EMP Pathway

Enzyme	**Rxn#**	**Gene**	**Reaction**	**EC Number**
Glucokinase	1	*glk*	GLC + ATP -> G6P + ADP	2.7.1.2
Glucokinase	586	*glk*	bDGLC + ATP -> bDG6P + ADP	2.7.1.2
Phosphoglucose isomerase	2	*pgi*	G6P <-> F6P	5.3.1.9
Phosphoglucose isomerase	3	*pgi*	bDG6P <-> G6P	5.3.1.9
Phosphoglucose isomerase	4	*pgi*	bDG6P <-> F6P	5.3.1.9
Aldose 1-epimerase	585	*galM*	bDGLC <-> GLC	5.1.3.3
Glucose-1-phophatase	587	*agp*	G1P -> GLC + PI	3.1.3.10
Phosphofructokinase	5	*pfkA*	F6P + ATP -> FDP + ADP	2.7.1.11
Phosphofructokinase B	624	*pfkB*	F6P + ATP -> FDP + ADP	2.7.1.11
Fructose-1,6-bisphosphatase	6	*fbp*	FDP -> F6P + PI	3.1.3.11
Fructose-1,6-bisphosphatate aldolase	7	*fba*	FDP <-> T3P1 + T3P2	4.1.2.13
Triosphosphate Isomerase	8	*tpiA*	T3P1 <-> T3P2	5.3.1.1
Methylglyoxal synthase		*mgsA*	T3P2 -> MTHGXL + PI	4.2.99.11
Glyceraldehyde-3-phosphate dehydrogenase-A complex	9	*gapA*	T3P1 + PI + NAD <-> NADH + 13PDG	1.2.1.12
Glyceraldehyde-3-phosphate dehydrogenase-C complex	714	*gapC1C2*	T3P1 + PI + NAD <-> NADH + 13PDG	1.2.1.12
Phosphoglycerate kinase	10	*pgk*	13PDG + ADP <-> 3PG + ATP	2.7.2.3
Phosphoglycerate mutase 1	11	*gpmA*	3PG <-> 2PG	5.4.2.1
Phosphoglycerate mutase 2	715	*gpmB*	3PG <-> 2PG	5.4.2.1
Enolase	12	*eno*	2PG <-> PEP	4.2.1.11
Phosphoenolpyruvate synthase	13	*ppsA*	PYR + ATP -> PEP + AMP + PI	2.7.9.2
Pyruvate Kinase II	14	*pykA*	PEP + ADP -> PYR + ATP	2.7.1.40
Pyruvate Kinase I	625	*pykF*	PEP + ADP -> PYR + ATP	2.7.1.40
Pyruvate dehydrogenase	15	*lpdA, aceEF*	PYR + COA + NAD -> NADH + CO2 + ACCOA	1.2.4.1, 2.3.1.12, 1.8.6.4
Glucose-1-phosphate adenylytransferase	108	*glgC*	ATP + G1P -> ADPGLC + PPI	2.7.7.27
Glycogen synthase	685	*glgA*	ADPGLC -> ADP + GLYCOGEN	2.4.1.21
Glycogen phosphorylase	109	*glgP*	GLYCOGEN + PI -> G1P	2.4.1.1
Maltodextrin phosphorylase	686	*malP*	GLYCOGEN + PI -> G1P	2.4.1.1

Pentose Phosphate Pathway

Glucose 6-phosphate-1-dehydrogenase	59	*zwf*	G6P + NADP <-> D6PGL + NADPH	1.1.1.49
6-Phosphogluconolactonase	60	*pgl*	D6PGL -> D6PGC	3.1.1.31
6-Phosphogluconate dehydrogenase (decarboxylating)	61	*gnd*	D6PGC + NADP -> NADPH + CO2 + RL5P	1.1.1.44
Ribose-5-phosphate isomerase A	62	*rpiA*	RL5P <-> R5P	5.3.1.6
Ribose-5-phosphate isomerase B	628	*rpiB*	RL5P <-> R5P	5.3.1.6
Ribulose phosphate 3-epimerase	63	*rpe*	RL5P <-> X5P	5.1.3.1
Transketolase I	64	*tktA*	R5P + X5P <-> T3P1 + S7P	2.2.1.1
Transketolase II	690	*tktB*	R5P + X5P <-> T3P1 + S7P	2.2.1.1
Transketolase I	65	*tktA*	X5P + E4P <-> F6P + T3P1	2.2.1.1
Transketolase II	691	*tktB*	X5P + E4P <-> F6P + T3P1	2.2.1.1
Transaldolase B	629	*talB*	T3P1 + S7P <-> E4P + F6P	2.2.1.2
Phosphogluconate dehydratase	67	*edd*	D6PGC -> 2KD6PG	4.2.1.12
2-Keto-3-deoxy-6-phosphogluconate aldolase	68	*eda*	2KD6PG -> T3P1 + PYR	4.1.2.14

The Tricarboxylic Acid Cycle

Citrate synthase	69	*gltA*	ACCOA + OA -> COA + CIT	4.1.3.7
Aconitase A	70	*acnA*	CIT <-> ICIT	4.2.1.3
Aconitase B	630	*acnB*	CIT <-> ICIT	4.2.1.3
Isocitrate dehydrogenase	71	*icdA*	ICIT + NADP <-> CO2 + NADPH + AKG	1.1.1.42
2-Ketoglutarate dehyrogenase	72	*sucAB, lpdA*	AKG + NAD + COA -> CO2 + NADH + SUCCOA	1.2.4.2,2.3.1.61,1.8.1.4
Succinyl-CoA synthetase	73	*sucCD*	SUCCOA + ADP + PI <-> ATP + COA + SUCC	6.2.1.5
Succinate dehydrogenase	74	*sdhABCD*	SUCC + FAD -> FADH + FUM	1.3.99.1
Fumurate reductase	75	*frdABCD*	FUM + FADH -> SUCC + FAD	1.3.99.1
Fumarase A	76	*fumA*	FUM <-> MAL	4.2.1.2
Fumarase B	692	*fumB*	FUM <-> MAL	4.2.1.2
Fumarase C	693	*fumC*	FUM <-> MAL	4.2.1.2
Malate dehydrogenase	77	*mdh*	MAL + NAD <-> NADH + OA	1.1.1.37

Pyruvate Metabolism

D-Lactate dehydrogenase 1	589	*dld*	PYR + NADH <-> NAD + LAC	1.1.1.28
D-Lactate dehydrogenase 2	78	*ldhA*	PYR + NADH <-> NAD + LAC	1.1.1.28
Acetaldehyde dehydrogenase	79	*adhE*	ACCOA +2 NADH <-> ETH +2 NAD + COA	1.2.1.10
Pyruvate formate lyase 1	80	*pflAB*	PYR + COA -> ACCOA + FOR	2.3.1.54
Pyruvate formate lyase 2	694	*pflCD*	PYR + COA -> ACCOA + FOR	2.3.1.54

Formate hydrogen lyase	81	*fdhF, hycBEFG*	FOR -> CO2	1.2.1.2, 1.12.1.2
Phosphotransacetylase	82	*pta*	ACCOA + PI <-> ACTP + COA	2.3.1.8
Acetate kinase A	83	*ackA*	ACTP + ADP <-> ATP + AC	2.7.2.1
GAR transformylase T	717	*purT*	ACTP + ADP <-> ATP + AC	2.7.2.1
Acetyl-CoA synthetase	590	*acs*	ATP + AC + COA -> AMP + PPI + ACCOA	6.2.1.1
Anaplerotic Reactions				
Phosphoenolpyruvate carboxykinase	84	*pckA*	OA + ATP -> PEP + CO2 + ADP	4.1.1.49
Phosphoenolpyruvate carboxylase	85	*ppc*	PEP + CO2 -> OA + PI	4.1.1.31
Malic enzyme (NADP)	86	*maeB*	MAL + NADP -> CO2 + NADPH + PYR	1.1.1.40
Malic enzyme (NAD)	87	*maeA*	MAL + NAD -> CO2 + NADH + PYR	1.1.1.38
Isocitrate lyase	88	*aceA*	ICIT -> GLX + SUCC	4.1.3.1
Malate synthase A	89	*aceB*	ACCOA + GLX -> COA + MAL	4.1.3.2
Malate synthase G	695	*glcB*	ACCOA + GLX -> COA + MAL	4.1.3.2
Inorganic pyrophosphatase	721	*ppa*	PPI -> 2 PI	3.6.1.1
Respiration				
NADH dehydrogenase II	90	*ndh*	NADH + Q -> NAD + QH2	1.6.5.3
NADH dehydrogenase I	91	*nuoABEFGHIJKLMN*	NADH + Q -> NAD + QH2 +3.5 HEXT	1.6.5.3
Formate dehydrogenase-N	92	*fdnGHI*	FOR + Q -> QH2 + CO2 +2 HEXT	1.2.2.1
Formate dehydrogenase-O	696	*fdoIHG*	FOR + Q -> QH2 + CO2 +2 HEXT	1.2.2.1
Formate dehydrogenase	697	*fdhF*	FOR + Q -> QH2 + CO2 +2 HEXT	1.2.2.1
Pyruvate oxidase	93	*poxB*	PYR + Q -> AC + CO2 + QH2	1.2.2.2
L-Lactate dehydrogenase	94	*lctD*	LLAC + Q -> PYR + QH2	1.1.2.3
D-Lactate dehydrogenase (cyctochrome)		*dld*	LAC + Q -> PYR + QH2	1.1.2.4
Glycerol-3-phosphate dehydrogenase (aerobic)	95	*glpD*	GL3P + Q -> T3P2 + QH2	1.1.99.5
Glycerol-3-phosphate dehydrogenase (anaerobic)	631	*glpABC*	GL3P + Q -> T3P2 + QH2	1.1.99.5
Cytochrome oxidase bo3	96	*cyoABCD, cycBC, cydAB*	QH2 +.5 O2 -> Q +2.5 HEXT	1.10.2.2,1.9.3.1
Cytochrome oxidase bd	97	*cydABCD, appBC, cycBC*	QH2 +.5 O2 -> Q +2 HEXT	1.10.2.2,1.9.3.1
Succinate dehydrogenase complex	98	*sdhABCD*	FADH + Q <-> FAD + QH2	1.3.5.1
Thioredoxin reductase	99	*trxB*	OTHIO + NADPH -> NADP + RTHIO	1.6.4.5
Pyridine nucleotide transhydrogenase	100	*pntAB*	NADPH + NAD -> NADP + NADH	1.6.1.1
Pyridine nucleotide transhydrogenase	100	*pntAB*	NADP + NADH +2 HEXT -> NADPH + NAD	1.6.1.1
Hydrogenase I		*hyaABC*	2 Q+2 HEXT <-> 2 QH2 + H2	1.3.99.1
Hydrogenase 2		*hybAC*	2 Q+2 HEXT <-> 2 QH2 + H2	1.3.99.1
Hydrogenase 3		*hycFGBE*	2 Q+2 HEXT <-> 2 QH2 + H2	1.3.99.1
F0F1-ATPase	101	*atpABCDEFGHI*	ATP <-> ADP + PI +4 HEXT	3.6.1.34
Alternative Carbon Source				
Melibiose				
Alpha-galactosidase (melibiase)	16	*melA*	MELI -> GLC + GLAC	3.2.1.22
Galactose				
Galactokinase	17	*galK*	GLAC + ATP -> GAL1P + ADP	2.7.1.6
Galactose-1-phosphate uridylyltransferase	18	*galT*	GAL1P + UDPG <-> G1P + UDPGAL	2.7.7.10
UDP-glucose 4-epimerase	19	*galE*	UDPGAL <-> UDPG	5.1.3.2
UDP-glucose-1-phosphate uridylyltransferase	20	*galU*	G1P + UTP <-> UDPG + PPI	2.7.7.9
Phosphoglucomutase	21	*pgm*	G1P <-> G6P	5.4.2.2
Lactose				
Periplasmic beta-glucosidase precursor	22	*bglX*	LCTS -> GLC + GLAC	3.2.1.21
Beta-galactosidase (LACTase)	23	*lacZ*	LCTS -> GLC + GLAC	3.2.1.23
Trehalose				
trehalose-6-phosphate hydrolase	24	*treC*	TRE6P -> bDG6P + GLC	3.2.1.93
Sucrose				
Beta-fructofuranosidase	25		SUC6P -> G6P + FRU	3.2.1.26
Fructose				
1-Phosphofructokinase (Fructose 1-phosphate kinase)	26	*fruK*	F1P + ATP -> FDP + ADP	2.7.1.56
Xylose isomerase	27	*xylA*	FRU -> GLC	5.3.1.5
Mannose				

