Biochimica et Biophysica Acta, 429 (1976) 1—45

ENZYME NOMENCLATURE: Recommendations (1972) of the International Union of Pure and Applied Chemistry and the International Union of Biochemistry

Supplement 1: Corrections & Additions (1975)

Entries marked with • replace the entries of corresponding EC number in Enzyme Nomenclature (1972). All others are new entries.

References referred to by number are to be found in Enzyme Nomenclature (1972); references given in letter form (gb) are on pages 40-45 of this document.

A subcommittee is reviewing all the entries in sub-class 3.4; results were not available in time to be included in this supplement.

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Number	Recommended Name	Reaction
• 1.1.1.3	Homoserine dehydrogenase	L-Homoserine + $NAD(P)^+$ = L-aspartate β-semialdehyde + NAD(P)H
• 1.1.1.5	Acetoin dehydrogenase	Acetoin + NAD^+ = diacetyl + NADH
• 1.1.1.24	Quinate dehydrogenase	Quinate + NAD^+ = 3-dehydroquinate + NADH
• 1.1.1.25	Shikimate dehydrogenase	Shikimate + $NADP^+$ = 3-dehydroshikimate + NADPH
• 1.1.1.40	Malate dehydrogenase (oxaloacetate-decarboxylating) ($NADP^+$)	L-Malate + $NADP^+$ = pyruvate + CO_2 + NADPH
• 1.1.1.52	3α-Hydroxycholanate dehydrogenase	3α-Hydroxy-5β-cholanate + NAD^+ = 3-oxo-5β-cholanate + NADH
• 1.1.1.65	Pyridoxine 4-dehydrogenase	Pyridoxine + $NADP^+$ = pyridoxal + NADPH
• 1.1.1.69	Gluconate 5-dehydrogenase	D-Gluconate + $NAD(P)^+$ = 5-keto-D-gluconate + NAD(P)H
• *[1.1.1.74*	*Deleted entry: D-Aminopropanol dehydrogenase (reaction due to EC 1.1.1.4)]*	
• 1.1.1.85	3-Isopropylmalate dehydrogenase	2-Hydroxy-4-methyl-3-carboxyvalerate + NAD^+ = 2-oxo-4-methyl-3-carboxyvalerate + NADH
• 1.1.1.86	Ketol-acid reductoisomerase	2,3-Dihydroxyisovalerate + $NADP^+$ = 2-acetolactate + NADPH
• *[1.1.1.89*	*Deleted entry: Dihydroxyisovalerate dehydrogenase (isomerizing). Now included with EC 1.1.1.86]*	
• 1.1.1.100	3-Oxoacyl-[acyl-carrier-protein] reductase	D-3-Hydroxyacyl-[acyl-carrier protein] + $NADP^+$ = 3-oxoacyl-[acyl-carrier protein] + NADPH
• 1.1.1.101	Palmitoyldihydroxyacetone-phosphate reductase	1-Palmitoylglycerol 3-phosphate + $NADP^+$ = palmitoyldihydroxyacetone phosphate + NADPH
• 1.1.1.106	Pantoate dehydrogenase	D-Pantoate + NAD^+ = D-2-hydroxy-3,3-dimethyl-3-formylpropionate + NADH
• *[1.1.1.109*	*Transferred entry: now EC 1.3.1.28 – 2,3-Dihydro-2,3-dihydroxybenzoate dehydrogenase]*	
• 1.1.1.118	Glucose dehydrogenase (NAD^+)	D-Glucose + NAD^+ = D-glucono-δ-lactone + NADH
• 1.1.1.123	Sorbose dehydrogenase ($NADP^+$)	L-Sorbose + $NADP^+$ = 5-keto-D-fructose + NADPH
• 1.1.1.124	Fructose 5-dehydrogenase ($NADP^+$)	D-Fructose + $NADP^+$ = 5-keto-D-fructose + NADPH
• 1.1.1.127	2-Keto-3-deoxy-D-gluconate dehydrogenase ($NAD(P)^+$)	2-Keto-3-deoxy-D-gluconate + $NAD(P)^+$ = 3-deoxy-D-*glycero*-2,5-hexodiulosonate + NAD(P)H
• 1.1.1.128	L-Idonate dehydrogenase	L-Idonate + $NADP^+$ = 5-keto-D-gluconate + NADPH
• 1.1.1.135	GDP-6-deoxy-D-talose dehydrogenase	GDP-6-deoxy-D-talose + $NAD(P)^+$ = GDP-4-keto-6-deoxy-D-talose + NAD(P)H
1.1.1.154	Ureidoglycollate dehydrogenase	(*S*)-Ureidoglycollate + $NAD(P)^+$ = oxalureate + NAD(P)H

Number	Other Name	Basis for classification (Systematic Name)	Comments	Reference
1.1.1.3		L-Homoserine:$NAD(P)^+$ oxidoreductase	The yeast enzyme acts most rapidly with NAD^+; a purified enzyme from Neurospora acts more rapidly with $NADP^+$	216,2712
1.1.1.5	Diacetyl reductase	Acetoin:NAD^+ oxidoreductase	$NADP^+$ also acts	2310, bl
1.1.1.24		Quinate:NAD^+ 3-oxidoreductase		710, 1626
1.1.1.25		Shikimate:$NADP^+$ 3-oxido-reductase		131, 1626, 2685
1.1.1.40	'Malic' enzyme, Decarboxylating L-malate→PN transhydrogenase, Pyruvic-malic carboxylase	L-Malate:$NADP^+$ oxidoreductase (oxaloacetate-decarboxylating)	Also decarboxylates added oxaloacetate	864, 1781, 2055, 2313 2547
1.1.1.52		3α-Hydroxy-5β-cholanate:NAD^+ oxidoreductase	Also acts on other 3α-hydroxysteroids with an acidic side-chain	895
1.1.1.65	Pyridoxin dehydrogenase	Pyridoxine:$NADP^+$ 4-oxidoreductase	Also oxidizes pyridoxine phosphate	983
1.1.1.69	5-Keto-D-gluconate 5-reductase	D-Gluconate:$NAD(P)^+$ 5-oxidoreductase		1794, bg
1.1.1.85		2-Hydroxy-4-methyl-3-carboxy-valerate:NAD^+ oxidoreductase	The product decarboxylates to 2-oxo-4-methylvalerate	311,1835
1.1.1.86	Dihydroxyisovalerate dehydrogenase (isomerizing), Acetohydroxy acid isomeroreductase	2,3-Dihydroxyisovalerate:$NADP^+$ oxidoreductase (isomerizing)	Also catalyses the reduction of 2-aceto-2-hydroxybutyrate to 2,3-dihydroxy-3-methylvalerate	73, 1214, 2082
1.1.1.100		D-3-Hydroxyacyl-[acyl-carrier-protein] :$NADP^+$ oxidoreductase	Exhibits a marked preference for acyl-carrier-protein derivatives over CoA derivatives as substrates	2450,gy
1.1.1.101		1-Palmitoylglycerol-3-phosphate:$NADP^+$ oxidoreductase	Also acts on alkylglycerol 3-phosphate	850, eu
1.1.1.106		D-Pantoate:NAD^+ 4-oxidoreductase		780
1.1.1.118		D-Glucose:NAD^+ 1-oxidoreductase		1008
1.1.1.123	5-Keto-D-fructose reductase	L-Sorbose:$NADP^+$ 5-oxidoreductase		594
1.1.1.124	5-Keto-D-fructose reductase ($NADP^+$)	D-Fructose:$NADP^+$ 5-oxidoreductase		98
1.1.1.127		2-Keto-3-deoxy-D-gluconate:$NAD(P)^+$ 5-oxidoreductase		1901
1.1.1.128	5-Keto-D-gluconate 2-reductase	L-Idonate:$NADP^+$ 2-oxidoreductase		2373
1.1.1.135		GDP-6-deoxy-D-talose:$NAD(P)^+$ 4-oxidoreductase		1520,le
1.1.1.154		(*S*)-Ureidoglycollate:$NAD(P)^+$ oxidoreductase		kk

Number	Recommended Name	Reaction
1.1.1.155	Homoisocitrate dehydrogenase	1-Hydroxy-1,2,4-butanetricarboxylate + NAD^+ = 2-oxoadipate + CO_2 + NADH
1.1.1.156	Glycerol 2-dehydrogenase ($NADP^+$)	Glycerol + $NADP^+$ = dihydroxyacetone + NADPH
1.1.1.157	3-Hydroxybutyryl-CoA dehydrogenase	L-3-Hydroxybutyryl-CoA + $NADP^+$ = 3-acetoacetyl-CoA + NADPH
1.1.1.158	UDP-*N*-acetyl*enol*pyruvoylglucosamine reductase	UDP-*N*-acetylmuramate + $NADP^+$ = UDP-2-acetamido-2-deoxy-3-*enol*pyruvoylglucose + NADPH
1.1.1.159	7α-Hydroxysteroid dehydrogenase	3α,7α,12α-Trihydroxy-5β-cholanate + NAD^+ = 3α,12α-dihydroxy-7-oxo-5β-cholanate + NADH
1.1.1.160	Dihydrobunolol dehydrogenase	D,L-5-[(*tert*-Butylamino)-2'-hydroxypropoxy]-1,2,3,-tetrahydro-1-naphthol + $NADP^+$ = D,L-5-[(*tert*-butylamino)-2'-hydroxypropoxy]-3,4-dihydro-1(2H)-naphthalenone + NADPH
1.1.1.161	Cholestanetetraol 26-dehydrogenase	5β-Cholestane-3α,7α,12α,26-tetraol + NAD^+ = 5β-cholestane-3α,7α,12α-triol-26-al + NADH
1.1.1.162	D-Erythrulose reductase	Erythritol + $NADP^+$ = D-erythrulose + NADPH
1.1.1.163	Cyclopentanol dehydrogenase	Cyclopentanol + NAD^+ = cyclopentanone + NADH
1.1.1.164	Hexadecanol dehydrogenase	Hexadecanol + NAD^+ = hexadecanal + NADH
1.1.1.165	2-Alkyne-1-ol dehydrogenase	2-Butyne-1,4-diol + NAD^+ = 4-hydroxy-2-butynal + NADH
1.1.1.166	Hydroxycyclohexanecarboxylate dehydrogenase	(1*S*,3*R*,4*S*)-3,4-Dihydroxycyclohexane-1-carboxylate + NAD^+ = (1*S*,4*S*)-4-hydroxy-3-oxocyclohexane-1-carboxylate + NADH
1.1.1.167	Hydroxymalonate dehydrogenase	Hydroxymalonate + NAD^+ = oxomalonate + NADH
1.1.1.168	2-Oxopantoyl-lactone reductase	Pantoyl lactone + $NADP^+$ = 2-oxopantoyl lactone + NADPH
1.1.1.169	2-Oxopantoate reductase	D-Pantoate + $NADP^+$ = 2-oxopantoate + NADPH
• *[1.1.3.2*	*Transferred entry: now EC 1.13.12.4 - Lactate 2-monooxygenase]*	
• 1.1.3.5	Hexose oxidase	β-D-Glucose + O_2 = D-glucono-δ-lactone + H_2O_2
• 1.1.3.12	Pyridoxine 4-oxidase	Pyridoxine + O_2 = pyridoxal + H_2O_2
1.1.3.16	Ecdysone oxidase	Ecdysone + O_2 = 3-dehydroecdysone + (?)
• 1.1.99.3	Gluconate 2-dehydrogenase	D-Gluconate + acceptor = 2-keto-D-gluconate + reduced acceptor

Number	Other Name	Basis for classification (Systematic Name)	Comments	Reference
1.1.1.155		1-Hydroxy-1,2,4-butanetricarboxylate:NAD^+ oxidoreductase (decarboxylating)		hr
1.1.1.156	Dihydroxyacetone reductase	Glycerol:$NADP^+$ 2-oxidoreductase (dihydroxyacetone-forming)		v
1.1.1.157		L-3-Hydroxybutyryl-CoA:$NADP^+$ oxidoreductase		fg
1.1.1.158		UDP-*N*-acetylmuramate:$NADP^+$ oxidoreductase	A flavoprotein (FAD). Sodium thionite, sodium borohydride and, to a lesser extent, NADH can replace NADPH	jt, js
1.1.1.159		7α-Hydroxysteroid:NAD^+ 7-oxidoreductase	Catalyses the oxidation of the 7α-hydroxyl group of bile acids, bile alcohols and sulphates, both in their free and conjugated forms. The *Bacteroides fragilis* enzyme can also utilize $NADP^+$	fd, fe
1.1.1.160	Bunolol reductase	D,L-5-[(*tert*-Butylamino)-2'--hydroxypropoxy]-1,2,3,4--tetrahydro-1-naphthol:$NADP^+$ oxidoreductase	Also acts more slowly with NAD^+	fa
1.1.1.161		5β-Cholestane-3α,7α,12α,26--tetraol:NAD^+ 26-oxidoreductase		fl
1.1.1.162		Erythritol:$NADP^+$ oxidoreductase	NAD^+ is also utilized, more slowly	kf
1.1.1.163		Cyclopentanol:NAD^+ oxidoreductase		cl
1.1.1.164		Hexadecanol:NAD^+ oxidoreductase	The liver enzyme acts on long chain alcohols from C-8 to C-16. The Euglena enzyme also oxidizes the aldehydes to fatty acids	jh, el
1.1.1.165		2-Butyne-1,4-diol:NAD^+ 1-oxidoreductase	Acts on a variety of 2-alkyne-1-ols, and also 1,4-butanediol. $NADP^+$ also acts as acceptor, more slowly	fu
1.1.1.166		(1*S*,3*R*,4*S*)-3,4-Dihydroxycyclohexane-1-carboxylate:NAD^+ 3-oxidoreductase	Acts on (−)-hydroxycyclohexanecarboxylates having an equatorial carboxyl group at C-1, an axial hydroxyl group at C-3 and an equatorial hydroxyl or carbonyl group at C-4, including (−)-quinate and (−)-shikimate	lb
1.1.1.167		Hydroxymalonate:NAD^+ oxidoreductase		dq, gr
1.1.1.168		Pantoyl-lactone:$NADP^+$ oxidoreductase		ef
1.1.1.169		D-Pantoate:$NADP^+$ 2-oxidoreductase		ef
1.1.3.5		D-Hexose:oxygen 1-oxidoreductase	A cupro-glycoprotein. Also oxidizes D-galactose, D-mannose, maltose, lactose and cellobiose	162, 163, jl
1.1.3.12	Pyridoxin 4-oxidase	Pyridoxine:oxygen 4-oxidoreductase	A flavoprotein. Can also use 2,6-dichloroindophenol as an acceptor	2341
1.1.3.16		Ecdysone:oxygen 3-oxidoreductase	2,6-Dichloroindophenol can also act as an acceptor	lt
1.1.99.3		D-Gluconate:(acceptor) 2-oxidoreductase		1943

Number	Recommended Name	Reaction
• 1.1.99.9	Pyridoxine 5-dehydrogenase	Pyridoxine + acceptor = isopyridoxal + reduced acceptor
• 1.1.99.10	Glucose dehydrogenase (acceptor)	D-Glucose + acceptor = D-glucono-δ-lactone + reduced acceptor
1.2.1.39	Phenylacetaldehyde dehydrogenase	Phenylacetaldehyde + NAD^+ + H_2O = phenylacetate + NADH
1.2.1.40	Cholestanetriol-26-al 26-dehydrogenase	5β-Cholestane-3α,7α,12α-triol-26-al + NAD^+ + H_2O = 5β-cholestane-3α,7α,12α-triol-26-oate + NADH
1.2.1.41	Glutamate-semialdehyde dehydrogenase	L-Glutamate γ-semialdehyde + orthophosphate + $NADP^+$ = L-γ-glutamyl phosphate + NADPH
1.2.3.6	Pyruvate oxidase (CoA-acetylating)	Pyruvate + CoA + O_2 = acetyl-CoA + CO_2 + H_2O_2
1.3.1.25	3,5-Cyclohexadiene-1,2-diol-1-carboxylate dehydrogenase	3,5-Cyclohexadiene-1,2-diol-1-carboxylate + NAD^+ = catechol + CO_2 + NADH
1.3.1.26	Dihydrodipicolinate reductase	2,3,4,5-Tetrahydrodipicolinate + $NAD(P)^+$ = 2,3-dihydrodipicolinate + NAD(P)H
1.3.1.27	2-Hexadecenal reductase	Hexadecanal + $NADP^+$ = 2-*trans*-hexadecenal + NADPH
1.3.1.28	2,3-Dihydro-2,3-dihydroxybenzoate dehydrogenase	2,3-Dihydro-2,3-dihydroxybenzoate + NAD^+ = 2,3-dihydroxybenzoate + NADH
1.3.1.29	*cis*-1,2-Dihydro-1,2-dihydroxynaphthalene dehydrogenase	*cis*-1,2-Dihydro-1,2-dihydroxynaphthalene + NAD^+ = 1,2-dihydroxynaphthalene + NADH
1.3.99.8	2-Furoyl-CoA dehydrogenase	2-Furoyl-CoA + H_2O + acceptor = 5-hydroxy-2-furoyl-CoA + reduced acceptor
1.3.99.9	β-Cyclopiazonate dehydrogenase	β-Cyclopiazonate + acceptor = α-cyclopiazonate + reduced acceptor

• 1.4 ACTING ON THE CH-NH_2 GROUP OF DONORS

These are the amino-acid dehydrogenases and the amine oxidases. In most cases the imine formed is hydrolysed to give an oxo-group and NH_3. This is indicated as (deaminating). Sub-sub-classes are formed according to acceptor: 1.4.1 with $NAD(P)^+$, 1.4.2 with a cytochrome, 1.4.3 with oxygen, 1.4.4 with a disulphide compound, 1.4.7 with an iron-sulphur protein as acceptor, and 1.4.99 with other acceptors.

