The Enzyme List
Class 3 — Hydrolases

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

Generated from the ExplorEnz database, May 2023

© 2023 IUBMB

Contents

EC 3.1 Acting on ester bonds 3
EC 3.1.1 Carboxylic-ester hydrolases ......................................................... 3
EC 3.1.2 Thioester hydrolases ........................................................................... 29
EC 3.1.3 Phosphoric-monoester hydrolases .................................................... 35
EC 3.1.4 Phosphoric-diester hydrolases ........................................................... 60
EC 3.1.5 Triphosphoric-monoester hydrolases .................................................. 70
EC 3.1.6 Sulfuric-ester hydrolases ................................................................... 70
EC 3.1.7 Diphosphoric-monoester hydrolases .................................................. 75
EC 3.1.8 Phosphoric-triester hydrolases ........................................................... 77
EC 3.1.11 Exodeoxyribonucleases producing 5'-phosphomonoesters ......... 78
EC 3.1.12 Exodeoxyribonucleases producing 3'-phosphomonoesters ......... 79
EC 3.1.13 Exoribonucleases producing 5'-phosphomonoesters ................. 80
EC 3.1.14 Exoribonucleases producing 3'-phosphomonoesters ................. 81
EC 3.1.15 Exonucleases that are active with either ribo- or deoxyribonucleic acids and produce 5'-phosphomonoesters 81
EC 3.1.16 Exonucleases that are active with either ribo- or deoxyribonucleic acids and produce 3'-phosphomonoesters 81
EC 3.1.21 Endodeoxyribonucleases producing 5'-phosphomonoesters .... 82
EC 3.1.22 Endodeoxyribonucleases producing 3'-phosphomonoesters .... 84
EC 3.1.25 Site-specific endodeoxyribonucleases that are specific for altered bases .......... 92
EC 3.1.26 Endoribonucleases producing 5'-phosphomonoesters ............ 92
EC 3.1.27 Endoribonucleases producing 3'-phosphomonoesters ............ 95
EC 3.1.30 Endoribonucleases that are active with either ribo- or deoxyribonucleic acids and produce 5'-phosphomonoesters 96
EC 3.1.31 Endoribonucleases that are active with either ribo- or deoxyribonucleic acids and produce 3'-phosphomonoesters 97

EC 3.2 Glycosylases 97
EC 3.2.1 Glycosidases, i.e. enzymes that hydrolyse O- and S-glycosyl compounds ......................................................... 97
EC 3.2.2 Hydrolysing N-glycosyl compounds ............................................... 147

EC 3.3 Acting on ether bonds 155
EC 3.3.2 Ether hydrolases .............................................................................. 155
EC 3.1 Acting on ester bonds

This subclass contains the esterase enzymes. The esterases are subdivided into: carboxylic-ester hydrolases (EC 3.1.1), thioester hydrolases (EC 3.1.2), phosphoric-monoester hydrolases, the phosphatases (EC 3.1.3), phosphoric-diester hydrolases (EC 3.1.4), triphosphoric-monoester hydrolases (EC 3.1.5), sulfuric-ester hydrolases, the sulfatases (EC 3.1.6), diphosphoric monoesterases (EC 3.1.7) and phosphoric-triester hydrolases (EC 3.1.8). The nucleases, previously included under EC 3.1.4, are now placed in a number of new sub-subclasses: the exonucleases (EC 3.1.11-16) and the endonucleases (EC 3.1.21-31). EC 3.1.23 and EC 3.1.24

In a previous edition, site-specific endodeoxyribonucleases were set out individually in subclasses EC 3.1.23 and EC 3.1.24 (since deleted), with 113 separate entries. These are now included in three entries EC 3.1.21.3, EC 3.1.21.4 and EC 3.1.21.5. A complete listing of all of these enzymes has been produced by R.J. Roberts and is available at http://rebase.neb.com/rebase/rebase.html.

EC 3.1.1 Carboxylic-ester hydrolases

EC 3.1.1.1

Accepted name: carboxylesterase

Reaction: a carboxylic ester + H₂O = an alcohol + a carboxylate

Other name(s): ali-esterase; B-esterase; monobutyrase; cocaine esterase; procaine esterase; methylbutyrase; vitamin A esterase; butyryl esterase; carboxyesterase; carboxylate esterase; carboxylic esterase; methylbutyrate esterase; triacetin esterase; carboxyl ester hydrolase; butyrate esterase; methylbutyrase; α-carboxylesterase; propionyl esterase; nonspecific carboxylesterase; esterase D; esterase B; esterase A; serine esterase; carboxylic acid esterase; cocaine esterase

Systematic name: carboxylic-ester hydrolase

Comments: Wide specificity. The enzymes from microsomes also catalyse the reactions of EC 3.1.1.2 (arylesterase), EC 3.1.1.5 (lyso phospholipase), EC 3.1.1.6 (acytylesterase), EC 3.1.1.23 (acylglycerol lipase), EC 3.1.1.28 (acylcarnitine hydrolase), EC 3.1.2.2 (palmitoyl-CoA hydrolase), EC 3.5.1.4 (amidase) and EC 3.5.1.13 (aryl-acylamidase). Also hydrolyses vitamin A esters.

References: [104, 155, 224, 354, 1250, 1888, 1986, 2605]

[EC 3.1.1.1 created 1961]

EC 3.1.1.2

Accepted name: arylesterase

Reaction: a phenyl acetate + H₂O = a phenol + acetate

Other name(s): A-esterase (ambiguous); paraoxonase (ambiguous); aromatic esterase

Systematic name: aryl-ester hydrolase

Comments: Acts on many phenolic esters. The reactions of EC 3.1.8.1 aryldialkylphosphatase, were previously attributed to this enzyme. It is likely that the three forms of human paraoxonase are lactonases rather than aromatic esterases [1518, 689]. The natural substrates of the paraoxonases are lactones [1518, 689], with (±)-5-hydroxy-6E,8Z,11Z,4Z-eicostetraenoic-acid 1,5-lactone being the best substrate [689].

References: [33, 109, 293, 1528, 1866, 1, 1518, 689]

[EC 3.1.1.2 created 1961, modified 1989]

EC 3.1.1.3

Accepted name: triacylglycerol lipase

Reaction: triacylglycerol + H₂O = diacylglycerol + a carboxylate

3
**Other name(s):** lipase (ambiguous); butyrinase; tributyrinase; Tween hydrolase; steapsin; triacetinase; tributyrin esterase; Tweenase; amno N-AP; Takedo 1969-4-9; Meito MY 30; Tweenesterase; GA 56; capalase L; triglyceride hydrolase; triolein hydrolase; tween-hydrolyzing esterase; amano P; amano AP; PPL; glycerol-ester hydrolase; GEH; meito Sangyo OF lipase; hepatic lipase; lipazin; post-heparin plasma protamine-resistant lipase; salt-resistant post-heparin lipase; heparin releasable hepatic lipase; amano CES; amano B; tributyrase; triglyceride lipase; liver lipase; hepatic monoacylglycerol acyltransferase; PNLI P (gene name); LIPF (gene name)

**Systematic name:** triacylglycerol acylhydrolase

**Comments:** The enzyme is found in diverse organisms including animals, plants, fungi, and bacteria. It hydrolyses triglycerides into diglycerides and subsequently into monoglycerides and free fatty acids. The enzyme is highly soluble in water and acts at the surface of oil droplets. Access to the active site is controlled by the opening of a lid, which, when closed, hides the hydrophobic surface that surrounds the active site. The lid opens when the enzyme contacts an oil-water interface (interfacial activation). The pancreatic enzyme requires a protein cofactor, namely colipase, to counteract the inhibitory effects of bile salts.

**References:** [2806, 2807, 2656, 1858, 2367, 3064, 1212, 3350, 1535, 1654, 2490]

[EC 3.1.1.3 created 1961]

**EC 3.1.1.4**

**Accepted name:** phospholipase A₂

**Reaction:** \( \text{phosphatidylcholine} + \text{H}_2\text{O} = 1\text{-acylglycerophosphocholine} + \text{a carboxylate} \)

**Other name(s):** lecithinase A; phosphatidase; phosphatidolipase; phospholipase A

**Systematic name:** phosphatidylcholine 2-acylhydrolase

**Comments:** Also acts on phosphatidylethanolamine, choline plasmalogen and phosphatides, removing the fatty acid attached to the 2-position. Requires \( \text{Ca}^{2+} \).

**References:** [672, 853, 1103, 2058, 2623, 3181]

[EC 3.1.1.4 created 1961, modified 1976, modified 1983]

**EC 3.1.1.5**

**Accepted name:** lysophospholipase

**Reaction:** \( 2\text{-lysophosphatidylcholine} + \text{H}_2\text{O} = \text{glycerophosphocholine} + \text{a carboxylate} \)

**Other name(s):** lecithinase B; lysolecithinase; phospholipase B; lysophosphatidase; lecitholipase; phosphatidase B; lysophosphatidylcholine hydrolase; lysophospholipase A₁; lysophospholipase L₂; lysophospholipase transacylase; neuropathy target esterase; NTE; NTE-LysOPLA; NTE-lysophospholipase

**Systematic name:** 2-lysophosphatidylcholine acylhydrolase

**References:** [5, 523, 593, 783, 2755, 3182, 3197, 2464, 1854, 3352]

[EC 3.1.1.5 created 1961, modified 1976, modified 1983]

**EC 3.1.1.6**

**Accepted name:** acetyesterase

**Reaction:** an acetic ester + \( \text{H}_2\text{O} = \text{an alcohol} + \text{acetate} \)

**Other name(s):** C-esterase (in animal tissues); acetic ester hydrolase; chloroesterase; \( p \)-nitrophenyl acetate esterase; *Citrus* acetyesterase

**Systematic name:** acetic-ester acetylhydrolase

**References:** [33, 213, 1388]

[EC 3.1.1.6 created 1961]
EC 3.1.1.7

Accepted name: acetylcholinesterase
Reaction: acetylcholine + H₂O = choline + acetate
Other name(s): true cholinesterase; choline esterase I; cholinesterase; acetyltiocholinesterase; acetylcholine hydrolase; acetylβ-methylcholinesterase; AcCholE
Systematic name: acetylcholine acetylhydrolase
Comments: Acts on a variety of acetic esters; also catalyses transacytlations.
References: [105, 214, 492, 1744, 2123, 3511]

[EC 3.1.1.7 created 1961]

EC 3.1.1.8

Accepted name: cholinesterase
Reaction: an acylcholine + H₂O = choline + a carboxylate
Other name(s): pseudocholinesterase; butyrylcholine esterase; non-specific cholinesterase; choline esterase II (un-specific); benzoylcholinesterase; choline esterase; butyrylcholinesterase; propionylcholinesterase; BtChoEase
Systematic name: acylcholine acylhydrolase
Comments: Acts on a variety of choline esters and a few other compounds.
References: [105, 109, 1580, 2123, 2680, 2921]

[EC 3.1.1.8 created 1961]

[3.1.1.9 Deleted entry. benzoylcholinesterase; a side reaction of EC 3.1.1.8 cholinesterase]

[EC 3.1.1.9 created 1961, deleted 1972]

EC 3.1.1.10

Accepted name: tropinesterase
Reaction: atropine + H₂O = tropine + tropate
Other name(s): tropine esterase; atropinase; atropine esterase
Systematic name: atropine acylhydrolase
Comments: Also acts on cocaine and other tropine esters.
References: [984, 2057]

[EC 3.1.1.10 created 1961, deleted 1972, reinstated 1976]

EC 3.1.1.11

Accepted name: pectinesterase
Reaction: pectin + n H₂O = n methanol + pectate
Other name(s): pectin demethoxylase; pectin methoxylase; pectin methylesterase; pectase; pectin methyl esterase; pectinoesterase
Systematic name: pectin pectylhydrolase
References: [636, 1800, 2016]

[EC 3.1.1.11 created 1961]

[3.1.1.12 Deleted entry. vitamin A esterase, now believed to be identical with EC 3.1.1.1 carboxylesterase]

[EC 3.1.1.12 created 1961, deleted 1972]

EC 3.1.1.13

Accepted name: sterol esterase
Reaction: a steryl ester + H₂O = a sterol + a fatty acid
Other name(s): cholesterol esterase; cholesteryl ester synthase; triterpenol esterase; cholesteryl esterase; cholesteryl ester hydrolase; sterol ester hydrolase; cholesterol ester hydrolase; cholesteryl acylhydrolase

Systematic name: steryl-ester acylhydrolase

Comments: A group of enzymes of broad specificity, acting on esters of sterols and long-chain fatty acids, that may also bring about the esterification of sterols. Activated by bile salts.

References: [1292, 2294, 3177, 3278]

[EC 3.1.1.13 created 1961, modified 1990]

EC 3.1.1.14

Accepted name: chlorophyllase
Reaction: chlorophyll + H₂O = phytol + chlorophyllide
Other name(s): CLH, Chlase
Systematic name: chlorophyll chlorophyllidohydrolase

Comments: Chlorophyllase has been found in higher plants, diatoms, and in the green algae Chlorella [3122]. This enzyme forms part of the chlorophyll degradation pathway and is thought to take part in degreening processes such as fruit ripening, leaf senescence and flowering, as well as in the turnover and homeostasis of chlorophyll [2296]. This enzyme acts preferentially on chlorophyll a but will also accept chlorophyll b and pheophytins as substrates [1254]. Ethylene and methyl jasmonate, which are known to accelerate senescence in many species, can enhance the activity of the hormone-inducible form of this enzyme [1254].

References: [1235, 1559, 3122, 2296, 1254]

[EC 3.1.1.14 created 1961, modified 2007]

EC 3.1.1.15

Accepted name: L-arabinonolactonase
Reaction: L-arabinono-1,4-lactone + H₂O = L-arabinonate
Systematic name: L-arabinono-1,4-lactone lactonohydrolase

References: [3305]

[EC 3.1.1.15 created 1961]

[3.1.1.16 Deleted entry. 4-carboxymethyl-4-hydroxyisocrotonolactonolactonase. This reaction was due to a mixture of EC 5.3.3.4 (muconolactone Δ-isomerase) and EC 3.1.1.24 (3-oxoadipate enol-lactonase)]

[EC 3.1.1.16 created 1961, deleted 1972]

EC 3.1.1.17

Accepted name: gluconolactonase
Reaction: D-glucono-1,5-lactone + H₂O = D-gluconate
Other name(s): lactonase, aldolactonase, glucono-δ-lactonase, gulonolactonase
Systematic name: D-glucono-1,5-lactone lactonohydrolase

Comments: Acts on a wide range of hexose-1,5-lactones. The hydrolysis of L-gulono-1,5-lactone was previously listed separately.

References: [327, 351, 2954]

[EC 3.1.1.17 created 1961 (EC 3.1.1.18 created 1961, incorporated 1982)]

[3.1.1.18 Deleted entry. aldolactonase. Now included with EC 3.1.1.17 gluconolactonase]

[EC 3.1.1.18 created 1961, deleted 1982]
EC 3.1.1.19
Accepted name: uronolactonase
Reaction: D-glucurono-6,2-lactone + H₂O = D-glucuronate
Other name(s): glucuronolactonase
Systematic name: D-glucurono-6,2-lactone lactonohydrolase
References: [3348]

[EC 3.1.1.19 created 1961]

EC 3.1.1.20
Accepted name: tannase
Reaction: digallate + H₂O = 2 gallate
Other name(s): tannase S; tannin acetylhydrolase
Systematic name: tannin acylhydrolase
Comments: Also hydrolyses ester links in other tannins.
References: [716]

[EC 3.1.1.20 created 1961]

[3.1.1.21 Deleted entry. retinyl-palmitate esterase. Now known to be catalysed by EC 3.1.1.1, carboxylesterase and EC 3.1.1.3, triacylglycerol lipase.]

[EC 3.1.1.21 created 1972, deleted 2011]

EC 3.1.1.22
Accepted name: hydroxybutyrate-dimer hydrolase
Reaction: (R)-3-((R)-3-hydroxybutanoyloxy)butanoate + H₂O = 2 (R)-3-hydroxybutanoate
Other name(s): D-(-)-3-hydroxybutyrate-dimer hydrolase
Systematic name: (R)-3-((R)-3-hydroxybutanoyloxy)butanoate hydroxybutanoylhydrolase
References: [615]

[EC 3.1.1.22 created 1972]

EC 3.1.1.23
Accepted name: acylglycerol lipase
Reaction: Hydrolyses glycerol monoesters of long-chain fatty acids
Other name(s): monoaoylglycerol lipase; monoaoylglycerolipase; monoglyceride lipase; monoglyceride hydrolase; fatty acyl monoester lipase; monoclaylglycerol hydrolase; monoglyceridyllipase; monoglyceridase
Systematic name: glycerol-ester acylhydrolase
References: [1984, 2429]

[EC 3.1.1.23 created 1972]

EC 3.1.1.24
Accepted name: 3-oxoadipate enol-lactonase
Reaction: 3-oxoadipate enol-lactone + H₂O = 3-oxoadipate
Other name(s): carboxymethylbutenolide lactonase; β-ketoacidic enol-lactone hydrolase; 3-ketoacidic enol-lactone hydrolase; 3-oxoadipic enol-lactone hydrolase; β-ketoacidic enol-lactone hydrolase
Systematic name: 4-carboxymethylbut-3-en-4-olide enol-lactonohydrolase
Comments: The enzyme acts on the product of EC 4.1.1.44 4-carboxybutenolactone decarboxylase.
References: [2312, 2313]

[EC 3.1.1.24 created 1961 as EC 3.1.1.16, part transferred 1972 to EC 3.1.1.24]
EC 3.1.1.25

Accepted name: 1,4-lactonase
Reaction: a 1,4-lactone + H₂O = a 4-hydroxyacid
Other name(s): γ-lactonase
Systematic name: 1,4-lactone hydroxyacylhydrolase
Comments: The enzyme is specific for 1,4-lactones with 4-8 carbon atoms. It does not hydrolyse simple aliphatic esters, acetylcholine, sugar lactones or substituted aliphatic lactones, e.g. 3-hydroxy-4-butyrolactone; requires Ca²⁺.
References: [827, 828]

[EC 3.1.1.25 created 1972, modified 1981]

EC 3.1.1.26

Accepted name: galactolipase
Reaction: 1,2-diacyl-3-β-D-galactosyl-sn-glycerol + 2 H₂O = 3-β-D-galactosyl-sn-glycerol + 2 carboxylates
Other name(s): galactolipid lipase; polygalactolipase; galactolipid acylhydrolase
Systematic name: 1,2-diacyl-3-β-D-galactosyl-sn-glycerol acylhydrolase
Comments: Also acts on 2,3-di-O-acyl-1-O-(6-O-α-D-galactosyl-β-D-galactosyl)-D-glycerol, and phosphatidylcholine and other phospholipids.
References: [1177, 1221]

[EC 3.1.1.26 created 1972]

EC 3.1.1.27

Accepted name: 4-pyridoxolactonase
Reaction: 4-pyridoxolactone + H₂O = 4-pyridoxate
Systematic name: 4-pyridoxolactone lactonohydrolase
References: [356]

[EC 3.1.1.27 created 1972]

EC 3.1.1.28

Accepted name: acylcarnitine hydrolase
Reaction: O-acylcarnitine + H₂O = a fatty acid + L-carnitine
Other name(s): high activity acylcarnitine hydrolase; HACH; carnitine ester hydrolase; palmitoylcarnitine hydrolase; palmitoyl-L-carnitine hydrolase; long-chain acyl-L-carnitine hydrolase; palmitoyl carnitine hydrolase
Systematic name: O-acylcarnitine acylhydrolase
Comments: Acts on higher fatty acid (C₆ to C₁₈) esters of L-carnitine; highest activity is with O-decanoyl-L-carnitine.
References: [1871, 1985]

[EC 3.1.1.28 created 1972]

EC 3.1.1.29

Accepted name: aminocyl-tRNA hydrolase
Reaction: N-substituted aminocyl-tRNA + H₂O = N-substituted amino acid + tRNA
Other name(s): aminocyl-transfer ribonucleate hydrolase; N-substituted aminocyl transfer RNA hydrolase; peptidyl-tRNA hydrolase
Systematic name: aminocyl-tRNA aminocarbonylhydrolase
References: [1425]

[EC 3.1.1.29 created 1972]
EC 3.1.1.30
Accepted name: D-arabinonolactonase
Reaction: D-arabinono-1,4-lactone + H₂O = D-arabinonate
Systematic name: D-arabinono-1,4-lactone lactonohydrolase
References: [2338]

[EC 3.1.1.30 created 1972]

EC 3.1.1.31
Accepted name: 6-phosphogluconolactonase
Reaction: 6-phospho-D-glucono-1,5-lactone + H₂O = 6-phospho-D-gluconate
Other name(s): phosphogluconolactonase; 6-PGL
Systematic name: 6-phospho-D-glucono-1,5-lactone lactonohydrolase
References: [1488, 2003]

[EC 3.1.1.31 created 1972]

EC 3.1.1.32
Accepted name: phospholipase A₁
Reaction: phosphatidylethanolamine + H₂O = 2-acylglycerophosphatidylethanolamine + a carboxylate
Systematic name: phosphatidylethanolamine 1-acylhydrolase
Comments: This enzyme has a much broader specificity than EC 3.1.1.4 phospholipase A₂. Requires Ca²⁺.
References: [940, 2681, 3181, 3183]

[EC 3.1.1.32 created 1972, modified 1976]

EC 3.1.1.33
Accepted name: 6-acetylglucose deacetylase
Reaction: 6-acetyl-D-glucose + H₂O = D-glucose + acetate
Other name(s): 6-O-acetylglucose deacetylase
Systematic name: 6-acetyl-D-glucose acetylhydrolase
References: [707]

[EC 3.1.1.33 created 1972]

EC 3.1.1.34
Accepted name: lipoprotein lipase
Reaction: triacylglycerol + H₂O = diacylglycerol + a carboxylate
Other name(s): clearing factor lipase; diacylglycerol lipase; postheparin esterase; diglyceride lipase; postheparin lipase; diacylglycerol hydrolase; lipemia-clearing factor; hepatic triacylglycerol lipase; LIPC (gene name); LPL (gene name); triacylglycerol-protein acylhydrolase
Systematic name: triacylglycerol acylhydrolase (lipoprotein-dependent)
Comments: Hydrolyses triacylglycerols and diacylglycerol in chylomicrons and low-density lipoprotein particles. Human protein purified from post-heparin plasma (LPL) shows no activity against triglyceride in the absence of added lipoprotein. The principal reaction sequence of that enzyme is triglyceride → 1,2-diglyceride → 2-monoglyceride. The hepatic enzyme (LIPC) also hydrolyses triglycerides and phospholipids present in circulating plasma lipoproteins.
References: [725, 817, 1033, 2082, 2196, 2654]

[EC 3.1.1.34 created 1972, modified 1976]
EC 3.1.1.35
Accepted name: dihydrocoumarin hydrolase
Reaction: dihydrocoumarin + H₂O = melilotate
Systematic name: dihydrocoumarin lactonohydrolase
Comments: Also hydrolyses some other benzenoid 1,4-lactones.
References: [1605]

[EC 3.1.1.35 created 1972]

EC 3.1.1.36
Accepted name: limonin-D-ring-lactonase
Reaction: limonoate D-ring-lactone + H₂O = limonoate
Other name(s): limonin-D-ring-lactone hydrolase; limonin lactone hydrolase
Systematic name: limonoate-D-ring-lactone lactonohydrolase
Comments: Limonoate is a triterpenoid.
References: [1874]

[EC 3.1.1.36 created 1972]

EC 3.1.1.37
Accepted name: steroid-lactonase
Reaction: testololactone + H₂O = testolate
Systematic name: testololactone lactonohydrolase
References: [1237]

[EC 3.1.1.37 created 1972]

EC 3.1.1.38
Accepted name: triacetate-lactonase
Reaction: triacetate lactone + H₂O = triacetate
Other name(s): triacetic lactone hydrolase; triacetic acid lactone hydrolase; TAL hydrolase; triacetate lactone hydrolase
Systematic name: triacetolactone lactonohydrolase
References: [1484]

[EC 3.1.1.38 created 1972]

EC 3.1.1.39
Accepted name: actinomycin lactonase
Reaction: actinomycin + H₂O = actinomycinic monolactone
Systematic name: actinomycin lactonohydrolase
References: [1260]

[EC 3.1.1.39 created 1972]

EC 3.1.1.40
Accepted name: orsellinate-depside hydrolase
Reaction: orsellinate depside + H₂O = 2 orsellinate
Other name(s): lecanorate hydrolase
Systematic name: orsellinate-depside hydrolase
Comments: The enzyme will only hydrolyse those substrates based on the 2,4-dihydroxy-6-methylbenzoate structure that also have a free hydroxy group ortho to the depside linkage.
References: [2721]

EC 3.1.1.41

Accepted name: cephalosporin-C deacetylase
Reaction: cephalosporin C + H₂O = deacetylcephalosporin C + acetate
Other name(s): cephalosporin C acetyl-hydrolase; cephalosporin C acetylase; cephalosporin C acetyleresterase; cephalosporin C acetyl-esterase; cephalosporin C deacetylase
Systematic name: cephalosporin-C acetylhydrolase
Comments: Hydrolyses the acetyl ester bond on the 10-position of the antibiotic cephalosporin C.
References: [900]

EC 3.1.1.42

Accepted name: chlorogenate hydrolase
Reaction: chlorogenate + H₂O = caffeate + quinate
Other name(s): chlorogenase; chlorogenic acid esterase
Systematic name: chlorogenate hydrolase
Comments: Also acts, more slowly, on isochlorogenate. No other substrates are known.
References: [2709, 2710]

EC 3.1.1.43

Accepted name: α-amino-acid esterase
Reaction: an α-amino acid ester + H₂O = an α-amino acid + an alcohol
Other name(s): α-amino acid ester hydrolase
Systematic name: α-amino-acid-ester aminoacylhydrolase
Comments: Also catalyses α-aminoacyl transfer to a number of amine nucleophiles.
References: [1482, 1483, 2989]

EC 3.1.1.44

Accepted name: 4-methyloxaloacetate esterase
Reaction: oxaloacetate 4-methyl ester + H₂O = oxaloacetate + methanol
Systematic name: oxaloacetate-4-methyl-ester oxaloacetohydrolase
References: [683]

EC 3.1.1.45

Accepted name: carboxymethylenebutenolidase
Reaction: 4-carboxymethylenebut-2-en-4-olide + H₂O = 4-oxohex-2-enedioate
Other name(s): maleylacetate enol-lactonase; dienelactone hydrolase; carboxymethylene butenolide hydrolase
Systematic name: 4-carboxymethylenebut-2-en-4-olide lactonohydrolase
References: [2704]

[EC 3.1.1.40 created 1976]
[EC 3.1.1.41 created 1976]
[EC 3.1.1.42 created 1981]
[EC 3.1.1.43 created 1983]
[EC 3.1.1.44 created 1983]
[EC 3.1.1.45 created 1983]
EC 3.1.1.46
Accepted name: deoxylimonate A-ring-lactonase
Reaction: deoxylimonate + H₂O = deoxylimonic acid D-ring-lactone
Systematic name: deoxylimonate A-ring-lactonohydrolase
Comments: The enzyme opens the A-ring-lactone of the triterpenoid deoxylimonic acid, leaving the D-ring-lactone intact.
References: [1128]

[EC 3.1.1.46 created 1983]

EC 3.1.1.47
Accepted name: 1-alkyl-2-acetylglycerophosphocholine esterase
Reaction: 1-alkyl-2-acetyl-sn-glycero-3-phosphocholine + H₂O = 1-alkyl-sn-glycero-3-phosphocholine + acetate
Other name(s): 1-alkyl-2-acetyl-sn-glycero-3-phosphocholine acetylhydrolase; alkylacetyl-GPC:acylhydrolase
Systematic name: 1-alkyl-2-acetyl-sn-glycero-3-phosphocholine acetohydrolase
References: [265]

[EC 3.1.1.47 created 1984]

EC 3.1.1.48
Accepted name: fusarinine-C ornithinesterase
Reaction: \(N^5\)-acyl-L-ornithine ester + H₂O = \(N^5\)-acyl-L-ornithine + an alcohol
Other name(s): ornithine esterase; 5-N-acyl-L-ornithine-ester hydrolase
Systematic name: \(N^5\)-acyl-L-ornithine-ester hydrolase
Comments: Hydrolyses the three ornithine ester bonds in fusarinine C. Also acts on \(N^5\)-dinitrophenyl-L-ornithine methyl ester.
References: [742]

[EC 3.1.1.48 created 1984]

EC 3.1.1.49
Accepted name: sinapine esterase
Reaction: sinapoylcholine + H₂O = sinapate + choline
Other name(s): aromatic choline esterase
Systematic name: sinapoylcholine sinapohydrolase
References: [2228]

[EC 3.1.1.49 created 1984]

EC 3.1.1.50
Accepted name: wax-ester hydrolase
Reaction: a wax ester + H₂O = a long-chain alcohol + a long-chain carboxylate
Other name(s): jojoba wax esterase; WEH
Systematic name: wax-ester acylhydrolase
Comments: Also acts on long-chain acylglycerol, but not diacyl- or triacylglycerols.
References: [1275, 2064]

[EC 3.1.1.50 created 1984]
EC 3.1.1.51

Accepted name: phorbol-diester hydrolase
Reaction: phorbol 12,13-dibutanoate + \( \text{H}_2\text{O} \) = phorbol 13-butanoate + butanoate
Other name(s): diacylphorbate 12-hydrolase; diacylphorbate 12-hydrolase; phorbol-12,13-diester 12-ester hydrolase; PDEH
Systematic name: 12,13-diacylphorbate 12-acylhydrolase
Comments: Hydrolysates the 12-ester bond in a variety of 12,13-diacylphorbols (phorbol is a diterpenoid); this reaction inactivates the tumour promotor 12-O-tetradecanoylphorbol-13-acetate from croton oil.
References: [2783]

[EC 3.1.1.51 created 1984]

EC 3.1.1.52

Accepted name: phosphatidylinositol deacylase
Reaction: 1-phosphatidyl-\( \text{D}-\text{myo}-\)inositol + \( \text{H}_2\text{O} \) = 1-acylglycerophosphoinositol + a carboxylate
Other name(s): phosphatidylinositol phospholipase \( \text{A}_2 \); phospholipase \( \text{A}_2 \)
Systematic name: 1-phosphatidyl-\( \text{D}-\text{myo}-\)inositol 2-acylhydrolase
References: [1025, 1024]

[EC 3.1.1.52 created 1984]

EC 3.1.1.53

Accepted name: sialate \( \text{O}\)-acytylesterase
Reaction: \( \text{N-acetyl-O-acytyleuraminate} + \text{H}_2\text{O} = \text{N-acetyl-\( \text{O-acytyleuraminate} + \text{acetate} \)
Other name(s): \( \text{N-acetyl-\( \text{O-acytyleuraminate} \) acetyltransferase; sialate 9(4)-\( \text{O-acytylesterase; sialidase} \)
Systematic name: \( \text{N-acetyl-\( \text{O-acytyleuraminate} \) \( \text{O-acytylesterase} \)
Comments: Acts on free and glycosidically bound \( \text{N-acetyl-} \) or \( \text{N-glycoloyl-} \) neuraminic acid; acts mainly on the 4-\( \text{O-} \) and 9-\( \text{O-} \) acetyl groups. Also acts on some other \( \text{O-} \) acetyl esters, both cyclic and acyclic compounds, which are not sialic acids.
References: [934, 2784]

[EC 3.1.1.53 created 1984]

EC 3.1.1.54

Accepted name: acetoxybutynylbithiophene deacetylase
Reaction: 5-(4-acetoxybut-1-ynyl)-2,2'-bithiophene + \( \text{H}_2\text{O} = 5-(4-hydroxybut-1-ynyl)-2,2'-bithiophene + \text{acetate} \)
Other name(s): acetoxybutynylbithiophene esterase; 5-(4-acetoxy-1-butynyl)-2,2'-bithiophene:acetate esterase
Systematic name: 5-(4-acetoxybut-1-ynyl)-2,2'-bithiophene \( \text{O-acytylesterase} \)
Comments: The enzyme is highly specific.
References: [2949]

[EC 3.1.1.54 created 1986]

EC 3.1.1.55

Accepted name: acetylsalicylate deacetylase
Reaction: acetylsalicylate + \( \text{H}_2\text{O} = \text{salicylate} + \text{acetate} \)
Other name(s): aspirin esterase; aspirin esterase; acetylsalicylic acid esterase; aspirin hydrolase
Systematic name: acetylsalicylate \( \text{O-acytylesterase} \)

13
Comments: Not identical with EC 3.1.1.1 (carboxylesterase), EC 3.1.1.2 (arylesterase), EC 3.1.1.7 (acetylcholinesterase) or EC 3.1.1.8 (cholinesterase). The activity of the liver cytosol enzyme is highest with acetyl esters of aryl alcohols, and thiocarbamates are also hydrolysed; the microsomal enzyme also hydrolys some other negatively charged esters, with highest activity on esters of salicylate with long-chain alcohols.

References: [38, 1527, 3325]

[EC 3.1.1.55 created 1986, modified 1989]

EC 3.1.1.56

Accepted name: methylumbelliferyl-acetate deacylase
Reaction: 4-methylumbelliferyl acetate + H2O = 4-methylumbelliferone + acetate
Other name(s): esterase D
Systematic name: 4-methylumbelliferyl-acetate acylhydrolase
Comments: Acts on short-chain acyl esters of 4-methylumbelliferone, but not on naphthyl, indoxyl or thiocholine esters.
References: [1247]

[EC 3.1.1.56 created 1986]

EC 3.1.1.57

Accepted name: 2-pyrene-4,6-dicarboxylate lactonase
Reaction: 2-oxo-2H-pyran-4,6-dicarboxylate + H2O = (1E)-4-oxobut-1-ene-1,2,4-tricarboxylate
Other name(s): 2-pyrene-4,6-dicarboxylate hydrolase; 2-pyrene-4,6-dicarboxylate lactonohydrolase
Systematic name: 2-oxo-2H-pyran-4,6-dicarboxylate lactonohydrolase
Comments: The product is most likely the keto-form of 4-oxalomesaconate (as shown in the reaction) [1506, 1924]. It can be converted to the enol-form, 4-hydroxybuta-1,3-diene-1,2,4-trioate, either spontaneously or by EC 5.3.2.8, 4-oxalomesaconate tautomerase [2209].
References: [1506, 1924, 2209]

[EC 3.1.1.57 created 1986, modified 2010]

EC 3.1.1.58

Accepted name: N-acetylgalactosaminoglycan deacetylase
Reaction: N-acetyl-D-galactosaminoglycan + H2O = D-galactosaminoglycan + acetate
Other name(s): polysaccharide deacetylase (misleading); Vi-polysaccharide deacetylase; N-acetyl galactosaminoglycan deacetylase
Systematic name: N-acetyl-D-galactosaminoglycan acetylhydrolase
References: [1421]

[EC 3.1.1.58 created 1986]

EC 3.1.1.59

Accepted name: juvenile-hormone esterase
Reaction: (1) juvenile hormone I + H2O = juvenile hormone I acid + methanol
(2) juvenile hormone III + H2O = juvenile hormone III acid + methanol
Other name(s): JH-esterase; juvenile hormone analog esterase; juvenile hormone carboxyesterase; methyl-(2E,6E)-(10R,11S)-11-epoxy-3,7,11-trimethylnonadeca-2,6-dienoate acylhydrolase
Systematic name: methyl-(2E,6E,10R)-11-epoxy-3,7,11-trimethyltrideca-2,6-dienoate acylhydrolase
Comments: Demethylates the insect juvenile hormones JH1 and JH3, but does not hydrolyse the analogous ethyl or isopropyl esters.
References: [600, 2031]

[EC 3.1.1.59 created 1989, modified 2015]
EC 3.1.1.60

**Accepted name:** bis(2-ethylhexyl)phthalate esterase

**Reaction:** bis(2-ethylhexyl)phthalate + H₂O = 2-ethylhexyl phthalate + 2-ethylhexan-1-ol

**Other name(s):** DEHP esterase

**Systematic name:** bis(2-ethylhexyl)phthalate acylhydrolase

**Comments:** Also acts on 4-nitrophenyl esters, with optimum chain-length C₆ to C₈.

**References:** [1070]

[EC 3.1.1.60 created 1989]

EC 3.1.1.61

**Accepted name:** protein-glutamate methylesterase

**Reaction:** protein L-glutamate O⁵-methyl ester + H₂O = protein L-glutamate + methanol

**Other name(s):** chemotaxis-specific methylesterase; methyl-accepting chemotaxis protein methyl-esterase; CheB methylesterase; methylesterase CheB; protein methyl-esterase; protein carboxyl methylesterase; PME; protein methylesterase; protein-L-glutamate-5-O-methyl-ester acylhydrolase

**Systematic name:** protein-L-glutamate-O⁵-methyl-ester acylhydrolase

**Comments:** Hydrolyses the products of EC 2.1.1.77 (protein-L-isoaspartate(D-aspartate) O-methyltransferase), EC 2.1.1.78 (isororientin 3’-O-methyltransferase), EC 2.1.1.80 (protein-glutamate O-methyltransferase) and EC 2.1.1.100 (protein-S-isoprenylcysteine O-methyltransferase).

**References:** [925, 1495]

[EC 3.1.1.61 created 1989, modified 2002]

[3.1.1.62 Deleted entry. N-acetyldiaminopimelate deacylase. Now listed as EC 3.5.1.47, N-acetyldiaminopimelate deacetylase]

[EC 3.1.1.62 created 1989, deleted 1992]

EC 3.1.1.63

**Accepted name:** 11-cis-retinyl-palmitate hydrolase

**Reaction:** 11-cis-retinyl palmitate + H₂O = 11-cis-retinol + palmitate

**Other name(s):** 11-cis-retinol palmitate esterase; RPH

**Systematic name:** 11-cis-retinyl-palmitate acylhydrolase

**Comments:** Activated by bile salts.

**References:** [263, 264]

[EC 3.1.1.63 created 1989]

EC 3.1.1.64

**Accepted name:** retinoid isomerohydrolase

**Reaction:** an all-trans-retinyl ester + H₂O = 11-cis-retinol + a fatty acid

**Other name(s):** all-trans-retinyl-palmitate hydrolase (ambiguous); retinol isomerase (ambiguous); all-trans-retinol isomerase;hydrolase (ambiguous); all-trans-retinylester 11-cis isomerohydrolase; RPE65 (gene name)

**Systematic name:** all-trans-retinyl ester acylhydrolase, 11-cis retinol-forming

**Comments:** This enzyme, which operates in the retinal pigment epithelium (RPE), catalyses the cleavage and isomerization of all-trans-retinyl fatty acid esters to 11-cis-retinol, a key step in the regeneration of the visual chromophore in the vertebrate visual cycle [2047]. Interaction of the enzyme with the membrane is critical for its enzymic activity [996].

**References:** [263, 219, 317, 2047, 2193, 996]

[EC 3.1.1.64 created 1989 (EC 5.2.1.7 created 1989, incorporated 2011), modified 2011]
EC 3.1.1.65
Accepted name: L-rhamnono-1,4-lactonase
Reaction: L-rhamnono-1,4-lactone + H₂O = L-rhamnonate
Other name(s): L-rhamno-γ-lactonase; L-rhamnono-γ-lactonase; L-rhamnonate dehydratase
Systematic name: L-rhamnono-1,4-lactone lactonohydrolase
References: [2553]

EC 3.1.1.66
Accepted name: 5-(3,4-diacetoxybut-1-ynyl)-2,2′-bithiophene deacetylase
Reaction: 5-(3,4-diacetoxybut-1-ynyl)-2,2′-bithiophene + H₂O = 5-(3-hydroxy-4-acetoxybut-1-ynyl)-2,2′-bithiophene + acetate
Other name(s): diacetoxybutynylbithiophene acetate esterase; 3,4-diacetoxybutinylbithiophene:4-acetate esterase
Systematic name: 5-(3,4-diacetoxybut-1-ynyl)-2,2′-bithiophene acetylhydrolase
Comments: A highly specific enzyme from Tagetes patula.
References: [2373]

EC 3.1.1.67
Accepted name: fatty-acyl-ethyl-ester synthase
Reaction: a long-chain-fatty-acyl ethyl ester + H₂O = a long-chain-fatty acid + ethanol
Other name(s): FAEES
Systematic name: long-chain-fatty-acyl-ethyl-ester acylhydrolase
Comments: The reaction, forms ethyl esters from fatty acids and ethanol in the absence of coenzyme A or ATP. Best substrates are unsaturated octadecanoic acids; palmitate, stearate and arachidonate also act, but more slowly.
References: [2046]

EC 3.1.1.68
Accepted name: xylono-1,4-lactonase
Reaction: D-xylono-1,4-lactone + H₂O = D-xylonate
Other name(s): xylono-γ-lactonase; xylonolactonase
Systematic name: D-xylono-1,4-lactone lactonohydrolase
References: [353]

EC 3.1.1.69
Accepted name: xylono-1,4-lactonase
Reaction: D-xylono-1,4-lactone + H₂O = D-xylonate
Other name(s): xylono-γ-lactonase; xylonolactonase
Systematic name: D-xylono-1,4-lactone lactonohydrolase
References: [353]

EC 3.1.1.70
Accepted name: cetraxate benzylesterase
Reaction: cetraxate benzyl ester + H₂O = cetraxate + benzyl alcohol
Systematic name: cetraxate-benzyl-ester benzylydrolase
Comments: Acts on a number of benzyl esters of substituted phenyl propanoates, and on the benzyl esters of phenylalanine and tyrosine.
References: [1662]
EC 3.1.1.71

**Accepted name:** acetylylalkylglycerol acetylhydrolase  
**Reaction:** \(2\text{-acetyl-1-alkyl-}\text{sn-}\text{glycerol} + \text{H}_2\text{O} = 1\text{-alkyl-}\text{sn-}\text{glycerol} + \text{acetate}\)  
**Other name(s):** alkylacylglycerol acetylhydrolase  
**Systematic name:** 2-acetyl-1-alkyl-\text{sn-}\text{glycerol acetylhydrolase}  
**Comments:** Hydrolysis of the acetyl group from the 1-alkyl-2-acetyl and 1-alkyl-3-acetyl substrates occurs at apparently identical rates. The enzyme from Erlich ascites cells is membrane-bound. It differs from lipoprotein lipase (EC 3.1.1.34) since 1,2-diacyl-\text{sn-}\text{glycerols are not substrates. It also differs from EC 3.1.1.47, 1-acetyl-2-alkyl-glycerophosphocholine esterase.}  
**References:** [266]

EC 3.1.1.72

**Accepted name:** acetylxylan esterase  
**Reaction:** Deacetylation of xylans and xylo-oligosaccharides  
**Systematic name:** acetylxylan esterase  
**Comments:** Catalyses the hydrolysis of acetyl groups from polymeric xylan, acetylated xylose, acetylated glucose, \(\alpha\)-napthyl acetate, \(p\)-nitrophenyl acetate but not from triacylgllycerol. Does not act on acetylated mannur or pectin.  
**References:** [2944, 2437, 1908]

EC 3.1.1.73

**Accepted name:** feruloyl esterase  
**Reaction:** \(\text{feruloyl-polysaccharide} + \text{H}_2\text{O} = \text{ferulate} + \text{polysaccharide}\)  
**Other name(s):** ferulic acid esterase; hydroxycinnamoyl esterase; hemicellulase accessory enzyme; FAE-III; cinnamoyl ester hydrolase; FAEA; cinnAE; FAE-I; FAE-II  
**Systematic name:** 4-hydroxy-3-methoxycinnamoyl-sugar hydrolase  
**Comments:** Catalyses the hydrolysis of the 4-hydroxy-3-methoxycinnamoyl (feruloyl) group from an esterified sugar, which is usually arabinose in "natural" substrates. \(p\)-Nitrophenol acetate and methyl ferulate are poorer substrates. All microbial ferulate esterases are secreted into the culture medium. They are sometimes called hemicellulase accessory enzymes, since they help xylanases and pectinases to break down plant cell wall hemicellulose.  
**References:** [797, 798, 1627, 640, 410]

EC 3.1.1.74

**Accepted name:** cutinase  
**Reaction:** cutin + \(\text{H}_2\text{O} = \text{cutin monomers}\)  
**Systematic name:** cutin hydrolase  
**Comments:** Cutin, a polymeric structural component of plant cuticles, is a polymer of hydroxy fatty acids that are usually \(\text{C}_{16}\) or \(\text{C}_{18}\) and contain up to three hydroxy groups. The enzyme from several fungal sources also hydrolyses the \(p\)-nitrophenyl esters of hexadecanoic acid. It is however inactive towards several esters that are substrates for non-specific esterases.  
**References:** [933, 2449, 2448]
EC 3.1.1.75

**Accepted name:** poly(3-hydroxybutyrate) depolymerase  
**Reaction:** \([ (R)-3\text{-hydroxybutanoate}]_n + H_2O = [ (R)-3\text{-hydroxybutanoate}]_{n-x} + [ (R)-3\text{-hydroxybutanoate}]_x; x = 1-5\)  
**Other name(s):** PHB depolymerase; poly(3HB) depolymerase; poly\([ (R)-\text{hydroxyalkanoic acid}]\) depolymerase; poly\([ (R)-3\text{-hydroxybutyrate}]\) hydrolase  
**Systematic name:** poly\([ (R)-3\text{-hydroxybutanoate}]\) hydrolase  
**Comments:** Reaction also occurs with esters of other short-chain-length (C\(_1\)-C\(_5\)) hydroxyalkanoic acids (HA). There are two types of polymers: native (intracellular) granules are amorphous and have an intact surface layer; denatured (extracellular) granules either have no surface layer or a damaged surface layer and are partially crystalline.  
**References:** [1397, 931]

[EC 3.1.1.75 created 2001]

EC 3.1.1.76

**Accepted name:** poly(3-hydroxyoctanoate) depolymerase  
**Reaction:** Hydrolyses the polyester polyoxyxycarbonyl\([ (R)-2\text{-pentylethylene}]\) to oligomers  
**Other name(s):** PHO depolymerase; poly(3HO) depolymerase; poly\([ (R)-\text{hydroxyalkanoic acid}]\) depolymerase; poly\([ (R)-3\text{-hydroxyoctanoate}]\) hydrolase  
**Systematic name:** polyoxyxycarbonyl\([ (R)-2\text{-pentylethylene}]\) hydrolase  
**Comments:** The main product after prolonged incubation is the dimer [2698]. Besides hydrolysing polymers of 3-hydroxyoctanoic acid, the enzyme also hydrolyses other polymers derived from medium-chain-length (C\(_6\)-C\(_{12}\)) hydroxyalkanoic acids and copolymers of mixtures of these. It also hydrolysers p-nitrophenyl esters of fatty acids. Polymers of short-chain-length hydroxyalkanoic acids such as poly\([ (R)-3\text{-hydroxybutanoic acid}]\) and poly\([ (R)-3\text{-hydroxypentanoic acid}]\) are not hydrolysed.  
**References:** [1397, 931, 2698]

[EC 3.1.1.76 created 2001, modified 2005]

EC 3.1.1.77

**Accepted name:** acyloxyacyl hydrolase  
**Reaction:** 3-(acyloxy)acyl group of bacterial toxin + H\(_2\)O = 3-hydroxyacyl group of bacterial toxin + a fatty acid  
**Comments:** The substrate is lipid A on the reducing end of the toxic lipopolysaccharide (LPS) of *Salmonella typhimurium* and related organisms. It consists of diglucosamine, \(\beta\)-D-GlcN-(1→6)-D-GlcN, attached by glycosylation on O-6 of its non-reducing residue, phosphorylated on O-4 of this residue and on O-1 of its potentially reducing residue. Both residues carry 3-(acyloxy)acyl groups on N-2 and O-3. The enzyme from human leucocytes detoxifies the lipid by hydrolysing the secondary acyl groups from O-3 of the 3-hydroxyacyl groups on the disaccharide (LPS). It also possesses a wide range of phospholipase and acyltransferase activities [e.g. EC 3.1.1.4 (phospholipase A\(_2\)), EC 3.1.1.5 (lyso phospholipase), EC 3.1.1.32 (phospholipase A\(_1\)) and EC 3.1.1.52 (phosphatidylinositol decacylase)], hydrolysing diacylglycerol and phosphatidyl compounds, but not triacylglycerols. It has a preference for saturated C\(_{12}\)-C\(_{16}\) acyl groups.  
**References:** [762, 1081, 2104]

[EC 3.1.1.77 created 2001]

EC 3.1.1.78

**Accepted name:** polynucleotide-aldehyde esterase  
**Reaction:** polynucleotide aldehyde + H\(_2\)O = 16-epivellosimine + CO\(_2\) + methanol  
**Other name(s):** polynucleotide aldehyde esterase; PNAE  
**Systematic name:** polynucleotide aldehyde hydrolase (decarboxylating)
Following hydrolysis of this indole alkaloid ester the carboxylic acid decarboxylates spontaneously giving the sarpagan skeleton. The enzyme also acts on akuammidine aldehyde (the 16-epimer of polyneuridine aldehyde).

References: [2389, 2390, 673, 1941]

EC 3.1.1.79
Accepted name: hormone-sensitive lipase
Reaction: (1) diacylglycerol + H₂O = monoacylglycerol + a carboxylate
(2) triacylglycerol + H₂O = diacylglycerol + a carboxylate
(3) monoacylglycerol + H₂O = glycerol + a carboxylate
Other name(s): HSL
Systematic name: diacylglycerol acylhydrolase
Comments: This enzyme is a serine hydrolase. Compared with other lipases, hormone-sensitive lipase has a uniquely broad substrate specificity. It hydrolyses all acylglycerols (triacylglycerol, diacylglycerol and monoacylglycerol) [2,3,4] as well as cholesteryl esters [856, 2317], steroid fatty acid esters [1714], retinyl esters [3300] and p-nitrophenyl esters [2317, 3127]. It exhibits a preference for the 1- or 3-ester bond of its acylglycerol substrate compared with the 2-ester bond [3441]. The enzyme shows little preference for the fatty acids in the triacylglycerol, although there is some increase in activity with decreasing chain length. The enzyme activity is increased in response to hormones that elevate intracellular levels of cAMP.
References: [1236, 856, 3206, 2317, 1714, 3300, 3127, 3441]

EC 3.1.1.80
Accepted name: acetylajmaline esterase
Reaction: (1) 17-O-acetylajmaline + H₂O = ajmaline + acetate
(2) 17-O-acetylnorajmaline + H₂O = norajmaline + acetate
Other name(s): AAE; 2β-[R]-17-O-acetylajmalan:acetylesterase; acetylajmalan esterase
Systematic name: 17-O-acetylajmaline O-acyethylhydrolase
Comments: This plant enzyme is responsible for the last stages in the biosynthesis of the indole alkaloid ajmaline. The enzyme is highly specific for the substrates 17-O-acetylajmaline and 17-O-acetylnorajmaline as the structurally related acetylated alkaloids vinorine, vomilenine, 1,2-dihydropvinorine and 1,2-dihydrocaffricine cannot act as substrates [2606]. This is a novel member of the GDSL family of serine esterases/lipases.
References: [2426, 2606]

EC 3.1.1.81
Accepted name: quorum-quenching N-acyl-homoserine lactonase
Reaction: an N-acyl-L-homoserine lactone + H₂O = an N-acyl-L-homoserine
Other name(s): acyl homoserine degrading enzyme; acyl-homoserine lactone acylase; AHL lactonase; AHL-degrading enzyme; AHL-inactivating enzyme; AHLase; AhlD; AhlK; AiiA; AiiA lactonase; AiiA-like protein; AiiB; AiiC; AttM; delactonase; lactonase-like enzyme; N-acyl homoserine lactonase; N-acyl homoserine lactone hydrolase; N-acyl-homoserine lactone lactonase; N-acyl-L-homoserine lactone hydrolase; quorum-quenching lactonase; quorum-quenching N-acyl homoserine lactone hydrolase
Systematic name: N-acyl-L-homoserine-lactone lactonohydrolase
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 [681]. Plants or animals capable of degrading AHLs would have a therapeutic advantage in avoiding bacterial infection as they could prevent AHL-signalling and the expression of virulence genes in quorum-sensing bacteria [681].

N-(3-Oxohexanoyl)-L-homoserine lactone, N-(3-oxododecanoyl)-L-homoserine lactone, N-butanoyl-L-homoserine lactone and N-(3-oxooctanoyl)-L-homoserine lactone can act as substrates [681].

References:
[3057, 680, 3267, 682, 681, 1721, 2349, 3157, 1537, 1814, 3416]

EC 3.1.1.82
Accepted name: pheophorbidase
Reaction: pheophorbide $a + H_2O = pyropheophorbide \ a + \text{methanol} + CO_2$ (overall reaction)
(1a) pheophorbide $a + H_2O = C-13^2$-carboxypyropheophorbide $a + \text{methanol}
(1b) C-13^2$-carboxypyropheophorbide $a = pyropheophorbide a + CO_2$ (spontaneous)
Other name(s): phedase; PPD
Systematic name: pheophorbide-$a$ hydrolase
Comments: This enzyme forms part of the chlorophyll degradation pathway, and is found in higher plants and in algae. In higher plants it participates in de-greening processes such as fruit ripening, leaf senescence, and flowering. The enzyme exists in two forms: type 1 is induced by senescence whereas type 2 is constitutively expressed [2959, 2957]. The enzyme is highly specific for pheophorbide as substrate (with a preference for pheophorbide $a$ over pheophorbide $b$) as other chlorophyll derivatives such as protochlorophyllide $a$, pheophytin $a$ and $c$, chlorophyll $a$ and $b$, and chlorophyllide $a$ cannot act as substrates [2957]. Another enzyme, called pheophorbide demethoxycarbonylase (PDC), produces pyropheophorbide $a$ from pheophorbide $a$ without forming an intermediate although the precise reaction is not yet known [2959].

References: [2959, 2957, 1254]

EC 3.1.1.83
Accepted name: monoterpene $\epsilon$-lactone hydrolase
Reaction: (1) isoprop(en)ylmethyloxepan-2-one + H$_2$O = 6-hydroxyisoprop(en)ylmethylhexanoate (general reaction)
(2) 4-isopropenyl-7-methyloxepan-2-one + H$_2$O = 6-hydroxy-3-isopropenylheptanoate
(3) 7-isopropyl-4-methyloxepan-2-one + H$_2$O = 6-hydroxy-3,7-dimethyloctanoate
Other name(s): MLH
Systematic name: isoprop(en)ylmethyloxepan-2-one lactonohydrolase
Comments: The enzyme catalyses the ring opening of $\epsilon$-lactones which are formed during degradation of dihydrocarveol by the Gram-positive bacterium Rhodococcus erythropolis DCL14. The enzyme also acts on ethyl caproate, indicating that it is an esterase with a preference for lactones (internal cyclic esters). The enzyme is not stereoselective.

References: [3189]

EC 3.1.1.84
Accepted name: cocaine esterase
Reaction: cocaine + H$_2$O = ecgonine methyl ester + benzoate
Other name(s): CoE; hCE2; hCE-2; human carboxylesterase 2
Systematic name: cocaine benzoylhydrolase
Comments: *Rhodococcus* sp. strain MB1 and *Pseudomonas maltophilia* strain MB11L can utilize cocaine as sole source of carbon and energy [315, 323].
References: [928, 315, 323, 1697, 2403]

[EC 3.1.1.84 created 2010]

**EC 3.1.1.85**
Accepted name: pimelyl-[acyl-carrier protein] methyl ester esterase
Other name(s): BioH
Systematic name: pimeloyl-[acyl-carrier protein] methyl ester hydrolase
Comments: Involved in biotin biosynthesis in Gram-negative bacteria. The enzyme exhibits carboxylesterase activity, particularly toward substrates with short acyl chains [2645, 1735]. Even though the enzyme can interact with coenzyme A thioesters [3077], the *in vivo* role of the enzyme is to hydrolyse the methyl ester of pimeloyl-[acyl carrier protein], terminating the part of the biotin biosynthesis pathway that is catalysed by the fatty acid elongation enzymes [1789].
References: [2645, 1735, 3077, 1789]

[EC 3.1.1.85 created 2011]

**EC 3.1.1.86**
Accepted name: rhamnogalacturonan acetyl esterase
Reaction: Hydrolytic cleavage of 2-O-acetyl- or 3-O-acetyl groups of α-D-galacturonic acid in rhamnogalacturonan I.
Other name(s): RGAE
Systematic name: rhamnogalacturonan 2/3-O-acetyl-α-D-galacturonate O-acetylhydrolase
Comments: The degradation of rhamnogalacturonan by rhamnogalacturonases depends on the removal of the acetyl esters from the substrate [1487].
References: [1487, 2051]

[EC 3.1.1.86 created 2011]

**EC 3.1.1.87**
Accepted name: fumonisin B1 esterase
Reaction: fumonisin B1 + 2 H₂O = aminopentol + 2 propane-1,2,3-tricarboxylate
Other name(s): *fumD* (gene name)
Systematic name: fumonisin B1 acylhydrolase
Comments: The enzyme is involved in degradation of fumonisin B1 [1172].
References: [1172]

[EC 3.1.1.87 created 2011]

**EC 3.1.1.88**
Accepted name: pyrethroid hydrolase
Reaction: *trans*-permethrin + H₂O = (3-phenoxyphenyl)methanol + (1S,3R)-3-(2,2-dichloroethenyl)-2,2-dimethylcyclopropanecarboxylate
Other name(s): pyrethroid-hydrolyzing carboxylesterase; pyrethroid-hydrolysing esterase; pyrethroid-hydrolyzing esterase; pyrethroid-selective esterase; pyrethroid-cleaving enzyme; permethrinase; PytH; EstP
Systematic name: pyrethroid-ester hydrolase

21
The enzyme is involved in degradation of pyrethroid pesticides. The enzymes from *Sphingobium* sp., *Klebsiella* sp. and *Aspergillus niger* hydrolyse cis-permethrin at approximately equal rate to trans-permethrin [3256, 3374, 1768]. The enzyme from mouse hydrolys trans-permethrin at a rate about 22-fold higher than cis-permethrin [2919].

References: [3256, 3374, 1768, 2919, 1892, 1059]

[EC 3.1.1.88 created 2011]

**EC 3.1.1.89**

Accepted name: protein phosphatase methylesterase-1  
Reaction: [phosphatase 2A protein]-leucine methyl ester + H₂O = [phosphatase 2A protein]-leucine + methanol  
Other name(s): PME-1; PPME1  
Systematic name: [phosphatase 2A protein]-leucine ester acylhydrolase  
Comments: A key regulator of protein phosphatase 2A. The methyl ester is formed by EC 2.1.1.233 (leucine carboxy methyltransferase-1). Occurs mainly in the nucleus.  
References: [2262, 3385]

[EC 3.1.1.89 created 2011]

**EC 3.1.1.90**

Accepted name: all-trans-retinyl ester 13-cis isomerohydrolase  
Reaction: an all-trans-retinyl ester + H₂O = 13-cis-retinol + a fatty acid  
Systematic name: all-trans-retinyl ester acylhydrolase, 13-cis-retinol-forming  
Comments: All-trans-retinyl esters, which are a storage form of vitamin A, are generated by the activity of EC 2.3.1.135, phosphatidylcholine—retinol O-acyltransferase (LRAT). They can be hydrolysed to 11-cis-retinol by EC 3.1.1.64, retinoid isomerohydrolase (RPE65), or to 13-cis-retinol by this enzyme.  
References: [2990]

[EC 3.1.1.90 created 2011]

**EC 3.1.1.91**

Accepted name: 2-oxo-3-(5-oxofuran-2-ylidene)propanoate lactonase  
Reaction: 2-oxo-3-(5-oxofuran-2-ylidene)propanoate + H₂O = maleylpyruvate  
Other name(s): *naaC* (gene name)  
Systematic name: 2-oxo-3-(5-oxofuran-2-ylidene)propanoate lactonohydrolase  
Comments: This enzyme, characterized from the soil bacterium *Bradyrhizobium* sp. JS329, is involved in the pathway of 5-nitroanthranilate degradation.  
References: [2458]

[EC 3.1.1.91 created 2012]

**EC 3.1.1.92**

Accepted name: 4-sulfomuconolactone hydrolase  
Reaction: 4-sulfomuconolactone + H₂O = maleylacetate + sulfite  
Systematic name: 4-sulfomuconolactone sulfohydrolase  
Comments: The enzyme was isolated from the bacteria *Hydrogenophaga intermedia* and *Agrobacterium radiobacter* S2. It catalyses a step in the degradation of 4-sulfocatechol.  
References: [1085]

[EC 3.1.1.92 created 2012]
**EC 3.1.1.93**

**Accepted name:** mycophenolic acid acyl-glucuronide esterase  
**Reaction:** mycophenolic acid O-acyl-glucuronide + H₂O = mycophenolate + D-glucuronate  
**Other name(s):** mycophenolic acid acyl-glucuronide deacetylglucuronidase; AcMPAG deacetylglucuronidase  
**Systematic name:** mycophenolic acid O-acyl-glucuronide esterase  
**Comments:** This liver enzyme deacetylglucuronidates mycophenolic acid O-acyl-glucuronide, a metabolite of the immunosuppressant drug mycophenolate that is thought to be immunotoxic.  
**References:** [1359]

[EC 3.1.1.93 created 2012]

**EC 3.1.1.94**

**Accepted name:** versiconal hemiacetal acetate esterase  
**Reaction:**  
1. versiconal hemiacetal acetate + H₂O = versiconal + acetate  
2. versiconol acetate + H₂O = versiconol + acetate  
**Other name(s):** VHA esterase  
**Systematic name:** versiconal-hemiacetal-acetate O-acetimide hydrolyase  
**Comments:** Isolated from the mold Aspergillus parasiticus. Involved in a metabolic grid that leads to aflatoxin biosynthesis.  
**References:** [1668, 427]

[EC 3.1.1.94 created 2013]

**EC 3.1.1.95**

**Accepted name:** aclacinomycin methyl esterase  
**Reaction:** aclacinomycin T + H₂O = aclacinomycin T + methanol  
**Other name(s):** RdmC; aclacinomycin methyl esterase  
**Systematic name:** aclacinomycin T methyl esterase  
**Comments:** The enzyme is involved in the modification of the aclavinone skeleton in the biosynthesis of anthracyclines in Streptomyces species.  
**References:** [3274, 1389]

[EC 3.1.1.95 created 2013]

**EC 3.1.1.96**

**Accepted name:** D-aminoacyl-tRNA deacylase  
**Reaction:**  
1. D-aminoacyl-tRNA + H₂O = D-amino acid + tRNA  
2. glycyl-tRNAAla + H₂O = glycine + tRNAAla  
**Other name(s):** Dtd2; D-Tyr-tRNA(Tyr) deacylase; D-Tyr-tRNA Tyr deacylase; D-tyrosyl-tRNA Tyr aminoacylhydrodrolase; dtdA (gene name)  
**Systematic name:** D-aminoacyl-tRNA aminoacylhydrodrolase  
**Comments:** The enzyme, found in all domains of life, can cleave mischarged glycyyl-tRNAAla [2366]. The enzyme from Escherichia coli can cleave D-tyrosyl-tRNA Tyr, D-aspartyl-tRNA Asp and D-tryptophanyl-tRNA Trp [2872]. Whereas the enzyme from the archaeon Pyrococcus abyssi is a zinc protein, the enzyme from Escherichia coli does not carry any zinc [812].  
**References:** [2872, 812, 811, 3380, 2366]

[EC 3.1.1.96 created 2014, modified 2019]

**EC 3.1.1.97**

**Accepted name:** methylated diphthine methylhydrolase  
**Reaction:** diphthine methyl ester-[translation elongation factor 2] + H₂O = diphthine-[translation elongation factor 2] + methanol
Other name(s): Dph7; diphthine methyl esterase (incorrect)
Systematic name: diphthine methyl ester acylhydrolase
Comments: The protein is only present in eukaryotes.
References: [1794]

[EC 3.1.1.97 created 2014, modified 2015]

EC 3.1.1.98
Accepted name: [Wnt protein] O-palmitoleoyl-L-serine hydrolase
Reaction: [Wnt]-O-(9Z)-hexadec-9-enoyl-L-serine + H₂O = [Wnt]-L-serine + (9Z)-hexadec-9-enoate
Other name(s): Notum
Systematic name: [Wnt]-O-(9Z)-hexadec-9-enoyl-L-serine acylhydrolase
Comments: The enzyme removes the palmitoleate modification that is introduced to specific L-serine residues in Wnt proteins by EC 2.3.1.250, [Wnt protein]-O-palmitoleoyl transferase.
References: [1442]

[EC 3.1.1.98 created 2015]

EC 3.1.1.99
Accepted name: 6-deoxy-6-sulfogluconolactonase
Reaction: 6-deoxy-6-sulfo-D-glucono-1,5-lactone + H₂O = 6-deoxy-6-sulfo-D-gluconate
Other name(s): SGL lactonase
Systematic name: 6-deoxy-6-sulfo-D-glucono-1,5-lactone lactonohydrolase
Comments: The enzyme, characterized from the bacterium Pseudomonas putida SQ1, participates in a sulfoglucuronovose degradation pathway.
References: [805]

[EC 3.1.1.99 created 2016]

EC 3.1.1.100
Accepted name: chlorophyllide a hydrolase
Reaction: chlorophyllide a + H₂O = 8-ethyl-12-methyl-3-vinyl-bacteriochlorophyllide d + methanol + CO₂
Other name(s): bciC (gene name)
Systematic name: chlorophyllide-a hydrolase
Comments: This enzyme, found in green sulfur bacteria (Chlorobiaceae) and green filamentous bacteria (Chlororflexaceae), catalyses the first committed step in the biosynthesis of bacteriochlorophylls c, d and e, the removal of the C-13²-methylcarboxyl group from chlorophyllide a. The reaction is very similar to the conversion of pheophorbide a to pyropheophorbide a during chlorophyll a degradation, which is catalysed by EC 3.1.1.82, pheophorbidase.
References: [1824]

[EC 3.1.1.100 created 2016]

EC 3.1.1.101
Accepted name: poly(ethylene terephthalate) hydrolase
Reaction: (ethylene terephthalate)ₙ + H₂O = (ethylene terephthalate)ₙ₋₁ + 4-[(2-hydroxyethoxy)carbonyl]benzoate
Other name(s): PETase; PET hydrolase
Systematic name: poly(ethylene terephthalate) hydrolase
Comments: The enzyme, isolated from the bacterium Ideonella sakaiensis, also produces small amounts of terephthalate (cf. EC 3.1.1.102, mono(ethylene terephthalate) hydrolase). The reaction takes place on PET-film placed in solution.
References: [3461]
**EC 3.1.1.102**

**Accepted name:** mono(ethylene terephthalate) hydrolase

**Reaction:** 4-[(2-hydroxyethoxy)carbonyl]benzoate + H₂O = terephthalate + ethylene glycol

**Other name(s):** MHET hydrolase; MHETase

**Systematic name:** 4-[(2-hydroxyethoxy)carbonyl]benzoate acylhydrolase

**Comments:** The enzyme, isolated from the bacterium *Ideonella sakaiensis*, has no activity with poly(ethylene terephthalate) PET (cf. EC 3.1.1.101, poly(ethylene terephthalate) hydrolase).

**References:** [3461]

**EC 3.1.1.103**

**Accepted name:** teichoic acid D-alanine hydrolase

**Reaction:** [(4-D-Ala)-(2-GlcNAc)-Rib-ol-P]ₘ-[(Gro-P)ₘ-β-D-ManNAc-(1→4)-α-D-GlcNAc-P]-peptidoglycan + n H₂O = [(2-GlcNAc)-Rib-ol-P]ₘ-β-D-ManNAc-(1→4)-α-D-GlcNAc-P]-peptidoglycan + n D-alanine

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

**Systematic name:** teichoic acid D-alanylhydrolase

**Comments:** The enzyme, characterized from the bacterium *Staphylococcus aureus*, removes D-alanine groups from the teichoic acid produced by this organism, thus modulating the electrical charge of the bacterial surface. The activity greatly increases methicillin resistance in MRSA strains.

**References:** [1589, 2453, 2478]

**EC 3.1.1.104**

**Accepted name:** 5-phospho-D-xylono-1,4-lactonase

**Reaction:**
(1) D-xylono-1,4-lactone 5-phosphate + H₂O = 5-phospho-D-xylonate
(2) L-arabino-1,4-lactone 5-phosphate + H₂O = 5-phospho-L-arabinate

**Systematic name:** 5-phospho-D-xylono-1,4-lactone hydrolase

**Comments:** The enzyme, characterized from *Mycoplasma* spp., contains a binuclear metal center with two zinc cations. The enzyme is specific for the phosphorylated forms, and is unable to hydrolyze non-phosphorylated 1,4-lactones.

**References:** [1598]

**EC 3.1.1.105**

**Accepted name:** 3-O-acetylpapaveroxine carboxylesterase

**Reaction:** 3-O-acetylpapaveroxine + H₂O = narcotine hemiacetal + acetate

**Other name(s):** CXE1 (gene name)

**Systematic name:** 3-O-acetylpapaveroxine acetatehydrolase

**Comments:** The enzyme, characterized from the plant *Papaver somniferum* (opium poppy), participates in the biosynthesis of the isoquinoline alkaloid noscapine.

**References:** [575, 2347]

**EC 3.1.1.106**

**Accepted name:** O-acetyl-ADP-ribose deacetylase
Reaction:
(1) 3′′-O-acetyl-ADP-D-ribose + H$_2$O = ADP-D-ribose + acetate
(2) 2′′-O-acetyl-ADP-D-ribose + H$_2$O = ADP-D-ribose + acetate

Other name(s): ymdB (gene name); MACROD1 (gene name)

Systematic name: O-acetyl-ADP-D-ribose carboxylesterase

Comments: The enzyme, characterized from the bacterium *Escherichia coli* and from human cells, removes the acetyl group from either the 2′′ or 3′′ position of O-acetyl-ADP-ribose, which are formed by the action of EC 2.3.1.286, protein acetyllysine N-acetyltransferase. The human enzyme can also remove ADP-D-ribose from phosphorylated double stranded DNA adducts.

References:
[447, 3494, 24]

EC 3.1.1.107

Accepted name: apo-salmochelin esterase

Reaction:
(1) enterobactin + H$_2$O = N-(2,3-dihydroxybenzoyl)L-serine trimer
(2) triglucosyl-enterobactin + H$_2$O = triglucosyl-(2,3-dihydroxybenzoyl)serine$_3$
(3) diglucosyl-enterobactin + H$_2$O = diglucosyl-(2,3-dihydroxybenzoyl)serine$_3$
(4) monoglucosyl-enterobactin + H$_2$O = monoglucosyl-(2,3-dihydroxybenzoyl)serine$_3$

Other name(s): iroE (gene name)

Systematic name: apo-salmochelin esterase

Comments: This bacterial enzyme is present in pathogenic *Salmonella* species, uropathogenic and avian pathogenic *Escherichia coli* strains, and certain *Klebsiella* strains. Unlike EC 3.1.1.108, iron(III)-enterobactin esterase, which acts only on enterobactin, this enzyme can also act on the C-glucosylated forms known as salmochelins. Unlike EC 3.1.1.109, iron(III)-salmochelin esterase (IroD), IroE prefers apo siderophores as substrates, and is assumed to act before the siderophores are exported out of the cell. It hydrolyses the trilactone only once, producing linearized trimers.

References:
[1787]

EC 3.1.1.108

Accepted name: iron(III)-enterobactin esterase

Reaction:
iron(III)-enterobactin + 3 H$_2$O = iron(III)-N-(2,3-dihydroxybenzoyl)l-serine complex + 2 N-(2,3-dihydroxybenzoyl)l-serine (overall reaction)
(1a) iron(III)-enterobactin + H$_2$O = iron(III)-N-(2,3-dihydroxybenzoyl)l-serine trimer complex
(1b) iron(III)-N-(2,3-dihydroxybenzoyl)l-serine trimer complex + H$_2$O = iron(III)-N-(2,3-dihydroxybenzoyl)l-serine dimer complex + N-(2,3-dihydroxybenzoyl)l-serine
(1c) iron(III)-N-(2,3-dihydroxybenzoyl)l-serine dimer complex + H$_2$O = iron(III)-N-(2,3-dihydroxybenzoyl)l-serine complex + N-(2,3-dihydroxybenzoyl)l-serine

Other name(s): fes (gene name); pfeE (gene name); enterochelin hydrolase; enterochelin esterase; ferric enterobactin esterase

Systematic name: iron(III)-enterobactin hydrolase

Comments: The enzyme, isolated from the bacterium *Escherichia coli*, allows the bacterium to grow in limited iron conditions. It can also act on enterobactin (with no complexed iron) and the aluminium(III) analogue of iron(III)-enterobactin. The trimer formed is further hydrolysed to form the dimer and the monomer.

References:
[2233, 1031, 2388, 316, 3349, 2375]

EC 3.1.1.109

Accepted name: iron(III)-salmochelin esterase

Reaction:
(1) iron(III)-[diglucosyl-enterobactin] complex + H$_2$O = iron(III)-[salmochelin S2] complex
(2) \text{iron(III)-[monoglucosyl-enterobactin] complex} + H_2O = \text{iron(III)-[monoglucosyl-(2,3-dihydroxybenzoylserine)] complex}

(3) \text{iron(III)-[salmochelin S2] complex} + H_2O = \text{iron(III)-[diglucosyl-(2,3-dihydroxybenzoylserine)] complex} + \text{N-(2,3-dihydroxybenzoyl)-L-serine}

(4) \text{iron(III)-[salmochelin S2] complex} + H_2O = \text{iron(III)-[salmochelin S1] complex} + \text{salmochelin SX}

(5) \text{iron(III)-[monoglucosyl-(2,3-dihydroxybenzoylserine)] complex} + H_2O = \text{iron(III)-[salmochelin S1] complex} + \text{N-(2,3-dihydroxybenzoyl)-L-serine}

(6) \text{iron(III)-[diglucosyl-(2,3-dihydroxybenzoylserine)] complex} + H_2O = \text{iron(III)-[salmochelin SX] complex} + \text{salmochelin SX}

Other name(s): iroD (gene name); ferric-salmochelin esterase

Systematic name: iron(III)-salmochelin complex hydrolase

Comments: This bacterial enzyme is present in pathogenic \textit{Salmonella} species, uropathogenic and avian pathogenic \textit{Escherichia coli} strains, and certain \textit{Klebsiella} strains. The enzyme acts on iron(III)-bound enterobactin and C-glucosylated derivatives known as salmochelins. Unlike EC 3.1.1.107, apo-salmochelin esterase (IroE), IroD prefers iron(III)-bound siderophores as substrates, and is assumed to act after the iron-siderophore complexes are imported into the cell. It catalyses several hydrolytic reactions, producing a mixture of iron(III)-[N-(2,3-dihydroxybenzoyl)-L-serine] complex and salmochelin SX.

References: [1787]

[EC 3.1.1.109 created 2019]

EC 3.1.1.110

Accepted name: xylono-1,5-lactonase

Reaction: \text{d-xylono-1,5-lactone} + H_2O = \text{d-xylonate}

Other name(s): xyl\text{C} (gene name); \text{d-xylono-1,5-lactone lactonase}

Systematic name: \text{d-xylono-1,5-lactone lactonohydrolase}

Comments: The enzyme, found in bacteria, participates in the degradation of \text{d-xylose}. \textit{cf.} EC 3.1.1.68, xylono-1,4-lactonase.

References: [3072, 2230]

[EC 3.1.1.110 created 2019]

EC 3.1.1.111

Accepted name: phosphatidylserine \textit{sn}-1 acylhydrolase

Reaction: (1) a phosphatidylserine + H_2O = a 2-acyl-1-lyso-phosphatidylserine + a fatty acid

(2) a 1-acyl-2-lyso-phosphatidylserine + H_2O = glycerophosphoserine + a fatty acid

Other name(s): phosphatidylserine-specific phospholipase \text{A}_1; \text{PS-PLA1}; \text{PLA1A} (gene name)

Systematic name: 3-\textit{sn}-phosphatidyl-L-serine \textit{sn}-1 acylhydrolase

Comments: The enzyme, which has been described from mammals, is specific for phosphatidylserine and 2-lyso phosphatidylserine, and does not act on phosphatidylcholine, phosphatidylethanolamine, phosphatidic acid or phosphatidylinositol.

References: [2666, 2125, 1259, 64]

[EC 3.1.1.111 created 2019]

EC 3.1.1.112

Accepted name: isoamyl acetate esterase

Reaction: 3-methylbutyl acetate + H_2O = 3-methylbutanol + acetate

Other name(s): IAH1 (gene name)

Systematic name: 3-methylbutyl acetate acetohydrolase

Comments: The enzyme, characterized from the yeast \textit{Saccharomyces cerevisiae}, hydrolyses acetate esters. It acts preferentially on 3-methylbutyl acetate, a major determinant of sake flavor.
References: [912]

[EC 3.1.1.112 created 2019]

EC 3.1.1.113
Accepted name: ethyl acetate hydrolase
Reaction: ethyl acetate + H₂O = acetate + ethanol
Other name(s): mekB (gene name); estZ (gene name)
Systematic name: ethyl acetate acetohydrolase
Comments: The enzyme, characterized from Pseudomonas strains, is involved in degradation of short chain alkyl methyl ketones.
References: [1135, 2307]

[EC 3.1.1.113 created 2019]

EC 3.1.1.114
Accepted name: methyl acetate hydrolase
Reaction: methyl acetate + H₂O = acetate + methanol
Other name(s): acmB (gene name)
Systematic name: methyl acetate acetohydrolase
Comments: The enzyme, characterized from the bacterium Gordonia sp. TY-5, participates in a propane utilization pathway.
References: [1608]

[EC 3.1.1.114 created 2019]

EC 3.1.1.115
Accepted name: D-apionolactonase
Reaction: D-apionolactone + H₂O = D-apionate
Other name(s): apnL (gene name)
Systematic name: D-apionolactone lactonohydrolase
Comments: The enzyme, characterized from several bacterial species, is involved in a catabolic pathway for D-apiose.
References: [408]

[EC 3.1.1.115 created 2020]

EC 3.1.1.116
Accepted name: sn-1-specific diacylglycerol lipase
Reaction: a 1,2-diacyl-sn-glycerol + H₂O = a 2-acylglycerol + a fatty acid
Other name(s): DAGLA (gene name); DAGLB (gene name)
Systematic name: diacylglycerol sn-1-acylhydrolase
Comments: The enzyme, present in animals, is specific for the sn-1 position. When acting on 1-acyl-2-arachidonoyl-sn-glycerol, the enzyme forms 2-arachidonoylglycerol, the most abundant endocannabinoid in the mammalian brain.
References: [439, 244, 243]

[EC 3.1.1.116 created 2021]

EC 3.1.1.117
Accepted name: (4-O-methyl)-D-glucuronate—lignin esterase
Reaction: a 4-O-methyl-D-glucopyranuronate ester + H₂O = 4-O-methyl-D-glucuronic acid + an alcohol

[EC 3.1.1.117 created 2021]
Other name(s): glucuronoyl esterase (ambiguous); 4-O-methyl-glucuronoyl methylesterase; glucuronoyl-lignin ester hydrolase
Systematic name: (4-O-methyl)-D-glucuronate—lignin ester hydrolase
Comments: The enzyme occurs in microorganisms and catalyses the cleavage of the ester bonds between glucuronoyl or 4-O-methyl-glucuronoyl groups attached to xylan and aliphatic or aromatic alcohols in lignin polymers.
References: [2876, 434, 118, 1286, 1287, 119, 1954, 761]

EC 3.1.1.118
Accepted name: phospholipid sn-1 acylhydrolase
Reaction: (1) a 1-phosphatidyl-1D-myoinositol + H₂O = a 2-acyl-sn-glycero-3-phospho-1D-myoinositol + a fatty acid
(2) a 1,2-diacyl-sn-glycerol 3-phosphate + H₂O = a 2-acyl-sn-glycerol 3-phosphate + a fatty acid
Other name(s): phospholipase DDHD1; phosphatidic acid-preferring phospholipase A₁; PA-PLA₁; DDHD1 (gene name)
Systematic name: phospholipid sn-1 acylhydrolase
Comments: The human enzyme shows broad specificity, and has a preference for phosphatidate over other phospholipids. Unlike EC 3.1.1.32, phospholipase A₁, it is also active against phosphatidylinositol. It is not active towards acyl groups linked at the sn-2 position.
References: [3408, 120]

EC 3.1.1.119
Accepted name: L-fuco-no-1,5-lactonase
Reaction: L-fuco-no-1,5-lactone + H₂O = L-fuconate
Systematic name: L-fuco-no-1,5-lactone lactonohydrolase
Comments: The enzyme, characterized from the bacterium Burkholderia multivorans, participates in an L-fucose degradation pathway. The enzyme exhibits catalytic activity for the hydrolysis of several lactones, including L-fuco-no-1,4-lactone, D-arabinono-1,4-lactone, L-xylono-1,4-lactone, and L-galactono-1,4-lactone, but L-fuco-no-1,5-lactone is the best substrate.
References: [1229]

EC 3.1.2 Thioester hydrolases

EC 3.1.2.1
Accepted name: acetyl-CoA hydrolase
Reaction: acetyl-CoA + H₂O = CoA + acetate
Other name(s): acetyl-CoA decacylase; acetyl-CoA acylase; acetyl coenzyme A hydrolase; acetyl coenzyme A deacylase; acetyl coenzyme A acylase; acetyl-CoA thiol esterase
Systematic name: acetyl-CoA hydrolase
References: [948]
EC 3.1.2.2

Accepted name: palmitoyl-CoA hydrolase
Reaction: palmitoyl-CoA + H₂O = CoA + palmitate
Other name(s): long-chain fatty-acyl-CoA hydrolase; palmitoyl coenzyme A hydrolase; palmitoyl thioesterase; palmitoyl coenzyme A hydrolase; palmitoyl-CoA deacylase; palmitoyl thioesterase; palmityl-CoA deacylase; fatty acyl thioesterase I; palmityl thioesterase I
Systematic name: palmitoyl-CoA hydrolase
Comments: Also hydrolyses CoA thioesters of other long-chain fatty acids.
References: [160, 210, 2040, 2885, 3394]

[EC 3.1.2.2 created 1961]

EC 3.1.2.3

Accepted name: succinyl-CoA hydrolase
Reaction: succinyl-CoA + H₂O = CoA + succinate
Other name(s): succinyl-CoA acylase; succinyl coenzyme A hydrolase; succinyl coenzyme A deacylase
Systematic name: succinyl-CoA hydrolase
References: [948]

[EC 3.1.2.3 created 1961]

EC 3.1.2.4

Accepted name: 3-hydroxyisobutyryl-CoA hydrolase
Reaction: 3-hydroxy-2-methylpropanoyl-CoA + H₂O = CoA + 3-hydroxy-2-methylpropanoate
Other name(s): 3-hydroxy-isobutyryl CoA hydrolase; HIB CoA deacylase
Systematic name: 3-hydroxy-2-methylpropanoyl-CoA hydrolase
Comments: Also hydrolyses 3-hydroxypropanoyl-CoA.
References: [2535]

[EC 3.1.2.4 created 1961]

EC 3.1.2.5

Accepted name: hydroxymethylglutaryl-CoA hydrolase
Reaction: (S)-3-hydroxy-3-methylglutaryl-CoA + H₂O = CoA + 3-hydroxy-3-methylglutarate
Other name(s): β-hydroxy-β-methylglutaryl coenzyme A hydrolase; β-hydroxy-β-methylglutaryl coenzyme A deacylase; hydroxymethylglutaril coenzyme A hydrolase; hydroxymethylglutaril coenzyme A deacylase; 3-hydroxy-3-methylglutaryl-CoA hydrolase
Systematic name: (S)-3-hydroxy-3-methylglutaryl-CoA hydrolase
References: [612]

[EC 3.1.2.5 created 1961]

EC 3.1.2.6

Accepted name: hydroxyacylglutathione hydrolase
Reaction: S-(2-hydroxyacyl)glutathione + H₂O = glutathione + a 2-hydroxy carboxylate
Other name(s): glyoxalase II; S-2-hydroxylacetylglutathione hydrolase; hydroxyacylglutathione hydrolase; acetoacetyl-glutathione hydrolase
Systematic name: S-(2-hydroxyacyl)glutathione hydrolase
Comments: Also hydrolyses S-acetoacetylglutathione, but more slowly.
References: [2471, 3163, 3164]

[EC 3.1.2.6 created 1961 (EC 3.1.2.8 created 1961, incorporated 1978)]
EC 3.1.2.7
Accepted name: glutathione thiolesterase
Reaction: S-acylglutathione + H₂O = glutathione + a carboxylate
Other name(s): citrly-glutathione thioesterhydrolase
Systematic name: S-acylglutathione hydrolase
References: [1521]

[EC 3.1.2.7 created 1961]

[3.1.2.8 Deleted entry. S-acetoacylgulathtione hydrolase. Now included with EC 3.1.2.6 hydroxyacylglutathione hydrolase]

[EC 3.1.2.8 created 1961, deleted 1978]

[3.1.2.9 Deleted entry. S-acetoacetylhydrolipoate hydrolase]

[EC 3.1.2.9 created 1961, deleted 1964]

EC 3.1.2.10
Accepted name: formyl-CoA hydrolase
Reaction: formyl-CoA + H₂O = CoA + formate
Other name(s): formyl coenzyme A hydrolase
Systematic name: formyl-CoA hydrolase
References: [2830]

[EC 3.1.2.10 created 1965]

EC 3.1.2.11
Accepted name: acetoacetyl-CoA hydrolase
Reaction: acetoacetyl-CoA + H₂O = CoA + acetoacetate
Other name(s): acetoacetyl coenzyme A hydrolase; acetoacetyl CoA deacylase; acetoacetyl coenzyme A deacylase
Systematic name: acetoacetyl-CoA hydrolase
References: [68, 699]

[EC 3.1.2.11 created 1972]

EC 3.1.2.12
Accepted name: S-formylglutathione hydrolase
Reaction: S-formylglutathione + H₂O = glutathione + formate
Systematic name: S-formylglutathione hydrolase
Comments: Also hydrolyses S-acetylglutathione, but more slowly.
References: [3163, 3166, 1118]

[EC 3.1.2.12 created 1978]

EC 3.1.2.13
Accepted name: S-succinylglutathione hydrolase
Reaction: S-succinylglutathione + H₂O = glutathione + succinate
Systematic name: S-succinylglutathione hydrolase
References: [3163, 3165]

[EC 3.1.2.13 created 1978]
EC 3.1.2.14
**Accepted name:** oleoyl-[acyl-carrier-protein] hydrolase
**Reaction:** an oleoyl-[acyl-carrier protein] + H$_2$O = an [acyl-carrier protein] + oleate
**Other name(s):** acyl-[acyl-carrier-protein] hydrolase; acyl-ACP-hydrolase; acyl-acyl carrier protein hydrolase; oleoyl-ACP thioesterase; oleoyl-acyl carrier protein thioesterase; oleoyl-[acyl-carrier-protein] hydrolase
**Systematic name:** oleoyl-[acyl-carrier protein] hydrolase
**Comments:** Acts on acyl-carrier-protein thioesters of fatty acids from C$_{12}$ to C$_{18}$, but the derivative of oleic acid is hydrolysed much more rapidly than any other compound tested.
**References:** [2270, 2775]

[EC 3.1.2.14 created 1984]

[3.1.2.15 Deleted entry. This activity is covered by EC 3.4.19.12, ubiquitinyl hydrolase 1]

[EC 3.1.2.15 created 1986, deleted 2014]

EC 3.1.2.16
**Accepted name:** citrate-lyase deacetylase
**Reaction:** acetyl-[citrate-(pro-3S)-lyase] + H$_2$O = holo-[citrate-(pro-3S)-lyase] + acetate
**Other name(s):** [citrate-(pro-3S)-lyase] thiolesterase; acetyl-S-(acyl-carrier protein) enzyme thioester hydrolase; citrate lyase deacetylase; [citrate-(pro-3S)-lyase][acyethyl-form] hydrolase
**Systematic name:** acetyl-[citrate-(pro-3S)-lyase] hydrolase
**Comments:** In the proteobacterium *Rubrivivax gelatinosus*, this enzyme modulates the activity of EC 4.1.3.6, citrate (pro-3S)-lyase, by converting it from its active acetyl form into its inactive thiol form by removal of its acetyl groups [969]. The activity of citrate-lyase deacetylase is itself inhibited by L-glutamate [969].
**References:** [968, 969]

[EC 3.1.2.16 created 1989]

EC 3.1.2.17
**Accepted name:** (S)-methylmalonyl-CoA hydrolase
**Reaction:** (S)-methylmalonyl-CoA + H$_2$O = methylmalonate + CoA
**Other name(s):** D-methylmalonyl-coenzyme A hydrolase
**Systematic name:** (S)-methylmalonyl-CoA hydrolase
**References:** [1613]

[EC 3.1.2.17 created 1989]

EC 3.1.2.18
**Accepted name:** ADP-dependent short-chain-acyl-CoA hydrolase
**Reaction:** acyl-CoA + H$_2$O = CoA + a carboxylate
**Other name(s):** short-chain acyl coenzyme A hydrolase; propionyl coenzyme A hydrolase; propionyl-CoA hydrolase; propionyl-CoA thioesterase; short-chain acyl-CoA hydrolase; short-chain acyl-CoA thioesterase
**Systematic name:** ADP-dependent-short-chain-acyl-CoA hydrolase
**Comments:** Requires ADP; inhibited by NADH. Maximum activity is shown with propionyl-CoA.
**References:** [35, 36]

[EC 3.1.2.18 created 1992]

EC 3.1.2.19
**Accepted name:** ADP-dependent medium-chain-acyl-CoA hydrolase
**Reaction:** acyl-CoA + H$_2$O = CoA + a carboxylate

32
Other name(s): medium-chain acyl coenzyme A hydrolase; medium-chain acyl-CoA hydrolase; medium-chain acyl-thioester hydrolase; medium-chain hydrolase; myristoyl-CoA thioesterase
Systematic name: ADP-dependent-medium-chain-acyl-CoA hydrolase
Comments: Requires ADP; inhibited by NADH. Maximum activity is shown with nonanoyl-CoA.
References: [35]

[EC 3.1.2.19 created 1992]

**EC 3.1.2.20**

Accepted name: acyl-CoA hydrolase
Reaction: acyl-CoA + H$_2$O = CoA + a carboxylate
Other name(s): acyl coenzyme A thioesterase; acyl-CoA thioesterase; acyl coenzyme A hydrolase; thioesterase B; thioesterase II; acyl-CoA thioesterase
Systematic name: acyl-CoA hydrolase
Comments: Broad specificity for medium- to long-chain acyl-CoA. Insensitive to NAD$^+$ (cf. EC 3.1.2.19 ADP-dependent medium-chain-acyl-CoA hydrolase)
References: [36]

[EC 3.1.2.20 created 1992]

**EC 3.1.2.21**

Accepted name: dodecanoyl-[acyl-carrier-protein] hydrolase
Other name(s): lauryl-acyl-carrier-protein hydrolase; dodecanoyl-acyl-carrier-protein hydrolase; dodecyl-acyl-carrier protein hydrolase; dodecanoyl-[acyl-carrier protein] hydrolase; dodecanoyl-[acyl-carrier-protein] hydrolase
Systematic name: dodecanoyl-[acyl-carrier protein] hydrolase
Comments: Acts on the acyl-carrier-protein thioester of C$_{12}$ and, with a much lower activity, C$_{14}$ fatty acids. The derivative of oleic acid is hydrolysed very slowly (cf. EC 3.1.2.14, oleoyl-[acyl-carrier-protein] hydrolase).
References: [2423, 589]

[EC 3.1.2.21 created 1999]

**EC 3.1.2.22**

Accepted name: palmitoyl[protein] hydrolase
Reaction: palmitoyl[protein] + H$_2$O = palmitate + protein
Other name(s): palmitoyl-protein thioesterase; palmitoyl-(protein) hydrolase
Systematic name: palmitoyl[protein] hydrolase
Comments: Specific for long-chain thioesters of fatty acids. Hydrolyses fatty acids from S-acylated cysteine residues in proteins, palmitoyl cysteine and palmitoyl-CoA.
References: [388, 2717, 3211]

[EC 3.1.2.22 created 1999]

**EC 3.1.2.23**

Accepted name: 4-hydroxybenzoyl-CoA thioesterase
Reaction: 4-hydroxybenzoyl-CoA + H$_2$O = 4-hydroxybenzoate + CoA
Systematic name: 4-hydroxybenzoyl-CoA hydrolase
Comments: This enzyme is part of the bacterial 2,4-dichlorobenzoate degradation pathway.
References: [425, 710]

[EC 3.1.2.23 created 1999]
[3.1.2.24 Transferred entry. 2-(2-hydroxyphenyl)benzenesulfinate hydrolase. Now EC 3.13.1.3, 2'-hydroxybiphenyl-2-sulfinate desulfinase. The enzyme was incorrectly classified as a thioester hydrolase when the bond broken is a C-S bond, which is not an ester]

[EC 3.1.2.24 created 2000, deleted 2005]

EC 3.1.2.25

Accepted name: phenylacetyl-CoA hydrolase
Reaction: phenylglyoxylyl-CoA + H₂O = phenylglyoxylate + CoA
Systematic name: phenylglyoxylyl-CoA hydrolase
Comments: This is the second step in the conversion of phenylacetyl-CoA to phenylglyoxylate, the first step being carried out by EC 1.17.5.1, phenylacetyl-CoA dehydrogenase.
References: [2542, 2708]

[EC 3.1.2.25 created 2004]

[3.1.2.26 Transferred entry. bile-acid-CoA hydrolase. Now EC 2.8.3.25, bile acid CoA transferase]

[EC 3.1.2.26 created 2005, deleted 2016]

EC 3.1.2.27

Accepted name: choloyl-CoA hydrolase
Reaction: choloyl-CoA + H₂O = cholate + CoA
Other name(s): PTE-2 (ambiguous); choloyl-coenzyme A thioesterase; chenodeoxycholoyl-coenzyme A thioesterase; peroxisomal acyl-CoA thioesterase 2
Systematic name: choloyl-CoA hydrolase
Comments: Also acts on chenodeoxycholoyl-CoA and to a lesser extent on short- and medium- to long-chain acyl-CoAs, and other substrates, including trihydroxycoprostanoyl-CoA, hydroxymethylglutaryl-CoA and branched chain acyl-CoAs, all of which are present in peroxisomes. The enzyme is strongly inhibited by CoA and may be involved in controlling CoA levels in the peroxisome [1282].
References: [1282, 2850, 2607]

[EC 3.1.2.27 created 2005]

EC 3.1.2.28

Accepted name: 1,4-dihydroxy-2-naphthoyl-CoA hydrolase
Reaction: 1,4-dihydroxy-2-naphthoyl-CoA + H₂O = 1,4-dihydroxy-2-naphthoate + CoA
Other name(s): menI (gene name); ydiL (gene name)
Systematic name: 1,4-dihydroxy-2-naphthoyl-CoA hydrolase
Comments: This enzyme participates in the synthesis of menaquinones [449], phyloquinone [3332], as well as several plant pigments [2101, 728]. The enzyme from the cyanobacterium Synechocystis sp. PCC 6803 does not accept benzoyl-CoA or phenylacetyl-CoA as substrates [3332].
References: [2101, 728, 3332, 449]

[EC 3.1.2.28 created 2010]

EC 3.1.2.29

Accepted name: fluoroacetyl-CoA thioesterase
Reaction: fluoroacetyl-CoA + H₂O = fluoroacetate + CoA
Systematic name: fluoroacetyl-CoA hydrolase
Fluoroacetate is extremely toxic. It reacts with CoA to form fluoroacetyl-CoA, which substitutes for acetyl CoA and reacts with EC 2.3.3.1 (citrate synthase) to produce fluorocitrate, a metabolite of which binds very tightly to EC 4.2.1.3 (aconitase) and halts the TCA cycle. This enzyme hydrolyses fluoroacetyl-CoA before it can react with citrate synthase, and thus confers fluoroacetate resistance on the organisms that produce it. It has been described in the poisonous plant *Dichapetalum cymosum* and the bacterium *Streptomyces cattleya*, both of which are fluoroacetate producers.

References: [1992, 1276, 643]

EC 3.1.2.29

**Accepted name:** (3S)-malyl-CoA thioesterase

**Reaction:** (S)-malyl-CoA + H2O = (S)-malate + CoA

**Other name(s):** mcl2 (gene name)

**Systematic name:** (S)-malyl-CoA hydrolase

**Comments:** Stimulated by Mg2+ or Mn2+. The enzyme has no activity with (2R,3S)-2-methylmalyl-CoA (cf. EC 4.1.3.24, malyl-CoA lyase) or other CoA esters.

References: [756]

EC 3.1.2.30

**Accepted name:** dihydromonacolin L-[lovastatin nonaketide synthase] thioesterase

**Reaction:** dihydromonacolin L-[lovastatin nonaketide synthase] + H2O = holo-[lovastatin nonaketide synthase] + dihydromonacolin L acid

**Other name(s):** LovG

**Systematic name:** dihydromonacolin L-[lovastatin nonaketide synthase] hydrolase

**Comments:** Dihydromonacolin L acid is synthesized while bound to an acyl-carrier protein domain of the lovastatin nonaketide synthase (EC 2.3.1.161). Since that enzyme lacks a thioesterase domain, release of the dihydromonacolin L acid moiety from the polyketide synthase requires this dedicated enzyme.

References: [3391]

EC 3.1.2.31

**Accepted name:** 2-aminobenzoylacetyl-CoA thioesterase

**Reaction:** (2-aminobenzoyl)acetyl-CoA + H2O = (2-aminobenzoyl)acetate + CoA

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

**Systematic name:** (2-aminobenzoyl)acetyl-CoA hydrolase

**Comments:** The enzyme, characterized from the bacterium *Pseudomonas aeruginosa*, participates in the production of the signal molecule 2-heptyl-4(1H)-quinolone (HHQ).

References: [3470, 695]

EC 3.1.3 Phosphoric-monoester hydrolases

EC 3.1.3.1

**Accepted name:** alkaline phosphatase

**Reaction:** a phosphate monoester + H2O = an alcohol + phosphate

**Other name(s):** alkaline phosphomonoesterase; phosphomonoesterase; glycerophosphatase; alkaline phosphohydrolase; alkaline phenyl phosphatase; orthophosphoric-monoester phosphohydrolase (alkaline optimum)
**Systematic name:** phosphate-monoester phosphohydrolase (alkaline optimum)  
**Comments:** Wide specificity. Also catalyses transphosphorylations. The human placental enzyme is a zinc protein. Some enzymes hydrolyse diphosphate (cf. EC 3.6.1.1 inorganic diphosphatase)  
**References:** [752, 1116, 1883, 2085, 2892]

[EC 3.1.3.1 created 1961]

**EC 3.1.3.2**  
**Accepted name:** acid phosphatase  
**Reaction:** a phosphate monoester + H₂O = an alcohol + phosphate  
**Other name(s):** acid phosphomonoesterase; phosphomonoesterase; glycerophosphatase; acid monophosphatase; acid phosphohydrolase; acid phosphomonoester hydrolase; uteroferrin; acid nucleoside diphosphate phosphatase; orthophosphoric-monoester phosphohydrolase (acid optimum)  
**Systematic name:** phosphate-monoester phosphohydrolase (acid optimum)  
**Comments:** Wide specificity. Also catalyses transphosphorylations.  
**References:** [1428, 1651, 3121]

[EC 3.1.3.2 created 1961]

**EC 3.1.3.3**  
**Accepted name:** phosphoserine phosphatase  
**Reaction:** O-phospho-L(or D)-serine + H₂O = L(or D)-serine + phosphate  
**Systematic name:** O-phosphoserine phosphohydrolase  
**References:** [291, 373, 2177]

[EC 3.1.3.3 created 1961]

**EC 3.1.3.4**  
**Accepted name:** phosphatidate phosphatase  
**Reaction:** a 1,2-diacylglycerol 3-phosphate + H₂O = a 1,2-diacyl-sn-glycerol + phosphate  
**Other name(s):** phosphatic acid phosphatase; acid phosphatidyl phosphatase; phosphatic acid phosphohydrolase; PAP; Lipin  
**Systematic name:** diacylglycerol-3-phosphate phosphohydrolase  
**Comments:** This enzyme catalyses the Mg²⁺-dependent dephosphorylation of a 1,2-diacylglycerol-3-phosphate, yielding a 1,2-diacyl-sn-glycerol (DAG), the substrate for de novo lipid synthesis via the Kennedy pathway and for the synthesis of triacylglycerol. In lipid signalling, the enzyme generates a pool of DAG to be used for protein kinase C activation. The mammalian enzymes are known as lipins.  
**References:** [2840, 403]

[EC 3.1.3.4 created 1961, modified 2010]

**EC 3.1.3.5**  
**Accepted name:** 5′-nucleotidase  
**Reaction:** a 5′-ribonucleotide + H₂O = a ribonucleoside + phosphate  
**Other name(s):** uridine 5′-nucleotidase; 5′-adenylic phosphatase; adenosine 5′-phosphatase; AMP phosphatase; adenosine monophosphatase; 5′-mononucleotidase; AMPase; UMPase; snake venom 5′-nucleotidase; thymidine monophosphate nucleotidase; 5′-AMPase; 5′-AMP nucleotidase; AMP phosphohydrolase; IMP 5′-nucleotidase  
**Systematic name:** 5′-ribonucleotide phosphohydrolase  
**Comments:** Wide specificity for 5′-nucleotides.  
**References:** [1057, 1190, 2736]

[EC 3.1.3.5 created 1961]
EC 3.1.3.6
Accepted name: 3′-nucleotidase
Reaction: a 3′-ribonucleotide + H₂O = a ribonucleoside + phosphate
Other name(s): 3′-mononucleotidase; 3′-phosphatase; 3′-ribonucleotidase
Systematic name: 3′-ribonucleotide phosphohydrolase
Comments: Wide specificity for 3′-nucleotides.
References: [2786]

[EC 3.1.3.6 created 1961]

EC 3.1.3.7
Accepted name: 3′(2′),5′-bisphosphate nucleotidase
Reaction: adenosine 3′,5′-bisphosphate + H₂O = AMP + phosphate
Other name(s): phosphoadenylate 3′-nucleotidase; 3′-phosphoadenylylsulfate 3′-phosphatase; 3′(2′),5′-bisphosphonucleoside 3′(2′)-phosphohydrolase
Systematic name: adenosine-3′(2′),5′-bisphosphate 3′(2′)-phosphohydrolase
Comments: Also acts on 3′-phosphoadenylyl sulfate, and on the corresponding 2′-phosphates.
References: [347, 791, 2486, 3116]

[EC 3.1.3.7 created 1961]

EC 3.1.3.8
Accepted name: 3-phytase
Reaction: myo-inositol hexakisphosphate + H₂O = 1D-myo-inositol 1,2,4,5,6-pentakisphosphate + phosphate
Other name(s): 1-phytase; phytase; phytate 1-phosphatase; phytate 6-phosphatase
Systematic name: myo-inositol-hexakisphosphate 3-phosphohydrolase
References: [532, 1410, 1332, 533]

[EC 3.1.3.8 created 1961, modified 1976, modified 2002]

EC 3.1.3.9
Accepted name: glucose-6-phosphatase
Reaction: D-glucose 6-phosphate + H₂O = D-glucose + phosphate
Other name(s): glucose 6-phosphate phosphatase
Systematic name: D-glucose-6-phosphate phosphohydrolase
Comments: Wide distribution in animal tissues. Also catalyses potent transphosphorylations from carbamoyl phosphate, hexose phosphates, diphosphate, phosphoenolpyruvate and nucleoside di- and triphosphates, to D-glucose, D-mannose, 3-methyl-D-glucose or D-deoxy-D-glucose [cf. EC 2.7.1.62 (phosphoramidate—hexose phosphotransferase), EC 2.7.1.79 (diphosphate—glycerol phosphotransferase) and EC 3.9.1.1 (phosphoamidase)].
References: [53, 506, 2216, 2217]

[EC 3.1.3.9 created 1961]

EC 3.1.3.10
Accepted name: glucose-1-phosphatase
Reaction: α-D-glucose 1-phosphate + H₂O = D-glucose + phosphate
Systematic name: α-D-glucose-1-phosphate phosphohydrolase
Comments: Also acts, more slowly, on D-galactose 1-phosphate.
References: [799, 3146]

[EC 3.1.3.10 created 1961]
EC 3.1.3.11

Accepted name: fructose-bisphosphatase
Reaction: \( \text{D-fructose 1,6-bisphosphate} + \text{H}_2\text{O} = \text{D-fructose 6-phosphate} + \text{phosphate} \)
Other name(s): hexose diphosphatase; FBPase; fructose 1,6-diphosphatase; fructose 1,6-diphosphate phosphatase; D-fructose 1,6-diphosphatase; fructose 1,6-bisphosphatase; fructose diphosphatase; fructose bisphosphate phosphatase; fructose 1,6-bisphosphate 1-phosphatase; fructose 1,6-bisphosphate phosphatase; hexose bisphosphatase; D-fructose-1,6-bisphosphate phosphatase
Systematic name: D-fructose-1,6-bisphosphate 1-phosphohydrolase
Comments: The animal enzyme also acts on sedoheptulose 1,7-bisphosphate.
References: [734, 1008, 2050, 2428]

[EC 3.1.3.11 created 1961, modified 1976]

EC 3.1.3.12

Accepted name: trehalose-phosphatase
Reaction: \( \alpha,\alpha\text{-trehalose 6-phosphate} + \text{H}_2\text{O} = \alpha,\alpha\text{-trehalose} + \text{phosphate} \)
Other name(s): trehalose 6-phosphatase; trehalose 6-phosphate phosphatase; trehalose-6-phosphate phosphohydrolase
Systematic name: \( \alpha,\alpha\text{-trehalose-6-phosphate phosphohydrolase} \)
References: [377, 395]

[EC 3.1.3.12 created 1961]

EC 3.1.3.13 Deleted entry. bisphosphoglycerate phosphatase. Recent studies have shown that this is a partial activity of EC 5.4.2.11, phosphoglycerate mutase (2,3-diphosphoglycerate-dependent)]

[EC 3.1.3.13 created 1961, deleted 2016]

EC 3.1.3.14

Accepted name: methylphosphothioglycerate phosphatase
Reaction: \( S\text{-methyl-3-phospho-1-thio-\text{D}-glycerate} + \text{H}_2\text{O} = S\text{-methyl-1-thio-\text{D}-glycerate} + \text{phosphate} \)
Other name(s): methylthiophosphoglycerate phosphatase
Systematic name: \( S\text{-methyl-3-phospho-1-thio-\text{D}-glycerate phosphohydrolase} \)
References: [254]

[EC 3.1.3.14 created 1961]

EC 3.1.3.15

Accepted name: histidinol-phosphatase
Reaction: \( \text{L-histidinol phosphate} + \text{H}_2\text{O} = \text{L-histidinol} + \text{phosphate} \)
Other name(s): histidinol phosphate phosphatase; L-histidinol phosphate phosphatase; histidinolphosphate phosphatase; HPpase; histidinolphosphatase
Systematic name: \( \text{L-histidinol-phosphate phosphohydrolase} \)
References: [49]

[EC 3.1.3.15 created 1961]

EC 3.1.3.16

Accepted name: protein-serine/threonine phosphatase
Reaction: \( \text{[a protein]-serine/threonine phosphate} + \text{H}_2\text{O} = \text{[a protein]-serine/threonine} + \text{phosphate} \)

38
**Other name(s):** phosphoprotein phosphatase (ambiguous); protein phosphatase-1; protein phosphatase-2A; protein phosphatase-2B; protein phosphatase-2C; protein D phosphatase; phosphospectrin phosphatase; casein phosphatase; Aspergillus awamori acid protein phosphatase; calcineurin; phosphatase 2A; phosphatase 2B; phosphatase II; phosphatase IB; phosphatase C-II; polycation modulated (PCM-) phosphatase; phosphopyruvate dehydrogenase phosphatase; phosphatase SP; branched-chain α-keto acid dehydrogenase phosphatase; BCKDH phosphatase; 3-hydroxy 3-methylglutaryl coenzymeA reductase phosphatase; HMG-CoA reductase phosphatase; phosphatase H-II; phosphatase III; phosphatase I; protein phosphatase; phosphatase IV; phosphoprotein phosphohydrolase

**Systematic name:** protein-serine/threonine-phosphate phosphohydrolase

**Comments:** A group of enzymes removing the serine- or threonine-bound phosphate group from a wide range of phosphoproteins, including a number of enzymes that have been phosphorylated under the action of a kinase (cf. EC 3.1.3.48 protein-tyrosine-phosphatase). The spleen enzyme also acts on phenolic phosphates and phosphamides (cf. EC 3.9.1.1, phosphomimidase).

**References:** [638, 1326, 2943, 3089]

[EC 3.1.3.16 created 1961, modified 1989, modified 2013]

**EC 3.1.3.17**

**Accepted name:** [phosphorylase] phosphatase

**Reaction:** [phosphorylase a] + 4 H₂O = [phosphorylase b] + 4 phosphate

**Other name(s):** PR-enzyme; phosphorylase a phosphatase; glycogen phosphorylase phosphatase; protein phosphatase C; type 1 protein phosphatase

**Systematic name:** [phosphorylase a] phosphohydrolase

**References:** [305, 1021, 2483]

[EC 3.1.3.17 created 1961]

**EC 3.1.3.18**

**Accepted name:** phosphoglycolate phosphatase

**Reaction:** 2-phosphoglycolate + H₂O = glycolate + phosphate

**Other name(s):** phosphoglycolate hydrolase; 2-phosphoglycolate phosphatase; P-glycolate phosphatase; phosphoglycolate phosphatase

**Systematic name:** 2-phosphoglycolate phosphohydrolase

**References:** [450]

[EC 3.1.3.18 created 1965]

**EC 3.1.3.19**

**Accepted name:** glycerol-2-phosphatase

**Reaction:** glycerol 2-phosphate + H₂O = glycerol + phosphate

**Other name(s):** β-glycerophosphatase; β-glycerophosphate phosphatase; 2-glycerophosphatase

**Systematic name:** glycerol-2-phosphate phosphohydrolase

**References:** [2706, 3121]

[EC 3.1.3.19 created 1965]

**EC 3.1.3.20**

**Accepted name:** phosphoglycerate phosphatase

**Reaction:** D-glycerate 2-phosphate + H₂O = D-glycerate + phosphate

**Other name(s):** D-2-phosphoglycerate phosphatase; glycerophosphate phosphatase

**Systematic name:** D-glycerate-2-phosphate phosphohydrolase

**References:** [786]

[EC 3.1.3.20 created 1972]
EC 3.1.3.21
Accepted name: glycerol-1-phosphatase
Reaction: glycerol 1-phosphate + H₂O = glycerol + phosphate
Other name(s): α-glycerophosphatase; α-glycerol phosphatase; glycerol 3-phosphatase; glycerol-3-phosphate phosphatase; glycerol 3-phosphate phosphohydrolase
Systematic name: glycerol-1-phosphate phosphohydrolase
Comments: The *Dunaliella* enzyme acts more rapidly on *sn*-glycerol 1-phosphate than on the 3-phosphate. The enzyme from yeast also acts on propane-1,2-diol 1-phosphate, but not on a variety of other phosphate esters.
References: [2948]

[EC 3.1.3.21 created 1972, modified 1986]

EC 3.1.3.22
Accepted name: mannitol-1-phosphatase
Reaction: D-mannitol 1-phosphate + H₂O = D-mannitol + phosphate
Other name(s): mannitol-1-phosphate phosphatase
Systematic name: D-mannitol-1-phosphate phosphohydrolase
References: [2603, 3398]

[EC 3.1.3.22 created 1972]

EC 3.1.3.23
Accepted name: sugar-phosphatase
Reaction: sugar phosphate + H₂O = sugar + phosphate
Systematic name: sugar-phosphate phosphohydrolase
Comments: Has a wide specificity, acting on aldohexose 1-phosphates, ketohexose 1-phosphates, aldohexose 6-phosphates, ketohexose 6-phosphates, both phosphate ester bonds of fructose 1,6-bisphosphate, phosphoric esters of disaccharides, and on pentose and triose phosphates, but at a slower rate.
References: [1728]

[EC 3.1.3.23 created 1972]

EC 3.1.3.24
Accepted name: sucrose-phosphate phosphatase
Reaction: sucrose 6F-phosphate + H₂O = sucrose + phosphate
Other name(s): sucrose 6-phosphate hydrodrolase; sucrose-phosphate hydrodrolase; sucrose-phosphate phosphohydrolase; sucrose-6-phosphatase; sucrose phosphatase; sucrose-6-phosphate phosphatase; SPP
Systematic name: sucrose-6F-phosphate phosphohydrolase
Comments: Requires Mg²⁺ for maximal activity [1852]. This is the final step in the sucrose-biosynthesis pathway. The enzyme is highly specific for sucrose 6-phosphate, with fructose 6-phosphate unable to act as a substrate [1852]. Belongs in the haloacid dehydrogenase (HAD) superfamily. The F of sucrose 6F-phosphate is used to indicate that the fructose residue of sucrose carries the substituent.
References: [1145, 1852, 1853, 819]

[EC 3.1.3.24 created 1972, modified 2008]

EC 3.1.3.25
Accepted name: inositol-phosphate phosphatase
Reaction: myo-inositol phosphate + H₂O = myo-inositol + phosphate

[EC 3.1.3.25 created 1972]
Other name(s): myo-inositol-1(or 4)-monophosphatase; inositol 1-phosphatase; L-myo-inositol-1-phosphate phosphatase; myo-inositol 1-phosphatase; inositol phosphatase; inositol monophosphate phosphatase; inositol-1(or 4)-monophosphatase; myo-inositol-1(or 4)-phosphate phosphohydrolase; myo-inositol monophosphatase; myo-inositol-1-phosphatase

Systematic name: myo-inositol-phosphate phosphohydrolase

Comments: Acts on five of the six isomers of myo-inositol phosphate, all except myo-inositol 2-phosphate, but does not act on myo-inositol bearing more than one phosphate group. It also acts on adenosine 2′-phosphate (but not the 3′- or 5′- phosphates), sn-glycerol 3-phosphate and glycerol 2-phosphate. Two isoforms are known [3462].

References: [731, 944, 1089, 3462, 3368, 13]


EC 3.1.3.26

Accepted name: 4-phytase

Reaction: myo-inositol hexakisphosphate + H₂O = 1D-my/o-inositol 1,2,3,5,6-pentakisphosphate + phosphate

Other name(s): 6-phytase (name based on 1L-numbering system and not 1D-numbering); phytase; phytate 6-phosphatase; myo-inositol-hexakisphosphate 6-phosphohydrolase (name based on 1L-numbering system and not 1D-numbering)

Systematic name: myo-inositol-hexakisphosphate 4-phosphohydrolase

References: [1410, 3082, 1782, 533]

[EC 3.1.3.26 created 1972, modified 1976, modified 2002]

EC 3.1.3.27

Accepted name: phosphatidylglycerophosphatase

Reaction: phosphatidylglycerophosphate + H₂O = phosphatidylglycerol + phosphate

Other name(s): phosphatidylglycerol phosphate phosphatase; phosphatidylglycerol phosphatase; PGP phosphatase

Systematic name: phosphatidylglycerophosphate phosphohydrolase

References: [430]

[EC 3.1.3.27 created 1972]

EC 3.1.3.28

Accepted name: ADP-phosphoglycerate phosphatase

Reaction: 3-(ADP)-2-phosphoglycerate + H₂O = 3-(ADP)-glycerate + phosphate

Other name(s): adenosine diphosphate phosphoglycerate phosphatase

Systematic name: 3-(ADP)-2-phosphoglycerate phosphohydrolase

Comments: Also acts on 2,3-bisphosphoglycerate.

References: [3477]

[EC 3.1.3.28 created 1972]

EC 3.1.3.29

Accepted name: N-acyleuraminate-9-phosphatase

Reaction: N-acyleuraminate 9-phosphate + H₂O = N-acyleuraminate + phosphate

Other name(s): acyleuraminate 9-phosphatase; N-acyleuraminic acid 9-phosphate phosphatase; N-acyleuraminic (sialic) acid 9-phosphatase

Systematic name: N-acyleuraminate-9-phosphate phosphohydrolase

References: [1427]

[EC 3.1.3.29 created 1972]

[3.1.3.30 Deleted entry. 3′-phosphoadenylylsulfate 3′-phosphatase. The activity may be that of an acid phosphatase.]
EC 3.1.3.32

**Accepted name:** polynucleotide $3'$-phosphatase  
**Reaction:** $a\ 3'$-phosphopolynucleotide + $H_2O \rightarrow a\ polynucleotide + phosphate$  
**Other name(s):** $2'(3')$-polynucleotidase; DNA $3'$-phosphatase; deoxyribonucleate $3'$-phosphatase; $5'$-polynucleotidekinase $3'$-phosphatase  
**Systematic name:** polynucleotide $3'$-phosphohydrolase  
**Comments:** Also hydrolyses nucleoside $2'$-, $3'$- and $5'$-monophosphates, but only $2'$- and $3'$-phosphopolynucleotides.  
**References:** [195]

[EC 3.1.3.32 created 1972]

EC 3.1.3.33

**Accepted name:** polynucleotide $5'$-phosphatase  
**Reaction:** $a\ 5'$-phosphopolynucleotide + $H_2O \rightarrow a\ polynucleotide + phosphate$  
**Other name(s):** $5'$-polynucleotidase  
**Systematic name:** polynucleotide $5'$-phosphohydrolase  
**Comments:** Does not act on nucleoside monophosphates. Induced in *Escherichia coli* by T-even phages.  
**References:** [195]

[EC 3.1.3.33 created 1972]

EC 3.1.3.34

**Accepted name:** deoxynucleotide $3'$-phosphatase  
**Reaction:** $a\ 2'$-deoxyribonucleoside $3'$-phosphate + $H_2O \rightarrow a\ 2'$-deoxyribonucleoside + phosphate$  
**Other name(s):** $3'$-deoxynucleotidase; $3'$-deoxyribonucleotidase  
**Systematic name:** $2'$-deoxyribonucleotide $3'$-phosphohydrolase  
**Comments:** Also catalyses the selective removal of $3'$-phosphate groups from DNA and oligodeoxyribonucleotides. Induced in *Escherichia coli* by T-even phages.  
**References:** [195]

[EC 3.1.3.34 created 1972]

EC 3.1.3.35

**Accepted name:** thymidylate $5'$-phosphatase  
**Reaction:** $thymidylate + H_2O \rightarrow thymidine + phosphate$  
**Other name(s):** thymidylate $5'$-nucleotidase; deoxythymidylate $5'$-nucleotidase; thymidylate nucleotidase; deoxythymidylic $5'$-nucleotidase; deoxythymidylate phosphohydrolase; dTMPase  
**Systematic name:** thymidylate $5'$-phosphohydrolase  
**Comments:** Acts on 5-methyl-dCMP and on TMP, but more slowly than on dTMP.  
**References:** [67]

[EC 3.1.3.35 created 1972]

EC 3.1.3.36

**Accepted name:** phosphoinositide $5'$-phosphatase
**Reaction:**
1-phosphatidyl-1D-myoinositol 4,5-bisphosphate + H₂O = 1-phosphatidyl-1D-myoinositol 4-phosphate + phosphate

**Other name(s):**
type II inositol polyphosphate 5-phosphatase; triphosphoinositide phosphatase; IP₃ phosphatase; PtdIns(4,5)P₂ phosphatase; triphosphoinositide phosphomonoesterase; diphosphoinositide phosphatase; inositol 1,4,5-triphosphate 5-phosphomonoesterase; inositol triphosphate 5-phosphomonoesterase; phosphatidylinositol-bisphosphatase; phosphatidyl-myoinositol-4,5-bisphosphate phosphatase; phosphatidyl-inositol 4,5-bisphosphate phosphatase; polyphosphoinositol lipid 5-phosphatase; phosphatidyl-inositol-bisphosphate phosphatase

**Systematic name:**
phosphatidyl-myoinositol-4,5-bisphosphate 4-phosphohydrolase

**Comments:**
These enzymes can also remove the 5-phosphate from Ins(1,4,5)P₃ and/or Ins(1,3,4,5)P₄. They are a diverse family of enzymes, with differing abilities to catalyse two or more of the four reactions listed. They are thought to use inositol lipids rather than inositol phosphates as substrates in vivo. All of them can use either or both of PtdIns(4,5)P₂ and PtdIns(3,4,5)P₃ as substrates; this is the main property that distinguishes them from EC 3.1.3.56, inositol-polyposphate 5-phosphatase.

**References:**
[598, 2559, 3368]

[EC 3.1.3.36 created 1972, modified 2002]

---

**EC 3.1.3.37**

**Accepted name:** sedoheptulose-bisphosphatase

**Reaction:**
sedoheptulose 1,7-bisphosphate + H₂O = sedoheptulose 7-phosphate + phosphate

**Other name(s):** SBPase; sedoheptulose 1,7-diphosphate phosphatase; sedoheptulose 1,7-diphosphatase; sedoheptulose diphosphatase; sedoheptulose bisphosphatase

**Systematic name:**
sedoheptulose-1,7-bisphosphate 1-phosphohydrolase

**References:**
[2472, 3104]

[EC 3.1.3.37 created 1976]

---

**EC 3.1.3.38**

**Accepted name:** 3-phosphoglycerate phosphatase

**Reaction:**
D-glycerate 3-phosphate + H₂O = D-glycerate + phosphate

**Other name(s):** D-3-Phosphoglycerate phosphatase; 3-PGA phosphatase

**Systematic name:**
D-glycerate-3-phosphate phosphohydrolase

**Comments:**
Wide specificity, but 3-phosphoglycerate is the best substrate.

**References:**
[2491]

[EC 3.1.3.38 created 1976]

---

**EC 3.1.3.39**

**Accepted name:** streptomycin-6-phosphatase

**Reaction:**
streptomycin 6-phosphate + H₂O = streptomycin + phosphate

**Other name(s):** streptomycin 6-phosphate phosphatase; streptomycin 6-phosphate phosphohydrolase; streptomycin-6-P phosphohydrolase

**Systematic name:**
streptomycin-6-phosphate phosphohydrolase

**Comments:**
Also acts on dihydrostreptomycin 3′α,6-bisphosphate and streptidine 6-phosphate.

**References:**
[3247, 3248]

[EC 3.1.3.39 created 1976]

---

**EC 3.1.3.40**

**Accepted name:** guanidinodeoxy-scyllo-inositol-4-phosphatase

**Reaction:**
1-guanidino-1-deoxy-scyllo-inositol 4-phosphate + H₂O = 1-guanidino-1-deoxy-scyllo-inositol + phosphate
Other name(s): 1-guanidino-scyllo-inositol 4-phosphatase; 1-guanidino-1-deoxy-scyllo-inositol-4-P phosphohydrolase  
Systematic name: 1-guanidino-1-deoxy-scyllo-inositol-4-phosphate 4-phosphohydrolase  
References: [3248]

[EC 3.1.3.40 created 1976]

EC 3.1.3.41  
Accepted name: 4-nitrophenylphosphatase  
Reaction: 4-nitrophenyl phosphate + H₂O = 4-nitrophenol + phosphate  
Other name(s): nitrophenyl phosphatase; p-nitrophenylphosphatase; para-nitrophenyl phosphatase; K-pNPPase; NPPase; Ecto-p-nitrophenyl phosphatase; p-nitrophenylphosphate phosphohydrolase  
Systematic name: 4-nitrophenylphosphate phosphohydrolase  
Comments: A number of other substances, including phenyl phosphate, 4-nitrophenyl sulfate, acetyl phosphate and glycerol phosphate, are not substrates.  
References: [100, 101]

[EC 3.1.3.41 created 1976]

EC 3.1.3.42  
Accepted name: [glycogen-synthase-D] phosphatase  
Other name(s): uridine diphosphoglucone-glycogen glucosyltransferase phosphatase; UDP-glycogen glucosyltransferase phosphatase; UDPglucose-glycogen glucosyltransferase phosphatase; glycogen glucosyltransferase phosphatase; glycogen synthase phosphatase; glycogen synthase phosphatase; glycogen synthase D phosphatase; Mg²⁺ dependent glycogen synthase phosphatase; phosphatase type 2°C  
Systematic name: [UDP-glucose:glycogen 4-α-D-glucosyltransferase-D] phosphohydrolase  
Comments: The product is EC 2.4.1.11 glycogen(starch) synthase.  
References: [7]

[EC 3.1.3.42 created 1976]

EC 3.1.3.43  
Accepted name: [pyruvate dehydrogenase (acetyl-transferring)]-phosphatase  
Reaction: [pyruvate dehydrogenase (acetyl-transferring)] phosphate + H₂O = [pyruvate dehydrogenase (acetyl-transferring)] + phosphate  
Other name(s): pyruvate dehydrogenase phosphatase; phosphopyruvate dehydrogenase phosphatase; [pyruvate dehydrogenase (lipoamide)]-phosphatase; [pyruvate dehydrogenase (lipoamide)]-phosphate phosphohydrolase  
Systematic name: [pyruvate dehydrogenase (acetyl-transferring)]-phosphate phosphohydrolase  
Comments: A mitochondrial enzyme associated with EC 1.2.4.1 pyruvate dehydrogenase (acetyl-transferring), in the pyruvate dehydrogenase complex.  
References: [1804, 2521]

[EC 3.1.3.43 created 1978]

EC 3.1.3.44  
Accepted name: [acyl-CoA carboxylase]-phosphatase  
Reaction: [acyl-CoA carboxylase] phosphate + H₂O = [acyl-CoA carboxylase] + phosphate  
Systematic name: [acyl-CoA:carbon-dioxide ligase (ADP-forming)]-phosphate phosphohydrolase
Simultaneously dephosphorylates and activates EC 6.4.1.2 acetyl-CoA carboxylase. Acts similarly on EC 1.1.1.88 (hydroxymethylglutaryl-CoA reductase), EC 2.4.1.1 (phosphorylase), EC 2.4.1.11 [glycogen(starch) synthase], and dephosphorylates phosphoprotamine and 4-nitrophenyl phosphate.

Not identical to EC 3.1.3.17 ([phosphorylase] phosphatase) or EC 3.1.3.43 [pyruvate dehydrogenase (acetyl-transferring)]-phosphatase.

References: [1616]

[EC 3.1.3.44 created 1983]

**EC 3.1.3.45**

**Accepted name:** 3-deoxy-

**Systematic name:** 3-deoxy-

**Reaction:** 3-deoxy-

References: [2509]

[EC 3.1.3.45 created 1983]

**EC 3.1.3.46**

**Accepted name:** fructose-2,6-bisphosphate 2-phosphatase

**Reaction:** β-D-fructose 2,6-bisphosphate + H₂O = D-fructose 6-phosphate + phosphate

**Other name(s):** fructose-2,6-bisphosphatase; D-fructose-2,6-bisphosphate 2-phosphohydrolase

**Systematic name:** β-D-fructose-2,6-bisphosphate 2-phosphohydrolase

**Comments:** The enzyme copurifies with EC 2.7.1.105 6-phosphofructo-2-kinase. (cf. EC 3.1.3.54 fructose-2,6-bisphosphate 6-phosphatase).

References: [2685]

[EC 3.1.3.46 created 1984]

**EC 3.1.3.47**

**Accepted name:** [hydroxymethylglutaryl-CoA reductase (NADPH)]-phosphatase

**Reaction:** [hydroxymethylglutaryl-CoA reductase (NADPH)] phosphate + H₂O = [hydroxymethylglutaryl-CoA reductase (NADPH)] + phosphate

**Other name(s):** reductase phosphatase

**Systematic name:** [hydroxymethylglutaryl-CoA reductase (NADPH)]-phosphate phosphohydrolase

**Comments:** Acts on the product of the reaction catalysed by EC 2.7.11.31 [hydroxymethylglutaryl-CoA reductase (NADPH)] kinase, simultaneously dephosphorylating and activating EC 1.1.1.34 hydroxymethylglutaryl-CoA reductase (NADPH).

References: [971, 972]

[EC 3.1.3.47 created 1984]

**EC 3.1.3.48**

**Accepted name:** protein-tyrosine-phosphatase

**Reaction:** [a protein]-tyrosine phosphate + H₂O = [a protein]-tyrosine + phosphate

**Other name(s):** phosphotyrosine phosphatase; phosphoprotein phosphatase (phosphotyrosine); phosphotyrosine histone phosphatase; protein phosphotyrosine phosphatase; tyrosylprotein phosphatase; phosphotyrosine protein phosphatase; phosphotyrosylprotein phosphatase; tyrosine O-phosphate phosphatase; PPT-phosphatase; PPTase; [phosphotyrosine]protein phosphatase; PTP-phosphatase

**Systematic name:** protein-tyrosine-phosphate phosphohydrolase

**Comments:** Dephosphorylates O-phosphotyrosine groups in phosphoproteins, such as the products of EC 2.7.10.2, non-specific protein-tyrosine kinase.

References: [850, 927]

[EC 3.1.3.48 created 1984]
EC 3.1.3.49
Accepted name: [pyruvate kinase]-phosphatase
Reaction: [pyruvate kinase] phosphate + H$_2$O = [pyruvate kinase] + phosphate
Other name(s): pyruvate kinase phosphatase
Systematic name: [ATP:pyruvate 2-O-phosphotransferase]-phosphatase phosphohydrolase
Comments: Simultaneously dephosphorylates and activates EC 2.7.1.40 pyruvate kinase, that has been inactivated by protein kinase.
References: [1402]

[EC 3.1.3.49 created 1984]

EC 3.1.3.50
Accepted name: sorbitol-6-phosphatase
Reaction: sorbitol 6-phosphate + H$_2$O = sorbitol + phosphate
Other name(s): sorbitol-6-phosphate phosphatase
Systematic name: sorbitol-6-phosphate phosphohydrolase
Comments: Acts, very slowly, on hexose 6-phosphates.
References: [1019]

[EC 3.1.3.50 created 1984]

EC 3.1.3.51
Accepted name: dolichyl-phosphatase
Reaction: dolichyl phosphate + H$_2$O = dolichol + phosphate
Other name(s): dolichyl phosphate phosphatase; dolichol phosphatase; dolichol monophosphatase; dolichyl monophosphate phosphatase; dolichyl phosphate phosphatase; polyisoprenyl phosphate phosphatase; polyrenylphosphate phosphatase; Dol-P phosphatase
Systematic name: dolichyl-phosphate phosphohydrolase
References: [19, 2555, 3298]

[EC 3.1.3.51 created 1984]

EC 3.1.3.52
Accepted name: [3-methyl-2-oxobutanoate dehydrogenase (2-methylpropanoyl-transferring)]-phosphatase
Reaction: [3-methyl-2-oxobutanoate dehydrogenase (2-methylpropanoyl-transferring)] phosphate + H$_2$O = [3-methyl-2-oxobutanoate dehydrogenase (2-methylpropanoyl-transferring)] + phosphate
Other name(s): branched-chain oxo-acid dehydrogenase phosphatase; branched-chain 2-keto acid dehydrogenase phosphatase; branched-chain α-keto acid dehydrogenase phosphatase; BCKDH (ambiguous); [3-methyl-2-oxobutanoate dehydrogenase (lipoamide)]-phosphatase; [3-methyl-2-oxobutanoate dehydrogenase (lipoamide)]-phosphate phosphohydrolase
Systematic name: [3-methyl-2-oxobutanoate dehydrogenase (2-methylpropanoyl-transferring)]-phosphate phosphohydrolase
Comments: A mitochondrial enzyme associated with the 3-methyl-2-oxobutanoate dehydrogenase complex. Simultaneously dephosphorylates and activates EC 1.2.4.4 3-methyl-2-oxobutanoate dehydrogenase (2-methylpropanoyl-transferring), that has been inactivated by phosphorylation.
References: [794, 2521]

[EC 3.1.3.52 created 1986]

EC 3.1.3.53
Accepted name: [myosin-light-chain] phosphatase
Reaction: [myosin light-chain] phosphate + H$_2$O = [myosin light-chain] + phosphate
Other name(s): myosin light chain kinase phosphatase; myosin phosphatase; myosin phosphatase; protein phosphatase 2A; myosin-light-chain-phosphatase

Systematic name: [myosin-light-chain]-phosphate phosphohydrolase

Comments: The enzyme is composed of three subunits. The holoenzyme dephosphorylates myosin light chains and EC 2.7.11.18, myosin-light-chain kinase, but not myosin; the catalytic subunit acts on all three substrates.

References: [2358]

[EC 3.1.3.53 created 1986]

EC 3.1.3.54
Accepted name: fructose-2,6-bisphosphate 6-phosphatase
Reaction: \( \beta-D\)-fructose 2,6-bisphosphate + H\(_2\)O = \( \beta-D\)-fructofuranose 2-phosphate + phosphate
Other name(s): fructose 2,6-bisphosphate-6-phosphohydrolase; fructose-2,6-bisphosphate 6-phosphohydrolase; D-fructose-2,6-bisphosphate 6-phosphohydrolase
Systematic name: \( \beta-D\)-fructose-2,6-bisphosphate 6-phosphohydrolase
Comments: cf. EC 3.1.3.46 fructose-2,6-bisphosphate 2-phosphatase.
References: [2450, 2451]

[EC 3.1.3.54 created 1989]

EC 3.1.3.55
Accepted name: caldesmon-phosphatase
Reaction: caldesmon phosphate + H\(_2\)O = caldesmon + phosphate
Other name(s): SMP-I; smooth muscle caldesmon phosphatase
Systematic name: caldesmon-phosphate phosphohydrolase
Comments: Dephosphorylation activates the calmodulin- and actin-binding ability of the protein caldesmon.
References: [2185]

[EC 3.1.3.55 created 1989]

EC 3.1.3.56
Accepted name: inositol-polyphosphate 5-phosphatase
Reaction: (1) 1-D\(-\)myo-inositol 1,4,5-trisphosphate + H\(_2\)O = myo-inositol 1,4-bisphosphate + phosphate
(2) 1D-myoinositol 1,3,4,5-tetrakisphosphate + H\(_2\)O = 1\(D\)-myo-inositol 1,3,4-trisphosphate + phosphate
Other name(s): type I inositol-polyphosphate phosphatase; inositol trisphosphate phosphomonoesterase; Ins\(P_3\)/Ins(1,3,4,5)\(P_4\) 5-phosphatase; inositol triphosphatase; \(D\)-myo-inositol 1,4,5-trisphosphate 5-phosphatase; \(D\)-myo-inositol 1,4,5-trisphosphate 5-phosphatase; \(1\)-myo-inositol 1,4,5-trisphosphate-5-phosphatase; \(1\)-myo-inositol 1,4,5-trisphosphate-5-phosphatase; inositol phosphate 5-phosphomonoesterase; inositol-1,4,5-trisphosphate/1,3,4,5-tetrakisphosphate 5-phosphatase; Ins(1,4,5)\(P_3\) 5-phosphatase; \(D\)-myo-inositol(1,4,5)/(1,3,4,5)-polyphosphate 5-phosphatase; inositol 1,4,5-trisphosphate phosphatase; inositol polyphosphate-5-phosphatase; \(myo\)-inositol-1,4,5-trisphosphate 5-phosphatase; inositol-1,4,5-trisphosphate 5-phosphatase
Systematic name: 1D-myoinositol-1,4,5-trisphosphate 5-phosphohydrolase
Comments: One mammalian isoform is known. This enzyme is distinguished from the family of enzymes classified under EC 3.1.3.36, phosphoinositide 5-phosphatase, by its inability to dephosphorylate inositol lipids.
References: [687, 760, 3368, 3210]

[EC 3.1.3.56 created 1989, modified 2002]
EC 3.1.3.57
Accepted name: inositol-1,4-bisphosphate 1-phosphatase
Reaction: 1D-my-o-inositol 1,4-bisphosphate + H₂O = 1D-my-o-inositol 4-phosphate + phosphate
Other name(s): inositol-polyphosphate 1-phosphatase
Systematic name: 1D-my-o-inositol-1,4-bisphosphate 1-phosphohydrolase
Comments: The enzyme acts on inositol 1,4-bisphosphate and inositol 1,3,4-trisphosphate (forming inositol 3,4-bisphosphate) with similar $V_{max}$ values for both substrates, but with a five-times higher affinity for the bisphosphate. Does not act on inositol 1-phosphate, inositol 1,4,5-trisphosphate or inositol 1,3,4,5-tetrakisphosphate.
References: [220, 521, 1328]

[EC 3.1.3.57 created 1989, modified 2002]

EC 3.1.3.58
Accepted name: sugar-terminal-phosphatase
Reaction: D-glucose 6-phosphate + H₂O = D-glucose + phosphate
Other name(s): xylitol-5-phosphatase
Systematic name: sugar-ω-phosphate phosphohydrolase
Comments: Acts on sugars and polyols phosphorylated on the terminal carbon, with a preference for sugars with a D-erythro-configuration, e.g. good substrates are glucose 6-phosphate, mannose 6-phosphate, 6-phosphogluconate, erythrose 4-phosphate and xylitol 5-phosphate.
References: [1831]

[EC 3.1.3.58 created 1989]

EC 3.1.3.59
Accepted name: alkylacetylglycerophosphatase
Reaction: 1-alkyl-2-acetyl-sn-glycero-3-phosphate + H₂O = 1-alkyl-2-acetyl-sn-glycerol + phosphate
Other name(s): 1-alkyl-2-lyso-sn-glycero-3-P:acetyl-CoA acetyltransferase; alkylacetylglycerophosphate phosphatase
Systematic name: 1-alkyl-2-acetyl-sn-glycero-3-phosphate phosphohydrolase
Comments: Involved in the biosynthesis of thrombocyte activating factor in animal tissues.
References: [1723]

[EC 3.1.3.59 created 1989]

EC 3.1.3.60
Accepted name: phosphoenolpyruvate phosphatase
Reaction: phosphoenolpyruvate + H₂O = pyruvate + phosphate
Other name(s): PEP phosphatase
Systematic name: phosphoenolpyruvate phosphohydrolase
Comments: Also acts, but more slowly, on a wide range of other monophosphates.
References: [708, 1886, 1887]

[EC 3.1.3.60 created 1992]

[3.1.3.61  Deleted entry. inositol-1,4,5-trisphosphate 1-phosphatase, as its existence has not been established]

[EC 3.1.3.61 created 1992, deleted 2002]

EC 3.1.3.62
Accepted name: multiple inositol-polyphosphate phosphatase
Reaction: myo-inositol hexakisphosphate + H₂O = myo-inositol pentakisphosphate (mixed isomers) + phosphate

48
Other name(s): inositol (1,3,4,5)-tetrakisphosphate 3-phosphatase; inositol 1,3,4,5-tetrakisphosphate 3-phosphomonoesterase; inositol 1,3,4,5-tetrakisphosphate-5-phosphomonoesterase; inositol tetrakisphosphate phosphomonoesterase; inositol-1,3,4,5-tetrakisphosphate 3-phosphatase; MIPP

Systematic name: 1D-my-o-inositol-hexakisphosphate 5-phosphohydrolase

Comments: This enzyme exists in two isoforms. It also acts on Ins(1,3,4,5)P4 to yield Ins(1,4,5)P3.

References: [557, 542]

[EC 3.1.3.62 created 1992, modified 2002]

EC 3.1.3.63

Accepted name: 2-carboxy-D-arabinitol-1-phosphatase

Reaction: 2-carboxy-D-arabinitol 1-phosphate + H2O = 2-carboxy-D-arabinitol + phosphate

Other name(s): 2-carboxy-D-arabinitol 1-phosphatase; 2-carboxy-D-arabinitol 1-phosphate phosphohydrolase

Systematic name: 2-carboxy-D-arabinitol-1-phosphate 1-phosphohydrolase

References: [2640]

[EC 3.1.3.63 created 1992]

EC 3.1.3.64

Accepted name: phosphatidylinositol-3-phosphatase

Reaction: 1-phosphatidyl-D-my-o-inositol 3-phosphate + H2O = 1-phosphatidyl-1D-my-o-inositol + phosphate

Other name(s): inositol-1,3-bisphosphate 3-phosphatase; inositol 1,3-bisphosphate phosphatase; inositol-polyphosphate 3-phosphatase; D-my-o-inositol-1,3-bisphosphate 3-phosphohydrolase; phosphatidylinositol-3-phosphatase

Systematic name: 1-phosphatidyl-D-my-o-inositol-3-phosphate 3-phosphohydrolase

Comments: This enzyme still works when the 2,3-bis(acyloxy)propyl group is removed, i.e., it hydrolyses Ins(1,3)P2 to Ins-1-P.