Phosphomannomutase	588	*cpsG*	MAN6P <-> MAN1P	5.4.2.8
Mannose-6-phosphate isomerase	28	*manA*	MAN1P <-> F6P	5.3.1.8
Sorbose				
N-Acetylglucosamine				
N-Acetylglucosamine-6-phosphate deacetylase	31	*nagA*	NAGP -> GA6P + AC	3.5.1.25
Glucosamine				
Glucosamine-6-phosphate deaminase	32	*nagB*	GA6P -> F6P + NH3	5.3.1.10
Sialic Acid				
N-Acetylneuraminate lyase		*nanA*	SLA -> PYR + NAMAN	4.1.3.3
Fucose				
L-Fucose isomerase	33	*fucI*	FUC <-> FCL	5.3.1.-
L-Fuculokinase	34	*fucK*	FCL + ATP -> FCL1P + ADP	2.7.1.51
L-Fuculose phosphate aldolase	35	*fucA*	FCL1P <-> LACAL + T3P2	4.1.2.17
Lactaldehyde reductase	36	*fucO*	LACAL + NADH <-> 12PPD + NAD	1.1.1.77
Aldehyde dehydrogenase A	37	*aldA*	LACAL + NAD <-> LLAC + NADH	1.2.1.22
Aldehyde dehydrogenase B	687	*aldB*	LACAL + NAD <-> LLAC + NADH	1.2.1.22
Aldehyde dehydrogenase	722	*adhC*	LACAL + NAD <-> LLAC + NADH	1.1.1.1
Aldehyde dehydrogenase	725	*adhC*	GLAL + NADH <-> GL + NAD	1.1.1.1
Aldehyde dehydrogenase	723	*adhE*	LACAL + NAD -> LLAC + NADH	1.1.1.1
Aldehyde dehydrogenase	724	*aldH*	LACAL + NAD <-> LLAC + NADH	1.2.1.3
Aldehyde dehydrogenase	726	*aldH*	ACAL + NAD -> AC + NADH	1.2.1.3
Gluconate				
Gluconokinase I	38	*gntV*	GLCN + ATP -> D6PGC + ADP	
Gluconokinase II	626	*gntK*	GLCN + ATP -> D6PGC + ADP	
Rhamnose				
L-Rhamnose isomerase	39	*rhaA*	RMN <-> RML	5.3.1.14
Rhamnulokinase	40	*rhaB*	RML + ATP -> RML1P + ADP	2.7.1.5
Rhamnulose-1-phosphate aldolase	41	*rhaD*	RML1P <-> LACAL + T3P2	4.1.2.19
Arabinose				
L-Arabinose isomerase	42	*araA*	ARAB <-> RBL	5.3.1.4
Arabinose-5-phosphate isomerase	43		RL5P <-> A5P	5.3.1.13
L-Ribulokinase	44	*araB*	RBL + ATP -> RL5P + ADP	2.7.1.16
L-Ribulose-phosphate 4-epimerase	45	*araD*	RL5P <-> X5P	5.1.3.4
Xylose				
Xylose isomerase	46	*xylA*	XYL <-> XUL	5.3.1.5
Xylulokinase	47	*xylB*	XUL + ATP -> X5P + ADP	2.7.1.17
Ribose				
Ribokinase	48	*rbsK*	RIB + ATP -> R5P + ADP	2.7.1.15
Mannitol				
Mannitol-1-phosphate 5-dehydrogenase	49	*mtlD*	MNT6P + NAD <-> F6P + NADH	1.1.1.17
Glucitol				
Glucitol-6-phosphate dehydrogenase	50	*srlD*	GLT6P + NAD <-> F6P + NADH	1.1.1.140
Galacitol				
Galactitol-1-phosphate dehydrogenase	51	*gatD*	GLTL1P + NAD <-> TAG6P + NADH	1.1.1.-
Phosphofructokinase B	52	*pfkB*	TAG6P + ATP -> TAG16P + ADP	2.7.1.11
1-Phosphofructokinase	627	*fruK*	TAG6P + ATP -> TAG16P + ADP	2.7.1.56
Tagatose-6-phosphate kinase	688	*agaZ*	TAG6P + ATP -> TAG16P + ADP	2.7.1.-
Tagatose-bisphosphate aldolase 2	53	*gatY*	TAG16P <-> T3P2 + T3P1	4.1.2.-
Tagatose-bisphosphate aldolase 1	689	*agaY*	TAG16P <-> T3P2 + T3P1	4.1.2.-
Glycerol				
Glycerol kinase	54	*glpK*	GL + ATP -> GL3P + ADP	2.7.1.30
Glycerol-3-phosphate-dehydrogenase-[NAD(P)+]	55	*gpsA*	GL3P + NADP <-> T3P2 + NADPH	1.1.1.94
Nucleosides and Deoxynucleosides				
Phosphopentomutase	56	*deoB*	DR1P <-> DR5P	5.4.2.7
Phosphopentomutase	57	*deoB*	R1P <-> R5P	5.4.2.7
Deoxyribose-phosphate aldolase	58	*deoC*	DR5P -> ACAL + T3P1	4.1.2.4

Aspartate & Asparagine Biosynthesis

Asparate transaminase	102	*aspC*	OA + GLU <-> ASP + AKG	2.6.1.1
Asparagine synthetase (Glutamate dependent)	103	*asnB*	ASP + ATP + GLN -> GLU + ASN + AMP + PPI	6.3.5.4
Aspartate-ammonia ligase	104	*asnA*	ASP + ATP + NH3 -> ASN + AMP + PPI	6.3.1.1

Glutamate and Glutamine Biosynthesis

Glutamate dehydrogenase	105	*gdhA*	AKG + NH3 + NADPH <-> GLU + NADP	1.4.1.4
Glutamate-ammonia ligase	106	*glnA*	GLU + NH3 + ATP -> GLN + ADP + PI	6.3.1.2
Glutamate synthase	107	*gltBD*	AKG + GLN + NADPH -> NADP + 2 GLU	1.4.1.13

Alanine Biosynthesis

Alanine transaminase	110	*alaB*	PYR + GLU <-> AKG + ALA	2.6.1.2
Valine-pyruvate aminotransferase	632	*avtA*	OIVAL + ALA -> PYR + VAL	2.6.1.66
Alanine racemase, biosynthetic	112	*alr*	ALA <-> DALA	5.1.1.1

