.99 Transferring other nitrogenous groups

EC 2.6.99.1
Accepted name: dATP(dGTP)—DNA purinetransferase
Reaction: (1) dATP + depurinated DNA = deoxyribose triphosphate + DNA
(2) dGTP + depurinated DNA = deoxyribose triphosphate + DNA
Systematic name: dATP(dGTP):depurinated-DNA purine transferase
Comments: The purine residue is transferred on to the apurinic site forming a normal glycosylic bond. dATP reacts at sites of the double-stranded depurinated DNA that lack adenine, and dGTP at sites that lack guanine.
References: [724, 2015]

[EC 2.6.99.1 created 1984]

EC 2.6.99.2
Accepted name: pyridoxine 5′-phosphate synthase
Reaction: 1-deoxy-D-xylulose 5-phosphate + 3-amino-2-oxopropyl phosphate = pyridoxine 5′-phosphate + phosphate + **2** H_2O
Other name(s): pyridoxine 5-phosphate phospho lyase; PNP synthase; PdxJ
Systematic name: 1-deoxy-D-xylulose-5-phosphate:3-amino-2-oxopropyl phosphate 3-amino-2-oxopropyltransferase (phosphate-hydrolysing; cyclizing)

Comments: In *Escherichia coli*, the coenzyme pyridoxal $5'$-phosphate is synthesized de novo by a pathway that involves EC 1.2.1.72 (erythrose-4-phosphate dehydrogenase), EC 1.1.1.290 (4-phosphoerythronate dehydrogenase), EC 2.6.1.52 (phosphoserine transaminase), EC 1.1.1.262 (4-hydroxythreonine-4-phosphate dehydrogenase), EC 2.6.99.2 (pyridoxine $5'$-phosphate synthase) and EC 1.4.3.5 (with pyridoxine $5'$-phosphate as substrate). 1-Deoxy-D-xylulose cannot replace 1-deoxy-D-xylulose 5-phosphate as a substrate [1836].

References: [1019, 1020, 1836, 945]

[EC 2.6.99.2 created 2006]

EC 2.6.99.3

Accepted name: *O*-ureido-L-serine synthase

Reaction: *O*-acetyl-L-serine + hydroxyurea = *O*-ureido-L-serine + acetate

Other name(s): *dcsD* (gene name)

Systematic name: *O*-acetyl-L-serine:hydroxyurea 2-amino-2-carboxyethyltransferase

Comments: The enzyme participates in the biosynthetic pathway of D-cycloserine, an antibiotic substance produced by several *Streptomyces* species. Also catalyses EC 2.5.1.47, cysteine synthase.

References: [1813, 3597]

[EC 2.6.99.3 created 2013]

[2.6.99.4 Transferred entry. N^6-L-threonylcarbamoyladenine synthase. Now EC 2.3.1.234, N^6-L-threonylcarbamoyladenine synthase.]

[EC 2.6.99.4 created 2014, deleted 2014]

EC 2.7 Transferring phosphorus-containing groups

This subclass contains a rather large group of enzymes that transfer not only phosphate but also diphosphate, nucleotidyl residues and other groups. The phosphotransferases are subdivided according to the acceptor group, which may be an alcohol group (EC 2.7.1), a carboxy group (EC 2.7.2), a nitrogenous group, such as that of creatine (EC 2.7.3), or a phosphate group, as in the case of adenylate kinase (EC 2.7.4). Other sub-subclasses are for: diphosphotransferases (EC 2.7.6), nucleotidyltransferases (EC 2.7.7) and transferases for other substituted phosphate groups (EC 2.7.8). With the enzymes of sub-subclass EC 2.7.9, two phosphate groups are transferred from a donor such as ATP to two different acceptors. The protein kinases are divided into the sub-subclasses protein-tyrosine kinases (EC 2.7.10), protein-serine/threonine kinases (EC 2.7.11), dual-specificity kinases (EC 2.7.12), protein-histidine kinases (EC 2.7.13) and other protein kinases (EC 2.7.99).

EC 2.7.1 Phosphotransferases with an alcohol group as acceptor

EC 2.7.1.1

Accepted name: hexokinase

Reaction: ATP + D-hexose = ADP + D-hexose 6-phosphate

Other name(s): hexokinase type IV glucokinase; hexokinase D; hexokinase type IV; hexokinase (phosphorylating); ATP-dependent hexokinase; glucose ATP phosphotransferase

Systematic name: ATP:D-hexose 6-phosphotransferase

Comments: D-Glucose, D-mannose, D-fructose, sorbitol and D-glucosamine can act as acceptors; ITP and dATP can act as donors. The liver isoenzyme has sometimes been called glucokinase.

References: [164, 280, 1820, 2738, 3618, 475]

[EC 2.7.1.1 created 1961]

EC 2.7.1.2

Accepted name: glucokinase
Reaction: ATP + D-glucose = ADP + D-glucose 6-phosphate
Other name(s): glucokinase (phosphorylating)
Systematic name: ATP:D-glucose 6-phosphotransferase
Comments: A group of enzymes found in invertebrates and microorganisms that are highly specific for glucose.
References: [239, 419, 2743]

[EC 2.7.1.2 created 1961]

EC 2.7.1.3

Accepted name: ketohexokinase
Reaction: ATP + D-fructose = ADP + D-fructose 1-phosphate
Other name(s): ketohexokinase (phosphorylating)
Systematic name: ATP:D-fructose 1-phosphotransferase
Comments: D-Sorbose, D-tagatose and 5-dehydro-D-fructose and a number of other ketoses and their analogues can also act as substrates [2825].
References: [616, 1306, 2627, 2825]

[EC 2.7.1.3 created 1961]

EC 2.7.1.4

Accepted name: fructokinase
Reaction: ATP + D-fructose = ADP + D-fructose 6-phosphate
Other name(s): fructokinase (phosphorylating); D-fructokinase; D-fructose(D-mannose)kinase
Systematic name: ATP:D-fructose 6-phosphotransferase
References: [419, 2204]

[EC 2.7.1.4 created 1961]

EC 2.7.1.5

Accepted name: rhamnulokinase
Reaction: ATP + L-rhamnulose = ADP + L-rhamnulose 1-phosphate
Other name(s): RhuK; rhamnulokinase (phosphorylating); L-rhamnulokinase; L-rhamnulose kinase; rhamnulose kinase
Systematic name: ATP:L-rhamnulose 1-phosphotransferase
References: [3867]

[EC 2.7.1.5 created 1961]

EC 2.7.1.6

Accepted name: galactokinase
Reaction: ATP + α-D-galactose = ADP + α-D-galactose 1-phosphate
Other name(s): galactokinase (phosphorylating); ATP:D-galactose-1-phosphotransferase
Systematic name: ATP:α-D-galactose 1-phosphotransferase
Comments: Part of the Leloir pathway for galactose metabolism. The enzymes from mammals and from the bacterium *Escherichia coli* have no activity with *N*-acetyl-α-D-galactosamine [3961, 3535, 3518].
References: [476, 2438, 3851, 3961, 3535, 3518]

[EC 2.7.1.6 created 1961]

EC 2.7.1.7

Accepted name: mannokinase

Reaction: ATP + D-mannose = ADP + D-mannose 6-phosphate
Other name(s): mannokinase (phosphorylating); D-fructose (D-mannose) kinase
Systematic name: ATP:D-mannose 6-phosphotransferase
References: [419]

[EC 2.7.1.7 created 1961]

EC 2.7.1.8

Accepted name: glucosamine kinase
Reaction: ATP + D-glucosamine = ADP + D-glucosamine 6-phosphate
Other name(s): glucosamine kinase (phosphorylating); ATP:2-amino-2-deoxy-D-glucose-6-phosphotransferase; aminodeoxyglucose kinase; ATP:D-glucosamine phosphotransferase
Systematic name: ATP:D-glucosamine 6-phosphotransferase
Comments: The enzyme has been studied in the bacterium *Vibrio cholerae*, where it participates in a chitin degradation pathway.
References: [419, 2622]

[EC 2.7.1.8 created 1961, modified 2014]

[2.7.1.9 Deleted entry. acetylaminodeoxyglucose kinase]

[EC 2.7.1.9 created 1961, deleted 1965]

EC 2.7.1.10

Accepted name: phosphoglucokinase
Reaction: ATP + α-D-glucose 1-phosphate = ADP + α-D-glucose 1,6-bisphosphate
Other name(s): glucose-phosphate kinase; phosphoglucokinase (phosphorylating); ATP:D-glucose-1-phosphate 6-phosphotransferase
Systematic name: ATP:α-D-glucose-1-phosphate 6-phosphotransferase
References: [2601]

[EC 2.7.1.10 created 1961]

EC 2.7.1.11

Accepted name: 6-phosphofructokinase
Reaction: ATP + D-fructose 6-phosphate = ADP + D-fructose 1,6-bisphosphate
Other name(s): phosphohexokinase; phosphofructokinase I; phosphofructokinase (phosphorylating); 6-phosphofructose 1-kinase; ATP-dependent phosphofructokinase; D-fructose-6-phosphate 1-phosphotransferase; fructose 6-phosphate kinase; fructose 6-phosphokinase; nucleotide triphosphate-dependent phosphofructokinase; phospho-1,6-fructokinase; PFK
Systematic name: ATP:D-fructose-6-phosphate 1-phosphotransferase
Comments: D-Tagatose 6-phosphate and sedoheptulose 7-phosphate can act as acceptors. UTP, CTP and ITP can act as donors. Not identical with EC 2.7.1.105 6-phosphofructo-2-kinase.
References: [136, 1978, 2115, 2508, 2628, 2786, 3283, 3621]

[EC 2.7.1.11 created 1961]

EC 2.7.1.12

Accepted name: gluconokinase
Reaction: ATP + D-gluconate = ADP + 6-phospho-D-gluconate
Other name(s): gluconokinase (phosphorylating); gluconate kinase
Systematic name: ATP:D-gluconate 6-phosphotransferase
References: [587, 1885, 2419, 2986]

[EC 2.7.1.12 created 1961]

EC 2.7.1.13

Accepted name: dehydrogluconokinase
Reaction: ATP + 2-dehydro-D-gluconate = ADP + 6-phospho-2-dehydro-D-gluconate
Other name(s): ketogluconokinase; 2-ketogluconate kinase; ketogluconokinase (phosphorylating); 2-ketogluconokinase
Systematic name: ATP:2-dehydro-D-gluconate 6-phosphotransferase
References: [942]

[EC 2.7.1.13 created 1961]

EC 2.7.1.14

Accepted name: sedoheptulokinase
Reaction: ATP + sedoheptulose = ADP + sedoheptulose 7-phosphate
Other name(s): heptulokinase; sedoheptulokinase (phosphorylating)
Systematic name: ATP:sedoheptulose 7-phosphotransferase
References: [800]

[EC 2.7.1.14 created 1961]

EC 2.7.1.15

Accepted name: ribokinase
Reaction: ATP + D-ribose = ADP + D-ribose 5-phosphate
Other name(s): deoxyribokinase; ribokinase (phosphorylating); D-ribokinase
Systematic name: ATP:D-ribose 5-phosphotransferase
Comments: 2-Deoxy-D-ribose can also act as acceptor.
References: [25, 1063]

[EC 2.7.1.15 created 1961]

EC 2.7.1.16

Accepted name: ribulokinase
Reaction: ATP + L(or D)-ribulose = ADP + L(or D)-ribulose 5-phosphate
Other name(s): ribulokinase (phosphorylating); L-ribulokinase
Systematic name: ATP:L(or D)-ribulose 5-phosphotransferase
Comments: Ribitol and L-arabinitol can also act as acceptors.
References: [431, 1896, 3237]

[EC 2.7.1.16 created 1961]

EC 2.7.1.17

Accepted name: xylulokinase
Reaction: ATP + D-xylulose = ADP + D-xylulose 5-phosphate
Other name(s): xylulokinase (phosphorylating); D-xylulokinase
Systematic name: ATP:D-xylulose 5-phosphotransferase
References: [1318, 3236, 3254, 3377]

[EC 2.7.1.17 created 1961]

EC 2.7.1.18

Accepted name: phosphoribokinase

Reaction: ATP + D-ribose 5-phosphate = ADP + α-D-ribose 1,5-bisphosphate
Other name(s): phosphoribokinase (phosphorylating)
Systematic name: ATP:D-ribose-5-phosphate 1-phosphotransferase
References: [1778, 3053]

[EC 2.7.1.18 created 1961]

EC 2.7.1.19

Accepted name: phosphoribulokinase
Reaction: ATP + D-ribulose 5-phosphate = ADP + D-ribulose 1,5-bisphosphate
Other name(s): phosphopentokinase; ribulose-5-phosphate kinase; phosphopentokinase; phosphoribulokinase (phosphorylating); 5-phosphoribulose kinase; ribulose phosphate kinase; PKK; PRuK; PRK
Systematic name: ATP:D-ribulose-5-phosphate 1-phosphotransferase
References: [1414, 1495]

[EC 2.7.1.19 created 1961]

EC 2.7.1.20

Accepted name: adenosine kinase
Reaction: ATP + adenosine = ADP + AMP
Other name(s): adenosine kinase (phosphorylating)
Systematic name: ATP:adenosine 5′-phosphotransferase
Comments: 2-Aminoadenosine can also act as acceptor.
References: [1976, 474, 1759]

[EC 2.7.1.20 created 1961]

EC 2.7.1.21

Accepted name: thymidine kinase
Reaction: ATP + thymidine = ADP + dTMP
Other name(s): thymidine kinase (phosphorylating); 2′-deoxythymidine kinase; deoxythymidine kinase (phosphorylating)
Systematic name: ATP:thymidine 5′-phosphotransferase
Comments: Deoxyuridine can also act as acceptor, and dGTP can act as a donor. The deoxypyrimidine kinase complex induced by *Herpes simplex* virus catalyses this reaction as well as those of EC 2.7.1.114 (AMP—thymidine kinase), EC 2.7.1.118 (ADP—thymidine kinase) and EC 2.7.4.9 (dTMP-kinase).
References: [870, 1702, 2554]

[EC 2.7.1.21 created 1961, deleted 1972, reinstated 1976 (EC 2.7.1.75 created 1972, incorporated 1976)]

EC 2.7.1.22

Accepted name: ribosylnicotinamide kinase
Reaction: ATP + 1-(β-D-ribofuranosyl)-nicotinamide = ADP + β-nicotinamide D-ribonucleotide
Other name(s): ribosylnicotinamide kinase (phosphorylating); ATP:*N*-ribosylnicotinamide 5′-phosphotransferase
Systematic name: ATP:1-(β-D-ribofuranosyl)-nicotinamide 5′-phosphotransferase
References: [2948]

[EC 2.7.1.22 created 1961]

EC 2.7.1.23

Accepted name: NAD$^+$ kinase
Reaction: ATP + NAD$^+$ = ADP + NADP$^+$

Other name(s): DPN kinase; nicotinamide adenine dinucleotide kinase (phosphorylating); nicotinamide adenine dinucleotide kinase; NAD kinase; NADK
Systematic name: ATP:NAD^+ 2′-phosphotransferase
References: [442, 564, 1755, 3757]

[EC 2.7.1.23 created 1961]

EC 2.7.1.24

Accepted name: dephospho-CoA kinase
Reaction: ATP + 3′-dephospho-CoA = ADP + CoA
Other name(s): dephosphocoenzyme A kinase (phosphorylating); 3′-dephospho-CoA kinase; dephosphocoenzyme A kinase; ATP:dephospho-CoA 3′-phosphotransferase
Systematic name: ATP:3′-dephospho-CoA 3′-phosphotransferase
References: [6, 1345, 3757]

[EC 2.7.1.24 created 1961]

EC 2.7.1.25

Accepted name: adenylyl-sulfate kinase
Reaction: ATP + adenylyl sulfate = ADP + 3′-phosphoadenylyl sulfate
Other name(s): adenylylsulfate kinase (phosphorylating); 5′-phosphoadenosine sulfate kinase; adenosine 5′-phosphosulfate kinase; adenosine phosphosulfate kinase; adenosine phosphosulfokinase; adenosine-5′-phosphosulfate-3′-phosphokinase; APS kinase
Systematic name: ATP:adenylyl-sulfate 3′-phosphotransferase
Comments: The human phosphoadenosine-phosphosulfate synthase (PAPSS) system is a bifunctional enzyme (fusion product of two catalytic activities). In a first step, sulfate adenylyltransferase catalyses the formation of adenosine 5′-phosphosulfate (APS) from ATP and inorganic sulfate. The second step is catalysed by the adenylylsulfate kinase portion of 3′-phosphoadenosine 5′-phosphosulfate (PAPS) synthase, which involves the formation of PAPS from enzyme-bound APS and ATP. In contrast, in bacteria, yeast, fungi and plants, the formation of PAPS is carried out by two individual polypeptides, sulfate adenylyltransferase (EC 2.7.7.4) and adenylyl-sulfate kinase (EC 2.7.1.25).
References: [178, 2892, 3660]

[EC 2.7.1.25 created 1961, modified 1999]

EC 2.7.1.26

Accepted name: riboflavin kinase
Reaction: ATP + riboflavin = ADP + FMN
Other name(s): flavokinase; FK; RFK
Systematic name: ATP:riboflavin 5′-phosphotransferase
Comments: The cofactors FMN and FAD participate in numerous processes in all organisms, including mitochondrial electron transport, photosynthesis, fatty-acid oxidation, and metabolism of vitamin B_6, vitamin B_{12} and folates [3018]. While monofunctional riboflavin kinase is found in eukaryotes, some bacteria have a bifunctional enzyme that exhibits both this activity and that of EC 2.7.7.2, FMN adenylyltransferase [3018]. A divalent metal cation is required for activity (with different species preferring Mg^{2+}, Mn^{2+} or Zn^{2+}). In *Bacillus subtilis*, ATP can be replaced by other phosphate donors but with decreasing enzyme activity in the order ATP $>$ dATP $>$ CTP $>$ UTP [3282].
References: [507, 1065, 1622, 2188, 3018, 3282, 3281]

[EC 2.7.1.26 created 1961, modified 2007]

EC 2.7.1.27

Accepted name: erythritol kinase (D-erythritol 4-phosphate-forming)

Reaction: ATP + erythritol = ADP + D-erythritol 4-phosphate
Other name(s): erythritol kinase (phosphorylating) (ambiguous)
Systematic name: ATP:erythritol 4-phosphotransferase
Comments: The enzyme has been characterized from the bacterium *Propionibacterium acidipropionici* (previously known as *Propionibacterium pentosaceum*). *cf.* EC 2.7.1.215, erythritol kinase (L-erythritol 4-phosphate-forming).
References: [3177, 1361]

[EC 2.7.1.27 created 1961, modified 2016]

EC 2.7.1.28

Accepted name: triokinase
Reaction: ATP + D-glyceraldehyde = ADP + D-glyceraldehyde 3-phosphate
Other name(s): triose kinase;
Systematic name: ATP:D-glyceraldehyde 3-phosphotransferase
References: [1307, 3226]

[EC 2.7.1.28 created 1961]

EC 2.7.1.29

Accepted name: glycerone kinase
Reaction: ATP + glycerone = ADP + glycerone phosphate
Other name(s): dihydroxyacetone kinase; acetol kinase; acetol kinase (phosphorylating)
Systematic name: ATP:glycerone phosphotransferase
References: [3136]

[EC 2.7.1.29 created 1961]

EC 2.7.1.30

Accepted name: glycerol kinase
Reaction: ATP + glycerol = ADP + *sn*-glycerol 3-phosphate
Other name(s): glycerokinase; GK; ATP:glycerol-3-phosphotransferase; glycerol kinase (phosphorylating); glyceric kinase
Systematic name: ATP:glycerol 3-phosphotransferase
Comments: Glycerone and L-glyceraldehyde can act as acceptors; UTP (and, in the case of the yeast enzyme, ITP and GTP) can act as donors.
References: [283, 414, 3849]

[EC 2.7.1.30 created 1961]

EC 2.7.1.31

Accepted name: glycerate 3-kinase
Reaction: ATP + D-glycerate = ADP + 3-phospho-D-glycerate
Other name(s): glycerate kinase (phosphorylating) (ambiguous); D-glycerate 3-kinase; D-glycerate kinase (ambiguous); glycerate-kinase (ambiguous); GK (ambiguous); D-glyceric acid kinase (ambiguous); ATP:(*R*)-glycerate 3-phosphotransferase
Systematic name: ATP:D-glycerate 3-phosphotransferase
References: [761, 1426]

[EC 2.7.1.31 created 1961, modified 2012]

EC 2.7.1.32

Accepted name: choline kinase
Reaction: ATP + choline = ADP + phosphocholine
Other name(s): choline kinase (phosphorylating); choline phosphokinase; choline-ethanolamine kinase
Systematic name: ATP:choline phosphotransferase
Comments: Ethanolamine and its methyl and ethyl derivatives can also act as acceptors.
References: [1253, 3877]

[EC 2.7.1.32 created 1961]

EC 2.7.1.33

Accepted name: pantothenate kinase
Reaction: ATP + (*R*)-pantothenate = ADP + (*R*)-4′-phosphopantothenate
Other name(s): pantothenate kinase (phosphorylating); pantothenic acid kinase; ATP:pantothenate 4′-phosphotransferase; D-pantothenate kinase
Systematic name: ATP:(*R*)-pantothenate 4′-phosphotransferase
References: [7, 405, 2703]

[EC 2.7.1.33 created 1961]

EC 2.7.1.34

Accepted name: pantetheine kinase
Reaction: ATP + pantetheine = ADP + pantetheine 4′-phosphate
Other name(s): pantetheine kinase (phosphorylating)
Systematic name: ATP:pantetheine 4′-phosphotransferase
References: [2492]

[EC 2.7.1.34 created 1961]

EC 2.7.1.35

Accepted name: pyridoxal kinase
Reaction: ATP + pyridoxal = ADP + pyridoxal 5′-phosphate
Other name(s): pyridoxal kinase (phosphorylating); pyridoxal 5-phosphate-kinase; pyridoxal phosphokinase; pyridoxine kinase
Systematic name: ATP:pyridoxal 5′-phosphotransferase
Comments: Pyridoxine, pyridoxamine and various derivatives can also act as acceptors.
References: [2189, 3571]

[EC 2.7.1.35 created 1961]

EC 2.7.1.36

Accepted name: mevalonate kinase
Reaction: ATP + (*R*)-mevalonate = ADP + (*R*)-5-phosphomevalonate
Other name(s): mevalonate kinase (phosphorylating); mevalonate phosphokinase; mevalonic acid kinase; mevalonic kinase; mevalonate 5-phosphotransferase ; MVA kinase; ATP:mevalonate 5-phosphotransferase
Systematic name: ATP:(*R*)-mevalonate 5-phosphotransferase
Comments: CTP, GTP and UTP can also act as donors.
References: [1284, 1951, 2128, 3491]

[EC 2.7.1.36 created 1961]

[2.7.1.37 Transferred entry. protein kinase. Now divided into EC 2.7.11.1 (non-specific serine/threonine protein kinase), EC 2.7.11.8 (Fas-activated serine/threonine kinase), EC 2.7.11.9 (Goodpasture-antigen-binding protein kinase), EC 2.7.11.10 (IκB kinase), EC 2.7.11.11 (cAMP-dependent protein kinase), EC 2.7.11.12 (cGMP-dependent protein kinase), EC 2.7.11.13 (protein

kinase C), EC 2.7.11.21 (polo kinase), EC 2.7.11.22 (cyclin-dependent kinase), EC 2.7.11.24 (mitogen-activated protein kinase), EC 2.7.11.25 (mitogen-activated protein kinase kinase kinase), EC 2.7.11.30 (receptor protein serine/threonine kinase) and EC 2.7.12.1 (dual-specificity kinase)]

[EC 2.7.1.37 created 1961 (EC 2.7.1.70 incorporated 2004), deleted 2005]

[2.7.1.38 Transferred entry. phosphorylase kinase. Now EC 2.7.11.19, phosphorylase kinase]

[EC 2.7.1.38 created 1961, deleted 2005]

EC 2.7.1.39

Accepted name: homoserine kinase
Reaction: ATP + L-homoserine = ADP + *O*-phospho-L-homoserine
Other name(s): homoserine kinase (phosphorylating); HSK
Systematic name: ATP:L-homoserine *O*-phosphotransferase
References: [915, 3786]

[EC 2.7.1.39 created 1961]

EC 2.7.1.40

Accepted name: pyruvate kinase
Reaction: ATP + pyruvate = ADP + phospho*enol*pyruvate
Other name(s): phospho*enol*pyruvate kinase; phospho*enol* transphosphorylase
Systematic name: ATP:pyruvate 2-*O*-phosphotransferase
Comments: UTP, GTP, CTP, ITP and dATP can also act as donors. Also phosphorylates hydroxylamine and fluoride in the presence of CO_2.
References: [370, 1759, 1800, 3374, 3534]

[EC 2.7.1.40 created 1961]

EC 2.7.1.41

Accepted name: glucose-1-phosphate phosphodismutase
Reaction: **2** D-glucose 1-phosphate = D-glucose + D-glucose 1,6-bisphosphate
Systematic name: D-glucose-1-phosphate:D-glucose-1-phosphate 6-phosphotransferase
References: [1931, 3218]

[EC 2.7.1.41 created 1961]

EC 2.7.1.42

Accepted name: riboflavin phosphotransferase
Reaction: α-D-glucose 1-phosphate + riboflavin = D-glucose + FMN
Other name(s): riboflavine phosphotransferase; glucose-1-phosphate phosphotransferase; G-1-*P* phosphotransferase; D-glucose-1-phosphate:riboflavin 5′-phosphotransferase
Systematic name: α-D-glucose-1-phosphate:riboflavin 5′-phosphotransferase
References: [1594]

[EC 2.7.1.42 created 1961]

EC 2.7.1.43

Accepted name: glucuronokinase
Reaction: ATP + D-glucuronate = ADP + 1-phospho-α-D-glucuronate
Other name(s): glucuronokinase (phosphorylating); glucurono-glucuronokinase
Systematic name: ATP:D-glucuronate 1-phosphotransferase
References: [2437]

[EC 2.7.1.43 created 1965]

EC 2.7.1.44

Accepted name: galacturonokinase
Reaction: ATP + D-galacturonate = ADP + 1-phospho-α-D-galacturonate
Other name(s): galacturonokinase (phosphorylating) D-galacturonic acid kinase
Systematic name: ATP:D-galacturonate 1-phosphotransferase
References: [2439]

[EC 2.7.1.44 created 1965]

EC 2.7.1.45

Accepted name: 2-dehydro-3-deoxygluconokinase
Reaction: ATP + 2-dehydro-3-deoxy-D-gluconate = ADP + 2-dehydro-3-deoxy-6-phospho-D-gluconate
Other name(s): 2-keto-3-deoxygluconokinase; 2-keto-3-deoxy-D-gluconic acid kinase; 2-keto-3-deoxygluconokinase (phosphorylating); 2-keto-3-deoxygluconate kinase; ketodeoxygluconokinase
Systematic name: ATP:2-dehydro-3-deoxy-D-gluconate 6-phosphotransferase
Comments: The enzyme shows no activity with 2-dehydro-3-deoxy-D-galactonate [650]. *cf.* EC 2.7.1.178, 2-dehydro-3-deoxyglucono/2-dehydro-3-deoxygalactonokinase.
References: [650]

[EC 2.7.1.45 created 1965, modified 1976]

EC 2.7.1.46

Accepted name: L-arabinokinase
Reaction: ATP + L-arabinose = ADP + β-L-arabinose 1-phosphate
Other name(s): L-arabinokinase (phosphorylating)
Systematic name: ATP:L-arabinose 1-phosphotransferase
References: [2438]

[EC 2.7.1.46 created 1965]

EC 2.7.1.47

Accepted name: D-ribulokinase
Reaction: ATP + D-ribulose = ADP + D-ribulose 5-phosphate
Other name(s): D-ribulokinase (phosphorylating)
Systematic name: ATP:D-ribulose 5-phosphotransferase
References: [972]

[EC 2.7.1.47 created 1965]

EC 2.7.1.48

Accepted name: uridine kinase
Reaction: ATP + uridine = ADP + UMP
Other name(s): pyrimidine ribonucleoside kinase; uridine-cytidine kinase; uridine kinase (phosphorylating); uridine phosphokinase
Systematic name: ATP:uridine $5'$-phosphotransferase
Comments: Cytidine can act as acceptor; GTP and ITP can act as donors.
References: [2574, 3248]

[EC 2.7.1.48 created 1965]

EC 2.7.1.49

Accepted name: hydroxymethylpyrimidine kinase

Reaction: ATP + 4-amino-5-hydroxymethyl-2-methylpyrimidine = ADP + 4-amino-2-methyl-5-(phosphooxymethyl)pyrimidine

Other name(s): hydroxymethylpyrimidine kinase (phosphorylating)

Systematic name: ATP:4-amino-5-hydroxymethyl-2-methylpyrimidine 5-phosphotransferase

Comments: CTP, UTP and GTP can act as donors.

References: [1953]

[EC 2.7.1.49 created 1965]

EC 2.7.1.50

Accepted name: hydroxyethylthiazole kinase

Reaction: ATP + 4-methyl-5-(2-hydroxyethyl)thiazole = ADP + 4-methyl-5-(2-phosphooxyethyl)thiazole

Other name(s): hydroxyethylthiazole kinase (phosphorylating); 4-methyl-5-(β-hydroxyethyl)thiazole kinase

Systematic name: ATP:4-methyl-5-(2-hydroxyethyl)thiazole 2-phosphotransferase

References: [1953]

[EC 2.7.1.50 created 1965]

EC 2.7.1.51

Accepted name: L-fuculokinase

Reaction: ATP + L-fuculose = ADP + L-fuculose 1-phosphate

Other name(s): L-fuculokinase (phosphorylating); L-fuculose kinase

Systematic name: ATP:L-fuculose 1-phosphotransferase

References: [1265]

[EC 2.7.1.51 created 1965]

EC 2.7.1.52

Accepted name: fucokinase

Reaction: ATP + L-fucose = ADP + β-L-fucose 1-phosphate

Other name(s): fucokinase (phosphorylating); fucose kinase; L-fucose kinase; L-fucokinase; ATP:6-deoxy-L-galactose 1-phosphotransferase; ATP:L-fucose 1-phosphotransferase

Systematic name: ATP:β-L-fucose 1-phosphotransferase

Comments: Requires a divalent cation for activity, with Mg^{2+} and Fe^{2+} giving rise to the highest enzyme activity. Forms part of a salvage pathway for reutilization of L-fucose. Can also phosphorylate D-arabinose, but more slowly.

References: [1456, 443, 2625]

[EC 2.7.1.52 created 1972, modified 2004]

EC 2.7.1.53

Accepted name: L-xylulokinase

Reaction: ATP + L-xylulose = ADP + L-xylulose 5-phosphate

Other name(s): L-xylulokinase (phosphorylating)

Systematic name: ATP:L-xylulose 5-phosphotransferase

References: [79]

[EC 2.7.1.53 created 1972]

EC 2.7.1.54

Accepted name: D-arabinokinase
Reaction: ATP + D-arabinose = ADP + D-arabinose 5-phosphate
Other name(s): D-arabinokinase (phosphorylating)
Systematic name: ATP:D-arabinose 5-phosphotransferase
References: [3699]

[EC 2.7.1.54 created 1972]

EC 2.7.1.55

Accepted name: allose kinase
Reaction: ATP + D-allose = ADP + D-allose 6-phosphate
Other name(s): allokinase (phosphorylating); allokinase; D-allokinase; D-allose-6-kinase
Systematic name: ATP:D-allose 6-phosphotransferase
References: [1046]

[EC 2.7.1.55 created 1972]

EC 2.7.1.56

Accepted name: 1-phosphofructokinase
Reaction: ATP + D-fructose 1-phosphate = ADP + D-fructose 1,6-bisphosphate
Other name(s): fructose-1-phosphate kinase; 1-phosphofructokinase (phosphorylating); D-fructose-1-phosphate kinase; fructose 1-phosphate kinase; phosphofructokinase 1
Systematic name: ATP:D-fructose-phosphate 6-phosphotransferase
Comments: ITP, GTP or UTP can replace ATP.
References: [2856, 3025]

[EC 2.7.1.56 created 1972]

[2.7.1.57 Deleted entry. mannitol kinase]

[EC 2.7.1.57 created 1972, deleted 1984]

EC 2.7.1.58

Accepted name: 2-dehydro-3-deoxygalactonokinase
Reaction: ATP + 2-dehydro-3-deoxy-D-galactonate = ADP + 2-dehydro-3-deoxy-6-phospho-D-galactonate
Other name(s): 2-keto-3-deoxygalactonokinase; 2-keto-3-deoxygalactonate kinase (phosphorylating); 2-oxo-3-deoxygalactonate kinase
Systematic name: ATP:2-dehydro-3-deoxy-D-galactonate 6-phosphotransferase
References: [3359]

[EC 2.7.1.58 created 1972]

EC 2.7.1.59

Accepted name: *N*-acetylglucosamine kinase
Reaction: ATP + *N*-acetyl-D-glucosamine = ADP + *N*-acetyl-D-glucosamine 6-phosphate
Other name(s): acetylglucosamine kinase (phosphorylating); ATP:2-acetylamino-2-deoxy-D-glucose 6-phosphotransferase; 2-acetylamino-2-deoxy-D-glucose kinase; acetylaminodeoxyglucokinase
Systematic name: ATP:*N*-acetyl-D-glucosamine 6-phosphotransferase
Comments: The bacterial enzyme also acts on D-glucose.
References: [120, 198, 675]

[EC 2.7.1.59 created 1972]

EC 2.7.1.60

Accepted name: *N*-acylmannosamine kinase

Reaction: ATP + *N*-acyl-D-mannosamine = ADP + *N*-acyl-D-mannosamine 6-phosphate

Other name(s): acylmannosamine kinase (phosphorylating); acetylamidodeoxymannokinase; acetylmannosamine kinase; acylaminodeoxymannokinase; acylmannosamine kinase; *N*-acyl-D-mannosamine kinase; *N*-acetylmannosamine kinase; ATP:*N*-acetylmannosamine 6-phosphotransferase

Systematic name: ATP:*N*-acyl-D-mannosamine 6-phosphotransferase

Comments: Acts on the acetyl and glycolyl derivatives.

References: [179, 1045, 1819]

[EC 2.7.1.60 created 1972]

EC 2.7.1.61

Accepted name: acyl-phosphate—hexose phosphotransferase

Reaction: acyl phosphate + D-hexose = a carboxylate + D-hexose phosphate

Other name(s): hexose phosphate:hexose phosphotransferase

Systematic name: acyl-phosphate:D-hexose phosphotransferase

Comments: Phosphorylates D-glucose and D-mannose on O-6, and D-fructose on O-1 or O-6.

References: [78, 1572, 486]

[EC 2.7.1.61 created 1972, modified 2011]

EC 2.7.1.62

Accepted name: phosphoramidate—hexose phosphotransferase

Reaction: phosphoramidate + D-hexose = NH_3 + α-D-hexose 1-phosphate

Other name(s): phosphoramidate-hexose transphosphorylase; phosphoramidic-hexose transphosphorylase; phosphoramidate:hexose 1-phosphotransferase

Systematic name: phosphoramidate:D-hexose 1-phosphotransferase

Comments: Activity is observed with several hexoses; of these glucose is the best substrate and the product from it is α-D-glucose 1-phosphate. The phosphoramidate donor can be replaced by *N*-phosphoglycine and by an *N*-phosphohistidine. May be identical with EC 3.1.3.9 glucose-6-phosphatase.

References: [3263]

[EC 2.7.1.62 created 1972]

EC 2.7.1.63

Accepted name: polyphosphate—glucose phosphotransferase

Reaction: (phosphate)$_n$ + D-glucose = (phosphate)$_{n-1}$ + D-glucose 6-phosphate

Other name(s): polyphosphate glucokinase; polyphosphate-D-(+)-glucose-6-phosphotransferase; polyphosphate-glucose 6-phosphotransferase

Systematic name: polyphosphate:D-glucose 6-phosphotransferase

Comments: Requires a neutral salt, *e.g.* KCl, for maximum activity. Also acts on glucosamine.

References: [3419, 3420]

[EC 2.7.1.63 created 1972]

EC 2.7.1.64

Accepted name: inositol 3-kinase

Reaction: ATP + *myo*-inositol = ADP + 1D-*myo*-inositol 3-phosphate

Other name(s): inositol-1-kinase (phosphorylating); myoinositol kinase; *myo*-inositol 1-kinase

Systematic name: ATP:*myo*-inositol 1-phosphotransferase

References: [840, 2026, 3332]

[EC 2.7.1.64 created 1972, modified 2001]

EC 2.7.1.65

Accepted name: *scyllo*-inosamine 4-kinase

Reaction: ATP + 1-amino-1-deoxy-*scyllo*-inositol = ADP + 1-amino-1-deoxy-*scyllo*-inositol 4-phosphate

Other name(s): *scyllo*-inosamine kinase (phosphorylating); *scyllo*-inosamine kinase; ATP:inosamine phosphotransferase

Systematic name: ATP:1-amino-1-deoxy-*scyllo*-inositol 4-phosphotransferase

Comments: Also acts on streptamine, 2-deoxystreptamine and 1D-1-guanidino-3-amino-1,3-dideoxy-*scyllo*-inositol.

References: [3731, 3733]

[EC 2.7.1.65 created 1972, modified 1976]

EC 2.7.1.66

Accepted name: undecaprenol kinase

Reaction: ATP + undecaprenol = ADP + undecaprenyl phosphate

Other name(s): isoprenoid alcohol kinase; isoprenoid alcohol phosphokinase; C_{55}-isoprenoid alcohol phosphokinase; isoprenoid alcohol kinase (phosphorylating); C_{55}-isoprenoid alcohol kinase; C_{55}-isoprenyl alcohol phosphokinase; polyisoprenol kinase

Systematic name: ATP:undecaprenol phosphotransferase

References: [1324]

[EC 2.7.1.66 created 1972]

EC 2.7.1.67

Accepted name: 1-phosphatidylinositol 4-kinase

Reaction: ATP + 1-phosphatidyl-1D-*myo*-inositol = ADP + 1-phosphatidyl-1D-*myo*-inositol 4-phosphate

Other name(s): phosphatidylinositol kinase (phosphorylating); phosphatidylinositol 4-kinase; phosphatidylinositol kinase; type II phosphatidylinositol kinase; PI kinase; PI 4-kinase

Systematic name: ATP:1-phosphatidyl-1D-*myo*-inositol 4-phosphotransferase

Comments: This reaction is catalysed by at least two different isoforms.

References: [595, 1555, 3727, 3841, 213]

[EC 2.7.1.67 created 1972, modified 1982, modified 2002]

EC 2.7.1.68

Accepted name: 1-phosphatidylinositol-4-phosphate 5-kinase

Reaction: ATP + 1-phosphatidyl-1D-*myo*-inositol 4-phosphate = ADP + 1-phosphatidyl-1D-*myo*-inositol 4,5-bisphosphate

Other name(s): diphosphoinositide kinase; PIP kinase; phosphatidylinositol 4-phosphate kinase; phosphatidylinositol-4-phosphate 5-kinase; type I PIP kinase

Systematic name: ATP:1-phosphatidyl-1D-*myo*-inositol-4-phosphate 5-phosphotransferase

Comments: This enzyme can also phosphorylate PtdIns3*P* in the 4-position, and PtdIns, PtdIns3*P* and PtdIns(3,4)P_2 in the 5-position *in vitro*, but to a lesser extent. The last of these reactions occurs *in vivo* and is physiologically relevant. Three different isoforms are known.

References: [1553, 1554, 2805]

[EC 2.7.1.68 created 1972, modified 1980, modified 1982, modified 2002]

[2.7.1.69 Transferred entry. protein-N^{π}-phosphohistidine—sugar phosphotransferase, now covered by EC 2.7.1.191 protein-N^{π}-phosphohistidine—D-mannose phosphotransferase, EC 2.7.1.192 protein-N^{π}-phosphohistidine—N-acetylmuramate phosphotransferase, EC 2.7.1.193 protein-N^{π}-phosphohistidine—N-acetyl-D-glucosamine phosphotransferase, EC 2.7.1.194 protein-N^{π}-

phosphohistidine—L-ascorbate phosphotransferase, EC 2.7.1.195 protein-N^{π}-phosphohistidine—2-O-α-mannosyl-D-glycerate phosphotransferase, EC 2.7.1.196 protein-N^{π}-phosphohistidine—N,N′-diacetylchitobiose phosphotransferase, EC 2.7.1.197 protein-N^{π}-phosphohistidine—D-mannitol phosphotransferase, EC 2.7.1.198 protein-N^{π}-phosphohistidine—D-sorbitol phosphotransferase, EC 2.7.1.199 protein-N^{π}-phosphohistidine—D-glucose phosphotransferase, EC 2.7.1.200 protein-N^{π}-phosphohistidine—galactitol phosphotransferase, EC 2.7.1.201 protein-N^{π}-phosphohistidine—trehalose phosphotransferase, EC 2.7.1.202 protein-N^{π}-phosphohistidine—D-fructose phosphotransferase, EC 2.7.1.203 protein-N^{π}-phosphohistidine—D-glucosaminate phosphotransferase, EC 2.7.1.204 protein-N^{π}-phosphohistidine—D-galactose phosphotransferase, EC 2.7.1.205 protein-N^{π}-phosphohistidine—D-cellobiose phosphotransferase, EC 2.7.1.206 protein-N^{π}-phosphohistidine—L-sorbose phosphotransferase, EC 2.7.1.207 protein-N^{π}-phosphohistidine—lactose phosphotransferase and EC 2.7.1.208 protein-N^{π}-phosphohistidine—maltose phosphotransferase.]

[EC 2.7.1.69 created 1972, modified 2000, deleted 2016]

[2.7.1.70 Deleted entry. protamine kinase. Now included in EC 2.7.11.1, non-specific serine/threonine protein kinase]

[EC 2.7.1.70 created 1972, deleted 2004]

EC 2.7.1.71

Accepted name: shikimate kinase
Reaction: ATP + shikimate = ADP + 3-phosphoshikimate
Other name(s): shikimate kinase (phosphorylating); shikimate kinase II
Systematic name: ATP:shikimate 3-phosphotransferase
References: [2308]

[EC 2.7.1.71 created 1972]

EC 2.7.1.72

Accepted name: streptomycin 6-kinase
Reaction: ATP + streptomycin = ADP + streptomycin 6-phosphate
Other name(s): streptidine kinase; SM 6-kinase; streptomycin 6-kinase (phosphorylating); streptidine kinase (phosphorylating); streptomycin 6-*O*-phosphotransferase; streptomycin 6-phosphotransferase
Systematic name: ATP:streptomycin 6-phosphotransferase
Comments: dATP can replace ATP; and dihydrostreptomycin, streptidine and ¡BR¿ 2-deoxystreptidine can act as acceptors.
References: [3732, 3734]

[EC 2.7.1.72 created 1972, modified 1976]

EC 2.7.1.73

Accepted name: inosine kinase
Reaction: ATP + inosine = ADP + IMP
Other name(s): inosine-guanosine kinase; inosine kinase (phosphorylating)
Systematic name: ATP:inosine 5′-phosphotransferase
References: [2704]

[EC 2.7.1.73 created 1972]

EC 2.7.1.74

Accepted name: deoxycytidine kinase
Reaction: NTP + deoxycytidine = NDP + dCMP
Other name(s): deoxycytidine kinase (phosphorylating); 2′-deoxycytidine kinase; Ara-C kinase; arabinofuranosylcytosine kinase; deoxycytidine-cytidine kinase
Systematic name: NTP:deoxycytidine 5′-phosphotransferase
Comments: Cytosine arabinoside can act as acceptor; all natural nucleoside triphosphates (except dCTP) can act as donors.
References: [797, 1472, 1647, 2293]

[EC 2.7.1.74 created 1972]

[2.7.1.75 Deleted entry. thymidine kinase. Now EC 2.7.1.21 thymidine kinase]

[EC 2.7.1.75 created 1972, deleted 1976]

EC 2.7.1.76

Accepted name: 2′-deoxyadenosine kinase
Reaction: ATP + 2′-deoxyadenosine = ADP + dAMP
Other name(s): purine-deoxyribonucleoside kinase; deoxyadenosine kinase (phosphorylating) (ambiguous); purine-deoxyribonucleoside kinase (ambiguous); deoxyadenosine kinase (ambiguous); ATP:deoxyadenosine 5′-phosphotransferase (ambiguous)
Systematic name: ATP:2′-deoxyadenosine 5′-phosphotransferase
Comments: 2′-Deoxyguanosine can also act as acceptor. Possibly identical with EC 2.7.1.74 deoxycytidine kinase.
References: [502, 1797]

[EC 2.7.1.76 created 1972]

EC 2.7.1.77

Accepted name: nucleoside phosphotransferase
Reaction: a nucleotide + a 2′-deoxyribonucleoside = a nucleoside + a 2′-deoxyribonucleoside 5′-phosphate
Other name(s): nonspecific nucleoside phosphotransferase; nucleotide:3′-deoxynucleoside 5′-phosphotransferase
Systematic name: nucleotide:nucleoside 5′-phosphotransferase
Comments: Phenyl phosphate and nucleoside 3′-phosphates can act as donors, although not so well as nucleoside 5′-phosphates. Nucleosides as well as 2′-deoxyribonucleosides can act as acceptors.
References: [411, 2755]

[EC 2.7.1.77 created 1972]

EC 2.7.1.78

Accepted name: polynucleotide 5′-hydroxyl-kinase
Reaction: ATP + 5′-dephospho-DNA = ADP + 5′-phospho-DNA
Other name(s): ATP:5′-dephosphopolynucleotide 5′-phosphatase; PNK; polynucleotide 5′-hydroxyl kinase (phosphorylating); 5′-hydroxyl polynucleotide kinase; 5′-hydroxyl polyribonucleotide kinase; 5′-hydroxyl RNA kinase; DNA 5′-hydroxyl kinase; DNA kinase; polynucleotide kinase; polynucleotide 5′-hydroxy-kinase
Systematic name: ATP:5′-dephosphopolynucleotide 5′-phosphotransferase
Comments: Also acts on 5′-dephospho-RNA 3′-mononucleotides.
References: [2493, 2494]

[EC 2.7.1.78 created 1972]

EC 2.7.1.79

Accepted name: diphosphate—glycerol phosphotransferase
Reaction: diphosphate + glycerol = phosphate + glycerol 1-phosphate
Other name(s): PPi-glycerol phosphotransferase; pyrophosphate-glycerol phosphotransferase
Systematic name: diphosphate:glycerol 1-phosphotransferase
Comments: May be identical with EC 3.1.3.9 glucose-6-phosphatase.
References: [3339]

[EC 2.7.1.79 created 1972]

EC 2.7.1.80

Accepted name: diphosphate—serine phosphotransferase
Reaction: diphosphate + L-serine = phosphate + *O*-phospho-L-serine
Other name(s): pyrophosphate-serine phosphotransferase; pyrophosphate-L-serine phosphotransferase
Systematic name: diphosphate:L-serine *O*-phosphotransferase
References: [453]

[EC 2.7.1.80 created 1972]

EC 2.7.1.81

Accepted name: hydroxylysine kinase
Reaction: GTP + 5-hydroxy-L-lysine = GDP + 5-phosphooxy-L-lysine
Other name(s): hydroxylysine kinase (phosphorylating); guanosine triphosphate:5-hydroxy-L-lysine *O*-phosphotransferase
Systematic name: GTP:5-hydroxy-L-lysine *O*-phosphotransferase
Comments: Both the natural 5-hydroxy-L-lysine and its 5-epimer act as acceptors.
References: [1328]

[EC 2.7.1.81 created 1972]

EC 2.7.1.82

Accepted name: ethanolamine kinase
Reaction: ATP + ethanolamine = ADP + *O*-phosphoethanolamine
Other name(s): ethanolamine kinase (phosphorylating); ethanolamine phosphokinase
Systematic name: ATP:ethanolamine *O*-phosphotransferase
References: [882, 3388, 3806]

[EC 2.7.1.82 created 1976]

EC 2.7.1.83

Accepted name: pseudouridine kinase
Reaction: ATP + pseudouridine = ADP + pseudouridine 5′-phosphate
Other name(s): pseudouridine kinase (phosphorylating)
Systematic name: ATP:pseudouridine 5′-phosphotransferase
References: [3280]

[EC 2.7.1.83 created 1976]

EC 2.7.1.84

Accepted name: alkylglycerone kinase
Reaction: ATP + *O*-alkylglycerone = ADP + *O*-alkylglycerone phosphate
Other name(s): alkyldihydroxyacetone kinase (phosphorylating); alkyldihydroxyacetone kinase
Systematic name: ATP:*O*-alkylglycerone phosphotransferase
References: [495]

[EC 2.7.1.84 created 1976]

EC 2.7.1.85

Accepted name: β-glucoside kinase
Reaction: ATP + cellobiose = ADP + 6-phospho-β-D-glucosyl-(1→4)-D-glucose
Other name(s): β-D-glucoside kinase (phosphorylating)
Systematic name: ATP:cellobiose 6-phosphotransferase

Comments: Phosphorylates a number of β-D-glucosides; GTP, CTP, ITP and UTP can also act as donors.
References: [2606]

[EC 2.7.1.85 created 1976]

EC 2.7.1.86

Accepted name: NADH kinase
Reaction: ATP + NADH = ADP + NADPH
Other name(s): reduced nicotinamide adenine dinucleotide kinase (phosphorylating); DPNH kinase; reduced diphosphopyridine nucleotide kinase; $NADH_2$ kinase
Systematic name: ATP:NADH 2′-phosphotransferase
Comments: CTP, ITP, UTP and GTP can also act as phosphate donors (in decreasing order of activity). The enzyme is specific for NADH. Activated by acetate.
References: [1139]

[EC 2.7.1.86 created 1976 (EC 2.7.1.96 created 1978, incorporated 1978)]

EC 2.7.1.87

Accepted name: streptomycin 3″-kinase
Reaction: ATP + streptomycin = ADP + streptomycin 3″-phosphate
Other name(s): streptomycin 3″-kinase (phosphorylating); streptomycin 3″-phosphotransferase
Systematic name: ATP:streptomycin 3″-phosphotransferase
Comments: Also phosphorylates dihydrostreptomycin, 3′-deoxydihydrostreptomycin and their 6-phosphates.
References: [3732]

[EC 2.7.1.87 created 1976]

EC 2.7.1.88

Accepted name: dihydrostreptomycin-6-phosphate 3′α-kinase
Reaction: ATP + dihydrostreptomycin 6-phosphate = ADP + dihydrostreptomycin 3′α,6-bisphosphate
Other name(s): dihydrostreptomycin 6-phosphate kinase (phosphorylating); ATP:dihydrostreptomycin-6-P 3′α-phosphotransferase
Systematic name: ATP:dihydrostreptomycin-6-phosphate 3′α-phosphotransferase
Comments: 3′-Deoxydihydrostreptomycin 6-phosphate can also act as acceptor.
References: [3732]

[EC 2.7.1.88 created 1976]

EC 2.7.1.89

Accepted name: thiamine kinase
Reaction: ATP + thiamine = ADP + thiamine phosphate
Other name(s): thiamin kinase (phosphorylating); thiamin phosphokinase; ATP:thiamin phosphotransferase; thiamin kinase
Systematic name: ATP:thiamine phosphotransferase
References: [1475]

[EC 2.7.1.89 created 1976]

EC 2.7.1.90

Accepted name: diphosphate—fructose-6-phosphate 1-phosphotransferase
Reaction: diphosphate + D-fructose 6-phosphate = phosphate + D-fructose 1,6-bisphosphate

Other name(s): 6-phosphofructokinase (pyrophosphate); pyrophosphate-fructose 6-phosphate 1-phosphotransferase; inorganic pyrophosphate-dependent phosphofructokinase; inorganic pyrophosphate-phosphofructokinase; pyrophosphate-dependent phosphofructo-1-kinase; pyrophosphate-fructose 6-phosphate phosphotransferase

Systematic name: diphosphate:D-fructose-6-phosphate 1-phosphotransferase

Comments: The enzyme catalyses a similar reaction to EC 2.7.1.11, 6-phosphofructokinase, but utilizes diphosphate instead of ATP as the the phosphate donor. It has been described in higher plants, primitive eukaryotes, bacteria, and archaea.

References: [2853, 2855, 478, 1840, 3221]

[EC 2.7.1.90 created 1976]

EC 2.7.1.91

Accepted name: sphingosine kinase

Reaction: ATP + a sphingoid base = ADP + a sphingoid base 1-phosphate

Other name(s): SPHK1 (gene name); SPHK2 (gene name); dihydrosphingosine kinase; dihydrosphingosine kinase (phosphorylating); sphingosine kinase (phosphorylating); sphingoid base kinase; sphinganine kinase; ATP:sphinganine 1-phosphotransferase

Systematic name: ATP:sphingoid base 1-phosphotransferase

Comments: The enzyme is involved in the production of sphingolipid metabolites. It phosphorylates various sphingoid long-chain bases, such as sphingosine, D-*erythro*-dihydrosphingosine (sphinganine), phytosphingosine (4-hydroxysphinganine), 4-hydroxy-8-sphingenine, 4,8-sphingadienine and D-*threo*-dihydrosphingosine and L-*threo*-dihydrosphingosine. The exact substrate range depends on the species.

