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

Proposed Changes to the Enzyme List

The entries below are proposed additions and amendments to the Enzyme Nomenclature list. They were prepared for the NC-IUBMB by Keith Tipton, Sinéad Boyce, Gerry Moss and Hal Dixon, with occasional help from other Committee members. Comments and suggestions on these draft entries should be sent to Professor K.F. Tipton and Dr S. Boyce (Department of Biochemistry, Trinity College Dublin, Dublin 2, Ireland). The date on which an enzyme will be made official is appended after the EC number.

Many thanks to those of you who have submitted details of new enzymes or updates to existing enzymes.

An asterisk before 'EC' indicates that this is an amendment to an existing enzyme rather than a new enzyme entry.

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***EC 1.1.1.95 – public review until 16 August 2006** **(1-1)** [Last modified: 19/07/2006] [Edit]

Accepted name: phosphoglycerate dehydrogenase

Reaction: (1) 3-phospho-D-glycerate + NAD$^+$ = 3-phosphonooxypyruvate + NADH + H$^+$
(2) 2-hydroxyglutarate + NAD$^+$ = 2-oxoglutarate + NADH + H$^+$
For diagram of the phosphoserine pathway of serine biosynthesis, click here

Other name(s): D-3-phosphoglycerate:NAD$^+$ oxidoreductase; α-phosphoglycerate dehydrogenase; 3-phosphoglycerate dehydrogenase; 3-phosphoglyceric acid dehydrogenase; D-3-

phosphoglycerate dehydrogenase; glycerate 3-phosphate dehydrogenase; glycerate-1,3-phosphate dehydrogenase; phosphoglycerate oxidoreductase; phosphoglyceric acid dehydrogenase; SerA; 3-phosphoglycerate:NAD$^+$ 2-oxidoreductase; SerA 3PG dehydrogenase; 3PHP reductase; αKG reductase; D- and L-HGA

Systematic name: 3-phospho-D-glycerate:NAD$^+$ 2-oxidoreductase

Comments: This enzyme catalyses the first committed step in the phosphoserine pathway of serine biosynthesis in *Escherichia coli* [2,3]. Reaction (1) occurs predominantly in the reverse direction and is inhibited by serine and glycine. The enzyme is unusual in that it also acts as a D- and L-2-hydroxyglutarate dehydrogenase (with the D-form being the better substrate) and as a 2-oxoglutarate reductase [3]. It has been postulated [3] that the cellular 2-oxoglutarate concentration may regulate serine biosynthesis and one-carbon metabolism directly by modulating the activity of this enzyme.

Links to other databases: BRENDA, ERGO, EXPASY, GO, GTD, IUBMB, KEGG, PDB, CAS registry number: 9075-29-0

References:

1. Sugimoto, E. and Pizer, L.I. The mechanism of end product inhibition of serine biosynthesis. I. Purification and kinetics of phosphoglycerate dehydrogenase. *J. Biol. Chem.* **243** (1968) 2081–1089. [PMID: 4384871]
2. Pizer, L.I. The pathway and control of serine biosynthesis in *Escherichia coli*. *J. Biol. Chem.* **238** (1963) 3934–3944. [PMID: 14086727]
3. Zhao, G. and Winkler, M.E. A novel α-ketoglutarate reductase activity of the *serA*-encoded 3-phosphoglycerate dehydrogenase of *Escherichia coli* K-12 and its possible implications for human 2-hydroxyglutaric aciduria. *J. Bacteriol.* **178** (1996) 232–239. [PMID: 8550422]
4. Schuller, D.J., Grant, G.A. and Banaszak, L.J. The allosteric ligand site in the V_{max}-type cooperative enzyme phosphoglycerate dehydrogenase. *Nat. Struct. Biol.* **2** (1995) 69–76. [PMID: 7719856]

[EC 1.1.1.95 created 1972, modified 2006]

*EC 1.2.3.3 – public review until 16 August 2006 **(1-1)** [Last modified: 19/07/2006] [Edit]

Accepted name: pyruvate oxidase

Reaction: pyruvate + phosphate + O_2 = acetyl phosphate + CO_2 + H_2O_2

Glossary: thiamine diphosphate = 3-[(4-amino-2-methylpyrimidin-5-yl)methyl]-5-(2-diphosphoethyl)-4-methyl-1,3-thiazolium

Other name(s): pyruvic oxidase; phosphate-dependent pyruvate oxidase

Systematic name: pyruvate:oxygen 2-oxidoreductase (phosphorylating)

Comments: A flavoprotein (FAD) requiring thiamine diphosphate. Two reducing equivalents are transferred from the resonant carbanion/enamine forms of 2-hydroxyethyl-thiamine-diphosphate to the adjacent flavin cofactor, yielding 2-acetyl-thiamine diphosphate (AcThDP) and reduced flavin. $FADH_2$ is reoxidized by O_2 to yield H_2O_2 and FAD and AcThDP is cleaved phosphorolytically to acetyl phosphate and thiamine diphosphate [2].

Links to other databases: BRENDA, ERGO, EXPASY, GO, IUBMB, KEGG, PDB, CAS registry number: 9001-96-1

References:

1. Williams, F.R. and Hager, L.P. Crystalline flavin pyruvate oxidase from *Escherichia coli*. I. Isolation and properties of the flavoprotein. *Arch. Biochem. Biophys.* **116** (1966) 168–176. [PMID: 5336022]
2. Tittmann, K., Wille, G., Golbik, R., Weidner, A., Ghisla, S. and Hübner, G. Radical phosphate transfer mechanism for the thiamin diphosphate- and FAD-dependent pyruvate oxidase from *Lactobacillus plantarum*. Kinetic coupling of intercofactor electron transfer with phosphate transfer to acetyl-thiamin diphosphate via a transient FAD semiquinone/hydroxyethyl-ThDP radical pair. *Biochemistry* **44** (2005) 13291–13303. [PMID: 16201755]

[EC 1.2.3.3 created 1961]

*EC 1.4.1.18 – public review until 01 September 2006 **(1-1)** [Last modified: 04/08/2006] [Edit]

Accepted name: lysine 6-dehydrogenase

Reaction: (1a) L-lysine + NAD$^+$ + H_2O = (*S*)-2-amino-6-oxohexanoate + NADH + H$^+$ + NH_3
(1b) (*S*)-2-amino-6-oxohexanoate = (*S*)-2,3,4,5-tetrahydropyridine-2-carboxylate + H_2O (spontaneous)

For diagram of reactions, click here

Glossary: (*S*)-2-amino-6-oxohexanoate = (*S*)-2-aminoadipate 6-semialdehyde = L-allysine
(*S*)-2,3,4,5-tetrahydropyridine-2-carboxylate = (*S*)-1,6-didehydropiperidine-2-carboxylate

Other name(s): L-lysine ε-dehydrogenase; L-lysine 6-dehydrogenase; LysDH

Systematic name: L-lysine:NAD^+ 6-oxidoreductase (deaminating)

Comments: The enzyme is highly specific for L-lysine as substrate, although (*S*)-(β-aminoethyl)-L-cysteine can act as a substrate, but more slowly. While the enzyme from *Agrobacterium tumefaciens* can use only NAD^+, that from the thermophilic bacterium *Geobacillus stearothermophilus* can also use $NADP^+$, but more slowly [1,4].

Links to other databases: BRENDA, ERGO, EXPASY, GO, IUBMB, KEGG, CAS registry number: 89400-30-6

References:

1. Misono, H. and Nagasaki, S. Occurrence of L-lysine ε-dehydrogenase in *Agrobacterium tumefaciens*. *J. Bacteriol.* **150** (1982) 398–401. [PMID: 6801024]
2. Misono, H., Uehigashi, H., Morimoto, E. and Nagasaki, S. Purification and properties of L-lysine ε-dehydrogenase from *Agrobacterium tumefaciens*. *Agric. Biol. Chem.* **49** (1985) 2253–2255.
3. Misono, H., Hashimoto, H., Uehigashi, H., Nagata, S. and Nagasaki, S. Properties of L-lysine ε-dehydrogenase from *Agrobacterium tumefaciens*. *J. Biochem. (Tokyo)* **105** (1989) 1002–1008. [PMID: 2768207]
4. Heydari, M., Ohshima, T., Nunoura-Kominato, N. and Sakuraba, H. Highly stable L-lysine 6-dehydrogenase from the thermophile *Geobacillus stearothermophilus* isolated from a Japanese hot spring: characterization, gene cloning and sequencing, and expression. *Appl. Environ. Microbiol.* **70** (2004) 937–942. [PMID: 14766574]

[EC 1.4.1.18 created 1989, modified 2006]

EC 1.5.1.35 – public review until 16 August 2006 **(2-1)** [Last modified: 19/07/2006] [Edit]

Accepted name: 1-pyrroline dehydrogenase

Reaction: 1-pyrroline + NAD^+ + **2** H_2O = 4-aminobutanoate + NADH + **2** H^+

For diagram of the arginine-catabolism pathway, click here

Glossary: 1-pyrroline = 3,4-dihydro-2*H*-pyrrole

Other name(s): γ-aminobutyraldehyde dehydrogenase; ABALDH; YdcW

Systematic name: 1-pyrroline:NAD^+ oxidoreductase

Comments: 1-Pyrroline forms spontaneously from 4-aminobutanal, produced by EC 2.6.1.82, putrescine aminotransferase. This enzyme forms part of the arginine-catabolism pathway [3].

References:

1. Prieto-Santos, M.I., Martin-Checa, J., Balaña-Fouce, R. and Garrido-Pertierra, A. A pathway for putrescine catabolism in *Escherichia coli*. *Biochim. Biophys. Acta* **880** (1986) 242–244. [PMID: 3510672]
2. Prieto, M.I., Martin, J., Balaña-Fouce, R. and Garrido-Pertierra, A. Properties of γ-aminobutyraldehyde dehydrogenase from *Escherichia coli*. *Biochimie* **69** (1987) 1161–1168. [PMID: 3129020]
3. Samsonova, N.N., Smirnov, S.V., Novikova, A.E. and Ptitsyn, L.R. Identification of *Escherichia coli* K12 YdcW protein as a γ-aminobutyraldehyde dehydrogenase. *FEBS Lett.* **579** (2005) 4107–4112. [PMID: 16023116]

[EC 1.5.1.35 created 2006]

EC 1.8.4.5 – public review until 16 August 2006 **(4-1)** [Last modified: 19/07/2006] [Edit]

Transferred entry: methionine-*S*-oxide reductase. Now EC 1.8.4.13, L-methionine (*S*)-*S*-oxide reductase and EC 1.8.4.14, L-methionine (*R*)-*S*-oxide reductase.

[EC 1.8.4.5 created 1984, deleted 2006]

EC 1.8.4.6 – public review until 16 August 2006 **(4-1)** [Last modified: 19/07/2006] [Edit]

Transferred entry: protein-methionine-*S*-oxide reductase. Proved to be due to EC 1.8.4.11, peptide-methionine (*S*)-*S*-oxide reductase.