Alanine racemase, catabolic	113	*dadX*	ALA -> DALA	5.1.1.1
Arginine, Putriscine, and Spermidine Biosynthesis				
N-Acetylglutamate synthase	114	*argA*	GLU + ACCOA -> COA + NAGLU	2.3.1.1
N-Acetylglutamate kinase	115	*argB*	NAGLU + ATP -> ADP + NAGLUYP	2.7.2.8
N-Acetylglutamate phosphate reductase	116	*argC*	NAGLUYP + NADPH <-> NADP + PI + NAGLUSAL	1.2.1.38
Acetylornithine transaminase	117	*argD*	NAGLUSAL + GLU <-> AKG + NAARON	2.6.1.11
Acetylornithine deacetylase	118	*argE*	NAARON -> AC + ORN	3.5.1.16
Carbamoyl phosphate synthetase	119	*carAB*	GLN +2 ATP + CO2 -> GLU + CAP +2 ADP + PI	6.3.5.5
Ornithine carbamoyl transferase 1	120	*argF*	ORN + CAP <-> CITR + PI	2.1.3.3
Ornithine carbamoyl transferase 2	633	*argI*	ORN + CAP <-> CITR + PI	2.1.3.3
Ornithine transaminase		*ygjGH*	ORN + AKG -> GLUGSAL + GLU	2.6.1.13
Argininosuccinate synthase	121	*argG*	CITR + ASP + ATP -> AMP + PPI + ARGSUCC	6.3.4.5
Argininosuccinate lyase	122	*argH*	ARGSUCC <-> FUM + ARG	4.3.2.1
Arginine decarboxylase, biosynthetic	123	*speA*	ARG -> CO2 + AGM	4.1.1.19
Arginine decarboxylase, degradative	634	*adi*	ARG -> CO2 + AGM	4.1.1.19
Agmatinase	124	*speB*	AGM -> UREA + PTRC	3.5.3.11
Ornithine decarboxylase, biosynthetic	125	*speC*	ORN -> PTRC + CO2	4.1.1.17
Ornithine decarboxylase, degradative	635	*speF*	ORN -> PTRC + CO2	4.1.1.17
Adenosylmethionine decarboxylase	126	*speD*	SAM <-> DSAM + CO2	4.1.1.50
Spermidine synthase	127	*speE*	PTRC + DSAM -> SPMD + 5MTA	2.5.1.16
Methylthioadenosine nucleosidase	128		5MTA -> AD + 5MTR	3.2.2.16
5-Methylthioribose kinase	129		5MTR + ATP -> 5MTRP + ADP	2.7.1.100
5-Methylthioribose-1-phosphate isomerase	130		5MTRP <-> 5MTR1P	5.3.1.23
E-1 (Enolase-phosphatase)	131		5MTR1P -> DKMPP	
E-3 (Unknown)	132		DKMPP -> FOR + KMB	
Transamination (Unknown)	133		KMB + GLN -> GLU + MET	
Proline biosynthesis				
γ-Glutamyl kinase	134	*proB*	GLU + ATP -> ADP + GLUP	2.7.2.11
Glutamate-5-semialdehyde dehydrogenase	135	*proA*	GLUP + NADPH -> NADP + PI + GLUGSAL	1.2.1.41
N-Acetylornithine deacetylase	136	*argE*	NAGLUSAL -> GLUGSAL + AC	
Pyrroline-5-carboxylate reductase	137	*proC*	GLUGSAL + NADPH -> PRO + NADP	1.5.1.2
Branched Chain Amino Acid Biosynthesis				
Threonine dehydratase, biosynthetic	138	*ilvA*	THR -> NH3 + OBUT	4.2.1.16
Threonine dehydratase, catabolic	718	*tdcB*	THR -> NH3 + OBUT	4.2.1.16
Acetohydroxybutanoate synthase I	139	*ilvBN*	OBUT + PYR -> ABUT + CO2	4.1.3.18
Acetohydroxybutanoate synthase II	698	*ilvG(12)M*	OBUT + PYR -> ABUT + CO2	4.1.3.18
Acetohydroxybutanoate synthase III	699	*ilvIH*	OBUT + PYR -> ABUT + CO2	4.1.3.18
Acetohydroxy Acid isomeroreductase	140	*ilvC*	ABUT + NADPH -> NADP + DHMVA	1.1.1.86
Dihydroxy acid dehydratase	141	*ilvD*	DHMVA -> OMVAL	4.2.1.9
Branched chain amino acid aminotransferase	142	*ilvE*	OMVAL + GLU <-> AKG + ILE	4.6.1.42
Acetolactate synthase I	143	*ilvBN*	2 PYR -> CO2 + ACLAC	4.1.3.18
Acetolactate synthase II	700	*ilvG(12)M*	2 PYR -> CO2 + ACLAC	4.1.3.18
Acetolactate synthase III	701	*ilvIH*	2 PYR -> CO2 + ACLAC	4.1.3.18
Acetohydroxy acid isomeroreductase	144	*ilvC*	ACLAC + NADPH -> NADP + DHVAL	1.1.1.86
Dihydroxy acid dehydratase	145	*ilvD*	DHVAL -> OIVAL	4.2.1.9
Branched chain amino acid aminotransferase	146	*ilvE*	OIVAL + GLU -> AKG + VAL	2.6.1.42
Valine-pyruvate aminotransferase	636	*avtA*	OIVAL + ALA -> PYR + VAL	2.6.1.66
Isopropylmalate synthase	148	*leuA*	ACCOA + OIVAL -> COA + CBHCAP	4.1.3.12
Isopropylmalate isomerase	149	*leuCD*	CBHCAP <-> IPPMAL	4.2.1.33
3-Isopropylmalate dehydrogenase	150	*leuB*	IPPMAL + NAD -> NADH + OICAP + CO2	1.1.1.85
Branched chain amino acid aminotransferase	151	*ilvE*	OICAP + GLU -> AKG + LEU	2.6.1.42
Aromatic amino acid transaminase	152	*tyrB*	OICAP + GLU -> AKG + LEU	2.6.1.42
Aromatic Amino Acids				
2-Dehydro-3-deoxyphosphoheptonate aldolase F	153	*aroF*	E4P + PEP -> PI + 3DDAH7P	4.1.2.15
2-Dehydro-3-deoxyphosphoheptonate aldolase G	702	*aroG*	E4P + PEP -> PI + 3DDAH7P	4.1.2.15
2-Dehydro-3-deoxyphosphoheptonate aldolase H	154	*aroH*	E4P + PEP -> PI + 3DDAH7P	4.1.2.15
3-Dehydroquinate synthase	155	*aroB*	3DDAH7P -> DQT + PI	4.6.1.3
3-Dehydroquinate dehydratase	156	*aroD*	DQT <-> DHSK	4.2.1.10
Shikimate dehydrogenase	157	*aroE*	DHSK + NADPH <-> SME + NADP	1.1.1.25
Shikimate kinase I	158	*aroK*	SME + ATP -> ADP + SME5P	2.7.1.71
Shikimate kinase II	637	*aroL*	SME + ATP -> ADP + SME5P	2.7.1.71
3-Phosphoshikimate-1-carboxyvinyltransferase	159	*aroA*	SME5P + PEP <-> 3PSME + PI	2.5.1.19
Chorismate synthase	160	*aroC*	3PSME -> PI + CHOR	4.6.1.4
Chorismate mutase 1	161	*pheA*	CHOR -> PHEN	5.4.99.5

Prephenate dehydratase	162	*pheA*	PHEN -> CO2 + PHPYR	4.2.1.51
Aromatic amino acid transaminase	163	*tyrB*	PHPYR + GLU <-> AKG + PHE	2.6.1.57
Chorismate mutase 2	164	*tyrA*	CHOR -> PHEN	5.4.99.5
Prephanate dehydrogenase	165	*tyrA*	PHEN + NAD -> HPHPYR + CO2 + NADH	1.3.1.12
Aromatic amino acid transaminase	166	*tyrB*	HPHPYR + GLU <-> AKG + TYR	2.6.1.5
Asparate transaminase	102	*aspC*	HPHPYR + GLU <-> AKG + TYR	2.6.1.1
Anthranilate synthase	167	*trpDE*	CHOR + GLN -> GLU + PYR + AN	4.1.3.27
Anthranilate synthase component II	168	*trpD*	AN + PRPP -> PPI + NPRAN	2.4.2.18
Phosphoribosyl anthranilate isomerase	169	*trpC*	NPRAN -> CPAD5P	5.3.1.24
Indoleglycerol phosphate synthase	170	*trpC*	CPAD5P -> CO2 + IGP	4.1.1.48
Tryptophan synthase	171	*trpAB*	IGP + SER -> T3P1 + TRP	4.2.1.20
Histidine Biosynthesis				
Phosphoribosyl pyrophosphate synthase	172	*prsA*	R5P + ATP <-> PRPP + AMP	2.7.6.1
ATP phosphoribosyltransferase	173	*hisG*	PRPP + ATP -> PPI + PRBATP	2.4.2.17
Phosphoribosyl-ATP pyrophosphatase	174	*hisIE*	PRBATP -> PPI + PRBAMP	3.6.1.31
Phosphoribosyl-AMP cyclohydrolase	175	*hisIE*	PRBAMP -> PRFP	3.5.4.19
Phosphoribosylformimino-5-amino-1-phosphoribosyl-4-imidazole c	176	*hisA*	PRFP -> PRLP	5.3.1.16
Imidazoleglycerol phosphate synthase	177	*hisFH*	PRLP + GLN -> GLU + AICAR + DIMGP	2.4.2.-
Imidazoleglycerol phosphate dehydratase	178	*hisB*	DIMGP -> IMACP	4.2.1.19
L-Histidinol phosphate aminotransferase	179	*hisC*	IMACP + GLU -> AKG + HISOLP	2.6.1.9
Histidinol phosphatase	180	*hisB*	HISOLP -> PI + HISOL	3.1.3.15
Histidinol dehydrogenase	181	*hisD*	HISOL + 3 NAD -> HIS + 3 NADH	1.1.1.23
Serine & Glycine Biosynthesis				
3-Phosphoglycerate dehydrogenase	182	*serA*	3PG + NAD -> NADH + PHP	1.1.1.95
Phosphoserine transaminase	183	*serC*	PHP + GLU -> AKG + 3PSER	2.6.1.52
Phosphoserine phosphatase	184	*serB*	3PSER -> PI + SER	3.1.3.3
Glycine hydroxymethyltransferase	185	*glyA*	THF + SER -> GLY + METTHF	2.1.2.1
Threonine dehydrogenase	186	*tdh*	THR + COA -> GLY + ACCOA	1.1.1.103
Amino ketobutyrate CoA ligase	638	*kbl*	THR + COA -> GLY + ACCOA	2.3.1.29
Cysteine Biosynthesis				
Sulfate adenylyltransferase	187	*cysDN*	SLF + ATP + GTP -> PPI + APS + GDP + PI	2.7.7.4
Adenylylsulfate kinase	188	*cysC*	APS + ATP -> ADP + PAPS	2.7.1.25
3'-Phospho-adenylylsulfate reductase	189	*cysH*	PAPS + RTHIO -> OTHIO + H2SO3 + PAP	1.8.99.-
Sulfite reductase	190	*cysIJ*	H2SO3 + 3 NADPH <-> H2S + 3 NADP	1.8.1.2
Serine transacetylase	191	*cysE*	SER + ACCOA <-> COA + ASER	2.3.1.30
O-Acetylserine (thiol)-lyase A	192	*cysK*	ASER + H2S -> AC + CYS	4.2.99.8
O-Acetylserine (thiol)-lyase B	639	*cysM*	ASER + H2S -> AC + CYS	4.2.99.8
3' - 5' Bisphosphate nucleotidase	193		PAP -> AMP + PI	3.1.3.7
Threonine and Lysine Biosynthesis				
Aspartate kinase I	194	*thrA*	ASP + ATP <-> ADP + BASP	2.7.2.4
Aspartate kinase II	640	*metL*	ASP + ATP <-> ADP + BASP	2.7.2.4
Aspartate kinase III	641	*lysC*	ASP + ATP <-> ADP + BASP	2.7.2.4
Aspartate semialdehyde dehydrogenase	195	*asd*	BASP + NADPH <-> NADP + PI + ASPSA	1.2.1.11
Homoserine dehydrogenase I	196	*thrA*	ASPSA + NADPH <-> NADP + HSER	1.1.1.3
Homoserine dehydrogenase II	642	*metL*	ASPSA + NADPH <-> NADP + HSER	1.1.1.3
Homoserine kinase	197	*thrB*	HSER + ATP -> ADP + PHSER	2.7.1.39
Threonine synthase	198	*thrC*	PHSER -> PI + THR	4.2.99.2
Dihydrodipicolinate synthase	199	*dapA*	ASPSA + PYR -> D23PIC	4.2.1.52
Dihydrodipicolinate reductase	200	*dapB*	D23PIC + NADPH -> NADP + PIP26DX	1.3.1.26
Tetrahydrodipicolinate succinylase	201	*dapD*	PIP26DX + SUCCOA -> COA + NS2A6O	2.3.1.117
Succinyl diaminopimelate aminotransferase	202	*dapC*	NS2A6O + GLU <-> AKG + NS26DP	2.6.1.17
Succinyl diaminopimelate desuccinylase	203	*dapE*	NS26DP -> SUCC + D26PIM	3.5.1.18
Diaminopimelate epimerase	204	*dapF*	D26PIM <-> MDAP	5.1.1.7
Diaminopimelate decarboxylase	205	*lysA*	MDAP -> CO2 + LYS	4.1.1.20
Lysine decarboxylase 1	591	*cadA*	LYS -> CO2 + CADV	4.1.1.18
Lysine decarboxylase 2	643	*ldcC*	LYS -> CO2 + CADV	4.1.1.18
Methionine Biosynthesis				
Homoserine transsuccinylase	206	*metA*	HSER + SUCCOA -> COA + OSLHSER	2.3.1.46
O-succinlyhomoserine lyase	207	*metB*	OSLHSER + CYS -> SUCC + LLCT	4.2.99.9
Cystathionine-β-lyase	208	*metC*	LLCT -> HCYS + PYR + NH3	4.4.1.8
Adenosyl homocysteinase (Unknown)	209	*Unknown*	HCYS + ADN <-> SAH	3.3.1.1 ?
Cobalamin-dependent methionine synthase	210	*metH*	HCYS + MTHF -> MET + THF	2.1.1.13
Cobalamin-independent methionine synthase	211	*metE*	HCYS + MTHF -> MET + THF	2.1.1.14
S-Adenosylmethionine synthetase	212	*metK*	MET + ATP -> PPI + PI + SAM	2.5.1.6