Number	Recommended Name	Reaction
1.4.1.11	L-*erythro*-3,5-Diaminohexanoate dehydrogenase	L-*erythro*-3,5-Diaminohexanoate + H_2O + NAD^+ = 5-amino-3-oxohexanoate + NH_3 + NADH
1.4.1.12	2,4-Diaminopentanoate dehydrogenase	2,4-Diaminopentanoate + H_2O + $NAD(P)^+$ = 2-amino-4-oxopentanoate + NH_3 + NAD(P)H
1.4.1.13	Glutamate synthase (NADPH)	2 L-Glutamate + $NADP^+$ = L-glutamine + 2-oxoglutarate + NADPH

Number	Other Name	Basis for classification (Systematic Name)	Comments	Reference
1.1.99.9	Pyridoxol 5-dehydrogenase	Pyridoxine:(acceptor) 5-oxidoreductase	A flavoprotein (FAD)	2341
1.1.99.10	Glucose dehydrogenase (Aspergillus)	D-Glucose:(acceptor) 1-oxidoreductase	2,6-Dichloroindophenol can act as acceptor; enzyme contains one mole of FAD per mole of enzyme and is a glycoprotein (24% carbohydrate)	127
1.2.1.39		Phenylacetaldehyde:NAD^+ oxidoreductase		cc, cd
1.2.1.40		5β-Cholestane-3α,7α,12α-triol-26-al:NAD^+ oxidoreductase		fl
1.2.1.41	γ-Glutamylphosphate reductase	L-Glutamate-γ-semialdehyde:$NADP^+$ oxidoreductase (phosphorylating)		k
1.2.3.6		Pyruvate:oxygen oxidoreductase (CoA-acetylating)	A flavoprotein (FAD)	mc
1.3.1.25		3,5-Cyclohexadiene-1,2-diol-1-carboxylate:NAD^+ oxidoreductase (decarboxylating)		hh
1.3.1.26		2,3,4,5-Tetrahydrodipicolinate:NAD(P)$^+$ oxidoreductase		ju, bx
1.3.1.27	2-Alkenal reductase	Hexadecanal:$NADP^+$ oxidoreductase	Enzyme is specific for long chain 2-*trans*- and 2-*cis*-alkenals, with chain length optimum around 14 to 16 carbon atoms	je
1.3.1.28		2,3-Dihydro-2,3-dihydroxybenzoate:NAD^+ oxidoreductase	Formerly EC 1.1.1.109	2705
1.3.1.29		*cis*-1,2-Dihydro-1,2-dihydroxynaphthalene:NAD^+ 1,2-oxidoreductase	Also acts, at half the rate, on *cis*-anthracene dihydrodiol and *cis*-phenanthrene dihydrodiol	gm
1.3.99.8	Furoyl-CoA hydroxylase	2-Furoyl-CoA:(acceptor) oxidoreductase (hydroxylating)	A cuproprotein. The oxygen atom of the -OH produced is derived from water, not O_2; the actual oxidative step is probably C-CHOH- to C=C(OH)-. The product of the reaction tautomerizes non-enzymically to form 5-oxo-Δ^2-dihydro-2-furoyl-CoA. Methylene blue, nitro blue tetrazolium and a membrane fraction from *P. putida* can act as acceptors	eh
1.3.99.9	β-Cyclopiazonate oxidocyclase	β-Cyclopiazonate:(acceptor) oxidoreductase (cyclizing)	A flavoprotein (FAD). Cytochrome *c* and various dyes can act as acceptor	ic, ib
1.4.1.11		L-*erythro*-3,5-Diaminohexanoate:NAD^+ oxidoreductase (deaminating)		*l*
1.4.1.12		2,4-Diaminopentanoate:NAD(P)$^+$ oxidoreductase (deaminating)	Also acts, more slowly, on 2,5-diaminohexanoate forming 2-amino-5-oxohexanoate, which then cyclizes non-enzymically to 1-pyrroline-2-methyl-5-carboxylate	jb, iw, kb
1.4.1.13		L-Glutamate:$NADP^+$ oxidoreductase (transaminating)	An iron-sulphur-flavoprotein. Formerly EC 2.6.1.53	2406a, fp

Number	Recommended Name	Reaction
	1.4.2 WITH A CYTOCHROME AS ACCEPTOR	
1.4.2.1	Glycine dehydrogenase (cytochrome)	Glycine + H_2O + 2 ferricytochrome *c* = glyoxylate + NH_3 + 2 ferrocytochrome *c*
1.4.3.10	Putrescine oxidase	Putrescine + O_2 + H_2O = 4-aminobutyraldehyde + NH_3 + H_2O_2
1.4.3.11	L-Glutamate oxidase	2 L-Glutamate + O_2 + H_2O = 2 2-oxoglutarate + 2 NH_3 + H_2O
	1.4.7 WITH AN IRON-SULPHUR PROTEIN AS ACCEPTOR	
1.4.7.1	Glutamate synthase (ferredoxin)	2 L-Glutamate + 2 oxidized ferredoxin = L-glutamine + 2-oxoglutarate + 2 reduced ferredoxin
1.4.99.2	Taurine dehydrogenase	Taurine + H_2O + acceptor = sulphoacetaldehyde + NH_3 + reduced acceptor
• 1.5.1.3	Tetrahydrofolate dehydrogenase	5,6,7,8-Tetrahydrofolate + $NADP^+$ = 7,8-dihydrofolate + NADPH
• *[1.5.1.4*	*Deleted entry:Dihydrofolate dehydrogenase. Now included with EC 1.5.1.3]*	
1.5.1.14	1,2-Didehydropipecolate reductase	L-Pipecolate + $NADP^+$ = 1,2-didehydropipecolate + NADPH
1.5.99.5	Methylglutamate dehydrogenase	*N*-Methyl-L-glutamate + acceptor + H_2O = L-glutamate + formaldehyde + reduced acceptor
1.5.99.6	Spermidine dehydrogenase	Spermidine + acceptor + H_2O = 1,3-diaminopropane + 4-aminobutyraldehyde + reduce acceptor
1.5.99.7	Trimethylamine dehydrogenase	Trimethylamine + H_2O + acceptor = dimethylamine + formaldehyde + reduced acceptor
• 1.6.4.3	Lipoamide reductase (NADH)	NADH + lipoamide = NAD^+ + dihydrolipoamide
• 1.6.99.1	NADPH dehydrogenase	NADPH + acceptor = $NADP^+$ + reduced acceptor
• 1.7.2.1	Nitrite reductase (cytochrome)	Nitric oxide + H_2O + 2 ferricytochrome *c* = nitrite + 2 ferrocytochrome *c*
• 1.7.99.2	Nitric-oxide reductase	Nitrogen + acceptor = 2 nitric oxide + reduced acceptor
• 1.7.99.3	Nitrite reductase	2 Nitric oxide + 2 H_2O + acceptor = 2 nitrite + reduced acceptor

Number	Other Name	Basis for classification (Systematic Name)	Comments	Reference
1.4.2.1	Glycine–cytochrome *c* reductase	Glycine:ferricytochrome *c* oxidoreductase (deaminating)		hw
1.4.3.10		Putrescine:oxygen oxidoreductase (deaminating)	A flavoprotein (FAD). 4-Aminobutyraldehyde condenses non-enzymically to 1-pyrroline	lk, bi
1.4.3.11		L-Glutamate:oxygen oxidoreductase (deaminating)	Can also use phenazine methosulphate and ferricyanide as electron acceptors	dr
1.4.7.1		L-Glutamate:ferredoxin oxidoreductase (transaminating)	An iron-sulphur-flavoprotein	fo
1.4.99.2		Taurine:(acceptor) oxidoreductase (deaminating)		em
1.5.1.3	Dihydrofolate reductase	5,6,7,8-Tetrahydrofolate:$NADP^+$ oxidoreductase	The animal enzyme also slowly oxidizes 7,8-dihydrofolate to folate	2715, 225, dx, eb
1.5.1.14		L-Pipecolate:$NADP^+$ 2-oxidoreductase		ao
1.5.99.5		*N*-Methyl-L-glutamate:(acceptor) oxidoreductase (demethylating)	A number of *N*-methyl-substituted amino acids can act as donor; 2,6-dichloroindophenol is the best acceptor	cx
1.5.99.6		Spermidine:(acceptor) oxidoreductase	A flavohaemoprotein (FAD). Ferricyanide, dichloroindophenol and cytochrome *c* can act as acceptor. 4-Aminobutyraldehyde condenses non-enzymically to 1-pyrroline	jq, jp
1.5.99.7		Trimethylamine:(acceptor) oxidoreductase (demethylating)	A number of alkyl-substituted derivatives of trimethylamine can also act as electron donor; phenazine methosulphate and 2,6-dichloroindophenol can act as electron acceptors	ar
1.6.4.3	Diaphorase, Lipoyl dehydrogenase, Dihydro-α-lipoic acid→DPN transhydrogenase, Lipoamide dehydrogenase (NADH)	NADH:lipoamide oxidoreductase	A flavoprotein (FAD)	1536, 1537, 2085, 2303, ek, lg
1.6.99.1	'Old Yellow enzyme', $TPN.H_2 \rightarrow O_2$ transhydrogenase, NADPH diaphorase	NADPH:(acceptor) oxidoreductase	A flavoprotein (FMN in yeast, FAD in plants)	23, 2412, 2413, dm, i
1.7.2.1		Nitric-oxide:ferricytochrome *c* oxidoreductase	A cuproprotein. Cytochrome *c*-552 or cytochrome *c*-553 from *Pseudomonas denitrificans* acts as acceptor	1628
1.7.99.2		Nitrogen:(acceptor) oxidoreductase	A flavoprotein. Reduced pyocyanine acts as donor for the reduction of NO	392, 626
1.7.99.3		Nitric-oxide:(acceptor) oxidoreductase	A cuproprotein; the Pseudomonas enzyme also contains FAD. Reduced pyocyanine, flavins, *etc.* act as donor for the reduction of nitrite. Formerly EC 1.6.6.5	391, 2550 dj

Number	Recommended Name	Reaction
• 1.7.99.4	Nitrate reductase	Nitrite + acceptor = nitrate + reduced acceptor
• *[1.8.6.1*	*Deleted entry: Nitrate-ester reductase. Now included with EC 2.5.1.18]*	

• 1.10 ACTING ON DIPHENOLS AND RELATED SUBSTANCES AS DONORS

These enzymes oxidize diphenols or ascorbate. There are three sub-sub-groups: 1.10.1, with NAD^+ or $NADP^+$, 1.10.2, with cytochromes, and 1.10.3 with oxygen as acceptor. Some enzymes oxidizing phenols are oxygenases (sub-sub-group 1.14.4).

Number	Recommended Name	Reaction
1.10.1.1	*trans*-Acenaphthene-1,2-diol dehydrogenase	($\pm$)-*trans*-Acenaphthene 1,2-diol + $NADP^+$ = acenaphthenequinone + NADPH
• 1.13.11.14	2,3-Dihydroxybenzoate 3,4-dioxygenase	2,3-Dihydroxybenzoate + O_2 = 3-carboxy-2-hydroxymuconate semialdehyde
• 1.13.11.20	Cysteine dioxygenase	L-Cysteine + O_2 = cysteine sulphinate
1.13.12.5	Renilla luciferin 2-monooxygenase	Renilla luciferin + O_2 = oxidized Renilla luciferin + CO_2 + $h\nu$
1.13.12.6	Cypridina luciferin 2-monooxygenase	Cypridina luciferin + O_2 = oxidized Cypridina luciferin + CO_2 + $h\nu$
1.13.12.7	Photinus luciferin 4-monooxygenase (ATP-hydrolysing)	Photinus luciferin + O_2 + ATP = oxidized Photinus luciferin + CO_2 + H_2O + AMP + pyrophosphate + $h\nu$
• 1.14.11.3	Thymidine,2-oxoglutarate dioxygenase	Thymidine + 2-oxoglutarate + O_2 = thymine ribonucleoside + succinate + CO_2
• *[1.14.11.5*	*Deleted entry: 5-Hydroxymethyluracil,2-oxoglutarate dioxygenase. Now included with EC 1.14.11.6]*	
• 1.14.11.6	Thymine,2-oxoglutarate dioxygenase	Thymine + 2-oxoglutarate + O_2 = 5-hydroxymethyluracil + succinate + CO_2
1.14.13.10	2,6-Dihydroxypyridine 3-monooxygenase	2,6-Dihydroxypyridine + NADH + O_2 = 2,3,6-trihydroxypyridine + NAD^+ + H_2O
1.14.13.11	*trans*-Cinnamate 4-monooxygenase	*trans*-Cinnamate + NADPH + O_2 = 4-hydroxycinnamate + $NADP^+$ + H_2O
1.14.13.12	Benzoate 4-monooxygenase	Benzoate + NADPH + O_2 = 4-hydroxybenzoate + $NADP^+$ + H_2O
1.14.13.13	25-Hydroxycholecalciferol 1-monooxygenase	25-Hydroxycholecalciferol + NADPH + O_2 = 1,25-dihydroxycholecalciferol + $NADP^+$ + H_2O
1.14.13.14	*trans*-Cinnamate 2-monooxygenase	*trans*-Cinnamate + NADPH + O_2 = 2-hydroxycinnamate + $NADP^+$ + H_2O
1.14.13.15	Cholestanetriol 26-monooxygenase	5β-Cholestane-$3\alpha,7\alpha,12\alpha$-triol + NADPH + O_2 = 5β-cholestane-$3\alpha,7\alpha,12\alpha$,26-tetraol + $NADP^+$ + H_2O