[EC 1.8.4.6 created 1984, deleted 2006]

EC 1.8.4.11 – public review until 16 August 2006 **(2-1)** [Last modified: 30/08/2006] [Edit]

Accepted name: peptide-methionine (*S*)-*S*-oxide reductase

Reaction: (1) peptide-L-methionine + thioredoxin disulfide + H_2O = peptide-L-methionine (*S*)-*S*-oxide + thioredoxin
(2) L-methionine + thioredoxin disulfide + H_2O = L-methionine (*S*)-*S*-oxide + thioredoxin

For diagram of reaction, click here and for mechanism of reaction, click here

Other name(s): MsrA; methionine sulfoxide reductase (ambiguous); methionine sulphoxide reductase A; methionine *S*-oxide reductase (ambiguous); methionine *S*-oxide reductase (*S*-form oxidizing); methionine sulfoxide reductase A; peptide methionine sulfoxide reductase

Systematic name: peptide-L-methionine:thioredoxin-disulfide *S*-oxidoreductase [L-methionine (*S*)-*S*-oxide-forming]

Comments: The reaction occurs in the reverse direction to that shown above. The enzyme exhibits high specificity for the reduction of the *S*-form of L-methionine *S*-oxide, acting faster on the residue in a peptide than on the free amino acid [9]. On the free amino acid, it can also reduce D-methionine (*S*)-*S*-oxide but more slowly [9]. The enzyme plays a role in preventing oxidative-stress damage caused by reactive oxygen species by reducing the oxidized form of methionine back to methionine and thereby reactivating peptides that had been damaged. In some species, e.g. *Neisseria meningitidis*, both this enzyme and EC 1.8.4.12, methionine (*R*)-*S*-oxide reductase, are found within the same protein whereas, in other species, they are separate proteins [1,4]. The reaction proceeds via a sulfenic-acid intermediate [5,10].

References:

1. Moskovitz, J., Singh, V.K., Requena, J., Wilkinson, B.J., Jayaswal, R.K. and Stadtman, E.R. Purification and characterization of methionine sulfoxide reductases from mouse and *Staphylococcus aureus* and their substrate stereospecificity. *Biochem. Biophys. Res. Commun.* **290** (2002) 62–65. [PMID: 11779133]
2. Taylor, A.B., Benglis, D.M., Jr., Dhandayuthapani, S. and Hart, P.J. Structure of *Mycobacterium tuberculosis* methionine sulfoxide reductase A in complex with protein-bound methionine. *J. Bacteriol.* **185** (2003) 4119–4126. [PMID: 12837786]
3. Singh, V.K. and Moskovitz, J. Multiple methionine sulfoxide reductase genes in *Staphylococcus aureus*: expression of activity and roles in tolerance of oxidative stress. *Microbiology* **149** (2003) 2739–2747. [PMID: 14523107]
4. Boschi-Muller, S., Olry, A., Antoine, M. and Branlant, G. The enzymology and biochemistry of methionine sulfoxide reductases. *Biochim. Biophys. Acta* **1703** (2005) 231–238. [PMID: 15680231]
5. Ezraty, B., Aussel, L. and Barras, F. Methionine sulfoxide reductases in prokaryotes. *Biochim. Biophys. Acta* **1703** (2005) 221–229. [PMID: 15680230]
6. Weissbach, H., Resnick, L. and Brot, N. Methionine sulfoxide reductases: history and cellular role in protecting against oxidative damage. *Biochim. Biophys. Acta* **1703** (2005) 203–212. [PMID: 15680228]
7. Kauffmann, B., Aubry, A. and Favier, F. The three-dimensional structures of peptide methionine sulfoxide reductases: current knowledge and open questions. *Biochim. Biophys. Acta* **1703** (2005) 249–260. [PMID: 15680233]
8. Vougier, S., Mary, J. and Friguet, B. Subcellular localization of methionine sulphoxide reductase A (MsrA): evidence for mitochondrial and cytosolic isoforms in rat liver cells. *Biochem. J.* **373** (2003) 531–537. [PMID: 12693988]
9. Olry, A., Boschi-Muller, S., Marraud, M., Sanglier-Cianferani, S., Van Dorsselear, A. and Branlant, G. Characterization of the methionine sulfoxide reductase activities of PILB, a probable virulence factor from *Neisseria meningitidis*. *J. Biol. Chem.* **277** (2002) 12016–12022. [PMID: 11812798]
10. Brot, N., Weissbach, L., Werth, J. and Weissbach, H. Enzymatic reduction of protein-bound methionine sulfoxide. *Proc. Natl. Acad. Sci. USA* **78** (1981) 2155–2158. [PMID: 7017726]

[EC 1.8.4.11 created 2006]

EC 1.8.4.12 – public review until 16 August 2006 **(2-1)** [Last modified: 30/08/2006] [Edit]

Accepted name: peptide-methionine (*R*)-*S*-oxide reductase

Reaction: peptide-L-methionine + thioredoxin disulfide + H_2O = peptide-L-methionine (*R*)-*S*-oxide + thioredoxin

For diagram of reaction, click here and for mechanism of reaction, click here

Other name(s): MsrB; methionine sulfoxide reductase (ambiguous); pMSR; methionine *S*-oxide reductase (ambiguous); selenoprotein R; methionine *S*-oxide reductase (*R*-form oxidizing); methionine sulfoxide reductase B; SelR; SelX; PilB; pRMsr

Systematic name: peptide-methionine:thioredoxin-disulfide *S*-oxidoreductase [methionine (*R*)-*S*-oxide-forming]

Comments: The reaction occurs in the reverse direction to that shown above. The enzyme exhibits high specificity for reduction of the *R*-form of methionine *S*-oxide, with higher activity being observed with L-methionine *S*-oxide than with D-methionine *S*-oxide [9]. While both free and protein-bound methionine (*R*)-*S*-oxide act as substrates, the activity with the peptide-bound form is far greater [10]. The enzyme plays a role in preventing oxidative-stress damage caused by reactive oxygen species by reducing the oxidized form of methionine back to methionine and thereby reactivating peptides that had been damaged. In some species, e.g. *Neisseria meningitidis*, both this enzyme and EC 1.8.4.11, peptide-methionine (*S*)-*S*-oxide reductase, are found within the same protein whereas in other species, they are separate proteins [3,5]. The reaction proceeds via a sulfenic-acid intermediate [5,10]. For MsrB2 and MsrB3, thioredoxin is a poor reducing agent but thionein works well [11]. The enzyme from some species contains selenocysteine and Zn^{2+}.

References:

1. Moskovitz, J., Singh, V.K., Requena, J., Wilkinson, B.J., Jayaswal, R.K. and Stadtman, E.R. Purification and characterization of methionine sulfoxide reductases from mouse and *Staphylococcus aureus* and their substrate stereospecificity. *Biochem. Biophys. Res. Commun.* **290** (2002) 62–65. [PMID: 11779133]
2. Taylor, A.B., Benglis, D.M., Jr., Dhandayuthapani, S. and Hart, P.J. Structure of *Mycobacterium tuberculosis* methionine sulfoxide reductase A in complex with protein-bound methionine. *J. Bacteriol.* **185** (2003) 4119–4126. [PMID: 12837786]
3. Singh, V.K. and Moskovitz, J. Multiple methionine sulfoxide reductase genes in *Staphylococcus aureus*: expression of activity and roles in tolerance of oxidative stress. *Microbiology* **149** (2003) 2739–2747. [PMID: 14523107]
4. Boschi-Muller, S., Olry, A., Antoine, M. and Branlant, G. The enzymology and biochemistry of methionine sulfoxide reductases. *Biochim. Biophys. Acta* **1703** (2005) 231–238. [PMID: 15680231]
5. Ezraty, B., Aussel, L. and Barras, F. Methionine sulfoxide reductases in prokaryotes. *Biochim. Biophys. Acta* **1703** (2005) 221–229. [PMID: 15680230]
6. Weissbach, H., Resnick, L. and Brot, N. Methionine sulfoxide reductases: history and cellular role in protecting against oxidative damage. *Biochim. Biophys. Acta* **1703** (2005) 203–212. [PMID: 15680228]
7. Kauffmann, B., Aubry, A. and Favier, F. The three-dimensional structures of peptide methionine sulfoxide reductases: current knowledge and open questions. *Biochim. Biophys. Acta* **1703** (2005) 249–260. [PMID: 15680233]
8. Vougier, S., Mary, J. and Friguet, B. Subcellular localization of methionine sulphoxide reductase A (MsrA): evidence for mitochondrial and cytosolic isoforms in rat liver cells. *Biochem. J.* **373** (2003) 531–537. [PMID: 12693988]
9. Olry, A., Boschi-Muller, S., Marraud, M., Sanglier-Cianferani, S., Van Dorsselear, A. and Branlant, G. Characterization of the methionine sulfoxide reductase activities of PILB, a probable virulence factor from *Neisseria meningitidis*. *J. Biol. Chem.* **277** (2002) 12016–12022. [PMID: 11812798]
10. Sagher, D., Brunell, D., Hejtmancik, J.F., Kantorow, M., Brot, N. and Weissbach, H. Thionein can serve as a reducing agent for the methionine sulfoxide reductases. *Proc. Natl. Acad. Sci. USA* **103** (2006) 8656–8661. [PMID: 16735467]

[EC 1.8.4.12 created 2006]

EC 1.8.4.13 – public review until 16 August 2006 **(2-1)** [Last modified: 19/07/2006] [Edit]

Accepted name: L-methionine (*S*)-*S*-oxide reductase

Reaction: L-methionine + thioredoxin disulfide + H_2O = L-methionine (*S*)-*S*-oxide + thioredoxin

For diagram of reaction, click here and for mechanism of reaction, click here

Other name(s): fSMsr; methyl sulfoxide reductase I and II; acetylmethionine sulfoxide reductase; methionine sulfoxide reductase; L-methionine:oxidized-thioredoxin *S*-oxidoreductase; methionine-*S*-oxide reductase; free-methionine (*S*)-*S*-oxide reductase

Systematic name: L-methionine:thioredoxin-disulfide *S*-oxidoreductase

Comments: Requires NADPH [2]. The reaction occurs in the opposite direction to that given above. Dithiothreitol can replace reduced thioredoxin. L-Methionine (*R*)-*S*-oxide is not a substrate [see EC 1.8.4.14, L-methionine (*R*)-*S*-oxide reductase].