Amino Acid Degradation

Alanine				
D-Amino acid dehydrogenase	213	*dadA*	DALA + FAD -> PYR + NH3 + FADH	1.4.99.1
Arginine				
Putrescine transaminase	214	*pat*	PTRC + AKG -> GABAL + GLU	
Amino oxidase	703	*tynA*	PTRC -> GABAL + NH3	1.4.3.6
Aminobutyraldehyde dehydrogenase	215	*prr*	GABAL + NAD -> GABA + NADH	1.2.1.19
Aldehyde dehydrogenase	704	*aldH*	GABAL + NAD -> GABA + NADH	1.2.1.3
Aminobutyrate aminotransaminase 1	216	*gabT*	GABA + AKG -> SUCCSAL + GLU	2.6.1.19
Aminobutyrate aminotransaminase 2	705	*goaG*	GABA + AKG -> SUCCSAL + GLU	2.6.1.19
Succinate semialdehyde dehydrogenase –NAD	217	*sad*	SUCCSAL + NAD -> SUCC + NADH	1.2.1.16
Succinate semialdehyde dehydrogenase –NADP	218	*gabD*	SUCCSAL + NADP -> SUCC + NADPH	1.2.1.16
Asparagine				
Asparininase I	219	*ansA*	ASN -> ASP + NH3	3.5.1.1
Asparininase II	706	*ansB*	ASN -> ASP + NH3	3.5.1.1
Aspartate				
Aspartate ammonia-lyase	220	*aspA*	ASP -> FUM + NH3	4.3.1.1
Cysteine				
Tryptophanase	221	*tnaA*	CYS -> PYR + NH3 + H2S	4.1.99.1
L-Cysteine desulfhydrase	222		CYS -> PYR + NH3 + H2S	
Glutamate				
Glutamate decarboxylase A	592	*gadA*	GLU -> GABA + CO2	4.1.1.15
Glutamate decarboxylase B	719	*gadB*	GLU -> GABA + CO2	4.1.1.15
Glutamine				
Glutaminase A	223		GLN -> GLU + NH3	3.5.1.2
Glutaminase B	707		GLN -> GLU + NH3	3.5.1.2
Glycine – Does not utilize				
Histidine – Does not utilize				
Isoleucine – Does not utilize				
Leucine – Does not utilize				
Lysine – Does not utilize				
Methionine – Does not utilize				
Phenylalanine – Does not utilize				
Proline				
Proline dehydrogenase	224	*putA*	PRO + FAD -> FADH + GLUGSAL	1.5.99.8
Pyrroline-5-carboxylate dehydrogenase	225	*putA*	GLUGSAL + NAD -> NADH + GLU	1.5.1.12
Serine				
Serine deaminase 1	226	*sdaA*	SER -> PYR + NH3	4.2.1.13
Serine deaminase 2	644	*sdaB*	SER -> PYR + NH3	4.2.1.13
Trypothanase	227	*tnaA*	SER -> PYR + NH3	
D-Serine deaminase	593	*dsdA*	DSER -> PYR + NH3	4.2.1.14
Threonine				
Threonine dehydrogenase	228	*tdh*	THR + NAD -> 2A3O + NADH	1.1.1.103
Amino ketobutyrate ligase	229	*kbl*	2A3O + COA -> ACCOA + GLY	2.3.1.29
Threonine dehydratase catabolic	594	*tdcB*	THR -> OBUT + NH3	4.2.1.16
Threonine deaminase 1	720	*sdaA*	THR -> OBUT + NH3	
Threonine deaminase 2	366	*sdaB*	THR -> OBUT + NH3	
Tryptophan				
Tryptophanase	230	*tnaA*	TRP <-> INDOLE + PYR + NH3	4.1.99.1
Tyrosine – Does not utilize				
Valine – Does not utilize				

Purine Biosynthesis

Amidophosphoribosyl transferase	231	*purF*	PRPP + GLN -> PPI + GLU + PRAM	2.4.2.14
Phosphoribosylamine-glycine ligase	232	*purD*	PRAM + ATP + GLY <-> ADP + PI + GAR	6.3.4.13
Phosphoribosylglycinamide formyltransferase	233	*purN*	GAR + FTHF -> THF + FGAR	2.1.2.2
GAR transformylase T	234	*purT*	GAR + FOR + ATP -> ADP + PI + FGAR	2.1.2.-
Phosphoribosylformylglycinamide synthetase	235	*purL*	FGAR + ATP + GLN -> GLU + ADP + PI + FGAM	6.3.5.3
Phosphoribosylformylglycinamide cyclo-ligase	236	*purM*	FGAM + ATP -> ADP + PI + AIR	6.3.3.1
Phosphoribosylaminoimidazole carboxylase 1	237	*purK*	AIR + CO2 + ATP <-> NCAIR + ADP + PI	4.1.1.21
Phosphoribosylaminoimidazole carboxylase 2	238	*purE*	NCAIR <-> CAIR	4.1.1.21
Phosphoribosylaminoimidazole-succinocarboxamide synthetase	239	*purC*	CAIR + ATP + ASP <-> ADP + PI + SAICAR	6.3.2.6
5'-Phosphoribosyl-4-(N-succinocarboxamide)-5-aminoimidazole lya	240	*purB*	SAICAR <-> FUM + AICAR	4.3.2.2
AICAR transformylase	241	*purH*	AICAR + FTHF <-> THF + PRFICA	2.1.2.3
IMP cyclohydrolase	242	*purH*	PRFICA <-> IMP	3.5.4.10
Adenylosuccinate synthetase	243	*purA*	IMP + GTP + ASP -> GDP + PI + ASUC	6.3.4.4
Adenylosucinate lyase	244	*purB*	ASUC <-> FUM + AMP	4.3.2.2
IMP dehydrogenase	245	*guaB*	IMP + NAD -> NADH + XMP	1.1.1.205
GMP synthase	246	*guaA*	XMP + ATP + GLN -> GLU + AMP + PPI + GMP	6.3.4.1
GMP reductase	247	*guaC*	GMP + NADPH -> NADP + IMP + NH3	1.6.6.8

Pyrimidine Biosynthesis

Aspartate-carbamoyltransferase	248	*pyrBI*	CAP + ASP -> CAASP + PI	2.1.3.2
Dihydroorotase	249	*pyrC*	CAASP <-> DOROA	3.5.2.3
Dihydroorotate dehydrogenase	250	*pyrD*	DOROA + Q <-> QH2 + OROA	1.3.3.1
Orotate phosphoribosyl transferase	251	*pyrE*	OROA + PRPP <-> PPI + OMP	2.4.2.10
OMP decarboxylase	252	*pyrF*	OMP -> CO2 + UMP	4.1.1.23
CTP synthetase	253	*pyrG*	UTP + GLN + ATP -> GLU + CTP + ADP + PI	6.3.4.2

Salvage Pathways

Adenylate kinase	254	*adk*	ATP + AMP <-> 2 ADP	2.7.4.3
Adenylate kinase		*adk*	GTP + AMP <-> ADP + GDP	2.7.4.3
Adenylate kinase		*adk*	ITP + AMP <-> ADP + IDP	2.7.4.3
Adenylate kinase	255	*adk*	DAMP + ATP <-> ADP + DADP	2.7.4.11
Guanylate kinase	256	*gmk*	GMP + ATP <-> GDP + ADP	2.7.4.8
Deoxyguanylate kinase	257	*gmk*	DGMP + ATP <-> DGDP + ADP	2.7.4.8
Nucleoside-diphosphate kinase	258	*ndk*	GDP + ATP <-> GTP + ADP	2.7.4.6
Nucleoside-diphosphate kinase	259	*ndk*	UDP + ATP <-> UTP + ADP	2.7.4.6
Nucleoside-diphosphate kinase	260	*ndk*	CDP + ATP <-> CTP + ADP	2.7.4.6
Nucleoside-diphosphate kinase	262	*ndk*	DGDP + ATP <-> DGTP + ADP	2.7.4.6
Nucleoside-diphosphate kinase	263	*ndk*	DUDP + ATP <-> DUTP + ADP	2.7.4.6
Nucleoside-diphosphate kinase	264	*ndk*	DCDP + ATP <-> DCTP + ADP	2.7.4.6
Nucleoside-diphosphate kinase	266	*ndk*	DADP + ATP <-> DATP + ADP	2.7.4.6
Nucleoside-diphosphate kinase	267	*ndk*	DTDP + ATP <-> DTTP + ADP	2.7.4.6
AMP Nucleosidse	268	*amn*	AMP -> AD + R5P	3.2.2.4
Adenosine deaminase	269	*add*	ADN -> INS + NH3	3.5.4.4
Deoxyadenosine deaminase	678	*add*	DA -> DIN + NH3	3.5.4.4
Adenine deaminase	270	*yicP*	AD -> NH3 + HYXN	3.5.4.2
Inosine kinase	271	*gsk*	INS + ATP -> IMP + ADP	2.7.1.73
Guanosine kinase	272	*gsk*	GSN + ATP -> GMP + ADP	2.7.1.73
Adenosine kinase		*adk*	ADN + ATP -> AMP + ADP	2.7.1.20
Adenine phosphoryltransferase	273	*apt*	AD + PRPP -> PPI + AMP	2.4.2.7
Xanthine-guanine phosphoribosyltransferase	274	*gpt*	XAN + PRPP -> XMP + PPI	2.4.2.22
Xanthine-guanine phosphoribosyltransferase	275	*gpt*	HYXN + PRPP -> PPI + IMP	2.4.2.22
Hypoxanthine phosphoribosyltransferase	645	*hpt*	HYXN + PRPP -> PPI + IMP	2.4.2.8
Xanthine-guanine phosphoribosyltransferase	276	*gpt*	GN + PRPP -> PPI + GMP	2.4.2.22
Hypoxanthine phosphoribosyltransferase	646	*hpt*	GN + PRPP -> PPI + GMP	2.4.2.8
Xanthosine phosphorylase	277	*xapA*	DIN + PI <-> HYXN + DR1P	2.4.2.1
Purine nucleotide phosphorylase	647	*deoD*	DIN + PI <-> HYXN + DR1P	2.4.2.1
Xanthosine phosphorylase	278	*xapA*	DA + PI <-> AD + DR1P	2.4.2.1
Purine nucleotide phosphorylase	648	*deoD*	DA + PI <-> AD + DR1P	2.4.2.1
Xanthosine phosphorylase	279	*xapA*	DG + PI <-> GN + DR1P	2.4.2.1
Purine nucleotide phosphorylase	649	*deoD*	DG + PI <-> GN + DR1P	2.4.2.1
Xanthosine phosphorylase	280	*xapA*	HYXN + R1P <-> INS + PI	2.4.2.1
Purine nucleotide phosphorylase	650	*deoD*	HYXN + R1P <-> INS + PI	2.4.2.1
Xanthosine phosphorylase	281	*xapA*	AD + R1P <-> PI + ADN	2.4.2.1
Purine nucleotide phosphorylase	651	*deoD*	AD + R1P <-> PI + ADN	2.4.2.1
Xanthosine phosphorylase	282	*xapA*	GN + R1P <-> PI + GSN	2.4.2.1
Purine nucleotide phosphorylase	652	*deoD*	GN + R1P <-> PI + GSN	2.4.2.1
Xanthosine phosphorylase	283	*xapA*	XAN + R1P <-> PI + XTSN	2.4.2.1
Purine nucleotide phosphorylase	653	*deoD*	XAN + R1P <-> PI + XTSN	2.4.2.1
Uridine phosphorylase	284	*udp*	URI + PI <-> URA + R1P	2.4.2.3
Thymidine (deoxyuridine) phosphorylase	285	*deoA*	DU + PI <-> URA + DR1P	2.4.2.4
Purine nucleotide phosphorylase	654	*deoD*	DU + PI <-> URA + DR1P	2.4.2.4
Thymidine (deoxyuridine) phosphorylase	286	*deoA*	DT + PI <-> THY + DR1P	2.4.2.4
Cytidylate kinase	287	*cmkA*	DCMP + ATP <-> ADP + DCDP	2.7.4.14
Cytidylate kinase	288	*cmkA*	CMP + ATP <-> ADP + CDP	2.7.4.14
Cytidylate kinase	265	*cmkB*	DCMP + ATP <-> ADP + DCDP	2.7.4.14
Cytidylate kinase	261	*cmkB*	CMP + ATP <-> ADP + CDP	2.7.4.14
Cytidylate kinase	729	*cmkA*	UMP + ATP <-> ADP + UDP	2.7.4.14
Cytidylate kinase	730	*cmkB*	UMP + ATP <-> ADP + UDP	2.7.4.14
dTMP kinase	289	*tmk*	DTMP + ATP <-> ADP + DTDP	2.7.4.9
Uridylate kinase	290	*pyrH*	UMP + ATP <-> UDP + ADP	2.1.4.-
Uridylate kinase	291	*pyrH*	DUMP + ATP <-> DUDP + ADP	2.1.4.-
Thymidine (deoxyuridine) kinase	292	*tdk*	DU + ATP -> DUMP + ADP	2.7.1.21
Uracil phosphoribosyltransferase	293	*upp*	URA + PRPP -> UMP + PPI	2.4.2.9
Cytosine deaminase	294	*codA*	CYTS -> URA + NH3	3.5.4.1
Uridine kinase	295	*udk*	URI + GTP -> GDP + UMP	2.7.1.48
Cytodine kinase	296	*udk*	CYTD + GTP -> GDP + CMP	2.7.1.48
CMP glycosylase	297		CMP -> CYTS + R5P	3.2.2.10
Cytidine deaminase	298	*cdd*	CYTD -> URI + NH3	3.5.4.5
Thymidine (deoxyuridine) kinase	299	*tdk*	DT + ATP -> ADP + DTMP	2.7.1.21