References: [3348, 3347, 2396, 1736, 1997, 3895]

[EC 2.7.1.91 created 1976, modified 1980, modified 2016]

EC 2.7.1.92

Accepted name: 5-dehydro-2-deoxygluconokinase

Reaction: ATP + 5-dehydro-2-deoxy-D-gluconate = ADP + 6-phospho-5-dehydro-2-deoxy-D-gluconate

Other name(s): 5-keto-2-deoxygluconokinase; 5-keto-2-deoxyglucono kinase (phosphorylating); DKH kinase

Systematic name: ATP:5-dehydro-2-deoxy-D-gluconate 6-phosphotransferase

References: [80]

[EC 2.7.1.92 created 1976]

EC 2.7.1.93

Accepted name: alkylglycerol kinase

Reaction: ATP + 1-*O*-alkyl-*sn*-glycerol = ADP + 1-*O*-alkyl-*sn*-glycerol 3-phosphate

Other name(s): 1-alkylglycerol kinase (phosphorylating); ATP-alkylglycerol phosphotransferase; alkylglycerol phosphotransferase; ATP: 1-alkyl-*sn*-glycerol phosphotransferase

Systematic name: ATP:1-*O*-alkyl-*sn*-glycerol 3-phosphotransferase

References: [2907]

[EC 2.7.1.93 created 1976]

EC 2.7.1.94

Accepted name: acylglycerol kinase

Reaction: ATP + acylglycerol = ADP + acyl-*sn*-glycerol 3-phosphate

Other name(s): monoacylglycerol kinase; monoacylglycerol kinase (phosphorylating); *sn*-2-monoacylglycerol kinase; MGK; monoglyceride kinase; monoglyceride phosphokinase

Systematic name: ATP:acylglycerol 3-phosphotransferase

Comments: Acts on both 1- and 2-acylglycerols.
References: [2701, 2702]

[EC 2.7.1.94 created 1976]

EC 2.7.1.95

Accepted name: kanamycin kinase
Reaction: ATP + kanamycin = ADP + kanamycin 3′-phosphate
Other name(s): neomycin-kanamycin phosphotransferase;
Systematic name: ATP:kanamycin 3′-*O*-phosphotransferase
Comments: Also acts on the antibiotics neomycin, paromomycin, neamine, paromamine, vistamycin and gentamicin A. An enzyme from *Pseudomonas aeruginosa* also acts on butirosin.
References: [747, 748]

[EC 2.7.1.95 created 1976]

[2.7.1.96 Deleted entry. NADH kinase. Now included with EC 2.7.1.86 NADH kinase]

[EC 2.7.1.96 created 1978, deleted 1978]

[2.7.1.97 Deleted entry. opsin kinase. Identical with EC 2.7.11.14, rhodopsin kinase]

[EC 2.7.1.97 created 1978, deleted 1992]

[2.7.1.98 Deleted entry. phosphoenolpyruvate—fructose phosphotransferase]

[EC 2.7.1.98 created 1978, deleted 1984]

[2.7.1.99 Transferred entry. [pyruvate dehydrogenase (lipoamide)] kinase. Now EC 2.7.11.2, [pyruvate dehydrogenase (acetyl-transferring)] kinase]

[EC 2.7.1.99 created 1978, deleted 2005]

EC 2.7.1.100

Accepted name: *S*-methyl-5-thioribose kinase
Reaction: ATP + *S*-methyl-5-thio-D-ribose = ADP + *S*-methyl-5-thio-α-D-ribose 1-phosphate
Other name(s): 5-methylthioribose kinase (phosphorylating); methylthioribose kinase; 5-methylthioribose kinase; ATP:S^5-methyl-5-thio-D-ribose 1-phosphotransferase
Systematic name: ATP:*S*-methyl-5-thio-D-ribose 1-phosphotransferase
Comments: CTP also acts, but more slowly.
References: [900, 1181]

[EC 2.7.1.100 created 1980]

EC 2.7.1.101

Accepted name: tagatose kinase
Reaction: ATP + D-tagatose = ADP + D-tagatose 6-phosphate
Other name(s): AtuFK
Systematic name: ATP:D-tagatose 6-phosphotransferase
Comments: The enzyme from *Agrobacterium fabrum* C58 is part of D-altritol and galactitol degradation pathways.
References: [3417, 3844]

[EC 2.7.1.101 created 1983]

EC 2.7.1.102

Accepted name: hamamelose kinase
Reaction: ATP + D-hamamelose = ADP + D-hamamelose 2′-phosphate
Other name(s): hamamelose kinase (phosphorylating); hamamelosekinase (ATP: hamamelose 2′-phosphotransferase); ATP/hamamelose 2′-phosphotransferase
Systematic name: ATP:D-hamamelose 2′-phosphotransferase
Comments: Also acts, more slowly, on D-hamamelitol.
References: [246]

[EC 2.7.1.102 created 1983]

EC 2.7.1.103

Accepted name: viomycin kinase
Reaction: ATP + viomycin = ADP + *O*-phosphoviomycin
Other name(s): viomycin phosphotransferase; capreomycin phosphotransferase
Systematic name: ATP:viomycin *O*-phosphotransferase
Comments: Acts also on capreomycins. A serine residue in the peptide antibiotics acts as phosphate-acceptor.
References: [3247]

[EC 2.7.1.103 created 1983]

[2.7.1.104 Transferred entry. diphosphate—protein phosphotransferase. Now EC 2.7.99.1, triphosphate—protein phosphotransferase]

[EC 2.7.1.104 created 1987, deleted 2005]

EC 2.7.1.105

Accepted name: 6-phosphofructo-2-kinase
Reaction: ATP + β-D-fructose 6-phosphate = ADP + β-D-fructose 2,6-bisphosphate
Other name(s): phosphofructokinase 2; 6-phosphofructose 2-kinase; 6-phosphofructo-2-kinase (phosphorylating); fructose 6-phosphate 2-kinase; ATP:D-fructose-6-phosphate 2-phosphotransferase
Systematic name: ATP:β-D-fructose-6-phosphate 2-phosphotransferase
Comments: Not identical with EC 2.7.1.11 6-phosphofructokinase. The enzyme co-purifies with EC 3.1.3.46 fructose-2,6-bisphosphate 2-phosphatase.
References: [3062]

[EC 2.7.1.105 created 1984]

EC 2.7.1.106

Accepted name: glucose-1,6-bisphosphate synthase
Reaction: 3-phospho-D-glyceroyl phosphate + α-D-glucose 1-phosphate = 3-phospho-D-glycerate + α-D-glucose 1,6-bisphosphate
Other name(s): glucose 1,6-diphosphate synthase; glucose-1,6-bisphosphate synthetase; 3-phospho-D-glyceroyl-phosphate:D-glucose-1-phosphate 6-phosphotransferase
Systematic name: 3-phospho-D-glyceroyl-phosphate:α-D-glucose-1-phosphate 6-phosphotransferase
Comments: D-Glucose 6-phosphate can act as acceptor, forming α-D-glucose 1,6-bisphosphate.
References: [2933]

[EC 2.7.1.106 created 1984]

EC 2.7.1.107

Accepted name: diacylglycerol kinase (ATP)
Reaction: ATP + 1,2-diacyl-*sn*-glycerol = ADP + 1,2-diacyl-*sn*-glycerol 3-phosphate

Other name(s): diglyceride kinase (ambiguous); 1,2-diacylglycerol kinase (phosphorylating) (ambiguous); 1,2-diacylglycerol kinase (ambiguous); *sn*-1,2-diacylglycerol kinase (ambiguous); DG kinase (ambiguous); DGK (ambiguous); ATP:diacylglycerol phosphotransferase; arachidonoyl-specific diacylglycerol kinase; diacylglycerol:ATP kinase; ATP:1,2-diacylglycerol 3-phosphotransferase; diacylglycerol kinase (ATP dependent)
Systematic name: ATP:1,2-diacyl-*sn*-glycerol 3-phosphotransferase
Comments: Involved in synthesis of membrane phospholipids and the neutral lipid triacylglycerol. Activity is stimulated by certain phospholipids [3742, 3875]. In plants and animals the product 1,2-diacyl-*sn*-glycerol 3-phosphate is an important second messenger. *cf.* EC 2.7.1.174, diacylglycerol kinase (CTP).
References: [1356, 3814, 660, 3742, 2975, 3743, 3875]

[EC 2.7.1.107 created 1984, modified 2013]

EC 2.7.1.108

Accepted name: dolichol kinase
Reaction: CTP + dolichol = CDP + dolichyl phosphate
Other name(s): dolichol phosphokinase
Systematic name: CTP:dolichol *O*-phosphotransferase
References: [437, 2888]

[EC 2.7.1.108 created 1984]

[2.7.1.109 Transferred entry. [hydroxymethylglutaryl-CoA reductase (NADPH)] kinase. Now EC 2.7.11.31, [hydroxymethylglutaryl-CoA reductase (NADPH)] kinase]

[EC 2.7.1.109 created 1984, deleted 2005]

[2.7.1.110 Transferred entry. dephospho-[reductase kinase] kinase. Now EC 2.7.11.3, dephospho-[reductase kinase] kinase]

[EC 2.7.1.110 created 1984, deleted 2005]

[2.7.1.111 Deleted entry. [acetyl-CoA carboxylase] kinase. Now listed as EC 2.7.11.27, [acetyl-CoA carboxylase] kinase]

[EC 2.7.1.111 created 1984, deleted 1992]

[2.7.1.112 Transferred entry. protein-tyrosine kinase. Now EC 2.7.10.2, non-specific protein-tyrosine kinase]

[EC 2.7.1.112 created 1984, deleted 2005]

EC 2.7.1.113

Accepted name: deoxyguanosine kinase
Reaction: ATP + deoxyguanosine = ADP + dGMP
Other name(s): deoxyguanosine kinase (phosphorylating); (dihydroxypropoxymethyl)guanine kinase; 2′-deoxyguanosine kinase; NTP-deoxyguanosine 5′-phosphotransferase
Systematic name: ATP:deoxyguanosine 5′-phosphotransferase
Comments: Deoxyinosine can also act as acceptor.
References: [194, 1120]

[EC 2.7.1.113 created 1984]

EC 2.7.1.114

Accepted name: AMP—thymidine kinase
Reaction: AMP + thymidine = adenosine + dTMP
Other name(s): adenylate-nucleoside phosphotransferase
Systematic name: AMP:thymidine 5′-phosphotransferase

Comments: The deoxypyrimidine kinase complex induced by *Herpes simplex* virus catalyses this reaction as well as those of EC 2.7.1.21 (thymidine kinase), EC 2.7.1.118 (ADP—thymidine kinase) and EC 2.7.4.9 (dTMP kinase).

References: [870, 871]

[EC 2.7.1.114 created 1984]

[2.7.1.115 Transferred entry. [3-methyl-2-oxobutanoate dehydrogenase (lipoamide)] kinase. Now EC 2.7.11.4, [3-methyl-2-oxobutanoate dehydrogenase (acetyl-transferring)] kinase]

[EC 2.7.1.115 created 1986, deleted 2005]

[2.7.1.116 Transferred entry. [isocitrate dehydrogenase (NADP$^+$)] kinase. Now EC 2.7.11.5, [isocitrate dehydrogenase (NADP$^+$)] kinase]

[EC 2.7.1.116 created 1986, deleted 2005]

[2.7.1.117 Transferred entry. myosin-light-chain kinase. Now EC 2.7.11.18, myosin-light-chain kinase]

[EC 2.7.1.117 created 1986, deleted 2005]

EC 2.7.1.118

Accepted name: ADP—thymidine kinase

Reaction: ADP + thymidine = AMP + dTMP

Other name(s): ADP:dThd phosphotransferase; adenosine diphosphate-thymidine phosphotransferase

Systematic name: ADP:thymidine 5′-phosphotransferase

Comments: The deoxypyrimidine kinase complex induced by *Herpes simplex* virus catalyses this reaction as well as those of EC 2.7.1.21 (thymidine kinase), EC 2.7.1.114 (AMP—thymidine kinase) and EC 2.7.4.9 (dTMP kinase).

References: [870]

[EC 2.7.1.118 created 1986]

EC 2.7.1.119

Accepted name: hygromycin-B 7″-*O*-kinase

Reaction: ATP + hygromycin B = ADP + 7″-*O*-phosphohygromycin B

Other name(s): hygromycin B phosphotransferase; hygromycin-B kinase (ambiguous)

Systematic name: ATP:hygromycin-B 7″-*O*-phosphotransferase

Comments: Phosphorylates the antibiotics hygromycin B, 1-*N*-hygromycin B and destomycin, but not hygromycin B2, at the 7″-hydroxy group in the destomic acid ring.

References: [4024]

[EC 2.7.1.119 created 1989, modified 2009, modified 2011]

[2.7.1.120 Transferred entry. caldesmon kinase. Now EC 2.7.11.17, Ca^{2+}/calmodulin-dependent protein kinase]

[EC 2.7.1.120 created 1989, modified 1990, deleted 2005]

EC 2.7.1.121

Accepted name: phospho*enol*pyruvate—glycerone phosphotransferase

Reaction: phospho*enol*pyruvate + glycerone = pyruvate + glycerone phosphate

Systematic name: phospho*enol*pyruvate:glycerone phosphotransferase

References: [1514]

[EC 2.7.1.121 created 1989]

EC 2.7.1.122

Accepted name: xylitol kinase
Reaction: ATP + xylitol = ADP + xylitol 5-phosphate
Systematic name: ATP:xylitol 5-phosphotransferase
References: [122]

[EC 2.7.1.122 created 1989]

[2.7.1.123 Transferred entry. Ca^{2+}/calmodulin-dependent protein kinase. Now EC 2.7.11.17, Ca^{2+}/calmodulin-dependent protein kinase]

[EC 2.7.1.123 created 1989, deleted 2005]

[2.7.1.124 Transferred entry. [tyrosine 3-monooxygenase] kinase. Now EC 2.7.11.6, [tyrosine 3-monooxygenase] kinase]

[EC 2.7.1.124 created 1989, deleted 2005]

[2.7.1.125 Transferred entry. rhodopsin kinase. Now EC 2.7.11.14, rhodopsin kinase]

[EC 2.7.1.125 created 1989 (EC 2.7.1.97 created 1978, incorporated 1992), deleted 2005]

[2.7.1.126 Transferred entry. [β-adrenergic-receptor] kinase. Now EC 2.7.11.15, β-adrenergic-receptor kinase]

[EC 2.7.1.126 created 1989, deleted 2005]

EC 2.7.1.127

Accepted name: inositol-trisphosphate 3-kinase
Reaction: ATP + 1D-*myo*-inositol 1,4,5-trisphosphate = ADP + 1D-*myo*-inositol 1,3,4,5-tetrakisphosphate
Other name(s): 1D-*myo*-inositol-trisphosphate 3-kinase; Ins(1,4,5)P_3 3-kinase
Systematic name: ATP:1D-*myo*-inositol-1,4,5-trisphosphate 3-phosphotransferase
Comments: Activated by Ca^{2+}. Three isoforms have been shown to exist [1451].
References: [1213, 1450, 1451]

[EC 2.7.1.127 created 1989, modified 2002]

[2.7.1.128 Transferred entry. [acetyl-CoA carboxylase] kinase. Now EC 2.7.11.27, [acetyl-CoA carboxylase] kinase]

[EC 2.7.1.128 created 1990 (EC 2.7.1.111 created 1984, incorporated 1992), deleted 2005]

[2.7.1.129 Transferred entry. [myosin-heavy-chain] kinase. Now EC 2.7.11.7, myosin-heavy-chain kinase]

[EC 2.7.1.129 created 1990, deleted 2005]

EC 2.7.1.130

Accepted name: tetraacyldisaccharide 4′-kinase
Reaction: ATP + 2-*N*,3-*O*-bis[(3*R*)-3-hydroxytetradecanoyl]-β-D-glucosaminyl-(1→6)-2-*N*,3-*O*-bis[(3*R*)-3-hydroxytetradecanoyl]-α-D-glucosaminyl phosphate = ADP + 2-*N*,3-*O*-bis[(3*R*)-3-hydroxytetradecanoyl]-4-*O*-phospho-β-D-glucosaminyl-(1→6)-2-*N*,3-*O*-bis[(3*R*)-3-hydroxytetradecanoyl]-α-D-glucosaminyl phosphate
Other name(s): lipid-A 4′-kinase
Systematic name: ATP:2,2′,3,3′-tetrakis[(3*R*)-3-hydroxytetradecanoyl]-β-D-glucosaminyl-(1→6)-α-D-glucosaminyl-phosphate 4′-*O*-phosphotransferase
Comments: Involved with EC 2.3.1.129 (acyl-[acyl-carrier- protein]—UDP-*N*-acetylglucosamine *O*-acyltransferase) and EC 2.4.1.182 (lipid-A-disaccharide synthase) in the biosynthesis of the phosphorylated glycolipid, lipid A, in the outer membrane of *Escherichia coli*.
References: [2831]

[EC 2.7.1.130 created 1990]

[2.7.1.131 Transferred entry. [low-density-lipoprotein] kinase. Now EC 2.7.11.29, low-density-lipoprotein receptor kinase]

[EC 2.7.1.131 created 1990, deleted 2005]

[2.7.1.132 Transferred entry. tropomyosin kinase. Now EC 2.7.11.28, tropomyosin kinase]

[EC 2.7.1.132 created 1990, deleted 2005]

[2.7.1.133 Deleted entry. inositol-trisphosphate 6-kinase. Now included with EC 2.7.1.134, inositol-tetrakisphosphate 1-kinase]

[EC 2.7.1.133 created 1990, deleted 2002]

EC 2.7.1.134

Accepted name: inositol-tetrakisphosphate 1-kinase

Reaction: ATP + 1D-*myo*-inositol 3,4,5,6-tetrakisphosphate = ADP + 1D-*myo*-inositol 1,3,4,5,6-pentakisphosphate

Other name(s): 1D-*myo*-inositol-tetrakisphosphate 1-kinase; inositol-trisphosphate 6-kinase; 1D-*myo*-inositol-trisphosphate 6-kinase; ATP:1D-*myo*-inositol-1,3,4-trisphosphate 6-phosphotransferase; inositol-trisphosphate 5-kinase; 1D-*myo*-inositol-trisphosphate 5-kinase; ATP:1D-*myo*-inositol-1,3,4-trisphosphate 5-phosphotransferase

Systematic name: ATP:1D-*myo*-inositol-3,4,5,6-tetrakisphosphate 1-phosphotransferase

Comments: This enzyme also phosphorylates Ins(1,3,4)P_3 on O-5 and O-6. The phosphotransfer from ATP to either inositol 1,3,4-trisphosphate or inositol 3,4,5,6-tetrakisphosphate appears to be freely reversible to the extent that the enzyme can act like an inositol polyphosphate phosphatase in the presence of ADP. It can also catalyse an isomerization between Ins(1,3,4,5)P_4 and Ins(1,3,4,6)P_4 in the presence of ADP.

References: [3331, 173, 3168, 3166, 3965, 1344]

[EC 2.7.1.134 created 1990, (EC 2.7.1.133 created 1989, incorporated 2002; EC 2.7.1.139 created 1992, incorporated 2002), modified 2002]

[2.7.1.135 Transferred entry. [tau-protein] kinase. Now EC 2.7.11.26, tau-protein kinase]

[EC 2.7.1.135 created 1990, deleted 2005]

EC 2.7.1.136

Accepted name: macrolide 2′-kinase

Reaction: ATP + oleandomycin = ADP + oleandomycin 2′-*O*-phosphate

Systematic name: ATP:macrolide 2′-*O*-phosphotransferase

Comments: Erythromycin, spiramycin and some other macrolide antibiotics can also act as acceptors.

References: [2531]

[EC 2.7.1.136 created 1992]

EC 2.7.1.137

Accepted name: phosphatidylinositol 3-kinase

Reaction: ATP + 1-phosphatidyl-1D-*myo*-inositol = ADP + 1-phosphatidyl-1D-*myo*-inositol 3-phosphate

Other name(s): 1-phosphatidylinositol 3-kinase; type III phosphoinositide 3-kinase; Vps34p; type I phosphatidylinositol kinase

Systematic name: ATP:1-phosphatidyl-1D-*myo*-inositol 3-phosphotransferase

Comments: One mammalian isoform is known.

References: [3841, 3649]

[EC 2.7.1.137 created 1992, modified 2002]

EC 2.7.1.138

Accepted name: ceramide kinase
Reaction: ATP + ceramide = ADP + ceramide 1-phosphate
Other name(s): acylsphingosine kinase
Systematic name: ATP:ceramide 1-phosphotransferase
References: [171]

[EC 2.7.1.138 created 1992]

[2.7.1.139 Deleted entry. inositol-trisphosphate 5-kinase. Now included with EC 2.7.1.134, inositol-tetrakisphosphate 1-kinase]

[EC 2.7.1.139 created 1992, deleted 2002]

EC 2.7.1.140

Accepted name: inositol-tetrakisphosphate 5-kinase
Reaction: ATP + 1D-*myo*-inositol 1,3,4,6-tetrakisphosphate = ADP + 1D-*myo*-inositol 1,3,4,5,6-pentakisphosphate
Other name(s): 1D-*myo*-inositol-tetrakisphosphate 5-kinase
Systematic name: ATP:1D-*myo*-inositol-1,3,4,6-tetrakisphosphate 5-phosphotransferase
Comments: The enzyme from plants and yeast can also use Ins(1,2,3,4,6)P_5 as a substrate [3340].
References: [3166, 3340]

[EC 2.7.1.140 created 1992]

[2.7.1.141 Transferred entry. [RNA-polymerase]-subunit kinase. Now EC 2.7.11.23, [RNA-polymerase]-subunit kinase]

[EC 2.7.1.141 created 1992, deleted 2005]

EC 2.7.1.142

Accepted name: glycerol-3-phosphate—glucose phosphotransferase
Reaction: *sn*-glycerol 3-phosphate + D-glucose = glycerol + D-glucose 6-phosphate
Systematic name: *sn*-glycerol-3-phosphate:D-glucose 6-phosphotransferase
Comments: Involved in the anaerobic metabolism of sugars in the bloodstream of trypanosomes.
References: [1666]

[EC 2.7.1.142 created 1992]

EC 2.7.1.143

Accepted name: diphosphate-purine nucleoside kinase
Reaction: diphosphate + a purine nucleoside = phosphate + a purine mononucleotide
Other name(s): pyrophosphate-purine nucleoside kinase
Systematic name: diphosphate:purine nucleoside phosphotransferase
Comments: The enzyme from the Acholeplasma class of *Mollicutes* catalyses the conversion of adenosine, guanosine and inosine to AMP, GMP and IMP. ATP cannot substitute for diphosphate as a substrate.
References: [3572, 3573]

[EC 2.7.1.143 created 1999]

EC 2.7.1.144

Accepted name: tagatose-6-phosphate kinase
Reaction: ATP + D-tagatose 6-phosphate = ADP + D-tagatose 1,6-bisphosphate
Systematic name: ATP:D-tagatose-6-phosphate 1-phosphotransferase
References: [2476]

[EC 2.7.1.144 created 1999]

EC 2.7.1.145

Accepted name: deoxynucleoside kinase

Reaction: ATP + a 2′-deoxyribonucleoside = ADP + a 2′-deoxyribonucleoside 5′-phosphate

Other name(s): multispecific deoxynucleoside kinase; ms-dNK; multisubstrate deoxyribonucleoside kinase; multifunctional deoxynucleoside kinase; D. melanogaster deoxynucleoside kinase; Dm-dNK; ATP:deoxynucleoside 5′-phosphotransferase

Systematic name: ATP:deoxyribonucleoside 5′-phosphotransferase

Comments: The enzyme from embryonic cells of the fruit fly *Drosophila melanogaster* differs from other 2′-deoxyribonucleoside kinases [EC 2.7.1.76 (deoxyadenosine kinase) and EC 2.7.1.113 (deoxyguanosine kinase)] in its broad specificity for all four common 2′-deoxyribonucleosides.

References: [2360, 2359]

[EC 2.7.1.145 created 2001]

EC 2.7.1.146

Accepted name: ADP-specific phosphofructokinase

Reaction: ADP + D-fructose 6-phosphate = AMP + D-fructose 1,6-bisphosphate

Other name(s): ADP-6-phosphofructokinase, ADP-dependent phosphofructokinase

Systematic name: ADP:D-fructose-6-phosphate 1-phosphotransferase

Comments: ADP can be replaced by GDP, ATP and GTP, to a limited extent. Divalent cations are necessary for activity, with Mg^{2+} followed by Co^{2+} being the most effective.

References: [3590]

[EC 2.7.1.146 created 2001]

EC 2.7.1.147

Accepted name: ADP-specific glucokinase

Reaction: ADP + D-glucose = AMP + D-glucose 6-phosphate

Other name(s): ADP-dependent glucokinase

Systematic name: ADP:D-glucose 6-phosphotransferase

Comments: Requires Mg^{2+}. The enzyme from *Pyrococcus furiosus* is highly specific for D-glucose; there is some activity with 2-deoxy-D-glucose, but no activity with D-fructose, D-mannose or D-galactose as the substrate. No activity is detected when ADP is replaced by ATP, GDP, phospho*enol*pyruvate, diphosphate or polyphosphate.

References: [1638]

[EC 2.7.1.147 created 2001]

EC 2.7.1.148

Accepted name: 4-(cytidine 5′-diphospho)-2-*C*-methyl-D-erythritol kinase

Reaction: ATP + 4-(cytidine 5′-diphospho)-2-*C*-methyl-D-erythritol = ADP + 2-phospho-4-(cytidine 5′-diphospho)-2-*C*-methyl-D-erythritol

Other name(s): CDP-ME kinase

Systematic name: ATP:4-(cytidine 5′-diphospho)-2-*C*-methyl-D-erythritol 2-phosphotransferase

Comments: The enzyme from *Escherichia coli* requires Mg^{2+} or Mn^{2+}. Forms part of an alternative nonmevalonate pathway for terpenoid biosynthesis (for diagram, click here).

References: [2075, 1834]

[EC 2.7.1.148 created 2001]

EC 2.7.1.149

Accepted name: 1-phosphatidylinositol-5-phosphate 4-kinase
Reaction: ATP + 1-phosphatidyl-1D-*myo*-inositol 5-phosphate = ADP + 1-phosphatidyl-1D-*myo*-inositol 4,5-bisphosphate
Other name(s): type II PIP kinase
Systematic name: ATP:1-phosphatidyl-1D-*myo*-inositol-5-phosphate 4-phosphotransferase
References: [2805]

[EC 2.7.1.149 created 2002]

EC 2.7.1.150

Accepted name: 1-phosphatidylinositol-3-phosphate 5-kinase
Reaction: ATP + 1-phosphatidyl-1D-*myo*-inositol 3-phosphate = ADP + 1-phosphatidyl-1D-*myo*-inositol 3,5-bisphosphate
Other name(s): type III PIP kinase; phosphatidylinositol 3-phosphate 5-kinase
Systematic name: ATP:1-phosphatidyl-1D-*myo*-inositol-3-phosphate 5-phosphotransferase
References: [605]

[EC 2.7.1.150 created 2002]

EC 2.7.1.151

Accepted name: inositol-polyphosphate multikinase
Reaction: **2** ATP + 1D-*myo*-inositol 1,4,5-trisphosphate = **2** ADP + 1D-*myo*-inositol 1,3,4,5,6-pentakisphosphate (overall reaction)
(1a) ATP + 1D-*myo*-inositol 1,4,5-trisphosphate = ADP + 1D-*myo*-inositol 1,4,5,6-tetrakisphosphate
(1b) ATP + 1D-*myo*-inositol 1,4,5,6-tetrakisphosphate = ADP + 1D-*myo*-inositol 1,3,4,5,6-pentakisphosphate
Other name(s): IpK2; IP$_3$/IP4 6-/3-kinase; IP$_3$/IP4 dual-specificity 6-/3-kinase; IpmK; ArgRIII; AtIpk2α; AtIpk2β; inositol polyphosphate 6-/3-/5-kinase
Systematic name: ATP:1D-*myo*-inositol-1,4,5-trisphosphate 6-phosphotransferase
Comments: This enzyme also phosphorylates Ins(1,4,5)P_3 to Ins(1,3,4,5)P_4, Ins(1,3,4,5)P_4 to Ins(1,3,4,5,6)P_5, and Ins(1,3,4,5,6)P_4 to Ins(PP)P_4, isomer unknown. The enzyme from the plant *Arabidopsis thaliana* can also phosphorylate Ins(1,3,4,6)P_4 and Ins(1,2,3,4,6)P_5 at the D-5-position to produce 1,3,4,5,6-pentakisphosphate and inositol hexakisphosphate (InsP_6), respectively [3340]. Yeast produce InsP_6 from Ins(1,4,5)P_3 by the actions of this enzyme and EC 2.7.1.158, inositol-pentakisphosphate 2-kinase [3666].
References: [2996, 2509, 3340, 3666]

[EC 2.7.1.151 created 2002, modified 2006]

[2.7.1.152 Transferred entry. inositol-hexakisphosphate kinase. Now EC 2.7.4.21, inositol-hexakisphosphate kinase]

[EC 2.7.1.152 created 2002, deleted 2003]

EC 2.7.1.153

Accepted name: phosphatidylinositol-4,5-bisphosphate 3-kinase
Reaction: ATP + 1-phosphatidyl-1D-*myo*-inositol 4,5-bisphosphate = ADP + 1-phosphatidyl-1D-*myo*-inositol 3,4,5-trisphosphate
Other name(s): type I phosphoinositide 3-kinase
Systematic name: ATP:1-phosphatidyl-1D-*myo*-inositol-4,5-bisphosphate 3-phosphotransferase
Comments: This enzyme also catalyses the phosphorylation of PtdIns4P to PtdIns(3,4)P_2, and of PtdIns to PtdIns3P. Four mammalian isoforms are known to exist.
References: [3649]

[EC 2.7.1.153 created 2002]

EC 2.7.1.154

Accepted name: phosphatidylinositol-4-phosphate 3-kinase

Reaction: ATP + 1-phosphatidyl-1D-*myo*-inositol 4-phosphate = ADP + 1-phosphatidyl-1D-*myo*-inositol 3,4-bisphosphate

Other name(s): type II phosphoinositide 3-kinase; C^2-domain-containing phosphoinositide 3-kinase; phosphoinositide 3-kinase

Systematic name: ATP:1-phosphatidyl-1D-*myo*-inositol-4-phosphate 3-phosphotransferase

Comments: This enzyme also phosphorylates PtdIns to PtdIns3*P*. Three mammalian isoforms have been found to date.

References: [3649]

[EC 2.7.1.154 created 2002]

[2.7.1.155 Transferred entry. diphosphoinositol-pentakisphosphate kinase. Now EC 2.7.4.24, diphosphoinositol-pentakisphosphate kinase. The enzyme had been incorrectly classified as the reaction involves transfer of a phospho group to another phospho group (EC 2.7.4) rather than to an hydroxy group (EC 2.7.1)]

[EC 2.7.1.155 created 2003, deleted 2007]

EC 2.7.1.156

Accepted name: adenosylcobinamide kinase

Reaction: RTP + adenosylcobinamide = adenosylcobinamide phosphate + RDP [where RTP is either ATP or GTP (for symbol definitions, click here)]

Other name(s): CobU; adenosylcobinamide kinase/adenosylcobinamide-phosphate guanylyltransferase; AdoCbi kinase/AdoCbi-phosphate guanylyltransferase

Systematic name: RTP:adenosylcobinamide phosphotransferase

Comments: In *Salmonella typhimurium* LT2, under anaerobic conditions, CobU (EC 2.7.7.62 and EC 2.7.1.156), CobT (EC 2.4.2.21), CobC (EC 3.1.3.73) and CobS (EC 2.7.8.26) catalyse reactions in the nucleotide loop assembly pathway, which convert adenosylcobinamide (AdoCbi) into adenosylcobalamin (AdoCbl). CobT and CobC are involved in 5,6-dimethylbenzimidazole activation whereby 5,6-dimethylbenzimidazole is converted to its riboside, α-ribazole. The second branch of the nucleotide loop assembly pathway is the cobinamide (Cbi) activation branch where AdoCbi or adenosylcobinamide-phosphate is converted to the activated intermediate AdoCbi-GDP by Cob U. The final step in adenosylcobalamin biosynthesis is the condensation of AdoCbi-GDP with α-ribazole, which is catalysed by EC 2.7.8.26, adenosylcobinamide-GDP ribazoletransferase (CobS), to yield adenosylcobalamin. CobU is a bifunctional enzyme that has both kinase (EC 2.7.1.156) and guanylyltransferase (EC 2.7.7.62, adenosylcobinamide-phosphate guanylyltransferase) activities. However, both activities are not required at all times. The kinase activity has been proposed to function only when S. typhimurium is assimilating cobinamide whereas the guanylyltransferase activity is required for both assimilation of exogenous cobinamide and for *de novo* synthesis of adenosylcobalamin [3520].

References: [2584, 3528, 3529, 3520, 3778]

[EC 2.7.1.156 created 2004]

EC 2.7.1.157

Accepted name: *N*-acetylgalactosamine kinase

Reaction: ATP + *N*-acetyl-α-D-galactosamine = ADP + *N*-acetyl-α-D-galactosamine 1-phosphate

Other name(s): GALK2; GK2; GalNAc kinase; *N*-acetylgalactosamine (GalNAc)-1-phosphate kinase; ATP:*N*-acetyl-D-galactosamine 1-phosphotransferase

Systematic name: ATP:*N*-acetyl-α-D-galactosamine 1-phosphotransferase

Comments: The enzyme is highly specific for GalNAc as substrate, but has slight activity with D-galactose [2634]. Requires Mg^{2+}, Mn^{2+} or Co^{2+} for activity, with Mg^{2+} resulting in by far the greatest stimulation of enzyme activity.

References: [2633, 2634, 3517]

[EC 2.7.1.157 created 2005]

EC 2.7.1.158

Accepted name: inositol-pentakisphosphate 2-kinase

Reaction: ATP + 1D-*myo*-inositol 1,3,4,5,6-pentakisphosphate = ADP + 1D-*myo*-inositol hexakisphosphate

Other name(s): IP5 2-kinase; Gsl1p; Ipk1p; inositol polyphosphate kinase; inositol 1,3,4,5,6-pentakisphosphate 2-kinase; Ins(1,3,4,5,6)P_5 2-kinase

Systematic name: ATP:1D-*myo*-inositol 1,3,4,5,6-pentakisphosphate 2-phosphotransferase

Comments: The enzyme can also use Ins(1,4,5,6)P_4 [2691] and Ins(1,4,5)P_3 [2692] as substrate. Inositol hexakisphosphate (phytate) accumulates in storage protein bodies during seed development and, when hydrolysed, releases stored nutrients to the developing seedling before the plant is capable of absorbing nutrients from its environment [2250].

References: [3997, 2691, 2692, 2566, 2250, 3340]

[EC 2.7.1.158 created 2006]

EC 2.7.1.159

Accepted name: inositol-1,3,4-trisphosphate 5/6-kinase

Reaction: (1) ATP + 1D-*myo*-inositol 1,3,4-trisphosphate = ADP + 1D-*myo*-inositol 1,3,4,5-tetrakisphosphate
(2) ATP + 1D-*myo*-inositol 1,3,4-trisphosphate = ADP + 1D-*myo*-inositol 1,3,4,6-tetrakisphosphate

Other name(s): Ins(1,3,4)P_3 5/6-kinase; inositol trisphosphate 5/6-kinase

Systematic name: ATP:1D-*myo*-inositol 1,3,4-trisphosphate 5-phosphotransferase

Comments: In humans, this enzyme, along with EC 2.7.1.127 (inositol-trisphosphate 3-kinase), EC 2.7.1.140 (inositol-tetrakisphosphate 5-kinase) and EC 2.7.1.158 (inositol pentakisphosphate 2-kinase) is involved in the production of inositol hexakisphosphate (InsP_6). InsP_6 is involved in many cellular processes, including mRNA export from the nucleus [3666]. Yeasts do not have this enzyme, so produce InsP_6 from Ins(1,4,5)P_3 by the actions of EC 2.7.1.151 (inositol-polyphosphate multikinase) and EC 2.7.1.158 (inositol-pentakisphosphate 2-kinase) [3666].

References: [3871, 3666, 2252]

[EC 2.7.1.159 created 2006]

EC 2.7.1.160

Accepted name: 2′-phosphotransferase

Reaction: 2′-phospho-[ligated tRNA] + NAD$^+$ = mature tRNA + ADP-ribose 1″,2″-phosphate + nicotinamide

Other name(s): yeast 2′-phosphotransferase; Tpt1; Tpt1p; 2′-phospho-tRNA:NAD$^+$ phosphotransferase

Systematic name: 2′-phospho-[ligated tRNA]:NAD$^+$ phosphotransferase

Comments: Catalyses the final step of tRNA splicing in the yeast *Saccharomyces cerevisiae* [3300]. The reaction takes place in two steps: in the first step, the 2′-phosphate on the RNA substrate is ADP-ribosylated, causing the relase of nicotinamide and the formation of the reaction intermediate, ADP-ribosylated tRNA [3324]. In the second step, dephosphorylated (mature) tRNA is formed along with ADP ribose 1″-2″-cyclic phosphate. Highly specific for oligonucleotide substrates bearing an internal 2′-phosphate. Oligonucleotides with only a terminal 5′- or 3′-phosphate are not substrates [3325].

References: [3325, 3300, 640, 2191, 1389, 3324, 3048, 1602]

[EC 2.7.1.160 created 2006]

EC 2.7.1.161

Accepted name: CTP-dependent riboflavin kinase

Reaction: CTP + riboflavin = CDP + FMN

Other name(s): *Methanocaldococcus jannaschii* Mj0056; Mj0056

Systematic name: CTP:riboflavin 5′-phosphotransferase

Comments: This archaeal enzyme differs from EC 2.7.1.26, riboflavin kinase, in using CTP as the donor nucleotide. UTP, but not ATP or GTP, can also act as a phosphate donor but it is at least an order of magnitude less efficient than CTP.

References: [71]

[EC 2.7.1.161 created 2008]

EC 2.7.1.162

Accepted name: *N*-acetylhexosamine 1-kinase

Reaction: ATP + *N*-acetyl-D-hexosamine = ADP + *N*-acetyl-α-D-hexosamine 1-phosphate

Other name(s): NahK; LnpB; *N*-acetylgalactosamine/*N*-acetylglucosamine 1-kinase

Systematic name: ATP:*N*-acetyl-D-hexosamine 1-phosphotransferase

Comments: This enzyme is involved in the lacto-*N*-biose I/galacto-*N*-biose degradation pathway in the probiotic bacterium *Bifidobacterium longum*. Differs from EC 2.7.1.157, *N*-acetylgalactosamine kinase, as it can phosphorylate both *N*-acetylgalactosamine and *N*-acetylglucosamine at similar rates. Also has some activity with *N*-acetyl-D-mannosamine, D-talose and D-mannose as substrate. ATP can be replaced by GTP or ITP but with decreased enzyme activity. Requires a divalent cation, with Mg^{2+} resulting in by far the greatest stimulation of enzyme activity.

References: [2466]

[EC 2.7.1.162 created 2008]

EC 2.7.1.163

Accepted name: hygromycin B 4-*O*-kinase

Reaction: ATP + hygromycin B = ADP + 4-*O*-phosphohygromycin B

Other name(s): hygromycin-B kinase (ambiguous)

Systematic name: ATP:hygromycin-B 4-*O*-phosphotransferase

Comments: Phosphorylates the antibiotic hygromycin B. Whereas the enzyme from *Streptomyces hygroscopicus* (EC 2.7.1.119; hygromycin-B $7''$-*O*-kinase) catalyses the formation of $7''$-*O*-phosphohygromycin B, this enzyme, found in *Escherichia coli* carrying a plasmid conferring resistance to hygromycin-B, forms 4-*O*-phosphohygromycin B.

References: [2817]

[EC 2.7.1.163 created 2009]

EC 2.7.1.164

Accepted name: *O*-phosphoseryl-tRNA^{Sec} kinase

Reaction: ATP + L-seryl-tRNA^{Sec} = ADP + *O*-phospho-L-seryl-tRNA^{Sec}

Other name(s): PSTK; phosphoseryl-tRNA[Ser]Sec kinase; phosphoseryl-tRNA^{Sec} kinase

Systematic name: ATP:L-seryl-tRNA^{Sec} *O*-phosphotransferase

Comments: In archaea and eukarya selenocysteine formation is achieved by a two-step process: *O*-phosphoseryl-tRNA^{Sec} kinase (PSTK) phosphorylates the endogenous L-seryl-tRNA^{Sec} to *O*-phospho-L-seryl-tRNA^{Sec}, and then this misacylated amino acid-tRNA species is converted to L-selenocysteinyl-tRNA^{Sec} by EC 2.9.1.2 (Sep-tRNA:Sec-tRNA synthase).

References: [479, 3175, 1659]

[EC 2.7.1.164 created 2009]

EC 2.7.1.165

Accepted name: glycerate 2-kinase

Reaction: ATP + D-glycerate = ADP + 2-phospho-D-glycerate

Other name(s): D-glycerate-2-kinase; glycerate kinase (2-phosphoglycerate forming); ATP:(*R*)-glycerate 2-phosphotransferase

Systematic name: ATP:D-glycerate 2-phosphotransferase

Comments: A key enzyme in the nonphosphorylative Entner-Doudoroff pathway in archaea [1992, 2858]. In the bacterium *Hyphomicrobium methylovorum* GM2 the enzyme is involved in formaldehyde assimilation I (serine pathway) [4000]. In *Escherichia coli* the enzyme is involved in D-glucarate/D-galactarate degradation [1398]. The enzyme requires a divalent metal ion [1992].

References: [1992, 2858, 1989, 2485, 4000, 1398]

[EC 2.7.1.165 created 2010]

EC 2.7.1.166

Accepted name: 3-deoxy-D-*manno*-octulosonic acid kinase

Reaction: α-Kdo-(2→6)-lipid IV$_A$ + ATP = 4-*O*-phospho-α-Kdo-(2→6)-lipid IV$_A$ + ADP

Other name(s): *kdkA* (gene name); Kdo kinase

Systematic name: ATP:(Kdo)-lipid IV$_A$ 3-deoxy-α-D-*manno*-oct-2-ulopyranose 4-phosphotransferase

Comments: The enzyme phosphorylates the 4-OH position of Kdo in (Kdo)-lipid IV$_A$.

References: [373, 1229, 3833, 3834]

[EC 2.7.1.166 created 2010, modified 2011]

EC 2.7.1.167

Accepted name: D-*glycero*-β-D-*manno*-heptose-7-phosphate kinase

Reaction: D-*glycero*-β-D-*manno*-heptose 7-phosphate + ATP = D-*glycero*-β-D-*manno*-heptose 1,7-bisphosphate + ADP

Other name(s): heptose 7-phosphate kinase; D-β-D-heptose 7-phosphotransferase; D-β-D-heptose-7-phosphate kinase; HldE1 heptokinase; *glycero-manno*-heptose 7-phosphate kinase; D-β-D-heptose 7-phosphate kinase/D-β-D-heptose 1-phosphate adenylyltransferase; *hldE* (gene name); *rfaE* (gene name)

Systematic name: ATP:D-*glycero*-β-D-*manno*-heptose 7-phosphate 1-phosphotransferase

Comments: The bifunctional protein *hldE* includes D-*glycero*-β-D-*manno*-heptose-7-phosphate kinase and D-*glycero*-β-D-*manno*-heptose 1-phosphate adenylyltransferase activity (*cf.* EC 2.7.7.70). The enzyme is involved in biosynthesis of ADP-L-*glycero*-β-D-*manno*-heptose, which is utilized for assembly of the lipopolysaccharide inner core in Gram-negative bacteria. The enzyme selectively produces D-*glycero*-β-D-*manno*-heptose 1,7-bisphosphate [3753].

References: [2183, 1716, 3631, 1515, 3753]

[EC 2.7.1.167 created 2010]

EC 2.7.1.168

Accepted name: D-*glycero*-α-D-*manno*-heptose-7-phosphate kinase

Reaction: D-*glycero*-α-D-*manno*-heptose 7-phosphate + ATP = D-*glycero*-α-D-*manno*-heptose 1,7-bisphosphate + ADP

Other name(s): D-α-D-heptose-7-phosphate kinase; hdda (gene name)

Systematic name: ATP:D-*glycero*-α-D-*manno*-heptose 7-phosphate 1-phosphotransferase

Comments: The enzyme is involved in biosynthesis of GDP-D-*glycero*-α-D-*manno*-heptose, which is required for assembly of S-layer glycoprotein in Gram-positive bacteria. The enzyme is specific for the α-anomer.

References: [1715, 3631]

[EC 2.7.1.168 created 2010]

EC 2.7.1.169

Accepted name: pantoate kinase

Reaction: ATP + (*R*)-pantoate = ADP + (*R*)-4-phosphopantoate

Other name(s): PoK; TK2141 protein

Systematic name: ATP:(*R*)-pantoate 4-phosphotransferase

Comments: The conversion of (*R*)-pantoate to (*R*)-4′-phosphopantothenate is part of the pathway leading to biosynthesis of 4′-phosphopantetheine, an essential cofactor of coenzyme A and acyl-carrier protein. In bacteria and eukaryotes this conversion is performed by condensation with β-alanine, followed by phosphorylation (EC 6.3.2.1 and EC 2.7.1.33, respectively). In archaea the order of these two steps is reversed, and phosphorylation precedes condensation with β-alanine.

References: [3987]

[EC 2.7.1.169 created 2011]

EC 2.7.1.170

Accepted name: anhydro-*N*-acetylmuramic acid kinase

Reaction: ATP + 1,6-anhydro-*N*-acetyl-β-muramate + H_2O = ADP + *N*-acetylmuramate 6-phosphate

Other name(s): anhMurNAc kinase; AnmK

Systematic name: ATP:1,6-anhydro-*N*-acetyl-β-muramate 6-phosphotransferase

Comments: This enzyme, along with EC 4.2.1.126, *N*-acetylmuramic acid 6-phosphate etherase, is required for the utilization of anhydro-*N*-acetylmuramic acid in proteobacteria. The substrate is either imported from the medium or derived from the bacterium's own cell wall murein during cell wall recycling. The product *N*-acetylmuramate 6-phosphate is produced as a 7:1 mixture of the α- and β-anomers.

References: [3602, 3601, 151]

[EC 2.7.1.170 created 2011, modified 2011]

EC 2.7.1.171

Accepted name: protein-fructosamine 3-kinase

Reaction: ATP + [protein]-N^6-D-fructosyl-L-lysine = ADP + [protein]-N^6-(3-*O*-phospho-D-fructosyl)-L-lysine

Other name(s): FN3K; fructosamine 3-kinase

Systematic name: ATP:[protein]-N^6-D-fructosyl-L-lysine 3-phosphotransferase

Comments: Non-enzymic glycation is an important factor in the pathogenesis of diabetic complications. Key early intermediates in this process are fructosamines, such as [protein]-N^6-D-fructosyl-L-lysine. Fructosamine-3-kinase is part of an ATP-dependent system for removing carbohydrates from non-enzymically glycated proteins. The phosphorylation destablilizes the [protein]-N^6-D-fructosyl-L-lysine adduct and leads to its spontaneous decomposition. *cf.* EC 2.7.1.172, protein-ribulosamine 3-kinase.

References: [3418, 705]

[EC 2.7.1.171 created 2011]

EC 2.7.1.172

Accepted name: protein-ribulosamine 3-kinase

Reaction: ATP + [protein]-N^6-D-ribulosyl-L-lysine = ADP + [protein]-N^6-(3-*O*-phospho-D-ribulosyl)-L-lysine

Other name(s): Fn3KRP; FN3K-related protein; FN3K-RP; ketosamine 3-kinase 2; fructosamine-3-kinase-related protein; ribulosamine/erythrulosamine 3-kinase; ribulosamine 3-kinase

Systematic name: ATP:[protein]-N^6-D-ribulosyl-L-lysine 3-phosphotransferase

Comments: This enzyme plays a role in freeing proteins from ribulosamines or psicosamines, which might arise from the reaction of amines with glucose and/or glycolytic intermediates. This role is shared by EC 2.7.1.171 (protein-fructosamine 3-kinase), which has, in addition, the unique capacity to phosphorylate fructosamines [593]. The plant enzyme also phosphorylates [protein]-N^6-D-erythrulosyl-L-lysine [935]. No activity with [protein]-N^6-D-fructosyl-L-lysine [593, 935].

References: [593, 935, 2647]

[EC 2.7.1.172 created 2011]

EC 2.7.1.173

Accepted name: nicotinate riboside kinase
Reaction: ATP + β-D-ribosylnicotinate = ADP + nicotinate β-D-ribonucleotide
Other name(s): ribosylnicotinic acid kinase; nicotinic acid riboside kinase; NRK1 (ambiguous)
Systematic name: ATP:β-D-ribosylnicotinate 5-phosphotransferase
Comments: The enzyme from yeast and human also has the activity of EC 2.7.1.22 (ribosylnicotinamide kinase).
References: [3497]

[EC 2.7.1.173 created 2012]

EC 2.7.1.174

Accepted name: diacylglycerol kinase (CTP)
Reaction: CTP + 1,2-diacyl-*sn*-glycerol = CDP + 1,2-diacyl-*sn*-glycerol 3-phosphate
Other name(s): DAG kinase; CTP-dependent diacylglycerol kinase; diglyceride kinase (ambiguous); DGK1 (gene name); diacylglycerol kinase (CTP dependent)
Systematic name: CTP:1,2-diacyl-*sn*-glycerol 3-phosphotransferase
Comments: Requires Ca^{2+} or Mg^{2+} for activity. Involved in synthesis of membrane phospholipids and the neutral lipid triacylglycerol. Unlike the diacylglycerol kinases from bacteria, plants, and animals [*cf.* EC 2.7.1.107, diacylglycerol kinase (ATP)], the enzyme from *Saccharomyces cerevisiae* utilizes CTP. The enzyme can also use dCTP, but not ATP, GTP or UTP.
References: [1206, 1207, 866]

[EC 2.7.1.174 created 2012, modified 2013]

EC 2.7.1.175

Accepted name: maltokinase
Reaction: ATP + maltose = ADP + α-maltose 1-phosphate
Systematic name: ATP:α-maltose 1-phosphotransferase
Comments: Requires Mg^{2+} for activity.
References: [2212]

[EC 2.7.1.175 created 2012]

EC 2.7.1.176

Accepted name: UDP-*N*-acetylglucosamine kinase
Reaction: ATP + UDP-*N*-acetyl-α-D-glucosamine = ADP + UDP-*N*-acetyl-α-D-glucosamine 3′-phosphate
Other name(s): UNAG kinase; ζ toxin; toxin PezT; ATP:UDP-*N*-acetyl-D-glucosamine 3′-phosphotransferase
Systematic name: ATP:UDP-*N*-acetyl-α-D-glucosamine 3′-phosphotransferase
Comments: Toxic component of a toxin-antitoxin (TA) module. The phosphorylation of UDP-*N*-acetyl-D-glucosamine results in the inhibition of EC 2.5.1.7, UDP-*N*-acetylglucosamine 1-carboxyvinyltransferase, the first committed step in cell wall synthesis, which is then blocked. The activity of this enzyme is inhibited when the enzyme binds to the cognate ε antitoxin.
References: [1663, 2381]

[EC 2.7.1.176 created 2012]

EC 2.7.1.177

Accepted name: L-threonine kinase
Reaction: ATP + L-threonine = ADP + *O*-phospho-L-threonine
Other name(s): PduX
Systematic name: ATP:L-threonine O^3-phosphotransferase
Comments: The enzyme is involved in the *de novo* synthesis of adenosylcobalamin. It is specific for ATP and free L-threonine. In the bacterium *Salmonella enterica* the activity with CTP, GTP, or UTP is 6, 11, and 3% of the activity with ATP.
References: [873, 874]

[EC 2.7.1.177 created 2012]

EC 2.7.1.178

Accepted name: 2-dehydro-3-deoxyglucono/galactono-kinase

Reaction: (1) ATP + 2-dehydro-3-deoxy-D-gluconate = ADP + 2-dehydro-3-deoxy-6-phospho-D-gluconate
(2) ATP + 2-dehydro-3-deoxy-D-galactonate = ADP + 2-dehydro-3-deoxy-6-phospho-D-galactonate

Other name(s): KDG kinase (ambiguous); KDGK (ambiguous); 2-keto-3-deoxy-D-gluconate kinase (ambiguous)

Systematic name: ATP:2-dehydro-3-deoxy-D-gluconate/2-dehydro-3-deoxy-D-galactonate 6-phosphotransferase

Comments: The enzyme from the archaeon *Sulfolobus solfataricus* is involved in glucose and galactose catabolism via the branched variant of the Entner-Doudoroff pathway. It phosphorylates 2-dehydro-3-deoxy-D-gluconate and 2-dehydro-3-deoxy-D-galactonate with similar catalytic efficiency. *cf.* EC 2.7.1.45, 2-dehydro-3-deoxygluconokinase and EC 2.7.1.58, 2-dehydro-3-deoxygalactonokinase.

References: [1854, 2745, 1682]

[EC 2.7.1.178 created 2013]

EC 2.7.1.179

Accepted name: kanosamine kinase

Reaction: ATP + kanosamine = ADP + kanosamine 6-phosphate

Other name(s): *rifN* (gene name)

Systematic name: ATP:kanosamine 6-phosphotransferase

Comments: The enzyme from the bacterium *Amycolatopsis mediterranei* is specific for kanosamine.

References: [101]

[EC 2.7.1.179 created 2013]

EC 2.7.1.180

Accepted name: FAD:protein FMN transferase

Reaction: FAD + [protein]-L-threonine = [protein]-FMN-L-threonine + AMP

Other name(s): flavin transferase; *apbE* (gene name)

Systematic name: FAD:protein riboflavin-5′-phosphate transferase

Comments: The enzyme catalyses the transfer of the FMN portion of FAD and its covalent binding to the hydroxyl group of an L-threonine residue in a target flavin-binding protein such as the B and C subunits of EC 7.2.1.1, NADH:ubiquinone reductase (Na^+-transporting). Requires Mg^{2+}.

References: [295]

[EC 2.7.1.180 created 2013, modified 2018]

EC 2.7.1.181

Accepted name: polymannosyl GlcNAc-diphospho-*ditrans*,*octacis*-undecaprenol kinase

Reaction: ATP + α-D-Man-(1→2)-α-D-Man-(1→2)-[α-D-Man-(1→3)-α-D-Man-(1→3)-α-D-Man-(1→2)-α-D-Man-(1→2)]$_n$-α-D-Man-(1→3)-α-D-Man-(1→3)-α-D-Man-(1→3)-α-D-GlcNAc-diphospho-*ditrans*,*octacis*-undecaprenol = ADP + 3-*O*-phospho-α-D-Man-(1→2)-α-D-Man-(1→2)-[α-D-Man-(1→3)-α-D-Man-(1→3)-α-D-Man-(1→2)-α-D-Man-(1→2)]$_n$-α-D-Man-(1→3)-α-D-Man-(1→3)-α-D-Man-(1→3)-α-D-GlcNAc-diphospho-*ditrans*,*octacis*-undecaprenol

Other name(s): WbdD; ATP:α-D-Man-(1→2)-α-D-Man-(1→2)-α-D-Man-(1→3)-α-D-Man-(1→3)-[α-D-Man-(1→2)-α-D-Man-(1→2)-α-D-Man-(1→3)-α-D-Man-(1→3)]$_n$-α-D-Man-(1→3)-α-D-Man-(1→3)-α-D-GlcNAc-diphospho-*ditrans*,*octacis*-undecaprenol 3-phosphotransferase

Systematic name: ATP:α-D-Man-(1→2)-α-D-Man-(1→2)-[α-D-Man-(1→3)-α-D-Man-(1→3)-α-D-Man-(1→2)-α-D-Man-(1→2)]$_n$-α-D-Man-(1→3)-α-D-Man-(1→3)-α-D-Man-(1→3)-α-D-GlcNAc-diphospho-*ditrans*,*octacis*-undecaprenol 3-phosphotransferase

Comments: The enzyme is involved in the biosynthesis of the polymannose O-polysaccharide in the outer leaflet of the membrane of *Escherichia coli* serotype O9a. O-Polysaccharide structures vary extensively because of differences in the number and type of sugars in the repeat unit. The dual kinase/methylase WbdD also catalyses the methylation of 3-phospho-α-D-Man-(1→2)-α-D-Man-(1→2)-[α-D-Man-(1→3)-α-D-Man-(1→3)-α-D-Man-(1→2)-α-D-Man-(1→2)]$_n$-α-D-Man-(1→3)-α-D-Man-(1→3)-α-D-Man-(1→3)-α-D-GlcNAc-diphospho-*ditrans*,*octacis*-undecaprenol (*cf.* EC 2.1.1.294, 3-*O*-phospho-polymannosyl GlcNAc-diphospho-*ditrans*,*octacis*-undecaprenol 3-phospho-methyltransferase).
References: [574, 575, 576, 1986]

[EC 2.7.1.181 created 2014, modified 2017]

EC 2.7.1.182

Accepted name: phytol kinase
Reaction: CTP + phytol = CDP + phytyl phosphate
Other name(s): VTE5 (gene name)
Systematic name: CTP:phytol *O*-phosphotransferase
Comments: The enzyme is found in plants and photosynthetic algae [3626] and is involved in phytol salvage [1452]. It can use UTP as an alternative phosphate donor with lower activity [3626].
References: [1452, 3626]

[EC 2.7.1.182 created 2014]

EC 2.7.1.183

Accepted name: glycoprotein-mannosyl O^6-kinase
Reaction: ATP + O^3-[*N*-acetyl-β-D-galactosaminyl-(1→3)-*N*-acetyl-β-D-glucosaminyl-(1→4)-α-D-mannosyl]-L-threonyl/L-seryl-[protein] = ADP + O^3-[*N*-acetyl-β-D-galactosaminyl-(1→3)-*N*-acetyl-β-D-glucosaminyl-(1→4)-α-D-(6-phospho)mannosyl]-L-threonyl/L-seryl-[protein]
Other name(s): SGK196; protein *O*-mannose kinase
Systematic name: ATP:O^3-[*N*-acetyl-β-D-galactosaminyl-(1→3)-*N*-acetyl-β-D-glucosaminyl-(1→4)-α-D-mannosyl]-L-threonyl/L-seryl-[protein] 6-phosphotransferase
Comments: In humans this phosphorylated trisaccharide is attached to an L-threonine residue of α-dystroglycan, an extracellular peripheral glycoprotein that acts as a receptor for extracellular matrix proteins containing laminin-G domains, and is important for its activity.
References: [4001]

[EC 2.7.1.183 created 2014]

EC 2.7.1.184

Accepted name: sulfofructose kinase
Reaction: ATP + 6-deoxy-6-sulfo-D-fructose = ADP + 6-deoxy-6-sulfo-D-fructose 1-phosphate
Other name(s): *yihV* (gene name)
Systematic name: ATP:6-deoxy-6-sulfo-D-fructose 1-phosphotransferase
Comments: The enzyme, characterized from the bacterium *Escherichia coli*, is involved in the degradation pathway of sulfoquinovose, the polar headgroup of sulfolipids found in the photosynthetic membranes of all higher plants, mosses, ferns, algae, and most photosynthetic bacteria, as well as the surface layer of some archaea.
References: [711]

[EC 2.7.1.184 created 2014]

EC 2.7.1.185

Accepted name: mevalonate 3-kinase

Reaction: ATP + (*R*)-mevalonate = ADP + (*R*)-3-phosphomevalonate
Other name(s): ATP:(*R*)-MVA 3-phosphotransferase
Systematic name: ATP:(*R*)-mevalonate 3-phosphotransferase
Comments: Mevalonate 3-kinase and mevalonate-3-phosphate-5-kinase (EC 2.7.1.186) act sequentially in an alternate mevalonate pathway in the archaeon *Thermoplasma acidophilum*. Mevalonate 3-kinase is different from mevalonate kinase, EC 2.7.1.36, which transfers phosphate to position 5 of (*R*)-mevalonate and is part of the classical mevalonate pathway in eukaryotes and archaea.
References: [3685, 146]

[EC 2.7.1.185 created 2014]

EC 2.7.1.186

Accepted name: mevalonate-3-phosphate 5-kinase
Reaction: ATP + (*R*)-3-phosphomevalonate = ADP + (*R*)-3,5-bisphosphomevalonate
Systematic name: ATP:(*R*)-3-phosphomevalonate 5-phosphotransferase
Comments: Mevalonate 3-kinase (EC 2.7.1.185) and mevalonate-3-phosphate-5-kinase act sequentially in an alternate mevalonate pathway in the archaeon *Thermoplasma acidophilum*.
References: [3685]

[EC 2.7.1.186 created 2014]

EC 2.7.1.187

Accepted name: acarbose 7^{IV}-phosphotransferase
Reaction: ATP + acarbose = ADP + acarbose 7^{IV}-phosphate
Other name(s): acarbose 7-kinase; AcbK
Systematic name: ATP:acarbose 7^{IV}-phosphotransferase
Comments: The enzyme, characterized from the bacterium *Actinoplanes* sp. SE50/110, is specific for acarbose.
References: [774, 1085, 4037]

[EC 2.7.1.187 created 2015]

EC 2.7.1.188

Accepted name: 2-*epi*-5-*epi*-valiolone 7-kinase
Reaction: ATP + 2-*epi*-5-*epi*-valiolone = ADP + 2-*epi*-5-*epi*-valiolone 7-phosphate
Other name(s): AcbM
Systematic name: ATP:2-*epi*-5-*epi*-valiolone 7-phosphotransferase
Comments: The enzyme, characterized from the bacterium *Actinoplanes* sp. SE50/110, is involved in the biosynthesis of the oligosaccharide acarbose.
References: [4037]

[EC 2.7.1.188 created 2015]

EC 2.7.1.189

Accepted name: autoinducer-2 kinase
Reaction: ATP + (*S*)-4,5-dihydroxypentane-2,3-dione = ADP + (*S*)-4-hydroxypentane-2,3-dione 5-phosphate
Other name(s): *lsrK* (gene name)
Systematic name: ATP:(*S*)-4,5-dihydroxypentane-2,3-dione 5-phosphotransferase
Comments: The enzyme participates in a degradation pathway of the bacterial quorum-sensing autoinducer molecule AI-2.
References: [3916, 2954, 4079]

[EC 2.7.1.189 created 2015]

EC 2.7.1.190

Accepted name: aminoglycoside $2''$-phosphotransferase

Reaction: GTP + gentamicin = GDP + gentamicin $2''$-phosphate

Other name(s): *aphD* (gene name); APH($2''$); aminoglycoside ($2''$) kinase; gentamicin kinase (ambiguous); gentamicin phosphotransferase (ambiguous)

Systematic name: GTP:gentamicin $2''$-*O*-phosphotransferase

Comments: Requires Mg^{2+}. This bacterial enzyme phosphorylates many 4,6-disubstituted aminoglycoside antibiotics that have a hydroxyl group at position $2''$, including kanamycin A, kanamycin B, tobramycin, dibekacin, arbekacin, amikacin, gentamicin C, sisomicin and netilmicin. In most, but not all, cases the phosphorylation confers resistance against the antibiotic. Some forms of the enzyme use ATP as a phosphate donor in appreciable amount. The enzyme is often found as a bifunctional enzyme that also catalyses $6'$-aminoglycoside *N*-acetyltransferase activity. The bifunctional enzyme is the most clinically important aminoglycoside-modifying enzyme in Gram-positive bacteria, responsible for high-level resistance in both Enterococci and Staphylococci.