References: 1. Black, S., Harte, E.M., Hudson, B. and Wartofsky, L. A specific enzymatic reduction of L-(-)methionine sulfoxide and a related nonspecific reduction of diulfides. *J. Biol. Chem.* **235** (1960) 2910–2916.
2. Ejiri, S.-I., Weissbach, H. and Brot, N. Reduction of methionine sulfoxide to methionine by *Escherichia coli*. *J. Bacteriol.* **139** (1979) 161–164. [PMID: 37234]
3. Ejiri, S.-I., Weissbach, H. and Brot, N. The purification of methionine sulfoxide reductase from *Escherichia coli*. *Anal. Biochem.* **102** (1980) 393–398. [PMID: 6999943]
4. Weissbach, H., Resnick, L. and Brot, N. Methionine sulfoxide reductases: history and cellular role in protecting against oxidative damage. *Biochim. Biophys. Acta* **1703** (2005) 203–212. [PMID: 15680228]

[EC 1.8.4.13 created 1984 as EC 1.8.4.5, part-transferred 2006 to EC 1.8.4.13]

EC 1.8.4.14 – public review until 16 August 2006 **(2-1)** [Last modified: 19/07/2006] [Edit]

Accepted name: L-methionine (*R*)-*S*-oxide reductase

Reaction: L-methionine + thioredoxin disulfide + H_2O = L-methionine (*R*)-*S*-oxide + thioredoxin

For diagram of reaction, click here and for mechanism of reaction, click here

Other name(s): fRMsr; FRMsr; free met-R-(o) reductase; free-methionine (*R*)-*S*-oxide reductase

Systematic name: L-methionine:thioredoxin-disulfide *S*-oxidoreductase [L-methionine (*R*)-*S*-oxide-forming]

Comments: Requires NADPH. Unlike EC 1.8.4.12, peptide-methionine (*R*)-*S*-oxide reductase, this enzyme cannot use peptide-bound methionine (*R*)-*S*-oxide as a substrate [1]. Differs from EC 1.8.4.13, L-methionine (*S*)-*S*-oxide in that L-methionine (*S*)-*S*-oxide is not a substrate.

References: 1. Etienne, F., Spector, D., Brot, N. and Weissbach, H. A methionine sulfoxide reductase in *Escherichia coli* that reduces the R enantiomer of methionine sulfoxide. *Biochem. Biophys. Res. Commun.* **300** (2003) 378–382. [PMID: 12504094]

[EC 1.8.4.14 created 1984 as EC 1.8.4.5, part-transferred 2006 to EC 1.8.4.14]

*EC 1.10.3.4 – public review until 16 August 2006 **(1-1)** [Last modified: 19/07/2006] [Edit]

Accepted name: *o*-aminophenol oxidase

Reaction: (1a) **2** 2-aminophenol + O_2 = **2** 6-iminocyclohexa-2,4-dienone + **2** H_2O
(1b) **2** 6-iminocyclohexa-2,4-dienone + oxidant = 2-aminophenoxazin-3-one + reduced oxidant (spontaneous)

For diagram of reaction, click here

Glossary: 6-iminocyclohexa-2,4-dienone = 1,2-benzoquinone monoimine
isophenoxazine = 2-aminophenoxazin-3-one

Other name(s): isophenoxazine synthase; *o*-aminophenol:O_2 oxidoreductase; 2-aminophenol:O_2 oxidoreductase; GriF

Systematic name: 2-aminophenol:oxygen oxidoreductase

Comments: A flavoprotein. While the enzyme from the plant *Tecoma stans* is activated by Mn^{2+} [1], that from the bacterium *Streptomyces griseus* (GriF) requires Cu^{2+} for maximal activity. Two molecules of the product 6-iminocyclohexa-2,4-dienone (i.e. 1,2-benzoquinone monoimine) spontaneously condense with oxidation to yield 2-aminophenoxazin-3-one [4]. 3-Amino-4-hydroxybenzaldehyde, which has a -CHO group at the para-position with respect fo the hydroxy group of 2-aminophenol, was found to be the best substrate for GriF [4].

Links to other databases: BRENDA, ERGO, EXPASY, GO, IUBMB, KEGG, CAS registry number: 9013-85-8

References: 1. Nair, P.M. and Vaidynathan, C.S. Isophenoxazine synthase. *Biochim. Biophys. Acta* **81** (1964) 507–516.
2. Nair, P.M. and Vining, L.C. Isophenoxazine synthase apoenzyme from *Pycnoporus coccineus*. *Biochim. Biophys. Acta* **96** (1965) 318–327. [PMID: 14298835]
3. Subba Rao, P.V. and Vaidyanathan, C.S. Studies on the metabolism of *o*-aminophenol. Purification and properties of isophenoxazine synthase from *Bauhenia monandra*. *Arch. Biochem. Biophys.* **118** (1967) 388–394. [PMID: 4166439]
4. Suzuki, H., Furusho, Y., Higashi, T., Ohnishi, Y. and Horinouchi, S. A novel *o*-aminophenol oxidase responsible for formation of the phenoxazinone chromophore of grixazone. *J. Biol. Chem.* **281** (2006) 824–833. [PMID: 16282322]

[EC 1.10.3.4 created 1972, modified 2006]

EC 1.13.12.11 – public review until 16 August 2006 **(3-1)** [Last modified: 19/07/2006] [Edit]

Deleted entry: methylphenyltetrahydropyridine *N*-monooxygenase. The activity is due to EC 1.14.13.8, flavin monooxygenase.

[EC 1.13.12.11 created 1992, deleted 2006]

EC 1.14.11.27 – public review until 29 August 2006 **(2-1)** [Last modified: 01/08/2006] [Edit]

Accepted name: [histone-H3]-lysine-36 demethylase

Reaction: (1) protein 6-*N*,6-*N*-dimethyl-L-lysine + 2-oxoglutarate + O_2 = protein 6-*N*-methyl-L-lysine + succinate + formaldehyde + CO_2
(2) protein 6-*N*-methyl-L-lysine + 2-oxoglutarate + O_2 = protein L-lysine + succinate + formaldehyde + CO_2

Other name(s): JHDM1A; JmjC domain-containing histone demethylase 1A; H3-K36-specific demethylase; histone-lysine (H3-K36) demethylase; histone demethylase

Systematic name: protein-6-*N*,6-*N*-dimethyl-L-lysine,2-oxoglutarate:oxygen oxidoreductase

Comments: Requires iron(II). Of the seven potential methylation sites in histones H3 (K4, K9, K27, K36, K79) and H4 (K20, R3) from HeLa cells, the enzyme is specific for Lys-36. Lysine residues exist in three methylation states (mono-, di- and trimethylated). The enzyme preferentially demethylates the dimethyl form of Lys-36 (K36me2), which is its natural substrate, to form the monomethyl and unmethylated forms of Lys-36. It can also demethylate the monomethyl- but not the trimethyl form of Lys-36.

References:
1. Tsukada, Y., Fang, J., Erdjument-Bromage, H., Warren, M.E., Borchers, C.H., Tempst, P. and Zhang, Y. Histone demethylation by a family of JmjC domain-containing proteins. *Nature* **439** (2006) 811–816. [PMID: 16362057]

[EC 1.14.11.27 created 2006]

*EC 1.14.13.8 – public review until 16 August 2006 **(1-1)** [Last modified: 19/07/2006] [Edit]

Accepted name: flavin-containing monooxygenase

Reaction: *N*,*N*-dimethylaniline + NADPH + H^+ + O_2 = *N*,*N*-dimethylaniline *N*-oxide + $NADP^+$ + H_2O

Other name(s): dimethylaniline oxidase; dimethylaniline *N*-oxidase; FAD-containing monooxygenase; *N*,*N*-dimethylaniline monooxygenase; DMA oxidase; flavin mixed function oxidase; Ziegler's enzyme; mixed-function amine oxidase; FMO; FMO-I; FMO-II; FMO1; FMO_2; FMO3; FMO4; FMO5; flavin monooxygenase; methylphenyltetrahydropyridine *N*-monooxygenase; 1-methyl-4-phenyl-1,2,3,6-tetrahydropyridine:oxygen *N*-oxidoreductase; dimethylaniline monooxygenase (*N*-oxide-forming)

Systematic name: *N*,*N*-dimethylaniline,NADPH:oxygen oxidoreductase (*N*-oxide-forming)

Comments: A flavoprotein. A broad spectrum monooxygenase that accepts substrates as diverse as hydrazines, phosphines, boron-containing compounds, sulfides, selenides, iodide, as well as primary, secondary and tertiary amines [3,4]. This enzyme is distinct from other monooxygenases in that the enzyme forms a relatively stable hydroperoxy flavin intermediate [4,5]. This microsomal enzyme generally converts nucleophilic heteroatom-containing chemicals and drugs into harmless, readily excreted metabolites. For example, *N*-oxygenation is largely responsible for the detoxification of the dopaminergic neurotoxin 1-methyl-4-phenyl-1,2,3,6-tetrahydropyridine (MPTP) [2,6]

Links to other databases: BRENDA, ERGO, EXPASY, IUBMB, KEGG, PDB, CAS registry number: 37256-73-8

References:
1. Ziegler, D.M. and Pettit, F.H. Microsomal oxidases. I. The isolation and dialkylarylamine oxygenase activity of pork liver microsomes. *Biochemistry* **5** (1966) 2932–2938. [PMID: 4381353]
2. Chiba, K., Kubota, E., Miyakawa, T., Kato, Y. and Ishizaki, T. Characterization of hepatic microsomal metabolism as an in vivo detoxication pathway of 1-methyl-4-phenyl-1,2,3,6-tetrahydropyridine in mice. *J. Pharmacol. Exp. Ther.* **246** (1988) 1108–1115. [PMID: 3262153]
3. Cashman, J.R. Structural and catalytic properties of the mammalian flavin-containing monooxygenase. *Chem. Res. Toxicol.* **8** (1995) 165–181.

