

EMP Pathway

Enzyme	Rxn#	Gene	Reaction	EC Number
Glucokinase	1	<i>glk</i>	GLC + ATP -> G6P + ADP	2.7.1.2
Glucokinase	586	<i>glk</i>	bDGLC + ATP -> bDG6P + ADP	2.7.1.2
Phosphoglucose isomerase	2	<i>pgi</i>	G6P <-> F6P	5.3.1.9
Phosphoglucose isomerase	3	<i>pgi</i>	bDG6P <-> G6P	5.3.1.9
Phosphoglucose isomerase	4	<i>pgi</i>	bDG6P <-> F6P	5.3.1.9
Aldose 1-epimerase	585	<i>galM</i>	bDGLC <-> GLC	5.1.3.3
Glucose-1-phosphatase	587	<i>agp</i>	G1P -> GLC + PI	3.1.3.10
Phosphofructokinase	5	<i>pfkA</i>	F6P + ATP -> FDP + ADP	2.7.1.11
Phosphofructokinase B	624	<i>pfkB</i>	F6P + ATP -> FDP + ADP	2.7.1.11
Fructose-1,6-bisphosphatase	6	<i>fbp</i>	FDP -> F6P + PI	3.1.3.11
Fructose-1,6-bisphosphatase aldolase	7	<i>fba</i>	FDP <-> T3P1 + T3P2	4.1.2.13
Triosphosphate Isomerase	8	<i>tpiA</i>	T3P1 <-> T3P2	5.3.1.1
Methylglyoxal synthase		<i>mgsA</i>	T3P2 -> MTHGXL + PI	4.2.99.11
Glyceraldehyde-3-phosphate dehydrogenase-A complex	9	<i>gapA</i>	T3P1 + PI + NAD <-> NADH + 13PDG	1.2.1.12
Glyceraldehyde-3-phosphate dehydrogenase-C complex	714	<i>gapCIC2</i>	T3P1 + PI + NAD <-> NADH + 13PDG	1.2.1.12
Phosphoglycerate kinase	10	<i>pgk</i>	13PDG + ADP <-> 3PG + ATP	2.7.2.3
Phosphoglycerate mutase 1	11	<i>gpmA</i>	3PG <-> 2PG	5.4.2.1
Phosphoglycerate mutase 2	715	<i>gpmB</i>	3PG <-> 2PG	5.4.2.1
Enolase	12	<i>eno</i>	2PG <-> PEP	4.2.1.11
Phosphoenolpyruvate synthase	13	<i>ppsA</i>	PYR + ATP -> PEP + AMP + PI	2.7.9.2
Pyruvate Kinase II	14	<i>pykA</i>	PEP + ADP -> PYR + ATP	2.7.1.40
Pyruvate Kinase I	625	<i>pykF</i>	PEP + ADP -> PYR + ATP	2.7.1.40
Pyruvate dehydrogenase	15	<i>lpdA, aceEF</i>	PYR + COA + NAD -> NADH + CO2 + ACCOA	1.2.4.1, 2.3.1.12, 1.8.6.4
Glucose-1-phosphate adenyltransferase	108	<i>glgC</i>	ATP + G1P -> ADPGLC + PPI	2.7.7.27
Glycogen synthase	685	<i>glgA</i>	ADPGLC -> ADP + GLYCOGEN	2.4.1.21
Glycogen phosphorylase	109	<i>glgP</i>	GLYCOGEN + PI -> G1P	2.4.1.1
Maltodextrin phosphorylase	686	<i>malP</i>	GLYCOGEN + PI -> G1P	2.4.1.1

Pentose Phosphate Pathway

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

The Tricarboxylic Acid Cycle

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

Pyruvate Metabolism

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

Formate hydrogen lyase	81	<i>fdhF</i> , <i>hycBEFG</i>	FOR -> CO2	1.2.1.2, 1.12.1.2
Phosphotransacetylase	82	<i>pta</i>	ACCOA + PI <-> ACTP + COA	2.3.1.8
Acetate kinase A	83	<i>ackA</i>	ACTP + ADP <-> ATP + AC	2.7.2.1
GAR transformylase T	717	<i>purT</i>	ACTP + ADP <-> ATP + AC	2.7.2.1
Acetyl-CoA synthetase	590	<i>acs</i>	ATP + AC + COA -> AMP + PPI + ACCOA	6.2.1.1

Anaplerotic Reactions

Phosphoenolpyruvate carboxykinase	84	<i>pckA</i>	OA + ATP -> PEP + CO2 + ADP	4.1.1.49
Phosphoenolpyruvate carboxylase	85	<i>ppc</i>	PEP + CO2 -> OA + PI	4.1.1.31
Malic enzyme (NADP)	86	<i>maeB</i>	MAL + NADP -> CO2 + NADPH + PYR	1.1.1.40
Malic enzyme (NAD)	87	<i>maeA</i>	MAL + NAD -> CO2 + NADH + PYR	1.1.1.38
Isocitrate lyase	88	<i>aceA</i>	ICIT -> GLX + SUCC	4.1.3.1
Malate synthase A	89	<i>aceB</i>	ACCOA + GLX -> COA + MAL	4.1.3.2
Malate synthase G	695	<i>glcB</i>	ACCOA + GLX -> COA + MAL	4.1.3.2
Inorganic pyrophosphatase	721	<i>ppa</i>	PPI -> 2 PI	3.6.1.1