References: [899, 949]

[EC 2.7.1.190 created 2015]

EC 2.7.1.191

Accepted name: protein-N^{π}-phosphohistidine—D-mannose phosphotransferase

Reaction: [protein]-N^{π}-phospho-L-histidine + D-mannose$_{\text{[side 1]}}$ = [protein]-L-histidine + D-mannose 6-phosphate$_{\text{[side 2]}}$

Other name(s): manXYZ (gene names); mannose PTS permease; EII$^{\text{Man}}$; Enzyme II$^{\text{Man}}$

Systematic name: protein-N^{π}-phospho-L-histidine:D-mannose N^{π}-phosphotransferase

Comments: This enzyme is a component (known as enzyme II) of a phospho*enol*pyruvate (PEP)-dependent, sugar transporting phosphotransferase system (PTS). The system, which is found only in prokaryotes, simultaneously transports its substrate from the periplasm or extracellular space into the cytoplasm and phosphorylates it. The phosphate donor, which is shared among the different systems, is a phospho-carrier protein of low molecular mass that has been phosphorylated by EC 2.7.3.9 (phospho*enol*pyruvate—protein phosphotransferase). Enzyme II, on the other hand, is specific for a particular substrate, although in some cases alternative substrates can be transported with lower efficiency. The reaction involves a successive transfer of the phosphate group to several amino acids within the enzyme before the final transfer to the substrate.

References: [850, 3858, 852, 3352, 2877, 1399]

[EC 2.7.1.191 created 1972 as EC 2.7.1.69, part transferred 2016 to EC 2.7.1.191]

EC 2.7.1.192

Accepted name: protein-N^{π}-phosphohistidine—*N*-acetylmuramate phosphotransferase

Reaction: [protein]-N^{π}-phospho-L-histidine + *N*-acetyl-D-muramate$_{\text{[side 1]}}$ = [protein]-L-histidine + *N*-acetyl-D-muramate 6-phosphate$_{\text{[side 2]}}$

Other name(s): *murP* (gene name); *N*-acetylmuramic acid PTS permease; EII$^{\text{NAcMur}}$; Enzyme II$^{\text{NAcMur}}$

Systematic name: protein-N^{π}-phospho-L-histidine:*N*-acetyl-D-muramate N^{π}-phosphotransferase

Comments: This enzyme is a component (known as enzyme II) of a phospho*enol*pyruvate (PEP)-dependent, sugar transporting phosphotransferase system (PTS). The system, which is found only in prokaryotes, simultaneously transports its substrate from the periplasm or extracellular space into the cytoplasm and phosphorylates it. The phosphate donor, which is shared among the different systems, is a phospho-carrier protein of low molecular mass that has been phosphorylated by EC 2.7.3.9 (phospho*enol*pyruvate—protein phosphotransferase). Enzyme II, on the other hand, is specific for a particular substrate, although in some cases alternative substrates can be transported with lower efficiency. The reaction involves a successive transfer of the phosphate group to several amino acids within the enzyme before the final transfer to the substrate.

References: [655]

[EC 2.7.1.192 created 1972 as EC 2.7.1.69, part transferred 2016 to EC 2.7.1.192]

EC 2.7.1.193

Accepted name: protein-N^{π}-phosphohistidine—N-acetyl-D-glucosamine phosphotransferase

Reaction: [protein]-N^{π}-phospho-L-histidine + N-acetyl-D-glucosamine$_{\text{[side 1]}}$ = [protein]-L-histidine + N-acetyl-D-glucosamine 6-phosphate$_{\text{[side 2]}}$

Other name(s): *nagE* (gene name); N-acetyl-D-glucosamine PTS permease; EII$^{\text{Nag}}$; Enzyme II$^{\text{Nag}}$; EIICBA$^{\text{Nag}}$

Systematic name: protein-N^{π}-phospho-L-histidine:N-acetyl-D-glucosamine N^{π}-phosphotransferase

Comments: This enzyme is a component (known as enzyme II) of a phospho*enol*pyruvate (PEP)-dependent, sugar transporting phosphotransferase system (PTS). The system, which is found only in prokaryotes, simultaneously transports its substrate from the periplasm or extracellular space into the cytoplasm and phosphorylates it. The phosphate donor, which is shared among the different systems, is a phospho-carrier protein of low molecular mass that has been phosphorylated by EC 2.7.3.9 (phospho*enol*pyruvate—protein phosphotransferase). Enzyme II, on the other hand, is specific for a particular substrate, although in some cases alternative substrates can be transported with lower efficiency. The reaction involves a successive transfer of the phosphate group to several amino acids within the enzyme before the final transfer to the substrate.

References: [3839, 2917, 2666, 2729]

[EC 2.7.1.193 created 1972 as EC 2.7.1.69, part transferred 2016 to EC 2.7.1.193]

EC 2.7.1.194

Accepted name: protein-N^{π}-phosphohistidine—L-ascorbate phosphotransferase

Reaction: [protein]-N^{π}-phospho-L-histidine + L-ascorbate$_{\text{[side 1]}}$ = [protein]-L-histidine + L-ascorbate 6-phosphate$_{\text{[side 2]}}$

Other name(s): ulaABC (gene names); L-ascorbate PTS permease; EII$^{\text{Sga}}$; Enzyme II$^{\text{Sga}}$; Enzyme II$^{\text{Ula}}$

Systematic name: protein-N^{π}-phospho-L-histidine:L-ascorbate N^{π}-phosphotransferase

Comments: This enzyme is a component (known as enzyme II) of a phospho*enol*pyruvate (PEP)-dependent, sugar transporting phosphotransferase system (PTS). The system, which is found only in prokaryotes, simultaneously transports its substrate from the periplasm or extracellular space into the cytoplasm and phosphorylates it. The phosphate donor, which is shared among the different systems, is a phospho-carrier protein of low molecular mass that has been phosphorylated by EC 2.7.3.9 (phospho*enol*pyruvate—protein phosphotransferase). Enzyme II, on the other hand, is specific for a particular substrate, although in some cases alternative substrates can be transported with lower efficiency. The reaction involves a successive transfer of the phosphate group to several amino acids within the enzyme before the final transfer to the substrate.

References: [4057, 1418, 2072]

[EC 2.7.1.194 created 1972 as EC 2.7.1.69, part transferred 2016 to EC 2.7.1.194]

EC 2.7.1.195

Accepted name: protein-N^{π}-phosphohistidine—2-O-α-mannosyl-D-glycerate phosphotransferase

Reaction: [protein]-N^{π}-phospho-L-histidine + 2-O-(α-D-mannopyranosyl)-D-glycerate $_{\text{[side 1]}}$ = [protein]-L-histidine + 2-O-(6-phospho-α-D-mannopyranosyl)-D-glycerate $_{\text{[side 2]}}$

Other name(s): *mngA* (gene names); 2-O-α-mannosyl-D-glycerate PTS permease; EII$^{\text{MngA}}$; Enzyme II$^{\text{MngA}}$; Enzyme II$^{\text{HrsA}}$; EII$^{\text{mannosylglycerate}}$; Frx

Systematic name: protein-N^{π}-phospho-L-histidine:2-O-α-mannopyranosyl-D-glycerate N^{π}-phosphotransferase

Comments: This enzyme is a component (known as enzyme II) of a phospho*enol*pyruvate (PEP)-dependent, sugar transporting phosphotransferase system (PTS). The system, which is found only in prokaryotes, simultaneously transports its substrate from the periplasm or extracellular space into the cytoplasm and phosphorylates it. The phosphate donor, which is shared among the different systems, is a phospho-carrier protein of low molecular mass that has been phosphorylated by EC 2.7.3.9 (phospho*enol*pyruvate—protein phosphotransferase). Enzyme II, on the other hand, is specific for a particular substrate, although in some cases alternative substrates can be transported with lower efficiency. The reaction involves a successive transfer of the phosphate group to several amino acids within the enzyme before the final transfer to the substrate.

References: [3013]

[EC 2.7.1.195 created 1972 as EC 2.7.1.69, part transferred 2016 to EC 2.7.1.195]

EC 2.7.1.196

Accepted name: protein-N^{π}-phosphohistidine—N,N'-diacetylchitobiose phosphotransferase

Reaction: [protein]-N^{π}-phospho-L-histidine + N,N'-diacetylchitobiose$_{\text{[side 1]}}$ = [protein]-L-histidine + N,N'-diacetylchitobiose 6′-phosphate$_{\text{[side 2]}}$

Other name(s): chbABC (gene names); N,N'-diacetylchitobiose PTS permease; chitobiose PTS permease; EII$^{\text{cel}}$; EII$^{\text{chb}}$; Enzyme II$^{\text{cel}}$; Enzyme II$^{\text{chb}}$

Systematic name: protein-N^{π}-phospho-L-histidine:N,N'-diacetylchitobiose N^{π}-phosphotransferase

Comments: This enzyme is a component (known as enzyme II) of a phospho*enol*pyruvate (PEP)-dependent, sugar transporting phosphotransferase system (PTS). The system, which is found only in prokaryotes, simultaneously transports its substrate from the periplasm or extracellular space into the cytoplasm and phosphorylates it. The phosphate donor, which is shared among the different systems, is a phospho-carrier protein of low molecular mass that has been phosphorylated by EC 2.7.3.9 (phospho*enol*pyruvate—protein phosphotransferase). Enzyme II, on the other hand, is specific for a particular substrate, although in some cases alternative substrates can be transported with lower efficiency. The reaction involves a successive transfer of the phosphate group to several amino acids within the enzyme before the final transfer to the substrate.

References: [1652, 2866, 1651, 1650]

[EC 2.7.1.196 created 1972 as EC 2.7.1.69, part transferred 2016 to EC 2.7.1.196]

EC 2.7.1.197

Accepted name: protein-N^{π}-phosphohistidine—D-mannitol phosphotransferase

Reaction: [protein]-N^{π}-phospho-L-histidine + D-mannitol$_{\text{[side 1]}}$ = [protein]-L-histidine + D-mannitol 1-phosphate$_{\text{[side 2]}}$

Other name(s): *mtlA* (gene name); D-mannitol PTS permease; EII$^{\text{Mtl}}$

Systematic name: protein-N^{π}-phospho-L-histidine:D-mannitol N^{π}-phosphotransferase

Comments: This enzyme is a component (known as enzyme II) of a phospho*enol*pyruvate (PEP)-dependent, sugar transporting phosphotransferase system (PTS). The system, which is found only in prokaryotes, simultaneously transports its substrate from the periplasm or extracellular space into the cytoplasm and phosphorylates it. The phosphate donor, which is shared among the different systems, is a phospho-carrier protein of low molecular mass that has been phosphorylated by EC 2.7.3.9 (phospho*enol*pyruvate—protein phosphotransferase). Enzyme II, on the other hand, is specific for a particular substrate, although in some cases alternative substrates can be transported with lower efficiency. The reaction involves a successive transfer of the phosphate group to several amino acids within the enzyme before the final transfer to the substrate.

References: [1483, 1484, 447, 827, 3645, 342]

[EC 2.7.1.197 created 1972 as EC 2.7.1.69, part transferred 2016 to EC 2.7.1.197]

EC 2.7.1.198

Accepted name: protein-N^{π}-phosphohistidine—D-sorbitol phosphotransferase

Reaction: [protein]-N^{π}-phospho-L-histidine + D-sorbitol$_{[side\ 1]}$ = [protein]-L-histidine + D-sorbitol 6-phosphate$_{[side\ 2]}$

Other name(s): srlABE (gene names); D-sorbitol PTS permease; sorbitol PTS permease; glucitol PTS permease; EII^{Gut}; Enzyme II^{Gut}

Systematic name: protein-N^{π}-phospho-L-histidine:D-sorbitol N^{π}-phosphotransferase

Comments: This enzyme is a component (known as enzyme II) of a phospho*enol*pyruvate (PEP)-dependent, sugar transporting phosphotransferase system (PTS). The system, which is found only in prokaryotes, simultaneously transports its substrate from the periplasm or extracellular space into the cytoplasm and phosphorylates it. The phosphate donor, which is shared among the different systems, is a phospho-carrier protein of low molecular mass that has been phosphorylated by EC 2.7.3.9 (phospho*enol*pyruvate—protein phosphotransferase). Enzyme II, on the other hand, is specific for a particular substrate, although in some cases alternative substrates can be transported with lower efficiency. The reaction involves a successive transfer of the phosphate group to several amino acids within the enzyme before the final transfer to the substrate.

References: [1933, 2867]

[EC 2.7.1.198 created 1972 as EC 2.7.1.69, part transferred 2016 to EC 2.7.1.198]

EC 2.7.1.199

Accepted name: protein-N^{π}-phosphohistidine—D-glucose phosphotransferase

Reaction: [protein]-N^{π}-phospho-L-histidine + D-glucose$_{[side\ 1]}$ = [protein]-L-histidine + D-glucose 6-phosphate$_{[side\ 2]}$

Other name(s): *ptsG* (gene name); D-glucose PTS permease; EII^{Glc}; Enzyme II^{Glc}

Systematic name: protein-N^{π}-phospho-L-histidine:D-glucose N^{π}-phosphotransferase

Comments: This enzyme is a component (known as enzyme II) of a phospho*enol*pyruvate (PEP)-dependent, sugar transporting phosphotransferase system (PTS). The system, which is found only in prokaryotes, simultaneously transports its substrate from the periplasm or extracellular space into the cytoplasm and phosphorylates it. The phosphate donor, which is shared among the different systems, is a phospho-carrier protein of low molecular mass that has been phosphorylated by EC 2.7.3.9 (phospho*enol*pyruvate—protein phosphotransferase). Enzyme II, on the other hand, is specific for a particular substrate, although in some cases alternative substrates can be transported with lower efficiency. The reaction involves a successive transfer of the phosphate group to several amino acids within the enzyme before the final transfer to the substrate.

References: [3346, 851]

[EC 2.7.1.199 created 1972 as EC 2.7.1.69, part transferred 2016 to EC 2.7.1.199]

EC 2.7.1.200

Accepted name: protein-N^{π}-phosphohistidine—galactitol phosphotransferase

Reaction: [protein]-N^{π}-phospho-L-histidine + galactitol$_{[side\ 1]}$ = [protein]-L-histidine + galactitol 1-phosphate$_{[side\ 2]}$

Other name(s): gatABC (gene names); galactitol PTS permease; EII^{Gat}; Enzyme II^{Gat}

Systematic name: protein-N^{π}-phospho-L-histidine:galactitol N^{π}-phosphotransferase

Comments: This enzyme is a component (known as enzyme II) of a phospho*enol*pyruvate (PEP)-dependent, sugar transporting phosphotransferase system (PTS). The system, which is found only in prokaryotes, simultaneously transports its substrate from the periplasm or extracellular space into the cytoplasm and phosphorylates it. The phosphate donor, which is shared among the different systems, is a phospho-carrier protein of low molecular mass that has been phosphorylated by EC 2.7.3.9 (phospho*enol*pyruvate—protein phosphotransferase). Enzyme II, on the other hand, is specific for a particular substrate, although in some cases alternative substrates can be transported with lower efficiency. The reaction involves a successive transfer of the phosphate group to several amino acids within the enzyme before the final transfer to the substrate.

References: [1933, 2476, 2477]

[EC 2.7.1.200 created 1972 as EC 2.7.1.69, part transferred 2016 to EC 2.7.1.200]

EC 2.7.1.201

Accepted name: protein-N^{π}-phosphohistidine—trehalose phosphotransferase

Reaction: [protein]-N^{π}-phospho-L-histidine + α,α-trehalose$_{\text{[side 1]}}$ = [protein]-L-histidine + α,α-trehalose 6-phosphate$_{\text{[side 2]}}$

Other name(s): *treB* (gene name); trehalose PTS permease; EII$^{\text{Tre}}$; Enzyme II$^{\text{Tre}}$

Systematic name: protein-N^{π}-phospho-L-histidine:α,α-trehalose N^{π}-phosphotransferase

Comments: This enzyme is a component (known as enzyme II) of a phospho*enol*pyruvate (PEP)-dependent, sugar transporting phosphotransferase system (PTS). The system, which is found only in prokaryotes, simultaneously transports its substrate from the periplasm or extracellular space into the cytoplasm and phosphorylates it. The phosphate donor, which is shared among the different systems, is a phospho-carrier protein of low molecular mass that has been phosphorylated by EC 2.7.3.9 (phospho*enol*pyruvate—protein phosphotransferase). Enzyme II, on the other hand, is specific for a particular substrate, although in some cases alternative substrates can be transported with lower efficiency. The reaction involves a successive transfer of the phosphate group to several amino acids within the enzyme before the final transfer to the substrate.

References: [354, 1708]

[EC 2.7.1.201 created 1972 as EC 2.7.1.69, part transferred 2016 to EC 2.7.1.201]

EC 2.7.1.202

Accepted name: protein-N^{π}-phosphohistidine—D-fructose phosphotransferase

Reaction: [protein]-N^{π}-phospho-L-histidine + D-fructose$_{\text{[side 1]}}$ = [protein]-L-histidine + D-fructose 1-phosphate$_{\text{[side 2]}}$

Other name(s): *fruAB* (gene names); fructose PTS permease; EII$^{\text{Fru}}$; Enzyme II$^{\text{Fru}}$

Systematic name: protein-N^{π}-phospho-L-histidine:D-fructose N^{π}-phosphotransferase

Comments: This enzyme is a component (known as enzyme II) of a phospho*enol*pyruvate (PEP)-dependent, sugar transporting phosphotransferase system (PTS). The system, which is found only in prokaryotes, simultaneously transports its substrate from the periplasm or extracellular space into the cytoplasm and phosphorylates it. The phosphate donor, which is shared among the different systems, is usually a phospho-carrier protein of low molecular mass that has been phosphorylated by EC 2.7.3.9 (phospho*enol*pyruvate—protein phosphotransferase). The enzyme from the bacterium *Escherichia coli* is an exception, since it is phosphorylated directly by EC 2.7.3.9. The reaction involves a successive transfer of the phosphate group to several amino acids within the enzyme before the final transfer to the substrate.

References: [3793, 1760, 1030, 1761]

[EC 2.7.1.202 created 1972 as EC 2.7.1.69, part transferred 2016 to EC 2.7.1.202]

EC 2.7.1.203

Accepted name: protein-N^{π}-phosphohistidine—D-glucosaminate phosphotransferase

Reaction: [protein]-N^{π}-phospho-L-histidine + 2-amino-2-deoxy-D-gluconate$_{\text{[side 1]}}$ = [protein]-L-histidine + 2-amino-2-deoxy-D-gluconate 6-phosphate$_{\text{[side 2]}}$

Other name(s): dgaABCD (gene names); 2-amino-2-deoxy-D-gluconate PTS permease

Systematic name: protein-N^{π}-phospho-L-histidine:2-amino-2-deoxy-D-gluconate N^{π}-phosphotransferase

Comments: This enzyme is a component (known as enzyme II) of a phospho*enol*pyruvate (PEP)-dependent, sugar transporting phosphotransferase system (PTS). The system, which is found only in prokaryotes, simultaneously transports its substrate from the periplasm or extracellular space into the cytoplasm and phosphorylates it. The phosphate donor, which is shared among the different systems, is a phospho-carrier protein of low molecular mass that has been phosphorylated by EC 2.7.3.9 (phospho*enol*pyruvate—protein phosphotransferase). Enzyme II, on the other hand, is specific for a particular substrate, although in some cases alternative substrates can be transported with lower efficiency. The reaction involves a successive transfer of the phosphate group to several amino acids within the enzyme before the final transfer to the substrate.

References: [2255]

[EC 2.7.1.203 created 1972 as EC 2.7.1.69, part transferred 2016 to EC 2.7.1.203]

EC 2.7.1.204

Accepted name: protein-N^{π}-phosphohistidine—D-galactose phosphotransferase

Reaction: [protein]-N^{π}-phospho-L-histidine + D-galactose$_{[side\ 1]}$ = [protein]-L-histidine + D-galactose 6-phosphate$_{[side\ 2]}$

Other name(s): D-galactose PTS permease; EII^{Gal}; Enzyme II^{Gal}

Systematic name: protein-N^{π}-phospho-L-histidine:D-galactose N^{π}-phosphotransferase

Comments: This enzyme is a component (known as enzyme II) of a phospho*enol*pyruvate (PEP)-dependent, sugar transporting phosphotransferase system (PTS). The system, which is found only in prokaryotes, simultaneously transports its substrate from the periplasm or extracellular space into the cytoplasm and phosphorylates it. The phosphate donor, which is shared among the different systems, is a phospho-carrier protein of low molecular mass that has been phosphorylated by EC 2.7.3.9 (phospho*enol*pyruvate—protein phosphotransferase). Enzyme II, on the other hand, is specific for a particular substrate, although in some cases alternative substrates can be transported with lower efficiency. The reaction involves a successive transfer of the phosphate group to several amino acids within the enzyme before the final transfer to the substrate.

References: [4029, 4030]

[EC 2.7.1.204 created 1972 as EC 2.7.1.69, part transferred 2016 to EC 2.7.1.204]

EC 2.7.1.205

Accepted name: protein-N^{π}-phosphohistidine—cellobiose phosphotransferase

Reaction: [protein]-N^{π}-phospho-L-histidine + cellobiose$_{[side\ 1]}$ = [protein]-L-histidine + 6-phospho-β-D-glucosyl-(1→4)-D-glucose$_{[side\ 2]}$

Other name(s): *celB* (gene name); cellobiose PTS permease; EII^{Cel}; Enzyme II^{Cel}

Systematic name: protein-N^{π}-phospho-L-histidine:cellobiose N^{π}-phosphotransferase

Comments: This enzyme is a component (known as enzyme II) of a phospho*enol*pyruvate (PEP)-dependent, sugar transporting phosphotransferase system (PTS). The system, which is found only in prokaryotes, simultaneously transports its substrate from the periplasm or extracellular space into the cytoplasm and phosphorylates it. The phosphate donor, which is shared among the different systems, is a phospho-carrier protein of low molecular mass that has been phosphorylated by EC 2.7.3.9 (phospho*enol*pyruvate—protein phosphotransferase). Enzyme II, on the other hand, is specific for a particular substrate, although in some cases alternative substrates can be transported with lower efficiency. The reaction involves a successive transfer of the phosphate group to several amino acids within the enzyme before the final transfer to the substrate.

References: [1847, 1846, 3351, 3904]

[EC 2.7.1.205 created 1972 as EC 2.7.1.69, part transferred 2016 to EC 2.7.1.205]

EC 2.7.1.206

Accepted name: protein-N^{π}-phosphohistidine—L-sorbose phosphotransferase

Reaction: [protein]-N^{π}-phospho-L-histidine + L-sorbose$_{[side\ 1]}$ = [protein]-L-histidine + L-sorbose 1-phosphate$_{[side\ 2]}$

Other name(s): sorABFM (gene names); L-sorbose PTS permease; EII^{Sor}; Enzyme II^{Sor}

Systematic name: protein-N^{π}-phospho-L-histidine:L-sorbose N^{π}-phosphotransferase

Comments: This enzyme is a component (known as enzyme II) of a phospho*enol*pyruvate (PEP)-dependent, sugar transporting phosphotransferase system (PTS). The system, which is found only in prokaryotes, simultaneously transports its substrate from the periplasm or extracellular space into the cytoplasm and phosphorylates it. The phosphate donor, which is shared among the different systems, is a phospho-carrier protein of low molecular mass that has been phosphorylated by EC 2.7.3.9 (phospho*enol*pyruvate—protein phosphotransferase). Enzyme II, on the other hand, is specific for a particular substrate, although in some cases alternative substrates can be transported with lower efficiency. The reaction involves a successive transfer of the phosphate group to several amino acids within the enzyme before the final transfer to the substrate.

References: [3802, 3973]

[EC 2.7.1.206 created 1972 as EC 2.7.1.69, part transferred 2016 to EC 2.7.1.206]

EC 2.7.1.207

Accepted name: protein-N^{π}-phosphohistidine—lactose phosphotransferase

Reaction: [protein]-N^{π}-phospho-L-histidine + lactose$_{[\text{side 1}]}$ = [protein]-L-histidine + lactose $6'$-phosphate$_{[\text{side 2}]}$

Other name(s): *lacEF* (gene names); lactose PTS permease; EII$^{\text{Lac}}$; Enzyme II$^{\text{Lac}}$

Systematic name: protein-N^{π}-phospho-L-histidine:lactose N^{π}-phosphotransferase

Comments: This enzyme is a component (known as enzyme II) of a phospho*enol*pyruvate (PEP)-dependent, sugar transporting phosphotransferase system (PTS). The system, which is found only in prokaryotes, simultaneously transports its substrate from the periplasm or extracellular space into the cytoplasm and phosphorylates it. The phosphate donor, which is shared among the different systems, is a phospho-carrier protein of low molecular mass that has been phosphorylated by EC 2.7.3.9 (phospho*enol*pyruvate—protein phosphotransferase). Enzyme II, on the other hand, is specific for a particular substrate, although in some cases alternative substrates can be transported with lower efficiency. The reaction involves a successive transfer of the phosphate group to several amino acids within the enzyme before the final transfer to the substrate.

References: [1295, 3623, 384, 3704, 2672]

[EC 2.7.1.207 created 1972 as EC 2.7.1.69, part transferred 2016 to EC 2.7.1.207]

EC 2.7.1.208

Accepted name: protein-N^{π}-phosphohistidine—maltose phosphotransferase

Reaction: [protein]-N^{π}-phospho-L-histidine + maltose$_{[\text{side 1}]}$ = [protein]-L-histidine + maltose $6'$-phosphate$_{[\text{side 2}]}$

Other name(s): *malT* (gene name); maltose PTS permease; EII$^{\text{Mal}}$; Enzyme II$^{\text{Mal}}$

Systematic name: protein-N^{π}-phospho-L-histidine:maltose N^{π}-phosphotransferase

Comments: This enzyme is a component (known as enzyme II) of a phospho*enol*pyruvate (PEP)-dependent, sugar transporting phosphotransferase system (PTS). The system, which is found only in prokaryotes, simultaneously transports its substrate from the periplasm or extracellular space into the cytoplasm and phosphorylates it. The phosphate donor, which is shared among the different systems, is a phospho-carrier protein of low molecular mass that has been phosphorylated by EC 2.7.3.9 (phospho*enol*pyruvate—protein phosphotransferase). Enzyme II, on the other hand, is specific for a particular substrate, although in some cases alternative substrates can be transported with lower efficiency. The reaction involves a successive transfer of the phosphate group to several amino acids within the enzyme before the final transfer to the substrate.

References: [2905, 3795]

[EC 2.7.1.208 created 1972 as EC 2.7.1.69, part transferred 2016 to EC 2.7.1.208]

EC 2.7.1.209

Accepted name: L-erythrulose 1-kinase

Reaction: ATP + L-erythrulose = ADP + L-erythrulose 1-phosphate

Other name(s): *lerK* (gene name); L-erythrulose 1-kinase [incorrect]

Systematic name: ATP:L-erythrulose 1-phosphotransferase

Comments: The enzyme, characterized from the bacterium *Mycobacterium smegmatis*, participates in the degradation of L-threitol.
References: [1392, 1393]

[EC 2.7.1.209 created 2016, modified 2018]

EC 2.7.1.210

Accepted name: D-erythrulose 4-kinase
Reaction: ATP + D-erythrulose = ADP + D-erythrulose 4-phosphate
Other name(s): *derK* (gene name)
Systematic name: ATP:D-erythrulose 4-phosphotransferase
Comments: The enzyme, characterized from the bacterium *Mycobacterium smegmatis*, participates in the degradation of erythritol and D-threitol.
References: [1392]

[EC 2.7.1.210 created 2016]

EC 2.7.1.211

Accepted name: protein-N^{π}-phosphohistidine—sucrose phosphotransferase
Reaction: [protein]-N^{π}-phospho-L-histidine + sucrose$_{[\text{side 1}]}$ = [protein]-L-histidine + sucrose 6^{G}-phosphate$_{[\text{side 2}]}$
Other name(s): *scrAB* (gene names); sucrose PTS permease; EII^{Scr}; Enzyme II^{Scr}
Systematic name: protein-N^{π}-phospho-L-histidine:sucrose N^{π}-phosphotransferase
Comments: This enzyme is a component (known as enzyme II) of a phospho*enol*pyruvate (PEP)-dependent, sugar transporting phosphotransferase system (PTS). The system, which is found only in prokaryotes, simultaneously transports its substrate from the periplasm or extracellular space into the cytoplasm and phosphorylates it. The phosphate donor, which is shared among the different systems, is a phospho-carrier protein of low molecular mass that has been phosphorylated by EC 2.7.3.9 (phospho*enol*pyruvate—protein phosphotransferase). Enzyme II, on the other hand, is specific for a particular substrate, although in some cases alternative substrates can be transported with lower efficiency. The reaction involves a successive transfer of the phosphate group to several amino acids within the enzyme before the final transfer to the substrate.
References: [2134, 2070, 939, 3036, 3537, 1512]

[EC 2.7.1.211 created 1972 as EC 2.7.1.69, part transferred 2016 to EC 2.7.1.211]

EC 2.7.1.212

Accepted name: α-D-ribose-1-phosphate 5-kinase (ADP)
Reaction: ADP + α-D-ribose-1-phosphate = AMP + α-D-ribose 1,5-bisphosphate
Systematic name: ADP:α-D-ribose-1-phosphate 5-phosphotransferase
Comments: The enzyme, characterized from the archaeon *Thermococcus kodakarensis*, participates in an archaeal pathway for nucleoside degradation.
References: [97]

[EC 2.7.1.212 created 2016]

EC 2.7.1.213

Accepted name: cytidine kinase
Reaction: ATP + cytidine = ADP + CMP
Systematic name: ATP:cytidine 5′-phosphotransferase
Comments: The enzyme, characterized from the archaeon *Thermococcus kodakarensis*, participates in a pathway for nucleoside degradation. The enzyme can also act on deoxycytidine and uridine, but unlike EC 2.7.1.48, uridine kinase, it is most active with cytidine.
References: [97]

[EC 2.7.1.213 created 2016]

EC 2.7.1.214

Accepted name: C_7-cyclitol 7-kinase

Reaction: (1) ATP + valienone = ADP + valienone 7-phosphate
(2) ATP + validone = ADP + validone 7-phosphate

Other name(s): *valC* (gene name); *vldC* (gene name)

Systematic name: ATP:C_7-cyclitol 7-phosphotransferase

Comments: The enzyme, characterized from the bacterium *Streptomyces hygroscopicus var. jinggangensis*, is involved in the biosynthesis of the antifungal agent validamycin A.

References: [2259]

[EC 2.7.1.214 created 2016]

EC 2.7.1.215

Accepted name: erythritol kinase (D-erythritol 1-phosphate-forming)

Reaction: ATP + erythritol = ADP + D-erythritol 1-phosphate

Other name(s): *eryA* (gene name)

Systematic name: ATP:erythritol 1-phosphotransferase

Comments: The enzyme, characterized from the pathogenic bacterium *Brucella abortus*, which causes brucellosis in livestock, participates in erythritol catabolism. *cf.* EC 2.7.1.27, erythritol kinase (D-erythritol 4-phosphate-forming).

References: [3298, 1968]

[EC 2.7.1.215 created 2016]

EC 2.7.1.216

Accepted name: farnesol kinase

Reaction: CTP + (2*E*,6*E*)-farnesol = CDP + (2*E*,6*E*)-farnesyl phosphate

Other name(s): FOLK (gene name)

Systematic name: CTP:(2*E*,6*E*)-farnesol phosphotransferase

Comments: The enzyme, found in plants and animals, can also use other nucleotide triphosphates as phosphate donor, albeit less efficiently. The plant enzyme can also use geraniol and geranylgeraniol as substrates with lower activity, but not farnesyl phosphate (*cf.* EC 2.7.4.32, farnesyl phosphate kinase) [912].

References: [273, 912]

[EC 2.7.1.216 created 2017]

EC 2.7.1.217

Accepted name: 3-dehydrotetronate 4-kinase

Reaction: (1) ATP + 3-dehydro-L-erythronate = ADP + 3-dehydro-4-phospho-L-erythronate
(2) ATP + 3-dehydro-D-erythronate = ADP + 3-dehydro-4-phospho-D-erythronate

Other name(s): *otnK* (gene name)

Systematic name: ATP:3-dehydrotetronate 4-phosphotransferase

Comments: The enzyme, characterized from bacteria, is involved in D-erythronate and L-threonate catabolism.

References: [4049]

[EC 2.7.1.217 created 2017]

EC 2.7.1.218

Accepted name: fructoselysine 6-kinase

Reaction: ATP + N^6-(D-fructosyl)-L-lysine = ADP + N^6-(6-phospho-D-fructosyl)-L-lysine

Other name(s): *frlD* (gene name)
Systematic name: ATP:D-fructosyl-L-lysine 6-phosphotransferase
Comments: The enzyme, characterized from the bacterium *Escherichia coli*, has very little activity with fructose.
References: [3842, 3843]

[EC 2.7.1.218 created 2017]

EC 2.7.1.219

Accepted name: D-threonate 4-kinase
Reaction: ATP + D-threonate = ADP + 4-phospho-D-threonate
Other name(s): *dtnK* (gene name)
Systematic name: ATP:D-threonate 4-phosphotransferase
Comments: The enzyme, characterized from bacteria, is involved in a pathway for D-threonate catabolism.
References: [4049]

[EC 2.7.1.219 created 2017]

EC 2.7.1.220

Accepted name: D-erythronate 4-kinase
Reaction: ATP + D-erythronate = ADP + 4-phospho-D-erythronate
Other name(s): *denK* (gene name)
Systematic name: ATP:D-erythronate 4-phosphotransferase
Comments: The enzyme, characterized from bacteria, is involved in a pathway for D-erythronate catabolism.
References: [4049]

[EC 2.7.1.220 created 2017]

EC 2.7.1.221

Accepted name: *N*-acetylmuramate 1-kinase
Reaction: ATP + *N*-acetyl-D-muramate = ADP + *N*-acetyl-α-D-muramate 1-phosphate
Other name(s): *amgK* (gene name)
Systematic name: ATP:*N*-acetyl-D-muramate 1-phosphotransferase
Comments: The enzyme, characterized from *Pseudomonas* species, participates in a peptidoglycan salvage pathway.
References: [1068]

[EC 2.7.1.221 created 2017]

EC 2.7.1.222

Accepted name: 4-hydroxytryptamine kinase
Reaction: ATP + 4-hydroxytryptamine = ADP + 4-hydroxytryptamine 4-phosphate
Other name(s): PsiK
Systematic name: ATP:4-hydroxytryptamine 4-phosphotransferase
Comments: Also acts on 4-hydroxy-L-tryptophan *in vitro*. Isolated from the fungus *Psilocybe cubensis*. Involved in the biosynthesis of the psychoactive compound psilocybin.
References: [961]

[EC 2.7.1.222 created 2017]

EC 2.7.1.223

Accepted name: aminoimidazole riboside kinase
Reaction: ATP + 5-amino-1-(β-D-ribosyl)imidazole = ADP + 5-amino-1-(5-phospho-β-D-ribosyl)imidazole

Other name(s): STM4066 (locus name)
Systematic name: ATP:5-amino-1-(β-D-ribosyl)imidazole 5′-phosphotransferase
Comments: The enzyme, characterized from the bacterium *Salmonella enterica*, can phosphorylate exogeneously-provided 5-amino-1-(β-D-ribosyl)imidazole to form 5-amino-1-(5-phospho-β-D-ribosyl)imidazole (AIR), an important intermediate in the production of both purine mononucleotides and the hydroxymethyl pyrimidine moiety of thiamine.
References: [760, 4052]

[EC 2.7.1.223 created 2018]

EC 2.7.1.224

Accepted name: cytidine diphosphoramidate kinase
Reaction: ATP + cytidine 5′-diphosphoramidate = ADP + cytidine 3′-phospho-5′-diphosphoramidate
Systematic name: ATP:cytidine 5′-diphosphoramidate 3′-phosphotransferase
Comments: The enzyme, characterized from the bacterium *Campylobacter jejuni*, is involved in formation of a unique *O*-methyl phosphoramidate modification on specific sugar residues within the bacterium's capsular polysaccharides.
References: [3490]

[EC 2.7.1.224 created 2018]

EC 2.7.2 Phosphotransferases with a carboxy group as acceptor

EC 2.7.2.1

Accepted name: acetate kinase
Reaction: ATP + acetate = ADP + acetyl phosphate
Other name(s): acetokinase; AckA; AK; acetic kinase; acetate kinase (phosphorylating)
Systematic name: ATP:acetate phosphotransferase
Comments: Requires Mg^{2+} for activity. While purified enzyme from *Escherichia coli* is specific for acetate [941], others have found that the enzyme can also use propanoate as a substrate, but more slowly [1446]. Acetate can be converted into the key metabolic intermediate acetyl-CoA by coupling acetate kinase with EC 2.3.1.8, phosphate acetyltransferase. Both this enzyme and EC 2.7.2.15, propionate kinase, play important roles in the production of propanoate [1312].
References: [2922, 2923, 3338, 941, 1720, 440, 1446, 1103, 1312]

[EC 2.7.2.1 created 1961, modified 2005]

EC 2.7.2.2

Accepted name: carbamate kinase
Reaction: ATP + NH_3 + hydrogencarbonate = ADP + carbamoyl phosphate + H_2O (overall reaction)
(1a) ATP + carbamate = ADP + carbamoyl phosphate
(1b) NH_3 + hydrogencarbonate = carbamate + H_2O (spontaneous)
Other name(s): CKase; carbamoyl phosphokinase; carbamyl phosphokinase
Systematic name: ATP:carbamate phosphotransferase
Comments: The enzyme catalyses the reversible conversion of carbamoyl phosphate and ADP to ATP and carbamate, which hydrolyses to ammonia and hydrogencarbonate. The physiological role of the enzyme is to generate ATP.
References: [1531, 682, 1073, 312, 3311]

[EC 2.7.2.2 created 1961, modified 2018]

EC 2.7.2.3

Accepted name: phosphoglycerate kinase
Reaction: ATP + 3-phospho-D-glycerate = ADP + 3-phospho-D-glyceroyl phosphate
Other name(s): PGK; 3-PGK; ATP-3-phospho-D-glycerate-1-phosphotransferase; ATP:D-3-phosphoglycerate 1-phosphotransferase; 3-phosphoglycerate kinase; 3-phosphoglycerate phosphokinase; 3-phosphoglyceric acid kinase; 3-phosphoglyceric acid phosphokinase; 3-phosphoglyceric kinase; glycerate 3-phosphate kinase; glycerophosphate kinase; phosphoglyceric acid kinase; phosphoglyceric kinase; phosphoglycerokinase
Systematic name: ATP:3-phospho-D-glycerate 1-phosphotransferase
References: [135, 416, 1241, 2814]

[EC 2.7.2.3 created 1961]

EC 2.7.2.4

Accepted name: aspartate kinase
Reaction: ATP + L-aspartate = ADP + 4-phospho-L-aspartate
Other name(s): aspartokinase; AK; β-aspartokinase; aspartic kinase
Systematic name: ATP:L-aspartate 4-phosphotransferase
Comments: The enzyme from *Escherichia coli* is a multifunctional protein, which also catalyses the reaction of EC 1.1.1.3 homoserine dehydrogenase. This is also the case for two of the four isoenzymes in *Arabidopsis thaliana*. The equilibrium constant strongly favours the reaction from right to left, i.e. the non-physiological direction of reaction.
References: [317, 2643, 3320, 3671, 506, 647]

[EC 2.7.2.4 created 1961]

[2.7.2.5 Deleted entry. carbamoyl-phosphate synthase (ammonia). Now EC 6.3.4.16, carbamoyl-phosphate synthase (ammonia)]

[EC 2.7.2.5 created 1965, deleted 1978]

EC 2.7.2.6

Accepted name: formate kinase
Reaction: ATP + formate = ADP + formyl phosphate
Systematic name: ATP:formate phosphotransferase
References: [3256]

[EC 2.7.2.6 created 1965]

EC 2.7.2.7

Accepted name: butyrate kinase
Reaction: ATP + butanoate = ADP + butanoyl phosphate
Systematic name: ATP:butanoate 1-phosphotransferase
Comments: The enzyme from *Clostridium* sp. also acts, more slowly, on pentanoate and propanoate, and on some branched-chain fatty acids (*cf.* EC 2.7.1.14 sedoheptulokinase).
References: [1235, 3595]

[EC 2.7.2.7 created 1972, modified 1986, modified 1990]

EC 2.7.2.8

Accepted name: acetylglutamate kinase
Reaction: ATP + *N*-acetyl-L-glutamate = ADP + *N*-acetyl-L-glutamyl 5-phosphate
Other name(s): *N*-acetylglutamate 5-phosphotransferase; acetylglutamate phosphokinase; *N*-acetylglutamate phosphokinase; *N*-acetylglutamate kinase; *N*-acetylglutamic 5-phosphotransferase
Systematic name: ATP:*N*-acetyl-L-glutamate 5-phosphotransferase

References: [162, 876, 3695]

[EC 2.7.2.8 created 1972]

[2.7.2.9 Transferred entry. carbamoyl-phosphate synthase (glutamine). Now EC 6.3.5.5, carbamoyl-phosphate synthase (glutamine-hydrolysing)]

[EC 2.7.2.9 created 1972, deleted 1978]

EC 2.7.2.10

Accepted name: phosphoglycerate kinase (GTP)
Reaction: GTP + 3-phospho-D-glycerate = GDP + 3-phospho-D-glyceroyl phosphate
Systematic name: GTP:3-phospho-D-glycerate 1-phosphotransferase
References: [2854]

[EC 2.7.2.10 created 1976]

EC 2.7.2.11

Accepted name: glutamate 5-kinase
Reaction: ATP + L-glutamate = ADP + L-glutamate 5-phosphate
Other name(s): ATP-L-glutamate 5-phosphotransferase; ATP:γ-L-glutamate phosphotransferase; γ-glutamate kinase; γ-glutamyl kinase; glutamate kinase
Systematic name: ATP:L-glutamate 5-phosphotransferase
Comments: In the absence of downstream enzymes, the product rapidly cyclizes to 5-oxo-L-proline and phosphate.
References: [161]

[EC 2.7.2.11 created 1976]

EC 2.7.2.12

Accepted name: acetate kinase (diphosphate)
Reaction: diphosphate + acetate = phosphate + acetyl phosphate
Other name(s): pyrophosphate-acetate phosphotransferase
Systematic name: diphosphate:acetate phosphotransferase
References: [2851]

[EC 2.7.2.12 created 1976]

EC 2.7.2.13

Accepted name: glutamate 1-kinase
Reaction: ATP + L-glutamate = ADP + α-L-glutamyl phosphate
Systematic name: ATP:L-glutamate 1-phosphotransferase
References: [3759]

[EC 2.7.2.13 created 1984]

EC 2.7.2.14

Accepted name: branched-chain-fatty-acid kinase
Reaction: ATP + 2-methylpropanoate = ADP + 2-methylpropanoyl phosphate
Other name(s): isobutyrate kinase
Systematic name: ATP:branched-chain-fatty-acid 1-phosphotransferase
Comments: 3-Methylbutanoate, 2-methylbutanoate, pentanoate, butanoate and propanoate can also act as acceptors (*cf.* EC 2.7.2.7 butyrate kinase).

References: [1239]

[EC 2.7.2.14 created 1990]

EC 2.7.2.15

Accepted name: propionate kinase
Reaction: ATP + propanoate = ADP + propanoyl phosphate
Other name(s): PduW; TdcD; propionate/acetate kinase
Systematic name: ATP:propanoate phosphotransferase
Comments: Requires Mg^{2+}. Acetate can also act as a substrate. Involved in the anaerobic degradation of L-threonine in bacteria [1312]. Both this enzyme and EC 2.7.2.1, acetate kinase, play important roles in the production of propanoate [1312].
References: [1312, 2600, 3803, 1446, 3230, 3231]

[EC 2.7.2.15 created 2005]

EC 2.7.3 Phosphotransferases with a nitrogenous group as acceptor

EC 2.7.3.1

Accepted name: guanidinoacetate kinase
Reaction: ATP + guanidinoacetate = ADP + phosphoguanidinoacetate
Other name(s): glycocyamine kinase
Systematic name: ATP:guanidinoacetate *N*-phosphotransferase
References: [1346, 2753, 2754, 3513]

[EC 2.7.3.1 created 1961]

EC 2.7.3.2

Accepted name: creatine kinase
Reaction: ATP + creatine = ADP + phosphocreatine
Other name(s): ATP:creatine phosphotransferase; CK; MM-CK; MB-CK; BB-CK; creatine phosphokinase; creatine phosphotransferase; phosphocreatine kinase; adenosine triphosphate-creatine transphosphorylase; Mi-CK; CK-BB; CK-MM; CK-MB; CKMiMi; MiMi-CK
Systematic name: ATP:creatine *N*-phosphotransferase
Comments: *N*-Ethylglycocyamine can also act as acceptor.
References: [841, 1649, 1801, 1802]

[EC 2.7.3.2 created 1961]

EC 2.7.3.3

Accepted name: arginine kinase
Reaction: ATP + L-arginine = ADP + N^{ω}-phospho-L-arginine
Other name(s): arginine phosphokinase; adenosine $5'$-triphosphate: L-arginine phosphotransferase; adenosine $5'$-triphosphate-arginine phosphotransferase; ATP:L-arginine *N*-phosphotransferasel ATP:L-arginine ω-*N*-phosphotransferase
Systematic name: ATP:L-arginine N^{ω}-phosphotransferase
References: [831, 2324, 3416, 3686]

[EC 2.7.3.3 created 1961]

EC 2.7.3.4

Accepted name: taurocyamine kinase
Reaction: ATP + taurocyamine = ADP + *N*-phosphotaurocyamine
Other name(s): taurocyamine phosphotransferase; ATP:taurocyamine phosphotransferase
Systematic name: ATP:taurocyamine *N*-phosphotransferase
References: [1346, 1593, 3513, 3515]

[EC 2.7.3.4 created 1965]

EC 2.7.3.5

Accepted name: lombricine kinase
Reaction: ATP + lombricine = ADP + *N*-phospholombricine
Systematic name: ATP:lombricine *N*-phosphotransferase
Comments: Also acts on methylated lombricines such as thalassemine; the specificity varies with the source species.
References: [1002, 1593, 2614, 3516]

[EC 2.7.3.5 created 1965, modified 1976]

EC 2.7.3.6

Accepted name: hypotaurocyamine kinase
Reaction: ATP + hypotaurocyamine = ADP + N^{ω}-phosphohypotaurocyamine
Systematic name: ATP:hypotaurocyamine *N*-phosphotransferase
Comments: Also acts, more slowly, on taurocyamine.
References: [3515]

[EC 2.7.3.6 created 1965]

EC 2.7.3.7

Accepted name: opheline kinase
Reaction: ATP + guanidinoethyl methyl phosphate = ADP + N'-phosphoguanidinoethyl methylphosphate
Systematic name: ATP:guanidinoethyl-methyl-phosphate phosphotransferase
Comments: Has a little activity on taurocyamine, lombricine and phosphotaurocyamine.
References: [3514]

[EC 2.7.3.7 created 1972]

EC 2.7.3.8

Accepted name: ammonia kinase
Reaction: ATP + NH_3 = ADP + phosphoramide
Other name(s): phosphoramidate-adenosine diphosphate phosphotransferase; phosphoramidate-ADP-phosphotransferase
Systematic name: ATP:ammonia phosphotransferase
Comments: Has a wide specificity. In the reverse direction, *N*-phosphoglycine and *N*-phosphohistidine can also act as phosphate donors, and ADP, dADP, GDP, CDP, dTDP, dCDP, IDP and UDP can act as phosphate acceptors (in decreasing order of activity).
References: [771]

[EC 2.7.3.8 created 1972]

EC 2.7.3.9

Accepted name: phospho*enol*pyruvate—protein phosphotransferase
Reaction: phospho*enol*pyruvate + protein histidine = pyruvate + protein N^{π}-phospho-L-histidine

Other name(s): phospho*enol*pyruvate sugar phosphotransferase enzyme I; phosphopyruvate-protein factor phosphotransferase; phosphopyruvate-protein phosphotransferase; sugar-PEP phosphotransferase enzyme I; phospho*enol*pyruvate:protein-L-histidine *N*-*pros*-phosphotransferase
Systematic name: phospho*enol*pyruvate:protein-L-histidine N^{π}-phosphotransferase
Comments: Enzyme I of the phosphotransferase system (*cf.* EC 2.7.1.69 protein-N^{π}-phosphohistidine—sugar phosphotransferase). Acts only on histidine residues in specific phosphocarrier proteins of low molecular mass (9.5 kDa) involved in bacterial sugar transport. A similar reaction, where the protein is the enzyme EC 2.7.9.2 pyruvate, water dikinase, is part of the mechanism of that enzyme.
References: [2744]

[EC 2.7.3.9 created 1972]

EC 2.7.3.10
Accepted name: agmatine kinase
Reaction: ATP + agmatine = ADP + N^4-phosphoagmatine
Other name(s): phosphagen phosphokinase; ATP:agmatine 4-*N*-phosphotransferase
Systematic name: ATP:agmatine N^4-phosphotransferase
Comments: L-Arginine can act as acceptor, but more slowly.
References: [2698]

[EC 2.7.3.10 created 1984]

[2.7.3.11 Transferred entry. protein-histidine pros-kinase. Now EC 2.7.13.1, protein-histidine pros-kinase]

[EC 2.7.3.11 created 1989, deleted 2005]

[2.7.3.12 Transferred entry. protein-histidine tele-kinase. Now EC 2.7.13.2, protein-histidine tele-kinase]

[EC 2.7.3.12 created 1989, deleted 2005]

EC 2.7.3.13
Accepted name: glutamine kinase
Reaction: ATP + L-glutamine + H_2O = AMP + phosphate + N^5-phospho-L-glutamine
Systematic name: ATP:L-glutamine N^5-phosphotransferase
Comments: The enzyme, characterized from the bacterium *Campylobacter jejuni*, is involved in formation of a unique *O*-methyl phosphoramidate modification on specific sugar residues within the bacterium's capsular polysaccharides.
References: [3489]

[EC 2.7.3.13 created 2017]

EC 2.7.4 Phosphotransferases with a phosphate group as acceptor

EC 2.7.4.1
Accepted name: polyphosphate kinase
Reaction: ATP + $(\text{phosphate})_n$ = ADP + $(\text{phosphate})_{n+1}$
Other name(s): polyphosphoric acid kinase
Systematic name: ATP:polyphosphate phosphotransferase
References: [1353, 1756, 2342]

[EC 2.7.4.1 created 1961]

EC 2.7.4.2

Accepted name: phosphomevalonate kinase
Reaction: ATP + (*R*)-5-phosphomevalonate = ADP + (*R*)-5-diphosphomevalonate
Other name(s): ATP:5-phosphomevalonate phosphotransferase; 5-phosphomevalonate kinase; mevalonate phosphate kinase; mevalonate-5-phosphate kinase; mevalonic acid phosphate kinase
Systematic name: ATP:(*R*)-5-phosphomevalonate phosphotransferase
References: [332, 1296, 1951]

[EC 2.7.4.2 created 1961]

EC 2.7.4.3

Accepted name: adenylate kinase
Reaction: ATP + AMP = **2** ADP
Other name(s): myokinase; 5′-AMP-kinase; adenylic kinase; adenylokinase
Systematic name: ATP:AMP phosphotransferase
Comments: Inorganic triphosphate can also act as donor.
References: [542, 1067, 2480, 2481, 2482, 2483, 2558]

[EC 2.7.4.3 created 1961]

EC 2.7.4.4

Accepted name: nucleoside-phosphate kinase
Reaction: ATP + nucleoside phosphate = ADP + nucleoside diphosphate
Other name(s): NMP-kinase
Systematic name: ATP:nucleoside-phosphate phosphotransferase
Comments: Many nucleotides can act as acceptors; other nucleoside triphosphates can act instead of ATP.
References: [1050, 1303, 1965, 2481]

[EC 2.7.4.4 created 1961]

[2.7.4.5 Deleted entry. deoxycytidylate kinase. Now included with EC 2.7.4.14 cytidylate kinase]

[EC 2.7.4.5 created 1961, deleted 1972]

EC 2.7.4.6

Accepted name: nucleoside-diphosphate kinase
Reaction: ATP + nucleoside diphosphate = ADP + nucleoside triphosphate
Other name(s): nucleoside 5′-diphosphate kinase; nucleoside diphosphate (UDP) kinase; nucleoside diphosphokinase; nucleotide phosphate kinase; UDP kinase; uridine diphosphate kinase
Systematic name: ATP:nucleoside-diphosphate phosphotransferase
Comments: Many nucleoside diphosphates can act as acceptors, while many ribo- and deoxyribonucleoside triphosphates can act as donors.
References: [278, 1050, 1692, 1781, 2404, 2821]

[EC 2.7.4.6 created 1961]

EC 2.7.4.7

Accepted name: phosphooxymethylpyrimidine kinase
Reaction: ATP + 4-amino-2-methyl-5-(phosphooxymethyl)pyrimidine = ADP + 4-amino-2-methyl-5-(diphosphooxymethyl)pyrimidine
Other name(s): hydroxymethylpyrimidine phosphokinase; ATP:4-amino-2-methyl-5-phosphooxymethylpyrimidine phosphotransferase; ATP:(4-amino-2-methylpyrimidin-5-yl)methyl-phosphate phosphotransferase; phosphomethylpyrimidine kinase
Systematic name: ATP:4-amino-2-methyl-5-(phosphooxymethyl)pyrimidine phosphotransferase
References: [1953]

[EC 2.7.4.7 created 1965, modified 2016]

EC 2.7.4.8

Accepted name: guanylate kinase

Reaction: ATP + GMP = ADP + GDP

Other name(s): deoxyguanylate kinase; $5'$-GMP kinase; GMP kinase; guanosine monophosphate kinase; ATP:GMP phosphotransferase

Systematic name: ATP:(d)GMP phosphotransferase

Comments: dGMP can also act as acceptor, and dATP can act as donor.

References: [415, 1338, 1138, 2511, 3196]

[EC 2.7.4.8 created 1965]

EC 2.7.4.9

Accepted name: dTMP kinase

Reaction: ATP + dTMP = ADP + dTDP

Other name(s): thymidine monophosphate kinase; thymidylate kinase; thymidylate monophosphate kinase; thymidylic acid kinase; thymidylic kinase; deoxythymidine $5'$-monophosphate kinase; TMPK; thymidine $5'$-monophosphate kinase

Systematic name: ATP:dTMP phosphotransferase

References: [1412, 1626, 2431]

[EC 2.7.4.9 created 1965]

EC 2.7.4.10

Accepted name: nucleoside-triphosphate—adenylate kinase

Reaction: nucleoside triphosphate + AMP = nucleoside diphosphate + ADP

Other name(s): guanosine triphosphate-adenylate kinase; nucleoside triphosphate-adenosine monophosphate transphosphorylase; GTP:AMP phosphotransferase; isozyme 3 of adenylate kinase

Systematic name: nucleoside-triphosphate:AMP phosphotransferase

Comments: Many nucleoside triphosphates can act as donors.