Number	Other Name	Basis for classification (Systematic Name)	Comments	Reference
.7.99.4	Respiratory nitrate reductase	Nitrite:(acceptor) oxidoreductase	The Pseudomonas enzyme is a cytochrome, but the enzyme from *Micrococcus halodentrificans* is a non-haem-iron protein containing Mo. Reduced benzyl viologen and other dyes bring about the reduction of nitrate	1721, 1933, hp
1.10.1.1		($\pm$)-*trans*-Acenaphthene-1,2-diol:$NADP^+$ oxidoreductase	Some preparations also utilize NAD^+	da
1.13.11.14	*o*-Pyrocatechuate oxygenase	2,3-Dihydroxybenzoate:oxygen 3,4-oxidoreductase (decyclizing)		1991
1.13.11.20		L-Cysteine:oxygen oxidoreductase	Requires ferrous ion and NAD(P)H	1432
1.13.12.5		Renilla luciferin:oxygen 2-oxidoreductase (decarboxylating)	The 'alkyl' group, unidentified, has a M.W. of $\sim$ 200; a benzyl group in the same position yields a fully active compound. Luciferases of other coelenterates (Ptilosarcus, Stylatula) also react with Renilla luciferin	ay, ii, dc
1.13.12.6		Cypridina luciferin:oxygen 2-oxidoreductase (decarboxylating)	The luciferins (and presumably the luciferases, since they cross-react) of some luminous fish (*e.g.* Apogon, Parapriacanthus, Porichthys) are apparently identical or closely similar	eg, dv, kc, ax
1.13.12.7		Photinus luciferin:oxygen 4-oxidoreductase (decarboxylating, ATP-hydrolysing)	The first step in the reaction is the formation of an acid anhydride between the carboxylic group and AMP, with the release of pyrophosphate	kz, db, la
1.14.11.3	Thymidine 2′-hydroxylase, Pyrimidine deoxyribonucleoside 2′-hydroxylase	Thymidine,2-oxoglutarate:oxygen oxidoreductase (2′-hydroxylating)	Requires ferrous ion and ascorbate	2145, m
1.14.11.6	Thymine 7-hydroxylase	Thymine,2-oxoglutarate:oxygen oxidoreductase (7-hydroxylating)	Requires ferrous ion and ascorbate. Also acts on 5-hydroxymethyluracil	1, fc
1.14.13.10		2,6-Dihydroxypyridine,NADH:oxygen oxidoreductase (3-hydroxylating)	A flavoprotein	cy, cz
1.14.13.11		*trans*-Cinnamate,NADPH:oxygen oxidoreductase (4-hydroxylating)	NADH also acts, more slowly. Involves cytochrome *P*-450	hs, gx
1.14.13.12		Benzoate,NADPH:oxygen oxidoreductase (4-hydroxylating)	Requires ferrous ion and tetrahydropteridine	he
1.14.13.13	25-Hydroxycholecalciferol 1-hydroxylase	25-Hydroxycholecalciferol,NADPH:oxygen oxidoreductase (1-hydroxylating)		ck
1.14.13.14	Cinnamic acid 2-hydroxylase	*trans*-Cinnamate,NADPH:oxygen oxidoreductase (2-hydroxylating)		ch
1.14.13.15		5β-Cholestane-3α,7α,12α-triol,NADPH:oxygen oxidoreductase (26-hydroxylating)		gf

Number	Recommended Name	Reaction
1.14.13.16	Cyclopentanone monooxygenase	Cyclopentanone + NADPH + O_2 = 5-valerolactone + $NADP^+$ + H_2O
1.14.13.17	Cholesterol 7α-monooxygenase	Cholesterol + NADPH + O_2 = 7α-hydroxycholesterol + $NADP^+$ + H_2O
1.14.13.18	4-Hydroxyphenylacetate 1-monooxygenase	4-Hydroxyphenylacetate + NAD(P)H + O_2 = homogentisate + $NAD(P)^+$ + H_2O
1.14.13.19	Taxifolin 8-monooxygenase	Taxifolin + NAD(P)H + O_2 = 2,3-dihydrogossypetin + $NAD(P)^+$ + H_2O
• 1.14.14.1	Flavoprotein-linked monooxygenase	RH + reduced flavoprotein + O_2 = ROH + oxidized flavoprotein + H_2O
• *[1.14.14.2*	*Deleted entry:Benzopyrene 3-monooxygenase. Now included with EC 1.14.14.1]*	
1.14.16.5	Glyceryl-ether monooxygenase	1-Alkyl-*sn*-glycerol + tetrahydropteridine + O_2 = 1-hydroxyalkyl-*sn*-glycerol + dihydropteridine + H_2O
• 1.14.18.1	Monophenol monooxygenase	Tyrosine+ dihydroxyphenylalanine + O_2 = dihydroxyphenylalanine + dioxophenylalanine + H_2O
• *[1.14.99.17*	*Transferred entry:now EC 1.14.16.5:Glyceryl-ether monooxygenase]*	
1.14.99.18	*N*-Acetylneuraminate monooxygenase	*N*-Acetylneuraminate + AH_2 + O_2 = *N*-glycoloylneuraminate + A + H_2O
1.14.99.19	Alkylacylglycerophosphoethanolamine desaturase	*O*-1-Alkyl-2-acyl-*sn*-glycero-3-phosphoethanolamine + AH_2 + O_2 = *O*-1-alk-1-enyl-2-acyl-*sn*-glycero-3-phosphoethanolamine + A + 2 H_2O
1.14.99.20	Phylloquinone monooxygenase (2,3-epoxidizing)	Phylloquinone + AH_2 + O_2 = 2,3-epoxyphylloquinone + A + H_2O
1.14.99.21	Latia luciferin monooxygenase (demethylating)	Latia luciferin + AH_2 + 2 O_2 = oxidized Latia luciferin + CO_2 + formate + A + H_2O + $h\nu$
• 2.1.1.23	Protein(arginine) methyltransferase	*S*-Adenosyl-L-methionine + protein = *S*-adenosyl-L-homocysteine + protein containing ω-*N*-methylarginine
2.1.1.42	Luteolin methyltransferase	*S*-Adenosyl-L-methionine + 5,7,3′,4′-tetrahydroxyflavone = *S*-adenosyl-L-homocysteine + 5,7,4′-trihydroxy-3′-methoxyflavone
2.1.1.43	Protein(lysine) methyltransferase	*S*-Adenosyl-L-methionine + protein = *S*-adenosyl-L-homocysteine + protein containing ε-*N*-methyllysine

Number	Other Name	Basis for classification (Systematic Name)	Comments	Reference
1.14.13.16		Cyclopentanone,NADPH:oxygen oxidoreductase (5-hydroxylating, lactonizing)		cl
1.14.13.17		Cholesterol,NADPH:oxygen oxidoreductase (7α-hydroxylating)	A cytochrome *P*-450 enzyme	ft, af
1.14.13.18	4-Hydroxyphenylacetate 1-hydroxylase	4-Hydroxyphenyl-acetate,NAD(P)H:oxygen oxidoreductase (1-hydroxylating)	A flavoprotein (FAD). Also acts on 4-hydroxyhydratropate (forming 2-methylhomogentisate) and on 4--hydroxyphenoxyacetate (forming hydroquinone and glycollate)	cq
1.14.13.19		Taxifolin,NAD(P)H:oxygen oxidoreductase (8-hydroxylating)	A flavoprotein. Also acts on fustin, but not on catechin, quercetin or mollisacacidin	dp
1.14.14.1	Aryl 4-hydroxylase, Aryl 4-monooxygenase, Benzopyrene 3-mono-oxygenase, Mixed-function oxidase, RH hydroxylase	RH,reduced-flavoprotein:oxygen oxidoreductase (RH-hydroxylating)	Reactions catalysed by a family of spectrally similar cytochromes *P*-450 with different or overlapping substrate specificities. Types of substrates include steroids, fatty acids, alkanes, drugs and many xenobiotics. Formerly EC 1.14.1.1 and 1.99.1.1	240, 1441a, 1623, fs, 701 1727
1.14.16.5	Glyceryl ether cleaving enzyme	1-Alkyl-*sn*-glycerol,tetrahydro-pteridine:oxygen oxidoreductase	The product spontaneously breaks down to form a fatty aldehyde and glycerol. Formerly EC 1.14.99.17	jx, gq, ix, ir
1.14.18.1	Tyrosinase, Phenolase, Catechol oxidase, Polyphenol oxidase, Monophenol oxidase, Laccase, *o*- and *p*-Diphenol oxidase, Orthophenolase, Urushiol oxidase	Monophenol,dihydroxy-phenylalanine:oxygen oxidoreductase	A copper-protein. Ascorbate is stimulating in the absence of dihydroxyphenylalanine. The classification of this group of enzymes here is controversial; they were previously listed as EC 1.10.3.1 and 1.10.3.2, *i.e.* as enzymes acting on diphenols as donors, with O_2 as acceptor	284, 486, 650, 813, 1532, 1709, 1884, ea, bd, gn, gw, go
1.14.99.18		*N*-Acetylneuraminate,hydrogen--donor:oxygen oxidoreductase (*N*-acetyl-hydroxylating)	Requires ferrous ion. Either NADPH or ascorbate can act as AH_2	id, ie
1.14.99.19		*O*-1-Alkyl-2-acyl-*sn*-glycero-3--phosphoethanolamine,hydrogen--donor:oxygen oxidoreductase	Requires NADPH or NADH. May involve cytochrome b_5. Activated by Mg^{2+} and ATP	gl, li
1.14.99.20	Phylloquinone epoxidase	Phylloquinone,hydrogen-donor:oxygen oxidoreductase (2,3-epoxidizing)		ld
1.14.99.21		Latia luciferin,hydrogen-donor: oxy-gen oxidoreductase (demethylating)	A flavoprotein. The reaction possibly involves two enzymes, an oxygenase followed by a monooxygenase for the actual light-emitting step	ih, ij
2.1.1.23	Protein methylase I	*S*-Adenosyl-L-methionine:pro-tein(arginine) *N*-methyltransferase		1824
2.1.1.42	*o*-Dihydric phenol methyltransferase	*S*-Adenosyl-L-methionine:5,7,3′,4′--tetrahydroxyflavone 3′-*O*-methyl-transferase	Also acts on luteolin-7-*O*-β-D-glucoside	br
2.1.1.43	Protein methylase III	*S*-Adenosyl-L-methionine:protein-(lysine) *N*-methyltransferase		1825

Number	Recommended Name	Reaction
2.1.1.44	Dimethylhistidine methyltransferase	*S*-Adenosyl-L-methionine + N^{α},N^{α}-dimethyl-L-histidine = *S*-adenosyl-L-homocysteine + N^{α},N^{α},N^{α}-trimethyl-L-histidine
2.1.1.45	Thymidylate synthase	5,10-Methylenetetrahydrofolate + dUMP = dihydrofolate + dTMP
2.1.1.46	Isoflavone methyltransferase	*S*-Adenosyl-L-methionine + isoflavone = *S*-adenosyl-L-homocysteine + 4′-*O*-methylisoflavone
2.1.1.47	Indolepyruvate methyltransferase	*S*-Adenosyl-L-methionine + indolepyruvate = *S*-adenosyl-L-homocysteine + β-methylindolepyruvate
2.1.1.48	rRNA (adenine-6-)-methyltransferase	*S*-Adenosyl-L-methionine + rRNA = *S*-adenosyl-L-homocysteine + rRNA containing N^6-methyladenine
2.1.1.49	Tryptamine *N*-methyltransferase	*S*-Adenosyl-L-methionine + tryptamine = *S*-adenosyl-L-homocysteine + *N*-methyltryptamine
2.1.1.50	Loganate methyltransferase	*S*-Adenosyl-L-methionine + loganate = *S*-adenosyl-L-homocysteine + loganin
2.1.1.51	rRNA (guanine-1-)-methyltransferase	*S*-Adenosyl-L-methionine + rRNA = *S*-adenosyl-L-homocysteine + rRNA containing 1-methylguanine
2.1.1.52	rRNA (guanine-2-)-methyltransferase	*S*-Adenosyl-L-methionine + rRNA = *S*-adenosyl-L-homocysteine + rRNA containing N^2-methylguanine
2.1.1.53	Putrescine methyltransferase	*S*-Adenosyl-L-methionine + putrescine = *S*-adenosyl-L-homocysteine + *N*-methylputrescine
2.1.3.5	Oxamate carbamoyltransferase	Carbamoylphosphate + oxamate = orthophosphate + oxalureate
2.1.3.6	Putrescine carbamoyltransferase	Carbamoylphosphate + putrescine = orthophosphate + *N*-carbamoylputrescine
2.1.4.2	Inosamine-phosphate amidinotransferase	L-Arginine + 1-amino-1-deoxy-*scyllo*-inositol 4-phospha L-ornithine + 1-guanidino-1-deoxy-*scyllo*-inositol 4-phosphate
• 2.3.1.8	Phosphate acetyltransferase	Acetyl-CoA + orthophosphate = CoA + acetylphosphate
• 2.3.1.15	Glycerophosphate acyltransferase	Acyl-CoA + *sn*-glycerol 3-phosphate = CoA + acylglycerol 3-phosphate
• 2.3.1.43	Lecithin--cholesterol acyltransferase	A lecithin + cholesterol = 1-acylglycerophosphocholine + cholesterol ester
2.3.1.46	Homoserine succinyltransferase	Succinyl-CoA + L-homoserine = CoA + *O*-succinyl-L-homoserine
2.3.1.47	7-Oxo-8-aminononanoate synthase	Pimelyl-CoA + L-alanine = 7-oxo-8-aminononanoate + CoA + CO_2
2.3.1.48	Histone acetyltransferase	Acetyl-CoA + histone = CoA + acetylhistone
2.3.1.49	Deacetyl-[citrate-(*pro*-3*S*)-lyase] acetyltransferase	*S*-Acetylphosphopantetheine + deacetyl-[citrate-oxaloacetate-lyase(*pro*-3*S*-CH_2COO^-→acetate)] = phosphopantetheine + [citrate oxaloacetate-lyase(*pro*-3*S*-CH_2COO^-→acetate)]

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2.1.1.44		*S*-Adenosyl-L-methionine:N^{α},N^{α}-dimethyl-L-histidine N^{α}-methyltransferase	Methylhistidine and histidine can also act as methyl acceptors, trimethylhistidine being formed in both cases	di
2.1.1.45		5,10-Methylenetetrahydrofolate:dUMP *C*-methyltransferase		ad, kp
2.1.1.46		*S*-Adenosyl-L-methionine:isoflavone 4′-*O*-methyltransferase		ky
2.1.1.47		*S*-Adenosyl-L-methionine:indolepyruvate *C*-methyltransferase		dd
2.1.1.48		*S*-Adenosyl-L-methionine:rRNA (adenine-6-)-methyltransferase	Also methylates 9-β-D-ribosyl 2,6-diaminopurine to 9-β-D-ribosyl-6-amino-2-methylaminopurine	ip
2.1.1.49		*S*-Adenosyl-L-methionine:tryptamine *N*-methyltransferase	5-Methyltetrahydrofolate can also act as donor	de
2.1.1.50		*S*-Adenosyl-L-methionine:loganate 11-*O*-methyltransferase	Also acts on secologanate. Methylates the 11-carboxyl group of loganate	fh
2.1.1.51		*S*-Adenosyl-L-methionine:rRNA (guanine-1-)-methyltransferase		dg
2.1.1.52		*S*-Adenosyl-L-methionine:rRNA (guanine-2-)-methyltransferase		dg
2.1.1.53		*S*-Adenosyl-L-methionine:putrescine *N*-methyltransferase		fv
2.1.3.5	Oxamic transcarbamylase	Carbamoylphosphate:oxamate carbamoyltransferase		ae
2.1.3.6		Carbamoylphosphate:putrescine carbamoyltransferase		ho
2.1.4.2		L-Arginine:1-amino-1-deoxy-*scyllo*-inositol-4-phosphate amidinotransferase	1D-1-Guanidino-3-amino-1,3-dideoxy-*scyllo*-inositol 6-phosphate, streptamine phosphate and 2-deoxystreptamine phosphate can also act as acceptor; canavanine can act as donor	kt
2.3.1.8	Phosphotransacetylase, Phosphoacylase	Acetyl-CoA:orthophosphate acetyltransferase	Also acts with other short-chain acyl-CoA's	190, 2258 iz
2.3.1.15	Stearyl-CoA→L-α-glycerophosphate transstearylase	Acyl-CoA:*sn*-glycerol-3-phosphate *O*-acyltransferase	Acts only with CoA derivatives of fatty acids of chain length above C-10	1266
2.3.1.43	Lecithin acyltransferase	Lecithin:cholesterol acyltransferase		766a
2.3.1.46	Homoserine *O*-transsuccinylase	Succinyl-CoA:L-homoserine *O*-succinyltransferase		hq
2.3.1.47		Pimelyl-CoA:L-alanine *C*-pimelyltransferase (decarboxylating)	A pyridoxal-phosphate-protein	bt
2.3.1.48		Acetyl-CoA:histone acetyltransferase	A group of enzymes with differing specificity towards histone acceptors	cg
2.3.1.49		*S*-Acetylphosphopantetheine:deacetyl-[citrate-oxaloacetate-lyase(*pro*-3*S*-CH_2COO^{-}→acetate)] *S*-acetyltransferase		in