Respiration

NADH dehydrogenase II	90	<i>ndh</i>	NADH + Q -> NAD + QH2	1.6.5.3
NADH dehydrogenase I	91	<i>nuoABEF</i> <i>GHIJKLM</i> <i>N</i>	NADH + Q -> NAD + QH2 +3.5 HEXT	1.6.5.3
Formate dehydrogenase-N	92	<i>fdhGHI</i>	FOR + Q -> QH2 + CO2 +2 HEXT	1.2.2.1
Formate dehydrogenase-O	696	<i>fdoIHG</i>	FOR + Q -> QH2 + CO2 +2 HEXT	1.2.2.1
Formate dehydrogenase	697	<i>fdhF</i>	FOR + Q -> QH2 + CO2 +2 HEXT	1.2.2.1
Pyruvate oxidase	93	<i>poxB</i>	PYR + Q -> AC + CO2 + QH2	1.2.2.2
L-Lactate dehydrogenase	94	<i>lctD</i>	LLAC + Q -> PYR + QH2	1.1.2.3
D-Lactate dehydrogenase (cytochrome)		<i>dld</i>	LAC + Q -> PYR + QH2	1.1.2.4
Glycerol-3-phosphate dehydrogenase (aerobic)	95	<i>glpD</i>	GL3P + Q -> T3P2 + QH2	1.1.99.5
Glycerol-3-phosphate dehydrogenase (anaerobic)	631	<i>glpABC</i>	GL3P + Q -> T3P2 + QH2	1.1.99.5
Cytochrome oxidase bo3	96	<i>cyoABCD</i> , <i>cycBC</i> , <i>cydAB</i>	QH2 +5 O2 -> Q +2.5 HEXT	1.10.2.2,1.9.3.1
Cytochrome oxidase bd	97	<i>cydABCD</i> , <i>appBC</i> , <i>cycBC</i>	QH2 +5 O2 -> Q +2 HEXT	1.10.2.2,1.9.3.1
Succinate dehydrogenase complex	98	<i>sdhABCD</i>	FADH + Q <-> FAD + QH2	1.3.5.1
Thioredoxin reductase	99	<i>trxB</i>	OTHIO + NADPH -> NADP + RTHIO	1.6.4.5
Pyridine nucleotide transhydrogenase	100	<i>pntAB</i>	NADPH + NAD -> NADP + NADH	1.6.1.1
Pyridine nucleotide transhydrogenase	100	<i>pntAB</i>	NADP + NADH +2 HEXT -> NADPH + NAD	1.6.1.1
Hydrogenase 1		<i>hyaABC</i>	2 Q+2 HEXT <-> 2 QH2 + H2	1.3.99.1
Hydrogenase 2		<i>hybAC</i>	2 Q+2 HEXT <-> 2 QH2 + H2	1.3.99.1
Hydrogenase 3		<i>hycFGBE</i>	2 Q+2 HEXT <-> 2 QH2 + H2	1.3.99.1
FOF1-ATPase	101	<i>atpABCD</i> <i>EFGHI</i>	ATP <-> ADP + PI +4 HEXT	3.6.1.34

Alternative Carbon Source

Melibiose				
Alpha-galactosidase (melibiase)	16	<i>melA</i>	MELI -> GLC + GLAC	3.2.1.22
Galactose				
Galactokinase	17	<i>galK</i>	GLAC + ATP -> GALIP + ADP	2.7.1.6
Galactose-1-phosphate uridylyltransferase	18	<i>galT</i>	GALIP + UDPG <-> G1P + UDPGAL	2.7.7.10
UDP-glucose 4-epimerase	19	<i>galE</i>	UDPGAL <-> UDPG	5.1.3.2
UDP-glucose-1-phosphate uridylyltransferase	20	<i>galU</i>	G1P + UTP <-> UDPG + PPI	2.7.7.9
Phosphoglucomutase	21	<i>pgm</i>	G1P <-> G6P	5.4.2.2
Lactose				
Periplasmic beta-glucosidase precursor	22	<i>bglX</i>	LCTS -> GLC + GLAC	3.2.1.21
Beta-galactosidase (LACTase)	23	<i>lacZ</i>	LCTS -> GLC + GLAC	3.2.1.23
Trehalose				
trehalose-6-phosphate hydrolase	24	<i>treC</i>	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	<i>fruK</i>	F1P + ATP -> FDP + ADP	2.7.1.56
Xylose isomerase	27	<i>xyIA</i>	FRU -> GLC	5.3.1.5
Mannose				