4. Cashman, J.R. and Zhang, J. Human flavin-containing monooxygenases. *Annu. Rev. Pharmacol. Toxicol.* **46** (2006) 65–100. [PMID: 16402899]
5. Jones, K.C. and Ballou, D.P. Reactions of the 4a-hydroperoxide of liver microsomal flavin-containing monooxygenase with nucleophilic and electrophilic substrates. *J. Biol. Chem.* **261** (1986) 2553–2559. [PMID: 3949735]
6. Chiba, K., Kobayashi, K., Itoh, K., Itoh, S., Chiba, T., Ishizaki, T. and Kamataki, T. *N*-Oxygenation of 1-methyl-4-phenyl-1,2,3,6-tetrahydropyridine by the rat liver flavin-containing monooxygenase expressed in yeast cells. *Eur. J. Pharmacol.* **293** (1995) 97–100. [PMID: 7672012]

[EC 1.14.13.8 created 1972 (EC 1.13.12.11 created 1992, part-incorporated 2006), modified 2006]

*EC 2.4.1.79 – public review until 16 August 2006 (1-1) [Last modified: 19/07/2006] [Edit]

Accepted name: globotriaosylceramide 3-β-*N*-acetylgalactosaminyltransferase

Reaction: UDP-*N*-acetyl-D-galactosamine + α-D-galactosyl-(1→4)-β-D-galactosyl-(1→4)-β-D-glucosylceramide = UDP + β-*N*-acetyl-D-galactosaminyl-(1→3)-α-D-galactosyl-(1→4)-β-D-galactosyl-(1→4)-β-D-glucosylceramide

Glossary: globotriaosylceramide = P^k antigen = α-D-galactosyl-(1→4)-β-D-galactosyl-(1→4)-β-D-glucosylceramide
globotetraosylceramide = globoside = P antigen = β-*N*-acetyl-D-galactosaminyl-(1→3)-α-D-galactosyl-(1→4)-β-D-galactosyl-(1→4)-β-D-glucosylceramide

Other name(s): uridine diphosphoacetylgalactosamine-galactosylgalactosylglucosylceramide acetylgalactosaminyltransferase; globoside synthetase; UDP-*N*-acetylgalactosamine:globotriaosylceramide β-3-*N*-acetylgalactosaminyltransferase; galactosylgalactosylglucosylceramide β-D-acetylgalactosaminyltransferase; UDP-*N*-acetylgalactosamine:globotriaosylceramide β1,3-*N*-acetylgalactosaminyltransferase; globoside synthase; galactosylgalactosylglucosylceramide β-D-acetylgalactosaminyltransferase; UDP-*N*-acetyl-D-galactosamine:D-galactosyl-1,4-D-galactosyl-1,4-D-glucosylceramide β-*N*-acetyl-D-galactosaminyltransferase; β3GalNAc-T1

Systematic name: UDP-*N*-acetyl-D-galactosamine:α-D-galactosyl-(1→4)-β-D-galactosyl-(1→4)-β-D-glucosylceramide 3^{III}-β-*N*-acetyl-D-galactosaminyltransferase

Comments: Globoside is a neutral glycosphingolipid in human erythrocytes and has blood-group-*P*-antigen activity [4]. The enzyme requires a divalent cation for activity, with Mn^{2+} required for maximal activity [3]. UDP-GalNAc is the only sugar donor that is used efficiently by the enzyme: UDP-Gal and UDP-GlcNAc result in very low enzyme activity [3]. Lactosylceramide, globoside and gangliosides GM3 and GD3 are not substrates [4]. For explanation of the superscripted 'III' in the systematic name, see 2-carb.37.

Links to other databases: BRENDA, ERGO, EXPASY, GO, IUBMB, KEGG, CAS registry number: 62213-46-1

References:

1. Chien, J.-L., Williams, T. and Basu, S. Biosynthesis of a globoside-type glycosphingolipid by a β-*N*-acetylgalactosaminyltransferase from embryonic chicken brain. *J. Biol. Chem.* **248** (1973) 1778–1785. [PMID: 4632917]
2. Ishibashi, T., Kijimoto, S. and Makita, A. Biosynthesis of globoside and Forssman hapten from trihexosylceramide and properties of β-*N*-acetyl-galactosaminyltransferase of guinea pig kidney. *Biochim. Biophys. Acta* **337** (1974) 92–106. [PMID: 4433547]
3. Taniguchi, N. and Makita, A. Purification and characterization of UDP-*N*-acetylgalactosamine: globotriaosylceramide β-3-*N*-acetylgalactosaminyltransferase, a synthase of human blood group P antigen, from canine spleen. *J. Biol. Chem.* **259** (1984) 5637–5642. [PMID: 6425294]
4. Okajima, T., Nakamura, Y., Uchikawa, M., Haslam, D.B., Numata, S.I., Furukawa, K., Urano, T. and Furukawa, K. Expression cloning of human globoside synthase cDNAs. Identification of β3Gal-T3 as UDP-*N*-acetylgalactosamine:globotriaosylceramide β1,3-*N*-acetylgalactosaminyltransferase. *J. Biol. Chem.* **275** (2000) 40498–40503. [PMID: 10993897]

[EC 2.4.1.79 created 1976, modified 2006]

*EC 2.4.1.92 – public review until 16 August 2006 (1-1) [Last modified: 19/07/2006] [Edit]

Accepted name: (*N*-acetylneuraminyl)-galactosylglucosylceramide *N*-acetylgalactosaminyltransferase

Reaction: UDP-*N*-acetyl-D-galactosamine + 1-*O*-[*O*-(*N*-acetyl-α-neuraminosyl)-(2→3)-*O*-β-D-galactopyranosyl-(1→4)-β-D-glucopyranosyl]-ceramide = UDP + 1-*O*-[*O*-2-(acetylamino)-2-

deoxy-β-D-galactopyranosyl-(1→4)-*O*-[*N*-acetyl-α-neuraminosyl-(2→3)]-*O*-β-D-galactopyranosyl-(1→4)-β-D-glucopyranosyl]-ceramide

Glossary: ganglioside GM2 = 1-*O*-[*O*-2-(acetylamino)-2-deoxy-β-D-galactopyranosyl-(1→4)-*O*-[*N*-acetyl-α-neuraminosyl-(2→3)]-*O*-β-D-galactopyranosyl-(1→4)-β-D-glucopyranosyl]-ceramide
ganglioside GM3 = 1-*O*-[*O*-(*N*-acetyl-α-neuraminosyl)-(2→3)-*O*-β-D-galactopyranosyl-(1→4)-β-D-glucopyranosyl]-ceramide
ganglioside GD3 = 1-*O*-[*O*-(*N*-acetyl-α-neuraminosyl)-(2→8)-*O*-(*N*-acetyl-α-neuraminosyl)-(2→3)-*O*-β-D-galactopyranosyl-(1→4)-β-D-glucopyranosyl]-ceramide
ganglioside GD2 = 1-*O*-[*O*-(*N*-acetyl-α-neuraminosyl)-(2→8)-*O*-(*N*-acetyl-α-neuraminosyl)-(2→3)-*O*-[2-(acetylamino)-2-deoxy-β-D-galactopyranosyl-(1→4)]-*O*-β-D-galactopyranosyl-(1→4)-β-D-glucopyranosyl]-ceramide
ganglioside SM3 = 1-*O*-[4-*O*-(3-*O*-sulfo-β-D-galactopyranosyl)-β-D-glucopyranosyl]-ceramide
ganglioside SM2 = 1-*O*-[*O*-2-(acetylamino)-2-deoxy-β-D-galactopyranosyl-(1→4)-*O*-3-*O*-sulfo-β-D-galactopyranosyl-(1→4)-β-D-glucopyranosyl]-ceramide

Other name(s): uridine diphosphoacetylgalactosamine-ganglioside GM3 acetylgalactosaminyltransferase; ganglioside GM2 synthase; ganglioside GM3 acetylgalactosaminyltransferase; GM2 synthase; UDP acetylgalactosamine-(*N*-acetylneuraminyl)-D-galactosyl-D-glucosylceramide acetylgalactosaminyltransferase; UDP-*N*-acetylgalactosamine GM3 *N*-acetylgalactosaminyltransferase; uridine diphosphoacetylgalactosamine-acetylneuraminylgalactosylglucosylceramide acetylgalactosaminyltransferase; uridine diphosphoacetylgalactosamine-hematoside acetylgalactosaminyltransferase; GM2/GD2-synthase; β-1,4*N*-aetylgalactosaminyltransferase; asialo-GM2 synthase; GalNAc-T; UDP-*N*-acetyl-D-galactosamine:(*N*-acetylneuraminyl)-D-galactosyl-D-glucosylceramide *N*-acetyl-D-galactosaminyltransferase

Systematic name: UDP-*N*-acetyl-D-galactosamine:1-*O*-[*O*-(*N*-acetyl-α-neuraminosyl)-(2→3)-*O*-β-D-galactopyranosyl-(1→4)-β-D-glucopyranosyl]-ceramide 1,4-β-*N*-acetyl-D-galactosaminyltransferase

Comments: This enzyme catalyses the formation of the gangliosides (i.e. sialic-acid-containing glycosphingolipids) GM2, GD2 and SM2 from GM3, GD3 and SM3, respectively. Asialo-GM3 [3] and lactosylceramide [2] are also substrates, but glycoproteins and oligosaccharides are not substrates.

Links to other databases: BRENDA, ERGO, EXPASY, IUBMB, KEGG, CAS registry number: 67338-98-1

References:

1. Dicesare, J.L. and Dain, J.A. The enzymic synthesis of ganglioside. IV. UDP-*N*-acetylgalactosamine: (*N*-acetylneuraminyl)-galactosylglucosyl ceramide *N*-acetylgalactosaminyltransferase in rat brain. *Biochim. Biophys. Acta* **231** (1971) 385–393. [PMID: 5554906]
2. Pohlentz, G., Klein, D., Schwarzmann, G., Schmitz, D. and Sandhoff, K. Both GA2, GM2, and GD2 synthases and GM1b, GD1a, and GT1b synthases are single enzymes in Golgi vesicles from rat liver. *Proc. Natl. Acad. Sci. USA* **85** (1988) 7044–7048. [PMID: 3140234]
3. Kazuya, I.-P., Hidari, J.K., Ichikawa, S., Furukawa, K., Yamasaki, M. and Hirabayashi, Y. β1-4*N*-Acetylgalactosaminyltransferase can synthesize both asialoglycosphingolipid GM2 and glycosphingolipid GM2 in vitro and in vivo: isolation and characterization of a β1-4*N*-acetylgalactosaminyltransferase cDNA clone from rat ascites hepatoma cell line AH7974F. *Biochem. J.* **303** (1994) 957–965. [PMID: 7980468]
4. Hashimoto, Y., Sekine, M., Iwasaki, K. and Suzuki, A. Purification and characterization of UDP-*N*-acetylgalactosamine G_{M3}/G_{D3} *N*-acetylgalactosaminyltransferase from mouse liver. *J. Biol. Chem.* **268** (1993) 25857–25864. [PMID: 8245020]
5. Nagai, K. and Ishizuka, I. Biosynthesis of monosulfogangliotriaosylceramide and GM2 by *N*-acetylgalactosaminyltransferase from rat brain. *J. Biochem. (Tokyo)* **101** (1987) 1115–1127. [PMID: 3115968]
6. Furukawa, K., Takamiya, K. and Furukawa, K. β1,4-*N*-Acetylgalactosaminyltransferase—GM2/GD2 synthase: a key enzyme to control the synthesis of brain-enriched complex gangliosides. *Biochim. Biophys. Acta* **1573** (2002) 356–362. [PMID: 12417418]
7. Yamashita, T., Wu, Y.P., Sandhoff, R., Werth, N., Mizukami, H., Ellis, J.M., Dupree, J.L., Geyer, R., Sandhoff, K. and Proia, R.L. Interruption of ganglioside synthesis produces central nervous system degeneration and altered axon-glial interactions. *Proc. Natl. Acad. Sci. USA* **102** (2005) 2725–2730. [PMID: 15710896]

[EC 2.4.1.92 created 1976, modified 2006]

*EC 2.4.1.116 – public review until 16 August 2006 **(1-1)** [Last modified: 19/07/2006] [Edit]

Accepted name: cyanidin 3-*O*-rutinoside 5-*O*-glucosyltransferase

Reaction: UDP-glucose + cyanidin 3-*O*-rutinoside = UDP + cyanidin 3-*O*-rutinoside 5-*O*-β-D-glucoside

For diagram of anthocyanidin glycoside biosynthesis, click here

Other name(s): uridine diphosphoglucose-cyanidin 3-rhamnosylglucoside 5-*O*-glucosyltransferase; cyanidin-3-rhamnosylglucoside 5-*O*-glucosyltransferase; UDP-glucose:cyanidin-3-*O*-D-rhamnosyl-1,6-D-glucoside 5-*O*-D-glucosyltransferase

Systematic name: UDP-glucose:cyanidin-3-*O*-β-L-rhamnosyl-(1→6)-β-D-glucoside 5-*O*-β-D-glucosyltransferase

Comments: Also acts on pelargonidin-3-rutinoside. The enzyme does not catalyse the glucosylation of the 5-hydroxy group of cyanidin-3-glucoside.