Number	Recommended Name	Reaction
2.3.1.50	Serine palmitoyltransferase	Palmitoyl-CoA + L-serine = CoA + 3-oxo-D-dihydrosphingosine + CO_2
2.3.1.51	1-Acylglycerophosphate acyltransferase	Acyl-CoA + 1-acyl-*sn*-glycerol 3-phosphate = CoA + 1,2-diacyl-*sn*-glycerol 3-phosphate
2.3.1.52	2-Acylglycerophosphate acyltransferase	Acyl-CoA + 2-acyl-*sn*-glycerol 3-phosphate = CoA + 1,2-diacyl-*sn*-glycerol 3-phosphate
2.3.1.53	Phenylalanine acetyltransferase	Acetyl-CoA + L-phenylalanine = CoA + *N*-acetyl-L-phenylalanine
2.3.1.54	Formate acetyltransferase	Acetyl-CoA + formate = CoA + pyruvate
2.3.1.55	Kanamycin 6′-acetyltransferase	Acetyl-CoA + kanamycin = CoA + $N^{6'}$-acetylkanamycin
2.3.1.56	Aromatic-hydroxylamine acetyltransferase	*N*-Hydroxy-4-acetylaminobiphenyl + *N*-hydroxy-4-aminobiphenyl = *N*-hydroxy-4-aminobiphenyl + *N*-acetoxy-4-aminobiphenyl
2.3.1.57	Putrescine acetyltransferase	Acetyl-CoA + putrescine = CoA + monoacetylputrescine
2.3.1.58	2,3-Diaminopropionate oxalyltransferase	Oxalyl-CoA + L-2,3-diaminopropionate = CoA + N^3-oxalyl-L-2,3-diaminopropionate
2.3.1.59	Gentamicin 2′-acetyltransferase	Acetyl-CoA + gentamicin C_{1a} = CoA + $N^{2'}$-acetylgentamicin C_{1a}
2.3.1.60	Gentamicin 3-acetyltransferase	Acetyl-CoA + gentamicin C = CoA + N^3-acetylgentamicin C
• 2.3.2.1	D-Glutamyltransferase	L(or D)-Glutamine + D-glutamyl-peptide = NH_3 + 5-glutamyl-D-glutamyl-peptide
• 2.3.2.2	γ-Glutamyltransferase	(5-L-Glutamyl)-peptide + an amino acid = peptide + 5-L-glutamyl-amino acid
• 2.3.2.6	Leucyltransferase	L-Leucyl-tRNA + protein = tRNA + L-leucyl-protein
• 2.3.2.8	Arginyltransferase	L-Arginyl-tRNA + protein = tRNA + arginyl-protein
2.3.2.12	Peptidyltransferase	Peptidyl-$tRNA^1$ + aminoacyl-$tRNA^2$ = $tRNA^1$ + peptidyl-aminoacyl-$tRNA^2$
• 2.4.1.38	Glycoprotein β-D-galactosyltransferase	UDPgalactose + 2-acetamido-2-deoxy-D-glucosyl-glycopeptide = UDP + 4-*O*-β-D-galactosyl-2-acetamido-2-deoxy-D-glucosyl-glycopeptide
• *[2.4.1.72*	*Transferred entry: now EC 2.4.2.24 – 1,4-β-D-Xylan synthase]*	
2.4.1.75	UDPgalacturonosyltransferase	UDPgalacturonate + acceptor = UDP + acceptor β-galacturonide
2.4.1.76	UDPglucuronate—bilirubin glucuronosyltransferase	UDPglucuronate + bilirubin = UDP + bilirubin glucuronoside

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2.3.1.50		Palmitoyl-CoA:L-serine *C*-palmitoyltransferase (decarboxylating)	A pyridoxal-phosphate-protein	2294, ag
2.3.1.51		Acyl-CoA:1-acyl-*sn*-glycerol-3-phosphate *O*-acyltransferase	Specific for the transfer of mono- and dienoic fatty-acyl-CoA thioesters	lm
2.3.1.52		Acyl-CoA:2-acyl-*sn*-glycerol-3-phosphate *O*-acyltransferase	Saturated acyl-CoA thioesters are the most effective acyl donors	lm
2.3.1.53		Acetyl-CoA:L-phenylalanine *N*-acetyltransferase	Also acts, more slowly, on L-histidine and L-alanine	ep
2.3.1.54	Pyruvate formate-lyase	Acetyl-CoA:formate *C*-acetyltransferase		ja, ej
2.3.1.55		Acetyl-CoA:kanamycin $N^{6'}$-acetyltransferase	Kanamycin A, kanamycin B, neomycin, gentamicin C_{1a}, gentamicin C_2 and sisomicin are substrates	w, ey
2.3.1.56		*N*-Hydroxy-4-acetylaminobiphenyl:*N*-hydroxy-4-aminobiphenyl *O*-acetyltransferase	Transfers the *N*-acetyl group of some aromatic acethydroxamates to the *O*-position of some aromatic hydroxylamines	n
2.3.1.57		Acetyl-CoA:putrescine *N*-acetyltransferase		ig
2.3.1.58	Oxalyldiaminopropionate synthase	Oxalyl-CoA:L-2,3-diaminopropionate N^3-oxalyltransferase		fj
2.3.1.59	Gentamicin acetyltransferase II	Acetyl-CoA:gentamicin-C_{1a} $N^{2'}$-acetyltransferase	Gentamicin A, sisomicin, tobramycin, paromomycin, neomycin B, kanamycin B and kanamycin C can also act as acceptors	y
2.3.1.60	Gentamicin acetyltransferase I	Acetyl-CoA:gentamicin-C N^3-acetyltransferase	Also acetylates sisomicin	aj
2.3.2.1	D-Glutamyl transpeptidase	Glutamine:D-glutamyl-peptide glutamyltransferase		2626
2.3.2.2	Glutamyl transpeptidase	(5-Glutamyl)-peptide:amino-acid 5-glutamyltransferase		784, 1365
2.3.2.6		L-Leucyl-tRNA:protein leucyltransferase	Also transfers phenylalanyl groups. Requires a monovalent cation. Peptides and proteins containing an *N*-terminal arginine, lysine or histidine residue can act as acceptors	1366, 1367, it
2.3.2.8		L-Arginyl-tRNA:protein arginyltransferase	Requires mercaptoethanol and a monovalent cation. Peptides and proteins containing an *N*-terminal glutamate, aspartate or cystine residue can act as acceptors	2233, 2234, is
2.3.2.12		Peptidyl-tRNA:aminoacyl-tRNA *N*-peptidyltransferase		hu, ka, ht
2.4.1.38	Thyroid galactosyltransferase, UDPgalactose–glycoprotein galactosyltransferase	UDPgalactose:2-acetamido-2-deoxy-D-glucosyl-glycopeptide galactosyltransferase	This enzyme may be a component of EC 2.4.1.22	2246
2.4.1.75	*p*-Nitrophenol conjugating enzyme	UDPgalacturonate β-galacturonosyltransferase (acceptor-unspecific)		ko
2.4.1.76		UDPglucuronate:bilirubin glucuronosyltransferase		do

Number	Recommended Name	Reaction
2.4.1.77	UDPglucuronate bilirubin-glucuronoside glucuronosyl-transferase	UDPglucuronate + bilirubin-glucuronoside = UDP + bilirubin bis-glucuronoside
2.4.1.78	UDPglucose phosphopolyprenol glucosyltransferase	UDPglucose + polyprenol phosphate = UDP + polyprenolphosphate-glucose
2.4.1.79	UDPacetylgalactosamine galactosyl-galactosyl-glucosyl-ceramide β-*N*-acetyl-D-galactosaminyltransferase	UDP-2-acetamido-2-deoxy-D-galactose + D-galactosyl-(1,4)-D-galactosyl-(1,4)-D-glucosylceramide = UDP + 2-acetamido-2-deoxy-D-galactosyl-(1,3)-D-galactosyl-(1,4)-D-galactosyl-(1,4)-D-glucosylceramide
2.4.1.80	UDPglucose ceramide glucosyltransferase	UDPglucose + *N*-acylsphingosine = UDP + D-glucosyl-*N*-acylsphingosine
2.4.1.81	UDPglucose luteolin β-D-glucosyltransferase	UDPglucose + 5,7,3′,4′-tetrahydroxyflavone = UDP + 7-*O*-β-D-glucosyl-5,7,3′,4′-tetrahydroxyflavone
2.4.1.82	Galactinol sucrose galactosyltransferase	1-*O*-α-D-Galactosyl-*myo*-inositol + sucrose = *myo*-inositol + raffinose
2.4.1.83	GDPmannose dolicholphosphate mannosyltransferase	GDPmannose + dolichol phosphate = GDP + dolichol phosphate mannose
2.4.1.84	UDPglucuronate 1,2-diacylglycerol glucuronosyl-transferase	UDPglucuronate + 1,2-diacylglycerol = UDP + 1,2-diacylglycerol 3-D-glucuronoside
2.4.1.85	Cyanohydrin glucosyltransferase	UDPglucose + (*S*)-4-hydroxymandelonitrile = UDP + (*S*)-4-hydroxymandelonitrile β-D-glucoside
2.4.1.86	UDPgalactose glucosaminyl-galactosyl-glucosylceramide β-D-galactosyltransferase	UDPgalactose + 2-acetamido-2-deoxy-D-glucosyl-(1,3)-D-galactosyl-(1,4)-D-glucosylceramide = UDP + D-galactosyl-2-acetamido-2-deoxy-D-glucosyl-(1,3)-D-galactosyl-(1,4)-D-glucosylceramide
2.4.1.87	UDPgalactose galactosyl-glucosaminyl-galactosyl-glucosyl-ceramide α-D-galactosyltransferase	UDPgalactose + D-galactosyl-(1,4)-2-acetamido-2-deoxy-D-glucosyl-(1,3)-D-galactosyl-(1,4)-D-glucosylceramide = UDP + D-galactosyl-D-galactosyl-(1,4)-2-acetamido-2-deoxy-D-glucosyl-(1,3)-D-galactosyl-(1,4)-D-glucosylceramide
2.4.1.88	UDPacetylgalactosamine globoside α-*N*-acetyl-D-galactosaminyltransferase	UDP-2-acetamido-2-deoxy-D-galactose + 2-acetamido-2-deoxy-D-galactosyl-(1,3)-D-galactosyl-(1,4)-D-galactosyl-(1,4)-D-glucosylceramide = UDP + 2-acetamido-2-deoxy-D-galactosyl-2-acetamido-2-deoxy-D-galactosyl-(1,3)-D-galactosyl-(1,4)-D-galactosyl-(1,4)-D-glucosylceramide
2.4.1.89	GDPfucose galactosyl-glucosaminyl-galactosyl-glucosyl-ceramide α-L-fucosyltransferase	GDPfucose + D-galactosyl-(1,4)-2-acetamido-2-deoxy-D-glucosyl-(1,3)-D-galactosyl-(1,4)-D-glucosylceramide = GDP + fucosyl-D-galactosyl-(1,4)-2-acetamido-2-deoxy-D-glucosyl-(1,3)-D-galactosyl-(1,4)-D-glucosylceramide
2.4.1.90	*N*-Acetyllactosamine synthase	UDPgalactose + 2-acetamido-2-deoxy-D-glucose = UDP + 4-*O*-β-D-galactosyl-2-acetamido-2-deoxy-D-glucose
2.4.1.91	UDPglucose flavonol glucosyltransferase	UDPglucose + a flavonol = UDP + flavonol 3-*O*-glucoside
2.4.1.92	UDPacetylgalactosamine (*N*-acetylneuraminyl)-D-galactosyl-D-glucosylceramide acetylgalactosaminyl-transferase	UDP-2-acetamido-2-deoxy-D-galactose + (*N*-acetylneuraminyl)-D-galactosyl-D-glucosylceramide = UDP + 2-acetamido-2-deoxy-D-galactosyl-(*N*-acetylneuraminyl)-D-galactosyl-D-glucosylceramide

Number	Other Name	Basis for classification (Systematic Name)	Comments	Reference
2.4.1.77		UDPglucuronate:bilirubin-glucuronoside glucuronosyltransferase		do
2.4.1.78		UDPglucose:phosphopolyprenol glucosyltransferase	Ficaprenol is the best substrate; other polyprenols act, more slowly	dn
2.4.1.79		UDP-2-acetamido-2-deoxy-D-galactose:D-galactosyl-(1,4)-D-galactosyl-(1,4)-D-glucosylceramide β-N-acetamidodeoxy-D-galactosyltransferase		dh, aq
2.4.1.80		UDPglucose:N-acylsphingosine glucosyltransferase	Sphingosine and dihydrosphingosine can also act as acceptor; CDPglucose can act as donor	s
2.4.1.81	UDPglucose--apigenin β-glucosyltransferase	UDPglucose:5,7,3′,4′-tetrahydroxyflavone β-D-glucosyltransferase	A number of flavones, flavanones and flavonols can function as acceptors	jo
2.4.1.82		1-O-α-D-Galactosyl-myo-inositol:sucrose 6-galactosyltransferase	4-Nitrophenyl-α-D-galactopyranoside can also act as donor. Enzyme also catalyses an exchange reaction between raffinose and sucrose	ez
2.4.1.83		GDPmannose:dolichol-phosphate mannosyltransferase		ah
2.4.1.84		UDPglucuronate:1,2-diacylglycerol 3-glucuronosyltransferase		jc
2.4.1.85		UDPglucose:(S)-4-hydroxymandelonitrile β-D-glucosyltransferase	Also acts on (S)-mandelonitrile	hd
2.4.1.86		UDPgalactose:2-acetamido-2-deoxy-D-glucosyl-(1,3)-D-galactosyl-(1,4)-D-glucosylceramide β-D-galactosyltransferase		p
2.4.1.87		UDPgalactose:D-galactosyl-(1,4)-2-acetamido-2-deoxy-D-glucosyl-(1,3)-D-galactosyl-(1,4)-D-glucosylceramide α-D-galactosyltransferase		q
2.4.1.88		UDP-2-acetamido-2-deoxy-D-galactose:2-acetamido-2-deoxy-D-galactosyl-(1,3)-D-galactosyl-(1,4)-D-galactosyl-(1,4)-D-glucosylceramide α-N-acetamidodeoxy-D-galactosyltransferase		ec
2.4.1.89		GDPfucose:D-galactosyl-(1,4)-2-acetamido-2-deoxy-D-glucosyl-(1,3)-D-galactosyl-(1,4)-D-glucosylceramide α-L-fucosyltransferase		r
2.4.1.90		UDPgalactose:2-acetamido-2-deoxy-D-glucose 4-β-D-galactosyltransferase		cu
2.4.1.91		UDPglucose:flavonol 3-O-glucosyltransferase	Acts on a variety of flavonols, including quercetin and quercetin 7-O-glucoside	jn
2.4.1.92		UDP-2-acetamido-2-deoxy-D-galactose:(N-acetylneuraminyl)-D-galactosyl-D-glucosylceramide acetamidodeoxygalactosyltransferase		bk