Phosphomannomutase	588	<i>cpsG</i>	MAN6P <-> MAN1P	5.4.2.8
Mannose-6-phosphate isomerase	28	<i>mana</i>	MAN1P <-> F6P	5.3.1.8
Sorbose				
<i>N-Acetylglucosamine</i>				
N-Acetylglucosamine-6-phosphate deacetylase	31	<i>nagA</i>	NAGP -> GA6P + AC	3.5.1.25
<i>Glucosamine</i>				
Glucosamine-6-phosphate deaminase	32	<i>nagB</i>	GA6P -> F6P + NH3	5.3.1.10
<i>Sialic Acid</i>				
N-Acetylneuraminatase lyase		<i>nanA</i>	SLA -> PYR + NAMAN	4.1.3.3
Fucose				
L-Fucose isomerase	33	<i>fucI</i>	FUC <-> FCL	5.3.1.-
L-Fuculokinase	34	<i>fucK</i>	FCL + ATP -> FCL1P + ADP	2.7.1.51
L-Fuculose phosphate aldolase	35	<i>fucA</i>	FCL1P <-> LACAL + T3P2	4.1.2.17
Lactaldehyde reductase	36	<i>fucO</i>	LACAL + NADH <-> 12PPD + NAD	1.1.1.77
Aldehyde dehydrogenase A	37	<i>aldA</i>	LACAL + NAD <-> LLAC + NADH	1.2.1.22
Aldehyde dehydrogenase B	687	<i>aldB</i>	LACAL + NAD <-> LLAC + NADH	1.2.1.22
Aldehyde dehydrogenase	722	<i>adhC</i>	LACAL + NAD <-> LLAC + NADH	1.1.1.1
Aldehyde dehydrogenase	725	<i>adhE</i>	GLAL + NADH <-> GL + NAD	1.1.1.1
Aldehyde dehydrogenase	723	<i>adhE</i>	LACAL + NAD -> LLAC + NADH	1.1.1.1
Aldehyde dehydrogenase	724	<i>aldH</i>	LACAL + NAD <-> LLAC + NADH	1.2.1.3
Aldehyde dehydrogenase	726	<i>aldH</i>	ACAL + NAD -> AC + NADH	1.2.1.3
<i>Gluconate</i>				
Gluconokinase I	38	<i>gntV</i>	GLCN + ATP -> D6PGC + ADP	
Gluconokinase II	626	<i>gntK</i>	GLCN + ATP -> D6PGC + ADP	
Rhamnose				
L-Rhamnose isomerase	39	<i>rhaA</i>	RMN <-> RML	5.3.1.14
Rhamnulokinase	40	<i>rhaB</i>	RML + ATP -> RML1P + ADP	2.7.1.5
Rhamnulose-1-phosphate aldolase	41	<i>rhaD</i>	RML1P <-> LACAL + T3P2	4.1.2.19
<i>Arabinose</i>				
L-Arabinose isomerase	42	<i>araA</i>	ARAB <-> RBL	5.3.1.4
Arabinose-5-phosphate isomerase	43		RL5P <-> A5P	5.3.1.13
L-Ribulokinase	44	<i>araB</i>	RBL + ATP -> RL5P + ADP	2.7.1.16
L-Ribulose-phosphate 4-epimerase	45	<i>araD</i>	RL5P <-> X5P	5.1.3.4
<i>Xylose</i>				
Xylose isomerase	46	<i>xylA</i>	XYL <-> XUL	5.3.1.5
Xylulokinase	47	<i>xylB</i>	XUL + ATP -> X5P + ADP	2.7.1.17
Ribose				