References: [1807, 384]

[EC 3.1.3.64 created 1992, [EC 3.1.3.65 created 1992, incorporated 2002], modified 2002]

[3.1.3.65 Deleted entry. inositol-1,3-bisphosphate 3-phosphatase. Now included with EC 3.1.3.64, phosphatidylinositol-3-phosphatase]

[EC 3.1.3.65 created 1992, deleted 2002]

EC 3.1.3.66

Accepted name: phosphatidylinositol-3,4-bisphosphate 4-phosphatase

Reaction: 1-phosphatidyl-my-o-inositol 3,4-bisphosphate + H2O = 1-phosphatidyl-1D-my-o-inositol 3-phosphate + phosphate

Other name(s): inositol-3,4-bisphosphate 4-phosphatase; D-my-o-inositol-3,4-bisphosphate 4-phosphohydrolase; phosphoinositide 4-phosphatase; inositol polyphosphate 4-phosphatase; inositol polyphosphate 4-phosphatase type II

Systematic name: 1-phosphatidyl-D-my-o-inositol-3,4-bisphosphate 4-phosphohydrolase

Comments: Mg2+-independent. This enzyme still works when the 2,3-bis(acyloxy)propyl group is removed, i.e., it hydrolyses Ins(1,3,4)P3 to Ins(1,3)P2. It also converts Ins(3,4)P2 into Ins-3-P.

References: [1268, 2220, 2219]

[EC 3.1.3.66 created 1992, modified 2002]

EC 3.1.3.67

Accepted name: phosphatidylinositol-3,4,5-trisphosphate 3-phosphatase
Reaction: 1-phosphatidyl-1D-myoinositol 3,4,5-trisphosphate + H₂O = 1-phosphatidyl-1D-myoinositol 4,5-bisphosphate + phosphate

Other name(s): PTEN; MMAC1; phosphatidylinositol-3,4,5-trisphosphate 3-phosphohydrolase

Systematic name: 1-phosphatidyl-1D-myoinositol-3,4,5-trisphosphate 3-phosphohydrolase

Comments: Requires Mg²⁺. Does not dephosphorylate inositol 4,5-bisphosphate. This enzyme still works when the 2,3-bis(acyloxy)propyl group is removed, i.e., it hydrolyses Ins(1,3,4,5)P₄ to Ins(1,4,5)P₃

References: [1434, 2966]

---

EC 3.1.3.67
Accepted name: 2-deoxyglucose-6-phosphatase
Reaction: 2-deoxy-D-glucose 6-phosphate + H₂O = 2-deoxy-D-glucose + phosphate
Other name(s): 2-deoxyglucose-6-phosphate phosphatase
Systematic name: 2-deoxy-D-glucose-6-phosphate phosphohydrolase
Comments: Also active towards fructose 1-phosphate
References: [1414, 2493]

---

EC 3.1.3.69
Accepted name: glucosylglycerol 3-phosphatase
Reaction: 2-O-(α-D-glucosyl)-sn-glycerol-3-phosphate + H₂O = 2-O-(α-D-glucopyranosyl)glycerol + phosphate
Other name(s): salt tolerance protein A; StpA; 2-(β-D-glucosyl)-sn-glycerol-3-phosphate phosphohydrolase (incorrect)
Systematic name: 2-O-(α-D-glucopyranosyl)-sn-glycerol-3-phosphate phosphohydrolase
Comments: Acts with EC 2.4.1.213 (glucosylglycerol-phosphate synthase) to form glucosylglycerol, an osmolyte that endows cyanobacteria with resistance to salt.
References: [1078, 1079, 1080]

---

EC 3.1.3.70
Accepted name: mannosyl-3-phosphoglycerate phosphatase
Reaction: 2-O-(α-D-mannosyl)-3-phosphoglycerate + H₂O = 2-O-(α-D-mannosyl)-D-glycerate + phosphate
Systematic name: 2-O-(α-D-mannosyl)3-phosphoglycerate phosphohydrolase
Comments: Requires Mg²⁺. The enzyme from Pyrococcus horikoshii is specific for α-D-mannosyl-3-phosphoglycerate and forms part of the pathway for the synthesis of mannosylglycerate.
References: [746]

---

EC 3.1.3.71
Accepted name: 2-phosphosulfolactate phosphatase
Reaction: (2R)-2-phospho-3-sulfolactate + H₂O = (2R)-3-sulfolactate + phosphate
Other name(s): (2R)-phosphosulfolactate phosphohydrolase; ComB phosphatase
Systematic name: (R)-2-phospho-3-sulfolactate phosphohydrolase
Comments: Requires Mg²⁺. The enzyme from Methanococcus jannaschii acts on both stereoisoimers of the substrate and also hydrolyses a number of phosphate monoesters of (S)-2-hydroxycarboxylic acids, including 2-phosphomalate, 2-phosphoacetate and 2-phosphoglycolate. This enzyme can also hydrolyse phosphate monoesters of (R)-2-hydroxycarboxylic acids such as (S)-2-phospho-3-sulfolactate and (R)-2-phosphomalate, which, presumably, bind to the enzyme in opposite orientations.
EC 3.1.3.72

Accepted name: 5-phytase
Reaction: myo-inositol hexakisphosphate + H₂O = 1L-myoinositol 1,2,3,4,6-pentakisphosphate + phosphate
Systematic name: myo-inositol-hexakisphosphate 5-phosphohydrolase
Comments: The enzyme attacks the product of the above reaction more slowly to yield Ins(1,2,3)P₃.
References: [1017, 177]

EC 3.1.3.73

Accepted name: adenosylcobalamin/α-ribazole phosphatase
Reaction: (1) adenosylcobalamin 5′-phosphate + H₂O = coenzyme B₁₂ + phosphate
(2) α-ribazole 5'-phosphate + H₂O = α-ribazole + phosphate
Other name(s): CobC; adenosylcobalamin phosphatase; α-ribazole phosphatase
Systematic name: adenosylcobalamin/α-ribazole-5′-phosphate phosphohydrolase
Comments: This enzyme catalyses the last step in the anaerobic (early cobalt insertion) pathway of adenosylcobalamin biosynthesis, characterized in Salmonella enterica [3478]. It also participates in a salvage pathway that recycles cobinamide into adenosylcobalamin [2323].
References: [2323, 3282, 3478]

EC 3.1.3.74

Accepted name: pyridoxal phosphatase
Reaction: pyridoxal 5′-phosphate + H₂O = pyridoxal + phosphate
Other name(s): vitamine B₆ (pyridoxine) phosphatase; PLP phosphatase; vitamin B₆-phosphate phosphatase; PNP phosphatase
Systematic name: pyridoxal-5′-phosphate phosphohydrolase
Comments: Requires Mg²⁺. This enzyme is specific for phosphorylated vitamin B₆ compounds: it acts not only on pyridoxal phosphate (PLP), but also on pyridoxine phosphate (PNP), pyridoxamine phosphate (PMP), 4-pyridoxic acid phosphate and 4-deoxypyridoxine phosphate. This reaction can also be carried out by EC 3.1.3.1 (alkaline phosphatase) and EC 3.1.3.2 (acid phosphatase), but these enzymes have very broad substrate specificities.
References: [846, 847, 1387]

EC 3.1.3.75

Accepted name: phosphoethanolamine/phosphocholine phosphatase
Reaction: (1) O-phosphoethanolamine + H₂O = ethanolamine + phosphate
(2) phosphocholine + H₂O = choline + phosphate
Other name(s): PHOSPHO1; 3X11A
Systematic name: phosphoethanolamine phosphohydrolase
Comments: Requires active site Mg²⁺ but also works, to a lesser extent, with Co²⁺ and Mn²⁺. The enzyme is highly specific for phosphoethanolamine and phosphocholine.
References: [1263, 2912, 2565]
EC 3.1.3.76

Accepted name: lipid-phosphate phosphatase

Reaction: (9S,10S)-10-hydroxy-9-(phosphoxy)octadecanoate + H₂O = (9S,10S)-9,10-dihydroxyoctadecanoate
+ phosphate

Other name(s): hydroxy fatty acid phosphatase; dihydroxy fatty acid phosphatase; hydroxy lipid phosphatase; sEH (ambiguous); soluble epoxide hydrolase (ambiguous); (9S,10S)-10-hydroxy-9-phosphonoxy)octadecanoyl phosphohydrolase

Systematic name: (9S,10S)-10-hydroxy-9-(phosphoxy)octadecanoyl phosphohydrolase

Comments: Requires Mg²⁺ for maximal activity. The enzyme from mammals is a bifunctional enzyme: the N-terminal domain exhibits lipid-phosphate-phosphatase activity and the C-terminal domain has the activity of EC 3.3.2.10, soluble epoxide hydrolase (sEH) [2181]. The best substrates for this enzyme are 10-hydroxy-9-(phosphoxy)octadecanoates, with the threo-form being a better substrate than the erythro-form [2181]. The phosphatase activity is not found in plant sEH or in EC 3.3.2.9, microsomal epoxide hydrolase, from mammals [2181].

References: [2181, 549, 2078, 3103, 2180, 2889, 1006]

[EC 3.1.3.76 created 2006]

EC 3.1.3.77

Accepted name: acireductone synthase

Reaction: 5-(methylsulfanyl)-2,3-dioxopentyl phosphate + H₂O = 1,2-dihydroxy-5-(methylsulfonyl)pent-1-en-3-one + phosphate (overall reaction)

(1a) 5-(methylsulfanyl)-2,3-dioxopentyl phosphate = 2-hydroxy-5-(methylsulfanyl)-3-oxopent-1-enyl phosphate (probably spontaneous)

(1b) 2-hydroxy-5-(methylsulfanyl)-3-oxopent-1-enyl phosphate + H₂O = 1,2-dihydroxy-5-(methylsulfanyl)pent-1-en-3-one + phosphate

Other name(s): E1; E-1 enolase-phosphatase; 5-(methylthio)-2,3-dioxopentyl-phosphate phosphohydrolase (isomerizing)

Systematic name: 5-(methylsulfanyl)-2,3-dioxopentyl-phosphate phosphohydrolase (isomerizing)

Comments: This bifunctional enzyme first enolizes the substrate to form the intermediate 2-hydroxy-5-(methylsulfanyl)-3-oxopent-1-enyl phosphate, which is then dephosphorylated to form the acireductone 1,2-dihydroxy-5-(methylsulfanyl)pent-1-en-3-one [3369]. The acireductone represents a branch point in the methionine-salvage pathway as it is used in the formation of formate, CO and 3-(methylsulfanyl)propanoate by EC 1.13.11.53 [acireductone dioxygenase (Ni²⁺-requiring)] and of formate and 4-(methylsulfanyl)-2-oxobutanoate either by a spontaneous reaction under aerobic conditions or by EC 1.13.11.54 acireductone dioxygenase [iron(II)-requiring] [2118, 3369].

References: [2118, 3369, 3260]

[EC 3.1.3.77 created 2006]

EC 3.1.3.78

Accepted name: phosphatidylinositol-4,5-bisphosphate 4-phosphatase

Reaction: 1-phosphatidyl-1D-myoinositol 4,5-bisphosphate + H₂O = 1-phosphatidyl-1D-myoinositol 5-phosphate + phosphate

Other name(s): phosphatidylinositol-4,5-bisphosphate 4-phosphatase I; phosphatidylinositol-4,5-bisphosphate 4-phosphatase II; type I PtdIns-4,5-P₂ 4-Phae; type II PtdIns-4,5-P₂ 4-Phae; 1pgD; PtdIns-4,5-P₂ 4-phosphatase type I; PtdIns-4,5-P₂ 4-phosphatase type II; type I phosphatidylinositol-4,5-bisphosphate 4-phosphatase; type 1 4-phosphatase

Systematic name: 1-phosphatidyl-1D-myoinositol-4,5-bisphosphate 4-phosphohydrolase

52
Comments: Two pathways exist in mammalian cells to degrade 1-phosphatidyl-1-D-myo-inositol 4,5-bisphosphate [PtdIns(4,5)P₂] [3162]. One is catalysed by this enzyme and the other by EC 3.1.3.36, phospho-inositide 5-phosphatase, where the product is PtdIns4P. The enzyme from human is specific for PtdIns(4,5)P₂ as substrate, as it cannot use PtdIns(3,4,5)P₃, PtdIns(3,4)P₂, PtdIns(3,5)P₂, PtdIns5P, PtdIns4P or PtdIns3P [3162]. In humans, the enzyme is localized to late endosomal/lysosomal membranes [3162]. It can control nuclear levels of PtdIns5P and thereby control p53-dependent apoptosis [3516].

References: [2189, 3162, 3516, 1930]

EC 3.1.3.79

Accepted name: mannosylfructose-phosphate phosphatase
Reaction: β-D-fructofuranosyl-α-D-mannopyranoside 6F-phosphate + H₂O = β-D-fructofuranosyl-α-D-mannopyranoside + phosphate
Other name(s): mannosylfructose-6-phosphate phosphatase; MFPP
Systematic name: β-D-fructofuranosyl-α-D-mannopyranoside-6F-phosphate phosphohydrolase
Comments: This enzyme, from the soil proteobacterium and plant pathogen Agrobacterium tumefaciens strain C58, requires Mg²⁺ for activity. Mannosylfructose is the major endogenous osmolyte produced by several α-proteobacteria in response to osmotic stress and is synthesized by the sequential action of EC 2.4.1.246 (mannosylfructose-phosphate synthase) followed by this enzyme. While mannosylfructose 6-phosphate is the physiological substrate, the enzyme can use sucrose 6-phosphate very efficiently. The F in mannosylfructose 6F-phosphate is used to indicate that the fructose residue of sucrose carries the substituent.

References: [3092]

EC 3.1.3.80

Accepted name: 2,3-bisphosphoglycerate 3-phosphatase
Reaction: 2,3-bisphospho-D-glycerate + H₂O = 2-phospho-D-glycerate + phosphate
Other name(s): MIPP1; 2,3-BPG 3-phosphatase
Systematic name: 2,3-bisphospho-D-glycerate 3-phosphohydrolase
Comments: This reaction is a shortcut in the Rapoport-Luebering shunt. It bypasses the reactions of EC 5.4.2.11/EC 5.4.2.12 [phosphoglycerate mutases (2,3-diphosphoglycerate-dependent and independent)] and directly forms 2-phospho-D-glycerate by removing the 3-phospho-group of 2,3-diphospho-D-glycerate [472]. The MIPP1 protein also catalyses the reaction of EC 3.1.3.62 (multiple inositol-polyphosphate phosphatase).

References: [472]

[3.1.3.81 Transferred entry. diacylglycerol diphosphate phosphatase. Now EC 3.6.1.75, diacylglycerol diphosphate phosphatase]

[EC 3.1.3.81 created 2010, deleted 2022]

EC 3.1.3.82

Accepted name: D-glycero-β-D-manno-heptose 1,7-bisphosphate 7-phosphatase
Reaction: D-glycero-β-D-manno-heptose 1,7-bisphosphate + H₂O = D-glycero-β-D-manno-heptose 1-phosphate + phosphate
Other name(s): gmbB (gene name); yaeD (gene name)
Systematic name: D-glycero-β-D-manno-heptose 1,7-bisphosphate 7-phosphohydrolase
Comments: The enzyme is involved in biosynthesis of ADP-L-glycero-\(\beta\)-d-manno-heptose, which is utilized for assembly of the lipopolysaccharide inner core in Gram-negative bacteria. In vitro the catalytic efficiency with the \(\beta\)-anomer is 100-200-fold higher than with the \(\alpha\)-anomer [3264].

References: [1569, 3180, 3264]

[EC 3.1.3.82 created 2010]

**EC 3.1.3.83**

**Accepted name:** d-glycero-\(\alpha\)-d-manno-heptose 1,7-bisphosphate 7-phosphatase  
**Reaction:** d-glycero-\(\alpha\)-d-manno-heptose 1,7-bisphosphate + H\(_2\)O = d-glycero-\(\alpha\)-d-manno-heptose 1-phosphate + phosphate  
**Other name(s):**  
**Systematic name:** d-glycero-\(\alpha\)-d-manno-heptose 1,7-bisphosphate 7-phosphohydrolase  
**Comments:** The enzyme is involved in biosynthesis of GDP-d-glycero-\(\alpha\)-d-manno-heptose, which is required for assembly of S-layer glycoprotein in some Gram-positive bacteria. The in vitro catalytic efficiency of the enzyme from *Bacteroides thetaiotaomicron* is 6-fold higher with the \(\alpha\)-anomer than with the \(\beta\)-anomer [3264].

References: [3264]

[EC 3.1.3.83 created 2010]

**EC 3.1.3.84**

**Accepted name:** ADP-ribose 1\(^{\prime}\prime\)-phosphate phosphatase  
**Reaction:** ADP-D-ribose 1\(^{\prime}\prime\)-phosphate + H\(_2\)O = ADP-D-ribose + phosphate  
**Other name(s):** POA1; Appr1p phosphatase; Poa1p; ADP-ribose 1\(^{\prime}\prime\)-phosphate phosphohydrolase  
**Systematic name:** ADP-D-ribose 1\(^{\prime}\)-phosphate phosphohydrolase  
**Comments:** The enzyme is highly specific for ADP-D-ribose 1\(^{\prime}\)-phosphate. Involved together with EC 3.1.4.37, 2',3'-cyclic-nucleotide 3'-phosphodiesterase, in the breakdown of adenosine diphosphate ribose 1\(^{\prime}\),2\(^{\prime}\)-cyclic phosphate (Appr\(\beta\)p), a by-product of tRNA splicing.

References: [2785]

[EC 3.1.3.84 created 2011]

**EC 3.1.3.85**

**Accepted name:** glucosyl-3-phosphoglycerate phosphatase  
**Reaction:** 2-O-(\(\alpha\)-D-glucopyranosyl)-3-phospho-D-glycerate + H\(_2\)O = 2-O-(\(\alpha\)-D-glucopyranosyl)-D-glycerate + phosphate  
**Other name(s):** GpgP protein  
**Systematic name:** \(\alpha\)-D-glucosyl-3-phospho-D-glycerate phosphohydrolase  
**Comments:** The enzyme is involved in biosynthesis of 2-O-(\(\alpha\)-D-glucopyranosyl)-D-glycerate via the two-step pathway in which EC 2.4.1.266 (glucosyl-3-phosphoglycerate synthase) catalyses the conversion of GDP-glucose and 3-phospho-D-glycerate into 2-O-(\(\alpha\)-D-glucopyranosyl)-3-phospho-D-glycerate, which is then converted to 2-O-(\(\alpha\)-D-glucopyranosyl)-D-glycerate by glucosyl-3-phosphoglycerate phosphatase. *In vivo* the enzyme catalyses the dephosphorylation of 2-O-(\(\alpha\)-D-mannopyranosyl)-3-phospho-D-glycerate with lower efficiency [534, 535]. Divalent metal ions (Mg\(^{2+}\), Mn\(^{2+}\) or Co\(^{2+}\)) stimulate activity [534, 535].

References: [534, 535, 1981]

[EC 3.1.3.85 created 2011]

**EC 3.1.3.86**

**Accepted name:** phosphatidylinositol-3,4,5-trisphosphate 5-phosphatase

54
Reaction: 1-phosphatidyl-1-D-myo-inositol 3,4,5-trisphosphate + H₂O = 1-phosphatidyl-1-D-myo-inositol 3,4-bisphosphate + phosphate

Other name(s): SHIP1; SHIP2; SHIP; p150Ship

Systematic name: 1-phosphatidyl-1-D-myo-inositol-3,4,5-trisphosphate 5-phosphohydrolase

Comments: This enzyme hydrolyses 1-phosphatidyl-1-D-myo-inositol 3,4,5-trisphosphate (PtdIns(3,4,5)P₃) to produce PtdIns(3,4)P₂, thereby negatively regulating the PI3K (phosphoinositide 3-kinase) pathways. The enzyme also shows activity toward (PtdIns(1,3,4,5)P₄) [2376]. The enzyme is involved in several signal transduction pathways in the immune system leading to an adverse range of effects.

References: [1805, 574, 979, 694, 2376]

[EC 3.1.3.86 created 2011]

EC 3.1.3.87

Accepted name: 2-hydroxy-3-keto-5-methylthiopentenyl-1-phosphate phosphatase

Reaction: 2-hydroxy-5-(methylsulfanyl)-3-oxopent-1-en-1-yl phosphate + H₂O = 1,2-dihydroxy-5-(methylsulfanyl)pent-1-en-3-one + phosphate

Other name(s): HK-MTPenyl-1-P phosphatase; MtnX; YkrX; 2-hydroxy-5-(methylthio)-3-oxopent-1-enyl phosphate phosphohydrolase; 2-hydroxy-5-(methylsulfanyl)-3-oxopent-1-enyl phosphate phosphohydrolase

Systematic name: 2-hydroxy-5-(methylsulfanyl)-3-oxopent-1-en-1-yl phosphate phosphohydrolase

Comments: The enzyme participates in the methionine salvage pathway in Bacillus subtilis [93]. In some species a single bifunctional enzyme, EC 3.1.3.77, acireductone synthase, catalyses both this reaction and EC 5.3.2.5, 2,3-diketo-5-methylthiopentyl-1-phosphate enolase [2118].

References: [2118, 93]

[EC 3.1.3.87 created 2012]

EC 3.1.3.88

Accepted name: 5′-phosphoribostamycin phosphatase

Reaction: 5′-phosphoribostamycin + H₂O = ribostamycin + phosphate

Other name(s): btrP (gene name); neoI (gene name)

Systematic name: 5′-phosphoribostamycin phosphohydrolase

Comments: Involved in the biosynthetic pathways of several clinically important aminocyclitol antibiotics, including ribostamycin, neomycin and butirosin. No metal is required for activity.

References: [1631]

[EC 3.1.3.88 created 2012]

EC 3.1.3.89

Accepted name: 5′-deoxynucleotidase

Reaction: a 2′-deoxyribonucleoside 5′-monophosphate + H₂O = a 2′-deoxyribonucleoside + phosphate

Other name(s): yfbR (gene name)

Systematic name: 2′-deoxyribonucleoside 5′-monophosphate phosphohydrolase

Comments: The enzyme, characterized from the bacterium Escherichia coli, shows strict specificity towards deoxyribonucleoside 5′-monophosphates and does not dephosphorylate 5′-ribonucleotides or ribonucleoside 3′-monophosphates. A divalent metal cation is required for activity, with cobalt providing the highest activity.

References: [2445, 3509]

[EC 3.1.3.89 created 2013]

EC 3.1.3.90

Accepted name: maltose 6′-phosphate phosphatase

Reaction: maltose 6′-phosphate + H₂O = maltose + phosphate
Other name(s): maltose 6′-P phosphatase; mapP (gene name)
Systematic name: maltose 6′-phosphate phosphohydrolase
Comments: The enzyme from the bacterium Enterococcus faecalis also has activity with the sucrose isomer turanose 6′-phosphate (α-D-glucopyranosyl-(1→3)-D-fructose 6-phosphate).
References: [2048]

[EC 3.1.3.90 created 2013]

EC 3.1.3.91
Accepted name: 7-methylguanosine nucleotidase
Reaction:
1. \( N^7 \)-methyl-GMP + H\(_2\)O = \( N^7 \)-methyl-guanosine + phosphate
2. CMP + H\(_2\)O = cytidine + phosphate
Other name(s): cytosolic nucleotidase III-like; cNIII-like; \( N^7 \)-methylguanylate 5′-phosphatase
Systematic name: \( N^7 \)-methyl-GMP phosphohydrolase
Comments: The enzyme also has low activity with \( N^7 \)-methyl-GDP, producing \( N^7 \)-methyl-GMP. Does not accept AMP or GMP, and has low activity with UMP.
References: [363]

[EC 3.1.3.91 created 2013]

EC 3.1.3.92
Accepted name: kanosamine-6-phosphate phosphatase
Reaction: kanosamine 6-phosphate + H\(_2\)O = kanosamine + phosphate
Other name(s): ntdB (gene name)
Systematic name: kanosamine-6-phosphate phosphohydrolase
Comments: The enzyme, found in the bacterium Bacillus subtilis, is involved in a kanosamine biosynthesis pathway.
References: [3214]

[EC 3.1.3.92 created 2013]

EC 3.1.3.93
Accepted name: L-galactose 1-phosphate phosphatase
Reaction: \( \beta \)-L-galactose 1-phosphate + H\(_2\)O = L-galactose + phosphate
Other name(s): VTC4 (gene name) (ambiguous); IMPL2 (gene name) (ambiguous)
Systematic name: \( \beta \)-L-galactose-1-phosphate phosphohydrolase
Comments: The enzyme from plants also has the activity of EC 3.1.3.25, inositol-phosphate phosphatase. The enzymes have very low activity with D-galactose 1-phosphate (cf. EC 3.1.3.94, D-galactose 1-phosphate phosphatase).
References: [1681, 3091, 2380]

[EC 3.1.3.93 created 2014]

EC 3.1.3.94
Accepted name: D-galactose 1-phosphate phosphatase
Reaction: \( \alpha \)-D-galactose 1-phosphate + H\(_2\)O = D-galactose + phosphate
Systematic name: \( \alpha \)-D-galactose-1-phosphate phosphohydrolase
Comments: The human enzyme also has the activity of EC 3.1.3.25, inositol-phosphate phosphatase. The enzyme has very low activity with L-galactose 1-phosphate (cf. EC 3.1.3.93, L-galactose 1-phosphate phosphatase).
References: [2354]

[EC 3.1.3.94 created 2014]
EC 3.1.3.95
Accepted name: phosphatidylinositol-3,5-bisphosphate 3-phosphatase
Reaction: 1-phosphatidyl-1D-myoinositol 3,5-bisphosphate + H₂O = 1-phosphatidyl-1D-myoinositol 5-phosphate + phosphate
Other name(s): MTMR; PtdIns-3,5-P₂ 3-Ptase
Systematic name: 1-phosphatidyl-1D-myoinositol-3,5-bisphosphate 3-phosphohydrolase
Comments: The enzyme is found in both plants and animals. It also has the activity of EC 3.1.3.64 (phosphatidylinositol-3-phosphatase).
References: [3244, 211, 663]

[EC 3.1.3.95 created 2014]

EC 3.1.3.96
Accepted name: pseudouridine 5′-phosphatase
Reaction: pseudouridine 5′-phosphate + H₂O = pseudouridine + phosphate
Other name(s): pseudouridine 5′-monophosphatase; 5′-PsiMPase; HDHD1
Systematic name: pseudouridine 5′-phosphohydrolase
Comments: Requires Mg²⁺ for activity.
References: [2442]

[EC 3.1.3.96 created 2014]

EC 3.1.3.97
Accepted name: 3′,5′-nucleoside bisphosphate phosphatase
Reaction: nucleoside 3′,5′-bisphosphate + H₂O = nucleoside 5′-phosphate + phosphate
Systematic name: nucleoside-3′,5′-bisphosphate 3′-phosphohydrolase
Comments: The enzyme, characterized from the bacterium Chromobacterium violaceum, has similar catalytic efficiencies with all the bases. The enzyme has similar activity with ribonucleoside and 2′-deoxyribonucleoside 3′,5′-bisphosphates, but shows no activity with nucleoside 2′,5′-bisphosphates (cf. EC 3.1.3.7, 3′(2′),5′-bisphosphate nucleotidase).
References: [558]

[EC 3.1.3.97 created 2015]

[3.1.3.98 Transferred entry. geranyl diphosphate phosphohydrolase, transferred to EC 3.6.1.68, geranyl diphosphate phosphohydrolase]

[EC 3.1.3.98 created 2015, deleted 2016]

EC 3.1.3.99
Accepted name: IMP-specific 5′-nucleotidase
Reaction: IMP + H₂O = inosine + phosphate
Other name(s): ISN1 (gene name)
Systematic name: inosine 5′-phosphate phosphohydrolase
Comments: The enzyme, isolated from the yeast Saccharomyces cerevisiae, is highly specific for inosine 5′-phosphate, and has no detectable activity with other purine and pyrimidine nucleotides. Requires divalent metals, such as Mg²⁺, Co²⁺ or Mn²⁺.
References: [1349, 1350]

[EC 3.1.3.99 created 2016]

EC 3.1.3.100
Accepted name: thiamine phosphate phosphatase
**Reaction:** thiamine phosphate + H₂O = thiamine + phosphate  
**Systematic name:** thiamine phosphate phosphohydrolase  
**Comments:** The enzyme participates in the thiamine biosynthesis pathway in eukaryotes and a few prokaryotes. These organisms lack EC 2.7.4.16, thiamine-phosphate kinase, and need to convert thiamine phosphate to thiamine diphosphate, the active form of the vitamin, by first removing the phosphate group, followed by diphosphorylation by EC 2.7.6.2, thiamine diphosphokinase.  
**References:** [2644, 1592, 2729, 2099, 1588, 2018]

**EC 3.1.3.101**  
**Accepted name:** validoxylamine A 7′-phosphate phosphatase  
**Reaction:** validoxylamine A 7′-phosphate + H₂O = validoxylamine A + phosphate  
**Other name(s):** vldH (gene name)  
**Systematic name:** validoxylamine-A 7′-phosphate phosphohydrolase  
**Comments:** The enzyme, characterized from the bacterium *Streptomyces hygroscopicus* subsp. *limoneus*, is involved in the biosynthesis of the antifungal agent validamycin A.  
**References:** [88]

**EC 3.1.3.102**  
**Accepted name:** FMN hydrolase  
**Reaction:** FMN + H₂O = riboflavin + phosphate  
**Other name(s):** FMN phosphatase; AtcpFHy1  
**Systematic name:** FMN phosphohydrolase  
**Comments:** Requires Mg²⁺. The enzyme, found in many isoforms purified from both bacteria and plants, is a member of the haloacid dehalogenase superfamily. Most of the isoforms have a wide substrate specificity [1670], but isoforms specific for FMN also exist [2505].  
**References:** [2643, 1670, 2505]

**EC 3.1.3.103**  
**Accepted name:** 3-deoxy-D-glycero-D-galacto-nonulopyranosonate 9-phosphatase  
**Reaction:** 3-deoxy-D-glycero-D-galacto-nonulopyranosonate 9-phosphate + H₂O = 3-deoxy-D-glycero-D-galacto-non-2-ulopyranosonate + phosphate  
**Other name(s):** 3-deoxy-D-glycero-D-galacto-non-2-ulopyranosonate-9-phosphate phosphatase  
**Systematic name:** 3-deoxy-D-glycero-D-galacto-non-2-ulopyranosonate 9-phosphohydrolase  
**Comments:** The enzyme, characterized from the bacterium *Bacteroides thetaiotaomicron*, 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:** [3265, 1845]

**EC 3.1.3.104**  
**Accepted name:** 5-amino-6-(5-phospho-D-ribitylamino)uracil phosphatase  
**Reaction:** 5-amino-6-(5-phospho-D-ribitylamino)uracil + H₂O = 5-amino-6-(D-ribitylamino)uracil + phosphate  
**Other name(s):** 5-amino-6-ribitylaminoc-2,4(1H,3H)-pyrimidinedione 5'-phosphate phosphatase  
**Systematic name:** 5-amino-6-(5-phospho-D-ribitylamino)uracil phosphohydrolase
Comments: Requires Mg\(^{2+}\). The enzyme, which is found in plants and bacteria, is part of a pathway for riboflavin biosynthesis. Most forms of the enzyme has a broad substrate specificity [1072, 2657].

References: [1072, 1832, 2657]

[EC 3.1.3.104 created 2016]

EC 3.1.3.105
Accepted name: N-acetyl-D-muramate 6-phosphate phosphatase
Reaction: N-acetyl-D-muramate 6-phosphate + H\(_2\)O = N-acetyl-D-muramate + phosphate
Other name(s): mapP (gene name)
Systematic name: N-acetyl-D-muramate 6-phosphate phosphohydrolase
Comments: The enzyme, characterized from Pseudomonas species, participates in a peptidoglycan salvage pathway.
References: [290]

[EC 3.1.3.105 created 2017]

EC 3.1.3.106
Accepted name: 2-lysophosphatidylate phosphatase
Reaction: a 1-acyl-sn-glycerol 3-phosphate + H\(_2\)O = a 1-acyl-sn-glycerol + phosphate
Other name(s): 1-acyl-sn-glycerol 3-phosphatase; CPC3 (gene name); PHM8 (gene name)
Systematic name: 1-acyl-sn-glycerol 3-phosphate phosphohydrolase
Comments: The enzyme has been studied from the plants Arachis hypogaea (peanut) and Arabidopsis thaliana (thale cress) and from the yeast Saccharomyces cerevisiae. The enzyme from yeast, but not from the plants, requires Mg\(^{2+}\).
References: [2759, 2519, 2518]

[EC 3.1.3.106 created 2019]

EC 3.1.3.107
Accepted name: amicoumacin phosphatase
Reaction: amicoumacin A 2-phosphate + H\(_2\)O = amicoumacin A + phosphate
Other name(s): amiO (gene name)
Systematic name: amicoumacin 2-phosphate phosphohydrolase
Comments: This bacterial enzyme activates the antibiotic amicoumacin A by removing a phosphate group that is added by EC 2.7.1.230, amicoumacin kinase.
References: [3045]

[EC 3.1.3.107 created 2019]

EC 3.1.3.108
Accepted name: nocturnin
Reaction: (1) NADPH + H\(_2\)O = NADH + phosphate
(2) NADP\(^+\) + H\(_2\)O = NAD\(^+\) + phosphate
Other name(s): NOCT (gene name); nocturnin (curled); MJ0109 (gene name); NADP phosphatase; NADPase
Systematic name: NADPH 2\(^-\)-phosphohydrolase
Comments: The mammalian mitochondrial enzyme is a rhythmically expressed protein that regulates metabolism under the control of circadian clock. It has a slight preference for NADPH over NADP\(^+\). The archaeal enzyme, identified in Methanocaldococcus jannaschii, is bifunctional acting as NAD\(^+\) kinase (EC 2.7.1.23) and NADP\(^+\) phosphatase with a slight preference for NADP\(^+\) over NADPH.
References: [1489, 9, 772, 771]

[EC 3.1.3.108 created 2020]
EC 3.1.3.109

Accepted name: ribulose-1,5-bisphosphate 5-phosphatase
Reaction: D-ribulose-1,5-bisphosphate + H₂O = D-ribulose 1-phosphate + phosphate
Other name(s): RuBP 5-phosphatase
Systematic name: D-ribulose-1,5-bisphosphate 5-phosphohydrolase
Comments: The enzyme, characterized from the halophilic archaeon *Halopiger xanaduensis*, participates in a non-carboxylating pentose bisphosphate pathway for nucleoside degradation, which is found in some halophilic archaea. The enzyme requires both monovalent and divalent ions for optimal activity.
References: [2667]

[EC 3.1.3.109 created 2022]

EC 3.1.4 Phosphoric-diester hydrolases

EC 3.1.4.1

Accepted name: phosphodiesterase I
Reaction: Hydrolytically removes 5′-nucleotides successively from the 3′-hydroxy termini of 3′-hydroxy-terminated oligonucleotides
Other name(s): 5′-exonuclease; 5′-phosphodiesterase; 5′-nucleotide phosphodiesterase; oligonucleotide 5′-nucleotidohydrolase; 5′-nucleotide phosphodiesterase/alkaline phosphodiesterase I; 5′-NPDase; 5′-PDE; 5′NPDE; alkaline phosphodiesterase; nucleotide pyrophosphatase/phosphodiesterase I; orthophosphoric diester phosphohydrolase; PDE I; phosphodiesterase (ambiguous); exonuclease I
Systematic name: oligonucleotide 5′-nucleotidohydrolase
Comments: Hydrolyses both ribonucleotides and deoxyribonucleotides. Has low activity towards polynucleotides. A 3′-phosphate terminus on the substrate inhibits hydrolysis.
References: [1519]

[EC 3.1.4.1 created 1961]

EC 3.1.4.2

Accepted name: glycerophosphocholine phosphodiesterase
Reaction: sn-glycero-3-phosphocholine + H₂O = choline + sn-glycerol 3-phosphate
Other name(s): glycerophosphinicococile diesterase; glycerylphosphorylcholinediesterase; sn-glycerol-3-phosphorylcholine diesterase; glycerolphosphorylcholine phosphodiesterase; glycerophosphohydrolase
Systematic name: sn-glycero-3-phosphocholine glycerophosphohydrolase
Comments: Also acts on sn-glycerol-3-phosphoethanolamine.
References: [592, 1148, 3296]

[EC 3.1.4.2 created 1961, modified 1976]

EC 3.1.4.3

Accepted name: phospholipase C
Reaction: a phosphatidylycerine + H₂O = 1,2-diacyl-sn-glycerol + phosphocholine
Other name(s): lipophosphodiesterase I; lecithinase C; *Clostridium welchii* α-toxin; *Clostridium oedematiens* β- and γ-toxins; lipophosphodiesterase C; phosphatidase C; heat-labile hemolysin; α-toxin
Systematic name: phosphatidylycerine cholinephosphohydrolase
Comments: The bacterial enzyme, which is a zinc protein, also acts on sphingomyelin and phosphatidylinositol; that from seminal plasma does not act on phosphatidylinositol.
References: [700, 1808, 2758, 2987]

[EC 3.1.4.3 created 1961]
EC 3.1.4.4

**Accepted name:** phospholipase D  
**Reaction:** a phosphatidylcholine + H\(_2\)O = choline + a phosphatidate  
**Other name(s):** lipophosphodiesterase II; lecithinase D; choline phosphatase  
**Systematic name:** phosphatidylcholine phosphatidohydrolase  
**Comments:** Also acts on other phosphatidyl esters.  
**References:** [98, 730, 1104, 3090]

[EC 3.1.4.4 created 1961]

3.1.4.5  
**Transferred entry. deoxyribonuclease. Now EC 3.1.21.1, deoxyribonuclease I**

[EC 3.1.4.5 created 1961, deleted 1978]

3.1.4.6  
**Transferred entry. deoxyribonuclease II. Now EC 3.1.22.1, deoxyribonuclease II**

[EC 3.1.4.6 created 1961, deleted 1978]

3.1.4.7  
**Transferred entry. micrococal nuclease. Now EC 3.1.31.1, micrococal nuclease**

[EC 3.1.4.7 created 1961, deleted 1978]

3.1.4.8  
**Transferred entry. Aspergillus oryzae ribonuclease. Now EC 3.1.27.3, ribonuclease T1**

[EC 3.1.4.8 created 1961, transferred 1965 to EC 2.7.7.26, reinstated 1972, deleted 1978]

3.1.4.9  
**Transferred entry. nucleate endonuclease. Now EC 3.1.30.2, Serratia marcescens nuclease**

[EC 3.1.4.9 created 1965, deleted 1978]

3.1.4.10  
**Transferred entry. 1-phosphatidylinositol phosphodiesterase. Now EC 4.6.1.13, phosphatidylinositol diacylglycerol-lyase. As there is no hydrolysis of the inositol 1,2-cyclic phosphate formed, previous classification of the enzyme as a hydrolase was incorrect**

[EC 3.1.4.10 created 1972, modified 1976, deleted 2002]

EC 3.1.4.11

**Accepted name:** phosphoinositide phospholipase C  
**Reaction:** 1-phosphatidyl-1D-myoinositol 4,5-bisphosphate + H\(_2\)O = 1D-myoinositol 1,4,5-trisphosphate + diacylglycerol  
**Other name(s):** triphosphoinositide phosphodiesterase; phosphoinositidase C; 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase; monophosphatidylinositol phosphodiesterase; phosphatidylinositol phospholipase C; PI-PLC; 1-phosphatidyl-1D-myoinositol-4,5-bisphosphate inositoltrisphosphohydrolase  
**Systematic name:** 1-phosphatidyl-1D-myoinositol-4,5-bisphosphate inositoltrisphosphohydrolase  
**Comments:** These enzymes form some of the cyclic phosphate Ins(cyclic1,2)P(4,5)P\(_2\) as well as Ins(1,4,5)P\(_3\). They show activity towards phosphatidylinositol, i.e., the activity of EC 4.6.1.13, phosphatidylinositol diacylglycerol-lyase, in vitro at high [Ca\(_{2+}\)]. Four \(\beta\)-isoforms regulated by G-proteins, two \(\gamma\)-forms regulated by tyrosine kinases, four \(\delta\)-forms regulated at least in part by calcium and an \(\epsilon\)-form, probably regulated by the oncogene ras, have been found.  
**References:** [686, 3059, 2541]

[EC 3.1.4.11 created 1972, modified 2002]

EC 3.1.4.12

**Accepted name:** sphingomyelin phosphodiesterase  
**Reaction:** a sphingomyelin + H\(_2\)O = a ceramide + phosphocholine  
**Other name(s):** neutral sphingomyelinase

61
**Systematic name:** sphingomyelin cholinephosphohydrolase  
**Comments:** Has very little activity on phosphatidylcholine.  
**References:** [163, 438, 1176, 1467]

[EC 3.1.4.12 created 1972]

**EC 3.1.4.13**  
**Accepted name:** serine-ethanolaminephosphate phosphodiesterase  
**Reaction:** serine phosphoethanolamine + H₂O = serine + ethanolamine phosphate  
**Other name(s):** serine ethanolamine phosphodiester phosphodiesterase; SEP diesterase  
**Systematic name:** serine-phosphoethanolamine ethanolaminophosphohydrolase  
**Comments:** Acts only on those phosphodiesters that have ethanolamine as a component part of the molecule.  
**References:** [1082]

[EC 3.1.4.13 created 1972, modified 1976]

**EC 3.1.4.14**  
**Accepted name:** [acyl-carrier-protein] phosphodiesterase  
**Reaction:** holo-[acyl-carrier protein] + H₂O = 4′-phosphopantetheine + apo-[acyl-carrier protein]  
**Other name(s):** ACP hydrolyase; ACP phosphodiesterase; AcpH; [acyl-carrier-protein] 4′-pantetheine-phosphohydrolase  
**Systematic name:** holo-[acyl-carrier protein] 4′-pantetheine-phosphohydrolase  
**Comments:** The enzyme cleaves acyl-[acyl-carrier-protein] species with acyl chains of 6-16 carbon atoms although it appears to demonstrate a preference for the unacylated acyl-carrier protein (ACP) and short-chain ACPs over the medium- and long-chain species [3055]. Deletion of the gene encoding this enzyme abolishes ACP prosthetic-group turnover in vivo [3055]. Activation of apo-ACP to form the holoenzyme is carried out by EC 2.7.8.7, holo-[acyl-carrier-protein] synthase.  
**References:** [2846, 3176, 3055]

[EC 3.1.4.14 created 1972, modified 2006]

**3.1.4.15  Transferred entry. adenylyl-[glutamateammonia ligase] hydrolase. As it has been shown that the enzyme catalyses a transfer of the adenylyl group to phosphate, the enzyme has been transferred to EC 2.7.7.89, adenylyl-[glutamateammonia ligase] phosphorylase**

[EC 3.1.4.15 created 1972, deleted 2015]

**EC 3.1.4.16**  
**Accepted name:** 2′,3′-cyclic-nucleotide 2′-phosphodiesterase  
**Reaction:** nucleoside 2′,3′-cyclic phosphate + H₂O = nucleoside 3′-phosphate  
**Other name(s):** ribonucleoside 2′,3′-cyclic phosphate diesterase; 2′,3′ : -cyclic AMP phosphodiesterase; 2′,3′-cyclic nucleotidase; cyclic 2′,3′-nucleotide 2′-phosphodiesterase; cyclic 2′,3′-nucleotide phosphodiesterase; 2′,3′-cyclic nucleoside monophosphate phosphodiesterase; 2′,3′-cyclic AMP 2′-phosphohydrolase; cyclic phosphodiesterase; 2′,3′-cyclic nucleotide phosphohydrolase; 2′,3′-cyclic phosphodiesterase; 2′,3′-cyclic nucleotide phosphodiesterase; 3′-nucleotidase  
**Systematic name:** nucleoside-2′,3′-cyclic-phosphate 3′-nucleotidohydrolase  
**Comments:** Also hydrolyses 3′-nucleoside monophosphates and bis-4-nitrophenyl phosphate, but not 3′-deoxynucleotides. Similar reactions are carried out by EC 4.6.1.24 (ribonuclease T₁) and EC 4.6.1.18 (pancreatic ribonuclease).  
**References:** [61, 62, 416, 2300, 3160]

[EC 3.1.4.16 created 1972, modified 1976]
EC 3.1.4.17

**Accepted name:** 3′,5′-cyclic-nucleotide phosphodiesterase

**Reaction:** nucleoside 3′,5′-cyclic phosphate + H₂O = nucleoside 5′-phosphate

**Other name(s):** cyclic 3′,5′-mononucleotide phosphodiesterase; PDE; cyclic 3′,5′-nucleotide phosphodiesterase; cyclic 3′,5′-nucleotide phosphodiesterase; 3′:5′-cyclic nucleotide 5′-nucleotidohydrolase; 3′,5′-cyclonucleotide phosphodiesterase; cyclic nucleotide phosphodiesterase; 3′, 5′-cyclic nucleoside monophosphate phosphodiesterase; 3′: 5′-monophosphate phosphodiesterase (cyclic CMP); cytidine 3′:5′-monophosphate phosphodiesterase (cyclic CMP); cyclic 3′,5′-nucleotide monophosphate phosphodiesterase; nucleoside 3′,5′-cyclic phosphate diesterase; nucleoside-3′,5′-monophosphate phosphodiesterase

**Systematic name:** 3′,5′-cyclic-nucleotide 5′-nucleotidohydrolase

**Comments:** Acts on 3′,5′-cyclic AMP, 3′,5′-cyclic dAMP, 3′,5′-cyclic IMP, 3′,5′-cyclic GMP and 3′,5′-cyclic CMP.

**References:** [825, 2132]

[EC 3.1.4.17 created 1972, modified 1976]
**3.1.4.30** Transferred entry. endodeoxyribonuclease. Now EC 3.1.21.2, deoxyribonuclease IV (phage-T4-induced)

[EC 3.1.4.30 created 1972, deleted 1978]

**3.1.4.31** Transferred entry. DNA 5′-dinucleotidohydrolase. Now EC 3.1.11.4, exodeoxyribonuclease (phage SP3-induced)

[EC 3.1.4.31 created 1972, deleted 1978]

**3.1.4.32** Deleted entry. endodeoxyribonuclease (ATP- and S-adenosylmethionine-dependent). See EC 3.1.21.3 type 1 site-specific deoxyribonuclease and EC 3.1.21.5 type III site-specific deoxyribonuclease

[EC 3.1.4.32 created 1972, deleted 1978]

**3.1.4.33** Deleted entry. endodeoxyribonuclease (ATP-hydrolysing). See EC 3.1.21.3 type 1 site-specific deoxyribonuclease and EC 3.1.21.5 type III site-specific deoxyribonuclease

[EC 3.1.4.33 created 1972, deleted 1978]

**3.1.4.34** Deleted entry. hybrid nuclease. See sub-subclasses EC 3.1.15, EC 3.1.16, EC 3.1.30 and EC 3.1.31.

[EC 3.1.4.34 created 1972, deleted 1978]

**3.1.4.35**

Accepted name: 3′,5′-cyclic-GMP phosphodiesterase

Reaction: guanosine 3′,5′-cyclic phosphate + H₂O = GMP

Other name(s): guanosine cyclic 3′,5′-phosphate phosphodiesterase; cyclic GMP phosphodiesterase; cyclic 3′,5′-GMP phosphodiesterase; cyclic guanosine 3′,5′-monophosphate phosphodiesterase; cyclic guanosine 3′,5′-phosphate phosphodiesterase; cGMP phosphodiesterase; cGMP-PDE

Systematic name: 3′,5′-cyclic-GMP 5′-nucleotidohydrolase

References: [1912]

[EC 3.1.4.35 created 1976]

**3.1.4.36**

Deleted entry. 1,2-cyclic-inositol-phosphate phosphodiesterase. Now included with EC 3.1.4.43, glycerophosphoinositol inositolphosphodiesterase

[EC 3.1.4.36 created 1976, deleted 2002]

**3.1.4.37**

Accepted name: 2′,3′-cyclic-nucleotide 3′-phosphodiesterase

Reaction: nucleoside 2′,3′-cyclic phosphate + H₂O = nucleoside 2′-phosphate

Other name(s): cyclic-CMP phosphodiesterase; 2′,3′-cyclic AMP phosphodiesterase; cyclic 2′,3′-nucleotide 3′-phosphodiesterase; cyclic 2′,3′-nucleotide phosphodiesterase; cyclic 2′,3′-cyclic monophosphate phosphodiesterase; cyclic 2′,3′-cyclic nucleotide 3′-phosphohydrolase; CNPase; 2′,3′-cyclic nucleotide phosphohydrolase; 2′,3′-cyclic nucleotide 3′-phosphodiesterase; 2′,3′-CNMP-3′-ase

Systematic name: nucleoside-2′,3′-cyclic-phosphate 2′-nucleotidohydrolase

Comments: The brain enzyme acts on 2′,3′-cyclic AMP more rapidly than on the UMP or CMP derivatives. An enzyme from liver acts on 2′,3′-cyclic CMP more rapidly than on the purine derivatives; it also hydrolyses the corresponding 3′,5′-cyclic phosphates, but more slowly. This latter enzyme has been called cyclic-CMP phosphodiesterase.

References: [698, 1174, 1175, 1659, 2205]

[EC 3.1.4.37 created 1976]

**3.1.4.38**

Accepted name: glycerophosphocholine cholinephosphodiesterase

Reaction: \(sn\)-glycero-3-phosphocholine + H₂O = glycerol + phosphocholine

[EC 3.1.4.38 created 1976]
### Other name(s): L-3-glycerolphosphinicocholine cholinephosphohydrolase
**Systematic name:** \( sn-glycero-3 \)-phosphocholine cholinephosphohydrolase
**Comments:** No activity on \( sn-3 \)-glycerophosphoethanolamine.
**References:** [8]

[EC 3.1.4.38 created 1976]

### EC 3.1.4.39
**Accepted name:** alkylglycerolphosphoethanolamine phosphodiesterase
**Reaction:** 1-alkyl-\( sn \)-glycero-3-phosphoethanolamine + H\(_2\)O = 1-alkyl-\( sn \)-glycerol 3-phosphate + ethanolamine
**Other name(s):** lysophospholipase D
**Systematic name:** 1-alkyl-\( sn \)-glycero-3-phosphoethanolamine ethanolaminehydrolase
**Comments:** Also acts on acyl and choline analogues.
**References:** [3381]

[EC 3.1.4.39 created 1976]

### EC 3.1.4.40
**Accepted name:** CMP-N-acylneuraminate phosphodiesterase
**Reaction:** CMP-N-acylneuraminate + H\(_2\)O = CMP + N-acylneuraminate
**Other name(s):** CMP-sialate hydrolase; CMP-sialic acid hydrolase; CMP-N-acylneuraminic acid hydrolase; cytidine monophosphosialic hydrolase; cytidine monophosphosialolate hydrolase; cytidine monophosphate-N-acylneuraminic acid hydrolase; CMP-N-acetylneuraminic acid hydrolase
**Systematic name:** CMP-N-acylneuraminate N-acylneuraminohydrolase
**References:** [1493]

[EC 3.1.4.40 created 1976]

### EC 3.1.4.41
**Accepted name:** sphingomyelin phosphodiesterase D
**Reaction:** sphingomyelin + H\(_2\)O = ceramide phosphate + choline
**Other name(s):** sphingomyelinase D
**Systematic name:** sphingomyelin ceramide-phosphohydrolase
**Comments:** Does not act on phosphatidylcholine, but hydrolyses 2-lysophosphatidylcholine to choline and 2-lysophosphatidate.
**References:** [405, 2870]

[EC 3.1.4.41 created 1978]

### EC 3.1.4.42
**Accepted name:** glycerol-1,2-cyclic-phosphate 2-phosphodiesterase
**Reaction:** glycerol 1,2-cyclic phosphate + H\(_2\)O = glycerol 1-phosphate
**Other name(s):** rac-glycerol 1:2-cyclic phosphate 2-phosphodiesterase
**Systematic name:** rac-glycerol-1,2-cyclic-phosphate 2-glycerophosphohydrolase
**Comments:** Acts on both stereoisomers of the substrate and also, more slowly, on 3′,5′-cyclic AMP and on 2′,3′-cyclic AMP.
**References:** [498]

[EC 3.1.4.42 created 1984]

### EC 3.1.4.43
**Accepted name:** glycerophosphoinositol inositolphosphodiesterase
Reaction: 1-(sn-glycero-3-phospho)-1D-myoinositol + H₂O = glycerol + 1D-myoinositol 1-phosphate

Other name(s): 1,2-cyclic-inositol-phosphate phosphodiesterase; D-myoinositol 1,2-cyclic phosphate 2-phosphohydrolase; D-myoinositol 1,2-cyclic phosphate 2-phosphohydrolase; 1-D-myoinositol-1,2-cyclic-phosphate 2-inositolphosphohydrolase; inositol-1,2-cyclic-phosphate 2-inositolphosphohydrolase

Systematic name: 1-(sn-glycero-3-phospho)-1D-myoinositol inositolphosphohydrolase

Comments: This enzyme also hydrolysates Ins(cyclic1,2)P to Ins-1-P

References: [596, 599, 595, 2590]

EC 3.1.4.43 created 1984, (EC 3.1.4.36 created 1976, incorporated 2002), modified 2002

EC 3.1.4.44

Accepted name: glycerophosphoinositol glycerophosphodiesterase

Reaction: 1-(sn-glycero-3-phospho)-1D-myoinositol + H₂O = myoinositol + sn-glycerol 3-phosphate

Other name(s): sn-glycero(3)phosphoinositol glycerophosphohydrolase; sn-glycero-3-phospho-1-inositol glycerophosphohydrolase

Systematic name: 1-(sn-glycero-3-phospho)-1D-myoinositol glycerophosphohydrolase

References: [597]

[EC 3.1.4.44 created 1984, modified 2002]

EC 3.1.4.45

Accepted name: N-acetylglucosamine-1-phosphodiester α-N-acetylglucosaminidase

Reaction: glycoprotein N-acetyl-D-glucosaminyl-phospho-D-mannose + H₂O = N-acetyl-D-glucosamine + glycoprotein phospho-D-mannose

Other name(s): α-N-acetylglucosaminyl phosphodiesterase; lysosomal α-N-acetylglucosaminidase; phosphodiester glycosidase; α-N-acetyl-D-glucosamine-1-phosphodiester N-acetylglucosaminidase; 2-acetamido-2-deoxy-α-D-glucose 1-phosphodiester acetamido-2-deoxyglucohydrolase

Systematic name: glycoprotein-N-acetyl-D-glucosaminyl-phospho-D-mannose N-acetyl-D-glucosaminylphosphohydrolase

Comments: Acts on a variety of compounds in which N-acetyl-D-glucosamine is α-linked to a phosphate group, including the biosynthetic intermediates of the high mannose oligosaccharide components of some lysosomal enzymes and the products of EC 2.7.8.17 UDP-N-acetylglucosamine—lysosomal-enzyme N-acetylglucosaminephosphotransferase.

References: [623, 3186, 3188, 3234]

[EC 3.1.4.45 created 1984]

EC 3.1.4.46

Accepted name: glycerophosphodiester phosphodiesterase

Reaction: a glycerophosphodiester + H₂O = an alcohol + sn-glycerol 3-phosphate

Other name(s): gene hpd protein; glycerophosphoryl diester phosphodiesterase; IgD-binding protein D

Systematic name: glycerophosphodiester glycerophosphohydrolase

Comments: Broad specificity for glycerophosphodiesters; glycerophosphocholine, glycerophosphoethanolamine, glycerophosphoglycerol and bis(glycerophospho)-glycerol are hydrolysed.

References: [1698]

[EC 3.1.4.46 created 1986]

[3.1.4.47 Transferred entry. variant-surface-glycoprotein phospholipase C. Now EC 4.6.1.14, glycosylphosphatidylinositol diacylglycerol-lyase]

[EC 3.1.4.47 created 1989, deleted 2002]
EC 3.1.4.48  
**Accepted name:** dolichylphosphate-glucose phosphodiesterase  
**Reaction:** dolichyl β-D-glucosyl phosphate + H_2O = dolichyl phosphate + D-glucose  
**Other name(s):** dolichol phosphoglucone phosphodiesterase; Dol-P-Glc phosphodiesterase  
**Systematic name:** dolichyl-β-D-glucosyl-phosphate dolichylphosphohydrolase  
**References:** [543]  

[EC 3.1.4.48 created 1989]

EC 3.1.4.49  
**Accepted name:** dolichylphosphate-mannose phosphodiesterase  
**Reaction:** dolichyl β-D-mannosyl phosphate + H_2O = dolichyl phosphate + D-mannose  
**Other name(s):** mannosylphosphodolichol phosphodiesterase  
**Systematic name:** dolichyl-β-D-mannosyl-phosphate dolichylphosphohydrolase  
**References:** [3080]  

[EC 3.1.4.49 created 1990]

EC 3.1.4.50  
**Accepted name:** glycosylphosphatidylinositol phospholipase D  
**Reaction:** 6-(α-D-glucosaminyl)-1-phosphatidyl-D-myo-inositol + H_2O = 6-(α-D-glucosaminyl)-1-D-myo-inositol + 3-sn-phosphatidate  
**Other name(s):** GPI-PLD; glycoprotein phospholipase D; phosphatidylinositol phospholipase D; phosphatidylinositol-specific phospholipase D  
**Systematic name:** glycoprotein-phosphatidylinositol phosphatidohydrolase  
**Comments:** This enzyme is also active when O-4 of the glucosamine is substituted by carrying the oligosaccharide that can link a protein to the structure. It therefore cleaves proteins from the lipid part of the glycosylphosphatidylinositol (GPI) anchors, but does so by hydrolysis, whereas glycosylphosphatidylinositol diacylglycerol-lyase (EC 4.6.1.14) does so by elimination. It acts on plasma membranes only after solubilization of the substrate with detergents or solvents, but it may act on intracellular membranes.  
**References:** [1840, 1889, 1756, 609]  

[EC 3.1.4.50 created 1990, modified 2002]

EC 3.1.4.51  
**Accepted name:** glucose-1-phospho-D-mannosylglycoprotein phosphodiesterase  
**Reaction:** 6-(D-glucose-1-phospho)-D-mannosylglycoprotein + H_2O = α-D-glucose 1-phosphate + D-mannosylglycoprotein  
**Other name(s):** α-glucose-1-phosphate phosphodiesterase  
**Systematic name:** 6-(D-glucose-1-phospho)-D-mannosylglycoprotein glucose-1-phosphohydrolase  
**Comments:** The enzyme is specific for the product of EC 2.7.8.19 UDP-glucose—glycoprotein glucose phosphotransferase.  
**References:** [2888]  

[EC 3.1.4.51 created 1992]

EC 3.1.4.52  
**Accepted name:** cyclic-guanylate-specific phosphodiesterase  
**Reaction:** cyclic di-3′,5′-guanylate + H_2O = 5′-phosphoguananylyl(3′→5′)guanosine  
**Other name(s):** cyclic bis(3′→5′)guanylate phosphodiesterase; c-di-GMP-specific phosphodiesterase; c-di-GMP phosphodiesterase; phosphodiesterase (misleading); phosphodiesterase A1; PDEA1; VieA  
**Systematic name:** cyclic bis(3′→5′)guanylate 3′-guanylylhydrolase
Comments: Requires Mg\(^{2+}\) or Mn\(^{2+}\) for activity and is inhibited by Ca\(^{2+}\) and Zn\(^{2+}\). Contains a heme unit. This enzyme linearizes cyclic di-3',5'-guanylate, the product of EC 2.7.7.65, diguanylate cyclase and an allosteric activator of EC 2.4.1.12, cellulose synthase (UDP-forming), rendering it inactive [423]. It is the balance between these two enzymes that determines the cellular level of c-di-GMP [423].

References: [423, 481, 2701, 3007]

EC 3.1.4.53

Accepted name: 3',5'-cyclic-AMP phosphodiesterase

Reaction: adenosine 3',5'-cyclic phosphate + H\(_2\)O = AMP

Other name(s): cAMP-specific phosphodiesterase; cAMP-specific PDE; PDE1; PDE2A; PDE2B; PDE4; PDE7; PDE8; PDEB1; PDEB2

Systematic name: 3',5'-cyclic-AMP 5'-nucleotidohydrolase

Comments: Requires Mg\(^{2+}\) or Mn\(^{2+}\) for activity [129]. This enzyme is specific for 3',5'-cAMP and does not hydrolyse other nucleoside 3',5'-cyclic phosphates such as cGMP (cf. EC 3.1.4.17, 3,5-cyclic-nucleotide phosphodiesterase and EC 3.1.4.35, 3,5-cyclic-GMP phosphodiesterase). It is involved in modulation of the levels of cAMP, which is a mediator in the processes of cell transformation and proliferation [2500].

References: [42, 129, 2500, 1406, 1849, 1318]

EC 3.1.4.54

Accepted name: N-acetylphosphatidylethanolamine-hydrolysing phospholipase D

Reaction: N-acylphosphatidylethanolamine + H\(_2\)O = N-acylethanolamine + a 1,2-diacylglycerol 3-phosphate

Other name(s): NAPE-PLD; anandamide-generating phospholipase D; N-acyl phosphatidylethanolamine phospholipase D; NAPE-hydrolyzing phospholipase D

Systematic name: N-acetylphosphatidylethanolamine phosphatidohydrolase

Comments: This enzyme is involved in the biosynthesis of anandamide. It does not hydrolyse phosphatidylcholine and phosphatidylethanolamine [2293]. No transphosphatidation [2293]. The enzyme contains Zn\(^{2+}\) and is activated by Mg\(^{2+}\) or Ca\(^{2+}\) [3262].

References: [2293, 3262]

EC 3.1.4.55

Accepted name: phosphoribosyl 1,2-cyclic phosphate phosphodiesterase

Reaction: 5-phospho-\(\alpha\)-D-ribose 1,2-cyclic phosphate + H\(_2\)O = \(\alpha\)-D-ribose 1,5-bisphosphate

Other name(s): phnP (gene name)

Systematic name: 5-phospho-\(\alpha\)-D-ribose 1,2-cyclic phosphate 2-phosphohydrolase (\(\alpha\)-D-ribose 1,5-bisphosphate-forming)

Comments: Binds Mn\(^{2+}\) and Zn\(^{2+}\). Isolated from the bacterium Escherichia coli, where it participates in the degradation of methylphosphonate.

References: [2414, 1264, 1158]

EC 3.1.4.56

Accepted name: 7,8-dihydroneopterin 2',3'-cyclic phosphate phosphodiesterase

Reaction: (1) 7,8-dihydroneopterin 2',3'-cyclic phosphate + H\(_2\)O = 7,8-dihydroneopterin 3'-phosphate
(2) 7,8-dihydroneopterin 2',3'-cyclic phosphate + H\(_2\)O = 7,8-dihydroneopterin 2'-phosphate

References: [2414, 1264, 1158]
Other name(s): MptB
Systematic name: 7,8-dihydroneopterin 2′,3′-cyclic phosphate 2′/3′-phosphodiesterase
Comments: Contains one zinc atom and one iron atom per subunit of the dodecameric enzyme. It hydrolyses 7,8-dihydroneopterin 2′,3′-cyclic phosphate, a step in tetrahydromethanopterin biosynthesis. *In vitro* the enzyme forms 7,8-dihydroneopterin 2′-phosphate and 7,8-dihydroneopterin 3′-phosphate at a ratio of 4:1.
References: [1929]

[EC 3.1.4.56 created 2013]

**EC 3.1.4.57**

Accepted name: phosphoribosyl 1,2-cyclic phosphate 1,2-diphosphodiesterase
Reaction: (1) 5-phospho-α-D-ribose 1,2-cyclic phosphate + H₂O = D-ribofuranose 2,5-bisphosphate
(2) D-ribofuranose 2,5-bisphosphate + H₂O = D-ribofuranose 5-phosphate + phosphate
Other name(s): cyclic phosphate dihydrolase; phnPP (gene name)
Systematic name: 5-phospho-α-D-ribose 1,2-cyclic phosphate 1,2-diphosphophosphohydrolase
Comments: The enzyme, characterized from the bacterium *Eggerthella lenta*, is involved in degradation of methylphosphonate.
References: [958]

[EC 3.1.4.57 created 2014]

**EC 3.1.4.58**

Accepted name: RNA 2′,3′-cyclic 3′-phosphodiesterase
Reaction: (ribonucleotide)ₙ-2′,3′-cyclic phosphate + H₂O = (ribonucleotide)ₙ-2′-phosphate
Other name(s): thpR (gene name); ligT (gene name)
Systematic name: (ribonucleotide)ₙ-2′,3′-cyclic phosphate 3′-nucleotidohydrolase
Comments: The enzyme hydrolyses RNA 2′,3′-cyclic phosphodiester to an RNA 2′-phosphomonoester. *In vitro* the enzyme can also ligate tRNA molecules with 2′,3′-cyclic phosphate to tRNA with 5′-hydroxyl termini, forming a 2′-5′ phosphodiester linkage. However, the ligase activity is unlikely to be relevant *in vivo*.
References: [1460, 2533]

[EC 3.1.4.58 created 2017]

**EC 3.1.4.59**

Accepted name: cyclic-di-AMP phosphodiesterase
Reaction: cyclic di-3′,5′-adenylate + H₂O = 5′-O-phosphonoadenylyl-(3′→5′)-adenosine
Other name(s): gdpP (gene name)
Systematic name: cyclic bis(3′→5′)diadenylate 3′-adenylylhydrolase
Comments: The enzyme, described from Gram-positive bacteria, degrades the second messenger cyclic di-3′,5′-adenylate. It is a membrane-bound protein that contains a cytoplasmic facing Per-Arnt-Sim (PAS) domain, a modified GGDEF domain, and a DHH/DHHA₁ domain, which confers the phosphodiesterase activity. Activity requires Mn²⁺ and is inhibited by pApA.
References: [2497, 530, 1034, 301]

[EC 3.1.4.59 created 2019]

**EC 3.1.4.60**

Accepted name: pApA phosphodiesterase
Reaction: 5′-O-phosphonoadenylyl-(3′→5′)-adenosine + H₂O = 2 AMP
Other name(s): pde2 (gene name); pApA hydrolase
Systematic name: 5′-O-phosphonoadenylyl-(3′→5′)-adenosine phosphohydrolase

69
Comments: The enzyme, characterized from the Gram-positive bacterium *Staphylococcus aureus*, is a cytoplasmic protein that contains a DHH/DHHA$_1$ domain. It can act on cyclic di-$3',5'$-adenylate with a much lower activity (cf. EC 3.1.4.59, cyclic-di-AMP phosphodiesterase). Activity requires Mn$^{2+}$ and is inhibited by ppGpp.

References: [131, 3440, 3024, 1632, 301]

[EC 3.1.4.60 created 2019]

EC 3.1.4.61

Accepted name: cyclic 2,3-diphosphoglycerate hydrolase

Reaction: cyclic 2,3-bisphosphoglycerate + H$_2$O = 2,3-diphosphoglycerate

Systematic name: cyclic 2,3-diphosphoglycerate phosphohydrolyase

Comments: The enzyme degrades cyclic 2,3-bisphosphoglycerate, a thermoprotectant that is produced by certain archaeal genera. Two different enzymes that catalyse this activity, one soluble and one membrane-bound, have been characterized from the archaeon *Methanothermobacter thermautotrophicus.*

References: [2665, 922]

[EC 3.1.4.61 created 2021]

EC 3.1.5 Triphosphoric-monoester hydrolases

EC 3.1.5.1

Accepted name: dGTPase

Reaction: dGTP + H$_2$O = deoxyguanosine + triphosphate

Other name(s): deoxy-GTPase; deoxyguanosine 5-triphosphate triphosphohydrolase; deoxyguanosine triphosphatase; deoxyguanosine triphosphohydrolase

Systematic name: dGTP triphosphohydrolase

Comments: Also acts on GTP.

References: [1601]

[EC 3.1.5.1 created 1961]

EC 3.1.6 Sulfuric-ester hydrolases

EC 3.1.6.1

Accepted name: arylsulfatase (type I)

Reaction: an aryl sulfate + H$_2$O = a phenol + sulfate

Other name(s): sulfatase; nitro catechol sulfatase; phenol sulfatase; phenylsulfatase; p-nitrophenyl sulfatase; arylsulfate hydrolase; 4-methylumbelliferyl sulfatase; estrogen sulfatase; type I sulfatase; arylsulfatase

Systematic name: aryl-sulfate sulfohydrolase

Comments: Sulfatase enzymes are classified as type I, in which the key catalytic residue is 3-oxo-L-alanine, type II, which are non-heme iron-dependent dioxygenases, or type III, whose catalytic domain adopts a metallo-β-lactamase fold and binds two zinc ions as cofactors. Arylsulfatas are type I enzymes, found in both prokaryotes and eukaryotes, with rather similar specificities. The key catalytic residue 3-oxo-L-alanine initiates the reaction through a nucleophilic attack on the sulfur atom in the substrate. This residue is generated by posttranslational modification of a conserved cysteine or serine residue by EC 1.8.3.7, formylglycine-generating enzyme, EC 1.1.98.7, serine-type anaerobic sulfatase-maturating enzyme, or EC 1.8.98.7, cysteine-type anaerobic sulfatase-maturating enzyme.

References: [669, 3293, 2598, 2599, 2702, 651]

[EC 3.1.6.1 created 1961, modified 2011, modified 2021]
EC 3.1.6.2
Accepted name: sterol-sulfatase
Reaction: $3\beta$-hydroxyandrost-5-en-17-one 3-sulfate + H$_2$O = $3\beta$-hydroxyandrost-5-en-17-one + sulfate
Other name(s): arylsulfatase; steroid sulfatase; sterol sulfatase; dehydroepiandrosterone sulfatase sulfatase; arylsulfatase C; steroid 3-sulfatase; steroid sulfate sulfohydrolase; dehydroepiandrosterone sulfatase; pregnenolone sulfatase; phenolic steroid sulfatase; 3-$\beta$-hydroxysteroid sulfate sulfatase
Systematic name: sterol-sulfate sulfohydrolase
Comments: Also acts on some related sterol sulfates.
References: [2597, 2598, 2913]

[EC 3.1.6.2 created 1961]

EC 3.1.6.3
Accepted name: glycosulfatase
Reaction: D-glucose 6-sulfate + H$_2$O = D-glucose + sulfate
Other name(s): glucosulfatase
Systematic name: sugar-sulfate sulfohydrolase
Comments: Also acts on other sulfates of monosaccharides and disaccharides and on adenosine 5'-sulfate.
References: [668, 723, 2598]

[EC 3.1.6.3 created 1961]

EC 3.1.6.4
Accepted name: N-acetylgalactosamine-6-sulfatase
Reaction: Hydrolysis of the 6-sulfate groups of the N-acetyl-D-galactosamine 6-sulfate units of chondroitin sulfate and of the D-galactose 6-sulfate units of keratan sulfate
Other name(s): chondroitin sulfatase; chondroitinase; galactose-6-sulfate sulfatase; acetylgalactosamine 6-sulfatase; N-acetylgalactosamine-6-sulfate sulfatase; N-acetylgalactosamine 6-sulfatase
Systematic name: N-acetyl-D-galactosamine-6-sulfate 6-sulfohydrolase
References: [755, 985, 1781, 2865, 3476]

[EC 3.1.6.4 created 1961]

[3.1.6.5 Deleted entry. sinigrin sulfohydrolase; myrosulfatase]

[EC 3.1.6.5 created 1961, deleted 1964]

EC 3.1.6.6
Accepted name: choline-sulfatase
Reaction: choline sulfate + H$_2$O = choline + sulfate
Systematic name: choline-sulfate sulfohydrolase
References: [2995]

[EC 3.1.6.6 created 1965]

EC 3.1.6.7
Accepted name: cellulose-polysulfatase
Reaction: Hydrolysis of the 2- and 3-sulfate groups of the polysulfates of cellulose and charonin
Systematic name: cellulose-sulfate sulfohydrolase
References: [2983]

[EC 3.1.6.7 created 1965]
<table>
<thead>
<tr>
<th>EC</th>
<th>Accepted name</th>
<th>Reaction</th>
<th>Other name(s)</th>
<th>Systematic name</th>
<th>Comments</th>
<th>References</th>
</tr>
</thead>
<tbody>
<tr>
<td>EC 3.1.6.8</td>
<td>cerebroside-sulfatase</td>
<td>a cerebroside 3-sulfate + H₂O = a cerebroside + sulfate</td>
<td>arylsulfatase A; cerebroside sulfate sulfatase</td>
<td>cerebroside-3-sulfate 3-sulfohydrolase</td>
<td>Hydrolyses galactose-3-sulfate residues in a number of lipids. Also hydrolyses ascorbate 2-sulfate and many phenol sulfates.</td>
<td>[1973, 2599]</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td>[EC 3.1.6.8 created 1972]</td>
</tr>
<tr>
<td>EC 3.1.6.9</td>
<td>chondro-4-sulfatase</td>
<td>4-deoxy-β-D-gluc-4-enuronosyl-(1→3)-N-acetyl-D-galactosamine 4-sulfate + H₂O = 4-deoxy-β-D-gluc-4-enuronosyl-(1→3)-N-acetyl-D-galactosamine + sulfate</td>
<td>chondroitin-4-sulfatase; 4-deoxy-β-D-gluc-4-enuronosyl-(1,3)-N-acetyl-D-galactosamine-4-sulfate 4-sulfohydrolase</td>
<td>4-deoxy-β-D-gluc-4-enuronosyl-(1→3)-N-acetyl-D-galactosamine-4-sulfate 4-sulfohydrolase</td>
<td>Also acts on the saturated analogue but not on higher oligosaccharides, nor any 6-sulfates.</td>
<td>[1173, 2599, 3400]</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td>[EC 3.1.6.9 created 1972]</td>
</tr>
<tr>
<td>EC 3.1.6.10</td>
<td>chondro-6-sulfatase</td>
<td>4-deoxy-β-D-gluc-4-enuronosyl-(1→3)-N-acetyl-D-galactosamine 6-sulfate + H₂O = 4-deoxy-β-D-gluc-4-enuronosyl-(1→3)-N-acetyl-D-galactosamine + sulfate</td>
<td>4-deoxy-β-D-gluc-4-enuronosyl-(1,3)-N-acetyl-D-galactosamine-6-sulfate 6-sulfohydrolase</td>
<td>4-deoxy-β-D-gluc-4-enuronosyl-(1→3)-N-acetyl-D-galactosamine-6-sulfate 6-sulfohydrolase</td>
<td>Also acts on the saturated analogue and N-acetyl-D-galactosamine 4,6-disulfate, but not higher oligosaccharides, nor any 4-sulfate</td>
<td>[3400]</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td>[EC 3.1.6.10 created 1972]</td>
</tr>
<tr>
<td>EC 3.1.6.11</td>
<td>disulfoglucosamine-6-sulfatase</td>
<td>2-N,6,0-disulfo-D-glucosamine + H₂O = 2-N-sulfo-D-glucosamine + sulfate</td>
<td></td>
<td>2-N,6,0-disulfo-D-glucosamine 6-sulfatase; 6-N-disulfoglucosamine 6-O-sulfohydrolase; N,6-O-disulfo-D-glucosamine 6-sulfohydrolase</td>
<td>May be identical with EC 3.1.6.14 N-acetylglucosamine-6-sulfatase.</td>
<td>[653]</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td>[EC 3.1.6.11 created 1972, modified 1989]</td>
</tr>
<tr>
<td>EC 3.1.6.12</td>
<td>N-acetylgalactosamine-4-sulfatase</td>
<td>Hydrolysis of the 4-sulfate groups of the N-acetyl-D-galactosamine 4-sulfate units of chondroitin sulfate and dermatan sulfate</td>
<td>chondroitin sulfatase; chondroitinase; arylsulfatase B; acetylgalactosamine 4-sulfatase; N-acetylgalactosamine-4-sulfate sulfatase</td>
<td>N-acetyl-D-galactosamine-4-sulfate 4-sulfohydrolase</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

72
Comments: Acts also on N-acetylgalactosamine 4-sulfate.
References: [790, 1014, 3124]

[EC 3.1.6.12 created 1984]

EC 3.1.6.13
Accepted name: iduronate-2-sulfatase
Reaction: Hydrolysis of the 2-sulfate groups of the L-iduronate 2-sulfate units of dermatan sulfate, heparan sulfate and heparin
Other name(s): chondroitinsulfatase; idurono-2-sulfatase; iduronide-2-sulfate sulfatase; L-iduronosulfatase; L-iduronate sulfate sulfatase; iduronate sulfate sulfatase; sulfo-L-iduronate sulfatase; L-iduronate 2-sulfate sulfatase; sulfo-iduronate sulfohydrolase; 2-sulfo-L-iduronate 2-sulfatase; iduronate-2-sulfate sulfatase; iduronate sulfate sulfatase
Systematic name: L-iduronate-2-sulfate 2-sulfohydrolase
References: [75, 125, 660, 3475]

[EC 3.1.6.13 created 1984]

EC 3.1.6.14
Accepted name: N-acetylgalactosamine-6-sulfatase
Reaction: Hydrolysis of the 6-sulfate groups of the N-acetyl-D-glucosamine 6-sulfate units of heparan sulfate and keratan sulfate
Other name(s): chondroitinsulfatase; O.N-disulfate O-sulfohydrolase; acetylgalactosamine 6-sulfatase; N-acetylgalactosamine 6-sulfate sulfatase; acetylgalactosamine 6-sulfatase; 2-acetamido-2-deoxy-D-glucose 6-sulfate sulfatase
Systematic name: N-acetyl-D-glucosamine-6-sulfate 6-sulfohydrolase
Comments: May be identical with EC 3.1.6.11 disulfoglucosamine-6-sulfatase.
References: [183, 1623, 3308]

[EC 3.1.6.14 created 1984]

EC 3.1.6.15
Accepted name: N-sulfoglucosamine-3-sulfatase
Reaction: Hydrolysis of the 3-sulfate groups of the N-sulfo-D-glucosamine 3-O-sulfate units of heparin
Other name(s): chondroitinsulfatase
Systematic name: N-sulfo-3-sulfoglucosamine 3-sulfohydrolase
Comments: The enzyme from Flavobacterium heparinum also hydrolyses N-acetyl-D-glucosamine 3-O-sulfate; the mammalian enzyme acts only on the disulfated residue.
References: [344, 1708]

[EC 3.1.6.15 created 1984, modified 1989]

EC 3.1.6.16
Accepted name: monomethyl-sulfatase
Reaction: monomethyl sulfate + H₂O = methanol + sulfate
Systematic name: monomethyl-sulfate sulfohydrolase
Comments: Highly specific; does not act on monoethyl sulfate, monoisopropyl sulfate or monododecyl sulfate.
References: [957]

[EC 3.1.6.16 created 1989]
EC 3.1.6.17

Accepted name: D-lactate-2-sulfatase
Reaction: \((R)-2-O\text{-sulfolactate} + \text{H}_2\text{O} = (R)\text{-lactate} + \text{sulfate}\)
Other name(s): (S)-2-O-sulfolactate 2-sulfohydrolase (incorrect stereochemistry)
Systematic name: (R)-2-O-sulfolactate 2-sulfohydrolase
Comments: Highly specific.
References: [545]

[EC 3.1.6.17 created 1989]

EC 3.1.6.18

Accepted name: glucuronate-2-sulfatase
Reaction: Hydrolysis of the 2-sulfate groups of the 2-O-sulfo-D-glucuronate residues of chondroitin sulfate, heparin and heparitin sulfate
Other name(s): glucurono-2-sulfatase
Systematic name: polysaccharide-2-O-sulfo-D-glucuronate 2-sulfohydrolase
Comments: Does not act on iduronate 2-sulfate residues (cf. EC 3.1.6.13 iduronate-2-sulfatase)
References: [2750]

[EC 3.1.6.18 created 1989]

EC 3.1.6.19

Accepted name: (R)-specific secondary-alkylsulfatase (type III)
Reaction: an \((R)\)-secondary-alkyl sulfate + \text{H}_2\text{O} = an \((S)\)-secondary-alcohol + \text{sulfate}
Other name(s): S3 secondary alkylsulphohydrolase; PIsa1; secondary alkylsulphohydrolase; \((R)\)-specific sec-alkylsulfatase; sec-alkylsulfatase; \((R)\)-specific secondary-alkylsulfatase; type III \((R)\)-specific secondary-alkylsulfatase
Systematic name: \((R)\)-secondary-alkyl sulfate sulfohydrolase [(S)-secondary-alcohol-forming]
Comments: Sulfatase enzymes are classified as type I, in which the key catalytic residue is 3-oxo-L-alanine, type II, which are non-heme iron-dependent dioxygenases, or type III, whose catalytic domain adopts a metallo-β-lactamase fold and binds two zinc ions as cofactors. This enzyme belongs to the type III sulfatase family. The enzyme from the bacterium Rhodococcus ruber prefers linear secondary-alkyl sulfate esters, particularly octan-2-yl, octan-3-yl, and octan-4-yl sulfates [2417]. The enzyme from the bacterium Pseudomonas sp. DSM6611 utilizes a range of secondary-alkyl sulfate esters bearing aromatic, olefinic and acetylenic moieties. Hydrolysis proceeds through inversion of the configuration at the stereogenic carbon atom, resulting in perfect enantioselectivity. cf. EC 3.1.6.1, arylsulfatase (type I), and EC 1.14.11.77, alkyl sulfatase (type II).
References: [2417, 3251, 1568, 2711]

[EC 3.1.6.19 created 2013, modified 2021]

EC 3.1.6.20

Accepted name: S-sulfsulfanyl-L-cysteine sulfohydrolase
Reaction: (1) \([\text{SoxY protein}]\)-S-sulfsulfanyl-L-cysteine + \text{H}_2\text{O} = \([\text{SoxY protein}]\)-S-sulfanyl-L-cysteine + \text{sulfate}  
(2) \([\text{SoxY protein}]\)-S-(2-sulfsulfanyl)-L-cysteine + \text{H}_2\text{O} = \([\text{SoxY protein}]\)-S-disulfanyl-L-cysteine + \text{sulfate}
Other name(s): SoxB
Systematic name: [SoxY protein]-S-sulfosulfanyl-L-cysteine sulfohydrolase
Comments: Contains Mn\(^{2+}\). 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. In both cases the enzyme hydrolyses a sulfonate moiety that is bound (either directly or via a sulfane) to a cysteine residue of a SoxY protein, releasing sulfate. The enzyme from Paracoccus pantotrophus contains a pyroglutamate (cycloglutamate) at its N-terminus.

References: [2417, 3251, 1568, 2711]
EC 3.1.6.21

**Accepted name:** linear primary-alkylsulfatase

**Reaction:** a primary alkyl sulfate ester + $\text{H}_2\text{O} = \text{an alcohol} + \text{sulfate}$

**Other name(s):** *sdsA1* (gene name); *yjcS* (gene name); type III linear primary-alkylsulfatase

**Systematic name:** primary alkyl sulfate ester sulfohydrolase

**Comments:** Sulfatase enzymes are classified as type I, in which the key catalytic residue is 3-oxo-$\alpha$-alanine, type II, which are non-heme iron-dependent dioxygenases, or type III, whose catalytic domain adopts a metallo-$\beta$-lactamase fold and binds two zinc ions as cofactors. This enzyme belongs to the type III sulfatase family. It is active against linear primary-alkyl sulfate esters, such as dodecyl sulfate, decyl sulfate, octyl sulfate, and hexyl sulfate. The enzyme from *Pseudomonas aeruginosa* is secreted out of the cell. The catalytic mechanism begins with activation of a water molecule by the binuclear Zn$^{2+}$ cluster, resulting in a nucleophilic attack on the carbon atom. *cf.* EC 3.1.6.22, branched primary-alkylsulfatase, and EC 3.1.6.19, ($R$)-specific secondary-alkylsulfatase (type III).

**References:** [1077, 1833, 1769, 2942]

[EC 3.1.6.21 created 2021]

EC 3.1.6.22

**Accepted name:** branched primary-alkylsulfatase

**Reaction:** 2-butyloctyl sulfate + $\text{H}_2\text{O} = 2$-butyloctan-1-ol + sulfate

**Other name(s):** DP1 (gene name); type III branched primary-alkylsulfatase

**Systematic name:** branched primary-alkyl sulfate ester sulfohydrolase

**Comments:** Sulfatase enzymes are classified as type I, in which the key catalytic residue is 3-oxo-$\alpha$-alanine, type II, which are non-heme iron-dependent dioxygenases, or type III, whose catalytic domain adopts a metallo-$\beta$-lactamase fold and binds two zinc ions as cofactors. This enzyme belongs to the type III family. The enzyme, characterized from a *Pseudomonas* strain, is specific for branched primary-alkyl sulfate esters and does not act on linear substrates such as dodecyl sulfate. *cf.* EC 3.1.6.1, arylsulfatase (type I), EC 1.14.11.77, alkyl sulfatase, EC 3.1.6.19, ($R$)-specific secondary-alkylsulfatase (type III) and EC 3.1.6.21, linear primary-alkylsulfatase.

**References:** [738, 3070]

[EC 3.1.6.22 created 2021]

EC 3.1.7 Diphosphoric-monoester hydrolases

EC 3.1.7.1

**Accepted name:** prenyl-diphosphatase

**Reaction:** prenyl diphosphate + $\text{H}_2\text{O} = \text{prenol} + \text{diphosphate}$

**Other name(s):** prenyl-pyrophosphatase; prenol pyrophosphatase; prenylphosphatase

**Systematic name:** prenyl-diphosphate diphosphohydrolase

**Comments:** Farnesyl diphosphate is the best substrate tested to date.

**References:** [3114]

[EC 3.1.7.1 created 1972]

EC 3.1.7.2

**Accepted name:** guanosine-$3',5'-$bis(diphosphate) 3'$-diphosphatase

**Reaction:** guanosine $3',5'$-bis(diphosphate) + $\text{H}_2\text{O} = \text{GDP} + \text{diphosphate}$
Other name(s): guanosine-3′,5′′-bis(diphosphate) 3′-pyrophosphatase; PpGpp-3′-pyrophosphohydrolase; PpGpp phosphohydrolase
Systematic name: guanosine-3′,5′′-bis(diphosphate) 3′-diphosphohydrolase
References: [1171, 2549]

EC 3.1.7.2
Accepted name: monoterpenyl-diphosphatase
Reaction: a monoterpenyl diphosphate + H₂O = a monoterpenol + diphosphate
Other name(s): bornyl pyrophosphate hydrolase; monoterpenyl-pyrophosphatase
Systematic name: monoterpenyl-diphosphate diphosphohydrolase
Comments: A group of enzymes with varying specificity for the monoterpenol moiety. One has the highest activity on sterically hindered compounds such as (+)-bornyl diphosphate; another has highest activity on the diphosphates of primary allylic alcohols such as geraniol.
References: [552]

EC 3.1.7.3
Accepted name: monoterpenyl-diphosphatase
Reaction: a monoterpenyl diphosphate + H₂O = a monoterpenol + diphosphate
Other name(s): bornyl pyrophosphate hydrolase; monoterpenyl-pyrophosphatase
Systematic name: monoterpenyl-diphosphate diphosphohydrolase
Comments: A group of enzymes with varying specificity for the monoterpenol moiety. One has the highest activity on sterically hindered compounds such as (+)-bornyl diphosphate; another has highest activity on the diphosphates of primary allylic alcohols such as geraniol.
References: [552]

EC 3.1.7.5
Accepted name: geranylgeranyl diphosphatase
Reaction: geranylgeranyl diphosphate + H₂O = geranylgeraniol + diphosphate
Other name(s): geranylgeranyl diphosphate phosphatase
Systematic name: geranyl-diphosphate diphosphohydrolase
Comments: Involved in the biosynthesis of plaunotol. There are two isoenzymes with different ion requirements. Neither require Mg²⁺ but in addition PI is inhibited by Zn²⁺, Mn²⁺ and Co²⁺. It is not known which isoenzyme is involved in plaunotol biosynthesis.
References: [2226]

EC 3.1.7.6
Accepted name: farnesyl diphosphatase
Reaction: (2E,6E)-farnesyl diphosphate + H₂O = (2E,6E)-farnesol + diphosphate
Other name(s): FPP phosphatase
Systematic name: (2E,6E)-farnesyl-diphosphate diphosphohydrolase
Comments: The enzyme is involved in the biosynthesis of acyclic sesquiterpenoids [2857].
References: [2857, 3114]

EC 3.1.7.7
Accepted name: (−)-drimenol synthase. Now EC 4.2.3.194, (−)-drimenol synthase
Reaction: (−)-drimenol synthase. Now EC 4.2.3.194, (−)-drimenol synthase
Other name(s): (−)-drimenol synthase. Now EC 4.2.3.194, (−)-drimenol synthase
Systematic name: (−)-drimenol synthase. Now EC 4.2.3.194, (−)-drimenol synthase
Comments: The enzyme is involved in the biosynthesis of acyclic sesquiterpenoids [2857].
References: [2857, 3114]

EC 3.1.7.8
Accepted name: tuberculosinol synthase. Now known to be partial activity of EC 2.5.1.153, adenosine tuberculosinyltransferase.
Reaction: tuberculosinol synthase. Now known to be partial activity of EC 2.5.1.153, adenosine tuberculosinyltransferase.
Other name(s): tuberculosinol synthase. Now known to be partial activity of EC 2.5.1.153, adenosine tuberculosinyltransferase.
Systematic name: tuberculosinol synthase. Now known to be partial activity of EC 2.5.1.153, adenosine tuberculosinyltransferase.
Comments: The enzyme is involved in the biosynthesis of acyclic sesquiterpenoids [2857].
References: [2857, 3114]
EC 3.1.7.10

Accepted name: (13E)-labda-7,13-dien-15-ol synthase
Reaction: geranylgeranyl diphosphate + H₂O = (13E)-labda-7,13-dien-15-ol + diphosphate
Other name(s): labda-7,13E-dien-15-ol synthase
Comments: The enzyme from the lycophyte Selaginella moellendorffii is bifunctional, initially forming (13E)-labda-7,13-dien-15-yl diphosphate, which is hydrolysed to the alcohol.
References: [1868]

EC 3.1.7.11

Accepted name: geranyl diphosphate diphosphatase
Reaction: geranyl diphosphate + H₂O = geraniol + diphosphate
Other name(s): geraniol synthase; geranyl pyrophosphate pyrophosphatase; GES; CtGES
Systematic name: geranyl-diphosphate diphosphohydrolase
Comments: Isolated from Ocimum basilicum (basil) and Cinnamomum tenuipile (camphor tree). Requires Mg²⁺ or Mn²⁺. Geraniol is labelled when formed in the presence of [¹⁸O]H₂O. Thus mechanism involves a geranyl cation [1302]. Neryl diphosphate is hydrolysed more slowly. May be the same as EC 3.1.7.3 monoterpenyl-diphosphatase.
References: [1302, 3418]

EC 3.1.7.12

Accepted name: (+)-kolavelool synthase
Reaction: (+)-kolavenyl diphosphate + H₂O = (+)-kolavelool + diphosphate
Other name(s): Haur_2146
Systematic name: kolavenyl-diphosphate diphosphohydrolase
Comments: Isolated from the bacterium Herpetosiphon aurantiacus.
References: [2153]

EC 3.1.7.13

Accepted name: neryl diphosphate diphosphatase
Reaction: neryl diphosphate + H₂O = nerol + diphosphate
Other name(s): NES (gene name); nerol synthase
Systematic name: neryl-diphosphate diphosphohydrolase
Comments: The enzyme, characterized from Glycine max (soybeans), is specific for neryl diphosphate.
References: [3491]

EC 3.1.8 Phosphoric-triester hydrolases

EC 3.1.8.1

Accepted name: aryl dialkylphosphatase
Reaction: an aryl dialkyl phosphate + H₂O = dialkyl phosphate + an aryl alcohol
Other name(s): organophosphate hydrolase; paraoxonase; A-esterase; aryltriphosphatase; organophosphate esterase; esterase B1; esterase E4; paraoxon esterase; pirimiphos-methyl oxon esterase; OPA anhydrase (ambiguous); organophosphorus hydrolase; phosphotriesterase; paraoxon hydrolase; OPH; organophosphorus acid anhydrase

Systematic name: aryltriphosphate dialkylphosphohydrolase

Comments: Acts on organophosphorus compounds (such as paraoxon) including esters of phosphonic and phosphinic acids. Inhibited by chelating agents; requires divalent cations for activity. Previously regarded as identical with EC 3.1.1.2 arylesterase.

References: [33, 293, 1866, 1875, 1]

EC 3.1.8.2

Accepted name: diisopropyl-fluorophosphatase

Reaction: DI Pase + H2O = DI P + F

Other name(s): DF Pase; tabunase; somanase; organophosphorus acid anhydrolase; organophosphate acid anhydrase; OPA anhydrase (ambiguous); diisopropylphosphofluoridase; dialkylfluorophosphatase; diisopropyl phosphorofluoridate hydrolase; isopropylphosphorofluoridase; diisopropylfluorophosphonate dehalogenase

Systematic name: diisopropyl-fluorophosphate fluorohydrolase

Comments: Acts on phosphorus anhydride bonds (such as phosphorus-halide and phosphorus-cyanide) in organophosphorus compounds (including 'nerve gases'). Inhibited by chelating agents; requires divalent cations. Related to EC 3.1.8.1 aryldialkylphosphatase.

References: [106, 107, 108, 503, 2092, 1]

EC 3.1.11 Exodeoxyribonucleases producing 5'-phosphomonoesters

EC 3.1.11.1

Accepted name: exodeoxyribonuclease I

Reaction: Exonucleolytic cleavage in the 3' to 5'-direction to yield nucleoside 5'-phosphates

Other name(s): Escherichia coli exonuclease I; E. coli exonuclease I; exonuclease I

Comments: Preference for single-stranded DNA. The Escherichia coli enzyme hydrolyses glucosylated DNA.

References: [261, 1500, 1731]

EC 3.1.11.2

Accepted name: exodeoxyribonuclease III

Reaction: Exonucleolytic cleavage in the 3'- to 5'-direction to yield nucleoside 5'-phosphates

Other name(s): Escherichia coli exonuclease III; E. coli exonuclease III; endoribonuclease III

Comments: Preference for double-stranded DNA. Has endonucleolytic activity near apurinic sites on DNA.

References: [1796, 2546, 2547]

EC 3.1.11.3

Accepted name: exodeoxyribonuclease (lambda-induced)

Reaction: Exonucleolytic cleavage in the 5’- to 3’-direction to yield nucleoside 5'-phosphates

Other name(s): lambda exonuclease; phage lambda-induced exonuclease; Escherichia coli exonuclease IV; E. coli exonuclease IV; exodeoxyribonuclease IV; exonuclease IV
Comments: Preference for double-stranded DNA. Does not attack single-strand breaks.
References: [1795, 1809]

[EC 3.1.11.3 created 1972 as EC 3.1.4.28, transferred 1978 to EC 3.1.11.3]

EC 3.1.11.4
Accepted name: exodeoxyribonuclease (phage SP$_3$-induced)
Reaction: Exonucleolytic cleavage in the $5'\rightarrow 3'$-direction to yield nucleoside $5'$-phosphates
Other name(s): phage SP$_3$ DNase; DNA $5'$-dinucleotidohydrolase; deoxyribonucleate $5'$-dinucleotidase; deoxyri-
bonucleic $5'$-dinucleotidohydrolase; bacteriophage SP$_3$ deoxyribonuclease; deoxyribonucleate $5'$-
dinucleotidase
Comments: Preference for single-stranded DNA.
References: [3110]

[EC 3.1.11.4 created 1972 as EC 3.1.4.31, transferred 1978 to EC 3.1.11.4]

EC 3.1.11.5
Accepted name: exodeoxyribonuclease V
Reaction: Exonucleolytic cleavage (in the presence of ATP) in either $5'\rightarrow 3'$- to $3'\rightarrow 5'$-direction to yield $5'$-
phosphooligonucleotides
Other name(s): *Escherichia coli* exonuclease V; *E. coli* exonuclease V; gene recBC endoenzyme; RecBC deoxy-
ribonuclease; gene recBC Dnase; exonuclease V; gene recBCD enzymes
Comments: Preference for double-stranded DNA. Possesses DNA-dependent ATPase activity. Acts endonucle-
olytically on single-stranded circular DNA.
References: [729, 1005, 2285, 3370]

[EC 3.1.11.5 created 1978]

EC 3.1.11.6
Accepted name: exodeoxyribonuclease VII
Reaction: Exonucleolytic cleavage in either $5'\rightarrow 3'$- to $3'\rightarrow 5'$- to $5'\rightarrow 3'$-direction to yield nucleoside $5'$-
phosphates
Other name(s): *Escherichia coli* exonuclease VII; *E. coli* exonuclease VII; endodeoxyribonuclease VII; exonuclease
VII
Comments: Preference for single-stranded DNA.
References: [436, 435]

[EC 3.1.11.6 created 1978]

[3.1.11.7 Transferred entry. adenosine-$5'$-diphospho-$5'$-[DNA] diphosphatase. Now EC 3.6.1.71, adenosine-$5'$-diphospho-
$5'$-[DNA] diphosphatase]

[EC 3.1.11.7 created 2017, deleted 2019]

[3.1.11.8 Transferred entry. guanosine-$5'$-diphospho-$5'$-[DNA] diphosphatase. Now EC 3.6.1.70, guanosine-$5'$-diphospho-
$5'$-[DNA] diphosphatase]

[EC 3.1.11.8 created 2017, deleted 2019]

EC 3.1.12 Exodeoxyribonucleases producing $3'$-phosphomonoesters

EC 3.1.12.1
Accepted name: $5'$ to $3'$ exodeoxyribonuclease (nucleoside $3'$-phosphate-forming)
Reaction: exonucleolytic cleavage in the $5'\rightarrow 3'$-direction to yield nucleoside $3'$-phosphates

79
Other name(s): Cas4; 5′ to 3′ single stranded DNA exonuclease
Comments: Preference for single-stranded DNA. The enzyme from the archaeon *Sulfolobus solfataricus* contains a [4Fe-4S] cluster and requires a divalent metal cation, such as Mg$^{2+}$ or Mn$^{2+}$, for activity.
References: [3487, 1733]

EC 3.1.12.1 created 2014

[3.1.12.2 Transfered entry. DNA-3-diphospho-5-guanosine diphosphatase. Now EC 3.6.1.72, DNA-3-diphospho-5-guanosine diphosphatase]

EC 3.1.13 Exoribonucleases producing 5′-phosphomonoesters

EC 3.1.13.1
Accepted name: exoribonuclease II
Reaction: Exonucleolytic cleavage in the 3′- to 5′-direction to yield nucleoside 5′-phosphates
Other name(s): ribonuclease II; ribonuclease Q; BN ribonuclease; *Escherichia coli* exo-RNase II; RNase II; exoribonuclease (misleading); 5′-exoribonuclease (misleading)
Comments: Preference for single-stranded RNA. The enzyme processes 3′-terminal extra-nucleotides of monomeric tRNA precursors, following the action of EC 3.1.26.5 ribonuclease P.
References: [2224, 2705, 2771, 2882]

[EC 3.1.13.1 created 1972 as EC 3.1.4.20, transferred 1978 to EC 3.1.13.1]

EC 3.1.13.2
Accepted name: exoribonuclease H
Reaction: 3′-end directed exonucleolytic cleavage of viral RNA-DNA hybrid
Comments: This is a secondary reaction to the RNA 5′-end directed cleavage 13-19 nucleotides from the RNA end performed by EC 3.1.26.13 (retroviral ribonuclease H).
References: [2687]

[EC 3.1.13.2 created 1978, modified 2010]

EC 3.1.13.3
Accepted name: oligonucleotidase
Reaction: Exonucleolytic cleavage of oligonucleotides to yield nucleoside 5′-phosphates
Other name(s): oligoribonuclease
Comments: Also hydrolyses NAD$^+$ to NMN and AMP.
References: [921]

[EC 3.1.13.3 created 1972 as EC 3.1.4.19, transferred 1978 to EC 3.1.13.3]

EC 3.1.13.4
Accepted name: poly(A)-specific ribonuclease
Reaction: Exonucleolytic cleavage of poly(A) to 5′-AMP
Other name(s): 3′-exoribonuclease; 2′,3′-exoribonuclease
Comments: Cleaves poly(A) in either the single- or double-stranded form.
References: [2719]

[EC 3.1.13.4 created 1984]
EC 3.1.13.5

**Accepted name:** ribonuclease D  
**Reaction:** Exonucleolytic cleavage that removes extra residues from the 3'-terminus of tRNA to produce 5'-mononucleotides  
**Other name(s):** R Nase D  
**Comments:** Requires divalent cations for activity (Mg$^{2+}$, Mn$^{2+}$ or Co$^{2+}$). Alteration of the 3'-terminal base has no effect on the rate of hydrolysis whereas modification of the 3'-terminal sugar has a major effect. tRNA terminating with a 3'-phosphate is completely inactive [554]. This enzyme can convert a tRNA precursor into a mature tRNA [555].  
**References:** [960, 555, 554, 3488]

[EC 3.1.13.5 created 2006]

### EC 3.1.14 Exoribonucleases producing 3'-phosphomonoesters

**EC 3.1.14.1**

**Accepted name:** yeast ribonuclease  
**Reaction:** Exonucleolytic cleavage to nucleoside 3'-phosphates  
**Comments:** Similar enzyme: RNase U$_4$.  
**References:** [2322]

[EC 3.1.14.1 created 1978]

### EC 3.1.15 Exonucleases that are active with either ribo- or deoxyribonucleic acids and produce 5'-phosphomonoesters

**EC 3.1.15.1**

**Accepted name:** venom exonuclease  
**Reaction:** Exonucleolytic cleavage in the 3'- to 5'- direction to yield nucleoside 5'-phosphates  
**Other name(s):** venom phosphodiesterase  
**Comments:** Preference for single-stranded substrate.  
**References:** [1699]

[EC 3.1.15.1 created 1978]

### EC 3.1.16 Exonucleases that are active with either ribo- or deoxyribonucleic acids and produce 3'-phosphomonoesters

**EC 3.1.16.1**

**Accepted name:** spleen exonuclease  
**Reaction:** Exonucleolytic cleavage in the 5'- to 3'-direction to yield nucleoside 3'-phosphates  
**Other name(s):** 3'-exonuclease; spleen phosphodiesterase; 3'-nucleotide phosphodiesterase; phosphodiesterase II  
**Comments:** Preference for single-stranded substrate.  
**References:** [216]

[EC 3.1.16.1 created 1972 as EC 3.1.4.18, transferred 1978 to EC 3.1.16.1]
EC 3.1.21 Endodeoxyribonucleases producing 5’-phosphomonoesters

EC 3.1.21.1

Accepted name: deoxyribonuclease I  
Reaction: Endonucleolytic cleavage to 5’-phosphodinucleotide and 5’-phosphooligonucleotide end-products  
Other name(s): pancreatic DNase; DNase; thymonuclease, dornase; dornava; dornavase; pancreatic deoxyribonuclease; pancreatic dornase; deoxyribonuclease (pancreatic); pancreatic DNase; DNAase; deoxyribonuclease I; alkaline deoxyribonuclease; alkaline DNase; endodeoxyribonuclease I; DNA depolymerase; Escherichia coli endonuclease I; deoxyribonuclease A; DNA endonuclease; DNA nuclease  
Comments: Preference for double-stranded DNA.  
References: [599, 1645, 1700]  


EC 3.1.21.2

Accepted name: deoxyribonuclease IV  
Reaction: Endonucleolytic cleavage of ssDNA at apurinic/apyrimidinic sites to 5’-phosphooligonucleotide end-products  
Other name(s): deoxyribonuclease IV (phage-T₄-induced) (misleading); endodeoxyribonuclease IV (phage T₄-induced) (misleading); E. coli endonuclease IV; endodeoxyribonuclease (misleading); redoxyendonuclease; deoxriboendonuclease (misleading); endonuclease II; endonuclease IV; DNA-adenine-transferase; nfo (gene name)  
Comments: The enzyme is an apurinic/apyrimidinic (AP) site endonuclease that primes DNA repair synthesis at AP sites. It specifically cleaves the DNA backbone at AP sites and also removes 3’ DNA-blocking groups such as 3’ phosphates, 3’ phosphoglycolates, and 3’ α,β-unsaturated aldehydes that arise from oxidative base damage and the activity of combined glycosylase/lyase enzymes. It is also the only known repair enzyme that is able to cleave the DNA backbone 5’ of the oxidative lesion α-deoxyadenosine. The enzyme has a strong preference for single-stranded DNA.  
References: [871, 872, 1075, 562, 1298, 1257]  

[EC 3.1.21.2 created 1972 as EC 3.1.4.30, transferred 1978 to EC 3.1.21.2, modified 2014]

EC 3.1.21.3

Accepted name: type I site-specific deoxyribonuclease  
Reaction: Endonucleolytic cleavage of DNA to give random double-stranded fragments with terminal 5’-phosphates; ATP is simultaneously hydrolysed  
Other name(s): type I restriction enzyme; deoxyribonuclease (ATP- and S-adenosyl-L-methionine-dependent); restriction-modification system; deoxyribonuclease (adenosine triphosphate-hydrolyzing); adenosine triphosphate-dependent deoxyribonuclease; ATP-dependent DNase; type 1 site-specific deoxyribonuclease  
Comments: This is a large group of enzymes which, together with those now listed as EC 3.1.21.4 (type II site-specific deoxyribonuclease) and EC 3.1.21.5 (type III site-specific deoxyribonuclease), were previously listed separately in sub-subclasses EC 3.1.23 and EC 3.1.24. They have an absolute requirement for ATP (or dATP) and S-adenosyl-L-methionine. They recognize specific short DNA sequences and cleave at sites remote from the recognition sequence. They are multifunctional proteins that also catalyse the reactions of EC 2.1.1.72 [site-specific DNA-methyltransferase (adenine-specific)] and EC 2.1.1.37  
References: [2564]  

[EC 3.1.21.3 created 1984 from EC 3.1.23 and EC 3.1.24]
EC 3.1.21.4
Accepted name: type II site-specific deoxyribonuclease
Reaction: Endonucleolytic cleavage of DNA to give specific double-stranded fragments with terminal 5′-phosphates
Other name(s): type II restriction enzyme
Comments: This is a large group of enzymes which, together with those now listed as EC 3.1.21.3 (type I site-specific deoxyribonuclease) and EC 3.1.21.5.
References: [2564]

EC 3.1.21.5
Accepted name: type III site-specific deoxyribonuclease
Reaction: Endonucleolytic cleavage of DNA to give specific double-stranded fragments with terminal 5′-phosphates
Other name(s): type III restriction enzyme; restriction-modification system
Comments: This is a large group of enzymes which, together with those now listed as EC 3.1.21.3 (type I site-specific deoxyribonuclease) and EC 3.1.21.4 (type II site-specific deoxyribonuclease), were previously listed separately in sub-subclasses EC 3.1.23 and EC 3.1.24. They have an absolute requirement for ATP but do not hydrolyse it; S-adenosyl-L-methionine stimulates the reaction, but is not absolutely required. They recognize specific, short DNA sequences and cleave a short distance away from the recognition sequence. These enzymes exist as complexes with enzymes of similar specificity listed under EC 2.1.1.72 [site-specific DNA-methyltransferase (adenine-specific)] or EC 2.1.1.73.
References: [2564]

EC 3.1.21.6
Accepted name: CC-preferring endodeoxyribonuclease
Reaction: Endonucleolytic cleavage to give 5′-phosphooligonucleotide end-products, with a preference for cleavage within the sequence CC
Other name(s): Streptomyces glaucescens exocytoplasmic dodeoxyribonuclease
Comments: Prefers CC sites in double-stranded circular and linear DNA. Greater affinity for double-stranded than single-stranded DNA. Produces nicks, generating double-stranded fragments with 5′- and/or 3′-protruding single-stranded tails. Requires magnesium ions for activity. The endonuclease from Chlorella-like green algae infected with NYs-1 virus 4[3384] may be the same enzyme.
References: [3384, 66]

EC 3.1.21.7
Accepted name: deoxyribonuclease V
Reaction: Endonucleolytic cleavage at apurinic or apyrimidinic sites to products with a 5′-phosphate
Other name(s): endodeoxyribonuclease V; DNase V; Escherichia coli endodeoxyribonuclease V
Comments: Previously classified erroneously as EC 3.1.22.3.
References: [939]

EC 3.1.21.8
Accepted name: T4 deoxyribonuclease II
Reaction: Endonucleolytic nicking and cleavage of cytosine-containing double-stranded DNA.
Other name(s): T4 endonuclease II; EndoII (ambiguous); denA (gene name)
Comments: Requires Mg\(^{2+}\). This phage T\(_4\) enzyme is involved in degradation of host DNA. The enzyme primarily catalyses nicking of the bottom strand of double stranded DNA between the first and second base pair to the right of a top-strand CCGC motif. Double-stranded breaks are produced 5- to 10-fold less frequently \[400\]. It does not cleave the T4 native DNA, which contains 5-hydroxymethylcytosine instead of cytosine.

References: [401, 399, 400, 56]

[EC 3.1.21.8 created 2014]

**EC 3.1.21.9**

Accepted name: T\(_4\) deoxyribonuclease IV

Reaction: Endonucleolytic cleavage of the 5' phosphodiester bond of deoxycytidine in single-stranded DNA.

Other name(s): T\(_4\) endonuclease IV; EndoIV (ambiguous); denB (gene name)

Comments: This phage T\(_4\) enzyme is involved in degradation of host DNA. The enzyme does not cleave double-stranded DNA or native T4 DNA, which contains 5-hydroxymethylcytosine instead of cytosine.

References: [2616, 1801, 2615, 217, 1218, 2275]

[EC 3.1.21.9 created 2014]

**EC 3.1.21.10**

Accepted name: crossover junction endodeoxyribonuclease

Reaction: Endonucleolytic cleavage at a junction such as a reciprocal single-stranded crossover between two homologous DNA duplexes (Holliday junction)

Other name(s): Hje endonuclease; Holliday junction endonuclease CCE1; Holliday junction resolvase; Holliday junction-cleaving endonuclease; Holliday junction-resolving endonuclease; RusA Holliday junction resolvase; RusA endonuclease; RuvC endonuclease; SpCCe1 Holliday junction resolvase; crossover junction endoribonuclease; cruciform-cutting endonuclease; endo X3; endonuclease RuvC; endonuclease VII; endonuclease X3; resolving enzyme CCE1

Comments: The enzyme from *Saccharomyces cerevisiae* has no endonuclease or exonuclease activity on single-stranded or double-stranded DNA molecules that do not contain Holliday junctions.

References: [2964, 2765, 2749, 839, 1780, 2004]

[EC 3.1.21.10 created 1989 as EC 3.1.22.4, modified 2003, transferred 2021 to EC 3.1.21.10]

**EC 3.1.22 Endodeoxyribonucleases producing 3’-phosphomonoesters**

**EC 3.1.22.1**

Accepted name: deoxyribonuclease II

Reaction: Endonucleolytic cleavage to nucleoside 3'-phosphates and 3'-phosphooligonucleotide end-products

Other name(s): DNase II; pancreatic DNase II; deoxyribonuclease 3'-nucleotidohydrolase; DNase II; pancreatic DNase II; acid deoxyribonuclease; acid DNase

Comments: Preference for double-stranded DNA.

References: [218]

[EC 3.1.22.1 created 1961 as EC 3.1.4.6, transferred 1978 to EC 3.1.22.1, modified 1981]

**EC 3.1.22.2**

Accepted name: *Aspergillus* deoxyribonuclease K\(_1\)

Reaction: Endonucleolytic cleavage to nucleoside 3'-phosphates and 3'-phosphooligonucleotide end-products

Other name(s): *Aspergillus* DNase K\(_1\)

Comments: Preference for single-stranded DNA.

References: [1859, 2780]
EC 3.1.22.5

Accepted name: deoxyribonuclease X

Reaction: Endonucleolytic cleavage of supercoiled plasma DNA to linear DNA duplexes

Other name(s): Escherichia coli endodeoxyribonuclease; Escherichia coli endodeoxyribonuclease X

Comments: Preference for supercoiled DNA; little activity on linear double-stranded DNA. Inhibited by single-stranded DNA, ATP and AMP.

References: [961]

[EC 3.1.22.5 created 1992]

EC 3.1.23 Site-specific endodeoxyribonucleases: cleavage is sequence specific (deleted sub-subclass)


[3.1.23.5] Transferred entry. endodeoxyribonuclease Ball. Now EC 3.1.21.4, type II site-specific deoxyribonuclease]

[3.1.23.6] Transferred entry. endodeoxyribonuclease BamHI. Now EC 3.1.21.4, type II site-specific deoxyribonuclease]


[3.1.23.8] Transferred entry. endodeoxyribonuclease BclI. Now EC 3.1.21.4, type II site-specific deoxyribonuclease]

[3.1.23.9] Transferred entry. endodeoxyribonuclease BglII. Now EC 3.1.21.4, type II site-specific deoxyribonuclease]

[3.1.23.10] Transferred entry. endodeoxyribonuclease BglIII. Now EC 3.1.21.4, type II site-specific deoxyribonuclease]


[EC 3.1.23.11 created 1978, deleted 1984]

[EC 3.1.23.12 created 1978, modified 1982, deleted 1984]

[EC 3.1.23.13 created 1978, deleted 1984]

[EC 3.1.23.14 created 1978, deleted 1984]

[EC 3.1.23.15 created 1978, deleted 1984]

[EC 3.1.23.16 created 1978, deleted 1984]

[EC 3.1.23.17 created 1978, deleted 1984]

[EC 3.1.23.18 created 1978, deleted 1984]

[EC 3.1.23.19 created 1978, deleted 1984]

[EC 3.1.23.20 created 1978, deleted 1984]

[EC 3.1.23.21 created 1978, deleted 1984]

[EC 3.1.23.22 created 1978, deleted 1984]

[EC 3.1.23.23 created 1978, deleted 1984]

[EC 3.1.23.24 created 1978, deleted 1984]

[EC 3.1.23.25 created 1978, deleted 1984]

[EC 3.1.23.26 created 1978, deleted 1984]

[EC 3.1.23.27 created 1978, deleted 1984]

[EC 3.1.23.28 created 1978, deleted 1984]
Transferred entry. endodeoxyribonuclease MnlI. Now EC 3.1.21.4, type II site-specific deoxyribonuclease

[EC 3.1.23.29 created 1978, deleted 1984]

Transferred entry. endodeoxyribonuclease PfaI. Now EC 3.1.21.4, type II site-specific deoxyribonuclease

[EC 3.1.23.30 created 1978, modified 1982, deleted 1984]

Transferred entry. endodeoxyribonuclease PstI. Now EC 3.1.21.4, type II site-specific deoxyribonuclease

[EC 3.1.23.31 created 1978, deleted 1984]

Transferred entry. endodeoxyribonuclease PvuI. Now EC 3.1.21.4, type II site-specific deoxyribonuclease

[EC 3.1.23.32 created 1978, modified 1982, deleted 1984]

Transferred entry. endodeoxyribonuclease PvuII. Now EC 3.1.21.4, type II site-specific deoxyribonuclease

[EC 3.1.23.33 created 1978, deleted 1984]

Transferred entry. endodeoxyribonuclease SacI. Now EC 3.1.21.4, type II site-specific deoxyribonuclease

[EC 3.1.23.34 created 1978, deleted 1984]

Transferred entry. endodeoxyribonuclease SacII. Now EC 3.1.21.4, type II site-specific deoxyribonuclease

[EC 3.1.23.35 created 1978, deleted 1984]

Transferred entry. endodeoxyribonuclease SacIII. Now EC 3.1.21.4, type II site-specific deoxyribonuclease

[EC 3.1.23.36 created 1978, deleted 1984]

Transferred entry. endodeoxyribonuclease SalI. Now EC 3.1.21.4, type II site-specific deoxyribonuclease

[EC 3.1.23.37 created 1978, deleted 1984]

Transferred entry. endodeoxyribonuclease SgrI. Now EC 3.1.21.4, type II site-specific deoxyribonuclease

[EC 3.1.23.38 created 1978, deleted 1984]

Transferred entry. endodeoxyribonuclease TaqI. Now EC 3.1.21.4, type II site-specific deoxyribonuclease

[EC 3.1.23.39 created 1978, deleted 1984]

Transferred entry. endodeoxyribonuclease TaqII. Now EC 3.1.21.4, type II site-specific deoxyribonuclease

[EC 3.1.23.40 created 1978, deleted 1984]

Transferred entry. endodeoxyribonuclease XbaI. Now EC 3.1.21.4, type II site-specific deoxyribonuclease

[EC 3.1.23.41 created 1978, deleted 1984]

Transferred entry. endodeoxyribonuclease XhoI. Now EC 3.1.21.4, type II site-specific deoxyribonuclease

[EC 3.1.23.42 created 1978, deleted 1984]

Transferred entry. endodeoxyribonuclease XhoII. Now EC 3.1.21.4, type II site-specific deoxyribonuclease

[EC 3.1.23.43 created 1978, modified 1982, deleted 1984]

Transferred entry. endodeoxyribonuclease XmaI. Now EC 3.1.21.4, type II site-specific deoxyribonuclease

[EC 3.1.23.44 created 1978, deleted 1984]

Transferred entry. endodeoxyribonuclease XniI. Now EC 3.1.21.4, type II site-specific deoxyribonuclease

[EC 3.1.23.45 created 1978, modified 1982, deleted 1984]

Transferred entry. endodeoxyribonuclease AimI. Now EC 3.1.21.4, type II site-specific deoxyribonuclease

[EC 3.1.23.46 created 1978, deleted 1984]
[EC 3.1.23.46 created 1982, deleted 1984]

[3.1.23.47 Transferred entry. endodeoxyribonuclease AccI. Now EC 3.1.21.4, type II site-specific deoxyribonuclease]

[EC 3.1.23.47 created 1982, deleted 1984]

[3.1.23.48 Transferred entry. endodeoxyribonuclease AccII. Now EC 3.1.21.4, type II site-specific deoxyribonuclease]

[EC 3.1.23.48 created 1982, deleted 1984]

[3.1.23.49 Transferred entry. endodeoxyribonuclease AtuAI. Now EC 3.1.21.4, type II site-specific deoxyribonuclease]

[EC 3.1.23.49 created 1982, deleted 1984]

[3.1.23.50 Transferred entry. endodeoxyribonuclease AtuBVI. Now EC 3.1.21.4, type II site-specific deoxyribonuclease]

[EC 3.1.23.50 created 1982, deleted 1984]

[3.1.23.51 Transferred entry. endodeoxyribonuclease AcaI. Now EC 3.1.21.4, type II site-specific deoxyribonuclease]

[EC 3.1.23.51 created 1982, deleted 1984]

[3.1.23.52 Transferred entry. endodeoxyribonuclease AcyI. Now EC 3.1.21.4, type II site-specific deoxyribonuclease]

[EC 3.1.23.52 created 1982, deleted 1984]

[3.1.23.53 Transferred entry. endodeoxyribonuclease AosI. Now EC 3.1.21.4, type II site-specific deoxyribonuclease]

[EC 3.1.23.53 created 1982, deleted 1984]

[3.1.23.54 Transferred entry. endodeoxyribonuclease AsuII. Now EC 3.1.21.4, type II site-specific deoxyribonuclease]

[EC 3.1.23.54 created 1982, deleted 1984]

[3.1.23.55 Transferred entry. endodeoxyribonuclease AvaIII. Now EC 3.1.21.4, type II site-specific deoxyribonuclease]

[EC 3.1.23.55 created 1982, deleted 1984]

[3.1.23.56 Transferred entry. endodeoxyribonuclease AvrII. Now EC 3.1.21.4, type II site-specific deoxyribonuclease]

[EC 3.1.23.56 created 1982, deleted 1984]

[3.1.23.57 Transferred entry. endodeoxyribonuclease BceI4579. Now EC 3.1.21.4, type II site-specific deoxyribonuclease. Assumed to be the same as endodeoxyribonuclease Bce4579I (see http://rebase.neb.com/rebase/rebase.html)]

[EC 3.1.23.57 created 1982, deleted 1984]

[3.1.23.58 Transferred entry. endodeoxyribonuclease Bce1229. Now EC 3.1.21.4, type II site-specific deoxyribonuclease. Assumed to be the same as endodeoxyribonuclease Bce1229I (see http://rebase.neb.com/rebase/rebase.html)]

[EC 3.1.23.58 created 1982, deleted 1984]

[3.1.23.59 Transferred entry. endodeoxyribonuclease Bme899. Now EC 3.1.21.4, type II site-specific deoxyribonuclease. Assumed to be the same as endodeoxyribonuclease Bme899I (see http://rebase.neb.com/rebase/rebase.html)]

[EC 3.1.23.59 created 1982, deleted 1984]

[3.1.23.60 Transferred entry. endodeoxyribonuclease Bme205. Now EC 3.1.21.4, type II site-specific deoxyribonuclease. Assumed to be the same as endodeoxyribonuclease Bme205I (see http://rebase.neb.com/rebase/rebase.html)]

[EC 3.1.23.60 created 1982, deleted 1984]

[3.1.23.61 Transferred entry. endodeoxyribonuclease Bmel. Now EC 3.1.21.4, type II site-specific deoxyribonuclease]

[EC 3.1.23.61 created 1982, deleted 1984]

[3.1.23.62 Transferred entry. endodeoxyribonuclease Bsp1286. Now EC 3.1.21.4, type II site-specific deoxyribonuclease. Assumed to be the same as endodeoxyribonuclease Bsp1286I (see http://rebase.neb.com/rebase/rebase.html)]

88


[3.1.23.67] Transferred entry. endodeoxyribonuclease BsuMI. Now EC 3.1.21.4, type II site-specific deoxyribonuclease. Assumed to be the same as endodeoxyribonuclease BsuMI (see http://rebase.neb.com/rebase/rebase.html)

[3.1.23.68] Transferred entry. endodeoxyribonuclease Bsu6633. Now EC 3.1.21.4, type II site-specific deoxyribonuclease. The name was misprinted in supplement 3 of the 1978 edition. Assumed to be the same as endodeoxyribonuclease Bsu6633I (see http://rebase.neb.com/rebase/rebase.html)


[3.1.23.70] Transferred entry. endodeoxyribonuclease Bsu1192. Now EC 3.1.21.4, type II site-specific deoxyribonuclease. Assumed to be the same as endodeoxyribonuclease Bsu1192I or see Bsu1192II (see http://rebase.neb.com/rebase/rebase.html)


[3.1.23.77 Created 1982, deleted 1984]

Transferred entry. endodeoxyribonuclease EclII. Now EC 3.1.21.4, type II site-specific deoxyribonuclease

[EC 3.1.23.77 created 1982, deleted 1984]

Transferred entry. endodeoxyribonuclease EcaI. Now EC 3.1.21.4, type II site-specific deoxyribonuclease

[EC 3.1.23.79 created 1982, deleted 1984]

Transferred entry. endodeoxyribonuclease EcoRf. Now EC 3.1.21.4, type II site-specific deoxyribonuclease. Assumed to be the same as endodeoxyribonuclease EcoRf (see http://rebase.neb.com/rebase/rebase.html)

[EC 3.1.23.80 created 1982, deleted 1984]

Transferred entry. endodeoxyribonuclease Fnu4HI. Now EC 3.1.21.4, type II site-specific deoxyribonuclease. Assumed to be the same as endodeoxyribonuclease Fnu4HI (see http://rebase.neb.com/rebase/rebase.html)

[EC 3.1.23.82 created 1982, deleted 1984]

Transferred entry. endodeoxyribonuclease HapI. Now EC 3.1.21.4, type II site-specific deoxyribonuclease

[EC 3.1.23.83 created 1982, deleted 1984]

Transferred entry. endodeoxyribonuclease Hin1056II. Now EC 3.1.21.4, type II site-specific deoxyribonuclease

[EC 3.1.23.84 created 1982, deleted 1984]

Transferred entry. endodeoxyribonuclease HinfIII. Now EC 3.1.21.4, type II site-specific deoxyribonuclease

[EC 3.1.23.85 created 1982, deleted 1984]

Transferred entry. endodeoxyribonuclease HgiAI. Now EC 3.1.21.4, type II site-specific deoxyribonuclease

[EC 3.1.23.86 created 1982, deleted 1984]

Transferred entry. endodeoxyribonuclease HgiCI. Now EC 3.1.21.4, type II site-specific deoxyribonuclease

[EC 3.1.23.87 created 1982, deleted 1984]

Transferred entry. endodeoxyribonuclease HgiDI. Now EC 3.1.21.4, type II site-specific deoxyribonuclease

[EC 3.1.23.88 created 1982, deleted 1984]

Transferred entry. endodeoxyribonuclease HgiEII. Now EC 3.1.21.4, type II site-specific deoxyribonuclease

[EC 3.1.23.89 created 1982, deleted 1984]

Transferred entry. endodeoxyribonuclease MstI. Now EC 3.1.21.4, type II site-specific deoxyribonuclease

[EC 3.1.23.90 created 1982, deleted 1984]

Transferred entry. endodeoxyribonuclease MstII. Now EC 3.1.21.4, type II site-specific deoxyribonuclease

[EC 3.1.23.91 created 1982, deleted 1984]

Transferred entry. endodeoxyribonuclease MglII. Now EC 3.1.21.4, type II site-specific deoxyribonuclease

[EC 3.1.23.92 created 1982, deleted 1984]

Transferred entry. endodeoxyribonuclease MglIII. Now EC 3.1.21.4, type II site-specific deoxyribonuclease

[EC 3.1.23.93 created 1982, deleted 1984]

Transferred entry. endodeoxyribonuclease MnoII. Now EC 3.1.21.4, type II site-specific deoxyribonuclease

[EC 3.1.23.94 created 1982, deleted 1984]
[EC 3.1.23.94 created 1982, deleted 1984]


[EC 3.1.23.95 created 1982, deleted 1984]


[EC 3.1.23.96 created 1982, deleted 1984]


[EC 3.1.23.97 created 1982, deleted 1984]


[EC 3.1.23.98 created 1982, deleted 1984]


[EC 3.1.23.99 created 1982, deleted 1984]


[EC 3.1.23.100 created 1982, deleted 1984]


[EC 3.1.23.101 created 1982, deleted 1984]


[EC 3.1.23.102 created 1982, deleted 1984]


[EC 3.1.23.103 created 1982, deleted 1984]


[EC 3.1.23.104 created 1982, deleted 1984]


[EC 3.1.23.105 created 1982, deleted 1984]


[EC 3.1.23.106 created 1982, deleted 1984]


[EC 3.1.23.107 created 1982, deleted 1984]


[EC 3.1.23.108 created 1982, deleted 1984]


[EC 3.1.23.109 created 1982, deleted 1984]
EC 3.1.24 Site specific endodeoxyribonucleases: cleavage is not sequence specific (deleted sub-subclass)

[3.1.24.1 Transferred entry. endodeoxyribonuclease EcoB. Now EC 3.1.21.3, type I site-specific deoxyribonuclease. Assumed to be the same as endodeoxyribonuclease EcoBI (see http://rebase.neb.com/rebase/rebase.html)]

[EC 3.1.24.1 created 1978, modified 1982, deleted 1984]

[3.1.24.2 Transferred entry. endodeoxyribonuclease EcoK. Now EC 3.1.21.3, type I site-specific deoxyribonuclease. Assumed to be the same as endodeoxyribonuclease EcoKI (see http://rebase.neb.com/rebase/rebase.html)]

[EC 3.1.24.2 created 1978, modified 1982, deleted 1984]

[3.1.24.3 Transferred entry. endodeoxyribonuclease EcoPI. Now EC 3.1.21.5, type III site-specific deoxyribonuclease. The name is misprinted in supplement 3 of the 1978 edition]

[EC 3.1.24.3 created 1978, modified 1982, deleted 1984]

[3.1.24.4 Transferred entry. endodeoxyribonuclease EcoP15. Now EC 3.1.21.5, type III site-specific deoxyribonuclease. Assumed to be the same as endodeoxyribonuclease EcoP15I (see http://rebase.neb.com/rebase/rebase.html)]

[EC 3.1.24.4 created 1978, modified 1982, deleted 1984]

EC 3.1.25 Site-specific endodeoxyribonucleases that are specific for altered bases

EC 3.1.25.1

Accepted name: deoxyribonuclease (pyrimidine dimer)

Reaction: Endonucleolytic cleavage near pyrimidine dimers to products with 5′-phosphate

Other name(s): endodeoxyribonuclease (pyrimidine dimer); endodeoxyribonuclease (pyrimidine dimer); bacterio-phage T4 endodeoxyribonuclease V; T4 endonuclease V

Comments: Acts on a damaged strand, 5′ from the damaged site.

References: [307, 2543]

[EC 3.1.25.1 created 1978]

[3.1.25.2 Transferred entry. endodeoxyribonuclease (apurinic or apyrimidinic). Now EC 4.2.99.18, DNA-(apurinic or apyrimidinic site) lyase]

[EC 3.1.25.2 created 1978, deleted 1992]

EC 3.1.26 Endoribonucleases producing 5′-phosphomonoesters

EC 3.1.26.1

Accepted name: Physarum polycephalum ribonuclease

Reaction: Endonucleolytic cleavage to 5′-phosphomonoester

References: [1216]

[EC 3.1.26.1 created 1978]

EC 3.1.26.2

Accepted name: ribonuclease α

Reaction: Endonucleolytic cleavage to 5′-phosphomonoester

Other name(s): 2′-O-methyl RNase

Comments: Specific for O-methylated RNA.

References: [2223]

92
EC 3.1.26.3

Accepted name: ribonuclease III
Reaction: Endonucleolytic cleavage to a 5′-phosphomonoester
Other name(s): RNase III; ribonuclease 3
Comments: This is an endoribonuclease that cleaves double-stranded RNA molecules [1050]. The cleavage can be either a single-stranded nick or double-stranded break in the RNA, depending in part upon the degree of base-pairing in the region of the cleavage site [538]. Specificity is conferred by negative determinants, i.e., the presence of certain Watson-Crick base-pairs at specific positions that strongly inhibit cleavage [3489]. RNase III is involved in both rRNA processing and mRNA processing and decay.
References: [553, 2515, 2567, 1050, 538, 3489]

[EC 3.1.26.3 created 1978, modified 2006]

EC 3.1.26.4

Accepted name: ribonuclease H
Reaction: Endonucleolytic cleavage to 5′-phosphomonoester
Other name(s): endoribonuclease H (calf thymus); RNase H; RNA*DNA hybrid ribonucleotidohydrolase; hybrid ribonuclease; hybridase; hybridase (ribonuclease H); ribonuclease H; hybrid nuclease; calf thymus ribonuclease H
Comments: Acts on RNA-DNA hybrids.
References: [1073, 2898]

[EC 3.1.26.4 created 1978, modified 2010]

EC 3.1.26.5

Accepted name: ribonuclease P
Reaction: Endonucleolytic cleavage of RNA, removing 5′-extranucleotides from tRNA precursor
Other name(s): RNase P
Comments: An RNA-containing enzyme, essential for tRNA processing; generates 5′-termini or mature tRNA molecules.
References: [237, 238, 2566]

[EC 3.1.26.5 created 1978, modified 1982]

EC 3.1.26.6

Accepted name: ribonuclease IV
Reaction: Endonucleolytic cleavage of poly(A) to fragments terminated by 3′-hydroxy and 5′-phosphate groups
Other name(s): endoribonuclease IV; poly(A)-specific ribonuclease
Comments: Forms oligonucleotides with an average chain length of 10.
References: [2097, 2098]

[EC 3.1.26.6 created 1984]

EC 3.1.26.7

Accepted name: ribonuclease P4
Reaction: Endonucleolytic cleavage of RNA, removing 3′-extranucleotides from tRNA precursor
References: [2743]

[EC 3.1.26.7 created 1984]
EC 3.1.26.8
Accepted name: ribonuclease M5
Reaction: Endonucleolytic cleavage of RNA, removing 21 and 42 nucleotides, respectively, from the 5′- and 3′-termini of a 5S-rRNA precursor
Other name(s): RNase M5; 5S ribosomal maturation nuclease; 5S ribosomal RNA maturation endonuclease
Comments: Converts the 5S-rRNA precursor from Bacillus subtilis into 5S-rRNA, with 5′-phosphate and 3′-hydroxy groups.
References: [2848]

[EC 3.1.26.8 created 1986]

EC 3.1.26.9
Accepted name: ribonuclease [poly-(U)-specific]
Reaction: Endonucleolytic cleavage of poly(U) to fragments terminated by 3′-hydroxy and 5′-phosphate groups
Other name(s): ribonuclease (uracil-specific); uracil-specific endoribonuclease; uracil-specific RNase
Comments: Forms oligonucleotides with chain lengths of 6 to 12.
References: [127]

[EC 3.1.26.9 created 1986]

EC 3.1.26.10
Accepted name: ribonuclease IX
Reaction: Endonucleolytic cleavage of poly(U) or poly(C) to fragments terminated by 3′-hydroxy and 5′-phosphate groups
Other name(s): poly(U)- and poly(C)-specific endoribonuclease
Comments: Acts on poly(U) and poly(C), with a higher affinity for poly(C), but does not act on poly(A) or poly(G).
References: [2788]

[EC 3.1.26.10 created 1992]

EC 3.1.26.11
Accepted name: tRNase Z
Reaction: Endonucleolytic cleavage of RNA, removing extra 3′ nucleotides from tRNA precursor, generating 3′ termini of tRNAs. A 3′-hydroxy group is left at the tRNA terminus and a 5′-phosphoryl group is left at the trailer molecule
Other name(s): 3′ tRNase; tRNA 3 endonuclease; RNase Z; 3′ tRNase
Comments: No cofactor requirements. An homologous enzyme to that found in Arabidopsis thaliana has been found in Methanococcus janaschii.
References: [2697, 1949, 2696, 1648, 2080, 2019, 2992]

[EC 3.1.26.11 created 2002]

EC 3.1.26.12
Accepted name: ribonuclease E
Reaction: Endonucleolytic cleavage of single-stranded RNA in A- and U-rich regions
Other name(s): endoribonuclease E; RNase E; Rne protein
Comments: RNase E is a bacterial ribonuclease that plays a role in the processing of ribosomal RNA (9S to 5S rRNA), the chemical degradation of bulk cellular RNA, the decay of specific regulatory, messenger and structural RNAs and the control of plasmid DNA replication [806]. The enzyme binds to monophosphorylated 5′ ends of substrates but exhibits sequential cleavages in the 3′ to 5′ direction [806]. 2′-O-Methyl nucleotide substitutions at RNase E binding sites do not prevent binding but do prevent cleavage of non-modified target sequences 5′ to that locus [806]. In *Escherichia coli*, the enzyme is found in the RNA degradosome. The C-terminal half of the protein contains binding sites for the three other major degradosomal components, the DEAD-box RNA helicase Rh1B, enolase (EC 4.1.1.11) and polynucleotide phosphorylase (EC 2.7.7.8).

References: [806, 727, 527, 3200, 2899, 385]

[EC 3.1.26.12 created 2008]

**EC 3.1.26.13**

**Accepted name:** retroviral ribonuclease H

**Reaction:** Endohydrolysis of RNA in RNA/DNA hybrids. Three different cleavage modes: 1. sequence-specific internal cleavage of RNA [1-4]. Human immunodeficiency virus type 1 and Moloney murine leukemia virus enzymes prefer to cleave the RNA strand one nucleotide away from the RNA-DNA junction [5]. 2. RNA 5′-end directed cleavage 13-19 nucleotides from the RNA end [6,7]. 3. DNA 3′-end directed cleavage 15-20 nucleotides away from the primer terminus [8-10].

**Other name(s):** RT/RNase H; retroviral reverse transcriptase RNaseH; HIV RNase H

**Comments:** Retroviral reverse transcriptase is a multifunctional enzyme responsible for viral replication. To perform this task the enzyme combines two distinct activities. The polymerase domain (EC 2.7.7.49, RNA-directed DNA polymerase) occupies the N-terminal two-thirds of the reverse transcriptase whereas the ribonuclease H domain comprises the C-terminal remaining one-third [421, 2722]. The RNase H domain of Moloney murine leukemia virus and Human immunodeficiency virus display two metal binding sites [991, 590, 2344].

**References:** [2723, 2655, 2502, 314, 2724, 634, 1479, 2336, 880, 200, 1277, 1629, 421, 2722, 991, 590, 2344]

[EC 3.1.26.13 created 2009]

**EC 3.1.27 Endoribonucleases producing 3′-phosphomonoesters**

[3.1.27.1] Transferred entry. ribonuclease T2. Now EC 4.6.1.19, ribonuclease T2, since the primary reaction is that of a lyase]

[EC 3.1.27.1 created 1972 as EC 3.1.4.23, transferred 1978 to EC 3.1.27.1, modified 1981, deleted 2018]

[3.1.27.2] Transferred entry. Bacillus subtilis ribonuclease. Now EC 4.6.1.22, Bacillus subtilis ribonuclease, since the reaction catalysed is that of a lyase]

[EC 3.1.27.2 created 1978, deleted 2018]

[3.1.27.3] Transferred entry. ribonuclease T1. Now EC 4.6.1.24, ribonuclease T1, since the primary reaction is that of a lyase]

[EC 3.1.27.3 created 1961 as EC 3.1.4.8, transferred 1965 to EC 2.7.7.26, reinstated 1972 as EC 3.1.4.8, transferred 1978 to EC 3.1.27.3, deleted 2020]

[3.1.27.4] Transferred entry. ribonuclease U2. Now EC 4.6.1.20, ribonuclease U2, since the primary reaction is that of a lyase]

[EC 3.1.27.4 created 1978, modified 1981, deleted 2018]

[3.1.27.5] Transferred entry. pancreatic ribonuclease. Now EC 4.6.1.18, pancreatic ribonuclease. This reaction is now known to involve an internal-transfer (lyase) process to produce the cyclic derivative, followed by a reversal of that step with water in the "hydrolytic step"]
[EC 3.1.27.5 created 1972 as EC 3.1.4.22, transferred 1978 to EC 3.1.27.5, modified 1981, deleted 2018]

[3.1.27.6 Transferred entry. Enterobacter ribonuclease. Now EC 4.6.1.21, Enterobacter ribonuclease, since the primary reaction is that of a lyase]

[EC 3.1.27.6 created 1978, modified 1981, deleted 2018]

EC 3.1.27.7

Accepted name: ribonuclease F

Reaction: Endonucleolytic cleavage of RNA precursor into two, leaving 5’-hydroxy and 3’-phosphate groups

Other name(s): ribonuclease F (E. coli)

References: [1062, 3290]

[EC 3.1.27.7 created 1984]

EC 3.1.27.8

Accepted name: ribonuclease V

Reaction: Hydrolysis of poly(A), forming oligoribonucleotides and ultimately 3’-AMP

Other name(s): endoribonuclease V

Comments: Also hydrolyses poly(U).

References: [2718]

[EC 3.1.27.8 created 1984]

[3.1.27.9 Transferred entry. tRNA-intron endonuclease. Now EC 4.6.1.16, tRNA-intron lyase]

[EC 3.1.27.9 created 1992, deleted 2014]

[3.1.27.10 Transferred entry. rRNA endonuclease. Now EC 4.6.1.23, ribotoxin, since the primary reaction is that of a lyase.]

[EC 3.1.27.10 created 1992, deleted 2019]

EC 3.1.30 Endoribonucleases that are active with either ribo- or deoxyribonucleic acids and produce 5’-phosphomonoesters

EC 3.1.30.1

Accepted name: Aspergillus nuclease S1

Reaction: Endonucleolytic cleavage to 5’-phosphomononucleotide and 5’-phospho[oligonucleotide end-products

Other name(s): endonuclease S1 (Aspergillus); single-stranded-nucleate endonuclease; deoxyribonuclease S1; deoxyribonuclease S1; nuclease S1; Neurospora crassa single-strand specific endonuclease; S1 nuclease; single-strand endodeoxyribonuclease; single-stranded DNA specific endonuclease; single-strand-specific endodeoxyribonuclease; single strand-specific DNase; Aspergillus oryzae S1 nuclease

References: [58, 2951, 3227]

[EC 3.1.30.1 created 1972 as EC 3.1.4.21, transferred 1978 to EC 3.1.30.1, modified 1981]

EC 3.1.30.2

Accepted name: Serratia marcescens nuclease

Reaction: Endonucleolytic cleavage to 5’-phosphomononucleotide and 5’-phospho[oligonucleotide end-products

Other name(s): endonuclease (Serratia marcescens); barley nuclease; plant nuclease I; nucleate endonuclease

Comments: Hydrolyses double- or single-stranded substrate.

References: [2006, 2908, 2909, 3297]

[EC 3.1.30.2 created 1965 as EC 3.1.4.9, transferred 1978 to EC 3.1.30.2, modified 1981]
EC 3.1.31 Endoribonucleases that are active with either ribo- or deoxyribonucleic acids and produce 3'-phosphomonoesters

EC 3.1.31.1
Accepted name: micrococcal nuclease
Reaction: Endonucleolytic cleavage to nucleoside 3'-phosphates and 3'-phosphooligonucleotide end-products
Other name(s): spleen endonuclease; thermonuclease; nuclease T; micrococcal endonuclease; nuclease T'; staphylococcal nuclease; spleen phosphodiesterase; Staphylococcus aureus nuclease; Staphylococcus aureus nuclease B; ribonuclease (deoxynuclease) 3'-nucleotidohydrolase
Comments: Hydrolyses double- or single-stranded substrate.
References: [34, 60, 2517, 2939]

[EC 3.1.31.1 created 1961 as EC 3.1.4.7, transferred 1978 to EC 3.1.31.1, modified 1981]

EC 3.2 Glycosylases
This subclass contains the glycosylases, which are classified as hydrolases, although some of them can also transfer glycosyl residues to oligosaccharides, polysaccharides and other alcoholic acceptors. The glycosylases are subdivided into glycosidases, i.e., enzymes that hydrolyse O- and S-glycosyl compounds (EC 3.2.1) and those that hydrolyse N-glycosyl compounds (EC 3.2.2). Common names for enzymes acting on D-sugars or their derivatives do not normally contain ‘D’, unless ambiguity would result from the common existence of the corresponding L-sugar. Enzymes that hydrolyse a terminal, non-reducing-end glycosyl compound (or a well-defined di-, tri- or oligosaccharide) from a glycan, i.e. exoenzymes, are given systematic names based on ‘glycohydrolase’; enzymes that hydrolyse internal glycosidic bonds, i.e. endoenzymes, are given systematic names based on ‘glycanohydrolase’. The same structure is often used when providing accepted names for these enzymes.