References: [49, 543]

[EC 2.7.4.10 created 1965]

EC 2.7.4.11

Accepted name: (deoxy)adenylate kinase

Reaction: ATP + dAMP = ADP + dADP

Systematic name: ATP:(d)AMP phosphotransferase

Comments: AMP can also act as acceptor.

References: [1138]

[EC 2.7.4.11 created 1972]

EC 2.7.4.12

Accepted name: T_2-induced deoxynucleotide kinase

Reaction: ATP + dGMP (or dTMP) = ADP + dGDP (or dTDP)

Systematic name: ATP:(d)NMP phosphotransferase

Comments: dTMP and dAMP can act as acceptors; dATP can act as donor.

References: [260]

[EC 2.7.4.12 created 1972]

EC 2.7.4.13

Accepted name: (deoxy)nucleoside-phosphate kinase

Reaction: ATP + a $2'$-deoxyribonucleoside $5'$-phosphate = ADP + a $2'$-deoxyribonucleoside $5'$-diphosphate

Other name(s): deoxynucleoside monophosphate kinase; deoxyribonucleoside monophosphokinase; deoxynucleoside-$5'$-monophosphate kinase; ATP:deoxynucleoside-phosphate phosphotransferase

Systematic name: ATP:$2'$-deoxyribonucleoside-$5'$-phosphate phosphotransferase

Comments: dATP can substitute for ATP.

References: [296]

[EC 2.7.4.13 created 1972]

EC 2.7.4.14

Accepted name: UMP/CMP kinase

Reaction: (1) ATP + (d)CMP = ADP + (d)CDP
(2) ATP + UMP = ADP + UDP

Other name(s): cytidylate kinase; deoxycytidylate kinase; CTP:CMP phosphotransferase; dCMP kinase; deoxycytidine monophosphokinase; UMP-CMP kinase; ATP:UMP-CMP phosphotransferase; pyrimidine nucleoside monophosphate kinase; uridine monophosphate-cytidine monophosphate phosphotransferase

Systematic name: ATP:CMP(UMP) phosphotransferase

Comments: This eukaryotic enzyme is a bifunctional enzyme that catalyses the phosphorylation of both CMP and UMP with similar efficiency. dCMP can also act as acceptor. Different from the monofunctional prokaryotic enzymes EC 2.7.4.25, CMP kinase and EC 2.7.4.22, UMP kinase.

References: [1412, 2968, 3067, 4076, 2927]

[EC 2.7.4.14 created 1961 as EC 2.7.4.5, transferred 1972 to EC 2.7.4.14, modified 1980, modified 2011]

EC 2.7.4.15

Accepted name: thiamine-diphosphate kinase

Reaction: ATP + thiamine diphosphate = ADP + thiamine triphosphate

Other name(s): ATP:thiamin-diphosphate phosphotransferase; TDP kinase; thiamin diphosphate kinase; thiamin diphosphate phosphotransferase; thiamin pyrophosphate kinase; thiamine diphosphate kinase; protein bound thiamin diphosphate:ATP phosphoryltransferase

Systematic name: ATP:thiamine-diphosphate phosphotransferase

References: [1470, 1669]

[EC 2.7.4.15 created 1972]

EC 2.7.4.16

Accepted name: thiamine-phosphate kinase

Reaction: ATP + thiamine phosphate = ADP + thiamine diphosphate

Other name(s): thiamin-monophosphate kinase; thiamin monophosphatase; thiamin monophosphokinase

Systematic name: ATP:thiamine-phosphate phosphotransferase

References: [2470]

[EC 2.7.4.16 created 1976]

EC 2.7.4.17

Accepted name: 3-phosphoglyceroyl-phosphate—polyphosphate phosphotransferase

Reaction: 3-phospho-D-glyceroyl phosphate + (phosphate)$_n$ = 3-phosphoglycerate + (phosphate)$_{n+1}$

Other name(s): diphosphoglycerate-polyphosphate phosphotransferase; 1,3-diphosphoglycerate-polyphosphate phosphotransferase

Systematic name: 3-phospho-D-glyceroyl-phosphate:polyphosphate phosphotransferase

References: [1809, 1810]

[EC 2.7.4.17 created 1976]

EC 2.7.4.18

Accepted name: farnesyl-diphosphate kinase

Reaction: ATP + farnesyl diphosphate = ADP + farnesyl triphosphate

Other name(s): farnesyl pyrophosphate kinase

Systematic name: ATP:farnesyl-diphosphate phosphotransferase

Comments: ADP can also act as donor.

References: [3066]

[EC 2.7.4.18 created 1978]

EC 2.7.4.19

Accepted name: 5-methyldeoxycytidine-5′-phosphate kinase

Reaction: ATP + 5-methyldeoxycytidine 5′-phosphate = ADP + 5-methyldeoxycytidine diphosphate

Systematic name: ATP:5-methyldeoxycytidine-5′-phosphate phosphotransferase

Comments: The enzyme, from phage XP-12-infected *Xanthomonas oryzae*, converts m^{5}dCMP into m^{5}dCDP and then into m^{5}dCTP.

References: [3756]

[EC 2.7.4.19 created 1984]

EC 2.7.4.20

Accepted name: dolichyl-diphosphate—polyphosphate phosphotransferase

Reaction: dolichyl diphosphate + (phosphate)$_n$ = dolichyl phosphate + (phosphate)$_{n+1}$

Other name(s): dolichylpyrophosphate:polyphosphate phosphotransferase

Systematic name: dolichyl-diphosphate:polyphosphate phosphotransferase

References: [2423]

[EC 2.7.4.20 created 1989]

EC 2.7.4.21

Accepted name: inositol-hexakisphosphate kinase

Reaction: (1) ATP + 1D-*myo*-inositol hexakisphosphate = ADP + 1D-*myo*-inositol 5-diphosphate 1,2,3,4,6-pentakisphosphate
(2) ATP + 1D-*myo*-inositol 1-diphosphate 2,3,4,5,6-pentakisphosphate = ADP + 1D-*myo*-inositol 1,5-bis(diphosphate) 2,3,4,6-tetrakisphosphate

Other name(s): ATP:1D-*myo*-inositol-hexakisphosphate phosphotransferase; IP6K

Systematic name: ATP:1D-*myo*-inositol-hexakisphosphate 5-phosphotransferase

Comments: Three mammalian isoforms are known to exist.

References: [2996, 3069, 46, 1969, 3750]

[EC 2.7.4.21 created 2002 as EC 2.7.1.152, transferred 2003 to EC 2.7.4.21, modified 2013]

EC 2.7.4.22

Accepted name: UMP kinase

Reaction: ATP + UMP = ADP + UDP

Other name(s): uridylate kinase; UMPK; uridine monophosphate kinase; PyrH; UMP-kinase; SmbA

Systematic name: ATP:UMP phosphotransferase

Comments: This enzyme is strictly specific for UMP as substrate and is used by prokaryotes in the de novo synthesis of pyrimidines, in contrast to eukaryotes, which use the dual-specificity enzyme UMP/CMP kinase (EC 2.7.4.14) for the same purpose [2121]. This enzyme is the subject of feedback regulation, being inhibited by UTP and activated by GTP [3146].

References: [3146, 2121]

[EC 2.7.4.22 created 2006]

EC 2.7.4.23

Accepted name: ribose 1,5-bisphosphate phosphokinase

Reaction: ATP + α-D-ribose 1,5-bisphosphate = ADP + 5-phospho-α-D-ribose 1-diphosphate

Other name(s): ribose 1,5-bisphosphokinase; PhnN; ATP:ribose-1,5-bisphosphate phosphotransferase

Systematic name: ATP:α-D-ribose-1,5-bisphosphate phosphotransferase

Comments: This enzyme, found in NAD supression mutants of *Escherichia coli*, synthesizes 5-phospho-α-D-ribose 1-diphosphate (PRPP) without the participation of EC 2.7.6.1, ribose-phosphate diphosphokinase. Ribose, ribose 1-phosphate and ribose 5-phosphate are not substrates, and GTP cannot act as a phosphate donor.

References: [1383]

[EC 2.7.4.23 created 2006]

EC 2.7.4.24

Accepted name: diphosphoinositol-pentakisphosphate kinase

Reaction: (1) ATP + 1D-*myo*-inositol 5-diphosphate 1,2,3,4,6-pentakisphosphate = ADP + 1D-*myo*-inositol 1,5-bis(diphosphate) 2,3,4,6-tetrakisphosphate

(2) ATP + 1D-*myo*-inositol hexakisphosphate = ADP + 1D-*myo*-inositol 1-diphosphate 2,3,4,5,6-pentakisphosphate

Other name(s): *PP*-IP$_5$ kinase; diphosphoinositol pentakisphosphate kinase; ATP:5-diphospho-1D-*myo*-inositol-pentakisphosphate phosphotransferase; *PP*-InsP_5 kinase; PPIP5K; PPIP5K1; PPIP5K2; VIP1; VIP2

Systematic name: ATP:1D-*myo*-inositol-5-diphosphate-pentakisphosphate phosphotransferase

Comments: This enzyme is activated by osmotic shock [552]. Ins(1,3,4,5,6)P_5, 1D-*myo*-inositol diphosphate tetrakisphosphate and 1D-*myo*-inositol bisdiphosphate triphosphate are not substrates [552].

References: [3167, 46, 962, 552, 1969, 3750]

[EC 2.7.4.24 created 2003 as EC 2.7.1.155, transferred 2007 to EC 2.7.4.24, modified 2014]

EC 2.7.4.25

Accepted name: (d)CMP kinase

Reaction: ATP + (d)CMP = ADP + (d)CDP

Other name(s): prokaryotic cytidylate kinase; deoxycytidylate kinase; dCMP kinase; deoxycytidine monophosphokinase

Systematic name: ATP:(d)CMP phosphotransferase

Comments: The prokaryotic cytidine monophosphate kinase specifically phosphorylates CMP (or dCMP), using ATP as the preferred phosphoryl donor. Unlike EC 2.7.4.14, a eukaryotic enzyme that phosphorylates UMP and CMP with similar efficiency, the prokaryotic enzyme phosphorylates UMP with very low rates, and this function is catalysed in prokaryotes by EC 2.7.4.22, UMP kinase. The enzyme phosphorylates dCMP nearly as well as it does CMP [294].

References: [294, 3532]

[EC 2.7.4.25 created 2011]

EC 2.7.4.26

Accepted name: isopentenyl phosphate kinase

Reaction: ATP + isopentenyl phosphate = ADP + isopentenyl diphosphate

Systematic name: ATP:isopentenyl phosphate phosphotransferase

Comments: The enzyme is involved in the mevalonate pathway in Archaea [1143]. The activity has also been identified in the plant *Mentha piperita* (peppermint) [1860]. It is strictly specific for ATP but can use other phosphate acceptors such as dimethylallyl phosphate, geranyl phosphate, or fosfomycin.

References: [1143, 1860, 532, 2090]

[EC 2.7.4.26 created 2012]

EC 2.7.4.27

Accepted name: [pyruvate, phosphate dikinase]-phosphate phosphotransferase

Reaction: [pyruvate, phosphate dikinase] phosphate + phosphate = [pyruvate, phosphate dikinase] + diphosphate

Other name(s): PPDK regulatory protein (ambiguous); pyruvate, phosphate dikinase regulatory protein (ambiguous); bifunctional dikinase regulatory protein (ambiguous); PDRP1 (gene name)

Systematic name: [pyruvate, phosphate dikinase] phosphate:phosphate phosphotransferase

Comments: The enzyme from the plants maize and *Arabidopsis* is bifunctional and also catalyses the phosphorylation of pyruvate, phosphate dikinase (EC 2.7.9.1), *cf.* EC 2.7.11.32, [pyruvate, phosphate dikinase] kinase [435, 508, 433, 509].

References: [434, 435, 508, 433, 509]

[EC 2.7.4.27 created 2012]

EC 2.7.4.28

Accepted name: [pyruvate, water dikinase]-phosphate phosphotransferase

Reaction: [pyruvate, water dikinase] phosphate + phosphate = [pyruvate, water dikinase] + diphosphate

Other name(s): PSRP (ambiguous)

Systematic name: [pyruvate, water dikinase] phosphate:phosphate phosphotransferase

Comments: The enzyme from the bacterium *Escherichia coli* is bifunctional and catalyses both the phosphorylation and dephosphorylation of EC 2.7.9.2, pyruvate, water dikinase. *cf.* EC 2.7.11.33, [pyruvate, water dikinase] kinase [432].

References: [432]

[EC 2.7.4.28 created 2012]

EC 2.7.4.29

Accepted name: Kdo$_2$-lipid A phosphotransferase

Reaction: *ditrans*-*octacis*-undecaprenyl diphosphate + α-D-Kdo-(2→4)-α-D-Kdo-(2→6)-lipid A = *ditrans*-*octacis*-undecaprenyl phosphate + α-D-Kdo-(2→4)-α-D-Kdo-(2→6)-lipid A 1-diphosphate

Other name(s): lipid A undecaprenyl phosphotransferase; LpxT; YeiU

Systematic name: *ditrans*-*octacis*-undecaprenyl diphosphate:α-D-Kdo-(2→4)-α-D-Kdo-(2→6)-lipid-A phosphotransferase

Comments: An inner-membrane protein. The activity of the enzyme is regulated by PmrA. *In vitro* the enzyme can use diacylglycerol 3-diphosphate as the phosphate donor.

References: [3555, 1305]

[EC 2.7.4.29 created 2015]

[2.7.4.30 Transferred entry. lipid A phosphoethanolamine transferase. Now EC 2.7.8.43, lipid A phosphoethanolamine transferase]

[EC 2.7.4.30 created 2015, deleted 2016]

EC 2.7.4.31

Accepted name: [5-(aminomethyl)furan-3-yl]methyl phosphate kinase

Reaction: ATP + [5-(aminomethyl)furan-3-yl]methyl phosphate = ADP + [5-(aminomethyl)furan-3-yl]methyl diphosphate

Other name(s): MfnE

Systematic name: ATP:[5-(aminomethyl)furan-3-yl]methyl-phosphate phosphotransferase

Comments: Requires Mg^{2+}. The enzyme, isolated from the archaeon *Methanocaldococcus jannaschii*, participates in the biosynthesis of the methanofuran cofactor.
References: [3768]

[EC 2.7.4.31 created 2015]

EC 2.7.4.32
Accepted name: farnesyl phosphate kinase
Reaction: CTP + (2*E*,6*E*)-farnesyl phosphate = CDP + (2*E*,6*E*)-farnesyl diphosphate
Systematic name: CTP:(2*E*,6*E*)-farnesyl-phosphate phosphotransferase
Comments: The enzyme, found in plants and animals, is specific for CTP as phosphate donor. It does not use farnesol as substrate (*cf.* EC 2.7.1.216, farnesol kinase).
References: [273, 912]

[EC 2.7.4.32 created 2017]

EC 2.7.5 Phosphotransferases with regeneration of donors, apparently catalysing intramolecular transfers (deleted sub-subclass)

[2.7.5.1 Transferred entry. phosphoglucomutase. Now EC 5.4.2.2, phosphoglucomutase]

[EC 2.7.5.1 created 1961, deleted 1984]

[2.7.5.2 Transferred entry. acetylglucosamine phosphomutase. Now EC 5.4.2.3, phosphoacetylglucosamine mutase]

[EC 2.7.5.2 created 1961, deleted 1984]

[2.7.5.3 Transferred entry. phosphoglyceromutase. Now EC 5.4.2.1, phosphoglycerate mutase]

[EC 2.7.5.3 created 1961, deleted 1984]

[2.7.5.4 Transferred entry. bisphosphoglyceromutase. Now EC 5.4.2.4, bisphosphoglycerate mutase]

[EC 2.7.5.4 created 1961, deleted 1984]

[2.7.5.5 Transferred entry. phosphoglucomutase (glucose-cofactor). Now EC 5.4.2.5, phosphoglucomutase (glucose-cofactor)]

[EC 2.7.5.5 created 1972, deleted 1984]

[2.7.5.6 Transferred entry. phosphopentomutase. Now EC 5.4.2.7, phosphopentomutase]

[EC 2.7.5.6 created 1972, deleted 1984]

[2.7.5.7 Transferred entry. phosphomannomutase. Now EC 5.4.2.8, phosphomannomutase]

[EC 2.7.5.7 created 1981, deleted 1984]

EC 2.7.6 Diphosphotransferases

EC 2.7.6.1
Accepted name: ribose-phosphate diphosphokinase
Reaction: ATP + D-ribose 5-phosphate = AMP + 5-phospho-α-D-ribose 1-diphosphate
Other name(s): ribose-phosphate pyrophosphokinase; PRPP synthetase; phosphoribosylpyrophosphate synthetase; PPRibP synthetase; *PP*-ribose P synthetase; 5-phosphoribosyl-1-pyrophosphate synthetase; 5-phosphoribose pyrophosphorylase; 5-phosphoribosyl-α-1-pyrophosphate synthetase; phosphoribosyl-diphosphate synthetase; phosphoribosylpyrophosphate synthase; pyrophosphoribosylphosphate synthetase; ribophosphate pyrophosphokinase; ribose-5-phosphate pyrophosphokinase
Systematic name: ATP:D-ribose-5-phosphate diphosphotransferase
Comments: dATP can also act as donor.
References: [1403, 1411, 2870, 3411]

[EC 2.7.6.1 created 1961]

EC 2.7.6.2

Accepted name: thiamine diphosphokinase

Reaction: ATP + thiamine = AMP + thiamine diphosphate

Other name(s): thiamin kinase; thiamine pyrophosphokinase; ATP:thiamin pyrophosphotransferase; thiamin pyrophosphokinase; thiamin pyrophosphotransferase; thiaminokinase; thiamin:ATP pyrophosphotransferase; TPTase

Systematic name: ATP:thiamine diphosphotransferase

References: [1944, 3192, 3342]

[EC 2.7.6.2 created 1961]

EC 2.7.6.3

Accepted name: 2-amino-4-hydroxy-6-hydroxymethyldihydropteridine diphosphokinase

Reaction: ATP + 6-hydroxymethyl-7,8-dihydropterin = AMP + 6-hydroxymethyl-7,8-dihydropterin diphosphate

Other name(s): 2-amino-4-hydroxy-6-hydroxymethyldihydropteridine pyrophosphokinase; H_2-pteridine-CH_2OH pyrophosphokinase; 7,8-dihydroxymethylpterin-pyrophosphokinase; HPPK; 7,8-dihydro-6-hydroxymethylpterin pyrophosphokinase; hydroxymethyldihydropteridine pyrophosphokinase; ATP:2-amino-4-hydroxy-6-hydroxymethyl-7,8-dihydropteridine 6′-diphosphotransferase

Systematic name: ATP:6-hydroxymethyl-7,8-dihydropterin 6′-diphosphotransferase

Comments: Binds 2 Mg^{2+} ions that are essential for activity [2034]. The enzyme participates in the biosynthetic pathways for folate (in bacteria, plants and fungi) and methanopterin (in archaea). The enzyme exists in varying types of multifunctional proteins in different organisms. The enzyme from the bacterium *Streptococcus pneumoniae* also harbours the activity of EC 4.1.2.25, dihydroneopterin aldolase [2034], the enzyme from the plant *Arabidopsis thaliana* harbours the activity of EC 2.5.1.15, dihydropteroate synthase [3358], while the enzyme from yeast *Saccharomyces cerevisiae* is trifunctional with both of the two above mentioned activities [1174].

References: [3208, 2881, 2882, 2034, 329, 1174, 3358]

[EC 2.7.6.3 created 1972, modified 2015]

EC 2.7.6.4

Accepted name: nucleotide diphosphokinase

Reaction: ATP + nucleoside 5′-phosphate = AMP + 5′-phosphonucleoside 3′-diphosphate

Other name(s): nucleotide pyrophosphokinase; ATP:nucleotide pyrophosphotransferase; ATP nucleotide 3′-pyrophosphokinase; nucleotide 3′-pyrophosphokinase

Systematic name: ATP:nucleoside-5′-phosphate diphosphotransferase

Comments: The enzyme acts on the 5′-mono-, di- and triphosphate derivatives of purine nucleosides.

References: [2372, 2471, 2472]

[EC 2.7.6.4 created 1976]

EC 2.7.6.5

Accepted name: GTP diphosphokinase

Reaction: ATP + GTP = AMP + guanosine 3′-diphosphate 5′-triphosphate

Other name(s): stringent factor; guanosine 3′,5′-polyphosphate synthase; GTP pyrophosphokinase; ATP-GTP 3′-diphosphotransferase; guanosine 5′,3′-polyphosphate synthetase; (p)ppGpp synthetase I; (p)ppGpp synthetase II; guanosine pentaphosphate synthetase; GPSI; GPSII

Systematic name: ATP:GTP 3′-diphosphotransferase

Comments: GDP can also act as acceptor.

References: [884, 3412]

[EC 2.7.6.5 created 1981]

EC 2.7.7 Nucleotidyltransferases

EC 2.7.7.1

Accepted name: nicotinamide-nucleotide adenylyltransferase

Reaction: ATP + nicotinamide ribonucleotide = diphosphate + NAD^+

Other name(s): NAD^+ pyrophosphorylase; adenosine triphosphate-nicotinamide mononucleotide transadenylase; ATP:NMN adenylyltransferase; diphosphopyridine nucleotide pyrophosphorylase; nicotinamide adenine dinucleotide pyrophosphorylase; nicotinamide mononucleotide adenylyltransferase; NMN adenylyltransferase

Systematic name: ATP:nicotinamide-nucleotide adenylyltransferase

Comments: Nicotinate nucleotide can also act as acceptor. See also EC 2.7.7.18 nicotinate-nucleotide adenylyltransferase.

References: [124, 658, 1758]

[EC 2.7.7.1 created 1961]

EC 2.7.7.2

Accepted name: FAD synthetase

Reaction: ATP + FMN = diphosphate + FAD

Other name(s): FAD pyrophosphorylase; riboflavin mononucleotide adenylyltransferase; adenosine triphosphate-riboflavin mononucleotide transadenylase; adenosine triphosphate-riboflavine mononucleotide transadenylase; riboflavin adenine dinucleotide pyrophosphorylase; riboflavine adenine dinucleotide adenylyltransferase; flavin adenine dinucleotide synthetase; FADS; FMN adenylyltransferase

Systematic name: ATP:FMN adenylyltransferase

Comments: Requires Mg^{2+} and is highly specific for ATP as phosphate donor [392]. The cofactors FMN and FAD participate in numerous processes in all organisms, including mitochondrial electron transport, photosynthesis, fatty-acid oxidation, and metabolism of vitamin B_6, vitamin B_{12} and folates [3018]. While monofunctional FAD synthetase is found in eukaryotes and in some prokaryotes, most prokaryotes have a bifunctional enzyme that exhibits both this activity and that of EC 2.7.1.26, riboflavin kinase [3018, 392].

References: [1066, 3105, 3018, 2542, 392]

[EC 2.7.7.2 created 1961, modified 2007]

EC 2.7.7.3

Accepted name: pantetheine-phosphate adenylyltransferase

Reaction: ATP + pantetheine 4′-phosphate = diphosphate + 3′-dephospho-CoA

Other name(s): dephospho-CoA pyrophosphorylase; pantetheine phosphate adenylyltransferase; dephospho-coenzyme A pyrophosphorylase; 3′-dephospho-CoA pyrophosphorylase

Systematic name: ATP:pantetheine-4′-phosphate adenylyltransferase

Comments: The enzyme from several bacteria (e.g. *Escherichia coli*, *Bacillus subtilis* and *Haemophilus influenzae*) has been shown to be bifunctional and also to possess the activity of EC 2.3.1.157, glucosamine-1-phosphate *N*-acetyltransferase.

References: [1345, 2492, 2133, 1029, 1476]

[EC 2.7.7.3 created 1961, modified 2002]

EC 2.7.7.4

Accepted name: sulfate adenylyltransferase

Reaction: ATP + sulfate = diphosphate + adenylyl sulfate

Other name(s): ATP-sulfurylase; adenosine-5′-triphosphate sulfurylase; adenosinetriphosphate sulfurylase; adenylylsulfate pyrophosphorylase; ATP sulfurylase; ATP-sulfurylase; sulfurylase
Systematic name: ATP:sulfate adenylyltransferase
Comments: The human phosphoadenosine-phosphosulfate synthase (PAPS) system is a bifunctional enzyme (fusion product of two catalytic activities). In a first step, sulfate adenylyltransferase catalyses the formation of adenosine 5′-phosphosulfate (APS) from ATP and inorganic sulfate. The second step is catalysed by the adenylylsulfate kinase portion of 3′-phosphoadenosine 5′-phosphosulfate (PAPS) synthase, which involves the formation of PAPS from enzyme-bound APS and ATP. In contrast, in bacteria, yeast, fungi and plants, the formation of PAPS is carried out by two individual polypeptides, sulfate adenylyltransferase (EC 2.7.7.4) and adenylyl-sulfate kinase (EC 2.7.1.25).
References: [178, 1332, 3660]

[EC 2.7.7.4 created 1961, modified 1999]

EC 2.7.7.5

Accepted name: sulfate adenylyltransferase (ADP)
Reaction: ADP + sulfate = phosphate + adenylyl sulfate
Other name(s): ADP-sulfurylase; sulfate (adenosine diphosphate) adenylyltransferase; adenosine diphosphate sulfurylase
Systematic name: ADP:sulfate adenylyltransferase
References: [1157, 2892]

[EC 2.7.7.5 created 1961]

EC 2.7.7.6

Accepted name: DNA-directed RNA polymerase
Reaction: nucleoside triphosphate + RNA$_n$ = diphosphate + RNA$_{n+1}$
Other name(s): RNA polymerase; RNA nucleotidyltransferase (DNA-directed); RNA polymerase I; RNA polymerase II; RNA polymerase III; C RNA formation factors; deoxyribonucleic acid-dependent ribonucleic acid polymerase; DNA-dependent ribonucleate nucleotidyltransferase; DNA-dependent RNA nucleotidyltransferase; DNA-dependent RNA polymerase; ribonucleate nucleotidyltransferase; ribonucleate polymerase; C ribonucleic acid formation factors; ribonucleic acid nucleotidyltransferase; ribonucleic acid polymerase; ribonucleic acid transcriptase; ribonucleic polymerase; ribonucleic transcriptase; RNA nucleotidyltransferase; RNA transcriptase; transcriptase; RNA nucleotidyltransferase I
Systematic name: nucleoside-triphosphate:RNA nucleotidyltransferase (DNA-directed)
Comments: Catalyses DNA-template-directed extension of the 3′- end of an RNA strand by one nucleotide at a time. Can initiate a chain *de novo*. In eukaryotes, three forms of the enzyme have been distinguished on the basis of sensitivity to α-amanitin, and the type of RNA synthesized. See also EC 2.7.7.19 (polynucleotide adenylyltransferase) and EC 2.7.7.48 (RNA-directed RNA polymerase).
References: [1777, 2114, 2913, 3171, 3794]

[EC 2.7.7.6 created 1961, modified 1981, modified 1982, modified 1989]

EC 2.7.7.7

Accepted name: DNA-directed DNA polymerase
Reaction: a 2′-deoxyribonucleoside 5′-triphosphate + DNA$_n$ = diphosphate + DNA$_{n+1}$
Other name(s): DNA polymerase I; DNA polymerase II; DNA polymerase III; DNA polymerase α; DNA polymerase β; DNA polymerase γ; DNA nucleotidyltransferase (DNA-directed); deoxyribonucleate nucleotidyltransferase; deoxynucleate polymerase; deoxyribonucleic acid duplicase; deoxyribonucleic acid polymerase; deoxyribonucleic duplicase; deoxyribonucleic polymerase; deoxyribonucleic polymerase I; DNA duplicase; DNA nucleotidyltransferase; DNA polymerase; DNA replicase; DNA-dependent DNA polymerase; duplicase; Klenow fragment; sequenase; Taq DNA polymerase; Taq Pol I; Tca DNA polymerase
Systematic name: 2′-deoxyribonucleoside-5′-triphosphate:DNA deoxynucleotidyltransferase (DNA-directed)

Comments: Catalyses DNA-template-directed extension of the 3′- end of a DNA strand by one nucleotide at a time. Cannot initiate a chain *de novo*. Requires a primer, which may be DNA or RNA. See also EC 2.7.7.49 RNA-directed DNA polymerase.

References: [346, 869, 1914, 2879, 3055, 4082]

[EC 2.7.7.7 created 1961, modified 1981, modified 1982]

EC 2.7.7.8

Accepted name: polyribonucleotide nucleotidyltransferase

Reaction: RNA_{n+1} + phosphate = RNA_n + a nucleoside diphosphate

Other name(s): polynucleotide phosphorylase; PNPase; nucleoside diphosphate:polynucleotidyl transferase; polyribonucleotide nucleotidyltransferase; polynucleotide phosphorylase; polyribonucleotide phosphorylase

Systematic name: polyribonucleotide:phosphate nucleotidyltransferase

Comments: ADP, IDP, GDP, UDP and CDP can act as donors.

References: [1198, 1987, 2507]

[EC 2.7.7.8 created 1961]

EC 2.7.7.9

Accepted name: UTP—glucose-1-phosphate uridylyltransferase

Reaction: UTP + α-D-glucose 1-phosphate = diphosphate + UDP-glucose

Other name(s): UDP glucose pyrophosphorylase; glucose-1-phosphate uridylyltransferase; UDPG phosphorylase; UDPG pyrophosphorylase; uridine 5′-diphosphoglucose pyrophosphorylase; uridine diphosphoglucose pyrophosphorylase; uridine diphosphate-D-glucose pyrophosphorylase; uridine-diphosphate glucose pyrophosphorylase

Systematic name: UTP:α-D-glucose-1-phosphate uridylyltransferase

References: [1561, 1576, 2022, 3258, 3594]

[EC 2.7.7.9 created 1961]

EC 2.7.7.10

Accepted name: UTP—hexose-1-phosphate uridylyltransferase

Reaction: UTP + α-D-galactose 1-phosphate = diphosphate + UDP-α-D-galactose

Other name(s): galactose-1-phosphate uridylyltransferase; galactose 1-phosphate uridylyltransferase; α-D-galactose 1-phosphate uridylyltransferase; galactose 1-phosphate uridyltransferase; UDPgalactose pyrophosphorylase; uridine diphosphate galactose pyrophosphorylase; uridine diphosphogalactose pyrophosphorylase

Systematic name: UTP:α-D-hexose-1-phosphate uridylyltransferase

Comments: α-D-Glucose 1-phosphate can also act as acceptor, but more slowly.

References: [1462, 1561, 1894, 2022]

[EC 2.7.7.10 created 1961]

EC 2.7.7.11

Accepted name: UTP—xylose-1-phosphate uridylyltransferase

Reaction: UTP + α-D-xylose 1-phosphate = diphosphate + UDP-xylose

Other name(s): xylose-1-phosphate uridylyltransferase; uridylyltransferase, xylose 1-phosphate; UDP-xylose pyrophosphorylase; uridine diphosphoxylose pyrophosphorylase; xylose 1-phosphate uridylyltransferase

Systematic name: UTP:α-D-xylose-1-phosphate uridylyltransferase

References: [1064]

[EC 2.7.7.11 created 1961]

EC 2.7.7.12

Accepted name: UDP-glucose—hexose-1-phosphate uridylyltransferase
Reaction: UDP-α-D-glucose + α-D-galactose 1-phosphate = α-D-glucose 1-phosphate + UDP-α-D-galactose
Other name(s): uridyl transferase; hexose-1-phosphate uridylyltransferase; uridyltransferase; hexose 1-phosphate uridyltransferase; UDP-glucose:α-D-galactose-1-phosphate uridylyltransferase
Systematic name: UDP-α-D-glucose:α-D-galactose-1-phosphate uridylyltransferase
References: [1562, 1823, 2182, 3000, 3258]

[EC 2.7.7.12 created 1961]

EC 2.7.7.13

Accepted name: mannose-1-phosphate guanylyltransferase
Reaction: GTP + α-D-mannose 1-phosphate = diphosphate + GDP-mannose
Other name(s): GTP-mannose-1-phosphate guanylyltransferase; PIM-GMP (phosphomannose isomerase-guanosine $5'$-diphospho-D-mannose pyrophosphorylase); GDP-mannose pyrophosphorylase; guanosine $5'$-diphospho-D-mannose pyrophosphorylase; guanosine diphosphomannose pyrophosphorylase; guanosine triphosphate-mannose 1-phosphate guanylyltransferase; mannose 1-phosphate guanylyltransferase (guanosine triphosphate)
Systematic name: GTP:α-D-mannose-1-phosphate guanylyltransferase
Comments: The bacterial enzyme can also use ITP and dGTP as donors.
References: [2361, 2759]

[EC 2.7.7.13 created 1961, modified 1976]

EC 2.7.7.14

Accepted name: ethanolamine-phosphate cytidylyltransferase
Reaction: CTP + ethanolamine phosphate = diphosphate + CDP-ethanolamine
Other name(s): phosphorylethanolamine transferase; ET; CTP-phosphoethanolamine cytidylyltransferase; phosphoethanolamine cytidylyltransferase; ethanolamine phosphate cytidylyltransferase
Systematic name: CTP:ethanolamine-phosphate cytidylyltransferase
References: [1640, 3387, 3687]

[EC 2.7.7.14 created 1961]

EC 2.7.7.15

Accepted name: choline-phosphate cytidylyltransferase
Reaction: CTP + phosphocholine = diphosphate + CDP-choline
Other name(s): phosphorylcholine transferase; CDP-choline pyrophosphorylase; CDP-choline synthetase; choline phosphate cytidylyltransferase; CTP-phosphocholine cytidylyltransferase; CTP:phosphorylcholine cytidylyltransferase; cytidine diphosphocholine pyrophosphorylase; phosphocholine cytidylyltransferase; phosphorylcholine cytidylyltransferase; phosphorylcholine:CTP cytidylyltransferase
Systematic name: CTP:phosphocholine cytidylyltransferase
References: [359, 1640, 3861]

[EC 2.7.7.15 created 1961]

[2.7.7.16 Transferred entry. ribonuclease. Now EC 3.1.27.5, pancreatic ribonuclease]

[EC 2.7.7.16 created 1961, deleted 1972, [transferred to EC 3.1.4.22, deleted 1980]]

[2.7.7.17 Transferred entry. ribonuclease. Now EC 3.1.27.1, ribonuclease T_2]

[EC 2.7.7.17 created 1965, deleted 1972, [transferred to EC 3.1.4.23, deleted 1980]]

EC 2.7.7.18

Accepted name: nicotinate-nucleotide adenylyltransferase

Reaction: ATP + β-nicotinate D-ribonucleotide = diphosphate + deamido-NAD$^+$

Other name(s): deamido-NAD$^+$ pyrophosphorylase; nicotinate mononucleotide adenylyltransferase; deamidonicotinamide adenine dinucleotide pyrophosphorylase; NaMN-ATase; nicotinic acid mononucleotide adenylyltransferase

Systematic name: ATP:β-nicotinate-D-ribonucleotide adenylyltransferase

References: [1444]

[EC 2.7.7.18 created 1965]

EC 2.7.7.19

Accepted name: polynucleotide adenylyltransferase

Reaction: ATP + RNA$_n$ = diphosphate + RNA$_{n+1}$

Other name(s): NTP polymerase; RNA adenylating enzyme; AMP polynucleotidylexotransferase; ATP-polynucleotide adenylyltransferase; ATP:polynucleotidylexotransferase; poly(A) polymerase; poly(A) synthetase; polyadenylate nucleotidyltransferase; polyadenylate polymerase; polyadenylate synthetase; polyadenylic acid polymerase; polyadenylic polymerase; terminal riboadenylate transferase; poly(A) hydrolase; RNA formation factors, PF1; adenosine triphosphate:ribonucleic acid adenylyltransferase

Systematic name: ATP:polynucleotide adenylyltransferase

Comments: Also acts slowly with CTP. Catalyses template-independent extension of the 3′- end of a DNA strand by one nucleotide at a time. Cannot initiate a chain *de novo*. The primer, depending on the source of the enzyme, may be an RNA or DNA fragment, or oligo(A) bearing a 3′-OH terminal group. See also EC 2.7.7.6 DNA-directed RNA polymerase.

References: [128, 808, 1110, 1776, 2114, 3171]

[EC 2.7.7.19 created 1965]

[2.7.7.20 Deleted entry. sRNA nucleotidyl transferase. This entry was identical with EC 2.7.7.25, tRNA adenylyltransferase]

[EC 2.7.7.20 created 1965, deleted 1972]

[2.7.7.21 Transferred entry. tRNA cytidylyltransferase. Now EC 2.7.7.72, CCA tRNA nucleotidyltransferase]

[EC 2.7.7.21 created 1965, deleted 2010]

EC 2.7.7.22

Accepted name: mannose-1-phosphate guanylyltransferase (GDP)

Reaction: GDP + α-D-mannose 1-phosphate = phosphate + GDP-mannose

Other name(s): GDP mannose phosphorylase; mannose 1-phosphate (guanosine diphosphate) guanylyltransferase; GDP mannose phosphorylase; GDP-mannose 1-phosphate guanylyltransferase; guanosine diphosphate-mannose 1-phosphate guanylyltransferase; guanosine diphosphomannose phosphorylase; mannose 1-phosphate guanylyltransferase; GDP:D-mannose-1-phosphate guanylyltransferase

Systematic name: GDP:α-D-mannose-1-phosphate guanylyltransferase

References: [480]

[EC 2.7.7.22 created 1965, modified 1976]

EC 2.7.7.23

Accepted name: UDP-*N*-acetylglucosamine diphosphorylase

Reaction: UTP + *N*-acetyl-α-D-glucosamine 1-phosphate = diphosphate + UDP-*N*-acetyl-α-D-glucosamine

Other name(s): UDP-*N*-acetylglucosamine pyrophosphorylase; uridine diphosphoacetylglucosamine pyrophosphorylase; UTP:2-acetamido-2-deoxy-α-D-glucose-1-phosphate uridylyltransferase; UDP-GlcNAc pyrophosphorylase; GlmU uridylyltransferase; Acetylglucosamine 1-phosphate uridylyltransferase; UDP-acetylglucosamine pyrophosphorylase; uridine diphosphate-*N*-acetylglucosamine pyrophosphorylase; uridine diphosphoacetylglucosamine phosphorylase; acetylglucosamine 1-phosphate uridylyltransferase

Systematic name: UTP:*N*-acetyl-α-D-glucosamine-1-phosphate uridylyltransferase

Comments: Part of the pathway for acetamido sugar biosynthesis in bacteria and archaea. The enzyme from several bacteria (e.g., *Escherichia coli*, *Bacillus subtilis* and *Haemophilus influenzae*) has been shown to be bifunctional and also to possess the activity of EC 2.3.1.157, glucosamine-1-phosphate *N*-acetyltransferase [3,4,6]. The enzyme from plants and animals is also active toward *N*-acetyl-α-D-galactosamine 1-phosphate (*cf.* EC 2.7.7.83, UDP-*N*-acetylgalactosamine diphosphorylase) [3770, 2659], while the bacterial enzyme shows low activity toward that substrate [1033].

References: [2637, 3375, 2221, 1033, 3770, 2560, 2659]

[EC 2.7.7.23 created 1965, modified 2012]

EC 2.7.7.24

Accepted name: glucose-1-phosphate thymidylyltransferase

Reaction: dTTP + α-D-glucose 1-phosphate = diphosphate + dTDP-α-D-glucose

Other name(s): glucose 1-phosphate thymidylyltransferase; dTDP-glucose synthase; dTDP-glucose pyrophosphorylase; thymidine diphosphoglucose pyrophosphorylase; thymidine diphosphate glucose pyrophosphorylase; TDP-glucose pyrophosphorylase

Systematic name: dTTP:α-D-glucose-1-phosphate thymidylyltransferase

Comments: Involved in the biosynthesis of L-rhamnose in bacteria.

References: [1764, 2650, 4089]

[EC 2.7.7.24 created 1965]

[2.7.7.25 Transferred entry. tRNA adenylyltransferase. Now EC 2.7.7.72, CCA tRNA nucleotidyltransferase]

[EC 2.7.7.25 created 1965, deleted 2010]

[2.7.7.26 Transferred entry. nicotinate-nucleotide adenylyltransferase. Now EC 3.1.27.3, ribonuclease T_1]

[EC 2.7.7.26 created 1961 as EC 3.1.4.8, transferred 1965 to EC 2.7.7.26, deleted 1972]

EC 2.7.7.27

Accepted name: glucose-1-phosphate adenylyltransferase

Reaction: ATP + α-D-glucose 1-phosphate = diphosphate + ADP-α-D-glucose

Other name(s): ADP glucose pyrophosphorylase; glucose 1-phosphate adenylyltransferase; adenosine diphosphate glucose pyrophosphorylase; adenosine diphosphoglucose pyrophosphorylase; ADP-glucose pyrophosphorylase; ADP-glucose synthase; ADP-glucose synthetase; ADPG pyrophosphorylase; ADP:α-D-glucose-1-phosphate adenylyltransferase

Systematic name: ATP:α-D-glucose-1-phosphate adenylyltransferase

References: [1043, 3172]

[EC 2.7.7.27 created 1972]

EC 2.7.7.28

Accepted name: nucleoside-triphosphate-aldose-1-phosphate nucleotidyltransferase

Reaction: nucleoside triphosphate + α-D-aldose 1-phosphate = diphosphate + NDP-hexose

Other name(s): NDP hexose pyrophosphorylase; hexose 1-phosphate nucleotidyltransferase; hexose nucleotidylating enzyme; nucleoside diphosphohexose pyrophosphorylase; hexose-1-phosphate guanylyltransferase; GTP:α-D-hexose-1-phosphate guanylyltransferase; GDP hexose pyrophosphorylase; guanosine diphosphohexose pyrophosphorylase; nucleoside-triphosphate-hexose-1-phosphate nucleotidyltransferase; NTP:hexose-1-phosphate nucleotidyltransferase
Systematic name: NTP:α-D-aldose-1-phosphate nucleotidyltransferase
Comments: In decreasing order of activity, guanosine, inosine and adenosine diphosphate hexoses are substrates in the reverse reaction, with either glucose or mannose as the sugar.
References: [3665, 1216]

[EC 2.7.7.28 created 1972, modified 2004 (EC 2.7.7.29 created 1972, incorporated 2004)]

[2.7.7.29 Deleted entry. hexose-1-phosphate guanylyltransferase. Enzyme is not specific for GTP and therefore is identical to EC 2.7.7.28, nucleoside-triphosphate-aldose-1-phosphate nucleotidyltransferase]

[EC 2.7.7.29 created 1972, deleted 2004]

EC 2.7.7.30

Accepted name: fucose-1-phosphate guanylyltransferase
Reaction: GTP + β-L-fucose 1-phosphate = diphosphate + GDP-L-fucose
Other name(s): GDP fucose pyrophosphorylase; guanosine diphosphate L-fucose pyrophosphorylase; GDP-L-fucose pyrophosphorylase; GDP-fucose pyrophosphorylase; GTP:L-fucose-1-phosphate guanylyltransferase
Systematic name: GTP:β-L-fucose-1-phosphate guanylyltransferase
References: [1455]

[EC 2.7.7.30 created 1972]

EC 2.7.7.31

Accepted name: DNA nucleotidylexotransferase
Reaction: 2′-deoxyribonucleoside 5′-triphosphate + DNA$_n$ = diphosphate + DNA$_{n+1}$
Other name(s): terminal deoxyribonucleotidyltransferase; terminal addition enzyme; addase; deoxynucleotidyl terminal transferase; deoxyribonucleic acid nucleotidyltransferase; deoxyribonucleic nucleotidyltransferase; terminal deoxynucleotide transferase; TdT
Systematic name: 2′-deoxyribonucleoside-5′-triphosphate:DNA deoxynucleotidylexotransferase
Comments: Catalyses template-independent extension of the 3′- end of a DNA strand by one nucleotide at a time. Cannot initiate a chain *de novo*. Nucleoside may be ribo- or 2′-deoxyribo-.
References: [347, 1110, 1776]

[EC 2.7.7.31 created 1972]

EC 2.7.7.32

Accepted name: galactose-1-phosphate thymidylyltransferase
Reaction: dTTP + α-D-galactose 1-phosphate = diphosphate + dTDP-galactose
Other name(s): dTDP galactose pyrophosphorylase; galactose 1-phosphate thymidylyl transferase; thymidine diphosphogalactose pyrophosphorylase; thymidine triphosphate:α-D-galactose 1-phosphate thymidylyltransferase
Systematic name: dTTP:α-D-galactose-1-phosphate thymidylyltransferase
References: [2648]

[EC 2.7.7.32 created 1972]

EC 2.7.7.33

Accepted name: glucose-1-phosphate cytidylyltransferase
Reaction: CTP + α-D-glucose 1-phosphate = diphosphate + CDP-glucose

Other name(s): CDP glucose pyrophosphorylase; cytidine diphosphoglucose pyrophosphorylase; cytidine diphosphate glucose pyrophosphorylase; cytidine diphosphate-D-glucose pyrophosphorylase; CTP:D-glucose-1-phosphate cytidylyltransferase
Systematic name: CTP:α-D-glucose-1-phosphate cytidylyltransferase
References: [2181]

[EC 2.7.7.33 created 1972]

EC 2.7.7.34

Accepted name: glucose-1-phosphate guanylyltransferase
Reaction: GTP + α-D-glucose 1-phosphate = diphosphate + GDP-glucose
Other name(s): GDP glucose pyrophosphorylase; guanosine diphosphoglucose pyrophosphorylase
Systematic name: GTP:α-D-glucose-1-phosphate guanylyltransferase
Comments: Also acts, more slowly, on D-mannose 1-phosphate.
References: [668]

[EC 2.7.7.34 created 1972]

EC 2.7.7.35

Accepted name: ADP ribose phosphorylase
Reaction: ADP + D-ribose 5-phosphate = phosphate + ADP-D-ribose
Other name(s): ; ribose-5-phosphate adenylyltransferase (ambiguous); adenosine diphosphoribose phosphorylase (ambiguous)
Systematic name: ADP:D-ribose-5-phosphate adenylyltransferase
Comments: The enzyme, characterized from the single-celled alga *Euglena gracilis*, catalyses an irreversible reaction in the direction of ADP formation. *cf.* EC 2.7.7.96, ADP-D-ribose pyrophosphorylase.
References: [859, 3334]

[EC 2.7.7.35 created 1972, modified 2016]

EC 2.7.7.36

Accepted name: aldose-1-phosphate adenylyltransferase
Reaction: ADP + α-D-aldose 1-phosphate = phosphate + ADP-aldose
Other name(s): sugar-1-phosphate adenylyltransferase; ADPaldose phosphorylase; adenosine diphosphosugar phosphorylase; ADP sugar phosphorylase; adenosine diphosphate glucose:orthophosphate adenylyltransferase; ADP:aldose-1-phosphate adenylyltransferase
Systematic name: ADP:α-D-aldose-1-phosphate adenylyltransferase
References: [669, 2632]

[EC 2.7.7.36 created 1972, modified 1986]

EC 2.7.7.37

Accepted name: aldose-1-phosphate nucleotidyltransferase
Reaction: NDP + α-D-aldose 1-phosphate = phosphate + NDP-aldose
Other name(s): sugar-1-phosphate nucleotidyltransferase; NDPaldose phosphorylase; glucose 1-phosphate inosityltransferase; NDP sugar phosphorylase; nucleoside diphosphosugar phosphorylase; sugar phosphate nucleotidyltransferase; nucleoside diphosphate sugar:orthophosphate nucleotidyltransferase; sugar nucleotide phosphorylase; NDP:aldose-1-phosphate nucleotidyltransferase
Systematic name: NDP:α-D-aldose-1-phosphate nucleotidyltransferase
Comments: The enzyme works on a variety of α-D-aldose 1-phosphates and β-L-aldose 1-phosphates (which have the same anomeric configuration as the former; see 2-Carb-6.2).
References: [448]

[EC 2.7.7.37 created 1972, modified 1986]

EC 2.7.7.38

Accepted name: 3-deoxy-*manno*-octulosonate cytidylyltransferase

Reaction: CTP + 3-deoxy-D-*manno*-octulosonate = diphosphate + CMP-3-deoxy-D-*manno*-octulosonate

Other name(s): CMP-3-deoxy-D-*manno*-octulosonate pyrophosphorylase; 2-keto-3-deoxyoctonate cytidylyltransferase; 3-Deoxy-D-*manno*-octulosonate cytidylyltransferase; CMP-3-deoxy-D-*manno*-octulosonate synthetase; CMP-KDO synthetase; CTP:CMP-3-deoxy-D-*manno*-octulosonate cytidylyltransferase; cytidine monophospho-3-deoxy-D-*manno*-octulosonate pyrophosphorylase

Systematic name: CTP:3-deoxy-D-*manno*-octulosonate cytidylyltransferase

References: [1039]

[EC 2.7.7.38 created 1972]

EC 2.7.7.39

Accepted name: glycerol-3-phosphate cytidylyltransferase

Reaction: CTP + *sn*-glycerol 3-phosphate = diphosphate + CDP-glycerol

Other name(s): CDP-glycerol pyrophosphorylase; cytidine diphosphoglycerol pyrophosphorylase; cytidine diphosphate glycerol pyrophosphorylase; CTP:glycerol 3-phosphate cytidylyltransferase; Gro-PCT; *tagD* (gene name); *tarD* (gene name)

Systematic name: CTP:*sn*-glycerol-3-phosphate cytidylyltransferase

Comments: Involved in the biosynthesis of teichoic acid linkage units in bacterial cell walls.

References: [3162, 2626, 3022, 154, 2638]

[EC 2.7.7.39 created 1972]

EC 2.7.7.40

Accepted name: D-ribitol-5-phosphate cytidylyltransferase

Reaction: CTP + D-ribitol 5-phosphate = diphosphate + CDP-ribitol

Other name(s): CDP ribitol pyrophosphorylase; cytidine diphosphate ribitol pyrophosphorylase; ribitol 5-phosphate cytidylyltransferase; cytidine diphosphoribitol pyrophosphorylase

Systematic name: CTP:D-ribitol-5-phosphate cytidylyltransferase

References: [3162]

[EC 2.7.7.40 created 1972]

EC 2.7.7.41

Accepted name: phosphatidate cytidylyltransferase

Reaction: CTP + phosphatidate = diphosphate + CDP-diacylglycerol

Other name(s): CDP diglyceride pyrophosphorylase; CDP-diacylglycerol synthase; CDP-diacylglyceride synthetase; cytidine diphosphoglyceride pyrophosphorylase; phosphatidate cytidyltransferase; phosphatidic acid cytidylyltransferase; CTP:1,2-diacylglycerophosphate-cytidyl transferase; CTP-diacylglycerol synthetase; DAG synthetase; CDP-DG

Systematic name: CTP:phosphatidate cytidylyltransferase

References: [484, 2184, 2681]

[EC 2.7.7.41 created 1972]

EC 2.7.7.42

Accepted name: [glutamine synthetase] adenylyltransferase

Reaction: ATP + [glutamine synthetase]-L-tyrosine = diphosphate + [glutamine synthetase]-O^{4}-($5'$-adenylyl)-L-tyrosine

Other name(s): glutamine-synthetase adenylyltransferase; ATP:glutamine synthetase adenylyltransferase; adenosine triphosphate:glutamine synthetase adenylyltransferase; ATP:[L-glutamate:ammonia ligase (ADP-forming)] adenylyltransferase; ATP:[L-glutamate:ammonia ligase (ADP-forming)]-L-tyrosine adenylyltransferase; [glutamate—ammonia-ligase] adenylyltransferase
Systematic name: ATP:[glutamine synthetase]-L-tyrosine adenylyltransferase
Comments: This bacterial enzyme adenylates a tyrosine residue of EC 6.3.1.2, glutamine synthetase. The enzyme is bifunctional, and also catalyses a reaction that removes the adenyl group from the modified tyrosine residue (*cf.* EC 2.7.7.89, [glutamine synthetase]-adenylyl-L-tyrosine phosphorylase) [1486, 3930]. The two activities are present on separate domains.
References: [804, 1689, 2202, 2203, 3151, 3880, 1486, 3930]

[EC 2.7.7.42 created 1972, modified 2016]

EC 2.7.7.43

Accepted name: *N*-acylneuraminate cytidylyltransferase
Reaction: CTP + *N*-acylneuraminate = diphosphate + CMP-*N*-acylneuraminate
Other name(s): CMP-sialate pyrophosphorylase; CMP-sialate synthase; cytidine 5′-monophosphosialic acid synthetase; CMP-Neu5Ac synthetase; CMP-NeuAc synthetase; acylneuraminate cytidyltransferase; CMP-*N*-acetylneuraminate synthetase; CMP-*N*-acetylneuraminate synthase; CMP-*N*-acetylneuraminic acid synthase; CMP-NANA synthetase; CMP-sialate synthetase; CMP-sialic synthetase; cytidine 5′-monophospho-*N*-acetylneuraminic acid synthetase; cytidine 5-monophosphate *N*-acetylneuraminic acid synthetase; cytidine monophosphosialic acid synthetase; cytidine monophosphoacetylneuraminic synthetase; cytidine monophosphosialate pyrophosphorylase; cytidine monophosphosialate synthetase; acetylneuraminate cytidylyltransferase
Systematic name: CTP:*N*-acylneuraminate cytidylyltransferase
Comments: Acts on *N*-acetyl- and *N*-glycolyl- derivatives.
References: [1621]

[EC 2.7.7.43 created 1972]

EC 2.7.7.44

Accepted name: glucuronate-1-phosphate uridylyltransferase
Reaction: UTP + 1-phospho-α-D-glucuronate = diphosphate + UDP-α-D-glucuronate
Other name(s): UDP-glucuronate pyrophosphorylase; UDP-D-glucuronic acid pyrophosphorylase; UDP-glucuronic acid pyrophosphorylase; uridine diphosphoglucuronic pyrophosphorylase
Systematic name: UTP:1-phospho-α-D-glucuronate uridylyltransferase
Comments: Also acts slowly with CTP.
References: [2898]

[EC 2.7.7.44 created 1976]

EC 2.7.7.45

Accepted name: guanosine-triphosphate guanylyltransferase
Reaction: **2** GTP = diphosphate + P^1,P^4-bis(5′-guanosyl) tetraphosphate
Other name(s): diguanosine tetraphosphate synthetase; GTP-GTP guanylyltransferase; Gp4G synthetase; guanosine triphosphate-guanose triphosphate guanylyltransferase
Systematic name: GTP:GTP guanylyltransferase
Comments: Also acts, more slowly, on GDP to form P^1,P^3-bis(5′-guanosyl) triphosphate.
References: [3773]

[EC 2.7.7.45 created 1976]

EC 2.7.7.46

Accepted name: gentamicin 2″-nucleotidyltransferase
Reaction: nucleoside triphosphate + gentamicin = diphosphate + 2″-nucleotidylgentamicin
Other name(s): gentamicin 2″-adenylyltransferase; aminoglycoside adenylyltransferase; gentamycin 2″-nucleotidyltransferase
Systematic name: NTP:gentamicin 2″-nucleotidyltransferase
Comments: ATP, dATP, CTP, ITP and GTP can act as donors; kanamycin, tobramycin and sisomicin can also act as acceptors. The nucleotidyl residue is transferred to the 2-hydroxy of the 3-amino-3-deoxy-D-glucose moiety in the antibiotic.
References: [88, 2388, 3935]

[EC 2.7.7.46 created 1976]

EC 2.7.7.47

Accepted name: streptomycin 3″-adenylyltransferase
Reaction: ATP + streptomycin = diphosphate + 3″-adenylylstreptomycin
Other name(s): streptomycin adenylate synthetase; streptomycin adenyltransferase; streptomycin adenylylase; streptomycin adenylyltransferase; streptomycin-spectinomycin adenylyltransferase; AAD (3″); aminoglycoside 3″-adenylyltransferase
Systematic name: ATP:streptomycin 3″-adenylyltransferase
Comments: Also acts on spectinomycin.
References: [1237]

[EC 2.7.7.47 created 1976]

EC 2.7.7.48

Accepted name: RNA-directed RNA polymerase
Reaction: nucleoside triphosphate + RNA_n = diphosphate + RNA_{n+1}
Other name(s): RNA nucleotidyltransferase (RNA-directed); RNA nucleotidyltransferase (RNA-directed); RNA-dependent ribonucleate nucleotidyltransferase; 3D polymerase; PB1 proteins; PB2 proteins; phage f2 replicase; polymerase L; Q-β replicase; phage f2 replicase; ribonucleic acid replicase; ribonucleic acid-dependent ribonucleate nucleotidyltransferase; ribonucleic acid-dependent ribonucleic acid polymerase; ribonucleic replicase; ribonucleic synthetase; RNA replicase; RNA synthetase; RNA transcriptase; RNA-dependent ribonucleate nucleotidyltransferase; RDRP; RNA-dependent RNA polymerase; RNA-dependent RNA replicase; transcriptase
Systematic name: nucleoside-triphosphate:RNA nucleotidyltransferase (RNA-directed)
Comments: Catalyses RNA-template-directed extension of the 3′- end of an RNA strand by one nucleotide at a time. Can initiate a chain *de novo*. See also EC 2.7.7.6 DNA-directed RNA polymerase.
References: [127, 1238, 3810]

[EC 2.7.7.48 created 1981, modified 1982]

EC 2.7.7.49

Accepted name: RNA-directed DNA polymerase
Reaction: a 2′-deoxyribonucleoside 5′-triphosphate + DNA_n = diphosphate + DNA_{n+1}
Other name(s): DNA nucleotidyltransferase (RNA-directed); reverse transcriptase; revertase; RNA-dependent deoxyribonucleate nucleotidyltransferase; RNA revertase; RNA-dependent DNA polymerase; RNA-instructed DNA polymerase; RT
Systematic name: 2′-deoxyribonucleoside-5′-triphosphate:DNA deoxynucleotidyltransferase (RNA-directed)
Comments: Catalyses RNA-template-directed extension of the 3′- end of a DNA strand by one deoxynucleotide at a time. Cannot initiate a chain *de novo*. Requires an RNA or DNA primer. DNA can also serve as template. See also EC 2.7.7.7 DNA-directed DNA polymerase.
References: [175, 3496]

[EC 2.7.7.49 created 1981, modified 1982]

EC 2.7.7.50

Accepted name: mRNA guanylyltransferase

Reaction: GTP + (5′)ppPur-mRNA = diphosphate + G(5′)pppPur-mRNA

Other name(s): mRNA capping enzyme; messenger RNA guanylyltransferase; Protein λ2

Systematic name: GTP:mRNA guanylyltransferase

Comments: The enzyme can also modify synthetic poly(A) and poly(G) to form the structures m^{7}G(5′)pppAn and m^{7}G(5′)pppGn.