Ribokinase	48	<i>rbsK</i>	RIB + ATP -> R5P + ADP	2.7.1.15
<i>Mannitol</i>				
Mannitol-1-phosphate 5-dehydrogenase	49	<i>mltD</i>	MNT6P + NAD <-> F6P + NADH	1.1.1.17
<i>Glucitol</i>				
Glucitol-6-phosphate dehydrogenase	50	<i>srlD</i>	GLT6P + NAD <-> F6P + NADH	1.1.1.140
<i>Galactitol</i>				
Galactitol-1-phosphate dehydrogenase	51	<i>gatD</i>	GLTL1P + NAD <-> TAG6P + NADH	1.1.1.-
Phosphofruktokinase B	52	<i>pfkB</i>	TAG6P + ATP -> TAG16P + ADP	2.7.1.11
1-Phosphofruktokinase	627	<i>fruK</i>	TAG6P + ATP -> TAG16P + ADP	2.7.1.56
Tagatose-6-phosphate kinase	688	<i>agaZ</i>	TAG6P + ATP -> TAG16P + ADP	2.7.1.-
Tagatose-bisphosphate aldolase 2	53	<i>gatY</i>	TAG16P <-> T3P2 + T3P1	4.1.2.-
Tagatose-bisphosphate aldolase 1	689	<i>agaY</i>	TAG16P <-> T3P2 + T3P1	4.1.2.-
<i>Glycerol</i>				
Glycerol kinase	54	<i>glpK</i>	GL + ATP -> GL3P + ADP	2.7.1.30
Glycerol-3-phosphate-dehydrogenase-[NAD(P)+]	55	<i>gpsA</i>	GL3P + NADP <-> T3P2 + NADPH	1.1.1.94
<i>Nucleosides and Deoxynucleosides</i>				
Phosphopentomutase	56	<i>deoB</i>	DR1P <-> DR5P	5.4.2.7
Phosphopentomutase	57	<i>deoB</i>	R1P <-> R5P	5.4.2.7
Deoxyribose-phosphate aldolase	58	<i>deoC</i>	DR5P -> ACAL + T3P1	4.1.2.4
Aspartate & Asparagine Biosynthesis				
Aspartate transaminase	102	<i>aspC</i>	OA + GLU <-> ASP + AKG	2.6.1.1
Asparagine synthetase (Glutamate dependent)	103	<i>asnB</i>	ASP + ATP + GLN -> GLU + ASN + AMP + PPI	6.3.5.4
Aspartate-ammonia ligase	104	<i>asnA</i>	ASP + ATP + NH3 -> ASN + AMP + PPI	6.3.1.1
Glutamate and Glutamine Biosynthesis				
Glutamate dehydrogenase	105	<i>gdhA</i>	AKG + NH3 + NADPH <-> GLU + NADP	1.4.1.4
Glutamate-ammonia ligase	106	<i>glnA</i>	GLU + NH3 + ATP -> GLN + ADP + PI	6.3.1.2
Glutamate synthase	107	<i>glnBD</i>	AKG + GLN + NADPH -> NADP + 2 GLU	1.4.1.13
Alanine Biosynthesis				
Alanine transaminase	110	<i>alaB</i>	PYR + GLU <-> AKG + ALA	2.6.1.2
Valine-pyruvate aminotransferase	632	<i>avtA</i>	OIVAL + ALA -> PYR + VAL	2.6.1.66
Alanine racemase, biosynthetic	112	<i>alr</i>	ALA <-> DALA	5.1.1.1