EC 3.2.1 Glycosidases, i.e. enzymes that hydrolyse O- and S-glycosyl compounds

EC 3.2.1.1
Accepted name: α-amylase
Reaction: Endohydrolysis of (1→4)-α-D-glucosidic linkages in polysaccharides containing three or more (1→4)-α-linked D-glucose units
Other name(s): glycogenase; α amylase; endoamylase; Taka-amylase A; 1,4-α-D-glucan glucanohydrolase
Systematic name: 4-α-D-glucan glucanohydrolase
Comments: Acts on starch, glycogen and related polysaccharides and oligosaccharides in a random manner; reducing groups are liberated in the α-configuration. The term ”α” relates to the initial anomeric configuration of the free sugar group released and not to the configuration of the linkage hydrolysed.
References: [823, 1898, 2731]

[EC 3.2.1.1 created 1961]

EC 3.2.1.2
Accepted name: β-amylase
Reaction: Hydrolysis of (1→4)-α-D-glucosidic linkages in polysaccharides so as to remove successive maltose units from the non-reducing ends of the chains
Other name(s): saccharogen amylase; glycogenase; β amylase; 1,4-α-D-glucan maltohydrolase
Systematic name: 4-α-D-glucan maltohydrolase
Comments: Acts on starch, glycogen and related polysaccharides and oligosaccharides producing β-maltose by an inversion. The term ”β” relates to the initial anomeric configuration of the free sugar group released and not to the configuration of the linkage hydrolysed.
References: [143, 859, 1898]
EC 3.2.1.2

**Accepted name:** glucan 1,4-\(\alpha\)-glucosidase

**Reaction:** Hydrolysis of terminal (1→4)-linked \(\alpha\)-D-glucose residues successively from non-reducing ends of the chains with release of \(\beta\)-D-glucose

**Other name(s):** glucamylase; amyloglucosidase; \(\gamma\)-amylase; lysosomal \(\alpha\)-glucosidase; acid maltase; exo-1,4-\(\alpha\)-glucosidase; glucose amylase; \(\gamma\)-1,4-glucan glucohydrolase; acid maltase; 1,4-\(\alpha\)-D-glucan glucohydrolase

**Systematic name:** 4-\(\alpha\)-D-glucan glucohydrolase

**Comments:** Most forms of the enzyme can rapidly hydrolyse 1,6-\(\alpha\)-D-glucosidic bonds when the next bond in the sequence is 1,4, and some preparations of this enzyme hydrolyse 1,6- and 1,3-\(\alpha\)-D-glucosidic bonds in other polysaccharides. This entry covers all such enzymes acting on polysaccharides more rapidly than on oligosaccharides. EC 3.2.1.20 \(\alpha\)-glucosidase, from mammalian intestine, can catalyse similar reactions.

**References:** [860, 336, 1394, 1502, 2014, 3126]

EC 3.2.1.3

**Accepted name:** cellulase

**Reaction:** Endohydrolysis of (1→4)-\(\beta\)-D-glucosidic linkages in cellulose, lichenin and cereal \(\beta\)-D-glucans

**Other name(s):** endo-1,4-\(\beta\)-D-glucanase; \(\beta\)-1,4-endoglucan hydrolase; celluase A; cellulosin AP; endoglucanase D; alkali cellulase; cellulase A 3; celludextrinase; 9.5 cellulase; avicelase; pancellase SS; 1,4-(1,3;1,4)-\(\beta\)-D-glucan 4-glucanohydrolase

**Systematic name:** 4-\(\beta\)-D-glucan 4-glucanohydrolase

**Comments:** Will also hydrolyse 1,4-linkages in \(\beta\)-D-glucans also containing 1,3-linkages.

**References:** [582, 1695, 2117, 2203, 3321, 1141, 1142, 1329]

EC 3.2.1.4

**Accepted name:** endo-1,3(4)-\(\beta\)-glucanase

**Reaction:** Endohydrolysis of (1→3)- or (1→4)-linkages in \(\beta\)-D-glucans when the glucose residue whose reducing group is involved in the linkage to be hydrolysed is itself substituted at C-3

**Other name(s):** endo-1,3-\(\beta\)-D-glucanase; laminarinase; laminaranase; \(\beta\)-1,3-1,4-glucanase; endo-1,3-\(\beta\)-glucanase; endo-1,3-1,4-glucanase; endo-\(\beta\)-(1→3)-D-glucanase; endo-1,3-1,4-\(\beta\)-D-glucanase; endo-\(\beta\)-(1-3)-D-glucanase; endo-\(\beta\)-1,3-1,4-glucanase IV; endo-1,3-\(\beta\)-D-glucanase; 1,3-(1,3;1,4)-\(\beta\)-D-glucan 3(4)-glucanohydrolase

**Systematic name:** 3(or 4)-\(\beta\)-D-glucan 3(4)-glucanohydrolase

**Comments:** Substrates include laminarin, lichenin and cereal D-glucans; different from EC 3.2.1.52 \(\beta\)-N-acetylhexosaminidase.

**References:** [166, 167, 561, 2523, 2873]

EC 3.2.1.5

**Deleted entry. licheninase**

[3.2.1.5 created 1961, deleted 1964]

EC 3.2.1.6

**Accepted name:** inulinase

**Reaction:** Endohydrolysis of (2→1)-\(\beta\)-D-fructosidic linkages in inulin

**Other name(s):**

**Systematic name:**

**Comments:**

**References:** [166, 167, 561, 2523, 2873]

[EC 3.2.1.6 created 1961, modified 1976]
Other name(s): inulase; indoinulinase; endo-inulinase; exoinulinase; 2,1-β-D-fructan fructanohydrolase
Systematic name: 1-β-D-fructan fructanohydrolase
References: [18]

[EC 3.2.1.7 created 1961]

EC 3.2.1.8
Accepted name: endo-1,4-β-xylanase
Reaction: Endohydrolysis of (1→4)-β-D-xylosidic linkages in xylans
Other name(s): endo-(1→4)-β-xylan 4-xylanohydrolase; endo-1,4-xylanase; xylanase; β-1,4-xylanase; endo-1,4-xylanase; endo-β-1,4-xylanase; endo-1,4-β-D-xylanase; 1,4-β-xylan xylanohydrolase; β-xylanase; β-1,4-xylan xylanohydrolase; endo-1,4-β-xylanase; β-D-xylanase
Systematic name: 4-β-D-xylan xylanohydrolase
References: [1266, 3320]

[EC 3.2.1.8 created 1961]

[3.2.1.9 Deleted entry. amylopectin-1,6-glucosidase]

[EC 3.2.1.9 created 1961, deleted 1972]

EC 3.2.1.10
Accepted name: oligo-1,6-glucohydrolase
Reaction: Hydrolysis of (1→6)-α-D-glucosidic linkages in some oligosaccharides produced from starch and glycogen by EC 3.2.1.1 (α-amylase), and in isomaltose
Other name(s): limit dextrinase (erroneous); isomaltase; sucrase-isomaltase; exo-oligo-1,6-glucohydrolase; dextrin 6α-glucanohydrolase; α-limit dextrinase; dextrin 6-glucanohydrolase; oligosaccharide α-1,6-glucohydrolase; α-methylglucosidase
Systematic name: oligosaccharide 6α-glucohydrolase
Comments: This enzyme, like EC 3.2.1.33 (amylo-α-1,6-glucosidase), can release an α-1→6-linked glucose, whereas the shortest chain that can be released by EC 3.2.1.41 (pullulanase), EC 3.2.1.142 (limit dextrinase), and EC 3.2.1.68 (isoamylase) is maltose. It also hydrolyses isomaltulose (palatinose), isomaltotriose and panose, but has no action on glycogen or phosphorylase limit dextrin. The enzyme from intestinal mucosa is a single polypeptide chain that also catalyses the reaction of EC 3.2.1.48 (sucrose α-glucosidase). Differ from EC 3.2.1.33 (amylo-α-1,6-glucosidase) in its preference for short-chain substrates and in its not requiring the 6-glucosylated residue to be at a branch point, i.e. linked at both C-1 and C-4.
References: [1144, 2817, 2576, 1517, 3404]

[EC 3.2.1.10 created 1961, modified 2000, modified 2013]

EC 3.2.1.11
Accepted name: dextranase
Reaction: Endohydrolysis of (1→6)-α-D-glucosidic linkages in dextran
Other name(s): dextran hydrolase; endodextranase; dextranase DL 2; DL 2; endo-dextranase; α-D-1,6-glucan-6-glucanohydrolase; 1,6-α-D-glucan 6-glucanohydrolase
Systematic name: 6-α-D-glucan 6-glucanohydrolase
References: [134, 636, 824, 2601]

[EC 3.2.1.11 created 1961]

[3.2.1.12 Deleted entry. cycloheptaglucanase. Now included with EC 3.2.1.54 cyclomaltodextrinase]

[EC 3.2.1.12 created 1961, deleted 1976]

[3.2.1.13 Deleted entry. cyclohexaglucanase. Now included with EC 3.2.1.54 cyclomaltodextrinase]
EC 3.2.1.14

Accepted name: chitinase

Reaction: Random endo-hydrolysis of N-acetyl-\(\beta\)-D-glucosaminide \((1\rightarrow4)\)-\(\beta\)-linkages in chitin and chitodextrins

Other name(s): ChiC; chitodextrinase (ambiguous); 1,4-\(\beta\)-poly-N-acetylglucosaminidase; poly-\(\beta\)-glucosaminidase; \(\beta\)-1,4-poly-\(N\)-acetyl glucosaminidase; poly\([1,4-(N\text{-acetyl-}\beta\text{-D-glucosaminide})]\) glycanohydrolase

Systematic name: \((1\rightarrow4)\)-2-acetamido-2-deoxy-\(\beta\)-D-glucan glycanohydrolase

Comments: The enzyme binds to chitin and randomly cleaves glycosidic linkages in chitin and chitodextrins in a non-processive mode, generating chitooligosaccharides and free ends on which exo-chitinases and exo-chitodextrinases can act. Activity is greatly stimulated in the presence of EC 1.14.99.53, lytic chitin monoxygenase, which attacks the crystalline structure of chitin and makes the polymer more accessible to the chitinase. cf. EC 3.2.1.202, endo-chitodextrinase.

References: [3480, 3102, 824, 517, 854, 3519, 2592]

EC 3.2.1.15

Accepted name: endo-polygalacturonase

Reaction: \((1,4-\alpha\text{-D-galacturonosyl})_{n+m} + \text{H}_2\text{O} = (1,4-\alpha\text{-D-galacturonosyl})_{n} + (1,4-\alpha\text{-D-galacturonosyl})_{m}\)

Other name(s): pectin depolymerase (ambiguous); pectinase (ambiguous); endopolygalacturonase; pectolase (ambiguous); pectin hydrolase (ambiguous); pectin polygalacturonase (ambiguous); polygalacturonic acid glycanohydrolase (ambiguous); endogalacturonase; endo-D-galacturonanase; poly\([1,4-\alpha\text{-D-galacturonide}]\) glycanohydrolase (ambiguous)

Systematic name: \((1\rightarrow4)\)-\(\alpha\)-D-galacturonan glycanohydrolase (endo-cleaving)

Comments: The enzyme catalyses the random hydrolysis of \((1\rightarrow4)\)-\(\alpha\)-D-galactosiduronic linkages in pectate and other galacturonans. Different forms of the enzyme have different tolerances to methyl esterification of the substrate.

References: [1800, 1960, 2391, 636, 2008]

EC 3.2.1.16

Deleted entry. alginase

[3.2.1.16 created 1961, deleted 1972]

EC 3.2.1.17

Accepted name: lysozyme

Reaction: Hydrolysis of \((1\rightarrow4)\)-\(\beta\)-linkages between \(N\text{-acetyl-}L\text{-muramic acid and }N\text{-acetyl-D-glucosamine residues in a peptidoglycan and between }N\text{-acetyl-}D\text{-glucosamine residues in chitodextrins}

Other name(s): muramidase; globulin G; mucopeptide glycohydrolase; globulin G1; \(N,O\text{-diacetyl}L\text{-muramidase; lysozyme g; L-7001; }1,4-N\text{-acetyl}L\text{-muramidase; mucopeptide }N\text{-acetyl}L\text{-muramoylhydrolase; PR1-lysozyme}

Systematic name: peptidoglycan \(N\text{-acetyl}L\text{-muramoylhydrolase}

Comments: cf. also EC 3.2.1.14 chitinase.

References: [257, 259, 1416]

EC 3.2.1.18

Accepted name: exo-\(\alpha\)-sialidase

Reaction: Hydrolysis of \(\alpha\)-(2\rightarrow3)-, \(\alpha\)-(2\rightarrow6)-, \(\alpha\)-(2\rightarrow8)- glycosidic linkages of terminal sialic acid residues in oligosaccharides, glycoproteins, glycolipids, colominic acid and synthetic substrates
Other name(s): neuraminidase; sialidase; α-neuraminidase; acetylneuraminidase
Systematic name: acetylneuraminyl hydrolase
Comments: The enzyme does not act on 4-O-acetylated sialic acids. endo-α-Sialidase activity is listed as EC 3.2.1.129, endo-α-sialidase. See also EC 4.2.2.15 anhydrosialidase.
References: [2688, 376]

[EC 3.2.1.18 created 1961, modified 1999]

[3.2.1.19 Deleted entry. heparinase]

[EC 3.2.1.19 created 1961, deleted 1978]

EC 3.2.1.20
Accepted name: α-glucosidase
Reaction: Hydrolysis of terminal, non-reducing (1→4)-linked α-D-glucose residues with release of D-glucose
Other name(s): maltase; glucoinvertase; glucosidoseurase; maltase-glucoamylase; α-glucopyranosidase; glucosidoinvertase; α-D-glucosidase; α-glucose hydrolase; α-1,4-glucosidase
Systematic name: α-D-glucoside glucohydrolase
Comments: This single entry covers a group of enzymes whose specificity is directed mainly towards the exo-hydrolysis of (1→4)-α-glucosidic linkages, and that hydrolyse oligosaccharides rapidly, relative to polysaccharide, which are hydrolysed relatively slowly, or not at all. The intestinal enzyme also hydrolyses polysaccharides, catalysing the reactions of EC 3.2.1.3 glucan 1,4-α-glucosidase and, more slowly, hydrolyses (1→6)-α-D-glucose links.
References: [348, 833, 1695, 2814, 2865]

[EC 3.2.1.20 created 1961]

EC 3.2.1.21
Accepted name: β-glucosidase
Reaction: Hydrolysis of terminal, non-reducing β-D-glucosyl residues with release of β-D-glucose
Other name(s): gentiobiose; cellobiose; emulsin; elaterase; aryl-β-glucosidase; β-D-glucosidase; β-glucoside glycohydrolase; arbutinase; amygdalinase; p-nitrophenyl β-glucosidase; primeverosidase; amygdalase; linamarase; salicinase; β-1.6-glucosidase
Systematic name: β-D-glucoside glucohydrolase
Comments: Wide specificity for β-D-glucosides. Some examples also hydrolyse one or more of the following: β-D-galactosides, α-L-arabinosides, β-D-xylosides, β-D-fucosides.
References: [471, 511, 570, 1206, 1695, 2647]

[EC 3.2.1.21 created 1961]

EC 3.2.1.22
Accepted name: α-galactosidase
Reaction: Hydrolysis of terminal, non-reducing α-D-galactose residues in α-D-galactosides, including galactose oligosaccharides, galactomannans and galactolipids
Other name(s): melibiase; α-D-galactosidase; α-galactosidase A; α-galactosidase galactohydrolase
Systematic name: α-D-galactoside galactohydrolase
Comments: Also hydrolyses α-D-fucosides.
References: [2953, 3333]

[EC 3.2.1.22 created 1961]

EC 3.2.1.23
Accepted name: β-galactosidase

101
Reaction: Hydrolysis of terminal non-reducing \( \beta \)-D-galactose residues in \( \beta \)-D-galactosides

Other name(s): lactase (ambiguous); \( \beta \)-lactosidase; maxilact; hydrolact; \( \beta \)-D-lactosidase; S 2107; lactozym; trilactase; \( \beta \)-D-galactanase; oryzatym; sumiklat

Systematic name: \( \beta \)-D-galactoside galactohydrolase

Comments: Some enzymes in this group hydrolyse \( \alpha \)-L-arabinosides; some animal enzymes also hydrolyse \( \beta \)-D-fucosides and \( \beta \)-D-glucosides; cf. EC 3.2.1.108 lactase.

References: [260, 1630, 1649, 1826, 2054, 3250, 96]

[EC 3.2.1.23 created 1961, modified 1980]

---

EC 3.2.1.24

Accepted name: \( \alpha \)-mannosidase

Reaction: Hydrolysis of terminal, non-reducing \( \alpha \)-D-mannose residues in \( \alpha \)-D-mannosides

Other name(s): \( \alpha \)-D-mannosidase; \( p \)-nitrophenyl-\( \alpha \)-mannosidase; \( \alpha \)-D-mannopyranosidase; 1,2-\( \alpha \)-mannosidase; 1,2-\( \alpha \)-mannoside mannohydrolase

Systematic name: \( \alpha \)-D-mannoside mannohydrolase

Comments: Also hydrolyses \( \alpha \)-D-lyxosides and heptopyranosides with the same configuration at C-2, C-3 and C-4 as mannose.

References: [1766, 3346]

[EC 3.2.1.24 created 1961]

---

EC 3.2.1.25

Accepted name: \( \beta \)-mannosidase

Reaction: Hydrolysis of terminal, non-reducing \( \beta \)-D-mannose residues in \( \beta \)-D-mannosides

Other name(s): mannanase; mannanase; \( \beta \)-D-mannosidase; \( \beta \)-D-mannoside mannohydrolase; exo-\( \beta \)-D-mannanase

Systematic name: \( \beta \)-D-mannoside mannohydrolase

References: [18, 179, 635, 1291]

[EC 3.2.1.25 created 1961]

---

EC 3.2.1.26

Accepted name: \( \beta \)-fructofuranosidase

Reaction: Hydrolysis of terminal non-reducing \( \beta \)-D-fructofuranoside residues in \( \beta \)-D-fructofuranosides

Other name(s): invertase; saccharase; glucosucrase; \( \beta \)-h-fructosidase; \( \beta \)-fructosidase; invertin; sucrase; maxinvert L 1000; fructosylinvertase; alkaline invertase; acid invertase

Systematic name: \( \beta \)-D-fructofuranoside fructohydrolase

Comments: Substrates include sucrose; also catalyses fructotransferase reactions.

References: [2119, 2178]

[EC 3.2.1.26 created 1961]

---

3.2.1.27  Deleted entry. \( \alpha \)-1,3-glucosidase

[EC 3.2.1.27 created 1961, deleted 1972]

---

EC 3.2.1.28

Accepted name: \( \alpha \)-\( \alpha \)-trehalase

Reaction: \( \alpha \)-\( \alpha \)-trehalose + \( H_2 O \) = \( \beta \)-D-glucose + \( \alpha \)-D-glucose

Other name(s): trehalase

Systematic name: \( \alpha \)-\( \alpha \)-trehalose glucohydrolase

102
Comments: The enzyme is an anomer-inverting glucosidase that catalyses the hydrolysis of the α-glucosidic O-linkage of α,α-trehalose, releasing initially equimolar amounts of α- and β-D-glucose. It is widely distributed in microorganisms, plants, invertebrates and vertebrates.

References: [2120, 1446, 1168, 2066]

[EC 3.2.1.28 created 1961, modified 2012]

[3.2.1.29] Deleted entry. chitobiase. Now included with EC 3.2.1.52, β-N-acetylhexasaminidase]

[EC 3.2.1.29 created 1961, deleted 1972]

[3.2.1.30] Deleted entry. β-D-acethylglucosaminidase. Now included with EC 3.2.1.52, β-N-acetylhexasaminidase]

[EC 3.2.1.30 created 1961, deleted 1992]

EC 3.2.1.31
Accepted name: β-glucuronidase
Reaction: a β-D-glucuronoside + H₂O = D-glucuronate + an alcohol
Other name(s): β-glucuronide glucuronohydrolase glucuronidase; exo-β-D-glucuronidase; ketodase
Systematic name: β-D-glucuronoside glucuronosohydrolase
References: [656, 688, 829, 1748, 3236]

[EC 3.2.1.31 created 1961]
EC 3.2.1.35  
**Accepted name:** hyaluronoglucosaminidase  
**Reaction:** Random hydrolysis of (1→4)-linkages between N-acetyl-β-D-glucosamine and D-glucuronate residues in hyaluronate  
**Other name(s):** hyaluronidase; hyaluronoglucosidase; chondroitinase; chondroitinase I  
**Systematic name:** hyaluronate 4-glycanohydrolase  
**Comments:** Also hydrolys 1,4-β-D-glycosidic linkages between N-acetyl-galactosamine or N-acetylgalactosamine sulfate and glucuronic acid in chondroitin, chondroitin 4- and 6-sulfates, and dermatan.  
**References:** [1993, 2499, 3307]  

[EC 3.2.1.35 created 1965, modified 1976, modified 2001 (EC 3.2.1.34 created 1965, incorporated 1972)]

EC 3.2.1.36  
**Accepted name:** hyaluronoglucuronidase  
**Reaction:** Random hydrolysis of (1→3)-linkages between β-D-glucuronate and N-acetyl-D-glucosamine residues in hyaluronate  
**Other name(s):** hyaluronidase; glucuronoglucosaminoglycan hyaluronate lyase; orgelase  
**Systematic name:** hyaluronate 3-glycanohydrolase  
**References:** [1803, 1993]  

[EC 3.2.1.36 created 1965, modified 1980]

EC 3.2.1.37  
**Accepted name:** xylan 1,4-β-xylosidase  
**Reaction:** Hydrolysis of (1→4)-β-D-xylans, to remove successive D-xylose residues from the non-reducing termini  
**Other name(s):** xyobiase; β-xylosidase; exo-1,4-β-xylosidase; β-D-xylopyranosidase; β-xylosidase; β-xylosidase; exo-1,4-xylosidase; exo-1,4-β-D-xylosidase; 1,4-β-D-xylan xylohydrolase  
**Systematic name:** 4-β-D-xylan xylohydrolase  
**Comments:** Also hydrolys xylobiose. Some other exoglycosidase activities have been found associated with this enzyme in sheep liver.  
**References:** [471, 1266]  

[EC 3.2.1.37 created 1965]

EC 3.2.1.38  
**Accepted name:** β-D-fucosidase  
**Reaction:** Hydrolysis of terminal non-reducing β-D-fucose residues in β-D-fucosides  
**Other name(s):** β-fucosidase  
**Systematic name:** β-D-fucoside fucohydrolase  
**Comments:** Enzymes from some sources also hydrolyse β-D-galactosides and/or β-D-glucosides and/or α-L-arabinosides. The activity of EC 3.2.1.37 xylan 1,4-β-xylosidase, is an associated activity found in some sources (e.g. liver).  
**References:** [470, 471, 2577, 3334, 3335]  

[EC 3.2.1.38 created 1965, deleted 1972, reinstated 1978]

EC 3.2.1.39  
**Accepted name:** glucan endo-1,3-β-D-glucosidase  
**Reaction:** Hydrolysis of (1→3)-β-D-glucosidic linkages in (1→3)-β-D-glucans  

104
Other name(s): endo-1,3-β-glucanase; laminarinase; laminaranase; oligo-1,3-glucosidase; endo-1,3-β-glucanase; pullulanase; pullulan 3-glucanohydrolase; endo-1,3-β-D-glucanase; (1→3)-β-glucan 3-glucanohydrolase; endo-1,3-β-D-glucanase; endo-1,3-β-glucosidase; 1,3-β-D-glucan glucanohydrolase

Systematic name: 3-β-D-glucan glucanohydrolase

Comments: Different from EC 3.2.1.6 endo-1,3-(4)-β-glucanase. Very limited action on mixed-link (1→3,1→4)-β-D-glucans. Hydrolyses laminarin, paramylon and pachyman.

References: [464, 2523]

[EC 3.2.1.39 created 1965]

EC 3.2.1.40

Accepted name: α-L-rhamnosidase

Reaction: Hydrolysis of terminal non-reducing α-L-rhamnose residues in α-L-rhamnosides

Other name(s): α-L-rhamnosidase T; α-L-rhamnosidase N

Systematic name: α-L-rhamnoside rhamnohydrolase

Comments: The enzyme, found in animal tissues, plants, yeasts, fungi and bacteria, utilizes an inverting mechanism of hydrolysis, releasing β-L-rhamnose. Substrates include naringin, rutin, quercitrin, hesperidin, dioscin, terpenyl glycosides and many other natural glycosides containing terminal α-L-rhamnose.

References: [2588, 1666, 3520, 3413, 556, 2465]

[EC 3.2.1.40 created 1972]

EC 3.2.1.41

Accepted name: pullulanase

Reaction: Hydrolysis of (1→6)-α-D-glucosidic linkages in pullulan, amylopectin and glycogen, and in the α- and β-limit dextrans of amylopectin and glycogen

Other name(s): limit dextrinase (erroneous); amylopectin 6-glucanohydrolase; bacterial debranching enzyme; debranching enzyme; α-dextrin endo-1,6-α-glucosidase; R-enzyme; pullulan α-1,6-glucanohydrolase

Systematic name: pullulan 6-α-glucanohydrolase

Comments: Different from EC 3.2.1.142 (limit dextrinase) in its action on glycogen, and its rate of hydrolysis of limit dextrans. Its action on amylopectin is complete. Maltose is the smallest sugar that it can release from an α-(1→6)-linkage.

References: [1713, 207, 1899]

[EC 3.2.1.41 created 1972, modified 1976, modified 2000 (EC 3.2.1.69 created 1972, incorporated 1976)]

EC 3.2.1.42

Accepted name: GDP-glucosidase

Reaction: GDP-glucose + H₂O = D-glucose + GDP

Other name(s): guanosine diphosphoglucosidase; guanosine diphosphate D-glucose glucohydrolase

Systematic name: GDP-glucose glucohydrolase

References: [2862]

[EC 3.2.1.42 created 1972]

EC 3.2.1.43

Accepted name: β-L-rhamnosidase

Reaction: Hydrolysis of terminal, non-reducing β-L-rhamnose residues in β-L-rhamnosides

Systematic name: β-L-rhamnoside rhamnolohydrolase

References: [156]

[EC 3.2.1.43 created 1972]
EC 3.2.1.45

**Accepted name:** glucosylceramidase  
**Reaction:** a D-glucosyl-N-acylsphingosine + H₂O = D-glucose + a ceramide  
**Other name(s):** psychosine hydrolase; glucosphingosine glucosylhydrolase; GlcCer-β-glucosidase; β-D-glucoceribrosidase; glucosylcerebrosidase; β-glucosylceramidase; ceramide glucosidase; glucocerebrosidase; glucosylphosphoglycerol β-glucosidase; glucosylsphingosine β-D-glucosidase

**Systematic name:** d-glucosyl-N-acylsphingosine glucohydrolase  
**Comments:** Also acts on glucosylsphingosine (cf. EC 3.2.1.62 glycosylceramidase).  
**References:** [303, 3174]  

[EC 3.2.1.45 created 1972]

EC 3.2.1.46

**Accepted name:** galactosylceramidase  
**Reaction:** a D-galactosyl-N-acylsphingosine + H₂O = D-galactose + a ceramide  
**Other name(s):** cerebroside galactosidase; galactocerebroside β-galactosidase; galactosylcerebrosidase; galactocerebrosidase; ceramide galactosidase; galactocerebroside galactosidase; galactosylceramide β-galactosidase; cerebroside β-galactosidase; galactosylceramidase; galactocerebroside β-D-galactosidase; lactosylceramidase I; β-galactocerebrosidase; lactosylceramide  
**Systematic name:** d-galactosyl-N-acylsphingosine galactohydrolase  
**Comments:** cf. EC 3.2.1.62 glycosylceramidase.  
**References:** [302]  

[EC 3.2.1.46 created 1972]

EC 3.2.1.47  
**Deleted entry. galactosylgalactosylglucosylceramidase. Now known to be catalyzed by EC 3.2.1.22, α-galactosidase.**  
[EC 3.2.1.47 created 1972, modified 2011, deleted 2021]

EC 3.2.1.48

**Accepted name:** sucrose α-glucosidase  
**Reaction:** Hydrolysis of sucrose and maltose by an α-D-glucosidase-type action  
**Other name(s):** sucrose α-glucohydrolase; sucrase; sucrase-isomaltase; sucrose α-glucohydrolase; intestinal sucrase; sucrase (invertase)  
**Systematic name:** sucrose-α-D-glucohydrolase  
**Comments:** This enzyme is isolated from intestinal mucosa as a single polypeptide chain that also displays activity towards isomaltose (EC 3.2.1.10 oligo-1,6-glucosidase).  
**References:** [513, 1144, 1587, 2793, 2817, 3001]  

[EC 3.2.1.48 created 1972]

EC 3.2.1.49

**Accepted name:** α-N-acetylgalactosaminidase  
**Reaction:** Cleavage of non-reducing α-(1→3)-N-acetylgalactosamine residues from human blood group A and AB mucin glycoproteins, Forssman hapten and blood group A lacto series glycolipids  
**Other name(s):** α-acetylglactosaminidase; N-acetyl-α-D-galactosaminidase; N-acetyl-α-galactosaminidase; α-NAGAL; α-NAGA; α-GalNAcase  
**Systematic name:** α-N-acetyl-d-galactosamidase N-acetylgalactosaminohydrolase  
**Comments:** The human lysosomal enzyme is involved in the degradation of blood type A epitope.
EC 3.2.1.50
Accepted name: α-N-acetylglucosaminidase
Reaction: Hydrolysis of terminal non-reducing N-acetyl-D-glucosamine residues in N-acetyl-α-D-glucosaminides
Other name(s): α-acetylgalactosaminidase; N-acetyl-α-D-glucosaminidase; N-acetyl-α-D-glucosaminidase; α-D-2-acetamido-2-deoxyglucosidase
Systematic name: α-N-acetyl-D-glucosaminidase
Comments: Hydrolyses UDP-N-acetylglucosamine.
References: [3229, 3230, 3309, 3315]

EC 3.2.1.51
Accepted name: α-L-fucosidase
Reaction: an α-L-fucoside + H₂O = L-fucose + an alcohol
Other name(s): α-fucosidase
Systematic name: α-L-fucoside fucohydrolase

EC 3.2.1.52
Accepted name: β-N-acetylhexosaminidase
Reaction: Hydrolysis of terminal non-reducing N-acetyl-D-hexosamine residues in N-acetyl-β-D-hexosaminides
Other name(s): hexosaminidase; β-acetylamino-2-deoxyhexosidase; N-acetyl-β-D-hexosaminidase; N-acetyl-β-hexosaminidase; β-hexosaminidase; β-acetylhexitosaminidase; β-N-acetyl-d-hexosaminidase; β-N-acetylglucosaminidase; hexosaminidase A; N-acetylhexosaminidase; β-d-hexosaminidase; NAHase
Systematic name: β-N-acetyl-D-hexosaminidase N-acetylhexosaminohydrolase
References: [375, 386, 875, 1758]

EC 3.2.1.53
Accepted name: β-N-acetylgalactosaminidase
Reaction: Hydrolysis of terminal non-reducing N-acetyl-D-galactosamine residues in N-acetyl-β-D-galactosaminides
Other name(s): N-acetyl-β-galactosaminidase; N-acetyl-β-D-galactosaminidase; β-acetylgalactosaminidase; β-D-N-acetylgalactosaminidase; N-acetylgalactosaminidase
Systematic name: β-N-acetyl-D-galactosaminidase N-acetylgalactosaminohydrolase
References: [875, 1243]

EC 3.2.1.54
Accepted name: cyclomaltodextrinase
Reaction: cyclomaltodextrin + H₂O = linear maltodextrin

References: [91, 3505, 497, 1258, 1126, 3303, 94]
Other name(s): cycloheptaglucanase; cyclohexaglucanase; cyclodextrinase; cyclomaltodextrin dextrin-hydrolase (de-cyclizing)

Systematic name: cyclomaltodextrin dextrin-hydrolase (ring-opening)

Comments: Also hydrolyses linear maltodextrin.

References: [627]

EC 3.2.1.55

Accepted name: non-reducing end α-L-arabinofuranosidase

Reaction: Hydrolysis of terminal non-reducing α-L-arabinofuranoside residues in α-L-arabinosides.

Other name(s): arabinosidase (ambiguous); α-arabinosidase; α-L-arabinosidase; α-arabinofuranosidase; polysaccharide α-L-arabinofuranosidase; α-L-arabinofuranoside hydrolase; L-arabinosidase (ambiguous); α-L-arabinanase

Systematic name: α-L-arabinofuranoside non-reducing end α-L-arabinofuranosidase

Comments: The enzyme acts on α-L-arabinofuranosides, α-L-arabinans containing (1,3)- and/or (1,5)-linkages, arabinoxylans and arabinogalactans. Some β-galactosidases (EC 3.2.1.23) and β-D-fucosidases (EC 3.2.1.38) also hydrolyse α-L-arabinosides. cf. EC 3.2.1.185, non-reducing end β-L-arabinofuranosidase.

References: [2971, 1438, 1439, 1907, 1322]

EC 3.2.1.56

Accepted name: glucuronosyl-disulfoglucosamine glucuronidase

Reaction: 3-D-glucuronosyl-N^2,6-disulfo-β-D-glucosamine + H_2O = D-glucuronate + N^2,6-disulfo-D-glucosamine

Other name(s): glycuronidase; 3-D-glucuronosyl-2-N,6-disulfo-β-D-glucosamine glucuronohydrolase

Systematic name: 3-D-glucuronosyl-N^2,6-disulfo-β-D-glucosamine glucuronohydrolase

References: [652]

EC 3.2.1.57

Accepted name: isopullulanase

Reaction: Hydrolysis of pullulan to isopanose (6-α-maltosylglucose)

Systematic name: pullulan 4-glucohydrolase (isopanose-forming)

Comments: The enzyme has practically no action on starch. Panose (4-α-isomaltosylglucose) is hydrolysed to isomaltose and glucose. cf. EC 3.2.1.41 (pullulanase) and EC 3.2.1.135 (neopullulanase).

References: [2631]

EC 3.2.1.58

Accepted name: glucan 1,3-β-glucosidase

Reaction: Successive hydrolysis of β-D-glucose units from the non-reducing ends of (1→3)-β-D-glucans, releasing α-glucose

Other name(s): exo-1,3-β-glucosidase; β-1,3-glucan exo-hydrolase; exo (1→3)-glucanohydrolase; 1,3-β-glucan glucohydrolase

Systematic name: 3-β-D-glucan glucohydrolase

Comments: Acts on oligosaccharides, but very slowly on laminaribiose.

References: [166, 167]
EC 3.2.1.59

Accepted name: glucan endo-1,3-α-glucosidase

Reaction: Endohydrolysis of (1→3)-α-D-glucosidic linkages in isolichenin, pseudonigeran and nigeran

Other name(s): endo-1,3-α-glucanase; mutanase; endo-(1→3)-α-glucanase; cariogenase; cariogenanase; endo-1,3-α-D-glucanase; 1,3(1,3;1,4)-α-D-glucan 3-glucanohydrolase

Systematic name: 3-α-D-glucan 3-glucanohydrolase

Comments: Products from pseudonigeran (1,3-α-D-glucan) are nigerose and α-D-glucose.

References: [1130]

[EC 3.2.1.59 created 1972]

EC 3.2.1.60

Accepted name: glucan 1,4-α-maltotetraohydrolase

Reaction: Hydrolysis of (1→4)-α-D-glucosidic linkages in amylaceous polysaccharides, to remove successive maltotetraose residues from the non-reducing chain ends

Other name(s): exo-maltotetraohydrolase; 1,4-α-D-glucan maltotetraohydrolase

Systematic name: 4-α-D-glucan maltotetraohydrolase

Comments: Compare EC 3.2.1.2 β-amylase, which removes successive maltose residues, and EC 3.2.1.98 (glucan 1,4-α-maltohexaosidase) and EC 3.2.1.116 (glucan 1,4-α-maltotriohydrolase).

References: [2145, 2570]

[EC 3.2.1.60 created 1972]

EC 3.2.1.61

Accepted name: mycodextranase

Reaction: Endohydrolysis of (1→3)-(1→4)-α-D-glucosidic linkages in α-D-glucans containing both (1→3)- and (1→4)-bonds

Other name(s): 1,3-1,4-α-D-glucan 4-glucanohydrolase

Systematic name: (1→3)-(1→4)-α-D-glucan 4-glucanohydrolase

Comments: Products are nigerose and 4-α-D-nigerosylglucose. No hydrolysis of α-D-glucans containing only 1,3- or 1,4-bonds.

References: [3144]

[EC 3.2.1.61 created 1972]

EC 3.2.1.62

Accepted name: glycosylceramidase

Reaction: (1) a β-D-glucosyl-N-acylsphingosine + H₂O = a ceramide + β-D-glucose
(2) a β-D-galactosyl-N-acylsphingosine + H₂O = a ceramide + β-D-galactose
(3) a flavonoid-O-β-D-glucoside + H₂O = a flavonoid + β-D-glucose

Other name(s): phlorizin hydrolase; phloretin-glucosidase; glycosyl ceramidase glycosylhydrolase; cerebrosidase; phloridzin β-glucosidase; lactase-phlorizin hydrolase; phloridzin glucosidase; LPH (gene name); LCT (gene name); glycosyl-N-acylsphingosine glycohydrolase

Systematic name: β-D-glucosyl-N-acylsphingosine glycohydrolase (configuration-retaining)

Comments: The enzyme, found in the intestinal mucosa, hydrolyses β-D-glucosyl and β-D-galactosyl residues from a very broad range of substrates using a retaining mechanism. Characterized substrates include glucosyl- and galactosyl-ceramides [1730], O³⁻, O⁴⁻ and O⁷-glucosylated flavonoids [2176], and the 2′-O-glucosylated dihydrochalcone phlorizin [1884]. The enzyme includes two glycosyl hydrolase domains, both belonging to the GH1 family. While one domain is responsible for the activity described here, the other catalyses the reaction of EC 3.2.1.108, lactase [3479, 83]. cf. EC 3.2.1.45, glucosylceramidase and EC 3.2.1.46, galactosylceramidase.

[EC 3.2.1.62 created 1972]
References: [1884, 1834, 1730, 3479, 83, 2176]

[EC 3.2.1.62 created 1972, modified 1976, modified 2022]

EC 3.2.1.63

Accepted name: 1,2-α-L-fucosidase
Reaction: methyl-2-α-L-fucopyranosyl-β-D-galactoside + H₂O = L-fucose + methyl β-D-galactoside
Other name(s): almond emulsin fucosidase; α-(1→2)-L-fucosidase
Systematic name: 2-α-L-fucopyranosyl-β-D-galactoside fucohydrolase
Comments: Highly specific for non-reducing terminal L-fucose residues linked to D-galactose residues by a 1,2-α-linkage. Not identical with EC 3.2.1.111 1,3-α-L-fucosidase.
References: [130, 2253, 2526]

[EC 3.2.1.63 created 1972]

EC 3.2.1.64

Accepted name: 2,6-β-fructan 6-levanbiohydrolase
Reaction: Hydrolysis of (2→6)-β-D-fructofuranan, to remove successive disaccharide residues as levanbiose, i.e. 6-(β-D-fructofuranosyl)-D-fructose, from the end of the chain
Other name(s): β-2,6-fructan-6-levanbiohydrolase; 2,6-β-D-fructan 6-levanbiohydrolase; levanbiose-producing lev-anase; 2,6-β-D-fructan 6-β-D-fructofuranosylfructohydrolase
Systematic name: (2→6)-β-D-fructofuranan 6-(β-D-fructosyl)-D-fructose-hydrolase
References: [113, 2624, 2625, 2855, 1469]

[EC 3.2.1.64 created 1972, modified 2004]

EC 3.2.1.65

Accepted name: levanase
Reaction: Random hydrolysis of (2→6)-β-D-fructofuranosidic linkages in (2→6)-β-D-fructans (levans) containing more than 3 fructose units
Other name(s): levan hydrolase; 2,6-β-D-fructan fructanohydrolase
Systematic name: (2→6)-β-D-fructan fructanohydrolase
References: [112]

[EC 3.2.1.65 created 1972]

[3.2.1.66 Deleted entry. The activity is covered by EC 3.2.1.40, α-L-rhamnosidase]

[EC 3.2.1.66 created 1972, deleted 2021]

EC 3.2.1.67

Accepted name: galacturonan 1,4-α-galacturonidase
Reaction: [(1→4)-α-D-galacturonidide]ₙ + H₂O = [(1→4)-α-D-galacturonide]ₙ₋₁ + D-galacturonate
Other name(s): exo-polygalacturonase; poly(galacturonate) hydrolase (ambiguous); exo-D-galacturonase; exopoly-D-galacturonase; poly(1,4-α-D-galacturonide) galacturonohydrolase (ambiguous); pgaA (gene name); pgaB (gene name); pgaC (gene name); pgaD (gene name); pgaE (gene name); pgaH (gene name); pgaI (gene name); poly[(1→4)-α-D-galacturonide] galacturonohydrolase; galacturonan 1,4-α-galacturonidase (incorrect)
Systematic name: poly[(1→4)-α-D-galacturonide] non-reducing-end galacturonohydrolase
Comments: The enzyme hydrolyses the first glycosidic bond from the non-reducing end of the substrate. It is specific for saturated oligomers of D-homogalacturonan, and is unable to degrade unsaturated substrates or methyl-esterified substrates.
References: [1129, 1565, 1915, 2400]
EC 3.2.1.68

Accepted name: isoamylase
Reaction: Hydrolysis of (1→6)-α-D-glucosidic branch linkages in glycogen, amyllopectin and their β-limit dextrans
Other name(s): debranching enzyme; glycogen α-1,6-glucanohydrolase
Systematic name: glycogen 6-α-D-glucanohydrolase
Comments: Also readily hydrolyses amyllopectin. Differs from EC 3.2.1.41 (pullulanase) and EC 3.2.1.142 (limit dextrinase) by its inability to hydrolyse pullulan, and by limited action on α-limit dextrans. Maltose is the smallest sugar it can release from an α-(1→6)-linkage.
References: [3445]

[EC 3.2.1.68 created 1972, modified 2019]

[3.2.1.69 Deleted entry. amylopectin 6-glucanohydrolase. Now included with EC 3.2.1.41 pullulanase]

EC 3.2.1.70

Accepted name: glucan 1,6-α-glucosidase
Reaction: Hydrolysis of (1→6)-α-D-glucosidic linkages in (1→6)-α-D-glucans and derived oligosaccharides
Other name(s): exo-1,6-β-glucosidase; glucodextrinase; glucan 6-α-D-glucanohydrolase
Systematic name: glucan 6-α-D-glucanohydrolase
Comments: Hydrolysis is accompanied by inversion at C-1, so that new reducing ends are released in the β-configuration. Dextrins and isomaltosaccharides are hydrolysed, as is isomaltose, but very slowly. The enzyme from some sources also possesses the activity of EC 3.2.1.59 (glucan endo-1,3-α-glucosidase).
References: [2284, 2679, 3246]

[EC 3.2.1.70 created 1972, modified 2001]

EC 3.2.1.71

Accepted name: glucan endo-1,2-β-glucosidase
Reaction: Random hydrolysis of (1→2)-β-D-glucosidic linkages in (1→2)-β-D-glucans
Other name(s): endo-1,2-β-glucanase; β-D-1,2-glucanase; endo-(1→2)-β-D-glucanase; 1,2-β-D-glucan glucanohydrolase
Systematic name: 2-β-D-glucan glucanohydrolase
References: [2524]

[EC 3.2.1.71 created 1972]

EC 3.2.1.72

Accepted name: xylan 1,3-β-xylosidase
Reaction: Hydrolysis of successive xylose residues from the non-reducing termini of (1→3)-β-D-xylans
Other name(s): 1,3-β-D-xylosidase; exo-1,3-β-xylosidase; β-1,3’-xylanase; exo-β-1,3’-xylanase; 1,3-β-D-xylan xylohydrolase
Systematic name: 3-β-D-xylan xylohydrolase
References: [914]

[EC 3.2.1.72 created 1972]
### EC 3.2.1.73

<table>
<thead>
<tr>
<th><strong>Accepted name:</strong></th>
<th>licheninase</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Reaction:</strong></td>
<td>Hydrolysis of (1→4)-β-D-glucosidic linkages in β-D-glucans containing (1→3)- and (1→4)-bonds</td>
</tr>
<tr>
<td><strong>Other name(s):</strong></td>
<td>lichenase; β-(1→4)-D-glucan 4-glucanohydrolase; 1,3;1,4-β-glucan 4-glucanohydrolase; 1,3-1,4-β-D-glucan 4-glucanohydrolase</td>
</tr>
<tr>
<td><strong>Systematic name:</strong></td>
<td>(1→3)-(1→4)-β-D-glucan 4-glucanohydrolase</td>
</tr>
<tr>
<td><strong>Comments:</strong></td>
<td>Acts on lichenin and cereal β-D-glucans, but not on β-D-glucans containing only 1,3- or 1,4-bonds.</td>
</tr>
<tr>
<td><strong>References:</strong></td>
<td>[165]</td>
</tr>
</tbody>
</table>

[EC 3.2.1.73 created 1972]

### EC 3.2.1.74

<table>
<thead>
<tr>
<th><strong>Accepted name:</strong></th>
<th>glucan 1,4-β-glucosidase</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Reaction:</strong></td>
<td>Hydrolysis of (1→4)-linkages in (1→4)-β-D-glucans, to remove successive glucose units</td>
</tr>
<tr>
<td><strong>Other name(s):</strong></td>
<td>exo-1,4-β-glucosidase; exocellulase; exo-β-1,4-glucosidase; exo-β-1,4-glucanase; β-1,4-β-glucanase; β-glucosidase; exo-1,4-β-glucanase; 1,4-β-D-glucan glucohydrolase</td>
</tr>
<tr>
<td><strong>Systematic name:</strong></td>
<td>4-β-D-glucan glucohydrolase</td>
</tr>
<tr>
<td><strong>Comments:</strong></td>
<td>Acts on 1,4-β-D-glucans and related oligosaccharides. Cellobiose is hydrolysed, but very slowly.</td>
</tr>
<tr>
<td><strong>References:</strong></td>
<td>[165]</td>
</tr>
</tbody>
</table>

[EC 3.2.1.74 created 1972]

### EC 3.2.1.75

<table>
<thead>
<tr>
<th><strong>Accepted name:</strong></th>
<th>glucan endo-1,6-β-glucosidase</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Reaction:</strong></td>
<td>Random hydrolysis of (1→6)-linkages in (1→6)-β-D-glucans</td>
</tr>
<tr>
<td><strong>Other name(s):</strong></td>
<td>endo-1,6-β-glucanase; β-1→6)-β-D-glucanase; β-1,6-glucanase-pustulanase; β-1,6-glucan hydrolase; β-1,6-glucan 6-glucanohydrolase; 1,6-β-D-glucan glucohydrolase</td>
</tr>
<tr>
<td><strong>Systematic name:</strong></td>
<td>6-β-D-glucan glucohydrolase</td>
</tr>
<tr>
<td><strong>Comments:</strong></td>
<td>Acts on lutean, pustulan and 1,6-oligo-β-D-glucosides.</td>
</tr>
<tr>
<td><strong>References:</strong></td>
<td>[2525]</td>
</tr>
</tbody>
</table>

[EC 3.2.1.75 created 1972]

### EC 3.2.1.76

<table>
<thead>
<tr>
<th><strong>Accepted name:</strong></th>
<th>L-iduronidase</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Reaction:</strong></td>
<td>Hydrolysis of unsulfated α-L-iduronosidic linkages in dermatan sulfate</td>
</tr>
<tr>
<td><strong>Other name(s):</strong></td>
<td>α-L-iduronidase</td>
</tr>
<tr>
<td><strong>Systematic name:</strong></td>
<td>glycosaminoglycan α-L-iduronohydrolase</td>
</tr>
<tr>
<td><strong>References:</strong></td>
<td>[1931, 2582, 2890]</td>
</tr>
</tbody>
</table>

[EC 3.2.1.76 created 1972]

### EC 3.2.1.77

<table>
<thead>
<tr>
<th><strong>Accepted name:</strong></th>
<th>mannan 1,2-(1,3)-α-mannosidase</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Reaction:</strong></td>
<td>Hydrolysis of (1→2)- and (1→3)-linkages in yeast mannan, releasing mannose</td>
</tr>
<tr>
<td><strong>Other name(s):</strong></td>
<td>exo-1,2-1,3-α-mannosidase; 1,2-1,3-α-D-mannan mannohydrolase</td>
</tr>
<tr>
<td><strong>Systematic name:</strong></td>
<td>(1→2)-(1→3)-α-D-mannan mannohydrolase</td>
</tr>
<tr>
<td><strong>Comments:</strong></td>
<td>A 1,6-α-D-mannan backbone remains after action on yeast mannan. This is further attacked, but slowly.</td>
</tr>
<tr>
<td><strong>References:</strong></td>
<td>[1418, 1419]</td>
</tr>
</tbody>
</table>

[EC 3.2.1.77 created 1972]
EC 3.2.1.78
Accepted name: mannan endo-1,4-β-mannosidase
Reaction: Random hydrolysis of (1→4)-β-D-mannosidic linkages in mannans, galactomannans and glucomannans
Other name(s): endo-1,4-β-mannanase; endo-β-1,4-mannase; β-mannanase B; β-1,4-mannan 4-mannanohydrolase; endo-β-mannanase; β-D-mannanase; 1,4-β-D-mannan mannanohydrolase
Systematic name: 4-β-D-mannan mannanohydrolase
References: [758, 2522]

[EC 3.2.1.78 created 1972]

[3.2.1.79 Deleted entry. α-L-arabinofuranoside hydrolase. Now included with EC 3.2.1.55 α-N-arabinofuranosidase]

[EC 3.2.1.79 created 1972, deleted 1976]

EC 3.2.1.80
Accepted name: fructan β-fructosidase
Reaction: Hydrolysis of terminal, non-reducing (2→1)- and (2→6)-linked β-D-fructofuranose residues in fructans
Other name(s): exo-β-D-fructosidase; exo-β-fructosidase; polysaccharide β-fructofuranosidase; fructan exohydrolase
Systematic name: β-D-fructan fructohydrolase
Comments: Hydrolyses inulin and levan, and also sucrose.
References: [567, 1369]

[EC 3.2.1.80 created 1972]

EC 3.2.1.81
Accepted name: β-agarase
Reaction: Hydrolysis of (1→4)-β-D-galactosidic linkages in agarose, giving the tetramer as the predominant product
Other name(s): agarase (ambiguous); AgaA; AgaB; endo-β-agarase; agarose 3-glycanohydrolase (incorrect)
Systematic name: agarose 4-glycanohydrolase
Comments: Also acts on porphyran, but more slowly [703]. This enzyme cleaves the β-(1→4) linkages of agarose in a random manner with retention of the anomeric-bond configuration, producing β-anomers that give rise progressively to α-anomers when mutarotation takes place [1383]. The end products of hydrolysis are neoagarotetraose and neoagarohexaose in the case of AgaA from the marine bacterium Zobellia galactanivorans, and neoagarotetraose and neoagarobiase in the case of AgaB [1383].
References: [703, 40, 2280, 2279, 2933, 1383]

[EC 3.2.1.81 created 1972, modified 2006]

EC 3.2.1.82
Accepted name: exo-poly-α-digalacturonosidase
Reaction: [((1→4)-α-D-galacturonosyl)_n + H_2O = α-D-galacturonosyl-(1→4)-D-galacturate + [(1→4)-α-D-galacturonosyl]_n−2
Other name(s): pehX (gene name); poly(1,4-α-D-galactosiduronate) digalacturonohydrolase; exopolygalacturonosidase (misleading); poly[(1→4)-α-D-galactosiduronate] digalacturonohydrolase; exo-poly-α-galacturonosidase
Systematic name: poly[(1→4)-α-D-galactosiduronate] non-reducing-end-digalacturonohydrolase
Comments: The enzyme, characterized from bacteria, hydrolyses the second α-1,4-glycosidic bond from the non-reducing end of polygalacturonate, releasing digalacturate.
References: [1129, 1139, 1140, 1159]

[EC 3.2.1.82 created 1972, modified 2019]
EC 3.2.1.83

Accepted name: κ-carrageenase
Reaction: Endohydrolysis of (1→4)-β-D-linkages between D-galactose 4-sulfate and 3,6-anhydro-D-galactose in κ-carrageenans
Other name(s): κ-carrageenan 4→D-glycanohydrolase
Systematic name: κ-carrageenan 4→D-glycanohydrolase (configuration-retaining)
Comments: The main products of hydrolysis are neocarrabiose-sulfate and neocarratetraose-sulfate [2000]. Unlike EC 3.2.1.157 (ι-carrageenase), but similar to EC 3.2.1.81 (β-agarase), this enzyme proceeds with retention of the anomeric configuration.
References: [3302, 2436, 2434, 1999, 2000]

EC 3.2.1.84

Accepted name: glucan 1,3-α-glucosidase
Reaction: Hydrolysis of terminal (1→3)-α-D-glucosidic links in (1→3)-α-D-glucans
Other name(s): exo-1,3-α-glucanase; glucosidase II; 1,3-α-D-glucan 3-glucohydrolase
Systematic name: 3-α-D-glucan 3-glucohydrolase
Comments: Does not act on nigeran.
References: [3515]

EC 3.2.1.85

Accepted name: 6-phospho-β-galactosidase
Reaction: \[\text{a 6-phospho-β-D-galactoside} + \text{H}_2\text{O} = \text{6-phospho-D-galactose} + \text{an alcohol}\]
Other name(s): phospha-β-galactosidase; β-D-phosphogalactoside galactohydrolase; phospho-β-D-galactosidase; 6-phospho-β-D-galactosidase
Systematic name: 6-phospho-β-D-galactosyl-(1→4)-D-glucose glucohydrolase
References: [1180]

EC 3.2.1.86

Accepted name: 6-phospho-β-glucosidase
Reaction: \[\text{6-phospho-β-D-glucosyl-(1→4)-D-glucose} + \text{H}_2\text{O} = \text{D-glucose} + \text{D-glucose 6-phosphate}\]
Other name(s): phospha-β-glucosidase A; phospha-β-glucosidase; phospha-β-glucosidase; 6-phospho-β-D-glucosyl-(1,4)-D-glucose glucohydrolase
Systematic name: 6-phospho-β-D-glucosyl-(1→4)-D-glucose glucohydrolase
References: [2341]

EC 3.2.1.87

Accepted name: capsular-polysaccharide endo-1,3-α-galactosidase
Reaction: Random hydrolysis of (1→3)-α-D-galactosidic linkages in Aerobacter aerogenes capsular polysaccharide
Other name(s): polysaccharide depolymerase; capsular polysaccharide galactohydrolase
Systematic name: Aerobacter-capsular-polysaccharide galactohydrolase
Comments: Hydrolyses the galactosyl-α-1,3-D-galactose linkages only in the complex substrate, bringing about depolymerization.
References: [3473, 3474]
EC 3.2.1.88

**Accepted name:** non-reducing end β-L-arabinopyranosidase

**Reaction:** Removal of a terminal β-L-arabinopyranose residue from the non-reducing end of its substrate.

**Other name(s):** vicianosidase; β-L-arabinosidase (ambiguous); β-L-arabinoside arabinohydrolase (ambiguous)

**Systematic name:** β-L-arabinopyranoside non-reducing end β-L-arabinopyranosidase

**Comments:** The enzyme, which was characterized from dormant seeds of the plant *Cajanus cajan* (pigeon pea), has been shown to remove the terminal non-reducing β-L-arabinopyranoside residue from the artificial substrate p-nitrophenyl-β-L-arabinopyranose [642]. In the presence of methanol the enzyme demonstrates transglycosylase activity, transferring the arabinose moiety to methanol while retaining the anomeric configuration, generating 1-O-methyl-β-L-arabinopyranose [641].

**References:** [642, 641]

[EC 3.2.1.88 created 1976, modified 2013]

EC 3.2.1.89

**Accepted name:** arabinogalactan endo-β-1,4-galactanase

**Reaction:** The enzyme specifically hydrolyses (1→4)-β-D-galactosidic linkages in type I arabinogalactans.

**Other name(s):** endo-1,4-β-galactanase; galactanase (ambiguous); arabinogalactanase; ganB (gene name)

**Systematic name:** arabinogalactan 4-β-D-galactanohydrolase

**Comments:** This enzyme, isolated from the bacterium *Bacillus subtilis*, hydrolyses the β(1→4) bonds found in type I plant arabinogalactans, which are a component of the primary cell walls of dicots. The predominant product is a tetrasaccharide. cf. EC 3.2.1.181, galactan endo-β-1,3-galactanase.

**References:** [744, 1674, 2778]

[EC 3.2.1.89 created 1976, modified 2012]

[3.2.1.90 Deleted entry. arabinogalactan endo-1,3-β-galactosidase. The enzyme was not sufficiently characterized to warrant an EC number]

[EC 3.2.1.90 created 1976, deleted 2001]

EC 3.2.1.91

**Accepted name:** cellulose 1,4-β-cellobiosidase (non-reducing end)

**Reaction:** Hydrolysis of (1→4)-β-D-glucosidic linkages in cellulose and cellotetraose, releasing cellobiose from the non-reducing ends of the chains

**Other name(s):** exo-cellobiohydrolase; β-1,4-glucan cellobiohydrolase; β-1,4-glucan cellobiosylhydrolase; 1,4-β-glucan cellobiosidase; exoglucanase; avicelase; CBH 1; C1 cellulase; cellobiohydrolase I; cellobiohydrolase; exo-β-1,4-glucan cellobiohydrolase; 1,4-β-D-glucan cellobiohydrolase; cellobiosidase

**Systematic name:** 4-β-D-glucan cellobiohydrolase (non-reducing end)

**References:** [212, 759, 1091]

[EC 3.2.1.91 created 1976, modified 2011]

EC 3.2.1.92

**Accepted name:** peptidoglycan β-N-acetylmuramidase

**Reaction:** Hydrolysis of terminal, non-reducing N-acetylmuramic residues

**Other name(s):** exo-β-N-acetylmuramidase; exo-β-acetylmuramidase; β-2-acetamido-3-O-(D-1-carboxyethyl)-2-deoxy-D-glucoside acetamidodeoxyglucohydrolase

**Systematic name:** peptidoglycan β-N-acetylmuramoylhexahydrolase

**References:** [2554]

[EC 3.2.1.92 created 1976]
EC 3.2.1.93

Accepted name: α,α-phosphotrehalase
Reaction: \( \alpha,\alpha\text{-trehalose 6-phosphate} + \text{H}_2\text{O} = \text{D-glucose} + \text{D-glucose 6-phosphate} \)
Other name(s): phosphotrehalase
Systematic name: \( \alpha,\alpha\text{-trehalose-6-phosphate phosphoglucohydrolase} \)
References: [233]

[EC 3.2.1.93 created 1976]

EC 3.2.1.94

Accepted name: glucan 1,6-α-isomaltosidase
Reaction: Hydrolysis of (1 → 6)-α-D-glucosidic linkages in polysaccharides, to remove successive isomaltose units from the non-reducing ends of the chains
Other name(s): exo-isomaltohydrolase; isomalto-dextranase; isomaltoextranase; G2-dextranase; 1,6-α-D-glucan isomaltohydrolase
Systematic name: 6-α-D-glucan isomaltohydrolase
Comments: Optimum activity is on those 1,6-α-D-glucans containing 6, 7 and 8 glucose units; those containing 3, 4 and 5 glucose units are hydrolysed at slower rates.
References: [2678, 2677]

[EC 3.2.1.94 created 1976]

EC 3.2.1.95

Accepted name: dextran 1,6-α-isomaltotriosidase
Reaction: Hydrolysis of (1 → 6)-α-D-glucosidic linkages in dextrans, to remove successive isomaltotriose units from the non-reducing ends of the chains
Other name(s): exo-isomaltotriohydrolase; 1,6-α-D-glucan isomaltotriohydrolase
Systematic name: 6-α-D-glucan isomaltotriohydrolase
References: [2936]

[EC 3.2.1.95 created 1978]

EC 3.2.1.96

Accepted name: mannosyl-glycoprotein endo-β-N-acetylglucosaminidase
Reaction: Endohydrolysis of the \( N,N' \)-diacyethylchitobiosyl unit in high-mannose glycopeptides and glycoproteins containing the -(Man(GlcNAc)_2)-Asn- structure. One N-acetyl-D-glucosamine residue remains attached to the protein; the rest of the oligosaccharide is released intact
Other name(s): \( N,N' \)-diacyethylchitobiosyl β-N-acetylglucosaminidase; endo-β-N-acetylglucosaminidase; mannosyl-glycoprotein endo-β-N-acetylglucosaminidase; \( N,N' \)-diacyethylchitobiosyl β-N-acetylglucosaminidase; endo-β-acetylglucosaminidase; endo-β-(1→4)-N-acetylglucosaminidase; mannosyl-glycoprotein 1,4-N-acetamidoxy-β-D-glycohydrolase; endoglycosidase S; endo-β-N-acetyl-β-D-glucosaminidase L; glycopeptide-D-mannosyl-4-N-(N-acetyl-D-glucosaminyl)2-asparagine 1,4-N-acetyl-β-D-glucosaminohydrolase; endoglycosidase H
Systematic name: glycopeptide-D-mannosyl-\( N' \)-\( N \)-acyethyl-D-glucosaminyl)_2-asparagine 1,4-N-acetyl-β-D-glucosaminohydrolase
Comments: A group of related enzymes.
References: [467, 1585, 2395, 2396, 2973, 3029]

[EC 3.2.1.96 created 1978]
EC 3.2.1.97

Accepted name: endo-\(\alpha\)-N-acetylgalactosaminidase
Reaction: \(\beta\)-D-galactosyl-(1\(\rightarrow\)3)-N-acetyl-\(\alpha\)-D-galactosaminyl-[glycoprotein]-L-serine/L-threonine + H\(_2\)O = \(\beta\)-D-galactosyl-(1\(\rightarrow\)3)-N-acetyl-D-galactosamine + [glycoprotein]-L-serine/L-threonine
Other name(s): endo-\(\alpha\)-N-acetyl-D-galactosaminidase; mucinaminylserine mucinaminohydrolase; endo-\(\alpha\)-GalNAc-ase; glycopeptide \(\alpha\)-N-acetylgalactosaminidase; D-galactosyl-\(\beta\)-(GlcNAc-(1\(\rightarrow\)6)-\(\beta\))-GalNAc or the core 3 disaccharide GlcNAc-(1\(\rightarrow\)3)-\(\beta\)-GalNAc

Systematic name: glycopeptide-D-galactosyl-N-acetyl-\(\alpha\)-D-galactosaminohydrolase

Comments: The enzyme catalyses the liberation of Gal-(1\(\rightarrow\)3)-\(\beta\)-GalNAc \(\alpha\)-linked to serine or threonine residues of mucin-type glycoproteins. EngBF from the bacterium Bifidobacterium longum specifically acts on core 1-type O-glycan to release the disaccharide Gal-(1\(\rightarrow\)3)-\(\beta\)-GalNAc. The enzymes from the bacteria Clostridium perfringens, Enterococcus faecalis, Propionibacterium acnes and Alcaligenes faecalis show broader specificity (e.g. they can also release the core 2 trisaccharide Gal-(1\(\rightarrow\)3)-\(\beta\)-(GlcNAc-(1\(\rightarrow\)6)-\(\beta\))-GalNAc or the core 3 disaccharide GlcNAc-(1\(\rightarrow\)3)-\(\beta\)-GalNAc) [92, 1612]. The enzyme may play an important role in the degradation and utilization of mucins having core 1 O-glycan.

References: [92, 1612, 902, 2956, 1032, 95, 990]

[EC 3.2.1.97 created 1978 (EC 3.2.1.110 created 1984, incorporated 2008), modified 2008, modified 2011]

EC 3.2.1.98

Accepted name: glucan 1,4-\(\alpha\)-maltotetraohydrolase
Reaction: Hydrolysis of (1\(\rightarrow\)4)-\(\alpha\)-D-glucosidic linkages in amylaceous polysaccharides, to remove successive maltotetraose residues from the non-reducing chain ends
Other name(s): exo-maltotetraohydrolase; 1,4-\(\alpha\)-D-glucan maltotetraohydrolase
Systematic name: 4-\(\alpha\)-D-glucan maltotetraohydrolase

Comments: cf. EC 3.2.1.3 glucan 1,4-\(\alpha\)-glucosidase, which removes successive glucose residues; EC 3.2.1.2 \(\beta\)-amylase, which removes successive maltose residues; EC 3.2.1.116 glucan 1,4-\(\alpha\)-maltotriohydrolase, which removes successive maltotriose units and EC 3.2.1.60 glucan 1,4-\(\alpha\)-maltotetraohydrolase, which removes successive maltotetraose residues. The products have the \(\alpha\)-configuration.

References: [1436, 2145]

[EC 3.2.1.98 created 1978]

EC 3.2.1.99

Accepted name: arabinan endo-1,5-\(\alpha\)-L-arabinanase
Reaction: Endohydrolysis of (1\(\rightarrow\)5)-\(\alpha\)-arabinofuranosidic linkages in (1\(\rightarrow\)5)-arabinans
Other name(s): endo-1,5-\(\alpha\)-L-arabinanase; endo-\(\alpha\)-L-arabinanase; 1,5-\(\alpha\)-L-arabinan 1,5-\(\alpha\)-L-arabinohydrolase; arabinan endo-1,5-\(\alpha\)-L-arabinosidase (misleading)
Systematic name: 5-\(\alpha\)-L-arabinan 5-\(\alpha\)-L-arabinohydrolase

Comments: Acts best on linear 1,5-\(\alpha\)-L-arabinan. Also acts on branched arabinan, but more slowly.

References: [1437, 3306, 837, 1704]

[EC 3.2.1.99 created 1981, modified 2011]

EC 3.2.1.100

Accepted name: mannan 1,4-mannobiosidase
Reaction: Hydrolysis of (1\(\rightarrow\)4)-\(\beta\)-D-mannosidic linkages in (1\(\rightarrow\)4)-\(\beta\)-D-mannans, to remove successive manno-biose residues from the non-reducing chain ends
Other name(s): 1,4-\(\beta\)-D-mannan mannobiohydrolase; exo-\(\beta\)-mannanase; exo-1,4-\(\beta\)-mannobiohydrolase
Systematic name: 4-\(\beta\)-D-mannan mannobiohydrolase

References: [71]
EC 3.2.1.100

**Accepted name:** mannan endo-1,6-α-mannosidase  
**Reaction:** Random hydrolysis of (1→6)-α-D-mannosidic linkages in unbranched (1→6)-mannans  
**Other name(s):** endo-α-1→6-D-mannanase; endo-1,6-β-mannanase; mannan endo-1,6-β-mannosidase; 1,6-α-D-mannan mannanohydrolase  
**Systematic name:** 6-α-D-mannan mannanohydrolase  
**References:** [2143, 318, 2142]

[EC 3.2.1.100 created 1983, modified 2001]

EC 3.2.1.101

**Accepted name:** blood-group-substance endo-1,4-β-galactosidase  
**Reaction:** Endohydrolysis of (1→4)-β-D-galactosidic linkages in blood group A and B substances  
**Other name(s):** endo-β-galactosidase (ambiguous); blood-group-substance 1,4-β-D-galactanohydrolase  
**Systematic name:** blood-group-substance 4-β-D-galactanohydrolase  
**Comments:** Hydrolyses the 1,4-β-D-galactosyl linkages adjacent to a 1,3-α-D-galactosyl or N-acetylgalactosaminyl residues and a 1,2-α-D-fucosyl residue.  
**References:** [913, 2158, 2993]

[EC 3.2.1.101 created 1984, modified 2001]

EC 3.2.1.102

**Accepted name:** keratan-sulfate endo-1,4-β-galactosidase  
**Reaction:** Endohydrolysis of (1→4)-β-D-galactosidic linkages in keratan sulfate  
**Other name(s):** endo-β-galactosidase (ambiguous); keratan sulfate endogalactosidase; keratanase; keratan-sulfate 1,4-β-D-galactanohydrolase  
**Systematic name:** keratan-sulfate 4-β-D-galactanohydrolase  
**Comments:** Hydrolyses the 1,4-β-D-galactosyl linkages adjacent to 1,3-N-acetyl-α-D-glucosaminyl residues. Also acts on some non-sulfated oligosaccharides, but only acts on blood group substances when the 1,2-linked fucosyl residues have been removed (cf. EC 3.2.1.102 blood-group-substance endo-1,4-β-galactosidase).  
**References:** [913]

[EC 3.2.1.102 created 1984]

EC 3.2.1.103

**Accepted name:** steryl-β-glucosidase  
**Reaction:** cholesteryl-β-D-glucoside + H₂O = D-glucose + cholesterol  
**Systematic name:** cholesteryl-β-D-glucoside glucohydrolase  
**Comments:** Acts on glucosides of cholesterol and sitosterol, but not on some related sterols such as coprostanol.  
**References:** [1447]

[EC 3.2.1.103 created 1984]

EC 3.2.1.104

**Accepted name:** 3α(5)-strictosidine β-glucosidase  
**Reaction:** strictosidine + H₂O = D-glucose + strictosidine aglycone  
**Systematic name:** strictosidine β-D-glucohydrolase  
**Comments:** Does not act on a number of closely related glycosides. Strictosidine is a precursor of indole alkaloids.

[EC 3.2.1.104 created 1984]
**EC 3.2.1.106**

**Accepted name:** mannosyl-oligosaccharide glucosidase  
**Reaction:** \( \text{Glc}_3\text{Man}_9\text{GlcNAc}_2\text{[protein]} + \text{H}_2\text{O} = \text{Glc}_2\text{Man}_9\text{GlcNAc}_2\text{[protein]} + \beta\text{-d-glucopyranose} \)  
**Other name(s):** Glc3Man99NaC2 oligosaccharide glucosidase; trimming glucosidase I; CWH41 (gene name); MOGS (gene name); mannosyl-oligosaccharide glucohydrolase  
**Systematic name:** Glc3Man99NaC2-[protein] glucohydrolase (configuration-inverting)  
**Comments:** This enzyme catalyses the first step in the processing of the \( N \)-glycan tetradecasaccharide precursor \( \text{Glc}_3\text{Man}_9\text{GlcNAc}_2 \), which takes place in the endoplasmic reticulum, by removing the distal \( \alpha\text{-1,2-} \)linked glucose residue. This and subsequent processing steps are required before complex \( N \)-glycans can be synthesized.  
**References:** [741, 1037, 1524, 1038, 1909]

[EC 3.2.1.106 created 1984, modified 2018]

**EC 3.2.1.107**

**Accepted name:** protein-glucosylgalactosylhydroxylysine glucosidase  
**Reaction:** [collagen]-(5\( R \))-5-O-[\( \alpha\text{-d-glucosyl-(1\rightarrow2)}\]-\( \beta\text{-d-galactosyl\text{-}5-hydroxy-L-lysine + H}_2\text{O} = \text{D-glucose + [collagen]-(5\( R \))-5-O-(\( \beta\text{-d-galactosyl\text{-5-hydroxy-L-lysine}} \) glucohydrolase; protein-\( \alpha\text{-d-glucosyl-1,2-}\beta\text{-d-galactosyl-L-hydroxylysine glucohydrolase; protein-\( \alpha\text{-d-glucosyl-(1\rightarrow2)-}\beta\text{-d-galactosyl-L-hydroxylysine glucohydrolase} \)  
**Other name(s):** PGGHG (gene name); 2-O-\( \alpha\text{-d-glucopyranosyl-5-O-}\alpha\text{-d-galactopyranosylhydroxy-L-lysine glucohydrolase; protein-}\alpha\text{-d-glucosyl-1,2-}\beta\text{-d-galactosyl-L-hydroxylysine glucohydrolase; protein-}\alpha\text{-d-glucosyl-(1\rightarrow2)-}\beta\text{-d-galactosyl-L-hydroxylysine glucohydrolase} \)  
**Systematic name:** [collagen]-(5\( R \))-5-O-[\( \alpha\text{-d-glucosyl-(1\rightarrow2)}\]-\( \beta\text{-d-galactosyl\text{-}5-hydroxy-L-lysine glucohydrolase} \)  
**Comments:** The enzyme specifically hydrolyses glucose from \( \alpha\text{-d-glucosyl-(1\rightarrow2)}\]-\( \beta\text{-d-galactosyl disaccharide units that are linked to hydroxylysine residues of collagen and collagen-like proteins. Acetylation of the \( \varepsilon\)-amino group of the glycosylated hydroxylysine abolishes activity.} \)  
**References:** [1096, 1097, 2907, 1095]

[EC 3.2.1.106 created 1984, modified 2018]

**EC 3.2.1.108**

**Accepted name:** lactase  
**Reaction:** lactose + \( \text{H}_2\text{O} = \text{d-glucose + d-galactose} \)  
**Other name(s):** lactase-phlorizin hydrolase; LPH (gene name); LCT (gene name)  
**Systematic name:** lactate galactohydrolase (configuration-retaining)  
**Comments:** The enzyme from intestinal mucosa contains two glycosyl hydrolase domains, both of which belong to glycosyl hydrolase family 1 (GH1). While the first domain catalyses the activity described here, the second domain catalyses the reaction of EC 3.2.1.62 glycosylceramidase. cf. EC 3.2.1.33 amylo-\( \alpha\text{-1,6-glucosidase.} \)  
**References:** [96, 2699, 1834, 2485, 2825, 2824, 3479, 83]

[EC 3.2.1.106 created 1984, modified 2022]

**EC 3.2.1.109**

**Accepted name:** endogalactosaminidase  
**Reaction:** Endohydrolysis of (1\( \rightarrow4\))-\( \alpha\text{-d-galactosaminidic linkages in poly(d-galactosamine} \)  
**Systematic name:** galactosaminoglycan glycanohydrolase  
**References:** [2529, 3008]

[EC 3.2.1.109 created 1984]
EC 3.2.1.111

Accepted name: 1,3-α-L-fucosidase

Reaction: Hydrolysis of (1→3)-linkages between α-L-fucose and N-acetylglucosamine residues in glycoproteins

Other name(s): almond emulsin fucosidase I

Systematic name: 3-α-L-fucosyl-N-acetylglucosaminyl-glycoprotein fucohydrolase

Comments: Not identical with EC 3.2.1.63 1,2-α-L-fucosidase.

References: [1321, 2253, 3463]

EC 3.2.1.112

Accepted name: 2-deoxyglucosidase

Reaction: a 2-deoxy-α-D-glucoside + H₂O = 2-deoxy-α-D-glucose + an alcohol

Other name(s): 2-deoxy-α-glucosidase; 2-deoxy-α-D-glucosidase

Systematic name: 2-deoxy-α-D-glucoside deoxyglucohydrolase

References: [396]

EC 3.2.1.113

Accepted name: mannosyl-oligosaccharide 1,2-α-mannosidase

Reaction: (1) Man₉GlcNAc₂-[protein] + 4 H₂O = Man₈GlcNAc₂-[protein] + 4 β-D-mannopyranose (overall reaction)
(1a) Man₉GlcNAc₂-[protein] + H₂O = Man₈GlcNAc₂-[protein] (isomer 8A₁₂₃B₁₂) + β-D-mannopyranose
(1b) Man₈GlcNAc₂-[protein] (isomer 8A₁₂₃B₁₂) + H₂O = Man₇GlcNAc₂-[protein] (isomer 7A₁₂₃B₂) + β-D-mannopyranose
(1c) Man₇GlcNAc₂-[protein] (isomer 7A₁₂₃B₂) + H₂O = Man₆GlcNAc₂-[protein] (isomer 6A₁₂B₂) + β-D-mannopyranose
(1d) Man₆GlcNAc₂-[protein] (isomer 6A₁₂B₂) + H₂O = Man₅GlcNAc₂-[protein] + β-D-mannopyranose
(2) Man₈GlcNAc₂-[protein] (isomer 8A₁₂₃B₁₃) + 3 H₂O = Man₇GlcNAc₂-[protein] + 3 β-D-mannopyranose (overall reaction)
(2a) Man₇GlcNAc₂-[protein] (isomer 8A₁₂₃B₁₃) + H₂O = Man₆GlcNAc₂-[protein] (isomer 7A₁₂₃B₁) + β-D-mannopyranose
(2b) Man₆GlcNAc₂-[protein] (isomer 7A₁₂₃B₁) + H₂O = Man₅GlcNAc₂-[protein] (isomer 6A₁₂₃B) + β-D-mannopyranose
(2c) Man₅GlcNAc₂-[protein] (isomer 6A₁₂₃B) + H₂O = Man₄GlcNAc₂-[protein] + 3 β-D-mannopyranose (overall reaction)

Other name(s): mannosidase IA; mannosidase IB; 1,2-α-mannosidase; exo-α-1,2-mannanase; mannose-9 processing α-mannosidase; glycoprotein processing mannosidase I; mannosidase I; Man₉-mannosidase; ManI; 1,2-α-mannosyl-oligosaccharide α-D-mannohydrolase; MAN1A1 (gene name); MAN1A2 (gene name); MAN1C1 (gene name); 2-α-mannosyl-oligosaccharide α-D-mannohydrolase

Systematic name: Man₉GlcNAc₂-[protein] α-2-mannohydrolase (configuration-inverting)
This family of mammalian enzymes, located in the Golgi system, participates in the maturation process of N-glycans that leads to formation of hybrid and complex structures. The enzymes catalyse the hydrolysis of the four (1→2)-linked α-D-mannose residues from the Man9GlcNAc2 oligosaccharide attached to target proteins as described in reaction (1). Alternatively, the enzymes act on the Man8GlcNAc2 isomer formed by EC 3.2.1.209, endoplasmic reticulum Man9GlcNAc2 1,2-α-mannosidase, as described in reaction (2). The enzymes are type II membrane proteins, require Ca2+, and use an inverting mechanism. While all three human enzymes can catalyse the reactions listed here, some of the enzymes can additionally catalyse hydrolysis in an alternative order, generating additional isomeric intermediates, although the final product is the same. The names of the isomers listed here are based on a nomenclature system proposed by Prien et al [2443].

References:
[2968, 3141, 234, 3106, 1682, 3107, 2443]

[EC 3.2.1.113 created 1986, modified 2019]
EC 3.2.1.117

Accepted name: amygdalin β-glucosidase
Reaction: \((R)-\text{amygdalin} + \text{H}_2\text{O} = (R)-\text{prunasin} + \text{D-glucose}\)
Other name(s): amygdalase; amygdalinase; amygdalin hydrolase; amygdalin glucosidase
Systematic name: amygdalin \(\beta\)-D-glucohydrolase
Comments: Highly specific; does not act on prunasin, linamarin, gentiobiose or cellobiose (cf. EC 3.2.1.21 \(\beta\)-glucosidase).
References: [1663]

[EC 3.2.1.117 created 1989]

EC 3.2.1.118

Accepted name: prunasin β-glucosidase
Reaction: \((R)-\text{prunasin} + \text{H}_2\text{O} = \text{D-glucose} + \text{mandelonitrile}\)
Other name(s): prunasin hydrolase
Systematic name: prunasin \(\beta\)-D-glucohydrolase
Comments: Highly specific; does not act on amygdalin, linamarin or gentiobiose. (cf. EC 3.2.1.21 \(\beta\)-glucosidase).
References: [1663]

[EC 3.2.1.118 created 1989]

EC 3.2.1.119

Accepted name: vicianin β-glucosidase
Reaction: \((R)-\text{vicianin} + \text{H}_2\text{O} = \text{mandelonitrile} + \text{vicianose}\)
Other name(s): vicianin hydrolase
Systematic name: \((R)-\text{vicianin}\) \(\beta\)-D-glucohydrolase
Comments: Also hydrolyses, more slowly, \((R)-\text{amygdalin}\) and \((R)-\text{prunasin}\), but not gentiobiose, linamarin or cellobiose.
References: [1663]

[EC 3.2.1.119 created 1989]

EC 3.2.1.120

Accepted name: oligoxyloglucan \(\beta\)-glycosidase
Reaction: Hydrolysis of \((1\rightarrow4)\)-\(\beta\)-D-glucosidic links in oligoxyloglucans so as to remove successive isoprimeverose [i.e. \(\alpha\)-xylo-(1\rightarrow6)-\(\beta\)-D-glosylosyl-] residues from the non-reducing chain ends
Other name(s): isoprimeverose-producing oligoxyloglucan hydrolase; oligoxyloglucan hydrolase
Systematic name: oligoxyloglucan xyloglucohydrolase
References: [1485]

[EC 3.2.1.120 created 1989]

EC 3.2.1.121

Accepted name: polymannuronate hydrolase
Reaction: Endohydrolysis of the \(D\)-mannuronide linkages of polymannuronate
Other name(s): polymannuronic acid polymerase
Systematic name: poly(mannuronide) mannuronohydrolase
Comments: Does not act on alginic acid, which is a copolymer of polymannuronate.
References: [712]

[EC 3.2.1.121 created 1989]
EC 3.2.1.122
Accepted name: maltose-6\textsuperscript{\prime}-phosphate glucosidase
Reaction: \(\alpha\)-maltose 6\textsuperscript{\prime}-phosphate + H\textsubscript{2}O \rightarrow D\text{-}glucose + D\text{-}glucose 6-phosphate
Other name(s): phospho-\(\alpha\)-glucosidase; maltose-6\textsuperscript{\prime}-phosphate 6-phosphoglucohydrolase
Systematic name: \(\alpha\)-maltose-6\textsuperscript{\prime}-phosphate 6-phosphoglucohydrolase
Comments: Hydrolyses a variety of 6-phospho-\(\alpha\)-D-glucosides, including \(\alpha\)-maltose 6\textsuperscript{\prime}-phosphate, \(\alpha\)\(\alpha\)-trehalose 6-phosphate, sucrose 6-phosphate and \(p\)-nitrophenyl-\(\alpha\)-D-glucopyranoside 6-phosphate (as a chromogenic substrate). The enzyme is activated by Fe\textsuperscript{II}, Mn\textsuperscript{II}, Co\textsuperscript{II} and Ni\textsuperscript{II}. It is rapidly inactivated in air.
References: [3058]

[EC 3.2.1.122 created 1989, modified 1999]

EC 3.2.1.123
Accepted name: endoglycosylceramidase
Reaction: oligoglycosylglucosyl-(1\(\leftrightarrow\)1)-ceramide + H\textsubscript{2}O \rightarrow ceramide + oligoglycosylglucose
Other name(s): endoglycoceramidase; EGCase; glycosyl-N\text{-}acetyl-sphingosine 1,1-\(\beta\)-D-glcanohydrolase; oligoglycosylglucosylceramide glycohydrolase; oligoglycosylglucosyl(1\(\leftrightarrow\)1)ceramide glycohydrolase
Systematic name: oligoglycosylglucosyl-(1\(\leftrightarrow\)1)-ceramide glycohydrolase
Comments: An enzyme from \textit{Rhodococcus} sp. that degrades various acidic and neutral glycosphingolipids to oligosaccharides and ceramides, by cleaving a glucosyl bond. Does not act on monoglycosylceramides. \textit{cf.} EC 3.2.1.62 glycosylceramidase.
References: [1344]

[EC 3.2.1.123 created 1989]

EC 3.2.1.124
Accepted name: 3-deoxy-2-octulosonidase
Reaction: Endohydrolysis of the \(\beta\)-ketopyranosidic linkages of 3-deoxy-D\text{-}manno\text{-}2-octulosonate in capsular polysaccharides
Other name(s): 2-keto-3-deoxyoctonate hydrolase; octulosylono hydrolase; octulofuranosylono hydrolase; octulopyranosylono hydrolase
Systematic name: capsular-polysaccharide 3-deoxy-D\text{-}manno\text{-}2-octulosonohydrolase
Comments: The enzyme from a bacteriophage catalyses the depolymerization of capsular polysaccharides containing 3-deoxy-2-octulosonide in the cell wall of \textit{Escherichia coli}.
References: [45]

[EC 3.2.1.124 created 1989]

EC 3.2.1.125
Accepted name: raucaffricine \(\beta\)-glucosidase
Reaction: raucaffricine + H\textsubscript{2}O \rightarrow D\text{-}glucose + vomilenine
Other name(s): raucaffricine \(\beta\)-D-glucosidase; raucaffricine glucosidase
Systematic name: raucaffricine \(\beta\)-D-glucohydrolase
Comments: Highly specific; some other ajmalan glucoside alkaloids are hydrolysed, but more slowly.
References: [2720]

[EC 3.2.1.125 created 1989]

EC 3.2.1.126
Accepted name: coniferin \(\beta\)-glucosidase
Reaction: coniferin + H\textsubscript{2}O \rightarrow D\text{-}glucose + coniferol
Other name(s): coniferin-hydrolyzing \(\beta\)-glucosidase

123
**Systematic name:** coniferin β-D-glucosidase  
**Comments:** Also hydrolyses syringin, 4-cinnamyl alcohol β-glucoside and, more slowly, some other aryl β-glycosides. A plant cell-wall enzyme involved in the biosynthesis of lignin.  
**References:** [1256, 1904]

[EC 3.2.1.126 created 1989]

**EC 3.2.1.127**  
**Accepted name:** 1,6-α-L-fucosidase  
**Reaction:** Hydrolysis of (1→6)-linkages between α-L-fucose and N-acetyl-D-glucosamine in glycopeptides such as immunoglobulin G glycopeptide and fucosyl-asialo-agalacto-fetuin  
**Other name(s):** α-l-fucosidase; 1,6-L-fucosyl-N-acetyl-D-glucosaminylglycopeptide fucohydrolase  
**Systematic name:** 6-L-fucosyl-N-acetyl-D-glucosaminylglycopeptide fucohydrolase  
**Comments:** The enzyme from *Aspergillus niger* does not act on 1,2-, 1,3-, or 1,4-L-fucosyl linkages.  
**References:** [3438]

[EC 3.2.1.127 created 1989]

**EC 3.2.1.128**  
**Accepted name:** glycyrrhizin hydrolase  
**Reaction:** glycyrrhizin + H₂O = β-D-glucuronosyl-(1→2)-D-glucuronate + glycyrrhetinate  
**Other name(s):** glycyrrhizinate β-glucuronidase; glycyrrhizin β-hydrolase; glycyrrhizinic acid hydrolase  
**Systematic name:** glycyrrhizinate glucuronosylhydrolase  
**Comments:** The enzyme from *Aspergillus niger* is specific for the hydrolysis of the triterpenoid glycoside glycyrrhizin from roots of *Glycyrrhiza* sp.  
**References:** [2110]

[EC 3.2.1.128 created 1989]

**EC 3.2.1.129**  
**Accepted name:** endo-α-sialidase  
**Reaction:** Endohydrolysis of (2→8)-α-sialosyl linkages in oligo- or poly(sialic) acids  
**Other name(s):** endo-N-acetylneuraminidase; endoneuraminidase; endo-N-acetylneuraminidase; poly(α-2,8-sialosyl) endo-N-acetylneuraminidase; poly(α-2,8-sialosyl) α-2,8-sialosylhydrolase; endosomalidase; endo-N polysialoside (2→8)-α-sialosylhydrolase  
**Comments:** Although the name endo-N-acetylneuraminidase has also been used for this enzyme, this is misleading since its activity is not restricted to acetylated substrates. An exo-α-sialidase activity is listed as EC 3.2.1.18 exo-α-sialidase. See also EC 4.2.2.15 anhydrosialidase.  
**References:** [821, 1090, 1556, 1671, 2370, 3076, 376]

[EC 3.2.1.129 created 1990, modified 1999]

**EC 3.2.1.130**  
**Accepted name:** glycoprotein endo-α-1,2-mannosidase  
**Reaction:** GlcMan₉GlcNAc₂-[protein] + H₂O = Man₈GlcNAc₂-[protein] (isomer 8A₁,2,3B₁,2) + α-D-glucosyl-(1→3)-α-D-mannopyranose  
**Other name(s):** glucosylmannosidase; endo-α-D-mannosidase; endo-α-mannosidase; endomannosidase; glucosyl mannosidase; MANEA (gene name); glycoprotein glucosylmannohydrolase  
**Systematic name:** glycoprotein glucosylmannohydrolase (configuration-retaining)  
**Comments:** The enzyme catalyses the hydrolysis of the terminal α-D-glucosyl-(1→3)-D-mannosyl unit from the GlcMan₉(GlcNAc)₂ oligosaccharide component of N-glucosylated proteins during their processing in the Golgi apparatus. The name for the isomer is based on a nomenclature proposed by Prien et al [2443].

124
References: [1847, 3140, 1215, 2881, 1098, 1114, 2443]

[EC 3.2.1.130 created 1990, modified 2017]

EC 3.2.1.131
Accepted name: xylan α-1,2-glucuronosidase
Reaction: Hydrolysis of (1→2)-α-D-(4-O-methyl)glucuronosyl links in the main chain of hardwood xylans
Other name(s): 1,2-α-glucuronidase; α-(1→2)-glucuronidase; xylan α-D-1,2-(4-O-methyl)glucuronohydrolase
Systematic name: xylan 2-α-D-(4-O-methyl)glucuronohydrolase
References: [1339]

[EC 3.2.1.131 created 1990]

EC 3.2.1.132
Accepted name: chitosanase
Reaction: Endohydrolysis of β-(1→4)-linkages between D-glucosamine residues in a partly acetylated chitosan
Systematic name: chitosan N-acetylglucosaminohydrolase
Comments: A whole spectrum of chitosanases are now known (for more details, see http://rbrzezinski.recherche.usherbrooke.ca/). They can hydrolyse various types of links in chitosan. The only constant property is the endohydrolysis of GlcN-GlcN links, which is common to all known chitosanases. One known chitosanase is limited to this link recognition [1905], while the majority can also recognize GlcN-GlcNAc links or GlcNAc-GlcN links but not both. They also do not recognize GlcNAc-GlcNAc links in partly acetylated chitosan.
References: [807, 2622, 1363, 1905]

[EC 3.2.1.132 created 1990, modified 2004]

EC 3.2.1.133
Accepted name: glucan 1,4-α-maltohydrolase
Reaction: hydrolysis of (1→4)-α-D-glucosidic linkages in polysaccharides so as to remove successive α-maltose residues from the non-reducing ends of the chains
Other name(s): maltogenic α-amylase; 1,4-α-D-glucan α-maltohydrolase
Systematic name: 4-α-D-glucan α-maltohydrolase
Comments: Acts on starch and related polysaccharides and oligosaccharides. The product is α-maltose; cf. EC 3.2.1.2 β-amylase.
References: [650, 2329]

[EC 3.2.1.133 created 1992, modified 1999]

[3.2.1.134 Transferred entry. difructose-dianhydride-I hydrolase. Now EC 4.2.1.179, difructose-dianhydride-I hydro-lyase]

[EC 3.2.1.134 created 1992, deleted 2021]

EC 3.2.1.135
Accepted name: neopullulanase
Reaction: Hydrolysis of pullulan to panose (6-α-D-glucosylmaltose)
Other name(s): pullulase II
Systematic name: pullulan 4-α-D-glucanohydrolase (panose-forming)
Comments: cf. EC 3.2.1.41 (pullulanase ) and EC 3.2.1.57 (isopullulanase).
References: [1320]

[EC 3.2.1.135 created 1992]
EC 3.2.1.136
Accepted name: glucuronoarabinoxylan endo-1,4-β-xylanase
Reaction: Endohydrolysis of (1→4)-β-D-xylosyl links in some glucuronoarabinoxylans
Other name(s): feraxan endo-β-D-xylanase; feraxanase; endoarabinoxylanase; glucuronoarabinoxylanase; glucuronoarabinoxylan xylohydrolase; glucuronoarabin oxydase; glucuronoarabinoxylan 1,4-β-D-xylanohydrolase
Systematic name: glucuronoarabinoxylan 4-β-D-xylanohydrolase
Comments: High activity towards feruloylated arabinoxylans from cereal plant cell walls.
References: [2202]

[EC 3.2.1.136 created 1992]

EC 3.2.1.137
Accepted name: mannan exo-1,2-1,6-α-mannosidase
Reaction: Hydrolysis of (1→2)-α-D- and (1→6)-α-D- linkages in yeast mannan, releasing D-mannose
Other name(s): exo-1,2-1,6-α-mannosidase; 1,2-1,6-α-D-mannan D-mannohydrolase
Systematic name: (1→2)-(1→6)-α-D-mannan D-mannohydrolase
Comments: Mannose residues linked α-D-1,3- are also released, but very slowly.
References: [2997]

[EC 3.2.1.137 created 1992]

[3.2.1.138 Transferred entry. anhydrosialidase. Now EC 4.2.2.15, anhydrosialidase]

[EC 3.2.1.138 created 1992, deleted 2003]

EC 3.2.1.139
Accepted name: α-glucuronidase
Reaction: an α-D-glucuronic acid + H₂O = an alcohol + D-glucuronate
Other name(s): α-glucosiduronase
Systematic name: α-D-glucosiduronate glucuronohydrolase
Comments: Considerable differences in the specificities of the enzymes from different fungi for α-D-glucosiduronates have been reported. Activity is also found in the snail.
References: [2447, 3153]

[EC 3.2.1.139 created 1999]

EC 3.2.1.140
Accepted name: lacto-N-biosidase
Reaction: β-D-Gal-(1→3)-β-D-GlcNAc-(1→3)-β-D-Gal-(1→4)-D-Glc + H₂O = β-D-Gal-(1→3)-D-GlcNAc + β-D-Gal-(1→4)-D-Glc
Systematic name: oligosaccharide lacto-N-biosylhydrolase
Comments: The enzyme from Streptomyces specifically hydrolyses the terminal lacto-N-biosyl residue (β-D-Gal-(1→3)-D-GlcNAc) from the non-reducing end of oligosaccharides with the structure β-D-Gal-(1→3)-β-D-GlcNAc-(1→3)-β-D-Gal-(1→R). Lacto-N-hexaose (β-D-Gal-(1→3)-β-D-GlcNAc-(1→3)-β-D-Gal-(1→3)-β-D-GlcNAc-(1→3)-β-D-Gal-(1→4)-D-Glc) is hydrolysed to form first lacto-N-tetraose plus lacto-N-biose, with the subsequent formation of lactose. Oligosaccharides in which the non-reducing terminal Gal or the penultimate GlcNAc are replaced by fucose or sialic acid are not substrates. Asialo GM1 tetraose (β-D-Gal-(1→3)-β-D-GalNAc-(1→3)-β-D-Gal-(1→4)-D-Glc) is hydrolysed very slowly, but lacto-N-neotetraose (β-D-Gal-(1→4)-β-D-GalNAc-(1→3)-β-D-Gal-(1→4)-D-Glc) is not a substrate
References: [2648, 2649]

[EC 3.2.1.140 created 1999]
EC 3.2.1.141
Accepted name: 4-α-D-(1→4)-α-D-glucanotrehalase trehalohydrolase
Reaction: Hydrolysis of (1→4)-α-D-glucosidic linkage in 4-α-D-[(1→4)-α-D-glucanosyl]n trehalose to yield trehalose and (1→4)-α-D-glucan
Other name(s): malto-oligosyltrehalose trehalohydrolase
Systematic name: 4-α-D-[(1→4)-α-D-glucano]trehalose glucanohydrolase (trehalose-producing)
References: [1922, 2135, 2134]

EC 3.2.1.142
Accepted name: limit dextrinase
Reaction: Hydrolysis of (1→6)-α-D-glucosidic linkages in α- and β-limit dextrins of amylopectin and glycogen, and in amylpectin and pullulan
Other name(s): R-enzyme; amylpectin-1,6-glucosidase; dextrin α-1,6-glucanohydrolase
Systematic name: dextrin 6-α-glucanohydrolase
Comments: Plant enzymes with little or no action on glycogen. Action on amylopectin is incomplete, but action on α-limit dextrins is complete. Maltose is the smallest sugar it can release from an α-(1→6)-linkage.
References: [1013, 1899]

EC 3.2.1.143
Accepted name: poly(ADP-ribose) glycohydrolase
Reaction: hydrolyses poly(ADP-D-ribose) at glycosidic (1′′′-2′′) linkage of ribose-ribose bond to produce free ADP-D-ribose
Comments: Specific to (1′′′-2′′) linkage of ribose-ribose bond of poly(ADP-D-ribose).
References: [2034, 1790]

EC 3.2.1.144
Accepted name: 3-deoxyoctulosonase
Reaction: 3-deoxyoctulosonosyl-lipopolysaccharide + H₂O = 3-deoxyoctulosonic acid + lipopolysaccharide
Other name(s): α-Kdo-ase
Systematic name: 3-deoxyoctulosonosyl-lipopolysaccharide hydrolase
Comments: Releases Kdo (α- and β-linked 3-deoxy-D-manno-octulosonic acid) from different lipopolysaccharides, including Re-LPS from Escherichia coli and Salmonella, Rd-LPS from S. minnesota, and de-O-acyl-re-LPS. 4-Methylumbelliferyl-α-Kdo (α-Kdo-OMec) is also a substrate.
References: [1767]

EC 3.2.1.145
Accepted name: galactan 1,3-β-galactosidase
Reaction: Hydrolysis of terminal, non-reducing β-D-galactose residues in (1→3)-β-D-galactopyranans
Other name(s): galactan (1→3)-β-D-galactosidase
Systematic name: galactan 3-β-D-galactosidase
Comments: This enzyme removes not only free galactose, but also 6-glycosylated residues, e.g., (1→6)-β-D-galactobiose, and galactose bearing oligosaccharide chains on O-6. Hence, it releases branches from arabino-galacto-(1→6)-(1→3)-β-D-galactans.
References: [3130, 2371]
EC 3.2.1.146
Accepted name: β-galactofuranosidase
Reaction: Hydrolysis of terminal non-reducing β-D-galactofuranosides, releasing galactose
Other name(s): exo-β-galactofuranosidase; exo-β-D-galactofuranosidase; β-D-galactofuranosidase
Systematic name: β-D-galactofuranoside hydrolase
Comments: The enzyme from Helminthosporium sacchari detoxifies helminthosporoside, a bis(digalactosyl)terpene produced by this fungus, by releasing its four molecules of bound galactose.
References: [2552, 571, 539, 2007]

EC 3.2.1.147
Accepted name: thioglucosidase
Reaction: a thioglucoside + H₂O = a sugar + a thiol
Other name(s): myrosinase; sinigrinase; sinigrase
Systematic name: thioglucoside glucohydrolase
Comments: Has a wide specificity for thioglycosides.
References: [1011, 2399]

EC 3.2.1.148
Accepted name: β-primeverosidase
Reaction: a 6-O-(β-D-xylopyranosyl)-β-D-glucopyranoside + H₂O = 6-O-(β-D-xylopyranosyl)-β-D-glucopyranose + an alcohol
Systematic name: 6-O-(β-D-xylopyranosyl)-β-D-glucopyranoside 6-O-(β-D-xylosyl)-β-D-glucopyranoside 6-O-(β-D-apiofuranosyl)-β-D-glucopyranosides and, less rapidly, β-vicianosides and 6-O-(α-L-arabinofuranosyl)-β-D-glucopyranosides, but not β-glucosides. Geranyl-, linaloyl-, benzyl- and p-nitrophenol glycosides are all hydrolysed.
Comments: The enzyme is responsible for the formation of the alcoholic aroma in oolong and black tea. In addition to β-primeverosides [i.e. 6-O-(β-D-xylopyranosyl)-β-D-glucopyranosides], it also hydrolyses 6-O-(β-D-apiofuranosyl)-β-D-glucopyranosides and, less rapidly, β-vicianosides and 6-O-(α-L-arabinofuranosyl)-β-D-glucopyranosides, but not β-glucosides. Geranyl-, linaloyl-, benzyl- and p-nitrophenol glycosides are all hydrolysed.
References: [1304, 2258]

EC 3.2.1.150
Accepted name: oligoxyloglucan reducing-end-specific cellobiohydrolase
Reaction: Hydrolysis of cellobiose from the reducing end of xyloglucans consisting of a (1→4)-β-linked glucan carrying α-D-xylosyl groups on O-6 of the glucose residues. To be a substrate, the first residue must be unsubstituted, the second residue may bear a xylosyl group, whether further glycosylated or not, and the third residue, which becomes the new terminus by the action of the enzyme, is preferably xylosylated, but this xylose residue must not be further substituted.
Systematic name: oligoxyloglucan reducing-end cellobiohydrolase
Comments: The enzyme is found in the fungus Geotrichum sp. M128. The substrate is a hemicellulose found in plant cell walls.
References: [3424]
EC 3.2.1.151

**Accepted name:** xyloglucan-specific endo-β-1,4-glucanase

**Reaction:** xyloglucan + H₂O = xyloglucan oligosaccharides

**Other name(s):** XEG; xyloglucan endo-β-1,4-glucanase; xyloglucanase; xyloglucanendohydrolase; XH; 1,4-β-D-glucan glucanohydrolase

**Systematic name:** [(1→6)-α-D-xylo]-[(1→4)-β-D-glucan glucanohydrolase

**Comments:** The enzyme from *Aspergillus aculeatus* is specific for xyloglucan and does not hydrolyse other cell-wall components. The reaction involves endohydrolysis of 1,4-β-D-glucosidic linkages in xyloglucan with retention of the β-configuration of the glycosyl residues.

**References:** [2363, 1041]

[EC 3.2.1.151 created 2003]

EC 3.2.1.152

**Accepted name:** mannosylglycoprotein endo-β-mannosidase

**Reaction:** Hydrolysis of the α-D-mannosyl-(1→6)-β-D-mannosyl-(1→4)-N-acetyl-β-D-glucosaminyl-(1→4)-N-acetyl-β-D-glucosaminyl sequence of glycoprotein to α-D-mannosyl-(1→6)-D-mannose and N-acetyl-β-D-glucosaminyl-(1→4)-N-acetyl-β-D-glucosaminyl sequences

**Other name(s):** endo-β-mannosidase

**Comments:** The substrate group is a substituent on N-4 of an asparagine residue in the glycoprotein. The mannose residue at the non-reducing end of the sequence may carry further α-D-mannosyl groups on O-3 or O-6, but such a substituent on O-3 of the β-D-mannosyl group prevents the action of the enzyme. The enzyme was obtained from the lily, *Lilium longiflorum*.

**References:** [1341, 2661]

[EC 3.2.1.152 created 2005]

EC 3.2.1.153

**Accepted name:** fructan β-(2,1)-fructosidase

**Reaction:** Hydrolysis of terminal, non-reducing (2→1)-linked β-D-fructofuranose residues in fructans

**Other name(s):** β-(2,1)-fructan fructohydrolase; β-(2,1)fructan exohydrolase; inulinase; 1-FEH II; 1-fructan exohydrolase; 1-FEH w1; 1-FEH w2; β-(2,1)-linkage-specific fructan-β-fructosidase; β-(2,1)-D-fructan fructohydrolase

**Systematic name:** β-(2→1)-D-fructan fructohydrolase

**Comments:** Possesses one of the activities of EC 3.2.1.80, fructan β-fructosidase. While the best substrates are the inulin-type fructans, such as 1-kestose [β-D-fructofuranosyl-(2→1)-β-D-fructofuranosyl α-D-glucopyranoside] and 1-nystose [β-D-fructofuranosyl-(2→1)-β-D-fructofuranosyl-(2→1)-β-D-fructofuranosyl α-D-glucopyranoside], some (but not all) levan-type fructans can also be hydrolysed, but more slowly [see EC 3.2.1.154, fructan β-(2,6)-fructosidase]. Sucrose, while being a very poor substrate, can substantially inhibit enzyme activity in some cases.

**References:** [2585, 621]

[EC 3.2.1.153 created 2005]

EC 3.2.1.154

**Accepted name:** fructan β-(2,6)-fructosidase

**Reaction:** Hydrolysis of terminal, non-reducing (2→6)-linked β-D-fructofuranose residues in fructans

**Other name(s):** β-(2,6)-fructan exohydrolase; levanase; 6-FEH; β-(2,6)-D-fructan fructohydrolase

**Systematic name:** (2→6)-β-D-fructan fructohydrolase

129
Comments: Possesses one of the activities of EC 3.2.1.80, fructan β-fructosidase. While the best substrates are the levan-type fructans such as 6-kestotriose \([\beta-D-fructofuranosyl-(2\rightarrow6)\beta-D-fructofuranosyl \alpha-D\-glucopyranoside]\) and 6,6-kestotetraose \([\beta-D-fructofuranosyl-(2\rightarrow6)\beta-D-fructofuranosyl-(2\rightarrow6)\beta-D-fructofuranosyl \alpha-D\-glucopyranoside]\), some (but not all) inulin-type fructans can also be hydrolysed, but more slowly \([cf.\ EC\ 3.2.1.153,\ fructan\ \beta-(2,1)-fructosidase]\). Sucrose, while being a very poor substrate, can substantially inhibit enzyme activity in some cases.

References: [1926, 622, 1188]

[EC 3.2.1.154 created 2005]

EC 3.2.1.155
Accepted name: xyloglucan-specific endo-processive \(\beta\)-1,4-glucanase
Reaction: Hydrolysis of \((1\rightarrow4)\beta-D\)-glucosidic linkages in xyloglucans so as to successively remove oligosaccharides from the newly-formed chain end after endo-initiation on a polymer molecule
Other name(s): Cel74A; \([\{1\rightarrow6\}-\alpha-D-xylo\}-(1\rightarrow4)\beta-D\-glucan exo-glucohydrolase\) (ambiguous); xyloglucan-specific exo-\(\beta\)-1,4-glucanase (ambiguous)
Systematic name: \([\{1\rightarrow6\}-\alpha-D-xylo\}-(1\rightarrow4)\beta-D\-glucan endo-processive glucohydrolase
Comments: The enzyme removes branched oligosaccharides, containing preferentially four glucoside residues in the main chain, from xyloglucan molecules in a processive manner after the initial endo-type attack on a polysaccharide \([1041, 1295, 1939, 81, 80]\). Hydrolysis occurs at either the unsubstituted \(D\)-glucopyranose residue in the main backbone and/or the \(D\)-glucopyranose residue bearing a xylosyl group \([1041, 1295, 1939, 81, 80]\). The enzyme does not display activity, or shows very low activity, towards other \(\beta\)-D-glycans \([1,2,4,5]\).

References: [1041, 1295, 1939, 81, 80, 1065]

[EC 3.2.1.155 created 2005, withdrawn at public-review stage, modified and reinstated 2006, modified 2020]

EC 3.2.1.156
Accepted name: oligosaccharide reducing-end xylanase
Reaction: Hydrolysis of \((1\rightarrow4)\beta-D\)-xylose residues from the reducing end of oligosaccharides
Other name(s): Rex; reducing end xylose-releasing exo-oligoxylanase
Systematic name: \(\beta-D\-xylopyranosyl-(1\rightarrow4)\beta-D\-xylopyranose reducing-end xylanase
Comments: The enzyme, originally isolated from the bacterium \(Bacillus halodurans\) C-125, releases the xylose unit at the reducing end of oligosaccharides ending with the structure \(\beta-D\-xylopyranosyl-(1\rightarrow4)\beta-D\-xylopyranosyl-(1\rightarrow4)\beta-D\-xylopyranose\), leaving the new reducing end in the \(\alpha\) configuration. It is specific for the \(\beta\) anomers of xylooligosaccharides whose degree of polymerization is equal to or greater than 3. The penultimate residue must be \(\beta-D\-xylopyranose\), but replacing either of the flanking residues with glucose merely slows the rate greatly.

References: [1239, 920]

[EC 3.2.1.156 created 2005]

EC 3.2.1.157
Accepted name: \(\iota\)-carrageenase
Reaction: Endohydrolysis of \((1\rightarrow4)\beta-D\)-linkages between \(D\-galactose\ \text{4-sulfate}\) and \(3,6\text{-anhydro-}D\-galactose\ \text{2-sulfate}\) in \(\iota\)-carrageenans
Systematic name: \(\iota\)-carrageenan \(4\beta-D\)-glycanohydrolase (configuration-inverting)
Comments: The main products of hydrolysis are \(\iota\)-neocarratetraose sulfate and \(\iota\)-neocarrarhexaose sulfate. \(\iota\)-Neocarractaeose is the shortest substrate oligomer that can be cleaved. Unlike EC 3.2.1.81, \(\beta\)-agarase and EC 3.2.1.83, \(\kappa\)-carrageenase, this enzyme proceeds with inversion of the anomer configuration. \(\iota\)-Carrageenan differs from \(\kappa\)-carrageenan by possessing a sulfo group on \(O\)-2 of the 3,6-anhydro-\(D\)-galactose residues, in addition to that present in the \(\kappa\)-compound on \(O\)-4 of the \(D\)-galactose residues.

References: [151, 2001, 2002]
**EC 3.2.1.158**

**Accepted name:** α-agarase

**Reaction:** Endohydrolysis of (1→3)-α-L-galactosidic linkages in agarose, yielding agarotetraose as the major product

**Other name(s):** agarase (ambiguous); agaraseA3

**Systematic name:** agarase 3-glycanohydrolase

**Comments:** Requires Ca$^{2+}$. The enzyme from *Thalassomonas* sp. can use agarose, agarohexaose and neoaagarohexaose as substrate. The products of agarohexaose hydrolysis are dimers and tetramers, with agarotetraose being the predominant product, whereas hydrolysis of neoaagarohexaose gives rise to two types of trimer. While the enzyme can also hydrolyse the highly sulfated agarose porphyran very efficiently, it cannot hydrolyse the related compounds κ-carrageenan (see EC 3.2.1.83) and ι-carrageenan (see EC 3.2.1.157) [2278]. See also EC 3.2.1.81, β-agarase.

**References:** [2435, 2278]

[EC 3.2.1.158 created 2006]

**EC 3.2.1.159**

**Accepted name:** α-neoagaro-oligosaccharide hydrolase

**Reaction:** Hydrolysis of the (1→3)-α-L-galactosidic linkages that are smaller than a hexamer, yielding 3,6-anhydro-L-galactose and D-galactose

**Other name(s):** α-neoagaroooligosaccharide hydrolase; α-NAOS hydrolase

**Systematic name:** α-neoagaro-oligosaccharide 3-glycohydrolase

**Comments:** When neoagarohexaose is used as a substrate, the oligosaccharide is cleaved at the non-reducing end to produce 3,6-anhydro-L-galactose and agaropentaose, which is further hydrolysed to agarobiose and agarotriose. With neoagarotetraose as substrate, the products are predominantly agarotriose and 3,6-anhydro-L-galactose. In *Vibrio* sp. the actions of EC 3.2.1.81, β-agarase and EC 3.2.1.159 can be used to degrade agarose to 3,6-anhydro-L-galactose and D-galactose.

**References:** [2932]

[EC 3.2.1.159 created 2006]

[3.2.1.160 Deleted entry. xyloglucan-specific exo-β-1,4-glucanase. The enzyme was shown to be identical to EC 3.2.1.155, xyloglucan-specific exo-β-1,4-glucanase, during the public-review process so was withdrawn before being made official]

[EC 3.2.1.160 created 2006, deleted 2006]

**EC 3.2.1.161**

**Accepted name:** β-apiosyl-β-glucosidase

**Reaction:** 7-[β-D-apiofuranosyl-(1→6)-β-D-glucopyranosyloxy]isoflavonoid + H$_2$O = a 7-hydroxyisoflavonoid + β-D-apiofuranosyl-(1→6)-D-glucose

**Other name(s):** isoflavonoid-7-O-β[D-apiosyl-(1→6)-β-D-glucoside] disaccharidase; isoflavonoid 7-O-β-apiosyl-glucoside β-glucosidase; furcatin hydrolase

**Systematic name:** 7-[β-D-apiofuranosyl-(1→6)-β-D-glucopyranosyloxy]isoflavonoid β-D-apiofuranosyl-(1→6)-D-glucopyranohydrolase

**Comments:** The enzyme from the tropical tree *Dalbergia nigrescens* Kurz belongs in glycosyl hydrolase family 1. The enzyme removes disaccharides from the natural substrates dalpatein 7-O-β-D-apiofuranosyl-(1→6)-β-D-glucopyranoside and 7-hydroxy-2',4',5',6-tetramethoxy-7-O-β-D-apiofuranosyl-(1→6)-β-D-glucopyranoside (dalnigrein 7-O-β-D-apiofuranosyl-(1→6)-β-D-glucopyranoside) although it can also remove a single glucose residue from isoflavonoid 7-O-glucosides [484]. Daidzin and genistin are also substrates.

**References:** [1255, 484, 26]

[EC 3.2.1.161 created 2006]
EC 3.2.1.162
Accepted name: λ-carrageenase
Reaction: Endohydrolysis of (1→4)-β-linkages in the backbone of λ-carrageenan, resulting in the tetrasaccharide α-D-Galp2,6Sβ-(1→3)-β-D-Galp2S-(1→4)-α-D-Galp2,6Sβ-(1→3)-D-Galp2S
Other name(s): endo-β-1,4-carrageenose 2,6,2′-trisulfate-hydrolase
Systematic name: endo-(1→4)-β-carrageenose 2,6,2′-trisulfate-hydrolase
Comments: The enzyme from Pseudoalteromonas sp. is specific for λ-carrageenan. ι-Carrageenan (see EC 3.2.1.157, ι-carrageenase), κ-carrageenan (see EC 3.2.1.83, κ-carrageenase), agarose and porphyran are not substrates.
References: [2277]

EC 3.2.1.163
Accepted name: 1,6-α-D-mannosidase
Reaction: Hydrolysis of the (1→6)-linked α-D-mannose residues in α-D-Manp-(1→6)-D-Manp
Systematic name: (1→6)-α-mannosyl α-d-mannohydrolase
Comments: The enzyme is specific for (1→6)-linked mannobiose and has no activity towards any other linkages, or towards p-nitrophenyl-α-D-mannopyranoside or baker’s yeast mannan. It is strongly inhibited by Mn^{2+} but does not require Ca^{2+} or any other metal cofactor for activity.
References: [99]

EC 3.2.1.164
Accepted name: galactan endo-1,6-β-galactosidase
Reaction: Endohydrolysis of (1→6)-β-D-galactosidic linkages in arabinogalactan proteins and (1→3):(1→6)-β-galactans to yield galactose and (1→6)-β-galactobiose as the final products
Other name(s): endo-1,6-β-galactanase
Systematic name: endo-β-(1→6)-galactanase
Comments: The enzyme specifically hydrolysates 1,6-β-D-galactooligosaccharides with a degree of polymerization (DP) higher than 3, and their acidic derivatives with 4-O-methylglucosuronate or glucosuronate groups at the non-reducing terminals [2297]. 1,3-β-D- and 1,4-β-D-galactosyl residues cannot act as substrates. The enzyme can also hydrolyse α-L-arabinofuranosidase-treated arabinogalactan protein (AGP) extracted from radish roots [2297, 1607]. AGPs are thought to be involved in many physiological events, such as cell division, cell expansion and cell death [1607].
References: [322, 2297, 1607]

EC 3.2.1.165
Accepted name: exo-1,4-β-D-glucosaminidase
Reaction: Hydrolysis of chitosan or chitosan oligosaccharides to remove successive D-glucosamine residues from the non-reducing termini
Other name(s): CsxA; GlcNase; exochitosanase; GlmA; exo-β-1,4-D-glucosaminidase; chitosan exo-1,4-β-D-glucosaminidase
Systematic name: chitosan exo-(1→4)-β-D-glucosaminidase
Comments: Chitosan is a partially or totally N-deacetylated chitin derivative that is found in the cell walls of some phytopathogenic fungi and comprises D-glucosamine residues with a variable content of GlcNAc residues [537]. Acts specifically on chitooligosaccharides and chitosan, having maximal activity on chitotetraose, chitopentaose and their corresponding alcohols [2159]. The enzyme can degrade GlcN-GlcNAc but not GlcNAc-GlcNAc [907]. A member of the glycoside hydrolase family 2 (GH-2) [537].
References: [2159, 2210, 907, 537, 1305]
**EC 3.2.1.166**

**Accepted name:** heparanase  
**Reaction:** endohydrolysis of (1→4)-β-D-glycosidic bonds of heparan sulfate chains in heparan sulfate proteoglycan  
**Other name(s):** Hpa1 heparanase; Hpa1; heparanase 1; heparanase-1; C1A heparanase; HPSE  
**Systematic name:** heparan sulfate N-sulfo-D-glucosamine endoglucanase  
**Comments:** Heparanase cleaves the linkage between a glucuronic acid unit and an N-sulfo glucosamine unit carrying either a 3-O-sulfo or a 6-O-sulfo group [2383]. Heparanase-1 cuts macromolecular heparin into fragments of 5000–20000 Da [3231]. The enzyme cleaves the heparan sulfate glycosaminoglycans from proteoglycan core proteins and degrades them to small oligosaccharides. Inside cells, the enzyme is important for the normal catabolism of heparan sulfate proteoglycans, generating glycosaminoglycan fragments that are then transported to lysosomes and completely degraded. When secreted, heparanase degrades basement membrane heparan sulfate glycosaminoglycans at sites of injury or inflammation, allowing extravasion of immune cells into nonvascular spaces and releasing factors that regulate cell proliferation and angiogenesis [147].

**References:** [147, 2383, 2401, 2292, 3231, 1009, 3100, 1997, 1099]

**EC 3.2.1.167**

**Accepted name:** baicalin-β-D-glucuronidase  
**Reaction:** baicalin + H₂O = baicalein + D-glucuronate  
**Other name(s):** baicalinase  
**Systematic name:** 5,6,7-trihydroxyflavone-7-O-β-D-glucopyranosiduronate glucuronosylhydrolase  
**Comments:** The enzyme also hydrolysates wogonin 7-O-β-D-glucuronide and oroxylin 7-O-β-D-glucuronide with lower efficiency [2077]. Negligible activity with p-nitrophenyl-β-D-glucuronide [3485].

**References:** [1306, 3485, 2662, 2077]

**EC 3.2.1.168**

**Accepted name:** hesperidin 6-O-α-L-rhamnosyl-β-D-glucosidase  
**Reaction:** hesperetin + H₂O = hesperetin + rutinose  
**Systematic name:** hesperetin 7-(6-O-α-L-rhamnopyranosyl-β-D-glucopyranoside) 6-O-α-rhamnopyranosyl-β-D-glucopyranosiduronate glucuronosylhydrolase  
**Comments:** The enzyme exhibits high specificity towards 7-O-linked flavonoid β-rutinosides.

**References:** [1955, 1956]

**EC 3.2.1.169**

**Accepted name:** protein O-GlcNAcase  
**Reaction:** (1) [protein]-3-O-(N-acetyl-β-D-glucosaminyl)-L-serine + H₂O = [protein]-L-serine + N-acetyl-D-glucosamine  
(2) [protein]-3-O-(N-acetyl-β-D-glucosaminyl)-L-threonine + H₂O = [protein]-L-threonine + N-acetyl-D-glucosamine  
**Other name(s):** OGA; glycoside hydrolase O-GlcNAcase; O-GlcNAcase; BtGH84; O-GlcNAc hydrolase  
**Systematic name:** [protein]-3-O-(N-acetyl-β-D-glucosaminyl)-L-serine/threonine N-acetylglucosaminyl hydrolase
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: [930, 3312, 418, 626, 1530, 677]

[EC 3.2.1.169 created 2011]

EC 3.2.1.170

Accepted name: mannosylglycerate hydrolase
Reaction: \(2-O-(\alpha-D\text{-mannopyranosyl})-D\text{-glycerate} + H_2O = \alpha-D\text{-mannopyranose} + D\text{-glycerate}\)
Other name(s): MgH
Systematic name: 2-\(O-(\alpha-D\text{-mannopyranosyl})\)-d-glycerate d-mannohydrolase
Comments: The enzyme occurs in thermophilic bacteria and has been characterized in *Thermus thermophilus* and *Rubrobacter radiotolerans*. It has also been identified in the moss *Selaginella moellendorffii*.
References: [31, 2208]

[EC 3.2.1.170 created 2011, modified 2018]

EC 3.2.1.171

Accepted name: rhamnogalacturonan hydrolase
Reaction: Endohydrolysis of \(\alpha-D\text{-GalA-(1→2)}-\alpha-L\text{-Rha glycosidic bond in the rhamnogalacturonan I backbone with initial inversion of anomeric configuration releasing oligosaccharides with }\beta-D\text{-GalA at the reducing end.}\)
Other name(s): rhamnogalacturonase A; RGase A; RG-hydrolase
Systematic name: rhamnogalacturonan \(\alpha-D\text{-GalA-(1→2)}-\alpha-L\text{-Rha hydrolase}\)
Comments: The enzyme is part of the degradation system for rhamnogalacturonan I in *Aspergillus aculeatus*.
References: [2382, 1581, 116, 2381, 2407]

[EC 3.2.1.171 created 2011]

EC 3.2.1.172

Accepted name: unsaturated rhamnogalacturonyl hydrolase
Reaction: \(2-O-(4\text{-deoxy-}\beta-L\text{-threo-hex-4-enopyranuronosyl})-\alpha-L\text{-rhamnopyranose} + H_2O = 5\text{-dehydro-4-deoxy-}\beta-D\text{-glucuronate} + L\text{-rhamnopyranose}\)
Other name(s): YteR; YesR
Systematic name: 2-\(O-(4\text{-deoxy-}\beta-L\text{-threo-hex-4-enopyranuronosyl})\)-\(\alpha-L\text{-rhamnopyranose hydrolase}\)
Comments: The enzyme is part of the degradation system for rhamnogalacturonan I in *Bacillus subtilis* strain 168.
References: [1353, 3493, 1354]

[EC 3.2.1.172 created 2011, modified 2012]

EC 3.2.1.173

Accepted name: rhamnogalacturonan galacturonohydrolase
Reaction: Exohydrolysis of the \(\alpha-D\text{-GalA-(1→2)}-\alpha-L\text{-Rha bond in rhamnogalacturonan oligosaccharides with initial inversion of configuration releasing D-galacturonic acid from the non-reducing end of rhamnogalacturonan oligosaccharides.}\)
Other name(s): RG-galacturonohydrolase
Systematic name: rhamnogalacturonan oligosaccharide \(\alpha-D\text{-GalA-(1→2)}-\alpha-L\text{-Rha galacturonohydrolase}\)
Comments: The enzyme is part of the degradation system for rhamnogalacturonan I in *Aspergillus aculeatus*.
References: [2114]

[EC 3.2.1.173 created 2011]

134
EC 3.2.1.174

**Accepted name:** rhamnogalacturonan rhamnohydrolase

**Reaction:** Exohydrolysis of the α-L-Rha-(1→4)-α-D-GalA bond in rhamnogalacturonan oligosaccharides with initial inversion of configuration releasing β-L-rhamnose from the non-reducing end of rhamnogalacturonan oligosaccharides.

**Other name(s):** RG-rhamnohydrolase; RG α-L-rhamnopyranohydrolase

**Systematic name:** rhamnogalacturonan oligosaccharide α-L-Rha-(1→4)-α-D-GalA rhamnohydrolase

**Comments:** The enzyme is part of the degradation system for rhamnogalacturonan I in *Aspergillus aculeatus.*

**References:** [2407, 2115]

[EC 3.2.1.174 created 2011]

EC 3.2.1.175

**Accepted name:** β-D-glucopyranosyl abscisate β-glucosidase

**Reaction:** D-glucopyranosyl abscisate + H₂O = d-glucose + abscisate

**Other name(s):** AtBG1; ABA-β-D-glucosidase; ABA-specific β-glucosidase; ABA-GE hydrolase; β-D-glucopyranosyl abscisate hydrolase

**Systematic name:** β-D-glucopyranosyl abscisate glucohydrolase

**Comments:** The enzyme hydrolyzes the biologically inactive β-D-glucopyranosyl ester of abscisic acid to produce active abscisate. Abscisate is a phytohormone critical for plant growth, development and adaption to various stress conditions. The enzyme does not hydrolyse β-D-glucopyranosyl zeatin [1715].

**References:** [1715, 1486, 654]

[EC 3.2.1.175 created 2011]

EC 3.2.1.176

**Accepted name:** cellulose 1,4-β-cellobiosidase (reducing end)

**Reaction:** Hydrolysis of (1→4)-β-D-glucosidic linkages in cellulose and similar substrates, releasing cellobiose from the reducing ends of the chains.

**Other name(s):** CelS; CelSS; endoglucanase SS; cellulase SS; cellobiohydrolase CelS; Cel48A

**Systematic name:** 4-β-D-glucan cellobiohydrolase (reducing end)

**Comments:** Some exocellulases, most of which belong to the glycoside hydrolase family 48 (GH48, formerly known as cellulase family L), act at the reducing ends of cellulose and similar substrates. The CelS enzyme from *Clostridium thermocellum* is the most abundant subunit of the cellulosome formed by the organism. It liberates cellobiose units from the reducing end by hydrolysis of the glycosidic bond, employing an inverting reaction mechanism [2620]. Different from EC 3.2.1.91, which attacks cellulose from the non-reducing end.

**References:** [164, 2620]

[EC 3.2.1.176 created 2011]

EC 3.2.1.177

**Accepted name:** α-D-xyloside xylohydrolase

**Reaction:** Hydrolysis of terminal, non-reducing α-D-xylose residues with release of α-D-xylose.

**Other name(s):** α-xylosidase

**Systematic name:** α-D-xyloside xylohydrolase

**Comments:** The enzyme catalyses hydrolysis of a terminal, unsubstituted xyloside at the extreme reducing end of a xyloglucan-oligosaccharide. Representative α-xylosidases from glycoside hydrolase family 31 utilize a two-step (double-displacement) mechanism involving a covalent glycosyl-enzyme intermediate, and retain the anomeric configuration of the product.

**References:** [2062, 2641, 547, 1839, 1299, 2299, 1696]

[EC 3.2.1.177 created 2011]
EC 3.2.1.178

**Accepted name:** β-porphyranase
**Reaction:** Hydrolysis of β-D-galactopyranose-(1→4)-α-L-galactopyranose-6-sulfate linkages in porphyran porphyranase; PorA; PorB; endo-β-porphyranase
**Systematic name:** porphyran β-D-galactopyranose-(1→4)-α-L-galactopyranose-6-sulfate 4-glycanohydrolase
**Comments:** The backbone of porphyran consists largely (70%) of (1→3)-linked β-D-galactopyranose followed by (1→4)-linked α-L-galactopyranose-6-sulfate [the other 30% are mostly agarobiose repeating units of (1→3)-linked β-D-galactopyranose followed by (1→4)-linked 3,6-anhydro-α-L-galactopyranose] [529]. This enzyme cleaves the (1→4) linkages between β-D-galactopyranose and α-L-galactopyranose-6-sulfate, forming mostly the disaccharide α-L-galactopyranose-6-sulfate-(1→3)-β-D-galactose, although some longer oligosaccharides of even number of residues are also observed. Since the enzyme is inactive on the non-sulfated agarose portion of the porphyran backbone, some agarose fragments are also included in the products [1167]. Methylation of the D-galactose prevents the enzyme from Zobellia galactanivorans, but not that from Wenyonghuangia fucanilytica, from binding at subsite -1 [529, 3495].
**References:** [1167, 529, 3495]

EC 3.2.1.179

**Accepted name:** gellan tetrasaccharide unsaturated glucuronosyl hydrolase
**Reaction:** β-D-4-deoxy-Δ^4^-GlcAp-(1→4)-β-D-Glc-(1→4)-α-L-Rhap-(1→3)-D-Glc + H_2O = 5-dehydro-4-deoxy-D-glucurionate + β-D-Glc-(1→4)-α-L-Rhap-(1→3)-D-Glc
**Systematic name:** β-D-4-deoxy-Δ^4^-GlcAp-(1→4)-β-D-Glc-(1→4)-α-L-Rhap-(1→3)-D-Glc β-D-4-deoxy-Δ^4^-GlcAp hydrolase
**Comments:** The enzyme releases 4-deoxy-4(5)-unsaturated D-glucuronic acid from oligosaccharides produced by polysaccharide lyases, e.g. the tetrasaccharide β-D-4-deoxy-Δ^4^-GlcAp-(1→4)-β-D-Glc-(1→4)-α-L-Rhap-(1→3)-D-Glc produced by EC 4.2.2.25, gellan lyase. The enzyme can also hydrolyse unsaturated chondroitin and hyaluronate disaccharides (β-D-4-deoxy-Δ^4^-GlcAp-(1→3)-D-GalNAc, β-D-4-deoxy-Δ^4^-GlcAp-(1→3)-D-GalNAcS, β-D-4-deoxy-Δ^4^-GlcAp2S-(1→3)-D-GalNAc, β-D-4-deoxy-Δ^4^-GlcAp-(1→3)-D-GlcNAc), preferring the unsulfated disaccharides to the sulfated disaccharides.
**References:** [1351, 1133, 1352]

EC 3.2.1.180

**Accepted name:** unsaturated chondroitin disaccharide hydrolase
**Reaction:** β-D-4-deoxy-Δ^4^-GlcAp-(1→3)-β-D-GalNAc6S + H_2O = 5-dehydro-4-deoxy-D-glucurionate + N-acetyl-β-D-galactosamine-6-O-sulfate
**Systematic name:** β-D-4-deoxy-Δ^4^-GlcAp-(1→3)-β-D-GalNAc6S hydrolase
**Comments:** The enzyme releases 4-deoxy-4,5-didehydro D-glucuronic acid or 4-deoxy-4,5-didehydro L-iduronic acid from chondroitin disaccharides, hyaluronan disaccharides and heparin disaccharides and cleaves both glycosidic (1→3) and (1→4) bonds. It prefers the sulfated disaccharides to the unsulfated disaccharides.
**References:** [1925, 2146]

EC 3.2.1.181

**Accepted name:** galactan endo-β-1,3-galactanase
Reaction: The enzyme specifically hydrolyses β-1,3-galactan and β-1,3-galactooligosaccharides
Other name(s): endo-β-1,3-galactanase
Systematic name: arabinogalactan 3-β-D-galactanohydrolase
Comments: The enzyme from the fungus Flammulina velutipes (winter mushroom) hydrolyses the β(1→3) bonds found in type II plant arabinogalactans, which occur in cell walls of dicots and cereals. The enzyme is an endohydrolase, and requires at least 3 contiguous β-1,3-residues. cf. EC 3.2.1.89, arabinogalactan endo-β-1,4-galactanase and EC 3.2.1.145, galactan 1,3-β-D-galactosidase.
References: [1606]

[EC 3.2.1.181 created 2012]

EC 3.2.1.182
Accepted name: 4-hydroxy-7-methoxy-3-oxo-3,4-dihydro-2H-1,4-benzoazin-2-yl glucoside β-D-glucosidase
Reaction: (1) (2R)-4-hydroxy-7-methoxy-3-oxo-3,4-dihydro-2H-1,4-benzoazin-2-yl β-D-glucopyranoside + H₂O = 2,4-dihydroxy-7-methoxy-2H-1,4-benzoazin-3(4H)-one + d-glucose
(2) (2R)-4-hydroxy-3-oxo-3,4-dihydro-2H-1,4-benzoazin-2-yl β-D-glucopyranoside + H₂O = 2,4-dihydroxy-2H-1,4-benzoazin-3(4H)-one + d-glucose
Other name(s): DIMBOAGlc hydrolase; DIMBOA glucosidase
Systematic name: (2R)-4-hydroxy-7-methoxy-3-oxo-3,4-dihydro-2H-1,4-benzoazin-2-yl β-D-glucopyranoside β-D-glucosidase
Comments: The enzyme from Triticum aestivum (wheat) has a higher affinity for DIMBOA glucoside than DI-BOA glucoside. With Secale cereale (rye) the preference is reversed.
References: [2929, 2928, 566, 2194, 2931, 2930]

[EC 3.2.1.182 created 2012]

EC 3.2.1.183
Accepted name: UDP-N-acetylglucosamine 2-epimerase (hydrolysing)
Reaction: UDP-N-acetyl-α-D-glucosamine + H₂O = N-acetyl-D-mannosamine + UDP
Other name(s): UDP-N-acetylglucosamine 2-epimerase (ambiguous); GNE (gene name); siaA (gene name); neuC (gene name)
Systematic name: UDP-N-acetyl-α-D-glucosamine hydrolase (2-epimerising)
Comments: The enzyme is found in mammalian liver, as well as in some pathogenic bacteria including Neisseria meningitidis and Staphylococcus aureus. It catalyses the first step of siaic acid (N-acetylneuraminic acid) biosynthesis. The initial product formed is the α anomer, which rapidly mutarotates to a mixture of anomers [479]. The mammalian enzyme is bifunctional and also catalyses EC 2.7.1.60, N-acetylmannosamine kinase. cf. EC 5.1.3.14, UDP-N-acetylglucosamine 2-epimerase (non-hydrolysing).
References: [2897, 479, 272, 2109]

[EC 3.2.1.183 created 2012]

EC 3.2.1.184
Accepted name: UDP-N,N'-diacetylbacillosamine 2-epimerase (hydrolysing)
Reaction: UDP-N,N'-diacetylbacillosamine + H₂O = UDP + 2,4-diacetamido-2,4,6-trideoxy-D-mannopyranose
Other name(s): UDP-Bac2Ac,Ac 2-epimerase; NeuC
Systematic name: UDP-N,N'-diacetylbacillosamine hydrolase (2-epimerising)
Comments: Requires Mg$^{2+}$. Involved in biosynthesis of legionaminic acid, a nonulosonate derivative that is incorporated by some bacteria into assorted virulence-associated cell surface glycoconjugates. The initial product formed by the enzyme from *Legionella pneumophila*, which incorporates legionaminic acid into the O-antigen moiety of its lipopolysaccharide, is 2,4-diacetamido-2,4,6-trideoxy-\(\alpha\)-D-mannopyranose, which rapidly mutarotates to a mixture of anomers [982]. The enzyme from *Campylobacter jejuni*, which incorporates legionaminic acid into flagellin, prefers GDP-\(N,N'\)-diacetylbacillosamine [2714].

References: [982, 2714]
EC 3.2.1.188

Accepted name: avenacosidase
Reaction: avenacoside B + H₂O = 26-desgluco-avenacoside B + D-glucose
Other name(s): As-P60
Systematic name: avenacoside B 26-β-D-glucohydrolase
Comments: Isolated from oat (Avena sativa) seedlings. The product acts as a defense system against fungal infection. Also acts on avenacoside A.
References: [1064, 1063]

EC 3.2.1.189

Accepted name: dioscin glycosidase (diosgenin-forming)
Reaction: 3-O-[α-L-Rha-(1→4)-[α-L-Rha-(1→2)]]-β-D-Glc]diosgenin + 3 H₂O = D-glucose + 2 L-rhamnopyranose + diosgenin
Other name(s): dioscin glycosidase (aglycone-forming)
Systematic name: 3-O-[α-L-Rha-(1→4)-[α-L-Rha-(1→2)]]-β-D-Glc]diosgenin hydrolase (diosgenin-forming)
Comments: The enzyme is involved in degradation of the steroid saponin dioscin by some fungi of the Absidia genus. The enzyme can also hydrolyse 3-O-[α-L-Ara-(1→4)-[α-L-Rha-(1→2)]]-β-D-Glc]diosgenin into diosgenin and free sugars as the final products. cf. EC 3.2.1.190, dioscin glycosidase (3-O-β-D-Glc-diosgenin-forming).
References: [881]

EC 3.2.1.190

Accepted name: dioscin glycosidase (3-O-β-D-Glc-diosgenin-forming)
Reaction: 3-O-[α-L-Rha-(1→4)-[α-L-Rha-(1→2)]]-β-D-Glc]diosgenin + 2 H₂O = 2 L-rhamnopyranose + diosgenin 3-O-β-D-glucopyranoside
Other name(s): dioscin-α-L-rhamnosidase
Systematic name: 3-O-[α-L-Rha-(1→4)-[α-L-Rha-(1→2)]]-β-D-Glc]diosgenin (3-O-β-D-Glc-diosgenin-forming)
Comments: The enzyme is involved in the hydrolysis of the steroid saponin dioscin by the digestive system of Sus scrofa (pig). cf. EC 3.2.1.189, dioscin glycosidase (diosgenin-forming).
References: [2454]

EC 3.2.1.191

Accepted name: ginsenosidase type III
Reaction: a protopanaxadiol-type ginsenoside with two glucosyl residues at position 3 + 2 H₂O = a protopanaxadiol-type ginsenoside with no glycosidic modification at position 3 + 2 D-glucopyranose (overall reaction)
(1a) a protopanaxadiol-type ginsenoside with two glucosyl residues at position 3 + H₂O a protopanaxadiol-type ginsenoside with one glucosyl residue at position 3 + D-glucopyranose
(1b) a protopanaxadiol-type ginsenoside with one glucosyl residue at position 3 + H₂O = a protopanaxadiol-type ginsenoside with no glycosidic modification at position 3 + D-glucopyranose
Systematic name: protopanaxadiol-type ginsenoside 3-β-D-hydrolase
Comments: Ginsenosidase type III catalyses the sequential hydrolysis of the 3-O-β-D-(1→2)-glucopyranosyl bond followed by hydrolysis of the 3-O-β-D-glucopyranosyl bond of protopanaxadiol ginsenosides. When acting for example on ginsenoside Rb1 the enzyme first generates ginsenoside XVII, and subsequently ginsenoside LXXV.

References: [1405, 51, 1240]

[EC 3.2.1.191 created 2014]

EC 3.2.1.192
Accepted name: ginsenoside Rb1 β-glucosidase
Reaction: ginsenoside Rb1 + 2 H2O = ginsenoside Rg3 + 2 D-glucopyranose (overall reaction)
(1a) ginsenoside Rb1 + H2O = ginsenoside Rd + D-glucopyranose
(1b) ginsenoside Rd + H2O = ginsenoside Rg3 + D-glucopyranose

Systematic name: ginsenoside Rb1 glucohydrolase
Comments: Ginsenosidases catalyse the hydrolysis of glycosyl moieties attached to the C-3, C-6 or C-20 position of ginsenosides. They are specific with respect to the nature of the glycosidic linkage, the position and the order in which the linkages are cleaved. Ginsenoside Rb1 β-glucosidase specifically and sequentially hydrolyses the 20-[β-D-glucopyranosyl-(1→6)-β-D glucopyranosyloxy] residues attached to position 20 by first hydrolysing the (1→6)-glycosidic bond to generate ginsenoside Rd as an intermediate, followed by hydrolysis of the remaining 20-O-β-D-glucosidic bond.

References: [3409]

[EC 3.2.1.192 created 2014]

EC 3.2.1.193
Accepted name: ginsenosidase type I
Reaction: (1) a protopanaxadiol-type ginsenoside with two glucosyl residues at position 3 + H2O = a protopanaxadiol-type ginsenoside with one glucosyl residue at position 3 + D-glucopyranose
(2) a protopanaxadiol-type ginsenoside with one glucosyl residue at position 3 + H2O = a protopanaxadiol-type ginsenoside with no glycosidic modifications at position 3 + D-glucopyranose
(3) a protopanaxadiol-type ginsenoside with two glycosyl residues at position 20 + H2O = a protopanaxadiol-type ginsenoside with a single glucosyl residue at position 20 + a monosaccharide

Systematic name: ginsenoside glucohydrolase
Comments: Ginsenosidase type I is slightly activated by Mg2+ or Ca2+ [3469]. The enzyme hydrolyses the 3-O-β-D-(1→2)-glucosidic bond, the 3-O-β-D-glucopyranosyl bond and the 20-O-β-D-(1→6)-glycosidic bond of protopanaxadiol ginsenosides. It usually leaves a single glucosyl residue attached at position 20 and one or no glucosyl residues at position 3. Starting with a ginsenoside that is glycosylated at both positions (e.g. ginsenoside Rb1, Rb2, Rb3, Rc or Rd), the most common products are ginsenoside F2 and ginsenoside C-K, with low amounts of ginsenoside Rh2.