References: [842, 1146, 1468, 2141, 2142]

[EC 2.7.7.50 created 1981]

EC 2.7.7.51

Accepted name: adenylylsulfate—ammonia adenylyltransferase

Reaction: adenylyl sulfate + NH_3 = adenosine 5′-phosphoramidate + sulfate

Other name(s): APSAT; adenylylsulfate:ammonia adenylyltransferase

Systematic name: adenylyl-sulfate:ammonia adenylyltransferase

References: [875]

[EC 2.7.7.51 created 1982]

EC 2.7.7.52

Accepted name: RNA uridylyltransferase

Reaction: UTP + RNA_n = diphosphate + RNA_{n+1}

Other name(s): terminal uridylyltransferase; TUT

Systematic name: UTP:RNA uridylyltransferase

Comments: The enzyme requires an oligoribonucleotide or polyribonucleotide with a free terminal 3′-OH as a primer.

References: [4016]

[EC 2.7.7.52 created 1983]

EC 2.7.7.53

Accepted name: ATP adenylyltransferase

Reaction: ADP + ATP = phosphate + P^1,P^4-bis(5′-adenosyl) tetraphosphate

Other name(s): bis(5′-nucleosyl)-tetraphosphate phosphorylase (NDP-forming); diadenosinetetraphosphate αβ-phosphorylase; adenine triphosphate adenylyltransferase; diadenosine 5′,5‴-P^1,P^4-tetraphosphate αβ-phosphorylase (ADP-forming); dinucleoside oligophosphate αβ-phosphorylase

Systematic name: ADP:ATP adenylyltransferase

Comments: GTP and adenosine tetraphosphate can also act as adenylyl acceptors.

References: [1182]

[EC 2.7.7.53 created 1986]

[2.7.7.54 Deleted entry. phenylalanine adenylyltransferase. The activity is part of EC 6.3.2.40, cyclopeptine synthase.]

[EC 2.7.7.54 created 1989, deleted 2013]

[2.7.7.55 Deleted entry. anthranilate adenylyltransferase. The activity is part of EC 6.3.2.40, cyclopeptine synthase.]

[EC 2.7.7.55 created 1989, deleted 2013]

EC 2.7.7.56

Accepted name: tRNA nucleotidyltransferase

Reaction: $tRNA_{n+1}$ + phosphate = $tRNA_n$ + a nucleoside diphosphate

Other name(s): phosphate-dependent exonuclease; RNase PH; ribonuclease PH
Systematic name: tRNA:phosphate nucleotidyltransferase
Comments: Brings about the final exonucleolytic trimming of the $3'$-terminus of tRNA precursors in *Escherichia coli* by a phosphorolysis, producing a mature $3'$-terminus on tRNA and nucleoside diphosphate. Not identical with EC 2.7.7.8 polyribonucleotide nucleotidyltransferase.
References: [636, 725]

[EC 2.7.7.56 created 1992]

EC 2.7.7.57

Accepted name: *N*-methylphosphoethanolamine cytidylyltransferase
Reaction: CTP + *N*-methylethanolamine phosphate = diphosphate + CDP-*N*-methylethanolamine
Other name(s): monomethylethanolamine phosphate cytidylyltransferase; CTP:P-MEA cytidylyltransferase
Systematic name: CTP:*N*-methylethanolamine-phosphate cytidylyltransferase
References: [674]

[EC 2.7.7.57 created 1992]

EC 2.7.7.58

Accepted name: (2,3-dihydroxybenzoyl)adenylate synthase
Reaction: ATP + 2,3-dihydroxybenzoate = diphosphate + (2,3-dihydroxybenzoyl)adenylate
Other name(s): 2,3-dihydroxybenzoate-AMP ligase
Systematic name: ATP:2,3-dihydroxybenzoate adenylyltransferase
References: [2974]

[EC 2.7.7.58 created 1992]

EC 2.7.7.59

Accepted name: [protein-PII] uridylyltransferase
Reaction: UTP + [protein-PII] = diphosphate + uridylyl-[protein-PII]
Other name(s): PII uridylyl-transferase; uridyl removing enzyme
Systematic name: UTP:[protein-PII] uridylyltransferase
Comments: The enzyme uridylylates and de-uridylylates the small trimeric protein PII. The enzymes from *Escherichia coli* and *Salmonella typhimurium* have been wrongly identified, in some databases, as EC 2.7.7.12 (UDP-glucose—hexose-1-phosphate uridylyltransferase), from which it differs greatly in both reaction catalysed and sequence.
References: [1012, 1269]

[EC 2.7.7.59 created 1999]

EC 2.7.7.60

Accepted name: 2-*C*-methyl-D-erythritol 4-phosphate cytidylyltransferase
Reaction: CTP + 2-*C*-methyl-D-erythritol 4-phosphate = diphosphate + 4-(cytidine $5'$-diphospho)-2-*C*-methyl-D-erythritol
Other name(s): MEP cytidylyltransferase
Systematic name: CTP:2-*C*-methyl-D-erythritol 4-phosphate cytidylyltransferase
Comments: The enzyme from *Escherichia coli* requires Mg^{2+} or Mn^{2+}. ATP or UTP can replace CTP, but both are less effective. GTP and TTP are not substrates. Forms part of an alternative nonmevalonate pathway for terpenoid biosynthesis (for diagram, click here).
References: [2918, 1833]

[EC 2.7.7.60 created 2001]

EC 2.7.7.61

Accepted name: citrate lyase holo-[acyl-carrier protein] synthase

Reaction: 2′-(5-triphosphoribosyl)-3′-dephospho-CoA + apo-[citrate (*pro*-3*S*)-lyase] = diphosphate + holo-[citrate (*pro*-3*S*)-lyase]

Other name(s): 2′-(5″-phosphoribosyl)-3′-dephospho-CoA transferase; 2′-(5″-triphosphoribosyl)-3′-dephospho-CoA:apo-citrate lyase; CitX; holo-ACP synthase (ambiguous); 2′-(5″-triphosphoribosyl)-3′-dephospho-CoA:apo-citrate lyase adenylyltransferase; 2′-(5″-triphosphoribosyl)-3′-dephospho-CoA:apo-citrate lyase 2′-(5″-triphosphoribosyl)-3′-dephospho-CoA transferase; 2′-(5″-triphosphoribosyl)-3′-dephospho-CoA:apo-citrate-lyase adenylyltransferase; holo-citrate lyase synthase (incorrect); 2′-(5-triphosphoribosyl)-3′-dephospho-CoA:apo-citrate-lyase 2′-(5-phosphoribosyl)-3′-dephospho-CoA-transferase

Systematic name: 2′-(5-triphosphoribosyl)-3′-dephospho-CoA:apo-[citrate (*pro*-3*S*)-lyase] 2′-(5-phosphoribosyl)-3′-dephospho-CoA-transferase

Comments: The γ-subunit of EC 4.1.3.6, citrate (*pro*-3*S*) lyase, serves as an acyl-carrier protein (ACP) and contains the prosthetic group 2′-(5-triphosphoribosyl)-3′-dephospho-CoA [3091, 3093]. Synthesis and attachment of the prosthetic group requires the concerted action of this enzyme and EC 2.4.2.52, triphosphoribosyl-dephospho-CoA synthase [3091]. In the enzyme from *Escherichia coli*, the prosthetic group is attached to serine-14 of the ACP via a phosphodiester bond.

References: [3091, 3092, 3093]

[EC 2.7.7.61 created 2002, modified 2008]

EC 2.7.7.62

Accepted name: adenosylcobinamide-phosphate guanylyltransferase

Reaction: GTP + adenosylcobinamide phosphate = diphosphate + adenosylcobinamide-GDP

Other name(s): CobU; adenosylcobinamide kinase/adenosylcobinamide-phosphate guanylyltransferase; AdoCbi kinase/AdoCbi-phosphate guanylyltransferase

Systematic name: GTP:adenosylcobinamide-phosphate guanylyltransferase

Comments: In *Salmonella typhimurium* LT2, under anaerobic conditions, CobU (EC 2.7.7.62 and EC 2.7.1.156), CobT (EC 2.4.2.21), CobC (EC 3.1.3.73) and CobS (EC 2.7.8.26) catalyse reactions in the nucleotide loop assembly pathway, which convert adenosylcobinamide (AdoCbi) into adenosylcobalamin (AdoCbl). CobT and CobC are involved in 5,6-dimethylbenzimidazole activation whereby 5,6-dimethylbenzimidazole is converted to its riboside, α-ribazole. The second branch of the nuclotide loop assembly pathway is the cobinamide (Cbi) activation branch where AdoCbi or adenosylcobinamide-phosphate is converted to the activated intermediate AdoCbi-GDP by the bifunctional enzyme Cob U. The final step in adenosylcobalamin biosynthesis is the condensation of AdoCbi-GDP with α-ribazole, which is catalysed by EC 2.7.8.26, cobalamin synthase (CobS), to yield adenosylcobalamin. CobU is a bifunctional enzyme that has both kinase (EC 2.7.1.156) and guanylyltransferase (EC 2.7.7.62) activities. However, both activities are not required at all times.The kinase activity has been proposed to function only when S. typhimurium is assimilating cobinamide whereas the guanylyltransferase activity is required for both assimilation of exogenous cobinamide and for *de novo* synthesis of adenosylcobalamin [3520]. The guanylyltransferase reaction is a two-stage reaction with formation of a CobU-GMP intermediate [2584]. Guanylylation takes place at histidine-46.

References: [2584, 3528, 3529, 3520, 3778]

[EC 2.7.7.62 created 2004]

[2.7.7.63 Transferred entry. lipoate—protein ligase, now EC EC 6.3.1.20, lipoate—protein ligase.]

[EC 2.7.7.63 created 2006, deleted 2016]

EC 2.7.7.64

Accepted name: UTP-monosaccharide-1-phosphate uridylyltransferase

Reaction: UTP + a monosaccharide 1-phosphate = diphosphate + UDP-monosaccharide

Other name(s): UDP-sugar pyrophosphorylase; PsUSP

Comments: Requires Mg^{2+} or Mn^{2+} for maximal activity. The reaction can occur in either direction and it has been postulated that MgUTP and Mg-diphosphate are the actual substrates [1769, 2958]. The enzyme catalyses the formation of UDP-Glc, UDP-Gal, UDP-GlcA, UDP-L-Ara and UDP-Xyl, showing broad substrate specificity towards monosaccharide 1-phosphates. Mannose 1-phosphate, L-Fucose 1-phosphate and glucose 6-phosphate are not substrates and UTP cannot be replaced by other nucleotide triphosphates [1769].

References: [1769, 2958]

[EC 2.7.7.64 created 2006]

EC 2.7.7.65

Accepted name: diguanylate cyclase

Reaction: **2** GTP = **2** diphosphate + cyclic di-3′,5′-guanylate

Other name(s): DGC; PleD

Systematic name: GTP:GTP guanylyltransferase (cyclizing)

Comments: A GGDEF-domain-containing protein that requires Mg^{2+} or Mn^{2+} for activity. The enzyme can be activated by BeF3, a phosphoryl mimic, which results in dimerization [2640]. Dimerization is required but is not sufficient for diguanylate-cyclase activity [2640]. Cyclic di-3′,5′-guanylate is an intracellular signalling molecule that controls motility and adhesion in bacterial cells. It was first identified as having a positive allosteric effect on EC 2.4.1.12, cellulose synthase (UDP-forming) [2982].

References: [2982, 2213, 2640]

[EC 2.7.7.65 created 2008]

EC 2.7.7.66

Accepted name: malonate decarboxylase holo-[acyl-carrier protein] synthase

Reaction: 2′-(5-triphosphoribosyl)-3′-dephospho-CoA + malonate decarboxylase apo-[acyl-carrier protein] = malonate decarboxylase holo-[acyl-carrier protein] + diphosphate

Other name(s): holo ACP synthase (ambiguous); 2′-(5″-triphosphoribosyl)-3′-dephospho-CoA:apo ACP 2′-(5″-triphosphoribosyl)-3′-dephospho-CoA transferase; MdcG; 2′-(5″-triphosphoribosyl)-3′-dephospho-CoA:apo-malonate-decarboxylase adenylyltransferase; holo-malonate-decarboxylase synthase (incorrect)

Systematic name: 2′-(5-triphosphoribosyl)-3′-dephospho-CoA:apo-malonate-decarboxylase 2′-(5-phosphoribosyl)-3′-dephospho-CoA-transferase

Comments: The δ subunit of malonate decarboxylase serves as an an acyl-carrier protein (ACP) and contains the prosthetic group 2-(5-triphosphoribosyl)-3-dephospho-CoA. Two reactions are involved in the production of the holo-ACP form of this enzyme. The first reaction is catalysed by EC 2.4.2.52, triphosphoribosyl-dephospho-CoA synthase. The resulting prosthetic group is then attached to the ACP subunit via a phosphodiester linkage to a serine residue, thus forming the holo form of the enzyme, in a manner analogous to that of EC 2.7.7.61, citrate lyase holo-[acyl-carrier protein] synthase.

References: [1351, 1350]

[EC 2.7.7.66 created 2008]

EC 2.7.7.67

Accepted name: CDP-2,3-bis-(*O*-geranylgeranyl)-*sn*-glycerol synthase

Reaction: CTP + 2,3-bis-(*O*-geranylgeranyl)-*sn*-glycerol 1-phosphate = diphosphate + CDP-2,3-bis-(*O*-geranylgeranyl)-*sn*-glycerol

Other name(s): *carS* (gene name); CDP-2,3-di-*O*-geranylgeranyl-*sn*-glycerol synthase; CTP:2,3-GG-GP ether cytidylyltransferase; CTP:2,3-di-*O*-geranylgeranyl-*sn*-glycero-1-phosphate cytidyltransferase; CDP-2,3-bis-*O*-(geranylgeranyl)-*sn*-glycerol synthase; CTP:2,3-bis-*O*-(geranylgeranyl)-*sn*-glycero-1-phosphate cytidylyltransferase; CDP-unsaturated archaeol synthase; CDP-archaeol synthase (incorrect)

Systematic name: CTP:2,3-bis-(*O*-geranylgeranyl)-*sn*-glycerol 1-phosphate cytidylyltransferase

Comments: This enzyme catalyses one of the steps in the biosynthesis of polar lipids in archaea, which are characterized by having an *sn*-glycerol 1-phosphate backbone rather than an *sn*-glycerol 3-phosphate backbone as is found in bacteria and eukaryotes [2317]. The enzyme requires Mg^{2+} and K^{+} for maximal activity [2317].

References: [2317, 2316, 1490]

[EC 2.7.7.67 created 2009, modified 2014]

EC 2.7.7.68

Accepted name: 2-phospho-L-lactate guanylyltransferase

Reaction: (2*S*)-2-phospholactate + GTP = (2*S*)-lactyl-2-diphospho-5′-guanosine + diphosphate

Other name(s): CofC; MJ0887

Systematic name: GTP:2-phospho-L-lactate guanylyltransferase

Comments: This enzyme is involved in the biosynthesis of coenzyme F_{420}, a redox-active cofactor found in all methanogenic archaea, as well as some eubacteria.

References: [1144]

[EC 2.7.7.68 created 2010]

EC 2.7.7.69

Accepted name: GDP-L-galactose phosphorylase

Reaction: GDP-β-L-galactose + phosphate = β-L-galactose 1-phosphate + GDP

Other name(s): VTC2; VTC5

Systematic name: GDP:α-L-galactose 1-phosphate guanylyltransferase

Comments: The enzyme catalyses a reaction of the Smirnoff-Wheeler pathway, the major route to ascorbate biosynthesis in plants.

References: [1981, 1980, 769, 2353]

[EC 2.7.7.69 created 2010]

EC 2.7.7.70

Accepted name: D-*glycero*-β-D-*manno*-heptose 1-phosphate adenylyltransferase

Reaction: D-*glycero*-β-D-*manno*-heptose 1-phosphate + ATP = ADP-D-*glycero*-β-D-*manno*-heptose + diphosphate

Other name(s): D-β-D-heptose 7-phosphate kinase/D-β-D-heptose 1-phosphate adenylyltransferase; D-*glycero*-D-*manno*-heptose-1β-phosphate adenylyltransferase; *hldE* (gene name); *rfaE* (gene name)

Systematic name: ATP:D-*glycero*-β-D-*manno*-heptose 1-phosphate adenylyltransferase

Comments: The bifunctional protein *hldE* includes D-*glycero*-β-D-*manno*-heptose-7-phosphate kinase and D-*glycero*-β-D-*manno*-heptose 1-phosphate adenylyltransferase activity (*cf.* EC 2.7.1.167). The enzyme is involved in biosynthesis of ADP-L-*glycero*-β-D-*manno*-heptose, which is utilized for assembly of the lipopolysaccharide inner core in Gram-negative bacteria.

References: [3630, 1716, 3631, 3753]

[EC 2.7.7.70 created 2010]

EC 2.7.7.71

Accepted name: D-*glycero*-α-D-*manno*-heptose 1-phosphate guanylyltransferase

Reaction: D-*glycero*-α-D-*manno*-heptose 1-phosphate + GTP = GDP-D-*glycero*-α-D-*manno*-heptose + diphosphate

Other name(s): *hddC* (gene name); *gmhD* (gene name)

Systematic name: GTP:D-*glycero*-α-D-*manno*-heptose 1-phosphate guanylyltransferase

Comments: The enzyme is involved in biosynthesis of GDP-D-*glycero*-α-D-*manno*-heptose, which is required for assembly of S-layer glycoprotein in some Gram-positive bacteria.

References: [1715]

[EC 2.7.7.71 created 2010]

EC 2.7.7.72

Accepted name: CCA tRNA nucleotidyltransferase

Reaction: a tRNA precursor + **2** CTP + ATP = a tRNA with a 3′ CCA end + **3** diphosphate (overall reaction)
(1a) a tRNA precursor + CTP = a tRNA with a 3′ cytidine end + diphosphate
(1b) a tRNA with a 3′ cytidine + CTP = a tRNA with a 3′ CC end + diphosphate
(1c) a tRNA with a 3′ CC end + ATP = a tRNA with a 3′ CCA end + diphosphate

Other name(s): CCA-adding enzyme; tRNA adenylyltransferase; tRNA cytidylyltransferase; tRNA CCA-pyrophosphorylase; tRNA-nucleotidyltransferase; transfer-RNA nucleotidyltransferase; transfer ribonucleic acid nucleotidyl transferase; CTP(ATP):tRNA nucleotidyltransferase; transfer ribonucleate adenylyltransferase; transfer ribonucleate adenyltransferase; transfer RNA adenylyltransferase; transfer ribonucleate nucleotidyltransferase; ATP (CTP):tRNA nucleotidyltransferase; ribonucleic cytidylic cytidylic adenylic pyrophosphorylase; transfer ribonucleic adenylyl (cytidylyl) transferase; transfer ribonucleic-terminal trinucleotide nucleotidyltransferase; transfer ribonucleate cytidylyltransferase; ribonucleic cytidylyltransferase; -C-C-A pyrophosphorylase; ATP(CTP)-tRNA nucleotidyltransferase; tRNA adenylyl(cytidylyl)transferase; CTP:tRNA cytidylyltransferase

Systematic name: CTP,CTP,ATP:tRNA cytidylyl,cytidylyl,adenylyltransferase

Comments: The acylation of all tRNAs with an amino acid occurs at the terminal ribose of a 3′ CCA sequence. The CCA sequence is added to the tRNA precursor by stepwise nucleotide addition performed by a single enzyme that is ubiquitous in all living organisms. Although the enzyme has the option of releasing the product after each addition, it prefers to stay bound to the product and proceed with the next addition [1378].

References: [3101, 3181, 129, 3938, 1378]

[EC 2.7.7.72 created 1965 as EC 2.7.7.21 and EC 2.7.7.25, both transferred 2010 to EC 2.7.7.72]

EC 2.7.7.73

Accepted name: sulfur carrier protein ThiS adenylyltransferase

Reaction: ATP + [ThiS] = diphosphate + adenylyl-[ThiS]

Other name(s): *thiF* (gene name)

Systematic name: ATP:[ThiS] adenylyltransferase

Comments: Binds Zn^{2+}. The enzyme catalyses the adenylation of ThiS, a sulfur carrier protein involved in the biosynthesis of thiamine. The enzyme shows significant structural similarity to ubiquitin-activating enzyme [783, 1915]. In *Escherichia coli*, but not in *Bacillus subtilis*, the enzyme forms a cross link from Cys-184 to the ThiS carboxy terminus (the position that is also thiolated) via an acyldisulfide [3917].

References: [3487, 3917, 783, 1915]

[EC 2.7.7.73 created 2011]

EC 2.7.7.74

Accepted name: 1L-*myo*-inositol 1-phosphate cytidylyltransferase

Reaction: CTP + 1L-*myo*-inositol 1-phosphate = diphosphate + CDP-1L-*myo*-inositol

Other name(s): CTP:inositol-1-phosphate cytidylyltransferase (bifunctional CTP:inositol-1-phosphate cytidylyltransferase/CDP-inositol:inositol-1-phosphate transferase (IPCT/DIPPS)); IPCT (bifunctional CTP:inositol-1-phosphate cytidylyltransferase/CDP-inositol:inositol-1-phosphate transferase (IPCT/DIPPS)); L-*myo*-inositol-1-phosphate cytidylyltransferase

Systematic name: CTP:1L-*myo*-inositol 1-phosphate cytidylyltransferase

Comments: In many organisms this activity is catalysed by a bifunctional enzyme. The cytidylyltransferase domain of the bifunctional EC 2.7.7.74/EC 2.7.8.34 (CTP:inositol-1-phosphate cytidylyltransferase/CDP-inositol:inositol-1-phosphate transferase) is absolutely specific for CTP and 1L-*myo*-inositol 1-phosphate. The enzyme is involved in biosynthesis of bis(1L-*myo*-inositol) 1,3′-phosphate, a widespread organic solute in microorganisms adapted to hot environments.

References: [2909]

[EC 2.7.7.74 created 2011]

EC 2.7.7.75

Accepted name: molybdopterin adenylyltransferase
Reaction: ATP + molybdopterin = diphosphate + adenylyl-molybdopterin
Other name(s): MogA; Cnx1 (ambiguous)
Systematic name: ATP:molybdopterin adenylyltransferase
Comments: Catalyses the activation of molybdopterin for molybdenum insertion. In eukaryotes, this reaction is catalysed by the C-terminal domain of a fusion protein that also includes molybdopterin molybdotransferase (EC 2.10.1.1). The reaction requires a divalent cation such as Mg^{2+} or Mn^{2+}.
References: [2449, 1822, 2017]

[EC 2.7.7.75 created 2011]

EC 2.7.7.76

Accepted name: molybdenum cofactor cytidylyltransferase
Reaction: CTP + molybdenum cofactor = diphosphate + cytidylyl molybdenum cofactor
Other name(s): MocA; CTP:molybdopterin cytidylyltransferase; MoCo cytidylyltransferase; Mo-MPT cytidylyltransferase
Systematic name: CTP:molybdenum cofactor cytidylyltransferase
Comments: Catalyses the cytidylation of the molybdenum cofactor. This modification occurs only in prokaryotes. Divalent cations such as Mg^{2+} or Mn^{2+} are required for activity. ATP or GTP cannot replace CTP.
References: [2442, 2443]

[EC 2.7.7.76 created 2011]

EC 2.7.7.77

Accepted name: molybdenum cofactor guanylyltransferase
Reaction: GTP + molybdenum cofactor = diphosphate + guanylyl molybdenum cofactor
Other name(s): MobA; MoCo guanylyltransferase
Systematic name: GTP:molybdenum cofactor guanylyltransferase
Comments: Catalyses the guanylation of the molybdenum cofactor. This modification occurs only in prokaryotes.
References: [1848, 3498, 1183]

[EC 2.7.7.77 created 2011]

EC 2.7.7.78

Accepted name: GDP-D-glucose phosphorylase
Reaction: GDP-α-D-glucose + phosphate = α-D-glucose 1-phosphate + GDP
Systematic name: GDP:α-D-glucose 1-phosphate guanylyltransferase
Comments: The enzyme may be involved in prevention of misincorporation of glucose in place of mannose residues into glycoconjugates i.e. to remove accidentally produced GDP-α-D-glucose. Activities with GDP-L-galactose, GDP-D-mannose and UDP-D-glucose are all less than 3% that with GDP-D-glucose.
References: [18]

[EC 2.7.7.78 created 2011]

EC 2.7.7.79

Accepted name: tRNA^{His} guanylyltransferase
Reaction: p-tRNA^{His} + ATP + GTP + H_2O = pGp-tRNA^{His} + AMP + **2** diphosphate (overall reaction)
(1a) p-tRNA^{His} + ATP = App-tRNA^{His} + diphosphate

(1b) App-tRNA^{His} + GTP = pppGp-tRNA^{His} + AMP
(1c) pppGp-tRNA^{His} + H_2O = pGp-tRNA^{His} + diphosphate

Other name(s): histidine tRNA guanylyltransferase; Thg1p (ambiguous); Thg1 (ambiguous)

Systematic name: p-tRNA^{His}:GTP guanylyltransferase (ATP-hydrolysing)

Comments: In eukarya an additional guanosine residue is added post-transcriptionally to the $5'$-end of tRNA^{His} molecules. The addition occurs opposite a universally conserved adenosine^{73} and is thus the result of a non-templated $3'$-$5'$ addition reaction. The additional guanosine residue is an important determinant for aminoacylation by EC 6.1.1.21, histidine—tRNA ligase.The enzyme requires a divalent cation for activity [2611]. ATP activation is not required when the substrate contains a $5'$-triphosphate (ppp-tRNA^{His}) [1164].

References: [1487, 2611, 1164, 2722, 1481, 1421]

[EC 2.7.7.79 created 2011]

EC 2.7.7.80

Accepted name: molybdopterin-synthase adenylyltransferase

Reaction: ATP + [molybdopterin-synthase sulfur-carrier protein]-Gly-Gly = diphosphate + [molybdopterin-synthase sulfur-carrier protein]-Gly-Gly-AMP

Other name(s): MoeB; adenylyltransferase and sulfurtransferase MOCS3

Systematic name: ATP:molybdopterin-synthase adenylyltransferase

Comments: Adenylates the C-terminus of the small subunit of the molybdopterin synthase. This activation is required to form the thiocarboxylated C-terminus of the active molybdopterin synthase small subunit. The reaction occurs in prokaryotes and eukaryotes. In the human, the reaction is catalysed by the N-terminal domain of the protein MOCS3, which also includes a molybdopterin-synthase sulfurtransferase (EC 2.8.1.11) C-terminal domain.

References: [1923, 2169]

[EC 2.7.7.80 created 2011]

EC 2.7.7.81

Accepted name: pseudaminic acid cytidylyltransferase

Reaction: CTP + 5,7-diacetamido-3,5,7,9-tetradeoxy-L-*glycero*-α-L-*manno*-2-nonulopyranosonic acid = diphosphate + CMP-5,7-diacetamido-3,5,7,9-tetradeoxy-L-*glycero*-α-L-*manno*-2-nonulopyranosonic acid

Other name(s): PseF

Systematic name: CTP:5,7-diacetamido-3,5,7,9-tetradeoxy-L-*glycero*-α-L-*manno*-nonulosonic acid cytidylyltransferase

Comments: Mg^{2+} is required for activity.

References: [3098]

[EC 2.7.7.81 created 2012]

EC 2.7.7.82

Accepted name: CMP-*N*,*N*′-diacetyllegionaminic acid synthase

Reaction: CTP + *N*,*N*′-diacetyllegionaminate = CMP-*N*,*N*′-diacetyllegionaminate + diphosphate

Other name(s): CMP-*N*,*N*′-diacetyllegionaminic acid synthetase; *neuA* (gene name); *legF* (gene name)

Systematic name: CTP:*N*,*N*′-diacetyllegionaminate cytidylyltransferase

Comments: Isolated from the bacteria *Legionella pneumophila* and *Campylobacter jejuni*. Involved in biosynthesis of legionaminic acid, a sialic acid-like derivative that is incorporated into virulence-associated cell surface glycoconjugates which may include lipopolysaccharide (LPS), capsular polysaccharide, pili and flagella.

References: [1074, 3100]

[EC 2.7.7.82 created 2012]

EC 2.7.7.83

Accepted name: UDP-*N*-acetylgalactosamine diphosphorylase
Reaction: UTP + *N*-acetyl-α-D-galactosamine 1-phosphate = diphosphate + UDP-*N*-acetyl-α-D-galactosamine
Systematic name: UTP:*N*-acetyl-α-D-galactosamine-1-phosphate uridylyltransferase
Comments: The enzyme from plants and animals also has activity toward *N*-acetyl-α-D-glucosamine 1-phosphate (*cf.* EC 2.7.7.23, UDP-*N*-acetylglucosamine diphosphorylase) [3770, 2659].
References: [3770, 2659]

[EC 2.7.7.83 created 2012]

EC 2.7.7.84

Accepted name: 2′-5′ oligoadenylate synthase
Reaction: **3** ATP = pppA2′p5’A2′p5’A + **2** diphosphate
Other name(s): OAS
Systematic name: ATP:ATP adenylyltransferase (2′-5′ linkages-forming)
Comments: The enzyme is activated by binding to double-stranded RNA. The resulting product binds to and activates RNase L, which subsequently degrades the RNA. Oligoadenylates of chain lengths 2, 4 and 5 are also produced. The dimer does not have any known biological activity [2135].
References: [1646, 2135, 1236, 1381]

[EC 2.7.7.84 created 2013]

EC 2.7.7.85

Accepted name: diadenylate cyclase
Reaction: **2** ATP = **2** diphosphate + cyclic di-3′,5′-adenylate
Other name(s): cyclic-di-AMP synthase; *dacA* (gene name); *disA* (gene name)
Systematic name: ATP:ATP adenylyltransferase (cyclizing)
Comments: Cyclic di-3′,5′-adenylate is a bioactive molecule produced by some bacteria and archaea, which may function as a secondary signalling molecule [3876]. The intracellular bacterial pathogen *Listeria monocytogenes* secretes it into the host’s cytosol, where it triggers a cytosolic pathway of innate immunity [3892].
References: [3876, 3892]

[EC 2.7.7.85 created 2013]

EC 2.7.7.86

Accepted name: cyclic GMP-AMP synthase
Reaction: ATP + GTP = **2** diphosphate + cyclic Gp(2′-5′)Ap(3′-5′) (overall reaction)
(1a) ATP + GTP = pppGp(2′-5′)A + diphosphate
(1b) pppGp(2′-5′)A = cyclic Gp(2′-5′)Ap(3′-5′) + diphosphate
Other name(s): cGAMP synthase; cGAS
Systematic name: ATP:GTP adenylyltransferase (cyclizing)
Comments: Cyclic Gp(2′-5′)Ap(3′-5′) is a signalling molecule in mammalian cells that triggers the production of type I interferons and other cytokines.
References: [3386, 8]

[EC 2.7.7.86 created 2013, modified 2014]

EC 2.7.7.87

Accepted name: L-threonylcarbamoyladenylate synthase
Reaction: L-threonine + ATP + HCO_3^- = L-threonylcarbamoyladenylate + diphosphate + H_2O
Other name(s): *yrdC* (gene name); Sua5; *ywlC* (gene name); ATP:L-threonyl,bicarbonate adenylyltransferase
Systematic name: ATP:L-threonyl,HCO_3^- adenylyltransferase

Comments: The enzyme is involved in the synthesis of N^6-threonylcarbamoyladenosine^{37} in tRNAs, with the anticodon NNU, i.e. tRNA^{Ile}, tRNA^{Thr}, tRNA^{Asn}, tRNA^{Lys}, tRNA^{Ser} and tRNA^{Arg} [2668].

References: [3934, 1230, 1825, 1875, 723, 2668, 3744]

[EC 2.7.7.87 created 2013]

EC 2.7.7.88

Accepted name: GDP polyribonucleotidyltransferase

Reaction: 5′-triphospho-mRNA + GDP = diphosphate + guanosine 5′-triphospho-mRNA

Systematic name: 5′-triphospho-mRNA:GDP 5′-phosphopolyribonucleotidyltransferase [G(5′)ppp-mRNA-forming]

Comments: The enzyme from rhabdoviruses transfers 5′-monophosphorylated (*p*-)mRNA from 5′-triphosphorylated (ppp-)mRNA to GDP to form 5′-capped mRNA (GpppmRNA) in a viral mRNA-start sequence-dependent manner. The (*p*-)mRNA transfer reaction proceeds through a covalent enzyme-pmRNA intermediate.

References: [2522, 2523, 2521, 2520, 2519]

[EC 2.7.7.88 created 2015]

EC 2.7.7.89

Accepted name: [glutamine synthetase]-adenylyl-L-tyrosine phosphorylase

Reaction: [glutamine synthetase]-O^4-(5′-adenylyl)-L-tyrosine + phosphate = [glutamine synthetase]-L-tyrosine + ADP

Other name(s): adenylyl-[glutamine—synthetase]-deadenylase; [L-glutamate:ammonia ligase (ADP-forming)]-O^4-(5′-adenylyl)-L-tyrosine:phosphate adenylyltransferase; [glutamate—ammonia ligase]-adenylyl-L-tyrosine phosphorylase

Systematic name: [glutamine synthetase]-O^4-(5′-adenylyl)-L-tyrosine:phosphate adenylyltransferase

Comments: This bacterial enzyme removes an adenylyl group from a modified tyrosine residue of EC 6.3.1.2, glutamine synthetase. The enzyme is bifunctional, and also performs the adenylation of this residue (*cf.* EC 2.7.7.42, [glutamine synthetase] adenylyltransferase) [1486, 3930]. The two activities are present on separate domains.

References: [81, 82, 1486, 3929, 3930]

[EC 2.7.7.89 created 1972 as EC 3.1.4.15, transferred 2015 to EC 2.7.7.89, modified 2016]

EC 2.7.7.90

Accepted name: 8-amino-3,8-dideoxy-*manno*-octulosonate cytidylyltransferase

Reaction: CTP + 8-amino-3,8-dideoxy-α-D-*manno*-octulosonate = diphosphate + CMP-8-amino-3,8-dideoxy-α-D-*manno*-octulosonate

Other name(s): *kdsB* (gene name, ambiguous)

Systematic name: CTP:8-amino-3,8-dideoxy-α-D-*manno*-octulosonate cytidylyltransferase

Comments: The enzyme, characterized from the bacterium *Shewanella oneidensis* MR-1, acts on the 8-aminated from of 3-deoxy-α-D-*manno*-octulosonate (Kdo). *cf.* EC 2.7.7.38, 3-deoxy-*manno*-octulosonate cytidylyltransferase.

References: [1025]

[EC 2.7.7.90 created 2016]

EC 2.7.7.91

Accepted name: valienol-1-phosphate guanylyltransferase

Reaction: GTP + valienol 1-phosphate = diphosphate + GDP-valienol

Other name(s): *vldB* (gene name)

Systematic name: GTP:valienol 1-phosphate guanylyltransferase

Comments: The enzyme, characterized from the bacterium *Streptomyces hygroscopicus* subsp. *limoneus*, is involved in the biosynthesis of the antifungal agent validamycin A.

References: [3962, 118]

[EC 2.7.7.91 created 2016]

EC 2.7.7.92

Accepted name: 3-deoxy-D-*glycero*-D-*galacto*-nonulopyranosonate cytidylyltransferase

Reaction: CTP + 3-deoxy-D-*glycero*-D-*galacto*-non-2-ulopyranosonate = diphosphate + CMP-3-deoxy-D-*glycero*-D-*galacto*-non-2-ulopyranosonate

Systematic name: CTP:3-deoxy-D-*glycero*-D-*galacto*-non-2-ulopyranosonate cytidylyltransferase

Comments: The enzyme is part of the biosynthesis pathway of the sialic acid 3-deoxy-D-*glycero*-D-*galacto*-non-2-ulopyranosonate (Kdn). Kdn is abundant in extracellular glycoconjugates of lower vertebrates such as fish and amphibians, but is also found in the capsular polysaccharides of bacteria that belong to the *Bacteroides* genus.

References: [3502, 3501, 2414, 3536, 3754]

[EC 2.7.7.92 created 2016]

EC 2.7.7.93

Accepted name: phosphonoformate cytidylyltransferase

Reaction: CTP + phosphonoformate = CMP-5′-phosphonoformate + diphosphate

Other name(s): *phpF* (gene name)

Systematic name: CTP:phosphonoformate cytidylyltransferase

Comments: The enzyme, characterized from the bacterium *Streptomyces viridochromogenes*, participates in the biosynthesis of the herbicide antibiotic bialaphos. The enzyme from the bacterium *Kitasatospora phosalacinea* participates in the biosynthesis of the related compound phosalacine. Both compounds contain the nonproteinogenic amino acid L-phosphinothricin that acts as a potent inhibitor of EC 6.3.1.2, glutamine synthetase.

References: [333]

[EC 2.7.7.93 created 2016]

[2.7.7.94 Transferred entry. 4-hydroxyphenylalkanoate adenylyltransferase. Now EC 6.2.1.51, 4-hydroxyphenylalkanoate adenylyltransferase FadD29]

[EC 2.7.7.94 created 2016, deleted 2017]

[2.7.7.95 Transferred entry. mycocerosic acid adenylyltransferase. Now EC 6.2.1.49, long-chain fatty acid adenylyltransferase FadD28]

[EC 2.7.7.95 created 2016, deleted 2017]

EC 2.7.7.96

Accepted name: ADP-D-ribose pyrophosphorylase

Reaction: ATP + D-ribose 5-phosphate = diphosphate + ADP-D-ribose

Other name(s): NUDIX5; NUDT5 (gene name); diphosphate—ADP-D-ribose adenylyltransferase; diphosphate adenylyltransferase (ambiguous)

Systematic name: ATP:D-ribose 5-phosphate adenylyltransferase

Comments: The human enzyme produces ATP in nuclei in situations of high energy demand, such as chromatin remodeling. The reaction is dependent on the presence of diphosphate. In its absence the enzyme catalyses the reaction of EC 3.6.1.13, ADP-ribose diphosphatase. *cf.* EC 2.7.7.35, ADP ribose phosphorylase.

References: [3899]

[EC 2.7.7.96 created 2016]

EC 2.7.7.97

Accepted name: 3-hydroxy-4-methylanthranilate adenylyltransferase

Reaction: ATP + 3-hydroxy-4-methylanthranilate = diphosphate + 3-hydroxy-4-methylanthranilyl-adenylate

Other name(s): *acmA* (gene name); *sibE* (gene name); actinomycin synthase I; 4-MHA-activating enzyme; ACMS I; actinomycin synthetase I; 4-MHA pentapeptide lactone synthase AcmA

Systematic name: ATP:3-hydroxy-4-methylanthranilate adenylyltransferase

Comments: The enzyme, characterized from the bacteria *Streptomyces anulatus* and *Streptosporangium sibiricum*, activates 3-hydroxy-4-methylanthranilate, a precursor of actinomycin antibiotics and the antitumor antibiotic sibiromycin, to an adenylate form, so it can be loaded onto a dedicated aryl-carrier protein.

References: [2684, 1056]

[EC 2.7.7.97 created 2016]

[2.7.7.98 Transferred entry. 4-hydroxybenzoate adenylyltransferase. Now EC 6.2.1.50, 4-hydroxybenzoate adenylyltransferase FadD22]

[EC 2.7.7.98 created 2017, deleted 2017]

EC 2.7.7.99

Accepted name: *N*-acetyl-α-D-muramate 1-phosphate uridylyltransferase

Reaction: UDP + *N*-acetyl-α-D-muramate 1-phosphate = UDP-*N*-acetyl-α-D-muramate + phosphate

Other name(s): *murU* (gene name)

Systematic name: UDP:*N*-acetyl-α-D-muramate 1-phosphate uridylyltransferase

Comments: The enzyme, characterized from *Pseudomonas* species, participates in a peptidoglycan salvage pathway.

References: [1068, 2872]

[EC 2.7.7.99 created 2017]

EC 2.7.7.100

Accepted name: SAMP-activating enzyme

Reaction: ATP + [SAMP]-Gly-Gly = diphosphate + [SAMP]-Gly-Gly-AMP

Other name(s): UbaA (ambiguous); SAMP-activating enzyme E1 (ambiguous)

Systematic name: ATP:[SAMP]-Gly-Gly adenylyltransferase

Comments: Contains Zn^{2+}. The enzyme catalyses the activation of SAMPs (Small Archaeal Modifier Proteins), which are ubiquitin-like proteins found only in the Archaea, by catalysing the ATP-dependent formation of a SAMP adenylate in which the C-terminal glycine of SAMP is bound to AMP via an acyl-phosphate linkage. The product of this activity can accept a sulfur atom to form a thiocarboxylate moiety that acts as a sulfur carrier involved in thiolation of tRNA and other metabolites such as molybdopterin. Alternatively, the enzyme can also catalyse the transfer of SAMP from its activated form to an internal cysteine residue, leading to a process termed SAMPylation (see EC 6.2.1.55, E1 SAMP-activating enzyme).

References: [2266, 2173, 1301]

[EC 2.7.7.100 created 2018]

EC 2.7.7.101

Accepted name: DNA primase DnaG

Reaction: ssDNA + $\boldsymbol{n}$ NTP = ssDNA/pppN$(pN)_{n-1}$ hybrid + ($\boldsymbol{n}$**-1**) diphosphate

Other name(s): DnaG

Systematic name: nucleotide $5'$-triphosphate:single-stranded DNA nucleotidyltransferase (DNA-RNA hybrid synthesizing)

Comments: The enzyme catalyses the synthesis of short RNA sequences that are used as primers for EC 2.7.7.7, DNA-directed DNA polymerase. It is found in bacteria and archaea. The latter also have a second primase system (EC 2.7.7.102, DNA primase AEP).

References:	[2949, 1440, 960, 4090]

[EC 2.7.7.101 created 2018]

EC 2.7.7.102

Accepted name:	DNA primase AEP
Reaction:	(1) ssDNA + $\boldsymbol{n}$ NTP = ssDNA/pppN(pN)$_{n-1}$ hybrid + ($\boldsymbol{n}$-**1**) diphosphate (2) ssDNA + $\boldsymbol{n}$ dNTP = ssDNA/pppdN(pdN)$_{n-1}$ hybrid + ($\boldsymbol{n}$-**1**) diphosphate
Other name(s):	archaeo-eukaryotic primase; AEP; PrimPol
Systematic name:	(deoxy)nucleotide $5'$-triphosphate:single-stranded DNA (deoxy)nucleotidyltransferase (DNA or DNA-RNA hybrid synthesizing)
Comments:	The enzyme, which is found in eukaryota and archaea, catalyses the synthesis of short RNA or DNA sequences which are used as primers for EC 2.7.7.7, DNA-directed DNA polymerase.
References:	[722, 106, 2004, 1861, 187, 1173]

[EC 2.7.7.102 created 2018]

EC 2.7.7.103

Accepted name:	L-glutamine-phosphate cytidylyltransferase
Reaction:	CTP + N^5-phospho-L-glutamine = diphosphate + N^5-(cytidine $5'$-diphosphoramidyl)-L-glutamine
Systematic name:	CTP:phosphoglutamine cytidylyltransferase
Comments:	The enzyme, characterized from the bacterium *Campylobacter jejuni*, is involved in formation of a unique *O*-methyl phosphoramidate modification on specific sugar residues within the bacterium's capsular polysaccharides.
References:	[3488]

[EC 2.7.7.103 created 2018]

EC 2.7.8 Transferases for other substituted phosphate groups

EC 2.7.8.1

Accepted name:	ethanolaminephosphotransferase
Reaction:	CDP-ethanolamine + 1,2-diacyl-*sn*-glycerol = CMP + a phosphatidylethanolamine
Other name(s):	EPT; diacylglycerol ethanolaminephosphotransferase; CDPethanolamine diglyceride phosphotransferase; phosphorylethanolamine-glyceride transferase; CDP-ethanolamine:1,2-diacylglycerol ethanolaminephosphotransferase
Systematic name:	CDP-ethanolamine:1,2-diacyl-*sn*-glycerol ethanolaminephosphotransferase
References:	[1640]

[EC 2.7.8.1 created 1961]

EC 2.7.8.2

Accepted name:	diacylglycerol cholinephosphotransferase
Reaction:	CDP-choline + 1,2-diacyl-*sn*-glycerol = CMP + a phosphatidylcholine
Other name(s):	phosphorylcholine-glyceride transferase; alkylacylglycerol cholinephosphotransferase; 1-alkyl-2-acetylglycerol cholinephosphotransferase; cholinephosphotransferase; CPT; alkylacylglycerol choline phosphotransferase; diacylglycerol choline phosphotransferase; 1-alkyl-2-acetyl-*m*-glycerol:CDPcholine choline phosphotransferase; CDP-choline diglyceride phosphotransferase; cytidine diphosphocholine glyceride transferase; cytidine diphosphorylcholine diglyceride transferase; phosphocholine diacylglyceroltransferase; *sn*-1,2-diacylglycerol cholinephosphotransferase; 1-alkyl-2-acetyl-*sn*-glycerol cholinephosphotransferase; CDP choline:1,2-diacylglycerol cholinephosphotransferase; CDP-choline:1,2-diacylglycerol cholinephosphotransferase

Systematic name: CDP-choline:1,2-diacyl-*sn*-glycerol cholinephosphotransferase
Comments: 1-Alkyl-2-acylglycerol can act as acceptor; this activity was previously listed separately.
References: [591, 1903, 2629, 2873]

[EC 2.7.8.2 created 1961, modified 1986 (EC 2.7.8.16 created 1983, incorporated 1986)]

EC 2.7.8.3

Accepted name: ceramide cholinephosphotransferase
Reaction: CDP-choline + a ceramide = CMP + sphingomyelin
Other name(s): phosphorylcholine-ceramide transferase
Systematic name: CDP-choline:*N*-acylsphingosine cholinephosphotransferase
References: [1639, 3307]

[EC 2.7.8.3 created 1965]

EC 2.7.8.4

Accepted name: serine-phosphoethanolamine synthase
Reaction: CDP-ethanolamine + L-serine = CMP + L-serine-phosphoethanolamine
Other name(s): serine ethanolamine phosphate synthetase; serine ethanolamine phosphodiester synthase; serine ethanolaminephosphotransferase; serine-phosphinico-ethanolamine synthase; serinephosphoethanolamine synthase
Systematic name: CDP-ethanolamine:L-serine ethanolamine phosphotransferase
References: [59]

[EC 2.7.8.4 created 1972, modified 1976]

EC 2.7.8.5

Accepted name: CDP-diacylglycerol—glycerol-3-phosphate 1-phosphatidyltransferase
Reaction: CDP-diacylglycerol + *sn*-glycerol 3-phosphate = CMP + 1-(3-*sn*-phosphatidyl)-*sn*-glycerol 3-phosphate
Other name(s): glycerophosphate phosphatidyltransferase; 3-phosphatidyl-1′-glycerol-3′-phosphate synthase; CDPdiacylglycerol:glycerol-3-phosphate phosphatidyltransferase; cytidine 5′-diphospho-1,2-diacyl-*sn*-glycerol (CDP-diglyceride):*sn*-glycerol-3-phosphate phosphatidyltransferase; phosphatidylglycerophosphate synthase; phosphatidylglycerolphosphate synthase; PGP synthase; CDP-diacylglycerol-*sn*-glycerol-3-phosphate 3-phosphatidyltransferase; CDP-diacylglycerol:*sn*-glycero-3-phosphate phosphatidyltransferase; glycerol phosphate phosphatidyltransferase; glycerol 3-phosphate phosphatidyltransferase; phosphatidylglycerol phosphate synthase; phosphatidylglycerol phosphate synthetase; phosphatidylglycerophosphate synthetase; *sn*-glycerol-3-phosphate phosphatidyltransferase
Systematic name: CDP-diacylglycerol:*sn*-glycerol-3-phosphate 1-(3-*sn*-phosphatidyl)transferase
Comments: The enzyme catalyses the committed step in the biosynthesis of acidic phospholipids known by the common names phophatidylglycerols and cardiolipins.
References: [1336, 330, 770, 1615, 2351, 148]

[EC 2.7.8.5 created 1972, modified 1976, modified 2016]

EC 2.7.8.6

Accepted name: undecaprenyl-phosphate galactose phosphotransferase
Reaction: UDP-α-D-galactose + undecaprenyl phosphate = UMP + α-D-galactosyl-diphosphoundecaprenol
Other name(s): poly(isoprenol)-phosphate galactose phosphotransferase; poly(isoprenyl)phosphate galactosephosphatetransferase; undecaprenyl phosphate galactosyl-1-phosphate transferase; UDP-galactose:undecaprenyl-phosphate galactose phosphotransferase
Systematic name: UDP-α-D-galactose:undecaprenyl-phosphate galactose phosphotransferase
References: [2578, 3898]

[EC 2.7.8.6 created 1972]

EC 2.7.8.7

Accepted name: holo-[acyl-carrier-protein] synthase

Reaction: CoA-[4′-phosphopantetheine] + apo-[acyl-carrier protein] = adenosine 3′,5′-bisphosphate + holo-[acyl-carrier protein]

Other name(s): acyl carrier protein holoprotein (holo-ACP) synthetase; holo-ACP synthetase; coenzyme A:fatty acid synthetase apoenzyme 4′-phosphopantetheine transferase; holosynthase; acyl carrier protein synthetase; holo-ACP synthase; PPTase; AcpS; ACPS; acyl carrier protein synthase; P-pant transferase; CoA:apo-[acyl-carrier-protein] pantetheinephosphotransferase; CoA-[4′-phosphopantetheine]:apo-[acyl-carrier-protein] 4′-pantetheinephosphotransferase

Systematic name: CoA-[4′-phosphopantetheine]:apo-[acyl-carrier protein] 4′-pantetheinephosphotransferase

Comments: Requires Mg^{2+}. All polyketide synthases, fatty-acid synthases and non-ribosomal peptide synthases require post-translational modification of their constituent acyl-carrier-protein (ACP) domains to become catalytically active. The inactive apo-proteins are converted into their active holo-forms by transfer of the 4′-phosphopantetheinyl moiety of CoA to the sidechain hydroxy group of a conserved serine residue in each ACP domain [1853]. The enzyme from human can activate both the ACP domain of the human cytosolic multifunctional fatty acid synthase system (EC 2.3.1.85) and that associated with human mitochondria as well as peptidyl-carrier and acyl-carrier-proteins from prokaryotes [1539]. Removal of the 4-phosphopantetheinyl moiety from holo-ACP is carried out by EC 3.1.4.14, [acyl-carrier-protein] phosphodiesterase.

References: [832, 2761, 1853, 3741, 2303, 1539]

[EC 2.7.8.7 created 1972, modified 2006]

EC 2.7.8.8

Accepted name: CDP-diacylglycerol—serine *O*-phosphatidyltransferase

Reaction: CDP-diacylglycerol + L-serine = CMP + (3-*sn*-phosphatidyl)-L-serine

Other name(s): phosphatidylserine synthase; CDPdiglyceride-serine *O*-phosphatidyltransferase; PS synthase; cytidine 5′-diphospho-1,2-diacyl-*sn*-glycerol (CDPdiglyceride):L-serine *O*-phosphatidyltransferase; phosphatidylserine synthetase; CDP-diacylglycerol-L-serine *O*-phosphatidyltransferase; cytidine diphosphoglyceride-serine *O*-phosphatidyltransferase; CDP-diglyceride-L-serine phosphatidyltransferase; CDP-diglyceride:serine phosphatidyltransferase; cytidine 5′-diphospho-1,2-diacyl-*sn*-glycerol:L-serine *O*-phosphatidyltransferase; CDP-diacylglycerol:L-serine 3-*O*-phosphatidyltransferase

Systematic name: CDP-diacylglycerol:L-serine 3-*sn*-phosphatidyltransferase

References: [1868, 2791]

[EC 2.7.8.8 created 1972, modified 1976]

EC 2.7.8.9

Accepted name: phosphomannan mannosephosphotransferase

Reaction: GDP-mannose + $(\text{phosphomannan})_n$ = GMP + $(\text{phosphomannan})_{n+1}$

Systematic name: GDP-mannose:phosphomannan mannose phosphotransferase

References: [389]

[EC 2.7.8.9 created 1972]

EC 2.7.8.10

Accepted name: sphingosine cholinephosphotransferase

Reaction: CDP-choline + sphingosine = CMP + sphingosyl-phosphocholine

Other name(s): CDP-choline-sphingosine cholinephosphotransferase; phosphorylcholine-sphingosine transferase; cytidine diphosphocholine-sphingosine cholinephosphotransferase; sphingosine choline phosphotransferase

Systematic name: CDP-choline:sphingosine cholinephosphotransferase
References: [984]

[EC 2.7.8.10 created 1972, modified 1976]

EC 2.7.8.11

Accepted name: CDP-diacylglycerol—inositol 3-phosphatidyltransferase
Reaction: CDP-diacylglycerol + *myo*-inositol = CMP + 1-phosphatidyl-1D-*myo*-inositol
Other name(s): CDP-diglyceride-inositol phosphatidyltransferase; phosphatidylinositol synthase; CDP-diacylglycerol-inositol phosphatidyltransferase; CDP-diglyceride:inositol transferase; cytidine 5′-diphospho-1,2-diacyl-*sn*-glycerol:*myo*-inositol 3-phosphatidyltransferase; CDP-DG:inositol transferase; cytidine diphosphodiglyceride-inositol phosphatidyltransferase; CDP-diacylglycerol:*myo*-inositol-3-phosphatidyltransferase; CDP-diglyceride-inositol transferase; cytidine diphosphoglyceride-inositol phosphatidyltransferase; cytidine diphosphoglyceride-inositol transferase
Systematic name: CDP-diacylglycerol:*myo*-inositol 3-phosphatidyltransferase
References: [331, 2766, 3011, 3449]

[EC 2.7.8.11 created 1972, modified 1976]

EC 2.7.8.12

Accepted name: teichoic acid poly(glycerol phosphate) polymerase
Reaction: ***n*** CDP-glycerol + 4-*O*-[(2*R*)-glycerophospho]-*N*-acetyl-β-D-mannosaminyl-(1→4)-*N*-acetyl-α-D-glucosaminyl-diphospho-*ditrans*,*octacis*-undecaprenol = ***n*** CMP + 4-*O*-poly[(2*R*)-glycerophospho]-(2*R*)-glycerophospho-*N*-acetyl-β-D-mannosaminyl-(1→4)-*N*-acetyl-α-D-glucosaminyl-diphospho-*ditrans*,*octacis*-undecaprenol
Other name(s): teichoic-acid synthase; cytidine diphosphoglycerol glycerophosphotransferase; poly(glycerol phosphate) polymerase; teichoic acid glycerol transferase; glycerophosphate synthetase; CGPTase; CDP-glycerol glycerophosphotransferase (ambiguous); Tag polymerase; CDP-glycerol:poly(glycerophosphate) glycerophosphotransferase; *tagF* (gene name); *tarF* (gene name) (ambiguous)
Systematic name: CDP-glycerol:4-*O*-[(2*R*)-glycerophospho]-*N*-acetyl-β-D-mannosaminyl-(1→4)-*N*-acetyl-α-D-glucosaminyl-diphospho-*ditrans*,*octacis*-undecaprenol glycerophosphotransferase
Comments: Involved in the biosynthesis of poly glycerol phosphate teichoic acids in bacterial cell walls. This enzyme adds 30–50 glycerol units to the linker molecule, but only after it has been primed with the first glycerol unit by EC 2.7.8.44, teichoic acid poly(glycerol phosphate) primase. *cf.* EC 2.7.8.45, teichoic acid glycerol-phosphate transferase.
References: [424, 3072, 3071, 2663, 3148, 2045, 406]

[EC 2.7.8.12 created 1972, modified 1982, modified 2017]

EC 2.7.8.13

Accepted name: phospho-*N*-acetylmuramoyl-pentapeptide-transferase
Reaction: UDP-Mur2Ac(oyl-L-Ala-γ-D-Glu-L-Lys-D-Ala-D-Ala) + undecaprenyl phosphate = UMP + Mur2Ac(oyl-L-Ala-γ-D-Glu-L-Lys-D-Ala-D-Ala)-diphosphoundecaprenol
Other name(s): MraY transferase; UDP-MurNAc-L-Ala-D-γ-Glu-L-Lys-D-Ala-D-Ala:C_{55}-isoprenoid alcohol transferase; UDP-MurNAc-Ala-γDGlu-Lys-DAla-DAla:undecaprenylphosphate transferase; phospho-*N*-acetylmuramoyl pentapeptide translocase; phospho-MurNAc-pentapeptide transferase; phospho-NAc-muramoyl-pentapeptide translocase (UMP); phosphoacetylmuramoylpentapeptide translocase; phosphoacetylmuramoylpentapeptidetransferase
Systematic name: UDP-MurAc(oyl-L-Ala-γ-D-Glu-L-Lys-D-Ala-D-Ala):undecaprenyl-phosphate phospho-*N*-acetylmuramoyl-pentapeptide-transferase
Comments: In Gram-negative and some Gram-positive organisms the L-lysine is replaced by *meso*-2,6-diaminoheptanedioate (*meso*-2,6-diaminopimelate, A2pm), which is combined with adjacent residues through its L-centre. The undecaprenol involved is *ditrans*,*octacis*-undecaprenol (for definitions, click here).