dCTP deaminase	300	*dcd*	DCTP -> DUTP + NH3	3.5.4.13
Cytidine deaminase	301	*cdd*	DC -> NH3 + DU	3.5.4.5
5'-Nucleotidase	302	*ushA*	DUMP -> DU + PI	3.1.3.5
5'-Nucleotidase	303	*ushA*	DTMP -> DT + PI	3.1.3.5
5'-Nucleotidase	304	*ushA*	DAMP -> DA + PI	3.1.3.5
5'-Nucleotidase	305	*ushA*	DGMP -> DG + PI	3.1.3.5
5'-Nucleotidase	306	*ushA*	DCMP -> DC + PI	3.1.3.5
5'-Nucleotidase	307	*ushA*	CMP -> CYTD + PI	3.1.3.5
5'-Nucleotidase	308	*ushA*	AMP -> PI + ADN	3.1.3.5
5'-Nucleotidase	309	*ushA*	GMP -> PI + GSN	3.1.3.5
5'-Nucleotidase	310	*ushA*	IMP -> PI + INS	3.1.3.5
5'-Nucleotidase	311	*ushA*	XMP -> PI + XTSN	3.1.3.5
5'-Nucleotidase	312	*ushA*	UMP -> PI + URI	3.1.3.5
Ribonucleoside-diphosphate reductase	313	*nrdAB*	ADP + RTHIO -> DADP + OTHIO	1.17.4.1
Ribonucleoside-diphosphate reductase	314	*nrdAB*	GDP + RTHIO -> DGDP + OTHIO	1.17.4.1
Ribonucleoside-triphosphate reductase	315	*nrdD*	ATP + RTHIO -> DATP + OTHIO	1.17.4.2
Ribonucleoside-triphosphate reductase	316	*nrdD*	GTP + RTHIO -> DGTP + OTHIO	1.17.4.2
Ribonucleoside-diphosphate reductase	317	*nrdAB*	CDP + RTHIO -> DCDP + OTHIO	1.17.4.1
Ribonucleoside-diphosphate reductase II	655	*nrdEF*	CDP + RTHIO -> DCDP + OTHIO	
Ribonucleoside-diphosphate reductase	318	*nrdAB*	UDP + RTHIO -> DUDP + OTHIO	1.17.4.1
Ribonucleoside-triphosphate reductase	319	*nrdD*	CTP + RTHIO -> DCTP + OTHIO	1.17.4.2
Ribonucleoside-triphosphate reductase	320	*nrdD*	UTP + RTHIO -> OTHIO + DUTP	1.17.4.2
dUTP pyrophosphatase	321	*dut*	DUTP -> PPI + DUMP	3.6.1.23
Thymidilate synthetase	322	*thyA*	DUMP + METTHF -> DHF + DTMP	2.1.1.45
Nucleoside triphosphatase	595	*mutT*	GTP -> GSN + 3 PI	3.6.1.-
Nucleoside triphosphatase	596	*mutT*	DGTP -> DG + 3 PI	3.6.1.-
Deoxyguanosinetriphosphate triphophohydrolase	597	*dgt*	DGTP -> DG + 3 PI	3.1.5.1
Deoxyguanosinetriphosphate triphophohydrolase	598	*dgt*	GTP -> GSN + 3 PI	3.1.5.1

One Carbon Metabolism

Glycine cleavage system (Multi-component system)	323	*gcvHTP, lpdA*	GLY + THF + NAD -> METTHF + NADH + CO2 + NH3	Multi-Component System: 1.4.4.2, 2.1.2.10
Formyl tetrahydrofolate deformylase	325	*purU*	FTHF -> FOR + THF	3.5.1.10
Methylene tetrahydrofolate reductase	326	*metF*	METTHF + NADH -> NAD + MTHF	1.7.99.5
Methylene THF dehydrogenase	327	*folD*	METTHF + NADP <-> METHF + NADPH	1.5.1.5
Methenyl tetrahydrofolate cyclehydrolase	328	*folD*	METHF <-> FTHF	3.5.4.9

Membrane Lipid Biosynthesis

Acetyl-CoA carboxyltransferase	330	*accABD*	ACCOA + ATP + CO2 <-> MALCOA + ADP + PI	6.4.1.2, 6.3.4.14
Malonyl-CoA-ACP transacylase	331	*fabD*	MALCOA + ACP <-> MALACP + COA	2.3.1.39
Malonyl-ACP decarboxylase	332	*fadB*	MALACP -> ACACP + CO2	2.3.1.41
Acetyl-CoA-ACP transacylase	333	*fabH*	ACACP + COA <-> ACCOA + ACP	2.3.1.41

β-Ketoacyl-ACP synthase (C12,0)		*fab*	ACACP +5 MALACP +10 NADPH -> 10 NADP + C120ACP +5 CO2 +5 ACP	
β-Ketoacyl-ACP synthase (C14,0)		*fab*	ACACP +6 MALACP +12 NADPH -> 12 NADP + C140ACP +6 CO2 +6 ACP	
β-Ketoacyl-ACP synthase I (C14,1)		*fab*	ACACP +6 MALACP +11 NADPH -> 11 NADP + C141ACP +6 CO2 +6 ACP	
β-Ketoacyl-ACP synthase I (C16,0)		*fab*	ACACP +7 MALACP +14 NADPH -> 14 NADP + C160ACP +7 CO2 +7 ACP	
β-Ketoacyl-ACP synthase I (C16,1)		*fab*	ACACP +7 MALACP +13 NADPH -> 13 NADP + C161ACP +7 CO2 +7 ACP	
β-Ketoacyl-ACP synthase I (C18,1)		*fab*	ACACP +8 MALACP +15 NADPH -> 15 NADP +1 C181ACP +8 CO2 +8 ACP	

Glycerol-3-phosphate dehydrogenase	341	*gpsA*	NADPH + T3P2 <-> GL3P + NADP	1.1.1.94

Acyltransferase		*pls*	GL3P +0.035 C140ACP +0.102 C141ACP +0.717 C160ACP +0.142 C161ACP +1.004 C181ACP -> 2 ACP + PA	

CDP-Diacylglycerol synthetase	344	*cdsA*	PA + CTP <-> CDPDG + PPI	2.7.7.41
CDP-Diacylglycerol pyrophosphatase	600	*cdh*	CDPDG -> CMP + PA	3.6.1.26
Phosphatidylserine synthase	345	*pssA*	CDPDG + SER <-> CMP + PS	2.7.8.8
Phosphatidylserine decarboxylase	346	*psd*	PS -> PE + CO2	4.1.1.65
Phosphatidylglycerol phosphate synthase	347	*pgsA*	CDPDG + GL3P <-> CMP + PGP	2.7.8.5
Phosphatidylglycerol phosphate phosphatase A	348	*pgpA*	PGP -> PI + PG	3.1.3.27
Phosphatidylglycerol phosphate phosphatase B	708	*pgpB*	PGP -> PI + PG	3.1.3.27

Cardiolipin synthase	349	*cls*	2 PG <-> CL + GL	2.7.8.?