References: [3469]

[EC 3.2.1.193 created 2014]

EC 3.2.1.194
Accepted name: ginsenosidase type IV
Reaction: a protopanaxatriol-type ginsenoside with two glucosyl residues at position 6 + 2 H2O = a protopanaxatriol-type ginsenoside with no glycosidic modification at position 6 + D-glucopyranose + a monosaccharide (overall reaction)
(1a) a protopanaxatriol-type ginsenoside with two glucosyl residues at position 6 + H2O = a protopanaxatriol-type ginsenoside with a single glucosyl at position 6 + a monosaccharide
(1b) a protopanaxatriol-type ginsenoside with a single glucosyl at position 6 + H2O = a protopanaxatriol-type ginsenoside with no glycosidic modification at position 6 + D-glucopyranose

References: [3469]
Systematic name: protopanaxatriol-type ginsenoside 6-β-D-glucosidase
Comments: Ginsenosidase type IV catalyses the sequential hydrolysis of the 6-O-β-D-(1→2)-glycosidic bond or the 6-O-α-D-(1→2)-glycosidic bond in protopanaxatriol-type ginsenosides with a disacchride attached to the C6 position, followed by the hydrolysis of the remaining 6-O-β-D-glycosidic bond (e.g. ginsenoside Re → ginsenoside Rg1 → ginsenoside F1).
References: [3258, 3257]

[EC 3.2.1.194 created 2014]

EC 3.2.1.195
Accepted name: 20-O-multi-glycoside ginsenosidase
Reaction: a protopanaxadiol-type ginsenoside with two glycosyl residues at position 20 + H2O = a protopanaxadiol-type ginsenoside with a single glucosyl residue at position 20 + a monosaccharide
Other name(s): ginsenosidase type II (erroneous)
Systematic name: protopanaxadiol-type ginsenoside 20-β-D-glucosidase
Comments: The 20-O-multi-glycoside ginsenosidase catalyses the hydrolysis of the 20- O-α-(1→6)-glycosidic bond and the 20- O-β-(1→6)-glycosidic bond of protopanaxadiol-type ginsenosides. The enzyme usually leaves a single glucosyl residue attached at position 20, although it can cleave the remaining glucosyl residue with a lower efficiency. Starting with a ginsenoside that is glycosylated at positions 3 and 20, such as ginsenosides Rb1, Rb2, Rb3 and Rc, the most common product is ginsenoside Rd, with a low amount of ginsenoside Rg3 also formed.
References: [3468]

[EC 3.2.1.195 created 2014]

EC 3.2.1.196
Accepted name: limit dextrin α-1,6-maltotetraose-hydrolase
Reaction: Hydrolysis of (1→6)-α-D-glucosidic linkages to branches with degrees of polymerization of three or four glucose residues in limit dextrin.
Other name(s): glgX (gene name); glycogen debranching enzyme (ambiguous)
Systematic name: glycogen phosphorylase-limit dextrin maltotetraose-hydrolase
Comments: This bacterial enzyme catalyses a reaction similar to EC 3.2.1.33, amylo-α-1,6-glucosidase (one of the activities of the eukaryotic glycogen debranching enzyme). However, while EC 3.2.1.33 removes single glucose residues linked by 1,6-α-linkage, and thus requires the additional activity of 4-α-glucanotransferase (EC 2.4.1.25) to act on limit dextrins formed by glycogen phosphorylase (EC 2.4.1.1), this enzyme removes maltotriose and maltotetraose chains that are attached by 1,6-α-linkage to the limit dextrin main chain, generating a debranched limit dextrin without a need for another enzyme.
References: [1393, 583, 2856]

[EC 3.2.1.196 created 2016]

EC 3.2.1.197
Accepted name: β-1,2-mannosidase
Reaction: β-D-mannopyranosyl-(1→2)-β-D-mannopyranosyl-(1→2)-D-mannopyranose + H2O = β-D-mannopyranosyl-(1→2)-D-mannopyranose + α-D-mannopyranose
Systematic name: β-1,2-D-mannoside mannohydrolase
Comments: The enzyme, characterized from multiple bacterial species, catalyses the hydrolysis of terminal, non-reducing β-mannose residues from β-1,2-mannotriose and β-1,2-mannobiose. The mechanism involves anomeric inversion, resulting in the release of α-D-mannopyranose. Activity with β-1,2-mannotriose or higher oligosaccharides is higher than that with β-1,2-mannobiose.
References: [564, 2190]

[EC 3.2.1.197 created 2016]
**EC 3.2.1.198**

**Accepted name:** α-mannan endo-1,2-α-mannanase

**Reaction:** Hydrolysis of the terminal α-D-mannosyl-(1→3)-α-D-mannose disaccharide from α-D-mannosyl-(1→3)-α-D-mannosyl-(1→2)-α-D-mannosyl-(1→2)-α-D-mannosyl side chains in fungal cell wall α-mannans.

**Systematic name:** α-mannan 1,2-[α-D-mannosyl-(1→3)-α-D-mannose] hydrolase

**Comments:** The enzyme, characterized from the gut bacteria *Bacteroides thetaiotaomicron* and *Bacteroides xylanisolvens*, can also catalyse the reaction of EC 3.2.1.130, glycoprotein endo-α-1,2-mannosidase.

**References:** [1084, 565]

[EC 3.2.1.198 created 2016]

**EC 3.2.1.199**

**Accepted name:** sulfoquinovosidase

**Reaction:** a 6-sulfo-α-D-quinovosyl diacylglycerol + H₂O = 6-sulfo-α-D-quinovose + a 1,2-diacylglycerol

**Other name(s):** yihQ (gene name); 6-sulfo-α-D-quinovosyl diacylglycerol 6-sulfo-D-quinovohydrolase

**Systematic name:** 6-sulfo-α-D-quinovosyl diacylglycerol 6-sulfo-D-quinovohydrolase (configuration-retaining)

**Comments:** The enzyme, characterized from the bacteria *Escherichia coli* and *Pseudomonas putida*, hydrolyses terminal non-reducing α-sulfoquinovoside residues in α-sulfoquinovosyl diacylglycerides and α-sulfoquinovosyl glycerol using a retaining mechanism. The enzyme belongs to the glycosyl hydrolase GH31 family.

**References:** [2764, 2878]

[EC 3.2.1.199 created 2016]

**EC 3.2.1.200**

**Accepted name:** exo-chitinase (non-reducing end)

**Reaction:** Hydrolysis of N,N′-diacetylchitobiose from the non-reducing end of chitin and chitodextrins.

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

**Systematic name:** (1→4)-2-acetamido-2-deoxy-β-D-glucan diacetylchitobiohydrolase (non-reducing end)

**Comments:** The enzyme hydrolyses the second glycosidic (1→4) linkage from non-reducing ends of chitin and chitodextrin molecules, liberating N,N′-diacetylchitobiose disaccharides. cf. EC 3.2.1.201, exo-chitinase (reducing end).

**References:** [3015, 1281, 2274, 1066]

[EC 3.2.1.200 created 2017]

**EC 3.2.1.201**

**Accepted name:** exo-chitinase (reducing end)

**Reaction:** Hydrolysis of N,N′-diacetylchitobiose from the reducing end of chitin and chitodextrins.

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

**Systematic name:** (1→4)-2-acetamido-2-deoxy-β-D-glucan diacetylchitobiohydrolase (reducing end)

**Comments:** The enzyme hydrolyses the second glycosidic (1→4) linkage from reducing ends of chitin and chitodextrin molecules, liberating N,N′-diacetylchitobiose disaccharides. cf. EC 3.2.1.200, exo-chitinase (non-reducing end).

**References:** [1281, 2138, 1066, 350]

[EC 3.2.1.201 created 2017]

**EC 3.2.1.202**

**Accepted name:** endo-chitodextrinase

**Reaction:** Hydrolysis of chitodextrins, releasing N,N′-diacetylchitobiose and small amounts of N,N′,N′′-triacetylchitotriose.
**Other name(s):** endo I (gene name); chitodextrinase (ambiguous); endolytic chitodextrinase; periplasmic chitodextrinase

**Systematic name:** (1→4)-2-acetamido-2-deoxy-β-D-glucan diacetylchitobiodydrolylase (endo-cleaving)

**Comments:** The enzyme, characterized from the bacterium *Vibrio furnissii*, is an endo-cleaving chitodextrinase that participates in the chitin catabolic pathway found in members of the *Vibrionaceae*. Unlike EC 3.2.1.14, chitinase, it has no activity on chitin. The smallest substrate is a tetrasaccharide, and the final products are N,N′-diacetylchitobiose and small amounts of N,N′,N′′-triacetylchitotriose. *cf.* EC 3.2.1.200, exo-chitinase (non-reducing end), and EC 3.2.1.201, exo-chitinase (reducing end).

**References:** [184, 1516]

[EC 3.2.1.202 created 2017]

**EC 3.2.1.203**

**Accepted name:** carboxymethylcellulase

**Reaction:** Endohydrolysis of (1→4)-β-D-glucosidic linkages in (carboxymethyl)cellulose.

**Other name(s):** CMCase

**Systematic name:** 4-β-D-(carboxymethyl)glucan 4-(carboxymethyl)glucanohydrolase

**Comments:** The enzyme from the acidophilic bacterium *Alicyclobacillus acidocaldarius* is an endo-cleaving hydrolase that cleaves β(1→4)-linked residues. However, it is specific for (carboxymethyl)cellulose and does not act on cellulosic substrates such as avicel.

**References:** [2063]

[EC 3.2.1.203 created 2017]

**EC 3.2.1.204**

**Accepted name:** 1,3-α-isomaltosidase

**Reaction:** cyclobis-(1→6)-α-nigerosyl + 2 H₂O = 2 isomaltose (overall reaction)
(1a) cyclobis-(1→6)-α-nigerosyl + H₂O = α-isomaltosyl-(1→3)-isomaltose
(1b) α-isomaltosyl-(1→3)-isomaltose + H₂O = 2 isomaltose

**Systematic name:** 1,3-α-isomaltohydrolase (configuration-retaining)

**Comments:** The enzyme, characterized from the bacteria *Bacillus* sp. NRRL B-21195 and *Kribbella flavida*, participates in the degradation of starch. The cyclic tetrasaccharide cyclobis-(1→6)-α-nigerosyl is formed from starch extracellularly and imported into the cell, where it is degraded to glucose.

**References:** [1542, 2970]

[EC 3.2.1.204 created 2017]

**EC 3.2.1.205**

**Accepted name:** isomaltose glucohydrolase

**Reaction:** isomaltose + H₂O = β-D-glucose + D-glucose

**Systematic name:** isomaltose 6-α-glucohydrolase (configuration-inverting)

**Comments:** The enzyme catalyses the hydrolysis of α-1,6-glucosidic linkages from the non-reducing end of its substrate. Unlike EC 3.2.1.10, oligo-1,6-glucosidase, the enzyme inverts the anomeric configuration of the released residue. The enzyme can also act on panose and maltotriose at a lower rate.

**References:** [2970]

[EC 3.2.1.205 created 2017]

**EC 3.2.1.206**

**Accepted name:** oleuropein β-glucosidase

**Reaction:** oleuropein + H₂O = oleuropein aglycone + D-glucopyranose

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

**Systematic name:** oleuropein 2-β-D-glucohydrolase
Oleuropein is a glycosylated secoiridoid exclusively biosynthesized by members of the Oleaceae plant family where it is part of a defence system against herbivores. The enzyme also hydrolyses ligstroside and demethyloleuropein.

References: [490, 2583, 1067, 1609, 1610]

EC 3.2.1.207

Accepted name: mannosyl-oligosaccharide α-1,3-glucosidase
Reaction: (1) Glc$_2$Man$_9$GlcNAc$_2$-[protein] + H$_2$O = GlcMan$_9$GlcNAc$_2$-[protein] + β-D-glucopyranose
(2) GlcMan$_9$GlcNAc$_2$-[protein] + H$_2$O = Man$_9$GlcNAc$_2$-[protein] + β-D-glucopyranose
Other name(s): ER glucosidase II; α-glucosidase II; trimming glucosidase II; ROT2 (gene name); GTB1 (gene name); GANAB (gene name); PRKCSH (gene name)
Systematic name: Glc$_2$Man$_9$GlcNAc$_2$-[protein] 3-α-glucohydrolase (configuration-inverting)
Comments: This eukaryotic enzyme cleaves off sequentially the two α-1,3-linked glucose residues from the Glc$_2$Man$_9$GlcNAc$_2$ oligosaccharide precursor of immature N-glycosylated proteins.
References: [3111, 3507, 3342, 2061]

EC 3.2.1.208

Accepted name: glucosylglycerate hydrolase
Reaction: 2-O-(α-D-glucopyranosyl)-D-glycerate + H$_2$O = D-glucopyranose + D-glycerate
Other name(s): GG hydrolase; GgH
Systematic name: 2-O-(α-D-glucopyranosyl)-D-glycerate D-glucohydrolase
Comments: The enzyme has been isolated from nontuberculous mycobacteria (e.g. Mycobacterium hassiacum), which accumulate 2-O-(α-D-glucopyranosyl)-D-glycerate during growth under nitrogen deprivation.
References: [30, 417]

EC 3.2.1.209

Accepted name: endoplasmic reticulum Man$_9$GlcNAc$_2$ 1,2-α-mannosidase
Reaction: Man$_9$GlcNAc$_2$-[protein] + H$_2$O = Man$_8$GlcNAc$_2$-[protein] (isomer 8A$_{1,2,3}B_{1,3}$) + D-mannopyranose
Other name(s): MAN1B1 (gene name); MNS1 (gene name); MNS3 (gene name)
Systematic name: Man$_9$GlcNAc$_2$-[protein] 2-α-mannohydrolase (configuration-inverting)
Comments: The enzyme, located in the endoplasmic reticulum, primarily trims a single α-1,2-linked mannose residue from Man$_9$GlcNAc$_2$ to produce Man$_8$GlcNAc$_2$ isomer 8A$_{1,2,3}B_{1,3}$ (the names of the isomers listed here are based on a nomenclature system proposed by Prien et al [2443]). The removal of the single mannosyl residue occurs in all eukaryotes as part of the processing of N-glycosylated proteins, and is absolutely essential for further elongation of the outer chain of properly-folded N-glycosylated proteins in yeast. In addition, the enzyme is involved in glycoprotein quality control at the ER quality control compartment (ERQC), helping to target misfolded glycoproteins for degradation. When present at very high concentrations in the ERQC, the enzyme can trim the carbohydrate chain further to Man(5-6)GlcNAc$_2$.
References: [1396, 3508, 1010, 1201, 111, 1776, 2443]

EC 3.2.1.210

Accepted name: endoplasmic reticulum Man$_9$GlcNAc$_2$ 1,2-α-mannosidase
Reaction: Man$_9$GlcNAc$_2$-[protein] (isomer 8A$_{1,2,3}B_{1,3}$) + H$_2$O = Man$_7$GlcNAc$_2$-[protein] (isomer 7A$_{1,2,3}B_3$) + D-mannopyranose
Other name(s): MNL1 (gene name)
Systematic name: Man₈GlcNAc₂-[protein] 2-α-mannohydrolase (configuration-inverting)
Comments: In yeast this activity is catalysed by a dedicated enzyme that processes unfolded protein-bound Man₈GlcNAc₂ N-glycans within the endoplasmic reticulum to Man₇GlcNAc₂. The exposed α-1,6-linked mannose residue in the product enables the recognition by the YOS9 lectin, targeting the proteins for degradation. In mammalian cells this activity is part of the regular processing of N-glycosylated proteins, and is not associated with protein degradation. It is carried out by EC 3.2.1.113, Golgi mannosyl-oligosaccharide 1,2-α-mannosidase. The names of the isomers listed here are based on a nomenclature system proposed by Prien et al [2443].

References: [2154, 1377, 2459, 501, 2443, 431]

EC 3.2.1.211

Accepted name: endo-(1→3)-fucoidanase
Reaction: endohydrolysis of (1→3)-α-L-fucoside linkages in fucan
Other name(s): α-L-fucosidase (incorrect); poly(1,3-α-L-fucoside-2/4-sulfate) glycanohydrolase
Systematic name: poly[(1→3)-α-L-fucoside-2/4-sulfate] glycanohydrolase
Comments: The enzyme specifically hydrolyses (1→3)-α-L-fucoside linkages in fucan. Fucans are found mainly in different species of seaweed and are sulfated polysaccharides with a backbone of (1→3)-linked or alternating (1→3)- and (1→4)-linked α-L-fucopyranosyl residues. In the literature, the sulfated polysaccharides are often called fucoidans. Fucoidans include polysaccharides with a relatively low proportion of fucose and some polysaccharides that have a backbone composed of other saccharides with fucose in the branching side chains. The sulfation of the α-L-fucopyranosyl residues may occur at positions 2 and 4. The enzyme degrades fucan to sulfated α-L-fucoooligosaccharides but neither L-fucose nor small fucoooligosaccharides are produced.

References: [3048, 141, 222, 239]

[EC 3.2.1.211 created 1972 as EC 3.2.1.44, part transferred 2020 to EC 3.2.1.211 ]

EC 3.2.1.212

Accepted name: endo-(1→4)-fucoidanase
Reaction: endohydrolysis of (1→4)-α-L-fucoside linkages in fucan
Other name(s): α-L-fucosidase (incorrect); poly(1,4-α-L-fucoside-2/3-sulfate) glycanohydrolase
Systematic name: poly[(1→4)-α-L-fucoside-2/3-sulfate] glycanohydrolase
Comments: The enzyme specifically hydrolyses (1→4)-α-L-fucoside linkages in fucan. Fucans are found mainly in different species of seaweed and are sulfated polysaccharides with a backbone of (1→3)-linked or alternating (1→3)- and (1→4)-linked α-L-fucopyranosyl residues. In the literature, the sulfated polysaccharides are often called fucoidans. Fucoidans include polysaccharides with a relatively low proportion of fucose and some polysaccharides that have a backbone composed of other saccharides with fucose in the branching side chains. The sulfation of the α-L-fucopyranosyl residues may occur at positions 2 and 3. The enzyme degrades fucan to sulfated α-L-fucoooligosaccharides but neither L-fucose nor small fucoooligosaccharides are produced.

References: [3048, 222, 630, 1539, 2795, 2796, 2797]

[EC 3.2.1.212 created 1972 as EC 3.2.1.44, part transferred 2020 to EC 3.2.1.212]

EC 3.2.1.213

Accepted name: galactan exo-1,6-β-galactobiodyrolase (non-reducing end)
Reaction: Hydrolysis of (1→6)-β-D-galactosidic linkages in arabinogalactan proteins and (1→3):(1→6)-β-galactans to yield (1→6)-β-galactobiose as the final product.
Other name(s): exo-β-1,6-galactobiodyrolase; 1,6Gal (gene name)
Systematic name: exo-β-(1→6)-galactobiodyrolase (non-reducing end)
The enzyme, characterized from the bacterium *Bifidobacterium longum*, specifically hydrolyses (1→6)-β-galactobiose from the non-reducing terminal of (1→6)-β-D-galactooligosaccharides with a degree of polymerization (DP) of 3 or higher, using an exo mode of action. The enzyme cannot hydrolyse α-L-arabinofuranosylated (1→6)-β-galactans (as found in arabinogalactans) and does not act on (1→3)-β-D- or (1→4)-β-D-galactans. cf. EC 3.2.1.164, galactan endo-1,6-β-galactosidase.

References: [903]

EC 3.2.1.214

**Accepted name:** exo β-1,2-glucooligosaccharide sophorohydrolase (non-reducing end)

**Reaction:** [(1→2)-β-D-glucosyl]n + H2O = sophorose + [(1→2)-β-D-glucosyl]n−2

**Systematic name:** exo (1→2)-β-D-glucooligosaccharide sophorohydrolase (non-reducing end)

**Comments:** The enzyme, characterized from the bacterium *Parabacteroides distasonis*, specifically hydrolyses (1→2)-β-D-glucooligosaccharides to sophorose. The best substrates are the tetra- and pentasaccharides. The enzyme is not able to cleave the trisaccharide, and activity with longer linear (1→2)-β-D-glucans is quite low. This enzyme acts in exo mode and is not able to hydrolyse cyclic (1→2)-β-D-glucans.

References: [2769]

EC 3.2.1.215

**Accepted name:** arabinogalactan exo α-(1,3)-α-D-galactosyl-(1→3)-L-arabinofuranosidase (non-reducing end)

**Reaction:** Hydrolysis of α-D-Galp-(1→3)-L-Araf disaccharides from non-reducing terminals in branches of type II arabinogalactan attached to proteins.

**Other name(s):** 3-O-α-D-galactosyl-α-L-arabinofuranosidase

**Systematic name:** type II arabinogalactan exo α-(1,3)-[α-D-galactosyl-(1→3)-L-arabinofuranose] hydrolase (non-reducing end)

**Comments:** The enzyme, characterized from the bacterium *Parabacteroides distasonis*, specifically hydrolyses (1→2)-β-D-galactosyl-(1→3)-L-Araf disaccharides from the non-reducing terminal of arabinogalactan using an exo mode of action. It is particularly active with gum arabic arabinogalactan, a type II arabinogalactan produced by acacia trees. The enzyme can also hydrolyse β-L-Arap-(1→3)-L-Araf disaccharides, but this activity is significantly lower.

References: [2664]

EC 3.2.1.216

**Accepted name:** kojibiose hydrolase

**Reaction:** kojibiose + H2O = β-D-glucopyranose + D-glucopyranose

**Other name(s):** kojibiase

**Systematic name:** kojibiose glucohydrolase (configuration-inverting)

**Comments:** The enzyme, characterized from the bacteria *Flavobacterium johnsoniae* and *Mucilaginibacter mal-lensis*, uses anomer-inverting mechanism to release β-glucose from the non-reducing ends of kojibiose and α-1,2-oligoglucans with a higher degree of polymerization.

References: [2148, 236]

EC 3.2.1.217

**Accepted name:** exo-acting protein-α-N-acetylgalactosaminidase
### Reaction

\[ \text{a [protein]-N-acetyl-\(\alpha\)-D-galactosalaminyl-(L-serine/L-threonine) + H}_2\text{O} = \text{a [protein]-(L-serine/L-threonine) + N-acetyl-D-galactosamine} \]

### Other name(s)

Nag31

### Systematic name

[protein]-N-acetyl-\(\alpha\)-D-galactosalaminyl-(L-serine/L-threonine) \(N\)-acetylgalactosaminohydrolase

### Comments

The enzyme, which belongs to the glycosylhydrolase 31 (GH31) family, is an exo-acting \(\alpha\)-N-acetylgalactosaminidase that acts on the innermost \(\alpha\)-GalNAc residues at the core of O-glycans when no other saccharides are attached to it. Unlike EC 3.2.1.49, \(\alpha\)-N-acetylgalactosaminidase, it is not able to act on blood group A antigen.

### References

[2477, 2039, 1307, 2038]

---

### EC 3.2.2 Hydrolysing \(N\)-glycosyl compounds

#### EC 3.2.2.1

**Accepted name:** purine nucleosidase

**Reaction:** a purine nucleoside + H\(_2\)O = D-ribose + a purine base

**Other name(s):** nucleosidase (misleading); purine \(\beta\)-ribosidase; purine nucleoside hydrolase; purine ribonucleosidase; ribonucleoside hydrolase (misleading); nucleoside hydrolase (misleading); \(N\)-ribosyl purine ribohydrolase; nucleosidase g; \(N\)-D-ribosylpurine ribohydrolase; inosine-adenosine-guanosine preferring nucleoside hydrolase; purine-specific nucleoside \(N\)-ribohydrolase; IAG-nucleoside hydrolase; IAG-NH

**Systematic name:** purine-nucleoside ribohydrolase

**Comments:** The enzyme from the bacterium *Ochrobactrum anthropi* specifically catalyses the irreversible \(N\)-riboside hydrolysis of purine nucleosides. Pyrimidine nucleosides, purine and pyrimidine nucleotides, \(\text{NAD}^+\), \(\text{NADP}^+\) and nicotinamide mononucleotide are not substrates [2257].

**References:** [1191, 1445, 2976, 3031, 2350, 2257, 3213, 1953]
EC 3.2.2.2

**Accepted name:** inosine nucleosidase  
**Reaction:** inosine + H₂O = d-ribose + hypoxanthine  
**Other name(s):** inosinase; inosine-guanosine nucleosidase  
**Systematic name:** inosine ribohydrolase  
**References:** [1579, 3031]

[EC 3.2.2.2 created 1961]

EC 3.2.2.3

**Accepted name:** uridine nucleosidase  
**Reaction:** uridine + H₂O = d-ribose + uracil  
**Other name(s):** uridine hydrolase  
**Systematic name:** uridine ribohydrolase  
**References:** [407]

[EC 3.2.2.3 created 1961]

EC 3.2.2.4

**Accepted name:** AMP nucleosidase  
**Reaction:** AMP + H₂O = d-ribose 5-phosphate + adenine  
**Other name(s):** adenylate nucleosidase; adenosine monophosphate nucleosidase  
**Systematic name:** AMP phosphoribohydrolase  
**References:** [1285]

[EC 3.2.2.4 created 1961]

EC 3.2.2.5

**Accepted name:** NAD⁺ glycohydrolase  
**Reaction:** NAD⁺ + H₂O = ADP-d-ribose + nicotinamide  
**Other name(s):** NAD glycohydrolase; nicotinamide adenine dinucleotide glycohydrolase; β-NAD⁺ glycohydrolase; DPNase (ambiguous); NAD hydrolase (ambiguous); diphosphopyridine nucleosidase (ambiguous); nicotinamide adenine dinucleotide nucleosidase (ambiguous); NAD nucleosidase (ambiguous); DPN hydrolase (ambiguous); NADase (ambiguous); nga (gene name); NAD⁺ nucleosidase  
**Systematic name:** NAD⁺ glycohydrolase  
**Comments:** This enzyme catalyses the hydrolysis of NAD⁺, without associated ADP-ribosyl cyclase activity (unlike the metazoan enzyme EC 3.2.2.6, bifunctional ADP-ribosyl cyclase/cyclic ADP-ribose hydrolase). The enzyme from Group A streptococci has been implicated in the pathogenesis of diseases such as streptococcal toxic shock-like syndrome (STSS) and necrotizing fasciitis. The enzyme from the venom of the snake *Agkistrodon acutus* also catalyses EC 3.6.1.5, apyrase [3490].  
**References:** [802, 1051, 3490, 959, 2835]

[EC 3.2.2.5 created 1961, modified 2013]

EC 3.2.2.6

**Accepted name:** ADP-ribosyl cyclase/cyclic ADP-ribose hydrolase  
**Reaction:** NAD⁺ + H₂O = ADP-d-ribose + nicotinamide (overall reaction)  
(1a) NAD⁺ = cyclic ADP-ribose + nicotinamide  
(1b) cyclic ADP-ribose + H₂O = ADP-d-ribose

148
Other name(s): NAD$^+$ nucleosidase; NADase (ambiguous); DPNase (ambiguous); DPN hydrolase (ambiguous); NAD hydrolyase (ambiguous); nicotinamide adenine dinucleotide nucleosidase (ambiguous); NAD glycohydrolase (misleading); NAD nucleosidase (ambiguous); nicotinamide adenine dinucleotide glycohydrolase (misleading); CD38 (gene name); BST1 (gene name)

Systematic name: NAD$^+$ glycohydrolase (cyclic ADP-ribose-forming)

Comments: This multi-entrical enzyme acts on NAD$^+$, catalysing both the synthesis and hydrolysis of cyclic ADP-ribose, 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 2.4.99.20, 2'-phospho-ADP-ribosyl cyclase/2'-phospho-cyclic-ADP-ribose transferase. It is also able to act on $\beta$-nicotinamide $\beta$-ribonucleotide. cf. EC 3.2.2.5, NAD$^+$ glycohydrolase.

References: [1316, 1267, 2994, 3071, 879, 3406, 1821]

[EC 3.2.2.6 created 1961, modified 2004, modified 2014, modified 2018]

EC 3.2.2.7
Accepted name: adenosine nucleosidase
Reaction: adenosine + H$_2$O = D-ribose + adenine
Other name(s): adenosinase; N-ribosyladenine ribohydrolase; adenosine hydrolase; ANase
Systematic name: adenosine ribohydrolase
Comments: Also acts on adenosine N-oxide.
References: [1952]

[EC 3.2.2.7 created 1972]

EC 3.2.2.8
Accepted name: ribosylpyrimidine nucleosidase
Reaction: a pyrimidine nucleoside + H$_2$O = D-ribose + a pyrimidine base
Other name(s): N-ribosylpyrimidine nucleosidase; pyrimidine nucleosidase; N-ribosylpyrimidine ribohydrolase; pyrimidine nucleoside hydrolase; RihB; YeiK; nucleoside ribohydrolase
Systematic name: pyrimidine-nucleoside ribohydrolase
Comments: Also hydrolyses purine D-ribonucleosides, but much more slowly, 2', 3' and 5'-deoxynucleosides are not substrates [964].
References: [3041, 2378, 964, 965]

[EC 3.2.2.8 created 1972]

EC 3.2.2.9
Accepted name: adenosylhomocysteine nucleosidase
Reaction: (1) $\beta$-adenosyl-L-homocysteine + H$_2$O = $\beta$-(5-deoxy-D-ribo-5-yl)-L-homocysteine + adenine
(2) 5'-deoxyadenosine + H$_2$O = 5-deoxy-D-ribose + adenine
(3) $\beta$-methyl-5'-thioadenosine + H$_2$O = 5-(methylsulfanyl)-D-ribose + adenine
Other name(s): $\beta$-adenosylhomocysteine hydrolase (ambiguous); $\beta$-adenosylhomocysteine nucleosidase; 5'-methyladenosine nucleosidase; $\beta$-adenosylhomocysteine/5'-methylthioadenosine nucleosidase; AdoHcy/MTA nucleosidase; MTN2 (gene name); mtnN (gene name)
Systematic name: $\beta$-adenosyl-L-homocysteine homocysteinylribohydrolase
Comments: This enzyme, found in bacteria and plants, acts on three different substrates. It is involved in the $\beta$-adenosyl-L-methionine (SAM, Met) cycle, which recycles $\beta$-adenosyl-L-homocysteine back to SAM, and in salvage pathways for 5'-deoxyadenosine and $\beta$-methyl-5'-thioadenosine, which are produced from SAM during the action of many enzymes. cf. the plant enzyme EC 3.2.2.16, methylthioadenosine nucleosidase.
References: [706, 813, 528, 2346, 792, 2221]

[EC 3.2.2.9 created 1972, modified 2004, modified 2020]
EC 3.2.2.10
Accepted name: pyrimidine-5′-nucleotide nucleosidase
Reaction: a pyrimidine 5′-nucleotide + H₂O = d-ribose 5-phosphate + a pyrimidine base
Other name(s): pyrimidine nucleotide N-ribosidase; Pyr5N
Systematic name: pyrimidine-5′-nucleotide phosphoribo(deoxyribo)hydrolase
Comments: Also acts on dUMP, dTMP and dCMP.
References: [1311, 1312]

[EC 3.2.2.10 created 1972]

EC 3.2.2.11
Accepted name: β-aspartyl-βN-acetylglucosaminidase
Reaction: 1-β-aspartyl-βN-acetyl-D-glucosaminylamine + H₂O = L-asparagine + N-acetyl-D-glucosamine
Other name(s): β-aspartylacetetylglucosaminidase
Systematic name: 1-β-aspartyl-βN-acetyl-D-glucosaminylamine L-asparaginohydrolase
References: [779]

[EC 3.2.2.11 created 1972]

EC 3.2.2.12
Accepted name: inosinate nucleosidase
Reaction: IMP + H₂O = d-ribose 5-phosphate + hypoxanthine
Other name(s): 5′-inosinate phosphoribohydrolase
Systematic name: IMP phosphoribohydrolase
References: [1644]

[EC 3.2.2.12 created 1972]

EC 3.2.2.13
Accepted name: 1-methyladenosine nucleosidase
Reaction: 1-methyladenosine + H₂O = 1-methyladenine + d-ribose
Other name(s): 1-methyladenosine hydrolase
Systematic name: 1-methyladenosine ribohydrolase
References: [3032]

[EC 3.2.2.13 created 1976]

EC 3.2.2.14
Accepted name: NMN nucleosidase
Reaction: β-nicotinamide d-ribonucleotide + H₂O = d-ribose 5-phosphate + nicotinamide
Other name(s): NMNase; nicotinamide mononucleotide nucleosidase; nicotinamide mononucleotidase; NMN glycohydrolyse; NMNGhase
Systematic name: nicotinamide-nucleotide phosphoribohydrolase
Comments: The enzyme is thought to participate in an NAD⁺-salvage pathway. In eukaryotic organisms this activity has been attributed to EC 3.2.2.6, ADP-ribosyl cyclase/cyclic ADP-ribose hydrolase.
References: [59, 1314, 1315]

[EC 3.2.2.14 created 1976, modified 2018]

EC 3.2.2.15
Accepted name: DNA-deoxyinosine glycosylase
Reaction: Hydrolyses DNA and polynucleotides, releasing free hypoxanthine
Other name(s): DNA(hypoxanthine) glycohydrolase; deoxyribonucleic acid glycosylase; hypoxanthine-DNA glyco-
sylase

Systematic name: DNA-deoxyinosine deoxyribohydrolase

References: [1475]

[EC 3.2.2.15 created 1980, modified 1982, modified 2000]

EC 3.2.2.16

Accepted name: methylthioadenosine nucleosidase

Reaction: \( \delta \)-methyl-5'-thioadenosine + H\(_2\)O = 5-((methylsulfanyl)-d-ribose + adenine

Other name(s): 5'-methylthioadenosine nucleosidase; MTA nucleosidase; MeSAdo nucleosidase; methylthioaden-
sine methylthioribohydrolase; MTN1 (gene name)

Systematic name: \( \delta \)-methyl-5'-thioadenosine adeninehydrolase

Comments: Unlike EC 3.2.2.9, adenosylhomocysteine nucleosidase, this plant enzyme has little or no activity
with S-adenosyl-L-homocysteine.

References: [1061, 2609, 2813, 2346]

[EC 3.2.2.16 created 1983, modified 2004]

EC 3.2.2.17

Accepted name: deoxyribodipyrimidine endonucleosidase

Reaction: Cleaves the N-glycosidic bond between the 5'-pyrimidine residue in cyclobutadipyrimidin (in DNA)
and the corresponding deoxy-d-ribose residue

Other name(s): pyrimidine dimer DNA-glycosylase; endonuclease V; deoxyribonucleate pyrimidine dimer glycosi-
dase; pyrimidine dimer DNA glycosylase; T\(_4\)-induced UV endonuclease; PD-DNA glycosylase

Systematic name: deoxy-d-ribocyclobutadipyrimidine polynucleotidodeoxyribohydrolase

References: [1131]

[EC 3.2.2.17 created 1983]

[3.2.2.18 Deleted entry. glycopeptide N-glycosidase. Now included with EC 3.5.1.52, peptide-N\(^4\)-(N-acetyl-\(\beta\)-glucosaminyl)asparagine amidase]

[EC 3.2.2.18 created 1984, deleted 1989]

EC 3.2.2.19

Accepted name: [protein ADP-ribosylarginine] hydrolase

Reaction: (1) protein-N\(^\omega\)-(ADP-d-ribosyl)-L-arginine + H\(_2\)O = ADP-d-ribose + protein-L-arginine
(2) N\(^\omega\)-(ADP-d-ribosyl)-L-arginine + H\(_2\)O = ADP-d-ribose + L-arginine

Other name(s): ADP-ribose-L-arginine cleavage enzyme; ADP-ribosylarginine hydrolase; N\(^\omega\)-(ADP-d-ribosyl)-L-
arginine ADP-ribosylhydrodrolase; protein-\(\omega\)-N-(ADP-d-ribosyl)-L-arginine ADP-ribosylhydrodrolase

Systematic name: protein-N\(^\omega\)-(ADP-d-ribosyl)-L-arginine ADP-ribosylhydrodrolase

Comments: The enzyme will remove ADP-d-ribose from arginine residues in ADP-ribosylated proteins.

References: [2086, 2087, 1595, 2974, 2272]

[EC 3.2.2.19 created 1989, modified 2004]

EC 3.2.2.20

Accepted name: DNA-3-methyladenine glycosylase I

Reaction: Hydrolysis of alkylated DNA, releasing 3-methyladenine

Other name(s): deoxyribonucleate 3-methyladenine glycosidase I; 3-methyladenine DNA glycosylase I; DNA-3-
methyladenine glycosidase I

Systematic name: alkylated-DNA glycohydrolase (releasing methyladenine and methylguanine)
Comments: Involved in the removal of alkylated bases from DNA in *Escherichia coli* (cf. EC 2.1.1.63 methylated-DNA—[protein]-cysteine S-methyltransferase).

References: [776, 1474, 3056]

[EC 3.2.2.20 created 1990, modified 2000]

EC 3.2.2.21

Accepted name: DNA-3-methyladenine glycosylase II

Reaction: Hydrolysis of alkylated DNA, releasing 3-methyladenine, 3-methylguanine, 7-methylguanine and 7-methyladenine

Other name(s): deoxyribonucleate 3-methyladenine glycosidase II; 3-methyladenine DNA glycosylase II; DNA-3-methyladenine glycosidase II; AlkA

Systematic name: alkylated-DNA glycohydrolase (releasing methyladenine and methylguanine)

Comments: Involved in the removal of alkylated bases from DNA in *Escherichia coli* (cf. EC 2.1.1.63 methylated-DNA—[protein]-cysteine S-methyltransferase).

References: [776, 1474, 2544, 3056]

[EC 3.2.2.21 created 1990, modified 2000]

EC 3.2.2.22

Accepted name: rRNA N-glycosylase

Reaction: Hydrolysis of the N-glycosylic bond at A-4324 in 28S rRNA from rat ribosomes

Other name(s): ribosomal ribonucleate N-glycosidase; nigrin b; RNA N-glycosidase; rRNA N-glycosidase; ricin; momorcochin-S; Mirabilis antiviral protein; momorcochin-S; gelonin; saporins

Systematic name: rRNA N-glycohydrolase

Comments: Ricin A-chain and related toxins show this activity. Naked rRNA is attacked more slowly than rRNA in intact ribosomes. Naked rRNA from *Escherichia coli* is cleaved at a corresponding position.

References: [750]

[EC 3.2.2.22 created 1990, modified 2000]

EC 3.2.2.23

Accepted name: DNA-formamidopyrimidine glycosylase

Reaction: Hydrolysis of DNA containing ring-opened 7-methylguanine residues, releasing 2,6-diamino-4-hydroxy-5-(N-methyl)formamidopyrimidine

Other name(s): Fapy-DNA glycosylase; deoxyribonucleate glycosidase; 2,6-diamino-4-hydroxy-5N-formamidopyrimidine-DNA glycosylase; 2,6-diamino-4-hydroxy-5(N-methyl)formamidopyrimidine-DNA glycosylase; DNA-formamidopyrimidine-DNA glycosylase; DNA-formamidopyrimidine glycosidase; Fpg protein

Systematic name: DNA glycohydrolase [2,6-diamino-4-hydroxy-5-(N-methyl)formamidopyrimide releasing]

Comments: May play a significant role in processes leading to recovery from mutagenesis and/or cell death by alkylating agents. Also involved in the GO system responsible for removing an oxidatively damaged form of guanine (7,8-dihydro-8-oxoguanine) from DNA.

References: [280]

[EC 3.2.2.23 created 1990, modified 2000]

EC 3.2.2.24

Accepted name: ADP-ribosyl-[dinitrogen reductase] hydrolase

Reaction: [dinitrogen reductase]-N^6-α-(ADP-D-ribosyl)-L-arginine = ADP-D-ribose + [dinitrogen reductase]-L-arginine

Other name(s): azoferredoxin glycosidase; azoferredoxin-activating enzymes; dinitrogenase reductase-activating glycohydrolase; ADP-ribosyl glycohydrolase; *draG* (gene name)
Systematic name: ADP-D-ribose-[dinitrogen reductase] ADP-ribosylhydrolase
Comments: The enzyme restores the activity of EC 1.18.6.1, nitrogenase, by catalysing the removal of ADP-ribose from an arginine residue of the dinitrogenase reductase component of nitrogenase. This activity occurs only when the nitrogenase product, ammonium, is not available. The combined activity of this enzyme and EC 2.4.2.37, NAD⁺-dinitrogen-reductase ADP-D-ribose transferase, controls the level of activity of nitrogenase.
References: [831, 1765, 223]

[EC 3.2.2.24 created 1992]

EC 3.2.2.25
Accepted name: N-methyl nucleosidase
Reaction: 7-methylxanthosine + H₂O = 7-methylxanthine + D-ribose
Other name(s): 7-methylxanthosine nucleosidase; N-MeNase; N-methyl nucleoside hydrolase; methylpurine nucleosidase
Systematic name: 7-methylxanthosine ribohydrolase
Comments: The enzyme preferentially hydrolyses 3- and 7-methylpurine nucleosides, such as 3-methylxanthosine, 3-methyladenosine and 7-methylguanosine. Hydrolysis of 7-methylxanthosine to form 7-methylxanthine is the second step in the caffeine-biosynthesis pathway.
References: [2172]

[EC 3.2.2.25 created 2007]

EC 3.2.2.26
Accepted name: futalosine hydrolase
Reaction: futalosine + H₂O = dehypoxanthine futalosine + hypoxanthine
Other name(s): futalosine nucleosidase; MqnB (ambiguous)
Systematic name: futalosine ribohydrolase
Comments: This enzyme, which is specific for futalosine, catalyses the second step of a novel menaquinone biosynthetic pathway that is found in some prokaryotes.
References: [1220]

[EC 3.2.2.26 created 2008]

EC 3.2.2.27
Accepted name: uracil-DNA glycosylase
Reaction: Hydrolyses single-stranded DNA or mismatched double-stranded DNA and polynucleotides, releasing free uracil
Other name(s): UdgB (ambiguous); uracil-DNA N-glycosylase; UDG (ambiguous); uracil DNA glycohydrolase
Systematic name: uracil-DNA deoxyribohydrolase (uracil-releasing)
Comments: Uracil-DNA glycosylases are widespread enzymes that are found in all living organisms. EC 3.2.2.27 and double-stranded uracil-DNA glycosylase (EC 3.2.2.28) form a central part of the DNA-repair machinery since they initiate the DNA base-excision repair pathway by hydrolysing the N-glycosidic bond between uracil and the deoxyribose sugar thereby catalysing the removal of mis-incorporated uracil from DNA.
References: [1717, 1531, 2345, 2914]

[EC 3.2.2.27 created 2009]

EC 3.2.2.28
Accepted name: double-stranded uracil-DNA glycosylase
Reaction: Specifically hydrolyses mismatched double-stranded DNA and polynucleotides, releasing free uracil
Other name(s): Mug; double-strand uracil-DNA glycosylase; Dug; dsUDG; double-stranded DNA specific UDG; dsDNA specific UDG; UdgB (ambiguous); G:T/U mismatch-specific DNA glycosylase; UDG (ambiguous)

Systematic name: uracil-double-strand DNA deoxyribohydrolase (uracil-releasing)

Comments: No activity on DNA containing a T/G mispair or single-stranded DNA containing either a site-specific uracil or 3,N\(^4\)-ethenocytosine residue [2946], significant role for double-stranded uracil-DNA glycosylase in mutation avoidance in non-dividing *E. coli* [2049]. Uracil-DNA glycosylases are widespread enzymes that are found in all living organisms. Uracil-DNA glycosylase (EC 3.2.2.27) and EC 3.2.2.28 form a central part of the DNA-repair machinery since they initiate the DNA base-excision repair pathway by hydrolysing the *N*-glycosidic bond between uracil and the deoxyribose sugar thereby catalysing the removal of mis-incorporated uracil from DNA.

References: [175, 2946, 2049]

[EC 3.2.2.28 created 2009]

EC 3.2.2.29

Accepted name: thymine-DNA glycosylase

Reaction: Hydrolyses mismatched double-stranded DNA and polynucleotides, releasing free thymine.

Other name(s): mismatch-specific thymine-DNA glycosylase; mismatch-specific thymine-DNA N-glycosylase; hTDG; hsTDG; TDG; thymine DNA glycosylase; G/T glycosylase; uracil/thymine DNA glycosylase; T:G mismatch-specific thymidine-DNA glycosylase; G:T mismatch-specific thymine DNA-glycosylase

Systematic name: thymine-DNA deoxyribohydrolase (thymine-releasing)

Comments: Thymine-DNA glycosylase is part of the DNA-repair machinery. Thymine removal is fastest when it is from a G/T mismatch with a 5'-flanking C/G pair. The glycosylase removes uracil from G/U, C/U, and T/U base pairs faster than it removes thymine from G/T [3286].

References: [3287, 2168, 3286]

[EC 3.2.2.29 created 2009]

EC 3.2.2.30

Accepted name: aminodeoxyfutalosine nucleosidase

Reaction: 6-amino-6-deoxyfutalosine + H\(_2\)O = dehypoxanthine futalosine + adenine

Other name(s): AFL nucleosidase; aminofutalosine nucleosidase; methylthioadenosine nucleosidase; MqnB (ambiguous)

Systematic name: 6-amino-6-deoxyfutalosine ribohydrolase

Comments: The enzyme, found in several bacterial species, catalyses a step in a modified futalosine pathway for menaquinone biosynthesis. While the enzyme from some organisms also has the activity of EC 3.2.2.9, adenosylhomocysteine nucleosidase, the enzyme from *Chlamydia trachomatis* is specific for 6-amino-6-deoxyfutalosine [178].

References: [1220, 1763, 69, 3268, 2026, 1538, 178]

[EC 3.2.2.30 created 2014]

EC 3.2.2.31

Accepted name: adenine glycosylase

Reaction: Hydrolyses free adenine bases from 7,8-dihydro-8-oxoguanine:adenine mismatched double-stranded DNA, leaving an apurinic site.

Other name(s): *mutY* (gene name); A/G-specific adenine glycosylase

Systematic name: adenine-DNA deoxyribohydrolase (adenine-releasing)
The enzyme serves as a mismatch repair enzyme that works to correct 7,8-dihydro-8-oxoguanine:adenine mispairs that arise in DNA when error-prone synthesis occurs past 7,8-dihydro-8-oxoguanine (GO) lesions in DNA. The enzyme excises the adenine of the mispair, producing an apurinic site sensitive to AP endonuclease activity. After removing the undamaged adenine the enzyme remains bound to the site to prevent EC 3.2.2.23 (MutM) from removing the GO lesion, which could lead to a double strand break. In vitro the enzyme is also active with adenine:guanine, adenine:cytosine, and adenine:7,8-dihydro-8-oxoadenine (AO) mispairs, removing the adenine in all cases.

References: [103, 1998]

[EC 3.2.2.31 created 2018]

**EC 3.2.3 Hydrolysing S-glycosyl compounds (deleted sub-subclass)**

[3.2.3.1 Transferred entry. thiglucosidase. Now EC 3.2.1.147, thiglucosidase]

[EC 3.2.3.1 created 1972, deleted 2001]

**EC 3.3 Acting on ether bonds**

This subclass contains enzymes that act on ether bonds. It is subdivided into those hydrolysing thioether and trialkylsulfonium compounds (EC 3.3.1) and those acting on ethers (EC 3.3.2).

**EC 3.3.1 Thioether and trialkylsulfonium hydrolases (deleted sub-subclass)**

This sub-subclass is now listed as EC 3.13.2.

[3.3.1.1 Transferred entry. adenosylhomocysteinase, now classified as EC 3.13.2.1, adenosylhomocysteinase]

[EC 3.3.1.1 created 1961, modified 2004, deleted 2022]

[3.3.1.2 Transferred entry. S-adenosyl-L-methionine hydrolase (L-homoserine-forming), now classified as EC 3.13.2.2, S-adenosyl-L-methionine hydrolase (L-homoserine-forming)]

[EC 3.3.1.2 created 1972, modified 1976, modified 2018, deleted 2022]

[3.3.1.3 Deleted entry. ribosylhomocysteinase. This enzyme was transferred to EC 3.2.1.148, ribosylhomocysteinase, which has since been deleted. The activity is most probably attributable to EC 4.4.1.21, S-ribosylhomocysteine lyase]

[EC 3.3.1.3 created 1972, deleted 2001]

**EC 3.3.2 Ether hydrolases**

**EC 3.3.2.1**

**Accepted name:** isochorismatase  
**Reaction:** isochorismate + H₂O = (2S,3S)-2,3-dihydroxy-2,3-dihydrobenzoate + pyruvate  
**Other name(s):** 2,3-dihydro-2,3-dihydroxybenzoate synthase; 2,3-dihydroxy-2,3-dihydrobenzoate synthase; 2,3-dihydroxy-2,3-dihydrobenzoic synthase  
**Systematic name:** isochorismate pyruvate-hydrolase  
**Comments:** The enzyme is involved in the biosynthesis of several siderophores, such as 2,3-dihydroxybenzoylglycine, enterobactin, bacillibactin, and vibriobactin.  
**References:** [3466]

[EC 3.3.2.1 created 1972]
EC 3.3.2.2

Accepted name: lysoplasmalogenase

Reaction: (1) 1-(1-alkenyl)-sn-glycero-3-phosphocholine + H$_2$O = an aldehyde + sn-glycero-3-phosphocholine
(2) 1-(1-alkenyl)-sn-glycero-3-phosphoethanolamine + H$_2$O = an aldehyde + sn-glycero-3-phosphoethanolamine

Other name(s): alkenylglycerophosphocholine hydrolase; alkenylglycerophosphoethanolamine hydrolase; 1-(1-alkenyl)-sn-glycero-3-phosphocholine aldehydohydrolase

Systematic name: lysoplasmalogen aldehydohydrolase

Comments: Lysoplasmalogenase is specific for the sn-2-deacylated (lyso) form of plasmalogen and catalyses hydrolytic cleavage of the vinyl ether bond, releasing a fatty aldehyde and sn-glycero-3-phosphocholine or sn-glycero-3-phosphoethanolamine.

References: [3280, 735, 1058, 85, 3373]

[EC 3.3.2.2 created 1972, modified 1976, (EC 3.3.2.5 created 1984, incorporated 2016), modified 2016]

3.3.2.3 Transferred entry. epoxide hydrolase. Now known to comprise two enzymes, microsomal epoxide hydrolase (EC 3.3.2.9) and soluble epoxide hydrolase (EC 3.3.2.10)

[EC 3.3.2.3 created 1978, modified 1999, deleted 2006]

EC 3.3.2.4

Accepted name: trans-epoxysuccinate hydrolase

Reaction: trans-2,3-epoxysuccinate + H$_2$O = meso-tartrate

Other name(s): trans-epoxysuccinate hydratase; tartrate epoxydase

Systematic name: trans-2,3-epoxysuccinate hydrolase

Comments: Acts on both optical isomers of the substrate.

References: [39]

[EC 3.3.2.4 created 1984]

3.3.2.5 Transferred entry. alkenylglycerophosphoethanolamine hydrolase. Now included in EC 3.3.2.2, lysoplasmalogenase.

[EC 3.3.2.5 created 1984, deleted 2016]

EC 3.3.2.6

Accepted name: leukotriene-A$_4$ hydrolase

Reaction: leukotriene A$_4$ + H$_2$O = leukotriene B$_4$

Other name(s): LTA$_4$ hydrolase; LTA4H; leukotriene A$_4$ hydrolase

Systematic name: (7E,9E,11Z,14Z)-(5S,6S)-5,6-epoxyicos-7,9,11,14-tetraenoate hydrolase

Comments: This is a bifunctional zinc metalloprotease that displays both epoxide hydrolase and aminopeptidase activities [2180, 2311]. It preferentially cleaves tripeptides at an arginyl bond, with dipeptides and tetrapeptides being poorer substrates [2311] (see EC 3.4.11.6, aminopeptidase B). It also converts leukotriene A$_4$ into leukotriene B$_4$, unlike EC 3.3.2.10, soluble epoxide hydrolase, which converts leukotriene A$_4$ into 5,6-dihydroxy-7,9,11,14-icosatetraenoic acid [1076, 2180]. In vertebrates, five epoxide-hydrolase enzymes have been identified to date: EC 3.3.2.6 (leukotriene A$_4$ hydrolase), EC 3.3.2.7 (hepoxilin-epoxide hydrolase), EC 3.3.2.9 (microsomal epoxide hydrolase), EC 3.3.2.10 (soluble epoxide hydrolase) and EC 3.3.2.11 (cholesterol-5,6-oxide hydrolase) [864].

References: [775, 2020, 1076, 2180, 864, 2311, 2269]

[EC 3.3.2.6 created 1989, modified 2006]

EC 3.3.2.7

Accepted name: hepoxilin-epoxide hydrolase

Reaction: hepoxilin A$_3$ + H$_2$O = trioxilin A$_3$

[EC 3.3.2.7 created 1989]
Other name(s): hepoxilin epoxide hydrolase; hepoxilin hydrolase; hepoxilin A₃ hydrolase
Systematic name: (5Z,9E,14Z)-(8ξ,11R,12S)-11,12-epoxy-8-hydroxyicos-5,9,14-trienoate hydrolase
Comments: Converts hepoxilin A₃ into trioxilin A. Highly specific for the substrate, having only slight activity with other epoxides such as leukotriene A₄ and styrene oxide [2333]. Hepoxilin A₃ is an hydroxyepoxide derivative of arachidonic acid that is formed via the 12-lipoxygenase pathway [2333]. It is probable that this enzyme plays a modulatory role in inflammation, vascular physiology, systemic glucose metabolism and neurological function [2180]. In vertebrates, five epoxide-hydrolase enzymes have been identified to date: EC 3.3.2.6 (leukotriene-A₄ hydrolase), EC 3.3.2.7 (hepoxilin-epoxide hydrolase), EC 3.3.2.9 (microsomal epoxide hydrolase), EC 3.3.2.10 (soluble epoxide hydrolase) and EC 3.3.2.11 (cholesterol 5,6-oxide hydrolase) [864].

References: [2332, 2333, 864, 2180]

EC 3.3.2.7 created 1992, modified 2006

EC 3.3.2.8
Accepted name: limonene-1,2-epoxide hydrolase
Reaction: 1,2-epoxymenth-8-ene + H₂O = menth-8-ene-1,2-diol
Other name(s): limonene oxide hydrolase
Systematic name: 1,2-epoxymenth-8-ene hydrolase
Comments: Involved in the monoterpene degradation pathway of the actinomycete Rhodococcus erythropolis. The enzyme hydrolyses several alicyclic and 1-methyl-substituted epoxides, such as 1-methylecyclohexene oxide, indene oxide and cyclohexene oxide. It differs from the previously described epoxide hydrolases [EC 3.3.2.4 (trans-epoxysuccinate hydrolase), EC 3.3.2.6 (leukotriene-A₄ hydrolase), EC 3.3.2.7 (hepoxilin-epoxide hydrolase), EC 3.3.2.9 (microsomal epoxide hydrolase) and EC 3.3.2.10 (soluble epoxide hydrolase)] as it is not inhibited by 2-bromo-4′-nitroacetophenone, diethyl dicarbonate, 4-fluorochalcone oxide or 1,10-phenanthroline. Both enantiomers of menth-8-ene-1,2-diol [i.e. (1R,2R,4S)-menth-8-ene-1,2-diol and (1S,2S,4R)-menth-8-ene-1,2-diol] are metabolized.

References: [3190, 152, 3191]

[EC 3.3.2.8 created 2001]

EC 3.3.2.9
Accepted name: microsomal epoxide hydrolase
Reaction: (1) cis-stilbene oxide + H₂O = (1R,2R)-1,2-diphenylethane-1,2-diol
(2) 1-(4-methoxyphenyl)-N-methyl-N-[3-(3-methyloxetan-3-yl)methyl]methanamine + H₂O = 2-[(4-methoxyphenyl)methyl][methyl]aminomethyl]-2-methylpropane-1,3-diol
Other name(s): microsomal oxirane/oxetane hydrolase; epoxide hydratase (ambiguous); microsomal epoxide hydratase (ambiguous); epoxide hydrolase; microsomal epoxide hydrolase; arene-oxide hydratase (ambiguous); benzo[a]pyrene-4,5-oxide hydratase; benzo[a]pyrene-4,5-epoxide hydratase; aryl epoxide hydrase (ambiguous); cis-epoxide hydrolase; mEH; EPHX1 (gene name)
Systematic name: cis-stilbene-oxide hydrolase
Comments: This is a key hepatic enzyme that catalyses the hydrolytic ring opening of oxiranes (epoxides) and oxetanes to give the corresponding diols. The enzyme is involved in the metabolism of numerous substrates including the stereoselective hydrolytic ring opening of 7-oxabicyclo[4.1.0]hepta-2,4-dienes (arene oxides) to the corresponding trans-dihydirols. The reaction proceeds via a triad mechanism and involves the formation of an hydroxalkyl-enzyme intermediate. Five epoxide-hydrolase enzymes have been identified in vertebrates to date: EC 3.3.2.6 (leukotriene-A₄ hydrolase), EC 3.3.2.7 (hepoxilin-epoxide hydrolase), EC 3.3.2.9 (microsomal epoxide hydrolase), EC 3.3.2.10 (soluble epoxide hydrolase) and EC 3.3.2.11 (cholesterol 5,6-oxide hydrolase).

References: [2251, 1381, 2249, 2250, 1841, 203, 864, 2078, 2180, 3094]

[EC 3.3.2.9 created 2006 (EC 3.3.2.3 created 1978, modified 1999, part incorporated 2006), modified 2017]
EC 3.3.2.10

Accepted name: soluble epoxide hydrolase
Reaction: an epoxide + H₂O = a glycol
Other name(s): epoxide hydrase (ambiguous); epoxide hydratase (ambiguous); arene-oxide hydratase (ambiguous); aryl epoxide hydrase (ambiguous); trans-stilbene oxide hydrolase; sEH; cytosolic epoxide hydrolase
Systematic name: epoxide hydrolase
Comments: Catalyses the hydrolysis of trans-substituted epoxides, such as trans-stilbene oxide, as well as various aliphatic epoxides derived from fatty-acid metabolism [864]. It is involved in the metabolism of arachidonic epoxides (epoxyicosatrienoic acids; EETs) and linoleic acid epoxides. The EETs, which are endogenous chemical mediators, act at the vascular, renal and cardiac levels to regulate blood pressure [2078, 3472]. The enzyme from mammals is a bifunctional enzyme: the C-terminal domain exhibits epoxide-hydrolase activity and the N-terminal domain has the activity of EC 3.1.3.76, lipid-phosphate phosphatase [2181, 549]. Like EC 3.3.2.9, microsomal epoxide hydrolase, it is probable that the reaction involves the formation of an hydroxyalkyl—enzyme intermediate [2078, 1678]. The enzyme can also use leukotriene A₄, the substrate of EC 3.3.2.6, leukotriene-A₄ hydrolase, but it forms 5,6-dihydroxy-7,9,11,14-icosatetraenoic acid rather than leukotriene B₄ as the product [1076, 2180]. In vertebrates, five epoxide-hydrolase enzymes have been identified to date: EC 3.3.2.6 (leukotriene-A₄ hydrolase), EC 3.3.2.7 (hepoxilin-epoxide hydrolase), EC 3.3.2.9 (microsomal epoxide hydrolase), EC 3.3.2.10 (soluble epoxide hydrolase) and EC 3.3.2.11 (cholesterol 5,6-oxide hydrolase) [864].

References: [2181, 549, 2249, 2078, 3472, 1678, 864, 3481, 1076, 2180]

[EC 3.3.2.10 created 2006 (EC 3.3.2.3 created 1978, part incorporated 2006)]

EC 3.3.2.11

Accepted name: cholesterol-5,6-oxide hydrolase
Reaction: (1) 5,6α-epoxy-5α-cholestan-3β-ol + H₂O = 5α-cholestanene-3β,5α,6β-triol
(2) 5,6β-epoxy-5β-cholestan-3β-ol + H₂O = 5α-cholestanene-3β,5α,6β-triol
Other name(s): cholesterol-epoxide hydrolase; ChEH
Systematic name: 5,6α-epoxy-5α-cholestan-3β-ol hydrolase
Comments: The enzyme appears to work equally well with either epoxide as substrate [2747]. The product is a competitive inhibitor of the reaction. In vertebrates, five epoxide-hydrolase enzymes have been identified to date: EC 3.3.2.6 (leukotriene-A₄ hydrolase), EC 3.3.2.7 (hepoxilin-epoxide hydrolase), EC 3.3.2.9 (microsomal epoxide hydrolase), EC 3.3.2.10 (soluble epoxide hydrolase) and EC 3.3.2.11 (cholesterol 5,6-oxide hydrolase) [2747].

References: [1746, 2252, 2747, 864, 3481, 1076, 2180]

[EC 3.3.2.11 created 2006]

EC 3.3.2.12

Accepted name: oxepin-CoA hydrolase
Reaction: 2-oxepin-(2H)-ylideneacetyl-CoA + H₂O = 3-oxo-5,6-dehydrosuberyl-CoA semialdehyde
Other name(s): paaZ (gene name)
Systematic name: 2-oxepin-(2H)-ylideneacetyl-CoA hydrolase
Comments: The enzyme from Escherichia coli is a bifunctional fusion protein that also catalyses EC 1.17.1.7, 3-oxo-5,6-dehydrosuberyl-CoA semialdehyde dehydrogenase. Combined the two activities result in a two-step conversion of oxepin-CoA to 3-oxo-5,6-dehydrosuberyl-CoA, part of an aerobic phenylacetate degradation pathway [1,3,4]. The enzyme from Escherichia coli also exhibits enoyl-CoA hydratase activity utilizing crotonyl-CoA as a substrate [2348].

References: [810, 2348, 1343, 3047]

[EC 3.3.2.12 created 2011 as EC 3.7.1.16, transferred 2013 to EC 3.3.2.12]
EC 3.3.2.13
Accepted name: chorismatase
Reaction: chorismate + H_2O = (4R,5R)-4,5-dihydroxycyclohexa-1(6),2-diene-1-carboxylate + pyruvate
Other name(s): chorismate/3,4-dihydroxycyclohexa-1,5-dienoate synthase; fkbO (gene name); rapK (gene name)
Systematic name: chorismate pyruvate-hydrolase
Comments: The enzyme found in several bacterial species is involved in the biosynthesis of macrocyclic polyketides.
References: [57, 1431]

[EC 3.3.2.13 created 2013]

EC 3.3.2.14
Accepted name: 2,4-dinitroanisole O-demethylase
Reaction: 2,4-dinitroanisole + H_2O = methanol + 2,4-dinitrophenol
Other name(s): 2,4-dinitroanisole ether hydrolase; dnhA (gene name); dnhB (gene name); DNAN demethylase
Systematic name: 2,4-dinitroanisole methanol hydrolase
Comments: The enzyme, characterized from the bacterium Nocardoides sp. JS1661, is involved in the degradation of 2,4-dinitroanisole. Unlike other known O-demethylases, such as EC 1.14.99.15, 4-methoxybenzoate monoxygenase (O-demethylating), or EC 1.14.11.32, codeine 3-O-demethylase, it does not require oxygen or electron donors, and produces methanol rather than formaldehyde.
References: [814]

[EC 3.3.2.14 created 2015]

EC 3.3.2.15
Accepted name: trans-2,3-dihydro-3-hydroxyanthranilic acid synthase
Reaction: (2S)-2-amino-4-deoxychorismate + H_2O = (5S,6S)-6-amino-5-hydroxycyclohexa-1,3-diene-1-carboxylate + pyruvate
Other name(s): isochorismatase (ambiguous); phzD (gene name)
Systematic name: (2S)-2-amino-4-deoxychorismate pyruvate-hydrolase
Comments: Isolated from the bacterium Pseudomonas aeruginosa. Involved in phenazine biosynthesis.
References: [1948, 2355]

[EC 3.3.2.15 created 2016]

EC 3.4 Acting on peptide bonds (peptidases)

It is recommended that the term "peptidase" be used as being synonymous with "peptide hydrolase" for any enzyme that hydrolizes peptide bonds. Peptidases are recommended to be further divided into "exopeptidases" that act only near a terminus of a polypeptide chain and "endopeptidases" that act internally in polypeptide chains. The types of exopeptidases and endopeptidases are described more fully below. The usage of "peptidase", which is now recommended, is synonymous with "protease" as it was originally used [1] as a general term for both exopeptidases and endopeptidases, but it should be noted that previously, in Enzyme Nomenclature (1984), "peptidase" was restricted to the enzymes included in sub-subclasses EC 3.4.11 and EC 3.4.13-19, the exopeptidases. Also, the term "protease" used previously for the enzymes included in sub-subclasses EC 3.4.21-25 carried the same meaning as "endopeptidase", and has been replaced by "endopeptidase", for consistency.

The nomenclature of the peptidases is troublesome. Their specificity is commonly difficult to define, depending upon the nature of several amino-acid residues around the peptide bond to be hydrolysed and also on the conformation of the substrate’s polypeptide chain. A classification involving the additional criterion of catalytic mechanism is therefore used; a classification involving the additional criterion of catalytic mechanism is therefore used.

Two sets of sub-subclasses of peptidases are recognized, those of the exopeptidases (EC 3.4.11 and EC 3.4.13-19) and those of the endopeptidases (EC 3.4.21-25). The exopeptidases act only near the ends of polypeptide chains, and those acting at a free N-terminus liberate a single amino-acid residue (aminopeptidases; EC 3.4.11), or a dipeptide or a tripeptide (dipeptidyl-peptidases and tripeptidyl-peptidases; EC 3.4.14). The exopeptidases that act at a free C-terminus liberate a single residue (carboxypeptidases, EC 3.4.16-18), or a dipeptide (peptidyl-dipeptidases; EC 3.4.15). The carboxypeptidases are allocated to three groups on the basis of catalytic mechanism: the serine-type carboxypeptidases (EC 3.4.16), the metallo-carboxypeptidases
(EC 3.4.17) and the cysteine-type carboxypeptidases (EC 3.4.18). Other exopeptidases are specific for dipeptidases (dipeptidases, EC 3.4.13), or for removal of terminal residues that are substituted, cyclized or linked by isopeptide bonds (peptide linkages other than those of alpha-carboxyl to alpha-amino groups) (omega peptidases; EC 3.4.19).

The endopeptidases are divided into sub-subclasses on the basis of catalytic mechanism, and specificity is used only to identify individual enzymes within the groups. The sub-subclasses are: serine endopeptidases (EC 3.4.21), cysteine endopeptidases (EC 3.4.22), aspartic endopeptidases (EC 3.4.23), metalloendopeptidases (EC 3.4.24) and threonine endopeptidases (EC 3.4.25).

There are characteristic inhibitors of the members of each catalytic type of endopeptidase; to save space, these have not been listed separately for each individual enzyme but are reviewed in [2] and [3]. A general source of information on peptidases that similarly has not been cited for each individual enzyme is reference [4].

In describing the specificity of peptidases, use is made of a model in which the catalytic site is considered to be flanked on one or both sides by specificity subsites, each able to accommodate the sidechain of a single amino-acid residue (based on [5]). These sites are numbered from the catalytic site, S1...Sn towards the N-terminus of the substrate, and S1'...Sn' towards the C-terminus. The residues they accommodate are numbered P1...Pn and P1'...Pn', respectively, as follows:

Substrate: - P3 - P2 - P1 \( \rightarrow \) P1'- P2'- P3'-...;

Enzyme: - S3 - S2 - S1 * S1'- S2'- S3'-...;

In this representation, the catalytic site of the enzyme is marked by an asterisk (*). The peptide bond cleaved (the scissile bond) is indicated by the symbol ‘\( \rightarrow \)’ or a hyphen in the structural formula of the substrate, or a hyphen in the name of the enzyme.

Finally, in describing the specificity of endopeptidases, the term oligopeptidase’ is used to refer to those that act optimally on substrates smaller than proteins.

Families of peptidases are referred to by use of the numbering system of Rawlings & Barrett [6,7].

### References


### EC 3.4.1 α-Amino-acyl-peptide hydrolases (deleted sub-subclass)

- **[3.4.1.1] Transferred entry. leucyl aminopeptidase. Now EC 3.4.11.1, leucyl aminopeptidase**
  
  [EC 3.4.1.1 created 1961, deleted 1972]

- **[3.4.1.2] Transferred entry. aminopeptidase. Now EC 3.4.11.2, membrane alanyl aminopeptidase**
  
  [EC 3.4.1.2 created 1961, deleted 1972]

- **[3.4.1.3] Transferred entry. aminotripeptidase. Now EC 3.4.11.4, tripeptide aminopeptidase**
  
  [EC 3.4.1.3 created 1961, deleted 1972]

- **[3.4.1.4] Transferred entry. proline iminopeptidase. Now EC 3.4.11.5, prolyl aminopeptidase**
  
  [EC 3.4.1.4 created 1965, deleted 1972]
EC 3.4.2 Peptidyl-amino-acid hydrolases (deleted sub-subclass)

[3.4.2.1] Transferred entry. carboxypeptidase A. Now EC 3.4.17.1, carboxypeptidase A

[3.4.2.2] Transferred entry. carboxypeptidase B. Now EC 3.4.17.2, carboxypeptidase B

[3.4.2.3] Transferred entry. yeast carboxypeptidase. Now EC 3.4.17.4, Gly-Xaa carboxypeptidase

EC 3.4.3 Dipeptide hydrolases (deleted sub-subclass)

[3.4.3.1] Transferred entry. glycyl-glycine dipeptidase. Now EC 3.4.13.18, cytosol nonspecific dipeptidase

[3.4.3.2] Transferred entry. glycyl-leucine dipeptidase. Now EC 3.4.13.18, cytosol nonspecific dipeptidase

[3.4.3.3] Transferred entry. aminoacyl-histidine dipeptidase. Now EC 3.4.13.3, Xaa-His dipeptidase

[3.4.3.4] Transferred entry. aminoacyl-methylhistidine dipeptidase. Now EC 3.4.13.5, Xaa-methyl-His dipeptidase

[3.4.3.5] Transferred entry. cysteinylglycine dipeptidase. Now EC 3.4.11.2, membrane alanyl aminopeptidase

[3.4.3.6] Transferred entry. iminodipeptidase. Now EC 3.4.13.18, cytosol nonspecific dipeptidase

[3.4.3.7] Transferred entry. iminodipeptidase. Now EC 3.4.13.9, Xaa-Pro dipeptidase

EC 3.4.4 Peptidyl peptide hydrolases (deleted sub-subclass)

[3.4.4.1] Transferred entry. pepsin. Now EC 3.4.23.1, pepsin A

[3.4.4.2] Transferred entry. pepsin B. Now EC 3.4.23.2, pepsin B

[3.4.4.3] Transferred entry. rennin. Now EC 3.4.23.4, chymosin

[3.4.4.4] Transferred entry. trypsin. Now EC 3.4.21.4, trypsin

[3.4.4.5] Transferred entry. chymotrypsin. Now EC 3.4.21.1, chymotrypsin
[EC 3.4.4.5 created 1961, deleted 1972]

[3.4.4.6 Transferred entry. chymotrypsin B. Now EC 3.4.21.1, chymotrypsin]

[EC 3.4.4.6 created 1961, deleted 1972]

[3.4.4.7 Transferred entry. elastase. Now covered by EC 3.4.21.36, pancreatic elastase and EC 3.4.21.37, leukocyte elastase]

[EC 3.4.4.7 created 1961, deleted 1972]

[3.4.4.8 Transferred entry. enteropeptidase. Now EC 3.4.21.9, enteropeptidase]

[EC 3.4.4.8 created 1961, deleted 1972]

[3.4.4.9 Transferred entry. cathepsin C. Now EC 3.4.14.1, dipeptidyl-peptidase I]

[EC 3.4.4.9 created 1961, deleted 1972]

[3.4.4.10 Transferred entry. papain. Now EC 3.4.22.2, papain]

[EC 3.4.4.10 created 1961, deleted 1972]

[3.4.4.11 Transferred entry. chymopapain. Now EC 3.4.22.6, chymopapain]

[EC 3.4.4.11 created 1961, deleted 1972]

[3.4.4.12 Transferred entry. ficin. Now EC 3.4.22.3, ficain]

[EC 3.4.4.12 created 1961, deleted 1972]

[3.4.4.13 Transferred entry. thrombin. Now EC 3.4.21.5, thrombin]

[EC 3.4.4.13 created 1961, deleted 1972]

[3.4.4.14 Transferred entry. plasmin. Now EC 3.4.21.7, plasmin]

[EC 3.4.4.14 created 1961, deleted 1972]

[3.4.4.15 Transferred entry. renin. Now EC 3.4.23.15, renin]

[EC 3.4.4.15 created 1961, deleted 1972]

[3.4.4.16 Transferred entry. subtilopeptidase A. Now covered by the microbial serine proteinases EC 3.4.21.62 (subtilisin), EC 3.4.21.63 (oryzin), EC 3.4.21.64 (endopeptidase K), EC 3.4.21.65 (thermomycolin), EC 3.4.21.66 (thermitase) and EC 3.4.21.67 (ndopeptidase So)]

[EC 3.4.4.16 created 1961, deleted 1972]

[3.4.4.17 Transferred entry. aspergillopeptidase A. Now covered by the microbial aspartic proteinases EC 3.4.23.20 (penicillopepsin), EC 3.4.23.21 (rhizopuaspepsin), EC 3.4.23.22 (endothiapepsin), EC 3.4.23.23 (mucorpepsin), EC 3.4.23.24 (candidapepsin), EC 3.4.23.25 (saccharopepsin), EC 3.4.23.26 (rhodotorulapepsin), EC 3.4.21.103 (physarolisin), EC 3.4.23.28 (acrocylindropepsin), EC 3.4.23.29 (polyporopepsin) and EC 3.4.23.30 (pycnoporopepsin)]

[EC 3.4.4.17 created 1961, deleted 1972]

[3.4.4.18 Transferred entry. streptococcus peptidase A. Now EC 3.4.22.10, stretopain]

[EC 3.4.4.18 created 1961, deleted 1972]

[3.4.4.19 Transferred entry. clostridiopeptidase A. Now EC 3.4.24.3, microbial collagenase]

[EC 3.4.4.19 created 1961, deleted 1972]

[3.4.4.20 Transferred entry. clostridiopeptidase B. Now EC 3.4.22.8, clostripain]

[EC 3.4.4.20 created 1961, deleted 1972]

[3.4.4.21 Transferred entry. kallikrein. Now EC 3.4.21.34 (plasma kallikrein) and EC 3.4.21.35 (tissue kallikrein)]

162
EC 3.4.11 Aminopeptidases

EC 3.4.11.1

Accepted name: leucyl aminopeptidase
Reaction: Release of an N-terminal amino acid, Xaa—Yaa, in which Xaa is preferably Leu, but may be other amino acids including Pro although not Arg or Lys, and Yaa may be Pro. Amino acid amides and methyl esters are also readily hydrolysed, but rates on arylamides are exceedingly low
Other name(s): leucine aminopeptidase; leucyl peptidase; peptidase S; cytosol aminopeptidase; cathepsin III; L-leucine aminopeptidase; leucinaminopeptidase; leucinamide aminopeptidase; FTBL proteins; proteinates FTBL; aminopeptidase II; aminopeptidase III; aminopeptidase I
Comments: A zinc enzyme isolated from pig kidney and cattle lens; activated by heavy metal ions. Type example of peptidase family M17.
References: [1213, 616, 3196]

EC 3.4.11.2

Accepted name: membrane alanyl aminopeptidase
Reaction: Release of an N-terminal amino acid, Xaa—Yaa- from a peptide, amide or arylamide. Xaa is preferably Ala, but may be most amino acids including Pro (slow action). When a terminal hydrophobic residue is followed by a prolyl residue, the two may be released as an intact Xaa-Pro dipeptide
Other name(s): microsomal aminopeptidase; aminopeptidase M; aminopeptidase N; particle-bound aminopeptidase; amino-oligopeptidase; alanine aminopeptidase; membrane aminopeptidase I; pseudo leucine aminopeptidase; alanyl aminopeptidase; alanine-specific aminopeptidase; cysteinylglycinase dipeptidase; cysteinylglycinase; L-alanine aminopeptidase; CD13
Comments: A zinc enzyme, not activated by heavy metal ions. Type example of peptidase family M1.
References: [3232, 1543, 1023, 2818, 808]

EC 3.4.11.3

Accepted name: cystinyl aminopeptidase
Reaction: Release of an N-terminal amino acid, Cys—Xaa-, in which the half-cystine residue is involved in a disulfide loop, notably in oxytocin or vasopressin. Hydrolysis rates on a range of aminoacyl arylamides exceed that for the cystinyl derivative, however [4]
Other name(s): cystyl-aminopeptidase; oxytocinase; cystine aminopeptidase; L-cystine aminopeptidase; oxytocin peptidase; vasopressinase
Comments: A zinc-containing sialoglycoprotein in peptidase family M1 (membrane alanyl aminopeptidase family)
References: [2815, 2816, 3444, 2634]

[EC 3.4.11.3 created 1972]

EC 3.4.11.4
Accepted name: tripeptide aminopeptidase
Reaction: Release of the N-terminal residue from a tripeptide
Other name(s): tripeptidase; aminotripeptidase; aminoexotripeptidase; lymphopeptidase; imidoendopeptidase; peptidase B; alanine-phenylalanine-proline arylamidase; peptidase T
Comments: A zinc enzyme, widely distributed in mammalian tissues. Formerly EC 3.4.1.3
References: [685, 2613]

[EC 3.4.11.4 created 1961 as EC 3.4.1.3, transferred 1972 to EC 3.4.11.4]

EC 3.4.11.5
Accepted name: prolyl aminopeptidase
Reaction: Release of N-terminal proline from a peptide
Other name(s): proline aminopeptidase; Pro-X aminopeptidase; cytosol aminopeptidase V; proline iminopeptidase
Comments: A Mn$^{2+}$-requiring enzyme present in the cytosol of mammalian and microbial cells. In contrast to the mammalian form, the bacterial form of the enzyme (type example of peptidase family S33) hydrolyses both polyproline and prolyl-2-naphthylamide. The mammalian enzyme, which is not specific for prolyl bonds, is possibly identical with EC 3.4.11.1, leucyl aminopeptidase.
References: [2658, 2218, 3151]

[EC 3.4.11.5 created 1965 as EC 3.4.1.4, transferred 1972 to EC 3.4.11.5]

EC 3.4.11.6
Accepted name: aminopeptidase B
Reaction: Release of N-terminal Arg and Lys from oligopeptides when P1' is not Pro. Also acts on arylamides of Arg and Lys
Other name(s): arylamidase II; arginine aminopeptidase; arginyl aminopeptidase; Cl$^-$-activated arginine aminopeptidase; cytosol aminopeptidase IV; L-arginine aminopeptidase
Comments: Cytosolic or membrane-associated enzyme from mammalian tissues, activated by chloride ions and low concentrations of thiol compounds. This is one of the activities of the bifunctional enzyme EC 3.3.2.6 (membrane alanyl aminopeptidase family) [909, 378].
References: [926, 202, 379, 909, 378, 2311]

[EC 3.4.11.6 created 1972, modified 1997]

EC 3.4.11.7
Accepted name: glutamyl aminopeptidase
Reaction: Release of N-terminal glutamate (and to a lesser extent aspartate) from a peptide
Other name(s): aminopeptidase A; aspartate aminopeptidase; angiotensinase A; glutamyl peptidase; Ca$^{2+}$-activated glutamate aminopeptidase; membrane aminopeptidase II; antigen BP-1/6C3 of mouse B lymphocytes; L-aspartate aminopeptidase; angiotensinase A2
Comments: Ca$^{2+}$-activated and generally membrane-bound. A zinc-metallopeptidase in family M1 (membrane alanyl aminopeptidase family)
References: [983, 485, 578, 3068, 3375]

[EC 3.4.11.7 created 1972]
**EC 3.4.11.9**

**Accepted name:** Xaa-Pro aminopeptidase

**Reaction:** Release of any N-terminal amino acid, including proline, that is linked to proline, even from a dipeptide or tripeptide

**Other name(s):** proline aminopeptidase; aminopeptidase P; aminoaacetylproline aminopeptidase; X-Pro aminopeptidase

**Comments:** A Mn$^{2+}$-dependent, generally membrane-bound enzyme present in both mammalian and bacterial cells. In peptidase family M24 (methionyl aminopeptidase family)

**References:** [3427, 3426, 834, 2309, 1245]

[EC 3.4.11.9 created 1972]

**EC 3.4.11.10**

**Accepted name:** bacterial leucyl aminopeptidase

**Reaction:** Release of an N-terminal amino acid, preferentially leucine, but not glutamic or aspartic acids

**Other name(s):** Aeromonas proteolytica aminopeptidase

**Comments:** A zinc enzyme. Forms of the enzyme have been isolated from Aeromonas proteolytica, Escherichia coli and Streptococcus thermophilus. Examples are known from peptidase families M17 and M28 (of leucyl aminopeptidase and aminopeptidase Y, respectively)

**References:** [2441, 647, 2466]

[EC 3.4.11.10 created 1972]

**EC 3.4.11.11**

*Deleted entry. aminopeptidase*

[EC 3.4.11.11 created 1978, deleted 1992]

**EC 3.4.11.12**

*Deleted entry. thermophilic aminopeptidase*

[EC 3.4.11.12 created 1978, deleted 1997]

**EC 3.4.11.13**

**Accepted name:** clostridial aminopeptidase

**Reaction:** Release of any N-terminal amino acid, including proline and hydroxyproline, but no cleavage of Xaa-Pro-

**Other name(s):** Clostridium histolyticum aminopeptidase

**Comments:** A secreted enzyme from Clostridium histolyticum, requiring Mn$^{2+}$ or Co$^{2+}$. In peptidase family M9.

**References:** [1511, 1512, 1513]

[EC 3.4.11.13 created 1978]

**EC 3.4.11.14**

**Accepted name:** cytosol alanyl aminopeptidase

**Reaction:** Release of an N-terminal amino acid, preferentially alanine, from a wide range of peptides, amides and arylamides

**Other name(s):** arylamidase; aminopolypeptidase; thiol-activated aminopeptidase; human liver aminopeptidase; puromycin-sensitive aminopeptidase; soluble alanyl aminopeptidase; cytosol aminopeptidase III; alanine aminopeptidase

**Comments:** A puromycin-sensitive, Co$^{2+}$-activated zinc-sialoglycoprotein that is generally cytosolic. Multiple forms are widely distributed in mammalian tissues and body fluids. In peptidase family M1 (membrane alanyl aminopeptidase family)
EC 3.4.11.15
Accepted name: aminopeptidase Y
Reaction: Preferentially, release of N-terminal lysine
Other name(s): aminopeptidase Co; aminopeptidase (cobalt-activated); lysyl aminopeptidase
Comments: Requires Co$^{2+}$; inhibited by Zn$^{2+}$ and Mn$^{2+}$. An enzyme best known from *Saccharomyces cerevisiae* that hydrolyses Lys-NHPhNO$_2$ and, more slowly, Arg-NHPhNO$_2$. Type example of peptidase family M28
References: [10, 3428, 2204]

EC 3.4.11.16
Accepted name: Xaa-Trp aminopeptidase
Reaction: Release of a variety of N-terminal residues (especially glutamate and leucine) from peptides, provided tryptophan (or at least phenylalanine or tyrosine) is the penultimate residue. Also acts on Glu-Trp, Leu-Trp and a number of other dipeptides
Other name(s): aminopeptidase W; aminopeptidase X-Trp; X-Trp aminopeptidase
Comments: A glycoprotein containing Zn$^{2+}$, from renal and intestinal brush border membranes. In peptidase family M9.
References: [942, 943]

EC 3.4.11.17
Accepted name: tryptophanyl aminopeptidase
Reaction: Preferential release of N-terminal tryptophan
Other name(s): tryptophan aminopeptidase; L-tryptophan aminopeptidase
Comments: From *Trichosporon cutaneum*. Also acts on L-tryptophanamide. Requires Mn$^{2+}$
References: [1360]

EC 3.4.11.18
Accepted name: methionyl aminopeptidase
Reaction: Release of N-terminal amino acids, preferentially methionine, from peptides and arylamides
Other name(s): methionine aminopeptidase; peptidase M; L-methionine aminopeptidase; MAP
Comments: This membrane-bound enzyme, which is present in both prokaryotes and eukaryotes, releases the initiator methionine from nascent peptides. The activity is dependent on the identity of the second, third and fourth amino acid residues of the target protein, but in general the enzyme acts only when the penultimate residue is small and uncharged (e.g. Gly, Ala, Cys, Ser, Thr, and Val). In peptidase family M24.
References: [3457, 3132, 858, 204, 2573]

EC 3.4.11.19
Accepted name: D-stereospecific aminopeptidase
Reaction: Release of an N-terminal D-amino acid from a peptide, Xaa–Yaa–, in which Xaa is preferably D-Ala, D-Ser or D-Thr. D-Amino acid amides and methyl esters also are hydrolysed, as is glycine amide
Other name(s): D-aminopeptidase
Comments: Known from the bacterium Ochrobactrum anthropi. In peptidase family S12 (D-Ala-D-Ala carboxypeptidase family) [89]
References: [90, 89]

EC 3.4.11.20
Accepted name: aminopeptidase Ey
Reaction: Differs from other aminopeptidases in broad specificity for amino acids in the P1 position and the ability to hydrolyse peptides of four or five residues that contain Pro in the P1′ position
Comments: A zinc glycoprotein in peptidase family M1 (membrane alanyl aminopeptidase family), composed of two 150 kDa subunits. From the plasma fraction of hen egg yolk
References: [1297, 3017, 3016]

EC 3.4.11.21
Accepted name: aspartyl aminopeptidase
Reaction: Release of an N-terminal aspartate or glutamate from a peptide, with a preference for aspartate
Comments: Aminoacyl-arylamides are poor substrates. This is an abundant cytosolic enzyme in mammalian cells, in peptidase family M18 of aminopeptidase I
References: [1501, 3338]

EC 3.4.11.22
Accepted name: aminopeptidase I
Reaction: Release of an N-terminal amino acid, preferably a neutral or hydrophobic one, from a polypeptide. Aminoacyl-arylamides are poor substrates
Other name(s): aminopeptidase III; aminopeptidase yscI (gene name); leucine aminopeptidase IV; yeast aminopeptidase I
Comments: A 640-kDa, dodecameric enzyme best known as the major vacuolar aminopeptidase of yeast, Saccharomyces cervisiae, in which species it was first given the name aminopeptidase I (one), amongst others. Activity is stimulated by both Zn^{2+} and Cl^{-} ions. Type example of peptidase family M18
References: [1412, 1989, 429, 2246]

EC 3.4.11.23
Accepted name: PepB aminopeptidase
Reaction: Release of an N-terminal amino acid, Xaa, from a peptide or arylamide. Xaa is preferably Glu or Asp but may be other amino acids, including Leu, Met, His, Cys and Gln
Other name(s): Salmonella enterica serovar Typhimurium peptidase B
Comments: A 270-kDa protein composed of six 46.3-kDa subunits. The pH optimum is in the alkaline range and activity is stimulated by KCl. In peptidase family M17.
References: [1932]

[EC 3.4.11.19 created 1993]
[EC 3.4.11.20 created 1995]
[EC 3.4.11.21 created 2000]
[EC 3.4.11.22 created 1997]
[EC 3.4.11.23 created 2003]
EC 3.4.11.24
Accepted name: aminopeptidase S
Reaction: Release of an N-terminal amino acid with a preference for large hydrophobic amino-terminus residues
Other name(s): Mername-AA022 peptidase; SGAP; aminopeptidase (Streptomyces griseus); Streptomyces griseus aminopeptidase; S. griseus AP; double-zinc aminopeptidase
Comments: Aminopeptidases are associated with many biological functions, including protein maturation, protein degradation, cell-cycle control and hormone-level regulation [77, 918]. This enzyme contains two zinc molecules in its active site and is activated by Ca$^{2+}$ [918]. In the presence of Ca$^{2+}$, the best substrates are Leu-Phe, Leu-Ser, Leu-pNA (aminoacyl-p-nitroanilide), Phe-Phe-Phe and Phe-Phe [77]. Peptides with proline in the P1' position are not substrates [77]. Belongs in peptidase family M28.
References: [2884, 205, 77, 918, 975]

[EC 3.4.11.24 created 2008]

EC 3.4.11.25
Accepted name: β-peptidyl aminopeptidase
Reaction: Cleaves N-terminal β-homoamino acids from peptides composed of 2 to 6 amino acids
Other name(s): BapA (ambiguous)
Comments: Sphingosinicella xenopeptidilytica strain 3-2W4 is able to utilize the β-peptides β-homoVal-β-homoAla-β-homoLeu and β-homoAla-β-homoLeu as sole carbon and energy sources [952].

References: [1164, 952, 951, 1163]

[EC 3.4.11.25 created 2011]

EC 3.4.11.26
Accepted name: intermediate cleaving peptidase 55
Reaction: The enzyme cleaves the Pro$^{36}$-Pro$^{37}$ bond of cysteine desulfurase (EC 2.8.1.7) removing three amino acid residues (Tyr-Ser-Pro) from the N-terminus after cleavage by mitochondrial processing peptidase.
Other name(s): Icp55; mitochondrial intermediate cleaving peptidase 55 kDa
Comments: Icp55 removes the destabilizing N-terminal amino acid residues that are left after cleavage by the mitochondrial processing peptidase, leading to the stabilisation of the substrate. The enzyme can remove single amino acids or a short peptide, as in the case of cysteine desulfurase (EC 2.8.1.7), where three amino acids are removed.
References: [2122, 3228]

[EC 3.4.11.26 created 2011]

EC 3.4.12 Peptidylamino-acid hydrolases or acylamino-acid hydrolases (deleted sub-subclass)

[3.4.12.1] Transferred entry. now EC 3.4.16.5 (carboxypeptidase C) and EC 3.4.16.6 (carboxypeptidase D)

[EC 3.4.12.1 created 1972, deleted 1978]

[3.4.12.2] Transferred entry. now EC 3.4.17.1, carboxypeptidase A

[EC 3.4.12.2 created 1972, deleted 1978]

[3.4.12.3] Transferred entry. now EC 3.4.17.2, carboxypeptidase B

[EC 3.4.12.3 created 1972, deleted 1978]

[3.4.12.4] Transferred entry. now EC 3.4.16.2, lysosomal Pro-Xaa carboxypeptidase

[EC 3.4.12.4 created 1972, modified 1976, deleted 1978]

[3.4.12.5] Transferred entry. now EC 3.5.1.28, N-acetylmuramoyl-L-alanine amidase

168
EC 3.4.12.5 created 1972, deleted 1978

[3.4.12.6] Transferred entry. now EC 3.4.17.8, muramoyl-pentapeptidase carboxypeptidase]
[EC 3.4.12.6 created 1972, deleted 1978]

[3.4.12.7] Transferred entry. now EC 3.4.17.3, lysine carboxypeptidase]
[EC 3.4.12.7 created 1972, deleted 1978]

[3.4.12.8] Transferred entry. now EC 3.4.17.4, Gly-Xaa carboxypeptidase]
[EC 3.4.12.8 created 1972, deleted 1978]

[3.4.12.9] Deleted entry. aspartate carboxypeptidase]
[EC 3.4.12.9 created 1972, deleted 1978]

[3.4.12.10] Transferred entry. now EC 3.4.19.9, γ-glutamyl hydrolase]
[EC 3.4.12.10 created 1972, modified 1976, deleted 1978]

[3.4.12.11] Transferred entry. now EC 3.4.17.6, alanine carboxypeptidase]
[EC 3.4.12.11 created 1972, deleted 1978]

[3.4.12.12] Transferred entry. now EC 3.4.16.5 (carboxypeptidase C) and EC 3.4.16.6 (carboxypeptidase D)]
[EC 3.4.12.12 created 1972, deleted 1978]

[EC 3.4.12.13 created 1975, modified 1976, deleted 1978]

EC 3.4.13 Dipeptidases

[EC 3.4.13.1 created 1972, deleted 1978 [transferred to EC 3.4.13.11, deleted 1992]]

[3.4.13.2] Transferred entry. glycyl-leucine dipeptidase. Now EC 3.4.13.18, cytosol nonspecific dipeptidase]
[EC 3.4.13.2 created 1972, deleted 1978 [transferred to EC 3.4.13.11, deleted 1992]]

[3.4.13.3] Deleted entry. Xaa-Arg dipeptidase. The activity is covered by EC 3.4.13.18, cytosol nonspecific dipeptidase and EC 3.4.13.20, β-Ala-His dipeptidase.]
[EC 3.4.13.3 created 1961 as EC 3.4.3.3, transferred 1972 to EC 3.4.13.3, modified 1989 (EC 3.4.13.13 created 1981, incorporated 1992), deleted 2011]

EC 3.4.13.4

Accepted name: Xaa-Arg dipeptidase
Reaction: Preferential hydrolysis of Xaa→Arg, Xaa→Lys or Xaa→ornithine dipeptides
Other name(s): aminooacyl-lysine dipeptidase; N⁶-(4-amino-butryl)-L-lysine hydrolase; X-Arg dipeptidase
Comments: Widely distributed in mammals
References: [1642]

[EC 3.4.13.4 created 1972]
EC 3.4.13.5

Accepted name: Xaa-methyl-His dipeptidase
Reaction: Hydrolysis of anserine (β-alanyl-N°-methyl-L-histidine), carnosine, homocarnosine, glycyll-leucine and other dipeptides with broad specificity
Other name(s): anserinase; aminocetyl-methylhistidine dipeptidase; acetylhistidine deacetylase; N-acetylhistidine deacetylase; α-N-acetyl-L-histidine aminohydrolase; X-methyl-His dipeptidase
References: [1420, 182, 1736]

[EC 3.4.13.5 created 1961 as EC 3.4.3.4, transferred 1972 to EC 3.4.13.5, modified 1981 (EC 3.5.1.34 created 1972, incorporated 1981)]

[3.4.13.6 Transferred entry. Cys-Gly dipeptidase. Now EC 3.4.11.2, membrane alanyl aminopeptidase]

[EC 3.4.13.6 created 1961 as EC 3.4.3.5, transferred 1972 to EC 3.4.13.6]

EC 3.4.13.7

Accepted name: Glu-Glu dipeptidase
Reaction: Hydrolysis of the Glu-Glu dipeptide
Other name(s): α-glutamyl-glutamate dipeptidase; glutamylglutamic arylamidase
Comments: It is unclear whether the specificity of this enzyme extends to other α-glutamyl dipeptides
References: [2440]

[EC 3.4.13.7 created 1972]

[3.4.13.8 Transferred entry. Pro-X dipeptidase. Now EC 3.4.13.18, cytosol nonspecific dipeptidase]

[EC 3.4.13.8 created 1961 as EC 3.4.3.6, transferred 1972 to EC 3.4.13.8]

EC 3.4.13.9

Accepted name: Xaa-Pro dipeptidase
Reaction: Hydrolysis of Xaa-Pro dipeptides; also acts on aminoacyl-hydroxyproline analogs. No action on Pro-Pro
Other name(s): prolidase; imidodipeptidase; proline dipeptidase; peptidase D; γ-peptidase; X-Pro dipeptidase
Comments: A Mn²⁺-activated enzyme, in peptidase family M24 (methionyl aminopeptidase family); cytosolic from most animal tissues.
References: [591, 2819, 140, 340]

[EC 3.4.13.9 created 1961 as EC 3.4.3.7, transferred 1972 to EC 3.4.13.9]

[3.4.13.10 Transferred entry. β-aspartyl-dipeptidase. Now EC 3.4.19.5, β-aspartyl-peptidase]

[EC 3.4.13.10 created 1972, deleted 1992]

[3.4.13.11 Transferred entry. dipeptidase. Now EC 3.4.13.19, membrane dipeptidase]

[EC 3.4.13.11 created 1972, deleted 1992]

EC 3.4.13.12

Accepted name: Met-Xaa dipeptidase
Reaction: Hydrolysis of Met-Xaa dipeptides
Other name(s): methionyl dipeptidase; dipeptidase M; Met-X dipeptidase
Comments: A Mn²⁺-activated Escherichia coli enzyme with thiol dependence
References: [338]

[EC 3.4.13.12 created 1976]


[EC 3.4.13.13 created 1981, deleted 1992]

170
3.4.13.14  Deleted entry. γ-glutamyl dipeptidase

[EC 3.4.13.14 created 1989, deleted 1992]

3.4.13.15  Transferred entry. N^2-β-alanylarginine dipeptidase. Now EC 3.4.13.18, cytosol nonspecific dipeptidase

[EC 3.4.13.15 created 1989, deleted 1992]

3.4.13.16  Deleted entry. aspartylphenylalanine dipeptidase

[EC 3.4.13.16 created 1989, deleted 1992]

EC 3.4.13.17

Accepted name: non-stereospecific dipeptidase
Reaction: Hydrolysis of dipeptides containing either D- or L-amino acids or both
Other name(s): peptidyl-D-amino acid hydrolase; D-(or L-)aminoacyl-dipeptidase
Comments: A digestive enzyme of cephalopods
References: [577]

[EC 3.4.13.17 created 1990]

EC 3.4.13.18

Accepted name: cytosol nonspecific dipeptidase
Reaction: Hydrolysis of dipeptides, preferentially hydrophobic dipeptides including prolyl amino acids
Other name(s): N^2-β-alanylarginine dipeptidase; glycyl-glycine dipeptidase; glycyl-leucine dipeptidase; iminodipeptidase; peptidase A; Pro-X dipeptidase; prolinase; prolyl dipeptidase; prolylglycine dipeptidase; L-prolylglycine dipeptidase; diglycinase; Gly-Leu hydrolase; glycyl-L-leucine dipeptidase; glycyl-L-leucine hydrolase; glycyl-L-leucine peptidase; L-amino-acyl-L-amino-acid hydrolase; glycyleucine peptidase; glycyleucine hydrolase; glycyleucine dipeptide hydrolase; non-specific dipeptidase; human cytosolic non-specific dipeptidase
Comments: A zinc enzyme with broad specificity, varying somewhat with source species. Activated and stabilized by dithiothreitol and Mn^{2+}. Inhibited by bestatin and leucine.
References: [187]

[EC 3.4.13.18 created 1961 as EC 3.4.3.1 and EC 3.4.3.2, transferred 1972 to EC 3.4.13.1 and EC 3.4.13.2, transferred 1978 to EC 3.4.13.11, part transferred 1992 to EC 3.4.13.18, modified 2000 (EC 3.4.13.15 created 1989, incorporated 1992)]

EC 3.4.13.19

Accepted name: membrane dipeptidase
Reaction: Hydrolysis of dipeptides
Other name(s): renal dipeptidase; dehydropeptidase I (DPH I); dipeptidase (ambiguous); aminodipeptidase; dipeptidyl hydrolase (ambiguous); dipeptidyl hydrolase (ambiguous); nonspecific dipeptidase; glycosyl-phosphatidylinositol-anchored renal dipeptidase; MDP
References: [389, 390, 1628, 1246]

[EC 3.4.13.19 created 1961 as EC 3.4.3.1 and EC 3.4.3.2, transferred 1972 to EC 3.4.13.1 and EC 3.4.13.2, transferred 1978 to EC 3.4.13.11, part transferred 1992 to EC 3.4.13.18, modified 2000 (EC 3.4.13.15 created 1989, incorporated 1992)]

EC 3.4.13.20

Accepted name: β-Ala-His dipeptidase
Reaction: Preferential hydrolysis of the β-Ala-His dipeptide (carnosine), and also anserine, Xaa-His dipeptides and other dipeptides including homocarnosine
Other name(s): serum carnosinase


References: [1737, 1367]

[EC 3.4.13.20 created 1992]

EC 3.4.13.21

Accepted name: dipeptidase E

Reaction: Dipeptidase E catalyses the hydrolysis of dipeptides Asp-Xaa. It does not act on peptides with N-terminal Glu, Asn or Gln, nor does it cleave isoaspartyl peptides

Other name(s): aspartyl dipeptidase; peptidase E; PepE gene product (Salmonella typhimurium)

Comments: A free carboxy group is not absolutely required in the substrate since Asp-Phe-NH$_2$ and Asp-Phe-OMe are hydrolysed somewhat more slowly than dipeptides with free C-terminals. No peptide larger than a C-blocked dipeptide is known to be a substrate. Asp-NH-Np is hydrolysed and is a convenient substrate for routine assay. The enzyme is most active near pH 7.0, and is not inhibited by diisopropylfluorophosphate or phenylmethanesulfonyl fluoride. Belongs in peptidase family S51.

References: [1071, 1701]

[EC 3.4.13.21 created 2001]

EC 3.4.13.22

Accepted name: D-Ala-D-Ala dipeptidase

Reaction: D-Ala-D-Ala + H$_2$O $\rightarrow$ 2 D-Ala

Other name(s): D-alanyl-D-alanine dipeptidase; vanX D-Ala-D-Ala dipeptidase; VanX

Comments: A Zn$^{2+}$-dependent enzyme [364]. The enzyme protects Enterococcus faecium from the antibiotic vancomycin, which can bind to the D-Ala-D-Ala sequence at the C-terminus of the peptidoglycan pentapeptide (see diagram). This enzyme reduces the availability of the free dipeptide D-Ala-D-Ala, which is the precursor for this pentapeptide sequence, allowing D-Ala-(R)-lactate (for which vancomycin has much less affinity) to be added to the cell wall instead [3378, 1957]. The enzyme is stereospecific, as l-Ala-l-Ala, D-Ala-l-Ala and L-Ala-D-Ala are not substrates [3378]. Belongs in peptidase family M15.

References: [2540, 3378, 1957, 364, 3010, 1943]

[EC 3.4.13.22 created 2006]

EC 3.4.13.23

Accepted name: cysteinylglycine-S-conjugate dipeptidase

Reaction: an [L-cysteinylglycine]-S-conjugate + H$_2$O = an l-cysteine-S-conjugate + glycine

Other name(s): tpdA (gene name); LAP3 (gene name)

Systematic name: cysteinylglycine-S-conjugate dipeptide hydrolase

Comments: The enzyme participates in a widespread glutathione-mediated detoxification pathway. In animals the activity is usually catalysed by enzymes that have numerous additional activities, such as EC 3.4.11.1, leucyl aminopeptidase, EC 3.4.11.2, membrane alanly aminopeptidase, and EC 3.4.13.19, membrane dipeptidase. However, in the bacterium Corynebacterium sp. Ax20, which degrades axillary secretions, the enzyme appears to be specific for this task.

References: [923, 2495, 1222, 1423, 747]

[EC 3.4.13.23 created 2019]
EC 3.4.14 Dipeptidyl-peptidases and tripeptidyl-peptidases

EC 3.4.14.1

Accepted name: dipeptidyl-peptidase I

Reaction: Release of an N-terminal dipeptide, Xaa-Yaa—Zaa—, except when Xaa is Arg or Lys, or Yaa or Zaa is Pro.

Other name(s): cathepsin C; dipeptidyl aminopeptidase I; dipeptidyl transferase; dipeptide arylamidase I; DAP I

Comments: A Cl⁻-dependent, lysosomal cysteine-type peptidase maximally active at acidic pH. Also polymerizes dipeptide amides, arylamides and esters at neutral pH. In peptidase family C1 (papain family).

References: [2409, 1988, 1966, 1965]

EC 3.4.14.2

Accepted name: dipeptidyl-peptidase II

Reaction: Release of an N-terminal dipeptide, Xaa-Yaa, preferentially when Yaa is Ala or Pro. Substrates are oligopeptides, preferentially tripeptides.

Other name(s): dipeptidyl aminopeptidase II; dipeptidyl arylamidase II; carboxytripeptidase; dipeptidyl peptidase II; DAP II; dipeptidyl(amino)peptidase II; dipeptidylarylamidase

Comments: A lysosomal serine-type peptidase in family S28 (Pro-X carboxypeptidase family); maximally active at acidic pH

References: [1964, 1965]

EC 3.4.14.3

Accepted name: dipeptidyl-peptidase III

Reaction: Release of an N-terminal dipeptide from a peptide comprising four or more residues, with broad specificity. Also acts on dipeptidyl 2-naphthylamides.

Other name(s): dipeptidyl aminopeptidase III; dipeptidyl arylamidase III; enkephalinase B; red cell angiotensinase

Comments: A cytosolic peptidase that is active at neutral pH. It has broad activity on peptides, although it is highly selective for Arg-Arg-2-naphthylamide, at pH 9.2. Active in the hydrolysis of enkephalins. A metallopeptidase, the type example of peptidase family M49.

References: [1962, 908]

EC 3.4.14.4

Accepted name: dipeptidyl-peptidase IV

Reaction: Release of an N-terminal dipeptide, Xaa-Yaa—Zaa—, from a polypeptide, preferentially when Yaa is Pro, provided Zaa is neither Pro nor hydroxyproline.

Other name(s): dipeptidyl aminopeptidase IV; Xaa-Pro-dipeptidyl-aminopeptidase; Gly-Pro naphthylamidase; post-proline dipeptidyl aminopeptidase IV; lymphocyte antigen CD26; glycoprotein GP110; dipeptidyl peptidase IV; glycylproline aminopeptidase; X-prolyl dipeptidyl aminopeptidase; pep X; leucocyte antigen CD26; glycylprolyl dipeptidylaminopeptidase; dipeptidyl-peptide hydrolase; glycyl-prolyl aminopeptidase; dipeptidyl-aminopeptidase IV; DPP IV/CD26; amino acyl-prolyl dipeptidyl aminopeptidase; T cell triggering molecule Tp103; X-PDAP

References: [EC 3.4.14.4 created 1981, modified 2001]
Comments: A homodimer. An integral protein of the plasma membrane of lymphocytes and other mammalian cells, in peptidase family S9 (prolyl oligopeptidase family). The reaction is similar to that of the unrelated EC 3.4.14.11 Xaa-Pro dipeptidyl-peptidase of lactococci

References: [2029, 585, 1308]

[EC 3.4.14.5 created 1981, modified 1996]

EC 3.4.14.6
Accepted name: dipeptidyl-dipeptidase
Reaction: Preferential release of dipeptides from a tetrapeptide, e.g. Ala-Gly→Ala-Gly. Acts more slowly on Ala-Ala→Ala-Ala and Gly-Gly→Gly-Gly
Other name(s): dipeptidyl tetrapeptide hydrolase; dipeptidyl ligase; tetrapeptide dipeptidase
Comments: A thiol-activated peptidase from cabbage (Brassica oleracea). Tetrapeptides are formed from Ala-Ala, Gly-Gly, Ala-Gly and Gly-Ala
References: [751]

[EC 3.4.14.6 created 1989]

[3.4.14.7 Deleted entry. tetralysine endopeptidase]

[EC 3.4.14.7 created 1989, deleted 1992]


[EC 3.4.14.8 created 1989, deleted 1992]

EC 3.4.14.9
Accepted name: tripeptidyl-peptidase I
Reaction: Release of an N-terminal tripeptide from a polypeptide, but also has endopeptidase activity.
Other name(s): tripeptidyl aminopeptidase; tripeptidyl peptidase
References: [781, 2508, 780, 1430, 1788]


EC 3.4.14.10
Accepted name: tripeptidyl-peptidase II
Reaction: Release of an N-terminal tripeptide from a polypeptide
Other name(s): tripeptidyl aminopeptidase; tripeptidyl peptidase; tripeptidyl aminopeptidase II; tripeptidyl peptidase II; TPP
Comments: A cytosolic enzyme in peptidase family S8 (subtilisin family). Active at neutral pH. Inhibited by diisopropyl fluorophosphate. Formerly included in EC 3.4.14.8
References: [145, 146, 3081]


EC 3.4.14.11
Accepted name: Xaa-Pro dipeptidyl-peptidase
Reaction: Hydrolyses Xaa-Pro→ bonds to release unblocked, N-terminal dipeptides from substrates including Ala-Pro→p-nitroanilide and (sequentially) Tyr-Pro→Phe-Pro→Gly-Pro→Ile
Other name(s): X-prolyl dipeptidyl aminopeptidase; PepX; X-prolyl dipeptidyl peptidase; X-Pro dipeptidyl-peptidase
Comments: The intracellular enzyme from Lactococcus lactis (190-kDa) is the type example of peptidase family S15. The reaction is similar to that catalysed by dipeptidyl-peptidase IV of animals
EC 3.4.14.12

Accepted name: Xaa-Xaa-Pro tripeptidyl-peptidase

Reaction: Hydrolysis of Xaa-Xaa-Pro+Yaa- releasing the N-terminal tripeptide of a peptide with Pro as the third residue (position P1) and where Yaa is not proline

Other name(s): prolyltripeptidyl amino peptidase; prolyl tripeptidyl peptidase; prolyltripeptidyl aminopeptidase; PTP-A; TPP

Comments: This cell-surface-associated serine exopeptidase is found in the Gram-negative, anaerobic bacterium Porphyromonas gingivalis, which has been implicated in adult periodontal disease [148]. The enzyme releases the N-terminal tripeptide of peptides, such as interleukin-6. It has an absolute requirement for a proline residue at the P1 position but is completely inactivated by a proline residue at the P1′ position [148]. The size of the peptide does not affect the rate of reaction [148].

References: [148, 895]

[EC 3.4.14.12 created 2006]

EC 3.4.14.13

Accepted name: γ-D-glutamyl-L-lysine dipeptidyl-peptidase

Reaction: The enzyme releases L-Ala-γ-D-Glu dipeptides from cell wall peptides via cleavage of an L-Ala-γ-D-Glu+L-Lys bond.

Other name(s): YkfC

Comments: The enzyme, characterized from the bacterium Bacillus subtilis, is involved in the recycling of the murein peptide.

References: [2703, 3390]

[EC 3.4.14.13 created 2015]

EC 3.4.14.14

Accepted name: [mycofactocin precursor peptide] peptidase

Reaction: C-terminal [mycofactocin precursor peptide]-glycyl-3-amino-5-[(4-hydroxyphenyl)methyl]-4,4-dimethylpyrrolidin-2-one + H₂O = C-terminal [mycofactocin precursor peptide]-glycine + 3-amino-5-[(4-hydroxyphenyl)methyl]-4,4-dimethylpyrrolidin-2-one

Other name(s): mftE (gene name)

Systematic name: C-terminal [mycofactocin precursor peptide]-glycyl-3-amino-5-[(4-hydroxyphenyl)methyl]-4,4-dimethylpyrrolidin-2-one 3-amino-5-[(4-hydroxyphenyl)methyl]-4,4-dimethylpyrrolidin-2-one hydrolyase

Comments: Requires Fe²⁺ ad Zn²⁺. The enzyme participates in the biosynthesis of the enzyme cofactor mycofactocin. It catalyses cleavage of the mycofactocin precursor peptide following its modification by MftC to liberate its final two residues, which consist of a cross-linked valine-tyramine dipeptide.

References: [345, 115]

[EC 3.4.14.14 created 2021]

EC 3.4.15 Peptidyl-dipeptidases

EC 3.4.15.1

Accepted name: peptidyl-dipeptidase A
**Reaction:** Release of a C-terminal dipeptide, oligopeptide-Xaa-Yaa, when Xaa is not Pro, and Yaa is neither Asp nor Glu. Thus, conversion of angiotensin I to angiotensin II, with increase in vasoconstrictor activity, but no action on angiotensin II

**Other name(s):** dipeptidyl carboxypeptidase I; peptidase P; dipeptide hydrolase (ambiguous); peptidyl dipeptidase; angiotensin converting enzyme; kininase II; angiotensin I-converting enzyme; carboxycathepsin; dipeptidyl carboxypeptidase; peptidyl dipeptidase I; peptidyl-dipeptidase hydrolase; endothelial cell peptidyl dipeptidase; ACE; peptidyl dipeptidase-4; PDH; peptidyl dipeptide hydrolase; DCP

**Comments:** A Cl$^-$-dependent, zinc glycoprotein that is generally membrane-bound. A potent inhibitor is captopril. Important in elevation of blood pressure, through formation of angiotensin II (vasoconstrictor) and destruction of bradykinin (vasodilator). Two molecular forms exist in mammalian tissues, a widely-distributed somatic form of 150- to 180-kDa that contains two non-identical catalytic sites, and a testicular form of 90- to 100-kDa that contains only a single catalytic site. Type example of peptidase family M2

**References:** [2869, 726, 3299, 531]


**[3.4.15.2] Transferred entry. peptidyl carboxyamidase. Now EC 3.4.19.2, peptidyl-glycinamidase**

[EC 3.4.15.2 created 1978, deleted 1981]

**[3.4.15.3] Transferred entry. dipeptidyl carboxypeptidase. Now EC 3.4.15.5, peptidyl-dipeptidase Dcp**

[EC 3.4.15.3 created 1981, modified 1989, deleted 1996]

**EC 3.4.15.4**

**Accepted name:** peptidyl-dipeptidase B

**Reaction:** Release of a C-terminal dipeptide or exceptionally a tripeptide

**Other name(s):** dipeptidyl carboxyhydrolase; atriopeptin convertase; atrial di-(tri)peptidyl carboxyhydrolase; peptidyl-dipeptidase B; atrial dipeptidyl carboxyhydrolase; atrial peptide convertase

**Comments:** A membrane-bound, zinc metallopeptidase located in mammalian atrial, but not ventricular, myocytes. Although it is capable of converting the 126-residue atriopeptin III directly to atriopeptin I by releasing a C-terminal tripeptide Phe-Arg-Tyr, it is generally restricted to the release of dipeptides. In contrast to peptidyl-dipeptidase A (EC 3.4.15.1) it displays no Cl$^-$ dependence and shows no action on angiotensin I. Conversely, peptidyl-dipeptidase A is unable to release Phe-Arg from the C-terminus of atriopeptin II

**References:** [1123, 1124, 2851, 2852]

[EC 3.4.15.4 created 1992]

**EC 3.4.15.5**

**Accepted name:** peptidyl-dipeptidase Dcp

**Reaction:** Hydrolysis of unblocked, C-terminal dipeptides from oligopeptides, with broad specificity. Does not hydrolyse bonds in which P1’ is Pro, or both P1 and P1’ are Gly

**Other name(s):** dipeptidyl carboxypeptidase (Dcp); dipeptidyl carboxypeptidase

**Comments:** Known from *Escherichia coli* and *Salmonella typhimurium*. A zinc metallopeptidase in peptidase family M3 (thimet oligopeptidase family). Ac-Ala-Ala-Ala-Ala is a good test substrate [514]. Inhibited by captopril, as is peptidyl-dipeptidase A. Formerly EC 3.4.15.3, and included in EC 3.4.15.1, peptidyl-dipeptidase A.

**References:** [3425, 1183, 514]

[EC 3.4.15.5 created 1981 as EC 3.4.15.3, modified 1989, transferred 1996 to EC 3.4.15.5]
EC 3.4.15.6

Accepted name: cyanophycinase

Reaction: \[\text{[L-Asp(4-L-Arg)]\textsubscript{n} + H\textsubscript{2}O = [L-Asp(4-L-Arg)]\textsubscript{n-1} + L-Asp(4-L-Arg)}\]

Other name(s): cyanophycin degrading enzyme; β-Asp-Arg hydrolysing enzyme; CGPase; CphB; CphE; cyanophycin granule polypeptidase; extracellular CGPase

Comments: The enzyme is highly specific for the branched polypeptide cyanophycin and does not hydrolyse poly-L-aspartate or poly-L-arginine [2550]. A serine-type exopeptidase that belongs in peptidase family S51.

References: [2234, 2235, 2550]

[EC 3.4.15.6 created 2007]

EC 3.4.16 Serine-type carboxypeptidases

3.4.16.1 Transferred entry. serine carboxypeptidase. Now EC 3.4.16.6, carboxypeptidase D

[EC 3.4.16.1 created 1972 as EC 3.4.12.1 and EC 3.4.21.13, both transferred 1978 to EC 3.4.16.1, deleted 1993]

EC 3.4.16.2

Accepted name: lysosomal Pro-Xaa carboxypeptidase

Reaction: Cleavage of a-Pro-Xaa bond to release a C-terminal amino acid

Other name(s): angiotensinase C; lysosomal carboxypeptidase C; peptidylprolylamino acid carboxypeptidase; aminoacylproline carboxypeptidase; prolyl carboxypeptidase; carboxypeptidase P; proline-specific carboxypeptidase P; PCP

Comments: A lysosomal peptidase active at acidic pH that inactivates angiotensin II. Inhibited by diisopropyl fluorophosphate. In peptidase family S28 (Pro-X carboxypeptidase family).

References: [3253, 2248]

[EC 3.4.16.2 created 1972 as EC 3.4.12.4, transferred 1978 to EC 3.4.16.2]

3.4.16.3 Transferred entry. tyrosine carboxypeptidase. Now included with EC 3.4.16.5, carboxypeptidase C

[EC 3.4.16.3 created 1972 as EC 3.4.12.12, transferred 1978 to EC 3.4.16.3, deleted 1992]

EC 3.4.16.4

Accepted name: serine-type D-Ala-D-Ala carboxypeptidase

Reaction: Preferential cleavage: (Ac)\textsubscript{2}-L-Lys-D-Ala-D-Ala. Also transpeptidation of peptidyl-alanyl moieties that are N-acyl substituents of D-alanine

Other name(s): DD-peptidase; D-alanyl-D-alanine-carboxypeptidase; D-alanyl-D-alanine-cleaving-peptidase; D-alanyl-D-alanine-cleaving peptidase; DD-transpeptidase; D-alanine carboxypeptidase; DD-carboxypeptidase; D-alanyl carboxypeptidase

Comments: A membrane-bound, bacterial enzyme inhibited by penicillin and other β-lactam antibiotics, which acylate the active site serine. Examples are known from peptidase families S11, S12 and S13. Distinct from EC 3.4.17.14, zinc D-Ala-D-Ala carboxypeptidase

References: [963, 862]

[EC 3.4.16.4 created 1989]

EC 3.4.16.5

Accepted name: carboxypeptidase C

Reaction: Release of a C-terminal amino acid with broad specificity

Other name(s): carboxypeptidase Y; serine carboxypeptidase I; cathepsin A; lysosomal protective protein; deamidase; lysosomal carboxypeptidase A; phaseolin
Comments: A carboxypeptidase with optimum pH 4.5–6.0, inhibited by diisopropyl fluorophosphate, and sensitive to thiol-blocking reagents (reviewed in [311]). Widely distributed in eukaryotes. Type example of peptidase family S10.

References: [311, 3179, 1364, 2012]

[EC 3.4.16.5 created 1972 as EC 3.4.12.1, transferred 1978 to EC 3.4.16.1, part transferred 1993 to EC 3.4.16.5 (EC 3.4.16.3 created 1972 as EC 3.4.12.12, transferred 1978 to EC 3.4.16.3, transferred 1992 to EC 3.4.16.1), (EC 3.4.21.13 created 1972, transferred 1978 to EC 3.4.16.1)]

EC 3.4.16.6

Accepted name: carboxypeptidase D

Reaction: Preferential release of a C-terminal arginine or lysine residue

Other name(s): cereal serine carboxypeptidase II; Saccharomyces cerevisiae KEX1 gene product; carboxypeptidase Kex1; gene KEX1 serine carboxypeptidase; KEX1 carboxypeptidase; KEX1 proteinase; KEX1DELTA; CPDW-II; serine carboxypeptidase (misleading); Phaseolus proteinase

Comments: A carboxypeptidase with optimum pH 4.5-6.0, inhibited by diisopropyl fluorophosphatase, and sensitive to thiol-blocking reagents (reviewed in [311]). In peptidase family S10 (carboxypeptidase C family).

References: [311, 313, 665, 1770]

[EC 3.4.16.6 created 1972 as EC 3.4.12.1, transferred 1978 to EC 3.4.16.1, part transferred 1993 to EC 3.4.16.6 (EC 3.4.16.3 created 1972 as EC 3.4.12.12, transferred 1978 to EC 3.4.16.3, transferred 1992 to EC 3.4.16.1), modified 2011]

EC 3.4.17 Metallocarboxypeptidases

EC 3.4.17.1

Accepted name: carboxypeptidase A

Reaction: Release of a C-terminal amino acid, but little or no action with -Asp, -Glu, -Arg, -Lys or -Pro

Other name(s): carboxypolypeptidase; pancreatic carboxypeptidase A; tissue carboxypeptidase A

Comments: A zinc enzyme formed from procarboxypeptidase A. Isolated from cattle, pig and dogfish pancreas, and other sources including mast cells [777] and skeletal muscle [277]. Type example of peptidase family M14.

References: [2385, 2520, 777, 277]

[EC 3.4.17.1 created 1961 as EC 3.4.2.1, transferred 1972 to EC 3.4.12.2, transferred 1978 to EC 3.4.17.1]

EC 3.4.17.2

Accepted name: carboxypeptidase B

Reaction: Preferential release of a C-terminal lysine or arginine amino acid

Other name(s): protaminase; pancreatic carboxypeptidase B; tissue carboxypeptidase B; peptidyl-lysine [L-arginine] hydrolase

Comments: A zinc enzyme formed from procarboxypeptidase B. Isolated from cattle, pig and dogfish pancreas and other sources, including skin fibroblasts [367] and adrenal medulla [3249]. In peptidase family M14 (carboxypeptidase A family).

References: [840, 328, 367, 3249]

[EC 3.4.17.2 created 1961 as EC 3.4.2.2, transferred 1972 to EC 3.4.12.3, transferred 1978 to EC 3.4.17.2]

EC 3.4.17.3

Accepted name: lysine carboxypeptidase

Reaction: Release of a C-terminal basic amino acid, preferentially lysine
Other name(s): carboxypeptidase N; arginine carboxypeptidase; kininase I; anaphylatoxin inactivator; plasma carboxypeptidase B; creatine kinase conversion factor; bradykinase; kininase Ia; hippuryllysine hydrolase; bradykinin-decomposing enzyme; protaminase; CPase N; creatinine kinase convertase; peptidyl-L-lysine(-L-arginine) hydrolase; CPN

Comments: A zinc enzyme found in plasma. Inactivates bradykinin and anaphylatoxins in blood plasma. In peptidase family M14 (carboxypeptidase A family).

References: [2412, 1747, 2820]

[EC 3.4.17.3 created 1972 as EC 3.4.12.7, transferred 1978 to EC 3.4.17.3, modified 1989]

EC 3.4.17.4
Accepted name: Gly-Xaa carboxypeptidase
Reaction: Release of a C-terminal amino acid from a peptide in which glycine is the penultimate amino acid, e.g. Z-Gly-Leu
Other name(s): glycine carboxypeptidase; carboxypeptidase a; carboxypeptidase S; peptidase α; yeast carboxypeptidase; Gly-X carboxypeptidase
Comments: From yeast. In peptidase family M20 (glutamate carboxypeptidase family).
References: [803, 3360]

[EC 3.4.17.4 created 1961 as EC 3.4.2.3, transferred 1972 to EC 3.4.12.8, transferred 1978 to EC 3.4.17.4 (EC 3.4.17.9 created 1981, incorporated 1992)]

3.4.17.5 Deleted entry. aspartate carboxypeptidase]

[EC 3.4.17.5 created 1972 as EC 3.4.12.9, transferred 1978 to EC 3.4.17.5, deleted 1992]

EC 3.4.17.6
Accepted name: alanine carboxypeptidase
Reaction: Release of a C-terminal alanine from a peptide or a variety of pteroyl or acyl groups
Other name(s): N-benzyol-L-alanine-amidohydrolase
Comments: From soil bacteria. The enzyme from Corynebacterium equi also hydrolysates N-benzoyleglycine and N-benzyol-L-aminobutyric acid.
References: [1750, 2035]

[EC 3.4.17.6 created 1972 as EC 3.4.12.11, transferred 1978 to EC 3.4.17.6]

3.4.17.7 Transferred entry. acylmuramoyl-alanine carboxypeptidase. Now EC 3.5.1.28, N-acetylmuramoyl-L-alanine amidase]

[EC 3.4.17.7 created 1978, deleted 1992]

EC 3.4.17.8
Accepted name: muramylpentapeptide carboxypeptidase
Reaction: Cleavage of the bond UDP-N-acetylmuramoyl-L-alanyl-γ-D-glutamyl-6-carboxy-L-lysyl-D-alanyl-D-alanine
Other name(s): D-alanine carboxypeptidase I; DD-carboxypeptidase; D-alanine carboxypeptidase; D-alanyl-D-alanine carboxypeptidase; D-alanine-D-alanine-carboxypeptidase; carboxypeptidase D-alanyl-D-alanine; carboxypeptidase D; UDP-N-acetylmuramoyl-tetrapeptidyl-D-alanine alanine-hydrolase; D-alanyl-D-alanine peptidase; DD-peptidase; penicillin binding protein 5; PBPs; PdCAs; VanY
References: [1362]

[EC 3.4.17.8 created 1972 as EC 3.4.12.6, transferred 1978 to EC 3.4.17.8]
EC 3.4.17.10
Accepted name: carboxypeptidase E
Reaction: Release of C-terminal arginine or lysine residues from polypeptides
Other name(s): carboxypeptidase H; enkephalin convertase; cobalt-stimulated chromaffin granule carboxypeptidase; insulin granule-associated carboxypeptidase; enkephalin convertase; membrane-bound carboxypeptidase; carboxypeptidase E; enkephalin-precursor endopeptidase; enkephalin precursor carboxypeptidase; peptidyl-L-lysine(-L-arginine) hydrolase
References: [2455, 870, 869, 1901, 868]

EC 3.4.17.11
Accepted name: glutamate carboxypeptidase
Reaction: Release of C-terminal glutamate residues from a wide range of N-acylating moieties, including peptidyl, aminoacyl, benzoyl, benzylxycarbonyl, folyl and pteroyl groups
Other name(s): carboxypeptidase G; carboxypeptidase G\(_1\); carboxypeptidase G\(_2\); glutamyl carboxypeptidase; N-pteroyl-L-glutamate hydrolase
Comments: A zinc enzyme produced by pseudomonads, Flavobacterium sp. and Acinetobacter sp. Its ability to hydrolyse pteroyl-L-glutamate (folic acid) has led to its use as a folate-depleting, antitumour agent. Type example of peptidase family M20
References: [1001, 1961, 32, 2762]

EC 3.4.17.12
Accepted name: carboxypeptidase M
Reaction: Cleavage of C-terminal arginine or lysine residues from polypeptides
Other name(s): CPM
Comments: A membrane-bound enzyme optimally active at neutral pH. In peptidase family M14 (carboxypeptidase A family)
References: [2821, 608, 2822]

EC 3.4.17.13
Accepted name: muramoyltetrapeptide carboxypeptidase
Other name(s): carboxypeptidase IIW; carboxypeptidase II; lysyl-D-alanine carboxypeptidase; L-lysyl-D-alanine carboxypeptidase; LD-carboxypeptidase
Comments: Variants are known from various microorganisms. Involved in peptidoglycan synthesis, catalysing both decarboxylation and transpeptidation. Stimulated by divalent cations such as Mg\(^{2+}\) and Ca\(^{2+}\), but not by Zn\(^{2+}\). Inhibited by thiol-blocking reagents, but unaffected by penicillin
References: [581, 2594, 1990]
EC 3.4.17.14
Accepted name: zinc D-Ala-D-Ala carboxypeptidase
Reaction: Cleavage of the bond: (Ac)₂-L-lysyl-D-alanyl-D-alanine
Other name(s): Zn²⁺ G peptidase; D-alanyl-D-alanine hydrolase; D-alanyl-D-alanine-cleaving carboxypeptidase; DD-carboxypeptidase; G enzyme; DD-carboxypeptidase-transpeptidase
References: [649, 1422, 963]

[EC 3.4.17.14 created 1992]

EC 3.4.17.15
Accepted name: carboxypeptidase A₂
Reaction: Similar to that of carboxypeptidase A (EC 3.4.17.1), but with a preference for bulkier C-terminal residues
Other name(s): CPA2
References: [935]

[EC 3.4.17.15 created 1992]

EC 3.4.17.16
Accepted name: membrane Pro-Xaa carboxypeptidase
Reaction: Release of a C-terminal residue other than proline, by preferential cleavage of a prolyl bond
Other name(s): carboxypeptidase P; microsomal carboxypeptidase; membrane Pro-X carboxypeptidase
Comments: One of the renal brush border exopeptidases
References: [611, 288, 1165]

[EC 3.4.17.16 created 1992]

EC 3.4.17.17
Accepted name: tubulinylt-Yr carboxypeptidase
Reaction: Cleavage of the -Glu-Tyr bond to release the C-terminal tyrosine residue from the native tyrosinated tubulin. Inactive on Z-Glu-Tyr
Other name(s): carboxypeptidase-tubulin; soluble carboxypeptidase; tubulin-tyrosine carboxypeptidase; tubulin-carboxypeptidase; tubulinyltirosine carboxypeptidase; tyrosinotubulin carboxypeptidase; tyrosyltubulin carboxypeptidase; TTCPase; brain I carboxypeptidase
Comments: Active at neutral pH, from brain
References: [2121, 1639, 74]

[EC 3.4.17.17 created 1992]

EC 3.4.17.18
Accepted name: carboxypeptidase T
Reaction: Releases a C-terminal residue, which may be hydrophobic or positively charged
Other name(s): CPT (ambiguous)
Comments: Known from Thermoactinomyces vulgaris. In peptidase family M14 (carboxypeptidase A family)
References: [2318, 2843, 3039]

[EC 3.4.17.18 created 1993]
EC 3.4.17.19
Accepted name: carboxypeptidase Taq
Reaction: Release of a C-terminal amino acid with broad specificity, except for -Pro
Comments: A 56-kDa enzyme from *Thermus aquaticus*. Most active at 80° C. Type example of peptidase family M32
References: [1718, 1719]

[EC 3.4.17.19 created 1996]

EC 3.4.17.20
Accepted name: carboxypeptidase U
Reaction: Release of C-terminal Arg and Lys from a polypeptide
Other name(s): arginine carboxypeptidase; carboxypeptidase R; plasma carboxypeptidase B (misleading, since the term carboxypeptidase B is used for other enzymes); thrombin-activatable fibrinolysis inhibitor
Comments: Pro-carboxypeptidase U in (human) plasma is activated by thrombin or plasmin during clotting to form the unstable carboxypeptidase U, with activity similar to that of the more stable lysine carboxypeptidase, except that no preference is shown for Lys over Arg. A zinc enzyme, in peptidase family M14 (carboxypeptidase A family)
References: [718, 2776, 3272, 3009, 341]

[EC 3.4.17.20 created 1997]

EC 3.4.17.21
Accepted name: glutamate carboxypeptidase II
Reaction: Release of an unsubstituted, C-terminal glutamyl residue, typically from Ac-Asp-Glu or folylpoly-γ-glutamates
Other name(s): N-acetylated-γ-linked-acidic dipeptidase (NAALADase); folate hydrolase; prostate-specific membrane antigen; pteroylpoly-γ-glutamate carboxypeptidase; microsomal γ-glutamyl carboxypeptidase; pteroylpolyglutamate hydrolase; pteroylpolyglutamic acid hydrolase; PSM antigen; acetyl-γ-glutarylglutamyl hydrolase; folate hydrolase; prostate-specific membrane antigen; pteroylpolyglutamate hydrolase; folate hydrolase; prostate-specific membrane antigen; pteroylpolyglutamate hydrolase; pteroylpolygammaglutamyl hydrolase; pteroylpolyglutamic acid hydrolase; PSM antigen; acetyl-γ-glutarylglutamyl hydrolase; folate hydrolase; prostate-specific membrane antigen; pteroylpolyglutamate hydrolase; PSM antigen
Comments: A metallo-carboxypeptidase that is predominantly expressed as a membrane-bound enzyme of 94-100 kDa, but also exists in a soluble form. Hydrolyses α-peptide bonds in Ac-Asp-Glu, Asp-Glu, and Glu-Glu, but also γ-glutamyl bonds in γ-Glu-Glu, and folylpoly-γ-glutamates. With folylpoly-γ-glutamates, shows processive carboxypeptidase activity to produce pteroylmonoglutamate [1856]. Does not hydrolyse Ac-β-Asp-Glu. Known inhibitors: quisqualic acid, Ac-β-Asp-Glu, and 2-phosphonomethyl-pentanedioate. In peptidase family M28 of *Vibrio* leucyl aminopeptidase. The release of C-terminal glutamate from folylpoly-γ-glutamates is also catalysed by EC 3.4.17.11 (glutamate carboxypeptidase) and EC 3.4.19.9 (folate γ-glutamyl hydrolase).
References: [1204, 2507, 1093, 1856]

[EC 3.4.17.21 created 1997, modified 2000 (EC 3.4.13.8 created 1972 and EC 3.4.19.8 created 1992, incorporated 2000)]

EC 3.4.17.22
Accepted name: metallo-carboxypeptidase D
Reaction: Releases C-terminal Arg and Lys from polypeptides
Other name(s): carboxypeptidase D (cattle, human, mouse, rat); gp180 (duck)
Comments: Activated by Co$^{2+}$; inhibited by [(2-guanidinoethyl)sulfanyl]butanedioate. Large molecule (180 kDa) because of presence of three copies of metallopeptidase domain. The product of the silver gene (*Drosophila*) is similar. A zinc metallopeptidase in peptidase family M14 (carboxypeptidase A family)
References: [1664, 2858, 2859]

[EC 3.4.17.22 created 1997]

EC 3.4.17.23

Accepted name: angiotensin-converting enzyme 2
Reaction: angiotensin II + H₂O → angiotensin-(1–7) + L-phenylalanine
Other name(s): ACE-2; ACE2; angiotensin converting enzyme 2; angiotensin converting enzyme-2; Tmem27
Comments: A transmembrane glycoprotein with an extracellular catalytic domain. Angiotensin-converting enzyme 2 functions as a carboxypeptidase, cleaving a single C-terminal residue from a distinct range of substrates [1686]. Catalytic efficiency is 400-fold higher with angiotensin II (1–8) as a substrate than with angiotensin I (1–10). Angiotensin-converting enzyme 2 also efficiently hydrolyses des-Arg⁹-bradykinin, but it does not hydrolyse bradykinin [3216]. In peptidase family M2.
References: [3216, 1686, 3098]

[EC 3.4.17.23 created 2009]

EC 3.4.17.24

Accepted name: tubulin-glutamate carboxypeptidase
Reaction: This is a subfamily of enzymes that cleave C-terminal and/or side chain amino acids from tubulins. The dual-specificity enzymes can cleave both α- and γ-linked L-glutamate from tubulins, removing the posttranslationally added polyglutamyl side chains from the C-terminal regions. In addition, the enzyme removes two glutamate residues from the C-terminus of β-tubulin and detyrosinated α-tubulin (from which the C-terminal L-tyrosine has been removed by EC 3.4.17.17, tubulinyl-Tyr carboxypeptidase). The latter is cleaved to δ2-tubulin and further to δ3-tubulin.
Other name(s): cytosolic carboxypeptidase 1; cytosolic carboxypeptidase 5; CCP1; CCP5; Agtpbp1 (gene name); AGBL5 (gene name)
References: [2579, 1544, 209, 208, 2356]

[EC 3.4.17.24 created 2020]

EC 3.4.17.25

Accepted name: glutathione-S-conjugate glycine hydrolase
Reaction: a glutathione-S-conjugate + H₂O → a [γ-glutamyl-L-cysteine]-S-conjugate + glycine
Other name(s): PCS1 (gene name); PRC1 (gene name); CPC (gene name); ATG42 (gene name); alr0975 (locus name)
Systematic name: glutathione-S-conjugate glycine hydrolase
Comments: The enzyme participates in a glutathione-mediated detoxification pathway found in plants, algae, fungi, and some bacteria. The enzymes from the plant Arabidopsis thaliana and the yeast Saccharomyces cerevisiae also catalyse the activity of EC 2.3.2.15, glutathione γ-glutamylcysteinyltransferase (phytochelatin synthase).
References: [194, 1053, 1111, 3125, 3222, 3379]

[EC 3.4.17.25 created 2021]

EC 3.4.18 Cysteine-type carboxypeptidases

EC 3.4.18.1

Accepted name: cathepsin X
Reaction: Release of C-terminal amino acid residues with broad specificity, but lacks action on C-terminal proline. Shows weak endopeptidase activity
Other name(s): cathepsin B2; cysteine-type carboxypeptidase; cathepsin IV; cathepsin Z; acid carboxypeptidase; lysosomal carboxypeptidase B

Comments: Cathepsin X is a lysosomal cysteine peptidase of family C1 (papain family). The pH optimum is dependent on the substrate and is 5.0 for the carboxypeptidase activity. Unstable above pH 7.0. Compound E-64, leupeptin and antipain are inhibitors, but not cystatin C. Cathepsin X is ubiquitously distributed in mammalian tissues. The propeptide is extremely short (38 amino acid residues) and the proenzyme is catalytically active. Human gene locus: 20q13.

References: [2130, 2129, 2653, 1963, 2326, 2198]

[EC 3.4.18.1 created 1981, modified 2000]

EC 3.4.19 Omega peptidases

EC 3.4.19.1

Accepted name: acylaminoacyl-peptidase
Reaction: Cleavage of an N-acetyl or N-formyl amino acid from the N-terminus of a polypeptide

Other name(s): acylamino-acid-releasing enzyme; N-acylpeptide hydrolase; N-formylmethionine (fMet) aminopeptidase; α-N-acylpeptide hydrolase

Comments: Active at neutral pH. Several variants of this enzyme exist; the human erythrocyte enzyme is relatively specific for removal of N-acetylalanine from peptides. Displays dipeptidyl-peptidase activity on glycyl-peptides, perhaps as a result of mis-recognition of the glycyl residue as an uncharged N-acyl group. Inhibited by diisopropyl fluorophosphate. In peptidase family S9 (prolyl oligopeptidase family).

References: [3133, 3161, 1577]

[EC 3.4.19.1 created 1978 as EC 3.4.14.3, transferred 1981 to EC 3.4.19.1]

EC 3.4.19.2

Accepted name: peptidyl-glycinamidase
Reaction: Cleavage of C-terminal glycaminamide from polypeptides

Other name(s): carboxyamidase; peptidyl carboxy-amidase; peptidyl-aminoacylamidase; carboxamidopeptidase; peptidyl amino acid amide hydrolase

Comments: Inactivates vasopressin and oxytocin by splitting off glycaminamide. Also cleaves ester substrates of trypsin and chymotrypsin. Although glycaminamide is by far the preferred leaving group, other aminocarboxylamides may also be released, e.g. phenylalaninamide. The toad skin enzyme is inhibited by diisopropyl fluorophosphate.

References: [877, 2160, 2803]

[EC 3.4.19.2 created 1978 as EC 3.4.15.2, transferred 1981 to EC 3.4.19.2]

EC 3.4.19.3

Accepted name: pyroglutamyl-peptidase I
Reaction: Release of an N-terminal pyroglutamyl group from a polypeptide, the second amino acid generally not being Pro

Other name(s): 5-oxoprolyl-peptidase; pyrase; pyroglutamate aminopeptidase; pyroglutamyl aminopeptidase; L-pyroglutamyl peptide hydrolase; pyrrolidone-carboxyl peptide peptidase; pyrrolidone-carboxylate peptidase; pyrrolidonyl peptidase; L-pyrrolidinocarboxylate peptidase; pyroglutamidase; pyrrolidonecarboxylyl peptidase

Comments: A cysteine peptidase, known from bacteria, plants and animals. The enzyme from bacterial sources is used in protein sequencing, and is the type example of peptidase family C15.

References: [3135, 114, 2362, 2668]

[EC 3.4.19.3 created 1972 as EC 3.4.11.8, transferred 1981 to EC 3.4.19.3, modified 1997]
EC 3.4.19.5

Accepted name: \( \beta \)-aspartyl-peptidase

Reaction: Cleavage of a \( \beta \)-linked Asp residue from the N-terminus of a polypeptide

Other name(s): \( \beta \)-aspartyl dipeptidase; \( \beta \)-aspartylpeptidase

Comments: Other isopeptide bonds, e.g. \( \gamma \)-glutamyl and \( \beta \)-alanyl, are not hydrolysed. A mammalian, cytosolic enzyme.

References: [1086]

[EC 3.4.19.5 created 1972 as EC 3.4.13.10, transferred 1992 to EC 3.4.19.5, modified 1997]

EC 3.4.19.6

Accepted name: pyroglutamyl-peptidase II

Reaction: Release of the N-terminal pyroglutamyl group from pGlu—His-Xaa tripeptides and pGlu—His-Xaa-Gly tetrapeptides

Other name(s): thyroliberinase; pyroglutamyl aminopeptidase II; thyrotropin-releasing factor pyroglutamate aminopeptidase; pyroglutamate aminopeptidase II; pyroglutamyl peptidase II; thyroliberin-hydrolyzing pyroglutamate aminopeptidase; thyrotropin-releasing hormone-degrading pyroglutamate aminopeptidase; thyrotropin-releasing hormone-degrading peptidase; TRH aminopeptidase


References: [188, 2237, 3339]

[EC 3.4.19.6 created 1992]

EC 3.4.19.7

Accepted name: \( N \)-formylmethionyl-peptidase

Reaction: Release of an N-terminal, formyl-methionyl residue from a polypeptide

Other name(s): (fMet)-releasing enzyme; formylmethionine aminopeptidase

Comments: Highly specific for \( N \)-formylmethionyl peptides. Will not cleave methionyl peptides or \( N \)-formyl derivatives of amino acids other than methionine. Isolated from rat liver. Inhibited by heavy metals and activated by \( \text{Cl}^- \)

References: [2927]

[EC 3.4.19.7 created 1992]

EC 3.4.19.9

Accepted name: folate \( \gamma \)-glutamyl hydrolase

Reaction: tetrahydropteroyl-(\( \gamma \)-glutamyl)\(_n\) + (\( n \)-1) \( \text{H}_2\text{O} = 5,6,7,8\)-tetrahydrofolate + (\( n \)-1) \( \text{L} \)-glutamate

Other name(s): GGH (gene name); conjugase; folate conjugase; lysosomal \( \gamma \)-glutamyl carboxypeptidase; \( \gamma \)-Glu-X carboxypeptidase; pteroyl-poly-\( \gamma \)-glutamate hydrolase; carboxypeptidase G; folic acid conjugase; poly(\( \gamma \)-glutamic acid) endohydrolase; polyglutamate hydrolase; poly(glutamic acid) hydrolase II; pteroylpoly-\( \gamma \)-glutamyl hydrolase; \( \gamma \)-glutamyl hydrolase

Systematic name: tetrahydropteroyl-poly-\( \gamma \)-glutamyl \( \gamma \)-glutamyl hydrolase

[EC 3.4.19.8 created 1992, deleted 2000]
Comments: The enzyme, which occurs only in animals and plants, can be either endo- and/or exopeptidase. It acts on tetrahydropteroyl polyglutamates and their modified forms, as well as the polyglutamates of the folate breakdown product N-(4-aminobenzoyl)-L-glutamate (pABA-Glu). The initial cleavage may release either monoglutamate or poly-γ-glutamate of two or more residues, depending on the specific enzyme. For example, GGH1 from the plant Arabidopsis thaliana cleaves pentaglutamates, mainly to di- and triglutamates, whereas GGH2 from the same organism yields mainly monoglutamates. The enzyme is lysosomal (and secreted) in animals and vacuolar in plants. In peptidase family C26.