Links to other databases: BRENDA, ERGO, EXPASY, GO, IUBMB, KEGG, CAS registry number: 70248-66-7

References:

1. Kamsteeg, J., van Brederode, J. and van Nigtevecht, G. Identification, properties, and genetic control of UDP-glucose: cyanidin-3-rhamnosyl-(1→6)-glucoside-5-*O*-glucosyltransferase isolated from petals of the red campion (*Silene dioica*). *Biochem. Genet.* **16** (1978) 1059–1071. [PMID: 751641]

[EC 2.4.1.116 created 1984 (EC 2.4.1.235 created 2004, incorporated 2006), modified 2006]

EC 2.4.1.154 – public review until 16 August 2006 **(3-1)** [Last modified: 19/07/2006] [Edit]

Deleted entry: globotriosylceramide β-1,6-*N*-acetylgalactosaminyl-transferase. The enzyme is identical to EC 2.4.1.79, globotriaosylceramide 3-β-*N*-acetylgalactosaminyltransferase. The reference cited referred to a 1rarr3 linkage and not to a 1rarr6 linkage, as indicated in the enzyme entry.

[EC 2.4.1.154 created 1986, deleted 2006]

EC 2.4.1.235 – public review until 16 August 2006 **(3-1)** [Last modified: 19/07/2006] [Edit]

Deleted entry: Enzyme is identical to EC 2.4.1.116, cyanidin 3-*O*-rutinoside 5-*O*-glucosyltransferase

[EC 2.4.1.235 created 2004, deleted 2006]

*EC 2.4.2.31 – public review until 16 August 2006 **(1-1)** [Last modified: 19/07/2006] [Edit]

Accepted name: NAD(P)$^+$-protein-arginine ADP-ribosyltransferase

Reaction: NAD(P)$^+$ + protein L-arginine = nicotinamide + ω-*N*-(ADP-D-ribosyl)-protein-L-arginine

Other name(s): ADP-ribosyltransferase; mono(ADP-ribosyl)transferase; NAD$^+$:L-arginine ADP-D-ribosyltransferase; NAD(P)$^+$-arginine ADP-ribosyltransferase; NAD(P)$^+$-arginine ADP-ribosyltransferase; NAD(P)$^+$:L-arginine ADP-D-ribosyltransferase

Systematic name: NAD(P)$^+$:protein-L-arginine ADP-D-ribosyltransferase

Comments: Arginine residues in proteins act as acceptors. Free arginine, agmatine [(4-aminobutyl)guanidine], arginine methyl ester and guanidine can also do so. The enzyme catalyses the NAD$^+$-dependent activation of EC 4.6.1.1, adenylate cyclase. Some bacterial enterotoxins possess similar enzymatic activities. (cf. EC 2.4.2.36 NAD$^+$—diphthamide ADP-ribosyltransferase).

Links to other databases: BRENDA, ERGO, EXPASY, IUBMB, KEGG, PDB, CAS registry number: 81457-93-4

References:

1. Moss, J., Stanley, S.J. and Oppenheimer, N.J. Substrate specificity and partial purification of a stereospecific NAD- and guanidine-dependent ADP-ribosyltransferase from avian erythrocytes. *J. Biol. Chem.* **254** (1979) 8891–8894. [PMID: 225315]
2. Moss, J., Stanley, S.J. and Watkins, P.A. Isolation and properties of an NAD- and guanidine-dependent ADP-ribosyltransferase from turkey erythrocytes. *J. Biol. Chem.* **255** (1980) 5838–5840. [PMID: 6247348]
3. Ueda, K. and Hayaishi, O. ADP-ribosylation. *Annu. Rev. Biochem.* **54** (1985) 73–100. [PMID: 3927821]

[EC 2.4.2.31 created 1984, modified 1990]

EC 2.6.1.82 – public review until 16 August 2006 **(2-1)** [Last modified: 19/07/2006] [Edit]

Accepted name: putrescine aminotransferase

Reaction: (1a) putrescine + 2-oxoglutarate = 4-aminobutanal + L-glutamate

(1b) 4-aminobutanal = 1-pyrroline (spontaneous)

For diagram of the arginine-catabolism pathway, click here

Glossary: putrescine = butane-1,4-diamine
1-pyrroline = 3,4-dihydro-2*H*-pyrrole

Other name(s): putrescine-α-ketoglutarate transaminase; YgjG; putrescine:α-ketoglutarate aminotransferase; PAT; putrescine:2-oxoglutarate aminotransferase; putrescine transaminase

Systematic name: butane-1,4-diamine:2-oxoglutarate aminotransferase

Comments: A pyridoxal-phosphate protein [3]. The product, 4-aminobutanal, spontaneously cyclizes to form 1-pyrroline, which is a substrate for EC 1.5.1.35, 1-pyrroline dehydrogenase. Cadaverine and spermidine can also act as substrates [3]. Forms part of the arginine-catabolism pathway [2].

References:
1. Prieto-Santos, M.I., Martin-Checa, J., Balaña-Fouce, R. and Garrido-Pertierra, A. A pathway for putrescine catabolism in *Escherichia coli*. *Biochim. Biophys. Acta* **880** (1986) 242–244. [PMID: 3510672]
2. Samsonova, N.N., Smirnov, S.V., Novikova, A.E. and Ptitsyn, L.R. Identification of *Escherichia coli* K12 YdcW protein as a γ-aminobutyraldehyde dehydrogenase. *FEBS Lett.* **579** (2005) 4107–4112. [PMID: 16023116]
3. Samsonova, N.N., Smirnov, S.V., Altman, I.B. and Ptitsyn, L.R. Molecular cloning and characterization of *Escherichia coli* K12 *ygjG* gene. *BMC Microbiol.* **3** (2003) 2 only. [PMID: 12617754]

[EC 2.6.1.82 created 2006]

EC 2.6.1.83 – public review until 16 August 2006 (2-1) [Last modified: 19/07/2006] [Edit]

Accepted name: LL-diaminopimelate aminotransferase

Reaction: LL-2,6-diaminoheptanedioate + 2-oxoglutarate = (*S*)-2,3,4,5-tetrahydropyridine-2,6-dicarboxylate + L-glutamate + H_2O

Glossary: LL-diaminopimelate = LL-2,6-diaminoheptanedioate
tetrahydrodipicolinate = tetrahydropyridine-2,6-dicarboxylate

Other name(s): LL-diaminopimelate transaminase; LL-DAP aminotransferase; LL-DAP-AT

Systematic name: LL-2,6-diaminoheptanedioate:2-oxoglutarate aminotransferase

Comments: A pyridoxal-phosphate enzyme. In vivo, the reaction occurs in the opposite direction to that shown above. This is one of the final steps in the lysine-biosynthesis pathway of plants (ranging from mosses to flowering plants). *meso*-Diaminoheptanedioate, an isomer of LL-2,6-diaminoheptanedioate, and the structurally related compounds lysine and ornithine are not substrates. 2-Oxoglutarate cannot be replaced by oxaloacetate or pyruvate. It is not yet known if the substrate of the biosynthetic reaction is the cyclic or acyclic form of tetrahydropyridine-2,6-dicarboxylate.

References:
1. Hudson, A.O., Singh, B.K., Leustek, T. and Gilvarg, C. An LL-diaminopimelate aminotransferase defines a novel variant of the lysine biosynthesis pathway in plants. *Plant Physiol.* **140** (2006) 292–301. [PMID: 16361515]

[EC 2.6.1.83 created 2006]

EC 2.7.1.160 – public review until 16 August 2006 (2-1) [Last modified: 19/07/2006] [Edit]

Accepted name: 2′-phosphotransferase

Reaction: 2′-phospho-[ligated tRNA] + NAD^+ = mature tRNA + ADP-ribose 1′′,2′′-phosphate + nicotinamide + H_2O

For diagram of reaction, click here and for mechanism, click here

Glossary: ADP-ribose = adenosine 5′-(5-deoxy-D-ribofuranos-5-yl diphosphate)

Other name(s): yeast 2′-phosphotransferase; Tpt1; Tpt1p; 2′-phospho-tRNA:NAD^+ phosphotransferase

Systematic name: 2′-phospho-[ligated tRNA]:NAD^+ phosphotransferase

Comments: Catalyses the final step of tRNA splicing in the yeast *Saccharomyces cerevisiae* [2]. The reaction takes place in two steps: in the first step, the 2′-phosphate on the RNA substrate is ADP-ribosylated, causing the relase of nicotinamide and the formation of the reaction intermediate, ADP-ribosylated tRNA [6]. In the second step, dephosphorylated (mature) tRNA is formed along with ADP ribose 1′′-2′′-cyclic phosphate. Highly specific for oligonucleotide

substrates bearing an internal 2′-phosphate. Oligonucleotides with only a terminal 5′- or 3′-phosphate are not substrates [1].