References: [1316, 1325, 3376, 3640]

[EC 2.7.8.13 created 1972, modified 2002]

EC 2.7.8.14

Accepted name: CDP-ribitol ribitolphosphotransferase

Reaction: ***n*** CDP-ribitol + 4-*O*-di[(2*R*)-1-glycerophospho]-*N*-acetyl-β-D-mannosaminyl-(1→4)-*N*-acetyl-α-D-glucosaminyl-diphospho-*ditrans*,*octacis*-undecaprenol = ***n*** CMP + 4-*O*-(D-ribitylphospho)$_n$-di[(2*R*)-1-glycerophospho]-*N*-acetyl-β-D-mannosaminyl-(1→4)-*N*-acetyl-α-D-glucosaminyl-diphospho-*ditrans*,*octacis*-undecaprenol

Other name(s): teichoic-acid synthase (ambiguous); polyribitol phosphate synthetase (ambiguous); teichoate synthetase (ambiguous); poly(ribitol phosphate) synthetase (ambiguous); polyribitol phosphate polymerase (ambiguous); teichoate synthase (ambiguous); CDP-ribitol:poly(ribitol phosphate) ribitolphosphotransferase

Systematic name: CDP-ribitol:4-*O*-di[(2*R*)-1-glycerophospho]-*N*-acetyl-β-D-mannosaminyl-(1→4)-*N*-acetyl-α-D-glucosaminyl-diphospho-*ditrans*,*octacis*-undecaprenol ribitolphosphotransferase

Comments: Involved in the biosynthesis of poly ribitol phosphate teichoic acids in the cell wall of the bacterium *Staphylococcus aureus*. This enzyme adds around 40 ribitol units to the linker molecule.

References: [1460, 408, 2662, 406]

[EC 2.7.8.14 created 1972 as EC 2.4.1.55, transferred 1982 to EC 2.7.8.14, modified 2017]

EC 2.7.8.15

Accepted name: UDP-*N*-acetylglucosamine—dolichyl-phosphate *N*-acetylglucosaminephosphotransferase

Reaction: UDP-*N*-acetyl-α-D-glucosamine + dolichyl phosphate = UMP + *N*-acetyl-α-D-glucosaminyl-diphosphodolichol

Other name(s): UDP-D-*N*-acetylglucosamine *N*-acetylglucosamine 1-phosphate transferase; UDP-GlcNAc:dolichyl-phosphate GlcNAc-1-phosphate transferase; UDP-*N*-acetyl-D-glucosamine:dolichol phosphate *N*-acetyl-D-glucosamine-1-phosphate transferase; uridine diphosphoacetylglucosamine-dolichyl phosphate acetylglucosamine-1-phosphotransferase; chitobiosylpyrophosphoryldolichol synthase; dolichol phosphate *N*-acetylglucosamine-1-phosphotransferase; UDP-acetylglucosamine-dolichol phosphate acetylglucosamine phosphotransferase; UDP-acetylglucosamine-dolichol phosphate acetylglucosamine-1-phosphotransferase

Systematic name: UDP-*N*-α-acetyl-D-glucosamine:dolichyl-phosphate *N*-acetyl-D-glucosaminephosphotransferase (configuration-retaining)

References: [3156, 3683]

[EC 2.7.8.15 created 1983]

[2.7.8.16 Deleted entry. 1-alkyl-2-acetylglycerol choline phosphotransferase. Now included with EC 2.7.8.2 diacylglycerol cholinephosphotransferase]

[EC 2.7.8.16 created 1983, deleted 1986]

EC 2.7.8.17

Accepted name: UDP-*N*-acetylglucosamine—lysosomal-enzyme *N*-acetylglucosaminephosphotransferase

Reaction: UDP-*N*-acetyl-D-glucosamine + lysosomal-enzyme D-mannose = UMP + lysosomal-enzyme *N*-acetyl-D-glucosaminyl-phospho-D-mannose

Other name(s): *N*-acetylglucosaminylphosphotransferase; UDP-*N*-acetylglucosamine:lysosomal enzyme *N*-acetylglucosamine-1-phosphotransferase; UDP-GlcNAc:glycoprotein *N*-acetylglucosamine-1-phosphotransferase; uridine diphosphoacetylglucosamine-lysosomal enzyme precursor acetylglucosamine-1-phosphotransferase; uridine diphosphoacetylglucosamine-glycoprotein acetylglucosamine-1-phosphotransferase; lysosomal enzyme precursor acetylglucosamine-1-phosphotransferase; *N*-acetylglucosaminyl phosphotransferase; UDP-acetylglucosamine:lysosomal enzyme *N*-acetylglucosamine-1-phosphotransferase; UDP-GlcNAc:lysosomal enzyme *N*-acetylglucosamine-1-phosphotransferase; UDP-*N*-acetylglucosamine:glycoprotein *N*-acetylglucosamine-1-phosphotransferase; UDP-*N*-acetylglucosamine:glycoprotein *N*-acetylglucosaminyl-1-phosphotransferase

Systematic name: UDP-*N*-acetyl-D-glucosamine:lysosomal-enzyme *N*-acetylglucosaminephosphotransferase

Comments: Some other glycoproteins with high-mannose can act as acceptors, but much more slowly than lysosomal enzymes.

References: [2865, 2864, 3718, 3719]

[EC 2.7.8.17 created 1984]

EC 2.7.8.18

Accepted name: UDP-galactose—UDP-*N*-acetylglucosamine galactose phosphotransferase

Reaction: UDP-α-D-galactose + UDP-*N*-acetyl-α-D-glucosamine = UMP + UDP-*N*-acetyl-6-(α-D-galactose-1-phospho)-α-D-glucosamine

Other name(s): uridine diphosphogalactose-uridine diphosphoacetylglucosamine galactose-1-phosphotransferase; galactose-1-phosphotransferase; galactosyl phosphotransferase; UDP-galactose:UDP-*N*-acetyl-D-glucosamine galactose phosphotransferase

Systematic name: UDP-α-D-galactose:UDP-*N*-acetyl-α-D-glucosamine galactose phosphotransferase

Comments: *N*-Acetylglucosamine end-groups in glycoproteins can also act as acceptors.

References: [2407]

[EC 2.7.8.18 created 1986]

EC 2.7.8.19

Accepted name: UDP-glucose—glycoprotein glucose phosphotransferase

Reaction: UDP-glucose + glycoprotein D-mannose = UMP + glycoprotein 6-(D-glucose-1-phospho)-D-mannose

Other name(s): UDP-glucose:glycoprotein glucose-1-phosphotransferase; GlcPTase; Glc-phosphotransferase; uridine diphosphoglucose-glycoprotein glucose-1-phosphotransferase

Systematic name: UDP-glucose:glycoprotein-D-mannose glucosephosphotransferase

Comments: Penultimate mannose residues on oligo-mannose type glycoproteins can act as acceptors.

References: [1765]

[EC 2.7.8.19 created 1986]

EC 2.7.8.20

Accepted name: phosphatidylglycerol—membrane-oligosaccharide glycerophosphotransferase

Reaction: phosphatidylglycerol + membrane-derived-oligosaccharide D-glucose = 1,2-diacyl-*sn*-glycerol + membrane-derived-oligosaccharide 6-(glycerophospho)-D-glucose

Other name(s): phosphoglycerol transferase; oligosaccharide glycerophosphotransferase; phosphoglycerol transferase I

Systematic name: phosphatidylglycerol:membrane-derived-oligosaccharide-D-glucose glycerophosphotransferase

Comments: 1,2-β- and 1,6-β-linked glucose residues in membrane polysaccharides and in synthetic glucosides can act as acceptors.

References: [1482]

[EC 2.7.8.20 created 1986]

EC 2.7.8.21

Accepted name: membrane-oligosaccharide glycerophosphotransferase
Reaction: Transfer of a glycerophospho group from one membrane-derived oligosaccharide to another
Other name(s): periplasmic phosphoglycerotransferase; phosphoglycerol cyclase
Systematic name: membrane-derived-oligosaccharide-6-(glycerophospho)-D-glucose:membrane-derived-oligosaccharide-D-glucose glycerophosphotransferase
Comments: β-Linked glucose residues in simple glucosides, such as gentiobiose, can act as acceptors. In the presence of low concentrations of acceptor, free cyclic 1,2-phosphoglycerol is formed.
References: [1089]

[EC 2.7.8.21 created 1986]

EC 2.7.8.22

Accepted name: 1-alkenyl-2-acylglycerol choline phosphotransferase
Reaction: CDP-choline + 1-alkenyl-2-acylglycerol = CMP + plasmenylcholine
Other name(s): CDP-choline-1-alkenyl-2-acyl-glycerol phosphocholinetransferase
Systematic name: CDP-choline:1-alkenyl-2-acylglycerol cholinephosphotransferase
References: [3850]

[EC 2.7.8.22 created 1990]

EC 2.7.8.23

Accepted name: carboxyvinyl-carboxyphosphonate phosphorylmutase
Reaction: 1-carboxyvinyl carboxyphosphonate = 3-(hydroxyphosphinoyl)pyruvate + CO$_2$
Systematic name: 1-carboxyvinyl carboxyphosphonate phosphorylmutase (decarboxylating)
Comments: Catalyses the transfer and decarboxylation of the carboxy(hydroxy)phosphoryl group, HOOC-P(O)(OH)- (phosphoryl being a 3-valent group), in the formation of an unusual C-P bond that is involved in the biosynthesis of the antibiotic bialaphos.
References: [2737, 95]

[EC 2.7.8.23 created 1999]

EC 2.7.8.24

Accepted name: phosphatidylcholine synthase
Reaction: CDP-diacylglycerol + choline = CMP + phosphatidylcholine
Other name(s): CDP-diglyceride-choline *O*-phosphatidyltransferase
Systematic name: CDP-diacylglycerol:choline *O*-phosphatidyltransferase
Comments: Requires divalent cations, with Mn^{2+} being more effective than Mg^{2+}.
References: [689, 3278]

[EC 2.7.8.24 created 2001]

[2.7.8.25 Transferred entry. triphosphoribosyl-dephospho-CoA synthase. Now EC 2.4.2.52, triphosphoribosyl-dephospho-CoA synthase]

[EC 2.7.8.25 created 2002, modified 2008, deleted 2013]

EC 2.7.8.26

Accepted name: adenosylcobinamide-GDP ribazoletransferase
Reaction: (1) adenosylcobinamide-GDP + α-ribazole = GMP + adenosylcobalamin
(2) adenosylcobinamide-GDP + α-ribazole 5′-phosphate = GMP + adenosylcobalamin 5′-phosphate
Other name(s): CobS; cobalamin synthase; cobalamin-5′-phosphate synthase; cobalamin (5′-phosphate) synthase
Systematic name: adenosylcobinamide-GDP:α-ribazole ribazoletransferase

Comments: In *Salmonella typhimurium* LT2, under anaerobic conditions, CobU (EC 2.7.7.62 and EC 2.7.1.156), CobT (EC 2.4.2.21), CobC (EC 3.1.3.73) and CobS (EC 2.7.8.26) catalyse reactions in the nucleotide loop assembly pathway, which convert adenosylcobinamide (AdoCbi) into adenosylcobalamin (AdoCbl). CobT and CobC are involved in 5,6-dimethylbenzimidazole activation whereby 5,6-dimethylbenzimidazole is converted to its riboside, α-ribazole. The second branch of the nucleotide loop assembly pathway is the cobinamide activation branch where AdoCbi or adenosylcobinamide-phosphate is converted to the activated intermediate AdoCbi-GDP by the bifunctional enzyme Cob U. CobS catalyses the final step in adenosylcobalamin biosynthesis, which is the condensation of AdoCbi-GDP with α-ribazole to yield adenosylcobalamin.

References: [2096, 3778, 461]

[EC 2.7.8.26 created 2004]

EC 2.7.8.27

Accepted name: sphingomyelin synthase

Reaction: a ceramide + a phosphatidylcholine = a sphingomyelin + a 1,2-diacyl-*sn*-glycerol

Other name(s): SM synthase; SMS1; SMS2

Systematic name: ceramide:phosphatidylcholine cholinephosphotransferase

Comments: The reaction can occur in both directions [1406]. This enzyme occupies a central position in sphingolipid and glycerophospholipid metabolism [3431]. Up- and down-regulation of its activity has been linked to mitogenic and pro-apoptotic signalling in a variety of mammalian cell types [3431]. Unlike EC 2.7.8.3, ceramide cholinephosphotransferase, CDP-choline cannot replace phosphatidylcholine as the donor of the phosphocholine moiety of sphingomyelin [3692].

References: [3609, 3692, 1406, 3431, 3951]

[EC 2.7.8.27 created 2006]

EC 2.7.8.28

Accepted name: 2-phospho-L-lactate transferase

Reaction: (2*S*)-lactyl-2-diphospho-5′-guanosine + 7,8-didemethyl-8-hydroxy-5-deazariboflavin = GMP + coenzyme F_{420}-0

Other name(s): LPPG:Fo 2-phospho-L-lactate transferase; LPPG:7,8-didemethyl-8-hydroxy-5-deazariboflavin 2-phospho-L-lactate transferase; MJ1256; lactyl-2-diphospho-(5′)guanosine:Fo 2-phospho-L-lactate transferase; CofD

Systematic name: (2*S*)-lactyl-2-diphospho-5′-guanosine:7,8-didemethyl-8-hydroxy-5-deazariboflavin 2-phospho-L-lactate transferase

Comments: This enzyme is involved in the biosynthesis of coenzyme F_{420}, a redox-active cofactor found in all methanogenic archaea, as well as some eubacteria.

References: [1125, 932]

[EC 2.7.8.28 created 2010]

EC 2.7.8.29

Accepted name: L-serine-phosphatidylethanolamine phosphatidyltransferase

Reaction: L-1-phosphatidylethanolamine + L-serine = L-1-phosphatidylserine + ethanolamine

Other name(s): phosphatidylserine synthase 2; serine-exchange enzyme II; PTDSS2 (gene name)

Systematic name: L-1-phosphatidylethanolamine:L-serine phosphatidyltransferase

Comments: This mammalian enzyme catalyses an exchange reaction in which the polar head group of phosphatidylethanolamine is replaced by L-serine.

References: [3353, 3548]

[EC 2.7.8.29 created 2010]

*[2.7.8.30 Transferred entry. undecaprenyl-phosphate 4-deoxy-4-formamido-*L*-arabinose transferase. Now EC 2.4.2.53,*

*undecaprenyl-phosphate 4-deoxy-4-formamido-*L*-arabinose transferase]*

[EC 2.7.8.30 created 2010, modified 2011, deleted 2013]

EC 2.7.8.31

Accepted name: undecaprenyl-phosphate glucose phosphotransferase

Reaction: UDP-glucose + *ditrans*,*octacis*-undecaprenyl phosphate = UMP + α-D-glucopyranosyl-diphospho-*ditrans*,*octacis*-undecaprenol

Other name(s): GumD; undecaprenylphosphate glucosylphosphate transferase

Systematic name: UDP-glucose:*ditrans*,*octacis*-undecaprenyl-phosphate glucose phosphotransferase

Comments: The enzyme is involved in biosynthesis of xanthan.

References: [1430, 1609, 1684]

[EC 2.7.8.31 created 2011]

EC 2.7.8.32

Accepted name: 3-*O*-α-D-mannopyranosyl-α-D-mannopyranose xylosylphosphotransferase

Reaction: UDP-xylose + 3-*O*-α-D-mannopyranosyl-α-D-mannopyranose = UMP + 3-*O*-(6-*O*-α-D-xylosylphospho-α-D-mannopyranosyl)-α-D-mannopyranose

Other name(s): XPT1

Systematic name: UDP-D-xylose:3-*O*-α-D-mannopyranosyl-α-D-mannopyranose xylosylphosphotransferase

Comments: Mn^{2+} required for activity. The enzyme is specific for mannose as an acceptor but is flexible as to the structural context of the mannosyl disaccharide.

References: [2860]

[EC 2.7.8.32 created 2011]

EC 2.7.8.33

Accepted name: UDP-*N*-acetylglucosamine—undecaprenyl-phosphate *N*-acetylglucosaminephosphotransferase

Reaction: UDP-*N*-acetyl-α-D-glucosamine + *ditrans*,*octacis*-undecaprenyl phosphate = UMP + *N*-acetyl-α-D-glucosaminyl-diphospho-*ditrans*,*octacis*-undecaprenol

Other name(s): UDP-*N*-acetylglucosamine:undecaprenyl-phosphate GlcNAc-1-phosphate transferase; WecA; WecA transferase; UDP-GIcNAc:undecaprenyl phosphate *N*-acetylglucosaminyl 1-*P* transferase; GlcNAc-P-P-Und synthase; GPT (ambiguous); TagO; UDP-GlcNAc:undecaprenyl-phosphate GlcNAc-1-phosphate transferase; UDP-*N*-acetyl-D-glucosamine:*ditrans*,*octacis*-undecaprenyl phosphate *N*-acetylglucosaminephosphotransferase

Systematic name: UDP-*N*-acetyl-α-D-glucosamine:*ditrans*,*octacis*-undecaprenyl phosphate *N*-acetyl-α-D-glucosaminephosphotransferase

Comments: This enzyme catalyses the synthesis of *N*-acetyl-α-D-glucosaminyl-diphospho-*ditrans*,*octacis*-undecaprenol, an essential lipid intermediate for the biosynthesis of various bacterial cell envelope components. The enzyme also initiates the biosynthesis of enterobacterial common antigen and O-antigen lipopolysaccharide in certain *Escherichia coli* strains, including K-12 [1916] and of teichoic acid in certain Gram-positive bacteria [3279].

References: [41, 1916, 2972, 3279]

[EC 2.7.8.33 created 2011]

EC 2.7.8.34

Accepted name: CDP-L-*myo*-inositol *myo*-inositolphosphotransferase

Reaction: CDP-1L-*myo*-inositol + 1L-*myo*-inositol 1-phosphate = CMP + bis(1L-*myo*-inositol) 3,1′-phosphate 1-phosphate

Other name(s): CDP-inositol:inositol-1-phosphate transferase (bifunctional CTP:inositol-1-phosphate cytidylyltransferase/CDP-inositol:inositol-1-phosphate transferase (IPCT/DIPPS)); DIPPS (bifunctional CTP:inositol-1-phosphate cytidylyltransferase/CDP-inositol:inositol-1-phosphate transferase (IPCT/DIPPS))
Systematic name: CDP-1L-*myo*-inositol:1L-*myo*-inositol 1-phosphate *myo*-inositolphosphotransferase
Comments: In many organisms this activity is catalysed by a bifunctional enzyme. The di-*myo*-inositol-1,3′-phosphate-1′-phosphate synthase domain of the bifunctional EC 2.7.7.74/EC 2.7.8.34 (CTP:inositol-1-phosphate cytidylyltransferase/CDP-inositol:inositol-1-phosphate transferase) uses only 1L-*myo*-inositol 1-phosphate as an alcohol acceptor, but CDP-glycerol, as well as CDP-1L-*myo*-inositol and CDP-D-*myo*-inositol, are recognized as alcohol donors. The enzyme is involved in biosynthesis of bis(1L-*myo*-inositol) 1,3-phosphate, a widespread organic solute in microorganisms adapted to hot environments.
References: [2909]

[EC 2.7.8.34 created 2011]

EC 2.7.8.35
Accepted name: UDP-*N*-acetylglucosamine—decaprenyl-phosphate *N*-acetylglucosaminephosphotransferase
Reaction: UDP-*N*-acetyl-α-D-glucosamine + *trans*,*octacis*-decaprenyl phosphate = UMP + *N*-acetyl-α-D-glucosaminyl-diphospho-*trans*,*octacis*-decaprenol
Other name(s): GlcNAc-1-phosphate transferase; UDP-GlcNAc:undecaprenyl phosphate GlcNAc-1-phosphate transferase; WecA; WecA transferase
Systematic name: UDP-*N*-acetyl-α-D-glucosamine:*trans*,*octacis*-decaprenyl-phosphate *N*-acetylglucosaminephosphotransferase
Comments: Isolated from *Mycobacterium tuberculosis* and *Mycobacterium smegmatis*. This enzyme catalyses the synthesis of *monotrans*,*octacis*-decaprenyl-*N*-acetyl-α-D-glucosaminyl diphosphate (mycobacterial lipid I), an essential lipid intermediate for the biosynthesis of various bacterial cell envelope components. *cf.* EC 2.7.8.33, UDP-GlcNAc:undecaprenyl-phosphate GlcNAc-1-phosphate transferase.
References: [1516]

[EC 2.7.8.35 created 2012]

EC 2.7.8.36
Accepted name: undecaprenyl phosphate *N*,*N*′-diacetylbacillosamine 1-phosphate transferase
Reaction: UDP-*N*,*N*′-diacetylbacillosamine + *tritrans*,*heptacis*-undecaprenyl phosphate = UMP + *N*,*N*′-diacetyl-α-D-bacillosaminyl-diphospho-*tritrans*,*heptacis*-undecaprenol
Other name(s): PglC
Systematic name: UDP-*N*,*N*′-diacetylbacillosamine:*tritrans*,*heptacis*-undecaprenyl-phosphate *N*,*N*′-diacetylbacillosamine transferase
Comments: Isolated from *Campylobacter jejuni*. Part of a bacterial N-linked glycosylation pathway.
References: [1079]

[EC 2.7.8.36 created 2012]

EC 2.7.8.37
Accepted name: α-D-ribose 1-methylphosphonate 5-triphosphate synthase
Reaction: ATP + methylphosphonate = α-D-ribose 1-methylphosphonate 5-triphosphate + adenine
Systematic name: ATP:methylphosphonate 5-triphosphoribosyltransferase
Comments: Isolated from the bacterium *Escherichia coli*.
References: [1569]

[EC 2.7.8.37 created 2012]

EC 2.7.8.38

Accepted name: archaetidylserine synthase

Reaction: (1) CDP-2,3-bis-(*O*-geranylgeranyl)-*sn*-glycerol + L-serine = CMP + 2,3-bis-(*O*-geranylgeranyl)-*sn*-glycero-1-phospho-L-serine
(2) CDP-2,3-bis-(*O*-phytanyl)-*sn*-glycerol + L-serine = CMP + 2,3-bis-(*O*-phytanyl)-*sn*-glycero-1-phospho-L-serine

Systematic name: CDP-2,3-bis-(*O*-geranylgeranyl)-*sn*-glycerol:L-serine 2,3-bis-(*O*-geranylgeranyl)-*sn*-glycerol phosphotransferase

Comments: Requires Mn^{2+}. Isolated from the archaeon *Methanothermobacter thermautotrophicus*.

References: [2316]

[EC 2.7.8.38 created 2013, modified 2013]

EC 2.7.8.39

Accepted name: archaetidylinositol phosphate synthase

Reaction: CDP-2,3-bis-(*O*-phytanyl)-*sn*-glycerol + 1L-*myo*-inositol 1-phosphate = CMP + 1-archaetidyl-1D-*myo*-inositol 3-phosphate

Other name(s): AIP synthase

Systematic name: CDP-2,3-bis-(*O*-phytanyl)-*sn*-glycerol:1L-*myo*-inositol 1-phosphate 1-*sn*-archaetidyltransferase

Comments: Requires Mg^{2+} or Mn^{2+} for activity. The enzyme is involved in biosynthesis of archaetidyl-*myo*-inositol, a compound essential for glycolipid biosynthesis in archaea.

References: [2315]

[EC 2.7.8.39 created 2013]

EC 2.7.8.40

Accepted name: UDP-*N*-acetylgalactosamine-undecaprenyl-phosphate *N*-acetylgalactosaminephosphotransferase

Reaction: UDP-*N*-acetyl-α-D-galactosamine + *ditrans*,*octacis*-undecaprenyl phosphate = UMP + *N*-acetyl-α-D-galactosaminyl-diphospho-*ditrans*,*octacis*-undecaprenol

Other name(s): WecP; UDP-GalNAc:polyprenol-P GalNAc-1-*P* transferase; UDP-GalNAc:undecaprenyl-phosphate GalNAc-1-phosphate transferase

Systematic name: UDP-*N*-acetyl-α-D-galactosamine:*ditrans*,*octacis*-undecaprenyl phosphate *N*-acetyl-D-galactosaminephosphotransferase

Comments: The enzyme catalyses a step in the assembly of the repeating-unit of the O-antigen of the Gram-negative bacterium *Aeromonas hydrophila* AH-3. The enzyme shows no activity with UDP-*N*-acetyl-α-D-glucosamine (*cf.* EC 2.7.8.33, UDP-*N*-acetylglucosamine-undecaprenyl-phosphate *N*-acetylglucosaminephosphotransferase).

References: [2227]

[EC 2.7.8.40 created 2013]

EC 2.7.8.41

Accepted name: cardiolipin synthase (CMP-forming)

Reaction: a CDP-diacylglycerol + a phosphatidylglycerol = a cardiolipin + CMP

Systematic name: CDP-diacylglycerol:phosphatidylglycerol diacylglycerolphosphotransferase (CMP-forming)

Comments: The eukaryotic enzyme is involved in the biosynthesis of the mitochondrial phospholipid cardiolipin. It requires divalent cations for activity.

References: [3075, 2495, 1380, 3019]

[EC 2.7.8.41 created 2014]

EC 2.7.8.42

Accepted name: Kdo_2-lipid A phosphoethanolamine $7''$-transferase

Reaction: (1) diacylphosphatidylethanolamine + α-D-Kdo-(2→4)-α-D-Kdo-(2→6)-lipid A = diacylglycerol + 7-*O*-[2-aminoethoxy(hydroxy)phosphoryl]-α-D-Kdo-(2→4)-α-D-Kdo-(2→6)-lipid A
(2) diacylphosphatidylethanolamine + α-D-Kdo-(2→4)-α-D-Kdo-(2→6)-lipid IV$_A$ = diacylglycerol + 7-*O*-[2-aminoethoxy(hydroxy)phosphoryl]-α-D-Kdo-(2→4)-α-D-Kdo-(2→6)-lipid IV$_A$

Other name(s): *eptB* (gene name)

Systematic name: diacylphosphatidylethanolamine:α-D-Kdo-(2→4)-α-D-Kdo-(2→6)-lipid-A 7″-phosphoethanolaminetransferase

Comments: The enzyme has been characterized from the bacterium *Escherichia coli*. It is activated by Ca^{2+} ions and is silenced by the sRNA MgrR.

References: [1582, 2876, 2298]

[EC 2.7.8.42 created 2015]

EC 2.7.8.43

Accepted name: lipid A phosphoethanolamine transferase

Reaction: (1) diacylphosphatidylethanolamine + lipid A = diacylglycerol + lipid A 1-(2-aminoethyl diphosphate)
(2) diacylphosphatidylethanolamine + lipid A = diacylglycerol + lipid A 4′-(2-aminoethyl diphosphate)
(3) diacylphosphatidylethanolamine + lipid A 1-(2-aminoethyl diphosphate) = diacylglycerol + lipid A 1,4′-bis(2-aminoethyl diphosphate)

Other name(s): lipid A PEA transferase; LptA

Systematic name: diacylphosphatidylethanolamine:lipid-A ethanolaminephosphotransferase

Comments: The enzyme adds one or two ethanolamine phosphate groups to lipid A giving a diphosphate, sometimes in combination with EC 2.4.2.43 (lipid IV$_A$ 4-amino-4-deoxy-L-arabinosyltransferase) giving products with 4-amino-4-deoxy-β-L-arabinose groups at the phosphates of lipid A instead of diphosphoethanolamine groups. It will also act on lipid IV$_A$ and Kdo$_2$-lipid A.

References: [3560, 1305, 639, 72, 3771]

[EC 2.7.8.43 created 2015 as EC 2.7.4.30, transferred 2016 to EC 2.7.8.43]

EC 2.7.8.44

Accepted name: teichoic acid glycerol-phosphate primase

Reaction: CDP-glycerol + *N*-acetyl-β-D-mannosaminyl-(1→4)-*N*-acetyl-α-D-glucosaminyl-diphospho-*ditrans*,*octacis*-undecaprenol = CDP + 4-*O*-[(2*R*)-1-glycerophospho]-*N*-acetyl-β-D-mannosaminyl-(1→4)-*N*-acetyl-α-D-glucosaminyl-diphospho-*ditrans*,*octacis*-undecaprenol

Other name(s): Tag primase; CDP-glycerol:glycerophosphate glycerophosphotransferase; *tagB* (gene name); *tarB* (gene name)

Systematic name: CDP-glycerol:*N*-acetyl-β-D-mannosaminyl-(1→4)-*N*-acetyl-α-D-glucosaminyl-diphospho-*ditrans*,*octacis*-undecaprenol glycerophosphotransferase

Comments: Involved in the biosynthesis of teichoic acid linkage units in bacterial cell walls. This enzyme adds the first glycerol unit to the disaccharide linker of the teichoic acid.

References: [304, 1062, 408]

[EC 2.7.8.44 created 2016]

EC 2.7.8.45

Accepted name: teichoic acid glycerol-phosphate transferase

Reaction: CDP-glycerol + 4-*O*-[(2*R*)-1-glycerophospho]-*N*-acetyl-β-D-mannosaminyl-(1→4)-*N*-acetyl-α-D-glucosaminyl-diphospho-*ditrans*,*octacis*-undecaprenol = CDP + 4-*O*-di[(2*R*)-1-glycerophospho]-*N*-acetyl-β-D-mannosaminyl-(1→4)-*N*-acetyl-α-D-glucosaminyl-diphospho-*ditrans*,*octacis*-undecaprenol

Other name(s): *tarF* (gene name) (ambiguous); teichoic acid glycerol-phosphate primase

Systematic name: CDP-glycerol:4-*O*-[(2*R*)-1-glycerophospho]-*N*-acetyl-β-D-mannosaminyl-(1→4)-*N*-acetyl-α-D-glucosaminyl-diphospho-*ditrans*,*octacis*-undecaprenol glycerophosphotransferase

Comments: Involved in the biosynthesis of teichoic acid linkage units in the cell walls of some bacteria such as *Staphylococcus aureus*. This enzyme adds a second glycerol unit to the disaccharide linker of the teichoic acid. *cf.* EC 2.7.8.12, teichoic acid poly(glycerol phosphate) polymerase.

References: [408, 406]

[EC 2.7.8.45 created 2017]

EC 2.7.8.46

Accepted name: teichoic acid ribitol-phosphate primase

Reaction: CDP-ribitol + 4-*O*-[(2*R*)-1-glycerophospho]-*N*-acetyl-β-D-mannosaminyl-(1→4)-*N*-acetyl-α-D-glucosaminyl-diphospho-*ditrans*,*octacis*-undecaprenol = CMP + 4-*O*-[1-D-ribitylphospho-(2*R*)-1-glycerophospho]-*N*-acetyl-β-D-mannosaminyl-(1→4)-*N*-acetyl-α-D-glucosaminyl-diphospho-*ditrans*,*octacis*-undecaprenol

Other name(s): Tar primase; *tarK* (gene name)

Systematic name: CDP-ribitol:4-*O*-[(2*R*)-1-glycerophospho]-*N*-acetyl-β-D-mannosaminyl-(1→4)-*N*-acetyl-α-D-glucosaminyl-diphospho-*ditrans*,*octacis*-undecaprenol ribitylphosphotransferase

Comments: Involved in the biosynthesis of teichoic acid linkage units in the cell wall of *Bacillus subtilis* W23. This enzyme adds the first ribitol unit to the disaccharide linker of the teichoic acid.

References: [406]

[EC 2.7.8.46 created 2017]

EC 2.7.8.47

Accepted name: teichoic acid ribitol-phosphate polymerase

Reaction: ***n*** CDP-ribitol + 4-*O*-[1-D-ribitylphospho-(2*R*)-1-glycerophospho]-*N*-acetyl-β-D-mannosaminyl-(1→4)-*N*-acetyl-α-D-glucosaminyl-diphospho-*ditrans*,*octacis*-undecaprenol = ***n*** CMP + 4-*O*-[(1-D-ribitylphospho)$_n$-(1-D-ribitylphospho)-(2*R*)-1-glycerophospho]-*N*-acetyl-β-D-mannosaminyl-(1→4)-*N*-acetyl-α-D-glucosaminyl-diphospho-*ditrans*,*octacis*-undecaprenol

Other name(s): Tar polymerase (ambiguous); *tarL* (gene name) (ambiguous)

Systematic name: CDP-ribitol:4-*O*-[1-D-ribitylphospho-(2*R*)-1-glycerophospho]-*N*-acetyl-β-D-mannosaminyl-(1→4)-*N*-acetyl-α-D-glucosaminyl-diphospho-*ditrans*,*octacis*-undecaprenol ribitolphosphotransferase

Comments: Involved in the biosynthesis of teichoic acid linkage units in the cell wall of *Bacillus subtilis* W23. This enzyme adds the 25-35 ribitol units to the linker molecule.

References: [406]

[EC 2.7.8.47 created 2017]

EC 2.7.9 Phosphotransferases with paired acceptors

EC 2.7.9.1

Accepted name: pyruvate, phosphate dikinase

Reaction: ATP + pyruvate + phosphate = AMP + phospho*enol*pyruvate + diphosphate

Other name(s): pyruvate, orthophosphate dikinase; pyruvate-phosphate dikinase (phosphorylating); pyruvate, phosphate dikinase; pyruvate-inorganic phosphate dikinase; pyruvate-phosphate dikinase; pyruvate-phosphate ligase; pyruvic-phosphate dikinase; pyruvic-phosphate ligase; pyruvate, Pi dikinase; PPDK

Systematic name: ATP:pyruvate, phosphate phosphotransferase

References: [1244, 2849, 2850, 2852]

[EC 2.7.9.1 created 1972]

EC 2.7.9.2

Accepted name: pyruvate, water dikinase

Reaction: ATP + pyruvate + H_2O = AMP + phospho*enol*pyruvate + phosphate
Other name(s): phospho*enol*pyruvate synthase; pyruvate-water dikinase (phosphorylating); PEP synthetase; phosphoenolpyruvate synthase; phoephoenolpyruvate synthetase; phospho*enol*pyruvic synthase; phosphopyruvate synthetase
Systematic name: ATP:pyruvate, water phosphotransferase
Comments: A manganese protein.
References: [286, 287, 610, 611]

[EC 2.7.9.2 created 1976]

EC 2.7.9.3

Accepted name: selenide, water dikinase
Reaction: ATP + selenide + H_2O = AMP + selenophosphate + phosphate
Other name(s): selenophosphate synthase
Systematic name: ATP:selenide, water phosphotransferase
Comments: Mg^{2+}-dependent enzyme identified in *Escherichia coli*
References: [3667]

[EC 2.7.9.3 created 1999]

EC 2.7.9.4

Accepted name: α-glucan, water dikinase
Reaction: ATP + α-glucan + H_2O = AMP + phospho-α-glucan + phosphate
Other name(s): starch-related R1 protein, GWD
Systematic name: ATP:α-glucan, water phosphotransferase
Comments: Requires Mg^{2+}. ATP appears to be the only phosphate donor. No activity could be detected using GTP, UTP, phospho*enol*pyruvate or diphosphate [2890]. The protein phosphorylates glucans exclusively on O-6 of glucosyl residues [2889]. The protein phosphorylates itself with the β-phosphate of ATP, which is then transferred to the glucan [2890].
References: [2890, 2889]

[EC 2.7.9.4 created 2002]

EC 2.7.9.5

Accepted name: phosphoglucan, water dikinase
Reaction: ATP + [phospho-α-glucan] + H_2O = AMP + *O*-phospho-[phospho-α-glucan] + phosphate
Other name(s): PWD; OK1
Systematic name: ATP:phospho-α-glucan, water phosphotransferase
Comments: The enzyme phosphorylates granular starch that has previously been phosphorylated by EC 2.7.9.4, α-glucan, water dikinase; there is no activity with unphosphorylated glucans. It transfers the β-phosphate of ATP to the phosphoglucan, whereas the γ-phosphate is transferred to water [1771]. In contrast to EC 2.7.9.4, which phosphorylates glucose groups in glucans on O-6, this enzyme phosphorylates glucose groups in phosphorylated starch on O-3 [2889]. The protein phosphorylates itself with the β-phosphate of ATP, which is then transferred to the glucan [1771].
References: [1771, 2889]

[EC 2.7.9.5 created 2005]

EC 2.7.9.6

Accepted name: rifampicin phosphotransferase
Reaction: ATP + rifampicin + H_2O = AMP + 21-phosphorifampicin + phosphate
Other name(s): rifampin phosphotransferase; RPH
Systematic name: ATP:rifampicin, water 21-*O*-phosphotransferase

Comments: The enzyme, characterized from a diverse collection of Gram-positive bacteria, inactivates the antibiotic rifampicin by phosphorylating it at position 21. The enzyme comprises three domains: two substrate-binding domains (ATP-grasp and rifampicin-binding domains) and a smaller phosphate-carrying L-histidine swivel domain that transits between the spatially distinct substrate-binding sites during catalysis.

References: [3293, 3350]

[EC 2.7.9.6 created 2018]

EC 2.7.10 Protein-tyrosine kinases

EC 2.7.10.1

Accepted name: receptor protein-tyrosine kinase

Reaction: ATP + a [protein]-L-tyrosine = ADP + a [protein]-L-tyrosine phosphate

Other name(s): AATK; AATYK; AATYK2; AATYK3; ACH; ALK; anaplastic lymphoma kinase; ARK; ATP:protein-tyrosine *O*-phosphotransferase (ambiguous); AXL; Bek; Bfgfr; BRT; Bsk; C-FMS; CAK; CCK4; CD115; CD135; CDw135; Cek1; Cek10; Cek11; Cek2; Cek3; Cek5; Cek6; Cek7; CFD1; CKIT; CSF1R; DAlk; DDR1; DDR2; Dek; DKFZp434C1418; *Drosophila* Eph kinase; DRT; DTK; Ebk; ECK; EDDR1; Eek; EGFR; Ehk2; Ehk3; Elk; EPH; EPHA1; EPHA2; EPHA6; EPHA7; EPHA8; EPHB1; EPHB2; EPHB3; EPHB4; EphB5; ephrin-B3 receptor tyrosine kinase; EPHT; EPHT2; EPHT3; EPHX; ERBB; ERBB1; ERBB2; ERBB3; ERBB4; ERK; Eyk; FGFR1; FGFR2; FGFR3; FGFR4; FLG; FLK1; FLK2; FLT1; FLT2; FLT3; FLT4; FMS; Fv2; HBGFR; HEK11; HEK2; HEK3; HEK5; HEK6; HEP; HER2; HER3; HER4; HGFR; HSCR1; HTK; IGF1R; INSR; INSRR; insulin receptor protein-tyrosine kinase; IR; IRR; JTK12; JTK13; JTK14; JWS; K-SAM; KDR; KGFR; KIA0641; KIAA1079; KIAA1459; Kil; Kin15; Kin16; KIT; KLG; LTK; MCF3; Mdk1; Mdk2; Mdk5; MEhk1; MEN2A/B; Mep; MER; MERTK; MET; Mlk1; Mlk2; Mrk; MST1R; MTC1; MUSK; Myk1; *N*-SAM; NEP; NET; Neu; neurite outgrowth regulating kinase; NGL; NOK; nork; novel oncogene with kinase-domain; Nsk2; NTRK1; NTRK2; NTRK3; NTRK4; NTRKR1; NTRKR2; NTRKR3; Nuk; NYK; PCL; PDGFR; PDGFRA; PDGFRB; PHB6; protein-tyrosine kinase (ambiguous); protein tyrosine kinase (ambiguous); PTK; PTK3; PTK7; receptor protein tyrosine kinase; RET; RON; ROR1; ROR2; ROS1; RSE; RTK; RYK; SEA; Sek2; Sek3; Sek4; Sfr; SKY; STK; STK1; TEK; TIE; TIE1; TIE2; TIF; TKT; TRK; TRKA; TRKB; TRKC; TRKE; TYK1; TYRO10; Tyro11; TYRO3; Tyro5; Tyro6; TYRO7; UFO; VEGFR1; VEGFR2; VEGFR3; Vik; YK1; Yrk

Systematic name: ATP:[protein]-L-tyrosine *O*-phosphotransferase (receptor-type)

Comments: The receptor protein-tyrosine kinases, which can be defined as having a transmembrane domain, are a large and diverse multigene family found only in Metazoans [2902]. In the human genome, 58 receptor-type protein-tyrosine kinases have been identified and these are distributed into 20 subfamilies.

References: [2902, 1473, 2035]

[EC 2.7.10.1 created 1984 as EC 2.7.1.112, part transferred 2005 to EC 2.7.10.1]

EC 2.7.10.2

Accepted name: non-specific protein-tyrosine kinase

Reaction: ATP + a [protein]-L-tyrosine = ADP + a [protein]-L-tyrosine phosphate

Other name(s): ABL; ABL1; ABL2; ABLL; ACK1; ACK2; AGMX1; ARG; ATK; ATP:protein-tyrosine *O*-phosphotransferase (ambiguous); BLK; Bmk; BMX; BRK; Bruton's tyrosine kinase; Bsk; BTK; BTKL; CAKb; Cdgip; CHK; CSK; CTK; CYL; cytoplasmic protein tyrosine kinase; EMT; ETK; Fadk; FAK; FAK2; FER; Fert1/2; FES; FGR; focal adhesion kinase; FPS; FRK; FYN; HCK; HCTK; HYL; IMD1; ITK; IYK; JAK1; JAK2; JAK3; Janus kinase 1; Janus kinase 2; Janus kinase 3; JTK1; JTK9; L-JAK; LCK; LSK; LYN; MATK; Ntk; p60c-src protein tyrosine kinase; PKB; protein-tyrosine kinase (ambiguous); PSCTK; PSCTK1; PSCTK2; PSCTK4; PSCTK5; PTK2; PTK2B; PTK6; PYK2; RAFTK; RAK; Rlk; Sik; SLK; SRC; SRC2; SRK; SRM; SRMS; STD; SYK; SYN; Tck; TEC; TNK1; Tsk; TXK; TYK2; TYK3; YES1; YK2; ZAP70

Systematic name: ATP:[protein]-L-tyrosine *O*-phosphotransferase (non-specific)
Comments: Unlike EC 2.7.10.1, receptor protein-tyrosine kinase, this protein-tyrosine kinase does not have a transmembrane domain. In the human genome, 32 non-specific protein-tyrosine kinases have been identified and these can be divided into ten families [2902].
References: [2902, 2936]

[EC 2.7.10.2 created 1984 as EC 2.7.1.112, part transferred 2005 to EC 2.7.10.2]

EC 2.7.11 Protein-serine/threonine kinases

EC 2.7.11.1
Accepted name: non-specific serine/threonine protein kinase
Reaction: ATP + a protein = ADP + a phosphoprotein
Other name(s): A-kinase; AP50 kinase; ATP-protein transphosphorylase; calcium-dependent protein kinase C; calcium/phospholipid-dependent protein kinase; cAMP-dependent protein kinase; cAMP-dependent protein kinase A; casein kinase; casein kinase (phosphorylating); casein kinase 2; casein kinase I; casein kinase II; cGMP-dependent protein kinase; CK-2; CKI; CKII; cyclic AMP-dependent protein kinase; cyclic AMP-dependent protein kinase A; cyclic monophosphate-dependent protein kinase; cyclic nucleotide-dependent protein kinase; cyclin-dependent kinase; cytidine 3′,5′-cyclic monophosphate-responsive protein kinase; dsk1; glycogen synthase a kinase; glycogen synthase kinase; HIPK2; Hpr kinase; hydroxyalkyl-protein kinase; hydroxyalkyl-protein kinase; M phase-specific cdc2 kinase; mitogen-activated S6 kinase; p82 kinase; phosphorylase *b* kinase kinase; PKA; protein glutamyl kinase; protein kinase (phosphorylating); protein kinase A; protein kinase CK2; protein kinase p58; protein phosphokinase; protein serine kinase; protein serine-threonine kinase; protein-aspartyl kinase; protein-cysteine kinase; protein-serine kinase; Prp4 protein kinase; Raf kinase; Raf-1; ribosomal protein S6 kinase II; ribosomal S6 protein kinase; serine kinase; serine protein kinase; serine-specific protein kinase; serine(threonine) protein kinase; serine/threonine protein kinase; STK32; T-antigen kinase; threonine-specific protein kinase; twitchin kinase; type-2 casein kinase; βIIPKC; ε PKC; Wee 1-like kinase; Wee-kinase; WEE1Hu
Systematic name: ATP:protein phosphotransferase (non-specific)
Comments: This is a heterogeneous group of serine/threonine protein kinases that do not have an activating compound and are either non-specific or their specificity has not been analysed to date.
References: [666, 157, 1509, 1859, 3451, 1150, 3764]

[EC 2.7.11.1 created 2005 (EC 2.7.1.37 part-incorporated 2005)]

EC 2.7.11.2
Accepted name: [pyruvate dehydrogenase (acetyl-transferring)] kinase
Reaction: ATP + [pyruvate dehydrogenase (acetyl-transferring)] = ADP + [pyruvate dehydrogenase (acetyl-transferring)] phosphate
Other name(s): PDH kinase; PDHK; PDK; PDK1; PDK2; PDK3; PDK4; pyruvate dehydrogenase kinase; pyruvate dehydrogenase kinase (phosphorylating); pyruvate dehydrogenase kinase activator protein; STK1
Systematic name: ATP:[pyruvate dehydrogenase (acetyl-transferring)] phosphotransferase
Comments: The enzyme has no activating compound but is specific for its substrate. It is a mitochondrial enzyme associated with the pyruvate dehydrogenase complex in mammals. Phosphorylation inactivates EC 1.2.4.1, pyruvate dehydrogenase (acetyl-transferring).
References: [1979, 2843, 3556, 183, 2906]

[EC 2.7.11.2 created 1978 as EC 2.7.1.99, transferred 2005 to EC 2.7.11.2]

EC 2.7.11.3
Accepted name: dephospho-[reductase kinase] kinase
Reaction: ATP + dephospho-[hydroxymethylglutaryl-CoA reductase (NADPH)] kinase = ADP + [hydroxymethylglutaryl-CoA reductase (NADPH)] kinase

Other name(s): AMP-activated kinase; AMP-activated protein kinase kinase; hydroxymethylglutaryl coenzyme A reductase kinase kinase; hydroxymethylglutaryl coenzyme A reductase kinase kinase (phosphorylating); reductase kinase; reductase kinase kinase; STK30

Systematic name: ATP:dephospho-[hydroxymethylglutaryl-CoA reductase (NADPH)] kinase phosphotransferase

Comments: The enzyme is activated by AMP and is specific for its substrate. Phosphorylates and activates EC 2.7.11.31, [hydroxymethylglutaryl-CoA reductase (NADPH)] kinase, that has been inactivated by EC 3.1.3.16, protein-serine/threonine phosphatase.

References: [252, 1445, 253, 578, 3033]

[EC 2.7.11.3 created 1984 as EC 2.7.1.110, transferred 2005 to EC 2.7.11.3]

EC 2.7.11.4

Accepted name: [3-methyl-2-oxobutanoate dehydrogenase (acetyl-transferring)] kinase

Reaction: ATP + [3-methyl-2-oxobutanoate dehydrogenase (acetyl-transferring)] = ADP + [3-methyl-2-oxobutanoate dehydrogenase (acetyl-transferring)] phosphate

Other name(s): BCK; BCKD kinase; BCODH kinase; branched-chain α-ketoacid dehydrogenase kinase; branched-chain 2-oxo acid dehydrogenase kinase; branched-chain keto acid dehydrogenase kinase; branched-chain oxo acid dehydrogenase kinase (phosphorylating); STK2

Systematic name: ATP:[3-methyl-2-oxobutanoate dehydrogenase (acetyl-transferring)] phosphotransferase

Comments: The enzyme has no activating compound but is specific for its substrate. It is a mitochondrial enzyme associated with the branched-chain 2-oxoacid dehydrogenase complex. Phosphorylation inactivates EC 1.2.4.4, 3-methyl-2-oxobutanoate dehydrogenase (2-methylpropanoyl-transferring).

References: [2645, 3914, 563, 2741]

[EC 2.7.11.4 created 1986 as EC 2.7.1.115, transferred 2005 to EC 2.7.11.4]

EC 2.7.11.5

Accepted name: [isocitrate dehydrogenase (NADP$^+$)] kinase

Reaction: ATP + [isocitrate dehydrogenase (NADP$^+$)] = ADP + [isocitrate dehydrogenase (NADP$^+$)] phosphate

Other name(s): [isocitrate dehydrogenase (NADP)] kinase; ICDH kinase/phosphatase; IDH kinase; IDH kinase/phosphatase; IDH-K/P; IDHK/P; isocitrate dehydrogenase kinase (phosphorylating); isocitrate dehydrogenase kinase/phosphatase; STK3

Systematic name: ATP:[isocitrate dehydrogenase (NADP$^+$)] phosphotransferase

Comments: The enzyme has no activating compound but is specific for its substrate. Phosphorylates and inactivates EC 1.1.1.42, isocitrate dehydrogenase (NADP$^+$).

References: [1550, 2257, 3243, 2586]

[EC 2.7.11.5 created 1986 as EC 2.7.1.116, transferred 2005 to EC 2.7.11.5]

EC 2.7.11.6

Accepted name: [tyrosine 3-monooxygenase] kinase

Reaction: ATP + [tyrosine-3-monooxygenase] = ADP + phospho-[tyrosine-3-monooxygenase]

Other name(s): pheochromocytoma tyrosine hydroxylase-associated kinase; STK4; tyrosine 3-monooxygenase kinase (phosphorylating)

Systematic name: ATP:[tyrosine-3-monoxygenase] phosphotransferase

Comments: The enzyme has no activating compound but is specific for its substrate, with which it co-purifies. Requires Mg^{2+}. Activates EC 1.14.16.2, tyrosine 3-monooxygenase, by phosphorylation.

References: [2709, 2710]

[EC 2.7.11.6 created 1989 as EC 2.7.1.124, transferred 2005 to EC 2.7.11.6]

EC 2.7.11.7

Accepted name: myosin-heavy-chain kinase

Reaction: ATP + [myosin heavy-chain] = ADP + [myosin heavy-chain] phosphate

Other name(s): ATP:myosin-heavy-chain *O*-phosphotransferase; calmodulin-dependent myosin heavy chain kinase; MHCK; MIHC kinase; myosin heavy chain kinase; myosin I heavy-chain kinase; myosin II heavy-chain kinase; [myosin-heavy-chain] kinase; myosin heavy chain kinase A; STK6

Systematic name: ATP:[myosin heavy-chain] *O*-phosphotransferase

Comments: The enzyme from *Dictyostelium* sp. (slime moulds) brings about phosphorylation of the heavy chains of *Dictyostelium* myosin, inhibiting the actin-activated ATPase activity of the myosin. One threonine residue in each heavy chain acts as acceptor. While the enzyme from some species is activated by actin, in other cases Ca^{2+}/calmodulin are required for activity.

References: [622, 1205, 2885, 2828, 412, 2829, 1000, 3415, 812]

[EC 2.7.11.7 created 1990 as EC 2.7.1.129, transferred 2005 to EC 2.7.11.7]

EC 2.7.11.8

Accepted name: Fas-activated serine/threonine kinase

Reaction: ATP + [Fas-activated serine/threonine protein] = ADP + [Fas-activated serine/threonine phosphoprotein]

Other name(s): FAST; FASTK; STK10

Systematic name: ATP:[Fas-activated serine/threonine protein] phosphotransferase

Comments: This enzyme is activated during Fas-mediated apoptosis. Following Fas ligation, the enzyme, which is constitutively phosphorylated, is dephosphorylated, and it is the dephosphorylated form that causes phosphorylation of TIA-1, a nuclear RNA-binding protein. Phosphorylation of TIA-1 precedes the onset of DNA fragmentation.

References: [3533, 1961]

[EC 2.7.11.8 created 2005 (EC 2.7.1.37 part-incorporated 2005)]

EC 2.7.11.9

Accepted name: Goodpasture-antigen-binding protein kinase

Reaction: ATP + [Goodpasture antigen-binding protein] = ADP + [Goodpasture antigen-binding phosphoprotein]

Other name(s): GPBPK; GPBP kinase; STK11; Goodpasture antigen-binding protein kinase

Systematic name: ATP:[Goodpasture antigen-binding protein] phosphotransferase

Comments: This serine/threonine kinase specifically binds to and phosphorylates the N-terminal region of the human Goodpasture antigen, which is located on the α_3 chain of collagen IV and is involved in autoimmune disease.

References: [2833, 2834]

[EC 2.7.11.9 created 2005 (EC 2.7.1.37 part-incorporated 2005)]

EC 2.7.11.10

Accepted name: IκB kinase

Reaction: ATP + [IκB protein] = ADP + [IκB phosphoprotein]

Other name(s): CHUK; IKBKA; IKBKB; IKK; IKK-1; IKK-2; inhibitor of NFκB kinase; inhibitor of NF-κB kinase; STK12; TANK-binding kinase 1; TBK1

Systematic name: ATP:[IκB protein] phosphotransferase

Comments: The enzyme phosphorylates IκB proteins at specific serine residues, which marks them for destruction via the ubiquitination pathway. Subsequent degradation of the IkB complex (IKK) activates NF-κB, a translation factor that plays an important role in inflammation, immunity, cell proliferation and apoptosis. If the serine residues are replaced by threonine residues, the activity of the enzyme is decreased considerably.

References: [2857, 2226, 4026, 3678]

[EC 2.7.11.10 created 2005 (EC 2.7.1.37 part-incorporated 2005)]

EC 2.7.11.11

Accepted name: cAMP-dependent protein kinase
Reaction: ATP + a protein = ADP + a phosphoprotein
Other name(s): PKA; PKA C; protein kinase A; STK22
Systematic name: ATP:protein phosphotransferase (cAMP-dependent)
Comments: cAMP is required to activate this enzyme. The inactive holoenzyme of cAMP-dependent protein kinase is a tetramer composed of two regulatory (R) and two catalytic (C) subunits. cAMP causes the dissociation of the inactive holoenzyme into a dimer of regulatory subunits bound to four cAMP molecules and two free monomeric catalytic subunits [i.e. R2C2 + 4 cAMP = R2(cAMP)$_4$ + 2 C].
References: [3492, 73, 1523, 1219]

[EC 2.7.11.11 created 2005 (EC 2.7.1.37 part-incorporated 2005)]

EC 2.7.11.12

Accepted name: cGMP-dependent protein kinase
Reaction: ATP + a protein = ADP + a phosphoprotein
Other name(s): 3′:5′-cyclic GMP-dependent protein kinase; cGMP-dependent protein kinase Iβ; guanosine 3′:5′-cyclic monophosphate-dependent protein kinase; PKG; PKG 1α; PKG 1β; PKG II; STK23
Systematic name: ATP:protein phosphotransferase (cGMP-dependent)
Comments: CGMP is required to activate this enzyme. The enzyme occurs as a dimer in higher eukaryotes. The C-terminal region of each polypeptide chain contains the catalytic domain that includes the ATP and protein substrate binding sites. This domain catalyses the phosphorylation by ATP to specific serine or threonine residues in protein substrates [2883]. The enzyme also has two allosteric cGMP-binding sites (sites A and B). Binding of cGMP causes a conformational change that is associated with activation of the kinase [4063].
References: [1061, 2379, 2883, 4063]

[EC 2.7.11.12 created 2005 (EC 2.7.1.37 part-incorporated 2005)]

EC 2.7.11.13

Accepted name: protein kinase C
Reaction: ATP + a protein = ADP + a phosphoprotein
Other name(s): calcium-dependent protein kinase C; calcium-independent protein kinase C; calcium/phospholipid dependent protein kinase; cPKCα; cPKCβ; cPKCγ; nPKCδ; nPKCε; nPKC; nPKC; PKC; PKCα; PKCβ; PKCγ; PKCδ; PKCε; PKCζ; Pkc1p; protein kinase Cε; STK24
Systematic name: ATP:protein phosphotransferase (diacylglycerol-dependent)
Comments: A family of serine- and threonine-specific protein kinases that depend on lipids for activity. They can be activated by calcium but have a requirement for the second messenger diacylglycerol. Members of this group of enzymes phosphorylate a wide variety of protein targets and are known to be involved in diverse cell-signalling pathways. Members of the protein kinase C family also serve as major receptors for phorbol esters, a class of tumour promoters.
References: [1491, 2617, 3629, 1932, 400]

[EC 2.7.11.13 created 2005 (EC 2.7.1.37 part-incorporated 2005)]

EC 2.7.11.14

Accepted name: rhodopsin kinase
Reaction: ATP + rhodopsin = ADP + phosphorhodopsin
Other name(s): cone opsin kinase; G-protein-coupled receptor kinase 1; GPCR kinase 1; GRK1; GRK7; opsin kinase; opsin kinase (phosphorylating); rhodopsin kinase (phosphorylating); RK; STK14
Systematic name: ATP:rhodopsin phosphotransferase

Comments: Requires G-protein for activation and therefore belongs to the family of G-protein-dependent receptor kinases (GRKs). Acts on the bleached or activated form of rhodopsin; also phosphorylates the β-adrenergic receptor, but more slowly. Does not act on casein, histones or phosphvitin. Inhibited by Zn^{2+} and digitonin (*cf.* EC 2.7.11.15, β-adrenergic-receptor kinase and EC 2.7.11.16, G-protein-coupled receptor kinase).