Number	Recommended Name	Reaction
2.4.1.93	Inulin fructotransferase (depolymerizing)	Transfers a terminal fructosyl-fructofuranosyl group to the terminal 3-position, forming a cyclic anhydride
2.4.2.24	1,4-β-D-Xylan synthase	UDPxylose + (1,4-β-D-xylan)$_n$ = UDP + (1,4-β-D-xylan)$_{n+1}$
2.4.2.25	UDPapiose- flavone apiosyltransferase	UDPapiose + 7-*O*-β-D-glucosyl-5,7,4′-trihydroxyflavone = UDP + 7-*O*-(β-D-apiofuranosyl-1,2-β-D-glucosyl)-5,7,4′-trihydroxyflavone
2.4.2.26	UDPxylose protein xylosyltransferase	Transfers a D-xylosyl residue from UDPxylose to the serine hydroxyl group of an acceptor protein substrate
• 2.4.99.1	CMP-*N*-acetylneuraminate—galactosyl-glycoprotein sialyltransferase	CMP-*N*-acetylneuraminate + D-galactosyl-glycoprotein = CMP + *N*-acetylneuraminyl-D-galactosyl-glycoprotein
2.4.99.2	CMP-*N*-acetylneuraminate—monosialoganglioside sialyltransferase	CMP-*N*-acetylneuraminate + D-galactosyl-2-acetamido-2-deoxy-D-galactosyl-(*N*-acetylneuraminyl)-D-galactosyl-D-glucosylceramide = CMP + *N*-acetylneuraminyl-D-galactosyl-2-acetamido-2-deoxy-D-galactosyl-(*N*-acetylneuraminyl)-D-galactosyl-D-glucosylceramide
• 2.5.1.2	Thiamin pyridinylase	Thiamin + pyridine = heteropyrithiamin + 4-methyl-5-(2′-hydroxyethyl)-thiazole
• *[2.5.1.12*	*Deleted entry: Glutathione S-alkyltransferase. Now included with EC 2.5.1.18]*	
• *[2.5.1.13*	*Deleted entry: Glutathione S-aryltransferase. Now included with EC 2.5.1.18]*	
• *[2.5.1.14*	*Deleted entry: Glutathione S-aralkyltransferase. Now included with EC 2.5.1.18]*	
2.5.1.18	Glutathione transferase	RX + glutathione = HX + R-S-G
2.5.1.19	3-*enol* Pyruvoylshikimate-5-phosphate synthase	Phospho*enol*pyruvate + shikimate 5-phosphate = orthophosphate + 3-*enol*pyruvoylshikimate 5-phosphate
2.5.1.20	Rubber allyltransferase	(*cis*-1,4-Isoprene)$_n$ diphosphate + isopentenyl diphosphate = pyrophosphate + (*cis*-1,4-isoprene)$_{n+1}$ diphosphate
2.5.1.21	Farnesyltransferase	2 Farnesyl diphosphate = pyrophosphate + presqualene diphosphate
• 2.6.1.1	Aspartate aminotransferase	L-Aspartate + 2-oxoglutarate = oxaloacetate + L-glutamate
• 2.6.1.32	Valine—3-methyl-2-oxovalerate aminotransferase	L-Valine + 3-methyl-2-oxovalerate = 2-oxoisovalerate + L-isoleucine
• *[2.6.1.53*	*Transferred entry: now EC 1.4.1.13, Glutamate synthase (NADPH)]*	
2.6.1.54	Pyridoxamine-phosphate aminotransferase	Pyridoxamine 5′-phosphate + 2-oxoglutarate = pyridoxal 5′-phosphate + D-glutamate

Number	Other Name	Basis for classification (Systematic Name)	Comments	Reference
2.4.1.93	Inulase II	Inulin fructosyl-β-1,2-fructofuranosyl-transferase (cyclizing)	Inulin is depolymerized to di-D-fructofuranose 1,2′-2,3′-dianhydride	ke
2.4.2.24		UDPxylose:1,4-β-D-xylan 4-β-D-xylosyltransferase	Formerly EC 2.4.1.72	125
2.4.2.25		UDPapiose:7-*O*-β-D-glucosyl-5,7,4′-trihydroxyflavone apiofuranosyl-transferase	7-*O*-β-D-Glucosides of a number of flavonoids and of 4-substituted phenols can act as acceptor	gg
2.4.2.26		UDPxylose:protein xylosyl-transferase	Involved in the biosynthesis of chondromucoprotein	ji
2.4.99.1	Sialyltransferase	CMP-*N*-acetylneuraminate:D-galactosyl-glycoprotein *N*-acetyl-neuraminyltransferase		944, 2245, me
2.4.99.2		CMP-*N*-acetylneuraminate:D-galactosyl-2-acetamido-2-deoxy-D-galactosyl-(*N*-acetylneuraminyl)-D-galactosyl-D-glucosylceramide *N*-acetylneuraminyltransferase		lo
2.5.1.2	Pyrimidine transferase, Thiaminase I	Thiamin:base 2-methyl-4-amino-pyrimidine-5-methenyltransferase	Various bases and thiol compounds can act instead of pyridine	699, 1189, lf
2.5.1.18	Glutathione *S*-alkyl-transferase, Glutathione *S*-aryl-transferase, *S*-(Hydroxyalkyl)glutathione lyase Glutathione *S*-aralkyl-transferase	RX:glutathione R-transferase	A group of enzymes of broad specificity. R may be an aliphatic, aromatic or heterocyclic radical; X may be a sulphate, nitrite or halide radical. Also catalyses the addition of aliphatic epoxides and arene oxides to glutathione and the reduction of polyol nitrate by glutathione to polyol and nitrite	gh, cp, co
2.5.1.19		Phospho*enol*pyruvate:shikimate-5-phosphate *enol*pyruvoyltransferase		fn
2.5.1.20	Rubber transferase	$(cis\text{-}1,4\text{-Isoprene})_n$-diphosphate:isopentenyl-diphosphate *cis*-1,4-isoprenyltransferase	Rubber particles act as acceptor	f, ff
2.5.1.21	Presqualene synthase	Farnesyl-diphosphate:farnesyl-diphosphate farnesyltransferase	The polymeric form of the enzyme also catalyses the reduction of presqualene diphosphate by NADPH to squalene	gz
2.6.1.1	Glutamic-oxaloacetic transaminase, Glutamic-aspartic transaminase, Transaminase A	L-Aspartate:2-oxoglutarate aminotransferase	A pyridoxal-phosphate-protein. Acts also on L-tyrosine, L-phenylalanine and L-tryptophan	137, 200, 1087, 2117, cw, fm, ik, ca
2.6.1.32	Valine–isoleucine aminotransferase	L-Valine:3-methyl-2-oxovalerate aminotransferase		1115
2.6.1.54		Pyridoxamine-5′-phosphate:2-oxoglutarate aminotransferase (D-glutamate-forming)	Also acts, more slowly, on pyridoxamine	jv

Number	Recommended Name	Reaction
2.6.1.55	Taurine aminotransferase	Taurine + 2-oxoglutarate = sulphoacetaldehyde + L-glutamate
2.6.1.56	1D-1-Guanidino-3-amino-1,3-dideoxy-*scyllo*-inositol aminotransferase	1D-1-Guanidino-3-amino-1,3-dideoxy-*scyllo*-inositol + pyruvate = 1D-1-guanidino-1-deoxy-3-keto-*scyllo*-inositol + L-alanine
2.6.1.57	Aromatic-amino-acid aminotransferase	An aromatic amino acid + 2-oxoglutarate = an aromatic keto acid + L-glutamate
2.7.1.21 (reinstated)	Thymidine kinase	ATP + thymidine = ADP + thymidine 5′-phosphate
• 2.7.1.45	2-Keto-3-deoxygluconokinase	ATP + 2-keto-3-deoxy-D-gluconate = ADP + 6-phospho-2-keto-3-deoxy-D-gluconate
• 2.7.1.65	*scyllo*-Inosamine kinase	ATP + 1-amino-1-deoxy-*scyllo*-inositol = ADP + 1-amino-1-deoxy-*scyllo*-inositol 4-phosphate
• 2.7.1.72	Streptomycin 6-kinase	ATP + streptomycin = ADP + streptomycin 6-phosphate
• *[2.7.1.75*	*Deleted entry: Thymidine kinase. Now EC 2.7.1.21]*	
2.7.1.82	Ethanolamine kinase	ATP + ethanolamine = ADP + *O*-phosphoethanolamine
2.7.1.83	Pseudouridine kinase	ATP + pseudouridine = ADP + pseudouridine 5′-phosphate
2.7.1.84	Alkyldihydroxyacetone kinase	ATP + *O*-alkyldihydroxyacetone = ADP + *O*-alkyldihydroxyacetone phosphate
2.7.1.85	β-D-Glucoside kinase	ATP + cellobiose = ADP + 6-phospho-β-D-glucosyl-(1,4)-D-glucose
2.7.1.86	NADH kinase	ATP + NADH = ADP + NADPH
2.7.1.87	Streptomycin 3″-kinase	ATP + streptomycin = ADP + streptomycin 3″-phosphate
2.7.1.88	Dihydrostreptomycin-6-phosphate 3′α-kinase	ATP + dihydrostreptomycin 6-phosphate = ADP + dihydrostreptomycin 3′α,6-bisphosphate
2.7.1.89	Thiamin kinase	ATP + thiamin = ADP + thiamin monophosphate
2.7.1.90	Pyrophosphate- fructose-6-phosphate 1-phosphotransferase	Pyrophosphate + D-fructose 6-phosphate = orthophosphate + D-fructose 1,6-bisphosphate
2.7.1.91	Dihydrosphingosine kinase	ATP + D-*erythro*-dihydrosphingosine = ADP + dihydrosphingosine 1-phosphate
2.7.1.92	5-Keto-2-deoxygluconokinase	ATP + 5-keto-2-deoxy-D-gluconate = ADP + 6-phospho-5-keto-2-deoxy-D-gluconate
2.7.1.93	Alkylglycerol kinase	ATP + 1-*O*-alkyl-*sn*-glycerol = ADP + 1-*O*-alkyl-*sn*-glycerol 3-phosphate
2.7.1.94	Monoacylglycerol kinase	ATP + monoacylglycerol = ADP + monoacylglycerol 3-phosphate

Number	Other Name	Basis for classification (Systematic Name)	Comments	Reference
2.6.1.55		Taurine:2-oxoglutarate aminotransferase	A pyridoxal-phosphate-protein. Also acts on D,L-3-aminoisobutyrate, β-alanine and 3-aminopropanesulphonate	jy
2.6.1.56		1D-1-Guanidino-3-amino-1,3-dideoxy-*scyllo*-inositol:pyruvate aminotransferase	L-Glutamate and L-glutamine can also act as amino donor	kq, 2557
2.6.1.57		Aromatic-amino-acid:2-oxoglutarate aminotransferase	A pyridoxal-phosphate-protein. L-Methionine can also act as donor, more slowly; oxaloacetate can act as acceptor. Controlled proteolysis converts the enzyme to EC 2.6.1.1	fm
2.7.1.21		ATP:thymidine 5′-phosphotransferase	Deoxyuridine is also an acceptor, and dGTP is a donor	1795, ei
2.7.1.45		ATP:2-keto-3-deoxy-D-gluconate 6-phosphotransferase		455
2.7.1.65		ATP:1-amino-1-deoxy-*scyllo*-inositol 4-phosphotransferase	Also acts on streptamine, 2-deoxystreptamine and 1D-1-guanidino-3-amino-1,3-dideoxy-*scyllo*-inositol	2556, kq
2.7.1.72	Streptidine kinase	ATP:streptomycin 6-phosphotransferase	dATP can replace ATP and dihydrostreptomycin, streptidine and 2-deoxystreptidine can act as acceptors	2558, kr
2.7.1.82		ATP:ethanolamine *O*-phosphotransferase		kx, jm, by
2.7.1.83		ATP:pseudouridine 5′-phosphotransferase		iu
2.7.1.84		ATP:*O*-alkyldihydroxyacetone phosphotransferase		an
2.7.1.85		ATP:cellobiose 6-phosphotransferase	Phosphorylates a number of β-D-glucosides; GTP, CTP, ITP and UTP can also act as donor	gj
2.7.1.86		ATP:NADH 2′-phosphotransferase	CTP, ITP, UTP and GTP can also act as phosphate donors (in decreasing order of activity)	cm
2.7.1.87		ATP:streptomycin 3″-phosphotransferase	Also phosphorylates dihydrostreptomycin, 3′-deoxydihydrostreptomycin and their 6-phosphates	kr
2.7.1.88		ATP:dihydrostreptomycin-6-phosphate 3′α-phosphotransferase	3′-Deoxydihydrostreptomycin 6-phosphate can also act as acceptor	kr
2.7.1.89		ATP:thiamin phosphotransferase		dk
2.7.1.90	6-Phosphofructokinase (pyrophosphate)	Pyrophosphate:D-fructose-6-phosphate 1-phosphotransferase		hg
2.7.1.91		ATP:D-*erythro*-dihydrosphingosine 1-phosphotransferase		jd, jg
2.7.1.92		ATP:5-keto-2-deoxy-D-gluconate 6-phosphotransferase		c
2.7.1.93		ATP:1-*O*-alkyl-*sn*-glycerol 3-phosphotransferase		hn
2.7.1.94		ATP:monoacylglycerol 3-phosphotransferase	Acts on both 1- and 2-monoacylglycerol	gs, gt

Number	Recommended Name	Reaction
2.7.1.95	Kanamycin kinase	ATP + kanamycin = ADP + kanamycin 3′-phosphate
2.7.2.10	Phosphoglycerate kinase (GTP)	GTP + 3-phospho-D-glycerate = GDP + 3-phospho-D-glyceroyl phosphate
2.7.2.11	Glutamate kinase	ATP + L-glutamate = ADP + γ-L-glutamyl phosphate
2.7.2.12	Acetate kinase (pyrophosphate)	Pyrophosphate + acetate = orthophosphate + acetyl phosphate
• 2.7.3.5	Lombricine kinase	ATP + lombricine = ADP + N^{ω}-phospholombricine
2.7.4.16	Thiamin-monophosphate kinase	ATP + thiamin monophosphate = ADP + thiamin diphosphate
2.7.4.17	3-Phosphoglyceroyl-phosphate–polyphosphate phosphotransferase	3-Phospho-D-glyceroyl phosphate + $(\text{phosphate})_n$ = 3-phosphoglycerate + $(\text{phosphate})_{n+1}$
2.7.6.4	Nucleotide pyrophosphokinase	ATP + nucleoside 5′-monophosphate = AMP + 5′-phosphonucleoside 3′-diphosphate
• 2.7.7.13	Mannose-1-phosphate guanylyltransferase	GTP + α-D-mannose 1-phosphate = pyrophosphate + GDPmannose
• 2.7.7.22	Mannose-1-phosphate guanylyltransferase (GDP)	GDP + D-mannose 1-phosphate = orthophosphate + GDPmannose
2.7.7.44	Glucuronate-1-phosphate uridylyltransferase	UTP + 1-phospho-α-D-glucuronate = pyrophosphate + UDP-D-glucuronate
2.7.7.45	Guanosinetriphosphate guanylyltransferase	2 GTP = pyrophosphate + P^1,P^4-bis(5′-guanosyl) tetraphosphate
2.7.7.46	Gentamicin 2″-nucleotidyltransferase	Nucleoside triphosphate + gentamicin = pyrophosphate + 2″-nucleotidylgentamicin
2.7.7.47	Streptomycin 3″-adenylyltransferase	ATP + streptomycin = pyrophosphate + 3″-adenylylstreptomycin
• 2.7.8.4	Serine-phosphoethanolamine synthase	CDPethanolamine + L-serine = CMP + L-serine-phosphoethanolamine
• 2.7.8.5	Glycerophosphate phosphatidyltransferase	CDPdiacylglycerol + *sn*-glycerol 3-phosphate = CMP + 3-phosphatidyl-phospho-*sn*-glycerol
• 2.7.8.8	Phosphatidylserine synthase	CDPdiacylglycerol + L-serine = CMP + phosphatidylserine
• 2.7.8.10	Sphingosine cholinephosphotransferase	CDPcholine + sphingosine = CMP + sphingosyl-phosphocholine
• 2.7.8.11	CDPdiacylglycerol–inositol phosphatidyltransferase	CDPdiacylglycerol + *myo*-inositol = CMP + *myo*-inositol phosphatide
2.7.9.2	Pyruvate,water dikinase	ATP + pyruvate + H_2O = AMP + phospho*enol*pyruvate + orthophosphate
• 2.8.2.11	Galactosylceramide sulphotransferase	3′-Phosphoadenylylsulphate + a galactosylceramide = adenosine 3′,5′-bisphosphate + galactosylceramidesulphate
2.8.2.13	Psychosine sulphotransferase	3′-Phosphoadenylylsulphate + galactosylsphingosine = adenosine 3′,5′-bisphosphate + psychosine sulphate