References: [1969, 3275, 3422, 3423, 3421, 2314, 28]

[EC 3.4.19.9 created 1972 as EC 3.4.12.10, transferred 1978 to EC 3.4.22.12, transferred 1992 to EC 3.4.19.9, modified 1997, modified 2018]

[3.4.19.10 Transferred entry. acylmuramoyl-Ala peptidase. Now EC 3.5.1.28, N-acetylmuramoyl-L-alanine amidase]


EC 3.4.19.11
Accepted name: γ-D-glutamyl-meso-diaminopimelate peptidase
Reaction: Hydrolysis of γ-D-glutamyl bonds to the L-terminus (position 7) of meso-diaminopimelic acid (meso-A2pm) in 7-(L-Ala-γ-D-Glu)-meso-A2pm and 7-(L-Ala-γ-D-Glu)-7-(D-Ala)-meso-A2pm. It is required that the D-terminal amino and carboxy groups of meso-A2pm are unsubstituted
Other name(s): endopeptidase I; γ-D-glutamyl-diaminopimelate endopeptidase; γ-D-glutamyl-L-meso-diaminopimelate peptidoglycan hydrolase; γ-glutamyl-L-meso-diaminopimelyl endopeptidase; γ-D-glutamyl-meso-diaminopimelate endopeptidase; γ-D-glutamyl-meso-diaminopimelic peptidoglycan hydrolase; γ-D-glutamyl-meso-diaminopimelic endopeptidase
Comments: A 45-kDa metallopeptidase from Bacillus sphaericus, the substrates being components of the bacterial spore wall. A member of peptidase family M14 (carboxypeptidase A family). Endopeptidase II has similar activity, but differs in cellular location, molecular mass and catalytic mechanism [1262]
References: [79, 937, 1262]

[EC 3.4.19.11 created 1996]

EC 3.4.19.12
Accepted name: ubiquitinyl hydrolase I
Reaction: Thiol-dependent hydrolysis of ester, thioester, amide, peptide and isopeptide bonds formed by the C-terminal Gly of ubiquitin (a 76-residue protein attached to proteins as an intracellular targeting signal)
Other name(s): ubiquitin C-terminal hydrolase; yeast ubiquitin hydrolase
Comments: Links to polypeptides smaller than 60 residues are hydrolysed more readily than those to larger polypeptides. Isoforms exist with quantitatively different specificities, amongst the best known being UCH-L1 and UCH-L3, which are major proteins of the brain of mammals [1415]. Inhibited by ubiquitin aldehyde (in which Gly76 is replaced by aminoacetaldehyde). Ubiquitinyl hydrolase I is the type example of peptidase family C12, with a similar protein fold to papain and catalytic amino acids Cys, His and Asp. There is a separate family (C19) of enzymes that also hydrolyse ubiquitinyl bonds, and it is thought that all the ubiquitinyl hydrolases are also ubiquitin thiolesterases (EC 3.1.2.15)
References: [1415, 3343]

[EC 3.4.19.12 created 2000]

EC 3.4.19.13
Accepted name: glutathione γ-glutamate hydrolase
Reaction: (1) glutathione + H2O = L-cysteinylglycine + L-glutamate
(2) a glutathione-S-conjugate + H2O = an (L-cysteinylglycine)-S-conjugate + L-glutamate
Other name(s): glutathionase; γ-glutamyltranspeptidase (ambiguous); glutathione hydrolase; GGT (gene name); ECM38 (gene name)
Comments: This is a bifunctional protein that also has the activity of EC 2.3.2.2, γ-glutamyltransferase. The enzyme binds its substrate by forming an initial γ-glutamyl-enzyme intermediate, releasing the L-cysteinylglycine part of the molecule. The enzyme then reacts with either a water molecule or a different acceptor substrate (usually an L-amino acid or a dipeptide) to form L-glutamate or a product containing a new γ-glutamyl isopeptide bond, respectively. The enzyme acts on glutathione, glutathione-S-conjugates, and, at a lower level, on other substrates with an N-terminal L-γ-glutamyl residue. It plays a crucial part in the glutathione-mediated xenobiotic detoxification pathway. The enzyme consists of two chains that are created by the proteolytic cleavage of a single precursor polypeptide.

References: [1105, 406, 2952, 2288, 273, 2289, 1052, 3329, 1497]

[EC 3.4.19.13 created 2011, modified 2019]

**EC 3.4.19.14**

**Accepted name:** leukotriene-C<sub>4</sub> hydrolase

**Reaction:** leukotriene C<sub>4</sub> + H<sub>2</sub>O = leukotriene D<sub>4</sub> + L-glutamate

**Other name(s):** γ-glutamyl leukotrienase; GGT5

**Comments:** The mouse enzyme is specific for leukotriene C<sub>4</sub>, while the human enzyme also has considerable activity towards glutathione and oxidized glutathione (cf. EC 3.4.19.13, glutathione hydrolase) [1100, 3329].

References: [406, 2763, 1100, 3329]

[EC 3.4.19.14 created 2012]

**EC 3.4.19.15**

**Accepted name:** desampylase

**Reaction:** an N<sup>6</sup>-[small archaeal modifier protein]-[protein]-L-lysine + H<sub>2</sub>O = a [protein]-L-lysine + a small archaeal modifier protein

**Other name(s):** SAMP-protein conjugate cleaving protease; HvJAMM1

**Systematic name:** N<sup>6</sup>-[small archaeal modifier protein]-[protein]-L-lysine hydrolase

**Comments:** The enzyme, characterized from the archaeon *Halofex volcanii*, specifically cleaves the ubiquitin-like small modifier proteins SAMP1 and SAMP2 from protein conjugates, hydrolysing the isopeptide bond between a lysine residue of the target protein and the C-terminal glycine of the modifier protein. The enzyme contains Zn<sup>2+</sup>. cf. EC 3.4.19.12, ubiquitinyl hydrolase 1. In peptidase family M67.

References: [1189]

[EC 3.4.19.15 created 2015 as EC 3.4.24.88, transferred 2016 to EC 3.4.19.15]

**EC 3.4.19.16**

**Accepted name:** glucosinolate γ-glutamyl hydrolase

**Reaction:**

1. (E)-1-(glutathion-S-yl)-N-hydroxy-ω-(methyalsulfanyl)alkan-1-imine + H<sub>2</sub>O = an (E)-1-(L-cysteinylglycin-S-yl)-N-hydroxy-ω-(methylsulfanyl)alkan-1-imine + L-glutamate

2. (E)-1-(glutathion-S-yl)-N-hydroxy-2-(1H-indol-3-yl)ethan-1-imine + H<sub>2</sub>O = (E)-1-(L-cysteinylglycin-S-yl)-N-hydroxy-2-(1H-indol-3-yl)ethan-1-imine + L-glutamate

3. (glutathion-S-yl)(1H-indol-3-yl)acetonitrile + H<sub>2</sub>O = (L-cysteinylglycin-S-yl)(1H-indol-3-yl)acetonitrile + L-glutamate

4. (Z)-1-(glutathion-S-yl)-N-hydroxy-2-phenylethan-1-imine + H<sub>2</sub>O = (Z)-1-(L-cysteinylglycin-S-yl)-N-hydroxy-2-phenylethan-1-imine + L-glutamate

**Other name(s):** GGIP1 (gene name); GGIP3 (gene name)

**Comments:** This enzyme, characterized from the plant *Arabidopsis thaliana*, participates in the biosynthesis of the plant defense compounds glucosinolates and camalexin. It is the only known plant enzyme capable of hydrolysing the γ-glutamyl residue of glutathione in the cytosol.

References: [950]

[EC 3.4.19.16 created 2017]
EC 3.4.21 Serine endopeptidases

EC 3.4.21.1
Accepted name: chymotrypsin
Reaction: Preferential cleavage: Tyr⁺, Trp⁺, Phe⁺, Leu⁺
Other name(s): chymotrypsins A and B; α-chymar ophth; avazyme; chymar; chymotest; enzeon; quimar; quimotrase; α-chymar; α-chymotrypsin A; α-chymotrypsin
Comments: Chymotrypsin A is formed from cattle and pig chymotrypsinogen A, several iso-forms being produced according to the number of bonds hydrolysed in the precursor. Chymotrypsin B (formerly listed as EC 3.4.4.6), formed from chymotrypsinogen B, is homologous with chymotrypsin A. Enzymes with specificity similar to that of chymotrypsins A and B have been isolated from many species. In peptidase family S1 (trypsin family)
References: [3336, 270, 186, 2421, 3079]

[EC 3.4.21.1 created 1961 as EC 3.4.4.5 and EC 3.4.4.6, transferred 1972 to EC 3.4.21.1]

EC 3.4.21.2
Accepted name: chymotrypsin C
Reaction: Preferential cleavage: Leu⁺, Tyr⁺, Phe⁺, Met⁺, Trp⁺, Gln⁺, Asn⁺
Comments: Formed from pig chymotrypsinogen C, and from cattle subunit II of procarboxypeptidase A. Reacts more readily with Tos-Leu-CH2Cl than Tos-Phe-CH2Cl in contrast to chymotrypsin. In peptidase family S1 (trypsin family)
References: [2368, 841, 3336]

[EC 3.4.21.2 created 1972]

EC 3.4.21.3
Accepted name: metridin
Reaction: Preferential cleavage: Leu⁺, Tyr⁺, Phe⁺, Met⁺, Trp⁺, Gln⁺, Asn⁺
Other name(s): Metridium proteinase A; sea anemone protease A; sea anemone proteinase A
Comments: Digestive enzyme from the sea anemone Metridium senile.
References: [966, 2910]

[EC 3.4.21.3 created 1972]

EC 3.4.21.4
Accepted name: trypsin
Reaction: Preferential cleavage: Arg⁺, Lys⁺
Other name(s): α-trypsin; β-trypsin; cocoonase; parenzyme; parenzymol; tryptar; trypure; pseudotrypsin; tryptase; tripellim; sperm receptor hydrolase
Comments: The single polypeptide chain cattle β-trypsin is formed from trypsinogen by cleavage of one peptide bond. Further peptide bond cleavages produce α and other iso-forms. Isolated as multiple cationic and anionic trypsins [835] from the pancreas of many vertebrates and from lower species including crayfish, insects (cocoonase) and microorganisms (Streptomyces griseus) [2513]. Type example of peptidase family S1.
References: [1279, 3252, 2513, 815, 835, 2421, 3025]

[EC 3.4.21.4 created 1961 as EC 3.4.4.4, transferred 1972 to EC 3.4.21.4]

EC 3.4.21.5
Accepted name: thrombin
Reaction: Selective cleavage of Arg$\rightarrow$Gly bonds in fibrinogen to form fibrin and release fibrinopeptides A and B.

Other name(s): fibrinogenase; thrombase; thrombofot; topical; thrombin-C; tropostasin; activated blood-coagulation factor II; blood-coagulation factor IIa; factor IIa; E thrombin; β-thrombin; γ-thrombin.

Comments: Formed from prothrombin. More selective than trypsin and plasmin. In peptidase family S1 (trypsin family).

References: [189, 1870, 2013, 1851, 1897, 588, 474, 1862]

EC 3.4.21.6
Accepted name: coagulation factor Xa.

Reaction: Selective cleavage of Arg$\rightarrow$Thr and then Arg$\rightarrow$Ile bonds in prothrombin to form thrombin.

Other name(s): thrombokinase; prothrombase; prothrombinase; activated blood-coagulation factor X; autoprotrombin-C; thromboplastin; plasma thromboplastin; factor Xa; activated Stuart-Prower factor; activated factor X.

Comments: A blood coagulation factor formed from the proenzyme factor X by limited proteolysis. Factor X is a glycoprotein composed of a heavy chain and a light chain, which are generated from a precursor protein by the excision of the tripeptide RKR and held together by one or more disulfide bonds. The activated factor Xa converts prothrombin to thrombin in the presence of factor Va, Ca$^{2+}$ and phospholipids. Scutelarin (EC 3.4.21.60) has similar specificity, but does not require factor Va.

References: [888, 1401, 588, 1366, 1970, 474]

[EC 3.4.21.6 created 1972, modified 2011]

EC 3.4.21.7
Accepted name: plasmin.

Reaction: Selective cleavage of Arg$\rightarrow$Thr and then Arg$\rightarrow$Ile bonds in prothrombin to form thrombin.

Other name(s): fibrinase; fibrinolysin; actase; serum tryptase; thrombolysin.

Comments: Formed from plasminogen by proteolysis which results in multiple forms of the active plasmin. In peptidase family S1 (trypsin family).

References: [412, 411, 2560]

[EC 3.4.21.7 created 1961 as EC 3.4.4.14, transferred 1972 to EC 3.4.21.7]

EC 3.4.21.8

[3.4.21.8 Transferred entry. kallikrein. Now EC 3.4.21.34 (plasma kallikrein) and EC 3.4.21.35 (tissue kallikrein)]

[EC 3.4.21.8 created 1972, deleted 1981]

EC 3.4.21.9
Accepted name: enteropeptidase.

Reaction: Activation of trypsinogen by selective cleavage of Lys$^6$$\rightarrow$Ile bond.

Other name(s): enterokinase.

Comments: Is not inhibited by protein inhibitors of trypsin. In peptidase family S1 (trypsin family).

References: [1778]

[EC 3.4.21.9 created 1961 as EC 3.4.4.8, transferred 1972 to EC 3.4.21.9]

EC 3.4.21.10
Accepted name: acrosin.

Reaction: Preferential cleavage: Arg$\rightarrow$, Lys$\rightarrow$.

Other name(s): acrosomal proteinase; acrozonase; α-acrosin; β-acrosin; upsilon-acrosin; acrosomal protease; acrosin amidase.
Comments: Occurs in spermatozoa; formed from proacrosin by limited proteolysis. Inhibited by naturally occurring trypsin inhibitors. In peptidase family S1 (trypsin family)

References: [2103, 2823, 1498]

[EC 3.4.21.10 created 1972]

[3.4.21.11 Transferred entry. elastase. Now EC 3.4.21.37, leukocyte elastase]

[EC 3.4.21.11 created 1972, deleted 1981]

EC 3.4.21.12
Accepted name: α-lytic endopeptidase

Reaction: Preferential cleavage: Ala—, Val— in bacterial cell walls, elastin and other proteins

Other name(s): myxobacter α-lytic proteinase; α-lytic proteinase; α-lytic protease; Mycobacterium sorangium α-lytic proteinase; Myxobacter 495 α-lytic proteinase; Myxobacter α-lytic proteinase

Comments: From the myxobacterium Lysobacter enzymogenes. In peptidase family S1 (trypsin family)

References: [2304, 2421, 754, 287]

[EC 3.4.21.12 created 1972]

[3.4.21.13 Transferred entry. Phaseolus proteinase. Now EC 3.4.16.6, carboxypeptidase D]

[EC 3.4.21.13 created 1972, deleted 1978]

[3.4.21.14 Transferred entry. now EC 3.4.21.67 endopeptidase So]


[EC 3.4.21.15 created 1972, deleted 1978 (transferred to EC 3.4.21.14, deleted 1992)]

[3.4.21.16 Deleted entry. Alternaria serine proteinase]

[EC 3.4.21.16 created 1972, deleted 1992]

[3.4.21.17 Deleted entry. Arthrobacter serine proteinase]


[3.4.21.18 Deleted entry. Tenebrio α-proteinase]

[EC 3.4.21.18 created 1972 [EC 3.4.99.24 created 1972, incorporated 1978], deleted 1992]

EC 3.4.21.19
Accepted name: glutamyl endopeptidase

Reaction: Preferential cleavage: Glu—, Asp—

Other name(s): V8 proteinase; endoproteinase Glu-C; staphylococcal serine proteinase

Comments: From Staphylococcus aureus strain V8. In appropriate buffer the specificity is restricted to Glu—. In peptidase family S1 (trypsin family)

References: [690, 692, 404]

[EC 3.4.21.19 created 1978]

EC 3.4.21.20
Accepted name: cathepsin G

Reaction: Specificity similar to chymotrypsin C

Other name(s): chymotrypsin-like proteinase; neutral proteinase
Comments: From azurophil granules of polymorphonuclear leukocytes. In peptidase family S1 (trypsin family)
References: [169, 3021, 1232]

[EC 3.4.21.20 created 1978]

EC 3.4.21.21

Accepted name: coagulation factor VIIa
Reaction: Selective cleavage of Arg—Ile bond in factor X to form factor Xa
Other name(s): blood-coagulation factor VIIa; activated blood coagulation factor VII
Comments: Formed from the precursor factor VII. The cattle enzyme is more readily inhibited by diisopropyl fluorophosphate than the human [2175]. In peptidase family S1 (trypsin family)
References: [2175, 588, 1366, 342]

[EC 3.4.21.21 created 1978]

EC 3.4.21.22

Accepted name: coagulation factor IXa
Reaction: Selective cleavage of Arg—Ile bond in factor X to form factor Xa
Other name(s): activated Christmas factor; blood-coagulation factor IXa; activated blood-coagulation factor IX; autoprotrombin II; blood platelet cofactor II; activated blood coagulation factor XI
Comments: A chymotrypsin homologue, and one of the γ-carboxyglutamic acid-containing blood coagulation factors. The proenzyme factor IX is activated by factor XIa. In peptidase family S1 (trypsin family)
References: [887, 588, 1802, 474]

[EC 3.4.21.22 created 1978]

[3.4.21.23 Deleted entry. Vipera russelli proteinase]

[EC 3.4.21.23 created 1978, deleted 1992]

[3.4.21.24 Deleted entry. red cell neutral endopeptidase]

[EC 3.4.21.24 created 1978, deleted 1992]

EC 3.4.21.25

Accepted name: cucumisin
Reaction: Hydrolysis of proteins with broad specificity
Other name(s): euphorbain; solanain; hurain; tabernamontanain
Comments: From the sarcocarp of the musk melon (Cucumis melo). In peptidase family S8 (subtilisin family). Other endopeptidases from plants, which are less well characterized but presumably of serine-type, include euphorbain from Euphorbia cerifera [1857], solanain from horse-nettle Solanum elaeagnifolium [1028], hurain from Hura crepitans [1375] and tabernamontanain from Tabernamontana grandiflora [1374].
References: [1028, 1375, 1374, 1464, 1463, 1857, 1465]


EC 3.4.21.26

Accepted name: prolyl oligopeptidase
Reaction: Hydrolysis of —Pro— and to a lesser extent —Ala— in oligopeptides
Other name(s): post-proline cleaving enzyme; proline-specific endopeptidase; post-proline endopeptidase; proline endopeptidase; endoprollypeptidase; prolyl endopeptidase
**Comments:**
Found in vertebrates, plants and *Flavobacterium*. Generally cytosolic, commonly activated by thiol compounds. Type example of peptidase family S9.

**References:**
[3254, 2213, 2079, 2536]


**EC 3.4.21.27**

**Accepted name:** coagulation factor XIa

**Reaction:** Selective cleavage of Arg–Ala and Arg–Val bonds in factor IX to form factor IXa

**Other name(s):** blood-coagulation factor XIa; activated blood-coagulation factor XI; activated plasma thromboplastin antecedent

**Comments:** In peptidase family S1 (trypsin family), and one of the γ-carboxyglutamic acid-containing blood coagulation factors. The proenzyme factor XI is activated by factor XIIa

**References:**
[1653, 474, 886]

[EC 3.4.21.27 created 1978]


[EC 3.4.21.28 created 1978, deleted 1992]


[EC 3.4.21.29 created 1978, deleted 1992]


[EC 3.4.21.30 created 1978, deleted 1992]

[3.4.21.31] Transferred entry. urokinase. Now EC 3.4.21.73, u-plasminogen activator]

[EC 3.4.21.31 created 1972 as EC 3.4.99.26, transferred 1978 to EC 3.4.21.31, deleted 1992]

**EC 3.4.21.32**

**Accepted name:** brachyurin

**Reaction:** Hydrolysis of proteins, with broad specificity for peptide bonds. Native collagen is cleaved about 75% of the length of the molecule from the N-terminus. Low activity on small molecule substrates of both trypsin and chymotrypsin

**Other name(s):** *Uca pugilator* collagenolytic proteinase; crab protease I; crab protease II

**Comments:** From hepatopancreas of the fiddler crab, *Uca pugilator*. In peptidase family S1 (trypsin family). Other serine endopeptidases that degrade collagen, but are not listed separately here, include a second endopeptidase from *Uca pugilator* [3310], digestive enzymes from other decapod crustacea [1561, 1843], and an enzyme from the fungus *Entomophthora coronata* [1284].

**References:**
[1284, 1020, 3311, 3310, 1561, 1843]

[EC 3.4.21.32 created 1978]


[EC 3.4.21.33 created 1978, deleted 1992]

**EC 3.4.21.34**

**Accepted name:** plasma kallikrein

**Reaction:** Selective cleavage of some Arg| and Lys| bonds, including Lys|Arg and Arg|Ser in (human) kininogen to release bradykinin

192
Other name(s): serum kallikrein; kininogenin; kallikrein I; kallikrein II; kininogenase; kallikrein; callicrein; glumorin; padreatin; padutin; kallidinogenase; bradykininogenase; pancreatic kallikrein; onokrein P; dilminal D; depot-Padutin; urokallikrein; urinary kallikrein

Comments: Formed from plasma prokallikrein (Fletcher factor) by factor XIIa. Activates coagulation factors XII, VII and plasminogen. Selective for Arg > Lys in P1, in small molecule substrates.

References: [1169, 1972, 2800, 2741, 3123]

[EC 3.4.21.34 created 1965 as EC 3.4.4.21, transferred 1972 to EC 3.4.21.8, part transferred 1981 to EC 3.4.21.34]

EC 3.4.21.35
Accepted name: tissue kallikrein
Reaction: Preferential cleavage of Arg bonds in small molecule substrates. Highly selective action to release kallidin (lysyl-bradykinin) from kininogen involves hydrolysis of Met or Leu. The rat enzyme is unusual in liberating bradykinin directly from autologous kininogens by cleavage at two Arg bonds

Other name(s): glandular kallikrein; pancreatic kallikrein; submandibular kallikrein; submaxillary kallikrein; kidney kallikrein; urinary kallikrein; salivary kallikrein; kininogenin; kininogenase; callicrein; glumorin; padreatin; padutin; kallidinogenase; bradykininogenase; depot-padutin; urokallikrein; dilminal D; onokrein P

Comments: Formed from tissue prokallikrein by activation with trypsin. In peptidase family S1 (trypsin family). A large number of tissue kallikrein-related sequences have been reported for rats [3347] and mice [774], though fewer seem to exist in other mammals. The few that have been isolated and tested on substrates include mouse γ-renin (EC 3.4.21.54), submandibular proteinase A [63, 227], epidermal growth-factor-binding protein, nerve growth factor γ-subunit, rat tonin [3,4,9], submaxillary proteinases A and B [1481], T-kininogenase [3386], kallikreins k7 and k8 [739] and human prostate-specific antigen (γ-seminoprotein, [29])

References: [816, 63, 2377, 1068, 129, 251, 432, 945, 227, 3347, 739, 3386]

[EC 3.4.21.35 created 1965 as EC 3.4.4.21, transferred 1972 to EC 3.4.21.8, part transferred 1981 to EC 3.4.21.35]

EC 3.4.21.36
Accepted name: pancreatic elastase
Reaction: Hydrolysis of proteins, including elastin. Preferential cleavage: Ala

Other name(s): pancreatopeptidase E; pancreatic elastase I; elastase; elaszym; serine elastase

Comments: Formed by activation of proelastase from mammalian pancreas by trypsin. In peptidase family S1 (trypsin family). Formerly included in EC 3.4.21.11

References: [2782, 1121, 1491, 236, 276]

[EC 3.4.21.36 created 1981 (EC 3.4.4.7 created 1961, transferred 1972 to EC 3.4.21.11 created 1972, part incorporated 1984)]

EC 3.4.21.37
Accepted name: leukocyte elastase
Reaction: Hydrolysis of proteins, including elastin. Preferential cleavage Val > Ala

Other name(s): lysosomal elastase; neutrophil elastase; polymorphonuclear leukocyte elastase; elastase; elaszym; serine elastase; granulocyte elastase

Comments: Differs from pancreatic elastase in specificity on synthetic substrates and in inhibitor sensitivity. In peptidase family S1 (trypsin family). Formerly included in EC 3.4.21.11

References: [170, 1121, 2901, 276]

[EC 3.4.21.37 created 1981 (EC 3.4.4.7 created 1961, transferred 1972 to EC 3.4.21.11 created 1972, part incorporated 1984)]

EC 3.4.21.38
Accepted name: coagulation factor XIIa
Reaction: Selective cleavage of Arg—Ile bonds in factor VII to form factor VIIa and factor XI to form factor XIa
Other name(s): Hageman factor (activated); blood-coagulation factor XIII; activated β blood-coagulation factor XII; prealbumin activator; Hageman factor β-fragment; Hageman factor fragment HFI; blood-coagulation factor XIIib; prekallikrein activator; kallikreinogen activator
Comments: Also activates plasminogen and plasma prokallikrein. Formed from the proenzyme, factor XII, by plasma kallikrein or factor XIIa. In peptidase family S1 (trypsin family)
References: [889, 474, 2461, 885, 2799]

[EC 3.4.21.38 created 1981]

EC 3.4.21.39
Accepted name: chymase
Reaction: Preferential cleavage: Phe—Tyr—Trp—Leu
Other name(s): mast cell protease I; skeletal muscle protease; skin chymotryptic proteinase; mast cell serine proteinase; skeletal muscle (SK) protease
Comments: In mast cell granules. In peptidase family S1 (trypsin family)
References: [3366, 2439, 1409]

[EC 3.4.21.39 created 1981]

[3.4.21.40  Deleted entry. submandibular proteinase A]

[EC 3.4.21.40 created 1981, deleted 1992]

EC 3.4.21.41
Accepted name: complement subcomponent C₁ʳ
Reaction: Selective cleavage of Lys(or Arg)—Ile bond in complement subcomponent C₁ˢ to form C₁ˢ (EC 3.4.21.42)
Other name(s): activated complement C₁ʳ; C₁ʳ esterase
Comments: Activated from proenzyme C₁ʳ in plasma by complement subcomponent C₁ˢ during activation of the complement system by the "classical" route. In peptidase family S1 (trypsin family)
References: [2801, 1753, 2102]

[EC 3.4.21.41 created 1981]

EC 3.4.21.42
Accepted name: complement subcomponent C₁ʳ
Reaction: Cleavage of Arg—Ala bond in complement component C₄ to form C₄a and C₄b, and Lys(or Arg)—Lys bond in complement component C₂ to form C₂a and C₂b: the "classical" pathway C₃ convertase
Other name(s): C₁ esterase; activated complement C₁ˢ; complement C₁ʳ
Comments: Activated from proenzyme C₁ˢ in plasma by complement subcomponent C₁ʳ. In peptidase family S1 (trypsin family)
References: [2801, 1865, 2102, 2823]

[EC 3.4.21.42 created 1981]

EC 3.4.21.43
Accepted name: classical-complement-pathway C₃/C₅ convertase
Reaction: Selective cleavage of Arg—Ser bond in complement component C₃ α-chain to form C₃a and C₃b, and Arg—bond in complement component C₅ α-chain to form C₅a and C₅b
Other name(s): C3 convertase; C₄₂; C₄b,2a; C₅ convertase; C₄₂₃; C₄b,2a,3b; C₄₂; C₄₂₃; complement C₃ convertase; C₄₂₃; C₄b,2a; C₅ convertase

Comments: A complex of complement fragments C₄b, C₂a and C₂b. C₂a contains the active site, C₂b the site for C₄b binding. C₂a and C₂b are formed by cleavage of proenzyme C₂ by complement subcomponent C₁₅. Cleavage of C₃ requires complement fragment C₃b which binds C₅ and renders it susceptible to cleavage by the C₄b,2a complex. Includes former EC 3.4.21.44. Complement component C₂a is in peptidase family S1 (trypsin family)

References: [1505, 2102]

[EC 3.4.21.43 created 1981 (EC 3.4.21.44 created 1981, incorporated 1984)]

[3.4.21.44 Transferred entry. complement component C₅ convertase. Now EC 3.4.21.43, classical-complement-pathway C₃/C₅ convertase]

[EC 3.4.21.44 created 1981, deleted 1984]

EC 3.4.21.45

Accepted name: complement factor I

Reaction: Inactivates complement subcomponents C₃b, iC₃b and C₄b by proteolytic cleavage

Other name(s): complement component C₃b inactivator; C₃b inactivator; C₃b/C₄b inactivator; C₃bINA; complement C₃b/C₄b inactivator; complement C₄b inactivator; conglutinin-activating factor C; complement C₃b inactivator; factor I; complement C₄bi

Comments: Cleavage of complement subcomponent C₃b requires its binding to cofactor factor H or complement receptor CR1; cleavage of iC₃b requires complement receptor CR1; cleavage of C₄b requires C₄b-binding protein. In peptidase family S1 (trypsin family)

References: [2126, 551, 2102]

[EC 3.4.21.45 created 1981]

EC 3.4.21.46

Accepted name: complement factor D

Reaction: Selective cleavage of Arg-Lys bond in complement factor B when in complex with complement subcomponent C₃b or with cobra venom factor

Other name(s): C₃ proactivator convertase; properdin factor D esterase; factor D; factor D (complement)

Comments: A component of the alternative pathway of complement activation. This reaction is analogous to the activation of complement component C₂ by complement subcomponent C₁₅. In peptidase family S1 (trypsin family)

References: [2527, 2102]

[EC 3.4.21.46 created 1981]

EC 3.4.21.47

Accepted name: alternative-complement-pathway C₃/C₅ convertase

Reaction: Cleavage of Arg-Ser bond in complement component C₃ α-chain to yield C₃a and C₃b, and Arg bond in complement component C₅ α-chain to yield C₅a and C₅b

Other name(s): complement component C₃/C₅ convertase (alternative); proenzyme factor B; properdin factor B; C₃ proactivator; glycine-rich β-glycoprotein; heat-labile factor; C₃ convertase; C₃b,Bb,CVF,Bb,C₅ convertase; (C₃b)n,Bb; complement C 3(C 5) convertase (amplification); alternative complement pathway C₃(C₅) convertase; C₅ convertase; CVF,Bb; (CVF)-dependent glycine-rich-β-glucoprotein; cobra venom factor-dependent C₃ convertase

195
A bimolecular complex of complement fragment Bb with either C3b or cobra venom factor; Bb contains the active site. Bb is formed by cleavage of proenzyme factor B by factor D. Cleavage of complement component C5 requires additional C3b which binds C5 and renders it susceptible to cleavage by C3b,Bb complex. C3b,Bb is stabilized in plasma by factor P. Complement factor B is in peptidase family S1 (trypsin family)

Comments: A bimolecular complex of complement fragment Bb with either C3b or cobra venom factor; Bb contains the active site. Bb is formed by cleavage of proenzyme factor B by factor D. Cleavage of complement component C5 requires additional C3b which binds C5 and renders it susceptible to cleavage by C3b,Bb complex. C3b,Bb is stabilized in plasma by factor P. Complement factor B is in peptidase family S1 (trypsin family)

References: [1504, 2081, 2102]

EC 3.4.21.48
Accepted name: cerevisin
Reaction: Hydrolysis of proteins with broad specificity, and of Bz-Arg-OEt Ac-Tyr-OEt. Does not hydrolyse peptide amides
Other name(s): yeast proteinase B; proteinase yscB (gene name); baker’s yeast proteinase B; brewer’s yeast proteinase; peptidase β
Comments: From Saccharomyces cerevisiae (baker’s yeast, brewer’s yeast). In peptidase family S8 (subtilisin family), but contains a Cys residue near the active site His, and is inhibited by mercurials. Proteinase yscB is a similar enzyme from the yeast Candida albicans [789]
References: [803, 1593, 789, 2045]

EC 3.4.21.49
Accepted name: hypodermin C
Reaction: Hydrolysis of proteins including native collagen at Ala bond leaving an N-terminal (75%) and a C-terminal (25%) fragment
Other name(s): Hypoderma collagenase
Comments: From the larva of a warble fly, Hypoderma lineatum. Little action on small molecule substrates of trypsin, chymotrypsin, elastase or microbial collagenases. In peptidase family S1 (trypsin family)
References: [1705, 1707, 1706]

EC 3.4.21.50
Accepted name: lysyl endopeptidase
Reaction: Preferential cleavage: Lys, including -Lys-Pro-
Other name(s): Achromobacter proteinase I (also see Comment); Achromobacter lyticus alkaline proteinase I; protease I; achromopeptidase; lysyl bond specific proteinase
Comments: From Achromobacter lyticus [3131]. Enzymes with similar specificity are produced by Lysobacter enzymogenes (Endopeptinase Lys-C; [1395]) and Pseudomonas aeruginosa (Ps-1; [736]). In peptidase family S1 (trypsin family)
References: [1928, 1927, 1395, 736, 2266, 3131]

[3.4.21.51 Deleted entry. Leukocyte-membrane neutral endopeptidase]

[EC 3.4.21.51 created 1984, deleted 1992]

[3.4.21.52 Deleted entry. Cathepsin R]

[EC 3.4.21.52 created 1981 as EC 3.4.99.33, transferred 1984 to EC 3.4.21.52, deleted 1992]
EC 3.4.21.53

Accepted name: endopeptidase La

Reaction: Hydrolysis of proteins in presence of ATP

Other name(s): ATP-dependent serine proteinase; lon protease La; proteinase La; ATP-dependent lon proteinase; ATP-dependent protease La; Escherichia coli proteinase La; Escherichia coli serine protease La; gene lon protease; gene lon proteins; PIM1 protease; PIM1 proteinase; serine protease La

Comments: Product of the lon gene in Escherichia coli. ATP hydrolysis is linked with peptide bond hydrolysis; vanadate inhibits both reactions. Type example of peptidase family S16. A similar enzyme occurs in animal mitochondria

References: [629, 1694, 468]

[EC 3.4.21.53 created 1986]

EC 3.4.21.54

Accepted name: γ-renin

Reaction: Cleavage of the Leu-Leu bond in synthetic tetradecapeptide renin substrate (horse), to produce angiotensin I, but not active on natural angiotensinogen, unlike renin (EC 3.4.23.15). Also hydrolyses Bz-Arg-p-nitroanilide

Comments: A member of the tissue kallikrein family, from submandibular glands of male mice. In peptidase family S1 (trypsin family)

References: [2416, 697]

[EC 3.4.21.54 created 1986]

EC 3.4.21.55

Accepted name: venombin AB

Reaction: Selective cleavage at Arg bonds in fibrinogen to form fibrin and release fibrinopeptides A and B

Other name(s): gabonase; okinaxobin II; Bitis gabonica venom serine proteinase; afacötin

Comments: From the venom of the Gaboon viper Bitis gabonica. Activates Factor XIII. Not inhibited by antithrombin III/heparin or hirudin, unlike EC 3.4.21.5, thrombin

References: [2404]

[EC 3.4.21.55 created 1989]

[3.4.21.56 Deleted entry. euphorbain. Now considered EC 3.4.21.25, cucumisin]

[EC 3.4.21.56 created 1972 as EC 3.4.99.7, transferred 1989 to EC 3.4.21.56, deleted 1992]

EC 3.4.21.57

Accepted name: leucyl endopeptidase

Reaction: Hydrolysis of proteins. Preferential cleavage: Leu in small molecule substrates

Other name(s): plant Leu-proteinase; leucine-specific serine proteinase; leucine endopeptidase; spinach serine proteinase (leucine specific); spinach leucine-specific serine proteinase; Leu-proteinase

Comments: From leaves of the spinach plant (Spinacia oleracea)

References: [21, 20]

[EC 3.4.21.57 created 1989]

[3.4.21.58 Deleted entry. prohormone serine proteinase]

[EC 3.4.21.58 created 1989, deleted 1992]
EC 3.4.21.59

Accepted name: tryptase

Reaction: Preferential cleavage: Arg↓↓, Lys↓↓, but with more restricted specificity than trypsin

Other name(s): mast cell tryptase; mast cell protease II; skin tryptase; lung tryptase; pituitary tryptase; mast cell neutral proteinase; mast cell serine proteinase II; mast cell proteinase II; mast cell serine proteinase tryptase; rat mast cell protease II; tryptase M

Comments: Occurs as a tetrameric molecule with high affinity for heparin, in mast cell granules. In peptidase family S1 (trypsin family). Not inhibited by α1-proteinase inhibitor or α2-macroglobulin

References: [3020, 1520, 548, 1127, 3199]

EC 3.4.21.60

Accepted name: scutelarin

Reaction: Selective cleavage of Arg↓↓Thr and Arg↓↓Ile in prothrombin to form thrombin and two inactive fragments

Other name(s): taipan activator; Oxyuranus scutellatus prothrombin-activating proteinase

Comments: From the venom of the Taipan snake (Oxyuranus scutellatus). Converts prothrombin to thrombin. Specificity is similar to that of Factor Xa (EC 3.4.21.6). However, unlike Factor Xa this enzyme can cleave its target in the absence of coagulation Factor Va. Activity is potentiated by phospholipid and Ca^{2+} which binds via γ-carboxyglutamatic acid residues. Similar enzymes are known from the venom of other Australian elapid snakes, including Pseudonaja textilis textilis, Oxyuranus microlepidotus and Demansia nuchalis affinis. A member of peptidase family S1.

References: [3245, 2879]

EC 3.4.21.61

Accepted name: kexin

Reaction: Cleavage of -Lys-Arg↓↓ and -Arg-Arg↓↓ bonds to process yeast α-factor pheromone and killer toxin precursors

Other name(s): yeast KEX2 protease; proteinase yseF (gene name); prohormone-processing endoprotease; paired-basic endopeptidase; yeast cysteine proteinase F (misleading); andrenorphin-Gly-generating enzyme; endoproteinase Kex2p; gene KEX2 dibasic proteinase; Kex2p proteinase; Kex2 endopeptidase; Kex2 endoproteinase; Kex2 protease; proteinase Kex2p; Kex2-like precursor protein processing endoprotease; prohormone-processing KEX2 proteinase; prohormone-processing proteinase; proprotein convertase; protease KEX2; Kex2 proteinase; Kex2-like endoproteinase

Comments: A Ca^{2+}-activated peptidase of peptidase family S8, containing Cys near the active site His, and inhibited by p-mercuribenzoate. Similar enzymes occur in mammals.

References: [1429, 12, 2041, 917, 2042]

EC 3.4.21.62

Accepted name: subtilisin

Reaction: Hydrolysis of proteins with broad specificity for peptide bonds, and a preference for a large uncharged residue in P1. Hydrolyses peptide amides
Other name(s): alcalase; alcalase 0.6L; alcalase 2.5L; ALK-enzyme; bacillopeptidase A; bacillopeptidase B; _Bacillus subtilis_ alkaline proteinase bioprase; bioprase AL 15; bioprase APL 30; colistinase; (see also comments); subtilisin J; subtilisin S41; subtilisin Sendai; subtilisin GX; subtilisin E; subtilisin BL; gene-nase I; esperase; maxatase; thermoase PC 10; protease XXVII; thermoase; superase; subtilisin DY; subtilopeptidase; SP 266; savinase 8.0L; savinase 4.0T; kazusase; protease VIII; opticlean; _Bacillus subtilis_ alkaline proteinase; protin A 3L; savinase; savinase 16.0L; savinase 32.0 L EX; orientase 10B; protease S

Comments: Subtilisin is a serine endopeptidase, type example of peptidase family S8. It contains no cysteine residues (although these are found in homologous enzymes). Species variants include subtilisin BP' (also subtilisin B, subtilopeptidase B, subtilopeptidase C, Nagarse, Nagarse proteinase, subtilisin Novo, bacterial proteinase Novo) and subtilisin Carlsberg (subtilisin A, subtilopeptidase A, alcalase Novo). Similar enzymes are produced by various _Bacillus subtilis_ strains and other _Bacillus_ species.

References: [2325, 2393]

EC 3.4.21.63
Accepted name: oryzin
Reaction: Hydrolysis of proteins with broad specificity, and of Bz-Arg-OEt > Ac-Tyr-OEt. Does not hydrolyse peptide amides

Other name(s): _Aspergillus_ alkaline proteinase; aspergillopeptidase B; API 21; aspergillopsin B; aspergillopsin F; _Aspergillus candidus_ alkaline proteinase; _Aspergillus flavus_ alkaline proteinase; _Aspergillus melleus_ semi-alkaline proteinase; _Aspergillus oryzae_ alkaline proteinase; _Aspergillus parasiticus_ alkaline proteinase; _Aspergillus serine proteinase; Aspergillus sydowi_ alkaline proteinase; _Aspergillus soya_ alkaline proteinase; _Aspergillus melleus_ alkaline proteinase; _Aspergillus sulphureus_ alkaline proteinase; prozyme; P 5380; kyorinase; seaprose S; semi-alkaline protease; sumizyme MP; prozyme 10; onoprose; onoprose SA; protease P; promelase

Comments: A peptidase of family S8 (subtilisin family), not containing cysteine, that is the predominant extracellular alkaline endopeptidase of the mold _Aspergillus oryzae_. Identical or closely related enzymes are produced by _A. flavus_ and _A. sojae_.

References: [2137, 1154, 3145, 2070, 2874]

EC 3.4.21.64
Accepted name: peptidase K
Reaction: Hydrolysis of keratin, and of other proteins with subtilisin-like specificity. Hydrolyses peptide amides

Other name(s): _Tririchtrium_ alkaline proteinase; _Tririchtrium album_ serine proteinase; proteinase K; _Tririchtrium album_ proteinase K; endopeptidase K

Comments: From the mold _Tririchtrium album_ Limber. A peptidase of family S8 (subtilisin family) containing two disulfide bridges and one free Cys near the active site His. Formerly included in EC 3.4.21.14

References: [721, 2073, 1619, 1390, 229]

EC 3.4.21.65
Accepted name: thermomycolin
Reaction: Rather nonspecific hydrolysis of proteins. Preferential cleavage: Ala→, Tyr→, Phe→ in small molecule substrates

References: [2325, 1911, 2393, 2169, 1310, 2421]
Other name(s): thermomycolase
Comments: A peptidase of family S8 (subtilisin family) from the thermophilic fungus *Malbranchea pulchella* var. *sulfurea* containing Cys, but not inhibited by *p*-mercuribenzoate. Very thermostable. Formerly included in EC 3.4.21.14
References: [941]


**EC 3.4.21.66**

Accepted name: thermitase
Reaction: Hydrolysis of proteins, including collagen
Other name(s): thermophilic Streptomyces serine proteinase; *Thermoactinomyces vulgaris* serine proteinase
Comments: A peptidase of family S8 (subtilisin family) from *Thermoactinomyces vulgaris* containing a single Cys, near the active site His, and inhibited by *p*-mercuribenzoate. The N-terminal extension of the polypeptide chain relative to subtilisin contributes to Ca\(^{2+}\)-binding and the high thermostability. The amino acid composition and properties of the thermostable enzyme from *Streptomyces rectus* var. *proteolyticus* (formerly included in EC 3.4.21.14) are closely similar [2043, 289].
References: [2043, 289, 1560, 1979, 3040]

[EC 3.4.21.66 created 1992]

**EC 3.4.21.67**

Accepted name: endopeptidase So
Reaction: Hydrolysis of proteins, but not Bz-Tyr-OEt, Ac-Phe-β-naphthylester, or Bz-Arg-OEt
Other name(s): *E. coli* cytoplasmic proteinase; proteinase So; *Escherichia coli* serine proteinase So
Comments: An *Escherichia coli* cytoplasmic endopeptidase formerly included in EC 3.4.21.14. Inhibited by Tos-Phe-CH\(_2\)Cl, but not by Tos-Lys-CH\(_2\)Cl
References: [997, 486]


**EC 3.4.21.68**

Accepted name: *t*-plasminogen activator
Reaction: Specific cleavage of Arg-Val bond in plasminogen to form plasmin
Other name(s): tissue plasminogen activator; plasminogen activator, tissue-type; tissue-type plasminogen activator; tPA; *t*-PA
Comments: A peptidase of family S1 (trypsin family) from a wide variety of mammalian tissues, especially endothelial cells. Secreted as a single chain precursor which is cleaved to a two-chain form by plasmin. Activity is considerably enhanced by fibrin. Formerly included in EC 3.4.21.31 and EC 3.4.99.26
References: [2372, 1836, 2379, 3209, 946, 507]

[EC 3.4.21.68 created 1972 as EC 3.4.99.26, transferred 1978 as EC 3.4.21.31, part transferred 1992 to EC 3.4.21.68]

**EC 3.4.21.69**

Accepted name: protein C (activated)
Reaction: Degradation of blood coagulation factors Va and VIIIa
Other name(s): blood-coagulation factor XIa; activated blood coagulation factor XIV; activated protein C; autoprothrombin II-A; protein Ca; APC; GSAPC
Comments: A peptidase of family S1 (trypsin family), one of the γ-carboxyglutamic acid-containing coagulation factors. Formed from protein C, the proenzyme that circulates in plasma, by the action of a complex of thrombin with thrombomodulin, or by serine endopeptidases present in several snake venoms

References: [2372, 1836, 2379, 3209, 946, 507]
EC 3.4.21.70
Accepted name: pancreatic endopeptidase E
Reaction: Preferential cleavage: Ala. Does not hydrolyse elastin
Other name(s): cholesterol-binding proteinase; proteinase E; cholesterol-binding serine proteinase; pancreatic protease E; pancreatic proteinase E; cholesterol-binding pancreatic proteinase; CBPP; pancreas E proteinase
Comments: A peptidase of family S1 (trypsin family) from pancreatic juice. Unlike elastases, has an acidic pI. Binds cholesterol
References: [1890, 2760]

EC 3.4.21.71
Accepted name: pancreatic elastase II
Reaction: Preferential cleavage: Leu, Met and Phe. Hydrolyses elastin
Other name(s): pancreatic elastase 2
Comments: A peptidase of family S1 (trypsin family) formed by activation of proelastase II from mammalian pancreas by trypsin. Usually, only one of the pancreatic elastases (see also EC 3.4.21.36) is expressed in a given species; human pancreatic elastase is of type II
References: [836, 2779]

EC 3.4.21.72
Accepted name: IgA-specific serine endopeptidase
Reaction: Cleavage of immunoglobulin A molecules at certain Pro bonds in the hinge region. No small molecule substrates are known
Other name(s): IgA protease; IgA proteinase; IgA-specific proteinase; immunoglobulin A protease; immunoglobulin A proteinase
Comments: Species variants differing slightly in specificity are secreted by Gram-negative bacteria Neisseria gonorrhoeae and Haemophilus influenzae. Type example of peptidase family S6. Some other bacterial endopeptidases with similar specificity are of metallo-type (see EC 3.4.24.13, IgA-specific metalloendopeptidase)
References: [2410, 128]

EC 3.4.21.73
Accepted name: u-plasminogen activator
Reaction: Specific cleavage of Arg-Val bond in plasminogen to form plasmin
Other name(s): urokinase; urinary plasminogen activator; cellular plasminogen activator; urokinase-type plasminogen activator; double-chain urokinase-type plasminogen activator; two-chain urokinase-type plasminogen activator; urokinase plasminogen activator; uPA; u-PA; abbokinase; urinary esterase A
Comments: Formed from the inactive precursor by action of plasmin or plasma kallikrein. Differs in structure from t-plasminogen activator (EC 3.4.21.68), and does not bind to fibrin. In peptidase family S1 (trypsin family). Formerly included in EC 3.4.21.31 and EC 3.4.99.26
References: [1838, 1836, 2632, 507, 1779]

[EC 3.4.21.70 created 1992]
[EC 3.4.21.71 created 1992]
[EC 3.4.21.72 created 1992]
[EC 3.4.21.73 created 1972 as EC 3.4.99.26, transferred 1978 as EC 3.4.21.31, part transferred 1992 to EC 3.4.21.73]
EC 3.4.21.74

Accepted name: venombin A

Reaction: Selective cleavage of Arg bond in fibrinogen, to form fibrin, and release fibrinopeptide A. The specificity of further degradation of fibrinogen varies with species origin of the enzyme

Other name(s): α-fibrinogenase; habutobin; zinc metalloproteinase Cbfib1.1; zinc metalloproteinase Cbfib1.2; zinc metalloproteinase Cbfib2; ancrod; (see also Comments)

Comments: A somewhat thrombin-like enzyme from venoms of snakes of the viper/rattlesnake group. Species variants of the enzyme include ancrod from Agkistrodon rhodostoma (Malayan pit viper) (formerly EC 3.4.21.28) [2212], batroxobin from Bothrops atrox (South American pit viper) (formerly EC 3.4.21.29) [2915, 1348] and crotalase from Crotalus adamanteus (Eastern diamondback rattlesnake) (formerly EC 3.4.21.30) [1910, 2802]. In peptidase family S1 (trypsin family). Does not require activation by Ca$^{2+}$.

References: [2212, 2915, 1910, 2802, 1348]

[EC 3.4.21.74 created 1992 (EC 3.4.21.28, EC 3.4.21.29 and 3.4.21.30 all created 1978 and incorporated 1992)]

EC 3.4.21.75

Accepted name: furin

Reaction: Release of mature proteins from their proproteins by cleavage of -Arg-Xaa-Yaa-Arg bonds, where Xaa can by any amino acid and Yaa is Arg or Lys. Releases albumin, complement component C3 and von Willebrand factor from their respective precursors

Other name(s): prohormone convertase; dibasic processing enzyme; PACE; paired basic amino acid cleaving enzyme; paired basic amino acid converting enzyme; serine proteinase PACE; PC1; SPC3; proprotein convertase

Comments: One of a group of peptidases in peptidase family S8 (subtilisin family) that is structurally and functionally similar to kexin. All are activated by Ca$^{2+}$, contain Cys near the active site His, and are inhibited by p-mercuribenzoate. At least three related enzymes are recognized in mammals: PC2, PC3 and PC4, which have somewhat different specificities

References: [606, 605, 1143, 2737, 2902]

[EC 3.4.21.75 created 1993]

EC 3.4.21.76

Accepted name: myeloblastin

Reaction: Hydrolysis of proteins, including elastin, by preferential cleavage: -Ala-Val-

Other name(s): leukocyte proteinase 3; leukocyte proteinase 4; Wegener’s granulomatosis autoantigen; proteinase PR-3; proteinase-3; PMNL proteinase

Comments: From polymorphonuclear leukocyte granules. In peptidase family S1 (trypsin family). Not inhibited by secretory leukocyte proteinase inhibitor

References: [1675, 2498, 343, 1450]

[EC 3.4.21.76 created 1993]

EC 3.4.21.77

Accepted name: semenogelase

Reaction: Preferential cleavage: -Tyr-

Other name(s): prostate-specific antigen; α-seminoprotein; seminin; P-30 antigen; antigen (human clone HPSA-1 prostate-specific protein moiety reduced); γ-seminoglycoprotein (human protein moiety reduced); γ-SM; antigen PSA (human prostate-specific); human glandular kallikrein; antigen PSA (human clone 5P1 protein moiety reduced)

Comments: A peptidase of family S1 (trypsin family) from seminal plasma. Slowly inhibited by α1-antichymotrypsin

References: [657, 482]
EC 3.4.21.78
Accepted name: granzyme A
Reaction: Hydrolysis of proteins, including fibronectin, type IV collagen and nucleolin. Preferential cleavage: -Arg, -Lys >> -Phe in small molecule substrates
Other name(s): CTLA3; HuTPS; T-cell associated protease 1; cytotoxic T lymphocyte serine protease; TSP-1; T-cell derived serine proteinase
Comments: From cytotoxic T lymphocyte granules. In peptidase family S1 (trypsin family). The human enzyme does not cleave Phe-
References: [2804, 949, 2247]

EC 3.4.21.79
Accepted name: granzyme B
Reaction: Preferential cleavage: -Asp >> -Asn >> -Met, -Ser
Other name(s): CTLA1; CCPII; cytotoxic cell proteinase-1; granzyme G; granzyme H; CCP1 proteinase
Comments: From cytotoxic T lymphocyte granules. In peptidase family S1 (trypsin family)
References: [2700, 2247, 2415]

EC 3.4.21.80
Accepted name: streptogrisin A
Reaction: Hydrolysis of proteins with specificity similar to chymotrypsin
Other name(s): Streptomyces griseus protease A; protease A; proteinase A; Streptomyces griseus proteinase A; Streptomyces griseus serine proteinase 3; Streptomyces griseus serine proteinase A
Comments: From Streptomyces griseus. A component of Pronase, in family S1 (trypsin family). Not inhibited by Tos-Phe-CH2Cl or ovomucoid
References: [1413, 2792, 1386, 618, 1179]

EC 3.4.21.81
Accepted name: streptogrisin B
Reaction: Hydrolysis of proteins with trypsin-like specificity
Other name(s): Streptomyces griseus protease B; pronase B; serine proteinase B; Streptomyces griseus proteinase B; Streptomyces griseus serine proteinase 1; Streptomyces griseus serine proteinase B
Comments: From Streptomyces griseus. A component of Pronase, in peptidase family S1 (trypsin family), distinct from Streptomyces trypsin
References: [1433, 897, 2514, 1179, 1030]

EC 3.4.21.82
Accepted name: glutamyl endopeptidase II
Reaction: Preferential cleavage: -Glu >> -Asp. Preference for Pro or Leu at P2 and Phe at P3. Cleavage of -Glu-Asp- and -Glu-Pro- bonds is slow
Other name(s): GluSGP
Comments: From Streptomyces griseus. A peptidase of family S1 (trypsin family). Inhibited by [Leu→Glu]-modified turkey ovomucoid third domain

References: [1433, 897, 2514, 1179, 1030]
EC 3.4.21.83
Accepted name: oligopeptidase B
Reaction: Hydrolysis of -Arg\textsubscript{1} -Lys\textsubscript{1} bonds in oligopeptides, even when P1\textsuperscript{′} residue is proline
Other name(s): protease II; *Escherichia coli* alkaline proteinase II
Comments: Known from *Escherichia coli*. Inhibited by Tos-Lys-CH2Cl. In peptidase family S9 (prolyl oligopeptidase family)
References: [1462]

[EC 3.4.21.83 created 1993]

EC 3.4.21.84
Accepted name: limulus clotting factor C
Reaction: Selective cleavage of -Arg\textsubscript{103} -Ser- and -Ile\textsubscript{124} -Ile- bonds in limulus clotting factor B to form factor B. Cleavage of -Pro-Arg- bonds in synthetic substrates
Other name(s): factor C; limulus factor C
Comments: From the hemocyte granules of the horseshoe crabs *Limulus* and *Tachypleus*. Factor C is activated by Gram-negative bacterial lipopolysaccharides and chymotrypsin. Inhibited by antithrombin III. In peptidase family S1 (trypsin family)
References: [2151, 2113, 3075]

[EC 3.4.21.84 created 1993]

EC 3.4.21.85
Accepted name: limulus clotting factor B
Reaction: Selective cleavage of -Arg\textsubscript{98} -Ile- bond in limulus proclotting enzyme to form active clotting enzyme
Comments: From the hemocyte granules of the horseshoe crabs *Limulus* and *Tachypleus*. Factor B is activated by limulus clotting factor C. In peptidase family S1 (trypsin family)
References: [2149]

[EC 3.4.21.85 created 1993]

EC 3.4.21.86
Accepted name: limulus clotting enzyme
Reaction: Selective cleavage of -Arg\textsubscript{18} and -Arg\textsubscript{37} bonds in coagulogen to form coagulin and fragments
Other name(s): clotting enzyme
Comments: From the hemocyte granules of horseshoe crabs *Limulus* and *Tachypleus*. Proclotting enzyme is activated by limulus clotting factor C. In peptidase family S1 (trypsin family)
References: [2112, 3075]

[EC 3.4.21.86 created 1993]

[3.4.21.87 Transferred entry. omptin. Now EC 3.4.23.49, omptin. The enzyme is not a serine protease, as thought previously, but an aspartate protease]

[EC 3.4.21.87 created 1993, deleted 2006]
EC 3.4.21.88

Accepted name: repressor LexA
Reaction: Hydrolysis of Ala
Gly bond in repressor LexA
Other name(s): LexA repressor
Comments: RecA protein and single-stranded DNA are required for activity, which is attributed to a Ser/Lys dyad [2829]. The LexA protein represses the SOS regulon, which regulates the genes involved in DNA repair. In the presence of single-stranded DNA, the RecA protein interacts with repressor LexA, causing it to undergo an autocatalytic cleavage which disrupts the DNA-binding part of the repressor, and inactivates it. The consequent derepression of the SOS regulon leads to DNA repair. This peptidase activity of LexA was previously attributed to the RecA protein. Type example of peptidase family S24
References: [1252, 2829, 1525, 1810]

EC 3.4.21.89

Accepted name: signal peptidase I
Reaction: Cleavage of hydrophobic, N-terminal signal or leader sequences
Other name(s): leader peptidase I; signal proteinase; Escherichia coli leader peptidase; eukaryotic signal peptidase; eukaryotic signal proteinase; leader peptidase; leader peptide hydrolase; leader proteinase; signal peptidase; pilin leader peptidase; SPC; prokaryotic signal peptidase; prokaryotic leader peptidase; HOSP; prokaryotic signal proteinase; propeptidase; PuIO prepilin peptidase; signal peptide hydrolase; signal peptide peptidase; signalase; bacterial leader peptidase 1
Comments: The enzyme is found in bacterial membranes and in chloroplast thylakoid membranes. Unaffected by inhibitors of most serine peptidases, but site-directed mutagenesis implicates a Ser/Lys catalytic dyad in activity [252, 3118]. Hydrolyses a single bond -Ala-Ala- in M13 phage procoat protein, producing free signal peptide and coat protein. Formerly included in EC 3.4.99.36. Eukaryote signal peptidases that may have somewhat different specificity are known from the endoplasmic reticulum membrane [1825] and mitochondrial inner membrane [2227]. Type example of peptidase family S26
References: [252, 2227, 3118, 1825, 3117, 419, 1330]

EC 3.4.21.90

Accepted name: togavirin
Reaction: Autocatalytic release of the core protein from the N-terminus of the togavirus structural polyprotein by hydrolysis of a -Trp-Ser- bond
Other name(s): Sindbis virus protease; Sindbis virus core protein; NsP2 proteinase
Comments: Known from the Sindbis and Semliki forest togaviruses. Once released, the core protein does not retain catalytic activity. Togavirin is the type example of peptidase family S3 and has a similar tertiary structure to chymotrypsin [3087]
References: [1620, 2920, 3087]

EC 3.4.21.91

Accepted name: flavivirin
Reaction: Selective hydrolysis of -Xaa-Xaa-Yaa- bonds in which each of the Xaa can be either Arg or Lys and Yaa can be either Ser or Ala
Other name(s): Yellow fever virus (flavivirus) protease; NS2B-3 proteinase
Comments: Known from classical flaviviruses (yellow fever, dengue fever). The functional viral peptidase is part of the NS2B protein. Catalytic His, Asp and Ser residues are arranged as in chymotrypsin, but flavivirin is the type example of peptidase family S7.
References: [420, 382, 1785]
EC 3.4.21.92

**Accepted name:** endopeptidase Clp

**Reaction:** Hydrolysis of proteins to small peptides in the presence of ATP and Mg\(^{2+}\). \(\alpha\)-Casein is the usual test substrate. In the absence of ATP, only oligopeptides shorter than five residues are hydrolysed (such as succinyl-Leu-Tyr-NHMe; and Leu-Tyr-Leu-Tyr-Trp, in which cleavage of the -Tyr-Leu- and -Tyr-Trp bonds also occurs)

**Other name(s):** endopeptidase Ti; caseinolytic protease; protease Ti; ATP-dependent Clp protease; ClpP; Clp protease

**Comments:** An enzyme from bacteria that contains subunits of two types, ClpP, with peptidase activity, and ClpA, with ATPase activity. The ClpAP complex, which displays ATP-dependent endopeptidase activity, has the composition (ClpP\(_{14}\)ClpA\(_{6}\))\(_2\) [1509]. ClpP is the type example of peptidase family S14

**References:** [1015, 1946, 1947, 1509]

---

EC 3.4.21.93

**Accepted name:** proprotein convertase 1

**Reaction:** Release of protein hormones, neuropeptides and renin from their precursors, generally by hydrolysis of -Lys-Arg- bonds

**Other name(s):** prohormone convertase 3; neuroendocrine convertase 1; PC1

**Comments:** A Ca\(^{2+}\)-dependent enzyme, maximally active at about pH 5.5. Substrates include pro-opiomelanocortin, proenkephalin, prodynorphin, proinsulin. Unlike prohormone convertase 2, does not hydrolyse proluteinizing-hormone-releasing-hormone. Unusually, processing of prodynorphin occurs at a bond in which P2 is Thr. Present in the regulated secretory pathway of neuroendocrine cells, commonly acting co-operatively with prohormone convertase 2. In peptidase family S8 (subtilisin family)

**References:** [2740, 2832, 2902, 2738, 1392]

---

EC 3.4.21.94

**Accepted name:** proprotein convertase 2

**Reaction:** Release of protein hormones and neuropeptides from their precursors, generally by hydrolysis of -Lys-Arg- bonds

**Other name(s):** neuroendocrine convertase 2; PC2

**Comments:** A Ca\(^{2+}\)-dependent enzyme, maximally active at about pH 5.5. Specificity is broader than that of prohormone convertase 1. Substrates include pro-opiomelanocortin, proenkephalin, prodynorphin, proglucagon, proinsulin and proluteinizing-hormone-releasing-hormone. Does not hydrolyse prorenin or prosomatostatin, however. Unusually, processing of prodynorphin occurs at a bond in which P2 is Thr. Present in the regulated secretory pathway of neuroendocrine cells, commonly acting co-operatively with prohormone convertase 1. In peptidase family S8 (subtilisin family)

**References:** [2740, 2833, 2593, 2738]

---

EC 3.4.21.95

**Accepted name:** snake venom factor V activator

**Reaction:** Fully activates human clotting factor V by a single cleavage at the Trp-Tyr-Leu-Arg\(^\text{1545}\)Ser-Asn-Asn-Gly bond. Cattle, but not rabbit, factor V is cleaved, and no other proteins of the clotting system are attacked. Esterase activity is observed on Bz-Arg-OEt and Tos-Arg-OMe, and amidase activity on Phe-pippecolyl-Arg-NHPhNO\(_2\)

206
Comments: Known from venom of Vipera russelli. Inhibited by di-isopropyl fluorophosphate, unlike the metalloendopeptidase russellysin (EC 3.4.24.58) that is specific for factor X [1554]. In peptidase family S1 (trypsin family) [3074].

References: [1554, 3074]

[EC 3.4.21.95 created 1997]

EC 3.4.21.96
Accepted name: lactocep
Reaction: Endopeptidase activity with very broad specificity, although some subsite preferences have been noted, e.g. large hydrophobic residues in the P1 and P4 positions, and Pro in the P2 position [1,2]. Best known for its action on caseins, although it has been shown to hydrolyse hemoglobin and oxidized insulin B chain

Other name(s): CEP; extracellular lactococcal proteinase; lactococcal cell wall-associated proteinase; lactococcal cell envelope-associated proteinase; lactococcal proteinase; PrtP

Comments: Associated with the cell envelope of Lactococcus lactis and attached via a C-terminal membrane anchor sequence. Responsible for the hydrolysis of casein in milk and the provision of peptides essential to cell growth. Important in cheese making and the production of lactic casein, being required for rapid growth to high cell densities with concomitant production of adequate levels of lactic acid. Specificity differences between lactocepins from different starter strains may be partly responsible for imparting different flavour qualities to cheese [2444]. In peptidase family S8 (subtilisin family)

References: [3219, 2053, 778, 2444]

[EC 3.4.21.96 created 1997]

EC 3.4.21.97
Accepted name: assemblin
Reaction: Cleaves -Ala-Ser- and -Ala-Ala- bonds in the scaffold protein

Comments: Involved in the breakdown of the scaffold protein during the late stages of assembly of the herpesvirus virion. Inhibited by diisopropyl fluorophosphate. Type example of peptidase family S21. Catalytic residues are His, Ser, His, a combination not known for any other peptidase, and the protein fold also is unique. Known from herpes viruses of several types, cytomegalovirus, Epstein-Barr virus and human herpesvirus 3

References: [451, 579]

[EC 3.4.21.97 created 2000]

EC 3.4.21.98
Accepted name: hepacivirin
Reaction: Hydrolysis of four peptide bonds in the viral precursor polyprotein, commonly with Asp or Glu in the P6 position, Cys or Thr in P1 and Ser or Ala in P1’

Other name(s): Cpro-2; hepatitis C virus NS3 serine proteinase; NS3-4A serine proteinase complex

Comments: Encoded by the genome of the viruses of the hepatitis C group, and contributes to the maturation of the precursor polyproteins. The enzyme is greatly activated by binding of the 54-residue NS4A ‘co-factor’ protein also derived from the viral polyprotein. Type example of peptidase family S29. The crystallographic structure shows a chymotrypsin-like fold.

References: [1533, 2545]

[EC 3.4.21.98 created 2000]

EC 3.4.21.99
Accepted name: spermosin
Reaction: Hydrolyses arginyl bonds, preferably with Pro in the P2 position

207
Comments: The enzyme from the ascidian (Prochordate) *Halocynthia roretzi* is localized in the sperm head, and released during sperm activation. A proline-rich region is involved in binding to the vitelline coat of the egg. Belongs in peptidase family S1 (trypsin family).

References: [2673, 2674, 2671, 2672]

[EC 3.4.21.99 created 2001]

EC 3.4.21.100

Accepted name: sedolisin

Reaction: Hydrolysis of the B chain of insulin at -Glu$^{13}$ Ala-, -Leu$^{15}$ Tyr- and -Phe$^{25}$ Tyr-, and angiotensin I at -Tyr$^{4}$ Ile-. A good synthetic substrate is Lys-Pro-Ile-Glu-Phe-Phe(NO$_2$)-Arg-Leu.

Other name(s): *Pseudomonas* sp. pepstatin-insensitive carboxyl proteinase; pseudomonapepsin; pseudomonalisin; sedolysin

Comments: An enzyme secreted by *Pseudomonas* sp. No. 101. Optimum pH is 4. It is distinguished from xanthomonapepsin by its insensitivity to EPNP and from scytalidopepsin B by this property and by its unrelated amino-acid sequence. Inhibited by tyrostatin, a peptide aldehyde [2242]. Type example of peptidase family S53.

References: [2244, 2242, 3357, 3358]

[EC 3.4.21.100 created 1995 as EC 3.4.23.37, transferred 2001 to EC 3.4.21.100, modified 2003]

EC 3.4.21.101

Accepted name: xanthomonalisin

Reaction: Cleavage of casein

Other name(s): *Xanthomonas* aspartic proteinase; xanthomonapepsin; sedolisin-B

Comments: Secreted by the bacterium *Xanthomonas* sp. Belongs in peptidase family S53.

References: [2243, 3358]

[EC 3.4.21.101 created 1995 as EC 3.4.23.33, transferred 2001 to EC 3.4.21.101, modified 2003]

EC 3.4.21.102

Accepted name: C-terminal processing peptidase

Reaction: The enzyme shows specific recognition of a C-terminal tripeptide, Xaa-Yaa-Zaa, in which Xaa is preferably Ala or Leu, Yaa is preferably Ala or Tyr, and Zaa is preferably Ala, but then cleaves at a variable distance from the C-terminus. A typical cleavage is -Ala-Ala-Arg-Ala-Ala-Lys-Glu-Asn-Tyr-Ala-Leu-Ala-Ala. In the plant chloroplast, the enzyme removes the C-terminal extension of the D1 polypeptide of photosystem II

Other name(s): CtpA gene product (*Synechocystis* sp.); photosystem II D1 protein processing peptidase; protease Re; tail-specific protease; Tsp protease

Comments: Proteolytic processing of the D1 protein of photosystem II is necessary to allow the light-driven assembly of the tetranuclear manganese cluster, which is responsible for photosynthetic water oxidation. The recognition of the substrate is mediated by a PDZ domain, a small protein module that promotes protein-protein interactions by binding to internal or C-terminal sequences of their partner proteins. Type example of peptidase family S41.

References: [1496, 199, 1771]

[EC 3.4.21.102 created 2001]

EC 3.4.21.103

Accepted name: physarolisin

Reaction: Milk clotting activity. Preferential cleavage of Gly$^{8}$ Ser in B chain of insulin most rapidly, followed by Leu$^{11}$ Val, Cys(SO$_3$)H$^{19}$ Gly and Phe$^{24}$ Phe. No action on Ac-Phe-Tyr(II)$_2$.
Other name(s): Dictyostelium discoideum aspartic proteinase; Dictyostelium discoideum aspartic proteinase E; Physarum flavicomum aspartic proteinase; Physarum polycephalum acid proteinase; Physarum aspartic proteinase; physaropepsin

Comments: Belongs in peptidase family S53. From the slime mold Physarum polycephalum. Is not inhibited by pepstatin, but is blocked by methyl 2-diazoacetamidohexanoate. Closely similar enzymes are found in Dictyostelium discoideum and P. flavicomum. Formerly included in EC 3.4.23.6.

References: [1182, 2105, 2222, 3358, 2200]

[EC 3.4.21.103 created 1992 as EC 3.4.23.27 (EC 3.4.23.6 created 1992 (EC 3.4.23.6 created 1961 as EC 3.4.4.17, transferred 1972 to EC 3.4.23.6, modified 1981 [EC 3.4.23.7, EC 3.4.23.8, EC 3.4.23.9, EC 3.4.23.10, EC 3.4.99.1, EC 3.4.99.15 and EC 3.4.99.25 all created 1972 and incorporated 1978], part incorporated 1992), transferred 2003 to EC 3.4.21.103]

EC 3.4.21.104

Accepted name: mannan-binding lectin-associated serine protease-2

Reaction: Selective cleavage after Arg$^{223}$ in complement component C2 (-Ser-Leu-Gly-Arg$^{223}$-Lys-Ile-Gln-Ile) and after Arg$^{76}$ in complement component C4 (-Gly-Leu-Gln-Arg$^{76}$-Ala-Leu-Glu-Ile)

Other name(s): MASP-2; MASP2; MBP-associated serine protease-2; mannos-binding lectin-associated serine protease-2; p100; mannan-binding lectin-associated serine peptidase 2

Comments: Mannan-binding lectin (MBL) recognizes patterns of neutral carbohydrates, such as mannose and N-acetylglucosamine, on a wide range of microbial surfaces and is able to initiate activation of the lectin pathway of complement [3038]. This enzyme displays C$_{1s}$-like esterolytic activity (cf. EC 3.4.21.42, complement subcomponent C$_{1s}$). It also cleaves C4 and C2 with efficiencies that are relatively higher than those of EC 3.4.21.42 [2591]. Belongs in peptidase family S1A.

References: [1936, 3051, 2591, 48, 1117, 445, 3038]

[EC 3.4.21.104 created 2005]

EC 3.4.21.105

Accepted name: rhomboid protease

Reaction: Cleaves type-1 transmembrane domains using a catalytic dyad composed of serine and histidine that are contributed by different transmembrane domains

Comments: These endopeptidases are multi-spanning membrane proteins. Their catalytic site is embedded within the membrane and they cleave type-1 transmembrane domains. A catalytic dyad is involved in proteolysis rather than a catalytic triad, as was thought previously [1734]. They are important for embryo development in Drosophila melanogaster. Rhomboid is a key regulator of EGF receptor signalling and is responsible for cleaving Spitz, the main ligand of the Drosophila EGF receptor pathway. Belongs in peptidase family S54. Parasite-encoded rhomboid enzymes are also important for invasion of host cells by Toxoplasma and the malaria parasite. Rhomboids are widely conserved from bacteria to archaea to humans [1597, 3169].

References: [3172, 335, 1197, 1391, 2794, 3168, 1198, 1597, 3167, 3171, 3170, 3169, 1734, 3276]

[EC 3.4.21.105 created 2005]

EC 3.4.21.106

Accepted name: hepsin

Reaction: Cleavage after basic amino-acid residues, with Arg strongly preferred to Lys

Comments: This type-II membrane-associated serine peptidase has been implicated in cell growth and development [3506, 3093]. The enzyme has been shown to activate blood coagulation factor VII by cleavage of the Arg$^{152}$-Ile$^{157}$ peptide bound in BHK cells, thus indicating a possible role in the initiation of blood coagulation [1492]. There is no cleavage after aromatic or aliphatic residues [3506]. The occupancy of the S2 site is an absolute requirement for catalysis and a basic residue at that site is preferred to an aliphatic residue. The nature of the residue at S3 also affects hydrolysis, with Gln being much more favourable than Ala [3506]. Belongs in peptidase family S1A.

References: [3093, 3506, 3093, 1597, 3169, 1734, 3276]
References: [3506, 1492, 3093]

[EC 3.4.21.106 created 2006]

EC 3.4.21.107
Accepted name: peptidase Do
Reaction: Acts on substrates that are at least partially unfolded. The cleavage site P1 residue is normally between a pair of hydrophobic residues, such as Val-Val
Other name(s): DegP; DegP protease; HtrA; high temperature requirement protease A; HtrA heat shock protein; protease Do; Do protease
Comments: This serine endopeptidase is essential for the clearance of denatured or aggregated proteins from the inner-membrane and periplasmic space in *Escherichia coli*. Natural substrates of the enzyme include colicin A lysis protein, pilin subunits and MalS from *E. coli* [1417]. The enzyme has weak peptidase activity with casein and other non-native substrates [1417]. The peptidase acts as a chaperone at low temperatures but switches to a peptidase (heat shock protein) at higher temperatures [1806, 1626]. Molecular chaperones and peptidases control the folded state of proteins by recognizing hydrophobic stretches of polypeptide that become exposed by misfolding or unfolding. They then bind these hydrophobic substrates to prevent aggregation or assist in protein refolding. If attempts at refolding fail, then irreversibly damaged proteins are degraded by peptidases such as this enzyme [1626]. Belongs in peptidase family S1C.

References: [1806, 2744, 1417, 2962, 2337, 1626]

[EC 3.4.21.107 created 2006]

EC 3.4.21.108
Accepted name: HtrA2 peptidase
Reaction: Cleavage of non-polar aliphatic amino-acids at the P1 position, with a preference for Val, Ile and Met. At the P2 and P3 positions, Arg is selected most strongly with a secondary preference for other hydrophilic residues
Other name(s): high temperature requirement protein A2; HtrA2; Omi stress-regulated endoprotease; serine proteinase OMI; HtrA2 protease; OMI/HtrA2 protease; HtrA2/Omi; Omi/HtrA2
Comments: This enzyme is upregulated in mammalian cells in response to stress induced by both heat shock and tunicamycin treatment [1022]. It can induce apoptosis in a caspase-independent manner through its peptidase activity and in a caspase-dependent manner by disrupting the interaction between caspase and the inhibitor of apoptosis (IAP) [1921]. Belongs in peptidase family S1C.

References: [2886, 2670, 1921, 1022, 1762]

[EC 3.4.21.108 created 2006]

EC 3.4.21.109
Accepted name: matriptase
Reaction: Cleave various synthetic substrates with Arg or Lys at the P1 position and prefers small side-chain amino acids, such as Ala and Gly, at the P2 position
Other name(s): serine protease 14; membrane-type serine protease 1; MT-SP1; prostatin; serine protease TADG-15; tumor-associated differentially-expressed gene 15 protein; ST14; breast cancer 80 kDa protease; epithelin; serine endopeptidase SNC19; matriptase-1; matriptase-2; matriptase-3; TMPRSS6 (gene name)
Comments: This trypsin-like integral-membrane serine peptidase has been implicated in breast cancer invasion and metastasis [1722, 1786]. The enzyme can activate hepatocyte growth factor/scattering factor (HGF/SF) by cleavage of the two-chain form at an Arg residue to give active α- and β-HGF, but it does not activate plasminogen, which shares high homology with HGF [1722]. The enzyme can also activate urokinase plasminogen activator (uPA), which initiates the matrix-degrading peptidase cascade [1722, 1786]. Hemojuvelin has been shown to be a physiologic substrate for matriptase-2 [3383]. Belongs in peptidase family S1A.

References: [1722, 1786]
EC 3.4.21.110

Accepted name: C5a peptidase

Reaction: The primary cleavage site is at His^{67}→Lys^{68} in human C5a with a minor secondary cleavage site at Ala^{58}→Ser^{59}

Other name(s): streptococcal C5a peptidase; ScpA; ScpB; SCPA

Comments: This enzyme is a surface-associated subtilisin-like serine peptidase with very specific substrate specificity. Virulent strains of streptococci, including *Streptococcus pyogenes*, can evade human detection and phagocytosis by destroying the complement chemotaxin C5a. Cleavage of human C5a by this enzyme reduces the ability of C5a to bind receptors on the surface of polymorphonuclear neutrophil leukocytes (PMNLs) and thereby abolishes its chemotactic properties [3319, 55]. Belongs in peptidase family S8A.

References: [3319, 279, 500, 55, 2893, 3042]

[EC 3.4.21.110 created 2006]

EC 3.4.21.111

Accepted name: aqualysin 1

Reaction: Exhibits low specificity towards esters of amino acids with small hydrophobic or aromatic residues at the P1 position

Other name(s): caldolysin

Comments: This enzyme from the extreme thermophile, *Thermus aquaticus*, is an alkaline serine peptidase. It has three subsites, S1, S2, and S3, in the substrate binding site. The preferred amino acids at the S1 site are Ala and Phe, at the S2 site are Ala and norleucine and at the S3 site are Phe and Ile [3019]. These specificities are similar to those of EC 3.4.21.64 (peptidase K) and EC 3.4.21.62 (subtilisin BPN′) [3019]. The enzyme displays broad specificity for cleavage of insulin B-chain and hydrolyses elastin substrates such as succinyl-(Ala)<sub>n</sub>-p-nitroanilide (<sub>n</sub>=1,2,3) and some peptide esters [1938, 3019]. Belongs in peptidase family S8A.

References: [1938, 3018, 3019]

[EC 3.4.21.111 created 2006]

EC 3.4.21.112

Accepted name: site-1 protease

Reaction: Processes precursors containing basic and hydrophobic/aliphatic residues at P4 and P2, respectively, with a relatively relaxed acceptance of amino acids at P1 and P3

Other name(s): mammalian subtilisin/kexin isozyme 1; membrane-bound transcription factor site-1 protease; proprotein convertase SKI-1; proprotein convertase SKI-1/S1P1S1; S1P endopeptidase; S1P protease; site-1 peptidase; site-1 protease; SKI-1; SREBP proteinase; SREBP S1 protease; SREBP-1 proteinase; SREBP-2 proteinase; sterol regulatory element-binding protein proteinase; sterol regulatory element-binding protein site 1 protease; sterol-regulated luminal protease; subtilase SKI-1; subtilase SKI-1/S1P; subtilisin/kexin-isozyme 1

Comments: Cleaves sterol regulatory element-binding proteins (SREBPs) and thereby initiates a process by which the active fragments of the SREBPs translocate to the nucleus and activate genes controlling the synthesis and uptake of cholesterol and unsaturated fatty acids into the bloodstream [765]. The enzyme also processes pro-brain-derived neurotrophic factor and undergoes autocatalytic activation in the endoplasmic reticulum through sequential cleavages [1738]. The enzyme can also process the unfolded protein response stress factor ATF6 at an Arg-His-Lys-Lys<sup>+</sup> site [3439, 2739], and the envelope glycoprotein of the highly infectious Lassa virus [1738, 2739] and Crimean Congo hemorrhagic fever virus at Arg-Arg-Lys-Lys<sup>+</sup> [3217, 2739]. Belongs in peptidase family S8A.

References: [1722, 1786, 2489, 1586, 3383]

[EC 3.4.21.109 created 2006, modified 2022]
**EC 3.4.21.113**

**Accepted name:** pestivirus NS3 polyprotein peptidase  

**Reaction:** Leu is conserved at position P1 for all four cleavage sites. Alanine is found at position P1’ of the NS4A-NS4B cleavage site, whereas serine is found at position P1’ of the NS3-NS4A, NS4B-NS5A and NS5A-NS5B cleavage sites  

**Other name(s):** border disease virus NS3 endopeptidase; BDV NS3 endopeptidase; bovine viral diarrhea virus NS3 endopeptidase; BVDV NS3 endopeptidase; classical swine fever virus NS3 endopeptidase; CSFV NS3 endopeptidase; p80  

**Comments:** The polyprotein of noncytopathogenic pestiviruses is cleaved co- and post-translationally into at least 11 proteins (Npro, C, E1m, E1, E2, p7, NS2-3, NS4A, NS4B, NS5A, and NS5B) [3034]. The genomes of cytopathogenic pestivirus strains express at least one additional protein, called NS3 (p80) [3034]. This enzyme, which resides in the N-terminal region of NS3 (nonstructural protein 3), is essential for generation of its own C-terminus and for processing of the downstream cleavage sites, leading to the release of the pestivirus nonstructural proteins NS4A, NS4B, NS5A and NS5B [3354, 3034]. Belongs in peptidase family S31.

**References:** [3354, 3034, 3388, 3035]

---

**EC 3.4.21.114**

**Accepted name:** equine arterivirus serine peptidase  

**Reaction:** Cleavage of (Glu/Gln)-(Gly/Ser/Ala) in arterivirus replicase translation products ORF1a and ORF1ab  

**Comments:** In the equine arterivirus (EAV), the replicase gene is translated into open reading frame 1a (ORF1a) and ORF1ab polyproteins. This enzyme is the main viral protease and processes five cleavage sites in the ORF1a protein and three in the ORF1b-encoded part of the ORF1ab protein to yield nonstructural proteins (nsp5-nsp12) [176]. It combines the catalytic system of a chymotrypsin-like serine peptidase (His-Asp-Ser catalytic triad) with the substrate specificity of a 3C-like serine peptidase (Glu or Gln) at the P1 position and a small amino-acid residue (Gly, Ser or Ala) at the P1’ position [2844]. Cleavage of ORF1ab by this enzyme is essential for viral replication [3195]. Belongs in peptidase family S32.

**References:** [2844, 3195, 176]

---

**EC 3.4.21.115**

**Accepted name:** infectious pancreatic necrosis birnavirus Vp4 peptidase  

**Reaction:** Cleaves the (Ser/Thr)-Xaa-Ala-(Ser/Ala)-Gly motif in the polyprotein NH₂-pVP2-VP4-VP3-COOH of infectious pancreatic necrosis virus at the pVP2-VP4 and VP4-VP3 junctions  

**Other name(s):** infectious pancreatic necrosis virus protease; IPNV Vp4 protease; IPNV Vp4 peptidase; NS protease; NS-associated protease; Vp4 protease  

**Comments:** Infectious pancreatic necrosis virus (IPNV) is a birnavirus that causes an acute, contagious disease in young salmonid fish [2384]. As with most viruses that infect eukaryotic cells, the proteolytic processing of viral precursor proteins is a crucial step in the life cycle of this virus [2384]. pVP2 is converted into VP2 by cleavage near the carboxy end of pVP2. This cleavage is most likely due to host-cell proteases rather than VP4 [2384, 666]. Differs from most serine peptidases in not having the catalytic triad Ser-His-Asp [2384]. Belongs in peptidase family S50.

**References:** [1900, 2384, 666]
EC 3.4.21.116

Accepted name: SpoIVB peptidase

Reaction: Self-cleaves Val\textsuperscript{52}→Asn\textsuperscript{53}, Ala\textsuperscript{62}→Phe\textsuperscript{63} and Val\textsuperscript{74}→Thr\textsuperscript{75} at the N-terminus of SpoIVB

Other name(s): sporulation factor IV B protease

Comments: This enzyme plays a central role in a regulatory checkpoint (the σ\textsuperscript{K} checkpoint), which coordinates gene expression during the later stages of spore formation in Bacillus subtilis [3243, 1228]. The enzyme activates proteolytic processing of a sporulation-specific sigma factor, pro-σ\textsuperscript{K}, to its mature and active form, σ\textsuperscript{K}, by self-cleavage [3243, 1228]. The enzyme is also subject to secondary proteolysis, which presumably inactivates SpoIVB [1228]. The enzyme is also essential for the formation of heat-resistant spores. Belongs in peptidase family S55.

References: [3243, 1227, 1228, 679]

[EC 3.4.21.116 created 2006]

EC 3.4.21.117

Accepted name: stratum corneum chymotryptic enzyme

Reaction: Cleavage of proteins with aromatic side chains in the P1 position

Other name(s): kallikrein 7; SCCE; KLK7; PRSS6; hK7

Comments: This enzyme has wide substrate specificity, being able to degrade heat-denatured bovine casein and the α-chain of native human fibrinogen. It cleaves the B chain of bovine insulin at Leu\textsuperscript{6}→Cys\textsuperscript{7}, Tyr\textsuperscript{16}→Leu\textsuperscript{17}, Phe\textsuperscript{25}→Tyr\textsuperscript{26} and Tyr\textsuperscript{26}→Thr\textsuperscript{27} [2826]. It is thought to play a role in the desquamation (skin-shedding) of the outer layer of skin, the stratum corneum, by degrading intercellular cohesive structures [2826, 724]. Belongs in peptidase family S1A.

References: [2826, 724, 1107, 3467, 3205]

[EC 3.4.21.117 created 2006]

EC 3.4.21.118

Accepted name: kallikrein 8

Reaction: Cleavage of amide substrates following the basic amino acids Arg or Lys at the P1 position, with a preference for Arg over Lys

Other name(s): KLK8; PRSS19; human kallikrein 8; hK8; mK8; ovasin; tumor-associated differentially expressed gene 14; TADG-14; NP; neuropsin

Comments: The enzyme is activated by removal of an N-terminal prepropeptide [2768, 1552]. The highest amidolytic activity is observed using Boc-Val-Pro-Arg→7-amido-4-methylcoumarin, which is a substrate of α-thrombin [2768, 1552]. Substrates lacking basic amino acids in the P1 position are not cleaved [1552]. The enzyme degrades casein, fibronectin, gelatin, collagen type IV, fibrinogen, and high-molecular-mass kininogen [2482] and is associated with diseases such as ovarian cancer and Alzheimer’s disease [1552]. Belongs in peptidase family S1A.

References: [457, 2768, 2482, 1552]

[EC 3.4.21.118 created 2006]

EC 3.4.21.119

Accepted name: kallikrein 13

Reaction: Hydrolyses mouse Ren2 protein (a species of prorenin present in the submandibular gland) on the carboxy side of the arginine residue at the Lys-Arg pair in the N-terminus, to yield mature renin

Other name(s): KLK13; kallikrein mK13; mGK-13; mK13; mKLK13; prorenin converting enzyme 1; PRECE-1; prorenin-converting enzyme; PRECE; proteinase P

References:

[EC 3.4.21.119 created 2006]
Comments: The enzyme is specific for prorenin from the mouse submandibular gland, as prorenin from the mouse kidney (Ren1) and human prorenin are not substrates [2156]. Site-directed mutagenesis studies have shown that the enzyme will also cleave prorenin when Lys-Arg is replaced by Arg-Arg or Gln-Arg but the rate of reaction is much slower when Lys-Lys is used. This enzyme is also able to process pro-interleukin-1β (pro-IL-1β) in mouse submandibular gland to form IL-1β [3419]. Belongs in peptidase family S1A.

References: [2156, 1540, 1522, 3419]

[EC 3.4.21.119 created 2006]

EC 3.4.21.120
Accepted name: oviductin
Reaction: Preferential cleavage at Gly-Ser-Arg^{373} of glycoprotein gp43 in Xenopus laevis coelemic egg envelope to yield gp41
Other name(s): oviductal protease
Comments: The egg envelope of the South African clawed frog (Xenopus laevis) is modified during transit of the egg through the pars rectus oviduct, changing the egg envelope from an unfertilizable form to a fertilizable form. This process involves the conversion of glycoprotein gp43 to gp41 (ZPC) by the pars recta protease oviductin. It is thought that the enzymically active protease molecule comprises the N-terminal protease domain coupled to two C-terminal CUB domains, which are related to the mammalian spermidhesin molecules implicated in mediating sperm-envelope interactions [1799]. The enzyme is also found in the Japanese toad (Bufo japonicus) [1225]. Belongs in peptidase family S1.

References: [1115, 1799, 1225]

[EC 3.4.21.120 created 2007]

EC 3.4.21.121
Accepted name: Lys-Lys/Arg-Xaa endopeptidase
Other name(s): ASP (Aeromonas sobria)-type peptidase; Aeromonas extracellular serine protease
Comments: The enzyme is a serine peptidase, which has been shown to cleave prothrombin and prekallikrein. It hydrolyses the complement component C5 releasing complement component C5a.

References: [1576, 2207, 1575, 1319, 2206]

[EC 3.4.21.121 created 2013]

EC 3.4.21.122
Accepted name: transmembrane protease serine 2
Reaction: The enzyme cleaves angiotensin-converting enzyme 2 (EC 3.4.17.23) and cleaves influenza A and B virus and coronavirus spike glycoproteins at arginine residues.
Other name(s): TMPRSS2 (gene name); epitheliasin
Comments: The enzyme, present in mammalia, cleaves and inactivates EC 3.4.17.23, angiotensin-converting enzyme 2 (ACE2), at arginine residues in the region R697 to R716, which enhances influenza and coronavirus uptake [1205]. The enzyme also cleaves and activates influenza and coronavirus spike glycoproteins and thus facilitates virus-cell membrane fusions. The cleavage of SARS-COV2 spike glycoprotein occurs between the S2 and S2' site at SKPSKR/SFIEDL, while the cleavage of MERS-COV glycoprotein occurs at GSRSAR/SAIEDL.

References: [1371, 1372, 295, 226, 223, 6, 1205, 1784, 228]

[EC 3.4.21.122 created 2020]
EC 3.4.22 Cysteine endopeptidases

EC 3.4.22.1
Accepted name: cathepsin B
Reaction: Hydrolysis of proteins with broad specificity for peptide bonds. Preferentially cleaves -Arg-Arg bonds in small molecule substrates (thus differing from cathepsin L). In addition to being an endopeptidase, shows peptidyl-dipeptidase activity, liberating C-terminal dipeptides
Other name(s): cathepsin B1 (obsolete); cathepsin II
Comments: An intracellular (lysosomal) enzyme in peptidase family C1 (papain family)
References: [283, 173, 2422, 172, 1550]

[EC 3.4.22.1 created 1972]

EC 3.4.22.2
Accepted name: papain
Reaction: Hydrolysis of proteins with broad specificity for peptide bonds, but preference for an amino acid bearing a large hydrophobic side chain at the P2 position. Does not accept Val in P1
Other name(s): papayotin; summetrin; velardon; papaine; Papaya peptidase I
Comments: Type example of peptidase family C1 from latex of the papaya (Carica papaya) fruit. Inhibited by compound E-64 and proteins of the cystatin family.
References: [1459, 1980]

[EC 3.4.22.2 created 1961 as EC 3.4.4.10, transferred 1972 to EC 3.4.22.2, modified 1976, modified 2000]

EC 3.4.22.3
Accepted name: ficain
Reaction: Similar to that of papain
Other name(s): ficin; debricin; higueroxyloxdelabarre
Comments: The major proteolytic component of the latex of fig, Ficus glabrata. Cysteine endopeptidases with similar properties are present in other members of the large genus Ficus. In peptidase family C1 (papain family).
References: [1777, 326]

[EC 3.4.22.3 created 1961 as EC 3.4.4.12, transferred 1972 to EC 3.4.22.3]

[3.4.22.4 Transferred entry. bromelain (stem). Now EC 3.4.22.32 (stem bromelain) and EC 3.4.22.33 (fruit bromelain)]

[EC 3.4.22.4 created 1972, deleted 1992 [EC 3.4.22.5 created 1972, incorporated 1978]]

[3.4.22.5 Transferred entry. bromelain (juice). Now EC 3.4.22.32 (stem bromelain) and EC 3.4.22.33 (fruit bromelain)]

[EC 3.4.22.5 created 1972, deleted 1978]

EC 3.4.22.6
Accepted name: chymopapain
Reaction: Similar to that of papain
Other name(s): chymopapain A; chymopapain B; chymopapain S
Comments: The major endopeptidase of papaya (Carica papaya) latex. It has multiple chromatographic forms. In peptidase family C1 (papain family).
References: [326, 1370, 368]

[EC 3.4.22.6 created 1961 as EC 3.4.4.11, transferred 1972 to EC 3.4.22.6]
EC 3.4.22.7

**Accepted name:** asclepain

**Reaction:** Similar to that of papain

**Comments:** From the latex of milkweed, *Asclepias syriaca*. It has multiple forms, and is in peptidase family C1 (papain family)

**References:** [324]

[EC 3.4.22.7 created 1972]

EC 3.4.22.8

**Accepted name:** clostripain

**Reaction:** Preferential cleavage: Arg, including Arg-Pro, but not Lys-

**Other name(s):** clostridiopeptidase B; clostridium histolyticum proteinase B; α-clostripain; clostridiopeptidase

**Comments:** From the bacterium *Clostridium histolyticum*. It requires Ca$^{2+}$ ions and is inhibited by EDTA. Type example of peptidase family C11.

**References:** [2030, 976, 977]

[EC 3.4.22.8 created 1961 as EC 3.4.4.20, transferred 1972 to EC 3.4.22.8]

[3.4.22.9] Transferred entry. yeast proteinase B. Now EC 3.4.21.48, cerevisin]

[EC 3.4.22.9 created 1972, deleted 1981]

EC 3.4.22.10

**Accepted name:** streptopain

**Reaction:** Preferential cleavage with hydrophobic residues at P2, P1 and P1′

**Other name(s):** *Streptococcus* peptidase A; streptococcal cysteine proteinase; *Streptococcus* protease

**Comments:** From the bacterium, group A *Streptococcus*. Formed from the proenzyme by limited proteolysis. Type example of peptidase family C10.

**References:** [737, 1823, 2972, 1827]

[EC 3.4.22.10 created 1961 as EC 3.4.4.18, transferred 1972 to EC 3.4.22.10]


[EC 3.4.22.11 created 1976, deleted 1978 [transferred to EC 3.4.99.45, deleted 1993]]

[3.4.22.12] Transferred entry. γ-glutamyl hydrolase. Now EC 3.4.19.9, γ-glutamyl hydrolase]

[EC 3.4.22.12 created 1978, deleted 1992]

[3.4.22.13] Deleted entry. staphylococcal cysteine proteinase]


EC 3.4.22.14

**Accepted name:** actinidain

**Reaction:** Similar to that of papain

**Other name(s):** actinidin; Actinidia anionic protease; proteinase A$_2$ of *Actinidia chinensis*

**Comments:** From the kiwi fruit or Chinese gooseberry (*Actinidia chinensis*). In peptidase family C1 (papain family)

**References:** [138, 1459, 139]

[EC 3.4.22.14 created 1978]
**EC 3.4.22.15**

**Accepted name:** cathepsin L  
**Reaction:** Similar to that of papain. As compared to cathepsin B, cathepsin L exhibits higher activity towards protein substrates, but has little activity on Z-Arg-Arg-NHMec, and no peptidyl-dipeptidase activity  
**Other name(s):** Aldrichina grahami cysteine proteinase  
**Comments:** A lysosomal enzyme in peptidase family C1 (papain family) that is readily inhibited by the diazomethane inhibitor Z-Phe-Phe-CHN2 or the epoxide inhibitor E-64  
**References:** [173, 172, 1424, 1550]

[EC 3.4.22.15 created 1978 (EC 3.4.99.19 created 1972, incorporated 1981)]

**EC 3.4.22.16**

**Accepted name:** cathepsin H  
**Reaction:** Hydrolysis of proteins, acting as an aminopeptidase (notably, cleaving Arg→ bonds) as well as an endopeptidase  
**Other name(s):** cathepsin B3; benzoylarginine-naphthylamide (BANA) hydrolase (obsolete); cathepsin Ba; aleurain; N-benzoylarginine-β-naphthylamide hydrolase  
**Comments:** Present in lysosomes of mammalian cells. In peptidase family C1 (papain family)  
**References:** [173, 329, 882]

[EC 3.4.22.16 created 1981, modified 1989]

[3.4.22.17 Transferred entry. calpain. Now EC 3.4.22.53, calpain-2]  
[EC 3.4.22.17 created 1981 [EC 3.4.24.5 created 1978, part incorporated 1989], deleted 2003]

[3.4.22.18 Transferred entry. prolyl endopeptidase (thiol-dependent). Now EC 3.4.21.26, prolyl oligopeptidase]  
[EC 3.4.22.18 created 1981, deleted 1992]

[3.4.22.19 Transferred entry. endo-oligopeptidase. Now EC 3.4.24.15, thimet oligopeptidase]  
[EC 3.4.22.19 created 1989, deleted 1992]

[3.4.22.20 Deleted entry. dinorphin-converting enzyme]  
[EC 3.4.22.20 created 1989, deleted 1992]

[3.4.22.21 Transferred entry. yeast cysteine proteinase E. Now EC 3.4.25.1, proteasome endopeptidase complex]  
[EC 3.4.22.21 created 1989, deleted 1992]

[3.4.22.22 Transferred entry. yeast cysteine proteinase D. Now EC 3.4.24.37, saccharolysin]  
[EC 3.4.22.22 created 1989, deleted 1992]

[3.4.22.23 Transferred entry. yeast cysteine proteinase F. Now EC 3.4.21.61, kexin]  
[EC 3.4.22.23 created 1989, deleted 1992]

**EC 3.4.22.24**

**Accepted name:** cathepsin T  
**Reaction:** Interconversion of the three forms of tyrosine aminotransferase, EC 2.6.1.5  
**Comments:** Degrades azocasein and denatured hemoglobin; the only native protein on which it has been shown to act is tyrosine aminotransferase  
**References:** [995, 994, 2406]

[EC 3.4.22.24 created 1990]
EC 3.4.22.25
Accepted name: glycyl endopeptidase
Reaction: Preferential cleavage: Gly−, in proteins and small molecule substrates
Other name(s): papaya peptidase B; papaya proteinase IV; glycine-specific proteinase; chymopapain; Papaya protei
 Comments: From the papaya plant, Carica papaya. Not inhibited by chicken cystatin, unlike most other homologi
ges of papain, but in peptidase family C1 (papain family)
References: [2419, 369, 2556, 371, 370]

EC 3.4.22.26
Accepted name: cancer procoagulant
Reaction: Specific cleavage of Arg−Ile bond in Factor X to form Factor Xa
Comments: Apparently produced only by malignant and fetal cells
References: [784, 785]

EC 3.4.22.27
Accepted name: cathepsin S
Reaction: Similar to cathepsin L, but with much less activity on Z-Phe-Arg−NHMec, and more activity on the Z-Val-Val-Arg−
Comments: A lysosomal cysteine endopeptidase that is unusual amongst such enzymes for its stability to neutral
pH. In peptidase family C1 (papain family)
References: [3150, 333, 1549]

EC 3.4.22.28
Accepted name: picornain 3C
Reaction: Selective cleavage of Gln−Gly bond in the poliovirus polyprotein. In other picornavirus reactions Glu may be substituted for Gln, and Ser or Thr for Gly
Other name(s): picornavirus endopeptidase 3C; poliovirus protease 3C; rhinovirus protease 3C; foot-and-mouth protease 3C; poliovirus proteinase 3C; rhinovirus proteinase 3C; coxsackievirus 3C proteinase; foot-and-mouth-disease virus proteinase 3C; 3C protease; 3C proteinase; cysteine proteinase 3C; hepatitis A virus 3C proteinase; protease 3C; tomato ringspot nepovirus 3C-related protease
Comments: From entero-, rhino-, aphto- and cardioviruses. Larger than the homologous virus picornain 2A. Type example of peptidase family C3
References: [1357, 193, 1620, 2188]

EC 3.4.22.29
Accepted name: picornain 2A
Reaction: Selective cleavage of Tyr−Gly bond in picornavirus polyprotein
Other name(s): picornavirus endopeptidase 2A; poliovirus protease 2A; rhinovirus protease 2A; 2A protease; 2A protei
Comments: From entero-, rhino-, aphto- and cardioviruses. Smaller than the homologous picornain 3C, which is also in peptidase family C3 (picornain 3C family)
References: [193, 1596, 1620]
EC 3.4.22.30
Accepted name: caricain
Reaction: Hydrolysis of proteins with broad specificity for peptide bonds, similar to those of papain and chymopapain
Other name(s): papaya peptidase A; papaya peptidase II; papaya proteinase; papaya proteinase III; papaya proteinase 3; proteinase 0; papaya proteinase A; chymopapain S; Pp
Comments: From papaya plant, *Carica papaya*. In peptidase family C1 (papain family)
References: [2684, 2568, 2420, 325, 3517, 702]

[EC 3.4.22.30 created 1992]

EC 3.4.22.31
Accepted name: ananain
Reaction: Hydrolysis of proteins with broad specificity for peptide bonds. Best reported small molecule substrate Bz-Phe-Val-Arg-NHMec, but broader specificity than fruit bromelain
Other name(s): stem bromelain; fruit bromelain
Comments: From stem of pineapple plant, *Ananas comosus*. Differs from stem and fruit bromelains in being inhibited by chicken cystatin. In peptidase family C1 (papain family)
References: [2595, 2596]

[EC 3.4.22.31 created 1992]

EC 3.4.22.32
Accepted name: stem bromelain
Reaction: Broad specificity for cleavage of proteins, but strong preference for Z-Arg-Arg-NHMec amongst small molecule substrates
Other name(s): bromelain; pineapple stem bromelain
Comments: The most abundant of the cysteine endopeptidases of the stem of the pineapple plant, *Ananas comosus*. Distinct from the bromelain found in the pineapple fruit (EC 3.4.22.33). Scarcely inhibited by chicken cystatin and also very slowly inactivated by E-64. In peptidase family C1 (papain family).
References: [326, 2595, 2557, 2596]

[EC 3.4.22.32 created 1965 as EC 3.4.4.24, transferred 1972 to EC 3.4.22.4, part transferred 1992 to EC 3.4.22.32]

EC 3.4.22.33
Accepted name: fruit bromelain
Reaction: Hydrolysis of proteins with broad specificity for peptide bonds. Bz-Phe-Val-Arg-NHMec is a good synthetic substrate, but there is no action on Z-Arg-Arg-NHMec (c.f. stem bromelain)
Other name(s): juice bromelain; ananase; bromelase; bromelin; extranase; pinase; pineapple enzyme; traumanase; fruit bromelain FA2
Comments: From the pineapple plant, *Ananas comosus*. Scarcely inhibited by chicken cystatin. Another cysteine endopeptidase, with similar action on small molecule substrates, pinguinain, is obtained from the related plant, *Bromelia pinguin*, but pinguinain differs from fruit bromelain in being inhibited by chicken cystatin [2596].
References: [2663, 3397, 2321, 2596]

[EC 3.4.22.33 created 1965 as EC 3.4.4.24, transferred 1972 to EC 3.4.22.4, part transferred 1992 to EC 3.4.22.33]

EC 3.4.22.34
Accepted name: legumain
Reaction: Hydrolysis of proteins and small molecule substrates at Asn-Xaa bonds
Other name(s): asparaginyl endopeptidase; citvac; proteinase B (ambiguous); hemoglobinase (ambiguous); PRSC1 gene product (*Homo sapiens*); vicilin peptidohydrolase; bean endopeptidase
Comments: Best known from legume seeds, the trematode *Schistosoma mansoni* and mammalian lysosomes. Not inhibited by compound E-64. Type example of peptidase family C13

References: [1110, 572, 448]

[EC 3.4.22.34 created 1992, modified 2000]

**EC 3.4.22.35**

**Accepted name:** histolysain  
**Reaction:** Hydrolysis of proteins, including basement membrane collagen and azocasein. Preferential cleavage: Arg-Arg in small molecule substrates including Z-Arg-Arg-NHMe

**Other name(s):** histolysin; *Entamoeba histolytica* cysteine proteinase; amebapain; *Entamoeba histolytica* cysteine protease; *Entamoeba histolytica* neutral thiol proteinase

**Comments:** From the protozoan, *Entamoeba histolytica*. In peptidase family C1 (papain family)

References: [1855, 1846]

[EC 3.4.22.35 created 1992]

**EC 3.4.22.36**

**Accepted name:** caspase-1  
**Reaction:** Strict requirement for an Asp residue at position P1 and has a preferred cleavage sequence of Tyr-Val-Ala-Asp

**Other name(s):** interleukin-1β-converting enzyme; protease VII; protease A; interleukin-1β precursor proteinase; interleukin-1 converting enzyme; interleukin-1β-converting endopeptidase; interleukin-1β convertase; interleukin-1β converting enzyme; interleukin-1β precursor proteinase; prointerleukin-1β protease; precursor interleukin-1β converting enzyme; pro-interleukin-1β proteinase; ICE

**Comments:** From mammalian monocytes. This enzyme is part of the family of inflammatory caspases, which also includes caspase-4 (EC 3.4.22.57) and caspase-5 (EC 3.4.22.58) in humans and caspase-11 (EC 3.4.22.64), caspase-12, caspase-13 and caspase-14 in mice. Contains a caspase-recruitment domain (CARD) in its N-terminal prodomain, which plays a role in procaspase activation [1920, 424]. Cleaves pro-interleukin-1β (pro-IL-1β) to form mature IL-1β, a potent mediator of inflammation. Also activates the proinflammatory cytokine, IL-18, which is also known as interferon-γ-inducing factor [1920]. Inhibited by Ac-Tyr-Val-Ala-Asp-CHO. Caspase-11 plays a critical role in the activation of caspase-1 in mice, whereas caspase-4 enhances its activation in humans [424]. Belongs in peptidase family C14.

References: [1265, 3061, 3060, 41, 1906, 1920, 424]

[EC 3.4.22.36 created 1993, modified 1997, modified 2007]

**EC 3.4.22.37**

**Accepted name:** gingipain R  
**Reaction:** Hydrolysis of proteins and small molecule substrates, with a preference for Arg in P1

**Other name(s):** Arg-gingipain; gingipain-1; argingipain; Arg-gingivain-55 proteinase; Arg-gingivain-70 proteinase; Arg-gingivain-75 proteinase; arginine-specific cysteine protease; arginine-specific gingipain; arginine-specific gingivain; RGP-1; RGP

**Comments:** A secreted endopeptidase from the bacterium *Porphyromonas gingivalis*. Strongly activated by glycine [456], and stabilized by Ca²⁺. Precursor molecule contains a hemagglutinin domain [1551, 2365]. Misleadingly described in some literature as "trypsin-like", being a cysteine peptidase, type example of peptidase family C25.

References: [456, 1551, 2365]

[EC 3.4.22.37 created 1996]
EC 3.4.22.38

Accepted name: cathepsin K

Reaction: Broad proteolytic activity. With small-molecule substrates and inhibitors, the major determinant of specificity is P2, which is preferably Leu, Met, Phe, and not Arg

Other name(s): cathepsin O and cathepsin X (both misleading, having been used for other enzymes); cathepsin O

Comments: Prominently expressed in mammalian osteoclasts, and believed to play a role in bone resorption. In peptidase family C1 (papain family)

References: [1325, 294, 330, 3497, 1968]

[EC 3.4.22.38 created 1997]

EC 3.4.22.39

Accepted name: adenain

Reaction: Cleaves proteins of the adenovirus and its host cell at two consensus sites: -Yaa-Xaa-Gly-Gly+Xaa- and -Yaa-Xaa-Gly-Xaa-Gly- (in which Yaa is Met, Ile or Leu, and Xaa is any amino acid)

Comments: A cysteine endopeptidase from adenoviruses, the type example of peptidase family C5, with a protein fold unlike that known for any other peptidase [661]. Activity is greatly stimulated by the binding to the enzyme of an 11-residue peptide from the adenovirus capsid protein pre-VI at a site separate from the active site [3295]

References: [3295, 661, 3294]

[EC 3.4.22.39 created 2000]

EC 3.4.22.40

Accepted name: bleomycin hydrolase

Reaction: Inactivates bleomycin B2 (a cytotoxic glycometallopeptide) by hydrolysis of a carboxyamide bond of β-aminoalanine, but also shows general aminopeptidase activity. The specificity varies somewhat with source, but amino acid arylamides of Met, Leu and Ala are preferred [1]

Other name(s): aminopeptidase C (Lactococcus lactis) [4]

Comments: The molecule is a homohexamer in which the monomers have a papain-like tertiary structure (in peptidase family C1). The active sites are on the walls of a central channel through the molecule, and access of substrate molecules to them is obstructed by this and by the C-terminus of each polypeptide chain [3501]. Bleomycin can scarcely be the natural substrate, and there are reports of limited endopeptidase activity. Known from bacteria as well as eukaryotic organisms. Hydrolase H from chicken muscle has many similarities to bleomycin hydrolase, but hydrolyses Ph-CO-Arg-2-naphthylamine as well as aminopeptidase substrates [15].

References: [332, 15, 3501, 2028]

[EC 3.4.22.40 created 2000]

EC 3.4.22.41

Accepted name: cathepsin F

Reaction: The recombinant enzyme cleaves synthetic substrates with Phe and Leu (better than Val) in P2, with high specificity constant (k_cat/K_m) comparable to that of cathepsin L

Comments: Cathepsin F is a lysosomal cysteine endopeptidase of family C1 (papain family), most active at pH 5.9. The enzyme is unstable at neutral pH values and is inhibited by compound E-64. Cathepsin F is expressed in most tissues of human, mouse and rat. Human gene locus: 11q13.1-13.3

References: [2652, 2131, 3318, 3255]

[EC 3.4.22.41 created 2000]

EC 3.4.22.42

Accepted name: cathepsin O
Reaction: The recombinant human enzyme hydrolyses synthetic endopeptidase substrates including Z-Phe-Arg-NHMeC and Z-Arg-Arg-NHMeC

Comments: Cathepsin O is a lysosomal cysteine peptidase of family C1 (papain family). The recombinant human enzyme is catalytically active at pH 6.0 and is inhibited by compound E-64. Cathepsin O is ubiquitously expressed in human tissues and the human gene locus is 4q31-32

References: [2650, 3207]

[EC 3.4.22.42 created 2000]

EC 3.4.22.43

Accepted name: cathepsin V

Reaction: The recombinant enzyme hydrolyses proteins (serum albumin, collagen) and synthetic substrates (Z-Phe-Arg-NHMeC > Z-Leu-Arg-NHMeC > Z-Val-Arg-NHMeC)

Other name(s): Cathepsin L2, cathepsin U

Comments: Cathepsin V is a human lysosomal cysteine endopeptidase of family C1 (papain family) that is maximally active at pH 5.7 and unstable at neutral pH. Compound E-64, leupeptin and chicken cystatin are inhibitors. Human cathepsin V shows expression restricted to thymus, testis, corneal epithelium and some colon and breast carcinomas. Human gene locus: 9q22.2

References: [331, 16, 2651]

[EC 3.4.22.43 created 2000]

EC 3.4.22.44

Accepted name: nuclear-inclusion-a endopeptidase

Reaction: Hydrolyses glutaminyl bonds, and activity is further restricted by preferences for the amino acids in P6 - P1′ that vary with the species of potyvirus, e.g. Glu-Xaa-Xaa-Tyr-Xaa-Gln-(Ser or Gly) for the enzyme from tobacco etch virus. The natural substrate is the viral polyprotein, but other proteins and oligopeptides containing the appropriate consensus sequence are also cleaved.

Other name(s): potyvirus NIa protease

Comments: The potyviruses cause diseases in plants, and inclusion bodies appear in the host cell nuclei; protein a of the inclusion bodies is the endopeptidase. The enzyme finds practical use when encoded in vectors for the artificial expression of recombinant fusion proteins, since it can confer on them the capacity for autolytic cleavage. It is also reported that transgenic plants expressing the enzyme are resistant to viral infection. Type example of peptidase family C4.

References: [804, 1526, 2985, 1529]

[EC 3.4.22.44 created 2000]

EC 3.4.22.45

Accepted name: helper-component proteinase

Reaction: Hydrolyses a Gly-Gly bond at its own C-terminus, commonly in the sequence -Tyr-Xaa-Val-Gly-Gly, in the processing of the potyviral polyprotein

Other name(s): HC-Pro

Comments: Known from many potyviruses. The helper component-proteinase of the tobacco etch virus is a multifunctional protein with several known activities: the N-terminal region is required for aphid transmission and efficient genome amplification, the central region is required for long-distance movement in plants, and the C-terminal domain has cysteine endopeptidase activity. Type example of peptidase family C6.

References: [1476, 3208]

[EC 3.4.22.45 created 2001]
EC 3.4.22.46
Accepted name: L-peptidase
Reaction: Autocatalytically cleaves itself from the polypeptide of the foot-and-mouth disease virus by hydrolysis of a Lys→Gly bond, but then cleaves host cell initiation factor eIF-4G at bonds -Gly→Arg- and -Lys→Arg-
Comments: Best known from foot-and-mouth disease virus, but occurs in other aphthoviruses and cardioviruses. Destruction of initiation factor eIF-4G has the effect of shutting off host-cell protein synthesis while allowing synthesis of viral proteins to continue. The tertiary structure reveals a distant relationship to papain and, consistent with this, compound E-64 is inhibitory. Type example of peptidase family C28.
References: [2394, 1055]

[EC 3.4.22.46 created 2001]

EC 3.4.22.47
Accepted name: gingipain K
Reaction: Endopeptidase with strict specificity for lysyl bonds
Other name(s): Lys-gingipain; PrtP proteinase
Comments: Activity is stimulated by glycine. Known from the bacterium Porphyromonas gingivalis and contributes to the pathogenicity of the organism. In peptidase family C25.
References: [2402, 563]

[EC 3.4.22.47 created 2003]

EC 3.4.22.48
Accepted name: staphopain
Reaction: Broad endopeptidase action on proteins including elastin, but rather limited hydrolysis of small-molecule substrates. Assays are conveniently made with hemoglobin, casein or Z-Phe-Arg-NHMec as substrate
Other name(s): staphylopain
Comments: Known from species of Staphylococcus. Type example of peptidase family C47.
References: [1230, 2432, 701]

[EC 3.4.22.48 created 2003]

EC 3.4.22.49
Accepted name: separase
Reaction: All bonds known to be hydrolysed by this endopeptidase have arginine in P1 and an acidic residue in P4. P6 is often occupied by an acidic residue or by an hydroxy-amino-acid residue, the phosphorylation of which enhances cleavage
Other name(s): separin
Comments: In both budding yeast and human cells, cleavage of the cohesin subunit Scc1 by separase is required for sister chromatid separation in mitosis. Budding yeast separase is also known to cleave the Rec8 subunit of a meiotic cohesin complex and the kinetochore protein Slk19. Type example of peptidase family C50.
References: [3235]

[EC 3.4.22.49 created 2003]

EC 3.4.22.50
Accepted name: V-cath endopeptidase
Reaction: Endopeptidase of broad specificity, hydrolysing substrates of both cathepsin L and cathepsin B
Other name(s): AcNPV protease; BmNPV protease; NPV protease; baculovirus cathepsin; nucleopolyhedrosis virus protease; viral cathepsin
Comments: In peptidase family C1. Contributes to the liquefaction of the tissues of the insect host in the late stages of infection by the baculovirus.

References: [2827, 1146]

[EC 3.4.22.50 created 2003]

EC 3.4.22.51

Accepted name: cruzipain

Reaction: Broad endopeptidase specificity similar to that of cathepsin L

Other name(s): congopain; cruzain; evansain; trypanopain

Comments: In peptidase family C1. Is located in the digestive vacuoles of the parasitic trypanosome and contributes to the nutrition of the organism by digestion of host proteins.

References: [414]

[EC 3.4.22.51 created 2003]

EC 3.4.22.52

Accepted name: calpain-1

Reaction: Broad endopeptidase specificity

Other name(s): µ-calpain; calcium-activated neutral protease I

Comments: In peptidase family C2. Requires Ca\(^{2+}\) at micromolar concentrations for activity. Cytosolic in animal cells. The active enzyme molecule is a heterodimer in which the large subunit contains the peptidase unit, and the small subunit is also a component of EC 3.4.22.53, calpain-2.

References: [715]

[EC 3.4.22.52 created 1981 as EC 3.4.22.17, transferred 2003 to EC 3.4.22.52]

EC 3.4.22.53

Accepted name: calpain-2

Reaction: Broad endopeptidase specificity

Other name(s): calcium-activated neutral protease II; m-calpain; milli-calpain

Comments: Type example of peptidase family C2. Requires Ca\(^{2+}\) at millimolar concentrations for activity. Cytosolic in animal cells. The active enzyme molecule is a heterodimer in which the large subunit contains the peptidase unit, and the small subunit is also a component of EC 3.4.22.52, calpain-1.

References: [2924, 715]

[EC 3.4.22.53 created 1981 as EC 3.4.22.17, transferred 2003 to EC 3.4.22.53]

EC 3.4.22.54

Accepted name: calpain-3

Reaction: Broad endopeptidase activity

Other name(s): p94; calpain p94; CAPN3; muscle calpain; calpain 3; calcium-activated neutral proteinase 3; muscle-specific calcium-activated neutral protease 3; CANP 3; calpain 1.3

Comments: This Ca\(^{2+}\)-dependent enzyme is found in skeletal muscle and is genetically linked to limb girdle muscular dystrophy type 2A [2866, 644]. The enzyme is activated by autoproteolytic cleavage of insertion sequence 1 (IS1), which allows substrates and inhibitors gain access to the active site [644]. Substrates include the protein itself [2539, 644] and connectin/titin [2867, 2308]. Belongs in peptidase family C2.

References: [2866, 2867, 2539, 644, 2308]

[EC 3.4.22.54 created 2007]
EC 3.4.22.55

Accepted name: caspase-2

Reaction: Strict requirement for an Asp residue at P1, with Asp\textsuperscript{316} being essential for proteolytic activity and has a preferred cleavage sequence of Val-Asp-Val-Ala-Asp→

Other name(s): ICH-1; NEDD-2; caspase-2L; caspase-2S; neural precursor cell expressed developmentally down-regulated protein 2; CASP-2; NEDD2 protein

Comments: Caspase-2 is an initiator caspase, as are caspase-8 (EC 3.4.22.61), caspase-9 (EC 3.4.22.62) and caspase-10 (EC 3.4.22.63) [424]. Contains a caspase-recruitment domain (CARD) in its N-terminal prodomain, which plays a role in procaspase activation [424]. Two forms of caspase-2 with antagonistic effects exist: caspase-2L induces programmed cell death and caspase-2S suppresses cell death [2,3,5]. Caspase-2 is activated by caspase-3 (EC 3.4.22.56), or by a caspase-3-like protease. Activation involves cleavage of the N-terminal prodomain, followed by self-proteolysis between the large and small subunits of pro-caspase-2 and further proteolysis into smaller fragments [1754]. Proteolysis occurs at Asp residues and the preferred substrate for this enzyme is a pentapeptide rather than a tetrapeptide [3502]. Apart from itself, the enzyme can cleave golgin-16, which is present in the Golgi complex and has a cleavage site that is unique for caspase-2 [1894, 3502]. αII-Spectrin, a component of the membrane cytoskeleton, is a substrate of the large isoform of pro-caspase-2 (caspase-2L) but not of the short isoform (caspase-2S). Belongs in peptidase family C14.

References: [1640, 3266, 1754, 1894, 3502, 424]

[EC 3.4.22.55 created 2007]

EC 3.4.22.56

Accepted name: caspase-3

Reaction: Strict requirement for an Asp residue at positions P1 and P4. It has a preferred cleavage sequence of Asp-Xaa-Xaa-Xaa-Asp→ with a hydrophobic amino-acid residue at P2 and a hydrophilic amino-acid residue at P3, although Val or Ala are also accepted at this position

Other name(s): CPP32; apopain; yama protein

Comments: Caspase-3 is an effector/executioner caspase, as are caspase-6 (EC 3.4.22.59) and caspase-7 (EC 3.4.22.60) [424]. These caspases are responsible for the proteolysis of the majority of cellular polypeptides [e.g. poly(ADP-ribose) polymerase (PARP)], which leads to the apoptotic phenotype [2186, 424]. Procaspase-3 can be activated by caspase-1 (EC 3.4.22.36), caspase-8 (EC 3.4.22.61), caspase-9 (EC 3.4.22.62) and caspase-10 (EC 3.4.22.63) as well as by the serine protease granzyme B [1622]. Caspase-3 can activate procaspase-2 (EC 3.4.22.55) [1754]. Activation occurs by inter-domain cleavage followed by removal of the N-terminal prodomain [1918]. Although Asp-Glu-(Val/Ile)-Asp is thought to be the preferred cleavage sequence, the enzyme can accommodate different residues at P2 and P3 of the substrate [788]. Like caspase-2, a hydrophobic residue at P5 of caspase-3 leads to more efficient hydrolysis, e.g. (Val/Leu)-Asp-Val-Ala-Asp→ is a better substrate than Asp-Val-Ala-Asp→. This is not the case for caspase-7 [788]. Belongs in peptidase family C14.

References: [1622, 1754, 2186, 788, 424, 1918]

[EC 3.4.22.56 created 2007]

EC 3.4.22.57

Accepted name: caspase-4

Reaction: Strict requirement for Asp at the P1 position. It has a preferred cleavage sequence of Tyr-Val-Ala-Asp→ but also cleaves at Asp-Glu-Val-Ala-Asp→

Other name(s): ICE\textsubscript{rel}II; ICE\textsubscript{rel}-II; Ich-2; transcript X; TX; TX protease; caspase 4; CASP-4
Comments: This enzyme is part of the family of inflammatory caspases, which also includes caspase-1 (EC 3.4.22.36) and caspase-5 (EC 3.4.22.58) in humans and caspase-11 (EC 3.4.22.64), caspase-12, caspase-13 and caspase-14 in mice. Contains a caspase-recruitment domain (CARD) in its N-terminal prodomain, which plays a role in procaspase activation [3,5,6]. The enzyme is able to cleave itself and the p30 caspase-1 precursor, but, unlike caspase-1, it is very inefficient at generating mature interleukin-1β (IL-1β) from pro-IL-1β [796, 793]. Both this enzyme and caspase-5 can cleave pro-caspase-3 to release the small subunit (p12) but not the large subunit (p17) [1452]. The caspase-1 inhibitor Ac-Tyr-Val-Ala-Asp-CHO can also inhibit this enzyme, but more slowly [793]. Belongs in peptidase family C14.

References: [796, 1454, 1452, 793, 1920, 424]

[EC 3.4.22.57 created 2007]

EC 3.4.22.58

Accepted name: caspase-5

Reaction: Strict requirement for Asp at the P1 position. It has a preferred cleavage sequence of Tyr-Val-Ala-Asp but also cleaves at Asp-Glu-Val-Asp

Other name(s): Icerel-III; Ich-3; ICH-3 protease; transcript Y; TY; CASP-5

Comments: This enzyme is part of the family of inflammatory caspases, which also includes caspase-1 (EC 3.4.22.36) and caspase-4 (EC 3.4.22.57) in humans and caspase-11 (EC 3.4.22.64), caspase-12, caspase-13 and caspase-14 in mice. Contains a caspase-recruitment domain (CARD) in its N-terminal prodomain, which plays a role in procaspase activation [3,5,6]. The enzyme is able to cleave itself and the p30 caspase-1 precursor, but is very inefficient at generating mature interleukin-1β (IL-1β) from pro-IL-1β [795, 793]. Both this enzyme and caspase-4 can cleave pro-caspase-3 to release the small subunit (p12) but not the large subunit (p17) [1792]. Unlike caspase-4, this enzyme can be induced by lipopolysaccharide [1792]. Belongs in peptidase family C14.

References: [795, 1452, 1792, 793, 1920, 424]

[EC 3.4.22.58 created 2007]

EC 3.4.22.59

Accepted name: caspase-6

Reaction: Strict requirement for Asp at position P1 and has a preferred cleavage sequence of Val-Glu-His-Asp

Other name(s): CASP-6; apoptotic protease Mch-2; Mch2

Comments: Caspase-6 is an effector/executioner caspase, as are caspase-3 (EC 3.4.22.56) and caspase-7 (EC 3.4.22.60) [424]. These caspases are responsible for the proteolysis of the majority of cellular polypeptides [e.g. poly(ADP-ribose) polymerase (PARP)], which leads to the apoptotic phenotype [424]. Caspase-6 can cleave its prodomain to produce mature caspase-6, which directly activates caspase-8 (EC 3.4.22.61) and leads to the release of cytochrome c from the mitochondria. The release of cytochrome c is an essential component of the intrinsic apoptosis pathway [541]. The enzyme can also cleave and inactivate laminins, the intermediate filament scaffold proteins of the nuclear envelope, leading to nuclear fragmentation in the final phases of apoptosis [2,4,5,6]. Belongs in peptidase family C14.

References: [541, 424, 1468, 1720, 1867, 2978]

[EC 3.4.22.59 created 2007]

EC 3.4.22.60

Accepted name: caspase-7

Reaction: Strict requirement for an Asp residue at position P1 and has a preferred cleavage sequence of Asp-Glu-Val-Asp

Other name(s): CASP-7; ICE-like apoptotic protease 3; ICE-LAP3; apoptotic protease Mch-3; Mch3; CMH-1
Caspase-7 is an effector/executioner caspase, as are caspase-3 (EC 3.4.22.56) and caspase-6 (EC 3.4.22.59) [424]. These caspases are responsible for the proteolysis of the majority of cellular polypeptides [e.g. poly(ADP-ribose) polymerase (PARP)], which leads to the apoptotic phenotype [2186]. Although a hydrophobic residue at P5 of caspase-2 (EC 3.4.22.55) and caspase-3 leads to more efficient hydrolysis, the amino-acid residue at this location in caspase-7 has no effect [788]. Caspase-7 is activated by the initiator caspases [caspase-8 (EC 3.4.22.61), caspase-9 (EC 3.4.22.62) and caspase-10 (EC 3.4.22.63)]. Removal of the N-terminal prodomain occurs before cleavage in the linker region between the large and small subunits [624]. Belongs in peptidase family C14.

References: [424, 2186, 788, 624]
EC 3.4.22.63

**Accepted name:** caspase-10  
**Reaction:** Strict requirement for Asp at position P1 and has a preferred cleavage sequence of Leu-Gln-Thr-Asp-Gly  
**Other name(s):** FLICE2; Mch4; CASP-10; ICE-like apoptotic protease 4; apoptotic protease Mch-4; FAS-associated death domain protein interleukin-1β-converting enzyme 2  
**Comments:** Caspase-10 is an initiator caspase, as are caspase-2 (EC 3.4.22.55), caspase-8 (EC 3.4.22.61) and caspase-9 (EC 3.4.22.62) [424]. Like caspase-8, caspase-10 contains two tandem death effector domains (DEDs) in its N-terminal prodomain, and these play a role in procaspase activation [424]. The enzyme has many overlapping substrates in common with caspase-8, such as RIP (the cleavage of which impairs NF-κB survival signalling and starts the cell-death process) and PAK2 (associated with some of the morphological features of apoptosis, such as cell rounding and apoptotic body formation) [826]. Bid, a Bcl2 protein, can be cleaved by caspase-3 (EC 3.4.22.56), caspase-8 and caspase-10 at Lys-Gln-Thr-Asp to yield the pro-apoptotic p15 fragment. The p15 fragment is N-myristoylated and enhances the release of cytochrome c from mitochondria (which, in turn, initiates the intrinsic apoptosis pathway). Bid can be further cleaved by caspase-10 and granzyme B but not by caspase-3 or caspase-8 at Ile-Glu-Thr-Asp to yield a p13 fragment that is not N-myristoylated [826]. Belongs in peptidase family C14.  
**References:** [424, 826, 2766, 274]

[EC 3.4.22.63 created 2007]

EC 3.4.22.64

**Accepted name:** caspase-11  
**Reaction:** Strict requirement for Asp at the P1 position and has a preferred cleavage sequence of (Ile/Leu/Val/Phe)-Gly-His-Asp  
**Other name(s):** CASP-11  
**Comments:** This murine enzyme is part of the family of inflammatory caspases, which also includes caspase-1 (EC 3.4.22.36), caspase-4 (EC 3.4.22.57) and caspase-5 (EC 3.4.22.58) in humans and caspase-12, caspase-13 and caspase-14 in mice. Contains a caspase-recruitment domain (CARD) in its N-terminal prodomain, which plays a role in procaspase activation. Like caspase-5, but unlike caspase-4, this enzyme can be induced by lipopolysaccharide [1470]. This enzyme not only activates caspase-1, which is required for the maturation of proinflammatory cytokines such as interleukin-1β (IL-1β) and IL-18, but it also activates caspase-3 (EC 3.4.22.56), which leads to cellular apoptosis under pathological conditions [1470, 1283]. Belongs in peptidase family C14.  
**References:** [1470, 1283, 3269, 749, 424]

[EC 3.4.22.64 created 2007]

EC 3.4.22.65

**Accepted name:** peptidase 1 (mite)  
**Reaction:** Broad endopeptidase specificity  
**Other name(s):** allergen Der f 1; allergen Der p 1; antigen Der p 1; antigen Eur m 1; antigen Pso o 1; major mite fecal allergen Der p 1; Der p 1; Der f 1; Eur m 1; endopeptidase 1 (mite)  
**Comments:** This enzyme, derived from the house dust mite, is a major component of the allergic immune response [1449]. The substrate specificity of this enzyme is not altogether clear. It cleaves the low-affinity IgE receptor CD23 at Glu298-Ser299 and Ser155-Ser156 [1975]. It also cleaves the pulmonay structural proteins occulmin and claudin at Leu-Leu, Asp-Leu and at Gly-Thr bonds [1975, 1449]. It can also cleave the α subunit of the interleukin-2 (IL-2) receptor (CD25) [2726]. Using a positional scanning combinatorial library, it was found that the major substrate-specificity determinant is for Ala in the P2 position [1122]. The enzyme shows only a slight preference for basic amino acids in the P1 and P3 positions and a preference for aliphatic amino acids such as Ile, Pro, Val, Leu and norleucine in the P4 position [1122]. Belongs in peptidase family C1A.  
**References:** [1975, 1449, 1122, 2726, 2725, 2991]
EC 3.4.22.66

Accepted name: calicivirin

Reaction: Endopeptidase with a preference for cleavage when the P1 position is occupied by Glu and the P1′ position is occupied by Gly.

Other name(s): Camberwell virus processing peptidase; Chiba virus processing peptidase; Norwalk virus processing peptidase; Southampton virus processing peptidase; norovirus virus processing peptidase; calicivirus trypsin-like cysteine protease; calicivirus TCP; calicivirus 3C-like protease; calicivirus endopeptidase; rabbit hemorrhagic disease virus 3C endopeptidase

Comments: Viruses that are members of the Norovirus genus (Caliciviridae family) are a major cause of epidemic acute viral gastroenteritis [1811]. The nonstructural proteins of these viruses are produced by proteolytic cleavage of a large precursor polyprotein, performed by a protease that is incorporated into the polyprotein [1]. Cleavage sites are apparently defined by features based on both sequence and structure since several sites in the polyprotein fulfilling the identified sequence requirements are not cleaved [1996]. The presence of acidic (Asp), basic (Arg), aromatic (Tyr) or aliphatic (Leu) amino acids at the P1′ position results in only minor differences in cleavage efficiency, suggesting that steric or conformational constraints may play a role in determining specificity [1996]. Changes to the amino acid at the P2 position do not alter cleavage efficiency [1996, 3353]. Belongs in peptidase family C37.

References: [1996, 3353, 43, 1811, 1812]

EC 3.4.22.67

Accepted name: zingipain

Reaction: Preferential cleavage of peptides with a proline residue at the P2 position

Other name(s): ginger protease; GP-I; GP-II; ginger protease II (Zingiber officinale); zingibain

Comments: This enzyme is found in ginger (Zingiber officinale) rhizome and is a member of the papain family. GP-II contains two glycosylation sites. The enzyme is inhibited by some divalent metal ions, such as Hg²⁺, Cu²⁺, Cd²⁺ and Zn²⁺ [2282]. Belongs in peptidase family C1.

References: [475, 2282, 476]

EC 3.4.22.68

Accepted name: Ulp1 peptidase

Reaction: Hydrolysis of the α-linked peptide bond in the sequence Gly-Gly-Ala-Thr-Tyr at the C-terminal end of the small ubiquitin-like modifier (SUMO) propeptide, Smt3, leading to the mature form of the protein. A second reaction involves the cleavage of an ε-linked peptide bond between the C-terminal glycine of the mature SUMO and the lysine ε-amino group of the target protein

Other name(s): Smt3-protein conjugate proteinase; Ubl-specific protease 1; Ulp1; Ulp1 endopeptidase; Ulp1 protease

Comments: The enzyme from Saccharomyces cerevisiae can also recognize small ubiquitin-like modifier 1 (SUMO-1) from human as a substrate in both SUMO-processing (α-linked peptide bonds) and SUMO-deconjugation (ε-linked peptide bonds) reactions [1,2,3]. Ulp1 has several functions, including an essential role in chromosomal segregation and progression of the cell cycle through the G2/M phase of the cell cycle. Belongs in peptidase family C48.

References: [1783, 1759, 3036, 1760, 1300, 2093]

EC 3.4.22.69

Accepted name: SARS coronavirus main proteinase
**EC 3.4.22.69**

**Accepted name:** sortase A  
**Reaction:** The enzyme catalyses a cell wall sorting reaction in which a surface protein with a sorting signal containing a LPXTG motif is cleaved between the Thr and Gly residue. The resulting threonine carboxyl end of the protein is covalently attached to a pentaglycine cross-bridge of peptidoglycan.  
**Other name(s):** SrtA; SrtA protein; SrtA sortase  
**Comments:** In peptidase family C60.  
**References:** [3085, 3513, 2470]

**EC 3.4.22.70**

**Accepted name:** sortase B  
**Reaction:** The enzyme catalyses a cell wall sorting reaction in which a surface protein with a sorting signal containing a NPXTN motif is cleaved between the Thr and Asn residue. The resulting threonine carboxyl end of the protein is covalently attached to a pentaglycine cross-bridge of peptidoglycan.  
**Other name(s):** SrtB  
**Comments:** In peptidase family C60.  
**References:** [3514, 235, 510]

**EC 3.4.22.71**

**Accepted name:** sortase A  
**Reaction:** The enzyme catalyses a cell wall sorting reaction in which a surface protein with a sorting signal containing a LPXTG motif is cleaved between the Thr and Gly residue. The resulting threonine carboxyl end of the protein is covalently attached to a pentaglycine cross-bridge of peptidoglycan.  
**Other name(s):** SrtA; SrtA protein; SrtA sortase  
**Comments:** In peptidase family C60.  
**References:** [3085, 3513, 2470]

**EC 3.4.23** Aspartic endopeptidases

**EC 3.4.23.1**

**Accepted name:** pepsin A  
**Reaction:** Preferential cleavage: hydrophobic, preferably aromatic, residues in P1 and P1′ positions. Cleaves Phe1→Val, Gln4→His, Glu13→Ala, Ala14→Leu, Leu15→Tyr, Tyr16→Leu, Gly23→Phe, Phe24→Phe and Phe25→Tyr bonds in the B chain of insulin  
**Other name(s):** pepsin; lactated pepsin; pepsin fortior; fundus-pepsin; elixir lactate of pepsin; P I; lactated pepsin elixir; P II; pepsin R; pepsin D  
**Comments:** The predominant endopeptidase in the gastric juice of vertebrates, formed from pepsinogen A by limited proteolysis. Human pepsin A occurs in five molecular forms. Pig pepsin D [1711, 1710] is unphosphorylated pepsin A. Type example of peptidase family A1.  
**References:** [1711, 1710, 845, 1385, 878, 3023, 2418]
EC 3.4.23.2
Accepted name: pepsin B
Reaction: Degradation of gelatin; little activity on hemoglobin. Specificity on B chain of insulin more restricted than that of pepsin A; does not cleave at Phe\(^1\)-Val, Gln\(^4\)-His or Gly\(^23\)-Phe
Other name(s): parapepsin I; pig gelatinase
Comments: Formed from pig pepsinogen B. In peptidase family A1 (pepsin A family)
References: [2608]

[EC 3.4.23.2 created 1961 as EC 3.4.4.2, transferred 1972 to EC 3.4.23.2, modified 1986]

EC 3.4.23.3
Accepted name: gastricsin
Reaction: More restricted specificity than pepsin A, but shows preferential cleavage at Tyr bonds. High activity on hemoglobin
Other name(s): pepsin C; pig parapepsin II; parapepsin II
Comments: Formed from progastricsin, apparently in the gastric juice of most vertebrates. In addition to the fundus, progastricsin is also secreted in antrum and proximal duodenum. Seminal plasma contains a zymogen that is immunologically identical with progastricsin [2528]. In peptidase family A1 (pepsin A family).
References: [2608, 3022, 843, 844, 1917, 2528, 1153]

[EC 3.4.23.3 created 1965 as EC 3.4.4.22, transferred 1972 to EC 3.4.23.3, modified 1986]

EC 3.4.23.4
Accepted name: chymosin
Reaction: Broad specificity similar to that of pepsin A. Clots milk by cleavage of a single Ser-Phe\(^{105}\)-Met-Ala bond in \(\kappa\)-chain of casein
Other name(s): rennin (but this should be avoided since it leads to confusion with rennin)
Comments: Neonatal gastric enzyme with high milk clotting and weak general proteolytic activity, formed from prochymosin. Found among mammals with postnatal uptake of immunoglobulins. In peptidase family A1 (pepsin A family)
References: [842, 1125, 3220]

[EC 3.4.23.4 created 1961 as EC 3.4.4.3, transferred 1972 to EC 3.4.23.4, modified 1986]

EC 3.4.23.5
Accepted name: cathepsin D
Reaction: Specificity similar to, but narrower than, that of pepsin A. Does not cleave the Gln\(^4\)-His bond in B chain of insulin
Comments: Occurs intracellularly, in lysosomes. A zymogen form is known [518]. In peptidase family A1 (pepsin A family)
References: [168, 2988, 800, 518]

[EC 3.4.23.5 created 1965 as EC 3.4.4.23, transferred 1972 to EC 3.4.23.5, modified 1986]

[3.4.23.6 Transferred entry. now EC 3.4.23.30 pycnoporopepsin]

[EC 3.4.23.6 created 1961 as EC 3.4.4.17, transferred 1972 to EC 3.4.23.6, modified 1981, deleted 1992 [EC 3.4.23.7, EC 3.4.23.8, EC 3.4.23.9, EC 3.4.23.10, EC 3.4.99.1, EC 3.4.99.15 and EC 3.4.99.25 all created 1972 and incorporated 1978]]

[3.4.23.7 Transferred entry. Penicillium janthinellum acid protease. Now EC 3.4.23.20, penicillopepsin]

[EC 3.4.23.7 created 1972, modified 1981, deleted 1978 [transferred to EC 3.4.23.6, deleted 1992]]

[3.4.23.8 Transferred entry. yeast proteinase A. Now EC 3.4.23.25, saccharopepsin]
[EC 3.4.23.8 created 1972, modified 1981, deleted 1978 [transferred to EC 3.4.23.6, deleted 1992]]

[3.4.23.9] Transferred entry. Rhizopus acid proteinase. Now EC 3.4.23.21, rhizopuspepsin

[EC 3.4.23.9 created 1972, modified 1981, deleted 1978 [transferred to EC 3.4.23.6, deleted 1992]]


[EC 3.4.23.10 created 1972, modified 1981, deleted 1978 [transferred to EC 3.4.23.6, deleted 1992]]

[3.4.23.11] Deleted entry. thyroid aspartic proteinase

[EC 3.4.23.11 created 1978, modified 1981, deleted 1992]

EC 3.4.23.12

Accepted name: nepenthesin

Reaction: Similar to pepsin, but also cleaves on either side of Asp and at Lys—Arg

Other name(s): Nepenthes aspartic proteinase; Nepenthes acid proteinase; nepenthacin; nepenthasin; aspartyl endopeptidase

Comments: From the insectivorous plants Nepenthes spp. (secretions) and Drosera peltata (ground-up leaves). Aspartic endopeptidases are probably present in many other plants, including Lotus [2774] and sorghum [936]. In peptidase family A1 (pepsin A family)

References: [47, 936, 2774, 46, 2980, 3073]

[EC 3.4.23.12 created 1972 as EC 3.4.99.4, transferred 1978 to EC 3.4.23.12, modified 1981]

[3.4.23.13] Deleted entry. Lotus aspartic proteinase


[3.4.23.14] Deleted entry. sorghum aspartic proteinase


EC 3.4.23.15

Accepted name: renin

Reaction: Cleavage of Leu—bond in angiotensinogen to generate angiotensin I

Other name(s): angiotensin-forming enzyme; angiotensinogenase


References: [1324, 2828, 1323, 2791]

[EC 3.4.23.15 created 1961 as EC 3.4.4.15, transferred 1972 to EC 3.4.99.19, transferred 1981 to EC 3.4.23.15]

EC 3.4.23.16

Accepted name: HIV-1 retropepsin

Reaction: Specific for a P1 residue that is hydrophobic, and P1′ variable, but often Pro

Other name(s): human immunodeficiency virus type 1 protease; gag protease; HIV aspartyl protease; HIV proteinase; retroproteinase; HIV-1 protease; HIV-2 protease

Comments: Present in human immunodeficiency virus type 1. Contributes to the maturation of the viral particle, and is a target of antiviral drugs. Active enzyme is a dimer of identical 11-kDa subunits. Similar enzymes occur in other retroviruses [1650]. Type example of peptidase family A2

References: [1650, 711]

[EC 3.4.23.16 created 1992, modified 2000]
EC 3.4.23.17

Accepted name: pro-opiomelanocortin converting enzyme
Reaction: Cleavage at paired basic residues in certain prohormones, either between them, or on the carboxyl side
Other name(s): prohormone converting enzyme; pro-opiomelanocortin-converting enzyme; proopiomelanocortin proteinase; PCE
Comments: A 70 kDa membrane-bound enzyme isolated from cattle pituitary secretory vesicle.
References: [1830, 1829, 770]

[EC 3.4.23.17 created 1989 as EC 3.4.99.38, transferred 1992 to EC 3.4.23.17]

EC 3.4.23.18

Accepted name: aspargillopepsin I
Reaction: Hydrolysis of proteins with broad specificity. Generally favours hydrophobic residues in P1 and P1', but also accepts Lys in P1, which leads to activation of trypsinogen. Does not clot milk
Other name(s): Aspergillus acid protease; Aspergillus acid proteinase; Aspergillus aspartic proteinase; Aspergillus awamori acid proteinase; Aspergillus carboxyl proteinase; (see also Comments); carboxyl proteinase; Aspergillus kawachii aspartic proteinase; Aspergillus saitoi acid proteinase; pepsin-type aspartic proteinase; Aspergillus niger acid proteinase; sumizyme AP; proctase P; denapsin; denapsin XP 271; proctase
Comments: Found in a variety of Aspergillus species (imperfect fungi): Aspergillus awamori (awamorin, aspargillopepsin A: [2320]), A. foetidus (aspargillopepsin F: [2319]), A. fumigatus [2342], A. kawachii [3395], A. niger (proteinase B, proctase B: [2069, 428]), A. oryzae (trypsinogen kinase: [587, 1880]), A. saitoi (aspargillopeptidase A: [1880]), and A. sojae [3012, 1880]. In peptidase family A1 (pepsin A family). Formerly included in EC 3.4.23.6
References: [1614, 2069, 587, 428, 3012, 2319, 2342, 2320, 3395, 1880]

[EC 3.4.23.18 created 1992 (EC 3.4.23.6 created 1961 as EC 3.4.4.17, transferred 1972 to EC 3.4.23.6, modified 1981 [EC 3.4.23.7, EC 3.4.23.8, EC 3.4.23.9, EC 3.4.23.10, EC 3.4.99.1, EC 3.4.99.15 and EC 3.4.99.25 all created 1972 and incorporated 1978], part incorporated 1992)]

EC 3.4.23.19

Accepted name: aspargillopepsin II
Reaction: Preferential cleavage in B chain of insulin: Asn3→Gln, Gly13→Ala, Tyr26→Thr
Other name(s): protease A; proctase A; Aspergillus niger var. macrosporus aspartic proteinase
Comments: Isolated from Aspergillus niger var. macrosporus, distinct from proteinase B (see aspargillopepsin I) in specificity and insensitivity to pepstatin. In peptidase family G1 (scytalidopepsin B family). Formerly included in EC 3.4.23.6
References: [428, 1303]

[EC 3.4.23.19 created 1992 (EC 3.4.23.6 created 1961 as EC 3.4.4.17, transferred 1972 to EC 3.4.23.6, modified 1981 [EC 3.4.23.7, EC 3.4.23.8, EC 3.4.23.9, EC 3.4.23.10, EC 3.4.99.1, EC 3.4.99.15 and EC 3.4.99.25 all created 1972 and incorporated 1978], part incorporated 1992)]

EC 3.4.23.20

Accepted name: penicillopepsin
Reaction: Hydrolysis of proteins with broad specificity similar to that of pepsin A, preferring hydrophobic residues at P1 and P1', but also cleaving Gly20→Glu in the B chain of insulin. Clots milk, and activates trypsinogen

References: [428, 1303]
Other name(s): peptidase A; *Penicillium janthinellum* aspartic proteinase; acid protease A; *Penicillium citrinum* acid proteinase; *Penicillium cyclopium* acid proteinase; *Penicillium expansum* acid protease; *Penicillium asparagi* aspartic proteinase; *Penicillium caseicolum* aspartic proteinase; *Penicillium roqueforti* acid proteinase; *Penicillium duponti* aspartic proteinase; *Penicillium citrinum* aspartic proteinase

Comments: From the imperfect fungus *Penicillium janthinellum*. In peptidase family A1 (pepsin A family). Closely related enzymes have been isolated from *P. roqueforti* [3482] and *P. duponti* [743].