References: 1. Steiger, M.A., Kierzek, R., Turner, D.H. and Phizicky, E.M. Substrate recognition by a yeast 2′-phosphotransferase involved in tRNA splicing and by its *Escherichia coli* homolog. *Biochemistry* **40** (2001) 14098–14105. [PMID: 11705403]
2. Spinelli, S.L., Kierzek, R., Turner, D.H. and Phizicky, E.M. Transient ADP-ribosylation of a 2′-phosphate implicated in its removal from ligated tRNA during splicing in yeast. *J. Biol. Chem.* **274** (1999) 2637–2644. [PMID: 9915792]
3. Culver, G.M., McCraith, S.M., Consaul, S.A., Stanford, D.R. and Phizicky, E.M. A 2′-phosphotransferase implicated in tRNA splicing is essential in *Saccharomyces cerevisiae*. *J. Biol. Chem.* **272** (1997) 13203–13210. [PMID: 9148937]
4. McCraith, S.M. and Phizicky, E.M. An enzyme from *Saccharomyces cerevisiae* uses NAD^+ to transfer the splice junction 2′-phosphate from ligated tRNA to an acceptor molecule. *J. Biol. Chem.* **266** (1991) 11986–11992. [PMID: 2050693]
5. Hu, Q.D., Lu, H., Huo, K., Ying, K., Li, J., Xie, Y., Mao, Y. and Li, Y.Y. A human homolog of the yeast gene encoding tRNA 2′-phosphotransferase: cloning, characterization and complementation analysis. *Cell. Mol. Life Sci.* **60** (2003) 1725–1732. [PMID: 14504659]
6. Steiger, M.A., Jackman, J.E. and Phizicky, E.M. Analysis of 2′-phosphotransferase (Tpt1p) from *Saccharomyces cerevisiae*: evidence for a conserved two-step reaction mechanism. *RNA* **11** (2005) 99–106. [PMID: 15611300]
7. Sawaya, R., Schwer, B. and Shuman, S. Structure-function analysis of the yeast NAD^+-dependent tRNA 2′-phosphotransferase Tpt1. *RNA* **11** (2005) 107–113. [PMID: 15611301]
8. Kato-Murayama, M., Bessho, Y., Shirouzu, M. and Yokoyama, S. Crystal structure of the RNA 2′-phosphotransferase from *Aeropyrum pernix* K1. *J. Mol. Biol.* **348** (2005) 295–305. [PMID: 15811369]

[EC 2.7.1.160 created 2006]

EC 2.7.4.23 – public review until 16 August 2006 **(2-1)** [Last modified: 19/07/2006] [Edit]

Accepted name: ribose 1,5-bisphosphate phosphokinase

Reaction: ATP + ribose 1,5-bisphosphate = ADP + 5-phospho-α-D-ribose 1-diphosphate

Glossary: PRPP = 5-phospho-α-D-ribose 1-diphosphate

Other name(s): ribose 1,5-bisphosphokinase; PhnN

Systematic name: ATP:ribose-1,5-bisphosphate phosphotransferase

Comments: This enzyme, found in NAD supression mutants of *Escherichia coli*, synthesizes 5-phospho-α-D-ribose 1-diphosphate (PRPP) without the participation of EC 2.7.6.1, ribose-phosphate diphosphokinase. Ribose, ribose 1-phosphate and ribose 5-phosphate are not substrates, and GTP cannot act as a phosphate donor.

References: 1. Hove-Jensen, B., Rosenkrantz, T.J., Haldimann, A. and Wanner, B.L. *Escherichia coli phnN*, encoding ribose 1,5-bisphosphokinase activity (phosphoribosyl diphosphate forming): dual role in phosphonate degradation and NAD biosynthesis pathways. *J. Bacteriol.* **185** (2003) 2793–2801. [PMID: 12700258]

[EC 2.7.4.23 created 2006]

*EC 2.7.8.7 – public review until 16 August 2006 **(1-1)** [Last modified: 19/07/2006] [Edit]

Accepted name: holo-[acyl-carrier-protein] synthase

Reaction: CoA-[4′-phosphopantetheine] + apo-[acyl-carrier-protein] = adenosine 3′,5′-bisphosphate + holo-[acyl-carrier-protein]

Other name(s): acyl carrier protein holoprotein (holo-ACP) synthetase; holo-ACP synthetase; coenzyme A:fatty acid synthetase apoenzyme 4′-phosphopantetheine transferase; holosynthase; acyl carrier protein synthetase; holo-ACP synthase; PPTase; AcpS; ACPS; acyl carrier protein synthase; P-pant transferase; CoA:apo-[acyl-carrier-protein] pantetheinephosphotransferase

Systematic name: CoA-[4′-phosphopantetheine]:apo-[acyl-carrier-protein] 4′-pantetheinephosphotransferase

Comments: Requires Mg^{2+}. All polyketide synthases, fatty-acid synthases and non-ribosomal peptide synthases require post-translational modification of their constituent acyl-carrier-protein (ACP) domains to become catalytically active. The inactive apo-proteins are converted into their active holo-forms by transfer of the 4′-phosphopantetheinyl moiety of CoA to the sidechain hydroxy group of a conserved serine residue in each ACP domain [3]. The enzyme from

human can activate both the ACP domain of the human cytosolic multifunctional fatty acid synthase and that associated with human mitochondria as well as peptidyl-carrier and acyl-carrier-proteins from prokaryotes [6]. Removal of the 4-phosphopantetheinyl moiety from holo-ACP is carried out by EC 3.1.4.14, [acyl-carrier-protein] phosphodiesterase.

Links to other databases: BRENDA, ERGO, EXPASY, IUBMB, KEGG, PDB, CAS registry number: 37278-30-1

References:

1. Elovson, J. and Vagelos, P.R. Acyl carrier protein. X. Acyl carrier protein synthetase. *J. Biol. Chem.* **243** (1968) 3603–3611. [PMID: 4872726]
2. Prescott, D.J. and Vagelos, P.R. Acyl carrier protein. *Adv. Enzymol. Relat. Areas Mol. Biol.* **36** (1972) 269–311. [PMID: 4561013]
3. Lambalot, R.H., Gehring, A.M., Flugel, R.S., Zuber, P., LaCelle, M., Marahiel, M.A., Reid, R., Khosla, C. and Walsh, C.T. A new enzyme superfamily - the phosphopantetheinyl transferases. *Chem. Biol.* **3** (1996) 923–936. [PMID: 8939709]
4. Walsh, C.T., Gehring, A.M., Weinreb, P.H., Quadri, L.E.N. and Flugel, R.S. Post-translational modification of polyketide and nonribosomal peptide synthases. *Curr. Opin. Chem. Biol.* **1** (1997) 309–315. [PMID: 9667867]
5. Mootz, H.D., Finking, R. and Marahiel, M.A. 4′-Phosphopantetheine transfer in primary and secondary metabolism of *Bacillus subtilis*. *J. Biol. Chem.* **276** (2001) 37289–37298. [PMID: 11489886]
6. Joshi, A.K., Zhang, L., Rangan, V.S. and Smith, S. Cloning, expression, and characterization of a human 4′-phosphopantetheinyl transferase with broad substrate specificity. *J. Biol. Chem.* **278** (2003) 33142–33149. [PMID: 12815048]

[EC 2.7.8.7 created 1972, modified 2006]

EC 3.1.1.80 – public review until 18 August 2006 **(2-1)** [Last modified: 21/07/2006] [Edit]

Accepted name: acetylajmaline esterase

Reaction: (1) 17-*O*-acetylajmaline + H_2O = ajmaline + acetate
(2) 17-*O*-acetylnorajmaline + H_2O = norajmaline + acetate

For diagram of ajmaline, vinorine, vomilenine and raucaffricine biosynthesis, click here

Other name(s): AAE; 2β(*R*)-17-*O*-acetylajmalan:acetylesterase; acetylajmalan esterase

Systematic name: 17-*O*-acetylajmaline *O*-acetylhydrolase

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-dihydrovomilenine and 1,2-dihydroraucaffricine cannot act as substrates [2]. This is a novel member of the GDSL family of serine esterases/lipases.

References:

1. Polz, L., Schübel, H. and Stöckigt, J. Characterization of 2β(*R*)-17-*O*-acetylajmalan:acetylesterase—a specific enzyme involved in the biosynthesis of the *Rauwolfia* alkaloid ajmaline. *Z. Naturforsch. [C]* **42** (1987) 333–342. [PMID: 2955586]
2. Ruppert, M., Woll, J., Giritch, A., Genady, E., Ma, X. and Stöckigt, J. Functional expression of an ajmaline pathway-specific esterase from *Rauvolfia* in a novel plant-virus expression system. *Planta* **222** (2005) 888–898. [PMID: 16133216]

[EC 3.1.1.80 created 2006]

EC 3.1.3.77 – public review until 16 August 2006 **(2-1)** [Last modified: 19/07/2006] [Edit]

Accepted name: acireductone synthase

Reaction: 5-(methylthio)-2,3-dioxopentyl phosphate + H_2O = 1,2-dihydroxy-5-(methylthio)pent-1-en-3-one + phosphate
(1a) 5-(methylthio)-2,3-dioxopentyl phosphate = 2-hydroxy-5-(methylthio)-3-oxopent-1-enyl phosphate
(1b) 2-hydroxy-5-(methylthio)-3-oxopent-1-enyl phosphate + H_2O = 1,2-dihydroxy-5-(methylthio)pent-1-en-3-one + phosphate

For diagram of the methionine-salvage pathway, click here

Glossary: acireductone = 1,2-dihydroxy-5-(methylthio)pent-1-en-3-one

Other name(s): E1; E-1 enolase-phosphatase

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

Comments: This bifunctional enzyme first enolizes the substrate to form the intermediate 2-hydroxy-5-

(methylthio)-3-oxopent-1-enyl phosphate, which is then dephosphorylated to form the acireductone 1,2-dihydroxy-5-(methylthio)pent-1-en-3-one [2]. The acireductone represents a branch point in the methione-salvage pathway as it is used in the formation of formate, CO and 3-(methylthio)propanoate by EC 1.13.11.53 [acireductone dioxygenase (Ni^{2+}-requiring)] and of formate and 4-methylthio-2-oxobutanoate either by a spontaneous reaction under aerobic conditions or by EC 1.13.11.54 {acireductone dioxygenase [iron(II)-requiring]} [1,2].

References:

1. Myers, R.W., Wray, J.W., Fish, S. and Abeles, R.H. Purification and characterization of an enzyme involved in oxidative carbon-carbon bond cleavage reactions in the methionine salvage pathway of *Klebsiella pneumoniae*. *J. Biol. Chem.* **268** (1993) 24785–24791. [PMID: 8227039]
2. Wray, J.W. and Abeles, R.H. The methionine salvage pathway in *Klebsiella pneumoniae* and rat liver. Identification and characterization of two novel dioxygenases. *J. Biol. Chem.* **270** (1995) 3147–3153. [PMID: 7852397]

[EC 3.1.3.77 created 2006]

*EC 3.1.4.14 – public review until 16 August 2006 **(1-1)** [Last modified: 19/07/2006] [Edit]

Accepted name: [acyl-carrier-protein] phosphodiesterase

Reaction: holo-[acyl-carrier-protein] + H_2O = 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 [3]. Deletion of the gene encoding this enzyme abolishes ACP prosthetic-group turnover in vivo [3]. Activation of apo-ACP to form the holoenzyme is carried out by EC 2.7.8.7, holo-[acyl-carrier-protein] synthase.