Number	Other Name	Basis for classification (Systematic Name)	Comments	Reference
2.7.1.95	Neomycin-kanamycin phosphotransferase	ATP:kanamycin 3′-*O*-phosphotransferase	Also acts on neomycin, paromomycin, neamine, paromamine, vistamycin, and gentamicin A. An enzyme from *Pseudomonas aeruginosa* also acts on butirosin	bo, bn
2.7.2.10		GTP:3-phospho-D-glycerate 1-phosphotransferase		hf
2.7.2.11		ATP:L-glutamate γ-phosphotransferase	Product rapidly cyclizes to 2-pyrrolidone 5-carboxylate and orthophosphate	j
2.7.2.12		Pyrophosphate:acetate phosphotransferase		lz
2.7.3.5		ATP:lombricine N^{ω}-phosphotransferase	Also acts on methylated lombricines such as thalassemine; the specificity varies with the species	1830, cf, dw, kn
2.7.4.16		ATP:thiamin-monophosphate phosphotransferase		ga
2.7.4.17		3-Phospho-D-glyceroyl-phosphate:polyphosphate phosphotransferase		eq, er
2.7.6.4		ATP:nucleoside-5′-monophosphate pyrophosphotransferase	Enzyme acts on the 5′-mono-, di- and triphosphate derivatives of purine nucleosides	lv, lx, ly
2.7.7.13	GTP—mannose-1-phosphate guanylyltransferase	GTP:α-D-mannose-1-phosphate guanylyltransferase	Bacterial enzyme can also use ITP and dGTP as donor	1679, 1904
2.7.7.22	GDPmannose phosphorylase	GDP:D-mannose-1-phosphate guanylyltransferase		348
2.7.7.44		UTP:1-phospho-α-D-glucuronate uridylyltransferase	Also acts slowly with CTP	hm
2.7.7.45		GTP:GTP guanylyltransferase	Also acts to a lesser degree on GDP to form P^1,P^3-bis(5′-guanosyl) triphosphate	kv
2.7.7.46		NTP:gentamicin 2″-nucleotidyltransferase	ATP, dATP, CTP, TTP and GTP can act as donors; kanamycin, tobramycin and sisomicin can also act as acceptors	x, fy
2.7.7.47		ATP:streptomycin 3″-adenylyltransferase	Also acts on spectinomycin	cs
2.7.8.4		CDPethanolamine:L-serine ethanolaminephosphotransferase		39
2.7.8.5		CDPdiacylglycerol:*sn*-glycerol-3--phosphate phosphatidyltransferase		364
2.7.8.8	CDPdiglyceride—serine *O*-phosphatidyltransferase	CDPdiacylglycerol:L-serine *O*-phosphatidyltransferase		1141
2.7.8.10		CDPcholine:sphingosine cholinephosphotransferase		694
2.7.8.11		CDPdiacylglycerol:*myo*-inositol phosphatidyltransferase		1843, 1908, 2072
2.7.9.2	Phospho*enol*pyruvate synthase	ATP:pyruvate,water phosphotransferase	Contains Mn	av, au, aa, aw
2.8.2.11		3′-Phosphoadenylylsulphate:galactosylceramide 3′-sulphotransferase		1474
2.8.2.13		3′-Phosphoadenylylsulphate:galactosylsphingosine sulphotransferase		ge

Number	Recommended Name	Reaction
• 3.1.1.4	Phospholipase A_2	A lecithin + H_2O = 1-acylglycerophosphocholine + an unsaturated fatty acid anion
• 3.1.1.5	Lysophospholipase	A lysolecithin + H_2O = glycerophosphocholine + a fatty acid anion
3.1.1.10 (reinstated)	Tropinesterase	Atropine + H_2O = tropine + tropate
• 3.1.1.32	Phospholipase A_1	A lecithin + H_2O = 2-acylglycerophosphocholine + a fatty acid anion
• 3.1.1.34	Lipoprotein lipase	Triacylglycerol + H_2O = diacylglycerol + a fatty acid anion
3.1.1.40	Orsellinate-depside hydrolase	Orsellinate depside + H_2O = 2 orsellinate
3.1.1.41	Cephalosporin C deacetylase	Cephalosporin C + H_2O = deacetylcephalosporin C + acetate
• 3.1.3.8	3-Phytase	*myo*-Inositol hexakisphosphate + H_2O = D-*myo*-inositol 1,2,4,5,6-pentakisphosphate + orthophosphate
• 3.1.3.11	Fructose-bisphosphatase	D-Fructose 1,6-bisphosphate + H_2O = D-fructose 6-phosphate + orthophosphate
• 3.1.3.26	6-Phytase	*myo*-Inositol hexakisphosphate + H_2O = 1L-*myo*-inositol 1,2,3,4,5-pentakisphosphate + orthophosphate
3.1.3.37	Sedoheptulose-bisphosphatase	Sedoheptulose 1,7-bisphosphate + H_2O = sedoheptulose 7-phosphate + orthophosphate
3.1.3.38	3-Phosphoglycerate phosphatase	D-Glycerate 3-phosphate + H_2O = D-glycerate + orthophosphate
3.1.3.39	Streptomycin-6-phosphatase	Streptomycin 6-phosphate + H_2O = streptomycin + orthophosphate
3.1.3.40	Guanidinodeoxy-*scyllo*-inositol-4-phosphatase	1-Guanidino-1-deoxy-*scyllo*-inositol 4-phosphate + H_2O = 1-guanidino-1-deoxy-*scyllo*-inositol + orthophosphate
3.1.3.41	4-Nitrophenylphosphatase	4-Nitrophenylphosphate + H_2O = 4-nitrophenol + orthophosphate
3.1.3.42	Glycogen-synthase-D phosphatase	Glycogen-synthase D = glycogen-synthase I + orthophosphate
• 3.1.4.2	Glycerophosphocholine phosphodiesterase	L-3-Glycerophosphocholine + H_2O = choline + glycerol 1-phosphate
• 3.1.4.10	Monophosphatidylinositol phosphodiesterase	Monophosphatidylinositol + H_2O = D-*myo*-inositol 1:2-cyclic phosphate + diacylglycerol
• 3.1.4.13	Serine-ethanolamine-phosphate phosphodiesterase	Serine-phosphoethanolamine + H_2O = serine + ethanolamine phosphate

Number	Other Name	Basis for classification (Systematic Name)	Comments	Reference
3.1.1.4	Lecithinase A, Phosphatidase, Phosphatidolipase	Phosphatide 2-acylhydrolase	Also acts on phosphatidylethanolamine, choline plasmalogen and phosphatides, removing the fatty acid attached to the 2-position	498, 534, 662, 854, fx, hv
3.1.1.5	Lecithinase B, Lysolecithinase, Phospholipase B	Lysolecithin acylhydrolase		420, 488, 611, kj
3.1.1.10		Atropine acylhydrolase	Also acts on cocaine and other tropine esters	ci, fw
3.1.1.32		Phosphatidate 1-acylhydrolase		715
3.1.1.34	Clearing factor lipase, Diglyceride lipase, Diacylglycerol lipase	Triacylglycero-protein acyl-hydrolase	Hydrolyses triacylglycerols in chylomicrons and low-density lipoproteins. Also hydrolyses diacylglycerol	630, 814, md, lu, lw
3.1.1.40	Lecanorate hydrolase	Orsellinate-depside hydrolase	Enzyme will only hydrolyse those substrates based on the 2,4-dihydroxy-6-methyl-benzoate structure that also have a free hydroxyl *ortho* to the depside linkage	if
3.1.1.41		Cephalosporin-C acetylhydrolase	Hydrolyses the acetyl ester bond on the 10-position	ce
3.1.3.8		*myo*-Inositol-hexakisphosphate 3-phosphohydrolase		435, 1092
3.1.3.11	Hexosediphosphatase	D-Fructose-1,6-bisphosphate 1-phosphohydrolase	The animal enzyme also acts on sedo-heptulose 1,7-bisphosphate	779, 1634, 1887, bu
3.1.3.26	Phytase, Phytate 6-phosphatase	*myo*-Inositol-hexakisphosphate 6-phosphohydrolase		1092
3.1.3.37		Sedoheptulose-1,7-bisphosphate 1-phosphohydrolase		jz, ha
3.1.3.38		D-Glycerate-3-phosphate phosphohydrolase	Wide specificity, but 3-phosphoglycerate is the best substrate	hc
3.1.3.39		Streptomycin-6-phosphate phosphohydrolase	Also acts on dihydrostreptomycin 3′α,6-bisphosphate and streptidine 6-phosphate	ku, ks
3.1.3.40		1-Guanidino-1-deoxy-*scyllo*-inositol-4-phosphate 4-phospho-hydrolase		ku
3.1.3.41		4-Nitrophenylphosphate phosphohydrolase	A number of other substrates including phenyl phosphate, 4-nitrophenyl sulphate, acetyl phosphate and glycerol phosphate are inactive	g, h
3.1.3.42		[UDPglucose–glycogen glucosyl-transferase-D] phosphohydrolase		a
3.1.4.2		L-3-Glycerophosphocholine glycerophosphohydrolase	Also acts on L-3-glycerophospho-ethanolamine	487, 892, 2579
3.1.4.10		Monophosphatidylinositol inositolphosphohydrolase		674
3.1.4.13		Serine-phosphoethanolamine ethanolaminephosphohydrolase	Acts only on those phosphodiesters that have ethanolamine as a component part of the molecule	844

Number	Recommended Name	Reaction
• 3.1.4.16	2′:3′-Cyclic-nucleotide 2′-phosphodiesterase	Nucleoside 2′:3′-cyclic phosphate + H_2O = nucleoside 3′-phosphate
• 3.1.4.17	3′:5′-Cyclic-nucleotide phosphodiesterase	Nucleoside 3′:5′-cyclic phosphate + H_2O = nucleoside 5′-phosphate
3.1.4.35	3′:5′-Cyclic-GMP phosphodiesterase	Guanosine 3′:5′-cyclic phosphate + H_2O = guanosine 5′-phosphate
3.1.4.36	1:2-Cyclic-inositol-monophosphate phosphodiesterase	D-*myo*-Inositol 1:2-cyclic phosphate + H_2O = D-*myo*-inositol 1-phosphate
3.1.4.37	2′:3′-Cyclic-nucleotide 3′-phosphodiesterase	Nucleoside 2′:3′-cyclic phosphate + H_2O = nucleoside 2′-phosphate
3.1.4.38	Glycerophosphocholine cholinephosphodiesterase	L-3-Glycerophosphocholine + H_2O = glycerol + choline phosphate
3.1.4.39	Alkylglycerophosphoethanolamine phosphodiesterase	1-Alkyl-*sn*-glycero-3-phosphoethanolamine + H_2O = 1-alkyl-*sn*-glycerol 3-phosphate + ethanolamine
3.1.4.40	CMP-*N*-acylneuraminate phosphodiesterase	CMP-*N*-acylneuraminate + H_2O = CMP + *N*-acylneuraminate
• 3.2.1.6	Endo-1,3(4)-β-D-glucanase	Endohydrolysis of 1,3- or 1,4-linkages in β-D-glucans when the glucose residue whose reducing group is involved in the linkage to be hydrolysed is itself substituted at C-3
• *[3.2.1.12*	*Deleted entry: Cycloheptaglucanase. Now included with EC 3.2.1.54]*	
• *[3.2.1.13*	*Deleted entry: Cyclohexaglucanase. Now included with EC 3.2.1.54]*	
• 3.2.1.35	Hyaluronoglucosaminidase	Random hydrolysis of 1,4-linkages between 2-acetamido-2-deoxy-β-D-glucose and D-glucuronate residues in hyaluronate
• 3.2.1.41	Pullulanase	Hydrolysis of 1,6-α-D-glucosidic linkages in pullulan, amylopectin and glycogen, and in the α- and β-amylase limit dextrins of amylopectin and glycogen
• 3.2.1.55	α-L-Arabinofuranosidase	Hydrolysis of terminal non-reducing α-L-arabinofuranoside residues in α-L-arabinosides
• 3.2.1.62	Glycosylceramidase	Glycosyl-*N*-acylsphingosine + H_2O = a sugar + *N*-acylsphingosine
• 3.2.1.68	Isoamylase	Hydrolysis of 1,6-α-D-glucosidic branch linkages in glycogen, amylopectin and their β-limit dextrins
• *[3.2.1.69*	*Deleted entry: Amylopectin 6-glucanohydrolase. Now included with EC 3.2.1.41]*	
• *[3.2.1.79*	*Deleted entry: α-L-Arabinofuranoside hydrolase. Now included with EC 3.2.1.55]*	

Number	Other Name	Basis for classification (Systematic Name)	Comments	Reference
3.1.4.16	2′:3′-Cyclic-nucleoside-monophosphate phosphodiesterase	Nucleoside-2′:3′-cyclic-phosphate 3′-nucleotidohydrolase	Also hydrolyses 3′-nucleoside monophosphates and bis-*p*-nitrophenyl phosphate, but not 3′-deoxynucleotides. Similar reactions are carried out by EC 3.1.4.8 and EC 3.1.4.22	66, 359, 2494
3.1.4.17	3′:5′-Cyclic-AMP phosphodiesterase	3′:5′-Cyclic-nucleotide 5′-nucleotidohydrolase	Acts on 3′:5′-cyclic AMP, 3′:5′-cyclic dAMP, 3′:5′-cyclic IMP, 3′:5′-cyclic GMP and 3′:5′-cyclic CMP	1691, bz
3.1.4.35		3′:5′-Cyclic-GMP 5′-nucleotidohydrolase		fk
3.1.4.36		D-*myo*-Inositol-1:2-cyclic-phosphate 2-inositolphosphohydrolase		be, bf
3.1.4.37		Nucleoside-2′:3′-cyclic-phosphate 2′-nucleotidohydrolase		bp, jk
3.1.4.38		L-3-Glycerophosphocholine cholinephosphohydrolase	No activity on L-3-glycerophosphoethanolamine	b
3.1.4.39	Lysophospholipase D	1-Alkyl-*sn*-glycero-3-phosphoethanolamine ethanolaminehydrolase	Also acts on acyl and choline analogues	lj
3.1.4.40	CMP-sialate hydrolase	CMP-*N*-acylneuraminate *N*-acylneuraminohydrolase		dy
3.2.1.6	Endo-1,3-β-D-glucanase, Laminarinase	1,3-(1,3:1,4)-β-D-Glucan 3(4)-glucanohydrolase	Substrates include laminarin, lichenin and cereal β-D-glucans; different from EC 3.2.1.39	152, 153, 454, 1975, iy
3.2.1.35	Mucinase, Spreading factor, Hyaluronidase, Hyaluronoglucosidase	Hyaluronate 4-glycanohydrolase	Also hydrolyses 1,4-β-glycosidic linkages between *N*-acetylgalactosamine or *N*-acetylgalactosamine sulphate and glucuronic acid in chondroitin, chondroitin 4- and 6-sulphates and dermatan	1602, 1603, 1956, 2598
3.2.1.41	R-enzyme, Limit dextrinase, Debranching enzyme, Amylopectin 6-glucanohydrolase	Pullulan 6-glucanohydrolase		1354, bq
3.2.1.55	Arabinosidase	α-L-Arabinofuranoside arabinofuranohydrolase	The enzyme acts on α-L-arabinofuranosides, α-L-arabinans containing (1,3)- and/or (1,5)-linkages, arabinoxylans and arabinogalactans	1121, jr, dt
3.2.1.62	Phlorizin hydrolase, Phloretin-glucosidase	Glycosyl-*N*-acylsphingosine glycohydrolase	Broad specificity (*cf* EC 3.2.1.45 and EC 3.2.1.46). Also hydrolyses phlorizin to phloretin and glucose	1503, ex
3.2.1.68	Debranching enzyme	Glycogen 6-glucanohydrolase	Distinguished from pullulanase (EC 3.2.1.41) by the inability of isoamylase to attack pullulan, and by limited action on α-limit dextrins. Action of bacterial enzyme on glycogen however is complete in contrast to limited action by pullulanase. 1,6-Linkage hydrolysed only if at a branch point	2693