References: [1877, 3482, 743, 1231, 1271]

[EC 3.4.23.20 created 1992 (EC 3.4.23.6 created 1992 (EC 3.4.23.6 created 1961 as EC 3.4.4.17, transferred 1972 to EC 3.4.23.6, modified 1981 [EC 3.4.23.7, EC 3.4.23.8, EC 3.4.23.9, EC 3.4.23.10, EC 3.4.99.1, EC 3.4.99.15 and EC 3.4.99.25 all created 1972 and incorporated 1978], part incorporated 1992))]

EC 3.4.23.21

Accepted name: rhizopuspepsin

Reaction: Hydrolysis of proteins with broad specificity similar to that of pepsin A, preferring hydrophobic residues at P1 and P1′. Clots milk and activates trypsinogen. Does not cleave Gln14-His, but does cleave His10-Leu and Val12-Glu in B chain of insulin

Other name(s): *Rhizopus* aspartic proteinase; neurase; *Rhizopus* acid protease; *Rhizopus* acid proteinase

Comments: From the zygomycete fungus *Rhizopus chinensis*. A similar endopeptidase is found in *R. niveus* [1665]. In peptidase family A1 (pepsin A family).

References: [3134, 1665, 2283, 2937]

[EC 3.4.23.21 created 1992 (EC 3.4.23.6 created 1992 (EC 3.4.23.6 created 1961 as EC 3.4.4.17, transferred 1972 to EC 3.4.23.6, modified 1981 [EC 3.4.23.7, EC 3.4.23.8, EC 3.4.23.9, EC 3.4.23.10, EC 3.4.99.1, EC 3.4.99.15 and EC 3.4.99.25 all created 1972 and incorporated 1978], part incorporated 1992))]

EC 3.4.23.22

Accepted name: endothiapepsin

Reaction: Hydrolysis of proteins with specificity similar to that of pepsin A; prefers hydrophobic residues at P1 and P1′, but does not cleave Ala14-Leu in the B chain of insulin or Z-Glu-Tyr. Clots milk

Other name(s): *Endothia* aspartic proteinase; *Endothia* acid proteinase; *Endothia parasitica* acid proteinase

Comments: From the ascomycete *Endothia parasitica*. In peptidase family A1 (pepsin A family).

References: [3324, 3344, 157, 525]

[EC 3.4.23.22 created 1992 (EC 3.4.23.6 created 1992 (EC 3.4.23.6 created 1961 as EC 3.4.4.17, transferred 1972 to EC 3.4.23.6, modified 1981 [EC 3.4.23.7, EC 3.4.23.8, EC 3.4.23.9, EC 3.4.23.10, EC 3.4.99.1, EC 3.4.99.15 and EC 3.4.99.25 all created 1972 and incorporated 1978], part incorporated 1992))]

EC 3.4.23.23

Accepted name: mucorpepsin

Reaction: Hydrolysis of proteins, favouring hydrophobic residues at P1 and P1′. Clots milk. Does not accept Lys at P1, and hence does not activate trypsinogen

Other name(s): Mucor rennin; Mucor aspartic proteinase; Mucor acid proteinase; Mucor acid protease; *Mucor miehei* aspartic proteinase; *Mucor miehei* aspartic protease; *Mucor pusillus* emporase; Fromase 100; *Mucor pusillus* rennin; Fromase 46TL; *Mucor miehei* rennin

Comments: Isolated from the zygomycete fungi *Mucor pusillus* and M. miehei. The two species variants show 83% sequence identity and are immunologically crossreactive. In peptidase family A1 (pepsin A family). Formerly included in EC 3.4.23.6

References: [78, 2324, 2906, 2286, 185]

[EC 3.4.23.23 created 1992 (EC 3.4.23.6 created 1992 (EC 3.4.23.6 created 1961 as EC 3.4.4.17, transferred 1972 to EC 3.4.23.6, modified 1981 [EC 3.4.23.7, EC 3.4.23.8, EC 3.4.23.9, EC 3.4.23.10, EC 3.4.99.1, EC 3.4.99.15 and EC 3.4.99.25 all created 1972 and incorporated 1978], part incorporated 1992))]
**EC 3.4.23.24**  
**Accepted name:** candidapepsin  
**Reaction:** Preferential cleavage at the carboxyl of hydrophobic amino acids, but fails to cleave Leu\(^{15}\)-Tyr, Tyr\(^{16}\)-Leu and Phe\(^{24}\)-Phe of insulin B chain. Activates trypsinogen, and degrades keratin  
**Other name(s):** *Candida albicans* aspartic proteinase; *Candida albicans* carboxyl proteinase; *Candida albicans* secretory acid proteinase; *Candida* olea acid proteinase; *Candida* aspartic proteinase; *Candida* olea aspartic proteinase  
**Comments:** This endopeptidase from the imperfect yeast *Candida albicans* is inhibited by pepstatin, but not by methyl 2-diazoacetamidohexanoate or 1,2-epoxy-3-(p-nitrophenoxy)propane. In peptidase family A1 (pepsin A family). Formerly included in EC 3.4.23.6  
**References:** [2532, 2602, 2171, 1837]

**EC 3.4.23.25**  
**Accepted name:** saccharopepsin  
**Reaction:** Hydrolysis of proteins with broad specificity for peptide bonds. Cleaves -Leu-Leu-Val-Tyr bond in a synthetic substrate. Does not act on esters of Tyr or Arg  
**Other name(s):** yeast endopeptidase A; *Saccharomyces* aspartic proteinase; *Saccharomyces* aspartic proteinase yoga\(^{A}\) (gene name); proteinase A; proteinase yoga\(^{A}\) (gene name); yeast proteinase A; *Saccharomyces cerevisiae* aspartic proteinase A; PRA  
**Comments:** Located in the vacuole of the baker’s yeast (*Saccharomyces cerevisiae*) cell. In peptidase family A1 (pepsin A family).  
**References:** [1138, 1991, 50]

**EC 3.4.23.26**  
**Accepted name:** rhodotorulapepsin  
**Reaction:** Specificity similar to that of pepsin A. Cleaves Z-Lys-Ala-Ala-Ala and activates trypsinogen  
**Other name(s):** Rhodotorula aspartic proteinase; *Cladosporium* acid protease; *Cladosporium* acid proteinase; Pae-cilomyces proteinase; *Cladosporium* aspartic proteinase; Pae-cilomyces proteinase; *Rhodotorula glutinis* aspartic proteinase; *Rhodotorula glutinis* acid proteinase; *Rhodotorula glutinis* aspartic proteinase II; Rhodotorula acid proteinase  
**Comments:** From the imperfect yeast *Rhodotorula glutinis*. Somewhat similar enzymes have been isolated from the imperfect yeast-like organism *Cladosporium* sp. [2108, 2238] and the imperfect fungus *Pae-cilomyces variotii* [2675, 2676].  
**References:** [2675, 2676, 1451, 2108, 2239, 2238, 2979, 1880]

**EC 3.4.23.28**  
**Accepted name:** rhodotorulapepsin  
**Reaction:** Specificity similar to that of pepsin A. Cleaves Z-Lys-Ala-Ala-Ala and activates trypsinogen  
**Other name(s):** Rhodotorula aspartic proteinase; *Cladosporium* acid protease; *Cladosporium* acid proteinase; Pae-cilomyces proteinase; *Cladosporium* aspartic proteinase; Pae-cilomyces proteinase; *Rhodotorula glutinis* aspartic proteinase; *Rhodotorula glutinis* acid proteinase; *Rhodotorula glutinis* aspartic proteinase II; Rhodotorula acid proteinase  
**Comments:** From the imperfect yeast *Rhodotorula glutinis*. Somewhat similar enzymes have been isolated from the imperfect yeast-like organism *Cladosporium* sp. [2108, 2238] and the imperfect fungus *Pae-cilomyces variotii* [2675, 2676].  
**References:** [2675, 2676, 1451, 2108, 2239, 2238, 2979, 1880]
Accepted name: acrocylindropepsin
Reaction: Preference for hydrophobic residues at P1 and P1′. Action on the B chain of insulin is generally similar to that of pepsin A, but it also cleaves Leu^6-Cys(SO3H), Glu^21-Arg and Asn^3-Gln, although not Gln^4-His
Other name(s): Acrocylindrium protease; Acrocylindrium acid proteinase
Comments: From the imperfect fungus Acrocylindrium sp. Has a very low pH optimum on casein of 2.0. In peptidase family A1 (pepsin A family).
References: [3154, 1294, 2979]

[EC 3.4.23.28 created 1992 (EC 3.4.23.6 created 1961 as EC 3.4.4.17, transferred 1972 to EC 3.4.23.6, modified 1981 [EC 3.4.23.7, EC 3.4.23.8, EC 3.4.23.9, EC 3.4.23.10, EC 3.4.99.1, EC 3.4.99.15 and EC 3.4.99.25 all created 1972 and incorporated 1978], part incorporated 1992)]

EC 3.4.23.29
Accepted name: polyporopepsin
Reaction: Milk clotting activity, broad specificity, but fails to cleave Leu^15-Tyr or Tyr^16-Leu of insulin B chain
Other name(s): Polyporus aspartic proteinase; Irpex lacteus aspartic proteinase; Irpex lacteus carboxyl proteinase B
Comments: From the basidiomycete Polyporus tulipiferae (formerly Irpex lacteus). In peptidase family A1 (pepsin A family)
References: [1572, 1574]

[EC 3.4.23.29 created 1992]

EC 3.4.23.30
Accepted name: pycnoporopepsin
Reaction: Similar to pepsin A, but narrower, cleaving only three bonds in the B chain of insulin: Ala^14-Leu, Tyr^16-Leu, and Phe^24-Phe
Other name(s): proteinase Ia; Pycnoporus coccineus aspartic proteinase; Trametes acid proteinase
Comments: From the basidiomycete Pycnoporus sanguineus, formerly known as P. coccineus and Trametes sanguinea. Formerly included in EC 3.4.23.6
References: [3083, 3134, 1296]

[EC 3.4.23.30 created 1992 (EC 3.4.23.6 created 1961 as EC 3.4.4.17, transferred 1972 to EC 3.4.23.6, modified 1981 [EC 3.4.23.7, EC 3.4.23.8, EC 3.4.23.9, EC 3.4.23.10, EC 3.4.99.1, EC 3.4.99.15 and EC 3.4.99.25 all created 1972 and incorporated 1978], part incorporated 1992)]

EC 3.4.23.31
Accepted name: scytalidopepsin A
Reaction: Hydrolysis of proteins with specificity similar to that of pepsin A, but also cleaves Cys(SO3H)^7-Gly and Leu^17-Val in the B chain of insulin
Other name(s): Scytalidium aspartic proteinase A; Scytalidium lignicolum aspartic proteinase; Scytalidium lignicolum aspartic proteinase A-2; Scytalidium lignicolum aspartic proteinase A-I; Scytalidium lignicolum aspartic proteinase C; Scytalidium lignicolum carboxyl proteinase; Scytalidium lignicolum acid proteinase
Comments: Isolated from the imperfect fungus Scytalidium lignicolum. Not inhibited by pepstatin-Ac, methyl 2-diazoacetamidohexanoate or 1,2-epoxy-3-(p-nitrophenyl)propane. A related enzyme from the same organism, proteinase C, is also insensitive to these inhibitors and has M_r = 406,000 [2245]
References: [2240, 2241, 2245]

[EC 3.4.23.31 created 1992]

EC 3.4.23.32
Accepted name: scytalidopepsin B
Reaction: Hydrolysis of proteins with broad specificity, cleaving Phe$^{24}$→Phe, but not Leu$^{15}$-Tyr and Phe$^{25}$-Tyr in the B chain of insulin

Other name(s): Scytalidium aspartic proteinase B; Ganoderma lucidum carboxyl proteinase; Ganoderma lucidum aspartic proteinase; Scytalidium lignicolum aspartic proteinase B; SLB

Comments: A second endopeptidase from Scytalidium lignicolum (see scytalidopepsin A) that is insensitive to pepstatin and methyl 2-diazoacetamidohexanoate. 1,2-Epoxy-3-(p-nitrophenoxy)propane reacts with Glu$^{53}$, which replaces one of the aspartic residues at the active centre. One of the smallest aspartic endopeptidases active as the monomer, with $M_r$ about 22,000. Similarly inhibitor-resistant endopeptidases are found in the basidiomycetes Lentinus edodes [3043] and Ganoderma lucidum [3044], and in Polyporus tulipiferae [1573], a second endopeptidase distinct from polyporopepsin, but these are of typical aspartic endopeptidase size, $M_r$ about 36,000. Type example of peptidase family G1.

References: [3043, 1878, 3044, 1573, 3137]

[EC 3.4.23.32 created 1992]

[3.4.23.33 Transferred entry. xanthomonapepsin. Now EC 3.4.21.101, xanthomonalisin]

[EC 3.4.23.33 created 1992, deleted 2001]

EC 3.4.23.34

Accepted name: cathepsin E

Reaction: Similar to cathepsin D, but slightly broader specificity

Other name(s): slow-moving proteinase; erythrocyte membrane aspartic proteinase; SMP; EMAP; non-pepsin proteinase; cathepsin D-like acid proteinase; cathepsin E-like acid proteinase; cathepsin D-type proteinase

Comments: Found in stomach, spleen, erythrocyte membrane; not lysosomal. Pro-cathepsin E is an 86 kDa disulfide-linked dimer; activation or reduction produces monomer. In peptidase family A1 (pepsin A family)

References: [1691, 3449, 1432, 117]

[EC 3.4.23.34 created 1992]

EC 3.4.23.35

Accepted name: barrierpepsin

Reaction: Selective cleavage of -Leu$^6$→Lys- bond in the pheromone α-mating factor

Other name(s): barrier proteinase; Bar proteinase

Comments: A secreted endopeptidase known from baker’s yeast (Saccharomyces cerevisiae). In peptidase family A1 (pepsin A family)

References: [1864, 1863]

[EC 3.4.23.35 created 1993]

EC 3.4.23.36

Accepted name: signal peptidase II

Reaction: Release of signal peptides from bacterial membrane prolipoproteins including murein prolipoprotein. Hydrolyses -Xaa-Yaa-Zaa→(S,diaicylglyceryl)Cys-, in which Xaa is hydrophobic (preferably Leu), and Yaa (Ala or Ser) and Zaa (Gly or Ala) have small, neutral sidechains

Other name(s): premurein-leader peptidase; prolipoprotein signal peptidase; leader peptidase II; premurein leader proteinase

Comments: An 18-kDa enzyme present in bacterial inner membranes. Inhibited by pepstatin and the antibiotic globomycin. Type example of peptidase family A8.

References: [639, 3499, 2646]

[EC 3.4.23.36 created 1984 as EC 3.4.99.35, transferred 1995 to EC 3.4.23.36]

[3.4.23.37 Transferred entry. pseudomonapepsin. Now EC 3.4.21.100, pseudomonalisin]
EC 3.4.23.38

Accepted name: plasmepsin I
Reaction: Hydrolysis of the -Phe\textsuperscript{33}±Leu- bond in the \(\alpha\)-chain of hemoglobin, leading to denaturation of the molecule
Other name(s): aspartic hemoglobinase I; PFAPG; malaria aspartic hemoglobinase
Comments: Known from the malaria organism, \textit{Plasmodium}. About 37 kDa. In peptidase family A1 (pepsin A family), closest to cathepsin D and renin in structure. Inhibited by pepstatin. Formerly included in EC 3.4.23.6
References: [998, 855, 987]

EC 3.4.23.39

Accepted name: plasmepsin II
Reaction: Hydrolysis of the bonds linking certain hydrophobic residues in hemoglobin or globin. Also cleaves the small molecule substrates such as Ala-Leu-Glu-Arg-Thr-Phe±Phe(NO\textsubscript{2})-Ser-Phe-Pro-Thr [3]
Other name(s): aspartic hemoglobinase II; PFAPD
Comments: Known from the malaria organism, \textit{Plasmodium}. About 37 kDa. In peptidase family A1 (pepsin A family), and is 73\% identical in sequence to plasmepsin I. Inhibited by pepstatin. Formerly included in EC 3.4.23.6
References: [573, 987, 1211]

EC 3.4.23.40

Accepted name: phytpepsin
Reaction: Prefers hydrophobic residues Phe, Val, Ile, Leu, and Ala at P1 and P1\(^{\prime}\), but also cleaves -Phe±Asp- and -Asp±Asp- bonds in 2S albumin from plant seeds
Comments: Known particularly from barley grain, but present in other plants also. In peptidase family A1 (pepsin A family), but structurally distinct in containing an internal region of about 100 amino acids not generally present in the family
References: [2604, 1507, 87, 1508]

EC 3.4.23.41

Accepted name: yapsin 1
Reaction: Hydrolyses various precursor proteins with Arg or Lys in P1, and commonly Arg or Lys also in P2. The P3 amino acid is usually non-polar, but otherwise additional basic amino acids are favourable in both non-prime and prime positions
Other name(s): yeast aspartic protease 3; Yap3 gene product (\textit{Saccharomyces cerevisiae})
Comments: In peptidase family A1 of pepsin, and weakly inhibited by pepstatin. Can partially substitute for kexin in a deficient strain of yeast. The homologous product of the Mkc7 gene (\textit{Saccharomyces cerevisiae}) has similar catalytic activity and has been termed yapsin 2 [916]
References: [413, 916, 2303]

EC 3.4.23.42

Accepted name: thermopsin

238
Reaction: Similar in specificity to pepsin A preferring bulky hydrophobic amino acids in P1 and P1′
Comments: From the thermophilic archaeon *Sulfolobus acidocaldarius*. Maximally active at pH 2 and 90 °C. Weakly inhibited by pepstatin but shows no sequence similarity to pepsin. Type example of peptidase family A5.
References: [1791]

[EC 3.4.23.42 created 1992 as EC 3.4.99.43, transferred 2000 to EC 3.4.23.42]

**EC 3.4.23.43**

Accepted name: prepilin peptidase

Reaction: Typically cleaves a -Gly-Phe- bond to release an N-terminal, basic peptide of 5-8 residues from type IV prepilin, and then N-methylates the new N-terminal amino group, the methyl donor being S-adenosyl-L-methionine

Comments: Many species of bacteria carry pili on their cell surfaces. These are virulence determinants in pathogenic strains, and are assembled biosynthetically from type IV prepilin subunits. Before assembly, the prepilin molecules require proteolytic processing, which is done by the prepilin peptidase. Prepilin peptidase and its homologues play a central role not only in type IV pilus biogenesis but also in transport of macromolecules across cell membranes. Although both peptide-bond hydrolysis and N-methylation are catalysed by the same molecule, the methylation can be inhibited without affecting peptidase activity, and it is believed that the enzyme has two separate catalytic sites. Type example of peptidase family A24.

References: [1835, 1690]

[EC 3.4.23.43 created 2001]

**EC 3.4.23.44**

Accepted name: nodavirus endopeptidase

Reaction: Hydrolysis of an asparaginyl bond involved in the maturation of the structural protein of the virus, typically -Asn-Ala- or -Asn-Phe-

Other name(s): Black Beetle virus endopeptidase; Flock House virus endopeptidase

Comments: A single aspartic residue is critical for activity, and inhibition by EDTA indicates that a metal ion is also important. The enzyme is known from several nodaviruses that are pathogens of insects. Type example of peptidase family A6, and structurally related to the tetravirus endopeptidase in family A21, although in that family, the catalytic residue is thought to be Glu.

References: [3512, 1408]

[EC 3.4.23.44 created 2001]

**EC 3.4.23.45**

Accepted name: memapsin 1

Reaction: Broad endopeptidase specificity. Cleaves Glu-Val-Asn-Leu-Asp-Ala-Glu-Phe in the Swedish variant of Alzheimer’s amyloid precursor protein

Other name(s): β-secretase; β-site Alzheimer’s amyloid precursor protein cleaving enzyme 2 (BACE2); ASP1; Down region aspartic protease

Comments: Can cleave β-amyloid precursor protein to form the amyloidogenic β-peptide that is implicated in the pathology of Alzheimer’s disease, but is not significantly expressed in human brain. In peptidase family A1, but is atypical in containing a C-terminal membrane-spanning domain.

References: [3148]

[EC 3.4.23.45 created 2003]

**EC 3.4.23.46**

Accepted name: memapsin 2

[239]
Reaction: Broad endopeptidase specificity. Cleaves Glu-Val-Asn-Leu—Asp-Ala-Glu-Phe in the Swedish variant of Alzheimer’s amyloid precursor protein
Other name(s): β-secretase; β-site Alzheimer’s amyloid precursor protein cleaving enzyme 1 (BACE1)
Comments: Suggested to be the major “β-secretase” responsible for the cleavage of the β-amyloid precursor protein to form the amyloidogenic β-peptide that is implicated in the pathology of Alzheimer’s disease. In peptidase family A1 but is atypical in containing a C-terminal membrane-spanning domain.
References: [3149, 1241]

[EC 3.4.23.46 created 2003]

EC 3.4.23.47
Accepted name: HIV-2 retropepsin
Reaction: Endopeptidase for which the P1 residue is preferably hydrophobic
Comments: In peptidase family A2. Responsible for the post-translational processing of the human immunodeficiency virus polyprotein.
References: [3101, 455]

[EC 3.4.23.47 created 2003]

EC 3.4.23.48
Accepted name: plasminogen activator Pla
Reaction: Converts human Glu-plasminogen to plasmin by cleaving the Arg$_{560}$—Val peptide bond that is also hydrolysed by the mammalian u-plasminogen activator and t-plasminogen activator. Also cleaves arginyl bonds in other proteins
Comments: In peptidase family A26. From the bacterium Yersinia pestis that causes plague.
References: [1633]

[EC 3.4.23.48 created 2003]

EC 3.4.23.49
Accepted name: omptin
Reaction: Has a virtual requirement for Arg in the P1 position and a slightly less stringent preference for this residue in the P1’ position, which can also contain Lys, Gly or Val.
Other name(s): protease VII; protease A; gene ompT proteins; ompT protease; protein a; Pla; OmpT
Comments: A product of the ompT gene of Escherichia coli, and associated with the outer membrane. Omptin shows a preference for cleavage between consecutive basic amino acids, but is capable of cleavage when P1’ is a non-basic residue [3198, 1958]. Belongs in peptidase family A26.
References: [1045, 2935, 1106, 613, 3198, 1617, 1958]

[EC 3.4.23.49 created 1993 as EC 3.4.21.87, transferred 2006 to EC 3.4.23.49]

EC 3.4.23.50
Accepted name: human endogenous retrovirus K endopeptidase
Reaction: Processing at the authentic HIV-1 PR recognition site and release of the mature p17 matrix and the p24 capsid protein, as a result of the cleavage of the -SQNY—PIVQ- cleavage site.
Other name(s): human endogenous retrovirus K10 endopeptidase; endogenous retrovirus HERV-K10 putative protease; human endogenous retrovirus K retropepsin; HERV K10 endopeptidase; HERV K10 retropepsin; HERV-K PR; HERV-K protease; HERV-K113 protease; human endogenous retrovirus K113 protease; human retrovirus K10 retropepsin
Comments: In peptidase family A2.
References: [3097]

[EC 3.4.23.50 created 2009]
EC 3.4.23.51

Accepted name: HycI peptidase

Reaction: This enzyme specifically removes a 32-amino acid peptide from the C-terminus of the precursor of the large subunit of hydrogenase 3 in Escherichia coli by cleavage at the C-terminal side of Arg\textsubscript{537}.

Other name(s): HycI; HycE processing protein

Comments: The reaction requires nickel to be bound to the precursor of the large subunit of hydrogenase 3. The endopeptidase uses the metal in the large subunit of [NiFe]-hydrogenases as a recognition motif [3049]. In peptidase family A31.

References: [3049, 3415]

[EC 3.4.23.51 created 2009]

EC 3.4.23.52

Accepted name: preflagellin peptidase

Reaction: Cleaves the signal peptide of 3 to 12 amino acids from the N-terminal of preflagellin, usually at Arg-Gly\textsubscript{+} or Lys-Gly\textsubscript{+}, to release flagellin.

Other name(s): FlaK

Comments: An aspartic peptidase from Archaea but not bacteria. In peptidase family A24 (type IV prepilin peptidase family).

References: [153, 2184, 1272]

[EC 3.4.23.52 created 2011]

EC 3.4.24 Metalloendopeptidases

EC 3.4.24.1

Accepted name: atrolysin A

Reaction: Cleavage of Asn\textsubscript{3}Gln, His\textsubscript{5}Leu, His\textsubscript{10}Leu, Ala\textsubscript{14}Leu and Tyr\textsubscript{16}Leu in insulin B chain; removes C-terminal Leu from small peptides

Other name(s): Crotalus atrox metalloendopeptidase a; hemorrhagic toxin a; Crotalus atrox \(\alpha\)-proteinase; Crotalus atrox proteinase; bothropasin

Comments: A hemorrhagic endopeptidase of 68 kDa, one of six hemorrhagic toxins in the venom of western diamondback rattlesnake. The 60 kDa hemorrhagic toxin 1 of Crotalus ruber ruber shows identical specificity [2067]. In peptidase family M12 (astacin family). Related metalloendopeptidases from rattlesnake venoms are EC 3.4.24.41 (atrolysin B), EC 3.4.24.42 (atrolysin C), EC 3.4.24.43 (atroxase), EC 3.4.24.44 (atrolysin E), EC 3.4.24.45 (atrolysin F), EC 3.4.24.46 (adamalysin), EC 3.4.24.47 (horrilysin), and EC 3.4.24.48 (ruberlysin)

References: [249, 2067, 248, 247]

[EC 3.4.24.1 created 1972, modified 1986]

[3.4.24.2 Deleted entry. Sepia proteinase]

[EC 3.4.24.2 created 1972, deleted 1992]

EC 3.4.24.3

Accepted name: microbial collagenase

Reaction: Digestion of native collagen in the triple helical region at Gly bonds. With synthetic peptides, a preference is shown for Gly at P3 and P1', Pro and Ala at P2 and P2', and hydroxyproline, Ala or Arg at P3'

References: [249, 2067, 248, 247]
Other name(s): *Clostridium histolyticum* collagenase; clostridiopeptidase A; collagenase A; collagenase I; *Achromobacter iophagus* collagenase; collagenase; aspergillopeptidase C; nucleolysin; azocollase; metallocollagenase; soycollagestin; *Clostridium histolyticum* proteinase A; clostridiopeptidase II; MMP-8; clostridiopeptidase I; collagen peptidase; collagen protease; collagenase MMP-1; metalloproteinase-1; kollaza; matrix metalloproteinase-1; MMP-1; matrix metalloproteinase-8; matrix metalloproteinase-18; interstitial collagenase

Comments: Six species of metalloendopeptidase acting on native collagen can be isolated from the medium of *Clostridium histolyticum*. Class I has forms α (68 kDa), β (115 kDa) and γ (79 kDa); class II has δ (100 kDa), ε (110 kDa) and ζ (125 kDa). The two classes are immunologically crossreactive, but have significantly different sequences, and different specificities such that their actions on collagen are complementary. The enzymes also act as peptidyl-tripeptidases. Variants of the enzyme have been purified from *Bacillus cereus* [1881], *Empedobacter collagenolyticum* [1673], *Pseudomonas marinoglutinosa* [1102], and species of *Vibrio*, *Vibrio* B-30 (ATCC 21250) [1987] and V. alginolyticus (previously *Achromobacter iophagus*) [1170, 3088]. Also known from *Streptomyces* sp. [748]. The *Vibrio* enzyme is the type example of peptidase family M9.

References: [1102, 1987, 1170, 1673, 284, 285, 3283, 3088, 748, 1881]

[EC 3.4.24.3 created 1961 as EC 3.4.4.19, transferred 1972 to EC 3.4.24.3 (EC 3.4.24.8 created 1978, incorporated 1992, EC 3.4.99.5 created 1972, incorporated 1978)]

[3.4.24.4  Transferred entry. now EC 3.4.24.40 serralysin]

[EC 3.4.24.4 created 1972 [EC 3.4.99.13 and EC 3.4.99.22 both created 1972, incorporated 1978], deleted 1992]

[3.4.24.5  Deleted entry. lens neutral proteinase. Now included with EC 3.4.22.53 (calpain-2) and EC 3.4.25.1 (proteasome endopeptidase complex)]

[EC 3.4.24.5 created 1978, deleted 1989]

EC 3.4.24.6

Accepted name: leucolysin

Reaction: Cleavage of Phe1→Val, His5→Leu, Ala14→Leu, Gly20→Glu, Gly23→Phe and Phe24→Phe bonds in insulin B chain as well as N-blocked dipeptides

Other name(s): *Leucostoma* neutral proteinase; *Leucostoma* peptidase A

Comments: From the venom of the western cottonmouth moccasin snake (*Agkistrodon piscivorus leucostoma*).

References: [3233, 2880]

[EC 3.4.24.6 created 1978]

EC 3.4.24.7

Accepted name: interstitial collagenase

Reaction: Cleavage of the triple helix of collagen at about three-quarters of the length of the molecule from the N-terminus, at Gly775→Ile in the α1(I) chain. Cleaves synthetic substrates and α-macroglobulins at bonds where P1’ is a hydrophobic residue

Other name(s): vertebrate collagenase; matrix metalloproteinase 1

Comments: The enzyme takes its name from substrates of the interstitial collagen group - types I, II and III, all of which are cleaved in the helical domain. However, α-macroglobulins are cleaved much more rapidly. The enzyme is widely distributed in vertebrate animals. Type example of peptidase family M10

References: [999, 240, 818, 2868]

[EC 3.4.24.7 created 1978]

[3.4.24.8  Transferred entry. *Achromobacter iophagus* collagenase. Now EC 3.4.24.3, microbial collagenase]

[EC 3.4.24.8 created 1978, deleted 1992]

[3.4.24.9  Deleted entry. *Trichophyton schoenleinii* collagenase]
EC 3.4.24.11

Accepted name: nepriysin

Reaction: Preferential cleavage of polypeptides between hydrophobic residues, particularly with Phe or Tyr at P1′

Other name(s): neutral endopeptidase; endopeptidase 24.11; kidney-brush-border neutral peptidase; enkephalinase (misleading); endopeptidase-2; CALLA (common acute lymphoblastic leukemia-associated) antigens; CALLA antigen; endopeptidase; membrane metalloendopeptidase; kidney-brush-border neutral endopeptidase; kidney-brush-border neutral proteinase; CALLA glycoprotein; CALLA; common acute lymphoblastic leukemia antigen; CALLA glycoproteins; common acute lymphoblastic leukemia-associated antigens; neutral metalloendopeptidase; NEP; neutral endopeptidase 24.11; CD10; acute lymphoblastic leukemia antigen

Comments: A membrane-bound glycoprotein widely distributed in animal tissues. Inhibited by phosphoramidon and thiopran. Common acute lymphoblastic leukemia antigen (CALLA). Type example of peptidase family M13

References: [1933, 1885, 1743, 757]

EC 3.4.24.12

Accepted name: envelysin

Reaction: Hydrolysis of proteins of the fertilization envelope and dimethylcasein

Other name(s): sea-urchin-hatching proteinase; hatching enzyme; chorionase; chorion-digesting proteinase; chymotrypsin; sea urchin embryo hatching enzyme

Comments: A glycoprotein from various members of the class Echinoidea. Extracellular enzyme requiring Ca2+. In peptidase family M10 (interstitial collagenase family)

References: [174, 1740, 1741, 2214]

EC 3.4.24.13

Accepted name: IgA-specific metalloendopeptidase

Reaction: Cleavage of Pro-Thr bond in the hinge region of the heavy chain of human IgA

Other name(s): immunoglobulin A1 proteinase; IgA protease; IgA1-specific proteinase; IgA1 protease; IgA1 proteinase

Comments: A 190 kDa enzyme found in several pathogenic species of Streptococcus such as sanguis and pneumoniae. Type example of peptidase family M26. There is also an IgA-specific prolyl endopeptidase of the serine-type (see EC 3.4.21.72, IgA-specific serine endopeptidase)

References: [1602, 974, 973]

EC 3.4.24.14

Accepted name: procollagen N-endopeptidase

Reaction: Cleaves the N-propeptide of collagen chain α1(I) at Pro-Gln and of α1(II) and α2(I) at Ala-Gln

Other name(s): procollagen N-terminal peptidase; procollagen aminopeptidase; aminoprocollagen peptidase; aminoterminal procollagen peptidase; procollagen aminoterminal protease; procollagen N-terminal proteinase; type I/II procollagen N-proteinase; type III procollagen
Comments: Removes the propeptides of type I and II collagens prior to fibril assembly. Does not act on type III collagen. In peptidase family M12 (astacin family)

References: [1583, 1233]

[EC 3.4.24.14 created 1984]

EC 3.4.24.15
Accepted name: thimet oligopeptidase
Reaction: Preferential cleavage of bonds with hydrophobic residues at P1, P2 and P3′ and a small residue at P1′ in substrates of 5-15 residues
Other name(s): Pz-peptidase; soluble metalloendopeptidase; endo-oligopeptidase A; tissue-endopeptidase degrading collagenase-synthetic-substrate
Comments: Thiol compounds activate at low concentrations. Type example of peptidase family M3.
References: [491, 2310, 171, 2397, 3065]

[EC 3.4.24.15 created 1984 (EC 3.4.22.19 created 1989 and EC 3.4.99.31 created 1978 both incorporated 1992)]

EC 3.4.24.16
Accepted name: neurolysin
Reaction: Preferential cleavage in neurotensin: Pro^{10} Tyr
Other name(s): neurotensin endopeptidase; endopeptidase 24.16; endo-oligopeptidase B (proline-endopeptidase)
Comments: No absolute requirement for a prolyl bond: the enzyme acts on some peptides, such as dynorphin 1-8, that do not contain proline, and does not act on some others that do. In peptidase family M3 (thimet oligopeptidase family)
References: [443, 154, 442]

[EC 3.4.24.16 created 1989]

EC 3.4.24.17
Accepted name: stromelysin 1
Reaction: Preferential cleavage where P1′, P2′ and P3′ are hydrophobic residues
Other name(s): matrix metalloproteinase 3; proteoglycanase; collagenase activating protein; procollagenase activator; transsin; MMP-3; neutral proteoglycanase; stromelysin; collagen-activating protein
Comments: An extracellular endopeptidase of vertebrate tissues homologous with interstitial collagenase. Digests proteoglycan, fibronectin, collagen types III, IV, V, IX, and activates procollagenase. In peptidase family M10 (interstitial collagenase family)
References: [469, 2290, 667, 745]

[EC 3.4.24.17 created 1990]

EC 3.4.24.18
Accepted name: meprin A
Reaction: Hydrolysis of protein and peptide substrates preferentially on carboxyl side of hydrophobic residues
Other name(s): endopeptidase-2; meprin-a; meprin; N-benzoyl-L-tyrosyl-p-aminobenzoic acid hydrolase; PABA-peptide hydrolase; PPH
Comments: A membrane-bound metalloendopeptidase of rat and mouse kidney and intestinal brush borders, and salivary ducts. Differences from neprilysin (EC 3.4.24.11) (astacin family). Formerly included in EC 3.4.24.11
References: [232, 366, 2904, 2905, 161]

[EC 3.4.24.18 created 1992]
EC 3.4.24.19
Accepted name: procollagen C-endopeptidase
Reaction: Cleavage of the C-terminal propeptide at Ala→Asp in type I and II procollagens and at Arg→Asp in type III
Other name(s): procollagen C-terminal proteinase; carboxyprocollagen peptidase; procollagen C-terminal peptidase; procollagen C-proteinase; procollagen carboxypeptidase; procollagen carboxy-terminal proteinase; procollagen peptidase
Comments: A 100 kDa endopeptidase the activity of which is increased by Ca$^{2+}$ and by an enhancer glycoprotein. In peptidase family M12 (astacin family)
References: [1234, 1510]

EC 3.4.24.20
Accepted name: peptidyl-Lys metalloendopeptidase
Reaction: Preferential cleavage in proteins: -Xaa→Lys- (in which Xaa may be Pro)
Other name(s): Armillaria mellea neutral proteinase; peptidyllysine metalloproteinase
Comments: From the honey fungus Armillaria mellea. In peptidase family M35 (deuterolysin family).
References: [2610, 1752]

EC 3.4.24.21
Accepted name: astacin
Reaction: Hydrolysis of peptide bonds in substrates containing five or more amino acids, preferentially with Ala in P1′, and Pro in P2′
Other name(s): Astacus proteinase; crayfish small-molecule proteinase
Comments: A 22.6 kDa digestive endopeptidase from the cardia of the crayfish Astacus fluviatilis. Type example of peptidase family M12.
References: [1618, 3067, 2917, 2916]

EC 3.4.24.22
Accepted name: stromelysin 2
Reaction: Similar to stromelysin 1, but action on collagen types III, IV and V is weak
Other name(s): matrix metalloproteinase 10; transin 2; proteoglycanase 2
Comments: In peptidase family M10 (interstitial collagenase family). Digests gelatin types I, III, IV, V, fibronectin and proteoglycan
References: [310, 2096, 2187]

EC 3.4.24.23
Accepted name: matrilysin
Reaction: Cleavage of Ala$^{14}$→Leu and Tyr$^{16}$→Leu in B chain of insulin. No action on collagen types I, II, IV, V. Cleaves gelatin chain $\alpha_2$(I) $>$ $\alpha_1$(I)
Other name(s): matrin; uterine metalloendopeptidase; matrix metalloproteinase 7; putative (or punctuated) metalloproteinase-1; matrix metalloproteinase pump 1; MMP 7; PUMP-1 proteinase; PUMP; metalloproteinase pump-1; putative metalloproteinase; MMP
Comments: Found in rat uterus; at 19 kDa, the smallest member of peptidase family M10 (interstitial collagenase family). Similar in specificity to stromelysin, but more active on azocoll

245
EC 3.4.24.24

Accepted name: gelatinase A
Reaction: Cleavage of gelatin type I and collagen types IV, V, VII, X. Cleaves the collagen-like sequence Pro-Gln-Gly-Ile-Ala-Gly-Gln
Other name(s): 72-kDa gelatinase; matrix metalloproteinase 2; type IV collagenase (ambiguous); 3/4 collagenase (obsolete); matrix metalloproteinase 5 (obsolete); 72 kDa gelatinase type A; collagenase IV (ambiguous); collagenase type IV (ambiguous); MMP 2; type IV collagen metalloproteinase (ambiguous); type IV collagenase/gelatinase (ambiguous)
Comments: A secreted endopeptidase in peptidase family M10 (interstitial collagenase family), but possessing an additional fibronectin-like domain
References: [2096, 3359, 2460, 2037]

[EC 3.4.24.24 created 1992]

EC 3.4.24.25

Accepted name: vibriolysin
Reaction: Preferential cleavage of bonds with bulky hydrophobic groups in P2 and P1’. Phe at P1’ is the most favoured residue, which distinguished this enzyme from thermolysin
Other name(s): Aeromonas proteolytica neutral proteinase; aeromonolysin
Comments: Thermostable enzyme from Vibrio proteolyticus (formerly Aeromonas proteolytica). Specificity related to, but distinct from, those of thermolysin and bacillolysin [1238]. A zinc metallopeptidase in family M4 (thermolysin family). Formerly included in EC 3.4.24.4
References: [1238, 3341, 191, 3340, 586]


EC 3.4.24.26

Accepted name: pseudolysin
Reaction: Hydrolysis of proteins including elastin, collagen types III and IV, fibronectin and immunoglobulin A, generally with bulky hydrophobic group at P1’. Insulin B chain cleavage pattern identical to that of thermolysin, but specificity differs in other respects
Other name(s): Pseudomonas elastase; Pseudomonas aeruginosa neutral metalloproteinase
Comments: In peptidase family M4 (thermolysin family). From the pathogenic bacteria Pseudomonas aeruginosa and Legionella pneumophila, and causes tissue damage.
References: [2072, 2201, 696, 231, 256]

[EC 3.4.24.26 created 1972 as EC 3.4.24.4, part transferred 1992 to EC 3.4.24.26]

EC 3.4.24.27

Accepted name: thermolysin
Reaction: Preferential cleavage: Leu > Phe
Other name(s): Bacillus thermoproteolyticus neutral proteinase; thermose; thermose Y10; TLN
Comments: A thermostable extracellular metalloendopeptidase containing four calcium ions. Enzymes that may be species variants of thermolysin are reported from Micrococcus caseolyticus [631] and Aspergillus oryzae [2071]. Type example of peptidase family M4. Closely related but distinct enzymes are aeromonolysin, pseudolysin, bacillolysin, aureolysin and mycolysin
References: [2281, 2074, 1702, 631, 2071, 3066, 1942]

[EC 3.4.24.27 created 1972 as EC 3.4.24.4, part transferred 1992 to EC 3.4.24.27]

246
EC 3.4.24.28

Accepted name: bacillolysin
Reaction: Similar, but not identical, to that of thermolysin
Other name(s): Bacillus metalloendopeptidase; Bacillus subtilis neutral proteinase; anilozyme P 10; Bacillus metalloproteinase; Bacillus neutral proteinase; megateriopeptidase
Comments: Variants of this enzyme have been found in species of Bacillus including B. subtilis [2074, 3417], B. amyloliquefaciens [3203], B. megaterium (megateriopeptidase, [2015]), B. mesentericus [2918], B. cereus [3,8,9] and B. stearothermophilus [2975]. In peptidase family M4 (thermolysin family). Formerly included in EC 3.4.24.4
References: [2074, 2015, 801, 1238, 3203, 3417, 2975, 2789, 2364, 2918]

[EC 3.4.24.28 created 1972 as EC 3.4.24.4, part transferred 1992 to EC 3.4.24.28]

EC 3.4.24.29

Accepted name: aureolysin
Reaction: Cleavage of insulin B chain with specificity similar to that of thermolysin, preferring hydrophobic P1’ residue. Activates the glutamyl endopeptidase (EC 3.4.21.19) of Staphylococcus aureus
Other name(s): Staphylococcus aureus neutral proteinase; Staphylococcus aureus neutral protease
Comments: A metalloenzyme from S. aureus earlier confused with staphylokinase (a non-enzymic activator of plasminogen).
References: [86, 2621, 691, 2433]

[EC 3.4.24.29 created 1972 as EC 3.4.24.4, part transferred 1992 to EC 3.4.24.29]

EC 3.4.24.30

Accepted name: coccolysin
Reaction: Preferential cleavage: +Leu, +Phe, +Tyr, +Ala
Other name(s): Streptococcus thermophilus intracellular proteinase; EM 19000
Comments: A 30 kDa endopeptidase found intracellularly in S. thermophilus [632] and S. diacetilactis [633] and in the medium of S. faecalis [2839, 1882]. In peptidase family M4 (thermolysin family). Formerly included in EC 3.4.24.4
References: [632, 633, 2839, 1882]

[EC 3.4.24.30 created 1972 as EC 3.4.24.4, part transferred 1992 to EC 3.4.24.30]

EC 3.4.24.31

Accepted name: mycolysin
Reaction: Preferential cleavage of bonds with hydrophobic residues in P1’
Other name(s): pronase component; Streptomyces griseus neutral proteinase; actinase E; SGNPI
Comments: The enzyme has been characterized from the bacteria Streptomyces griseus, Streptomyces naraensis, and Streptomyces cacaoi. Specificity is similar to that of thermolysin, but the enzyme is much more sensitive to inhibition by sulfanylacetyl-Phe-Leu. Little structural similarity to other bacterial metalloendopeptidases. Type example of peptidase family M5.
References: [2074, 1217, 271, 426]

[EC 3.4.24.31 created 1972 as EC 3.4.24.4, part transferred 1992 to EC 3.4.24.31]

EC 3.4.24.32

Accepted name: β-lytic metalloendopeptidase
Reaction: Cleavage of N-acetylmuramoyl-Ala, and of the insulin B chain at Gly<sup>23</sup>Phe > Val<sup>18</sup>Cys
Other name(s): Myxobacter β-lytic proteinase; achromopeptidase component; β-lytic metalloproteinase; β-lytic protease; Myxobacterium sorangium β-lytic proteinase; Myxobacter<sup>495</sup> β-lytic proteinase
Comments: From *Achromobacter lyticus* and *Lysobacter enzymogenes*. Digests bacterial cell walls. Type example of peptidase family M23.

References: [3323, 3322, 1757]

[EC 3.4.24.32 created 1972 as EC 3.4.24.4, part transferred 1992 to EC 3.4.24.32]

**EC 3.4.24.33**

**Accepted name:** peptidyl-Asp metalloendopeptidase

**Reaction:** Cleavage of Xaa–Asp, Xaa–Glu and Xaa–cysteic acid bonds

**Other name(s):** endoproteinase Asp-N; peptidyl-Asp metalloproteinase

**Comments:** A metalloenzyme isolated from *Pseudomonas fragi*. Useful in protein sequencing applications because of its limited specificity. In peptidase family M72.

References: [2431, 693, 1327]

[EC 3.4.24.33 created 1992]

**EC 3.4.24.34**

**Accepted name:** neutrophil collagenase

**Reaction:** Cleavage of interstitial collagens in the triple helical domain. Unlike EC 3.4.24.7, interstitial collagenase, this enzyme cleaves type III collagen more slowly than type I

**Other name(s):** matrix metalloproteinase 8; PMNL collagenase; MMP-8

**Comments:** Similar to interstitial collagenase in specificity, but the product of a different gene and highly glycosylated. Stored in the specific granules of neutrophil leukocytes. In peptidase family M10 (interstitial collagenase family). Formerly included in EC 3.4.24.7

References: [1136, 1137, 1567]

[EC 3.4.24.34 created 1992]

**EC 3.4.24.35**

**Accepted name:** gelatinase B

**Reaction:** Cleavage of gelatin types I and V and collagen types IV and V

**Other name(s):** 92-kDa gelatinase; matrix metalloproteinase 9; type V collagenase; 92-kDa type IV collagenase; macrophage gelatinase; 95-kDa type IV collagenase/gelatinase; collagenase IV (ambiguous); collagenase type IV (ambiguous); gelatinase MMP 9; MMP 9; type IV collagen metalloproteinase (ambiguous)

**Comments:** Similar to gelatinase A, but possesses a further domain. In peptidase family M10 (interstitial collagenase family)

References: [1207, 3337, 1876]

[EC 3.4.24.35 created 1992]

**EC 3.4.24.36**

**Accepted name:** leishmanolysin

**Reaction:** Preference for hydrophobic residues at P1 and P1′ and basic residues at P2 and P3′. A model nonapeptide is cleaved at -Ala-Tyr–Leu-Lys-Lys-

**Other name(s):** promastigote surface endopeptidase; glycoprotein gp63; *Leishmania* metalloproteinase; surface acid proteinase; promastigote surface protease

**Comments:** A membrane-bound glycoprotein found on the promastigote of various species of *Leishmania* protozoans. Contains consensus sequence for a zinc-binding site; Z-Tyr-Leu-NHOH is a strong inhibitor. The enzyme can activate its proenzyme by cleavage of the Val100–Val bond. An acid pH optimum is found with certain protein substrates. Type example of peptidase family M8

References: [372, 299, 440, 300]

[EC 3.4.24.36 created 1992]
EC 3.4.24.37

Accepted name: saccharolysin
Reaction: Cleavage of Pro-Phe and Ala-Ala bonds
Other name(s): proteinase yscD (gene name) (gene name); yeast cysteine proteinase D (Misleading); Saccharomyces cerevisiae proteinase yscD (gene name)
Comments: An 83 kDa cytoplasmic thiol-dependent metalloendopeptidase from Saccharomyces cerevisiae. In peptidase family M3 (thimet oligopeptidase family).
References: [11, 932]

[EC 3.4.24.37 created 1989 as EC 3.4.22.22, transferred 1992 to EC 3.4.24.37]

EC 3.4.24.38

Accepted name: gametolysin
Reaction: Cleavage of the proline- and hydroxyproline-rich proteins of the Chlamydomonas cell wall; also cleaves azocasein, gelatin and Leu-Trp-Met-Arg-Phe-Ala
Other name(s): autolysin; Chlamydomonas cell wall degrading protease; lysin; Chlamydomonas reinhardtii metallo-proteinase; gamete lytic enzyme; gamete autolysin
Comments: A glycoprotein found in the periplasmic space of Chlamydomonas reinhardtii gametes in a 62 kDa inactive form; decreased to 60 kDa upon activation. A zinc enzyme, inhibited by phosphoramidon, but also thiol activated. Type example of peptidase family M11
References: [1373, 352, 1934]

[EC 3.4.24.38 created 1992, modified 2000]

EC 3.4.24.39

Accepted name: deuterolysin
Reaction: Preferential cleavage of bonds with hydrophobic residues in P1', also Asn\textsuperscript{3} --- Gln and Gly\textsuperscript{8} --- Ser bonds in insulin B chain
Other name(s): Penicillium roqueforti protease II; microbial neutral proteinase II; acid metalloproteinase; neutral proteinase II; Penicillium roqueforti metalloproteinase
Comments: Proteolytic activity found in Penicillium roqueforti [1040], P. caseicolum [1040], Aspergillus sojae [2742] and A. oryzae [2136, 3175]. Optimum pH of 5 for digesting various proteins. Strong action on protamine and histones. Insensitive to phosphoramidon. About 20 kDa. A distinct Aspergillus sojae endopeptidase is larger and has a neutral pH optimum. Type example of peptidase family M35. Formerly included in EC 3.4.24.4
References: [2136, 1039, 2742, 1040, 3175]

[EC 3.4.24.39 created 1972 as EC 3.4.24.4, part transferred 1992 to EC 3.4.24.39]

EC 3.4.24.40

Accepted name: serralysin
Reaction: Preferential cleavage of bonds with hydrophobic residues in P1'
Other name(s): Pseudomonas aeruginosa alkaline proteinase; Escherichia freundii proteinase; Serratia marcescens extracellular proteinase; Serratia marcescens metalloproteinase; Pseudomonas aeruginosa alk. proteinase; Serratia marcescens metalloproteinase
Comments: A 50 kDa extracellular endopeptidase from Pseudomonas aeruginosa [1,2,6], Escherichia freundii [2140], Serratia marcescens [4,5,6] and Erwinia chrysanthemi [568]. There is broad specificity in cleavage of the insulin B chain, with some species variations. The pH optimum for digesting various proteins is about 9 - 10. In peptidase family M10 (interstitial collagenase family). Formerly included in EC 3.4.24.4
References: [2074, 2075, 2140, 607, 671, 2139, 568, 2298]

[EC 3.4.24.40 created 1972 as EC 3.4.24.4, part transferred 1992 to EC 3.4.24.40]
EC 3.4.24.41

Accepted name: atrolysin B

Reaction: Cleavage of His\(^5\)\(\text{Leu}\), His\(^{10}\)\(\text{Leu}\), Ala\(^{14}\)\(\text{Leu}\), Tyr\(^{16}\)\(\text{Leu}\) and Gly\(^{23}\)\(\text{Phe}\) of insulin B chain; identical to the cleavage of insulin B chain by atrolysin C. Also cleaves \(\text{Ser}\) bonds in glucagon

Other name(s): *Crotalus atrox* metalloendopeptidase b; hemorrhagic toxin b; Ht-b

Comments: From the venom of the western diamondback rattlesnake (*Crotalus atrox*). In peptidase family M12 (astacin family)

References: [249, 248]

[EC 3.4.24.41 created 1992]

EC 3.4.24.42

Accepted name: atrolysin C

Reaction: Cleavage of His\(^5\)\(\text{Leu}\), His\(^{10}\)\(\text{Leu}\), Ala\(^{14}\)\(\text{Leu}\), Tyr\(^{16}\)\(\text{Leu}\) and Gly\(^{23}\)\(\text{Phe}\) bonds in B chain of insulin. With small molecule substrates prefers hydrophobic residue at P2' and small residue such as Ala, Gly at P1

Other name(s): *Crotalus atrox* metalloendopeptidase c; hemorrhagic toxin c and d

Comments: A 24 kDa hemorrhagic endopeptidase from the venom of the western diamondback rattlesnake (*Crotalus atrox*) that digests type IV collagen, and exists as two forms, c and d. Phosphoramidon inhibits in the 0.1 mM range. In peptidase family M12 (astacin family). Hemorrhagic toxin-2 of *C. ruber ruber* has the same \(M_r\) and specificity and is a homologue [2067, 3005].

References: [249, 851, 246, 2067, 2751, 3005]

[EC 3.4.24.42 created 1992]

EC 3.4.24.43

Accepted name: atroxase

Reaction: Cleavage of His\(^5\)\(\text{Leu}\), Ser\(^9\)\(\text{His}\), His\(^{10}\)\(\text{Leu}\), Ala\(^{14}\)\(\text{Leu}\) and Tyr\(^{16}\)\(\text{Leu}\) of insulin B chain

Comments: A nonhemorrhagic endopeptidase from the venom of the western diamondback rattlesnake (*Crotalus atrox*) that cleaves fibrinogen. In peptidase family M12 (astacin family)

References: [3345]

[EC 3.4.24.43 created 1992]

EC 3.4.24.44

Accepted name: atrolysin E

Reaction: Cleavage of Asn\(^3\)\(\text{Gln}\), Ser\(^9\)\(\text{His}\) and Ala\(^{14}\)\(\text{Leu}\) bonds in insulin B chain and Tyr\(^{16}\)\(\text{Leu}\) in \(\alpha\)(IV)

Other name(s): *Crotalus atrox* metalloendopeptidase e; hemorrhagic toxin e

Comments: A 25.7 kDa hemorrhagic endopeptidase from the venom of the western diamondback rattlesnake (*Crotalus atrox*) that digests basement membrane components, including the triple helix of type IV collagen. Such action is believed to contribute to the hemorrhagic property by weakening capillary walls. In peptidase family M12 (astacin family)

References: [249, 245, 150]

[EC 3.4.24.44 created 1992]

EC 3.4.24.45

Accepted name: atrolysin F

Reaction: Cleavage of Val\(^2\)\(\text{Asn}\), Gln\(^4\)\(\text{His}\), Leu\(^6\)\(\text{Cys}\), His\(^{10}\)\(\text{Leu}\), Ala\(^{14}\)\(\text{Leu}\) and Tyr\(^{16}\)\(\text{Leu}\) bonds in insulin B chain
Other name(s): *Crotalus atrox* metalloendopeptidase; hemorrhagic toxin f; *Crotalus atrox* metalloendopeptidase f

Comments: A 64 kDa hemorrhagic endopeptidase from the venom of the western diamondback rattlesnake (*Crotalus atrox*) that digests the γ chain of fibrinogen. Immunologically distinct from EC 3.4.24.1, atrolysin A.

References: [2192]

[EC 3.4.24.45 created 1992]

EC 3.4.24.46

Accepted name: adanalysin

Reaction: Cleavage of Phe$^1$–Val, His$^5$–Leu, His$^{10}$–Leu, Ala$^{14}$–Leu, Leu$^{15}$–Tyr, and Tyr$^{16}$–Leu of insulin B chain

Other name(s): *Crotalus adamanteus* metalloendopeptidase; proteinase I and II; *Crotalus adamanteus* venom proteinase II; adanalysin II

Comments: From the venom of the eastern diamondback rattlesnake (*Crotalus adamanteus*). Two isoenzymes of approx. 24 kDa that inactivate α$_1$-proteinase inhibitor by a single cleavage. In peptidase family M12 (astacin family)

References: [1656]

[EC 3.4.24.46 created 1992]

EC 3.4.24.47

Accepted name: horrilysin

Reaction: Cleavage of only the single bond Ala$^{14}$–Leu in the insulin B chain, Ser$^{12}$–Leu in the A chain, and Ile–Gly, Pro–Ala, and Ser–Trp in melittin

Other name(s): *Crotalus horridus* metalloendopeptidase; hemorrhagic proteinase IV; *Crotalus horridus horridus* venom hemorrhagic proteinase

Comments: A 56 kDa hemorrhagic endopeptidase from the venom of the timber rattlesnake (*Crotalus horridus horridus*) that cleaves basement membrane, hide powder and fibrinogen.

References: [493, 495]

[EC 3.4.24.47 created 1992]

EC 3.4.24.48

Accepted name: ruberlysin

Reaction: Cleavage of His$^{10}$–Leu, Ala$^{14}$–Leu, Tyr$^{16}$–Leu and Gly$^{23}$–Phe bonds in the B chain of insulin; His–Pro, Pro–Phe, and Trp–Ser of angiotensin I; and Gly–Phe of Met enkephalin

Other name(s): *Crotalus ruber* metalloendopeptidase II; hemorrhagic toxin II

Comments: A 25 kDa hemorrhagic endopeptidase from the venom of the red rattlesnake (*Crotalus ruber ruber*) that cleaves fibrinogen. In peptidase family M12 (astacin family)

References: [2067, 3005]

[EC 3.4.24.48 created 1992]

EC 3.4.24.49

Accepted name: bothropasin

Reaction: Cleavage of His$^5$–Leu, His$^{10}$–Leu, Ala$^{14}$–Leu, Tyr$^{16}$–Leu and Phe$^{24}$–Phe in insulin B chain

Other name(s): *Bothrops jararaca* venom metalloproteinase

Comments: Caseinolytic endopeptidase of jararaca snake (*Bothrops jararaca*) venom; 48 kDa. In peptidase family M12

References: [1895]

[EC 3.4.24.49 created 1992]
EC 3.4.24.50  
Accepted name: bothrolysin  
Reaction: Cleavage of Gln$^4$His, Ser$^9$His and Ala$^{14}$Leu of insulin B chain and Pro$^6$Phe of angiotensin I  
Other name(s): Bothrops metalloendopeptidase J; J protease  
Comments: A 22.5 kDa endopeptidase from the venom of the jararaca snake (Bothrops jararaca), insensitive to phosphoramidon at 0.5 mM. In peptidase family M12 (astacin family)  
References: [3026]

[EC 3.4.24.50 created 1992]

EC 3.4.24.51  
Accepted name: ophiolysin  
Reaction: Cleavage of Asn$^3$Gln, Gln$^4$His, His$^{10}$Leu, Ala$^{14}$Leu, and Tyr$^{16}$Leu in insulin B chain  
Other name(s): Ophiophagus metalloendopeptidase  
Comments: A 70 kDa endopeptidase from the venom of the king cobra (Ophiophagus hannah)  
References: [3402]

[EC 3.4.24.51 created 1992]

EC 3.4.24.52  
Accepted name: trimerelysin I  
Reaction: Cleavage of only two bonds His$^{10}$Leu and Ala$^{14}$Leu in the insulin B chain  
Other name(s): Trimeresurus metalloendopeptidase I; hemorrhagic proteinase HR1A; hemorrhagic metalloproteinase HR1A  
Comments: A 60 kDa hemorrhagic endopeptidase of pI 4.4 from the venom of the habu snake (Trimeresurus flavoviridis). In peptidase family M12 (astacin family)  
References: [2306, 3003, 3004]

[EC 3.4.24.52 created 1992]

EC 3.4.24.53  
Accepted name: trimerelysin II  
Reaction: Cleavage of Asn$^3$Gln, His$^{10}$Leu and Ala$^{14}$Leu in the insulin B chain, and the bond Z-Gly-Pro-Leu-Gly-Pro in a small molecule substrate of microbial collagenase  
Other name(s): Trimeresurus metalloendopeptidase II; proteinase H$_2$; H$_2$-proteinase  
Comments: A 24 kDa nonhemorrhagic endopeptidase from the venom of the habu snake (Trimeresurus flavoviridis). In peptidase family M12 (astacin family)  
References: [2986, 3002]

[EC 3.4.24.53 created 1992]

EC 3.4.24.54  
Accepted name: mucrolysin  
Reaction: Cleavage of Ser$^9$His, His$^{10}$Leu, Ala$^{14}$Leu, Leu$^{15}$Tyr and Tyr$^{16}$Leu bonds in insulin B chain  
Other name(s): Trimeresurus metalloendopeptidase A; mucrotoxin A  
Comments: A 94 kDa hemorrhagic and fibrinogenolytic endopeptidase from the Chinese habu snake (Trimeresurus mucrosquamatus) venom. In peptidase family M12 (astacin family)  
References: [2934, 1553]

[EC 3.4.24.54 created 1992]
EC 3.4.24.55

**Accepted name:** pitrilysin  
**Reaction:** Preferential cleavage of -Tyr\(^{16}\)–Leu- and -Phe\(^{25}\)–Tyr-bonds of oxidized insulin B chain. Also acts on other substrates of less than 7 kDa such as insulin and glucagon  
**Other name(s):** *Escherichia coli* protease III; protease P\(_i\); proteinase P\(_i\); PTR; *Escherichia coli* metalloproteinase P\(_i\)  
**Comments:** From the periplasmic space of *Escherichia coli*. Inhibited by EDTA and 1,10-phenanthroline; not thiol-dependent. Type example of peptidase family M16  
**References:** [820, 22, 198, 662, 52]


---

EC 3.4.24.56

**Accepted name:** insulysin  
**Reaction:** Degradation of insulin, glucagon and other polypeptides. No action on proteins  
**Other name(s):** insulinase; insulin-degrading enzyme; insulin protease; insulin proteinase; insulin-degrading neutral proteinase; insulin-specific protease; insulin-glucagon protease; metalloinsulinase; IDE  
**Comments:** A 110 kDa cytosolic enzyme, known from mammals and the fruit fly, *Drosophila melanogaster*. Inhibited by bacitracin, chelating agents EDTA and 1,10-phenanthroline, and by thiol-blocking reagents such as N-ethylmaleimide, but not by phosphoramidon. In peptidase family M16 (pitrilysin family).  
**References:** [704, 23, 705, 1652, 662]

[EC 3.4.24.56 created 1972 as EC 3.4.99.10, transferred 1976 EC 3.4.22.11, transferred 1978 to EC 3.4.99.45, transferred 1993 to to EC 3.4.24.56 (EC 3.4.99.46 created 1992, incorporated 2000)]

---

EC 3.4.24.57

**Accepted name:** O-sialoglycoprotein endopeptidase  
**Reaction:** Hydrolysis of O-sialoglycoproteins; cleaves -Arg\(^{31}\)–Asp- bond in glycophorin A. Does not cleave unglycosylated proteins, desialylated glycoproteins or glycoproteins that are only N-glycosylated  
**Other name(s):** glycoprotease; glycophorin A proteinase; glycoproteinase; sialoglycoprotease; sialoglycoproteinase  
**Comments:** An enzyme secreted by the bacterium *Pasteurella haemolytica*. Inhibited by EDTA (100 mM) and 1,10-phenanthroline. Type example of peptidase family M22  
**References:** [3, 4, 2950]

[EC 3.4.24.57 created 1993]

---

EC 3.4.24.58

**Accepted name:** russellysin  
**Reaction:** Specifically activates several components of the blood clotting system, including coagulation factor X, coagulation factor IX and protein C by cleavage of -Arg-bonds. Has no action on insulin B chain  
**Other name(s):** Russell’s viper venom factor X activator; RVV-X; blood-coagulation factor X activating enzyme; metalloproteinase RVV-x; *Vipera russelli* proteinase; Russell’s viper blood coagulation factor X activator; RVV-V  
**Comments:** This enzyme from the venom of Russell’s viper (*Vipera russelli*) of 79 kDa comprises a heavy (59 kDa) and a heterogeneous light (18-21 kDa) chain. Contains Ca\(^{2+}\) and Zn\(^{2+}\). The heavy chain contains the zinc-binding endopeptidase domain and a disintegrin. In peptidase family M12 (astacin family)  
**References:** [919, 1798, 3003]

[EC 3.4.24.58 created 1993]

---

EC 3.4.24.59

**Accepted name:** mitochondrial intermediate peptidase
Reaction: Release of an N-terminal octapeptide as second stage of processing of some proteins imported into the mitochondrion

Other name(s): mitochondrial intermediate precursor-processing proteinase; MIP

Comments: A homologue of thimet oligopeptidase. Natural substrates are precursor proteins that have already been processed by mitochondrial processing peptidase. In peptidase family M3 (thimet oligopeptidase family)

References: [1333, 1334]

[EC 3.4.24.59 created 1993]

EC 3.4.24.60
Accepted name: dactylysin

Reaction: Hydrolysis of peptides of at least six residues, with bulky hydrophobic residues in the P1’ position. Shows a preference for hydrophobic doublets such as -Phe-Phe- and -Phe-Leu- in somatostatin-(1-14)-peptide and dynorphin A-(1-6)-peptide, respectively

Other name(s): peptide hormone inactivating endopeptidase; PHIE

Comments: An endopeptidase of 100 kDa secreted from the skin of the amphibian, *Xenopus laevis* (Dactylêtre du Cap). Resembles neprilysin in insensitivity to 1 µM captopril, but differs from it in being insensitive to thiorphan (1 µM) and unable to digest [Met⁵]enkephalin, [Leu⁵]enkephalin, oxytocin, and substance P-(7-11)-peptide. A similar endopeptidase is found in human neuroblastoma cells [619]

References: [409, 619, 1426]

[EC 3.4.24.60 created 1995]

EC 3.4.24.61
Accepted name: nardilysin

Reaction: Hydrolysis of polypeptides, preferably at -Xaa-Arg-Lys-, and less commonly at -Arg-Arg-Xaa-, in which Xaa is not Arg or Lys

Other name(s): N-arginine dibasic convertase; NRD-convertase

Comments: Enzyme of 133 kDa from rat brain and testis. A homologue of pitrilysin containing the His-Phe-Leu-Glu-His zinc-binding sequence, and a highly acidic stretch of 71 residues. Unusually for a metalloendopeptidase, inhibited by bestatin, amastatin and N-ethylmaleimide. In peptidase family M16 (pitrilysin family)

References: [1007, 986, 461, 2398]

[EC 3.4.24.61 created 1995]

EC 3.4.24.62
Accepted name: magnolysin

Reaction: Hydrolysis of polypeptides with Arg or Lys in P1 and P2, e.g. to hydrolyse pro-oxytocin at -Lys-Arg-Ala-Val-. The specificity further depends on the organization of a β-turn-α-helix of nine or more residues containing the paired basic amino acids near the centre [3]

Other name(s): bovine neurosecretory granule protease cleaving pro-oxytocin/neurophysin; pro-oxytocin/neurophysin convertase; prooxyphysin proteinase; pro-oxytocin convertase

Comments: An endopeptidase of 58 kDa known from bovine pituitary neurosecretory granules and bovine and human corpus luteum [2411, 1056]. Inhibited by EDTA [496]

References: [496, 544, 304, 2411, 1056]

[EC 3.4.24.62 created 1995]

EC 3.4.24.63
Accepted name: meprin B

Other name(s): meprin-b

Comments: A brush border membrane-bound metalloendopeptidase known from the intestine of all mouse strains that have been tested, and the kidney of certain inbred strains. A tetramer of meprin β subunits (in contrast to meprin A, which contains both α and β subunits). Occurs in the kidney as a proenzyme that can be activated by trypsin. Meprin B is inhibited by both EDTA and 1,10-phenanthroline, but not by phosphoramidon, captopril or thiorphan. In peptidase family M12 (astacin family)

References: [1611, 1012, 1407, 3364]

[EC 3.4.24.63 created 1995]

EC 3.4.24.64

Accepted name: mitochondrial processing peptidase

Reaction: Release of N-terminal targetting peptides from precursor proteins imported into the mitochondrion, typically with Arg in position P2

Other name(s): processing enhancing peptidase (for one of two subunits); mitochondrial protein precursor-processing proteinase; matrix peptidase; matrix processing peptidase; matrix processing proteinase; MPP

Comments: Known from the mitochondrial matrix of fungi and mammals. Formed from two subunits, both homologous with pitrilysin [2506], and the products of the MAS1 and MAS2 genes in yeast. In peptidase family M16 (pitrilysin family).

References: [1400, 3356, 2506, 1448, 349]

[EC 3.4.24.64 created 1989/90 as EC 3.4.99.41, transferred 1995 to EC 3.4.24.64]

EC 3.4.24.65

Accepted name: macrophage elastase

Reaction: Hydrolysis of soluble and insoluble elastin [1]. Specific cleavages are also produced at -Ala^14-Leu- and -Tyr^16-Leu- in the B chain of insulin [2]

Other name(s): metalloelastase; human macrophage metalloelastase (HME)

Comments: This enzyme is synthesized as a proenzyme of 53 kDa that is converted to an active form of 22 kDa. cDNA sequences have been obtained for the mouse [2756] and human [2757] enzymes. In peptidase family M10 (interstitial collagenase family)

References: [149, 1514, 2756, 2757]

[EC 3.4.24.65 created 1995]

EC 3.4.24.66

Accepted name: choriolyisn L

Reaction: Hydrolysis of the inner layer of fish egg envelope. Also hydrolysis of casein and small molecule substrates such as succinyl-Leu-Leu-Val-Tyr^7-(4-methyl)coumarylamide

Other name(s): teleost hatching enzyme (component); low choriolytic enzyme (LCE)

Comments: Known from the teleost fish Orzyias latipes (medaka). Efficient dissolution of the egg membrane requires concerted action with choriolyisn H. A 24 kDa peptidase family M12 (astacin family)

References: [3430, 3431, 3433, 3435]

[EC 3.4.24.66 created 1995]

EC 3.4.24.67

Accepted name: choriolyisn H

Reaction: Hydrolysis of the inner layer of fish egg envelope. Also hydrolysis of casein and small molecule substrates such as succinyl-Leu-Leu-Val-Tyr^7-(4-methyl)coumarylamide
Other name(s): teleost hatching enzyme (component); high choriolytic enzyme (HCE)
Comments: Known from the teleost fish *Oryzias latipes* (medaka). Efficient dissolution of the egg membrane requires concerted action with choriolysin L. A 25.5 kDa peptidase in family M12 (astacin family)
References: [3399, 3432, 3434, 3435, 1716]

[EC 3.4.24.67 created 1995]

EC 3.4.24.68

Accepted name: tentoxilysin
Reaction: Hydrolysis of -Gln^{76}\\(\rightarrow\)Phe- bond in synaptobrevin (also known as neuronal vesicle-associated membrane protein, VAMP)
Other name(s): tetanus neurotoxin
Comments: Zinc enzyme produced by *Clostridium* tetani. Proenzyme of 150 kDa is processed to disulfide-linked subunits of 100 and 50 kDa, the latter being responsible for the endopeptidase activity. Weakly inhibited by captopril, and phosphoramidon. The clostridial neurotoxins disable the neuroexocytosis apparatus, and have been described as the most toxic substances known. Tentoxilysin acts at the spinal inhibitory interneurons, blocking the release of various neurotransmitters to produce spastic paralysis. Type example of peptidase family M27 (tentoxilysin family)
References: [884, 2689, 2693, 2055, 2691]

[EC 3.4.24.68 created 1995]

EC 3.4.24.69

Accepted name: bontoxilysin
Reaction: Limited hydrolysis of proteins of the neuroexocytosis apparatus, synaptobrevin (also known as neuronal vesicle-associated membrane protein, VAMP), synaptosome-associated protein of 25 kDa (SNAP25) or syntaxin. No detected action on small molecule substrates
Other name(s): botulinum neurotoxin; BoNT
Comments: This zinc enzyme, produced by *Clostridium* botulinum, occurs as forms A-G that differ in specificity of action on the proteins of the neuroexocytosis apparatus [2692, 2694, 2695, 2690, 2055]. The 150-kDa proenzymes of bontoxilysin are processed to disulfide-linked subunits of 100 and 50 kDa, the latter being responsible for the endopeptidase activities. Weakly inhibited by captopril, and phosphoramidon. Toxicity is due to action at the neuromuscular junctions that blocks release of acetylcholine, causing flaccid paralysis, in contrast to the spastic paralysis caused by tentoxilysin. In peptidase family M27 (tentoxilysin family)
References: [2692, 2694, 2695, 2690, 2055, 2691]

[EC 3.4.24.69 created 1995]

EC 3.4.24.70

Accepted name: oligopeptidase A
Reaction: Hydrolysis of oligopeptides, with broad specificity. Gly or Ala commonly occur as P1 or P1′ residues, but more distant residues are also important, as is shown by the fact that Z-Gly-Pro-Gly-Gly-Pro-Ala is cleaved, but not Z-(Gly)₃ [4]
Other name(s): 68000-M signalpeptide hydrolase
Comments: Known from *Escherichia coli* and *Salmonella typhimurium*. A zinc metallopeptidase, in peptidase family M3 (thimet oligopeptidase family), but differs from thimet oligopeptidase in lack of thiol-activation
References: [2225, 516, 515, 514]

[EC 3.4.24.70 created 1996]
EC 3.4.24.71
Accepted name: endothelin-converting enzyme 1
Reaction: Hydrolysis of the Trp<sup>21</sup>-Val bond in big endothelin to form endothelin 1
Other name(s): endothelin-converting enzyme; ECE-1
Comments: A phosphoramidon-sensitive metalloendopeptidase in peptidase family M13 (neprilysin family). An integral membrane protein predominantly of endothelial cells, which generates the potent vasoconstrictor endothelin 1 from its inactive precursor
References: [2981, 2767, 3387]

[EC 3.4.24.71 created 1996]

EC 3.4.24.72
Accepted name: fibrolase
Reaction: Hydrolysis of Ala<sup>14</sup>-Leu- in insulin B chain and Lys<sup>413</sup>-Leu- in A<sub>α</sub>-chain of fibrinogen
Other name(s): fibrinolytic proteinase; Agkistrodon contortrix contortrix metalloproteinase; Agkistrodon contortrix contortrix venom metalloproteinase
Comments: A 23-kDa, non-hemorrhagic enzyme from the venom of the southern copperhead snake (Agkistrodon contortrix). In peptidase family M12 (astacin family)
References: [14, 1054, 2494, 1828, 2538]

[EC 3.4.24.72 created 1996]

EC 3.4.24.73
Accepted name: jararhagin
Reaction: Hydrolysis of His<sup>10</sup>-Leu-, Ala<sup>14</sup>-Leu-, Tyr<sup>16</sup>-Leu-and Phe<sup>24</sup>-Phe- bonds in insulin B chain
Other name(s): HF2-proteinase; JF1
Comments: Hemorrhagic endopeptidase from the venom of the jararaca snake (Bothrops jararaca). The 52-kDa enzyme contains a disintegrin domain [2335]. In peptidase family M12 (astacin family)
References: [1896, 97, 2335]

[EC 3.4.24.73 created 1996]

EC 3.4.24.74
Accepted name: fragilysin
Reaction: Broad proteolytic specificity, bonds hydrolysed including Gly-Leu-, Met-Leu-, Phe-Leu-, Cys-Leu-, Leu-Gly
Other name(s): Bacteroides fragilis (entero)toxin
Comments: Thought to be a cause of diarrhoea in animals and humans. Hydrolyses extracellular matrix proteins, and disrupts tight junctions of intestinal epithelial cells. Also degrades intracellular, cytoskeletal proteins actin, myosin and others. In peptidase family M10 (interstitial collagenase family)
References: [2052, 2232, 676, 1604, 1562]

[EC 3.4.24.74 created 1997]

EC 3.4.24.75
Accepted name: lysostaphin
Reaction: Hydrolysis of the Gly-Gly- bond in the pentaglycine inter-peptide link joining staphylococcal cell wall peptidoglycans
Other name(s): glycy1-glycine endopeptidase
Comments: A zinc-dependent, 25-kDa endopeptidase from Staphylococcus simulans. Lyses cells of S. aureus, in particular, by its action on the cross-bridges of the cell wall. Type example of peptidase family M23.
References: [2516, 121, 3062]
EC 3.4.24.76
Accepted name: flavastacin
Reaction: Hydrolyses polypeptides on the amino-side of Asp in -Xaa—Asp-. Acts very slowly on -Xaa—Glu
Comments: A zinc metalloendopeptidase in peptidase family M12 (astacin family), secreted by the bacterium Flavobacterium meningosepticum. The specificity is similar to that of EC 3.4.24.33, peptidyl-Asp metalloendopeptidase from Pseudomonas fragi but the two are reported to be structurally dissimilar
References: [3030]

EC 3.4.24.77
Accepted name: snapalysin
Reaction: Hydrolyses proteins with a preference for Tyr or Phe in the P1′ position. Has no action on amino-acid p-nitroanilides
Other name(s): small neutral protease; SnpA gene product (Streptomyces lividans)
Comments: Type example of peptidase family M7.
References: [1661, 365, 1660]

EC 3.4.24.78
Accepted name: gpr endopeptidase
Reaction: Endopeptidase action with P4 Glu or Asp, P1 preferably Glu Asp, P1′ hydrophobic and P2′ Ala
Other name(s): germination proteinase
Comments: Initiates the degradation of small, acid-soluble proteins during spore germination in Bacillus megaterium. Type example of peptidase family A25.
References: [2427]

EC 3.4.24.79
Accepted name: pappalysin-1
Reaction: Cleavage of the Met$^{135}$–Lys bond in insulin-like growth factor binding protein (IGFBP)-4, and the Ser$^{143}$–Lys bond in IGFBP-5
Other name(s): insulin-like growth factor binding protein-4 protease; pregnancy-associated plasma protein-A
Comments: A 400-kDa disulfide-linked dimer. Circulates in human pregnancy mainly as a complex with the pro-form of eosinophil major basic protein, which acts as an inhibitor of the peptidase. The rate of hydrolysis of IGFBP-4 is increased about 20-fold by the presence of insulin-like growth factor (IGF), whereas that of IGFBP-5 is decreased about two-fold. In peptidase family M43.
References: [1703, 444]

EC 3.4.24.80
Accepted name: membrane-type matrix metalloproteinase-1
Reaction: Endopeptidase activity. Activates progelatinase A by cleavage of the propeptide at Asn$^{37}$–Leu. Other bonds hydrolysed include Gly$^{35}$–Ile in the propeptide of collagenase 3, and Asn$^{341}$–Phe, Asp$^{441}$–Leu and Gln$^{354}$–Thr in the aggrecan interglobular domain
Other name(s): matrix metalloproteinase 14
In peptidase family M10, but, unlike most members of the family, is membrane-anchored. Believed to play an important role in the activation of progelatinase A at cell surfaces.

References: [1356]

[EC 3.4.24.80 created 2003]

EC 3.4.24.81

Accepted name: ADAM10 endopeptidase
Reaction: Endopeptidase of broad specificity
Other name(s): Kuzbanian protein; myelin-associated disintegrin metalloproteinase
Comments: In peptidase family M12. Partially responsible for the \( \alpha \)-secretase" activity in brain that degrades the potentially harmful \( \beta \)-amyloid peptide. Work with ADAM10-deficient mice supports a role in Notch signalling.
References: [1069]

[EC 3.4.24.81 created 2003]

EC 3.4.24.82

Accepted name: ADAMTS-4 endopeptidase
Reaction: Glutamyl endopeptidase; bonds cleaved include -Thr-Glu-Gly-Glu\( ^{173} \)→Ala-Arg-Gly-Ser- in the interglobular domain of mammalian aggrecan
Other name(s): aggrecanase-1
Comments: In peptidase family M12. Thought to be biologically significant for the degradation of the aggrecan component of cartilage matrix.
References: [3317]

[EC 3.4.24.82 created 2003]

EC 3.4.24.83

Accepted name: anthrax lethal factor endopeptidase
Reaction: Preferred amino acids around the cleavage site can be denoted BBBBxHxH, in which B denotes Arg or Lys, H denotes a hydrophobic amino acid, and x is any amino acid. The only known protein substrates are mitogen-activated protein (MAP) kinase kinases
Other name(s): lethal toxin
Comments: From the bacterium Bacillus anthracis that causes anthrax. One of three proteins that are collectively termed anthrax toxin. Cleaves several MAP kinase kinases near their N-termini, preventing them from phosphorylating the downstream mitogen-activated protein kinases. In peptidase family M34.
References: [2343]

[EC 3.4.24.83 created 2003]

EC 3.4.24.84

Accepted name: Ste24 endopeptidase
Reaction: The peptide bond hydrolysed can be designated -C\( ^{-} \)aaX in which C is an S-isoprenylated cysteine residue, a is usually aliphatic and X is the C-terminal residue of the substrate protein, and may be any of several amino acids
Comments: Type example of peptidase family M48. One of two enzymes that can catalyse this processing step for mating a-factor in yeast. Subsequently, the S-isoprenylated cysteine residue that forms the new C-terminus is methyl-esterified and forms a hydrophobic membrane-anchor.
References: [3006]

[EC 3.4.24.84 created 2003]
EC 3.4.24.85
Accepted name: S2P endopeptidase
Reaction: Cleaves several transcription factors that are type-2 transmembrane proteins within membrane-spanning domains. Known substrates include sterol regulatory element-binding protein (SREBP)-1, SREBP-2 and forms of the transcriptional activator ATF6. SREBP-2 is cleaved at the site DRSR\underline{I}LL\underline{483}\underline{CVLTLCL\underline{5}PLTSLLLQWGGA}, in which the membrane-spanning segment is underlined. The residues NP (bold), 11 residues distal to the site of cleavage in the membrane-spanning domain, are important for cleavage by S2P endopeptidase. Replacement of either of these residues does not prevent cleavage, but there is no cleavage if both of these residues are replaced.
Comments: Type example of peptidase family M50. The transcription factors SREBP-1 and -2 are synthesized as precursor proteins that are attached to the membranes of the endoplasmic reticulum and two cleavages are needed to release the active factor so that it can move to the nucleus. This enzyme cleaves the second of these, and is thus the "site 2 protease", S2P.
References: [339]

EC 3.4.24.86
Accepted name: ADAM 17 endopeptidase
Reaction: Narrow endopeptidase specificity. Cleaves Pro-Leu-Ala-Gln-Ala\underline{Val-Arg-Ser-Ser-Ser} in the membrane-bound, 26-kDa form of tumour necrosis factor (TNF\alpha). Similarly cleaves other membrane-anchored, cell-surface proteins to "shed" the extracellular domains
Other name(s): tumor necrosis factor \alpha-converting enzyme; TACE
Comments: In peptidase family M12. In vivo, the cleavage of tumour necrosis factor \alpha precursor releases the soluble, 17-kDa TNF\alpha, which induces inflammation.
References: [253]

EC 3.4.24.87
Accepted name: ADAMTS13 endopeptidase
Reaction: The enzyme cleaves the von Willebrand factor at bond Tyr\underline{842}\underline{Met} within the A2 domain
Other name(s): ADAMTS VWF cleaving metalloprotease; ADAMTS-13; ADAMTS13; vWF-cleaving protease; VWF-CP; vWF-degrading protease; Upshaw factor; von Willebrand factor cleaving protease; ADAMTS13 peptidase
Comments: In peptidase family M12.
References: [893, 678]

EC 3.4.24.88
Accepted name: Pro-Pro endopeptidase
Reaction: The enzyme catalyses the hydrolytic cleavage of peptide bonds between two proline residues
Other name(s): metalloprotease CD2830
Comments: This metalloprotease, which is secreted by the bacterium Peptoclostridium difficile, contains zinc.
References: [380, 1185, 1184]

[3.4.24.88 Transferred entry. desampylase. Transferred to EC 3.4.19.15 desampylase]

[EC 3.4.24.88 created 2015, deleted 2016]

[EC 3.4.24.89 created 2015]
EC 3.4.25 Threonine endopeptidases

**EC 3.4.25.1**

**Accepted name:** proteasome endopeptidase complex

**Reaction:** Cleavage of peptide bonds with very broad specificity

**Other name(s):** ingensin; macropain; multicatalytic endopeptidase complex; prosome; multicatalytic proteinase (complex); MCP; proteasome; large multicatalytic protease; multicatalytic proteinase; proteasome organelle; alkaline protease; 26S protease; tricorn proteinase; tricorn protease

**Comments:** A 20-S protein composed of 28 subunits arranged in four rings of seven. The outer rings are composed of α subunits, but the β subunits forming the inner rings are responsible for peptidase activity. In eukaryotic organisms there are up to seven different types of β subunits, three of which may carry the N-terminal threonine residues that are the nucleophiles in catalysis, and show different specificities. The molecule is barrel-shaped, and the active sites are on the inner surfaces. Terminal apertures restrict access of substrates to the active sites. There is evidence that catalytic subunits are replaced by others under some conditions so as to alter the specificity of proteolysis, perhaps optimizing it for the formation of antigenic peptides. A complex of the 20-S proteasome endopeptidase complex with a 19-S regulatory unit is the 26-S proteasome that degrades ubiquitin-protein conjugates. Type example of peptidase family T1.

**References:** [2733, 540, 1047, 648]

[EC 3.4.25.1 created 1978 as EC 3.4.24.5, part transferred 1989 to EC 3.4.22.21, transferred 1992 to EC 3.4.99.46, transferred 2000 to EC 3.4.25.1]

**EC 3.4.25.2**

**Accepted name:** HslU—HslV peptidase

**Reaction:** ATP-dependent cleavage of peptide bonds with broad specificity.

**Other name(s):** HslUV; HslV-HslU; HslV peptidase; ATP-dependent HslV-HslU proteinase; caseinolytic protease X; caseinolytic proteinase X; ClpXP ATP-dependent protease; ClpXP protease; ClpXP serine proteinase; *Escherichia coli* ClpXP serine proteinase; HslUV protease; HslUV proteinase; HslVU protease; HslV protease; protease HslVU; proteinase HslUV

**Comments:** The HslU subunit of the HslU—HslV complex functions as an ATP dependent ‘unfoldase’. The binding of ATP and its subsequent hydrolysis by HslU are essential for unfolding of protein substrates subsequently hydrolysed by HslV [3450]. HslU recognizes the N-terminal part of its protein substrates and unfolds these before they are guided to HslV for hydrolysis [362]. In peptidase family T1.

**References:** [3263, 2199, 2484, 3451, 3450, 1466, 362]

[EC 3.4.25.2 created 2009, modified 2010]

**EC 3.4.99 Endopeptidases of unknown catalytic mechanism (sub-subclass is currently empty)**


[EC 3.4.99.1 created 1972, deleted 1978 [transferred to EC 3.4.23.6, deleted 1992]]

[3.499.2] Deleted entry. agavain]

[EC 3.4.99.2 created 1972, deleted 1992]

[3.499.3] Deleted entry. angiotensinase]

[EC 3.4.99.3 created 1972, deleted 1992]


[EC 3.4.99.4 created 1972, deleted 1978]
Transferred entry. Clostridium histolyticum collagenase 2. Now EC 3.4.24.3, microbial collagenase

Transferred entry. crayfish low-molecular-weight proteinase. Now EC 3.4.24.21, astacin

Deleted entry. euphorbain

Deleted entry. Gliocladium proteinase

Deleted entry. hurain. Now considered EC 3.4.21.25, cucumisin

Transferred entry. insulinase. Now EC 3.4.24.56, insulysin

Deleted entry. Streptomyces alkalophilic keratinase

Deleted entry. Trichophyton mentagrophytes keratinase

Transferred entry. β-lytic proteinase (Mycobacterium sorangium). Now EC 3.4.24.32, β-lytic metalloendopeptidase

Deleted entry. mexicanain

Deleted entry. Paecilomyces proteinase

Deleted entry. Penicillium notatum extracellular proteinase

Deleted entry. peptidoglycan endopeptidase

Deleted entry. pinguinain

Transferred entry. renin. Now EC 3.4.23.15, renin

Deleted entry. Scopulariopsis proteinase

Deleted entry. solanain. Now considered EC 3.4.21.25, cucumisin

[3.4.99.23] Deleted entry. tabernamontanain. Now considered EC 3.4.21.25, cucumisin
[EC 3.4.99.23 created 1972, deleted 1992]

[3.4.99.24] Deleted entry. Tenebrio α-proteinase
[EC 3.4.99.24 created 1972, deleted 1978 [transferred to EC 3.4.21.18, deleted 1992]]

[3.4.99.25] Transferred entry. trametes acid proteinase. Now EC 3.4.23.21, rhizopuspepsin
[EC 3.4.99.25 created 1972, deleted 1978 [transferred to EC 3.4.23.6, deleted 1992]]

[EC 3.4.99.26 created 1972, deleted 1978 [transferred to EC 3.4.21.31, deleted 1992]]

[3.4.99.27] Deleted entry. Echis carinatus prothrombin-activating proteinase
[EC 3.4.99.27 created 1978, deleted 1992]

[EC 3.4.99.28 created 1978, deleted 1992]

[3.4.99.29] Deleted entry. Myxobacter AL-1 proteinase I
[EC 3.4.99.29 created 1978, deleted 1992]

[EC 3.4.99.30 created 1978, deleted 1992]

[3.4.99.31] Transferred entry. tissue endopeptidase degrading collagenase synthetic substrate. Now EC 3.4.24.15, thimet oligopeptidase
[EC 3.4.99.31 created 1978, deleted 1992]

[EC 3.4.99.32 created 1978, deleted 1992]

[3.4.99.33] Deleted entry. cathepsin R
[EC 3.4.99.33 created 1981, deleted 1984 [transferred to EC 3.4.21.52, deleted 1992]]

[3.4.99.34] Deleted entry. mytilidase
[EC 3.4.99.34 created 1981, deleted 1992]

[EC 3.4.99.35 created 1984, deleted 1995]

[EC 3.4.99.36 created 1984, deleted 1995]

[3.4.99.37] Deleted entry. RecA peptidase
[EC 3.4.99.37 created 1989, deleted 1992]

[3.4.99.38] Transferred entry. pro-opiomelanotropin-converting proteinase. Now EC 3.4.23.17, pro-opiomelanocortin converting enzyme
[EC 3.4.99.38 created 1989, deleted 1992]
EC 3.4.99.39  Deleted entry. pseudomurein endopeptidase

EC 3.4.99.40  Deleted entry. Pro-gonadoliberin proteinase
[EC 3.4.99.40 created 1989, deleted 1992]

EC 3.4.99.41  Transferred entry. mitochondrial processing peptidase. Now EC 3.4.24.64, mitochondrial processing peptidase
[EC 3.4.99.41 created 1989/90, deleted 1995]

EC 3.4.99.42  Deleted entry. leucyllysine endopeptidase
[EC 3.4.99.42 created 1990, deleted 1992]

EC 3.4.99.43  Transferred entry. thermopsin. Now EC 3.4.23.42, thermopsin
[EC 3.4.99.43 created 1992, deleted 2000]

EC 3.4.99.44  Transferred entry. pitrilysin. Now EC 3.4.24.55, pitrilysin
[EC 3.4.99.44 created 1992, deleted 1993]

EC 3.4.99.45  Transferred entry. insulinase. Now EC 3.4.24.56, insulysin
[EC 3.4.99.45 created 1992, deleted 1993]

EC 3.4.99.46  Transferred entry. multicatalytic endopeptidase complex. Now EC 3.4.25.1, proteasome endopeptidase complex
[EC 3.4.99.46 created 1992, deleted 2000]

**EC 3.5 Acting on carbon-nitrogen bonds, other than peptide bonds**

This subclass contains those enzymes that hydrolyse amides, amidines and other C-N bonds. Sub-subclasses are based on the substrate: linear amides (EC 3.5.1), cyclic amides (EC 3.5.2), linear amidines (EC 3.5.3), cyclic amidines (EC 3.5.4), nitriles (EC 3.5.5) and other compounds (EC 3.5.99).

**EC 3.5.1 In linear amides**

**EC 3.5.1.1**

Accepted name: asparaginase
Reaction: \( \text{L-asparagine + H}_2\text{O} = \text{L-aspartate} + \text{NH}_3 \)
Other name(s): asparaginase II; \text{L-asparaginase}; colaspase; elspar; leunase; crasnitin; \( \alpha \)-asparaginase
Systematic name: \text{L-asparagine amidohydrolase}
References: [1092, 1226, 2938]

[EC 3.5.1.1 created 1961]

**EC 3.5.1.2**

Accepted name: glutaminase
Reaction: \( \text{L-glutamine + H}_2\text{O} = \text{L-glutamate} + \text{NH}_3 \)
Other name(s): glutaminase I; \text{L-glutaminase}; glutamine aminohydrolase
Systematic name: \text{L-glutamine amidohydrolase}
References: [1643, 2562]

[EC 3.5.1.2 created 1961]
EC 3.5.1.3
Accepted name: ω-amidase
Reaction: a monoamide of a dicarboxylate + H₂O = a dicarboxylate + NH₃
Other name(s): α-keto acid-ω-amidase
Systematic name: ω-amidodicarboxylate amidohydrolase
References: [1977, 1978]

[EC 3.5.1.3 created 1961]

EC 3.5.1.4
Accepted name: amidase
Reaction: a monocarboxylic acid amide + H₂O = a monocarboxylate + NH₃
Other name(s): acylamidase; acylase (misleading); amidohydrolase (ambiguous); deaminase (ambiguous); fatty acylamidase; N-acetylaminohydrolase (ambiguous)
Systematic name: acylamide amidohydrolase
References: [308, 309]

[EC 3.5.1.4 created 1961, modified 2011]

EC 3.5.1.5
Accepted name: urease
Reaction: urea + H₂O = CO₂ + 2 NH₃
Systematic name: urea amidohydrolase
Comments: A nickel protein.
References: [664, 2940, 3202]

[EC 3.5.1.5 created 1961]

EC 3.5.1.6
Accepted name: β-ureidopropionase
Reaction: 3-ureidopropanoate + H₂O = β-alanine + CO₂ + NH₃
Other name(s): N-carbamoyl-β-alanine amidohydrolase
Systematic name: 3-ureidopropanoate amidohydrolase
Comments: The animal enzyme also acts on β-ureidoisobutyrate.
References: [391, 398, 3105]

[EC 3.5.1.6 created 1961]

EC 3.5.1.7
Accepted name: ureidosuccinase
Reaction: N-carbamoyl-L-aspartate + H₂O = L-aspartate + CO₂ + NH₃
Systematic name: N-carbamoyl-L-aspartate amidohydrolase
References: [1775]

[EC 3.5.1.7 created 1961]

EC 3.5.1.8
Accepted name: formylaspartate deformylase
Reaction: N-formyl-L-aspartate + H₂O = formate + L-aspartate
Other name(s): formylaspartic formylase (formylase I, formylase II)
Systematic name: N-formyl-L-aspartate amidohydrolase
EC 3.5.1.9
Accepted name: arylformamidase
Reaction: \( N\text{-formyl-L-kynurenine} + H_2O = \text{formate} + L\text{-kynurenine} \)
Other name(s): kynurenine formamidase; formylase; formylkynureninase; formylkynurenine formamidase; formamidase I; formamidase II
Systematic name: aryl-formylamine amidohydrolase
Comments: Also acts on other aromatic formylamines.
References: [1150, 1378, 1974]

EC 3.5.1.10
Accepted name: formyltetrahydrofolate deformylase
Reaction: \( 10\text{-formyltetrahydrofolate} + H_2O = \text{formate} + \text{tetrahydrofolate} \)
Systematic name: 10-formyltetrahydrofolate amidohydrolase
References: [1280]

EC 3.5.1.11
Accepted name: penicillin amidase
Reaction: penicillin + H_2O = a carboxylate + 6-aminopenicillanate
Other name(s): penicillin acylase; benzylpenicillin acylase; novozym 217; semacylase; \( \alpha\)-acylamino-\( \beta\)-lactam acylhydrolase; ampicillin acylase
Systematic name: penicillin amidohydrolase
References: [2627]

EC 3.5.1.12
Accepted name: biotinidase
Reaction: biotin amide + H_2O = biotin + NH_3
Other name(s): amidohydrolase biotinidase
Systematic name: biotin-amide amidohydrolase
Comments: Also acts on biotin esters.
References: [1566, 3054]

EC 3.5.1.13
Accepted name: arylaclylamidase
Reaction: an anilide + H_2O = a carboxylate + aniline
Other name(s): AAA-1; AAA-2; brain acetylcholinesterase (is associated with AAA-2); pseudocholinesterase (associated with arylaclylamidase)
Systematic name: aryl-aclylamide amidohydrolase
Comments: Also acts on 4-substituted anilides.
References: [2197]
EC 3.5.1.14

Accepted name: N-acyl-aliphatic-L-amino acid amidohydrolase
Reaction: (1) an N-acyl-aliphatic-L-amino acid + H₂O = an aliphatic L-amino acid + a carboxylate
(2) an N-acetyl-L-cysteine-S-conjugate + H₂O = an L-cysteine-S-conjugate + acetate
Other name(s): aminooacylase I; aminooacylase I; dehydropeptidase II; histozyme; hippuricase; benzamidase; acylase I; hippurase; amido acid deacylase; L-aminoacylase; acylase; aminoacylase; L-amino-acid acylase; α-N-acylaminoacid hydrolase; long acyl amidoacylace; short acyl amidoacylace; ACY1 (gene name); N-acyl-L-amino-acid amidohydrolase
Systematic name: N-acyl-aliphatic-L-amino acid amidohydrolase (carboxylate-forming)
Comments: Contains Zn²⁺. The enzyme is found in animals and is involved in the hydrolysis of N-acylated or N-acetylated amino acids (except L-aspartate). It acts on mercapturic acids (S-conjugates of N-acetyl-L-cysteine) and neutral aliphatic N-acyl-α-amino acids. Some bacterial aminoacylases demonstrate substrate specificity of both EC 3.5.1.14 and EC 3.5.1.114. cf. EC 3.5.1.15, aspartoacylase and EC 3.5.1.114, N-acyl-aromatic-L-amino acid amidohydrolase.
References: [242, 848, 1186, 1166, 2339, 3173, 1797]

[EC 3.5.1.14 created 1965, modified 2013]

EC 3.5.1.15

Accepted name: aspartoacylase
Reaction: N-acyl-L-aspartate + H₂O = a carboxylate + L-aspartate
Other name(s): aminooacylase II; N-acetylaspartate amidohydrolase; acetyl-aspartic deaminase; acylase II
Systematic name: N-acyl-L-aspartate amidohydrolase
References: [241, 242]

[EC 3.5.1.15 created 1965]

EC 3.5.1.16

Accepted name: acetylornithine deacetylase
Reaction: N²-acetyl-L-ornithine + H₂O = acetate + L-ornithine
Other name(s): acetylornithinase; N-acetylornithinase; 2-N-acetyl-L-ornithine amidohydrolase
Systematic name: N²-acetyl-L-ornithine amidohydrolase
Comments: Also hydrolyses N-acetylmethionine.
References: [3223, 3224]

[EC 3.5.1.16 created 1965]

EC 3.5.1.17

Accepted name: acyl-lysine deacylase
Reaction: N⁶-acyl-L-lysine + H₂O = a carboxylate + L-lysine
Other name(s): ε-lysine acylase; 6-N-acyl-L-lysine amidohydrolase
Systematic name: N⁶-acyl-L-lysine amidohydrolase
References: [2334]

[EC 3.5.1.17 created 1965]

EC 3.5.1.18

Accepted name: succinyl-diaminopimelate desuccinylase
Reaction: N-succinyl-LL-2,6-diaminoheptanedioate + H₂O = succinate + LL-2,6-diaminoheptanedioate
Other name(s): N-succinyl-L-α,ε-diaminopimelic acid deacylase
Systematic name: N-succinyl-LL-2,6-diaminoheptanedioate amidohydrolase
References: [1545]

267
EC 3.5.1.18

**Accepted name:** nicotinamidase
**Reaction:** nicotinamide + H₂O = nicotinate + NH₃
**Other name(s):** nicotinamide deaminase; nicotinamide amidase; YNDase
**Systematic name:** nicotinamide amidohydrolase
**References:** [2386, 2660]

[EC 3.5.1.18 created 1965]

EC 3.5.1.19

**Accepted name:** nicotinamidase
**Reaction:** nicotinamide + H₂O = nicotinate + NH₃
**Other name(s):** nicotinamide deaminase; nicotinamide amidase; YNDase
**Systematic name:** nicotinamide amidohydrolase
**References:** [2386, 2660]

[EC 3.5.1.19 created 1972]

EC 3.5.1.20

**Accepted name:** citrullinase
**Reaction:** L-citrulline + H₂O = L-ornithine + CO₂ + NH₃
**Other name(s):** citrulline ureidase; citrulline hydrolase; L-citrulline 5-N-carbamoyldihydrolase
**Systematic name:** L-citrulline N⁵-carbamoyldihydrolase
**References:** [1210]

[EC 3.5.1.20 created 1972]

EC 3.5.1.21

**Accepted name:** N-acetyl-β-alanine deacetylase
**Reaction:** N-acetyl-β-alanine + H₂O = acetate + β-alanine
**Systematic name:** N-acetyl-β-alanine amidohydrolase
**References:** [894]

[EC 3.5.1.21 created 1972]

EC 3.5.1.22

**Accepted name:** pantothenase
**Reaction:** (R)-pantothenate + H₂O = (R)-pantoate + β-alanine
**Other name(s):** pantothenate hydrolase; pantothenate amidohydrolase
**Systematic name:** (R)-pantothenate amidohydrolase
**References:** [2229]

[EC 3.5.1.22 created 1972]

EC 3.5.1.23

**Accepted name:** ceramidase
**Reaction:** a ceramide + H₂O = a carboxylate + sphingosine
**Other name(s):** acylsphingosine deacylase; glycosphingolipid ceramide deacylase
**Systematic name:** N-acylsphingosine amidohydrolase
**References:** [2195, 3437]

[EC 3.5.1.23 created 1972, modified 1990]

EC 3.5.1.24

**Accepted name:** choloylglycine hydrolase
**Reaction:** glycocholate + H₂O = cholate + glycine
**Other name(s):** glycocholase; bile salt hydrolase; choioyltaurine hydrolase; 3α,7α,12α-trihydroxy-5β-cholan-24-oxylglycine amidohydrolase

[EC 3.5.1.24 created 1972]

268
Systematic name: glycocholate amidohydrolase
Comments: Also acts on the 3α,12α-dihydroxy-derivative, and on choloyl-taurine.
References: [2133, 2903]

EC 3.5.1.25

Accepted name: N-acetylgalcosamine-6-phosphate deacetylase
Reaction: N-acetyl-D-glucosamine 6-phosphate + H₂O = D-glucosamine 6-phosphate + acetate
Other name(s): acetylgalcosamine phosphate deacetylase; acetylaminoxyglucosephosphate acetylhydrolase; 2-acetamido-2-deoxy-D-glucose-6-phosphate amidohydrolase
Systematic name: N-acetyl-D-glucosamine-6-phosphate amidohydrolase
References: [3326, 3407]

EC 3.5.1.26

Accepted name: N⁴-(β-N-acetylglucosaminyl)-L-asparaginase
Reaction: N⁴-(β-N-acetyl-D-glucosaminyl)-L-asparagine + H₂O = N-acetyl-β-D-glucosaminylamine + L-aspartate
Other name(s): aspartyglucosylamine deasparylase; aspartyglucosylaminase; aspartyglucosaminidase; aspartyglucosylamine amidohydrolase; N-aspartyglucosaminidase; glucosylamidase; β-aspartyglucosylamine amidohydrolase; 4-N-(β-N-acetyl-D-glucosaminyl)-L-asparagine amidohydrolase
Systematic name: N⁴-(β-N-acetyl-D-glucosaminyl)-L-asparagine amidohydrolase
Comments: Acts only on asparagine-oligosaccharides containing one amino acid, i.e., the asparagine has free α-amino and α-carboxyl groups [cf. EC 3.5.1.52, peptide-⁴-N-(N-acetyl-β-glucosaminy)asparagine amidase]
References: [1584, 1872, 3028]

EC 3.5.1.28

Accepted name: N-acetylmuramoyl-L-alanine amidase
Reaction: Hydrolyses the link between N-acetylmuramoyl residues and L-amino acid residues in certain cell-wall glycopeptides
Other name(s): acetylmuramyl-L-alanine amidase; N-acetylmuramyl-L-alanine amidase; N-acetylmuramoyl-L-alanine amidase; acetylmuramoyl-alanine amidase; N-acetylmuramic acid L-alanine amidase; acetylmuramyl-alanine amidase; N-acetylmuramylalanine amidase; murein hydrolase; N-acetylmuramoyl-L-alanine amidase type I; N-acetylmuramoyl-L-alanine amidase type II
Systematic name: peptidoglycan amidohydrolase
References: [962, 1196, 1195, 3277]

EC 3.5.1.29

Accepted name: 2-(acetamidomethylene)succinate hydrolase
Reaction: 2-(acetamidomethylene)succinate + 2 H₂O = acetate + succinate semialdehyde + NH₃ + CO₂
Other name(s): α-(N-acetylamino)methylene)succinic acid hydrolase
Systematic name: 2-(acetamidomethylene)succinate amidohydrolase (deaminating, decarboxylating)
Comments: Involved in the degradation of pyridoxin in *Pseudomonas*.
References: [1288, 2231]

[EC 3.5.1.29 created 1972]

EC 3.5.1.30
Accepted name: 5-aminopentanamidase
Reaction: 5-aminopentanamide + H₂O = 5-aminopentanoate + NH₃
Other name(s): 5-aminovaleramidase; 5-aminonorvaleramidase
Systematic name: 5-aminopentanamide amidohydrolase
Comments: The enzyme from *Pseudomonas putida* also acts on 4-aminobutanamide and, more slowly, on 6-aminohexanamide.
References: [2530, 2996]

[EC 3.5.1.30 created 1972, modified 1976]

EC 3.5.1.31
Accepted name: formylmethionine deformylase
Reaction: N-formyl-L-methionine + H₂O = formate + L-methionine
Systematic name: N-formyl-L-methionine amidohydrolase
References: [82]

[EC 3.5.1.31 created 1972]

EC 3.5.1.32
Accepted name: hippurate hydrolase
Reaction: hippurate + H₂O = benzoate + glycine
Systematic name: N-benzoyletanoic-amidohydrolase
Comments: Acts on various N-benzyolamino acids.
References: [2580, 2581]

[EC 3.5.1.32 created 1972]

EC 3.5.1.33
Accepted name: N-acetylglucosamine deacetylase
Reaction: N-acetyl-D-glucosamine + H₂O = D-glucosamine + acetate
Other name(s): acetylaminodeoxyglucose acetylhydrolase; N-acetyl-D-glucosaminyl N-deacetylase
Systematic name: N-acetyl-D-glucosamine amidohydrolase
References: [2587]

[EC 3.5.1.33 created 1972]

[3.5.1.34 Deleted entry. acetylhistidine deacetylase. Identical with EC 3.4.13.5, Xaa-methyl-His dipeptidase]

[EC 3.5.1.34 created 1972, deleted 1981]

EC 3.5.1.35
Accepted name: D-glutaminase
Reaction: D-glutamine + H₂O = D-glutamate + NH₃
Systematic name: D-glutamine amidohydrolase
EC 3.5.1.36

Accepted name: N-methyl-2-oxoglutaramate hydrolase
Reaction: $\text{N-methyl-2-oxoglutarate} + \text{H}_2\text{O} = \text{2-oxoglutarate} + \text{methylamine}$
Other name(s): 5-hydroxy-$N$-methylpyroglutamate synthase
Systematic name: $N$-methyl-2-oxoglutaramate methylamidohydrolase
Comments: In the reverse reaction, the product cyclizes non-enzymically to 2-hydroxy-$N$-methyl-5-oxo-L-proline.
References: [1202, 1203]

EC 3.5.1.38

Accepted name: glutamin-(asparagin-)ase
Reaction: 
(1) $\text{L-glutamine} + \text{H}_2\text{O} = \text{L-glutamate} + \text{NH}_3$
(2) $\text{L-asparagine} + \text{H}_2\text{O} = \text{L-aspartate} + \text{NH}_3$
Other name(s): glutaminase-asparaginase; $\text{ansB}$ (gene name); L-asparagine/L-glutamine amidohydrolase; L-ASNase/L-GLNase
Systematic name: L-glutamine(L-asparagine) amidohydrolase
Comments: The enzyme from the bacterium *Achromobacter* hydrolyses L-asparagine at 0.8 of the rate of L-glutamine; the D-isomers are also hydrolysed, but more slowly. cf. EC 3.5.1.2, glutaminase and EC 3.5.1.1, asparaginase.
References: [2563, 3013, 1848, 2315]

EC 3.5.1.39

Accepted name: alkylamidase
Reaction: $\text{N-methylhexanamide} + \text{H}_2\text{O} = \text{hexanoate} + \text{methylamine}$
Systematic name: $N$-methylhexanamide amidohydrolase
Comments: The enzyme hydrolyses $N$-monosubstituted and $N,N$-disubstituted amides, and there is some activity towards primary amides. It has little or no activity towards short-chain substrates.
References: [452]

EC 3.5.1.40

Accepted name: acylagmatine amidase
Reaction: $\text{benzoylagmatine} + \text{H}_2\text{O} = \text{benzoate} + \text{agmatine}$
Other name(s): acylagmatine amidohydrolase; acylagmatine deacylase
Systematic name: benzoylagmatine amidohydrolase
Comments: Also acts on acetylagmatine, propanoylagmatine and bleomycin B2
References: [3158]
EC 3.5.1.41

Accepted name: chitin deacetylase
Reaction: chitin + H₂O = chitosan + acetate
Systematic name: chitin amidohydrolase
Comments: Hydrolyses the N-acetamido groups of N-acetyl-D-glucosamine residues in chitin.
References: [73]

[EC 3.5.1.41 created 1976]

EC 3.5.1.42

Accepted name: nicotinamide-nucleotide amidase
Reaction: β-nicotinamide D-ribonucleotide + H₂O = β-nicotinate D-ribonucleotide + NH₃
Other name(s): NMN deamidase; nicotinamide mononucleotide deamidase; nicotinamide mononucleotide amidohydrolase
Systematic name: nicotinamide-D-ribonucleotide amidohydrolase
Comments: Also acts more slowly on β-nicotinamide D-ribonucleoside.
References: [1313]

[EC 3.5.1.42 created 1976]

EC 3.5.1.43

Accepted name: peptidyl-glutaminase
Reaction: α-N-peptidyl-L-glutamine + H₂O = α-N-peptidyl-L-glutamate + NH₃
Other name(s): peptidoglutaminase I; peptideglutaminase; peptidoglutanaminase
Systematic name: peptidyl-L-glutamine amidohydrolase
Comments: Specific for the hydrolysis of the γ-amide of glutamine substituted at the α-amino group, e.g., glycyl-L-glutamine, N-acetyl-L-glutamine and L-leucylglycyl-L-glutamine.
References: [1523]

[EC 3.5.1.43 created 1976]

EC 3.5.1.44

Accepted name: protein-glutamine glutaminase
Reaction: protein L-glutamine + H₂O = protein L-glutamate + NH₃
Other name(s): peptidoglutaminase II; glutaminyl-peptide glutaminase; destabilase; peptidylglutaminase II
Systematic name: protein-L-glutamine amidohydrolase
Comments: Specific for the hydrolysis of the γ-amide of glutamine substituted at the carboxyl position or both the α-amino and carboxyl positions, e.g., L-glutaminylglycine and L-phenylalanyl-L-glutaminylglycine.
References: [1523]

[EC 3.5.1.44 created 1976, modified 1983]

[3.5.1.45 Deleted entry. urease (ATP-hydrolysing). Now listed only as EC 6.3.4.6 urea carboxylase]

[EC 3.5.1.45 created 1978, deleted 1986]

EC 3.5.1.46

Accepted name: 6-aminohexanoylate-oligomer exohydrolase
Reaction: (1) [N-(6-aminohexanoyl)]ₙ + H₂O = [N-(6-aminohexanoyl)]ₙ₋₁ + 6-aminohexanoylate (2) N-(6-aminohexanoyl)-6-aminohexanoylate + H₂O = 2 6-aminohexanoylate
Other name(s): 6-aminohexanoylate-dimer hydrolase; nyB (gene name); 6-aminohexanoic acid oligomer hydrolase (ambiguous); N-(6-aminohexanoyl)-6-aminohexanoylate amidohydrolase; nylon-6 hydrolase (ambiguous)
**Systematic name:** N-(6-aminohexanoyl)-6-aminohexanoate exoamidohydrolase

**Comments:** The enzyme is involved in degradation of nylon-6 oligomers. It degrades linear oligomers of 6-aminohexanoate with a degree of polymerization of 2–20 by exo-type cleavage, removing residues sequentially from the N-terminus. Activity decreases with the increase of the polymerization number of the oligomer. cf. EC 3.5.1.117, 6-aminohexanoate-oligomer endohydrolase and EC 3.5.2.12, 6-aminohexanoate-cyclic-dimer hydrolase.

**References:** [1547]

[EC 3.5.1.46 created 1983, modified 2014]

**EC 3.5.1.47**

**Accepted name:** N-acetyldiaminopimelate deacetylase

**Reaction:** N-acetyl-LL-2,6-diaminoheptanedioate + H₂O = acetate + LL-2,6-diaminoheptanedioate

**Other name(s):** N-acetyl-L-diaminopimelic acid deacetylase; N-acetyl-LL-diaminopimelate deacetylase; 6-N-acetyl-LL-2,6-diaminoheptanedioate amidohydrolase

**Systematic name:** N⁶-acetyl-LL-2,6-diaminoheptanedioate amidohydrolase

**References:** [180, 2636, 2945]

[EC 3.5.1.47 created 1984 (EC 3.1.1.62 created 1989, incorporated 1992)]

**EC 3.5.1.48**

**Accepted name:** acetylspermidine deacetylase

**Reaction:** N⁸-acetylspermidine + H₂O = acetate + spermidine

**Other name(s):** N⁸-monoaacetylspermidine deacetylase; N⁸-acetylspermidine deacetylase; N-acetylspermidine deacetylase; N¹-acetylspermidine amidohydrolase (incorrect); 8-N-acetylspermidine amidohydrolase

**Systematic name:** N⁸-acetylspermidine amidohydrolase

**Comments:** It was initially thought that N¹-acetylspermidine was the substrate for this deacetylase reaction [1772] but this has since been disproved by Marchant et al. [1903].

**References:** [1772, 267, 1903]

[EC 3.5.1.48 created 1984, modified 2005]

**EC 3.5.1.49**

**Accepted name:** formamidase

**Reaction:** formamide + H₂O = formate + NH₃

**Systematic name:** formamide amidohydrolase

**Comments:** Also acts, more slowly, on acetamide, propanamide and butanamide.

**References:** [499, 873]

[EC 3.5.1.49 created 1984]

**EC 3.5.1.50**

**Accepted name:** pentanamidase

**Reaction:** pentanamide + H₂O = pentanoate + NH₃

**Other name(s):** valeramidase

**Systematic name:** pentanamide amidohydrolase

**Comments:** Also acts, more slowly, on other short-chain aliphatic amides. Different from EC 3.5.1.49 formamidase.

**References:** [873]

[EC 3.5.1.50 created 1984]
EC 3.5.1.51

Accepted name: 4-acetamidobutyryl-CoA deacetylase
Reaction: 4-acetamidobutanoyl-CoA + H2O = acetate + 4-aminobutanoyl-CoA
Other name(s): aminobutyryl-CoA thiolesterase; deacetylase-thiolesterase
Systematic name: 4-acetamidobutanoyl-CoA amidohydrolase
Comments: The enzyme also hydrolyses 4-aminobutanoyl-CoA to aminobutanoate and coenzyme A.
References: [2276]

EC 3.5.1.52

Accepted name: peptide-N4-(N-acetyl-β-glucosaminyl)asparagine amidase
Reaction: Hydrolysis of an N4-(acetyl-β-D-glucosaminyl)asparagine residue in which the glucosamine residue may be further glycosylated, to yield a (substituted) N-acetyl-β-D-glucosaminylamine and a peptide containing an aspartate residue
Other name(s): glycopeptide N-glycosidase; glycopeptidase; N-oligosaccharide glycopeptidase; N-glycanase; Jack-bean glycopeptidase; PNGase A; PNGase F
Systematic name: N-linked-glycopeptide-(N-acetyl-β-D-glucosaminyl)-L-asparagine amidohydrolase
Comments: Does not act on (GlcNAc)Asn, because it requires the presence of more than two amino-acid residues in the substrate [cf. EC 3.5.1.26, N4-(β-N-acetylg glucosaminyl)-L-asparaginase]. The plant enzyme was previously erroneously listed as EC 3.2.2.18.
References: [2413, 2982, 2984, 3027]

EC 3.5.1.53

Accepted name: N-carbamoylputrescine amidase
Reaction: N-carbamoylputrescine + H2O = putrescine + CO2 + NH3
Other name(s): carbamoylputrescine hydrolase; NCP
Systematic name: N-carbamoylputrescine amidohydrolase
References: [3411]

EC 3.5.1.54

Accepted name: alloxanate hydrolase
Reaction: urea-1-carboxylate + H2O = 2 CO2 + 2 NH3
Other name(s): alloxanate lyase; AtzF; TrzF
Systematic name: urea-1-carboxylate amidohydrolase
Comments: Along with EC 3.5.2.15 (cyanuric acid amidohydrolase) and EC 3.5.1.84 (biuret amidohydrolase), this enzyme forms part of the cyanuric-acid metabolism pathway, which degrades s-triazide herbicides, such as atrazine [2-chloro-4-(ethylamino)-6-(isopropylamino)-1,3,5-triazine], in bacteria. The yeast enzyme (but not that from green algae) also catalyses the reaction of EC 6.3.4.6, urea carboxylase, thus bringing about the hydrolysis of urea to CO2 and NH3 in the presence of ATP and bicarbonate. The enzyme from Pseudomonas sp. strain ADP has a narrow substrate specificity, being unable to use the structurally analogous compounds urea, hydroxyurea or methylcarbamate as substrate [2754].
References: [1879, 2584, 2941, 1461, 459, 2754, 2752]

EC 3.5.1.55

Accepted name: long-chain-fatty-acyl-glutamate deacylase
**Reaction:** \( N\text{-long-chain-fatty-acyl-}L\text{-glutamate} + H_2O = \text{a long-chain carboxylate} + L\text{-glutamate} \)

**Other name(s):**
- long-chain aminocacylase
- long-chain-fatty-acyl-glutamate deacylase
- long-chain acylglutamate amidae
- \( N\text{-acyl-D-glutamate deacylase} \)

**Systematic name:** \( N\text{-long-chain-fatty-acyl-L-glutamate amidohydrolase} \)

**Comments:**
Does not act on acyl derivates of other amino acids. Optimum chain length of acyl residue is 12 to 16.

**References:** [911]

---

**EC 3.5.1.56**

**Accepted name:** \( N,N\text{-dimethylformamidase} \)

**Reaction:** \( N,N\text{-dimethylformamide} + H_2O = \text{dimethylamine} + \text{formate} \)

**Other name(s):**
- dimethylformamidase
- DMFase

**Systematic name:** \( N,N\text{-dimethylformamide amidohydrolase} \)

**Comments:**
An iron protein. Also acts on \( N\text{-ethylformamide} \) and \( N\text{-methyl-formamide} \) and, more slowly, on \( N,N\text{-diethylformamide}, N,N\text{-dimethylacetamide} \) and unsubstituted acyl amides.

**References:** [2686]

---

**EC 3.5.1.57**

**Accepted name:** tryptophanamidase

**Reaction:** \( L\text{-tryptophanamide} + H_2O = L\text{-tryptophan} + NH_3 \)

**Other name(s):**
- tryptophan aminopeptidase
- \( L\text{-tryptophan aminopeptidase} \)

**Systematic name:** \( L\text{-tryptophanamide amidohydrolase} \)

**Comments:**
Requires \( \text{Mn}^{2+} \). Also acts on \( \text{N-ethylformamide} \) and \( \text{L-tyrosinamide} \), and on some tryptophan dipeptides.

**References:** [1360]

---

**EC 3.5.1.58**

**Accepted name:** \( N\text{-benzyloxycarbonylglycine hydrolase} \)

**Reaction:** \( N\text{-benzyloxycarbonylglycine} + H_2O = \text{benzyl alcohol} + \text{CO}_2 + \text{glycine} \)

**Other name(s):**
- \( N\text{-benzyloxycarbonylglycine hydrolyase} \)
- \( N\text{-benzyloxycarbonylglycine amidohydrolase} \)
- \( N\text{-benzyloxycarbonylglycine urethane hydrolase} \)
- \( N\text{-benzyloxycarbonylglycine urethane hydrolase I} \)

**Systematic name:** \( N\text{-benzyloxycarbonylglycine urethanehydrolase} \)

**Comments:**
Also acts, more slowly, on \( N\text{-benzyloxycarbonylalanine} \), but not on the corresponding derivatives of other amino acids or on \( N\text{-benzyloxycarbonylpeptides} \). Requires \( \text{Co}^{2+} \) or \( \text{Zn}^{2+} \). cf. EC 3.5.1.64, \( N\text{-benzyloxycarbonylleucine hydrolase} \).

**References:** [2107]

---

**EC 3.5.1.59**

**Accepted name:** \( N\text{-carbamoylsarcosine amidase} \)

**Reaction:** \( N\text{-carbamoylsarcosine} + H_2O = \text{sarcosine} + \text{CO}_2 + \text{NH}_3 \)

**Other name(s):**
- carbamoylsarcosine amidase

**Systematic name:** \( N\text{-carbamoylsarcosine amidohydrolase} \)

**References:** [610]

---

[EC 3.5.1.55 created 1986]

[EC 3.5.1.56 created 1989]

[EC 3.5.1.57 created 1989]

[EC 3.5.1.58 created 1989]

[EC 3.5.1.59 created 1989]
EC 3.5.1.60

Accepted name: N-(long-chain-acyl)ethanolamine deacylase
Reaction: N-(long-chain-acyl)ethanolamine + H₂O = a long-chain carboxylate + ethanolamine
Other name(s): NAAA (gene name); N-acylethanolamine amidohydrolase; acylethanolamine amidase
Systematic name: N-(long-chain-acyl)ethanolamine amidohydrolase
Comments: This lysosomal enzyme acts best on palmitoyl ethanolamine, with lower activity on other N-(long-chain-acyl)ethanolamines. It is only active at acidic pH. Unlike EC 3.5.1.99, fatty acid amide hydrolase, it does not act on primary amides such as oleamide, and has only a marginal activity with anandamide. The enzyme is translated as an inactive proenzyme, followed by autocatalytic cleavage into two subunits that reassociate to form an active heterodimeric complex.

References: [3156, 3155, 3316, 3498]

[EC 3.5.1.60 created 1989, modified 2019]

[3.5.1.61 Transferred entry. mimosinase. Now EC 4.3.3.8, mimosinase]

[EC 3.5.1.61 created 1989, deleted 2022]

EC 3.5.1.62

Accepted name: acetylputrescine deacetylase
Reaction: N-acetylputrescine + H₂O = acetate + putrescine
Systematic name: N-acetylputrescine acetylhydrolase
Comments: The enzyme from Micrococcus luteus also acts on N⁸-acetylspermidine and acetylcadaverine, but more slowly.

References: [2955]

[EC 3.5.1.62 created 1989]

EC 3.5.1.63

Accepted name: 4-acetamidobutyrate deacetylase
Reaction: 4-acetamidobutanoate + H₂O = acetate + 4-aminobutanoate
Systematic name: 4-acetamidobutanoate amidohydrolase
Comments: Also acts on N-acetyl-β-alanine and N5-acetamidopentanoate.

References: [1157]

[EC 3.5.1.63 created 1989]

EC 3.5.1.64

Accepted name: N⁶-benzoxycarbonyl-L-leucine hydrolase
Reaction: N⁶-benzoxycarbonyl-L-leucine + H₂O = benzyl alcohol + CO₂ + L-leucine
Other name(s): benzoxycarbonylleucine hydrolase; N⁶-benzoxycarbonyl amino acid urethane hydrolase IV; α-N-benzoxycarbonyl-L-leucine urethanehydrolase
Systematic name: N⁶-benzoxycarbonyl-L-leucine urethanehydrolase
Comments: Also acts on N⁶-α-t-butoxycarbonyl-L-leucine, and, more slowly, on the corresponding derivatives of L-aspartate, L-methionine, L-glutamate and L-alanine. cf. EC 3.5.1.58 N-benzoxycarbonylglycine hydrolase.

References: [1935]

[EC 3.5.1.64 created 1989]

EC 3.5.1.65

Accepted name: theanine hydrolase
Reaction: N⁵-ethyl-L-glutamine + H₂O = L-glutamate + ethylamine

References: [1935]

[EC 3.5.1.65 created 1989]
Other name(s):  L-theanine amidohydrolase; 5-N-ethyl-L-glutamine amidohydrolase
Systematic name:  N^5-ethyl-L-glutamine amidohydrolase
Comments:  Also acts on other N-alkyl-L-glutamines.
References:  [3138]

[EC 3.5.1.65 created 1989]

EC 3.5.1.66
Accepted name:  2-(hydroxymethyl)-3-(acetamidomethylene)succinate hydrolase
Reaction:  2-(hydroxymethyl)-3-(acetamidomethylene)succinate + 2 H_2O = acetate + 2-(hydroxymethyl)-4-oxobutanoate + NH_3 + CO_2
Other name(s):  compound B hydrolase; α-hydroxymethyl-α’-(N-acetylamidomethylene)succinic acid hydrolase
Systematic name:  2-(hydroxymethyl)-3-(acetamidomethylene)succinate amidohydrolase (deaminating, decarboxylating)
Comments:  Involved in the degradation of pyridoxin by Pseudomonas and Arthrobacter.
References:  [1288]

[EC 3.5.1.66 created 1989]

EC 3.5.1.67
Accepted name:  4-methyleneglutaminase
Reaction:  4-methylene-L-glutamine + H_2O = 4-methylene-L-glutamate + NH_3
Other name(s):  4-methyleneglutamine deamidase; 4-methyleneglutamine amidohydrolase
Systematic name:  4-methylene-L-glutamine amidohydrolase
References:  [1293]

[EC 3.5.1.67 created 1989]

EC 3.5.1.68
Accepted name:  N-formylglutamate deformylase
Reaction:  N-formyl-L-glutamate + H_2O = formate + L-glutamate
Other name(s):  β-citryl-L-glutamate hydrolase; formylglutamate deformylase; N-formylglutamate hydrolase; β-citrylglutamate amidase; β-citryl-L-glutamate amidohydrolase; β-citryl-L-glutamate amidase; β-citryl-L-glutamate-hydrolyzing enzyme
Systematic name:  N-formyl-L-glutamate amidohydrolase
Comments:  The animal enzyme also acts on β-citryl-L-glutamate and β-citryl-L-glutamine.
References:  [1273, 2036]

[EC 3.5.1.68 created 1989]

EC 3.5.1.69
Accepted name:  glycosphingolipid deacylase
Reaction:  Hydrolysis of gangliosides and neutral glycosphingolipids, releasing fatty acids to form the lyso-derivatives
Other name(s):  glycosphingolipid ceramide deacylase
Systematic name:  glycosphingolipid amidohydrolase
Comments:  Does not act on sphingolipids such as ceramide. Not identical with EC 3.5.1.23 ceramidase.
References:  [1214]

[EC 3.5.1.69 created 1990]

EC 3.5.1.70
Accepted name:  aculeacin-A deacylase

277
**Reaction:** Hydrolysis of the amide bond in aculeacin A and related neutral lipopeptide antibiotics, releasing the long-chain fatty acid side-chain

**Other name(s):** aculeacin A acylase

**Systematic name:** aculeacin-A amidohydrolase

**References:** [3000]

[EC 3.5.1.70 created 1992]

**EC 3.5.1.71**

**Accepted name:** N-feruloylglycine deacylase

**Reaction:** \( \text{N-feruloylglycine} + \text{H}_2\text{O} = \text{ferulate} + \text{glycine} \)

**Other name(s):** N-feruloylglycine hydrolase

**Systematic name:** N-feruloylglycine amidohydrolase

**Comments:** Hydrolyses a range of L-amino acids from the cinnamoyl and substituted cinnamoyl series. Not identical with EC 3.5.1.14 aminoacylase.

**References:** [1914, 1913]

[EC 3.5.1.71 created 1992]

**EC 3.5.1.72**

**Accepted name:** \( \text{D-benzoylarginine-4-nitroanilide amidase} \)

**Reaction:** \( \text{N-benzoyl-D-arginine-4-nitroanilide} + \text{H}_2\text{O} = \text{N-benzoyl-D-arginine} + 4\text{-nitroaniline} \)

**Other name(s):** benzoyl-D-arginine arylamidase; D-BAPA-ase

**Systematic name:** N-benzoyl-D-arginine-4-nitroanilide amidohydrolase

**References:** [993]

[EC 3.5.1.72 created 1992]

**EC 3.5.1.73**

**Accepted name:** carnitinamidase

**Reaction:** \( \text{L-carnitinamide} + \text{H}_2\text{O} = \text{L-carnitine} + \text{NH}_3 \)

**Other name(s):** L-carnitinamidase; carnitine amidase; L-carnitine amidase

**Systematic name:** L-carnitinamide amidohydrolase

**Comments:** Does not act on D-carnitinamide.

**References:** [2155]

[EC 3.5.1.73 created 1992]

**EC 3.5.1.74**

**Accepted name:** chenodeoxycholoyltaurine hydrolase

**Reaction:** \( \text{chenodeoxycholoyltaurine} + \text{H}_2\text{O} = \text{chenodeoxycholate} + \text{taurine} \)

**Systematic name:** chenodeoxycholoyltaurine amidohydrolase

**Comments:** Some other taurine conjugates are hydrolysed, but not glycine conjugates of bile acids.

**References:** [1490]

[EC 3.5.1.74 created 1992]

**EC 3.5.1.75**

**Accepted name:** urethanase

**Reaction:** \( \text{urethane} + \text{H}_2\text{O} = \text{ethanol} + \text{CO}_2 + \text{NH}_3 \)

**Other name(s):** urethane hydrolase

**Systematic name:** urethane amidohydrolase (decarboxylating)
EC 3.5.1.76

Accepted name: arylalkyl acylamidase
Reaction: \[N\text{-acetylarylalkylamine} + H_2O = \text{arylalkylamine} + \text{acetate}\]
Other name(s): aralkyl acylamidase
Systematic name: \(N\text{-acytethylarylalkylamine amidohydrolase}\)
Comments: Identified in *Pseudomonas putida*. Strict specificity for \(N\text{-acetyl arylalkylamines}\), including \(N\text{-acetyl-2-phenylethylamine}, N\text{-acetyl-3-phenylpropylamine}, N\text{-acetyldopamine}, N\text{-acetyl-serotonin and melatonin}\). It also accepts arylalkyl acetates but not acetanilide derivatives, which are common substrates of EC 3.5.1.13, aryl acylamidase.
References: [1571, 2770]

[EC 3.5.1.76 created 1992]

EC 3.5.1.77

Accepted name: \(N\text{-carbamoyl-}D\text{-amino-acid hydrolase}\)
Reaction: \[\text{an } N\text{-carbamoyl-}D\text{-amino acid} + H_2O = D\text{-amino acid} + NH_3 + CO_2\]
Other name(s): \(D\text{-N-carbamoylase}; N\text{-carbamoylase (ambiguous); N\text{-carbamoyl-}D\text{-amino acid hydrolase}\)}
Systematic name: \(N\text{-carbamoyl-}D\text{-amino-acid amidohydrolase}\)
Comments: This enzyme, along with EC 3.5.1.87 (\(N\text{-carbamoyl-L-amino-acid hydrolase}\)), EC 5.1.99.5 (hydantoin racemase) and hydantoinase, forms part of the reaction cascade known as the "hydantoinase process", which allows the total conversion of \(D, L-5\text{-monosubstituted hydantoins}\) into optically pure \(D\)- or \(L\)-amino acids [44]. It has strict stereospecificity for \(N\text{-carbamoyl-}D\text{-amino acids}\) and does not act upon the corresponding \(L\)-amino acids or on the \(N\text{-formyl amino acids}, N\text{-carbamoyl-sarcosine, -citrulline, -allantoin and -ureidopropanoate}\), which are substrates for other amidohydrolases.
References: [2255, 44]

[EC 3.5.1.77 created 1999, modified 2008]

EC 3.5.1.78

Accepted name: glutathionylspermidine amidase
Reaction: \(\text{glutathionylspermidine} + H_2O = \text{glutathione} + \text{spermidine}\)
Other name(s): glutathionylspermidine amidohydrolase (spermidine-forming)
Systematic name: \(\gamma\text{-L-glutamyl-L-cysteinyl-glycine:spermidine amidase}\)
Comments: Spermidine is numbered so that atom N-1 is in the amino group of the aminopropyl part of the molecule. The enzyme from *Escherichia coli* is bifunctional and also catalyses the glutathionylspermidine synthase (EC 6.3.1.8) reaction, resulting in a net hydrolysis of ATP.
References: [282]

[EC 3.5.1.78 created 1999]

EC 3.5.1.79

Accepted name: phthalyl amidase
Reaction: \(\text{a phthalylamide} + H_2O = \text{phthalic acid} + \text{a substituted amine}\)
Systematic name: phthalyl-amide amidohydrolase
Comments: In the entry, "phthalyl" is used to mean "2-carboxybenzoyl". The enzyme from *Xanthobacter agilis* hydrolyses phthalylated amino acids, peptides, \(\beta\)-lactams, aromatic and aliphatic amines. The substituent on nitrogen may be an alkyl group, but may also be complex, giving an amino acid or peptide derivative. Substitutions on the phthalyl ring include 6-F, 6-NH\(_2\), 3-OH, and a nitrogen in the aromatic ring ortho to the carboxy group attached to the amine. No cofactors are required.