Fatty Acid Metabolism

Acetyl-CoA C-acetyltransferase	606	*atoB*	2 ACCOA <-> COA + AACCOA	2.3.1.9
β-Ketoacyl-ACP synthase (C14,0)		*fab*	C140 + ATP +7 COA +7 FAD +7 NAD -> AMP + PPI +7 FADH +7 NADH +7 ACCOA	
β-Ketoacyl-ACP synthase I (C14,1)		*fab*	C160 + ATP +8 COA +8 FAD +8 NAD -> AMP + PPI +8 FADH +8 NADH +8 ACCOA	
β-Ketoacyl-ACP synthase I (C16,0)		*fab*	C180 + ATP +9 COA +9 FAD +9 NAD -> AMP + PPI +9 FADH +9 NADH +9 ACCOA	

Isoprenoid Biosynthesis

Isoprenyl-pyrophosphate synthesis pathway	350 (657-663)		T3P1 + PYR + 2 NADPH + ATP -> IPPP + ADP + 2 NADP + CO2	8 rxns
Isoprenyl pyrophosphate isomerase	351		IPPP -> DMPP	5.3.3.2
Farnesyl pyrophosphate synthetase	352	*ispA*	DMPP + IPPP -> GPP + PPI	2.5.1.1
Geranyltranstransferase	353	*ispA*	GPP + IPPP -> FPP + PPI	2.5.1.10
Octoprenyl pyrophosphate synthase (5 reactions)	354(664-	*ispB*	5 IPPP + FPP -> OPP + 5 PPI	2.5.1.-
Undecaprenyl pyrophosphate synthase (8 reactions)	355(668-675)		8 IPPP + FPP -> UDPP + 8 PPI	2.5.1.31

Quinone Biosynthesis

Ubiquinone

Chorismate pyruvate-lyase	356	*ubiC*	CHOR -> 4HBZ + PYR	4.1.3.27
Hydroxybenzoate octaprenyltransferase	357	*ubiA*	4HBZ + OPP -> O4HBZ + PPI	2.5.1.-
Octaprenyl-hydroxybenzoate decarboxylase	358	*ubiD, ubiX*	O4HBZ -> CO2 + 2OPPP	4.1.1.-
2-Octaprenylphenol hydroxylase	359	*ubiB*	2OPPP + O2 -> 2O6H	1.13.14.-
Methylation reaction	361		2O6H + SAM -> 2OPMP + SAH	2.1.1.-
2-Octaprenyl-6-methoxyphenol hydroxylase	362	*ubiH*	2OPMP + O2 -> 2OPMB	1.14.3.-
2-Octaprenyl-6-methoxy-1,4-benzoquinone methylase	364	*ubiE*	2OPMB + SAM -> 2OPMMB + SAH	2.1.1.-
2-Octaprenyl-3-methyl-6-methoxy-1,4-benzoquinone hydroxylase	365	*ubiF*	2OPMMB + O2 -> 2OMHMB	1.14.13.-
3-Dimethylubiquinone 3-methyltransferase	367	*ubiG*	2OMHMB + SAM -> QH2 + SAH	2.1.1.64

Menaquinone

Isochorismate synthase 1	368	*menF*	CHOR -> ICHOR	5.4.99.6
α-Ketoglutarate decarboxylase	369	*menD*	AKG + TPP -> SSALTPP + CO2	4.1.1.71
SHCHC synthase	370	*menD*	ICHOR + SSALTPP -> PYR + TPP + SHCHC	
O-Succinylbenzoate-CoA synthase	371	*menC*	SHCHC -> OSB	
O-Succinylbenzoic acid-CoA ligase	372	*menE*	OSB + ATP + COA -> OSBCOA + AMP + PPI	6.2.1.26
Naphthoate synthase	373	*menB*	OSBCOA -> DHNA + COA	4.1.3.36
1,4-Dihydroxy-2-naphthoate octaprenyltransferase	374	*menA*	DHNA + OPP -> DMK + PPI + CO2	
S-Adenosylmethionine-2-DMK methyltransferase	375	*menG*	DMK + SAM -> MK + SAH	

Enterochelin Biosynthesis

Isochorismate synthase 2	607	*entC*	CHOR -> ICHOR	5.4.99.6
Isochorismatase	608	*entB*	ICHOR <-> 23DHDHB + PYR	3.3.2.1
2,3-Dihydo-2,3-dihydroxybenzoate dehydrogenase	609	*entA*	23DHDHB + NAD <-> 23DHB + NADH	1.3.1.28
ATP-dependent activation of 2,3-dihydroxybenzoate	610	*entE*	23DHB + ATP <-> 23DHBA + PPI	6.-.-.-
ATP-dependent serine activating enzyme	611	*entF*	SER + ATP <-> SERA + PPI	2.7.7.-
Enterochelin synthetase	612	*entD*	3 SERA +3 23DHBA -> ENTER +6 AMP	6.-.-.-

Riboflavin Biosynthesis

GTP cyclohydrolase II	376	*ribA*	GTP -> D6RP5P + FOR + PPI	3.5.4.25
Pryimidine deaminase	377	*ribD*	D6RP5P -> A6RP5P + NH3	3.5.4.26
Pyrimidine reductase	378	*ribD*	A6RP5P + NADPH -> A6RP5P2 + NADP	1.1.1.193
Pyrimidine phosphatase	379		A6RP5P2 -> A6RP + PI	
3,4 Dihydroxy-2-butanone-4-phosphate synthase	380	*ribB*	RL5P -> DB4P + FOR	
6,7-Dimethyl-8-ribityllumazine synthase	381	*ribE*	DB4P + A6RP -> D8RL + PI	
Riboflavin synthase	382	*ribH*	2 D8RL -> RIBFLV + A6RP	2.5.1.9
Riboflavin kinase	383	*ribF*	RIBFLV + ATP -> FMN + ADP	2.7.1.26
FAD synthetase	384	*ribF*	FMN + ATP -> FAD + PPI	2.7.7.2

Folate Biosynthesis

GTP cyclohydrolase I	385	*folE*	GTP -> FOR + AHTD	3.5.4.16
Dihydroneopterin triphosphate pyrophosphorylase	386	*ntpA*	AHTD -> PPI + DHPP	3.6.1.-
Nucleoside triphosphatase	676	*mutT*	AHTD -> DHP +3 PI	3.1.3.1
Dihydroneopterin monophosphate dephosphorylase	360		DHPP -> DHP + PI	3.6.1.-
Dihydroneopterin aldolase	387	*folB*	DHP -> AHHMP + GLAL	4.1.2.25
6-Hydroxymethyl-7,8 dihydropterin pyrophosphokinase	388	*folK*	AHHMP + ATP -> AMP + AHHMD	2.7.6.3
Aminodeoxychorismate synthase	389	*pabAB*	CHOR + GLN -> ADCHOR + GLU	4.1.3.-

Aminodeoxychorismate lyase	390	*pabC*	ADCHOR -> PYR + PABA	4.-.-.-
Dihydropteroate synthase	391	*folP*	PABA + AHHMD -> PPI + DHPT	2.5.1.15
Dihydrofolate synthetase	392	*folC*	DHPT + ATP + GLU -> ADP + PI + DHF	6.3.2.12
Dihydrofolate reductase	393	*folA*	DHF + NADPH -> NADP + THF	1.5.1.3

Coenzyme A Biosynthesis

Ketopentoate hydroxymethyl transferase	394	*panB*	OIVAL + METTHF -> AKP + THF	2.1.2.11
Ketopantoate reductase	395	*panE*	AKP + NADPH -> NADP + PANT	1.1.1.169
Acetohyoxyacid isomeroreductase	396	*ilvC*	AKP + NADPH -> NADP + PANT	1.1.1.86
Aspartate decarboxylase	397	*panD*	ASP -> CO2 + bALA	4.1.1.11
Pantoate-β-alanine ligase	398	*panC*	PANT + bALA + ATP -> AMP + PPI + PNTO	6.3.2.1
Pantothenate kinase	399	*coaA*	PNTO + ATP -> ADP + 4PPNTO	2.7.1.33
Phosphopantothenate-cysteine ligase	400		4PPNTO + CTP + CYS -> CMP + PPI + 4PPNCYS	6.3.2.5
Phosphopantothenate-cysteine decarboxylase	401		4PPNCYS -> CO2 + 4PPNTE	4.1.1.36
Phospho-pantethiene adenylyltransferase	402		4PPNTE + ATP -> PPI + DPCOA	2.7.7.3
DephosphoCoA kinase	403		DPCOA + ATP -> ADP + COA	2.7.1.24
ACP Synthase	404	*acpS*	COA -> PAP + ACP	2.7.8.7

NAD Biosynthesis

Aspartate oxidase	405	*nadB*	ASP + FAD -> FADH + ISUCC	1.4.3.-
Quinolate synthase	406	*nadA*	ISUCC + T3P2 -> PI + QA	1.4.3.16
Quinolate phosphoribosyl transferase	407	*nadC*	QA + PRPP -> NAMN + CO2 + PPI	2.4.2.19
NAMN adenylyl transferase	408	*nadD*	NAMN + ATP -> PPI + NAAD	2.7.7.18
NAMN adenylyl transferase	409	*nadD*	NMN + ATP -> NAD + PPI	2.7.7.18
Deamido-NAD ammonia ligase	410	*nadE*	NAAD + ATP + NH3 -> NAD + AMP + PPI	6.3.5.1
NAD kinase	411	*nadFG*	NAD + ATP -> NADP + ADP	2.7.1.23
NADP phosphatase	412		NADP -> NAD + PI	3.1.2.-

PNC IV

DNA ligase	413	*lig*	NAD -> NMN + AMP	6.5.1.2
NMN amidohydrolase	415	*pncC*	NMN -> NAMN + NH3	3.5.1.42

PNC VI

NMN glycohydrolase (cytoplasmic)	416		NMN -> R5P + NAm	3.2.2.14
NAm amidohydrolase	417	*pncA*	NAm -> NAC + NH3	3.5.1.19
NAPRTase	418	*pncB*	NAC + PRPP + ATP -> NAMN + PPI + PI + ADP	2.4.2.11

Uptake Pathways

NAD pyrophosphatase	681	*pnuE*	NADxt -> NMNxt + AMPxt	3.6.1.22
NMN permease	682	*pnuC*	NMNxt -> NMN	
NMN glycohydrolase (membrane bound)	683		NMNxt -> R5P + NAm	3.2.2.14
Nicotinic acid uptake	684		NACxt -> NAC	

Tetrapyrrole Biosynthesis

GSA synthetase	419	*hemM*	GLU + ATP -> GTRNA + AMP + PPI	6.1.1.17
Glutamyl-tRNA synthetase	677	*gltX*	GLU + ATP -> GTRNA + AMP + PPI	6.1.1.17
Glutamyl-tRNA reductase	420	*hemA*	GTRNA + NADPH -> GSA + NADP	1.2.1.-
Glutamate-1-semialdehyde aminotransferase	421	*hemL*	GSA -> ALAV	5.4.3.8
Porphobilinogen synthase	422	*hemB*	8 ALAV -> 4 PBG	4.2.1.24
Hydroxymethylbilane synthase	423	*hemC*	4 PBG -> HMB + 4 NH3	4.1.3.8
Uroporphyrinogen III synthase	424	*hemD*	HMB -> UPRG	4.2.1.75
Uroporphyrin-III C-methyltransferase 1	709	*hemX*	SAM + UPRG -> SAH + PC2	2.1.1.107
Uroporphyrin-III C-methyltransferase 2	425	*cysG*	SAM + UPRG -> SAH + PC2	2.1.1.107
1,3-Dimethyluroporphyrinogen III dehydrogenase	426	*cysG*	PC2 + NAD -> NADH + SHCL	
Siroheme ferrochelatase	427	*cysG*	SHCL -> SHEME	4.99.1.-
Uroporphyrinogen decarboxylase	428	*hemE*	UPRG -> 4 CO2 + CPP	4.1.1.37
Coproporphyrinogen oxidase, aerobic	429	*hemF*	O2 + CPP -> 2 CO2 + PPHG	1.3.3.3
Protoporphyrinogen oxidase	430	*hemG*	O2 + PPHG -> PPIX	1.3.3.4
Ferrochelatase	431	*hemH*	PPIX -> PTH	4.99.1.1
Heme O synthase	432	*cyoE*	PTH + FPP -> HO + PPI	