Number	Recommended Name	Reaction
3.2.1.85	6-Phospho-β-D-galactosidase	A 6-phospho-β-D-galactoside + H_2O = an alcohol + 6-phospho-D-galactose
3.2.1.86	6-Phospho-β-D-glucosidase	6-Phospho-β-D-glucosyl-(1,4)-D-glucose + H_2O = D-glucose 6-phosphate + D-glucose
3.2.1.87	Capsular-polysaccharide galactohydrolase	Random hydrolysis of 1,3-α-D-galactosidic linkages in *Aerobacter aerogenes* capsular polysaccharide
3.2.1.88	β-L-Arabinosidase	β-L-Arabinoside + H_2O = an alcohol + L-arabinose
3.2.1.89	Endo-1,4-β-D-galactanase	Endohydrolysis of 1,4-β-D-galactosidic linkages in arabinogalactans
3.2.1.90	Endo-1,3-β-D-galactanase	Endohydrolysis of 1,3-β-D-galactosidic linkages in arabinogalactans
3.2.1.91	Exo-cellobiohydrolase	Hydrolysis of 1,4-β-D-glucosidic linkages in cellulose and cellotetraose, releasing cellobiose from the non--reducing ends of the chains
3.2.1.92	Exo-β-*N*-acetylmuramidase	Hydrolysis of terminal, non-reducing *N*-acetylmuramic residues
3.2.1.93	α,α-Phosphotrehalase	α,α-Trehalose 6-phosphate + H_2O = D-glucose + D-glucose 6-phosphate
3.2.1.94	Exo-isomaltohydrolase	Hydrolysis of 1,6-α-D-glucosidic linkages in polysaccharides so as to remove successive isomaltose units from the non-reducing ends of the chains
3.2.2.13	1-Methyladenosine nucleosidase	1-Methyladenosine + H_2O = 1-methyladenine + D-ribose
3.2.2.14	NMN nucleosidase	Nicotinamide D-ribonucleotide + H_2O = nicotinamide + D-ribose 5-phosphate
• 3.3.1.2	Adenosylmethionine hydrolase	*S*-Adenosyl-L-methionine + H_2O = methylthioadenosine + L-homoserine
■ 3.3.2.2	Alkenyl-glycerophosphocholine hydrolase	*O*-1-Alk-1-enyl-glycero-3-phosphocholine + H_2O = an aldehyde + glycero-3-phosphocholine
• 3.4.12.4	Peptidylprolylaminoacid carboxypeptidase	Peptidylprolyl-amino acid + H_2O = peptidyl-proline + amino acid
• 3.4.12.10	Glutamate γ-carboxypeptidase	Peptidyl-L-glutamate + H_2O = peptide + L-glutamate
3.4.12.13	γ-Glutamylglutamate carboxypeptidase	Pteroyl-(L-glutamate)$_n$ + H_2O = pteroyl-(L-glutamate)$_{n-1}$ + L-glutamate
3.4.13.12	Methionyl dipeptidase	L-Methionyl-amino acid + H_2O = L-methionine + amino acid
•3.4.22.2	Papain	Preferential cleavage: Arg-, Lys-, Phe-X-(the peptide bond next-but-one to the carboxyl group of phenylalanine); limited hydrolysis of native immunoglobulins
3.4.22.11	Insulinase	Hydrolyses insulin

Number	Other Name	Basis for classification (Systematic Name)	Comments	Reference
3.2.1.85		6-Phospho-β-D-galactoside 6-phosphogalactohydrolase		cv
3.2.1.86		6-Phospho-β-D-glucosyl-(1,4)--D-glucose glucohydrolase	Also hydrolyses several other phospho--β-D-glucosides, but not their non--phosphorylated forms	gk
3.2.1.87	Polysaccharide depolymerase	Aerobacter-capsular-polysaccharide galactohydrolase	Hydrolyses the galactosyl-α-1,3-D-galactose linkages only in the complex substrate, bringing about depolymerization	lq, lr
3.2.1.88		β-L-Arabinoside arabinohydrolase		bj
3.2.1.89	Galactanase, Arabinogalactanase	Arabinogalactan 4-β-D-galactanohydrolase		bv
3.2.1.90	Galactanase, Arabinogalactanase	Arabinogalactan 3-β-D-galactanohydrolase		ct
3.2.1.91	C_1 enzyme	1,4-β-D-Glucan cellobiohydrolase		z, bw
3.2.1.92		Mucopolysaccharide β-*N*-acetylmuramoylexohydrolase		bh
3.2.1.93		α,α-Trehalose-6-phosphate phosphoglucohydrolase		ac
3.2.1.94	Isomalto-dextranase	1,6-α-D-Glucan isomaltohydrolase	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	mb, ma
3.2.2.13		1-Methyladenosine ribohydrolase		jw
3.2.2.14	NMNase	Nicotinamidenucleotide phosphoribohydrolase		d
3.3.1.2	*S*-Adenosylmethionine cleaving enzyme, Methylmethionine--sulphonium-salt hydrolase	*S*-Adenosyl-L-methionine hydrolase	Also hydrolyses methylmethionine sulphonium salt to dimethyl sulphide and homoserine	1563
3.3.2.2		*O*-1-Alk-1-enyl-glycero-3--phosphocholine aldehydohydrolase		583, 2568
3.4.12.4	Proline carboxypeptidase	Peptidylprolyl-amino-acid hydrolase	Releases the *C*-terminal amino acid only if proline is in the penultimate position. Inactivates angiotensin II by this action	2681, 2682
3.4.12.10	*N*-Pteroyl-L-glutamate hydrolase, Conjugase, Carboxypeptidase G	γ-Peptidyl-L-glutamate hydrolase	Peptide can be replaced by substituted pteridines or variety of acyl groups	772, 1168, 1346, 1391, 1895, t
3.4.12.13	γ-Glutamylcarboxypeptidase	Pteroyloligo-L-glutamate hydrolase	A metalloprotein. The smallest substrate hydrolysed is pteroyl-γ-triglutamate	ds
3.4.13.12	Dipeptidase M	L-Methionyl-amino-acid hydrolase		ai
3.4.22.2	Papainase		Papaya latex. Formerly EC 3.4.4.10. The enzyme from the Chinese Gooseberry is similar; it has been called actinidin	133a, 545, 2198, 2210
3.4.22.11			Also hydrolyses globin and casein. Formerly EC 3.4.99.10	ak, o

Number	Recommended Name	Reaction
• *[3.4.99.10*	*Transferred entry: now EC 3.4.22.11, Insulinase]*	
• 3.4.99.22	Staphylokinase	See comments
• 3.5.1.30	5-Aminovaleramidase	5-Amino-*n*-valeramide + H_2O = 5-amino-*n*-valerate + NH_3
• *[3.5.1.37*	*Deleted entry: 4-L-Aspartylglycosylamine amidohydrolase. Identical with EC 3.5.1.26]*	
3.5.1.38	Glutamin-(asparagin-)ase	L-Glutamine + H_2O = L-glutamate + NH_3
3.5.1.39	Alkylamidase	*N*-Methylhexanoamide + H_2O = hexanoate + methylamine
3.5.1.40	Acylagmatine amidase	Benzoylagmatine + H_2O = benzoate + agmatine
3.5.1.41	Chitin deacetylase	Chitin + H_2O = chitosan + acetate
3.5.1.42	Nicotinamidenucleotide amidase	β-Nicotinamide D-ribonucleotide + H_2O = β-nicotinate D-ribonucleotide + NH_3
3.5.1.43	Peptidyl-glutaminase	Peptidyl-L-glutamine + H_2O = peptidyl-L-glutamate + NH_3
3.5.1.44	Glutaminyl-peptide glutaminase	L-Glutaminyl-peptide + H_2O = L-glutamyl-peptide + NH_3
3.5.2.9	5-Oxoprolinase (ATP-hydrolysing)	ATP + 5-oxo-L-proline + 2 H_2O = ADP + orthophosphate + L-glutamate
3.5.3.13	Formiminoglutamate deiminase	*N*-Formimino-L-glutamate + H_2O = *N*-formyl-L-glutamate + NH_3
3.5.3.14	Amidinoaspartase	*N*-Amidino-L-aspartate + H_2O = L-aspartate + urea
• 3.5.4.19	Phosphoribosyl-AMP cyclohydrolase	1-*N*-(5′-phospho-D-ribosyl)-AMP + H_2O = 5-(5′-phospho-D-ribosyl-aminoformimino)-1-(5′ -phosphoribosyl)-imidazole-4-carboxamide
3.5.4.22	1-Pyrroline-4-hydroxy-2-carboxylate deaminase	1-Pyrroline-4-hydroxy-2-carboxylate + H_2O = 2,5-dioxovalerate + NH_3
3.5.4.23	Blasticidin-S deaminase	Blasticidin S + H_2O = deaminohydroxyblasticidin S + NH_3
3.5.4.24	Sepiapterin deaminase	Sepiapterin + H_2O = xanthopterin-B_2 + NH_3

Number	Other Name	Basis for classification (Systematic Name)	Comments	Reference
3.4.99.22	Streptokinase, Plasminokinase		Converts plasminogen to plasmin. In contrast to urokinase, it does not activate ox plasminogen	476a, 756a, 1325a, 2358
3.5.1.30		5-Amino-*n*-valeramide amidohydrolase	The enzyme from *Pseudomonas putida* also acts on 4-aminobutyramide and, more slowly, on 6-aminocaproamide	2380, hi
3.5.1.38		L-Glutamine(L-asparagine) amidohydrolase	L-Asparagine is hydrolysed at 0.8 of the rate of L-glutamine; the D-isomers are also hydrolysed, more slowly	hl
3.5.1.39		*N*-Methylhexanoamide amidohydrolase	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	ap
3.5.1.40		Benzoylagmatine amidohydrolase	Also acts on acetylagmatine, propionylagmatine and bleomycin B_2	kg
3.5.1.41		Chitin amidohydrolase	Hydrolyses the *N*-acetamido groups of 2-acetamido-2-deoxy-D-glucose residues in chitin	e
3.5.1.42		Nicotinamidenucleotide amidohydrolase	Also acts more slowly on β-nicotinamide D-ribonucleoside	df
3.5.1.43	Peptidoglutaminase I	Peptidyl-L-glutamine amidohydrolase	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	ee
3.5.1.44	Peptidoglutaminase II	L-Glutaminyl-peptide amidohydrolase	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	ce
3.5.2.9	Pyroglutamase (ATP-hydrolysing)	5-Oxo-L-proline amidohydrolase (ATP-hydrolysing)		km
3.5.3.13		*N*-Formimino-L-glutamate iminohydrolase		lc
3.5.3.14		*N*-Amidino-L-aspartate amidinohydrolase	Also acts slowly on *N*-amidino-L-glutamate	fq
3.5.4.19	Phosphoribosyl-ATP pyrophosphohydrolase, Phosphoribosyl-AMP pyrophosphorylase	1-*N*-(5′-Phospho-D-ribosyl)-AMP 1,6-hydrolase	The *Neurospora crassa* enzyme also catalyses the reaction of EC 1.1.1.23, and cleaves pyrophosphate from 1-*N*-(5′-phosphoribosyl)-ATP	1619
3.5.4.22		1-Pyrroline-4-hydroxy-2-carboxylate aminohydrolase (decyclizing)		io
3.5.4.23		Blasticidin-S aminohydrolase	Catalyses the deamination of the cytosine moiety of blasticidin S, cytomycin and acetylblasticidin S	*ll*
3.5.4.24		Sepiapterin aminohydrolase	Also acts on isosepiapterin, more slowly	kd

	Number	Recommended Name	Reaction
•	3.6.1.5	Apyrase	ATP + 2 H_2O = AMP + 2 orthophosphate
•	3.6.1.17	Bis(5′-guanosyl)tetraphosphatase	P^1,P^4-Bis(5′-guanosyl) tetraphosphate + H_2O = GTP + GMP
	3.6.1.25	Triphosphatase	Triphosphate + H_2O = pyrophosphate + orthophosphate
	3.6.1.26	CDPdiacylglycerol pyrophosphatase	CDPdiacylglycerol + H_2O = CMP + phosphatidate
	3.7.1.5	Acylpyruvate hydrolase	An acylpyruvate + H_2O = a fatty acid + pyruvate
•	3.8.2.1	Di-isopropyl-fluorophosphatase	Di-isopropyl fluorophosphate + H_2O = di-isopropyl phosphate + fluoride
•	3.10	**ACTING ON SULPHUR-NITROGEN BONDS**	
	3.10.1.2	Cyclamate sulphamidase	Cyclohexylsulphamate + H_2O = cyclohexylamine + sulphate
•	3.11.1.1	Phosphonoacetaldehyde hydrolase	Phosphonoacetaldehyde + H_2O = acetaldehyde + orthophosphate
•	4.1.1.12	Aspartate 4-decarboxylase	L-Aspartate = L-alanine + CO_2
	4.1.1.29 (reinstated)	Cysteine-sulphinate decarboxylase	L-Cysteine sulphinate = hypotaurine + CO_2
	4.1.1.65	Phosphatidylserine decarboxylase	Phosphatidylserine = phosphatidylethanolamine + CO_2
	4.1.1.66	Uracil-5-carboxylate decarboxylase	Uracil 5-carboxylate = uracil + CO_2
	4.1.2.5 (reinstated)	Threonine aldolase	L-Threonine = glycine + acetaldehyde
•	4.1.2.14	Phospho-2-keto-3-deoxy-gluconate aldolase	6-Phospho-2-keto-3-deoxy-D-gluconate = pyruvate + D-glyceraldehyde 3-phosphate
•	4.1.2.15	Phospho-2-keto-3-deoxy-heptonate aldolase	7-Phospho-2-keto-3-deoxy-D-*arabino*heptonate + orthophosphate = phospho*enol*pyruvate + D-erythrose 4-phosphate + H_2O
•	4.1.2.18	2-Keto-3-deoxy-L-pentonate aldolase	2-Keto-3-deoxy-L-pentonate = pyruvate + glycollaldehyde
	4.1.2.28	2-Keto-3-deoxy-D-pentonate aldolase	2-Keto-3-deoxy-D-pentonate = pyruvate + glycollaldehyde
	4.1.2.29	Phospho-5-keto-2-deoxy-gluconate aldolase	6-Phospho-5-keto-2-deoxy-D-gluconate = dihydroxyacetone phosphate + malonate semialdehyc
	4.1.2.30	17α-Hydroxyprogesterone aldolase	17α-Hydroxyprogesterone = 4-androstene-3,17-dione + acetaldehyde