References: [1571, 2770]

[EC 3.5.1.79 created 1999]
References: [320, 255, 536, 319]

[EC 3.5.1.79 created 1999]

[3.5.1.80 Deleted entry. N-acetylglactosamine-6-phosphate deacetylase. Identical to EC 3.5.1.25, N-acetylglucosamine-6-phosphate deacetylase]

[EC 3.5.1.80 created 1999, deleted 2002]

EC 3.5.1.81

Accepted name: N-acyl-D-amino-acid deacylase
Reaction: N-acyl-D-amino acid + H2O = a carboxylate + D-amino acid
Systematic name: N-acyl-D-amino acid amidohydrolase
Comments: The enzyme from Alcaligenes denitrificans subsp. xylosoxydans and Alcaligenes xylosoxydans subsp. xylosoxydans has wide specificity; hydrolyses N-acyl derivative of neutral D-amino acids. Used in separating D- and L-amino acids. Requires zinc.
References: [3239, 3238]

[EC 3.5.1.81 created 1999]

EC 3.5.1.82

Accepted name: N-acyl-D-glutamate deacylase
Reaction: N-acyl-D-glutamate + H2O = a carboxylate + D-glutamate
Systematic name: N-acyl-D-glutamate amidohydrolase
Comments: The enzyme from Alcaligenes xylosoxydans subsp. xylosoxydans and Pseudomonas sp. is specific for N-acyl-D-glutamate. Requires zinc.
References: [3237, 3240, 3241]

[EC 3.5.1.82 created 1999]

EC 3.5.1.83

Accepted name: N-acyl-D-aspartate deacylase
Reaction: N-acyl-D-aspartate + H2O = a carboxylate + D-aspartate
Systematic name: N-acyl-D-aspartate amidohydrolase
Comments: The enzyme from Alcaligenes xylosoxydans subsp. xylosoxydans is specific for N-acyl-D-aspartate. Requires zinc.
References: [2068, 3242]

[EC 3.5.1.83 created 1999]

EC 3.5.1.84

Accepted name: biuret amidohydrolase
Reaction: biuret + H2O = urea-1-carboxylate + NH3
Other name(s): biuH (gene name)
Systematic name: biuret amidohydrolase
Comments: The enzyme, characterized from the bacterium Rhizobium leguminosarum bv. viciae 3841, participates in the degradation of cyanuric acid, an intermediate in the degradation of s-triazide herbicides such as atrazine [2-chloro-4-(ethylamino)-6-(isopropylamino)-1,3,5-triazine]. The substrate, biuret, forms by the spontaneous decarboxylation of 1-carboxybiuret in the absence of EC 3.5.1.131, 1-carboxybiuret hydrolase.
References: [387, 767, 766]

[EC 3.5.1.84 created 2000, modified 2008, modified 2019]
**EC 3.5.1.85**

**Accepted name:** (S)-N-acetyl-1-phenylethylamine hydrolase  
**Reaction:** N-acetylphenylethylamine + H₂O = phenylethylamine + acetate  
**Systematic name:** (S)-N-acetylphenylethylamine:H₂O hydrolase  
**Comments:** Inhibited by phenylmethanesulfonyl fluoride. Some related acetylated compounds are hydrolysed with variable enantiomeric selectivities.  
**References:** [346]

[EC 3.5.1.85 created 2000, modified 2002]

**EC 3.5.1.86**

**Accepted name:** mandelamide amidase  
**Reaction:** (R)-mandelamide + H₂O = (R)-mandelate + NH₃  
**Other name(s):** Pseudomonas mandelamide hydrolase  
**Systematic name:** mandelamide hydrolase  
**References:** [3405]

[EC 3.5.1.86 created 2000]

**EC 3.5.1.87**

**Accepted name:** N-carbamoyl-L-amino-acid hydrolase  
**Reaction:** an N-carbamoyl-L-2-amino acid (a 2-ureido carboxylate) + H₂O = an L-2-amino acid + NH₃ + CO₂  
**Other name(s):** N-carbamyl-L-amino acid amidohydrolase; N-carbamoyl-L-amino acid amidohydrolase; L-N-carbamoylase; N-carbamoylase (ambiguous)  
**Systematic name:** N-carbamoyl-L-amino-acid amidohydrolase  
**Comments:** This enzyme, along with EC 3.5.1.77 (N-carbamoyl-D-amino-acid hydrolase), EC 5.1.99.5 (hydantoin racemase) and hydantoinase, forms part of the reaction cascade known as the "hydantoinase process", which allows the total conversion of D,L-5-monosubstituted hydantoins into optically pure D- or L-amino acids [44]. The enzyme from Alcaligenes xylosoxidans has broad specificity for carbamoyl-L-amino acids, although it is inactive on the carbamoyl derivatives of glutamate, aspartate, arginine, tyrosine or tryptophan. The enzyme from Sinorhizobium meliloti requires a divalent cation for activity and can hydrolyse N-carbamoyl-L-tryptophan as well as N-carbamoyl L-amino acids with aliphatic substituents [1919]. The enzyme is inactive on derivatives of D-amino acids. In addition to N-carbamoyl L-amino acids, the enzyme can also hydrolyse formyl and acetyl derivatives to varying degrees [2254, 1919].  
**References:** [2254, 1919, 44]

[EC 3.5.1.87 created 2001, modified 2008]

**EC 3.5.1.88**

**Accepted name:** peptide deformylase  
**Reaction:** formyl-L-methionyl peptide + H₂O = formate + methionyl peptide  
**Other name(s):** N-formylmethionylaminoacyl-tRNA deformylase  
**Systematic name:** formyl-L-methionyl peptide amidohydrolase  
**Comments:** Requires iron(II). Also requires at least a dipeptide for an efficient rate of reaction. N-terminal L-methionine is a prerequisite for activity but the enzyme has broad specificity at other positions. Differs in substrate specificity from EC 3.5.1.31 (formylmethionine deformylase).  
**References:** [17, 1951, 422, 197, 196, 2481, 1042, 2480, 1274, 2475, 970, 2369]

[EC 3.5.1.88 created 2001]

**EC 3.5.1.89**

**Accepted name:** N-acetylglucosaminylphosphatidylinositol deacetylase  

281
Reaction: 6-(N-acetyl-α-D-glucosaminy1)-1-phosphatidy1-1D-my0-inositol + H₂O = 6-(α-D-glucosaminy1)-1-phosphatidy1-1D-my0-inositol + acetate

Other name(s): N-acetyl-D-glucosaminylphosphatidylinositol acetylhydrolase; N-acetylglucosaminylphosphatidylinositol de-N-acetylase; GlcNAc-PI de-N-acetylase; acetylglucosaminylphosphatidylinositol deacetylase

Systematic name: 6-(N-acetyl-α-D-glucosaminy1)-1-phosphatidy1-1D-my0-inositol acetylhydrolase

Comments: Involved in the second step of glycosylphosphatidylinositol (GPI) anchor formation in all eukaryotes. The enzyme appears to be composed of a single subunit (PIG-L in mammalian cells and GPI12 in yeast). In some species, the long-chain sn-1-acyl group of the phosphatidy1 group is replaced by a long-chain alkyl or alk-1-enyl group.

References: [670, 2147, 3284, 2842]

[EC 3.5.1.89 created 1992 as EC 3.1.1.69, transferred 2002 to EC 3.5.1.89, modified 2002]
EC 3.5.1.93
Accepted name: glutaryl-7-aminocephalosporanic-acid acylase
Reaction: (7R)-7-(4-carboxybutanamido)cephalosporanate + H₂O = (7R)-7-aminocephalosporanate + glutarate
Other name(s): 7β-(4-carboxybutanamido)cephalosporanic acid acylase; cephalosporin C acylase; glutaryl-7-ACA acylase; CA; GCA; GA; cephalosporin acylase; glutaryl-7-aminocephalosporanic acid acylase; GL-7-ACA acylase
Systematic name: (7R)-7-(4-carboxybutanamido)cephalosporanate amidohydrolase
Comments: Forms 7-aminocephalosporanic acid, a key intermediate in the synthesis of cephem antibiotics. It reacts only weakly with cephalosporin C.
References: [1340, 1548, 2056, 1672, 1541, 1278, 1532]

[EC 3.5.1.93 created 2005]

EC 3.5.1.94
Accepted name: γ-glutamyl-γ-aminobutyrate hydrolase
Reaction: 4-(γ-L-glutamylamino)butanoate + H₂O = 4-aminobutanoate + L-glutamate
Other name(s): γ-glutamyl-GABA hydrolase; PuuD; YcjL; 4-(γ-glutamylamino)butanoate amidohydrolase; 4-(L-γ-glutamylamino)butanoate amidohydrolase
Systematic name: 4-(γ-L-glutamylamino)butanoate amidohydrolase
Comments: Forms part of a putrescine-utilizing pathway in Escherichia coli, in which it has been hypothesized that putrescine is first glutamylated to form γ-glutamylputrescine, which is oxidized to 4-(γ-glutamylamino)butanal and then to 4-(γ-glutamylamino)butanoate. The enzyme can also catalyse the reactions of EC 3.5.1.35 (D-glutaminase) and EC 3.5.1.65 (theanine hydrolase).
References: [1657]

[EC 3.5.1.94 created 2006, modified 2011]

EC 3.5.1.95
Accepted name: N-malonylurea hydrolase
Reaction: 3-oxo-3-ureidopropanoate + H₂O = malonate + urea
Other name(s): \textit{ureidomalonase}
Systematic name: 3-oxo-3-ureidopropanoate amidohydrolase (urea- and malonate-forming)
Comments: Forms part of the oxidative pyrimidine-degrading pathway in some microorganisms, along with EC 1.17.99.4 (uracil/thymine dehydrogenase) and EC 3.5.2.1 (barbiturase).
References: [2864, 2863]

[EC 3.5.1.95 created 2006]

EC 3.5.1.96
Accepted name: succinylglutamate desuccinylase
Reaction: N-succinyl-L-glutamate + H₂O = succinate + L-glutamate
Other name(s): N²-succinylglutamate desuccinylase; SGDS; AstE
Systematic name: N-succinyl-L-glutamate amidohydrolase
Comments: Requires Co²⁺ for maximal activity [3291]. N²-Acetylglutamate is not a substrate. This is the final enzyme in the arginine succinylltransferase (AST) pathway for the catabolism of arginine [3291]. 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 2.6.1.11 (acetylornithine transaminase), EC 1.2.1.71 (succinylglutamate-semialdehyde dehydrogenase) and EC 3.5.1.96 (succinylglutamate desuccinylase).
References: [3291, 559, 560, 1355, 2707]

[EC 3.5.1.96 created 2006]
EC 3.5.1.97

Accepted name: acyl-homoserine-lactone acylase
Reaction: an N-acyl-L-homoserine lactone + H₂O = l-homoserine lactone + a carboxylate

Other name(s): acyl-homoserine lactone acylase; AHL-acylase; AiiD; N-acyl-homoserine lactone acylase; PA2385 protein; quorum-quenching AHL acylase; quorum-quenching enzyme; QuiP

Systematic name: N-acyl-L-homoserine-lactone amidohydrolase
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. Plants or animals capable of degrading AHLs would have a therapeutic advantage in avoiding bacterial infection as they could prevent AHL-signalling and the expression of virulence genes in quorum-sensing bacteria. This quorum-quenching enzyme removes the fatty-acid side chain from the homoserine lactone ring of AHL-dependent quorum-sensing signal molecules. It has broad specificity for AHLs with side changes ranging in length from 11 to 14 carbons. Substituents at the 3′-position, as found in N-(3-oxododecanoyl)-L-homoserine lactone, do not affect this activity.

References: [1793, 2812]

[EC 3.5.1.97 created 2007]

EC 3.5.1.98

Accepted name: histone deacetylase
Reaction: Hydrolysis of an N⁶-acetyl-lysine residue of a histone to yield a deacetylated histone

Other name(s): HDAC

Systematic name: histone amidohydrolase
Comments: A class of enzymes that remove acetyl groups from N⁶-acetyl-lysine residues on a histone. The reaction of this enzyme is opposite to that of EC 2.3.1.48, histone acetyltransferase. Histone deacetylases (HDACs) can be organized into three classes, HDAC1, HDAC2 and HDAC3, depending on sequence similarity and domain organization. Histone acetylation plays an important role in regulation of gene expression. In eukaryotes, HDACs play a key role in the regulation of transcription and cell proliferation [2861]. May be identical to EC 3.5.1.17, acyl-lysine deacylase.

References: [1624, 614, 2327, 2861, 822, 2392, 602]

[EC 3.5.1.98 created 2008]

EC 3.5.1.99

Accepted name: fatty acid amide hydrolase
Reaction: (1) anandamide + H₂O = arachidonic acid + ethanolamine
(2) oleamide + H₂O = oleic acid + NH₃

Other name(s): FAAH; oleamide hydrolase; anandamide amidohydrolase

Systematic name: fatty acylamide amidohydrolase
Comments: Integral membrane protein, the enzyme is responsible for the catabolism of neuromodulatory fatty acid amides, including anandamide and oleamide, occurs in mammalia.

References: [278, 2360, 2359]

[EC 3.5.1.99 created 2009]

EC 3.5.1.100

Accepted name: (R)-amidase
Reaction: (1) (R)-piperazine-2-carboxamide + H₂O = (R)-piperazine-2-carboxylate + NH₃
(2) β-alaninamide + H₂O = β-alanine + NH₃

Other name(s): R-stereospecific amidase; R-amidase

Systematic name: (R)-piperazine-2-carboxamide amidohydrolase
In addition (R)-piperidine-3-carboxamide is hydrolysed to (R)-piperidine-3-carboxylic acid and NH₃, and (R)-N-tert-butylpiperazine-2-carboxamide is hydrolysed to (R)-piperazine-2-carboxylic acid and tert-butylamine with lower activity. The enzyme does not act on the other amide substrates which are hydrolysed by EC 3.5.1.4 (amidase).

References: [1590]

[EC 3.5.1.100 created 2009, modified 2011]

**EC 3.5.1.101**

**Accepted name:** L-proline amide hydrolase

**Reaction:**
1. \((S)-\text{piperidine-2-carboxamide} + \text{H}_2\text{O} = \text{(S)-piperidine-2-carboxylate} + \text{NH}_3\)
2. \(\text{L-prolinamide} + \text{H}_2\text{O} = \text{L-proline} + \text{NH}_3\)

**Other name(s):** S-stereoselective piperazine-2-tert-butylcarboxamide hydrolase; LaaA; L-amino acid amidase

**Systematic name:** (S)-piperidine-2-carboxamide amidohydrolase

**References:** [1591]

[EC 3.5.1.101 created 2009]

**EC 3.5.1.102**

**Accepted name:** 2-amino-5-formylamino-6-(5-phospho-D-ribosylamino)pyrimidin-4(3H)-one 5′-monophosphate deformylase

**Reaction:** 2-amino-5-formylamino-6-(5-phospho-D-ribosylamino)pyrimidin-4(3H)-one + H₂O = 2,5-diamino-6-(5-phospho-D-ribosylamino)pyrimidin-4(3H)-one + formate

**Other name(s):** ArfB

**Systematic name:** 2-amino-5-formylamino-6-(5-phospho-D-ribosylamino)pyrimidin-4(3H)-one amidohydrolase

**Comments:** The enzyme catalyses the second step in archaeal riboflavin and 7,8-didemethyl-8-hydroxy-5-deazariboflavin biosynthesis. The first step is catalysed by EC 3.5.4.29 (GTP cyclohydrolase IIα). The bacterial enzyme, EC 3.5.4.25 (GTP cyclohydrolase II) catalyses both reactions.

**References:** [1044]

[EC 3.5.1.102 created 2010, modified 2011]

**EC 3.5.1.103**

**Accepted name:** N-acetyl-1-D-myoinositol-2-amino-2-deoxy-α-D-glucopyranoside deacetylase

**Reaction:** 1-O-(2-acetamido-2-deoxy-α-D-glucopyranosyl)-1D-myoinositol + H₂O = 1-O-(2-amino-2-deoxy-α-D-glucopyranosyl)-1D-myoinositol + acetate

**Other name(s):** MshB

**Systematic name:** 1-(2-acetamido-2-deoxy-α-D-glucopyranosyl)-1D-myoinositol acetylhydrolase

**Comments:** This enzyme is considered the key enzyme and rate limiting step in the mycothiol biosynthesis pathway [2504]. In addition to acetylase activity, the enzyme possesses weak activity of EC 3.5.1.115, mycothiol S-conjugate amidase, and shares sequence similarity with that enzyme [2183]. The enzyme requires a divalent transition metal ion for activity, believed to be Zn²⁺ [1950].

**References:** [2504, 2183, 1950]

[EC 3.5.1.103 created 2010]

**EC 3.5.1.104**

**Accepted name:** peptidoglycan-N-acetylglucosamine deacetylase

**Reaction:** peptidoglycan-N-acetyl-D-glucosamine + H₂O = peptidoglycan-D-glucosamine + acetate

**Other name(s):** HP310; FgdA; SpPgdA; BC1960; peptidoglycan deacetylase; N-acetylglucosamine deacetylase; peptidoglycan GlcNAc deacetylase; peptidoglycan N-acetylglucosamine deacetylase; PG N-deacetylase

**Systematic name:** peptidoglycan-N-acetylglucosamine amidohydrolase

References:
Modification of peptidoglycan by N-deacetylation is an important factor in virulence of *Helicobacter pylori*, *Listeria monocytogenes* and *Streptococcus suis* [3259, 2430, 830]. The enzyme from *Streptococcus pneumoniae* is a metalloenzyme using a His-His-Asp zinc-binding triad with a nearby aspartic acid and histidine acting as the catalytic base and acid, respectively [258].

References: [2446, 3115, 258, 3259, 2430, 830]

[EC 3.5.1.104 created 2010]

EC 3.5.1.105

**Accepted name:** chitin disaccharide deacetylase

**Reaction:** \(\text{N},\text{N}'\)-diacetylchitobiose + H\(_2\)O = N-acetyl-\(\beta\)-D-glucosaminyl-(1\(\rightarrow\)4)-D-glucosamine + acetate

**Other name(s):** chitobiose amidohydrolase; COD; chitin oligosaccharide deacetylase; chitin oligosaccharide amidohydrolase; 2-(acetylamino)-4-O-[2-(acetylamino)-2-deoxy-\(\beta\)-D-glucopyranosyl]-2-deoxy-\(\beta\)-D-glucopyranose acetylhydrolase

**Systematic name:** \(\text{N},\text{N}'\)-diacetylchitobiose acetylhydrolase

**Comments:** Chitin oligosaccharide deacetylase is a key enzyme in the chitin catabolic cascade of chitinolytic *Vibrio* strains. Besides being a nutrient, the heterodisaccharide product 4-O-(N-acetyl-\(\beta\)-D-glucosaminyl)-D-glucosamine is a unique inducer of chitinase production in *Vibrio parahaemolyticus* [1219]. In contrast to EC 3.5.1.41 (chitin deacetylase) this enzyme is specific for the chitin disaccharide [1435, 2268]. It also deacetylates the chitin trisaccharide with lower efficiency [2268]. No activity with higher polymers of GlcNAc [1435, 2268].

References: [1435, 1219, 2268, 2267]

[EC 3.5.1.105 created 2010]

EC 3.5.1.106

**Accepted name:** N-formylmaleamate deformylase

**Reaction:** \(\text{N-formylmaleamic acid} + \text{H}_2\text{O} = \text{maleamate} + \text{formate}\)

**Other name(s):** NicD

**Systematic name:** \(\text{N-formylmaleamic acid amidohydrolase}\)

**Comments:** The reaction is involved in the aerobic catabolism of nicotinic acid.

References: [1404]

[EC 3.5.1.106 created 2010]

EC 3.5.1.107

**Accepted name:** maleamate amidohydrolase

**Reaction:** maleamate + H\(_2\)O = maleate + NH\(_3\)

**Other name(s):** NicF

**Systematic name:** maleamate amidohydrolase

**Comments:** The reaction is involved in the aerobic catabolism of nicotinic acid.

References: [1404]

[EC 3.5.1.107 created 2010]

EC 3.5.1.108

**Accepted name:** UDP-3-O-acyl-\(\text{N-acetylglucosamine deacetylase}\)

**Reaction:** \(\text{a UDP-3-O-[(3R)-3-hydroxyacyl]-N-acetyl-}\(\alpha\)-D-glucosamine} + \text{H}_2\text{O} = \text{a UDP-3-O-[(3R)-3-hydroxyacyl]-}\(\alpha\)-D-glucosamine + acetate\)

286
Other name(s): LpxC protein; LpxC enzyme; LpxC deacetylase; deacetylase LpxC; UDP-3-O-acyl-GlcNAc deacetylase; UDP-3-O-((R)-3-hydroxymyristoyl)-N-acetylglucosamine deacetylase; UDP-3-O-(3-O-acetyl)-N-acetylglucosaminide deacetylase; UDP-3-O-(R-3-hydroxymyristoyl)-N-acetylglucosamine deacetylase; UDP-(3-O-(R-3-hydroxymyristoyl))-N-acetylglucosamine deacetylase; UDP-3-O-[(3R)-3-hydroxyacyl]-N-acetylglucosamine amidohydrolase

Systematic name: UDP-3-O-[(3R)-3-hydroxyacyl]-N-acetyl-α-D-glucosamine amidohydrolase

Comments: A zinc protein. The enzyme catalyses a committed step in the biosynthesis of lipid A.
References: [1200, 1365, 1290, 3273, 3328, 2044]

EC 3.5.1.109
Accepted name: sphingomyelin deacylase
Reaction: (1) an N-acyl-sphingosylphosphorylcholine + H₂O = a fatty acid + sphingosylphosphorylcholine (2) a D-glucosyl-N-acylsphingosine + H₂O = a fatty acid + D-glucosyl-sphingosine
Other name(s): SM deacylase; GcSM deacylase; glucosylceramide sphingomyelin deacylase; sphingomyelin glucosylceramide deacylase; SM glucosylceramide GCer deacylase; SM-GCer deacylase; SMGCer deacylase
Systematic name: N-acyl-sphingosylphosphorylcholine amidohydrolase
Comments: The enzyme is involved in the sphingolipid metabolism in the epidermis.
References: [1109, 1209, 1335]

EC 3.5.1.110
Accepted name: ureidoacrylate amidohydrolase
Reaction: (1) (Z)-3-ureidoacrylate + H₂O = (Z)-3-aminoacrylate + CO₂ + NH₃ (overall reaction) (1a) (Z)-3-ureidoacrylate + H₂O = (Z)-3-aminoacrylate + carbamate (1b) carbamate = CO₂ + NH₃ (spontaneous) (2) (Z)-2-methylureidoacrylate + H₂O = (Z)-2-methylaminoacrylate + CO₂ + NH₃ (overall reaction) (2a) (Z)-2-methylureidoacrylate + H₂O = (Z)-2-methylaminoacrylate + carbamate (2b) carbamate = CO₂ + NH₃ (spontaneous)
Other name(s): peroxyureidoacrylate/ureidoacrylate amidohydrolase; rutB (gene name); (Z)-3-ureidoacrylate peracid amidohydrolase
Systematic name: (Z)-3-ureidoacrylate amidohydrolase
Comments: The enzyme participates in the Rut pyrimidine catabolic pathway.
References: [1536]

EC 3.5.1.111
Accepted name: 2-oxoglutaramate amidase
Reaction: 2-oxoglutaramate + H₂O = 2-oxoglutarate + NH₃
Other name(s): ω-amidase (ambiguous)
Systematic name: 5-amino-2,5-dioxopentanoate amidohydrolase
Comments: The enzyme, which is highly specific for its substrate, participates in the nicotine degradation pathway of several Gram-positive bacteria.
References: [502]

EC 3.5.1.112
Accepted name: 2′-N-acetylpromamine deacetylase
Reaction: $2'$-N-acetylparomamine + H$_2$O = paromamine + acetate

Other name(s): btrD (gene name); neoL (gene name); kanN (gene name)

Systematic name: $2'$-N-acetylparomamine hydrolase (acetate-forming)

Comments: Involved in the biosynthetic pathways of several clinically important aminocyclitol antibiotics, including kanamycin, butirosin, neomycin and ribostamycin. The enzyme from the bacterium *Streptomyces fradiae* can also accept $2''''$-acetyl-6$''''$-hydroxyneomycin C as substrate, cf. EC 3.5.1.113, $2''''$-acetyl-6$''''$-hydroxyneomycin C deacetylase [3447].

References: [3113, 3447]

(3) $2''''$-acyl-6$''''$-hydroxyneomycin C deacetylase

Accepted name: $2''''$-acyl-6$''''$-hydroxyneomycin C deacetylase

Reaction: $2''''$-acyl-6$''''$-deamino-6$''''$-hydroxyneomycin C + H$_2$O = 6$''''$-deamino-6$''''$-hydroxyneomycin C + acetate

Other name(s): neoL (gene name)

Systematic name: $2''''$-acyl-6$''''$-hydroxyneomycin C hydrolase (acetate-forming)

Comments: Involved in the biosynthetic pathway of aminoglycoside antibiotics of the neomycin family. The enzyme from the bacterium *Streptomyces fradiae* also catalyses EC 3.5.1.112, $2'$-N-acetylparomamine deacetylase.

References: [3447]

(4) N-acyl-aromatic-L-amino acid amidohydrolase

Accepted name: N-acyl-aromatic-L-amino acid amidohydrolase

Reaction: (1) an N-acyl-aromatic-L-amino acid + H$_2$O = an aromatic-L-amino acid + a carboxylate
(2) an N-acyl-L-cysteine-S-conjugate + H$_2$O = an L-cysteine-S-conjugate + acetate

Other name(s): aminoacylase III; aminoacylase III; ACY3 (gene name)

Systematic name: N-acyl-aromatic-L-amino acid amidohydrolase (carboxylate-forming)

Comments: This enzyme is found in animals and is involved in the hydrolysis of N-acylated or N-acetylated amino acids (except L-aspartate). It preferentially deacylates N$^\alpha$-acylated aromatic amino acids and mercapturic acids (S-conjugates of N-acyl-L-cysteine) that are usually not deacylated by EC 3.5.1.14, N-acyl-aliphatic-L-amino acid amidohydrolase. The enzyme is significantly activated by Co$^{2+}$ and Ni$^{2+}$ [3120]. Some bacterial aminoacylases demonstrate substrate specificity for both EC 3.5.1.14 and EC 3.5.1.114. cf. EC 3.5.1.14, N-acyl-aliphatic-L-amino acid amidohydrolase and EC 3.5.1.15, aspartoacylase.

References: [2452, 2179, 3120, 1270, 3119]

(5) Mycothiol S-conjugate amidase

Accepted name: mycothiol S-conjugate amidase

Reaction: a mycothiol S-conjugate + H$_2$O = an N-acyl L-cysteine-S-conjugate + 1-O-(2-amino-2-deoxy-α-D-glucopyranosyl)-1-D-myoinositol

Other name(s): MCA

Systematic name: mycothiol S-conjugate 1D-myoinositol 2-amino-2-deoxy-α-D-glucopyranosyl-hydrolase

Comments: The enzyme that is found in actinomycetes is involved in the detoxification of oxidizing agents and electrophilic antibiotics. The enzyme has low activity with 1-O-(2-acetamido-2-deoxy-α-D-glucopyranosyl)-1-D-myoinositol as substrate (cf. EC 3.5.1.103, N-acyetyl-1-D-myoinositol-2-amino-2-deoxy-α-D-glucopyranoside deacetylase) [2900].

References: [2182, 2900]
EC 3.5.1.116

**Accepted name:** ureidoglycolate amidohydrolase  
**Reaction:** \((\delta)-\text{ureidoglycolate} + \text{H}_2\text{O} = \text{glyoxylate} + 2\text{NH}_3 + \text{CO}_2\)  
**Other name(s):** ureidoglycolate hydrolase; UAH (gene name)  
**Systematic name:** \((\delta)-\text{ureidoglycolate amidohydrolase (decarboxylating)}\)  
**Comments:** This plant enzyme is involved in the degradation of ureidoglycolate, an intermediate of purine degradation. Not to be confused with EC 4.3.2.3, ureidoglycolate lyase, which releases urea rather than ammonia.  
**References:** [3351, 3313, 3314]

[EC 3.5.1.116 created 1992 as EC 3.5.3.19, transferred 2014 to EC 3.5.1.116]

EC 3.5.1.117

**Accepted name:** 6-aminohexanoate-oligomer endohydrolase  
**Reaction:** \([N-(6-\text{aminohexanoyl})_n + \text{H}_2\text{O} = [N-(6-\text{aminohexanoyl})_{n-x} + [N-(6-\text{aminohexanoyl})_x]\]  
**Other name(s):** endo-type 6-aminohexanoate oligomer hydrolase; Ahx endo-type-oligomer hydrolase; 6-aminohexanoate oligomer hydrolase; Ahx-oligomer hydrolase; nylon hydrolase; nylon-oligomer hydrolase; NylC; nylon-6 hydrolase (ambiguous)  
**Systematic name:** 6-aminohexanoate oligomer endoamidohydrolase  
**Comments:** The enzyme is involved in degradation of nylon-6 oligomers. It degrades linear or cyclic oligomers of poly(6-aminohexanoate) with a degree of polymerization greater than three \((n > 3)\) by endo-type cleavage, to oligomers of a length of two or more \((2 < x < n)\). It shows negligible activity with \(N-(6-\text{aminohexanoyl})-6-\text{aminohexanoate}\) (cf. EC 3.5.1.46, 6-aminohexanoate-oligomer exo hydrolase) or with 1,8-diazacyclotetradecane-2,9-dione (cf. EC 3.5.2.12, 6-aminohexanoate-cyclic-dimer hydrolase).  
**References:** [1441, 3429, 2173]

[EC 3.5.1.117 created 2014]

EC 3.5.1.118

**Accepted name:** γ-glutamyl hercynylcysteine S-oxide hydrolase  
**Reaction:** \(\gamma-L-\text{glutamyl}-S-(\text{hercyn-2-yl})-L-\text{cysteine} \cdot \text{S-oxide} + \text{H}_2\text{O} = S-(\text{hercyn-2-yl})-L-\text{cysteine} \cdot \text{S-oxide} + L-\text{glutamate}\)  
**Other name(s):** EgtC  
**Systematic name:** γ-glutamyl-S-(hercyn-2-yl)cysteine S-oxide amidohydrolase  
**Comments:** The enzyme is part of the biosynthesis pathway of ergothioneine in mycobacteria.  
**References:** [2732]

[EC 3.5.1.118 created 2015]

EC 3.5.1.119

**Accepted name:** Pup amidohydrolase  
**Reaction:** [prokaryotic ubiquitin-like protein]-L-glutamine + H₂O = [prokaryotic ubiquitin-like protein]-L-glutamate + NH₃  
**Other name(s):** dop (gene name); Pup deamidase; depupylase/deamidase; DPUP; depupylase  
**Systematic name:** [prokaryotic ubiquitin-like protein]-L-glutamine amidohydrolase  
**Comments:** The enzyme has been characterized from the bacterium *Mycobacterium tuberculosis*. It catalyses the hydrolysis of the amido group of the C-terminal glutamine of prokaryotic ubiquitin-like protein (Pup), thus activating it for ligation to target proteins, a process catalysed by EC 6.3.1.19, prokaryotic ubiquitin-like protein ligase. The reaction requires ATP as cofactor but not its hydrolysis. The enzyme also catalyses the hydrolytic cleavage of the bond formed by the ligase, between an ε-amino group of a lysine residue of the target protein and the γ-carboxylate of the C-terminal glutamate of the prokaryotic ubiquitin-like protein.

289
References: [2923, 360, 2922]

[EC 3.5.1.119 created 2015]

[3.5.1.120 Transferred entry. 2-aminomuconate deaminase (2-hydroxymuconate-forming). Now EC 3.5.99.11, 2-aminomuconate deaminase (2-hydroxymuconate-forming) ]

[EC 3.5.1.120 created 2016, deleted 2017]

EC 3.5.1.121
Accepted name: protein N-terminal asparagine amidohydrolase
Reaction: N-terminal L-asparaginyl-[protein] + H₂O = N-terminal L-aspartyl-[protein] + NH₃
Other name(s): NTAN1 (gene name)
Systematic name: protein N-terminal asparagine amidohydrolase
Comments: This enzyme participates in the eukaryotic ubiquitin-dependent Arg/N-end rule pathway of protein degradation, promoting the turnover of intracellular proteins that initiate with Met-Asn. Following the acetylation and removal of the initiator methionine, the exposed N-terminal asparagine is deaminated, resulting in its conversion to L-aspartate. The latter serves as a substrate for EC 2.3.2.8, arginyltransferase, making the protein susceptible to arginylation, polyubiquitination and degradation as specified by the N-end rule.
References: [2911, 1035, 397]

[EC 3.5.1.121 created 2016]

EC 3.5.1.122
Accepted name: protein N-terminal glutamine amidohydrolase
Reaction: N-terminal L-glutaminyl-[protein] + H₂O = N-terminal L-glutamyl-[protein] + NH₃
Other name(s): NTAQ1 (gene name)
Systematic name: protein N-terminal glutamine amidohydrolase
Comments: This enzyme participates in the eukaryotic ubiquitin-dependent Arg/N-end rule pathway of protein degradation, promoting the turnover of intracellular proteins that initiate with Met-Gln. Following the acetylation and removal of the initiator methionine, the exposed N-terminal glutamine is deaminated, resulting in its conversion to L-glutamate. The latter serves as a substrate for EC 2.3.2.8, arginyltransferase, making the protein susceptible to arginylation, polyubiquitination and degradation as specified by the N-end rule.
References: [3261]

[EC 3.5.1.122 created 2016]

EC 3.5.1.123
Accepted name: \(\gamma\)-glutamylanilide hydrolase
Reaction: \(\text{N}^3\text{-phenyl-L-glutamine} + \text{H}_2\text{O} = \text{L-glutamate} + \text{aniline}\)
Other name(s): atdA2 (gene name)
Systematic name: \(\text{N}^3\text{-phenyl-L-glutamine amidohydrolase}\)
Comments: The enzyme, characterized from the bacterium Acinetobacter sp. YAA, catalyses the opposite reaction from that catalysed by EC 6.3.1.18, \(\gamma\)-glutamylanilide synthase, which is part of an aniline degradation pathway. Its purpose is likely to maintain a low concentration of \(\text{N}^3\text{-phenyl-L-glutamine}\), which is potentially toxic.
References: [2999]

[EC 3.5.1.123 created 2016]
EC 3.5.1.124

Accepted name: protein deglycase

Reaction: (1) an $N^\omega$-(1-hydroxy-2-oxopropyl)-[protein]-L-arginine + H$_2$O = a [protein]-L-arginine + lactate
(2) an $N^6$-(1-hydroxy-2-oxopropyl)-[protein]-L-lysine + H$_2$O = a [protein]-L-lysine + lactate
(3) an $S$-(1-hydroxy-2-oxopropyl)-[protein]-L-cysteine + H$_2$O = a [protein]-L-cysteine + lactate

Other name(s): PARK7 (gene name); DJ-1 protein; $yhbO$ (gene name); $yajL$ (gene name); glyoxylase III (incorrect)

Systematic name: a [protein]-L-amino acid-1-hydroxypropan-2-one hydrolase [(R)-lactate-forming]

Comments: The enzyme, previously thought to be a glyoxalase, acts on glycated L-arginine, L-lysine, and L-cysteine residues within proteins that have been attacked and modified by glyoxal or 2-oxopropanal. The attack forms hemithioacetal in the case of cysteines and aminocarbinols in the case of arginines and lysines. The enzyme repairs the amino acids, releasing glycolate or lactate (70-80% (S)-lactate and 20-30% (R)-lactate), depending on whether the attacking agent was glyoxal or 2-oxopropanal, respectively [2548, 2005].

References: [2027, 2926, 2548, 2005, 2]

[EC 3.5.1.124 created 2016]

EC 3.5.1.125

Accepted name: $N^2$-acetyl-L-2,4-diaminobutanoate deacetylase

Reaction: (2S)-2-acetamido-4-aminobutanoate + H$_2$O = L-2,4-diaminobutanoate + acetate

Other name(s): doeB (gene name)

Systematic name: (2S)-2-acetamido-4-aminobutanoate amidohydrolase

Comments: The enzyme, found in bacteria, has no activity with (2S)-4-acetamido-2-aminobutanoate (cf. EC 3.5.4.44, ectoine hydrolase).

References: [2730]

[EC 3.5.1.125 created 2017]

EC 3.5.1.126

Accepted name: oxamate amidohydrolase

Reaction: oxamate + H$_2$O = oxalate + NH$_3$

Other name(s): HpxW

Systematic name: oxamate amidohydrolase

Comments: The enzyme has been characterized from the bacterium Klebsiella pneumoniae.

References: [1208]

[EC 3.5.1.126 created 2017]

EC 3.5.1.127

Accepted name: jasmonoyl-L-amino acid hydrolase

Reaction: a jasmonoyl-L-amino acid + H$_2$O = jasmonate + an L-amino acid

Other name(s): IAR3 (gene name); ILL4 (gene name); ILL6 (gene name)

Systematic name: jasmonoyl-L-amino acid amidohydrolase

Comments: This entry includes a family of enzymes that recyle jasmonoyl-amino acid conjugates back to jasmonates. The enzymes from Arabidopsis thaliana have been shown to also act on 12-hydroxyjasmonoyl-L-isoleucine, generating tuberonic acid.

References: [3331]

[EC 3.5.1.127 created 2017]

EC 3.5.1.128

Accepted name: deaminated glutathione amidase

References: [3331]
N-(4-oxoglutaryl)-L-cysteinylglycine + H₂O = 2-oxoglutarate + L-cysteinylglycine

Other name(s): dGSH deaminase; NIT1 (gene name)

Systematic name: N-(4-oxoglutaryl)-L-cysteinylglycine amidohydrolase

Comments: The enzyme, present in animals, fungi and bacteria, is involved in clearing cells of the toxic compound deaminated glutathione, which can be produced as an unwanted side product by several transaminases.

References: [2374]

[EC 3.5.1.128 created 2018]

EC 3.5.1.129

Accepted name: N⁵-(cytidine 5′-diphosphoramidyl)-L-glutamine hydrolase

Reaction: N⁵-(cytidine 5′-diphosphoramidyl)-L-glutamine + H₂O = cytidine 5′-diphosphoramidate + L-glutamate

Other name(s): N⁵-(cytidine 5′-diphosphoramidyl)-L-glutamine deacylase

Systematic name: N⁵-(cytidine 5′-diphosphoramidyl)-L-glutamine amidohydrolase

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: [3037]

[EC 3.5.1.129 created 2018]

EC 3.5.1.130

Accepted name: [amino group carrier protein]-lysine hydrolase

Reaction: [amino group carrier protein]-C-terminal-γ-(L-lysyl)-L-glutamate + H₂O = [amino group carrier protein]-C-terminal-L-glutamate + L-lysine

Other name(s): lysK (gene name)

Systematic name: [amino group carrier protein]-C-terminal-γ-L-lysyl-L-glutamate amidohydrolase

Comments: The enzyme participates in an L-lysine biosynthetic pathway in certain species of archaea and bacteria. In some organisms the enzyme also catalyses the activity of EC 3.5.1.132, [amino group carrier protein]-ornithine hydrolase.

References: [1251, 2328, 3458, 906]

[EC 3.5.1.130 created 2019]

EC 3.5.1.131

Accepted name: 1-carboxybiuret hydrolase

Reaction: 1-carboxybiuret + H₂O = urea-1,3-dicarboxylate + NH₃

Other name(s): atzEG (gene names)

Systematic name: 1-carboxybiuret amidohydrolase

Comments: The enzyme, characterized from the bacterium Pseudomonas sp. ADP, participates in the degradation of cyanuric acid, an intermediate in the degradation of s-triazine herbicides such as atrazine [2-chloro-4-(ethylamino)-6-(isopropylamino)-1,3,5-triazine]. The enzyme is a heterotetramer composed of a catalytic subunit (AtzE) and an accessory subunit (AtzG) that stabilizes the complex.

References: [766]

[EC 3.5.1.131 created 2019]

EC 3.5.1.132

Accepted name: [amino group carrier protein]-ornithine hydrolase

Reaction: [amino group carrier protein]-C-terminal-γ-(L-ornithyl)-L-glutamate + H₂O = [amino group carrier protein]-C-terminal-L-glutamate + L-ornithine
**Other name(s):** lysK (gene name)
**Systematic name:** [amino group carrier protein]-C-terminal-$\gamma$-L-ornithyl-L-glutamate amidohydrolase
**Comments:** The enzyme participates in an L-arginine biosynthetic pathways in certain species of archaea and bacteria. In all cases known so far the enzyme also catalyses the activity of EC 3.5.1.130, [amino group carrier protein]-lysine hydrolase.

**References:** [2328, 3458]

[EC 3.5.1.132 created 2019]

**EC 3.5.1.133**
**Accepted name:** $N^\alpha$-acyl-L-glutamine aminoacylase
**Reaction:** an $N^\alpha$-acyl-L-glutamine + $H_2O$ = L-glutamine + a carboxylate
**Other name(s):** agaA (gene name); axillary malodor releasing enzyme; AMRE
**Systematic name:** $N^\alpha$-acyl-L-glutamine amidohydrolase (carboxylate-forming)
**Comments:** Requires Zn$^{2+}$. The enzyme, characterized from the bacterium Corynebacterium sp. AxB0, hydrolyses odorless $N^\alpha$-acyl-L-glutamine conjugates of short- and medium-chain fatty acids, releasing axillary malodor compounds. While the enzyme is highly specific for the L-glutamine moiety, it is quite promiscuous regarding the acyl moiety. The two most common products of the enzyme’s activity in axillary secretions are $(2E)$-3-methylhex-2-enoate and 3-hydroxy-3-methylhexanoate.

**References:** [2163, 2162, 2161]

[EC 3.5.1.133 created 2019]

**EC 3.5.1.134**
**Accepted name:** (indol-3-yl)acetyl-L-aspartate hydrolase
**Reaction:** (indol-3-yl)acetyl-L-aspartate + $H_2O$ = (indol-3-yl)acetate + L-aspartate
**Other name(s):** indole-3-acetyl-L-aspartate hydrolase; iaaspH (gene name)
**Systematic name:** (indol-3-yl)acetyl-L-aspartate amidohydrolase
**Comments:** The enzyme, isolated from the bacterium Pantoea agglomerans, is specific for its substrate and does not act efficiently on other indole-3-acetate conjugates.

**References:** [477, 478]

[EC 3.5.1.134 created 2019]

**EC 3.5.1.135**
**Accepted name:** $N^4$-acetylcytidine amidohydrolase
**Reaction:** $N^4$-acetylcytidine + $H_2O$ = cytidine + acetate
**Other name(s):** yqfB (gene name)
**Systematic name:** $N^4$-acetylcytidine amidohydrolase
**Comments:** The enzyme from the bacterium Escherichia coli is one of the smallest known monomeric amidohydrolases (103-amino acids). The enzyme is active towards a wide range of $N^4$-acylcytosines/cytidines, but is by far most active against $N^4$-acetylcytidine.

**References:** [2761, 2895]

[EC 3.5.1.135 created 2020]

**EC 3.5.1.136**
**Accepted name:** $N,N'$-diacetylchitobiose non-reducing end deacetylase
**Reaction:** $N,N'$-diacetylchitobiose + $H_2O = \beta-D$-glucosaminyl-(1$\rightarrow$4)-$N$-acyl-$D$-glucosamine + acetate
**Other name(s):** diacetylchitobiose deacetylase (ambiguous); cda (gene name)
**Systematic name:** $N,N'$-diacetylchitobiose non-reducing end acetylhydrolase

293
Comments: The enzyme, characterized from the archaeons *Thermococcus kodakarensis* and *Pyrococcus horikoshii*, deacetylates the non-reducing residue of \(N,N'\)-diacetylchitobiose, the end product of the archaeal chitinase, to produce \(\beta\)-D-glucosaminyl-(1→4)-N-acetyl-D-glucosamine. This is in contrast to EC 3.5.1.105, chitin disaccharide deacetylase, which deacetylates \(N,N'\)-diacetylchitobiose at the reducing residue to produce \(N\)-acetyl-\(\beta\)-D-glucosaminyl-(1→4)-D-glucosamine.

References: [3014, 2022, 2152]

[EC 3.5.1.136 created 2020]

**EC 3.5.1.137**

**Accepted name:** \(N\)-methylcarbamate hydrolase

**Reaction:** an \(N\)-methyl carbamate ester + \(H_2O = \) an alcohol + methylamine + \(CO_2\)

**Other name(s):** *mcbA* (gene name); *cehA* (gene name); *cfdJ* (gene name); carbaryl hydrolase; carbofuran hydrolase

**Systematic name:** \(N\)-methyl carbamate ester hydrolase

**Comments:** The enzyme catalyses the first step in the degradation of several carbamate insecticides such as carbarly, carbofuran, isoprocarb, propoxur, aldicarb and oxamyl. It catalyses the cleavage of the ester bond to release \(N\)-methylcarbamate, which spontaneously hydrolyses to methylamine and \(CO_2\). The enzymes from several Gram-negative bacteria were shown to be located in the periplasm.

References: [2094, 1156, 433, 1155, 1132, 3492, 2330, 1455, 3410, 1403]

[EC 3.5.1.137 created 2021]

**EC 3.5.2 In cyclic amides**

**EC 3.5.2.1**

**Accepted name:** barbiturase

**Reaction:** barbiturate + \(H_2O = 3\)-oxo-3-ureidopropanoate

**Systematic name:** barbiturate amidohydrolase (3-oxo-3-ureidopropanoate-forming)

**Comments:** Contains zinc and is specific for barbiturate as substrate [2863]. Forms part of the oxidative pyrimidine-degrading pathway in some microorganisms, along with EC 1.17.99.4 (uracil/thymine dehydrogenase) and EC 3.5.1.95 (N-malonylurea hydrolase). It was previously thought that the end-products of the reaction were malonate and urea but this has since been disproved [2864]. May be involved in the regulation of pyrimidine metabolism, along with EC 2.4.2.9, uracil phosphoribosyltransferase.

References: [1147, 2864, 2863]

[EC 3.5.2.1 created 1961, modified 2006]

**EC 3.5.2.2**

**Accepted name:** dihydropyrimidinase

**Reaction:** 5,6-dihydrouracil + \(H_2O = 3\)-ureidopropanoate

**Other name(s):** hydantoinase; hydoppyrimidine hydrase; hydantoin peptidase; pyrimidine hydrase; \(D\)-hydantoinase

**Systematic name:** 5,6-dihydropyrimidine amidohydrolase

**Comments:** Also acts on dihydrothymine and hydantoin.

References: [334, 717]

[EC 3.5.2.2 created 1961]

**EC 3.5.2.3**

**Accepted name:** dihydroorotase

**Reaction:** (\(S\))-dihydroorotate + \(H_2O = N\)-carbamoyl-L-aspartate

**Other name(s):** carbamoylaspartic dehydrase; dihydroorotate hydrolase
Systematic name: (S)-dihydroorotate amidohydrolase

References: [524, 1774]

[EC 3.5.2.3 created 1961]

**EC 3.5.2.4**
Accepted name: carboxymethylhydantoinase
Reaction: L-5-carboxymethylhydantoin + H₂O = N-carbamoyl-L-aspartate
Other name(s): hydantoin hydrolase
Systematic name: L-5-carboxymethylhydantoin amidohydrolase

References: [1774]

[EC 3.5.2.4 created 1961]

**EC 3.5.2.5**
Accepted name: allantoinase
Reaction: (S)-allantoin + H₂O = allantoate
Systematic name: (S)-allantoin amidohydrolase

References: [838]

[EC 3.5.2.5 created 1961]

**EC 3.5.2.6**
Accepted name: β-lactamase
Reaction: a β-lactam + H₂O = a substituted β-amino acid
Other name(s): penicillinase; cephalosporinase; neutrapen; penicillin β-lactamase; exopenicillinase; ampicillinase; penicillin amido-β-lactamhydrolase; penicillinase I; penicillinase II; β-lactamase I; β-lactamase II; β-lactamase III; β-lactamase A; β-lactamase B; β-lactamase C; β-lactamase AME I; cephaparin β-lactamase; carbapenemase
Systematic name: β-lactam hydrolase
Comments: A group of enzymes of varying specificity hydrolysing β-lactams; some act more rapidly on penicillins, some more rapidly on cephalosporins. The latter were formerly listed as EC 3.5.2.8, cephalosporinase.
References: [493, 1181, 1669, 2424, 2425, 2589]

[EC 3.5.2.6 created 1961, modified 1981 (EC 3.5.2.8 created 1972, incorporated 1978)]

**EC 3.5.2.7**
Accepted name: imidazolonepropionase
Reaction: (S)-3-(5-oxo-4,5-dihydro-3H-imidazol-4-yl)propanoate + H₂O = N-formimidoyl-L-glutamate + H⁺
Other name(s): 4-(5)-imidazolone-5(4)-propionic acid hydrolase; imidazolone propionic acid hydrolase
Systematic name: 3-(5-oxo-4,5-dihydro-3H-imidazol-4-yl)propanoate amidohydrolase

References: [2496, 2845]

[EC 3.5.2.7 created 1965, modified 2001]

**3.5.2.8** Deleted entry. cephalosporinase. Now included with EC 3.5.2.6 β-lactamase

[EC 3.5.2.8 created 1972, deleted 1978]

**EC 3.5.2.9**
Accepted name: 5-oxoprolinase (ATP-hydrolysing)
Reaction: \[ \text{ATP} + 5\text{-oxo-L-proline} + 2\text{H}_2\text{O} = \text{ADP} + \text{phosphate} + \text{L-glutamate} \]

Other name(s): pyroglutamase (ATP-hydrolysing); oxoprolinase; pyroglutamase; 5-oxoprolinase; pyroglutamate hydrolase; pyroglutamic hydrolase; L-5-pyroglutamate hydrolase; 5-oxo-L-prolinase; pyroglutamase

Systematic name: 5-oxo-L-proline amidohydrolase (ATP-hydrolysing)

References: [3192]

[EC 3.5.2.9 created 1976]

EC 3.5.2.10

Accepted name: creatininase

Reaction: creatinine + H\text{2}O = creatine

Other name(s): creatinine hydrolase

Systematic name: creatinine amidohydrolase

References: [3136]

[EC 3.5.2.10 created 1978]

EC 3.5.2.11

Accepted name: L-lysine-lactamase

Reaction: (S)-2-aminohexano-6-lactam + H\text{2}O = L-lysine

Other name(s): L-\alpha-aminocaprolactam hydrolase; L-lysinamidase; L-lysine-1,6-lactam lactamhydrolase

Systematic name: (S)-2-aminohexano-6-lactam lactamhydrolase

Comments: Also hydrolyses L-lysinamide.

References: [915, 2787]

[EC 3.5.2.11 created 1981, modified 1989]

EC 3.5.2.12

Accepted name: 6-aminohexanoate-cyclic-dimer hydrolase

Reaction: 1,8-diazacyclotetradecane-2,9-dione + H\text{2}O = N-(6-aminohexanoyl)-6-aminohexanoate

Systematic name: 1,8-diazacyclotetradecane-2,9-dione lactamhydrolase

Comments: The cyclic dimer of 6-aminohexanoate is converted to the linear dimer.

References: [1546]

[EC 3.5.2.12 created 1983]

EC 3.5.2.13

Accepted name: 2,5-dioxopiperazine hydrolase

Reaction: 2,5-dioxopiperazine + \text{H}_2\text{O} = \text{glycylglycine}

Other name(s): cyclo(Gly-Gly) hydrolase; cyclo(glycylglycine) hydrolase

Systematic name: 2,5-dioxopiperazine amidohydrolase

Comments: Highly specific; does not hydrolyse other dioxopiperazines, glycylglycine, proteins or barbiturates.

References: [2960]

[EC 3.5.2.13 created 1989]

EC 3.5.2.14

Accepted name: N-methylhydantoinase (ATP-hydrolysing)

Reaction: ATP + N-methylhydantoin + 2\text{H}_2\text{O} = \text{ADP} + \text{phosphate} + \text{N-carbamoylsarcosine}

Other name(s): N-methylhydantoin amidohydrolase; methylhydantoin amidase; N-methylhydantoin hydrolase; N-methylhydantoinase; N-methylimidazolidine-2,4-dione amidohydrolase (ATP-hydrolysing)

Systematic name: N-methylhydantoin amidohydrolase (ATP-hydrolysing)

References: [2960]
Accepted name: cyanuric acid amidohydrolase  
Reaction: cyanuric acid + H₂O = 1-carboxybiuret  
Other name(s): atzD (gene name); trzD (gene name)  
Systematic name: cyanuric acid amidohydrolase  
Comments: The enzyme catalyses the ring cleavage of cyanuric acid, an intermediate in the degradation of s-triazide herbicides such as atrazine [2-chloro-4-(ethylamino)-6-(isopropylamino)-1,3,5-triazine]. The enzyme is highly specific for cyanuric acid. The product was initially thought to be biuret, but was later shown to be 1-carboxybiuret.

References: [720, 719, 1473, 876, 766]  

[EC 3.5.2.15 created 2000, modified 2008, modified 2019]
EC 3.5.2.19
Accepted name: streptothricin hydrolase
Reaction: streptothricin-F + H₂O = streptothricin-F acid
Other name(s): sttH (gene name)
Systematic name: streptothricin-F hydrolase
Comments: The enzyme also catalyses the hydrolysis of streptothricin-D to streptothricin-D acid [1923]. The enzyme is responsible for streptothricin resistance in *Streptomyces albulus* and *Streptomyces noursei* [1923, 1094].
References: [1923, 1094]

EC 3.5.2.20
Accepted name: isatin hydrolase
Reaction: isatin + H₂O = isatinate
Systematic name: isatin amidohydrolase
Comments: Requires Mn²⁺. This enzyme, found in several bacterial species, is involved in the degradation of indole-3-acetic acid.
References: [2853, 250]

EC 3.5.3 In linear amidines

EC 3.5.3.1
Accepted name: arginase
Reaction: L-arginine + H₂O = L-ornithine + urea
Other name(s): arginine amidinase; canavanase; L-arginase; arginine transamidinase
Systematic name: L-arginine amidinohydrolase
Comments: Also hydrolyses α-N-substituted L-arginines and canavanine.
References: [126, 374, 709, 1026, 1027]

EC 3.5.3.2
Accepted name: guanidinoacetase
Reaction: guanidinoacetate + H₂O = glycine + urea
Other name(s): glycocyaminase
Systematic name: guanidinoacetate amidinohydrolase
Comments: Requires Mn²⁺.
References: [2571, 3456]

EC 3.5.3.3
Accepted name: creatinase
Reaction: creatine + H₂O = sarcosine + urea
Systematic name: creatine amidinohydrolase
References: [2571, 3464]
EC 3.5.3.4
Accepted name: allantoicase
Reaction: allantoate + H₂O = (S)-ureidoglycolate + urea
Systematic name: allantoate amidinohydrolase
Comments: Also hydrolyses (R)-ureidoglycolate to glyoxylate and urea.
References: [838, 3109, 3187, 2611]

EC 3.5.3.5
Accepted name: formimidoylaspartate deiminase
Reaction: N-formimidoyl-L-aspartate + H₂O = N-formyl-L-aspartate + NH₃
Other name(s): formiminoaspartate deiminase
Systematic name: N-formimidoyl-L-aspartate iminohydrolase
References: [1151]

EC 3.5.3.6
Accepted name: arginine deiminase
Reaction: L-arginine + H₂O = L-citrulline + NH₃
Other name(s): arginine dihydrolase; citrulline iminase; L-arginine deiminase
Systematic name: L-arginine iminohydrolase
Comments: Also acts on canavanine.
References: [2261, 2387, 2501]

EC 3.5.3.7
Accepted name: guanidinobutyrase
Reaction: 4-guanidinobutanoate + H₂O = 4-aminobutanoate + urea
Other name(s): γ-guanidinobutyrase; 4-guanidinobutyrate amidinobutyrase; γ-guanidinobutyrate amidinohydrolase; G-Base; GBH; guanidinobutyrate ureahydrolase
Systematic name: 4-guanidinobutanoate amidinohydrolase
Comments: Requires Mn²⁺. Also acts, very slowly, on 5-guanidinopentanoate and 6-guanidinohexanoate.
References: [2060, 3053, 3453, 3454]

EC 3.5.3.8
Accepted name: formimidoylglutamase
Reaction: N-formimidoyl-L-glutamate + H₂O = L-glutamate + formamide
Other name(s): formiminoglutamase; N-formiminoglutamate hydrolase; N-formimino-L-glutamate formiminohydrolase
Systematic name: N-formimidoyl-L-glutamate formimidoylhydrolase
References: [1456, 1850]

[EC 3.5.3.3 created 1961]

[EC 3.5.3.4 created 1961]

[EC 3.5.3.5 created 1961, modified 2000]

[EC 3.5.3.6 created 1961]

[EC 3.5.3.7 created 1972]

[EC 3.5.3.8 created 1972, modified 2000, modified 2001]
EC 3.5.3.9
Accepted name: allantoate deiminase
Reaction: allantoate + H₂O = (S)-ureidoglycine + NH₃ + CO₂
Other name(s): allantoate amidohydrolase
Systematic name: allantoate amidinohydrolase (decarboxylating)
Comments: This enzyme is part of the ureide pathway, which permits certain organisms to recycle the nitrogen in purine compounds. This enzyme, which liberates ammonia from allantoate, is present in plants and bacteria. In plants it is localized in the endoplasmic reticulum. Requires manganese.
References: [3225, 2746]

[EC 3.5.3.9 created 1972, modified 2010]

EC 3.5.3.10
Accepted name: D-arginase
Reaction: D-arginine + H₂O = D-ornithine + urea
Systematic name: D-arginine amidinohydrolase
References: [2124]

[EC 3.5.3.10 created 1972]

EC 3.5.3.11
Accepted name: agmatinase
Reaction: agmatine + H₂O = putrescine + urea
Other name(s): agmatine ureohydrolase; SpeB
Systematic name: agmatine amidinohydrolase
References: [1223, 3215]

[EC 3.5.3.11 created 1972]

EC 3.5.3.12
Accepted name: agmatine deiminase
Reaction: agmatine + H₂O = N-carbamoylputrescine + NH₃
Other name(s): agmatine amidinohydrolase
Systematic name: agmatine iminohydrolase
Comments: The plant enzyme also catalyses the reactions of EC 2.1.3.3 (ornithine carbamoyltransferase), EC 2.1.3.6 (putrescine carbamoyltransferase) and EC 2.7.2.2 (carbamate kinase), thus functioning as a putrescine synthase, converting agmatine and ornithine into putrescine and citrulline, respectively.
References: [2841, 2891]

[EC 3.5.3.12 created 1972]

EC 3.5.3.13
Accepted name: formimidoylglutamate deiminase
Reaction: N-formimidoyl-L-glutamate + H₂O = N-formyl-L-glutamate + NH₃
Other name(s): formiminoglutamate deiminase; formiminoglutamic iminohydrolase
Systematic name: N-formimidoyl-L-glutamate iminohydrolase
References: [3330]

[EC 3.5.3.13 created 1975, modified 2000]

EC 3.5.3.14
Accepted name: amidinoaspartase

300
Reaction: \( N\text{-amidino-L-aspartate} + H_2O = \text{L-aspartate} + \text{urea} \)

Other name(s): amidinoaspartic amidinohydrolase

Systematic name: \( N\text{-amidino-L-aspartate amidinohydrolase} \)

Comments: Also acts slowly on \( N\text{-amidino-L-glutamate} \).

References: [2017]

[EC 3.5.3.14 created 1976]

**EC 3.5.3.15**

Accepted name: protein-arginine deiminase

Reaction: protein \( \text{L-arginine} + H_2O = \text{protein \ L-citrulline} + \text{NH}_3 \)

Other name(s): peptidylarginine deiminase; PAD

Systematic name: protein-\( \text{L-arginine iminohydrolase} \)

Comments: Also acts on \( N\text{-acyl-\ L-arginine} \) and, more slowly, on \( \text{L-arginine esters} \).

References: [899]

[EC 3.5.3.15 created 1983]

**EC 3.5.3.16**

Accepted name: methylguanidinase

Reaction: methylguanidine + \( H_2O = \text{methylamine} + \text{urea} \)

Other name(s): methylguanidine hydrolase

Systematic name: methylguanidine amidinohydrolase

Comments: Acts on some other alkylguanidines, but very slowly.

References: [2141]

[EC 3.5.3.16 created 1984]

**EC 3.5.3.17**

Accepted name: guanidinopropionase

Reaction: 3-guanidinopropanoate + \( H_2O = \beta\text{-alanine} + \text{urea} \)

Other name(s): GPase; GPH

Systematic name: 3-guanidinopropanoate amidinopropionase

Comments: Requires Mn\(^{2+}\). Also acts, more slowly, on taurocyamine and 4-guanidinobutanoate.

References: [3455]

[EC 3.5.3.17 created 1989]

**EC 3.5.3.18**

Accepted name: dimethylargininase

Reaction: \( N^{\omega},N^{\omega'}\text{-dimethyl-L-arginine} + H_2O = \text{dimethylamine} + \text{L-citrulline} \)

Other name(s): dimethylarginine dimethylaminohydrolase; \( N^{G},N^{G'}\text{-dimethylarginine dimethylaminohydrolase} \);
\( N^{G},N^{G'}\text{-dimethyl-L-arginine dimethylamidohydrolase} \); \( \omega,\omega'-\text{di-}N\text{-methyl-L-arginine dimethylamidohydrolase} \); \( N^{\omega},N^{\omega'}\text{-methyl-L-arginine dimethylamidohydrolase} \) (incorrect)

Systematic name: \( N^{\omega},N^{\omega'}\text{-dimethyl-L-arginine dimethylamidohydrolase} \)

Comments: Also acts on \( N^{\omega}\text{-methyl-L-arginine} \).

References: [2259]

[EC 3.5.3.18 created 1992]

**3.5.3.19** Transferred entry. ureidoglycolate hydrolase. Now EC 3.5.1.116, ureidoglycolate amidohydrolase

[EC 3.5.3.19 created 1992, deleted 2014]

301
EC 3.5.3.20

Accepted name: diguanidinobutanase
Reaction: 1,4-diguanidinobutane + H₂O = agmatine + urea
Systematic name: 1,4-diguanidinobutane amidinohydrolase
Comments: Other diguanidinoalkanes with 3 to 10 methylene groups can also act, but more slowly.
References: [3452]

[EC 3.5.3.20 created 1992]

EC 3.5.3.21

Accepted name: methylenediurea deaminase
Reaction: methylenediurea + 2 H₂O = N-(hydroxymethyl)urea + 2 NH₃ + CO₂ (overall reaction)
(1a) methylenediurea + H₂O = N-(carboxyaminomethyl)urea + NH₃
(1b) N-(carboxyaminomethyl)urea = N-(aminomethyl)urea + CO₂ (spontaneous)
(1c) N-(aminomethyl)urea + H₂O = N-(hydroxymethyl)urea + NH₃ (spontaneous)
Other name(s): methylenediurease
Systematic name: methylenediurea aminohydrolase
Comments: Methylendiamine is hydrolysed and decarboxylated to give an aminated methyleneurea, which then spontaneously hydrolyses to hydroxymethylurea. The enzyme from Ochrobactrum anthropi also hydrolyses dimethylenetriurea and trimethylenetetraurea as well as ureidoglycolate, which is hydrolysed to urea and glyoxylate, and allantoate, which is hydrolysed to ureidoglycolate, ammonia and carbon dioxide.
References: [1376]

[EC 3.5.3.21 created 1999]

EC 3.5.3.22

Accepted name: proclavaminate amidinohydrolase
Reaction: amidinoproclavaminate + H₂O = proclavaminate + urea
Other name(s): PAH; proclavaminate amidino hydrolase
Systematic name: amidinoproclavaminate amidinohydrolase
Comments: Forms part of the pathway for the biosynthesis of the β-lactamase inhibitor clavulanate in Streptomyces clavuligerus. It carries out an intermediary reaction between the first reaction of EC 1.14.11.21, clavaminate synthase, and the second and third reactions of that enzyme. Requires Mn²⁺.
References: [2637, 3503, 3099, 3376]

[EC 3.5.3.22 created 2003]

EC 3.5.3.23

Accepted name: N-succinylarginine dihydrolase
Reaction: N²-succinyl-L-arginine + 2 H₂O = N²-succinyl-L-ornithine + 2 NH₃ + CO₂
Other name(s): N²-succinylarginine dihydrolase; arginine succinylhydrolase; SADH; AruB; AstB; 2-N-succinyl-L-arginine iminohydrolase (decarboxylating)
Systematic name: N²-succinyl-L-arginine inomohydrolase (decarboxylating)
Comments: Arginine, N²-acetylarginine and N²-glutamylarginine do not act as substrates [3291]. This is the second enzyme in the arginine succinyltransferase (AST) pathway for the catabolism of arginine [2707]. 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).
References: [2707, 3069, 3291, 559, 1355]

[EC 3.5.3.23 created 2006]
EC 3.5.3.24

Accepted name: \( N^1 \)-aminopropylagmatine ureohydrolase

Reaction: \( N^1 \)-aminopropylagmatine + \( \text{H}_2\text{O} = \text{spermidine} + \text{urea} \)

Systematic name: \( N^1 \)-aminopropylagmatine amidinohydrolase

Comments: The enzyme, which has been characterized from the hyperthermophilic archaeon *Pyrococcus kodakarensis* and the thermophilic Gram-negative bacterium *Thermus thermophilus*, is involved in the biosynthesis of spermidine.

References: [2273, 2076]

[EC 3.5.3.24 created 2013]

EC 3.5.3.25

Accepted name: \( N^\omega \)-hydroxy-L-arginine amidinohydrolase

Reaction: \( N^\omega \)-hydroxy-L-arginine + \( \text{H}_2\text{O} = \text{L-ornithine} + \text{hydroxyurea} \)

Systematic name: \( N^\omega \)-hydroxy-L-arginine amidinohydrolase

Comments: The enzyme participates in the biosynthetic pathway of D-cycloserine, an antibiotic substance produced by several *Streptomyces* species.

References: [1637, 1638]

[EC 3.5.3.25 created 2013]

EC 3.5.3.26

Accepted name: (S)-ureidoglycine aminohydrolase

Reaction: (S)-2-ureidoglycine + \( \text{H}_2\text{O} = (S)-\text{ureidoglycolate} + \text{NH}_3 \)

Other name(s): UGlyAH; UGHY; \( \text{ylbA} \) (gene name)

Systematic name: (S)-ureidoglycine aminohydrolase

Comments: Binds Mn\(^{2+}\). This enzyme, found in plants and bacteria, is part of the ureide pathway, which enables the recycling of the nitrogen in purine compounds. In plants it is localized in the endoplasmic reticulum.

References: [2746, 3314, 2773]

[EC 3.5.3.26 created 2013]

EC 3.5.4 In cyclic amidines

EC 3.5.4.1

Accepted name: cytosine deaminase

Reaction: cytosine + \( \text{H}_2\text{O} = \text{uracil} + \text{NH}_3 \)

Other name(s): isocytosine deaminase

Systematic name: cytosine aminohydrolase

Comments: Also acts on 5-methylcytosine.

References: [505, 1621]

[EC 3.5.4.1 created 1961]

EC 3.5.4.2

Accepted name: adenine deaminase

Reaction: adenine + \( \text{H}_2\text{O} = \text{hypoxanthine} + \text{NH}_3 \)

Other name(s): adеназе; adenine aminase; ADase

Systematic name: adenine aminohydrolase

References: [268, 1193]
EC 3.5.4.3
Accepted name: guanine deaminase
Reaction: guanine + H₂O = xanthine + NH₃
Other name(s): guanase; guanine aminase; GAH
Systematic name: guanine aminohydrolase
References: [1224, 1444, 2467]

EC 3.5.4.4
Accepted name: adenine deaminase
Reaction: (1) adenosine + H₂O = inosine + NH₃
(2) 2′-deoxyadenosine + H₂O = 2′-deoxyinosine + NH₃
Other name(s): deoxyadenosine deaminase
Systematic name: adenine aminohydrolase
Comments: The enzyme, found in a wide variety of microorganisms, plants, invertebrates, and animals, plays a role in purine metabolism.
References: [1472, 2438, 2808, 546]

EC 3.5.4.5
Accepted name: cytosine deaminase
Reaction: (1) cytidine + H₂O = uridine + NH₃
(2) 2′-deoxycytidine + H₂O = 2′-deoxyuridine + NH₃
Other name(s): cytosine nucleoside deaminase; (deoxy)cytidine deaminase; cdd (gene name); CDA (gene name)
Systematic name: cytidine/2′-deoxycytidine aminohydrolase
Comments: Contains zinc. Catalyses the deamination of cytidine and 2′-deoxycytidine with similar efficiencies. The enzyme, which is widely distributed among organisms, is involved in salvage of both exogenous and endogenous cytidine and 2′-deoxycytidine for UMP synthesis.
References: [2561, 3271, 2854, 1683, 3218]

EC 3.5.4.6
Accepted name: AMP deaminase
Reaction: AMP + H₂O = IMP + NH₃
Other name(s): adenyllic acid deaminase; AMP aminase; adenyllic deaminase; adenylate deaminase; 5-AMP deaminase; adenosine 5-monophosphate deaminase; 5-adenylate deaminase; adenyln deaminase; 5-adenylic acid deaminase; adenosine monophosphate deaminase; adenylate aminohydrolase; adenylate deaminase; adenosine 5-phosphate aminohydrolase; 5-adenylate deaminase
Systematic name: AMP aminohydrolase
Comments: cf. EC 3.5.4.17 adenosine-phosphate deaminase.
References: [1444, 1725, 1726, 1727, 1982, 3147, 3304]

EC 3.5.4.7
Accepted name: ADP deaminase
Reaction: ADP + H₂O = IDP + NH₃
Other name(s): adenosine diphosphate deaminase; adenosinepyrophosphate deaminase
Systematic name: ADP aminohydrolase
References: [637]

[EC 3.5.4.7 created 1961]

**EC 3.5.4.8**

Accepted name: aminomidazolase
Reaction: 4-aminimidazole + H₂O = imidazol-4-one + NH₃
Other name(s): 4-aminimidazole hydrolase; 4-aminimidazole deaminase
Systematic name: 4-aminimidazole aminohydrolase
Comments: Requires Fe²⁺. This enzyme forms part of the xanthine-degradation pathway in some bacteria. The product of the reaction, imidazol-4-one, can be converted non-enzymically into formiminoglycine. An enzyme has been identified in *Clostridium cylindrosorum* that can perform this hydrolysis reaction [863, 3226].
References: [2468, 863, 3226, 620]

[EC 3.5.4.8 created 1961]

**EC 3.5.4.9**

Accepted name: methenyltetrahydrofolate cyclohydrolase
Reaction: 5,10-methenyltetrahydrofolate + H₂O = 10-formyltetrahydrofolate
Other name(s): Citrovorum factor cyclodehydrase; cyclohydrolase; formyl-methenyl-methylenetetrahydrofolate synthetase (combined); 5,10-methenyltetrahydrofolate 5-hydrolase (decelyzing)
Systematic name: 5,10-methenyltetrahydrofolate 5-hydrolase (ring-opening)
Comments: In eukaryotes, the enzyme occurs as a trifunctional enzyme that also has methylenetetrahydrofolate dehydrogenase (NADP⁺) (EC 1.5.1.5) and formate—tetrahydrofolate ligase (EC 6.3.4.3) activity. In some prokaryotes, it occurs as a bifunctional enzyme that also has dehydrogenase (EC 1.5.1.5) activity or formimidoyltetrahydrofolate cyclodeaminase (EC 4.3.1.4) activity.
References: [2469, 2969]

[EC 3.5.4.9 created 1961]

**EC 3.5.4.10**

Accepted name: IMP cyclohydrolase
Reaction: IMP + H₂O = 5-formamido-1-(5-phospho-D-ribosyl)imidazole-4-carboxamide
Other name(s): inosinicase; inosinate cyclohydrolase; IMP 1,2-hydrolase (decelyzing)
Systematic name: IMP 1,2-hydrolase (ring-opening)
References: [832]

[EC 3.5.4.10 created 1961, modified 2000]

**EC 3.5.4.11**

Accepted name: pterin deaminase
Reaction: a 2-amino-4-hydroxypteridine + H₂O = a 2,4-dihydroxypteridine + NH₃
Other name(s): atrasinase
Systematic name: 2-amino-4-hydroxypteridine aminohydrolase
Comments: The animal enzyme is specific for pterin, isoxanthopterin and tetrahydropterin.
References: [1745, 2531]

[EC 3.5.4.11 created 1965]
EC 3.5.4.12
Accepted name: dCMP deaminase
Reaction: dCMP + H$_2$O = dUMP + NH$_3$
Other name(s): deoxyctydylate deaminase; deoxy-CMP-deaminase; deoxycytidylate aminohydrolase; deoxycytidine monophosphate deaminase; deoxycytidine-5’-phosphate deaminase; deoxycytidine-5’-monophosphate aminohydrolase
Systematic name: dCMP aminohydrolase
Comments: Also acts on some 5-substituted dCMPs.
References: [2682, 2683, 2745]
[EC 3.5.4.12 created 1965]

EC 3.5.4.13
Accepted name: dCTP deaminase
Reaction: dCTP + H$_2$O = dUTP + NH$_3$
Other name(s): deoxyctydylate triphosphate deaminase; 5-methyl-dCTP deaminase
Systematic name: dCTP aminohydrolase
References: [3078]
[EC 3.5.4.13 created 1972]

[3.5.4.14 Transferred entry. deoxycytidine deaminase. Now included in EC 3.5.4.5, (deoxy)cytidine deaminase]

[EC 3.5.4.14 created 1972, transferred 2013 to EC 3.5.4.5., deleted 2013]

EC 3.5.4.15
Accepted name: guanosine deaminase
Reaction: guanosine + H$_2$O = xanthosine + NH$_3$
Other name(s): guanosine aminase
Systematic name: guanosine aminohydrolase
References: [1342]
[EC 3.5.4.15 created 1972]

EC 3.5.4.16
Accepted name: GTP cyclohydrolase I
Reaction: GTP + H$_2$O = formate + 7,8-dihydroneopterin 3’-triphosphate
Other name(s): GTP cyclohydrolase; guanosine triphosphate cyclohydrolase; guanosine triphosphate 8-deformylase; dihydroneopterin triphosphate synthase; GTP 8-formylhydrolase
Systematic name: GTP 7,8-8,9-dihydrolase
Comments: The reaction involves hydrolysis of two C-N bonds and isomerization of the pentose unit; the recylization may be non-enzymic. This enzyme is involved in the de novo synthesis of tetrahydrobiopterin from GTP, with the other enzymes involved being EC 1.1.1.153 (sepiapterin reductase) and EC 4.2.3.12 (6-pyruvoyltetrahydropterin synthase) [2947].
References: [355, 3362, 2947]
[EC 3.5.4.16 created 1972]

EC 3.5.4.17
Accepted name: adenosine-phosphate deaminase
Reaction: (1) AMP + H$_2$O = IMP + NH$_3$
(2) ADP + H$_2$O = IDP + NH$_3$
(3) ATP + H$_2$O = ITP + NH$_3$

306
Other name(s): adenylate deaminase; adenine nucleotide deaminase; adenosine (phosphate) deaminase  
Systematic name: adenosine-phosphate aminohydrolase  
Comments: Acts on AMP, ADP, ATP, NAD$^+$ and adenosine, in decreasing order of activity. The bacterial enzyme can also accept the deoxy derivatives. cf. EC 3.5.4.6, AMP deaminase.  
References: [2925, 3436]

[EC 3.5.4.17 created 1972, modified 1980, modified 2014]

EC 3.5.4.18  
Accepted name: ATP deaminase  
Reaction: ATP + H$_2$O = ITP + NH$_3$  
Other name(s): adenosine triphosphate deaminase  
Systematic name: ATP aminohydrolase  
References: [489]

[EC 3.5.4.18 created 1972]

EC 3.5.4.19  
Accepted name: phosphoribosyl-AMP cyclohydrase  
Reaction: 1-[(5-phospho-$\beta$-D-ribosyl)-AMP + H$_2$O = 1-[(5-phospho-$\beta$-D-ribosylamino)methylideneamino]imidazole-4-carboxamide  
Other name(s): PRAMP-cyclohydrase; phosphoribosyladenosine monophosphate cyclohydrase; 1-(5-phospho-D-ribosyl)-AMP 1,6-hydrolase  
Systematic name: 1-(5-phospho-$\beta$-D-ribosyl)-AMP 1,6-hydrolase  
Comments: The *Neurospora crassa* enzyme also catalyses the reactions of EC 1.1.1.23 (histidinol dehydrogenase) and EC 3.6.1.31 (phosphoribosyl-ATP diphosphatase).  
References: [2024]

[EC 3.5.4.19 created 1972, modified 1976, modified 1981, modified 2000]

EC 3.5.4.20  
Accepted name: pyrithiamine deaminase  
Reaction: 1-[(4-amino-2-methylpyrimid-5-ylmethyl)-3-(2-hydroxyethyl)-2-methylpyridinium + H$_2$O = 1-[(4-hydroxy-2-methylpyrimid-5-ylmethyl)-3-(2-hydroxyethyl)-2-methylpyridinium + NH$_3$  
Other name(s): 1-[(4-amino-2-methylpyrimid-5-ylmethyl)-3-(2-hydroxyethyl)-2-methylpyridinium-bromide aminohydrolase  
Systematic name: 1-(4-amino-2-methylpyrimid-5-ylmethyl)-3-(2-hydroxyethyl)-2-methylpyridinium aminohydrolase  
References: [2811]

[EC 3.5.4.20 created 1972, modified 2014]

EC 3.5.4.21  
Accepted name: creatinine deaminase  
Reaction: creatinine + H$_2$O = N-methylhydantoin + NH$_3$  
Other name(s): creatinine hydrolase; creatinine desiminase  
Systematic name: creatinine iminohydrolase  
References: [2965]

[EC 3.5.4.21 created 1972]

EC 3.5.4.22  
Accepted name: 1-pyrroline-4-hydroxy-2-carboxylate deaminase

307
Reaction: 1-pyrroline-4-hydroxy-2-carboxylate + H_2O = 2,5-dioxopentanoate + NH_3
Other name(s): HPC deaminase; 1-pyrroline-4-hydroxy-2-carboxylate aminohydrolase (decyclizing)
Systematic name: 1-pyrroline-4-hydroxy-2-carboxylate aminohydrolase (ring-opening)
References: [2809, 2810]

[EC 3.5.4.22 created 1976]

EC 3.5.4.23
Accepted name: blasticidin-S deaminase
Reaction: blasticidin S + H_2O = deaminohydroxyblasticidin S + NH_3
Systematic name: blasticidin-S aminohydrolase
Comments: Catalyses the deamination of the cytosine moiety of the antibiotics blasticidin S, cytomycin and acetylblasticidin S.
References: [3401]

[EC 3.5.4.23 created 1976]

EC 3.5.4.24
Accepted name: sepiapterin deaminase
Reaction: sepiapterin + H_2O = xanthopterin-B2 + NH_3
Systematic name: sepiapterin aminohydrolase
Comments: Also acts on isosepiapterin, but more slowly.
References: [3139]

[EC 3.5.4.24 created 1976]

EC 3.5.4.25
Accepted name: GTP cyclohydrolase II
Reaction: GTP + 4 H_2O = formate + 2,5-diamino-6-hydroxy-4-(5-phospho-D-ribosylamino)pyrimidine + 2 phosphate
Other name(s): guanosine triphosphate cyclohydrolase II; GTP-8-formylhydrolase; ribA (gene name); GTP 7,8-8,9-dihydrolase (diphosphate-forming)
Systematic name: GTP 7,8-8,9-dihydrolase (formate-releasing, phosphate-releasing)
Comments: The enzyme, found in prokaryotes and some eukaryotes, hydrolytically cleaves the C-N bond at positions 8 and 9 of GTP guanine, followed by a subsequent hydrolytic attack at the base, which liberates formate, and cleavage of the α-β phosphodiester bond of the triphosphate to form diphosphate. The enzyme continues with a slow cleavage of the diphosphate to form two phosphate ions. The enzyme requires zinc and magnesium ions for the cleavage reactions at the GTP guanine and triphosphate sites, respectively. It is one of the enzymes required for flavin biosynthesis in many bacterial species, lower eukaryotes, and plants. cf. EC 3.5.4.16, GTP cyclohydrolase I, EC 3.5.4.29, GTP cyclohydrolase IIa, and EC 3.5.4.39, GTP cyclohydrolase IV.
References: [849, 2558, 2716, 2534, 2838]

[EC 3.5.4.25 created 1984, modified 2011, modified 2022]

EC 3.5.4.26
Accepted name: diaminohydroxyphosphoribosylaminopurine deaminase
Reaction: 2,5-diamino-6-hydroxy-4-(5-phospho-D-ribosylamino)pyrimidine + H_2O = 5-amino-6-(5-phospho-D-ribosylamino)uracil + NH_3
Systematic name: 2,5-diamino-6-hydroxy-4-(5-phospho-D-ribosylamino)pyrimidine 2-aminohydrolase
Comments: The substrate is the product of EC 3.5.4.25 GTP cyclohydrolase II.
References: [361]

[EC 3.5.4.26 created 1984, modified 2011]
EC 3.5.4.27
Accepted name: methenyltetrahydromethanopterin cyclohydrolase
Reaction: 5,10-methenyl-5,6,7,8-tetrahydromethanopterin + H₂O = 5-formyl-5,6,7,8-tetrahydromethanopterin
Other name(s): 5,10-methenyltetrahydromethanopterin cyclohydrodase; N⁵,N¹⁰-methenyltetrahydromethanopterin cyclohydrolase; methenyl-H₂MPT cyclohydrolase; 5,10-methenyltetrahydromethanopterin 10-hydrolase (decyclizing)
Systematic name: 5,10-methenyltetrahydromethanopterin 10-hydrolase (ring-opening)
Comments: Methanopterin is a pterin analogue. The enzyme is involved in the formation of methane from CO₂ in *Methanobacterium thermoautotrophicum.*
References: [684]

[EC 3.5.4.27 created 1989]

EC 3.5.4.28
Accepted name: S-adenosylhomocysteine deaminase
Reaction: S-adenosyl-L-homocysteine + H₂O = S-inosyl-L-homocysteine + NH₃
Other name(s): adenosylhomocysteine deaminase
Systematic name: S-adenosyl-L-homocysteine aminohydrolase
References: [3518]

[EC 3.5.4.28 created 1992]

EC 3.5.4.29
Accepted name: GTP cyclohydrolase IIa
Reaction: GTP + 3 H₂O = 2-amino-5-formylamino-6-(5-phospho-D-ribosylamino)pyrimidin-4(3H)-one + 2 phosphate
Systematic name: GTP 8,9-hydrolase (phosphate-forming)
Comments: Requires Mg²⁺. This enzyme catalyses the hydrolysis of the imidazole ring of guanosine 5′-triphosphate, N⁷-methylguanosine 5′-triphosphate or inosine 5′-triphosphate. Xanthosine 5′-triphosphate and ATP are not substrates. It also catalyses the hydrolysis of diphosphate to form two equivalents of phosphate. Unlike GTP cyclohydrolase II (EC 3.5.4.25), this enzyme does not release formate, but does hydrolyse the diphosphate from GTP to phosphate.
References: [1018]

[EC 3.5.4.29 created 2003, modified 2011]

EC 3.5.4.30
Accepted name: dCTP deaminase (dUMP-forming)
Reaction: dCTP + 2 H₂O = dUMP + diphosphate + NH₃
Systematic name: dCTP aminohydrolase (dUMP-forming)
Comments: Requires Mg²⁺. Is highly specific for dCTP as substrate as dCMP, CTP, CDP, CMP, cytosine or deoxycytosine are not deaminated. While most bacteria require two enzymes to form dUMP from dCTP (EC 3.5.4.13, dCTP deaminase and EC 3.6.1.23, dUTP diphosphatase), the archaeon *Methanocalphilus jannaschii* uses a single enzyme to carry out both functions. This enzyme can also act as a dUTP diphosphatase, but more slowly.
References: [1755]

[EC 3.5.4.30 created 2003]

EC 3.5.4.31
Accepted name: S-methyl-5′-thioadenosine deaminase
Reaction: S-methyl-5′-thioadenosine + H₂O = S-methyl-5′-thioinosine + NH₃
Other name(s): MTA deaminase; 5-methylthioadenosine deaminase
Systematic name: 5-methyl-5′-thioadenosine amidohydrolase
Comments: The enzyme from Thermotoga maritima also functions as 5'-adenosylhomocysteine deaminase (EC 3.5.4.28) and has some activity against adenosine. Adenosine 5'-phosphate and 5'-adenosyl-L-methionine (SAM) are not substrates.

References: [1199]

[EC 3.5.4.31 created 2011]

EC 3.5.4.32
Accepted name: 8-oxoguanine deaminase
Reaction: 8-oxoguanine + H₂O = urate + NH₃
Other name(s): 8-OGD
Systematic name: 8-oxoguanine aminohydrolase
Comments: Zn²⁺ is bound in the active site. 8-Oxoguanine is formed via the oxidation of guanine within DNA by reactive oxygen species. If uncorrected, this modification leads to the incorporation of 8-oxoG:A mismatches and eventually to G:C to T:A transversions.
References: [1088]

[EC 3.5.4.32 created 2012]

EC 3.5.4.33
Accepted name: tRNA(adenine³⁴) deaminase
Reaction: adenine³⁴ in tRNA + H₂O = hypoxanthine³⁴ in tRNA + NH₃
Other name(s): tRNA:A³⁴ deaminase; tadA protein; ADAT2-ADAT3 complex; TADA; tRNA adenosine deaminase arginine; AtTadA; tadA/ecADAT2; tRNA A:34 deaminase
Systematic name: tRNA(adenine³⁴) aminohydrolase
Comments: The enzyme is involved in editing of tRNA. The active site contains Zn²⁺ [2877].
References: [2877, 617, 1655, 3361, 1724, 2476]

[EC 3.5.4.33 created 2013]

EC 3.5.4.34
Accepted name: tRNA⁸Ala(adenine³⁷) deaminase
Reaction: adenine³⁷ in tRNA⁸Ala + H₂O = hypoxanthine³⁷ in tRNA⁸Ala + NH₃
Other name(s): ADAT1; Tad1p
Systematic name: tRNA⁸Ala(adenine³⁷) aminohydrolase
Comments: The enzyme deaminates adenosine³⁷ to inosine in eukaryotic tRNA⁸Ala [1860]. tRNA editing is strictly dependent on Mg²⁺ [947].
References: [1860, 947, 1494]

[EC 3.5.4.34 created 2013]

EC 3.5.4.35
Accepted name: tRNA(cytosine⁸) deaminase
Reaction: cytosine⁸ in tRNA + H₂O = uracil⁸ in tRNA + NH₃
Other name(s): CDAT8
Systematic name: tRNA(cytosine⁸) aminohydrolase
Comments: The enzyme from Methanopyrus kandleri specifically catalyses the deamination of cytosine at position 8 of tRNA in 30 different tRNAs. This cytosine-to-uracil editing guarantees the proper folding and functionality of the tRNAs.
References: [2492]
EC 3.5.4.36

Accepted name: mRNA(cytosine$^{6666}$) deaminase
Reaction: cytosine$^{6666}$ in apolipoprotein B mRNA + H$_2$O = uracil$^{6666}$ in apolipoprotein B mRNA + NH$_3$
Other name(s): APOBEC-1 (catalytic component of an RNA-editing complex); APOBEC1 (catalytic subunit); apolipoprotein B mRNA-editing enzyme 1 (catalytic component of an RNA-editing complex); apoB mRNA-editing enzyme catalytic polypeptide 1 (catalytic component of an RNA-editing complex); apoB mRNA editing complex; apolipoprotein B mRNA editing enzyme; REPR
Systematic name: mRNA(cytosine$^{6666}$) aminohydrolase
Comments: The apolipoprotein B mRNA editing enzyme complex catalyses the editing of apolipoprotein B mRNA at cytidine$^{6666}$ to uridine, thereby transforming the codon for glutamine-2153 to a termination codon. Editing results in translation of a truncated apolipoprotein B isoform ($apoB$-48) with distinct functions in lipid transport. The catalytic component (APOBEC-1) contains zinc at the active site [159].
References: [463, 898, 159, 462]

EC 3.5.4.37

Accepted name: double-stranded RNA adenine deaminase
Reaction: adenine in double-stranded RNA + H$_2$O = hypoxanthine in double-stranded RNA + NH$_3$
Other name(s): ADAR; double-stranded RNA adenosine deaminase; dsRAD; dsRNA adenosine deaminase; DRADA1; double-stranded RNA-specific adenosine deaminase
Systematic name: double-stranded RNA adenine aminohydrolase
Comments: This eukaryotic enzyme is involved in RNA editing. It destabilizes double-stranded RNA through conversion of adenosine to inosine. Inositol hexakisphosphate is required for activity [1861].
References: [1261, 2236, 3365, 1861]

EC 3.5.4.38

Accepted name: single-stranded DNA cytosine deaminase
Reaction: cytosine in single-stranded DNA + H$_2$O = uracil in single-stranded DNA + NH$_3$
Other name(s): AID; activation-induced deaminase; AICDA (gene name); activation-induced cytidine deaminase
Systematic name: single-stranded DNA cytosine aminohydrolase
Comments: The enzyme exclusively catalyses deamination of cytosine in single-stranded DNA. It preferentially deaminates five-nucleotide bubbles. The optimal target consists of a single-stranded NWRCN motif ($W = A$ or $T$, $R = A$ or $G$) [1693]. The enzyme initiates antibody diversification processes by deaminating immunoglobulin sequences.
References: [2849, 1693, 306, 1692, 3212]

EC 3.5.4.39

Accepted name: GTP cyclohydrolase IV
Reaction: GTP + H$_2$O = 7,8-dihydroneopterin 2',3'-cyclic phosphate + formate + diphosphate
Other name(s): MptA; GTP cyclohydrolase MptA
Systematic name: GTP 7.8-8,9-dihydrolase (cyclizing, formate-releasing, diphosphate-releasing)
Comments: Requires Fe$^{2+}$. A zinc protein. The enzyme is involved in methanopterin biosynthesis in methanogenic archaea. cf. GTP cyclohydrolase I (EC 3.5.4.16), GTP cyclohydrolase II (EC 3.5.4.25) and GTP cyclohydrolase IIa (EC 3.5.4.29).
References: [1043]
EC 3.5.4.40

Accepted name: aminodeoxyfutalosine deaminase

Reaction: 6-amino-6-deoxyfutalosine + H₂O = futalosine + NH₃

Other name(s): AFL deaminase; aminofutalosine deaminase; mqnX (gene name)

Systematic name: 6-amino-6-deoxyfutalosine deaminase

Comments: The enzyme, found in several bacterial species, is part of the futalosine pathway for menaquinone biosynthesis.

References: [69, 989]

EC 3.5.4.41

Accepted name: 5′-deoxyadenosine deaminase

Reaction: 5′-deoxyadenosine + H₂O = 5′-deoxyinosine + NH₃

Other name(s): MJ1541 (gene name); DadD

Systematic name: 5′-deoxyadenosine aminohydrolase

Comments: The enzyme from the archaeon Methanocaldococcus jannaschii is involved in the recycling of 5′-deoxyadenosine.

References: [2009]

EC 3.5.4.42

Accepted name: N-isopropylammelide isopropylaminohydrolase

Reaction: N-isopropylammelide + H₂O = cyanuric acid + isopropylamine

Other name(s): atzC (gene name)

Systematic name: N-isopropylammelide isopropylaminohydrolase

Comments: Requires Zn²⁺. This bacterial enzyme is involved in degradation of the herbicide atrazine. It can hydrolyse other N-substituted amino dihydroxy-s-triazine molecules, and prefers substrates with linear N-alkyl groups to those with branched alkyl groups.

References: [2617, 2753, 144]

EC 3.5.4.43

Accepted name: hydroxydechloroatrazine ethylaminohydrolase

Reaction: hydroxyatrazine + H₂O = N-isopropylammelide + ethylamine

Other name(s): atzB (gene name); 2,4-dihydroxy-6-(isopropylamino)-1,3,5-triazine ethylaminohydrolase

Systematic name: hydroxyatrazine ethylaminohydrolase

Comments: Contains Zn²⁺. This bacterial enzyme is involved in degradation of the herbicide atrazine. The enzyme has a broad substrate range, and requires a monohydroxylated s-triazine ring with a minimum of one primary or secondary amine substituent and either a chloride or amine leaving group. It catalyses both deamination and dechlorination reactions.

References: [297, 2734]

EC 3.5.4.44

Accepted name: ectoine hydrolase

Reaction: ectoine + H₂O = (2S)-2-acetamido-4-aminobutanoate
Other name(s): doeA (gene name)
Systematic name: ectoine aminohydrolase
Comments: The enzyme, found in some halophilic bacteria, is involved in the degradation of the compatible solute ectoine. The enzyme, which belongs to peptidase family M24, only acts in the direction of ectoine hydrolysis. It also produces smaller amounts of (2S)-4-acetamido-2-aminobutanoate, which is recycled back to ectoine by EC 4.2.1.108, ectoine synthase.
References: [2730]

[EC 3.5.4.44 created 2017]

EC 3.5.4.45
Accepted name: melamine deaminase
Reaction: (1) melamine + H₂O = ammeline + NH₃
(2) ammeline + H₂O = ammelide + NH₃
Other name(s): triA (gene name)
Systematic name: melamine aminohydrolase
Comments: The enzyme, isolated from the bacterium Acidovorax citrulli, performs the deamination of melamine 15-fold faster than the deamination of ammeline. It also has activity with 2-chloro-4,6-diamino-s-triazine, but has no activity toward halo-substituted triazine ring compounds such as atrazine (cf. EC 3.8.1.8, atrazine chlorohydrolase).
References: [2735]

[EC 3.5.4.45 created 2017]

EC 3.5.4.46
Accepted name: cAMP deaminase
Reaction: 3′,5′-cyclic AMP + H₂O = 3′,5′-cyclic IMP + NH₃
Other name(s): cyclic adenylate deaminase; CadD
Systematic name: 3′,5′-cyclic AMP aminohydrolase
Comments: Requires Zn²⁺. The enzyme, isolated from the bacterium Leptospira interrogans, is specific for cAMP.
References: [988]

[EC 3.5.4.46 created 2017]

EC 3.5.5 In nitriles

EC 3.5.5.1
Accepted name: nitrilase
Reaction: a nitrile + 2 H₂O = a carboxylate + NH₃
Other name(s): acetonitrilase; benzonitrilase
Systematic name: nitrile aminohydrolase
Comments: Acts on a wide range of aromatic nitriles including (indol-3-yl)acetonitrile, and also on some aliphatic nitriles, and on the corresponding acid amides. cf. EC 4.2.1.84 nitrile hydratase.
References: [1120, 3052, 2331]

[EC 3.5.5.1 created 1965, modified 1989]

EC 3.5.5.2
Accepted name: ricinine nitrilase
Reaction: ricinine + 2 H₂O = 3-carboxy-4-methoxy-N-methyl-2-pyridone + NH₃
Systematic name: ricinine aminohydrolase
References: [2569, 1244, 2331]

[EC 3.5.5.2 created 1972]

[3.5.5.3 Transferred entry. cyanate hydrolase. Now EC 4.2.1.104, cyanate hydratase]

[EC 3.5.5.3 created 1972, deleted 1990]

EC 3.5.5.4
Accepted name: cyanoalanine nitrilase
Reaction: 3-cyano-L-alanine + 2 H₂O = L-aspartate + NH₃ (overall reaction)
(1a) 3-cyano-L-alanine + H₂O = L-asparagine
(1b) L-asparagine + H₂O = L-aspartate + NH₃
Other name(s): β-cyanoalanine nitrilase
Systematic name: 3-cyano-L-alanine aminohydrolase
Comments: L-Asparagine is formed as an intermediate. cf. EC 4.2.1.65, 3-cyanoalanine hydratase and EC 3.5.1.1, asparaginase.
References: [3414]

[EC 3.5.5.4 created 1986]

EC 3.5.5.5
Accepted name: arylacetonitrilase
Reaction: 4-chlorophenylacetonitrile + 2 H₂O = 4-chlorophenylacetate + NH₃
Systematic name: arylacetonitrile aminohydrolase
Comments: Requires thiol compounds. Also hydrolyses other 4-substituted phenylacetonitriles, thien-2-ylacetonitrile, tolylacetonitriles, and, more slowly, benzyl cyanide.
References: [1944, 2127]

[EC 3.5.5.5 created 1992]

EC 3.5.5.6
Accepted name: bromoxynil nitrilase
Reaction: 3,5-dibromo-4-hydroxybenzonitrile + 2 H₂O = 3,5-dibromo-4-hydroxybenzoate + NH₃
Systematic name: 3,5-dibromo-4-hydroxybenzonitrile aminohydrolase
Comments: Involved in the bacterial degradation of the herbicide bromoxynil. Highly specific.
References: [2894]

[EC 3.5.5.6 created 1992]

EC 3.5.5.7
Accepted name: aliphatic nitrilase
Reaction: R-CN + 2 H₂O = R-COOH + NH₃
Systematic name: aliphatic nitrile aminohydrolase
Comments: Preferentially hydrolyses aliphatic nitriles, some of which are apparently not substrates for other known nitrilases (EC 3.5.5.1). Substrates include crotononitrile, acrylonitrile and glutaronitrile.
References: [1578, 2331]

[EC 3.5.5.7 created 1999]

EC 3.5.5.8
Accepted name: thiocyanate hydrolase
Reaction: \[ \text{thiocyanate} + 2 \text{H}_2\text{O} = \text{carbonyl sulfide} + \text{NH}_3 + \text{HO}^- \]

Systematic name: thiocyanate aminohydrolase

Comments: The enzyme from *Thiobacillus thioparus* catalyses the first step in the degradation of thiocyanate.

References: [1477, 1478]

**EC 3.5.99 In other compounds**

**EC 3.5.99.1**

Accepted name: riboflavinase

Reaction: riboflavin + H\(_2\)O = ribitol + lumichrome

Systematic name: riboflavin hydrolase

References: [3412]

[EC 3.5.99.1 created 1961]

**EC 3.5.99.2**

Accepted name: aminopyrimidine aminohydrolase

Reaction: (1) 4-amino-5-aminomethyl-2-methylpyrimidine + H\(_2\)O = 4-amino-5-hydroxymethyl-2-methylpyrimidine + NH\(_3\)
(2) thiamine + H\(_2\)O = 4-amino-5-hydroxymethyl-2-methylpyrimidine + 5-(2-hydroxyethyl)-4-methylthiazole

Other name(s): thiaminase (ambiguous); thiaminase II; *tenA* (gene name)

Systematic name: 4-amino-5-aminomethyl-2-methylpyrimidine aminohydrolase

Comments: Previously known as thiaminase II, this enzyme is involved in the regeneration of the thiamine pyrimidine from degraded products, rather than in thiamine degradation, and participates in thiamine salvage pathways.

References: [901, 1309, 3084, 206, 1398, 1399, 861]

[EC 3.5.99.2 created 1961, modified 2011]

[3.5.99.3 Transferred entry. *hydroxydechloroatrazine ethylaminohydrolase*. Now EC 3.5.4.43, *hydroxydechloroatrazine ethylaminohydrolase*]

[EC 3.5.99.3 created 2000, deleted 2016]

[3.5.99.4 Transferred entry. *N-isopropylammelide isopropylaminohydrolase*. Now EC 3.5.4.42, *N-isopropylammelide isopropylaminohydrolase*]

[EC 3.5.99.4 created 2000, deleted 2016]

**EC 3.5.99.5**

Accepted name: 2-aminomuconate deaminase

Reaction: 2-aminomuconate + H\(_2\)O = (3E)-2-oxohex-3-enedioate + NH\(_3\)

Other name(s): amnD (gene name); *nbaF* (gene name)

Systematic name: 2-aminomuconate aminohydrolase

Comments: 2-Aminomuconate is an intermediate in the bacterial biodegradation of nitrobenzene. The enzyme has been isolated from several species, including *Pseudomonas pseudocaligenes* JS45, *Pseudomonas fluorescens* KU-7, *Pseudomonas* sp. AP3 and *Burkholderia cenocepacia* J2315. The reaction is spontaneous in acid conditions.

References: [1161, 1162, 2998, 2106]

[EC 3.5.99.5 created 2000, modified 2012]
EC 3.5.99.6

Accepted name: glucosamine-6-phosphate deaminase
Reaction: \( \alpha\)-D-glucosamine 6-phosphate + H\(_2\)O = D-fructose 6-phosphate + NH\(_3\)
Other name(s): glucosaminephosphate isomerase (ambiguous); glucosamine-6-phosphate isomerase (ambiguous); phosphoglucomaminisomerase (ambiguous); glucosamine phosphate deaminase; aminodeoxyglucososephosphate isomerase (ambiguous); phosphoglucomamine isomerase (ambiguous); 2-amino-2-deoxy-D-glucose-6-phosphate aminohydrolase (ketal isomerizing)
Systematic name: 2-amino-2-deoxy-\(\alpha\)-D-glucose-6-phosphate aminohydrolase (ketol isomerizing)
Comments: The enzyme uses ring opening and isomerization of the aldose-ketose type to convert the -CH(-NH\(_2\))-CH=O group of glucosamine 6-phosphate into -C(=NH)-CH\(_2\)-OH, forming 2-deoxy-2-imino-\(\alpha\)-arabino-hexitol, which then hydrolyses to yield fructose 6-phosphate and ammonia. N-Acetyl-D-glucosamine 6-phosphate, which is not broken down, activates the enzyme.
References: [3363, 509, 2361, 1813]

[EC 3.5.99.6 created 1961 as EC 5.3.1.10, transferred 2000 to EC 3.5.99.6]

EC 3.5.99.7

Accepted name: 1-aminocyclopropane-1-carboxylate deaminase
Reaction: 1-aminocyclopropane-1-carboxylate + H\(_2\)O = 2-oxobutanoate + NH\(_3\) (overall reaction)
(1a) 1-aminocyclopropane-1-carboxylate = 2-aminobut-2-enoate
(1b) 2-aminobut-2-enoate = 2-iminobutanoate (spontaneous)
(1c) 2-iminobutanoate + H\(_2\)O = 2-oxobutanoate + NH\(_3\) (spontaneous)
Other name(s): 1-aminocyclopropane-1-carboxylic acid deaminase
Systematic name: 1-aminocyclopropane-1-carboxylate aminohydrolase (isomerizing)
Comments: A pyridoxal 5\(^\prime\)-phosphate enzyme. The enzyme, found in certain soil bacteria and fungi, catalyses the ring opening of 1-aminocyclopropane-1-carboxylate, the immediate precursor to ethylene, an important plant hormone that regulates fruit ripening and other processes. The enzyme releases an unstable enamine product that tautomerizes to an imine form, which undergoes a hydrolytic deamination. The latter reaction, which can occur spontaneously, can also be catalysed by EC 3.5.99.10, 2-iminobutanoate/2-iminopropanoate deaminase. The enzyme has been used to make fruit ripening dependent on externally added ethylene, as it removes the substrate for endogenous ethylene formation.
References: [1242, 3420, 3050]

[EC 3.5.99.7 created 1981 as EC 4.1.99.4, transferred 2002 to EC 3.5.99.7, modified 2014]

EC 3.5.99.8

Accepted name: 5-nitroanthranilic acid aminohydrolase
Reaction: 5-nitroanthranilate + H\(_2\)O = 5-nitrosalicylate + NH\(_3\)
Other name(s): naaA (gene name); 5NAA deaminase
Systematic name: 5-nitroanthranilate amidohydrolase
Comments: The enzyme catalyses the initial step in biodegradation of 5-nitroanthranilic acid by Bradyrhizobium sp. strain JS329.
References: [2456]

[EC 3.5.99.8 created 2011]

EC 3.5.99.9

Accepted name: 2-nitroimidazole nitrohydrolase
Reaction: 2-nitroimidazole + H\(_2\)O = imidazol-2-one + nitrite
Other name(s): NhhA; 2NI nitrohydrolase; 2NI denitrase
Systematic name: 2-nitroimidazole nitrohydrolase

[EC 3.5.99.9 created 2011]
Comments: The enzyme catalyses the initial step in the biodegradation of 2-nitroimidazole by the soil bacterium Mycobacterium sp. JS330

References: [2457]  
[EC 3.5.99.9 created 2012]

EC 3.5.99.10

Accepted name: 2-iminobutanoate/2-iminopropanoate deaminase

Reaction:  
(1) 2-iminobutanoate + H₂O = 2-oxobutanoate + NH₃  
(2) 2-iminopropanoate + H₂O = pyruvate + NH₃

Other name(s): ygfF (gene name); ridA (gene name); enamine/imine deaminase (ambiguous)

Systematic name: 2-iminobutanoate aminohydrolase

Comments: This enzyme, which has been found in all species and tissues examined, catalyses the hydrolytic deamination of imine intermediates formed by several types of pyridoxal-5'-phosphate-dependent dehydratases, such as EC 4.3.1.19, threonine ammonia-lyase and EC 4.3.1.17, L-serine ammonia-lyase. The reactions, which can occur spontaneously, are accelerated to minimize the cellular damage that could be caused by these reactive intermediates.

References: [1687]  
[EC 3.5.99.10 created 2014]

EC 3.5.99.11

Accepted name: 2-aminomuconate deaminase (2-hydroxymuconate-forming)

Reaction: 2-aminomuconate + H₂O = (2Z,4E)-2-hydroxyhexa-2,4-dienedioate + NH₃

Other name(s): cnbZ (gene name)

Systematic name: 2-aminomuconate aminohydrolase [(2Z,4E)-2-hydroxyhexa-2,4-dienedioate-forming]

Comments: The enzyme, characterized from the bacterium Comamonas testosteroni CNB-1, converts 2-aminomuconate to 2-hydroxyhexa-2,4-dienedioate, unlike the enzymes from Pseudomonas, which produce (3E)-2-oxohex-3-enedioate (see EC 3.5.99.5, 2-aminomuconate deaminase). The enzyme also acts on 2-amino-5-chloromuconate.

References: [1820]

[EC 3.5.99.11 created 2016 as EC 3.5.1.120, transferred 2017 to EC 3.5.99.11]

EC 3.6 Acting on acid anhydrides

To this subclass belong mainly the enzymes acting on diphosphate bonds in compounds such as nucleoside di- and tri-phosphates (EC 3.6.1), on sulfonyl-containing anhydrides such as adenyllylsulfate (EC 3.6.2) and on acid anhydrides; catalysing transmembrane movement of substances (EC 3.6.3).

EC 3.6.1 In phosphorus-containing anhydrides

EC 3.6.1.1

Accepted name: inorganic diphosphatase

Reaction: diphosphate + H₂O = 2 phosphate

Systematic name: diphosphate phosphohydrolase

Comments: Specificity varies with the source and with the activating metal ion. The enzyme from some sources may be identical with EC 3.1.3.1 (alkaline phosphatase) or EC 3.1.3.9 (glucose-6-phosphatase). cf. EC 7.1.3.1, H⁺-exporting diphosphatase.

References: [133, 1646, 2474]

[EC 3.6.1.1 created 1961, modified 2000, modified 2018]

317
EC 3.6.1.2

Accepted name: trimetaphosphatase
Reaction: trimetaphosphate + H₂O = triphosphate
Other name(s): inorganic trimetaphosphatase
Systematic name: trimetaphosphate hydrolase
References: [1600, 1995]

[EC 3.6.1.2 created 1961]

[3.6.1.3 Deleted entry. adenosinetriphosphatase. Enzymes previously listed under this number are now listed separately under EC 5.6 and EC 7.]

[EC 3.6.1.3 created 1961 (EC 3.6.1.4 created 1961, incorporated 1965), deleted 2020]

[3.6.1.4 Deleted entry. adenosinetriphosphatase (Mg-activated). Now included with EC 3.6.1.3 adenosinetriphosphatase]

[EC 3.6.1.4 created 1961, deleted 1965]

EC 3.6.1.5

Accepted name: apyrase
Reaction: a nucleoside 5'-triphosphate + 2 H₂O = a nucleoside 5'-phosphate + 2 phosphate (overall reaction)
(1a) a nucleoside 5'-triphosphate + H₂O = a nucleoside 5'-diphosphate + phosphate
(1b) a nucleoside 5'-diphosphate + H₂O = a nucleoside 5'-phosphate + phosphate
Other name(s): ATP-diphosphatase (ambiguous); adenosine diphosphatase; ADPase; ATP diphosphohydrolase [ambiguous]
Systematic name: nucleoside triphosphate phosphohydrolase (nucleoside monophosphate-forming)
Comments: Apyrases are active against both di- and triphosphate nucleotides (NDPs and NTPs) and hydrolyse NTPs to nucleotide monophosphates (NMPs) in two distinct successive phosphate-releasing steps, with NDPs as intermediates. They differ from ATPases, which specifically hydrolyse ATP, by hydrolysing both ATP and ADP. The eukaryotic enzymes requires Ca²⁺, but Mg²⁺ can substitute. Most of the ecto-ATPases that occur on the cell surface and hydrolyse extracellular nucleotides belong to this enzyme family.
References: [1625, 1773, 454, 483, 3270, 929, 3393]

[EC 3.6.1.5 created 1961, modified 1976, modified 2000, modified 2013]

EC 3.6.1.6

Accepted name: nucleoside diphosphate phosphatase
Reaction: a nucleoside diphosphate + H₂O = a nucleoside phosphate + phosphate
Other name(s): nucleoside-diphosphatase; thiaminpyrophosphatase; UDPase; inosine diphosphatase; adenosine diphosphatase; IDPase; ADPase; adenosinepyrophosphatase; guanosine diphosphatase; guanosine 5'-diphosphatase; inosine 5'-diphosphatase; uridine diphosphatase; uridine 5'-diphosphatase; type B nucleoside diphosphatase; GDPase; CDPase; nucleoside 5'-diphosphatase; type L nucleoside diphosphatase; NDPase; nucleoside diphosphate phosphohydrolase
Systematic name: nucleoside diphosphate phosphohydrolase
Comments: The enzyme, which appears to be limited to metazoa, acts on multiple nucleoside diphosphates as well as on D-ribose 5'-diphosphate. Specificity depends on species and isoform.
References: [967, 1249, 3442, 782, 3152]

[EC 3.6.1.6 created 1961]

EC 3.6.1.7

Accepted name: acylphosphatase
Reaction: an acylphosphate + H₂O = a carboxylate + phosphate
Other name(s): acetylphosphatase; 1,3-diphosphoglycerate phosphatase; acetic phosphatase; Ho 1-3; GP 1-3

318
Systematic name: acylphosphate phosphohydrolase
References: [2479, 2487, 2488, 2777]

[EC 3.6.1.7 created 1961]

EC 3.6.1.8
Accepted name: ATP diphosphatase
Reaction: ATP + H₂O = AMP + diphosphate
Other name(s): ATPase (ambiguous); ATP pyrophosphatase; adenosine triphosphate pyrophosphatase; ATP diphosphohydrolase (ambiguous)
Systematic name: ATP diphosphohydrolase (diphosphate-forming)
Comments: Also acts on ITP, GTP, CTP and UTP.
References: [1192, 1411]

[EC 3.6.1.8 created 1961]

EC 3.6.1.9
Accepted name: nucleotide diphosphatase
Reaction: a nucleoside triphosphate + H₂O = a nucleotide + diphosphate
Other name(s): ENPP1 (gene name); nucleotide pyrophosphatase; nucleotide-sugar pyrophosphatase; nucleoside-triphosphate diphosphatase
Systematic name: nucleoside-triphosphate diphosphohydrolase
Comments: The enzyme preferentially hydrolyses ATP, but can also hydrolyse other nucleoside 5′ triphosphates such as GTP, CTP, TTP and UTP to their corresponding monophosphates. In vitro the enzyme also acts as a nucleotidohydrolase on ADP, NAD⁺, NADP⁺, FAD, and CoA.
References: [460, 1503, 1689, 3486]

[EC 3.6.1.9 created 1961 (EC 3.6.1.19 created 1972, incorporated 2016), modified 2016]

EC 3.6.1.10
Accepted name: endopolyphosphatase
Reaction: polyphosphate + n H₂O = (n+1) oligophosphate
Other name(s): polyphosphate depolymerase; metaphosphatase; polyphosphatase; polymetaphosphatase
Systematic name: polyphosphate polyphosphohydrolase
Comments: The product contains 4 or 5 phosphate residues.
References: [1891, 1940]

[EC 3.6.1.10 created 1961]

EC 3.6.1.11
Accepted name: exopolyphosphatase
Reaction: (polyphosphate)ₙ + H₂O = (polyphosphate)ₙ₋₁ + phosphate
Other name(s): metaphosphatase; acid phosphoanhydride phosphohydrolase; Gra-Pase
Systematic name: polyphosphate phosphohydrolase
References: [1049, 1625, 1891]

[EC 3.6.1.11 created 1965]

EC 3.6.1.12
Accepted name: dCTP diphosphatase
Reaction: dCTP + H₂O = dCMP + diphosphate

References:
Other name(s): DCTPP1 (gene name); deoxycytidine-triphosphatase; dCTPase; dCTP pyrophosphatase; deoxycytidine triphosphatase; deoxy-CTPase
Systematic name: dCTP nucleotidohydrolase
Comments: The mammalian enzyme also displays weak activity against dTTP and dATP, but none against dGTP. Activity is highest with analogs including 5-iodo-dCTP and 5-methyl-dCTP.
References: [3510, 2083, 3371, 2215, 2537]

[EC 3.6.1.12 created 1965]

EC 3.6.1.13
Accepted name: ADP-ribose diphosphatase
Reaction: ADP-D-ribose + H₂O = AMP + D-ribose 5-phosphate
Other name(s): ADPribose pyrophosphatase; adenosine diphosphoribose pyrophosphatase; ADPR-PPase; ADP-ribose ribophosphohydrolase
Systematic name: ADP-D-ribose ribophosphohydrolase
References: [674]

[EC 3.6.1.13 created 1965]

EC 3.6.1.14
Accepted name: adenosine-tetraphosphatase
Reaction: adenosine 5′-tetraphosphate + H₂O = ATP + phosphate
Systematic name: adenosine-tetraphosphate phosphohydrolase
Comments: Also acts on inosine tetraphosphate and tripolyphosphate but shows little or no activity with other nucleotides or polyphosphates.
References: [2831]

[EC 3.6.1.14 created 1972]

EC 3.6.1.15
Accepted name: nucleoside-triphosphate phosphatase
Reaction: a nucleoside triphosphate + H₂O = a nucleoside diphosphate + phosphate
Other name(s): nucleoside-triphosphatase; nucleoside triphosphate phosphohydrolase; nucleoside-5-triphosphate phosphohydrolase; nucleoside 5-triphosphatase; unspecific diphosphate phosphohydrolase
Systematic name: nucleoside-triphosphate phosphohydrolase
Comments: The enzyme is found in eukaryotes and thermophilic bacteria, but appears to be absent from mesophilic bacteria. Also hydrolyses nucleoside diphosphates, thiamine diphosphate and FAD. The enzyme from the plant *Pisum sativum* (garden pea) is regulated by calmodulin [1269].
References: [321, 1751, 1937, 3086, 1269, 1563, 2408]

[EC 3.6.1.15 created 1972]

EC 3.6.1.16
Accepted name: CDP-glycerol diphosphatase
Reaction: CDP-glycerol + H₂O = CMP + sn-glycerol 3-phosphate
Other name(s): CDP-glycerol pyrophosphatase; cytidine diphosphoglycerol pyrophosphatase
Systematic name: CDP-glycerol phosphoglycerohydrolase
References: [980]

[EC 3.6.1.16 created 1972]
EC 3.6.1.17
Accepted name: bis(5′-nucleosyl)-tetraphosphatase (asymmetrical)
Reaction: \( P_1^1, P_4^4 \)-bis(5′-guanosyl) tetraphosphate + H\(_2\)O = GTP + GMP
Other name(s): \( P_1^1, P_4^4 \)-bis(5′-adenosyl)-tetraphosphatase; \( P_1^1, P_4^4 \)-bis(5′-adenosyl)-tetraphosphate nucleotidohydrolase; \( P_1^1, P_4^4 \)-bis(5′-uridyl)-tetraphosphate nucleotidohydrolase; \( P_1^1, P_4^4 \)-bis(5′-guanosyl)-tetraphosphate nucleotidohydrolase; \( P_1^1, P_4^4 \)-bis(5′-adenosyl)-tetraphosphate nucleotidohydrolase; \( P_1^1, P_4^4 \)-bis(5′-uridyl)-tetraphosphate nucleotidohydrolase; \( P_1^1, P_4^4 \)-bis(5′-guanosyl)-tetraphosphate nucleotidohydrolase; \( P_1^1, P_4^4 \)-bis(5′-adenosyl)-tetraphosphate nucleotidohydrolase; \( P_1^1, P_4^4 \)-bis(5′-uridyl)-tetraphosphate nucleotidohydrolase
Systematic name: \( P_1^1, P_4^4 \)-bis(5′-nucleosyl)-tetraphosphate nucleotidohydrolase
Comments: Also acts on \( P_1^1, P_4^4 \)-bis(5′-xanthosyl)-tetraphosphate and, more slowly, on \( P_1^1, P_4^4 \)-bis(5′-adenosyl)-tetraphosphate and \( P_1^1, P_4^4 \)-bis(5′-uridyl)-tetraphosphate [cf. EC 3.6.1.41 bis(5′-nucleosyl)-tetraphosphatase (symmetrical)]
References: [1382, 3178, 3279]

[EC 3.6.1.17 created 1972, modified 1976, modified 1986]

EC 3.6.1.18
Accepted name: FAD diphosphatase
Reaction: FAD + H\(_2\)O = AMP + FMN
Other name(s): FAD pyrophosphatase; riboflavin adenine dinucleotide pyrophosphatase; flavin adenine dinucleotide pyrophosphatase; riboflavin adenine dinucleotide pyrophosphatase; flavin adenine dinucleotide pyrophosphatase
Systematic name: FAD nucleotidohydrolase
Comments: The plant enzyme also hydrolyses NAD\(^+\) and NADH; the animal enzyme hydrolyses NAD\(^+\) and CoA at about half of the rate of hydrolysis of FAD. May be identical with EC 3.6.1.9 nucleotide diphosphatase.
References: [2503, 2772]

[EC 3.6.1.18 created 1972]

[3.6.1.19 Transferred entry. nucleoside-triphosphate diphosphatase. Now EC 3.6.1.9, nucleotide diphosphatase]

[EC 3.6.1.19 created 1972, deleted 2016]

EC 3.6.1.20
Accepted name: 5′-acylphosphoadenosine hydrolase
Reaction: 5′-acylphosphoadenosine + H\(_2\)O = AMP + a carboxylate
Other name(s): 5′-phosphoadenosine hydrolase
Systematic name: 5′-acylphosphoadenosine acylhydrolase
Comments: Also acts on inosine and uridine compounds.
References: [1499]

[EC 3.6.1.20 created 1972]

EC 3.6.1.21
Accepted name: ADP-sugar diphosphatase
Reaction: ADP-sugar + H\(_2\)O = AMP + α-D-aldose 1-phosphate
Other name(s): ADP-sugar pyrophosphatase; adenosine diphosphosugar pyrophosphatase
Systematic name: ADP-sugar sugarphosphohydrolase
Comments: Has a specificity that is distinct from that of UDP-sugar diphosphatase (EC 3.6.1.45).
References: [2578]

[EC 3.6.1.21 created 1972, modified 1999]

EC 3.6.1.22
Accepted name: NAD\(^+\) diphosphatase
**Reaction:**  
\[ \text{NAD}(H) + H_2O = \text{AMP} + \text{NMN}(H) \]

**Other name(s):** NPY1 (gene name); *nadC* (gene name); NUDT7 (gene name); nicotinamide adenine dinucleotide pyrophosphatase; NADP pyrophosphatase; NADH pyrophosphatase; NAD\(^+\) phosphohydrolase

**Systematic name:** NAD(H) phosphohydrolase

**Comments:** This enzyme, described from plants, animals, and bacteria, can act on both reduced and oxidized forms of its substrate, although enzymes from different organisms have different preferences. Also acts on other dinucleotides, including NADP(H), FAD(H\(_2\)), and the thionicotinamide analogues of NAD\(^+\) and NADP\(^+\).

**References:** [1599, 1368, 2963, 1641, 54, 2144, 867, 3392, 1384]

[EC 3.6.1.22 created 1972]

---

**EC 3.6.1.23**

**Accepted name:** dUTP diphosphatase

**Reaction:** dUTP + H\(_2\)O = dUMP + diphosphate

**Other name(s):** DUT (gene name); deoxyuridine-triphosphatase; dUTPase; dUTP pyrophosphatase; deoxyuridine 5\(^\prime\)-triphosphate nucleotidohydrolase; deoxyuridine 5\(^\prime\)-triphosphatase

**Systematic name:** dUTP nucleotidohydrolase

**Comments:** The enzyme catalyses the Mg\(^{2+}\)-dependent hydrolysis of dUTP to dUMP, providing the substrate for EC 2.1.1.45, thymidylate synthase, leading to production of thymidine nucleotides. By reducing the effective ratio of dUTP to dTTP, the enzyme also reduces the possibility of dUTP incorporation into DNA.

**References:** [1029, 221, 1036, 2781, 978, 415, 1679, 136, 3201]

[EC 3.6.1.23 created 1972]

---

**EC 3.6.1.24**

**Accepted name:** nucleoside phosphoacylhydrolase

**Reaction:** Hydrolyses mixed phospho-anhydride bonds

**Systematic name:** nucleoside-5\(^\prime\)-phosphoacylate acylhydrolase

**Comments:** Attacks ribonucleoside 5\(^\prime\)-nitrophenylphosphates, but is inactive against phosphodiester.

**References:** [2875]

[EC 3.6.1.24 created 1972]

---

**EC 3.6.1.25**

**Accepted name:** triphosphatase

**Reaction:** triphosphate + H\(_2\)O = diphosphate + phosphate

**Other name(s):** inorganic triphosphatase

**Systematic name:** triphosphate phosphohydrolase

**References:** [1635, 3159]

[EC 3.6.1.25 created 1976]

---

**EC 3.6.1.26**

**Accepted name:** CDP-diacylglycerol diphosphatase

**Reaction:** CDP-diaclylglycerol + H\(_2\)O = CMP + phosphatidate

**Other name(s):** cytidine diphosphodiacylglycerol pyrophosphatase; CDP diacylglycerol hydrolase

**Systematic name:** CDP-diaclylglycerol phosphatidylhydrolase

**References:** [2473]

[EC 3.6.1.26 created 1976]
EC 3.6.1.27

Accepted name: undecaprenyl-diphosphate phosphatase
Reaction: \( \text{ditrans,octacis-undecaprenyl diphosphate} + \text{H}_2\text{O} = \text{ditrans,octacis-undecaprenyl phosphate} + \text{phosphate} \)
Other name(s): C\text{35}-isoprenyl diphosphatase; C\text{3}\text{5}-isoprenyl pyrophosphatase; isoprenyl pyrophosphatase (ambiguous); undecaprenyl pyrophosphate phosphatase; undecaprenyl pyrophosphate pyrophosphatase; UPP phosphatase; Und-PP pyrophosphatase; UppP (ambiguous); BacA; undecaprenyl-diphosphate phosphohydrolase; undecaprenyl-diphosphatase
Systematic name: \( \text{ditrans,octacis-undecaprenyl-diphosphate phosphohydrolase} \)
Comments: Isolated from the bacteria Micrococcus lysodeikticus [1004], Escherichia coli [2,3,5,6] and Bacillus subtilis [215]. The product of the reaction, d ditrans,octacis-undecaprenyl phosphate, is essential for cell wall polysaccharide biosynthesis in these strains.
References: [1004, 954, 955, 215, 3033, 3096]

[EC 3.6.1.27 created 1978, modified 2002, modified 2012]

EC 3.6.1.28

Accepted name: thiamine-triphosphatase
Reaction: \( \text{thiamine triphosphate} + \text{H}_2\text{O} = \text{thiamine diphosphate} + \text{phosphate} \)
Systematic name: thiamine-triphosphate phosphohydrolase
References: [1134]

[EC 3.6.1.28 created 1978]

EC 3.6.1.29

Accepted name: bis(5'-adenosyl)-triphosphatase
Reaction: \( P^1,P^3\text{-bis(5'-adenosyl) triphosphate} + \text{H}_2\text{O} = \text{ADP} + \text{AMP} \)
Other name(s): dinucleosidetriphosphatase; diadenosine 5,5-P\text{1},P\text{3}-triphosphatase; 1-P,3-P-bis(5'-adenosyl)-triphosphate adenylohydrolase
Systematic name: \( P^1,P^3\text{-bis(5'-adenosyl)-triphosphate adenylohydrolase} \)
References: [1382, 2798]

[EC 3.6.1.29 created 1978]

[3.6.1.30 Deleted entry. \( m^7\text{G}(5')\text{pppN} \) diphosphatase. Now covered by EC 3.6.1.59 [\( m^7\text{GpppX} \) diphosphatase] and EC 3.6.1.62 [\( m^7\text{GpppN-mRNA hydrolase} \)].]

[EC 3.6.1.30 created 1978, deleted 2012]

EC 3.6.1.31

Accepted name: phosphoribosyl-ATP diphosphatase
Reaction: \( 1-(5\text{-phospho-}\beta\text{-d-ribose})\text{-ATP} + \text{H}_2\text{O} = 1-(5\text{-phospho-}\beta\text{-d-ribose})\text{-AMP} + \text{diphosphate} \)
Other name(s): phosphoribosyl-ATP pyrophosphatase; phosphoribosyladenosine triphosphate pyrophosphatase; 1-(5-phosphoribosyl)-ATP diphosphohydrolase
Systematic name: \( 1-(5\text{-phospho-}\beta\text{-d-ribose})\text{-ATP diphosphohydrolase} \)
Comments: The Neurospora crassa enzyme also catalyses the reactions of EC 1.1.1.23 (histidinol dehydrogenase) and EC 3.5.4.19 (phosphoribosyl-AMP cyclohydrolase).
References: [2836]

[EC 3.6.1.31 created 1981]

[3.6.1.32 Transferred entry. myosin ATPase. Now EC 3.6.4.1, myosin ATPase]

[EC 3.6.1.32 created 1984, deleted 2000]

[3.6.1.33 Transferred entry. dynein ATPase. Now EC 3.6.4.2, dynein ATPase]
[EC 3.6.1.33 created 1984, deleted 2000]


[EC 3.6.1.34 created 1984, deleted 2000]


[EC 3.6.1.35 created 1984, deleted 2000]

3.6.1.36 Transferred entry. H⁺/K⁺ exchanging ATPase. Now EC 3.6.3.10, H⁺/K⁺-exchanging ATPase

[EC 3.6.1.36 created 1984, deleted 2000]

3.6.1.37 Transferred entry. Na⁺/K⁺ exchanging ATPase. Now EC 3.6.3.9, Na⁺/K⁺-exchanging ATPase

[EC 3.6.1.37 created 1984, deleted 2000]

3.6.1.38 Transferred entry. Ca²⁺-transporting ATPase. Now EC 3.6.3.8, Ca²⁺-transporting ATPase

[EC 3.6.1.38 created 1984, deleted 2000]

EC 3.6.1.39

Accepted name: thymidine-triphosphatase
Reaction: dTTP + H₂O = dTDP + phosphate
Other name(s): thymidine triphosphate nucleotidohydrolase; dTTPase; deoxythymidine-5′-triphosphatase
Systematic name: dTTP nucleotidohydrolase
Comments: Also acts, more slowly, on dUTP and UTP.
References: [569]

[EC 3.6.1.39 created 1984]

EC 3.6.1.40

Accepted name: guanosine-5′-triphosphate,3′-diphosphate phosphatase
Reaction: guanosine 5′-triphosphate 3′-diphosphate + H₂O = guanosine 3′,5′-bis(diphosphate) + phosphate
Other name(s): pppGpp 5′-phosphohydrolase; guanosine 5′-triphosphate-3′-diphosphate 5′-phosphohydrolase; guanosine pentaphosphatase; guanosine pentaphosphate phosphatase; guanosine 5′-triphosphate 3′-diphosphate 5′-phosphatase; guanosine pentaphosphate phosphohydrolase
Systematic name: guanosine-5′-triphosphate-3′-diphosphate 5′-phosphohydrolase
Comments: Also hydrolyses other guanosine 5′-triphosphate derivatives with at least one unsubstituted phosphate group on the 3′-position, but not GTP, ATP or adenosine 5′-triphosphate 3′-diphosphate.
References: [1108]

[EC 3.6.1.40 created 1986, modified 2010]

EC 3.6.1.41

Accepted name: bis(5′-nucleosyl)-tetraphosphatase (symmetrical)
Reaction: P₁₁,P₄₄-bis(5′-adenosyl) tetraphosphate + H₂O = 2 ADP
Other name(s): diadenosinetetraphosphatase (symmetrical); dinucleosidetetraphosphatease (symmetrical); symmetrical diadenosine tetraphosphate hydrolase; adenosine tetraphosphate phosphodiesterase; Ap₄A hydrolase; bis(5′-adenosyl) tetraphosphate; diadenosine tetraphosphate hydrolase; diadenosine polyphosphate hydrolase; diadenosine 5′,5″,P₁₄.P₄₄-tetraphosphatase; diadenosinetetraphosphatase (symmetrical); 1-P₄,A-P₄-bis(5′-nucleosyl)-tetraphosphate nucleosidebiphosphohydrolase
Systematic name: P₁₁,P₄₄-bis(5′-nucleosyl)-tetraphosphatase nucleosidebiphosphohydrolase
Comments: Also acts on bis(5′-guanosyl) tetraphosphate and bis(5′-adenosyl) pentaphosphate and, more slowly, on some other polyphosphates, forming a nucleoside bisphosphate as one product in all cases [cf. EC 3.6.1.17 bis(5′-nucleosyl)-tetraphosphatase (asymmetrical)].
EC 3.6.1.42
Accepted name: guanosine-diphosphatase
Reaction: GDP + H₂O = GMP + phosphate
Other name(s): GDPase
Systematic name: GDP phosphohydrolase
Comments: Also acts on UDP but not on other nucleoside diphosphates and triphosphates.
References: [2512]

[EC 3.6.1.42 created 1989]

EC 3.6.1.43
Accepted name: dolichydiphosphatase
Reaction: dolichyl diphosphate + H₂O = dolichyl phosphate + phosphate
Other name(s): dolichol diphosphatase; dolichyl pyrophosphatase; dolichyl pyrophosphate phosphatase; dolichyl diphosphate phosphohydrolase; Dol-P-P phosphohydrolase
Systematic name: dolichyl-diphosphate phosphohydrolase
References: [2164]

[EC 3.6.1.43 created 1989]

EC 3.6.1.44
Accepted name: oligosaccharide-diphosphodolichol diphosphatase
Reaction: oligosaccharide-diphosphodolichol + H₂O = oligosaccharide phosphate + dolichyl phosphate
Other name(s): oligosaccharide-diphosphodolichol pyrophosphatase
Systematic name: oligosaccharide-diphosphodolichol phosphodolichohydrolase
References: [201]

[EC 3.6.1.44 created 1992]

EC 3.6.1.45
Accepted name: UDP-sugar diphosphatase
Reaction: UDP-sugar + H₂O = UMP + α-D-aldose 1-phosphate
Other name(s): nucleosidediphosphate-sugar pyrophosphatase; nucleosidediphosphate-sugar diphosphatase; UDP-sugar hydrolase; UDP-sugar pyrophosphatase
Systematic name: UDP-sugar phosphohydrolase
Comments: A divalent cation is required for activity. UDP-sugar is the best substrate, although other nucleoside-sugar diphosphates are used as substrates with similar \( K_m \) values but much lower maximum velocities. Thus, this enzyme has a specificity distinct from that of ADP-sugar diphosphatase (EC 3.6.1.21). Some but not all enzymes of this class also appear to have 5′-nucleotidase (see EC 3.1.3.5) activity.
References: [938, 981]

[EC 3.6.1.45 created 1999]

[3.6.1.46 Transferred entry. heterotrimeric G-protein GTPase. Now EC 3.6.5.1, heterotrimeric G-protein GTPase]

[EC 3.6.1.46 created 2000, deleted 2003]

[3.6.1.47 Transferred entry. small monomeric GTPase. Now EC 3.6.5.2, small monomeric GTPase]

[EC 3.6.1.47 created 2000, deleted 2003]
[3.6.1.48] Transferred entry. protein-synthesizing GTPase. Now EC 3.6.5.3, protein-synthesizing GTPase

[EC 3.6.1.48 created 2000, deleted 200]


[EC 3.6.1.49 created 2000, deleted 2003]

[3.6.1.50] Transferred entry. dynamin GTPase. Now EC 3.6.5.5, dynamin GTPase

[EC 3.6.1.50 created 2000, deleted 2003]

[3.6.1.51] Transferred entry. tubulin GTPase. Now EC 3.6.5.6, tubulin GTPase

[EC 3.6.1.51 created 2000, deleted 2003]

**EC 3.6.1.52**

Accepted name: diphosphoinositol-polyphosphate diphosphatase

Reaction: diphospho-myoinositol polyphosphate + H₂O → myo-inositol polyphosphate + phosphate

Other name(s): diphosphoinositol-polyphosphate phosphohydrolase; DIPP

Systematic name: diphospho-myoinositol-polyphosphate diphosphohydrolase

Comments: This enzyme hydrolyses the diphosphate bond, leaving a phospho group where a diphospho group had been. It can also act on bis(adenosine) diphosphate.

References: [2618, 381]

[EC 3.6.1.52 created 2002]

**EC 3.6.1.53**

Accepted name: Mn²⁺-dependent ADP-ribose/CDP-alcohol diphosphatase

Reaction: (1) CDP-choline + H₂O = CMP + phosphocholine

(2) ADP-β-ribose + H₂O = AMP + β-ribose 5-phosphate

Other name(s): Mn²⁺-dependent ADP-ribose/CDP-alcohol pyrophosphatase; ADPRibase-Mn

Systematic name: CDP-choline phosphohydrolase

Comments: Requires Mn²⁺. Unlike EC 3.6.1.13, ADP-ribose diphosphatase, it cannot utilize Mg²⁺. ADP-β-ribose, CDP-choline, CDP-ethanolamine and ADP are substrates for this enzyme but ADP-β-glucose, UDP-β-glucose, CDP, CMP and AMP are not hydrolysed [392]. The mammalian enzyme hydrolyses cyclic ADP-ribose to 1-(5-phospho-β-D-ribosyl)-AMP with 100-fold lower efficiency than ADP-β-ribose [393]. In rat, the enzyme is found predominantly in thymus and spleen.

References: [394, 392, 393, 2575]

[EC 3.6.1.53 created 2008]

**EC 3.6.1.54**

Accepted name: UDP-2,3-diacylglucosamine diphosphatase

Reaction: a UDP-2-N₃-O₃-bis[(3R)-3-hydroxyacyl]-α-D-glucosamine + H₂O = a lipid X + UMP

Other name(s): lpxH (gene name); UDP-2,3-diacylglucosamine hydrolase; UDP-2,3-diacylglucosamine pyrophosphatase; ybbF (gene name); UDP-2,3-bis[(3R)-3-hydroxymyristoyl]-α-D-glucosamine 2,3-bis[(3R)-3-hydroxymyristoyl]-β-D-glucosaminyl 1-phosphate phosphohydrolase (incorrect); UDP-2-N₃-O₃-bis[(3R)-3-hydroxytetradecanoyl]-α-D-glucosamine 2-N₃-O₃-bis[(3R)-3-hydroxytetradecanoyl]-α-D-glucosaminyl 1-phosphate phosphohydrolase

Systematic name: UDP-2-N₃-O₃-bis[(3R)-3-hydroxyacyl]-α-D-glucosamine 2-N₃-O₃-bis[(3R)-3-hydroxyacyl]-α-D-glucosaminyl 1-phosphate phosphohydrolase

Comments: The enzyme catalyses a step in the biosynthesis of lipid A.

References: [123, 122, 2287, 473, 76]

[EC 3.6.1.54 created 2010, modified 2021]
EC 3.6.1.55
Accepted name: 8-oxo-dGTP diphosphatase
Reaction: 8-oxo-dGTP + H$_2$O = 8-oxo-dGMP + diphosphate
Other name(s): MutT; 7,8-dihydro-8-oxoguanine triphosphatase; 8-oxo-dGTPase; 7,8-dihydro-8-oxo-dGTP pyrophosphohydrolase
Systematic name: 8-oxo-dGTP diphosphohydrolase
Comments: This enzyme hydrolyses the phosphoanhydride bond between the $\alpha$ and $\beta$ phosphate of 8-oxoguanine-containing nucleoside di- and triphosphates thereby preventing misincorporation of the oxidized purine nucleoside triphosphates into DNA. It does not hydrolyse 2-hydroxy-dATP (cf. EC 3.6.1.56, 2-hydroxy-dATP diphosphatase) [3448]. Requires Mg$^{2+}$.
References: [1345, 3465, 2150, 3448]

[EC 3.6.1.55 created 2011]

EC 3.6.1.56
Accepted name: 2-hydroxy-dATP diphosphatase
Reaction: 2-hydroxy-dATP + H$_2$O = 2-hydroxy-dAMP + diphosphate
Other name(s): NUDT1; MTH1; MTH2; oxidized purine nucleoside triphosphatase; (2′-deoxy) ribonucleoside 5′-triphosphate pyrophosphohydrolase
Systematic name: 2-hydroxy-dATP diphosphohydrolase
Comments: The enzyme hydrolyses oxidized purine nucleoside triphosphates such as 2-hydroxy-dATP, thereby preventing their misincorporation into DNA. It can also recognize 8-oxo-dGTP and 8-oxo-dATP, but with lower efficiency (cf. EC 3.6.1.55, 8-oxo-dGTP diphosphatase) [890].
References: [2633, 1443, 890, 2630, 891]

[EC 3.6.1.56 created 2011]

EC 3.6.1.57
Accepted name: UDP-2,4-diacetamido-2,4,6-trideoxy-β-L-altropyranose hydrolase
Reaction: UDP-2,4-diacetamido-2,4,6-trideoxy-β-L-altropyranose + H$_2$O = 2,4-diacetamido-2,4,6-trideoxy-β-L-altropyranose + UDP
Other name(s): PseG; UDP-6-deoxy-AltdiNAc hydrolase; Cj1312; UDP-2,4-bis(acetamido)-2,4,6-trideoxy-β-L-altropyranose hydrolase
Systematic name: UDP-2,4-diacetamido-2,4,6-trideoxy-β-L-altropyranose hydrolase
Comments: The enzyme is involved in biosynthesis of pseudaminic acid.
References: [1815, 2713]

[EC 3.6.1.57 created 2011]

EC 3.6.1.58
Accepted name: 8-oxo-dGDP phosphatase
Reaction: (1) 8-oxo-dGDP + H$_2$O = 8-oxo-dGMP + phosphate
(2) 8-oxo-GDP + H$_2$O = 8-oxo-GMP + phosphate
Other name(s): NUDT5; MTH3 (gene name); NUDT18
Systematic name: 8-oxo-dGDP phosphohydrolase
Comments: The enzyme catalyses the hydrolysis of both 8-oxo-dGDP and 8-oxo-GDP thereby preventing translational errors caused by oxidative damage. The preferred in vivo substrate is not known. The enzyme does not degrade 8-oxo-dGTP and 8-oxo-GTP to the monophosphates (cf. EC 3.6.1.55, 8-oxo-dGTP diphosphatase) [1336, 1337]. Ribonucleotide diphosphates and deoxyribonucleotide diphosphates are hydrolysed with broad specificity. The bifunctional enzyme NUDT5 also hydrolyses ADP-ribose to AMP and D-ribose 5-phosphate (cf. EC 3.6.1.13, ADP-ribose diphosphatase) [1346]. The human enzyme NUDT18 also hydrolyses 8-oxo-dADP and 2-hydroxy-dADP, the latter at a slower rate [2977].
References: [1336, 1337, 1457, 1346, 3484, 2977]

327
EC 3.6.1.59

**Accepted name:** 5′-(N7-methyl 5′-triphosphoguanosine)-[mRNA] diphosphatase

**Reaction:**
a 5′-(N7-methyl 5′-triphosphoguanosine)-[mRNA] + H2O = N7-methylguanosine 5′-phosphate + a 5′-diphospho-[mRNA]

**Other name(s):** DcpS; m7GpppX pyrophosphatase; m7GpppN m7GMP phosphohydrolase; m7G5pp5′N m7GMP phosphohydrolase

**Systematic name:** 5′-(N7-methyl 5′-triphosphoguanosine)-[mRNA] N7-methylguanosine 5′-phosphate phosphohydrolase

**Comments:** The enzyme removes (decaps) the N7-methylguanosine 5-phosphate cap from an mRNA degraded to a maximal length of 10 nucleotides [1816, 504]. Decapping is an important process in the control of eukaryotic mRNA degradation. The enzyme functions to clear the cell of cap structure following decay of the RNA body [1822]. The nematode enzyme can also decap triply methylated substrates, 5′-(N2,N2,N7-trimethyl 5′-triphosphoguanosine)-[mRNA] [3194].

**References:** [1893, 1822, 1816, 3194, 450, 504, 3382]

EC 3.6.1.60

**Accepted name:** diadenosine hexaphosphate hydrolase (AMP-forming)

**Reaction:**
(1) P1,P6-bis(5′-adenosyl)hexaphosphate + H2O = adenosine 5′-pentaphosphate + AMP
(2) P1,P5-bis(5′-adenosyl)pentaphosphate + H2O = adenosine 5′-tetraphosphate + AMP

**Other name(s):** hAps1; NUDT11 (gene name); hAps2; NUDT10 (gene name)

**Systematic name:** P1,P6-bis(5′-adenosyl)hexaphosphate nucleotidohydrolase (AMP-forming)

**Comments:** A divalent cation is essential for activity. Mn2+ (2–6 mM) is most effective. The enzyme controls intracellular levels of P1,P6-bis(5′-adenosyl)pentaphosphate and P1,P6-bis(5′-adenosyl)hexaphosphate. Weak activity with P1,P4-bis(5′-adenosyl)tetraphosphate. Marked preference for adenine over guanine nucleotides.

**References:** [1742, 2619]

EC 3.6.1.61

**Accepted name:** diadenosine hexaphosphate hydrolase (ATP-forming)

**Reaction:**
(1) P1,P6-bis(5′-adenosyl)hexaphosphate + H2O = 2 ATP
(2) P1,P5-bis(5′-adenosyl)pentaphosphate + H2O = ATP + ADP
(3) P1,P4-bis(5′-adenosyl)tetraphosphate + H2O = ATP + AMP

**Other name(s):** Ndx1

**Systematic name:** P1,P6-bis(5′-adenosyl)hexaphosphate nucleotidohydrolase (ATP-forming)

**Comments:** The enzyme requires the presence of the divalent cations (Mn2+, Mg2+, Zn2+, and Co2+). It hydrolyses P1,P4-bis(5-guanosyl) tetraphosphate very slowly [cf. EC 3.6.1.17, bis(5-nucleosyl)-tetraphosphatase (asymmetrical)].

**References:** [1358]

EC 3.6.1.62

**Accepted name:** 5′-(N7-methylguanosine 5′-tripospho)-[mRNA] hydrolase

**Reaction:**
a 5′-(N7-methylguanosine 5′-tripospho)-[mRNA] + H2O = N7-methylguanosine 5′-diphosphate + a 5′-phospho-[mRNA]

**Other name(s):** Dcp2; NUDT16; D10 protein; D9 protein; D10 decapping enzyme; decapping enzyme; m7GpppN-mRNA hydrolase; m7GpppN-mRNA m7GDP phosphohydrolase

328
Decapping of mRNA is a critical step in eukaryotic mRNA turnover. The enzyme is unable to cleave a free cap structure \((m^7\text{GpppG})\) \cite{3193}. The enzyme from Vaccinia virus is synergistically activated in the presence of \(\text{Mg}^{2+}\) and \(\text{Mn}^{2+}\) \cite{2871}.