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

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

Asparinase I 219 *ansA* ASN -> ASP + NH3 3.5.1.1
Asparinase 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 desulhydrase 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
Tryptophanase 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 lyase 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
Adenylosuccinate 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	<i>pyrBI</i>	CAP + ASP -> CAASP + PI	2.1.3.2
Dihydroorotase	249	<i>pyrC</i>	CAASP <-> DOROA	3.5.2.3
Dihydroorotate dehydrogenase	250	<i>pyrD</i>	DOROA + Q <-> QH2 + OROA	1.3.3.1
Orotate phosphoribosyl transferase	251	<i>pyrE</i>	OROA + PRPP <-> PPI + OMP	2.4.2.10
OMP decarboxylase	252	<i>pyrF</i>	OMP -> CO2 + UMP	4.1.1.23
CTP synthetase	253	<i>pyrG</i>	UTP + GLN + ATP -> GLU + CTP + ADP + PI	6.3.4.2

Salvage Pathways

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

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

One Carbon Metabolism

Glycine cleavage system (Multi-component system)	323	<i>gcvHTP, lpdA</i>	GLY + THF + NAD -> METTHF + NADH + CO ₂ + NH ₃	Multi-Component System: 1.4.4.2, 2.1.2.10
Formyl tetrahydrofolate deformylase	325	<i>purU</i>	FTHF -> FOR + THF	3.5.1.10
Methylene tetrahydrofolate reductase	326	<i>metF</i>	METTHF + NADH -> NAD + MTHF	1.7.99.5
Methylene THF dehydrogenase	327	<i>folD</i>	METTHF + NADP <-> METHF + NADPH	1.5.1.5
Methenyl tetrahydrofolate cyclehydrase	328	<i>folD</i>	METHF <-> FTHF	3.5.4.9

Membrane Lipid Biosynthesis

Acetyl-CoA carboxyltransferase	330	<i>accABD</i>	ACCOA + ATP + CO ₂ <-> MALCOA + ADP + PI	6.4.1.2, 6.3.4.14
Malonyl-CoA-ACP transacylase	331	<i>fabD</i>	MALCOA + ACP <-> MALACP + COA	2.3.1.39
Malonyl-ACP decarboxylase	332	<i>fadB</i>	MALACP -> ACACP + CO ₂	2.3.1.41
Acetyl-CoA-ACP transacylase	333	<i>fabH</i>	ACACP + COA <-> ACCOA + ACP	2.3.1.41
β-Ketoacyl-ACP synthase (C12,0)		<i>fab</i>	ACACP +5 MALACP +10 NADPH -> 10 NADP + C120ACP +5 CO ₂ +5 ACP	
β-Ketoacyl-ACP synthase (C14,0)		<i>fab</i>	ACACP +6 MALACP +12 NADPH -> 12 NADP + C140ACP +6 CO ₂ +6 ACP	
β-Ketoacyl-ACP synthase I (C14,1)		<i>fab</i>	ACACP +6 MALACP +11 NADPH -> 11 NADP + C141ACP +6 CO ₂ +6 ACP	
β-Ketoacyl-ACP synthase I (C16,0)		<i>fab</i>	ACACP +7 MALACP +14 NADPH -> 14 NADP + C160ACP +7 CO ₂ +7 ACP	
β-Ketoacyl-ACP synthase I (C16,1)		<i>fab</i>	ACACP +7 MALACP +13 NADPH -> 13 NADP + C161ACP +7 CO ₂ +7 ACP	
β-Ketoacyl-ACP synthase I (C18,1)		<i>fab</i>	ACACP +8 MALACP +15 NADPH -> 15 NADP +1 C181ACP +8 CO ₂ +8 ACP	
Glycerol-3-phosphate dehydrogenase	341	<i>gpsA</i>	NADPH + T3P2 <-> GL3P + NADP	1.1.1.94
Acyltransferase		<i>pls</i>	GL3P +0.035 C140ACP +0.102 C141ACP +0.717 C160ACP +0.142 C161ACP +1.004 C181ACP -> 2 ACP + PA	
CDP-Diacylglycerol synthetase	344	<i>cdsA</i>	PA + CTP <-> CDPDG + PPI	2.7.7.41
CDP-Diacylglycerol pyrophosphatase	600	<i>cdh</i>	CDPDG -> CMP + PA	3.6.1.26
Phosphatidylserine synthase	345	<i>psaA</i>	CDPDG + SER <-> CMP + PS	2.7.8.8
Phosphatidylserine decarboxylase	346	<i>psd</i>	PS -> PE + CO ₂	4.1.1.65
Phosphatidylglycerol phosphate synthase	347	<i>pgsA</i>	CDPDG + GL3P <-> CMP + PGP	2.7.8.5
Phosphatidylglycerol phosphate phosphatase A	348	<i>pgpA</i>	PGP -> PI + PG	3.1.3.27
Phosphatidylglycerol phosphate phosphatase B	708	<i>pgpB</i>	PGP -> PI + PG	3.1.3.27