References: [270, 3185, 2604, 3818, 493, 1660, 521, 3853]

[EC 2.7.11.14 created 1989 as EC 2.7.1.125 (EC 2.7.1.97 created 1978, incorporated 1992), transferred 2005 to EC 2.7.11.14]

EC 2.7.11.15

Accepted name: β-adrenergic-receptor kinase

Reaction: ATP + [β-adrenergic receptor] = ADP + phospho-[β-adrenergic receptor]

Other name(s): ATP:β-adrenergic-receptor phosphotransferase; [β-adrenergic-receptor] kinase; β-adrenergic receptor-specific kinase; β-AR kinase; β-ARK; β-ARK 1; β-ARK 2; β-receptor kinase; GRK2; GRK3; β-adrenergic-receptor kinase (phosphorylating); β2ARK; βARK1; β-adrenoceptor kinase; β-adrenoceptor kinase 1; β-adrenoceptor kinase 2; ADRBK1; BARK1; adrenergic receptor kinase; STK15

Systematic name: ATP:[β-adrenergic receptor] phosphotransferase

Comments: Requires G-protein for activation and therefore belongs to the family of G-protein-dependent receptor kinases (GRKs). Acts on the agonist-occupied form of the receptor; also phosphorylates rhodopsin, but more slowly. Does not act on casein or histones. The enzyme is inhibited by Zn^{2+} and digitonin but is unaffected by cyclic-AMP (*cf.* EC 2.7.11.14, rhodopsin kinase and EC 2.7.11.16, G-protein-coupled receptor kinase).

References: [271, 1676, 1874, 893, 3853]

[EC 2.7.11.15 created 1989 as EC 2.7.1.126, transferred 2005 to EC 2.7.11.15]

EC 2.7.11.16

Accepted name: G-protein-coupled receptor kinase

Reaction: ATP + [G-protein-coupled receptor] = ADP + [G-protein-coupled receptor] phosphate

Other name(s): G protein-coupled receptor kinase; GPCR kinase; GPCRK; GRK4; GRK5; GRK6; STK16

Systematic name: ATP:[G-protein-coupled receptor] phosphotransferase

Comments: Requires G-protein for activation and therefore belongs to the family of G-protein-dependent receptor kinases (GRKs). All members of this enzyme subfamily possess a highly conserved binding site for 1-phosphatidylinositol 4,5-bisphosphate. (*cf.* EC 2.7.11.14, rhodopsin kinase and EC 2.7.11.15, β-adrenergic-receptor kinase).

References: [1818, 2760, 3853]

[EC 2.7.11.16 created 2005]

EC 2.7.11.17

Accepted name: Ca^{2+}/calmodulin-dependent protein kinase

Reaction: ATP + a protein = ADP + a phosphoprotein

Other name(s): ATP:caldesmon *O*-phosphotransferase; caldesmon kinase; caldesmon kinase (phosphorylating); Ca^{2+}/calmodulin-dependent microtubule-associated protein 2 kinase; Ca^{2+}/calmodulin-dependent protein kinase 1; Ca^{2+}/calmodulin-dependent protein kinase II; Ca^{2+}/calmodulin-dependent protein kinase IV; Ca^{2+}/calmodulin-dependent protein kinase kinase; Ca^{2+}/calmodulin-dependent protein kinase kinase β; calmodulin-dependent kinase II; CaM kinase; CaM kinase II; CAM PKII; CaM-regulated serine/threonine kinase; CaMKI; CaMKII; CaMKIV; CaMKKα; CaMKKβ; microtubule-associated protein 2 kinase; STK20

Systematic name: ATP:protein phosphotransferase (Ca^{2+}/calmodulin-dependent)

Comments: Requires calmodulin and Ca^{2+} for activity. A wide range of proteins can act as acceptor, including vimentin, synapsin, glycogen synthase, myosin light chains and the microtubule-associated *tau* protein. Not identical with EC 2.7.11.18 (myosin-light-chain kinase) or EC 2.7.11.26 (*tau*-protein kinase).

References: [19, 234, 3113, 76, 2167, 2536, 2885, 1474, 1098, 2104, 2447, 1434]

[EC 2.7.11.17 created 1989 as EC 2.7.1.123, transferred 2005 to EC 2.7.11.17 (EC 2.7.1.120 incorporated 2005)]

EC 2.7.11.18

Accepted name: myosin-light-chain kinase

Reaction: ATP + [myosin light chain] = ADP + [myosin light chain] phosphate

Other name(s): [myosin-light-chain] kinase; ATP:myosin-light-chain *O*-phosphotransferase; calcium/calmodulin-dependent myosin light chain kinase; MLCK; MLCKase; myosin kinase; myosin light chain kinase; myosin light chain protein kinase; myosin light-chain kinase (phosphorylating); smooth-muscle-myosin-light-chain kinase; STK18

Systematic name: ATP:[myosin light chain] *O*-phosphotransferase

Comments: Requires Ca^{2+} and calmodulin for activity. The 20-kDa light chain from smooth muscle myosin is phosphorylated more rapidly than any other acceptor, but light chains from other myosins and myosin itself can act as acceptors, but more slowly.

References: [17, 1246, 2718, 2497, 805, 2104, 3268, 3269, 988]

[EC 2.7.11.18 created 1986 as EC 2.7.1.117, transferred 2005 to EC 2.7.11.18]

EC 2.7.11.19

Accepted name: phosphorylase kinase

Reaction: **2** ATP + phosphorylase *b* = **2** ADP + phosphorylase *a*

Other name(s): dephosphophosphorylase kinase; glycogen phosphorylase kinase; PHK; phosphorylase *b* kinase; phosphorylase B kinase; phosphorylase kinase (phosphorylating); STK17

Systematic name: ATP:phosphorylase-*b* phosphotransferase

Comments: Requires Ca^{2+} and calmodulin for activity. The enzyme phosphorylates *a* specific serine residue in each of the subunits of the dimeric phosphorylase *b*. For muscle phosphorylase but not liver phosphorylase, this is accompanied by a further dimerization to form a tetrameric phosphorylase. The enzyme couples muscle contraction with energy production via glycogenolysis—glycolysis by catalysing the Ca^{2+}-dependent phosphorylation and activation of glycogen phosphorylase *b* [879]. The γ subunit of the tetrameric enzyme is the catalytic subunit.

References: [1779, 1780, 2798, 2461, 879, 673, 2047]

[EC 2.7.11.19 created 1961 as EC 2.7.1.38, transferred 2005 to EC 2.7.11.19]

EC 2.7.11.20

Accepted name: elongation factor 2 kinase

Reaction: ATP + [elongation factor 2] = ADP + [elongation factor 2] phosphate

Other name(s): Ca/CaM-kinase III; calmodulin-dependent protein kinase III; CaM kinase III; eEF2 kinase; eEF2K; EF2K; STK19

Systematic name: ATP:[elongation factor 2] phosphotransferase

Comments: Requires Ca^{2+} and calmodulin for activity. The enzyme can also be phosphorylated by the catalytic subunit of EC 2.7.11.11, cAMP-dependent protein kinase. Elongation factor 2 is phosphorylated in several cell types in response to various growth factors, hormones and other stimuli that raise intracellular Ca^{2+} [2272, 1333].

References: [2272, 1333, 1714, 3023, 409, 2979]

[EC 2.7.11.20 created 2005]

EC 2.7.11.21

Accepted name: polo kinase

Reaction: ATP + a protein = ADP + a phosphoprotein

Other name(s): Cdc5; Cdc5p; Plk; PLK; Plk1; Plo1; POLO kinase; polo serine-threonine kinase; polo-like kinase; polo-like kinase 1; serine/threonine-specific *Drosophila* kinase polo; STK21

Systematic name: ATP:protein phosphotransferase (spindle-pole-dependent)

Comments: The enzyme associates with the spindle pole during mitosis and is thought to play an important role in the dynamic function of the mitotic spindle during chromosome segregation. The human form of the enzyme, Plk1, does not phosphorylate histone H1, enolase and phosvitin but it can phosphorylate myelin basic protein and microtubule-associated protein MAP-2, although to a lesser extent than casein [1097].

References: [2019, 1097, 2357, 2535]

[EC 2.7.11.21 created 2005 (EC 2.7.1.37 part-incorporated 2005)]

EC 2.7.11.22

Accepted name: cyclin-dependent kinase

Reaction: ATP + a protein = ADP + a phosphoprotein

Other name(s): Bur1; Bur1 Cdk; Cak1; Cak1p; cdc2; cdc2 kinase; Cdc28p; CDK; cdk-activating kinase; Cdk-activating protein kinase; cdk1; cdk2; Cdk2; cdk3; cdk4; cdk5; cdk6; cdk7; cdk8; cdk9; cyclin A-activated cdc2; cyclin A-activated cdk2; cyclin D-cdk6 kinase; cyclin D-dependent kinase; cyclin E kinase; cyclin-A associated kinase; cyclin-dependent kinase 6; cyclin-dependent kinase-2; cyclin-dependent kinase-4; cyclin-dependent protein kinase activating kinase; cyk; D-type cyclin kinase; nclk; neuronal cdc2-like kinase; PCTAIRE-1; STK25

Systematic name: ATP:cyclin phosphotransferase

Comments: Activation of cyclin-dependent kinases requires association of the enzyme with a regulatory subunit referred to as a cyclin. It is the sequential activation and inactivation of cyclin-dependent kinases, through the periodic synthesis and destruction of cyclins, that provides the primary means of cell-cycle regulation.

References: [1522, 2610, 3974]

[EC 2.7.11.22 created 2005 (EC 2.7.1.37 part-incorporated 2005)]

EC 2.7.11.23

Accepted name: [RNA-polymerase]-subunit kinase

Reaction: ATP + [DNA-directed RNA polymerase] = ADP + phospho-[DNA-directed RNA polymerase]

Other name(s): CTD kinase; STK9

Systematic name: ATP:[DNA-directed RNA polymerase] phosphotransferase

Comments: The enzyme appears to be distinct from other protein kinases. It brings about multiple phosphorylations of the unique C-terminal repeat domain of the largest subunit of eukaryotic DNA-directed RNA polymerase (EC 2.7.7.6). The enzyme does not phosphorylate casein, phosvitin or histone.

References: [1890]

[EC 2.7.11.23 created 1992 as EC 2.7.1.141, transferred 2005 to EC 2.7.11.23]

EC 2.7.11.24

Accepted name: mitogen-activated protein kinase

Reaction: ATP + a protein = ADP + a phosphoprotein

Other name(s): c-Jun N-terminal kinase; Dp38; ERK; ERK1; ERK2; extracellular signal-regulated kinase; JNK; JNK3α1; LeMPK3; MAP kinase; MAP-2 kinase; MAPK; MBP kinase I; MBP kinase II; microtubule-associated protein 2 kinase; microtubule-associated protein kinase; myelin basic protein kinase; p38δ; p38-2; p42 mitogen-activated protein kinase; p42mapk; PMK-1; PMK-2; PMK-3; pp42; pp44mapk; p44mpk; SAPK; STK26; stress-activated protein kinase

Systematic name: ATP:protein phosphotransferase (MAPKK-activated)

Comments: Phosphorylation of specific tyrosine and threonine residues in the activation loop of this enzyme by EC 2.7.12.2, mitogen-activated protein kinase kinase (MAPKK) is necessary for enzyme activation. Once activated, the enzyme phosphorylates target substrates on serine or threonine residues followed by a proline [2946]. A distinguishing feature of all MAPKs is the conserved sequence Thr-Xaa-Tyr (TXY). Mitogen-activated protein kinase (MAPK) signal transduction pathways are among the most widespread mechanisms of cellular regulation. Mammalian MAPK pathways can be recruited by a wide variety of stimuli including hormones (e.g. insulin and growth hormone), mitogens (e.g. epidermal growth factor and platelet-derived growth factor), vasoactive peptides (e.g. angiotensin-II and endothelin), inflammatory cytokines of the tumour necrosis factor (TNF) family and environmental stresses such as osmotic shock, ionizing radiation and ischaemic injury.

References: [2832, 2940, 3133, 3326, 1985, 2946]

[EC 2.7.11.24 created 2005 (EC 2.7.1.37 part-incorporated 2005)]

EC 2.7.11.25

Accepted name: mitogen-activated protein kinase kinase kinase

Reaction: ATP + a protein = ADP + a phosphoprotein

Other name(s): cMos; cRaf; MAPKKK; MAP3K; MAP kinase kinase kinase; MEKK; MEKK1; MEKK2; MEKK3; MEK kinase; Mil/Raf; MLK-like mitogen-activated protein triple kinase; MLTK; MLTKa; MLTKb; REKS; STK28

Systematic name: ATP:protein phosphotransferase (MAPKKKK-activated)

Comments: This enzyme phosphorylates and activates its downstream protein kinase, EC 2.7.12.2, mitogen-activated protein kinase kinase (MAPKK) but requires MAPKKKK for activation. Some members of this family can be activated by p21-activated kinases (PAK/STE20) or Ras. While c-Raf and c-Mos activate the classical MAPK/ERK pathway, MEKK1 and MEKK2 preferentially activate the c-Jun N-terminal protein kinase(JNK)/stress-activated protein kinase (SAPK) pathway [1105]. Mitogen-activated protein kinase (MAPK) signal transduction pathways are among the most widespread mechanisms of cellular regulation. Mammalian MAPK pathways can be recruited by a wide variety of stimuli including hormones (e.g. insulin and growth hormone), mitogens (e.g. epidermal growth factor and platelet-derived growth factor), vasoactive peptides (e.g. angiotensin-II and endothelin), inflammatory cytokines of the tumour necrosis factor (TNF) family and environmental stresses such as osmotic shock, ionizing radiation and ischaemic injury.

References: [3763, 1105, 3698]

[EC 2.7.11.25 created 2005 (EC 2.7.1.37 part-incorporated 2005)]

EC 2.7.11.26

Accepted name: *tau*-protein kinase

Reaction: ATP + [*tau*-protein] = ADP + *O*-phospho-[*tau*-protein]

Other name(s): ATP:*tau*-protein *O*-hosphotransferase; brain protein kinase PK40erk; cdk5/p20; CDK5/p23; glycogen synthase kinase-3β; GSK; protein tau kinase; STK31; tau kinase; [*tau*-protein] kinase; *tau*-protein kinase I; *tau*-protein kinase II; tau-tubulin kinase; TPK; TPK I; TPK II; TTK

Systematic name: ATP:[*tau*-protein] *O*-phosphotransferase

Comments: Activated by tubulin. Involved in the formation of paired helical filaments, which are the main fibrous component of all fibrillary lesions in brain and are associated with Alzheimer's disease.

References: [1454, 2069, 2238, 96]

[EC 2.7.11.26 created 1990 as EC 2.7.1.135, transferred 2005 to EC 2.7.11.27]

EC 2.7.11.27

Accepted name: [acetyl-CoA carboxylase] kinase

Reaction: ATP + [acetyl-CoA carboxylase] = ADP + [acetyl-CoA carboxylase] phosphate

Other name(s): acetyl coenzyme A carboxylase kinase (phosphorylating); acetyl-CoA carboxylase bound kinase; acetyl-CoA carboxylase kinase; acetyl-CoA carboxylase kinase (cAMP-independent); acetyl-CoA carboxylase kinase 2; acetyl-CoA carboxylase kinase-2; acetyl-CoA carboxylase kinase-3 (AMP-activated); acetyl-coenzyme A carboxylase kinase; ACK2; ACK3; AMPK; I-peptide kinase; STK5
Systematic name: ATP:[acetyl-CoA carboxylase] phosphotransferase
Comments: Phosphorylates and inactivates EC 6.4.1.2, acetyl-CoA carboxylase, which can be dephosphorylated and reactivated by EC 3.1.3.17, [phosphorylase] phosphatase. The enzyme is more active towards the dimeric form of acetyl-CoA carboxylase than the polymeric form [1268]. Phosphorylates serine residues.
References: [1496, 1935, 2362, 2288, 1268]

[EC 2.7.11.27 created 1990 as EC 2.7.1.128 (EC 2.7.1.111 created 1984, incorporated 1992), transferred 2005 to EC 2.7.11.27]

EC 2.7.11.28

Accepted name: tropomyosin kinase
Reaction: ATP + tropomyosin = ADP + *O*-phosphotropomyosin
Other name(s): tropomyosin kinase (phosphorylating); STK
Systematic name: ATP:tropomyosin *O*-phosphotransferase
Comments: The enzyme phosphorylates casein equally well, and histone and phosvitin to a lesser extent. The acceptor is a serine residue in the protein.
References: [696, 2297, 3789]

[EC 2.7.11.28 created 1990 as EC 2.7.1.132, transferred 2005 to EC 2.7.11.28]

EC 2.7.11.29

Accepted name: low-density-lipoprotein receptor kinase
Reaction: ATP + [low-density-lipoprotein receptor]-L-serine = ADP + [low-density-lipoprotein receptor]-*O*-phospho-L-serine
Other name(s): ATP:low-density-lipoprotein-L-serine *O*-phosphotransferase; LDL receptor kinase; [low-density-lipoprotein] kinase; low-density lipoprotein kinase; low-density-lipoprotein receptor kinase (phosphorylating); STK7
Systematic name: ATP:[low-density-lipoprotein receptor]-L-serine *O*-phosphotransferase
Comments: Phosphorylates the last serine residue (Ser-833) in the cytoplasmic domain of the low-density lipoprotein receptor from bovine adrenal cortex. Casein can also act as a substrate but with lower affinity. GTP can act instead of ATP.
References: [1694, 1695]

[EC 2.7.11.29 created 1990 as EC 2.7.1.131, transferred 2005 to EC 2.7.11.29]

EC 2.7.11.30

Accepted name: receptor protein serine/threonine kinase
Reaction: ATP + [receptor-protein] = ADP + [receptor-protein] phosphate
Other name(s): activin receptor kinase; receptor type I serine/threonine protein kinase; receptor type II serine/threonine protein kinase; STK13; TGF-β kinase; receptor serine/threonine protein kinase
Systematic name: ATP:[receptor-protein] phosphotransferase
Comments: The transforming growth factor β (TGF-β) family of cytokines regulates cell proliferation, differentiation, recognition and death. Signalling occurs by the binding of ligand to the type II receptor, which is the constitutively active kinase. Bound TGF-β is then recognized by receptor I, which is phosphorylated and can propagate the signal to downstream substrates [3897, 683].
References: [3897, 2153, 683]

[EC 2.7.11.30 created 2005 (EC 2.7.1.37 part-incorporated 2005)]

EC 2.7.11.31

Accepted name: [hydroxymethylglutaryl-CoA reductase (NADPH)] kinase

Reaction: ATP + [hydroxymethylglutaryl-CoA reductase (NADPH)] = ADP + [hydroxymethylglutaryl-CoA reductase (NADPH)] phosphate

Other name(s): AMPK; AMP-activated protein kinase; HMG-CoA reductase kinase; β-hydroxy-β-methylglutaryl-CoA reductase kinase; [hydroxymethylglutaryl-CoA reductase ($NADPH_2$)] kinase; 3-hydroxy-3-methylglutaryl coenzyme A reductase kinase; 3-hydroxy-3-methylglutaryl-CoA reductase kinase; hydroxymethylglutaryl coenzyme A reductase kinase; hydroxymethylglutaryl coenzyme A reductase kinase (phosphorylating); hydroxymethylglutaryl-CoA reductase kinase; reductase kinase; STK29

Systematic name: ATP:[hydroxymethylglutaryl-CoA reductase (NADPH)] phosphotransferase

Comments: The enzyme is activated by AMP. EC 1.1.1.34, hydroxymethylglutaryl-CoA reductase (NADPH) is inactivated by the phosphorylation of the enzyme protein. Histones can also act as acceptors. The enzyme can also phosphorylate hepatic acetyl-CoA carboxylase (EC 6.4.1.2) and adipose hormone-sensitive lipase (EC 3.1.1.79) [3800]. Thr-172 within the catalytic subunit (α-subunit) is the major site phosphorylated by the AMP-activated protein kinase kinase [3327]. GTP can act instead of ATP [898]

References: [251, 1051, 1445, 898, 3800, 635, 3327]

[EC 2.7.11.31 created 1984 as EC 2.7.1.109, transferred 2005 to EC 2.7.11.31]

EC 2.7.11.32

Accepted name: [pyruvate, phosphate dikinase] kinase

Reaction: ADP + [pyruvate, phosphate dikinase] = AMP + [pyruvate, phosphate dikinase] phosphate

Other name(s): PPDK regulatory protein (ambiguous); pyruvate; phosphate dikinase regulatory protein (ambiguous); bifunctional dikinase regulatory protein (ambiguous)

Systematic name: ADP:[pyruvate, phosphate dikinase] phosphotransferase

Comments: The enzymes from the plants *Zea mays* (maize) and *Arabidopsis thaliana* are bifunctional and catalyse both the phosphorylation and dephosphorylation of EC 2.7.9.1 (pyruvate, phosphate dikinase). *cf.* EC 2.7.4.27, [pyruvate, phosphate dikinase]-phosphate phosphotransferase [435, 508, 433, 509]. The enzyme is specific for a reaction intermediate form of EC 2.7.9.1, and phosphorylates a threonine located adjacent to the catalytic histidine. The phosphorylation only takes place if the histidine is already phosphorylated [508, 433, 509].

References: [434, 435, 508, 433, 509]

[EC 2.7.11.32 created 2012]

EC 2.7.11.33

Accepted name: [pyruvate, water dikinase] kinase

Reaction: ADP + [pyruvate, water dikinase] = AMP + [pyruvate, water dikinase] phosphate

Other name(s): PSRP (ambiguous); PEPS kinase

Systematic name: ADP:[pyruvate, water dikinase] phosphotransferase

Comments: The enzyme from the bacterium *Escherichia coli* is bifunctional and catalyses both the phosphorylation and dephosphorylation of EC 2.7.9.2, pyruvate, water dikinase. *cf.* EC 2.7.4.28, ([pyruvate, water dikinase] phosphate) phosphotransferase [432]. The enzyme is specific for a reaction intermediate form of EC 2.7.9.2, where it phosphorylates an active site histidine [432]. It has no activity toward EC 2.7.9.1 pyruvate, phosphate dikinase (*cf.* EC 2.7.11.32, [pyruvate, phosphate dikinase] kinase).

References: [432]

[EC 2.7.11.33 created 2012]

EC 2.7.12 Dual-specificity kinases (those acting on Ser/Thr and Tyr residues)

EC 2.7.12.1

Accepted name: dual-specificity kinase
Reaction: ATP + a protein = ADP + a phosphoprotein
Other name(s): ADK1; *Arabidopsis* dual specificity kinase 1; CLK1; dDYRK2; Mps1p
Systematic name: ATP:protein phosphotransferase (Ser/Thr- and Tyr-phosphorylating)
Comments: This family of enzymes can phosphorylate both Ser/Thr and Tyr residues.
References: [58, 1878, 2217, 2023]

[EC 2.7.12.1 created 2005 (EC 2.7.1.37 part-incorporated 2005)]

EC 2.7.12.2

Accepted name: mitogen-activated protein kinase kinase
Reaction: ATP + a protein = ADP + a phosphoprotein
Other name(s): MAP kinase kinase; MAP kinase kinase 4; MAP kinase kinase 7; MAP kinase or ERK kinase; MAP2K; MAPKK; MAPKK1; MEK; MEK1; MEK2; MKK; MKK2; MKK4; MKK6; MKK7; STK27
Systematic name: ATP:protein phosphotransferase (MAPKKK-activated)
Comments: This enzyme is a dual-specific protein kinase and requires mitogen-activated protein kinase kinase kinase (MAPKKK) for activation. It is required for activation of EC 2.7.11.24, mitogen-activated protein kinase. Phosphorylation of MEK1 by Raf involves phosphorylation of two serine residues [2689]. Mitogen-activated protein kinase (MAPK) signal transduction pathways are among the most widespread mechanisms of cellular regulation. Mammalian MAPK pathways can be recruited by a wide variety of stimuli including hormones (e.g. insulin and growth hormone), mitogens (e.g. epidermal growth factor and platelet-derived growth factor), vasoactive peptides (e.g. angiotensin-II and endothelin), inflammatory cytokines of the tumour necrosis factor (TNF) family and environmental stresses such as osmotic shock, ionizing radiation and ischaemic injury.
References: [2306, 492, 3903, 53, 2689, 1208]

[EC 2.7.12.2 created 2005]

EC 2.7.13 Protein-histidine kinases

EC 2.7.13.1

Accepted name: protein-histidine *pros*-kinase
Reaction: ATP + protein L-histidine = ADP + protein N^{π}-phospho-L-histidine
Other name(s): ATP:protein-L-histidine *N*-*pros*-phosphotransferase; histidine kinase (ambiguous); histidine protein kinase (ambiguous); protein histidine kinase (ambiguous); protein kinase (histidine) (ambiguous); HK2
Systematic name: ATP:protein-L-histidine N^{π}-phosphotransferase
Comments: A number of histones can act as acceptor.
References: [990, 1402]

[EC 2.7.13.1 created 1989 as EC 2.7.3.11, transferred 2005 to EC 2.7.13.1]

EC 2.7.13.2

Accepted name: protein-histidine *tele*-kinase
Reaction: ATP + protein L-histidine = ADP + protein N^{τ}-phospho-L-histidine
Other name(s): ATP:protein-L-histidine *N*-*tele*-phosphotransferase; histidine kinase (ambiguous); histidine protein kinase (ambiguous); protein histidine kinase (ambiguous); protein kinase (histidine) (ambiguous); HK3
Systematic name: ATP:protein-L-histidine N^{τ}-phosphotransferase
Comments: A number of histones can act as acceptor.
References: [990, 1402]

[EC 2.7.13.2 created 1989 as EC 2.7.3.12, transferred 2005 to EC 2.7.13.2]

EC 2.7.13.3

Accepted name: histidine kinase

Reaction: ATP + protein L-histidine = ADP + protein *N*-phospho-L-histidine

Other name(s): EnvZ; histidine kinase (ambiguous); histidine protein kinase (ambiguous); protein histidine kinase (ambiguous); protein kinase (histidine) (ambiguous); HK1; HP165; Sln1p

Systematic name: ATP:protein-L-histidine *N*-phosphotransferase

Comments: This entry has been included to accommodate those protein-histidine kinases for which the phosphorylation site has not been established (i.e. either the *pros*- or *tele*-nitrogen of histidine). A number of histones can act as acceptor.

References: [1775, 4003, 255, 2686, 2893]

[EC 2.7.13.3 created 2005]

EC 2.7.14 Protein-arginine kinases

EC 2.7.14.1

Accepted name: protein arginine kinase

Reaction: ATP + a [protein]-L-arginine = ADP + a [protein]-N^{ω}-phospho-L-arginine

Other name(s): McsB

Systematic name: ATP:[protein]-L-arginine N^{ω}-phosphotransferase

Comments: The enzyme, characterized from Gram-positive bacteria, is involved in the regulation of the bacterial stress response.

References: [977, 833, 3086]

[EC 2.7.14.1 created 2014]

EC 2.7.99 Other protein kinases

EC 2.7.99.1

Accepted name: triphosphate—protein phosphotransferase

Reaction: triphosphate + [microsomal-membrane protein] = diphosphate + phospho-[microsomal-membrane protein]

Other name(s): diphosphate:microsomal-membrane-protein *O*-phosphotransferase (erroneous); DiPPT (erroneous); pyrophosphate:protein phosphotransferase (erroneous); diphosphate—protein phosphotransferase (erroneous); diphosphate:[microsomal-membrane-protein] *O*-phosphotransferase (erroneous)

Systematic name: triphosphate:[microsomal-membrane-protein] phosphotransferase

Comments: This enzyme was originally thought to use diphosphate as substrate [1849] but this has since been disproved [3588]. The activity is observed as the second part of a biphasic reaction after depletion of ATP. Tripolyphosphate is a contaminant of [γ-^{32}P]ATP.

References: [1849, 3588]

[EC 2.7.99.1 created 1983 as EC 2.7.1.104, transferred 2005 to EC 2.7.99.1]

EC 2.8 Transferring sulfur-containing groups

This subclass contains enzymes that transfer a sulfur-containing group from a donor to an acceptor. Sub-subclasses are based on the type of sulfur group transferred: sulfur atoms (sulfurtransferases; EC 2.8.1), sulfate groups (sulfotransferases; EC 2.8.2), CoA (EC 2.8.3), or alkylthio groups (EC 2.8.4).

EC 2.8.1 Sulfurtransferases

EC 2.8.1.1

Accepted name: thiosulfate sulfurtransferase
Reaction: thiosulfate + cyanide = sulfite + thiocyanate
Other name(s): thiosulfate cyanide transsulfurase; thiosulfate thiotransferase; rhodanese; rhodanase
Systematic name: thiosulfate:cyanide sulfurtransferase
Comments: A few other sulfur compounds can act as donors.
References: [3289, 3290, 3826]

[EC 2.8.1.1 created 1961]

EC 2.8.1.2

Accepted name: 3-mercaptopyruvate sulfurtransferase
Reaction: 3-mercaptopyruvate + reduced thioredoxin = pyruvate + hydrogen sulfide + oxidized thioredoxin (overall reaction)
(1a) 3-mercaptopyruvate + [3-mercaptopyruvate sulfurtransferase]-L-cysteine = pyruvate + [3-mercaptopyruvate sulfurtransferase]-*S*-sulfanyl-L-cysteine
(1b) [3-mercaptopyruvate sulfurtransferase]-*S*-sulfanyl-L-cysteine + reduced thioredoxin = hydrogen sulfide + [3-mercaptopyruvate sulfurtransferase]-L-cysteine + oxidized thioredoxin
Other name(s): β-mercaptopyruvate sulfurtransferase; TUM1 (gene name); MPST (gene name); 3-mercaptopyruvate:cyanide sulfurtransferase
Systematic name: 3-mercaptopyruvate:sulfide sulfurtransferase
Comments: The enzyme catalyses a transsulfuration reaction from 3-mercaptopyruvate to an internal cysteine residue. In the presence of a dithiol such as reduced thioredoxin or dihydrolipoate, the sulfanyl sulfur is released as hydrogen sulfide. The enzyme participates in a sulfur relay process that leads to the 2-thiolation of some tRNAs and to protein urmylation by transferring sulfur between the NFS1 cysteine desulfurase (EC 2.8.1.7) and the MOCS3 sulfurtransferase (EC 2.8.1.11).
References: [903, 3291, 1422, 3636, 3622, 2384, 3184, 2244]

[EC 2.8.1.2 created 1961, modified 2018]

EC 2.8.1.3

Accepted name: thiosulfate—thiol sulfurtransferase
Reaction: thiosulfate + **2** glutathione = sulfite + glutathione disulfide + sulfide
Other name(s): glutathione-dependent thiosulfate reductase; sulfane reductase; sulfane sulfurtransferase
Systematic name: thiosulfate:thiol sulfurtransferase
Comments: The primary product is glutathione hydrodisulfide, which reacts with glutathione to give glutathione disulfide and sulfide. L-Cysteine can also act as acceptor.
References: [2652, 3220, 3606]

[EC 2.8.1.3 created 1982]

EC 2.8.1.4

Accepted name: tRNA uracil 4-sulfurtransferase
Reaction: ATP + [ThiI sulfur-carrier protein]-*S*-sulfanyl-L-cysteine + uracil in tRNA + **2** reduced ferredoxin [iron-sulfur] cluster = AMP + diphosphate + 4-thiouracil in tRNA + [ThiI sulfur-carrier protein]-L-cysteine + **2** oxidized ferredoxin [iron-sulfur] cluster
Other name(s): *thiI* (gene name); transfer ribonucleate sulfurtransferase (ambiguous); RNA sulfurtransferase (ambiguous); ribonucleate sulfurtransferase (ambiguous); transfer RNA sulfurtransferase (ambiguous); transfer RNA thiolase (ambiguous); L-cysteine:tRNA sulfurtransferase (incorrect); tRNA sulfurtransferase (ambiguous)
Systematic name: [ThiI sulfur-carrier protein]-*S*-sulfanyl-L-cysteine:uracil in tRNA sulfurtransferase

Comments: The enzyme, found in bacteria and archaea, is activated by EC 2.8.1.7, cysteine desulfurase, which transfers a sulfur atom to an internal L-cysteine residue, forming a cysteine persulfide. The activated enzyme then transfers the sulfur to a uridine in a tRNA chain in a reaction that requires ATP. The enzyme from the bacterium *Escherichia coli* forms 4-thiouridine only at position 8 of tRNA. The enzyme also participates in the biosynthesis of the thiazole moiety of thiamine, but different domains are involved in the two processes.

References: [10, 1256, 1983, 3888, 1570, 2340, 1876, 2444, 2014]

[EC 2.8.1.4 created 1984, modified 2017]

EC 2.8.1.5

Accepted name: thiosulfate—dithiol sulfurtransferase

Reaction: thiosulfate + dithioerythritol = sulfite + 4,5-*cis*-dihydroxy-1,2-dithiacyclohexane (i.e. oxidized dithioerythritol) + sulfide

Other name(s): thiosulfate reductase; TSR

Systematic name: thiosulfate:dithioerythritol sulfurtransferase

Comments: The enzyme from *Chlorella* shows very little activity towards monothiols such as glutathione and cysteine (*cf*. EC 2.8.1.3 thiosulfate—thiolsulfurtransferase). The enzyme probably transfers the sulfur atom onto one thiol group to form -S-S-, and sulfide is spontaneously expelled from this by reaction with the other thiol group. May be identical with EC 2.8.1.1 thiosulfate sulfurtransferase.

References: [3084]

[EC 2.8.1.5 created 1989, modified 1999]

EC 2.8.1.6

Accepted name: biotin synthase

Reaction: dethiobiotin + sulfur-(sulfur carrier) + **2** *S*-adenosyl-L-methionine + **2** reduced [2Fe-2S] ferredoxin = biotin + (sulfur carrier) + **2** L-methionine + **2** 5′-deoxyadenosine + **2** oxidized [2Fe-2S] ferredoxin

Other name(s): dethiobiotin:sulfur sulfurtransferase

Systematic name: dethiobiotin:sulfur-(sulfur carrier) sulfurtransferase

Comments: The enzyme binds a [4Fe-4S] and a [2Fe-2S] cluster. In every reaction cycle, the enzyme consumes two molecules of AdoMet, each producing 5′-deoxyadenosine and a putative dethiobiotinyl carbon radical. Reaction with another equivalent of AdoMet results in abstraction of the C6 methylene *pro-S* hydrogen atom from 9-mercaptodethiobiotin, and the resulting carbon radical is quenched via formation of an intramolecular C-S bond, thus closing the biotin thiophane ring. The sulfur donor is believed to be the [2Fe-2S] cluster, which is sacrificed in the process, so that *in vitro* the reaction is a single turnover. *In vivo*, the [2Fe-2S] cluster can be reassembled by the Isc or Suf iron-sulfur cluster assembly systems, to allow further catalysis.

References: [3559, 3210, 4046, 3605, 285, 2042, 3483, 2875]

[EC 2.8.1.6 created 1999, modified 2006, modified 2011, modified 2014]

EC 2.8.1.7

Accepted name: cysteine desulfurase

Reaction: L-cysteine + acceptor = L-alanine + S-sulfanyl-acceptor (overall reaction)
(1a) L-cysteine + [enzyme]-cysteine = L-alanine + [enzyme]-*S*-sulfanylcysteine
(1b) [enzyme]-*S*-sulfanylcysteine + acceptor = [enzyme]-cysteine + S-sulfanyl-acceptor

Other name(s): IscS; NIFS; NifS; SufS; cysteine desulfurylase

Systematic name: L-cysteine:acceptor sulfurtransferase

Comments: A pyridoxal-phosphate protein. The sulfur from free L-cysteine is first transferred to a cysteine residue in the active site, and then passed on to various other acceptors. The enzyme is involved in the biosynthesis of iron-sulfur clusters, thio-nucleosides in tRNA, thiamine, biotin, lipoate and pyranopterin (molybdopterin) [2242]. In *Azotobacter vinelandii*, this sulfur provides the inorganic sulfide required for nitrogenous metallocluster formation [4071].

References: [4071, 2242, 951]

[EC 2.8.1.7 created 2003, modified 2011]

EC 2.8.1.8

Accepted name: lipoyl synthase

Reaction: [protein]-N^6-(octanoyl)-L-lysine + an [Fe-S] cluster scaffold protein carrying a [4Fe-4S]$^{2+}$ cluster + **2** *S*-adenosyl-L-methionine + **2** oxidized [2Fe-2S] ferredoxin + **6** H$^+$ = [protein]-N^6-[(*R*)-dihydrolipoyl]-L-lysine + an [Fe-S] cluster scaffold protein + **2** sulfide + **4** Fe^{3+} + **2** L-methionine + **2** 5′-deoxyadenosine + **2** reduced [2Fe-2S] ferredoxin

Other name(s): *lipA* (gene name); LS; lipoate synthase; protein 6-*N*-(octanoyl)lysine:sulfur sulfurtransferase; protein N^6-(octanoyl)lysine:sulfur sulfurtransferase; protein N^6-(octanoyl)lysine:sulfur-(sulfur carrier) sulfurtransferase

Systematic name: [protein]-N^6-(octanoyl)-L-lysine:an [Fe-S] cluster scaffold protein carrying a [4Fe-4S]$^{2+}$ cluster sulfurtransferase

Comments: This enzyme catalyses the final step in the *de-novo* biosynthesis of the lipoyl cofactor, the attachment of two sulfhydryl groups to C_6 and C_8 of a pendant octanoyl chain. It is a member of the 'AdoMet radical' (radical SAM) family, all members of which produce the 5′-deoxyadenosin-5′-yl radical and methionine from AdoMet (*S*-adenosylmethionine) by the addition of an electron from an iron-sulfur centre. The enzyme contains two [4Fe-4S] clusters. The first cluster produces the radicals, which are converted into 5′-deoxyadenosine when they abstract hydrogen atoms from C_6 and C_8, respectively, leaving reactive radicals at these positions that interact with sulfur atoms within the second (auxiliary) cluster. Having donated two sulfur atoms, the auxiliary cluster is degraded during catalysis, but is regenerated immediately by the transfer of a new cluster from iron-sulfur cluster carrier proteins [2185]. Lipoylation is essential for the function of several key enzymes involved in oxidative metabolism, as it converts apoprotein into the biologically active holoprotein. Examples of such lipoylated proteins include pyruvate dehydrogenase (E_2 domain), 2-oxoglutarate dehydrogenase (E_2 domain), the branched-chain 2-oxoacid dehydrogenases and the glycine cleavage system (H protein) [566, 352]. An alternative lipoylation pathway involves EC 6.3.1.20, lipoate—protein ligase, which can lipoylate apoproteins using exogenous lipoic acid (or its analogues) [567].

References: [566, 352, 4067, 567, 3409, 2254, 2665, 2185]

[EC 2.8.1.8 created 2006, modified 2014, modified 2018]

EC 2.8.1.9

Accepted name: molybdenum cofactor sulfurtransferase

Reaction: molybdenum cofactor + L-cysteine + reduced acceptor + **2** H$^+$ = thio-molybdenum cofactor + L-alanine + H_2O + oxidized acceptor

Other name(s): molybdenum cofactor sulfurase; ABA3; HMCS; MoCo sulfurase; MoCo sulfurtransferase

Systematic name: L-cysteine:molybdenum cofactor sulfurtransferase

Comments: Contains pyridoxal phosphate. Replaces the equatorial oxo ligand of the molybdenum by sulfur via an enzyme-bound persulfide. The reaction occurs in prokaryotes and eukaryotes but MoCo sulfurtransferases are only found in eukaryotes. In prokaryotes the reaction is catalysed by two enzymes: cysteine desulfurase (EC 2.8.1.7), which is homologous to the N-terminus of eukaryotic MoCo sulfurtransferases, and a molybdo-enzyme specific chaperone which binds the MoCo and acts as an adapter protein.

References: [314, 1275, 3885]

[EC 2.8.1.9 created 2011, modified 2015]

EC 2.8.1.10

Accepted name: thiazole synthase

Reaction: 1-deoxy-D-xylulose 5-phosphate + 2-iminoacetate + thiocarboxy-[sulfur-carrier protein ThiS] = 2-[(2*R*,5*Z*)-2-carboxy-4-methylthiazol-5(2*H*)-ylidene]ethyl phosphate + [sulfur-carrier protein ThiS] + **2** H_2O

Other name(s): *thiG* (gene name)
Systematic name: 1-deoxy-D-xylulose 5-phosphate:thiol sulfurtransferase
Comments: H_2S can provide the sulfur *in vitro*. Part of the pathway for thiamine biosynthesis.
References: [2620, 757, 758, 3147, 1257, 1258]

[EC 2.8.1.10 created 2011, modified 2016]

EC 2.8.1.11

Accepted name: molybdopterin synthase sulfurtransferase
Reaction: [molybdopterin-synthase sulfur-carrier protein]-Gly-Gly-AMP + [cysteine desulfurase]-*S*-sulfanyl-L-cysteine + reduced acceptor = AMP + [molybdopterin-synthase sulfur-carrier protein]-Gly-NH-CH$_2$-C(O)SH + [cysteine desulfurase]-L-cysteine + oxidized acceptor
Other name(s): adenylyltransferase and sulfurtransferase MOCS3; Cnx5 (gene name); molybdopterin synthase sulfurylase
Systematic name: [cysteine desulfurase]-*S*-sulfanyl-L-cysteine:[molybdopterin-synthase sulfur-carrier protein]-Gly-Gly sulfurtransferase
Comments: The enzyme transfers sulfur to form a thiocarboxylate moiety on the C-terminal glycine of the small subunit of EC 2.8.1.12, molybdopterin synthase. In the human, the reaction is catalysed by the rhodanese-like C-terminal domain (*cf*. EC 2.8.1.1) of the MOCS3 protein, a bifunctional protein that also contains EC 2.7.7.80, molybdopterin-synthase adenylyltransferase, at the N-terminal domain.
References: [2169, 1922, 1218, 654]

[EC 2.8.1.11 created 2011, modified 2016]

EC 2.8.1.12

Accepted name: molybdopterin synthase
Reaction: cyclic pyranopterin phosphate + **2** [molybdopterin-synthase sulfur-carrier protein]-Gly-NH-CH$_2$-C(O)SH + H_2O = molybdopterin + **2** molybdopterin-synthase sulfur-carrier protein
Other name(s): MPT synthase
Systematic name: thiocarboxylated molybdopterin synthase:cyclic pyranopterin phosphate sulfurtransferase
Comments: Catalyses the synthesis of molybdopterin from cyclic pyranopterin monophosphate. Two sulfur atoms are transferred to cyclic pyranopterin monophosphate in order to form the characteristic ene-dithiol group found in the molybdenum cofactor. Molybdopterin synthase consists of two large subunits forming a central dimer and two small subunits (molybdopterin-synthase sulfur-carrier proteins) that are thiocarboxylated at the C-terminus by EC 2.8.1.11, molybdopterin synthase sulfurtransferase. The reaction occurs in prokaryotes and eukaryotes.
References: [667, 3908]

[EC 2.8.1.12 created 2011]

EC 2.8.1.13

Accepted name: tRNA-uridine 2-sulfurtransferase
Reaction: a [protein]-*S*-sulfanyl-L-cysteine + uacil34 in tRNA + ATP + reduced acceptor = a [protein]-L-cysteine + 2-thiouracil^{34} in tRNA + AMP + diphosphate + acceptor
Other name(s): *mnmA* (gene name)
Systematic name: [protein]-*S*-sulfanyl-L-cysteine:tRNA (uracil^{34}-2-*O*)-sulfurtransferase
Comments: The enzyme, found in bacteria, catalyses formation of the 2-thiouridine modification in the wobble position of tRNA^{Gln}, tRNA^{Lys} and tRNA^{Glu}.
References: [1571, 1439]

[EC 2.8.1.13 created 2015]

EC 2.8.1.14

Accepted name: tRNA-5-taurinomethyluridine 2-sulfurtransferase

Reaction: a [protein]-*S*-sulfanyl-L-cysteine + 5-taurinomethyluracil^{34} in tRNA + ATP + reduced acceptor = a [protein]-L-cysteine + 5-taurinomethyl-2-thiouracil^{34} in tRNA + AMP + diphosphate + acceptor

Other name(s): MTU1 (gene name); SLM3 (gene name); MTO$_2$ (gene name)

Systematic name: [protein]-*S*-sulfanyl-L-cysteine:tRNA (5-taurinomethyluracil^{34} 2-*O*)-sulfurtransferase

Comments: The enzyme, found in mitochondria, catalyses formation of 5-taurinomethyl-2-thiouridine in the wobble position of mitochondrial tRNA$^{\text{Gln}}$, tRNA$^{\text{Lys}}$ and tRNA$^{\text{Glu}}$.

References: [3611, 3761]

[EC 2.8.1.14 created 2015]

EC 2.8.1.15

Accepted name: tRNA-5-methyluridine^{54} 2-sulfurtransferase

Reaction: ATP + [TtuB sulfur-carrier protein]-Gly-NH-CH2-C(O)SH + 5-methyluracil^{54} in tRNA + H_2O = AMP + diphosphate + 5-methyl-2-thiouracil^{54} in tRNA + [TtuB sulfur-carrier protein]-Gly-Gly

Other name(s): TtuA

Systematic name: [TtuB sulfur-carrier protein]-Gly-NH-CH2-C(O)SH:tRNA (5-methyluridine^{54}-2-*O*)-sulfurtransferase

Comments: The enzyme, found in thermophilic bacteria and archaea, modifies the ribothymidine (5-methyluridine) residue at position 54 of tRNAs. Contains zinc and an [4Fe-4S] cluster. Some organisms, such as the archaeon *Pyrococcus horikoshii*, do not have a TtuB sulfur-carrier protein, and appear to use sulfide as the sulfur source.

References: [3187, 3188, 2398, 531]

[EC 2.8.1.15 created 2017]

EC 2.8.2 Sulfotransferases

EC 2.8.2.1

Accepted name: aryl sulfotransferase

Reaction: 3′-phosphoadenylyl sulfate + a phenol = adenosine 3′,5′-bisphosphate + an aryl sulfate

Other name(s): phenol sulfotransferase; sulfokinase; 1-naphthol phenol sulfotransferase; 2-naphtholsulfotransferase; 4-nitrocatechol sulfokinase; arylsulfotransferase; dopamine sulfotransferase; *p*-nitrophenol sulfotransferase; phenol sulfokinase; ritodrine sulfotransferase; PST; 3′-phosphoadenylyl-sulfate:phenol sulfotransferase

Systematic name: 3′-phosphoadenylyl-sulfate:phenol sulfonotransferase

Comments: A number of aromatic compounds can act as acceptors. Organic hydroxylamines are not substrates (*cf.* EC 2.8.2.9 tyrosine-ester sulfotransferase).

References: [2922, 3134]

[EC 2.8.2.1 created 1961, modified 1980]

EC 2.8.2.2

Accepted name: alcohol sulfotransferase

Reaction: 3′-phosphoadenylyl sulfate + an alcohol = adenosine 3′,5′-bisphosphate + an alkyl sulfate

Other name(s): hydroxysteroid sulfotransferase; 3β-hydroxy steroid sulfotransferase; Δ^5-3β-hydroxysteroid sulfokinase; 3-hydroxysteroid sulfotransferase; HST; 5α-androstenol sulfotransferase; cholesterol sulfotransferase; dehydroepiandrosterone sulfotransferase; estrogen sulfokinase; estrogen sulfotransferase; steroid alcohol sulfotransferase; steroid sulfokinase; steroid sulfotransferase; sterol sulfokinase; sterol sulfotransferase; alcohol/hydroxysteroid sulfotransferase; 3β-hydroxysteroid sulfotransferase; 3′-phosphoadenylyl-sulfate:alcohol sulfotransferase

Systematic name: 3′-phosphoadenylyl-sulfate:alcohol sulfonotransferase

Comments: Primary and secondary alcohols, including aliphatic alcohols, ascorbic acid, chloramphenicol, ephedrine and hydroxysteroids, but not phenolic steroids, can act as acceptors (*cf.* EC 2.8.2.15 steroid sulfotransferase).

References: [2080, 2081]

[EC 2.8.2.2 created 1961, modified 1980]

EC 2.8.2.3

Accepted name: amine sulfotransferase

Reaction: 3′-phosphoadenylyl sulfate + an amine = adenosine 3′,5′-bisphosphate + a sulfamate

Other name(s): arylamine sulfotransferase; amine *N*-sulfotransferase; 3′-phosphoadenylyl-sulfate:amine *N*-sulfotransferase

Systematic name: 3′-phosphoadenylyl-sulfate:amine *N*-sulfonotransferase

Comments: A large number of primary and secondary amines can act as acceptors, including aniline, 2-naphthylamine, cyclohexylamine and octylamine.

References: [2803, 2952]

[EC 2.8.2.3 created 1965]

EC 2.8.2.4

Accepted name: estrone sulfotransferase

Reaction: 3′-phosphoadenylyl sulfate + estrone = adenosine 3′,5′-bisphosphate + estrone 3-sulfate

Other name(s): 3′-phosphoadenylyl sulfate-estrone 3-sulfotransferase; estrogen sulfotransferase; estrogen sulphotransferase; oestrogen sulphotransferase; 3′-phosphoadenylylsulfate:oestrone sulfotransferase; 3′-phosphoadenylyl-sulfate:estrone 3-sulfotransferase

Systematic name: 3′-phosphoadenylyl-sulfate:estrone 3-sulfonotransferase

References: [15, 2957, 13]

[EC 2.8.2.4 created 1965]

EC 2.8.2.5

Accepted name: chondroitin 4-sulfotransferase

Reaction: 3′-phosphoadenylyl sulfate + chondroitin = adenosine 3′,5′-bisphosphate + chondroitin 4′-sulfate

Other name(s): chondroitin sulfotransferase; 3′-phosphoadenylyl-sulfate:chondroitin 4′-sulfotransferase

Systematic name: 3′-phosphoadenylyl-sulfate:chondroitin 4′-sulfonotransferase

Comments: The sulfation takes place at the 4-position of *N*-acetyl-galactosamine residues of chondroitin. Not identical with EC 2.8.2.17 chondroitin 6-sulfotransferase.