Number	Other Name	Basis for classification (Systematic Name)	Comments	Reference
3.6.1.5	ATP-diphosphatase, Adenosine diphosphatase, ADPase	ATP diphosphohydrolase	Activated by Ca. Also acts on ADP. Acts on other nucleoside triphosphates and diphosphates	1288,1403
3.6.1.17	Diguanosinetetraphosphatase	P^1,P^4-Bis(5′-guanosyl)-tetraphosphate guanylohydrolase		2567
3.6.1.25		Triphosphate phosphohydrolase		es, kh
3.6.1.26		CDPdiacylglycerol phosphatidyl-hydrolase		hb
3.7.1.5		Acylpyruvate acylhydrolase	Acts on formylpyruvate, 2,4-dioxovalerate, 2,4-dioxohexanoate and 2,4-dioxoheptanoate	kw
3.8.2.1	Diisopropylfluorophos-phonate halogenase, Tabunase, DFPase, Di-isopropyl phosphoro-fluoridase	Di-isopropyl-fluorophosphate fluorohydrolase	Acts on other organophosphorus compounds and 'nerve' gases	91, 400 1667
3.10.1.2	Cyclamate sulphamatase	Cyclohexylsulphamate sulphamidase	Also readily hydrolyses aliphatic sulphamates with 3 to 8 carbons	fz
3.11.1.1		(2-Oxoethyl)phosphonate phosphono-hydrolase		ew, 1333
4.1.1.12	Desulphinase	L-Aspartate 4-carboxy-lyase	A pyridoxal-phosphate-protein. Also catalyses the decarboxylation of amino-malonate (formerly listed as EC 4.1.1.10) and the desulphination of L-cysteine-sulphinate to sulphite and alanine	1122, 1773, 1827, 2634
4.1.1.29		L-Cysteine-sulphinate carboxy-lyase	A pyridoxal-phosphate-protein. Also acts on L-cysteate	dl, cn
4.1.1.65		Phosphatidylserine carboxy-lyase		1141
4.1.1.66		Uracil-5-carboxylate carboxy-lyase		gi
4.1.2.5		L-Threonine acetaldehyde-lyase	A pyridoxal-phosphate-protein	du, u, 1295a
4.1.2.14		6-Phospho-2-keto-3-deoxy-D-gluconate D-glyceraldehyde-3-phosphate-lyase	Also acts on 2-oxobutyrate	1590
4.1.2.15	DAHP synthase, KDHP synthetase	7-Phospho-2-keto-3-deoxy-D-*arabino*heptonate D-erythrose-4-phosphate-lyase (pyruvate-phosphorylating)		2255
4.1.2.18	2-Keto-3-deoxy-L-arabonate aldolase	2-Keto-3-deoxy-L-pentonate glycollaldehyde-lyase		465
4.1.2.28		2-Keto-3-deoxy-D-pentonate glycollaldehyde-lyase		ba
4.1.2.29		6-Phospho-5-keto-2-deoxy-D-gluconate malonate-semialdehyde-lyase		c
4.1.2.30		17α-Hydroxyprogesterone acetaldehyde-lyase		gc

Number	Recommended Name	Reaction
4.1.3.29	Decylhomocitrate synthase	Decylhomocitrate + CoA = lauroyl-CoA + H_2O + 2-oxoglutarate
4.2.1.7 (reinstated)	Altronate dehydratase	D-Altronate = 2-keto-3-deoxy-D-gluconate + H_2O
• 4.2.1.8	Mannonate dehydratase	D-Mannonate = 2-keto-3-deoxy-D-gluconate + H_2O
• 4.2.1.10	3-Dehydroquinate dehydratase	3-Dehydroquinate = 3-dehydroshikimate + H_2O
• 4.2.1.20	Tryptophan synthase	L-Serine + indoleglycerol phosphate = L-tryptophan + glyceraldehyde phosphate
• 4.2.1.33	3-Isopropylmalate dehydratase	2-Hydroxy-4-methyl-3-carboxyvalerate = dimethylcitraconate + H_2O
4.2.1.65	3-Cyanoalanine hydratase	L-Asparagine = 3-cyanoalanine + H_2O
4.2.1.66	Cyanide hydratase	Formamide = hydrogen cyanide + H_2O
4.2.1.67	D-Fuconate dehydratase	D-Fuconate = 2-keto-3-deoxy-D-fuconate + H_2O
4.2.1.68	L-Fuconate dehydratase	L-Fuconate = 2-keto-3-deoxy-L-fuconate + H_2O
4.2.1.69	Cyanamide hydratase	Urea = cyanamide + H_2O
• 4.2.99.8	Cysteine synthase	*O*-Acetyl-L-serine + hydrogen sulphide = L-cysteine + acetate
4.2.99.12	Carboxymethyloxysuccinate lyase	Carboxymethyloxysuccinate = fumarate + glycollate
4.3.1.12	Ornithine cyclodeaminase	L-Ornithine = L-proline + NH_3
4.3.1.13	Carbamoylserine ammonia-lyase	*O*-Carbamoyl-L-serine + H_2O = pyruvate + 2 NH_3 + CO_2
4.4.1.6 (reinstated)	*S*-Alkylcysteine lyase	An *S*-alkyl-L-cysteine + H_2O = pyruvate + NH_3 + an alkyl thiol
• *[4.4.1.7*	*Deleted entry: S-(Hydroxyalkyl)glutathione lyase. Now included with EC 2.5.1.18]*	
• *[4.4.1.9*	*Deleted entry: β-Cyanoalanine synthase (reaction due to EC 4.2.99.8)]*	
4.4.1.11	L-Methionine γ-lyase	L-Methionine = methanethiol + NH_3 + 2-oxobutyrate
4.4.1.12	Sulphoacetaldehyde lyase	Sulphoacetaldehyde + H_2O = sulphite + acetate
5.1.1.12	Ornithine racemase	L-Ornithine = D-ornithine

Number	Other Name	Basis for classification (Systematic Name)	Comments	Reference
4.1.3.29		Decylhomocitrate 2-oxoglutarate-lyase (CoA-acylating)	In the reverse reaction decanoyl-CoA can act instead of lauroyl-CoA, but 2-oxoglutarate cannot be replaced by oxalo-acetate or pyruvate	fi
4.2.1.7		D-Altronate hydro-lyase		iq
4.2.1.8		D-Mannonate hydro-lyase		83, hk
4.2.1.10		3-Dehydroquinate hydro-lyase		1625, 1626
4.2.1.20		L-Serine hydro-lyase (adding indoleglycerol-phosphate)	A pyridoxal-phosphate-protein. Also catalyses the conversion of serine and indole to tryptophan and water and of indoleglycerol phosphate to indole and glyceraldehyde phosphate (the latter reaction formerly listed as EC 4.1.2.8)	446
4.2.1.33		2-Hydroxy-4-methyl-3-carboxy-valerate hydro-lyase	The enzyme also hydrates the product to 3-hydroxy-4-methyl-3-carboxyvalerate thus bringing about an interconversion between the two isomers	823
4.2.1.65		L-Asparagine hydro-lyase		am
4.2.1.66		Formamide hydro-lyase		cb
4.2.1.67		D-Fuconate hydro-lyase	Also acts on L-arabonate	bb
4.2.1.68		L-Fuconate hydro-lyase	Also acts, slowly, on D-arabonate	lp
4.2.1.69		Urea hydro-lyase		jj
4.2.99.8		*O*-Acetyl-L-serine acetate-lyase (adding hydrogen-sulphide)	A pyridoxal-phosphate-protein. Also uses some alkyl thiols as replacing agents. Also forms 3-cyanoalanine from cysteine and HCN	167, al, 2426
4.2.99.12		Carboxymethyloxysuccinate glycollate-lyase		gp
4.3.1.12		L-Ornithine ammonia-lyase (cyclizing)	Requires NAD^+	az
4.3.1.13	*O*-Carbamoyl-L-serine deaminase	*O*-Carbamoyl-L-serine ammonia-lyase (pyruvate-forming)	A pyridoxal-phosphate-protein	at
4.4.1.6		*S*-Alkyl-L-cysteine alkylthiol-lyase (deaminating)	A pyridoxal-phosphate-protein. Decomposes *S*-alkyl-L-cysteines by $\alpha\beta$-elimination. Possibly identical, in yeast, with EC 4.4.1.8	gb
4.4.1.11	L-Methioninase	L-Methionine methanethiol-lyase (deaminating)	A pyridoxal-phosphate-protein	en
4.4.1.12		Sulphoacetaldehyde sulpho-lyase	Requires thiamin diphosphate	ls
5.1.1.12		Ornithine racemase		iv

Number	Recommended Name	Reaction
5.1.1.13	Aspartate racemase	L- Aspartate = D-aspartate
5.1.3.14	UDPacetylglucosamine 2-epimerase	UDP-2-acetamido-2-deoxy-D-glucose = UDP-2-acetamido-2-deoxy-D-mannose
5.1.3.15	Glucose-6-phosphate 1-epimerase	α-D-Glucose 6-phosphate = β-D-glucose 6-phosphate
5.1.99.3	Allantoin racemase	(*S*)(+)-Allantoin = (*R*)(-)-allantoin
• 5.2.1.3	Retinal isomerase	all-*trans*-Retinal = 11-*cis*-retinal
• *[5.3.1.2*	*Deleted entry: Erythrose isomerase]*	
5.3.3.8	Dodecenoyl-CoA Δ-isomerase	3-*cis*-Dodecenoyl-CoA = 2-*trans*-dodecenoyl-CoA
5.3.3.9	Prostaglandin-A_1 Δ-isomerase	Prostaglandin A_1 = prostaglandin C_1
5.3.99.2	Prostaglandin R_2 D-isomerase	Prostaglandin R_2 = prostaglandin D_2
5.3.99.3	Prostaglandin R_2 E-isomerase	Prostaglandin R_2 = prostaglandin E_2
• *[5.4.3.1*	*Deleted entry: Ornithine 4,5-aminomutase. This reaction was due to a mixture of EC 5.1.1.12 and 5.4.3.5]*	
5.4.3.5	D-Ornithine 4,5-aminomutase	D-Ornithine = D-*threo*-2,4-diaminopentanoate
5.4.3.6	Tyrosine 2,3-aminomutase	L-Tyrosine = 3-amino-3-(4-hydroxyphenyl)propionate
6.1.1.22	Asparaginyl-tRNA synthetase	ATP + L-asparagine + tRNA = AMP + pyrophosphate + L-asparaginyl-tRNA
6.2.1.12	4-Coumaroyl-CoA synthetase	ATP + 4-coumarate + CoA = AMP + pyrophosphate + 4-coumaroyl-CoA
	• 6.3.1 ACID-AMMONIA (OR AMINE) LIGASES (AMIDE SYNTHETASES)	
6.3.1.6	N^5-Ethyl-L-glutamine synthetase	ATP + L-glutamate + ethylamine = ADP + orthophosphate + N^5-ethyl-L-glutamine
6.3.2.15	UDP-*N*-acetylmuramoyl-L-alanyl-D-glutamyl-*meso*-2,6-diaminopimeloyl-D-alanyl-D-alanine synthetase	ATP + UDP-*N*-acetylmuramoyl-L-alanyl-D-glutamyl-*meso*-2,6-diaminopimelate + D-alanyl-D-alanine = ADP + orthophosphate + UDP-*N*-acetylmuramoyl-L-alanyl-D-glutamyl-*meso*-2,6-diaminopimeloyl-D-alanyl-D-alanine
6.3.2.16	D-Alanyl-alanyl-poly(glycerophosphate) synthetase	ATP + D-alanine + alanyl-poly(glycerophosphate) = ADP + orthophosphate + D-alanyl-alanyl-poly(glycerophosphate)
6.3.3.3	Dethiobiotin synthetase	ATP + 7,8-diaminononanoate + CO_2 = ADP + orthophosphate + dethiobiotin
6.3.4.14	Biotin carboxylase	ATP + biotin-carboxyl-carrier protein + CO_2 = ADP + orthophosphate + carboxybiotin-carboxyl-carrier protei
• 6.5.1.1	Polydeoxyribonucleotide synthetase (ATP)	ATP + (deoxyribonucleotide)$_n$ + (deoxyribonucleotide)$_m$ = AMP + pyrophosphate + (deoxyribonucleotide)$_{n+m}$

Number	Other Name	Basis for classification (Systematic Name)	Comments	Reference
5.1.1.13		Aspartate racemase	Also acts, at half the rate, on L-alanine	ev
5.1.3.14		UDP-2-acetamido-2-deoxy-D-glucose 2-epimerase	The enzyme hydrolyses the product to UDP and 2-acetamido-2-deoxy-D-mannose	ed
5.1.3.15		Glucose-6-phosphate 1-epimerase		lh
5.1.99.3		Allantoin racemase		kl
5.2.1.3	Retinene isomerase	all-*trans*-Retinal 11-*cis-trans*-isomerase	Light shifts the equilibrium towards the *cis*-isomer	1011
5.3.3.8		Dodecenoyl-CoA Δ^3-*cis*–Δ^2-*trans*-isomerase		jf
5.3.3.9		Prostaglandin-A_1 Δ^{10}–Δ^{11}-isomerase		gv
5.3.99.2		Prostaglandin R_2 D-isomerase	Brings about the opening of the peroxide ring	gd
5.3.99.3		Prostaglandin R_2 E-isomerase	Brings about the opening of the peroxide ring	gd
5.4.3.5		D-Ornithine 4,5-aminomutase	A pyridoxal-phosphate-protein, which requires a cobamide coenzyme and dithiothreitol for activity	iv
5.4.3.6		L-Tyrosine 2,3-aminomutase	Requires ATP	et
6.1.1.22		L-Asparagine:tRNA ligase (AMP-forming)		bc
6.2.1.12		4-Coumarate:CoA ligase (AMP-forming)		fb
6.3.1.6	Theanine synthetase	L-Glutamate:ethylamine ligase (ADP-forming)		hy, hx, hz
6.3.2.15		UDP-*N*-acetylmuramoyl-L-alanyl-D-glutamyl-*meso*-2,6-diaminopimelate:D-alanyl-D-alanine ligase (ADP-forming)	The enzyme from *Bacillus subtilis* also catalyses the reverse, hydrolytic, reaction in the presence of ADP, orthophosphate and Co^{2+}. No formation of ATP, however, was observed	bs, as
6.3.2.16	D-Alanine:membrane-acceptor ligase	D-Alanine:alanyl-poly(glycerophosphate) ligase (ADP-forming)	Involved in the synthesis of teichoic acids	hj
6.3.3.3		7,8-Diaminononanoate:carbon-dioxide cyclo-ligase (ADP-forming)	CTP has half the activity of ATP	eo, ln
6.3.4.14		Biotin-carboxyl-carrier-protein:carbon-dioxide ligase (ADP-forming)		bm
6.5.1.1	Polynucleotide ligase, Sealase, DNA repair enzyme, DNA joinase, DNA ligase	Poly(deoxyribonucleotide):poly(deoxyribonucleotide) ligase (AMP-forming)	Catalyses the formation of a phosphodiester at the site of a single-strand break in duplex DNA. RNA can also act as substrate to some extent	166a, 2592 ab

Number	Recommended Name	Reaction
• 6.5.1.2	Polydeoxyribonucleotide synthetase (NAD^+)	NAD^+ + (deoxyribonucleotide)$_n$ + (deoxyribonucleotide)$_m$ = AMP + NMN + (deoxyribonucleotide)$_{n+m}$
6.5.1.3	Polyribonucleotide synthetase (ATP)	ATP + (ribonucleotide)$_n$ + (ribonucleotide)$_m$ = AMP + pyrophosphate + (ribonucleotide)$_{n+m}$

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Number	Other Name	Basis for classification (Systematic Name)	Comments	Reference
6.5.1.2	Polynucleotide ligase (NAD^+), DNA repair enzyme, DNA joinase, DNA ligase	Poly(deoxyribonucleotide):poly(deoxyribonucleotide) ligase (AMP-forming, NMN-forming)	Catalyses the formation of a phosphodiester at the site of a single-strand break in duplex DNA. RNA can also act as substrate to some extent	2735
6.5.1.3	RNA ligase	Poly(ribonucleotide):poly(ribonucleotide) ligase (AMP-forming)	Converts linear RNA to a circular form by transfer of the 5′-phosphate to the 3′-hydroxyl terminus	im

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