Cardiolipin synthase	349	<i>cls</i>	2 PG <-> CL + GL	2.7.8.?
Fatty Acid Metabolism				
Acetyl-CoA C-acetyltransferase	606	<i>atoB</i>	2 ACCOA <-> COA + AACCOA	2.3.1.9
β -Ketoacyl-ACP synthase (C14,0)		<i>fab</i>	C140 + ATP +7 COA +7 FAD +7 NAD -> AMP + PPI +7 FADH +7 NADH +7 ACCOA	
β -Ketoacyl-ACP synthase I (C14,1)		<i>fab</i>	C160 + ATP +8 COA +8 FAD +8 NAD -> AMP + PPI +8 FADH +8 NADH +8 ACCOA	
β -Ketoacyl-ACP synthase I (C16,0)		<i>fab</i>	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	<i>ispA</i>	DMPP + IPPP -> GPP + PPI	2.5.1.1
Geranyltranstransferase	353	<i>ispA</i>	GPP + IPPP -> FPP + PPI	2.5.1.10
Octaprenyl pyrophosphate synthase (5 reactions)	354(664- <i>ispB</i>)		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				
<i>Ubiquinone</i>				
Chorismate pyruvate-lyase	356	<i>ubiC</i>	CHOR -> 4HBZ + PYR	4.1.3.27
Hydroxybenzoate octaprenyltransferase	357	<i>ubiA</i>	4HBZ + OPP -> O4HBZ + PPI	2.5.1.-
Octaprenyl-hydroxybenzoate decarboxylase	358	<i>ubiD, ubiX</i>	O4HBZ -> CO2 + 2OPPP	4.1.1.-
2-Octaprenylphenol hydroxylase	359	<i>ubiB</i>	2OPPP + O2 -> 2O6H	1.13.14.-
Methylation reaction	361		2O6H + SAM -> 2OPMP + SAH	2.1.1.-
2-Octaprenyl-6-methoxyphenol hydroxylase	362	<i>ubiH</i>	2OPMP + O2 -> 2OPMB	1.14.3.-
2-Octaprenyl-6-methoxy-1,4-benzoquinone methylase	364	<i>ubiE</i>	2OPMB + SAM -> 2OPMMB + SAH	2.1.1.-
2-Octaprenyl-3-methyl-6-methoxy-1,4-benzoquinone hydroxylase	365	<i>ubiF</i>	2OPMMB + O2 -> 2OMHMB	1.14.13.-
3-Dimethylubiquinone 3-methyltransferase	367	<i>ubiG</i>	2OMHMB + SAM -> QH2 + SAH	2.1.1.64
<i>Menaquinone</i>				
Isochorismate synthase 1	368	<i>menF</i>	CHOR -> ICHOR	5.4.99.6
α -Ketoglutarate decarboxylase	369	<i>menD</i>	AKG + TPP -> SSALTTPP + CO2	4.1.1.71
SHCHC synthase	370	<i>menD</i>	ICHOR + SSALTTPP -> PYR + TPP + SHCHC	
O-Succinylbenzoate-CoA synthase	371	<i>menC</i>	SHCHC -> OSB	
O-Succinylbenzoic acid-CoA ligase	372	<i>menE</i>	OSB + ATP + COA -> OSBCOA + AMP + PPI	6.2.1.26
Naphthoate synthase	373	<i>menB</i>	OSBCOA -> DHNA + COA	4.1.3.36
1,4-Dihydroxy-2-naphthoate octaprenyltransferase	374	<i>menA</i>	DHNA + OPP -> DMK + PPI + CO2	
S-Adenosylmethionine-2-DMK methyltransferase	375	<i>menG</i>	DMK + SAM -> MK + SAH	
Enterochelin Biosynthesis				
Isochorismate synthase 2	607	<i>entC</i>	CHOR -> ICHOR	5.4.99.6
Isochorismatase	608	<i>entB</i>	ICHOR <-> 23DHDHB + PYR	3.3.2.1
2,3-Dihydro-2,3-dihydroxybenzoate dehydrogenase	609	<i>entA</i>	23DHDHB + NAD <-> 23DHB + NADH	1.3.1.28
ATP-dependent activation of 2,3-dihydroxybenzoate	610	<i>entE</i>	23DHB + ATP <-> 23DHBA + PPI	6.-.-
ATP-dependent serine activating enzyme	611	<i>entF</i>	SER + ATP <-> SERA + PPI	2.7.7.-
Enterochelin synthetase	612	<i>entD</i>	3 SERA +3 23DHBA -> ENTER +6 AMP	6.-.-
Riboflavin Biosynthesis				
GTP cyclohydrolase II	376	<i>ribA</i>	GTP -> D6RP5P + FOR + PPI	3.5.4.25
Pyrimidine deaminase	377	<i>ribD</i>	D6RP5P -> A6RP5P + NH3	3.5.4.26
Pyrimidine reductase	378	<i>ribD</i>	A6RP5P + NADPH -> A6RP5P2 + NADP	1.1.1.193
Pyrimidine phosphatase	379		A6RP5P2 -> A6RP + PI	
3,4 Dihydroxy-2-butanone-4-phosphate synthase	380	<i>ribB</i>	RL5P -> DB4P + FOR	
6,7-Dimethyl-8-ribityllumazine synthase	381	<i>ribE</i>	DB4P + A6RP -> D8RL + PI	
Riboflavin synthase	382	<i>ribH</i>	2 D8RL -> RIBFLV + A6RP	2.5.1.9
Riboflavin kinase	383	<i>ribF</i>	RIBFLV + ATP -> FMN + ADP	2.7.1.26
FAD synthetase	384	<i>ribF</i>	FMN + ATP -> FAD + PPI	2.7.7.2
Folate Biosynthesis				
GTP cyclohydrolase I	385	<i>folE</i>	GTP -> FOR + AHTD	3.5.4.16
Dihydroneopterin triphosphate pyrophosphorylase	386	<i>ntpA</i>	AHTD -> PPI + DHPP	3.6.1.-
Nucleoside triphosphatase	676	<i>mutT</i>	AHTD -> DHP +3 PI	3.1.3.1
Dihydroneopterin monophosphate dephosphorylase	360		DHPP -> DHP + PI	3.6.1.-
Dihydroneopterin aldolase	387	<i>folB</i>	DHP -> AHHMP + GLAL	4.1.2.25
6-Hydroxymethyl-7,8 dihydropterin pyrophosphokinase	388	<i>folK</i>	AHHMP + ATP -> AMP + AHHMD	2.7.6.3
Aminodeoxychorismate synthase	389	<i>pabAB</i>	CHOR + GLN -> ADCHOR + GLU	4.1.3.-