Links to other databases: BRENDA, ERGO, EXPASY, IUBMB, KEGG, CAS registry number: 37288-21-4

References:

1. Sobhy, C. Regulation of fatty acid synthetase activity. The 4′-phosphopantetheine hydrolase of rat liver. *J. Biol. Chem.* **254** (1979) 8561–8566. [PMID: 224058]
2. Vagelos, P.R. and Larrabee, A.R. Acyl carrier protein. IX. Acyl carrier protein hydrolase. *J. Biol. Chem.* **242** (1967) 1776–1781. [PMID: 4290442]
3. Thomas, J. and Cronan, J.E. The enigmatic acyl carrier protein phosphodiesterase of *Escherichia coli*: genetic and enzymological characterization. *J. Biol. Chem.* **280** (2005) 34675–34683. [PMID: 16107329]

[EC 3.1.4.14 created 1972, modified 2006]

*EC 3.2.2.1 – public review until 16 August 2006 **(1-1)** [Last modified: 19/07/2006] [Edit]

Accepted name: purine nucleosidase

Reaction: a purine nucleoside + H_2O = D-ribose + a purine base

Other name(s): nucleosidase; purine β-ribosidase; purine nucleoside hydrolase; purine ribonucleosidase; ribonucleoside hydrolase; nucleoside hydrolase; *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, NAD^+, $NADP^+$ and nicotinaminde mononucleotide are not substrates [6].

Links to other databases: BRENDA, ERGO, EXPASY, GO, IUBMB, KEGG, PDB, CAS registry number: 9025-44-9

References:

1. Heppel, L.A. and Hilmoe, R.J. Phosphorolysis and hydrolysis of purine ribosides from yeast. *J. Biol. Chem.* **198** (1952) 683–694. [PMID: 12999785]
2. Kalckar, H.M. Biosynthetic aspects of nucleosides and nucleic acids. *Pubbl. Staz. Zool. (Napoli)* (1951) 87–103.
3. Takagi, Y. and Horecker, B.L. Purification and properties of a bacterial riboside hydrolyase. *J. Biol. Chem.* **225** (1956) 77–86.
4. Tarr, H.L.A. Fish muscle riboside hydrolases. *Biochem. J.* **59** (1955) 386–391.
5. Parkin, D.W. Purine-specific nucleoside *N*-ribohydrolase from *Trypanosoma brucei brucei*.

Purification, specificity, and kinetic mechanism. *J. Biol. Chem.* **271** (1996) 21713–21719. [PMID: 8702965]
6. Ogawa, J., Takeda, S., Xie, S.X., Hatanaka, H., Ashikari, T., Amachi, T. and Shimizu, S. Purification, characterization, and gene cloning of purine nucleosidase from *Ochrobactrum anthropi*. *Appl. Environ. Microbiol.* **67** (2001) 1783–1787. [PMID: 11282633]
7. Versées, W., Decanniere, K., Van Holsbeke, E., Devroede, N. and Steyaert, J. Enzyme-substrate interactions in the purine-specific nucleoside hydrolase from *Trypanosoma vivax*. *J. Biol. Chem.* **277** (2002) 15938–15946. [PMID: 11854281]
8. Mazumder-Shivakumar, D. and Bruice, T.C. Computational study of IAG-nucleoside hydrolase: determination of the preferred ground state conformation and the role of active site residues. *Biochemistry* **44** (2005) 7805–7817. [PMID: 15909995]

[EC 3.2.2.1 created 1961, modified 2006]

EC 4.2.1.109 – public review until 16 August 2006 **(2-1)** [Last modified: 19/07/2006] [Edit]

Accepted name: methylthioribulose 1-phosphate dehydratase

Reaction: *S*-methyl-5-thio-D-ribulose 1-phosphate = 5-(methylthio)-2,3-dioxopentyl phosphate + H_2O

For diagram of the methionine-salvage pathway, click here

Other name(s): 1-PMT-ribulose dehydratase

Systematic name: *S*-methyl-5-thio-D-ribulose-1-phosphate hydro-lyase

Comments: This enzyme forms part of the methionine-salvage pathway.

References:

1. Furfine, E.S. and Abeles, R.H. Intermediates in the conversion of 5′-*S*-methylthioadenosine to methionine in *Klebsiella pneumoniae*. *J. Biol. Chem.* **263** (1988) 9598–9606. [PMID: 2838472]
2. Wray, J.W. and Abeles, R.H. The methionine salvage pathway in *Klebsiella pneumoniae* and rat liver. Identification and characterization of two novel dioxygenases. *J. Biol. Chem.* **270** (1995) 3147–3153. [PMID: 7852397]

[EC 4.2.1.109 created 2006]

EC 4.2.2.4 – public review until 16 August 2006 **(4-1)** [Last modified: 19/07/2006] [Edit]

Transferred entry: chondroitin ABC lyase. Now known to comprise two enzymes: EC 4.2.2.20, chondroitin-sulfate-ABC endolyase and EC 4.2.2.21, chondroitin-sulfate-ABC exolyase.

[EC 4.2.2.4 created 1972 (EC 4.2.99.6 created 1965, part incorporated 1976), deleted 2006]

EC 4.2.2.20 – public review until 16 August 2006 **(2-1)** [Last modified: 19/07/2006] [Edit]

Accepted name: chondroitin-sulfate-ABC endolyase

Reaction: Endolytic cleavage of β-1,4-galactosaminic bonds between *N*-acetylgalactosamine and either D-glucuronic acid or L-iduronic acid to produce a mixture of Δ^4-unsaturated oligosaccharides of different sizes that are ultimately degraded to Δ^4-unsaturated tetra- and disaccharides

For diagram, click here

Glossary: chondroitin sulfate A = chondroitin 4-sulfate
chondroitin sulfate B = dermatan sulfate
chondroitin sulfate C = chondroitin 6-sulfate
For the nomenclature of glycoproteins, glycopeptides and peptidoglycans, click here

Other name(s): chondroitinase (ambiguous); chondroitin ABC eliminase (ambiguous); chondroitinase ABC (ambiguous); chondroitin ABC lyase (ambiguous); chondroitin sulfate ABC lyase (ambiguous); ChS ABC lyase (ambiguous); chondroitin sulfate ABC endoeliminase; chondroitin sulfate ABC endolyase; ChS ABC lyase I

Systematic name: chondroitin-sulfate-ABC endolyase

Comments: This enzyme degrades a variety of glycosaminoglycans of the chondroitin-sulfate- and dermatan-sulfate type. Chondroitin sulfate, chondroitin-sulfate proteoglycan and dermatan sulfate are the best substrates but the enzyme can also act on hyaluronan at a much lower rate. Keratan sulfate, heparan sulfate and heparin are not substrates. In general, chondroitin sulfate (CS) and dermatan sulfate (DS) chains comprise a linkage region, a chain cap and a repeat region. The repeat region of CS is a repeating disaccharide of glucuronic acid (GlcA)

and *N*-acetylgalactosamine (GalNAc) [-4)GlcA(β1-3)GalNAc(β1-]n, which may be *O*-sulfated on the C-4 and/or C-6 of GalNAc and C-2 of GlcA. GlcA residues of CS may be epimerized to iduronic acid (IdoA) forming the repeating disaccharide [-4)IdoA(α1-3)GalNAc(β1-]n of DS. Both the concentrations and locations of sulfate-ester substituents vary with glucosaminoglycan source [5]. The related enzyme EC 4.2.2.21, chondroitin-sulfate-ABC exolyase, has the same substrate specificity but removes disaccharide residues from the non-reducing ends of both polymeric chondroitin sulfates and their oligosaccharide fragments produced by EC 4.2.2.20 [4].

References:

1. Yamagata, T., Saito, H., Habuchi, O. and Suzuki, S. Purification and properties of bacterial chondroitinases and chondrosulfatases. *J. Biol. Chem.* **243** (1968) 1523–1535. [PMID: 5647268]
2. Saito, H., Yamagata, T. and Suzuki, S. Enzymatic methods for the determination of small quantities of isomeric chondroitin sulfates. *J. Biol. Chem.* **243** (1968) 1536–1542. [PMID: 4231029]
3. Suzuki, S., Saito, H., Yamagata, T., Anno, K., Seno, N., Kawai, Y. and Furuhashi, T. Formation of three types of disulfated disaccharides from chondroitin sulfates by chondroitinase digestion. *J. Biol. Chem.* **243** (1968) 1543–1550. [PMID: 5647269]
4. Hamai, A., Hashimoto, N., Mochizuki, H., Kato, F., Makiguchi, Y., Horie, K. and Suzuki, S. Two distinct chondroitin sulfate ABC lyases. An endoeliminase yielding tetrasaccharides and an exoeliminase preferentially acting on oligosaccharides. *J. Biol. Chem.* **272** (1997) 9123–9130. [PMID: 9083041]
5. Huckerby, T.N., Nieduszynski, I.A., Giannopoulos, M., Weeks, S.D., Sadler, I.H. and Lauder, R.M. Characterization of oligosaccharides from the chondroitin/dermatan sulfates. ^{1}H-NMR and ^{13}C-NMR studies of reduced trisaccharides and hexasaccharides. *FEBS J.* **272** (2005) 6276–6286. [PMID: 16336265]

[EC 4.2.2.20 created 2006 (EC 4.2.2.4 created 1972, part-incorporated 2006 (EC 4.2.99.6 created 1965, part incorporated 1976))]

EC 4.2.2.21 – public review until 16 August 2006 **(2-1)** [Last modified: 19/07/2006] [Edit]

Accepted name: chondroitin-sulfate-ABC exolyase

Reaction: Exolytic cleavage of disaccharide residues from the non-reducing ends of both polymeric chondroitin sulfates and their oligosaccharide fragments

For diagram of reaction, click here

Glossary: chondroitin sulfate A = chondroitin 4-sulfate
chondroitin sulfate B = dermatan sulfate
chondroitin sulfate C = chondroitin 6-sulfate
For the nomenclature of glycoproteins, glycopeptides and peptidoglycans, click here

Other name(s): chondroitinase (ambiguous); chondroitin ABC eliminase (ambiguous); chondroitinase ABC (ambiguous); chondroitin ABC lyase (ambiguous); chondroitin sulfate ABC lyase (ambiguous); ChS ABC lyase (ambiguous); chondroitin sulfate ABC exoeliminase; chondroitin sulfate ABC exolyase; ChS ABC lyase II

Systematic name: chondroitin-sulfate-ABC exolyase

Comments: This enzyme degrades a variety of glycosaminoglycans of the chondroitin-sulfate- and dermatan-sulfate type. Chondroitin sulfate, chondroitin-sulfate proteoglycan and dermatan sulfate are the best substrates but the enzyme can also act on hyaluronan at a much lower rate. Keratan sulfate, heparan sulfate and heparin are not substrates. In general, chondroitin sulfate (CS) and dermatan sulfate (DS) chains comprise a linkage region, a chain cap and a repeat region. The repeat region of CS is a repeating disaccharide of glucuronic acid (GlcA) and *N*-acetylgalactosamine (GalNAc) [-4)GlcA(β1-3)GalNAc(β1-]n, which may be *O*-sulfated on the C-4 and/or C-6 of GalNAc and C-2 of GlcA. GlcA residues of CS may be epimerized to iduronic acid (IdoA) forming the repeating disaccharide [-4)IdoA(α1-3)GalNAc(β1-]n of DS. Both the concentrations and locations of sulfate-ester substituents vary with glucosaminoglycan source [5]. The related enzyme EC 4.2.2.20, chondroitin-sulfate-ABC endolyase, has the same substrate specificity but produces a mixture of Δ^4-unsaturated oligosaccharides of different sizes that are ultimately degraded to Δ^4-unsaturated tetra- and disaccharides [4].