References: [3389, 1842, 3193, 2352, 2871, 2351, 2860]

[EC 3.6.1.62 created 2012, modified 2013]

**EC 3.6.1.63**

**Accepted name:** α-D-ribose 1-methylphosphonate 5-triphosphate diphosphatase  
**Reaction:** \(\alpha\text{-d-ribose 1-methylphosphonate 5-triphosphate} + \text{H}_2\text{O} = \alpha\text{-d-ribose 1-methylphosphonate 5-phosphate} + \text{diphosphate}\)  
**Other name(s):** \(\text{phnM} \text{ (gene name)}\)  
**Systematic name:** α-D-ribose-1-methylphosphonate-5-triphosphate diphosphohydrolase  
**Comments:** Isolated from the bacterium \(\text{Escherichia coli}\).  
**References:** [1453]

[EC 3.6.1.63 created 2012]

**EC 3.6.1.64**

**Accepted name:** inosine diphosphate phosphatase  
**Reaction:**  
(1) \(\text{IDP} + \text{H}_2\text{O} = \text{IMP} + \text{phosphate}\)  
(2) \(\text{dIDP} + \text{H}_2\text{O} = \text{dIMP} + \text{phosphate}\)  
**Other name(s):** (deoxy)inosine diphosphatase; NUDT16  
**Systematic name:** inosine diphosphate phosphatase  
**Comments:** The human enzyme also hydrolyses GDP and dGDP, and to a lesser extent ITP, dITP and XTP.  
**References:** [1361]

[EC 3.6.1.64 created 2013]

**EC 3.6.1.65**

**Accepted name:** (d)CTP diphosphatase  
**Reaction:**  
(1) \(\text{CTP} + \text{H}_2\text{O} = \text{CMP} + \text{diphosphate}\)  
(2) \(\text{dCTP} + \text{H}_2\text{O} = \text{dCMP} + \text{diphosphate}\)  
**Other name(s):** (d)CTP pyrophosphohydrolase; (d)CTP diphosphohydrolase; \(\text{nuD}G\) (gene name)  
**Systematic name:** (deoxy)cytidine 5′-triphosphate diphosphohydrolase  
**Comments:** The enzyme, characterized from the bacterium \(\text{Escherichia coli}\), is specific for the pyrimidine nucleotides CTP and dCTP. It also acts on 5-methyl-dCTP, 5-hydroxy-dCTP and 8-hydroxy-dGTP.  
**References:** [2264, 892, 1458, 1301]

[EC 3.6.1.65 created 2013]

**EC 3.6.1.66**

**Accepted name:** XTP/dITP diphosphatase  
**Reaction:**  
(1) \(\text{XTP} + \text{H}_2\text{O} = \text{XMP} + \text{diphosphate}\)  
(2) \(\text{dITP} + \text{H}_2\text{O} = \text{dIMP} + \text{diphosphate}\)  
(3) \(\text{ITP} + \text{H}_2\text{O} = \text{IMP} + \text{diphosphate}\)  
**Other name(s):** hypoxanthine/xanthine dNTP pyrophosphatase; \(\text{rdg}B\) (gene name)  
**Systematic name:** XTP/dTTP phosphohydrolase (diphosphate-forming)  
**Comments:** The enzymes from the bacterium \(\text{Escherichia coli}\) and the archaea \(\text{Methanococcus jannaschii}\) and \(\text{Archaeoglobus fulgidus}\) are highly specific for XTP, dITP and ITP. The activity is dependent on divalent cations, \(\text{Mg}^{2+}\) is preferred.
EC 3.6.1.67
Accepted name: dihydroneopterin triphosphate diphosphatase
Reaction: 7,8-dihydroneopterin 3′-triphosphate + H₂O = 7,8-dihydroneopterin 3′-phosphate + diphosphate
Other name(s): folQ (gene name); nudB (gene name); NUDT1 (gene name); dihydroneopterin triphosphate pyrophosphohydrolase
Systematic name: 7,8-dihydroneopterin 3′-triphosphate diphosphohydrolase
Comments: The enzyme participates in a folate biosynthesis pathway, which is found in bacteria, fungi, and plants. Requires Mg²⁺.
References: [2958, 2265, 1558, 924]

EC 3.6.1.68
Accepted name: geranyl diphosphate phosphohydrolase
Reaction: geranyl diphosphate + H₂O = geranyl phosphate + phosphate
Other name(s): NUDX1 (gene name)
Systematic name: geranyl-diphosphate phosphohydrolase
Comments: The enzyme, characterized from roses, is involved in a cytosolic pathway for the biosynthesis of free monoterpene alcohols that contribute to fragrance. In vitro the enzyme also acts on (2E,6E)-farnesyl diphosphate.
References: [1869]

EC 3.6.1.69
Accepted name: 8-oxo-(d)GTP phosphatase
Reaction: (1) 8-oxo-GTP + H₂O = 8-oxo-GDP + phosphate
(2) 8-oxo-dGTP + H₂O = 8-oxo-dGDP + phosphate
Other name(s): mutT1 (gene name)
Systematic name: 8-oxo-dGTP diphosphohydrolase
Comments: The enzyme, characterized from the bacterium Mycobacterium tuberculosis, catalyses the hydrolysis of both 8-oxo-GTP and 8-oxo-dGTP, thereby preventing transcriptional and translational errors caused by oxidative damage. The enzyme is highly specific. Unlike EC 3.6.1.55, 8-oxo-dGTP diphosphatase, it removes only a single phosphate group. The nucleoside diphosphate products are hydrolysed further by EC 3.6.1.58, 8-oxo-dGDP phosphatase.
References: [2357]

EC 3.6.1.70
Accepted name: guanosine-5′-diphospho-5′-[DNA] diphosphatase
Reaction: guanosine-5′-diphospho-5′-[DNA] + H₂O = phospho-5′-[DNA] + GMP
Other name(s): aprataxin; pp5′G5′DNA diphosphatase; pp5′G5′-DNA guanylate hydrolase; APTX (gene name); HNT3 (gene name)
Systematic name: guanosine-5′-diphospho-5′-[DNA] hydrolase (guanosine 5′-phosphate-forming)
Aprataxin is a DNA-binding protein that catalyses (among other activities) the 5' decapping of Gpp-DNA (formed by homologs of RtcB3 from the bacterium Myxococcus xanthus). The enzyme binds the guanylate group to a histidine residue at its active site, forming a covalent enzyme-nucleotide phosphate intermediate, followed by the hydrolysis of the guanylate from the nucleic acid and eventual release. The enzyme forms a 5'-phospho terminus that can be efficiently joined by "classical" ligases. The enzyme also possesses the activity of EC 3.6.1.71, adenosine-5'-diphospho-5'-[DNA] diphosphatase and EC 3.6.1.72, DNA-3'-diphospho-5'-guanosine diphosphatase.

References:
[1945]

EC 3.6.1.71

Accepted name: adenosine-5'-diphospho-5'-[DNA] diphosphatase
Reaction:
(1) adenosine-5'-diphospho-5'-[DNA] + H2O = AMP + phospho-5'-[DNA]
(2) adenosine-5'-diphospho-5'-[DNA] + H2O = AMP + 5'-phospho-(ribonucleotide)-[DNA]
Other name(s): aprataxin; 5'-App5'-DNA adenylate hydrolase; APTX (gene name); HNT3 (gene name)
Systematic name: adenosine-5'-diphospho-5'-[DNA] hydrolase (adenosine 5'-phosphate-forming)
Comments: Aprataxin is a DNA-binding protein involved in different types of DNA break repair. The enzyme acts (among other activities) on abortive DNA ligation intermediates that contain an adenylate covalently linked to the 5'-phosphate DNA terminus. It also acts when the adenylate is covalently linked to the 5'-phosphate of a ribonucleotide linked to a DNA strand, which is the result of abortive ligase activity on products of EC 3.1.26.4, ribonuclease H, an enzyme that cleaves RNA-DNA hybrids on the 5' side of the ribonucleotide found in the 5'-RNA-DNA-3' junction. Aprataxin binds the adenylate group to a histidine residue within the active site, followed by its hydrolysis from the nucleic acid and eventual release, leaving a 5'-phosphate terminus that can be efficiently rejoined. The enzyme also possesses the activities of EC 3.6.1.70, guanosine-5'-diphospho-5'-[DNA] diphosphatase, and EC 3.6.1.72, DNA-3'-diphospho-5'-guanosine diphosphatase.
References: [25, 3143]

EC 3.6.1.72

Accepted name: DNA-3'-diphospho-5'-guanosine diphosphatase
Reaction: [DNA]-3'-diphospho-5'-guanosine + H2O = [DNA]-3'-phosphate + GMP
Other name(s): aprataxin; DNA-3'ppG guanylate hydrolase; APTX (gene name); HNT3 (gene name)
Systematic name: [DNA]-3'-diphospho-5'-guanosine hydrolase (guanosine 5'-phosphate-forming)
Comments: Aprataxin is a DNA-binding protein that catalyses (among other activities) the 3' decapping of DNA-ppG (formed by EC 6.5.1.8, 3'-phosphate/5'-hydroxy nucleic acid ligase) [580]. The enzyme binds the guanylate group to a histidine residue at its active site, forming a covalent enzyme-nucleotide phosphate intermediate, followed by the hydrolysis of the guanylate from the nucleic acid and its eventual release. The enzyme also possesses the activity of EC 3.6.1.71, adenosine-5'-diphospho-5'-[DNA] diphosphatase, and EC 3.6.1.70, guanosine-5'-diphospho-5'-[DNA] diphosphatase.
References: [580, 441]

EC 3.6.1.73

Accepted name: inosine/xanthosine triphosphatase
Reaction:
(1) inosine 5'-triphosphate + H2O = inosine 5'-diphosphate + phosphate
(2) xanthosine 5'-triphosphate + H2O = xanthosine 5'-diphosphate + phosphate
Other name(s): yjjX (gene name)
Systematic name: inosine/xanthosine 5'-triphosphate phosphohydrolase
The enzyme, characterized from the bacterium *Escherichia coli*, preferentially hydrolyses inosine triphosphate and xanthosine triphosphate, which are formed by oxidative deamination damage. By hydrolysing these damaged nucleotides, the enzyme prevents their incorporation into RNA.

References: [3500]

EC 3.6.1.74

**Accepted name:** mRNA 5′-phosphatase  
**Reaction:** a 5′-triphospho-[mRNA] + H2O = a 5′-diphospho-[mRNA] + phosphate  
**Other name(s):** 5′-polynucleotidase; polynucleotide 5′-phosphohydrolase; RNGTT (gene name); CET1 (gene name); mRNA 5′-triposphate monophosphatase  
**Systematic name:** 5′-triphospho-mRNA 5′-phosphohydrolase  
**Comments:** The enzyme, found in eukaryotes and some plus strand RNA viruses (e.g. alphavirus), is involved in mRNA capping. Unlike the eukaryotic enzyme, the viral enzyme requires a purine in the first position of the mRNA. The human enzyme is a multi domain protein that also has the activity of EC 2.7.7.50, mRNA guanylyltransferase.

References: [1347, 3129, 3204]

EC 3.6.1.75

**Accepted name:** diacylglycerol diphosphate phosphatase  
**Reaction:** 1,2-diacyl-sn-glycerol 3-diphosphate + H2O = 1,2-diacyl-sn-glycerol 3-phosphate + phosphate  
**Other name(s):** DGPP phosphatase; DGPP phosphohydrolase; DPP1, DPPL1, DPPL2, FAP2; pyrophosphate phosphatase  
**Systematic name:** 1,2-diacyl-sn-glycerol 3-phosphate phosphohydrolase  
**Comments:** The bifunctional enzyme catalyses the dephosphorylation of diacylglycerol diphosphate to phosphatidate and the subsequent dephosphorylation of phosphatidate to diacylglycerol (*cf.* phosphatidate phosphatase (EC 3.1.3.4)). It regulates intracellular levels of diacylglycerol diphosphate and phosphatidate, phospholipid molecules believed to play a signalling role in stress response [1101]. The phosphatase activity of the bifunctional enzyme is Mg2+-independent and N-ethylmaleimide-insensitive and is distinct from the Mg2+-dependent and N-ethylmaleimide-sensitive enzyme EC 3.1.3.4 (phosphatidate phosphatase) [402]. The diacylglycerol pyrophosphate phosphatase activity in *Saccharomyces cerevisiae* is induced by zinc depletion, by inositol supplementation, and when cells enter the stationary phase [2316].

References: [659, 658, 3377, 2316, 402, 1101]

EC 3.6.1.76

**Accepted name:** prenyl-diphosphate phosphatase  
**Reaction:** (1) prenyl diphosphate + H2O = prenyl phosphate + phosphate  
(2) 3-methylbut-3-en-1-yl diphosphate + H2O = 3-methylbut-3-en-1-yl phosphate + phosphate  
**Systematic name:** prenyl diphosphate/3-methylbut-3-en-1-yl diphosphate phosphohydrolase  
**Comments:** The enzyme, characterized from the methanogenic archaeon *Methanosarcina mazei*, belongs to the Nudix hydrolase family (a superfamily of hydrolytic enzymes capable of cleaving nucleoside diphosphates linked to a moiety). Its main purpose is to provide the substrate for EC 2.5.1.129, flavin prenyltransferase.

References: [1338]

[EC 3.6.1.73 created 2020]
[EC 3.6.1.74 created 2021]
[EC 3.6.1.75 created 2010 as EC 3.1.3.81, 2022 transferred to EC 3.6.1.75]
[EC 3.6.1.76 created 2022]
EC 3.6.2 In sulfonyl-containing anhydrides

EC 3.6.2.1
Accepted name: adenylylsulfatase
Reaction: adenylyl sulfatase + H₂O = AMP + sulfate
Other name(s): adenosine 5-phosphosulfate sulfohydrolase; adenylylsulfate sulfohydrolase
Systematic name: adenylyl-sulfate sulfohydrolase
References: [135]

[EC 3.6.2.1 created 1972]

EC 3.6.2.2
Accepted name: phosphoadenylylsulfatase
Reaction: 3′-phosphoadenylyl sulfatase + H₂O = adenosine 3′,5′-bisphosphate + sulfate
Other name(s): 3-phosphoadenylyl sulfatase; 3-phosphoadenosine 5-phosphosulfate sulfatase; PAPS sulfatase; 3′-phosphoadenylylsulfate sulfohydrolase
Systematic name: 3′-phosphoadenylyl-sulfate sulfohydrolase
Comments: Requires Mn²⁺.
References: [142]

[EC 3.6.2.2 created 1972]

EC 3.6.3 Acting on acid anhydrides to catalyse transmembrane movement of substances

Several types of ATP phosphohydrolase are listed here. Entries EC 3.6.3.1 to EC 3.6.3.12 and EC 3.6.3.53 are enzymes undergoing covalent phosphorylation of an aspartate residue during the transport cycle; entries EC 3.6.3.14 and EC 3.6.3.15 refer to enzymes of complicated membrane and non-membrane location that can also serve in ATP synthesis; entry EC 3.6.3.16 is a multisubunit enzyme that is involved in arsenite transport only; entries EC 3.6.3.17 to EC 3.6.3.50 are two-domain enzymes of the ABC family; entries EC 3.6.3.51 and EC 3.6.3.52 are parts of a complex protein-transporting machinery in mitochondria and chloroplasts.

[3.6.3.1 Transferred entry. phospholipid-translocating ATPase. Now EC 7.6.2.1, P-type phospholipid transporter] [EC 3.6.3.1 created 2000 (EC 3.6.3.13 created 2000, incorporated 2001), deleted 2018]

[3.6.3.2 Transferred entry. Mg²⁺-importing ATPase. Now EC 7.2.2.14, P-type Mg²⁺ transporter] [EC 3.6.3.2 created 2000, modified 2001, deleted 2018]

[3.6.3.3 Transferred entry. Cd²⁺-exporting ATPase. Now EC 7.2.2.21, Cd²⁺-exporting ATPase] [EC 3.6.3.3 created 2000, deleted 2019]

[3.6.3.4 Transferred entry. Cu²⁺-exporting ATPase. Now EC 7.2.2.9, Cu²⁺-exporting ATPase] [EC 3.6.3.4 created 2000, modified 2013, deleted 2018]

[3.6.3.5 Transferred entry. Zn²⁺-exporting ATPase. Now EC 7.2.2.12, Zn²⁺-exporting ATPase] [EC 3.6.3.5 created 2000, modified 2001, modified 2006, deleted 2018]

[3.6.3.6 Transferred entry. H⁺-exporting ATPase. Now EC 7.1.2.1, P-type H⁺-exporting transporter] [EC 3.6.3.6 created 1984 as EC 3.6.1.35, transferred 2000 to EC 3.6.3.6, deleted 2018]

[3.6.3.7 Transferred entry. Na⁺-exporting ATPase. Now EC 7.2.2.3, P-type Na⁺ transporter] [EC 3.6.3.7 created 2000, modified 2001, transferred 2018 to EC 7.2.2.3, deleted 2018]

[3.6.3.8 Transferred entry. Ca²⁺-transporting ATPase. Now EC 7.2.2.10, Ca²⁺-transporting ATPase]
[EC 3.6.3.8 created 1984 as EC 3.6.1.38, transferred 2000 to EC 3.6.3.8, modified 2001, modified 2011, deleted 2018]

[3.6.3.9] Transferred entry. Na\(^+\)/K\(^+\)-exchanging ATPase. Now EC 7.2.2.13, Na\(^+\)/K\(^+\)-exchanging ATPase

[EC 3.6.3.9 created 1984 as EC 3.6.1.37, transferred 2000 to EC 3.6.3.9, modified 2001, deleted 2018]

[3.6.3.10] Transferred entry. H\(^+\)/K\(^+\)-exchanging ATPase. Now EC 7.2.2.19, H\(^+\)/K\(^+\)-exchanging ATPase

[EC 3.6.3.10 created 1984 as EC 3.6.1.36, transferred 2000 to EC 3.6.3.10, deleted 2018]

[3.6.3.11] Deleted entry. Cl\(^-\)-transporting ATPase. The activity was only ever studied in crude extracts, and is an artifact.

[EC 3.6.3.11 created 2000, deleted 2020]

[3.6.3.12] Transferred entry. K\(^+\)-transporting ATPase. Now EC 7.2.2.6, K\(^+\)-transporting ATPase

[EC 3.6.3.12 created 2000, deleted 2018]

[3.6.3.13] Deleted entry. aminophospholipid-transporting ATPase. Identical to EC 3.6.3.1, phospholipid-translocating ATPase

[EC 3.6.3.13 created 2000, deleted 2001]


[EC 3.6.3.14 created 1984 as EC 3.6.1.34, transferred 2000 to EC 3.6.3.14, deleted 2018]


[EC 3.6.3.15 created 2000, transferred 2018 to EC 7.2.2.1, deleted 2018]

[3.6.3.16] Transferred entry. arsenite-transporting ATPase. Now EC 7.3.2.7, arsenite-transporting ATPase

[EC 3.6.3.16 created 2000, deleted 2019]


[EC 3.6.3.17 created 2000, deleted 2019]

[3.6.3.18] Transferred entry. oligosaccharide-transporting ATPase. Now EC 7.5.2.2, ABC-type oligosaccharide transporter

[EC 3.6.3.18 created 2000, deleted 2018]

[3.6.3.19] Transferred entry. maltose-transporting ATPase. Now EC 7.5.2.1, ABC-type maltose transporter

[EC 3.6.3.19 created 2000, deleted 2018]


[EC 3.6.3.20 created 2000, deleted 2018]

[3.6.3.21] Transferred entry. polar-amino-acid-transporting ATPase. Now EC 7.4.2.1, ABC-type polar-amino-acid transporter

[EC 3.6.3.21 created 2000, deleted 2018]

[3.6.3.22] Transferred entry. nonpolar-amino-acid-transporting ATPase. Now EC 7.4.2.2, ABC-type nonpolar-amino-acid transporter

[EC 3.6.3.22 created 2000, deleted 2018]

[3.6.3.23] Transferred entry. oligopeptide-transporting ATPase. Now EC 7.4.2.6, oligopeptide-transporting ATPase

[EC 3.6.3.23 created 2000, deleted 2018]

[3.6.3.24] Transferred entry. nickel-transporting ATPase. Now EC 7.2.2.11, nickel-transporting ATPase

334
[EC 3.6.3.24 created 2000, deleted 2018]

[3.6.3.25 Transferred entry. sulfate-transporting ATPase. Now EC 7.3.2.3, sulfate-transporting ATPase]

[EC 3.6.3.25 created 2000, deleted 2018]

[3.6.3.26 Transferred entry. nitrate-transporting ATPase. Now EC 7.3.2.4, nitrate-transporting ATPase]

[EC 3.6.3.26 created 2000, deleted 2018]

[3.6.3.27 Transferred entry. phosphate-transporting ATPase. Now EC 7.3.2.1, ABC-type phosphate transporter]

[EC 3.6.3.27 created 2000, deleted 2018]

[3.6.3.28 Transferred entry. phosphonate-transporting ATPase. Now EC 7.3.2.2, ABC-type phosphonate transporter]

[EC 3.6.3.28 created 2000, deleted 2018]

[3.6.3.29 Transferred entry. molybdate-transporting ATPase. Now EC 7.3.2.5, molybdate-transporting ATPase]

[EC 3.6.3.29 created 2000, deleted 2018]

[3.6.3.30 Transferred entry. Fe$^{3+}$-transporting ATPase. Now EC 7.2.2.7, Fe$^{3+}$-transporting ATPase]

[EC 3.6.3.30 created 2000, deleted 2018]

[3.6.3.31 Transferred entry. polyamine-transporting ATPase. Now EC 7.6.2.11, polyamine-transporting ATPase]

[EC 3.6.3.31 created 2000, deleted 2018]

[3.6.3.32 Transferred entry. quaternary-amine-transporting ATPase. Now EC 7.6.2.9, quaternary-amine-transporting ATPase]

[EC 3.6.3.32 created 2000, deleted 2018]

[3.6.3.33 Transferred entry. vitamin B$^{12}$-transporting ATPase. Now EC 7.6.2.8, vitamin B$^{12}$-transporting ATPase]

[EC 3.6.3.33 created 2000, deleted 2018]

[3.6.3.34 Transferred entry. iron-chelate-transporting ATPase; now recognized to be at least 3 separate enzymes EC 7.2.2.16, iron(III) hydroxamate ABC transporter, EC 7.2.2.17, ferric enterobactin ABC transporter, and EC 7.2.2.18, ferric citrate ABC transporter]

[EC 3.6.3.34 created 2000, deleted 2018]

[3.6.3.35 Transferred entry. manganese-transporting ATPase. Now EC 7.2.2.5, manganese-transporting ATPase]

[EC 3.6.3.35 created 2000, deleted 2018]

[3.6.3.36 Transferred entry. taurine-transporting ATPase. Now EC 7.6.2.7, taurine-transporting ATPase]

[EC 3.6.3.36 created 2000, deleted 2018]

[3.6.3.37 Transferred entry. guanine-transporting ATPase. Now EC 7.6.2.6, guanine-transporting ATPase]

[EC 3.6.3.37 created 2000, deleted 2018]

[3.6.3.38 Transferred entry. capsular-polysaccharide-transporting ATPase. Now EC 7.6.2.12, ABC-type capsular-polysaccharide transporter]

[EC 3.6.3.38 created 2000, deleted 2018]

[3.6.3.39 Transferred entry. lipopolysaccharide-transporting ATPase. Now EC 7.5.2.5, lipopolysaccharide-transporting ATPase]

[EC 3.6.3.39 created 2000, deleted 2018]

[3.6.3.40 Transferred entry. teichoic-acid-transporting ATPase. Now EC 7.5.2.4, teichoic-acid-transporting ATPase] 335
[3.6.3.40 created 2000, deleted 2018]

[3.6.3.41 Transferred entry. heme-transporting ATPase. Now EC 7.6.2.5, heme-transporting ATPase]

[3.6.3.41 created 2000, deleted 2018]

[3.6.3.42 Transferred entry. β-glucan-transporting ATPase. Now EC 7.5.2.3, β-glucan-transporting ATPase]

[3.6.3.42 created 2000, deleted 2018]

[3.6.3.43 Transferred entry. peptide-transporting ATPase. Now EC 7.4.2.5, peptide-transporting ATPase]

[3.6.3.43 created 2000, deleted 2018]

[3.6.3.44 Transferred entry. xenobiotic-transporting ATPase. Now EC 7.6.2.2, ABC-type xenobiotic transporter]

[EC 3.6.3.44 created 2000 (EC 3.6.3.45 incorporated 2006), modified 2006, deleted 2018]

[3.6.3.45 Deleted entry. steroid-transporting ATPase. Now included with EC 3.6.3.44, xenobiotic-transporting ATPase]

[EC 3.6.3.45 created 2000, deleted 2006]

[3.6.3.46 Transferred entry. cadmium-transporting ATPase. Now EC 7.2.2.2, ABC-type Cd²⁺ transporter]

[EC 3.6.3.46 created 2000, transferred 2018 to EC 7.2.2.2, deleted 2018]

[3.6.3.47 Transferred entry. fatty-acyl-CoA-transporting ATPase. Now EC 7.6.2.4, fatty-acyl-CoA-transporting ATPase]

[EC 3.6.3.47 created 2000, deleted 2018]

[3.6.3.48 Transferred entry. α-factor-transporting ATPase. Now EC 7.4.2.7 as α-factor-pheromone transporting ATPase]

[EC 3.6.3.48 created 2000, deleted 2018]

[3.6.3.49 Transferred entry. channel-conductance-controlling ATPase. Now EC 5.6.1.6, channel-conductance-controlling ATPase]

[EC 3.6.3.49 created 2000, deleted 2018]

[3.6.3.50 Transferred entry. protein-secreting ATPase. Now EC 7.4.2.8, protein-secreting ATPase]

[EC 3.6.3.50 created 2000, deleted 2018]

[3.6.3.51 Transferred entry. mitochondrial protein-transporting ATPase. Now EC 7.4.2.3, mitochondrial protein-transporting ATPase]

[EC 3.6.3.51 created 2000, deleted 2018]

[3.6.3.52 Transferred entry. chloroplast protein-transporting ATPase. Now EC 7.4.2.4, chloroplast protein-transporting ATPase]

[EC 3.6.3.52 created 2000, deleted 2018]

[3.6.3.53 Transferred entry. Ag⁺-exporting ATPase. Now EC 7.2.2.15, Ag⁺-exporting ATPase]

[EC 3.6.3.53 created 2000, deleted 2018]

[3.6.3.54 Transferred entry. Cu⁺-exporting ATPase. Now EC 7.2.2.8, Cu⁺-exporting ATPase]

[EC 3.6.3.54 created 2013, deleted 2018]

[3.6.3.55 Transferred entry. tungstate-importing ATPase. Now EC 7.3.2.6, tungstate-importing ATPase]

[EC 3.6.3.55 created 2013, deleted 2018]

336
EC 3.6.4 Acting on acid anhydrides to facilitate cellular and subcellular movement

[3.6.4.1] Transferred entry. myosin ATPase. Now EC 5.6.1.8, myosin ATPase

[EC 3.6.4.1 created 1984 as EC 3.6.1.32, transferred 2000 to EC 3.6.4.1, deleted 2018]

[3.6.4.2] Transferred entry. dynein ATPase. Now EC 5.6.1.2, dynein ATPase

[EC 3.6.4.2 created 1984 as EC 3.6.1.33, transferred 2000 to EC 3.6.4.2, deleted 2018]

[3.6.4.3] Transferred entry. microtubule-severing ATPase. Now EC 5.6.1.1, microtubule-severing ATPase

[EC 3.6.4.3 created 2000 as 3.6.4.3, deleted 2018]


[EC 3.6.4.4 created 2000, deleted 2018]

[3.6.4.5] Transferred entry. minus-end-directed kinesin ATPase. Now EC 5.6.1.4, minus-end-directed kinesin ATPase

[EC 3.6.4.5 created 2000, deleted 2018]

EC 3.6.4.6

Accepted name: vesicle-fusing ATPase
Reaction: ATP + H₂O = ADP + phosphate
Systematic name: ATP phosphohydrolase (vesicle-fusing)
Comments: A large family of ATP-hydrolysing enzymes involved in the heterotypic fusion of membrane vesicles with target membranes and the homotypic fusion of various membrane compartments. They belong to the AAA-type (ATPase associated with a variety of cell activities) ATPase superfamily. They include peroxin, which apparently is involved in Zellweger’s syndrome.

References: [512, 1317, 124]

[EC 3.6.4.6 created 2000]

EC 3.6.4.7

Accepted name: peroxisome-assembly ATPase
Reaction: ATP + H₂O = ADP + phosphate
Other name(s): peroxisome assembly factor-2
Systematic name: ATP phosphohydrolase (peroxisome-assembling)
Comments: An extremely diversified group of enzymes that use the energy of ATP hydrolysis to import and assemble peroxisome components into the organelle. Their molecular masses range from 25 to 600 kDa.

References: [1729, 3128, 3396]

[EC 3.6.4.7 created 2000]

[3.6.4.8] Transferred entry. proteasome ATPase. Now EC 5.6.1.5, proteasome ATPase

[EC 3.6.4.8 created 2000, deleted 2018]

[3.6.4.9] Transferred entry. chaperonin ATPase. Now EC 5.6.1.7, chaperonin ATPase

[EC 3.6.4.9 created 2000, deleted 2018]

EC 3.6.4.10

Accepted name: non-chaperonin molecular chaperone ATPase
Reaction: ATP + H₂O = ADP + phosphate
Other name(s): molecular chaperone Hsc70 ATPase
**Systematic name:** ATP phosphohydrolase (polypeptide-polymerizing)

**Comments:** This is a highly diverse group of enzymes that perform many functions that are similar to those of chaperonins. They comprise a number of heat-shock-cognate proteins. They are also active in clathrin uncoating and in the oligomerization of actin.

**References:** [2614, 269, 3292, 2887, 1764]

[EC 3.6.4.10 created 2000]

[3.6.4.11] *Deleted entry. nucleoplasm ATPase. The activity has been shown not to take place.* [EC 3.6.4.11 created 2000, deleted 2018]

[3.6.4.12] *Transferred entry. DNA helicase. Now EC 5.6.2.3, DNA 5-3 helicase and EC 5.6.2.4, DNA 3-5 helicase* [EC 3.6.4.12 created 2009, deleted 2021]

**EC 3.6.4.13**

**Accepted name:** RNA helicase

**Reaction:** ATP + H₂O = ADP + phosphate

**Other name(s):** CSFV NS3 helicase; DBP2; DbpA; DDX17; DDX25; DDX3; DDX3X; DDX3Y; DDX4; DDX5; DEAD-box protein DED1; DEAD-box RNA helicase; DEAH-box protein 2; DEAH-box RNA helicase; DED1; Dx(H/D) RNA helicase; EhDEAD1; EhDEAD1 RNA helicase; elf4A helicase; KOKV helicase; Mtr4p; nonstructural protein 3 helicase; NPH-II; RHA; RNA helicase A; RNA helicase DDX3; RNA helicase Hera; RNA-dependent ATPase; TGBp1 NTPase/helicase domain; VRH1; GRTH/DDX25

**Systematic name:** ATP phosphohydrolase (RNA helix unwinding)

**Comments:** RNA helicases utilize the energy from ATP hydrolysis to unwind RNA. Some of them unwind RNA with a 3′ to 5′ polarity [1709], other show 5′ to 3′ polarity [?]. Some helicases unwind DNA as well as RNA [866, ?]. May be identical with EC 3.6.4.12 (DNA helicase).

**References:** [526, 2572, 1709, 1761, 3372, 1048, 866, ?]

[EC 3.6.4.13 created 2009]

**EC 3.6.5 Acting on GTP to facilitate cellular and subcellular movement**

**EC 3.6.5.1**

**Accepted name:** heterotrimeric G-protein GT-Pase

**Reaction:** GTP + H₂O = GDP + phosphate

**Systematic name:** GTP phosphohydrolase (signalling)

**Comments:** This group comprises GTP-hydrolysing systems, where GTP and GDP alternate in binding. This group includes stimulatory and inhibitory G-proteins such as Gᵢ, Gₛ, Gₒ and Gₒᵣ, targeting adenylate cyclase and/or K⁺ and Ca²⁺ channels; Gₛ stimulating phospholipase C; transducin activating cGMP phosphodiesterase; gustducin activating cAMP phosphodiesterase. Gₒᵣ is instrumental in odour perception, transducin in vision and gustducin in taste recognition. At least 16 different α subunits (39-52 kDa), 5 β subunits (36 kDa) and 12 γ subunits (6-9 kDa) are known.

**References:** [2170, 2883, 286, 2023]

[EC 3.6.5.1 created 2000 as EC 3.6.1.46, transferred 2003 to EC 3.6.5.1]

**EC 3.6.5.2**

**Accepted name:** small monomeric GTPase

**Reaction:** GTP + H₂O = GDP + phosphate

**Systematic name:** GTP phosphohydrolase (cell-regulating)
Comments: A family of about 50 enzymes with a molecular mass of 21 kDa that are distantly related to the α-subunit of heterotrimeric G-protein GTPase (EC 3.6.5.1). They are involved in cell-growth regulation (Ras subfamily), membrane vesicle traffic and uncoating (Rab and ARF subfamilies), nuclear protein import (Ran subfamily) and organization of the cytoskeleton (Rho and Rac subfamilies).

References: [298, 1087, 953, 3221]

[EC 3.6.5.2 created 2000 as EC 3.6.1.47, transferred 2003 to EC 3.6.5.2]

EC 3.6.5.3

Accepted name: protein-synthesizing GTPase
Reaction: GTP + H₂O = GDP + phosphate
Other name(s): elongation factor (EF); initiation factor (IF); peptide-release or termination factor
Systematic name: GTP phosphohydrolase (mRNA-translation-assisting)
Comments: This enzyme comprises a family of proteins involved in prokaryotic as well as eukaryotic protein synthesis. In the initiation factor complex, it is IF-2b (98 kDa) that binds GTP and subsequently hydrolyses it in prokaryotes. In eukaryotes, it is eIF-2 (150 kDa) that binds GTP. In the elongation phase, the GTP-hydrolysing proteins are the EF-Tu polypeptide of the prokaryotic transfer factor (43 kDa), the eukaryotic elongation factor EF-1α (53 kDa), the prokaryotic EF-G (77 kDa), the eukaryotic EF-2 (70-110 kDa) and the signal recognition particle that play a role in endoplasmic reticulum protein synthesis (325 kDa). EF-Tu and EF-1α catalyse binding of aminoacyl-tRNA to the ribosomal A-site, while EF-G and EF-2 catalyse the translocation of peptidyl-tRNA from the A-site to the P-site. GTPase activity is also involved in polypeptide release from the ribosome with the aid of the pRFs and eRFs.

References: [1667, 1555, 2574, 857, 1615]

[EC 3.6.5.3 created 2000 as EC 3.6.1.48, transferred 2003 to EC 3.6.5.3]

EC 3.6.5.4

Accepted name: signal-recognition-particle GTPase
Reaction: GTP + H₂O = GDP + phosphate
Systematic name: GTP phosphohydrolase (protein-synthesis-assisting)
Comments: Activity is associated with the signal-recognition particle (a protein- and RNA-containing structure involved in endoplasmic-reticulum-associated protein synthesis).

References: [519, 520, 2011, 865]

[EC 3.6.5.4 created 2000 as EC 3.6.1.49, transferred 2003 to EC 3.6.5.4]

EC 3.6.5.5

Accepted name: dynamin GTPase
Reaction: GTP + H₂O = GDP + phosphate
Systematic name: GTP phosphohydrolase (vesicle-releasing)
Comments: An enzyme with a molecular mass of about 100 kDa that is involved in endocytosis and is instrumental in pinching off membrane vesicles.

References: [3281, 1959, 2263]

[EC 3.6.5.5 created 2000 as EC 3.6.1.50, transferred 2003 to EC 3.6.5.5]

EC 3.6.5.6

Accepted name: tubulin GTPase
Reaction: GTP + H₂O = GDP + phosphate
Systematic name: GTP phosphohydrolase (microtubule-releasing)
Comments: An intrinsic activity of α-tubulin involved in tubulin folding, division plane formation in prokaryotic cells and others.
EC 3.7 Acting on carbon-carbon bonds

This subclass contains a single sub-subclass for those enzymes that act on carbon-carbon bonds in ketonic substances (EC 3.7.1). There are relatively few carbon-carbon hydrolases and they mostly catalyse the hydrolysis of 3-oxo-carboxylic acids.

EC 3.7.1 In ketonic substances

EC 3.7.1.1
Accepted name: oxaloacetase
Reaction: oxaloacetate + H₂O = oxalate + acetate
Other name(s): oxalacetic hydrolase
Systematic name: oxaloacetate acetylhydrolase
References: [1149]

EC 3.7.1.2
Accepted name: fumarylacetoacetase
Reaction: 4-fumarylacetoacetate + H₂O = acetoacetate + fumarate
Other name(s): β-diketonase; fumarylacetoacetate hydrolase
Systematic name: 4-fumarylacetoacetate fumarylhydrolase
Comments: Also acts on other 3,5- and 2,4-dioxo acids.
References: [522, 722, 1976]

EC 3.7.1.3
Accepted name: kynureninase
Reaction: L-kynurenine + H₂O = anthranilate + L-alanine
Systematic name: L-kynurenine hydrolase
Comments: A pyridoxal-phosphate protein. Also acts on 3′-hydroxy-L-kynurenine and some other (3-arylcarbonyl)-alanines.
References: [1380, 1379, 1570, 3355]

EC 3.7.1.4
Accepted name: phloretin hydrolase
Reaction: phloretin + H₂O = phloretate + phloroglucinol
Other name(s): ErPh; lactase-phlorerin hydrolase; C-acylphenol hydrolase; 2′,4,4′,6′-tetrahydroxydehydrochalcone 1,3,5-trihydroxybenzeneydrolase (incorrect)
Systematic name: phloretin acylhydrolase (phloroglucinol-forming)
Comments: Also hydrolyses other C-acylated phenols related to phloretin. Isolated from the fungus Aspergillus niger and the bacteria Pantoea agglomerans and Eubacterium ramulus.
References: [437, 2021, 2712]
EC 3.7.1.5
Accepted name: acylpyruvate hydrolase
Reaction: a 3-acylpyruvate + H₂O = a carboxylate + pyruvate
Systematic name: 3-acylpyruvate acylhydrolase
Comments: Acts on formylpyruvate, 2,4-dioxopentanoate, 2,4-dioxohexanoate and 2,4-dioxoheptanoate.
References: [3289]

[EC 3.7.1.5 created 1976]

EC 3.7.1.6
Accepted name: acetylpyruvate hydrolase
Reaction: acetylpyruvate + H₂O = acetate + pyruvate
Systematic name: 2,4-dioxopentanoate acetylhydrolase
Comments: Highly specific; does not act on pyruvate, oxaloacetate, maleylpyruvate, fumarlypyruvate or acetylacetone.
References: [584]

[EC 3.7.1.6 created 1984]

EC 3.7.1.7
Accepted name: β-diketone hydrolase
Reaction: nonane-4,6-dione + H₂O = pentan-2-one + butanoate
Other name(s): oxidized PVA hydrolase
Systematic name: nonane-4,6-dione acylhydrolase
Comments: Also acts on the product of the action of EC 1.1.3.18 secondary-alcohol oxidase, on polyvinyl alcohols; involved in the bacterial degradation of polyvinyl alcohol.
References: [2628, 2629]

[EC 3.7.1.7 created 1989]

EC 3.7.1.8
Accepted name: 2,6-dioxo-6-phenylhexa-3-enoate hydrolase
Reaction: 2,6-dioxo-6-phenylhexa-3-enoate + H₂O = benzoate + 2-oxopent-4-enoate
Other name(s): HOHPDA hydrolase
Systematic name: 2,6-dioxo-6-phenylhexa-3-enoate benzoylhydrolase
Comments: Cleaves the products from biphenol, 3-isopropylcatechol and 3-methylcatechol produced by EC 1.13.11.39 biphenyl-2,3-diol 1,2-dioxygenase, by ring-fission at a -CO-C bond. Involved in the breakdown of biphenyl-related compounds by Pseudomonas sp.
References: [2305]

[EC 3.7.1.8 created 1989]

EC 3.7.1.9
Accepted name: 2-hydroxymuconate-6-semialdehyde hydrolase
Reaction: 2-hydroxymuconate-6-semialdehyde + H₂O = formate + 2-oxopent-4-enoate
Other name(s): 2-hydroxymuconate-6-semialdehyde formylhydrolase; HMSH; HOD hydrolase; xyF (gene name); 2-hydroxymuconate-semialdehyde formylhydrolase; 2-hydroxymuconate-semialdehyde hydrolase
Systematic name: 2-hydroxymuconate-6-semialdehyde formylhydrolase
Comments: The enzyme is involved in the degradation of catechols.
References: [2635, 1112, 646]

[EC 3.7.1.9 created 1990, modified 2013]
EC 3.7.1.10
Accepted name: cyclohexane-1,3-dione hydrolase
Reaction: cyclohexane-1,3-dione + H₂O = 5-oxohexanoate
Other name(s): 1,3-cyclohexanedione hydrolase; cyclohexane-1,3-dione acylhydrolase (decyclizing)
Systematic name: cyclohexane-1,3-dione acylhydrolase (ring-opening)
Comments: Highly specific; does not act on other dione derivatives of cyclohexane, cyclopentane or cycloheptane.
References: [576]

[EC 3.7.1.10 created 1992]

EC 3.7.1.11
Accepted name: cyclohexane-1,2-dione hydrolase
Reaction: cyclohexane-1,2-dione + H₂O = 6-oxohexanoate
Other name(s): cyclohexane-1,2-dione acylhydrolase (decyclizing)
Systematic name: cyclohexane-1,2-dione acylhydrolase (ring-opening)
Comments: Highly specific; does not act on cyclohexanone or cyclohexane-1,3-dione as substrate.
References: [1113, 852]

[EC 3.7.1.11 created 2009]

EC 3.7.1.12
Accepted name: cobalt-precorrin 5A hydrolase
Reaction: cobalt-precorrin-5A + H₂O = cobalt-precorrin-5B + acetaldehyde + 2 H⁺
Other name(s): CbiG
Systematic name: cobalt-precorrin 5A acylhydrolase
Comments: This enzyme hydrolyses the ring A acetate δ-lactone of cobalt-precorrin-5A resulting in the loss of the C-20 carbon and its attached methyl group in the form of acetaldehyde. This is a key reaction in the contraction of the porphyrin-type tetrapyrrole ring and its conversion to a corrin ring in the anaerobic (early cobalt insertion) adenosylcobalamin biosynthesis pathway.
References: [1440, 2059]

[EC 3.7.1.12 created 2010]

EC 3.7.1.13
Accepted name: 2-hydroxy-6-oxo-6-(2-aminophenyl)hexa-2,4-dienoate hydrolase
Reaction: (2E,4E)-6-(2-aminophenyl)-2-hydroxy-6-oxohexa-2,4-dienoate + H₂O = anthranilate + (2E)-2-hydroxypenta-2,4-dienoate
Other name(s): mhpC (gene name)
Systematic name: (2E,4E)-6-(2-aminophenyl)-2-hydroxy-6-oxohexa-2,4-dienoate acylhydrolase
Comments: This enzyme catalyses the third step in the aerobic degradation pathway of carbazole. The effect of the presence of an amino group or hydroxyl group at the 2-position of the substrate is small. The enzyme has no cofactor requirement [2551].
References: [2211, 2551]

[EC 3.7.1.13 created 2010]

EC 3.7.1.14
Accepted name: 2-hydroxy-6-oxonona-2,4-dienedioate hydrolase
Reaction: (1) (2Z,4E)-2-hydroxy-6-oxonona-2,4-diene-1,9-dioate + H₂O = (2Z)-2-hydroxypenta-2,4-dienoate + succinate
(2) (2Z,4E,7E)-2-hydroxy-6-oxonona-2,4,7-triene-1,9-dioate + H₂O = (2Z)-2-hydroxypenta-2,4-dienoate + fumarate
Other name(s): mhpC (gene name)
**Systematic name:** (2Z,4E)-2-hydroxy-6-oxona-2,4-dienedioate succinylhydrolase

**Comments:** This enzyme catalyses a step in a pathway of phenylpropanoid compounds degradation. The first step of the enzyme mechanism involves a reversible keto-enol tautomerization [1685].

**References:** [357, 358, 1684, 1685, 809, 645]

[EC 3.7.1.14 created 2011, modified 2012]


[EC 3.7.1.15 created 2011, deleted 2013]

[3.7.1.16] Transferred entry. oxepin-CoA hydrolase. Now EC 3.3.2.12, oxepin-CoA hydrolase

[EC 3.7.1.16 created 2011, deleted 2013]

EC 3.7.1.17

**Accepted name:** 4,5:9,10-diseco-3-hydroxy-5,9,17-trioxoandrosta-1(10),2-diene-4-oate hydrolase

**Reaction:** (1E,2Z)-3-hydroxy-5,9,17-trioxoandrosta-1(10),2-diene-4-oate + H_2O = 3-[(3α,4S,7αS)-7a-methyl-1,5-dioxo-octahydro-1H-inden-4-yl]propanoate + (2Z,4Z)-2-hydroxyhexa-2,4-dienoate

**Other name(s):** tesD (gene name); hsaD (gene name)

**Systematic name:** 4,5:9,10-diseco-3-hydroxy-5,9,17-trioxoandrosta-1(10),2-diene-4-oate hydrolase (2Z,4Z)-2-hydroxyhexa-2,4-dienoate-forming

**Comments:** The enzyme is involved in the bacterial degradation of the steroid ring structure, and is involved in degradation of multiple steroids, such as testosterone [1253], cholesterol [628], and sitosterol.

**References:** [1253, 628, 1676, 1677]

[EC 3.7.1.17 created 2012]

EC 3.7.1.18

**Accepted name:** 6-oxocamphor hydrolase

**Reaction:** bornane-2,6-dione + H_2O = [(1S)-4-hydroxy-2,2,3-trimethylcyclopent-3-enyl]acetate

**Other name(s):** OCH; camK (gene name)

**Systematic name:** bornane-2,6-dione hydrolase

**Comments:** Isolated from *Rhodococcus* sp. The bornane ring system is cleaved by a retro-Claisen reaction to give the enol of α-camphololate. When separate from the enzyme the enol is tautomerised to the keto form as a 6:1 mixture of [(1S,3R)-2,2,3-trimethyl-4-oxocyclopentyl]acetate and [(1S,3S)-2,2,3-trimethyl-4-oxocyclopentyl]acetate.

**References:** [1046, 3327, 1739]

[EC 3.7.1.18 created 2012]

EC 3.7.1.19

**Accepted name:** 2,6-dihydroxypseudooxynicotine hydrolase

**Reaction:** 1-(2,6-dihydroxypyridin-3-yl)-4-(methylamino)butan-1-one + H_2O = 2,6-dihydroxypyridine + 4-methylaminobutanoate

**Systematic name:** 1-(2,6-dihydroxypyridin-3-yl)-4-(methylamino)butan-1-one hydrolase

**Comments:** The enzyme, characterized from the soil bacterium *Arthrobacter nicotinovorans*, participates in nicotine degradation.

**References:** [956, 2612]

[EC 3.7.1.19 created 2012]

343
EC 3.7.1.20
Accepted name: 3-fumarylpyruvate hydrolase
Reaction: 3-fumarylpyruvate + H₂O = fumarate + pyruvate
Other name(s): nagK (gene name); naaD (gene name)
Systematic name: 3-fumarylpyruvate hydrolase
Comments: The enzyme is involved in bacterial degradation of 5-substituted salicylates, including gentisate (5-hydroxysalicylate), 5-nitrosalicylate and 5-halosalicylates.
References: [3504, 2458]

[EC 3.7.1.20 created 2012]

EC 3.7.1.21
Accepted name: 6-oxocyclohex-1-ene-1-carbonyl-CoA hydratase
Reaction: 6-oxocyclohex-1-ene-1-carbonyl-CoA + 2 H₂O = 3-hydroxypimeloyl-CoA (overall reaction)
(1a) 6-oxocyclohex-1-ene-1-carbonyl-CoA + H₂O = 2-hydroxy-6-oxocyclohexane-1-carbonyl-CoA
(1b) 2-hydroxy-6-oxocyclohexane-1-carbonyl-CoA + H₂O = 3-hydroxypimeloyl-CoA
Other name(s): 6-oxocyclohex-1-ene-1-carbonyl-CoA hydrolase; 6-oxocyclohex-1-ene-1-carbonyl-CoA hydrolase (decyclizing)
Systematic name: 6-oxocyclohex-1-ene-1-carbonyl-CoA hydrolase (ring-opening)
Comments: The enzyme, which participates in the anaerobic benzoyl-CoA degradation pathway in certain organisms, catalyses the addition of one molecule of water to the double bond of 6-oxocyclohex-1-ene-1-carbonyl-CoA followed by the hydrolytic C-C cleavage of the alicyclic ring.
References: [1680, 1647]

[EC 3.7.1.21 created 2014]

EC 3.7.1.22
Accepted name: 3D-(3,5/4)-trihydroxycyclohexane-1,2-dione acylhydrolase (ring-opening)
Reaction: 3D-3,5/4-trihydroxycyclohexa-1,2-dione + H₂O = 5-deoxy-D-glucuronate
Other name(s): IolD; THcHDO hydrolase; 3D-(3,5/4)-trihydroxycyclohexa-1,2-dione hydrolase (decyclizing); 3D-(3,5/4)-trihydroxycyclohexane-1,2-dione acylhydrolase (decyclizing)
Systematic name: 3D-3,5/4-trihydroxycyclohexa-1,2-dione hydrolase (ring-opening)
Comments: The enzyme, found in the bacterium Bacillus subtilis, is part of the myo-inositol degradation pathway leading to acetyl-CoA.
References: [3459]

[EC 3.7.1.22 created 2014, modified 2014]

EC 3.7.1.23
Accepted name: maleylpyruvate hydrolase
Reaction: 3-maleylpyruvate + H₂O = maleate + pyruvate
Other name(s): hhzF (gene name)
Systematic name: (2Z)-4,6-dioxohept-2-enedioate acylhydrolase
Comments: The enzyme, characterized from the bacterium Pseudomonas alcaligenes NCIMB 9867, catalyses the hydrolysis of 3-maleylpyruvate, the ring-cleavage product of gentisate. The enzyme can also act on a number of maleylpyruvate derivatives, such as (2E)-2-methyl-4,6-dioxohept-2-enedioate and (2E)-3-methyl-4,6-dioxohept-2-enedioate. Activated by Mn²⁺. May be identical to EC 3.7.1.5, acylpyruvate hydrolase.
References: [1248, 192, 1819]

[EC 3.7.1.23 created 2016]
EC 3.7.1.24

Accepted name: 2,4-diacetylphloroglucinol hydrolase
Reaction: 2,4-diacetylphloroglucinol + H₂O = 2-acetylphloroglucinol + acetate
Other name(s): PhlG
Systematic name: 2,4-diacetylphloroglucinol acetylhydrolase
Comments: Requires Zn²⁺. Isolated from the bacteria Pseudomonas fluorescens, Pseudomonas sp. YGJ3 and Mycobacterium abscessus 103. It reduces the antibiotic activity of 2,4-diacetylphloroglucinol.
References: [296, 1160, 2626, 3496]

EC 3.7.1.25

Accepted name: 2-hydroxy-6-oxohepta-2,4-dienoate hydrolase
Reaction: (2Z,4E)-2-hydroxy-6-oxohepta-2,4-dienoate + H₂O = (2Z)-2-hydroxyhexa-2,4-dienoate + acetate
Other name(s): todF (gene name)
Systematic name: (2Z,4E)-2-hydroxy-6-oxohepta-2,4-dienoate acetylhydrolase
Comments: A bacterial enzyme that participates in the degradation of toluene and 2-nitrotoluene.
References: [1634, 1983, 1083]

EC 3.7.1.26

Accepted name: 2,4-didehydro-3-deoxy-L-rhamnonate hydrolase
Reaction: 2,4-didehydro-3-deoxy-L-rhamnonate + H₂O = pyruvate + (S)-lactate
Other name(s): lra6 (gene name)
Systematic name: 2,4-didehydro-3-deoxy-L-rhamnonate hydrolase
Comments: The enzyme, characterized from the bacterium Sphingomonas sp. SKA58, participates in an L-rhamnose degradation pathway.
References: [3285]

EC 3.7.1.28

Accepted name: 3-oxoisoapionate-4-phosphate transcarboxylase/hydrolase
Reaction: 3-oxoisoapionate 4-phosphate + H₂O = glycolate + 3-phospho-D-glycerate
Other name(s): oiaT (gene name)
Systematic name: 3-oxoisoapionate-4-phosphate transcarboxylase/glycolyldihydroxydolase (3-phospho-D-glycerate-forming)
Comments: The enzyme, which belongs to the RuBisCO-like-protein (RLP) superfamily, has been characterized from several bacterial species. It participates in the degradation of D-apionate. The reaction is initiated by decarboxylation to generate a stabilized enediolate intermediate, with the sequestered CO₂ carboxylating the adjacent enediolate carbon atom. The resulting 3-ketose-1-phosphate intermediate is hydrolysed, as in the authentic RuBisCO-catalysed reaction, to generate glycolate and 3-phospho-D-glycerate. Stereospecificity of 3-oxoisoapionate 4-phosphate has not been determined.
References: [408]

EC 3.8 Acting on halide bonds

This subclass contains enzymes that hydrolyse carbon-halide compounds in a single sub-subclass (EC 3.8.1).
EC 3.8.1 In carbon-halide compounds

[3.8.1.1  Deleted entry. alkylhalidase. Covered by EC 3.8.1.5, haloalkane dehalogenase.]

[EC 3.8.1.1 created 1961, deleted 2020]

EC 3.8.1.2

Accepted name: (S)-2-haloacid dehalogenase
Reaction: (S)-2-haloacid + H₂O = (R)-2-hydroxyacid + halide
Other name(s): 2-haloacid dehalogenase[ambiguous]; 2-haloacid halidohydrolase [ambiguous][ambiguous]; 2-haloalkanoic acid dehalogenase; 2-haloalkanoid acid halidohydrolase; 2-halocarboxylic acid dehalogenase II; DL-2-haloacid dehalogenase[ambiguous]; L-2-haloacid dehalogenase; t.-DEX
Systematic name: (S)-2-haloacid halidohydrolase
Comments: Acts on acids of short chain lengths, C₂ to C₄, with inversion of configuration at C-2. [See also EC 3.8.1.9 (R)-2-haloacid dehalogenase, EC 3.8.1.10 2-haloacid dehalogenase (configuration-inverting) and EC 3.8.1.11 2-haloacid dehalogenase (configuration-retaining)]
References: [1003, 2091, 1557, 655, 2084, 1582, 2088, 1658, 2847]

[EC 3.8.1.2 created 1972, modified 2003]

EC 3.8.1.3

Accepted name: haloacetate dehalogenase
Reaction: haloacetate + H₂O = glycolate + halide
Other name(s): monohaloacetate dehalogenase
Systematic name: haloacetate halidohydrolase
References: [1000, 1002]

[EC 3.8.1.3 created 1972]

[3.8.1.4  Transferred entry. thyroxine deiodinase. Now EC 1.97.1.10, thyroxine 5'-deiodinase]

[EC 3.8.1.4 created 1984, deleted 2003]

EC 3.8.1.5

Accepted name: haloalkane dehalogenase
Reaction: 1-haloalkane + H₂O = a primary alcohol + halide
Other name(s): 1-chlorohexane halidohydrolase; 1-haloalkane dehalogenase
Systematic name: 1-haloalkane halidohydrolase
Comments: Acts on a wide range of 1-haloalkanes, haloalcohols, haloalkenes and some haloaromatic compounds.
References: [1515, 2715, 3446]

[EC 3.8.1.5 created 1989]

EC 3.8.1.6

Accepted name: 4-chlorobenzoate dehalogenase
Reaction: 4-chlorobenzoate + H₂O = 4-hydroxybenzoate + chloride
Other name(s): halobenzoate dehalogenase
Systematic name: 4-chlorobenzoate chlorohydrolase
Comments: Catalyses the first step in the degradation of chlorobenzoate in *Pseudomonas*. In many microorganisms, this activity comprises three separate enzymes, EC 6.2.1.33 (4-chlorobenzoate—CoA ligase), EC 3.8.1.7 (4-chlorobenzyol-CoA dehalogenase) and EC 3.1.2.23 (4-hydroxybenzyl-CoA thioesterase).
References: [2100, 1194]
EC 3.8.1.7

Accepted name: 4-chlorobenzoyl-CoA dehalogenase
Reaction: $4\text{-chlorobenzoyl-CoA} + \text{H}_2\text{O} = 4\text{-hydroxybenzoyl CoA} + \text{chloride}$
Systematic name: 4-chlorobenzoyl CoA chlorohydrolase
Comments: Specific for dehalogenation at the 4-position. Can dehalogenate substrates bearing fluorine, chlorine, bromine and iodine in the 4-position. This enzyme is part of the bacterial 2,4-dichlorobenzoate degradation pathway.
References: [425, 550]

EC 3.8.1.8

Accepted name: atrazine chlorohydrolase
Reaction: atrazine + $\text{H}_2\text{O} = \text{hydroxyatrazine} + \text{chloride}$
Other name(s): AtzA
Systematic name: atrazine chlorohydrolase
Comments: Involved in the degradation of the herbicide atrazine, 2-chloro-4-(ethylamino)-6-(isopropylamino)-1,3,5-triazine, in bacteria.
References: [604, 603]

EC 3.8.1.9

Accepted name: $(\text{R})$-2-haloacid dehalogenase
Reaction: $(\text{R})$-2-haloacid + $\text{H}_2\text{O} = (\text{S})$-2-hydroxyacid + halide
Other name(s): 2-haloalkanoic acid dehalogenase[ambiguous]; 2-haloalkanoid acid halidohydrolase[ambiguous]; D-2-haloacid dehalogenase; D-DEX
Systematic name: $(\text{R})$-2-haloacid halidohydrolase
Comments: Acts on acids of short chain lengths, $\text{C}_2$ to $\text{C}_4$, with inversion of configuration at C-2. [See also EC 3.8.1.2 $(\text{S})$-2-haloacid dehalogenase, EC 3.8.1.10 2-haloacid dehalogenase (configuration-inverting) and EC 3.8.1.11 2-haloacid dehalogenase (configuration-retaining)]
References: [2837, 1732, 2847]

EC 3.8.1.10

Accepted name: 2-haloacid dehalogenase (configuration-inverting)
Reaction: (1) $(\text{S})$-2-haloacid + $\text{H}_2\text{O} = (\text{R})$-2-hydroxyacid + halide
(2) $(\text{R})$-2-haloacid + $\text{H}_2\text{O} = (\text{S})$-2-hydroxyacid + halide
Other name(s): 2-haloalkanoic acid dehalogenase; 2-haloalkanoid acid halidohydrolase; DL-2-haloacid dehalogenase (inversion of configuration); DL-2-haloacid halidohydrolase (inversion of configuration); DL-DExi; $(\text{R},\text{S})$-2-haloacid dehalogenase (configuration-inverting)
Systematic name: $(\text{S})$-2-haloacid dehalogenase (configuration-inverting)
Comments: Dehalogenates both $(\text{S})$- and $(\text{R})$-2-haloalkanoic acids to the corresponding $(\text{R})$- and $(\text{S})$-hydroxyalkanoic acids, respectively, with inversion of configuration at C-2. The enzyme from Pseudomonas sp. 113 acts on 2-haloalkanoic acids whose carbon chain lengths are five or less. [See also EC 3.8.1.2 $(\text{S})$-2-haloacid dehalogenase, EC 3.8.1.9 $(\text{R})$-2-haloacid dehalogenase and EC 3.8.1.11 2-haloacid dehalogenase (configuration-retaining)]
References: [2088, 2090, 2089, 1658, 1818, 383, 1732, 3301, 2847]
EC 3.8.1.11

Accepted name: 2-haloacid dehalogenase (configuration-retaining)
Reaction: (1) (S)-2-haloacid + H₂O = (S)-2-hydroxyacid + halide
(2) (R)-2-haloacid + H₂O = (R)-2-hydroxyacid + halide
Other name(s): 2-haloalkanoic acid dehalogenase; 2-haloalkanoid acid halidohydrolase; DL-2-haloacid dehalogenase; DL-DEXr
Systematic name: (S)-2-haloacid dehalogenase (configuration-retaining)
Comments: Dehalogenates both (S)- and (R)-2-haloalkanoic acids to the corresponding (S)- and (R)-hydroxyalkanoic acids, respectively, with retention of configuration at C-2. [See also EC 3.8.1.2 (S)-2-haloacid dehalogenase, EC 3.8.1.9 (R)-2-haloacid dehalogenase and EC 3.8.1.10 2-haloacid dehalogenase (configuration-inverting)]
References: [3301, 2847]

[EC 3.8.1.11 created 2003]

EC 3.8.2 In phosphorus-halide compounds (deleted sub-subclass)

[3.8.2.1 Transferred entry. di-isopropyl-fluorophosphatase. Now EC 3.1.8.2, diisopropyl-fluorophosphatase]

[EC 3.8.2.1 created 1961, modified 1976, deleted 1992]

EC 3.9 Acting on phosphorus-nitrogen bonds

This subclass contains a single sub-subclass for enzymes that act on phosphorus-nitrogen bonds (EC 3.9.1).

EC 3.9.1 Acting on phosphorus-nitrogen bonds (only sub-subclass identified to date)

EC 3.9.1.1

Accepted name: phosphoamidase
Reaction: N-phosphocreatine + H₂O = creatine + phosphate
Other name(s): creatine phosphatase
Systematic name: phosphoramidase hydrolase
Comments: Also acts on N-phospho-arginine and other phosphoamides. Possibly identical with EC 3.1.3.9 (glucose-6-phosphatase) or EC 3.1.3.16 (protein-serine/threonine phosphatase).
References: [2355, 2805, 2943]

[EC 3.9.1.1 created 1961]

EC 3.9.1.2

Accepted name: protein arginine phosphatase
Reaction: a [protein]-N⁰-phospho-L-arginine + H₂O = a [protein]-L-arginine + phosphate
Other name(s): YwlE
Systematic name: [protein]-N⁰-phospho-L-arginine phosphohydrolase
Comments: The enzyme, characterized from Gram-positive bacteria, hydrolyses the phosphoramidate (P-N) bond of N⁰-phospho-L-arginine residues in proteins and peptides that were phosphorylated by EC 2.7.14.1, protein-arginine-kinase.
References: [883, 3108, 740]

[EC 3.9.1.2 created 2014]
EC 3.9.1.3

Accepted name: phosphohistidine phosphatase
Reaction: a [protein]-N-phospho-L-histidine + H₂O = a [protein]-L-histidine + phosphate
Other name(s): PHPT1 (gene name); protein histidine phosphatase; PHP
Systematic name: [protein]-N-phospho-L-histidine phosphohydrolase
Comments: This eukaryotic enzyme dephosphorylates phosphorylated histidine residues within proteins and peptides. The enzyme acts on phosphate groups attached to both the pros- and tele-nitrogen atoms, but the pros- position is somewhat preferred (by a factor of two at the most) [102]. The substrate specificity depends on the amino acid sequence or structural context of the phosphohistidine in a phosphoprotein. The enzyme is also active on free phosphoramidate [733, 102] and peptide-bound phospholysine [732].
References: [733, 1564, 190, 102, 732]

[EC 3.9.1.3 created 2016]

EC 3.10 Acting on sulfur-nitrogen bonds

This subclass contains a single sub-subclass for enzymes that act on sulfur-nitrogen bonds (EC 3.10.1).

EC 3.10.1 Acting on sulfur-nitrogen bonds (only sub-subclass identified to date)

EC 3.10.1.1

Accepted name: N-sulfoglucosamine sulfohydrolase
Reaction: N-sulfo-D-glucosamine + H₂O = D-glucosamine + sulfate
Other name(s): sulfoglucosamine sulfamidase; heparin sulfamidase; 2-desoxy-D-glucoside-2-sulphamate sulphohydrolase (sulphamate sulphohydrolase)
Systematic name: N-sulfo-D-glucosamine sulfohydrolase
References: [653, 1873]

[EC 3.10.1.1 created 1972, modified 1981, modified 1982]

EC 3.10.1.2

Accepted name: cyclamate sulfohydrolase
Reaction: cyclohexylsulfamate + H₂O = cyclohexylamine + sulfate
Other name(s): cyclamate sulfamidase; cyclamate sulfamidase; cyclohexylsulfamate sulfamidase
Systematic name: cyclamate sulfohydrolase
Comments: Also readily hydrolyses aliphatic sulfamates with 3 to 8 carbons.
References: [2191]

[EC 3.10.1.2 created 1976, modified 1981]

EC 3.11 Acting on carbon-phosphorus bonds

This subclass contains a single sub-subclass for enzymes that hydrolyse C-phosphono-groups (EC 3.11.1).

EC 3.11.1 Acting on carbon-phosphorus bonds (only sub-subclass identified to date)

EC 3.11.1.1

[349]
Accepted name: phosphonoacetaldehyde hydrolase
Reaction: phosphonoacetaldehyde + H₂O = acetaldehyde + phosphate
Other name(s): phosphonatase; 2-phosphonoacetylaldehyde phosphonohydrolase
Systematic name: 2-oxoethylphosphonate phosphonohydrolase
Comments: This enzyme destabilizes the C-P bond, by forming an imine between one of its lysine residues and the carbonyl group of the substrate, thus allowing this, normally stable, bond to be broken. The mechanism is similar to that used by EC 4.1.2.13, fructose-bisphosphate aldolase, to break a C-C bond. Belongs to the haloacetate dehalogenase family.
References: [2166, 2167, 2165, 2302, 137]

[EC 3.11.1.1 created 1972, modified 1976, modified 2001]

EC 3.11.1.2
Accepted name: phosphonoacetate hydrolase
Reaction: phosphonoacetate + H₂O = acetate + phosphate
Systematic name: phosphonoacetate phosphonohydrolase
Comments: A zinc-dependent enzyme. Belongs to the alkaline phosphatase superfamily of zinc-dependent hydrolases.
References: [1967]

[EC 3.11.1.2 created 1999]

EC 3.11.1.3
Accepted name: phosphonopyruvate hydrolase
Reaction: 3-phosphonopyruvate + H₂O = pyruvate + phosphate
Other name(s): PPH
Comments: Highly specific for phosphonopyruvate as substrate [1636]. The reaction is not inhibited by phosphate but is inhibited by the phosphonates phosphonoformic acid, hydroxymethylphosphonic acid and 3-phosphonopropanoic acid [1636]. The enzyme is activated by the divalent cations Co²⁺, Mg²⁺ and Mn²⁺. This enzyme is a member of the phosphoenolpyruvate mutase/isocitrate lyase superfamily [446].
References: [3046, 1636, 446]

[EC 3.11.1.3 created 2007]

EC 3.12 Acting on sulfur-sulfur bonds

This subclass contains a single sub-subclass for enzymes that act on sulfur-sulfur bonds (EC 3.12.1).

EC 3.12.1 Acting on sulfur-sulfur bonds (only sub-subclass identified to date)

EC 3.12.1.1
Accepted name: trithionate hydrolase
Reaction: trithionate + H₂O = thiosulfate + sulfate + 2 H⁺
Systematic name: trithionate thiosulfohydrolase
References: [1844, 3112]

[EC 3.12.1.1 created 1990]
EC 3.13 Acting on carbon-sulfur bonds

EC 3.13.1 Acting on carbon-sulfur bonds

EC 3.13.1.1

Accepted name: UDP-sulfoquinovose synthase
Reaction: UDP-α-D-sulfoquinovopyranose + H₂O = UDP-α-D-glucose + sulfite
Other name(s): sulfite:UDP-glucose sulfotransferase; UDPsulfoquinovose synthase; UDP-6-sulfo-6-deoxyglucose sulfohydrolase
Systematic name: UDP-6-sulfo-6-deoxy-α-D-glucose sulfohydrolase
Comments: Requires NAD⁺, which appears to oxidize UDP-α-D-glucose to UDP-4-dehydroglucose, which dehydrates to UDP-4-dehydro-6-deoxygluc-5-enose, to which sulfite is added. The reaction is completed when the substrate is rehydrogenated at C-4. The enzyme from Arabidopsis thaliana is specific for UDP-Glc and sulfite.
References: [768, 769, 2095, 2642]

[EC 3.13.1.1 created 2001, modified 2010]

EC 3.13.1.3

Accepted name: 2′-hydroxybiphenyl-2-sulfinate desulfinase
Reaction: 2′-hydroxybiphenyl-2-sulfinate + H₂O = 2-hydroxybiphenyl + sulfite
Other name(s): gene dszB-encoded hydrolase; 2-(2-hydroxyphenyl) benzenesulfinate-H₂O hydrolase; DszB; HBPSi desulfinase; 2-(2-hydroxyphenyl) benzencesulfinate sulfohydrolase; HPBS desulfinase; 2-(2-hydroxyphenyl) benzencesulfinate desulfinase
Systematic name: 2′-hydroxybiphenyl-2-sulfinate sulfohydrolase
Comments: The enzyme from Rhodococcus sp. strain IGTS8 is encoded by the plasmid-encoded dibenzothiophene-desulfurization (dsz) operon. The enzyme has a narrow substrate specificity with biphenyl-2-sulfinate being the only other substrate known to date [2157].
References: [2301, 2157, 3288]

[EC 3.13.1.3 created 2000 as EC 3.1.2.24, transferred 2005 to EC 3.13.1.3]

EC 3.13.1.4

Accepted name: 3-sulfinopropanoyl-CoA desulfinase
Reaction: 3-sulfinopropanoyl-CoA + H₂O = propanoyl-CoA + sulfite
Other name(s): 3SP-CoA desulfinase; AcdDPN7; 3-sulfinopropionyl-CoA desulfinase
Systematic name: 3-sulfinopropanoyl-CoA sulfinohydrolase
Comments: The enzyme from the β-proteobacterium Advenella mimigardefordensis contains one non-covalently bound FAD per subunit.
References: [2728, 2727]

[EC 3.13.1.4 created 2014]

EC 3.13.1.5

Accepted name: carbon disulfide hydrolase
Reaction: carbon disulfide + 2 H₂O = CO₂ + 2 hydrogen sulfide (overall reaction)
Carbon disulfide + H₂O = carbonyl sulfide + hydrogen sulfide
Carbon disulfide + H₂O = CO₂ + hydrogen sulfide

Other name(s):
- CS₂ hydrolase (misleading)
- Carbon disulfide lyase
- CS₂-converting enzyme
- Carbon disulphide-lyase (decarboxylating)

Systematic name:
Carbon-disulfide hydrogen-sulfide-lyase (decarboxylating)

Comments:
The enzyme contains Zn²⁺. The hyperthermophilic archaeon *Acidianus* sp. A1-3 obtains energy by the conversion of carbon disulfide to hydrogen sulfide, with carbonyl sulfide as an intermediate.

References: [2834]

**EC 3.13.1.6**

Accepted name: [CysO sulfur-carrier protein]-S-L-cysteine hydrolase

Reaction: [CysO sulfur-carrier protein]-Gly-NH-CH₂-C(O)-S-L-cysteine + H₂O = [CysO sulfur-carrier protein]-Gly-NH-CH₂-COOH + L-cysteine

Other name(s):
- mec (gene name)

Systematic name: [CysO sulfur-carrier protein]-S-L-cysteine sulfohydrolase

Comments: Requires Zn²⁺. The enzyme, characterized from the bacterium *Mycobacterium tuberculosis*, participates in an L-cysteine biosynthesis pathway. It acts on the product of EC 2.5.1.113, [CysO sulfur-carrier protein]-thiocarboxylate-dependent cysteine synthase.

References: [359]

**EC 3.13.1.7**

Accepted name: carbonyl sulfide hydrolase

Reaction: carbonyl sulfide + H₂O = hydrogen sulfide + CO₂

Other name(s):
- COSase
- COS hydrolase
- cos (gene name)

Systematic name: carbonyl sulfide hydrogen-sulfide-lyase (decarboxylating)

Comments: The enzyme, characterized from the bacterium *Thiobacillus thioparus*, catalyses a step in the degradation pathway of thiocyanate. This activity is also catalysed by the archaeanal EC 3.13.1.5, carbon disulfide lyase.

References: [2260]

**EC 3.13.1.8** Transferred entry: *S*-adenosyl-L-methionine hydrolase (adenosine-forming), now classified as EC 3.13.2.3, *S*-adenosyl-L-methionine hydrolase (adenosine-forming)

[EC 3.13.1.8 created 2018, deleted 2022]

**EC 3.13.1.9**

Accepted name: *S*-inosyl-L-homocysteine hydrolase

Reaction: *S*-inosyl-L-homocysteine + H₂O = inosine + L-homocysteine

Other name(s): SIHH

Systematic name: *S*-inosyl-L-homocysteine hydrolase (inosine-forming)

Comments: The enzyme, characterized from the methanogenic archaeon *Methanocaldococcus jannaschii*, binds an NAD⁺ cofactor. It participates in an alternative pathway for the regeneration of *S*-adenosyl-L-methionine from *S*-adenosyl-L-homocysteine that involves the deamination of the latter to *S*-inosyl-L-homocysteine.

References: [2010]

[EC 3.13.1.9 created 2020]
EC 3.13.2 Thioether andtrialkylsulfonium hydrolases

EC 3.13.2.1
Accepted name: adenosylhomocysteinase
Reaction: \( S\text{-adenosyl-L-homocysteine} + H_2O \rightarrow L\text{-homocysteine} + \text{adenosine} \)
Other name(s): \( S\text{-adenosylhomocysteine synthase}; S\text{-adenosylhomocysteine hydrolase (ambiguous); adenosylhomocysteine hydrolase; } S\text{-adenosylhomocysteinase; SAHase; AdoHcyase} \)
Systematic name: \( S\text{-adenosyl-L-homocysteine hydrolase} \)
Comments: The enzyme contains one tightly bound NAD\(^+\) per subunit. This appears to bring about a transient oxidation at C-3\(^\prime\) of the 5\(^\prime\)-deoxyadenosine residue, thus labilizing the thioether bond [2340] (for mechanism, click here), cf. EC 5.5.1.4, inositol-3-phosphate synthase.
References: [601, 2340]

[EC 3.13.2.1 created 1961 as EC 3.3.1.1, modified 2004, transferred 2022 to EC 3.13.2.1]

353

3.13.2.2 Transferred entry. \( S\text{-adenosyl-L-methionine hydrolase (L-homoserine-forming). Now classified as EC 4.4.1.42, } S\text{-adenosyl-L-methionine lyase} \)

[EC 3.13.2.2 created 1972 as EC 3.3.1.2, modified 1976, modified 2018, transferred 2022 to EC 3.13.2.2, deleted 2022]

EC 3.13.2.3
Accepted name: \((R)\text{-S-adenosyl-L-methionine hydrolase (adenosine-forming)}\)
Reaction: \((R)\text{-S-adenosyl-L-methionine} + H_2O \rightarrow \text{adenosine} + L\text{-methionine}\)
Other name(s): SAM hydroxide adenosyltransferase
Systematic name: \((R)\text{-S-adenosyl-L-methionine hydrolase (adenosine-forming)}\)
Comments: The enzyme, found in bacteria and archaea, is involved in removing the \((R)\) isomer of \( S\text{-adenosyl-L-methionine} \) from the cell. It catalyses a nucleophilic attack of water at the C5\(^\prime\) carbon of \( S\text{-adenosyl-L-methionine} \) to generate adenosine and L-methionine.
References: [773, 625, 1603]

[EC 3.13.2.3 created 2018 as EC 3.13.1.8, transferred 2022 to EC 3.13.2.3]
References


357


361


369


386


387


K.V. Druzhinina and M.G. Kritzman. [Lecithinase from animal tissues.]. Biokhimiya, 17:77–81, 1952.


408


422


[1697] [1698] [1699] [1700] [1701] [1702] [1703] [1704] [1705] [1706] [1707] [1708] [1709] [1710] [1711] [1712] [1713] [1714] [1715] [1716]


451


473


### Index

<table>
<thead>
<tr>
<th>Enzyme Name</th>
<th>EC Number</th>
</tr>
</thead>
<tbody>
<tr>
<td>α-3′-ketoglucosidase</td>
<td>145</td>
</tr>
<tr>
<td>α-N-acetylgalactosaminidase</td>
<td>104</td>
</tr>
<tr>
<td>α-N-acetylgulcosaminidase</td>
<td>105</td>
</tr>
<tr>
<td>α-d-ribose 1-methylphosphonate 5-triphosphate diphosphatase</td>
<td>327</td>
</tr>
<tr>
<td>α-d-xyloside xylolohydrolase</td>
<td>133</td>
</tr>
<tr>
<td>α-L-fucosidase</td>
<td>105</td>
</tr>
<tr>
<td>α-L-rhamnosidase</td>
<td>103</td>
</tr>
<tr>
<td>β-1,2-mannosidase</td>
<td>139</td>
</tr>
<tr>
<td>β-Ala-His dipeptidase</td>
<td>169</td>
</tr>
<tr>
<td>β-N-acetylgalactosaminidase</td>
<td>105</td>
</tr>
<tr>
<td>β-N-acetylhexosaminidase</td>
<td>105</td>
</tr>
<tr>
<td>β-D-fucosidase</td>
<td>102</td>
</tr>
<tr>
<td>β-D-glucopyranosyl arabinosidase</td>
<td>133</td>
</tr>
<tr>
<td>β-L-rhamnosidase</td>
<td>103</td>
</tr>
<tr>
<td>γ-D-glutamyl-meso-diaminopimelate peptidase</td>
<td>184</td>
</tr>
<tr>
<td>γ-D-glutamyl-L-lysine dipeptidyl-peptidase</td>
<td>173</td>
</tr>
<tr>
<td>(4-O-methyl)-d-glucurionate—lignin esterase</td>
<td>27</td>
</tr>
<tr>
<td>(R)-2-haloacid dehalogenase</td>
<td>345</td>
</tr>
<tr>
<td>(R)-S-adenosyl-L-methionine hydrolase (adenosine-forming)</td>
<td>351</td>
</tr>
<tr>
<td>(S)-2-haloacid dehalogenase</td>
<td>344</td>
</tr>
<tr>
<td>(S)-N-acetyl-1-phenylethylamine hydrolase</td>
<td>279</td>
</tr>
<tr>
<td>(+)-kolavelool synthase</td>
<td>75</td>
</tr>
<tr>
<td>Aspergillus deoxyribonuclease K1</td>
<td>82</td>
</tr>
<tr>
<td>Aspergillus nuclease S1</td>
<td>94</td>
</tr>
<tr>
<td>N′-(β-N-acetylgulosaminyl)-L-asparaginase</td>
<td>267</td>
</tr>
<tr>
<td>Physarum polycephalum ribonuclease</td>
<td>90</td>
</tr>
<tr>
<td>all-trans-retinyl ester 13-cis isomerohydrolase</td>
<td>20</td>
</tr>
<tr>
<td>endo-1,3,β-xylanase</td>
<td>101</td>
</tr>
<tr>
<td>sn-1-specific diacylglycerol lipase</td>
<td>27</td>
</tr>
<tr>
<td>trans-2,3-dihydro-3-hydroxyanthranilic acid synthase</td>
<td>157</td>
</tr>
<tr>
<td>D-Ala-D-Ala dipeptidase</td>
<td>170</td>
</tr>
<tr>
<td>D-glycerol-β-d-manno-heptose 1,7-bisphosphate 7-phosphatase</td>
<td>52</td>
</tr>
<tr>
<td>D-glycerol-β-d-manno-heptose 1,7-bisphosphate 7-phosphatase</td>
<td>52</td>
</tr>
<tr>
<td>1,2-α-L-fucosidase</td>
<td>108</td>
</tr>
<tr>
<td>1,3-α-L-fucosidase</td>
<td>118</td>
</tr>
<tr>
<td>1,3-α-isomaltosidase</td>
<td>141</td>
</tr>
<tr>
<td>1,6-α-d-mannosidase</td>
<td>130</td>
</tr>
<tr>
<td>1,6-α-L-fucosidase</td>
<td>122</td>
</tr>
<tr>
<td>11-cis-retinyl-palmitate hydrolase</td>
<td>13</td>
</tr>
<tr>
<td>2′-N-acetylparamomamine deacetylase</td>
<td>285</td>
</tr>
<tr>
<td>2,6-β-fructan 6-levanbiohydrolase</td>
<td>108</td>
</tr>
<tr>
<td>20-O-methylglycoside ginsenosidase</td>
<td>139</td>
</tr>
<tr>
<td>3-O-acetylphosphates-3-carboxyesterase</td>
<td>24</td>
</tr>
<tr>
<td>3D-(3,5,4)-trihydroxycyclohexane-1,2-dione acetylhydrolase (ring opening)</td>
<td>342</td>
</tr>
<tr>
<td>4-α-D-(1→4)-α-D-glucanotrehalose trehalohydrolase</td>
<td>125</td>
</tr>
<tr>
<td>5′ to 3′ exodeoxyribonuclease (nucleoside 3′-phosphate-forming)</td>
<td>77</td>
</tr>
<tr>
<td>5′-(N7-methyl 5′-triphosphoguanosine)-[mRNA] diphosphatase</td>
<td>326</td>
</tr>
<tr>
<td>5′-(N7-methylguanosine 5′-triphospho)-[mRNA] hydrolase</td>
<td>326</td>
</tr>
<tr>
<td>5-(3,4-diacetoxybut-1-ynyl)-2,2′-bithiophene deacetylase</td>
<td>14</td>
</tr>
<tr>
<td>4-acetamidobutyrate deacetylase</td>
<td>274</td>
</tr>
<tr>
<td>4-acetamidobutyryl-CoA deacetylase</td>
<td>272</td>
</tr>
<tr>
<td>2-(acetoamidomethylene)succinate hydrolase</td>
<td>267</td>
</tr>
<tr>
<td>acetoacetyl-CoA deacetylase</td>
<td>29</td>
</tr>
<tr>
<td>acetoxybutynylbithiophene deacetylase</td>
<td>11</td>
</tr>
<tr>
<td>N-acetyl-β-alanine deacetylase</td>
<td>266</td>
</tr>
<tr>
<td>N-acetyl-1-D-myo-inositol-2-amino-2-deoxy-α-2-glucopyranoside deacetylase</td>
<td>283</td>
</tr>
<tr>
<td>2″-acetyl-6″-hydroxynemycin C deacetylase</td>
<td>286</td>
</tr>
<tr>
<td>N-acetyl-d-muramate 6-phosphate phosphatase</td>
<td>57</td>
</tr>
<tr>
<td>N′2-acetyl-1-L-2,4-diaminobutanoate deacetylase</td>
<td>289</td>
</tr>
<tr>
<td>O-acetyl-ADP-ribose deacetylase</td>
<td>24</td>
</tr>
<tr>
<td>[acyl-CoA carboxylase]-phosphatase</td>
<td>43</td>
</tr>
<tr>
<td>acetyl-CoA deacetylase</td>
<td>28</td>
</tr>
<tr>
<td>acetyljanmaline esterase</td>
<td>17</td>
</tr>
<tr>
<td>acetyltalkylglycerol acetylhydrolase</td>
<td>15</td>
</tr>
<tr>
<td>acetylcholinesterase</td>
<td>3</td>
</tr>
<tr>
<td>N′4-acetylcytidine amidohydrolase</td>
<td>291</td>
</tr>
<tr>
<td>N-acetyldiaminopimelate deacetylase</td>
<td>271</td>
</tr>
<tr>
<td>acetylenesterase</td>
<td>3</td>
</tr>
<tr>
<td>N-acetylgalactosamine-4-sulfatase</td>
<td>70</td>
</tr>
<tr>
<td>N-acetylgalactosamine-6-sulfatase</td>
<td>69</td>
</tr>
<tr>
<td>N-acetylgalactosaminoglycan deacetylase</td>
<td>12</td>
</tr>
<tr>
<td>N-acetylgulcosamine deacetylase</td>
<td>268</td>
</tr>
<tr>
<td>N-acetylgulcosamine-1-phosphodiester α-N-acetylgulcosaminidase</td>
<td>64</td>
</tr>
<tr>
<td>N-acetylgulcosamine-6-phosphate deacetylase</td>
<td>267</td>
</tr>
<tr>
<td>N-acetylgulcosamine-6-sulfatase</td>
<td>71</td>
</tr>
<tr>
<td>N-acetylgulcosaminylphosphate dihydrolase</td>
<td>279</td>
</tr>
<tr>
<td>6-acetylglucose deacetylase</td>
<td>7</td>
</tr>
<tr>
<td>N-acetylmuramoyl-L-alanine amidase</td>
<td>267</td>
</tr>
<tr>
<td>acetylsorbinidin deacetylase</td>
<td>265</td>
</tr>
<tr>
<td>N-acetylphosphatidylethanolamine-hydrolysing phospholipase D</td>
<td>66</td>
</tr>
<tr>
<td>acetylpusretine deacetylase</td>
<td>274</td>
</tr>
<tr>
<td>acetylpyruvate hydrolase</td>
<td>339</td>
</tr>
<tr>
<td>acetyl-lysic bicycle deacetylase</td>
<td>12</td>
</tr>
<tr>
<td>acetyl spermidine deacetylase</td>
<td>271</td>
</tr>
<tr>
<td>acetylxylan esterase</td>
<td>15</td>
</tr>
<tr>
<td>acetyl isopterinase</td>
<td>34</td>
</tr>
<tr>
<td>aciderutonate synthase</td>
<td>50</td>
</tr>
<tr>
<td>acilacinomycin methyltransferase</td>
<td>21</td>
</tr>
<tr>
<td>acroyclindropepsin</td>
<td>233</td>
</tr>
<tr>
<td>acrosin</td>
<td>187</td>
</tr>
<tr>
<td>actinidain</td>
<td>214</td>
</tr>
<tr>
<td>actinomycin lactonase</td>
<td>9</td>
</tr>
<tr>
<td>aculeacin-A deacetylase</td>
<td>275</td>
</tr>
<tr>
<td>N-acetyl-d-amino-acid deacetylase</td>
<td>278</td>
</tr>
</tbody>
</table>

529
N-acyl-D-aspartate deacylase, 278
N-acyl-D-glutamate deacylase, 278
N\(^{\alpha}\)-acyl-L-glutamine aminoacylase, 291
N-acyl-aliphatic-L-amino acid amidohydrolase, 265
N-acyl-aromatic-L-amino acid amidohydrolase, 286
[acyl-carrier-protein] phosphodiesterase, 60
acyl-CoA hydrolase, 31
acyl-homoserine-lactone acylase, 282
acyl-lysine deacylase, 265
acylagmatine amidase, 269
acylaminoacyl-peptidase, 182
acylcarnitine hydrolase, 6
acylglycerol lipase, 5
N-acylneuraminate-9-phosphatase, 40
acyloxyacyl hydrolase, 16
acylphosphatase, 316
5′-acylphosphoadenosine hydrolase, 319
acylpyruvate hydrolase, 339
ADAM 17 endopeptidase, 258
ADAM10 endopeptidase, 257
adamalysin, 249
ADAMTS-4 endopeptidase, 257
ADAMTS13 endopeptidase, 258
adenain, 219
adenine deaminase, 301
adenine glycosylase, 152
adenosine deaminase, 302
adenosine nucleosidase, 147
adenosine-5′-diphospho-5′-[DNA] diphosphatase, 329
adenosine-phosphate deaminase, 304
adenosylcobinamide hydrolase, 280
adenosylhomocysteinase, 351
\(\alpha\)-adenosylhomocysteine deaminase, 307
adenosylhomocysteine nucleosidase, 147
adenylylsulfatase, 331
ADP deaminase, 302
ADP-dependent medium-chain-acyl-CoA hydrolase, 31
ADP-dependent short-chain-acyl-CoA hydrolase, 31
ADP-phosphoglycerate phosphatase, 39
ADP-ribose 1′-phosphate phosphatase, 52
ADP-ribose diphosphatase, 318
ADP-riboseyclase/cyclic ADP-ribose hydrolase, 146
ADP-[dinitrogen reductase] hydrolase, 150
ADP-sugar diphosphatase, 319
\(\alpha\)-agarase, 129
\(\beta\)-agarase, 111
agmatinase, 298
agmatine deiminase, 298
alanine carboxypeptidase, 177
aliphatic nitrilase, 312
alkaline phosphatase, 34
1-alkyl-2-acetlyglycerophosphocholine esterase, 10
alkylacylgllycerophosphatase, 46
alkylamidase, 269
alkylglycerophosphoethanolamine phosphodiesterase, 63
allantoate deiminase, 297
allantoicase, 297
allophanate hydrolase, 272
alternative-complement-pathway C3/C5 convertase, 193
amicoumacin phosphatase, 57
\(\omega\)-amidase, 263
\((R)\)-amidase, 282
amidase, 263
amidinoplasmin, 298
[amino group carrier protein]-lysine hydrolase, 290
[amino group carrier protein]-ornithine hydrolase, 290
2-amino-5-formylamino-6-ribosylaminopyrimidin-4(3\(H\))-one 5′-monophosphate deformylase, 283
5-amino-6-(5-phospho-D-ribitylamino)uracil phosphatase, 56
\(\alpha\)-amino-acid esterase, 9
D-aminoacyl-tRNA deacylase, 21
aminoacyl-tRNA hydrolase, 7
2-amino-6-D-arabinohexose-2-uronate 2-deaminase, 33
1-amincyclopropane-1-carboxylate deaminase, 314
aminodeoxyfutalosine deaminase, 310
aminodeoxyfutalosine nucleosidase, 152
6-amino-hexanoate-cyclic-dimer hydrolase, 294
6-amino-hexanoate-oligomer endohydrolase, 287
6-amino-hexanoate-oligomer exohydrolase, 270
aminomimidazolyl phosphate, 303
2-amino-muconate deaminase, 313
2-amino muconate deaminase (2-hydroxymuconate-forming), 315
5-amino pentanamidase, 268
aminopeptidase B, 162
aminopeptidase Ey, 165
aminopeptidase I, 165
aminopeptidase S, 166
aminopeptidase Y, 164
N\(^{1}\)-aminopropylagmatine ureohydrolase, 301
aminopyrimidine aminohydrolase, 313
AMP deaminase, 302
AMP nucleosidase, 146
amygdalin \(\beta\)-glucosidase, 120
\(\alpha\)-amylase, 95
\(\beta\)-amylase, 95
amylo-\(\alpha\)-1,6-glucosidase, 101
ananain, 217
angiotensin-converting enzyme 2, 181
anthrax lethal factor endopeptidase, 257
D-apionolactonase, 26
\(\beta\)-apiosyl-\(\beta\)-glucosidase, 129
apo-salmochelin esterase, 24
apyrase, 316
aqualesin 1, 209
(Ara-f)-Hyp \(\beta\)-1-arabinobiosidase, 136
arabinan endo-1,5-\(\alpha\)-1-arabinanase, 115
arabino-o-galactan endo-\(\beta\)-1,4-galactanase, 113
arabino-o-galactan exo \(\alpha\)-1,3-\(\alpha\)-D-galactosyl-(1→3)-L-arabinofuranosidase (non-reducing end), 144
<table>
<thead>
<tr>
<th>Enzyme Name</th>
<th>Reference Page</th>
</tr>
</thead>
<tbody>
<tr>
<td>D-arabinonolactonase</td>
<td>7</td>
</tr>
<tr>
<td>L-arabinonolactonase</td>
<td>4</td>
</tr>
<tr>
<td>D-arginase</td>
<td>298</td>
</tr>
<tr>
<td>arginase</td>
<td>296</td>
</tr>
<tr>
<td>arginine deiminase</td>
<td>297</td>
</tr>
<tr>
<td>aryl-acylamidase</td>
<td>264</td>
</tr>
<tr>
<td>arylacetoni trilase</td>
<td>312</td>
</tr>
<tr>
<td>arylalkyl acylamidase</td>
<td>277</td>
</tr>
<tr>
<td>aryldialkylphosphatase</td>
<td>75</td>
</tr>
<tr>
<td>arylesterase</td>
<td>264</td>
</tr>
<tr>
<td>arylformamidase</td>
<td>2</td>
</tr>
<tr>
<td>arylsulfatase (type I)</td>
<td>68</td>
</tr>
<tr>
<td>asclepain</td>
<td>213</td>
</tr>
<tr>
<td>asparaginase</td>
<td>262</td>
</tr>
<tr>
<td>aspartoacylase</td>
<td>265</td>
</tr>
<tr>
<td>aspartyl aminopeptidase</td>
<td>165</td>
</tr>
<tr>
<td>β-aspartyl-β-N-acetylglucosaminidase</td>
<td>148</td>
</tr>
<tr>
<td>β-aspartyl-peptidase</td>
<td>183</td>
</tr>
<tr>
<td>aspergillopepsin I</td>
<td>231</td>
</tr>
<tr>
<td>aspergillopepsin II</td>
<td>231</td>
</tr>
<tr>
<td>assemblin</td>
<td>205</td>
</tr>
<tr>
<td>ascin</td>
<td>243</td>
</tr>
<tr>
<td>ATP deaminase</td>
<td>305</td>
</tr>
<tr>
<td>ATP diphosphatase</td>
<td>317</td>
</tr>
<tr>
<td>atrazine chlorohydrolase</td>
<td>345</td>
</tr>
<tr>
<td>atrolysin A</td>
<td>239</td>
</tr>
<tr>
<td>atrolysin B</td>
<td>248</td>
</tr>
<tr>
<td>atrolysin C</td>
<td>248</td>
</tr>
<tr>
<td>atrolysin E</td>
<td>248</td>
</tr>
<tr>
<td>atrolysin F</td>
<td>248</td>
</tr>
<tr>
<td>atroxase</td>
<td>248</td>
</tr>
<tr>
<td>aureolysin</td>
<td>245</td>
</tr>
<tr>
<td>avenacosidase</td>
<td>136</td>
</tr>
<tr>
<td>bacilloysisin</td>
<td>244</td>
</tr>
<tr>
<td>bacterial leucyl aminopeptidase</td>
<td>163</td>
</tr>
<tr>
<td>baicilin-β-D-glucuronidase</td>
<td>131</td>
</tr>
<tr>
<td>barbiturase</td>
<td>292</td>
</tr>
<tr>
<td>barrierpepsin</td>
<td>235</td>
</tr>
<tr>
<td>D-benzoylarginine-4-nitroanilide amidase</td>
<td>276</td>
</tr>
<tr>
<td>N-benzoxycarbonylglycine hydrolase</td>
<td>273</td>
</tr>
<tr>
<td>Nα-benzoxycarboxylleucine hydrolase</td>
<td>274</td>
</tr>
<tr>
<td>biotinidase</td>
<td>264</td>
</tr>
<tr>
<td>bis(2-ethylhexyl)phthalate esterase</td>
<td>13</td>
</tr>
<tr>
<td>bis(5′-adenosyl)-triphosphatase</td>
<td>321</td>
</tr>
<tr>
<td>bis(5′-nucleosyl)-tetraphosphatase (asymmetrical)</td>
<td>319</td>
</tr>
<tr>
<td>bis(5′-nucleosyl)-tetraphosphatase (symmetrical)</td>
<td>322</td>
</tr>
<tr>
<td>3′(2′),5′-bisphosphate nucleotidase</td>
<td>35</td>
</tr>
<tr>
<td>2,3-bisphosphoglycerate 3-phosphatase</td>
<td>51</td>
</tr>
<tr>
<td>biuret amidohydrolase</td>
<td>278</td>
</tr>
<tr>
<td>blasticidin-S deaminase</td>
<td>306</td>
</tr>
<tr>
<td>bleomycin hydrolase</td>
<td>219</td>
</tr>
<tr>
<td>blood-group-substance endo-1,4-β-galactosidase</td>
<td>116</td>
</tr>
<tr>
<td>bontoxilysin</td>
<td>254</td>
</tr>
<tr>
<td>bothrolysin</td>
<td>250</td>
</tr>
<tr>
<td>bothropasin</td>
<td>249</td>
</tr>
<tr>
<td>brachyurin</td>
<td>190</td>
</tr>
<tr>
<td>branched primary-alkylsulfatase</td>
<td>73</td>
</tr>
<tr>
<td>branched-dextran exo-1,2-α-glucosidase</td>
<td>119</td>
</tr>
<tr>
<td>bromoxynil nitrilase</td>
<td>312</td>
</tr>
<tr>
<td>C-terminal processing peptidase</td>
<td>206</td>
</tr>
<tr>
<td>C5a peptidase</td>
<td>208</td>
</tr>
<tr>
<td>caldesmon-phosphatase</td>
<td>45</td>
</tr>
<tr>
<td>calicivirin</td>
<td>226</td>
</tr>
<tr>
<td>calpain-1</td>
<td>222</td>
</tr>
<tr>
<td>calpain-2</td>
<td>222</td>
</tr>
<tr>
<td>calpain-3</td>
<td>222</td>
</tr>
<tr>
<td>cAMP deaminase</td>
<td>311</td>
</tr>
<tr>
<td>cancer procoagulant</td>
<td>216</td>
</tr>
<tr>
<td>candidapepsin</td>
<td>232</td>
</tr>
<tr>
<td>capsular-polysaccharide endo-1,3-α-galactosidase</td>
<td>112</td>
</tr>
<tr>
<td>N-carbamoyl-D-amino-acid hydrolase</td>
<td>277</td>
</tr>
<tr>
<td>N-carbamoyl-L-amino-acid hydrolase</td>
<td>279</td>
</tr>
<tr>
<td>N-carbamoylputrescine amidase</td>
<td>272</td>
</tr>
<tr>
<td>N-carbamoylsarcosine amidase</td>
<td>273</td>
</tr>
<tr>
<td>carbon disulfide hydrolase</td>
<td>349</td>
</tr>
<tr>
<td>carbonyl sulfide hydrolase</td>
<td>350</td>
</tr>
<tr>
<td>2-carboxy-D-arabinitol-1-phosphatase</td>
<td>47</td>
</tr>
<tr>
<td>1-carboxybiuret hydrolase</td>
<td>290</td>
</tr>
<tr>
<td>carboxylesterase</td>
<td>1</td>
</tr>
<tr>
<td>carboxymethylcellulase</td>
<td>141</td>
</tr>
<tr>
<td>carboxymethylenebutenolidase</td>
<td>10</td>
</tr>
<tr>
<td>carboxymethylhydantoinase</td>
<td>293</td>
</tr>
<tr>
<td>carboxypeptidase A</td>
<td>176</td>
</tr>
<tr>
<td>carboxypeptidase A2</td>
<td>179</td>
</tr>
<tr>
<td>carboxypeptidase B</td>
<td>176</td>
</tr>
<tr>
<td>carboxypeptidase C</td>
<td>175</td>
</tr>
<tr>
<td>carboxypeptidase D</td>
<td>176</td>
</tr>
<tr>
<td>carboxypeptidase E</td>
<td>178</td>
</tr>
<tr>
<td>carboxypeptidase M</td>
<td>178</td>
</tr>
<tr>
<td>carboxypeptidase T</td>
<td>179</td>
</tr>
<tr>
<td>carboxypeptidase Taq</td>
<td>180</td>
</tr>
<tr>
<td>carboxypeptidase U</td>
<td>180</td>
</tr>
<tr>
<td>caricain</td>
<td>216</td>
</tr>
<tr>
<td>carnitnimidase</td>
<td>276</td>
</tr>
<tr>
<td>t-carrageenase</td>
<td>128</td>
</tr>
<tr>
<td>κ-carrageenase</td>
<td>112</td>
</tr>
<tr>
<td>λ-carrageenase</td>
<td>130</td>
</tr>
<tr>
<td>caspase-1</td>
<td>218</td>
</tr>
<tr>
<td>caspase-10</td>
<td>225</td>
</tr>
<tr>
<td>caspase-11</td>
<td>226</td>
</tr>
<tr>
<td>caspase-2</td>
<td>222</td>
</tr>
<tr>
<td>caspase-3</td>
<td>223</td>
</tr>
<tr>
<td>caspase-4</td>
<td>223</td>
</tr>
<tr>
<td>caspase-5</td>
<td>224</td>
</tr>
<tr>
<td>caspase-6</td>
<td>224</td>
</tr>
<tr>
<td>caspase-7</td>
<td>225</td>
</tr>
<tr>
<td>caspase-8</td>
<td>225</td>
</tr>
<tr>
<td>caspase-9</td>
<td>225</td>
</tr>
<tr>
<td>cathepsin B</td>
<td>212</td>
</tr>
<tr>
<td>cathepsin D</td>
<td>229</td>
</tr>
</tbody>
</table>
cathepsin E, 235
\( \text{cathepsin F, 219} \)
\( \text{cathepsin G, 188} \)
\( \text{cathepsin H, 215} \)
\( \text{cathepsin K, 218} \)
\( \text{cathepsin L, 214} \)
\( \text{cathepsin O, 219} \)
\( \text{cathepsin S, 216} \)
\( \text{cathepsin T, 215} \)
\( \text{cathepsin V, 219} \)
\( \text{cathepsin X, 181} \)
\( \text{CC-preferring endodeoxyribonuclease, 81} \)
\( \text{CDP-diacylglycerol diphosphatase, 320} \)
\( \text{CDP-glycerol diphosphatase, 318} \)
\( \text{cellulase, 96} \)
\( \text{cellulose 1,4-β-cellobiosidase (non-reducing end), 113} \)
\( \text{cellulose 1,4-β-cellobiosidase (reducing end), 133} \)
\( \text{cellulose-polysulfatase, 69} \)
\( \text{cephalosporin-C deacetylase, 9} \)
\( \text{ceramidase, 266} \)
\( \text{cerebroside-sulfatase, 70} \)
\( \text{cerevisin, 194} \)
\( \text{cetraxate benzylesterase, 15} \)
\( \text{chenodeoxycholoyltaurine hydrolase, 276} \)
\( \text{chitin deacetylase, 270} \)
\( \text{chitin disaccharide deacetylase, 284} \)
\( \text{chitinase, 98} \)
\( \text{chitosanase, 123} \)
\( \text{4-chlorobenzoate dehalogenase, 344} \)
\( \text{4-chlorobenzoyl-CoA dehalogenase, 345} \)
\( \text{chlorogenate hydrolase, 9} \)
\( \text{chlorophyllase, 4} \)
\( \text{chlorophyllide a hydrolase, 22} \)
\( \text{cholesterol-5,6-oxide hydrolase, 68} \)
\( \text{chondro-4-sulfatase, 70} \)
\( \text{chondro-6-sulfatase, 70} \)
\( \text{choriolysin H, 253} \)
\( \text{choriolysin L, 253} \)
\( \text{coniferin β-glucosidase, 121} \)
\( \text{creatinase, 296} \)
\( \text{creatininase, 294} \)
\( \text{creatinine deaminase, 305} \)
\( \text{crossover junction endodeoxyribonuclease, 82} \)
\( \text{cruzipain, 221} \)
\( \text{cucumisin, 189} \)
\( \text{cutinase, 16} \)
\( \text{cyanoalanine nitrilase, 312} \)
\( \text{cyanophycinase, 175} \)
\( \text{cyanuric acid amido-hydrolase, 295} \)
\( \text{cyclohexane-1,2-dione hydrolase, 340} \)
\( \text{cyclohexane-1,3-dione hydrolase, 340} \)
\( \text{cyclomaltooligosaccharide, 105} \)
\( \text{[CysO sulfur-carrier protein]-S-L-cysteine hydrolase, 350} \)
\( \text{cysteinylglycine-S-conjugate dipeptidase, 170} \)
\( \text{cystinyl aminopeptidase, 161} \)
\( \text{N^5-(cytidine 5'-diphosphoramidyl)-L-glutamine hydrolase, 290} \)
\( \text{cytidine deaminase, 302} \)
\( \text{cytosine deaminase, 301} \)
\( \text{cytosol alanyl aminopeptidase, 163} \)
\( \text{cytosol nonspecific dipeptidase, 169} \)
\( \text{dactylisin, 252} \)
\( \text{dCMP deaminase, 304} \)
\( \text{dCTP deaminase, 304} \)
\( \text{dCTP deaminase (dUMP-forming), 307} \)
\( \text{dCTP diphosphatase, 327} \)
\( \text{dCTP diphosphatase, 317} \)
\( \text{deaminated glutathione amidase, 289} \)
\( \text{3-deoxy-2-octulosonidase, 121} \)
\( \text{3-deoxy-6-sulfoglucuronolactonase, 22} \)
\( \text{3-deoxy-manno-octulosonate-8-phosphatase, 43} \)
\( \text{3-deoxy-D-glycer-D-galacto-nonulopyranosonate 9-phosphatase, 56} \)
\( \text{5'-deoxyadenosine deaminase, 310} \)
\( \text{2-deoxyglucose-6-phosphatase, 48} \)
\( \text{coagulation factor Xa, 187} \)
\( \text{coagulation factor Xla, 190} \)
\( \text{coagulation factor XIIa, 191} \)
\( \text{cobalt-precorrin 5A hydrolyase, 340} \)
\( \text{cocoxylin, 245} \)
\( \text{complement factor D, 193} \)
\( \text{complement factor I, 193} \)
\( \text{complement subcomponent C^1r, 192} \)
\( \text{complement subcomponent C^1s, 192} \)
\( \text{coniferin β-glucosidase, 121} \)
\( \text{creatine kinase, 192} \)
\( \text{dCMP deaminase, 304} \)
\( \text{dCTP deaminase, 304} \)
\( \text{dCTP deaminase (dUMP-forming), 307} \)
\( \text{dCTP diphosphatase, 327} \)
\( \text{dCTP diphosphatase, 317} \)
\( \text{deaminated glutathione amidase, 289} \)
\( \text{3-deoxy-2-octulosonidase, 121} \)
\( \text{6-deoxy-6-sulfoglucuronolactonase, 22} \)
\( \text{3-deoxy-manno-octulosonate-8-phosphatase, 43} \)
\( \text{3-deoxy-D-glycero-D-galacto-nonulopyranosonate 9-phosphatase, 56} \)
\( \text{5'-deoxyadenosine deaminase, 310} \)
\( \text{2-deoxyglucose-6-phosphatase, 48} \)
2-deoxyglucosidase, 118
deoxylimonate A-ring-lactonase, 10
5′-deoxynucleotidase, 53
deoxynucleotide 3′-phosphatase, 40
3′-deoxyctosolosanase, 125
deoxyribodipyrimidine endonucleosidase, 149
deoxyribonuclease I, 80
deoxyribonuclease II, 82
deoxyribonuclease IV, 80
deoxyribonuclease (pyrimidine dimer), 90
deoxyribonuclease V, 81
deoxyribonuclease X, 83
desampylase, 185
deuterolysin, 247
dextran 1,6-α-isomaltotriosidase, 114
dextranase, 97
dGTPase, 68
N,N′-diacetylchitobiose non-reducing end deacetylase, 291
2,4-diacetylphloroglucinol hydrolase, 343
diacylglycerol diphosphate phosphatase, 330
diadenosine hexaphosphate hydrolase (AMP-forming), 326
diadenosine hexaphosphate hydrolase (ATP-forming), 326
diaminohydroxyphosphoribosylaminopyrimidine deaminase, 306
2,4-didehydro-3-deoxy-L-rhamnonate hydrolase, 343
diguanidinobutanase, 300
dihydromonacolin L-[lovastatin nonaketide synthase] thioesterase, 33
7,8-dihydroneopterin 2′,3′-cyclic phosphate phosphodiesterase, 66
dihydrochomarin hydrolase, 8
dihydomonacolin L-[lovastatin nonaketide synthase] thioesterase, 33
7,8-dihydroneopterin 2′,3′-cyclic phosphate phosphodiesterase, 66
dihydrochomarin hydrolase, 8
dihydrochomarin hydrolase, 8
dihydroorotase, 292
dihydropyrimidinase, 292
1,4-dihydroxy-2-naphthoyl-CoA hydrolase, 33
2,6-dihydroxypseudooxynicotine hydrolase, 341
diisopropyl-fluorophosphatase, 76
β-diketone hydrolase, 339
dimethylargininase, 299
N,N′-dimethylformamidase, 273
2,4-dinitroanisole O-demethylase, 157
dioscin glycosidase (3-O-β-D-Glc-diosgenin-forming), 137
dioscin glycosidase (diosgenin-forming), 137
2,6-dioso-6-phenylhexa-3-enoate hydrolase, 339
2,5-dioxoipiperazine hydrolase, 294
dipeptidase E, 170
dipeptidyl-dipeptidase, 172
dipeptidyl-peptidase I, 171
dipeptidyl-peptidase II, 171
dipeptidyl-peptidase III, 171
dipeptidyl-peptidase IV, 171
diphosphoinositol-polyphosphate diphosphatase, 324
4,5:9,10-dieco-3-hydroxy-5,9,17-trioxoandrosta-1(10),2-diene-4-oate hydrolase, 341
disulfoglucosamine-6-sulfatase, 70
DNA-3′-diphospho-5′-guanosine diphosphatase, 329
DNA-3-methyladenine glycosylase I, 149
DNA-3-methyladenine glycosylase II, 150
DNA-deoxyinosine glycosylase, 148
DNA-formamidopyrimidinyl glycosylase, 150
dodecanoyl-[acyl-carrier-protein] hydrolase, 31
dolichyl-phosphatase, 44
dolichyldiphosphatase, 323
dolichylphosphate-glucose phosphodiesterase, 65
dolichylphosphate-mannose phosphodiesterase, 65
double-stranded RNA adenine deaminase, 309
double-stranded uracil-DNA glycosylase, 151
dUTP diphosphatase, 320
dynamin GTPase, 337
ectoine hydrolase, 310
enamidase, 295
endo-α-N-acetylglactosaminidase, 115
endo-α-sialidase, 122
endo-(1→3)-fucoidanase, 143
endo-(1→4)-fucoidanase, 143
endo-1,3(4)-β-glucanase, 96
endo-1,4-β-xylanase, 97
endo-chitodextrinase, 140
endo-polygalacturonase, 98
endogalactosaminidase, 117
endoglycosylceramidase, 121
endopeptidase Clp, 203
endopeptidase La, 194
endopeptidase So, 198
endoplasmic reticulum Man_8GlcNAc_2 1,2-α-mannosidase, 142
endoplasmic reticulum Man_9GlcNAc_2 1,2-α-mannosidase, 142
endopolyphosphatase, 317
double-stranded uracil-DNA glycosylase, 151
dequine arterivirus serine peptidase, 210
equine arterivirus serine peptidase, 210
equine arterivirus serine peptidase, 210
ethyl acetate hydrolase, 26
exo-β-1,2-gluco-oligosaccharide saporhydrase (non-reducing end), 144
exo-α-sialidase, 98
exo-1,4-β-D-glucosaminidase, 130
exo-acting protein-α-N-acetylglactosaminidase, 144
exo-chitinase (non-reducing end), 140
exo-chitinase (reducing end), 140
exo-poly-α-digalacturonosidase, 111
exodeoxyribonuclease I, 76
exodeoxyribonuclease III, 76
exodeoxyribonuclease (lambda-induced), 76
exodeoxyribonuclease (phage SP3-induced), 77
exodeoxyribonuclease V, 77
exodeoxyribonuclease VII, 77
exopolyphosphatase, 317
exoribonuclease H, 78
exoribonuclease II, 78
FAD diphosphatase, 319
farnesyl diphosphatase, 74
fatty acid amide hydrolase, 282
fatty-acyl-ethyl-ester synthase, 14
feruloyl esterase, 15
N-feruloylglycine deacylase, 276
fibrolase, 255
ficain, 213
flavastacin, 256
flavivirin, 203
fluoroacetyl-CoA thioesterase, 33
FMN hydrolase, 56
folate γ-glutamyl hydrolase, 183
formamidase, 271
formimidoylaspartate deiminase, 297
formimidoylglutamase, 297
formimidoylglutamate deiminase, 298
formyl-CoA hydrolase, 29
formylaspartate deformylase, 263
N-formylglutamate deformylase, 275
S-formylglutathione hydrolase, 30
formylmethionine deformylase, 268
N-formylmethionyl-peptidase, 183
formyltetrahydrofolate deformylase, 264
fragilysin, 255
fructan β-(2,1)-fructosidase, 127
fructan β-(2,6)-fructosidase, 127
fructan β-fructosidase, 111
β-fructofuranosidase, 100
fructose-2,6-bisphosphate 2-phosphatase, 43
fructose-2,6-bisphosphate 6-phosphatase, 45
fructose-bisphosphatase, 36
fruit bromelain, 217
L-fucono-1,5-lactonase, 27
fumarylacetoacetase, 338
3-fumarylpyruvate hydrolase, 342
fumonisin B1 esterase, 20
furin, 200
fusaramine-C ornithinesterase, 10
futalosine hydrolase, 151
galactan 1,3-β-galactosidase, 125
galactan endo-β-1,3-galactanase, 134
galactan endo-1,6-β-galactosidase, 130
galactan exo-1,6-β-galactobiophosphatase (non-reducing end), 143
β-galactofuranosidase, 126
galactolipase, 6
D-galactose 1-phosphate phosphatase, 54
L-galactose 1-phosphate phosphatase, 54
α-galactosidase, 99
β-galactosidase, 99
galactosylceramidase, 104
galacturonan 1,4-α-galacturonidase, 108
gametolysin, 247
gastricsin, 229
GDP-glucosidase, 103
gelatinase A, 243
gelatinase B, 246
gellan tetrasaccharide unsaturated glucuronosyl hydrolase, 134
geranyl diphosphate diphosphatase, 75
geranyl diphosphate phosphohydrolase, 328
geranylgeranyl diphosphate diphosphatase, 74
gingipain K, 221
gingipain R, 218
ginsenosidase type I, 138
ginsenosidase type III, 137
ginsenosidase type IV, 138
ginsenoside Rb1 β-glucosidase, 138
Gluc-Glu dipeptidase, 168
glucan 1,3-α-glucosidase, 112
glucan 1,3-β-glucosidase, 106
glucan 1,4-α-glucosidase, 96
glucan 1,4-α-maltotetraosidase, 115
glucan 1,4-α-maltotriohydrolase, 119
glucan 1,4-β-glucosidase, 110
glucan 1,6-α-glucosidase, 109
glucan 1,6-α-isomaltodiastase, 114
glucan 1,2,3-β-glucanase, 109
glucan 1,3-α-glucosidase, 107
glucan 1,3-β-glucosidase, 102
glucan 1,6-β-glucosidase, 110
gluconolactonase, 5
glucosamine-6-phosphate deaminase, 314
glucose-1-phosphatase, 36
glucose-1-phospho-d-mannosylglycoprotein phosphodiesterase, 65
glucose-6-phosphatase, 35
α-glucosidase, 99
β-glucosidase, 99
glucosinolate γ-glutamyl hydrolase, 185
glucosyl-3-phosphoglycerate phosphatase, 52
glucosylceramidase, 104
glucosylglycerate hydrolase, 142
glucosylglycerol 3-phosphatase, 48
glucuronate-2-sulfatase, 72
α-glucuronidase, 124
β-glucuronidase, 101
glucuronoarabinoxylan endo-1,4-β-xylanase, 124
glucuronosyl-disulfoglucoaminyl glucuronidase, 106
glutamate carboxypeptidase, 178
glutamate carboxypeptidase II, 180
glutamin-(asparagin-)-ase, 269
D-glutaminase, 268
glutaminase, 262
glutamyl aminopeptidase, 162
glucuronate hydrolase, 142
glutaryl-7-aminocephalosporanic-acid acylase, 281
glutathione γ-glutamate hydrolase, 184
glutathione thiolesterase, 29
glutathione-5-conjugate glycine hydrolase, 181
glutathionylspermidine amidase, 277
Gly-Xa carboxypeptidase, 177
glycerol-1,2-cyclic-phosphate 2-phosphodiesterase, 63
glycerol-1-phosphatase, 38
glycerol-2-phosphatase, 37
glycerophosphocholine cholinephosphodiesterase, 63
glycerophosphodiester phosphodiesterase, 58
glycerophosphodiester phosphodiesterase, 64
glycerophosphoinositol glycerophosphodiesterase, 64
[glycogen-synthase-D] phosphatase, 42
glycoprotein endo-α-1,2-mannosidase, 122
glycosphingolipid deacylase, 275
glycosulfatase, 69
glycosylceramidase, 107
glycosylphosphatidylinositol phospholipase D, 65
glycyl endopeptidase, 215
glycyrrhizin hydrolase, 122
gpr endopeptidase, 256
granzyme A, 200
granzyme B, 201
GTP cyclohydrolase I, 304
GTP cyclohydrolase II, 306
GTP cyclohydrolase IIa, 307
GTP cyclohydrolase IV, 309
guanidinoacetase, 296
guanidinobutyrase, 297
guanidinodexoxy-scyllol-inositol-4-phosphatase, 42
guanidinopropionase, 299
guaniine deaminase, 302
guanosine deaminase, 304
guanosine-3',5'-bis(diphosphate) 3'-diphosphatase, 73
guanosine-5'-diphospho-5'-[DNA] diphosphatase, 328
guanosine-5'-triphosphate, 3'-diphosphate phosphatase, 322
guanosine-diphosphatase, 323
haloacetate dehalogenase, 344
2-haloacid dehalogenase (configuration-inverting), 345
2-haloacid dehalogenase (configuration-retaining), 346
haloalkane dehalogenase, 344
helper-component proteinase, 220
hepacivirin, 205
heparanase, 131
hepsin, 207
hesperidin 6-O-α-L-rhamnopyranosyl-β-D-glucosidase, 131
heterotrimeric G-protein GTase, 336
hippurate hydrolase, 268
histidinol-phosphatase, 37
histolysain, 217
histone deacetylase, 282
HIV-1 retropepsin, 230
HIV-2 retropepsin, 237
hormone-sensitive lipase, 17
horrilysin, 249
HsI U—HsI V peptidase, 259
HtrA2 peptidase, 208
human endogenous retrovirus K endopeptidase, 238
hyaluronoglucosaminidase, 102
hyaluronoglucuronidase, 102
HycI peptidase, 238
2-hydroxy-3-keto-5-methylthiopentenyl-1-phosphate phosphatase, 53
2-hydroxy-6-oxo-6-(2-aminophenyl)hexa-2,4-dienoic acid hydrolase, 340
2-hydroxy-6-oxohepta-2,4-dienoic acid hydrolase, 343
2-hydroxy-6-oxonona-2,4-dienoic acid hydrolase, 340
4-hydroxy-7-methoxy-3-oxo-3,4-dihydro-2H-1,4-benzoxazin-2-yl glucoside β-D-glucosidase, 135
N-formyl-hydroxy-L-arginine amidinohydrolase, 301
2-hydroxy-dATP diphosphatase, 325
hydroxyacylglutathione hydrolase, 32
4-hydroxybenzoyl-CoA thioesterase, 32
2'-hydroxybiphenyl-2-sulfinate desulfinase, 349
hydroxybutyrate-dimer hydrolase, 5
hydroxydechloroatrazine ethylaminohydrolase, 310
3-hydroxyisobutyryl-CoA hydrolase, 28
hydroxyisourate hydrolase, 295
2-(hydroxymethyl)-3-(acetamidomethyl) succinic acid hydrolase, 275
hydroxymethylglutaryl-CoA hydrolase, 29
[hydroxymethylglutaryl-CoA reductase (NADPH)]-phosphatase, 43
2-hydroxymuconate-6-semialdehyde hydrolase, 339
hypoerin C, 194
iduronate-2-sulfatase, 71
1-L-iduronidase, 110
IgA-specific metalloendopeptidase, 241
IgA-specific serine endopeptidase, 199
imidazolonepropionase, 293
2-iminobutanamide-2-iminopropanoic deaminase, 315
IMP cyclohydrolase, 303
IMP-specific 5'-nucleotidase, 55
(indol-3-yl)acetamide dehydrogenase, 291
infectious pancreatic necrosis birnavirus Vp4 peptidase, 210
inorganic diphosphatase, 315
inosinate nucleosidase, 148
inosine diphosphate phosphatase, 327
inosine nucleosidase, 146
inosine/xanthosine triphosphatase, 329
inosine/xanthosine triphosphatase, 329
inositol-1,4-bisphosphate 1-phosphatase, 46
inositol-phosphate phosphatase, 39
inositol-5-phosphatase, 45
inositol-1,4-bisphosphate-1-phosphatase, 46
inositol-phosphate phosphatase, 39
inositol-polyphosphate 5-phosphatase, 45
intermediate cleaving peptidase 55, 166
interstitial collagenase, 240
inulinase, 96
iron(III)-enterobactin esterase, 24
iron(III)-salmochelin esterase, 25
isatin hydrolase, 296
isoamyl acetate esterase, 26
isoamylase, 109
isochorismatase, 153
isomaltose glucohydrolase, 141
N-isopropylammelide isopropylaminohydrolase, 310
isopullulanase, 106
jararhagin, 255
jasmonoyl-L-amino acid hydrolase, 289
juvenile-hormone esterase, 13
kallikrein 13, 211
kallikrein 8, 211
kanosamine-6-phosphate phosphatase, 54
keratan-sulfate endo-1,4-β-galactosidase, 116
kexin, 196
kojibiose hydrolase, 144
kynureninase, 338
(13E)-labda-7,13-dien-15-ol synthase, 75
β-lactamase, 293
lactase, 117
D-lactate-2-sulfatase, 72
lacto-N-biosidase, 124
lactopepin, 204
1,4-lactonase, 6
legumain, 217
leishmanolysin, 246
leucolysin, 240
leucyl aminopeptidase, 161
leucyl endopeptidase, 195
leukocyte elastase, 191
leukotriene-A₄ hydrolase, 154
leukotriene-C₄ hydrolase, 185
levanase, 108
licheninase, 110
limit dextrin α,1,6-maltotetraose-hydrolase, 139
limit dextrinase, 125
limonene-1,2-epoxide hydrolase, 155
limonin-1,2-ring-lactonase, 8
limulus clotting enzyme, 202
limulus clotting factor B, 202
limulus clotting factor C, 202
linear primary-alkylsulfatase, 73
lipid-phosphate phosphatase, 50
lipoprotein lipase, 8
N-(long-chain-acyl)ethanolamine deacylase, 274
long-chain-fatty-acyl-glutamate deacylase, 272
Lys-Lys/Arg-Xaa endopeptidase, 212
lysine carboxypeptidase, 176
L-lysine-lactamase, 294
2-lysophosphatidate phosphatase, 57
lysophospholipase, 2
lysoaminopeptidase, 154
lysosomal Pro-Xaa carboxypeptidase, 175
lysostaphin, 255
lysozyme, 98
lysyl endopeptidase, 194
α-lytic endopeptidase, 188
β-lytic metalloendopeptidase, 245
macrophage elastase, 253
magnolysin, 252
maleamate amidohydrolase, 284
maleimide hydrolase, 295
maleylpyruvate hydrolase, 342
N-malonylurea hydrolase, 281
maltose 6'-phosphate phosphotase, 54
maltose-6'-phosphate glycosidase, 121
(35S)-malyl-CoA thioesterase, 33
mandelamide amidase, 279
mannan 1,2-(1,3)-α-mannosidase, 110
mannan 1,4-mannobiosidase, 115
α-mannan endo-1,2-α-mannanase, 139
mannan endo-1,4-β-mannosidase, 111
mannan endo-1,6-α-mannosidase, 116
mannan exo-1,2,1,6-α-mannosidase, 124
mannan-binding lectin-associated serine protease-2, 207
mannitol-1-phosphatase, 38
α-mannosidase, 100
β-mannosidase, 100
mannosyl-3-phosphoglycerate phosphatase, 48
mannosyl-glycoprotein endo-β-N-acetylgalcosaminidase, 114
mannosyl-oligosaccharide α,1,3-glucosidase, 142
mannosyl-oligosaccharide 1,2,α-mannosidase, 118
mannosyl-oligosaccharide 1,3,1,6-α-mannosidase, 119
mannosyl-oligosaccharide glucosidase, 117
mannosylfructose-phosphate phosphatase, 51
mannosylglycerate hydrolase, 132
mannosylglycoprotein endo-β-mannosidase, 127
matrilysin, 243
matriptase, 208
melamine deaminase, 311
memapsin 1, 237
memapsin 2, 237
membrane alanyl aminopeptidase, 161
membrane dipeptidase, 169
membrane Pro-Xaa carboxypeptidase, 179
membrane-type matrix metalloproteinase-1, 256
meprin A, 242
meprin B, 252
Met-Xaa dipeptidase, 168
metallocarboxypeptidase D, 180
methenyltetrahydrofolate cyclohydrolase, 303
methenyltetrahydrodromethanopterin cyclohydrolase, 307
methionyl aminopeptidase, 164
methyl acetate hydrolase, 26
N-methyl nucleosidase, 151
[3-methyl-2-oxobutanoate dehydrogenase (2-methylpropanoyl-transferring)-phosphatase, 44
N-methyl-2-oxoglutarate hydrolase, 269
S-methyl-5′-thioadenosine deaminase, 307
1-methyladenosine nucleosidase, 148
methylated diphthine methylhydrolase, 22
N′-methylcarbamate hydrolase, 292
methylenediurea deaminase, 300
4-methyleneglutaminase, 275
methylguanidinase, 299
7-methylguanosine nucleotidase, 54
(S)-methylmalonyl-CoA hydrolase, 30
4-methyloxaloacetate esterase, 9
methylphosphothioglycerate phosphatase, 36
methylumbelliferyl-acetate deacetylase, 12
metridin, 186
microbial collagenase, 239
micrococcal nuclease, 95
microsomal epoxide hydrolase, 155
mitochondrial intermediate peptidase, 251
mitochondrial processing peptidase, 253
Mn2+-dependent ADP-ribose/CDP-alcohol diphosphatase, 324
mono(ethylene terephthalate) hydrolase, 23
monomethyl-sulfatase, 71
monoterpene ε-lactone hydrolase, 19
monoterpenyl-diphosphatase, 74
mRNA 5′-phosphatase, 330
mRNA(cytosine) deaminase, 309
mucorpepsin, 232
mucrolysin, 250
multiple inositol-polyphosphate phosphatase, 47
muramoylpentapeptide carboxypeptidase, 177
muramoyl-leucinecarboxypeptidase, 178
mycodextranase, 107
[mycofactocin precursor peptide] peptidase, 173
mycolysin, 245
mycophenolic acid acyl-glucuronide esterase, 21
mycothiol S-conjugate amidase, 286
mycoblastin, 200
[myosin-light-chain] phosphatase, 45
N-formylmaleamate deformylase, 284
N-methylhydantoinase (ATP-hydrolysing), 294
NAD+ diphosphatase, 319
NAD+ glycohydrolase, 146
naldilysin, 252
α-neogararo-oligosaccharide hydrolase, 129
neopullulanase, 123
neprthesin, 230
neprylisin, 240
neryl diphosphate diphosphatase, 75
nueroysin, 242
neutrophil collagenase, 246
nicotinamidase, 266
nicotinamide-nucleotide amidase, 270
nitrilase, 311
5-nitroantranilic acid aminohydrolase, 314
2-nitroimidazole nitrohydrodrolase, 314
4-nitrophenylphosphatase, 42
NMN nucleosidase, 148
nocturnin, 57
nodavirus endopeptidase, 237
non-chaperonin molecular chaperone ATPase, 335
non-reducing end α-L-arabinofuranosidase, 106
non-reducing end β-L-arabinofuranosidase, 136
non-reducing end β-L-arabinopyranosidase, 113
non-stereospecific dipeptidase, 169
nuclear-inclusion a endopeptidase, 220
3′-5′-nucleoside bisphosphate phosphatase, 55
nucleoside diphosphatase, 316
nucleoside phosphoacylhydrolase, 320
nucleoside-triphosphate phosphatase, 318
3′-nucleotidase, 35
5′-nucleotidase, 35
nucleotide diphosphatase, 317
oleoyl-[acyl-carrier-protein] hydrolase, 30
oleuropein β-glucosidase, 141
oligo-1,6-glucosidase, 97
oligonucleotidase, 78
oligopeptidase A, 254
oligopeptidase B, 201
oligosaccharide reducing-end xylanase, 128
oligosaccharide-diphosphodolichol diphosphatase, 323
oligoxyloglucan β-glucosidase, 120
oligoxyloglucan reducing-end-specific cellobiohydrolase, 126
omptin, 238
ophiolsin, 250
pro-oxymelancortin converting enzyme, 230
orsellinate-depside hydrolase, 9
oryzin, 197
oviductin, 212
oxaloacetase, 338
oxamatic amidohydrolase, 289
oxepin-CoA hydrolase, 156
2-oxo-3-(5-oxofuran-2-yldene)propanoate lactonase, 20
8-oxo-dGDP phosphatase, 325
8-oxo-dGTP diphosphatase, 325
8-oxo-(d)GTP phosphatase, 328
3-oxoadipate enol-lactonase, 6
6-oxocamphor hydrolase, 341
6-oxocyclohex-1-ene-1-carbonyl-CoA hydratase, 342
2-oxoglutaramate amidase, 285
8-oxoguanine deaminase, 308
3-oxoisopentionate-4-phosphate transcarboxylase/hydrolase, 343
5-oxoproline (ATP-hydrolysing), 293
palatinase, 145
palmitoyl-CoA hydrolase, 28
palmitoyl[protein] hydrolase, 32
pancreatic elastase, 191
pancreatic elastase II, 199
pancreatic endopeptidase E, 198
pantetheine hydrolase, 280
pantothenase, 266
pApA phosphodiesterase, 67
papain, 213
pappalysin-1, 256
pectinesterase, 4
penicillin amidase, 264
penicillopepsin, 231
pentanamidase, 271
PepB aminopeptidase, 165
pepsin A, 228
pepsin B, 228
L- peptidase, 220
peptidase 1 (mite), 226
peptidase Do, 207
peptidase K, 197
peptide deformylase, 279
peptide-N^4-(N-acetyl-β-glucosaminyl)asparagine amidase, 272
peptidoglycan β-N-acetylmuramidase, 113
peptidoglycan-β-N-acetylglucosamine deacetylase, 283
β-peptidyl aminopeptidase, 166
peptidyl-Asp metalloendopeptidase, 246
peptidyl-dipeptidase A, 173
peptidyl-dipeptidase B, 174
peptidyl-dipeptidase Dcp, 174
peptidyl-dipeptidase D, 174
peptidyl-glutaminase, 270
peptidyl-glycinamidase, 182
peptidylglycinamidase, 182
peptidyl-lysine amidohydrolase, 243
peroxisome-assembly ATPase, 335
pestivirus NS3 polyprotein peptidase, 209
phenylacetyl-CoA hydrolase, 32
pheophorbidase, 18
phloretin hydrolase, 338
phorbol-12-deoxy hydrolase, 11
phosphatidate phosphatase, 34
phosphatidylglycerophosphatase, 39
polynucleotide 3′-phosphatase, 40
polynucleotide 5′-phosphatase, 40
polyporopepsin, 234
β-porphyranase, 134
preflagellin peptidase, 236
prelimin peptidase, 236
prelmin peptidase, 280
proclavaminate amidinohydrolase, 305
proclavaminate amidinohydrolase, 300
pimelyl-[acyl-carrier protein] methyl ester esterase, 19
plasminogen activator, 198
plasminogen activator Pla, 238
poly(A)-specific ribonuclease, 78
poly(ADP-ribose) glycohydrolase, 125
poly(ethylene terephthalate) hydrolase, 23
polyphosphate hydrolase, 120
polyneuridine-aldehyde esterase, 17
polyneuridine-α-lactone esterase, 17
polyneuridin-β-aldehyde esterase, 17
polynucleotide 3′-phosphatase, 40
polynucleotide 5′-phosphatase, 40
polyphosphatase, 234
polyphosphatase, 234
polyphosphatase, 234
procollagen N-endopeptidase, 241
proclavaminate amidinohydrolase, 300
proclavaminate amidinohydrolase, 300
procollagen C-endopeptidase, 242
L-proline amide hydrolase, 283
prolyl aminopeptidase, 162
prolyl oligopeptidase, 189
proprotein convertase 1, 204
proprotein convertase 2, 204
proteasome endopeptidase complex, 259
protein O-GlcNAcase, 131
[protein ADP-ribosylarginine] hydrolase, 149
protein arginine phosphatase, 346
protein C (activated), 198
protein deglycase, 289
protein N-terminal asparagine amidohydrolase, 288
protein N-terminal glutamine amidohydrolase, 288
protein phosphatase methylesterase-1, 20
protein-arginine deiminase, 299
[protein ADP-ribosylarginine] hydrolase, 149
protein arginine phosphatase, 346
protein C (activated), 198
protein deglycase, 289
protein N-terminal asparagine amidohydrolase, 288
protein N-terminal glutamine amidohydrolase, 288
protein phosphatase methylesterase-1, 20
protein-arginine deiminase, 299
protein-glucosylgalactosylhydroxylysine glucosidase, 117
protein-glutamate methylesterase, 13
protein-serine/threonine phosphatase, 37
protein-synthesizing GTPase, 337
protein-tyrosine-phosphatase, 44
protodioscin 26-O-β-D-glucosidase, 136
prunasin β-glucosidase, 120
pseudolysin, 244
pseudouridine 5′-phosphatase, 55
pterin deaminase, 303
pullulanase, 103
Pup amidohydrolase, 287
purine nucleosidase, 145
pycnoporopepsin, 234
pyrethroid hydrolase, 20
pyridoxal phosphatase, 49
4-pyridoxolactonase, 6
pyrimidine-5′-nucleotide nucleosidase, 148
pyrithiamine deaminase, 305
pyroglutamyl-peptidase I, 182
pyroglutamyl-peptidase II, 183
2-pyrene-4,6-dicarboxylate lactonase, 12
1-pyruvlate-4-hydroxy-2-carboxylate deaminase, 305
[pyruvate dehydrogenase (acetyl-transferring)]-phosphatase, 42
[pyruvate kinase]-phosphatase, 44
quorum-quenching N-acyl-homoserine lactonase, 18
rhizopuspepsin, 232
rhodotorulapepsin, 233
rhomboid protease, 207
riboflavinase, 313
ribonuclease α, 90
ribonuclease D, 79
ribonuclease E, 92
ribonuclease F, 94
ribonuclease H, 91
ribonuclease III, 91
ribonuclease IV, 91
ribonuclease IX, 92
ribonuclease M5, 92
ribonuclease P, 91
ribonuclease P4, 91
ribonuclease [poly-(U)-specific], 92
ribonuclease V, 94
ribozymyridine nucleosidase, 147
ribulose-1,5-bisphosphate 5-phosphatase, 58
ricine nitrilase, 311
RNA 2′,3′-cyclic 3′-phosphodiesterase, 67
RNA helicase, 336
rRNA N-glycosylase, 150
ruberylsin, 249
russellysin, 251
S2P endopeptidase, 258
saccharolysin, 246
saccharopepsin, 233
SARS coronavirus main proteinase, 227
scutelarin, 196
scyrilaside A, 234
scyrilaside B, 234
sedoheptulose bisphosphatase, 41
sedoheptulose-bisphosphatase, 41
semenogelase, 200
separase, 221
sepiapterin deaminase, 306
serine-ethanolaminephosphate phosphodiesterase, 60
serine-type D-Ala-D-Ala carboxypeptidase, 175
serralyasin, 247
sialate O-acetylerase, 11
O-sialyglycoprotein endopeptidase, 251
signal peptidase I, 202
signal peptidase II, 235
signal-recognition-particle GTPase, 337
sinapine esterase, 10
single-stranded DNA cytosine deaminase, 309
site-1 protease, 209
small monomeric DNA cytosine deaminase, 309
snake venom factor V activator, 204
snapalysin, 256
soluble epoxide hydrolase, 156
sorbitol-6-phosphatase, 44
sortase A, 228
sortase B, 228
539
(R)-specific secondary-alkylsulfatase (type III), 72
spermosin, 205
sphingomyelin deacylase, 285
sphingomyelin phosphodiesterase, 60
sphingomyelin phosphodiesterase D, 63
spleen exonuclease, 79
SpoIVB peptidase, 210
staphopain, 221
Ste24 endopeptidase, 257
stem bromelain, 217
d-stereospecific aminopeptidase, 164
steroid-lactonase, 4
steryl-β-glucosidase, 116
steryl-sulfatase, 69
stratum corneum chymotryptic enzyme, 211
streptogrisin A, 201
streptogrisin B, 201
streptomycin-6-phosphatase, 41
streptopain, 214
streptothricin hydrolase, 296
α(3S)-strictosidine β-glucosidase, 116
stromelysin 1, 242
stromelysin 2, 243
N-substituted formamide deformylase, 280
subtilisin, 196
succinyl-CoA hydrolase, 28
succinyl-diaminopimelate desuccinylase, 265
N-succinylarginine dihydrolase, 300
succinylglutamate desuccinylase, 265
S-succinylglutathione hydrolase, 30
succrose-phosphate phosphatase, 38
sugar-phosphatase, 38
sugar-terminal-phosphatase, 46
3-sulfino propanoyl-CoA desulfinylase, 249
N-sulfoglucoasamine sulfohydrolase, 347
N-sulfoglucosamine-3-sulfatase, 71
4-sulfomuconolate hydrolase, 21
sulfoquinovosidase, 140
γ-sulfosulfanyl-L-cysteine sulfohydrolase, 72
T₄ deoxyribonuclease II, 81
T₄ deoxyribonuclease IV, 82
tannase, 5
tehanine dihydrolase, 23
tentoxylsin, 254
theanine hydrolase, 274
thermitase, 197
thermolysin, 244
thermomycolin, 197
thermopin, 236
thiamine phosphate phosphatase, 56
thiamine-triphosphatase, 321
thimet oligopeptidase, 241
thiocyanate hydrolase, 312
thioglucoasidase, 126
thrombin, 186
thymidine-triphosphatase, 322
thymidylate 5′-phosphatase, 41
thymine-DNA glycosylase, 152
tissue kallikrein, 191
togavirin, 203
transmembrane protease serine 2, 212
αα-trehalase, 100
trehalose-phosphatase, 36
triacetate-lactonase, 8
triacylglycerol lipase, 2
trimelysin I, 250
trimelysin II, 250
trimetaphosphatase, 316
tripeptide aminopeptidase, 162
tripeptidyl-peptidase I, 172
tripeptidyl-peptidase II, 172
triposphatase, 320
trithionate hydrolase, 348
rRNA(adenine34) deaminase, 308
rRNA(adenine31) deaminase, 308
rRNA(cytosine8) deaminase, 308
RNase Z, 92
tropinesterase, 3
tryptase, 195
tryptophanaminidase, 273
tryptophanyl aminopeptidase, 164
tubulin GTPase, 337
tubulin-glutamate carboxypeptidase, 181
tubulyl-Tyr carboxypeptidase, 179
type I site-specific deoxyribonuclease, 80
type II site-specific deoxyribonuclease, 81
type III site-specific deoxyribonuclease, 81
u-plasminogen activator, 199
ubiquitinyl hydrolase 1, 184
UDP-2,3-diacylglucosamine diphosphatase, 324
UDP-2,4-diactamido-2,4,6-trideoxy-β-L-altropyranose hydrolase, 325
UDP-3-O-acyl-N-acetylglucoasamine deacytelase, 284
UDP-N′-diamybacillosamine 2-epimerase (hydrolysing), 135
UDP-N-acetylglucoasamine 2-epimerase (hydrolysing), 135
UDP-sugar diphosphatase, 323
UDP-sulfoquinovosy synthase, 349
Ulp1 peptidase, 227
undecaprenyl-diphosphate synthase, 321
unsaturated chondroitin disaccharide hydrolase, 134
unsaturated rhamnogalacturonyl hydrolase, 132
uracil-DNA glycosylase, 151
urease, 263
ureidoacrylate amidohydrolase, 285
(S)-ureidoglycine aminohydrolase, 301
ureidoglycolate amidohydrolase, 287
β-ureidopropionase, 263
ureidosuccinase, 263
urethanase, 276
uridine nucleosidase, 146
uronolactonase, 5
V-cath endopeptidase, 221
validoxylamine A 7'-phosphate phosphatase, 56
venom exonuclease, 79
venombin A, 199
venombin AB, 195
versiconal hemiacetal acetate esterase, 21
vesicle-fusing ATPase, 335
vibriolysin, 244
vicianin β-glucosidase, 120
wax-ester hydrolase, 11
[Wnt protein] O-palmitoleoyl-L-serine hydrolase, 22
Xaa-Arg dipeptidase, 167
Xaa-methyl-His dipeptidase, 168
Xaa-Pro aminopeptidase, 163
Xaa-Pro dipeptidase, 168
Xaa-Pro dipeptidyl-peptidase, 172
Xaa-Trp aminopeptidase, 164
Xaa-Xaa-Pro tripeptidyl-peptidase, 173
xanthomonalsin, 206
XTP/dITP diphosphatase, 327
xylan α-1,2-glucuronosidase, 123
xylan 1,3-β-xylosidase, 109
xylan 1,4-β-xylosidase, 102
xyloglucan-specific endo-β-1,4-glucanase, 127
xyloglucan-specific endo-processive β-1,4-glucanase, 128
xylono-1,4-lactonase, 14
xylono-1,5-lactonase, 25
yapsin 1, 236
yeast ribonuclease, 79
zinc D-Ala-D-Ala carboxypeptidase, 179
zingipain, 227