Biotin Biosynthesis

8-Amino-7-oxononanoate synthase	433	*bioF*	ALA + CHCOA <-> CO2 + COA + AONA	2.3.1.47
Adenosylmethionine-8-amino-7-oxononanoate aminotransferase	434	*bioA*	SAM + AONA <-> SAMOB + DANNA	2.6.1.62
Dethiobiotin synthase	435	*bioD*	CO2 + DANNA + ATP <-> DTB + PI + ADP	6.3.3.3
Biotin synthase	436	*bioB*	DTB + CYS <-> BT	2.8.1.-

Glutathione Biosynthesis

Glutamate-cysteine ligase	437	*gshA*	CYS + GLU + ATP -> GC + PI + ADP	6.3.2.2
Glutathione synthase	438	*gshB*	GLY + GC + ATP -> RGT + PI + ADP	6.3.2.3
Glutathione reductase	613	*gor*	NADPH + OGT <-> NADP + RGT	1.6.4.2

Thiamin (Vitamin B1) Biosynthesis

thiC protein	439	*thiC*	AIR -> AHM	
HMP kinase	440	*thiN*	AHM + ATP -> AHMP + ADP	2.7.1.49
HMP-phosphate kinase	441	*thiD*	AHMP + ATP -> AHMPP + ADP	2.7.4.7
Hypothetical	442		T3P1 + PYR -> DTP	
thiG protein	443	*thiG*	DTP + TYR + CYS -> THZ + HBA + CO2	
thiE protein	710	*thiE*	DTP + TYR + CYS -> THZ + HBA + CO2	
thiF protein	711	*thiF*	DTP + TYR + CYS -> THZ + HBA + CO2	
thiH protein	712	*thiH*	DTP + TYR + CYS -> THZ + HBA + CO2	
THZ kinase	444	*thiM*	THZ + ATP -> THZP + ADP	2.7.1.50
Thiamin phosphate synthase	445	*thiB*	THZP + AHMPP -> THMP + PPI	2.5.1.3
Thiamin kinase	446	*thiK*	THMP + ADP <-> THIAMIN + ATP	2.7.1.89
Thiamin phosphate kinase	447	*thiL*	THMP + ATP <-> TPP + ADP	2.7.4.16

Vitamin B6 (Pyridoxine) Biosynthesis

Erythrose 4-phosphate dehydrogenase	448	*epd*	E4P + NAD <-> ER4P + NADH	1.1.1.-
Erythronate-4-phosphate dehydrogenase	449	*pdxB*	ER4P + NAD <-> OHB + NADH	1.1.1.-
Hypothetical transaminase/phosphoserine transaminase	450	*serC*	OHB + GLU <-> PHT + AKG	2.6.1.52
Pyridoxal-phosphate biosynthetic proteins pdxJ-pdxA	451	*pdxAJ*	PHT + DX5P -> P5P + CO2	4.2.99.2
Pyridoxine 5'-phosphate oxidase	452	*pdxH*	P5P + O2 <-> PL5P + H2O2	1.4.3.5
Threonine synthase	453	*thrC*	PHT -> 4HLT + PI	4.2.99.2
Hypothetical Enzyme	454		4HLT -> PYRDX	4.1.1.-
Pyridoxine kinase	455	*pdxK*	PYRDX + ATP -> P5P + ADP	2.7.1.35
Hypothetical Enzyme	456		P5P -> PYRDX + PI	3.1.3.-
Hypothetical Enzyme	457		PL5P -> PL + PI	3.1.3.-
Pyridoxine kinase	458	*pdxK*	PL + ATP -> PL5P + ADP	2.7.1.35
Pyridoxine 5'-phosphate oxidase	459	*pdxH*	PYRDX + O2 <-> PL + H2O2	1.4.3.5
Pyridoxine 5'-phosphate oxidase	460	*pdxH*	PL + O2 + NH3 <-> PDLA + H2O2	1.4.3.5
Pyridoxine kinase	461	*pdxK*	PDLA + ATP -> PDLA5P + ADP	2.7.1.35
Hypothetical Enzyme	462		PDLA5P -> PDLA + PI	3.1.3.-
Pyridoxine 5'-phosphate oxidase	463	*pdxH*	PDLA5P + O2 -> PL5P + H202 + NH3	1.4.3.5
Serine hydroxymethyltransferase (serine methylase)	464	*glyA*	PL5P + GLU -> PDLA5P + AKG	2.1.2.1
Serine hydroxymethyltransferase (serine methylase)	465	*glyA*	PL5P + ALA -> PDLA5P + PYR	2.1.2.1

Cell Envelope Biosynthesis

Glutamine fructose-6-phosphate Transaminase	466	*glmS*	F6P + GLN -> GLU + GA6P	2.6.1.16
Phosphoglucosamine mutase	467	*glmM*	GA6P <-> GA1P	
N-Acetylglucosamine-1-phosphate-uridyltransferase	468	*glmU*	UTP + GA1P + ACCOA -> UDPNAG + PPI + COA	2.7.7.23

Lipid A biosynthesis

UDP-N-acetylglucosamine acyltransferase	469	*lpxA*	C140ACP + UDPNAG -> ACP + UDPG2AA	2.3.1.129
UDP-3-O-acyl-N-acetylglucosamine deacetylase	470	*lpxC*	UDPG2AA -> UDPG2A + AC	3.5.1.-
UDP-3-O-(3-hydroxymyristoyl)glucosamine-acyltransferase	471	*lpxD*	UDPG2A + C140ACP -> ACP + UDPG23A	2.3.1.-
UDP-sugar hydrolase	472	*ushA*	UDPG23A -> UMP + LIPX	3.6.1.45
Lipid A disaccharide synthase	473	*lpxB*	LIPX + UDPG23A -> UDP + DISAC1P	2.4.1.182
Tetraacyldisaccharide 4’ kinase	474		DISAC1P + ATP -> ADP + LIPIV	2.7.1.130
3-Deoxy-D-manno-octulosonic-acid transferase (KDO transferase)	475	*kdtA*	LIPIV + CMPKDO -> KDOLIPIV + CMP	2.-.-.-
3-Deoxy-D-manno-octulosonic-acid transferase (KDO transferase)	476	*kdtA*	KDOLIPIV + CMPKDO -> K2LIPIV + CMP	
Endotoxin synthase	477	*htrB,* *msbB*	K2LIPIV + C140ACP + C120ACP -> LIPA +2 ACP	

LPS sugar biosynthesis

3-Deoxy-D-manno-octulosonic-acid 8-phosphate synthase	478	*kdsA*	PEP + A5P -> KDOP + PI	4.1.2.16
3-Deoxy-D-manno-octulosonic-acid 8-phosphate phosphatase	363		KDOP -> KDO + PI	3.1.3.45
CMP-2-keto-3-deoxyoctonate synthesis	479	*kdsB*	KDO + CTP -> PPI + CMPKDO	2.7.7.38
ADP-L-glycero-D-mannoheptose-6-epimerase	480	*lpcA,* *rfaED*	S7P + ATP -> ADPHEP + PPI	
UDP glucose-1-phosphate uridylyltransferase	481	*galU,* *galF*	G1P + UTP -> PPI + UDPG	2.7.7.9
Ethanolamine phosphotransferase	482		PE + CMP <-> CDPETN + DGR	
Phosphatidate phosphatase	483		PA -> PI + DGR	
Diacylglycerol kinase	484	*dgkA*	DGR + ATP -> ADP + PA	2.7.1.107
LPS Synthesis – truncated version of LPS (ref neid)	485	*rfaLJIGFC*	LIPA +3 ADPHEP +2 UDPG +2 CDPETN + 3 CMPKDO -> LPS +3 ADP +2 UDP +3 CMP +2 CDP	

Murein biosyntheis

UDP-N-acetylglucosamine-enolpyruvate transferase	486	*murA*	UDPNAG + PEP -> UDPNAGEP + PI	2.5.1.7
UDP-N-acetylglucosamine-enolpyruvate dehydrogenase	487	*murB*	UDPNAGEP + NADPH -> UDPNAM + NADP	1.1.1.158
UDP-N-acetylmuramate-alanine ligase	488	*murC*	UDPNAM + ALA + ATP -> ADP + PI + UDPNAMA	6.3.2.8

UDP-N-acetylmuramoylalanine-D-glutamate ligase	489	*murD*	UDPNAMA + DGLU + ATP -> UDPNAMAG + ADP + PI	6.3.2.9
UDP-N-acetylmuramoylalanyl-D-glutamate 2,6-diaminopimelate lig	490	*murE*	UDPNAMAG + ATP + MDAP -> UNAGD + ADP + PI	6.3.2.13
D-Alanine-D-alanine adding enzyme	491	*murF*	UNAGD + ATP + AA -> UNAGDA + ADP + PI	6.3.2.15
Glutamate racemase	492	*murI*	GLU <-> DGLU	5.1.1.3
D-ala:D-ala ligases	493	*ddlAB*	2 DALA <-> AA	6.3.2.4
Phospho-N-acetylmuramoylpentapeptide transferase	494	*mraY*	UNAGDA -> UMP + PI + UNPTDO	
N-Acetylglucosaminyl transferase	679	*murG*	UNPTDO + UDPNAG -> UDP + PEPTIDO	