References: [1191, 2407, 2408, 3401, 3402, 3403]

[EC 2.8.2.5 created 1965, modified 1986]

EC 2.8.2.6

Accepted name: choline sulfotransferase

Reaction: 3′-phosphoadenylyl sulfate + choline = adenosine 3′,5′-bisphosphate + choline sulfate

Other name(s): choline sulphokinase; 3′-phosphoadenylyl-sulfate:choline sulfotransferase

Systematic name: 3′-phosphoadenylyl-sulfate:choline sulfonotransferase

References: [2575]

[EC 2.8.2.6 created 1972]

EC 2.8.2.7

Accepted name: UDP-*N*-acetylgalactosamine-4-sulfate sulfotransferase

Reaction: 3′-phosphoadenylyl sulfate + UDP-*N*-acetyl-D-galactosamine 4-sulfate = adenosine 3′,5′-bisphosphate + UDP-*N*-acetyl-D-galactosamine 4,6-bissulfate
Other name(s): uridine diphosphoacetylgalactosamine 4-sulfate sulfotransferase; uridine diphospho-*N*-acetylgalactosamine 4-sulfate sulfotransferase; 3′-phosphoadenylyl-sulfate:UDP-*N*-acetyl-D-galactosamine-4-sulfate 6-sulfotransferase
Systematic name: 3′-phosphoadenylyl-sulfate:UDP-*N*-acetyl-D-galactosamine-4-sulfate 6-sulfonotransferase
References: [1224]

[EC 2.8.2.7 created 1972]

EC 2.8.2.8

Accepted name: [heparan sulfate]-glucosamine *N*-sulfotransferase
Reaction: 3′-phosphoadenylyl sulfate + [heparan sulfate]-glucosamine = adenosine 3′,5′-bisphosphate + [heparan sulfate]-*N*-sulfoglucosamine
Other name(s): heparin *N*-sulfotransferase; 3′-phosphoadenylylsulfate:*N*-desulfoheparin sulfotransferase; PAPS:*N*-desulfoheparin sulfotransferase; PAPS:DSH sulfotransferase; *N*-HSST; *N*-heparan sulfate sulfotransferase; heparan sulfate *N*-deacetylase/*N*-sulfotransferase; heparan sulfate 2-*N*-sulfotransferase; heparan sulfate *N*-sulfotransferase; heparan sulfate sulfotransferase; *N*-desulfoheparin sulfotransferase; desulfoheparin sulfotransferase; 3′-phosphoadenylyl-sulfate:*N*-desulfoheparin *N*-sulfotransferase; heparitin sulfotransferase; 3′-phosphoadenylyl-sulfate:heparitin *N*-sulfotransferase; 3′-phosphoadenylyl-sulfate:[heparan sulfate]-glucosamine *N*-sulfotransferase
Systematic name: 3′-phosphoadenylyl-sulfate:[heparan sulfate]-glucosamine *N*-sulfonotransferase
Comments: The enzyme also catalyses the sulfation of chondroitin 4-sulfate and dermatan sulfate, but to a much more limited extent.
References: [3404, 821, 1521]

[EC 2.8.2.8 created 1972, modified 2001 (EC 2.8.2.12 created 1972, incorporated 2001)]

EC 2.8.2.9

Accepted name: tyrosine-ester sulfotransferase
Reaction: 3′-phosphoadenylyl sulfate + L-tyrosine methyl ester = adenosine 3′,5′-bisphosphate + L-tyrosine methyl ester 4-sulfate
Other name(s): aryl sulfotransferase IV; L-tyrosine methyl ester sulfotransferase; 3′-phosphoadenylyl-sulfate:L-tyrosine-methyl-ester sulfotransferase
Systematic name: 3′-phosphoadenylyl-sulfate:L-tyrosine-methyl-ester sulfonotransferase
Comments: Phenols and organic hydroxylamines can act as acceptors (*cf.* EC 2.8.2.1 aryl sulfotransferase).
References: [786, 2170, 3135]

[EC 2.8.2.9 created 1972, deleted 1980, reinstated 1984]

EC 2.8.2.10

Accepted name: *Renilla*-luciferin sulfotransferase
Reaction: 3′-phosphoadenylyl sulfate + *Renilla* luciferin = adenosine 3′,5′-bisphosphate + luciferyl sulfate
Other name(s): luciferin sulfotransferase; luciferin sulfokinase; luciferin sulfokinase (3′-phosphoadenylyl sulfate:luciferin sulfotransferase); 3′-phosphoadenylyl-sulfate:*Renilla* luciferin sulfotransferase
Systematic name: 3′-phosphoadenylyl-sulfate:*Renilla* luciferin sulfonotransferase
Comments: The product may be identical with *Watasenia* luciferin.
References: [617]

[EC 2.8.2.10 created 1972, modified 1982]

EC 2.8.2.11

Accepted name: galactosylceramide sulfotransferase

Reaction: 3′-phosphoadenylyl sulfate + a galactosylceramide = adenosine 3′,5′-bisphosphate + a galactosylceramidesulfate
Other name(s): GSase; 3′-phosphoadenosine-5′-phosphosulfate-cerebroside sulfotransferase; galactocerebroside sulfotransferase; galactolipid sulfotransferase; glycolipid sulfotransferase; glycosphingolipid sulfotransferase; 3′-phosphoadenylyl-sulfate:galactosylceramide 3′-sulfotransferase
Systematic name: 3′-phosphoadenylyl-sulfate:galactosylceramide 3′-sulfonotransferase
Comments: Also acts on lactosylceramide.
References: [2199, 3003]

[EC 2.8.2.11 created 1972, modified 1976]

[2.8.2.12 Deleted entry. heparitin sulfotransferase. Enzyme identical to EC 2.8.2.8, [heparan sulfate]-glucosamine N-sulfotransferase]

[EC 2.8.2.12 created 1972, deleted 2001]

EC 2.8.2.13
Accepted name: psychosine sulfotransferase
Reaction: 3′-phosphoadenylyl sulfate + galactosylsphingosine = adenosine 3′,5′-bisphosphate + psychosine sulfate
Other name(s): PAPS:psychosine sulphotransferase; 3′-phosphoadenosine 5′-phosphosulfate-psychosine sulphotransferase; 3′-phosphoadenylyl-sulfate:galactosylsphingosine sulfotransferase
Systematic name: 3′-phosphoadenylyl-sulfate:galactosylsphingosine sulfonotransferase
References: [2498]

[EC 2.8.2.13 created 1976]

EC 2.8.2.14
Accepted name: bile-salt sulfotransferase
Reaction: (1) 3′-phosphoadenylyl sulfate + glycolithocholate = adenosine 3′,5′-bisphosphate + glycolithocholate 3-sulfate
(2) 3′-phosphoadenylyl sulfate + taurolithocholate = adenosine 3′,5′-bisphosphate + taurolithocholate sulfate
Other name(s): BAST I; bile acid:3′-phosphoadenosine-5′-phosphosulfate sulfotransferase; bile salt:3′phosphoadenosine-5′-phosphosulfate:sulfotransferase; bile acid sulfotransferase I; glycolithocholate sulfotransferase; 3′-phosphoadenylyl-sulfate:glycolithocholate sulfotransferase
Systematic name: 3′-phosphoadenylyl-sulfate:glycolithocholate sulfonotransferase
Comments: The formation of sulfate esters of bile acids is an essential step in the prevention of toxicity by monohydroxy bile acids in many species [199]. This enzyme is both a bile salt and a 3-hydroxysteroid sulfotransferase. In addition to the 5β-bile acid glycolithocholate, deoxycholate, 3β-hydroxy-5-cholenoate and dehydroepiandrosterone (3β-hydroxyandrost-5-en-17-one) also act as substrates [see also EC 2.8.2.2 (alcohol sulfotransferase) and EC 2.8.2.34 (glycochenodeoxycholate sulfotransferase)]. May be identical to EC 2.8.2.2 [199].
References: [530, 201, 199, 2976]

[EC 2.8.2.14 created 1978, modified 2005]

EC 2.8.2.15
Accepted name: steroid sulfotransferase
Reaction: 3′-phosphoadenylyl sulfate + a phenolic steroid = adenosine 3′,5′-bisphosphate + steroid *O*-sulfate
Other name(s): steroid alcohol sulfotransferase; 3′-phosphoadenylyl-sulfate:phenolic-steroid sulfotransferase
Systematic name: 3′-phosphoadenylyl-sulfate:phenolic-steroid sulfonotransferase
Comments: Broad specificity resembling EC 2.8.2.2 alcohol sulfotransferase, but also acts on estrone.
References: [14]

[EC 2.8.2.15 created 1984]

EC 2.8.2.16

Accepted name: thiol sulfotransferase
Reaction: 3′-phosphoadenylyl sulfate + a thiol = adenosine 3′,5′-bisphosphate + an *S*-alkyl thiosulfate
Other name(s): phosphoadenylylsulfate-thiol sulfotransferase; PAPS sulfotransferase; adenosine 3′-phosphate 5′-sulphatophosphate sulfotransferase; 3′-phosphoadenylyl-sulfate:thiol *S*-sulfotransferase
Systematic name: 3′-phosphoadenylyl-sulfate:thiol *S*-sulfonotransferase
Comments: Also acts on dithiols; substrates include glutathione, dithioerythritol and 2,3-mercaptopropanol.
References: [3082, 3083, 3577]

[EC 2.8.2.16 created 1984]

EC 2.8.2.17

Accepted name: chondroitin 6-sulfotransferase
Reaction: 3′-phosphoadenylyl sulfate + chondroitin = adenosine 3′,5′-bisphosphate + chondroitin 6′-sulfate
Other name(s): chondroitin 6-*O*-sulfotransferase; 3′-phosphoadenosine 5′-phosphosulfate (PAPS):chondroitin sulfate sulfotransferase; terminal 6-sulfotransferase; 3′-phosphoadenylyl-sulfate:chondroitin 6′-sulfotransferase
Systematic name: 3′-phosphoadenylyl-sulfate:chondroitin 6′-sulfonotransferase
Comments: The sulfation is at the 6-position of *N*-acetylgalactosamine residues of chondroitin. Not identical with EC 2.8.2.5 chondroitin 4-sulfotransferase.
References: [1191]

[EC 2.8.2.17 created 1986]

EC 2.8.2.18

Accepted name: cortisol sulfotransferase
Reaction: 3′-phosphoadenylyl sulfate + cortisol = adenosine 3′,5′-bisphosphate + cortisol 21-sulfate
Other name(s): glucocorticosteroid sulfotransferase; glucocorticoid sulfotransferase; 3′-phosphoadenylyl-sulfate:cortisol 21-sulfotransferase
Systematic name: 3′-phosphoadenylyl-sulfate:cortisol 21-sulfonotransferase
References: [3238, 3239]

[EC 2.8.2.18 created 1986]

EC 2.8.2.19

Accepted name: triglucosylalkylacylglycerol sulfotransferase
Reaction: 3′-phosphoadenylyl sulfate + α-D-glucosyl-(1→6)-α-D-glucosyl-(1→6)-α-D-glucosyl-(1→3)-1-*O*-alkyl-2-*O*-acylglycerol = adenosine 3′,5′-bisphosphate + 6-sulfo-α-D-glucosyl-(1→6)-α-D-glucosyl-(1→6)-α-D-glucosyl-(1→3)-1-*O*-alkyl-2-*O*-acylglycerol
Other name(s): triglucosylmonoalkylmonoacyl sulfotransferase; 3′-phosphoadenylyl-sulfate:triglucosyl-1-*O*-alkyl-2-*O*-acylglycerol 6-sulfotransferase
Systematic name: 3′-phosphoadenylyl-sulfate:triglucosyl-1-*O*-alkyl-2-*O*-acylglycerol 6-sulfonotransferase
References: [1964]

[EC 2.8.2.19 created 1986]

EC 2.8.2.20

Accepted name: protein-tyrosine sulfotransferase
Reaction: 3′-phosphoadenylyl sulfate + protein tyrosine = adenosine 3′,5′-bisphosphate + protein tyrosine-*O*-sulfate

Other name(s): tyrosylprotein sulfotransferase; 3′-phosphoadenylyl-sulfate:protein-tyrosine *O*-sulfotransferase
Systematic name: 3′-phosphoadenylyl-sulfate:protein-tyrosine *O*-sulfonotransferase
Comments: The tyrosine residues of some specific proteins of rat pheochromocytoma cells act as acceptors.
References: [1900]

[EC 2.8.2.20 created 1986]

EC 2.8.2.21

Accepted name: keratan sulfotransferase
Reaction: 3′-phosphoadenylyl sulfate + keratan = adenosine 3′,5′-bisphosphate + keratan 6′-sulfate
Other name(s): 3′-phosphoadenylyl keratan sulfotransferase; keratan sulfate sulfotransferase; 3′-phosphoadenylylsulfate:keratan sulfotransferase; 3′-phosphoadenylyl-sulfate:keratan 6′-sulfotransferase
Systematic name: 3′-phosphoadenylyl-sulfate:keratan 6′-sulfonotransferase
Comments: Sulfation takes place at the 6-position of galactosyl and *N*-acetylglucosaminyl residues in keratan, a proteoglycan. Not identical with EC 2.8.2.5 (chondroitin 4-sulfotransferase), EC 2.8.2.6 (choline sulfotransferase) or EC 2.8.2.17 (chondroitin 6-sulfotransferase).
References: [2977]

[EC 2.8.2.21 created 1989]

EC 2.8.2.22

Accepted name: aryl-sulfate sulfotransferase
Reaction: an aryl sulfate + a phenol = a phenol + an aryl sulfate
Other name(s): arylsulfate-phenol sulfotransferase; arylsulfotransferase; ASST; arylsulfate sulfotransferase; arylsulfate:phenol sulfotransferase; *astA* (gene name); aryl-sulfate:phenol sulfotransferase
Systematic name: aryl-sulfate:phenol sulfonotransferase
Comments: The enzyme, characterized from bacteria that colonize the human and mouse intestine, catalyses the transfer of a sulfate group from a phenol sulfate ester to other phenolic compounds. Activity is enhanced by Mg^{2+} and Mn^{2+} [1677]. Unlike EC 2.8.2.9, tyrosine-ester sulfotransferase and EC 2.8.2.1, aryl sulfotransferase, the enzyme does not act on 3′-phosphoadenylyl sulfate or adenosine 3′,5′-bisphosphate [1677].The level of sulfation of polyphenols depends on the positions of the hydroxyl groups [1742, 1741, 1750]. Hydroxy groups of tyrosine residues in peptides such as angiotensin can also act as acceptors [1724]. The reaction proceeds according to a ping pong bi bi mechanism [1897].
References: [1677, 1724, 1742, 1741, 1750, 1897, 1673]

[EC 2.8.2.22 created 1990]

EC 2.8.2.23

Accepted name: [heparan sulfate]-glucosamine 3-sulfotransferase 1
Reaction: 3′-phosphoadenylyl sulfate + [heparan sulfate]-glucosamine = adenosine 3′,5′-bisphosphate + [heparan sulfate]-glucosamine 3-sulfate
Other name(s): heparin-glucosamine 3-*O*-sulfotransferase; 3′-phosphoadenylyl-sulfate:heparin-glucosamine 3-*O*-sulfotransferase; glucosaminyl 3-*O*-sulfotransferase; heparan sulfate D-glucosaminyl 3-*O*-sulfotransferase; isoform/isozyme 1 (3-OST-1, HS3ST1); 3′-phosphoadenylyl-sulfate:[heparan sulfate]-glucosamine 3-sulfotransferase
Systematic name: 3′-phosphoadenylyl-sulfate:[heparan sulfate]-glucosamine 3-sulfonotransferase

Comments: This enzyme differs from the other [heparan sulfate]-glucosamine 3-sulfotransferases [EC 2.8.2.29 ([heparan sulfate]-glucosamine 3-sulfotransferase 2) and EC 2.8.2.30 ([heparan sulfate]-glucosamine 3-sulfotransferase 3)] by being the most selective for a precursor of the antithrombin-binding site. It has a minimal acceptor sequence of: $\rightarrow$ GlcNAc$_6$S$\rightarrow$ GlcA$\rightarrow$ GlcN$_2$S*+/-6S$\rightarrow$ IdoA2S$\rightarrow$ GlcN$_2$S$\rightarrow$, the asterisk marking the target (symbols as in 2-Carb-38) using +/- to mean the presence or absence of a substituent, and $>$ to separate a predominant structure from a minor one. Thus Glc(N$_2$S $>$ NAc) means a residue of glucosamine where the N carries a sulfo group mainly but occasionally an acetyl group. [1831, 3215, 2000, 3216]. It can also modify other precursor sequences within heparan sulfate but this action does not create functional antithrombin-binding sites. These precursors are variants of the consensus sequence: $\rightarrow$ Glc(N$_2$S $>$ NAc)+/-6S$\rightarrow$ GlcA$\rightarrow$ GlcN$_2$S*+/-6S$\rightarrow$ GlcA $>$ IdoA$^+$/-2S$\rightarrow$ Glc(N$_2$S/NAc)+/-6S$\rightarrow$ [4044]. If the heparan sulfate substrate lacks 2-*O*-sulfation of GlcA residues, then enzyme specificity is expanded to modify selected glucosamine residues preceded by IdoA as well as GlcA [4043].

References: [1831, 3215, 2000, 3216, 4044, 4043]

[EC 2.8.2.23 created 1992, modified 2001]

EC 2.8.2.24

Accepted name: aromatic desulfoglucosinolate sulfotransferase

Reaction: (1) 3′-phosphoadenylyl sulfate + desulfoglucotropeolin = adenosine 3′,5′-bisphosphate + glucotropeolin

(2) 3′-phosphoadenylyl sulfate + indolylmethyl-desulfoglucosinolate = adenosine 3′,5′-bisphosphate + glucobrassicin

Other name(s): desulfoglucosinolate sulfotransferase (ambiguous); PAPS-desulfoglucosinolate sulfotransferase (ambiguous); 3′-phosphoadenosine-5′-phosphosulfate:desulfoglucosinolate sulfotransferase (ambiguous); 3′-phosphoadenylyl-sulfate:aromatic desulfoglucosinolate sulfotransferase

Systematic name: 3′-phosphoadenylyl-sulfate:aromatic desulfoglucosinolate sulfonotransferase

Comments: This enzyme, characterized from cruciferous plants, catalyses the last step in the biosynthesis of tryptophan- and phenylalanine-derived glucosinolates. *cf.* EC 2.8.2.38, aliphatic desulfoglucosinolate sulfotransferase.

References: [1489, 1706, 1705]

[EC 2.8.2.24 created 1992, modified 2017]

EC 2.8.2.25

Accepted name: flavonol 3-sulfotransferase

Reaction: 3′-phosphoadenylyl sulfate + quercetin = adenosine 3′,5′-bisphosphate + quercetin 3-sulfate

Other name(s): 3′-phosphoadenylyl-sulfate:quercetin 3-sulfotransferase

Systematic name: 3′-phosphoadenylyl-sulfate:quercetin 3-sulfonotransferase

Comments: Also acts on some other flavonol aglycones.

References: [3652]

[EC 2.8.2.25 created 1992]

EC 2.8.2.26

Accepted name: quercetin-3-sulfate 3′-sulfotransferase

Reaction: 3′-phosphoadenylyl sulfate + quercetin 3-sulfate = adenosine 3′,5′-bisphosphate + quercetin 3,3′-bissulfate

Other name(s): flavonol 3′-sulfotransferase; 3′-Sulfotransferase; PAPS:flavonol 3-sulfate 3′-sulfotransferase; 3′-phosphoadenylyl-sulfate:quercetin-3-sulfate 3′-sulfotransferase

Systematic name: 3′-phosphoadenylyl-sulfate:quercetin-3-sulfate 3′-sulfonotransferase

References: [3652]

[EC 2.8.2.26 created 1992]

EC 2.8.2.27

Accepted name: quercetin-3-sulfate 4′-sulfotransferase

Reaction: 3′-phosphoadenylyl sulfate + quercetin 3-sulfate = adenosine 3′,5′-bisphosphate + quercetin 3,4′-bissulfate

Other name(s): flavonol 4′-sulfotransferase; PAPS:flavonol 3-sulfate 4′-sulfotransferase; 3′-phosphoadenylylsulfate:quercetin-3-sulfate 4′-sulfotransferase

Systematic name: 3′-phosphoadenylyl-sulfate:quercetin-3-sulfate 4′-sulfonotransferase

References: [3652]

[EC 2.8.2.27 created 1992]

EC 2.8.2.28

Accepted name: quercetin-3,3′-bissulfate 7-sulfotransferase

Reaction: 3′-phosphoadenylyl sulfate + quercetin 3,3′-bissulfate = adenosine 3′,5′-bisphosphate + quercetin 3,7,3′-trissulfate

Other name(s): flavonol 7-sulfotransferase; 7-sulfotransferase; PAPS:flavonol 3,3′/3,4′-disulfate 7-sulfotransferase; 3′-phosphoadenylyl-sulfate:quercetin-3,3′-bissulfate 7-sulfotransferase

Systematic name: 3′-phosphoadenylyl-sulfate:quercetin-3,3′-bissulfate 7-sulfonotransferase

Comments: Quercetin 3,4′-bissulfate can also act as acceptor.

References: [3651]

[EC 2.8.2.28 created 1992]

EC 2.8.2.29

Accepted name: [heparan sulfate]-glucosamine 3-sulfotransferase 2

Reaction: 3′-phosphoadenylyl sulfate + [heparan sulfate]-glucosamine = adenosine 3′,5′-bisphosphate + [heparan sulfate]-glucosamine 3-sulfate

Other name(s): glucosaminyl 3-*O*-sulfotransferase; heparan sulfate D-glucosaminyl 3-*O*-sulfotransferase; isoform/isozyme 2 (3-OST-2, HS3ST2); 3′-phosphoadenylyl-sulfate:[heparan sulfate]-glucosamine 3-sulfotransferase

Systematic name: 3′-phosphoadenylyl-sulfate:[heparan sulfate]-glucosamine 3-sulfonotransferase

Comments: This enzyme sulfates the residues marked with an asterisk in sequences containing at least → IdoA2S→ GlcN*→ or → GlcA2S→ GlcN*→ (symbols as in 2-Carb-38). Preference for GlcN$_2$S vs. unmodified GlcN has not yet been established. Additional structural features are presumably required for substrate recognition, since the 3-*O*-sulfated residue is of low abundance, whereas the above IdoA-containing sequence is quite abundant. This enzyme differs from the other [heparan sulfate]-glucosamine 3-sulfotransferases by modifying selected glucosamine residues preceded by GlcA2S; EC 2.8.2.23 ([heparan sulfate]-glucosamine 3-sulfotransferase 1) prefers GlcA or IdoA, whereas EC 2.8.2.30 ([heparan sulfate]-glucosamine 3-sulfotransferase 3) prefers IdoA2S.

References: [3217, 2001]

[EC 2.8.2.29 created 2001]

EC 2.8.2.30

Accepted name: [heparan sulfate]-glucosamine 3-sulfotransferase 3

Reaction: 3′-phosphoadenylyl sulfate + [heparan sulfate]-glucosamine = adenosine 3′,5′-bisphosphate + [heparan sulfate]-glucosamine 3-sulfate

Other name(s): 3′-phosphoadenylyl-sulfate:[heparan sulfate]-glucosamine 3-sulfotransferase

Systematic name: 3′-phosphoadenylyl-sulfate:[heparan sulfate]-glucosamine 3-sulfonotransferase

Comments: Two major substrates contain the tetrasaccharides: → undetermined 2-sulfo-uronic acid→ GlcN$_2$S→ IdoA2S→ GlcN*→ and → undetermined 2-sulfo-uronic acid→ GlcN$_2$S→ IdoA2S→ GlcN$_6$S*→ (symbols as in 2-Carb-38) with modification of the *N*-unsubstituted glucosamine residue (shown with an asterisk) [1999, 2001]. Modification of selected sequences containing *N*-sulfo-glucosamine residues cannot yet be excluded. The 3-*O*-sulfated heparan sulfate can be utilized by *Herpes simplex* virus type 1 as an entry receptor to infect the target cells [3214]. There are two isozymes, known as 3-OST-3A and 3-OST-3B, which have identical catalytic domains but are encoded by different mammalian genes [3217]. The specificity of this enzyme differs from that of the other [heparan sulfate]-glucosamine 3-sulfotransferases. It is inefficient at modifying precursors of the antithrombin binding site [in contrast to EC 2.8.2.23 ([heparan sulfate]-glucosamine 3-sulfotransferase 1)] and it does not modify glucosamine preceded by GlcA2S [unlike EC 2.8.2.29 ([heparan sulfate]-glucosamine 3-sulfotransferase 2)].

References: [1999, 3214, 3217, 2001]

[EC 2.8.2.30 created 2001]

EC 2.8.2.31

Accepted name: petromyzonol sulfotransferase

Reaction: 3′-phosphoadenylyl sulfate + 5α-cholan-3α,7α,12α,24-tetrol = adenosine 3′,5′-bisphosphate + 5α-cholan-3α,7α,12α-triol 24-sulfate

Other name(s): PZ-SULT; 3′-phosphoadenylyl-sulfate:5α-cholan-3α,7α,12α,24-tetrol sulfotransferase

Systematic name: 3′-phosphoadenylyl-sulfate:5α-cholan-3α,7α,12α,24-tetrol sulfonotransferase

Comments: The enzyme from the lamprey *Petromyzon marinus* can also use the corresponding 3-ketone as a substrate. It is stereoselective (5α-cholane) and regioselective, exhibiting a preference for an hydroxy group at C-24. The enzyme is inactive when allocholic acid, which has a carboxy group at C-24, is used as a substrate.

References: [3661]

[EC 2.8.2.31 created 2004]

EC 2.8.2.32

Accepted name: scymnol sulfotransferase

Reaction: 3′-phosphoadenylyl sulfate + 5β-scymnol = adenosine 3′,5′-bisphosphate + 5β-scymnol sulfate

Other name(s): 3′-phosphoadenylyl sulfate:5β-scymnol sulfotransferase

Systematic name: 3′-phosphoadenylyl sulfate:5β-scymnol sulfonotransferase

Comments: The enzyme from the shark *Heterodontus portusjacksoni* is able to sulfate the C$_{27}$ bile salts 5β-scymnol (the natural bile salt) and 5α-cyprinol (the carp bile salt). Enzyme activity is activated by Mg^{2+} but inhibited by the product 5β-scymnol sulfate.

References: [2093, 2680, 2679, 2678]

[EC 2.8.2.32 created 2005]

EC 2.8.2.33

Accepted name: *N*-acetylgalactosamine 4-sulfate 6-*O*-sulfotransferase

Reaction: (1) 3′-phospho-5′-adenylyl sulfate + [dermatan]-4-*O*-sulfo-*N*-acetyl-D-galactosamine = adenosine 3′,5′-bisphosphate + [dermatan]-4,6-di-*O*-sulfo-*N*-acetyl-D-galactosamine
(2) 3′-phospho-5′-adenylyl sulfate + [chondroitin]-4-*O*-sulfo-*N*-acetyl-D-galactosamine = adenosine 3′,5′-bisphosphate + [chondroitin]-4,6-di-*O*-sulfo-*N*-acetyl-D-galactosamine

Other name(s): GalNAc4S-6ST; CHST15 (gene name); 3′-phosphoadenylyl-sulfate:[dermatan]-4-*O*-sulfo-*N*-acetyl-D-galactosamine 6-*O*-sulfotransferase

Systematic name: 3′-phosphoadenylyl-sulfate:[dermatan]-4-*O*-sulfo-*N*-acetyl-D-galactosamine 6-*O*-sulfonotransferase

Comments: The enzyme is activated by divalent cations and reduced glutathione. The enzyme from human transfers sulfate to position 6 of both internal residues and non-reducing terminal GalNAc 4-sulfate residues of chondroitin sulfate and dermatan sulfate. Oligosaccharides derived from chondroitin sulfate also serve as acceptors but chondroitin sulfate E, keratan sulfate and heparan sulfate do not. Differs from EC 2.8.2.17, chondroitin 6-sulfotransferase, in being able to use both chondroitin and dermatan as effective substrates

References: [1466, 2541]

[EC 2.8.2.33 created 2005, modified 2010]

EC 2.8.2.34

Accepted name: glycochenodeoxycholate sulfotransferase

Reaction: 3′-phosphoadenylyl sulfate + glycochenodeoxycholate = adenosine 3′,5′-bisphosphate + glycochenodeoxycholate 7-sulfate

Other name(s): bile acid:3′-phosphoadenosine-5′-phosphosulfate sulfotransferase; bile acid:PAPS:sulfotransferase; BAST; 3′-phosphoadenylyl-sulfate:glycochenodeoxycholate 7-sulfotransferase

Systematic name: 3′-phosphoadenylyl-sulfate:glycochenodeoxycholate 7-sulfonotransferase

Comments: The enzyme specifically sulfates glycochenodeoxycholate at the 7α-position (see also EC 2.8.2.14 bile-salt sulfotransferase). The monohydroxy bile acids glycolithocholate, chenodeoxycholate and ursodeoxycholate act as inhibitors.

References: [200, 2976]

[EC 2.8.2.34 created 2005]

EC 2.8.2.35

Accepted name: dermatan 4-sulfotransferase

Reaction: 3′-phospho-5′-adenylyl sulfate + [dermatan]-*N*-acetyl-D-galactosamine = adenosine 3′,5′-bisphosphate + [dermatan]-4-*O*-sulfo-*N*-acetyl-D-galactosamine

Other name(s): dermatan-specific *N*-acetylgalactosamine 4-*O*-sulfotransferase; dermatan-4-sulfotransferase-1; dermatan-4-sulfotransferase 1; D4ST-1; dermatan *N*-acetylgalactosamine 4-*O*-sulfotransferase; CHST14 protein; CHST14; 3′-phospho-5′-adenylyl sulfate:[dermatan]-*N*-acetyl-D-galactosamine 4-sulfotransferase

Systematic name: 3′-phospho-5′-adenylyl sulfate:[dermatan]-*N*-acetyl-D-galactosamine 4-sulfonotransferase

Comments: The sulfation takes place at the 4-position of *N*-acetyl-D-galactosamine residues of dermatan. D4ST-1 shows a strong preference *in vitro* for sulfate transfer to IdoUAα(1,3)GalNAcβ(1,4) that is flanked by GlcUAβ(1,3)GalNAcβ(1,4) as compared with IdoUAα(1,3)GalNAcβ(1,4) flanked by IdoUAα(1,3)GalNAcβ(1,4) [860].

References: [860, 2243, 2590, 2273]

[EC 2.8.2.35 created 2010]

EC 2.8.2.36

Accepted name: desulfo-A47934 sulfotransferase

Reaction: 3′-phosphoadenylyl sulfate + desulfo-A47934 = adenosine 3′,5′-bisphosphate + A47934

Other name(s): StaL; 3′-phosphoadenylyl-sulfate:desulfo-A47934 sulfotransferase

Systematic name: 3′-phosphoadenylyl-sulfate:desulfo-A47934 sulfonotransferase

Comments: The enzyme from the bacterium *Streptomyces toyocaensis* catalyses the final step in the biosynthesis of the glycopeptide antibiotic A47934, a naturally occuring antibiotic of the vancomycin group.

References: [1852, 3182]

[EC 2.8.2.36 created 2014]

EC 2.8.2.37

Accepted name: trehalose 2-sulfotransferase
Reaction: 3′-phosphoadenylyl sulfate + α,α-trehalose = adenosine 3′,5′-bisphosphate + 2-*O*-sulfo-α,α-trehalose
Other name(s): Stf0 sulfotransferase; 3′-phosphoadenylyl-sulfate:α,α-trehalose 2-sulfotransferase
Systematic name: 3′-phosphoadenylyl-sulfate:α,α-trehalose 2-sulfonotransferase
Comments: The sulfation of trehalose in the bacterium *Mycobacterium tuberculosis* is required for the biosynthesis of sulfolipid-1.
References: [2332, 2697]

[EC 2.8.2.37 created 2014]

EC 2.8.2.38

Accepted name: aliphatic desulfoglucosinolate sulfotransferase
Reaction: 3′-phosphoadenylyl sulfate + an aliphatic desulfoglucosinolate = adenosine 3′,5′-bisphosphate + an aliphatic glucosinolate
Other name(s): SOT17 (gene name); SOT18 (gene name); 3′-phosphoadenylyl-sulfate:aliphatic desulfoglucosinolate sulfotransferase
Systematic name: 3′-phosphoadenylyl-sulfate:aliphatic desulfoglucosinolate sulfonotransferase
Comments: The enzyme catalyses the last step in the biosynthesis of aliphatic glucosinolate core structures. *cf.* EC 2.8.2.24, aromatic desulfoglucosinolate sulfotransferase.
References: [2717, 1706, 1705]

[EC 2.8.2.38 created 2017]

EC 2.8.2.39

Accepted name: hydroxyjasmonate sulfotransferase
Reaction: 3′-phosphoadenylyl-sulfate + 12-hydroxyjasmonate = adenosine 3′,5′-bisphosphate + 12-sulfooxyjasmonate
Other name(s): ST2A (gene name); 3′-phosphoadenylyl-sulfate:12-hydroxyjasmonate sulfotransferase
Systematic name: 3′-phosphoadenylyl-sulfate:12-hydroxyjasmonate sulfonotransferase
Comments: The enzyme, charaterized from the plant *Arabidopsis thaliana*, also acts on 11-hydroxyjasmonate.
References: [1055]

[EC 2.8.2.39 created 2017]

EC 2.8.3 CoA-transferases

EC 2.8.3.1

Accepted name: propionate CoA-transferase
Reaction: acetyl-CoA + propanoate = acetate + propanoyl-CoA
Other name(s): propionate coenzyme A-transferase; propionate-CoA:lactoyl-CoA transferase; propionyl CoA:acetate CoA transferase; propionyl-CoA transferase
Systematic name: acetyl-CoA:propanoate CoA-transferase
Comments: Butanoate and lactate can also act as acceptors.
References: [3313]

[EC 2.8.3.1 created 1961]

EC 2.8.3.2

Accepted name: oxalate CoA-transferase
Reaction: succinyl-CoA + oxalate = succinate + oxalyl-CoA
Other name(s): succinyl—β-ketoacyl-CoA transferase; oxalate coenzyme A-transferase
Systematic name: succinyl-CoA:oxalate CoA-transferase
References: [2781]

[EC 2.8.3.2 created 1961]

EC 2.8.3.3

Accepted name: malonate CoA-transferase
Reaction: acetyl-CoA + malonate = acetate + malonyl-CoA
Other name(s): malonate coenzyme A-transferase
Systematic name: acetyl-CoA:malonate CoA-transferase
Comments: The enzyme from *Pseudomonas ovalis* also catalyses the reaction of EC 4.1.1.9 malonyl-CoA decarboxylase.
References: [1250, 3445]

[EC 2.8.3.3 created 1961]

[2.8.3.4 Deleted entry. butyrate CoA-transferase]

[EC 2.8.3.4 created 1961, deleted 1964]

EC 2.8.3.5

Accepted name: 3-oxoacid CoA-transferase
Reaction: succinyl-CoA + a 3-oxo acid = succinate + a 3-oxoacyl-CoA
Other name(s): 3-oxoacid coenzyme A-transferase; 3-ketoacid CoA-transferase; 3-ketoacid coenzyme A transferase; 3-oxo-CoA transferase; 3-oxoacid CoA dehydrogenase; acetoacetate succinyl-CoA transferase; acetoacetyl coenzyme A-succinic thiophorase; succinyl coenzyme A-acetoacetyl coenzyme A-transferase; succinyl-CoA transferase
Systematic name: succinyl-CoA:3-oxo-acid CoA-transferase
Comments: Acetoacetate and, more slowly, 3-oxopropanoate, 3-oxopentanoate, 3-oxo-4-methylpentanoate or 3-oxohexanoate can act as acceptors; malonyl-CoA can act instead of succinyl-CoA.
References: [1309, 2079, 2223, 3336]

[EC 2.8.3.5 created 1961, modified 1980]

EC 2.8.3.6

Accepted name: 3-oxoadipate CoA-transferase
Reaction: succinyl-CoA + 3-oxoadipate = succinate + 3-oxoadipyl-CoA
Other name(s): 3-oxoadipate coenzyme A-transferase; 3-oxoadipate succinyl-CoA transferase
Systematic name: succinyl-CoA:3-oxoadipate CoA-transferase
Comments: The enzyme, often found in soil bacteria and fungi, is involved in the catabolism of a variety of aromatic compounds, including catechol and protocatechuate, which are degraded via 3-oxoadipate.
References: [1595, 1589, 1081]

[EC 2.8.3.6 created 1961]

*[2.8.3.7 Deleted entry. succinate—citramalate CoA-transferase. The activity has now been shown to be due to two separate enzymes described by EC 2.8.3.22, succinyl-CoA—*L*-malate CoA-transferase, and EC 2.8.3.20, succinyl-CoA—*D*-citramalate CoA-transferase]*

[EC 2.8.3.7 created 1972, deleted 2014]

EC 2.8.3.8

Accepted name: acetate CoA-transferase
Reaction: acyl-CoA + acetate = a fatty acid anion + acetyl-CoA
Other name(s): acetate coenzyme A-transferase; butyryl CoA:acetate CoA transferase; butyryl coenzyme A transferase; succinyl-CoA:acetate CoA transferase
Systematic name: acyl-CoA:acetate CoA-transferase

Comments: The enzyme belongs to family I of CoA-transferases, which operate with a ping-pong kinetic mechanism. The reaction takes place in two half-reactions and involves the formation of a CoA thioester intermediate with a glutamate residue. Unlike EC 2.8.3.9, butyrate—acetoacetate CoA-transferase, this enzyme exhibits maximal activity using acetate as the CoA acceptor. Substrate range depends on the specific enzyme. Typical substrates include butanoyl-CoA and pentanoyl-CoA.

References: [3648, 2807]

[EC 2.8.3.8 created 1972]

EC 2.8.3.9

Accepted name: butyrate—acetoacetate CoA-transferase

Reaction: butanoyl-CoA + acetoacetate = butanoate + acetoacetyl-CoA

Other name(s): butyryl coenzyme A-acetoacetate coenzyme A-transferase; butyryl-CoA-acetoacetate CoA-transferase

Systematic name: butanoyl-CoA:acetoacetate CoA-transferase

Comments: Butanoate, acetoacetate and their CoA thioesters are the preferred substrates, but the enzyme also acts, more slowly, on the derivatives of a number of C_2 to C_6 monocarboxylic acids.

References: [192]

[EC 2.8.3.9 created 1984]

EC 2.8.3.10

Accepted name: citrate CoA-transferase

Reaction: acetyl-CoA + citrate = acetate + (3*S*)-citryl-CoA

Systematic name: acetyl-CoA:citrate CoA-transferase

Comments: The enzyme is a component of EC 4.1.3.6 [citrate (*pro*-3*S*)-lyase]. Also catalyses the transfer of thioacyl carrier protein from its acetyl thioester to citrate.

References: [737]

[EC 2.8.3.10 created 1984]

EC 2.8.3.11

Accepted name: citramalate CoA-transferase

Reaction: acetyl-CoA + citramalate = acetate + (3*S*)-citramalyl-CoA

Systematic name: acetyl-CoA:citramalate CoA-transferase

Comments: The enzyme is a component of EC 4.1.3.22 citramalate lyase. Also catalyses the transfer of thioacyl carrier protein from its acetyl thioester to citramalate.

References: [735]

[EC 2.8.3.11 created 1984]

EC 2.8.3.12

Accepted name: glutaconate CoA-transferase

Reaction: acetyl-CoA + (*E*)-glutaconate = acetate + glutaconyl-1-CoA

Systematic name: acetyl-CoA:(*E*)-glutaconate CoA-transferase

Comments: Glutarate, (*R*)-2-hydroxyglutarate, propenoate and propanoate, but not (*Z*)-glutaconate, can also act as acceptors.

References: [417]

[EC 2.8.3.12 created 1984, modified 2002]

EC 2.8.3.13

Accepted name: succinate—hydroxymethylglutarate CoA-transferase

Reaction: succinyl-CoA + 3-hydroxy-3-methylglutarate = succinate + (*S*)-3-hydroxy-3-methylglutaryl-CoA
Other name(s): hydroxymethylglutarate coenzyme A-transferase; dicarboxyl-CoA:dicarboxylic acid coenzyme A transferase
Systematic name: succinyl-CoA:3-hydroxy-3-methylglutarate CoA-transferase
Comments: Malonyl-CoA can also act as donor, but more slowly.
References: [691]

[EC 2.8.3.13 created 1984]

EC 2.8.3.14

Accepted name: 5-hydroxypentanoate CoA-transferase
Reaction: acetyl-CoA + 5-hydroxypentanoate = acetate + 5-hydroxypentanoyl-CoA
Other name(s): 5-hydroxyvalerate CoA-transferase; 5-hydroxyvalerate coenzyme A transferase
Systematic name: acetyl-CoA:5-hydroxypentanoate CoA-transferase
Comments: Propanoyl-CoA, acetyl-CoA, butanoyl-CoA and some other acyl-CoAs can act as substrates, but more slowly than 5-hydroxypentanoyl-CoA.
References: [815]

[EC 2.8.3.14 created 1992]

EC 2.8.3.15

Accepted name: succinyl-CoA:(*R*)-benzylsuccinate CoA-transferase
Reaction: succinyl-CoA + (*R*)-2-benzylsuccinate = succinate + (*R*)-2-benzylsuccinyl-CoA
Other name(s): benzylsuccinate CoA-transferase
Systematic name: succinyl-CoA:(*R*)-2-benzylsuccinate CoA-transferase
Comments: Involved in anaerobic catabolism of toluene and is a strictly toluene-induced enzyme that catalyses the reversible regio- and enantio-selective synthesis of (*R*)-2-benzylsuccinyl-CoA. The enzyme from *Thauera aromatica* is inactive when (*R*)-benzylsuccinate is replaced by (*S*)-benzylsuccinate.
References: [1947, 1946, 1945, 1276]

[EC 2.8.3.15 created 2003]

EC 2.8.3.16

Accepted name: formyl-CoA transferase
Reaction: formyl-CoA + oxalate = formate + oxalyl-CoA
Other name(s): formyl-coenzyme A transferase; formyl-CoA oxalate CoA-transferase
Systematic name: formyl-CoA:oxalate CoA-transferase
Comments: The enzyme from *Oxalobacter formigenes* can also catalyse the transfer of CoA from formyl-CoA to succinate.
References: [156, 3219]

[EC 2.8.3.16 created 2003]

EC 2.8.3.17

Accepted name: cinnamoyl-CoA:phenyllactate CoA-transferase
Reaction: (*E*)-cinnamoyl-CoA + (*R*)-phenyllactate = (*E*)-cinnamate + (*R*)-phenyllactyl-CoA
Other name(s): FldA
Systematic name: (*E*)-cinnamoyl-CoA:(*R*)-phenyllactate CoA-transferase
Comments: 3-Phenylproprionate is a better CoA acceptor than (*R*)-phenyllactate in vitro. The enzyme from *Clostridium sporogenes* is specific for derivatives of 3-phenylpropionate and 4-phenylbutyrate.
References: [733]

[EC 2.8.3.17 created 2003]

EC 2.8.3.18

Accepted name: succinyl-CoA:acetate CoA-transferase
Reaction: succinyl-CoA + acetate = acetyl-CoA + succinate
Other name(s): *aarC* (gene name); SCACT
Systematic name: succinyl-CoA:acetate CoA-transferase
Comments: In acetic acid bacteria the enzyme, which is highly specific, catalyses the conversion of toxic acetate to acetyl-CoA [2354, 2355]. In the hydrogenosomes of some trichomonads the enzyme catalyses the production of acetate [3328].
References: [3328, 2354, 2355]

[EC 2.8.3.18 created 2013]

EC 2.8.3.19

Accepted name: CoA:oxalate CoA-transferase
Reaction: acetyl-CoA + oxalate = acetate + oxalyl-CoA
Other name(s): acetyl-coenzyme A transferase; acetyl-CoA oxalate CoA-transferase; ACOCT; YfdE; UctC
Systematic name: acetyl-CoA:oxalate CoA-transferase
Comments: The enzymes characterized from the bacteria *Escherichia coli* and *Acetobacter aceti* can also use formyl-CoA and oxalate (EC 2.8.3.16, formyl-CoA transferase) or formyl-CoA and acetate, with significantly reduced specific activities.
References: [2356]

[EC 2.8.3.19 created 2013]

EC 2.8.3.20

Accepted name: succinyl-CoA—D-citramalate CoA-transferase
Reaction: (1) succinyl-CoA + (*R*)-citramalate = succinate + (*R*)-citramalyl-CoA
(2) succinyl-CoA + (*R*)-malate = succinate + (*R*)-malyl-CoA
Other name(s): Sct
Systematic name: succinyl-CoA:(*R*)-citramalate CoA-transferase
Comments: The enzyme, purified from the bacterium *Clostridium tetanomorphum*, can also accept itaconate as acceptor, with lower efficiency.
References: [968]

[EC 2.8.3.20 created 2014]

EC 2.8.3.21

Accepted name: L-carnitine CoA-transferase
Reaction: (1) (*E*)-4-(trimethylammonio)but-2-enoyl-CoA + L-carnitine = (*E*)-4-(trimethylammonio)but-2-enoate + L-carnitinyl-CoA
(2) 4-trimethylammoniobutanoyl-CoA + L-carnitine = 4-trimethylammoniobutanoate + L-carnitinyl-CoA
Other name(s): CaiB; crotonobetainyl/γ-butyrobetainyl-CoA:carnitine CoA-transferase
Systematic name: (*E*)-4-(trimethylammonio)but-2-enoyl-CoA:L-carnitine CoA-transferase
Comments: The enzyme is found in gammaproteobacteria such as *Proteus* sp. and *Escherichia coli*. It has similar activity with both substrates.
References: [838, 834, 3330, 839, 2808]

[EC 2.8.3.21 created 2014]

EC 2.8.3.22

Accepted name: succinyl-CoA—L-malate CoA-transferase
Reaction: (1) succinyl-CoA + (*S*)-malate = succinate + (*S*)-malyl-CoA

(2) succinyl-CoA + (*S*)-citramalate = succinate + (*S*)-citramalyl-CoA
Other name(s): SmtAB
Systematic name: succinyl-CoA:(*S*)-malate CoA-transferase
Comments: The enzyme, purified from the bacterium *Chloroflexus aurantiacus*, can also accept itaconate as acceptor, with lower efficiency. It is part of the 3-hydroxypropanoate cycle for carbon assimilation.
References: [969]

[EC 2.8.3.22 created 2014]

EC 2.8.3.23

Accepted name: caffeate CoA-transferase
Reaction: 3-(3,4-dihydroxyphenyl)propanoyl-CoA + (2*E*)-3-(3,4-dihydroxyphenyl)prop-2-enoate = 3-(3,4-dihydroxyphenyl)propanoate + (2*E*)-3-(3,4-dihydroxyphenyl)prop-2-enoyl-CoA
Other name(s): CarA
Systematic name: 3-(3,4-dihydroxyphenyl)propanoyl-CoA:(2*E*)-3-(3,4-dihydroxyphenyl)prop-2-enoate CoA-transferase
Comments: The enzyme, isolated from the bacterium *Acetobacterium woodii*, catalyses an energy-saving CoA loop for caffeate activation. In addition to caffeate, the enzyme can utilize 4-coumarate or ferulate as CoA acceptor.
References: [1311]

[EC 2.8.3.23 created 2015]

EC 2.8.3.24

Accepted name: (*R*)-2-hydroxy-4-methylpentanoate CoA-transferase
Reaction: 4-methylpentanoyl-CoA + (*R*)-2-hydroxy-4-methylpentanoate = 4-methylpentanoate + (*R*)-2-hydroxy-4-methylpentanoyl-CoA
Other name(s): *hadA* (gene name)
Systematic name: 4-methylpentanoyl-CoA:(*R*)-2-hydroxy-4-methylpentanoate CoA-transferase
Comments: The enzyme, characterized from the bacterium *Peptoclostridium difficile*, participates in an L-leucine fermentation pathway. The reaction proceeds via formation of a covalent anhydride intermediate between a conserved aspartate residue and the acyl group of the CoA thioester substrate.
References: [1679]

[EC 2.8.3.24 created 2016]

EC 2.8.3.25

Accepted name: bile acid CoA-transferase
Reaction: (1) lithocholoyl-CoA + cholate = lithocholate + choloyl-CoA
(2) deoxycholoyl-CoA + cholate = deoxycholate + choloyl-CoA
Other name(s): *baiF* (gene name); *baiK* (gene name); bile acid coenzyme A transferase
Systematic name: lithocholoyl-CoA:cholate CoA-transferase
Comments: The enzyme, characterized from the gut bacterium *Clostridium scindens*, catalyses the last step in bile acid 7α-dehydroxylation, the removal of the CoA moiety from the products. By using a transferase rather than hydrolase, the bacteria conserve the thioester bond energy, saving ATP molecules. *Clostridium scindens* possesses two forms of the enzyme, encoded by the *baiF* and *baiK* genes. While the enzymes have a broad acceptor specificity and can use allocholate, ursodeoxycholate, and β-muricholate, the donor specificity is more strict. BaiF acts on lithocholoyl-CoA and deoxycholoyl-CoA, and BaiK acts only on the latter.
References: [2884]

[EC 2.8.3.25 created 2005 as EC 3.1.2.26, transferred 2016 to EC 2.8.3.25]

EC 2.8.4 Transferring alkylthio groups

EC 2.8.4.1

Accepted name: coenzyme-B sulfoethylthiotransferase

Reaction: methyl-CoM + CoB = CoM-S-S-CoB + methane

Other name(s): methyl-CoM reductase; methyl coenzyme M reductase

Systematic name: methyl-CoM:CoB *S*-(2-sulfoethyl)thiotransferase

Comments: This enzyme catalyses the final step in methanogenesis, the biological production of methane. This important anaerobic process is carried out only by methanogenic archaea. The enzyme can also function in reverse, for anaerobic oxidation of methane.The enzyme requires the hydroporphinoid nickel complex coenzyme F_{430}. Highly specific for coenzyme B with a heptanoyl chain; ethyl CoM and difluoromethyl CoM are poor substrates. The sulfide sulfur can be replaced by selenium but not by oxygen.

References: [338, 830, 849, 3224, 3070]

[EC 2.8.4.1 created 2001, modified 2011]

EC 2.8.4.2

Accepted name: arsenate-mycothiol transferase

Reaction: arsenate + mycothiol = arseno-mycothiol + H_2O

Other name(s): ArsC1; ArsC2; mycothiol:arsenate transferase

Systematic name: mycothiol:arsenate *S*-arsenotransferase

Comments: Reduction of arsenate is part of a defence mechanism of the cell against toxic arsenate. The product arseno-mycothiol is reduced by EC 1.20.4.3 (mycoredoxin) to arsenite and mycothiol-mycoredoxin disulfide. Finally, a second mycothiol recycles mycoredoxin and forms mycothione.

References: [2572]

[EC 2.8.4.2 created 2010]

EC 2.8.4.3

Accepted name: tRNA-2-methylthio-N^6-dimethylallyladenosine synthase

Reaction: N^6-dimethylallyladenine^{37} in tRNA + sulfur-(sulfur carrier) + **2** *S*-adenosyl-L-methionine + reduced electron acceptor = 2-(methylsulfanyl)-N^6-dimethylallyladenine^{37} in tRNA + *S*-adenosyl-L-homocysteine + (sulfur carrier) + L-methionine + 5′-deoxyadenosine + electron acceptor (overall reaction)

(1a) N^6-dimethylallyladenine^{37} in tRNA + sulfur-(sulfur carrier) + *S*-adenosyl-L-methionine + reduced electron acceptor = 2-sulfanyl-N^6-dimethylallyladenine^{37} in tRNA + (sulfur carrier) + L-methionine + 5′-deoxyadenosine + electron acceptor

(1b) *S*-adenosyl-L-methionine + 2-sulfanyl-N^6-dimethylallyladenine^{37} in tRNA = *S*-adenosyl-L-homocysteine + 2-(methylsulfanyl)-N^6-dimethylallyladenine^{37} in tRNA

Other name(s): MiaB; 2-methylthio-*N*-6-isopentenyl adenosine synthase; tRNA-i6A37 methylthiotransferase; tRNA (N^6-dimethylallyladenosine^{37}):sulfur-(sulfur carrier),*S*-adenosyl-L-methionine C^2-methylthiotransferase

Systematic name: tRNA (N^6-dimethylallyladenosine^{37}):sulfur-(sulfur carrier),*S*-adenosyl-L-methionine C^2-(methylsulfanyl)transferase

Comments: This bacterial enzyme binds two [4Fe-4S] clusters as well as the transferred sulfur [2707]. The enzyme is a member of the superfamily of *S*-adenosyl-L-methionine-dependent radical (radical AdoMet) enzymes. The sulfur donor is believed to be one of the [4Fe-4S] clusters, which is sacrificed in the process, so that *in vitro* the reaction is a single turnover. The identity of the electron donor is not known.

References: [2706, 2708, 2707, 1304, 1855]

[EC 2.8.4.3 created 2014, modified 2015]

EC 2.8.4.4

Accepted name: [ribosomal protein S12] (aspartate^{89}-C^3)-methylthiotransferase

Reaction: L-aspartate^{89}-[ribosomal protein S12] + sulfur-(sulfur carrier) + **2** *S*-adenosyl-L-methionine + reduced acceptor = 3-(methylsulfanyl)-L-aspartate^{89}-[ribosomal protein S12] + *S*-adenosyl-L-homocysteine + (sulfur carrier) + L-methionine + $5'$-deoxyadenosine + oxidized acceptor (overall reaction)
(1a) *S*-adenosyl-L-methionine + L-aspartate^{89}-[ribosomal protein S12] + sulfur-(sulfur carrier) = *S*-adenosyl-L-homocysteine + L-aspartate^{89}-[ribosomal protein S12]-methanethiol + (sulfur carrier)
(1b) L-aspartate^{89}-[ribosomal protein S12]-methanethiol + *S*-adenosyl-L-methionine + reduced acceptor = 3-(methylsulfanyl)-L-aspartate^{89}-[ribosomal protein S12] + L-methionine + $5'$-deoxyadenosine + oxidized acceptor

Other name(s): RimO; [ribosomal protein S12]-Asp^{89}:sulfur-(sulfur carrier),*S*-adenosyl-L-methionine C^3-methylthiotransferase; [ribosomal protein S12]-L-aspartate^{89}:sulfur-(sulfur carrier),*S*-adenosyl-L-methionine C^3-methylthiotransferase

Systematic name: [ribosomal protein S12]-L-aspartate^{89}:sulfur-(sulfur carrier),*S*-adenosyl-L-methionine C^3-(methylsulfanyl)transferase

Comments: This bacterial enzyme binds two [4Fe-4S] clusters [1892, 110]. A bridge of five sulfur atoms is formed between the free Fe atoms of the two [4Fe-4S] clusters [933]. In the first reaction the enzyme transfers a methyl group from AdoMet to the external sulfur ion of the sulfur bridge. In the second reaction the enzyme catalyses the reductive fragmentation of a second molecule of AdoMet, yielding a $5'$-deoxyadenosine radical, which then attacks the methylated sulfur atom of the polysulfide bridge, resulting in the transfer of a methylsulfanyl group to aspartate^{89} [1855, 933]. The enzyme is a member of the superfamily of *S*-adenosyl-L-methionine-dependent radical (radical AdoMet) enzymes.

References: [93, 1892, 110, 3367, 1855, 933]

[EC 2.8.4.4 created 2014, modified 2014]

EC 2.8.4.5

Accepted name: tRNA (N^6-L-threonylcarbamoyladenosine^{37}-C^2)-methylthiotransferase

Reaction: N^6-L-threonylcarbamoyladenine^{37} in tRNA + sulfur-(sulfur carrier) + **2** *S*-adenosyl-L-methionine + reduced electron acceptor = 2-(methylsulfanyl)-N^6-L-threonylcarbamoyladenine^{37} in tRNA + *S*-adenosyl-L-homocysteine + (sulfur carrier) + L-methionine + $5'$-deoxyadenosine + electron acceptor (overall reaction)
(1a) N^6-L-threonylcarbamoyladenine^{37} in tRNA + sulfur-(sulfur carrier) + *S*-adenosyl-L-methionine + reduced electron acceptor = 2-sulfanyl-N^6-L-threonylcarbamoyladenine^{37} in tRNA + (sulfur carrier) + L-methionine + $5'$-deoxyadenosine + electron acceptor
(1b) *S*-adenosyl-L-methionine + 2-sulfanyl-N^6-L-threonylcarbamoyladenine^{37} in tRNA = *S*-adenosyl-L-homocysteine + 2-(methylsulfanyl)-N^6-L-threonylcarbamoyladenine^{37} in tRNA

Other name(s): MtaB; methylthio-threonylcarbamoyl-adenosine transferase B; CDKAL1 (gene name); tRNA (N^6-L-threonylcarbamoyladenosine^{37}):sulfur-(sulfur carrier),*S*-adenosyl-L-methionine C^2-methylthiotransferase

Systematic name: tRNA (N^6-L-threonylcarbamoyladenosine^{37}):sulfur-(sulfur carrier),*S*-adenosyl-L-methionine C^2-(methylsulfanyl)transferase

Comments: The enzyme, which is a member of the *S*-adenosyl-L-methionine-dependent radical (radical AdoMet) enzymes superfamily, binds two [4Fe-4S] clusters as well as the transferred sulfur. The sulfur donor is believed to be one of the [4Fe-4S] clusters, which is sacrificed in the process, so that *in vitro* the reaction is a single turnover. The identity of the electron donor is not known.

References: [111]

[EC 2.8.4.5 created 2014, modified 2015]

EC 2.8.5 Thiosulfotransferases

EC 2.8.5.1

Accepted name: *S*-sulfo-L-cysteine synthase (3-phospho-L-serine-dependent)
Reaction: 3-phospho-L-serine + thiosulfate = *S*-sulfo-L-cysteine + phosphate
Other name(s): *cysK2* (gene name); thiosulfate:3-phospho-L-serine thiosulfotransferase
Systematic name: thiosulfate:3-phospho-L-serine thiosulfonotransferase
Comments: The enzyme, which has been characterized from the bacterium *Mycobacterium tuberculosis*, has no activity with *O*-acetyl-L-serine. Requires pyridoxal 5′-phosphate. *cf.* EC 2.5.1.144, *S*-sulfo-L-cysteine synthase (*O*-acetyl-L-serine-dependent).
References: [3329]

[EC 2.8.5.1 created 2018]

EC 2.8.5.2
Accepted name: L-cysteine *S*-thiosulfotransferase
Reaction: (1) [SoxY protein]-L-cysteine + thiosulfate + **2** ferricytochrome *c* = [SoxY protein]-*S*-sulfosulfanyl-L-cysteine + **2** ferrocytochrome *c* + **2** H$^+$
(2) [SoxY protein]-*S*-sulfanyl-L-cysteine + thiosulfate + **2** ferricytochrome *c* = [SoxY protein]-*S*-(2-sulfodisulfanyl)-L-cysteine + **2** ferrocytochrome *c* + **2** H$^+$
Other name(s): SoxXA; thiosulfate:[SoxY protein]-L-cysteine thiosulfotransferase
Systematic name: thiosulfate:[SoxY protein]-L-cysteine thiosulfonotransferase
Comments: The enzyme is part of the Sox enzyme system, which participates in a bacterial thiosulfate oxidation pathway that produces sulfate. It catalyses two reactions in the pathway - early in the pathway it attaches a thiosulfate molecule to the sulfur atom of an L-cysteine of a SoxY protein; later it transfers a second thiosulfate molecule to a sulfane group that is already attached to the same cysteine residue.
References: [970, 516, 2942, 176, 663, 1299, 1121]

[EC 2.8.5.2 created 2018]

EC 2.9 Transferring selenium-containing groups

This subclass currently contains a single sub-subclass, selenotransferase (EC 2.9.1).

EC 2.9.1 Selenotransferases

EC 2.9.1.1
Accepted name: L-seryl-tRNA^{Sec} selenium transferase
Reaction: L-seryl-tRNA^{Sec} + selenophosphate = L-selenocysteinyl-tRNA^{Sec} + phosphate
Other name(s): L-selenocysteinyl-tRNA^{Sel} synthase; L-selenocysteinyl-tRNA^{Sec} synthase selenocysteine synthase; cysteinyl-tRNA^{Sec}-selenium transferase; cysteinyl-tRNA^{Sec}-selenium transferase
Systematic name: selenophosphate:L-seryl-tRNA^{Sec} selenium transferase
Comments: A pyridoxal 5′-phosphate enzyme identified in *Escherichia coli*. Recognises specifically tRNA^{Sec}-species. Binding of tRNA^{Sec} also occurs in the absence of the seryl group. 2-Aminoacryloyl-tRNA, bound to the enzyme as an imine with the pyridoxal phosphate, is an intermediate in the reaction. Since the selenium atom replaces oxygen in serine, the product may also be referred to as L-selenoseryl-tRNA^{Sec}. The symbol Sel has also been used for selenocysteine but Sec is preferred.
References: [928]

[EC 2.9.1.1 created 1999]

EC 2.9.1.2
Accepted name: *O*-phospho-L-seryl-tRNA^{Sec}:L-selenocysteinyl-tRNA synthase
Reaction: *O*-phospho-L-seryl-tRNA^{Sec} + selenophosphate + H_2O = L-selenocysteinyl-tRNA^{Sec} + **2** phosphate

Other name(s): MMPSepSecS; SepSecS; SLA/LP; *O*-phosphoseryl-tRNA:selenocysteinyl-tRNA synthase; *O*-phospho-L-seryl-tRNA:L-selenocysteinyl-tRNA synthase

Systematic name: selenophosphate:*O*-phospho-L-seryl-tRNA^{Sec} selenium transferase

Comments: A pyridoxal-phosphate protein [4010]. In archaea and eukarya selenocysteine formation is achieved by a two-step process: EC 2.7.1.164 (*O*-phosphoseryl-tRNA^{Sec} kinase) phosphorylates the endogenous L-seryl-tRNA^{Sec} to *O*-phospho-L-seryl-tRNA^{Sec}, and then this misacylated amino acid-tRNA species is converted to L-selenocysteinyl-tRNA^{Sec} by Sep-tRNA:Sec-tRNA synthase.

References: [2605, 100, 20, 4010]

[EC 2.9.1.2 created 2009, modified 2014]

EC 2.10 Transferring molybdenum- or tungsten-containing groups

EC 2.10.1 Molybdenumtransferases or tungstentransferases with sulfide groups as acceptors

EC 2.10.1.1

Accepted name: molybdopterin molybdotransferase

Reaction: adenylyl-molybdopterin + molybdate = molybdenum cofactor + AMP + H_2O

Other name(s): MoeA; Cnx1 (ambiguous)

Systematic name: adenylyl-molybdopterin:molybdate molybdate transferase (AMP-forming)

Comments: Catalyses the insertion of molybdenum into the ene-dithiol group of molybdopterin. In eukaryotes this reaction is catalysed by the N-terminal domain of a fusion protein whose C-terminal domain catalyses EC 2.7.7.75, molybdopterin adenylyltransferase. Requires divalent cations such as Mg^{2+} or Zn^{2+} for activity.

References: [2449, 2450, 2018]

[EC 2.10.1.1 created 2011]

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Index