Aminodeoxychorismate lyase	390	<i>pabC</i>	ADCHOR -> PYR + PABA	4.-.-
Dihydropterolate synthase	391	<i>folP</i>	PABA + AHHMD -> PPI + DHPT	2.5.1.15
Dihydrofolate synthetase	392	<i>folC</i>	DHPT + ATP + GLU -> ADP + PI + DHF	6.3.2.12
Dihydrofolate reductase	393	<i>folA</i>	DHF + NADPH -> NADP + THF	1.5.1.3
Coenzyme A Biosynthesis				
Ketopantoate hydroxymethyl transferase	394	<i>panB</i>	OIVAL + METTHF -> AKP + THF	2.1.2.11
Ketopantoate reductase	395	<i>panE</i>	AKP + NADPH -> NADP + PANT	1.1.1.169
Acetohydroxyacid isomeroreductase	396	<i>ilvC</i>	AKP + NADPH -> NADP + PANT	1.1.1.86
Aspartate decarboxylase	397	<i>panD</i>	ASP -> CO2 + bALA	4.1.1.11
Pantoate-β-alanine ligase	398	<i>panC</i>	PANT + bALA + ATP -> AMP + PPI + PNT0	6.3.2.1
Pantothenate kinase	399	<i>coaA</i>	PNT0 + ATP -> ADP + 4PPNT0	2.7.1.33
Phosphopantothenate-cysteine ligase	400		4PPNT0 + CTP + CYS -> CMP + PPI + 4PPNCYS	6.3.2.5
Phosphopantothenate-cysteine decarboxylase	401		4PPNCYS -> CO2 + 4PPNTE	4.1.1.36
Phospho-pantethiene adenyltransferase	402		4PPNTE + ATP -> PPI + DPCOA	2.7.7.3
DephosphoCoA kinase	403		DPCOA + ATP -> ADP + COA	2.7.1.24
ACP Synthase	404	<i>acpS</i>	COA -> PAP + ACP	2.7.8.7
NAD Biosynthesis				
Aspartate oxidase	405	<i>nadB</i>	ASP + FAD -> FADH + ISUCC	1.4.3.-
Quinolinate synthase	406	<i>nadA</i>	ISUCC + T3P2 -> PI + QA	1.4.3.16
Quinolinate phosphoribosyl transferase	407	<i>nadC</i>	QA + PRPP -> NAMN + CO2 + PPI	2.4.2.19
NAMN adenyl transferase	408	<i>nadD</i>	NAMN + ATP -> PPI + NAAD	2.7.7.18
NAMN adenyl transferase	409	<i>nadE</i>	NMN + ATP -> NAD + PPI	2.7.7.18
Deamido-NAD ammonia ligase	410	<i>nadE</i>	NAAD + ATP + NH3 -> NAD + AMP + PPI	6.3.5.1
NAD kinase	411	<i>nadFG</i>	NAD + ATP -> NADP + ADP	2.7.1.23
NADP phosphatase	412		NADP -> NAD + PI	3.1.2.-
PNC IV				
DNA ligase	413	<i>lig</i>	NAD -> NMN + AMP	6.5.1.2
NMN amidohydrolase	415	<i>pncC</i>	NMN -> NAMN + NH3	3.5.1.42
PNC VI				
NMN glycohydrolase (cytoplasmic)	416		NMN -> R5P + NAm	3.2.2.14
NAm amidohydrolase	417	<i>pncA</i>	NAm -> NAC + NH3	3.5.1.19
NAPRTase	418	<i>pncB</i>	NAC + PRPP + ATP -> NAMN + PPI + PI + ADP	2.4.2.11
Uptake Pathways				
NAD pyrophosphatase	681	<i>pnuE</i>	NADxt -> NMNxt + AMPxt	3.6.1.22
NMN permease	682	<i>pnuC</i>	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	<i>hemM</i>	GLU + ATP -> GTRNA + AMP + PPI	6.1.1.17
Glutamyl-tRNA synthetase	677	<i>gltX</i>	GLU + ATP -> GTRNA + AMP + PPI	6.1.1.17
Glutamyl-tRNA reductase	420	<i>hemA</i>	GTRNA + NADPH -> GSA + NADP	1.2.1.-
Glutamate-1-semialdehyde aminotransferase	421	<i>hemL</i>	GSA -> ALAV	5.4.3.8
Porphobilinogen synthase	422	<i>hemB</i>	8 ALAV -> 4 PBG	4.2.1.24
Hydroxymethylbilane synthase	423	<i>hemC</i>	4 PBG -> HMB + 4 NH3	4.1.3.8
Uroporphyrinogen III synthase	424	<i>hemD</i>	HMB -> UPRG	4.2.1.75
Uroporphyrin-III C-methyltransferase 1	709	<i>hemX</i>	SAM + UPRG -> SAH + PC2	2.1.1.107
Uroporphyrin-III C-methyltransferase 2	425	<i>cysG</i>	SAM + UPRG -> SAH + PC2	2.1.1.107
1,3-Dimethyluroporphyrinogen III dehydrogenase	426	<i>cysG</i>	PC2 + NAD -> NADH + SHCL	
Siroheme ferrochelatase	427	<i>cysG</i>	SHCL -> SHEME	4.99.1.-
Uroporphyrinogen decarboxylase	428	<i>hemE</i>	UPRG -> 4 CO2 + CPP	4.1.1.37
Coproporphyrinogen oxidase, aerobic	429	<i>hemF</i>	O2 + CPP -> 2 CO2 + PPHG	1.3.3.3
Protoporphyrinogen oxidase	430	<i>hemG</i>	O2 + PPHG -> PPIX	1.3.3.4
Ferrochelatase	431	<i>hemH</i>	PPIX -> PTH	4.99.1.1
Heme O synthase	432	<i>cyoE</i>	PTH + FPP -> HO + PPI	
Biotin Biosynthesis				
8-Amino-7-oxononanoate synthase	433	<i>bioF</i>	ALA + CHCOA <-> CO2 + COA + AONA	2.3.1.47
Adenosylmethionine-8-amino-7-oxononanoate aminotransferase	434	<i>bioA</i>	SAM + AONA <-> SAMOB + DANNA	2.6.1.62
Dethiobiotin synthase	435	<i>bioD</i>	CO2 + DANNA + ATP <-> DTB + PI + ADP	6.3.3.3
Biotin synthase	436	<i>bioB</i>	DTB + CYS <-> BT	2.8.1.-
Glutathione Biosynthesis				
Glutamate-cysteine ligase	437	<i>gshA</i>	CYS + GLU + ATP -> GC + PI + ADP	6.3.2.2
Glutathione synthase	438	<i>gshB</i>	GLY + GC + ATP -> RGT + PI + ADP	6.3.2.3
Glutathione reductase	613	<i>gor</i>	NADPH + OGT <-> NADP + RGT	1.6.4.2