References:

1. Yamagata, T., Saito, H., Habuchi, O. and Suzuki, S. Purification and properties of bacterial chondroitinases and chondrosulfatases. *J. Biol. Chem.* **243** (1968) 1523–1535. [PMID: 5647268]
2. Saito, H., Yamagata, T. and Suzuki, S. Enzymatic methods for the determination of small quantities of isomeric chondroitin sulfates. *J. Biol. Chem.* **243** (1968) 1536–1542. [PMID:

4231029]
3. Suzuki, S., Saito, H., Yamagata, T., Anno, K., Seno, N., Kawai, Y. and Furuhashi, T. Formation of three types of disulfated disaccharides from chondroitin sulfates by chondroitinase digestion. *J. Biol. Chem.* **243** (1968) 1543–1550. [PMID: 5647269]
4. Hamai, A., Hashimoto, N., Mochizuki, H., Kato, F., Makiguchi, Y., Horie, K. and Suzuki, S. Two distinct chondroitin sulfate ABC lyases. An endoeliminase yielding tetrasaccharides and an exoeliminase preferentially acting on oligosaccharides. *J. Biol. Chem.* **272** (1997) 9123–9130. [PMID: 9083041]
5. Huckerby, T.N., Nieduszynski, I.A., Giannopoulos, M., Weeks, S.D., Sadler, I.H. and Lauder, R.M. Characterization of oligosaccharides from the chondroitin/dermatan sulfates. ^{1}H-NMR and ^{13}C-NMR studies of reduced trisaccharides and hexasaccharides. *FEBS J.* **272** (2005) 6276–6286. [PMID: 16336265]

[EC 4.2.2.21 created 2006 (EC 4.2.2.4 created 1972, part-incorporated 2006 (EC 4.2.99.6 created 1965, part incorporated 1976))]

EC 6.3.2.28 – public review until 16 August 2006 **(2-1)** [Last modified: 19/07/2006] [Edit]

Accepted name: L-amino-acid α-ligase

Reaction: ATP + an L-amino acid + an L-amino acid = ADP + phosphate + L-aminoacyl-L-amino acid

Other name(s): L-amino acid α-ligase; bacilysin synthetase; YwfE; L-amino acid ligase

Comments: The enzyme from *Bacillus* sp. requires Mg^{2+} or Mn^{2+} for activity. While the enzyme has extremely broad substrate specificity, it does not accept highly charged amino acids, such as Lys, Arg, Glu and Asp, nor does it react with secondary amines such as Pro. The N-terminal residue of the α-dipeptide formed seems to be limited to Ala, Gly, Ser, Thr and Met (with Ala and Ser being the most preferred), whereas the C-terminal residue seems to allow for a wider variety of amino acids (but with a preference for Met and Phe). However, not all combinations or dipeptides are formed. For example, while Ser is acceptable for the N-terminus and Thr for the C-terminus, a Ser-Thr dipeptide is not formed. D-Ala, D-Ser and D-Phe are not substrates. Belongs in the ATP-dependent carboxylate-amine/thiol ligase superfamily.

References:
1. Tabata, K., Ikeda, H. and Hashimoto, S. *ywfE* in *Bacillus subtilis* codes for a novel enzyme, L-amino acid ligase. *J. Bacteriol.* **187** (2005) 5195–5202. [PMID: 16030213]

[EC 6.3.2.28 created 2006]

*EC 6.3.5.4 – public review until 16 August 2006 **(1-1)** [Last modified: 19/07/2006] [Edit]

Accepted name: asparagine synthase (glutamine-hydrolysing)

Reaction: ATP + L-aspartate + L-glutamine + H_2O = AMP + diphosphate + L-asparagine + L-glutamate
(1a) L-glutamine + H_2O = L-glutamate + NH_3
(1b) ATP + L-aspartate + NH_3 = AMP + diphosphate + L-asparagine

Other name(s): asparagine synthetase (glutamine-hydrolysing); glutamine-dependent asparagine synthetase; asparagine synthetase B; AS; AS-B

Systematic name: L-aspartate:L-glutamine amido-ligase (AMP-forming)

Comments: The enzyme from *Escherichia coli* has two active sites [4] that are connected by an intramolecular ammonia tunnel [6,7]. The enzyme catalyses three distinct chemical reactions: glutamine hydrolysis to yield ammonia takes place in the N-terminal domain. The C-terminal active site mediates both the synthesis of a β-aspartyl-AMP intermediate and its subsequent reaction with ammonia. The ammonia released is channeled to the other active site to yield asparagine [7].

Links to other databases: BRENDA, ERGO, EXPASY, IUBMB, KEGG, PDB, CAS registry number: 37318-72-2

References:
1. Patterson, M.K., Jr. and Orr, G.R. Asparagine biosynthesis by the Novikoff hepatoma. Isolation, purification, property, and mechanism studies of the enzyme system. *J. Biol. Chem.* **243** (1968) 376–380. [PMID: 4295091]
2. Boehlein, S.K., Richards, N.G. and Schuster, S.M. Glutamine-dependent nitrogen transfer in *Escherichia coli* asparagine synthetase B. Searching for the catalytic triad. *J. Biol. Chem.* **269** (1994) 7450–7457. [PMID: 7907328]
3. Richards, N.G. and Schuster, S.M. Mechanistic issues in asparagine synthetase catalysis. *Adv. Enzymol. Relat. Areas Mol. Biol.* **72** (1998) 145–198. [PMID: 9559053]
4. Larsen, T.M., Boehlein, S.K., Schuster, S.M., Richards, N.G., Thoden, J.B., Holden, H.M. and Rayment, I. Three-dimensional structure of *Escherichia coli* asparagine synthetase B: a short journey from substrate to product. *Biochemistry* **38** (1999) 16146–16157. [PMID:

10587437]
5. Larsen, T.M., Boehlein, S.K., Schuster, S.M., Richards, N.G., Thoden, J.B., Holden, H.M. and Rayment, I. Erratum to: Three-dimensional structure of escherichia coli asparagine synthetase B: A short journey from substrate to product. *Biochemistry* **39** (2000) 7330 only. [PMID: 10852734]
6. Huang, X., Holden, H.M. and Raushel, F.M. Channeling of substrates and intermediates in enzyme-catalyzed reactions. *Annu. Rev. Biochem.* **70** (2001) 149–180. [PMID: 11395405]
7. Tesson, A.R., Soper, T.S., Ciustea, M. and Richards, N.G. Revisiting the steady state kinetic mechanism of glutamine-dependent asparagine synthetase from *Escherichia coli*. *Arch. Biochem. Biophys.* **413** (2003) 23–31. [PMID: 12706338]

[EC 6.3.5.4 created 1972, modified 2006]

*EC 6.3.5.5 – public review until 16 August 2006 (1-1) [Last modified: 19/07/2006] [Edit]

Accepted name: carbamoyl-phosphate synthase (glutamine-hydrolysing)

Reaction: **2** ATP + L-glutamine + HCO_3^- + H_2O = **2** ADP + phosphate + L-glutamate + carbamoyl phosphate

(1a) L-glutamine + H_2O = L-glutamate + NH_3

(1b) **2** ATP + HCO_3^- = **2** ADP + phosphate + carbamoyl phosphate

For diagram of pyrimidine biosynthesis, click here

Other name(s): carbamoyl-phosphate synthetase (glutamine-hydrolysing); carbamyl phosphate synthetase (glutamine); carbamoylphosphate synthetase II; glutamine-dependent carbamyl phosphate synthetase; carbamoyl phosphate synthetase; CPS; carbon-dioxide:L-glutamine amido-ligase (ADP-forming, carbamate-phosphorylating)

Systematic name: hydrogen-carbonate:L-glutamine amido-ligase (ADP-forming, carbamate-phosphorylating)

Comments: The product carbamoyl phosphate is an intermediate in the biosynthesis of arginine and the pyrimidine nucleotides [4]. The enzyme from *Escherichia coli* has three separate active sites, which are connected by a molecular tunnel that is almost 100 Å in length [8]. The amidotransferase domain within the small subunit of the enzyme hydrolyses glutamine to ammonia via a thioester intermediate. The ammonia migrates through the interior of the protein, where it reacts with carboxy phosphate to produce the carbamate intermediate. The carboxy-phosphate intermediate is formed by the phosphorylation of bicarbonate by ATP at a site contained within the N-terminal half of the large subunit. The carbamate intermediate is transported through the interior of the protein to a second site within the C-terminal half of the large subunit, where it is phosphorylated by another ATP to yield the final product, carbamoyl phosphate [6].

Links to other databases: BRENDA, ERGO, EXPASY, IUBMB, KEGG, PDB, CAS registry number: 37233-48-0

References:

1. Anderson, P.M. and Meister, A. Evidence for an activated form of carbon dioxide in the reaction catalysed by *Escherichia coli* carbamyl phosphate synthetase. *Biochemistry* **4** (1965) 2803–2809.
2. Kalman, S.M., Duffield, P.H. and Brzozowski, T. Purification and properties of a bacterial carbamyl phosphate synthetase. *J. Biol. Chem.* **241** (1966) 1871–1877. [PMID: 5329589]
3. Yip, M.C.M. and Knox, W.E. Glutamine-dependent carbamyl phosphate synthetase. Properties and distribution in normal and neoplastic rat tissues. *J. Biol. Chem.* **245** (1970) 2199–2204. [PMID: 5442268]
4. Stapleton, M.A., Javid-Majd, F., Harmon, M.F., Hanks, B.A., Grahmann, J.L., Mullins, L.S. and Raushel, F.M. Role of conserved residues within the carboxy phosphate domain of carbamoyl phosphate synthetase. *Biochemistry* **35** (1996) 14352–14361. [PMID: 8916922]
5. Holden, H.M., Thoden, J.B. and Raushel, F.M. Carbamoyl phosphate synthetase: a tunnel runs through it. *Curr. Opin. Struct. Biol.* **8** (1998) 679–685. [PMID: 9914247]
6. Raushel, F.M., Thoden, J.B., Reinhart, G.D. and Holden, H.M. Carbamoyl phosphate synthetase: a crooked path from substrates to products. *Curr. Opin. Chem. Biol.* **2** (1998) 624–632. [PMID: 9818189]
7. Raushel, F.M., Thoden, J.B. and Holden, H.M. The amidotransferase family of enzymes: molecular machines for the production and delivery of ammonia. *Biochemistry* **38** (1999) 7891–7899. [PMID: 10387030]
8. Thoden, J.B., Huang, X., Raushel, F.M. and Holden, H.M. Carbamoyl-phosphate synthetase. Creation of an escape route for ammonia. *J. Biol. Chem.* **277** (2002) 39722–39727. [PMID: 12130656]

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