Membrane Transport

Carbohydrates

Arabinose (low affinity)	495	*araE*	ARABxt + HEXT <-> ARAB
Arabinose (high affinity)	571	*araFGH*	ARABxt + ATP -> ARAB + ADP + PI
Dihydroxyacetone	496		DHAxt + PEP -> T3P2 + PYR
Fructose	497	*fruABF*	FRUxt + PEP -> F1P + PYR
Fucose	498	*fucP*	FUCxt + HEXT <-> FUC
Galacitol	499	*gatABC*	GLTLxt + PEP -> GLTL1P + PYR
Galactose (low affinity)	500	*galP*	GLACxt + HEXT -> GLAC
Galactose (low affinity)		*galP*	GLCxt + HEXT -> GLC
Galactose (high affinity)	572	*mglABC*	GLACxt + ATP -> GLAC + ADP + PI
Glucitol	501	*srlA1A2B*	GLTxt + PEP -> GLT6P + PYR
Gluconate	502	*gntST*	GLCNxt + ATP -> GLCN + ADP + PI
Glucose	504	*ptsG, crr*	GLCxt + PEP -> G6P + PYR
Glycerol	505	*glpF*	GLxt <-> GL
Lactose	506	*lacY*	LACxt + HEXT <-> LAC
Maltose	507	*malX, crr, malEFGK, lamB*	MLTxt + PEP -> MLT6P + PYR
Mannitol	508	*mtlA, cmtAB*	MNTxt + PEP -> MNT6P + PYR
Mannose	509	*manXYZ, ptsPAI*	MANxt + PEP -> MAN1P + PYR
Melibiose	510	*melB*	MELIxt + HEXT -> MELI
N-Acetylglucosamine	511	*nagE, ptsN*	NAG + PEP -> NAGP + PYR
Rhamnose	512	*rhaT*	RMNxt + ATP -> RMN + ADP + PI
Ribose	513	*rbsABCD, xylH*	RIBxt + ATP -> RIB + ADP + PI
Sucrose	515	*scr*	SUCxt + PEP -> SUC6P + PYR
Trehalose	516	*treAB*	TRExt + PEP -> TRE6P + PYR
Xylose (low affinity)	517	*xylE*	XYLxt + HEXT -> XYL
Xylose (high affinity)	573	*xylFG, rbsB*	XYLxt + ATP -> XYL + ADP + PI

Amino Acids

Alanine	518	*cycA*	ALAxt + ATP -> ALA + ADP + PI
Arginine	519	*artPMQJI, argT hisMQP*	ARGxt + ATP -> ARG + ADP + PI
Asparagine (low Affinity)	520		ASNxt + HEXT <-> ASN
Asparagine (high Affinity)	574		ASNxt + ATP -> ASN + ADP + PI
Aspartate	521	*gltP*	ASPxt + HEXT -> ASP
Aspartate	575	*gltJKL*	ASPxt + ATP -> ASP + ADP + PI
Branched chain amino acid transport	522	*brnQ*	BCAAxt + HEXT <-> BCAA
Branched chain amino acid transport		*braB*	
Cysteine	523	*not identified*	CYSxt + ATP -> CYS + ADP + PI
D-Alanine	524	*cycA*	DALAxt + ATP -> DALA + ADP + PI
D-Alanine glycine permease		*cycA*	DALAxt + HEXT <-> DALA
D-Alanine glycine permease		*cycA*	DSERxt + HEXT <-> DSER
D-Alanine glycine permease		*cycA*	GLYxt + HEXT <-> GLY
Diaminopimelic acid	525		MDAPxt + ATP -> MDAP + ADP + PI
γ-Aminobutyrate transport	614	*gabP*	GABAxt + ATP -> GABA + ADP + PI
Glutamate	526	*gltP*	GLUxt + HEXT <-> GLU
Glutamate	576	*gltS*	GLUxt + HEXT <-> GLU
Glutamate	680	*gltJKL*	GLUxt + ATP -> GLU + ADP + PI
Glutamine	527	*glnHPQ*	GLNxt + ATP -> GLN + ADP + PI

Glycine	528	*cycA, proVWX*	GLYxt + ATP -> GLY + ADP + PI
Histidine	529	*hisJMPQ*	HISxt + ATP -> HIS + ADP + PI
Isoleucine	530	*livJ*	ILExt + ATP -> ILE + ADP + PI
Leucine	531	*livHKM/livFGJ*	LEUxt + ATP -> LEU + ADP + PI
Lysine	532	*lysP*	LYSxt + HEXT <-> LYS
Lysine	577	*argT, hisMPQ*	LYSxt + ATP -> LYS + ADP + PI
Lysine/Cadaverine	615	*cadB*	LYSxt + ATP -> LYS + ADP + PI
Methionine	533	*metD*	METxt + ATP -> MET + ADP + PI
Ornithine	534	*argT, hisMPQ*	ORNxt + ATP -> ORN + ADP + PI
Phenlyalanine	535	*aroP/mtr/pheP*	PHExt + HEXT <-> PHE
Proline	536	*putP, proPWX*	PROxt + HEXT <-> PRO
Proline		*cycA, proVW*	PROxt + ATP -> PRO + ADP + PI
Putrescine	537	*potEFHIG*	PTRCxt + ATP -> PTRC + ADP + PI
Serine	538	*sdaC*	SERxt + HEXT <-> SER
Serine	578	*cycA*	SERxt + ATP -> SER + ADP + PI
Spermidine & putrescine	539	*potABCD*	SPMDxt + ATP -> SPMD + ADP + PI
Spermidine & **putrescine**	539	*potABCD*	PTRCxt + ATP -> PTRC + ADP + PI
Threonine	540	*livJ*	THRxt + ATP -> THR + ADP + PI
Threonine	579	*tdcC*	THRxt + HEXT <-> THR
Tryptophan	541	*tnaB*	TRPxt + HEXT <-> TRP
Tyrosine	542	*tyrP*	TYRxt + HEXT <-> TYR
Valine	543	*livJ*	VALxt + ATP -> VAL + ADP + PI
Dipeptide	616	*dppABCDF*	DIPEPxt + ATP -> DIPEP + ADP + PI
Oligopeptide	617	*oppABCDF*	OPEPxt + ATP -> OPEP + ADP + PI
Peptide		*sapABD*	PEPTxt + ATP -> PEPT + ADP + PI
Purines & Pyrimidines			
Ribonucleotide transport	544	*mkl*	
Uracil	545	*uraA*	URAxt + HEXT -> URA
Nicotinamide mononucleotide transporter	546	*pnuC*	NMNxt + HEXT -> + NMN
Cytosine	547	*codB*	CYTSxt + HEXT -> CYTS
Adenine	548	*purB*	ADxt + HEXT -> AD
Guanine	549	*gpt, hpt*	GNxt <-> GN
Hypoxanthine	550	*gpt, hpt*	HYXNxt <-> HYXN
Xanthosine	618	*xapB*	XTSNxt <-> XTSN
Xanthine	551	*gpt*	XANxt <-> XAN
G-system	552	*nupG*	ADNxt + HEXT -> ADN
G-system		*nupG*	GSNxt + HEXT -> GSN
G-system		*nupG*	URIxt + HEXT -> URI
G-system		*nupG*	CYTDxt + HEXT -> CYTD
G-system (transports all nucleosides)		*nupG*	INSxt + HEXT -> INS
G-system		*nupG*	XTSNxt + HEXT -> XTSN
G-system		*nupG*	DTxt + HEXT -> DT
G-system		*nupG*	DINxt + HEXT -> DIN
G-system		*nupG*	DGxt + HEXT -> DG
G-system		*nupG*	DAxt + HEXT -> DA
G-system		*nupG*	DCxt + HEXT -> DC
G-system		*nupG*	DUxt + HEXT -> DU
C-system	553	*nupC*	ADNxt + HEXT -> ADN
C-system		*nupC*	URIxt + HEXT -> URI
C-system		*nupC*	CYTDxt + HEXT -> CYTD
C-system		*nupC*	DTxt + HEXT -> DT
C-system		*nupC*	DAxt + HEXT -> DA
C-system		*nupC*	DCxt + HEXT -> DC
C-system		*nupC*	DUxt + HEXT -> DU
Nucleosides and deoxynucleoside	554	*tsx*	ADNxt + HEXT -> ADN
Nucleosides and deoxynucleoside		*tsx*	GSNxt + HEXT -> GSN
Nucleosides and deoxynucleoside		*tsx*	URIxt + HEXT -> URI

Nucleosides and deoxynucleoside		*tsx*	CYTDxt + HEXT -> CYTD
Nucleosides and deoxynucleoside		*tsx*	INSxt + HEXT -> INS
Nucleosides and deoxynucleoside		*tsx*	XTSNxt + HEXT -> XTSN
Nucleosides and deoxynucleoside		*tsx*	DTxt + HEXT -> DT
Nucleosides and deoxynucleoside		*tsx*	DINxt + HEXT -> DIN
Nucleosides and deoxynucleoside		*tsx*	DGxt + HEXT -> DG
Nucleosides and deoxynucleoside		*tsx*	DAxt + HEXT -> DA
Nucleosides and deoxynucleoside		*tsx*	DCxt + HEXT -> DC
Nucleosides and deoxynucleoside		*tsx*	DUxt + HEXT -> DU

Metabolic By-Products

Acetate transport	555		ACxt + HEXT <-> AC
L-Lactate	619	*lldP*	LACxt + HEXT <-> LAC
Formate transport	557	*focA*	FORxt <-> FOR
Ethanol transport	558		ETHxt + HEXT <-> ETH
Succinate transport	559	*dcuAB*	SUCCxt + HEXT <-> SUCC
Pyruvate transport	559		PYRxt + HEXT <-> PYR

Other Compounds

Ammonia transport	560	*amtB*	NH3xt + HEXT <-> NH3
Potassium transport	561	*kdpABC*	Kxt + ATP -> K + ADP + PI
Potassium transport	580	*trkAEHG*	Kxt + HEXT <-> K
Sulfate transport	562	*cysPTUW AZ, sbp*	SLFxt + ATP -> SLF + ADP + PI
Phosphate transport	563	*pstABCS*	PIxt + ATP -> ADP + 2 PI
Phosphate transport	581	*pitAB*	PIxt + HEXT <-> PI
Hexose phosphate transport	620	*uhpT*	
Glycerol-3-phosphate	564	*glpT, ugpABCE*	GL3Pxt + PI -> GL3P
Nitrate transport	621	*narK*	
Vitamin B12	622	*btuBCDE*	
Dicarboxylates	566	*dcuAB, dctA*	SUCCxt + HEXT <-> SUCC
Dicarboxylates	582	*dcuAB, dctA*	FUMxt + HEXT <-> FUM
Dicarboxylates	583	*dcuAB, dctA*	MALxt + HEXT <-> MAL
Dicarboxylates	584	*dcuAB, dctA*	ASPxt + HEXT <-> ASP
Fatty acid transport	623	*fadL*	C140xt -> C140
Fatty acid transport	623	*fadL*	C160xt -> C160
Fatty acid transport	623	*fadL*	C180xt -> C180
α-Ketoglutarate	567	*kgtP*	AKGxt + HEXT <-> AKG
D-Glyceraldehyde transport	568		
Na/H antiporter	569	*nhaABC*	NAxt + <-> NA + HEXT
Na/H antiporter	713	*chaABC*	NAxt + <-> NA + HEXT
Na/H antiporter		*napA*	NAxt + <-> NA + HEXT
Pantothenate	570	*panF*	PNTOxt + HEXT <-> PNTO
Sialic acid permease		*nanT*	SLAxt + ATP -> SLA + ADP + PI
Oxygen transport			O2xt <-> O2
Carbon dioxide transport			CO2xt <-> CO2
Urea transport			UREAxt +2 HEXT <-> UREA
ATP drain flux for constant maintanence requirements			ATP -> ADP + PI
Glyceraldehyde transport		*gufP*	GLALxt <-> GLAL
Acetaldehyde transport			ACALxt <-> ACAL