Thiamin (Vitamin B1) Biosynthesis

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

Vitamin B6 (Pyridoxine) Biosynthesis

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

Cell Envelope Biosynthesis

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

Lipid A biosynthesis

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

LPS sugar biosynthesis

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

Murein biosynthesis

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

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

Membrane Transport

Carbohydrates

Arabinose (low affinity)	495	<i>araE</i>	ARABxt + HEXT <-> ARAB	
Arabinose (high affinity)	571	<i>araFGH</i>	ARABxt + ATP -> ARAB + ADP + PI	
Dihydroxyacetone	496		DHAXt + PEP -> T3P2 + PYR	
Fructose	497	<i>fruABF</i>	FRUxt + PEP -> FIP + PYR	
Fucose	498	<i>fucP</i>	FUCxt + HEXT <-> FUC	
Galacitol	499	<i>gatABC</i>	GLTLxt + PEP -> GLTLIP + PYR	
Galactose (low affinity)	500	<i>galP</i>	GLACxt + HEXT -> GLAC	
Galactose (low affinity)		<i>galP</i>	GLCxt + HEXT -> GLC	
Galactose (high affinity)	572	<i>mglABC</i>	GLACxt + ATP -> GLAC + ADP + PI	
Glucitol	501	<i>srlAIA2B</i>	GLTxt + PEP -> GLT6P + PYR	
Gluconate	502	<i>gntST</i>	GLCNxt + ATP -> GLCN + ADP + PI	
Glucose	504	<i>ptsG, crr</i>	GLCxt + PEP -> G6P + PYR	
Glycerol	505	<i>glpF</i>	GLxt <-> GL	
Lactose	506	<i>lacY</i>	LACxt + HEXT <-> LAC	
Maltose	507	<i>malX, crr, malEFGK, lamB</i>	MLTxt + PEP -> MLT6P + PYR	
Mannitol	508	<i>mtlA, cmtAB</i>	MNTxt + PEP -> MNT6P + PYR	
Mannose	509	<i>manXYZ, ptsPAI</i>	MANxt + PEP -> MAN1P + PYR	
Melibiose	510	<i>melB</i>	MELIxt + HEXT -> MELI	
N-Acetylglucosamine	511	<i>nagE, ptsN</i>	NAG + PEP -> NAGP + PYR	
Rhamnose	512	<i>rhaT</i>	RMNxt + ATP -> RMN + ADP + PI	
Ribose	513	<i>rhsABCD, xylH</i>	RIBxt + ATP -> RIB + ADP + PI	
Sucrose	515	<i>scr</i>	SUCxt + PEP -> SUC6P + PYR	
Trehalose	516	<i>treAB</i>	TRExt + PEP -> TRE6P + PYR	
Xylose (low affinity)	517	<i>xylE</i>	XYLxt + HEXT -> XYL	
Xylose (high affinity)	573	<i>xylFG, rhsB</i>	XYLxt + ATP -> XYL + ADP + PI	

Amino Acids

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

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

Nucleosides and deoxynucleoside
 Nucleosides and deoxynucleoside
 Nucleosides and deoxynucleoside
 Nucleosides and deoxynucleoside
 Nucleosides and deoxynucleoside
 Nucleosides and deoxynucleoside
 Nucleosides and deoxynucleoside
 Nucleosides and deoxynucleoside
 Nucleosides and deoxynucleoside

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

Metabolic By-Products

Acetate transport 555
 L-Lactate 619
 Formate transport 557
 Ethanol transport 558
 Succinate transport 559
 Pyruvate transport 559

ACxt + HEXT <-> AC
lldP LACxt + HEXT <-> LAC
focA FORxt <-> FOR
 ETHxt + HEXT <-> ETH
dcuAB SUCCxt + HEXT <-> SUCC
 PYRxt + HEXT <-> PYR

Other Compounds

Ammonia transport 560
 Potassium transport 561
 Potassium transport 580
 Sulfate transport 562
 Phosphate transport 563
 Phosphate transport 581
 Hexose phosphate transport 620
 Glycerol-3-phosphate 564
 Nitrate transport 621
 Vitamin B12 622
 Dicarboxylates 566
 Dicarboxylates 582
 Dicarboxylates 583
 Dicarboxylates 584
 Fatty acid transport 623
 Fatty acid transport 623
 Fatty acid transport 623
 α-Ketoglutarate 567
 D-Glyceraldehyde transport 568
 Na/H antiporter 569
 Na/H antiporter 713
 Na/H antiporter
 Pantothenate 570
 Sialic acid permease
 Oxygen transport
 Carbon dioxide transport
 Urea transport
 ATP drain flux for constant maintenance requirements
 Glyceraldehyde transport
 Acetaldehyde transport

amtB NH3xt + HEXT <-> NH3
kdpABC Kxt + ATP -> K + ADP + PI
trkAEHG Kxt + HEXT <-> K
cysPTUW SLFxt + ATP -> SLF + ADP + PI
AZ, sbp
pstABCS PIxt + ATP -> ADP + 2 PI
pitAB PIxt + HEXT <-> PI
uhpT
glpT, ugpABCE GL3Pxt + PI -> GL3P
narK
btuBCDE
dcuAB, dctA SUCCxt + HEXT <-> SUCC
dcuAB, dctA FUMxt + HEXT <-> FUM
dcuAB, dctA MALxt + HEXT <-> MAL
dcuAB, dctA ASPxt + HEXT <-> ASP
fadL C140xt -> C140
fadL C160xt -> C160
fadL C180xt -> C180
kgtP AKGxt + HEXT <-> AKG
nhaABC NAxt + <-> NA + HEXT
chaABC NAxt + <-> NA + HEXT
napA NAxt + <-> NA + HEXT
panF PNTOxt + HEXT <-> PNTO
nanT SLAxt + ATP -> SLA + ADP + PI
 O2xt <-> O2
 CO2xt <-> CO2
 UREAxt + 2 HEXT <-> UREA
 ATP -> ADP + PI
gufP GLALxt <-> GLAL
 ACALxt <-> ACAL