Enzyme Abundance Sp (Log transformed)
10
8
6
4
2
0
coenzyme A biosynthesis I (prokaryotic): phosphopantothenate−−−cysteine ligase (CTP)
coenzyme A biosynthesis I (prokaryotic): phosphopantothenoylcysteine decarboxylase
coenzyme A biosynthesis I (prokaryotic): pantetheine−phosphate adenylyltransferase
coenzyme A biosynthesis I (prokaryotic): dephospho−CoA kinase
peptidoglycan biosynthesis I (meso−diaminopimelate containing): undecaprenyldiphospho−muramoylpentapeptide beta−N−acetylglucosaminyltransferase
peptidoglycan biosynthesis I (meso−diaminopimelate containing): phospho−N−acetylmuramoyl−pentapeptide−transferase
peptidoglycan biosynthesis I (meso−diaminopimelate containing): UDP−N−acetylmuramoyl−tripeptide−−−D−alanyl−D−alanine ligase
peptidoglycan biosynthesis I (meso−diaminopimelate containing): glutamate racemase
peptidoglycan biosynthesis I (meso−diaminopimelate containing): D−alanine−−−D−alanine ligase
peptidoglycan biosynthesis I (meso−diaminopimelate containing): UDP−N−acetylmuramate−−−L−alanine ligase
peptidoglycan biosynthesis I (meso−diaminopimelate containing): UDP−N−acetylmuramoyl−L−alanine−−−D−glutamate ligase
peptidoglycan biosynthesis I (meso−diaminopimelate containing): UDP−N−acetylglucosamine 1−carboxyvinyltransferase
peptidoglycan biosynthesis I (meso−diaminopimelate containing): UDP−N−acetylmuramate dehydrogenase
tRNA charging: alanine−−−tRNA ligase
tRNA charging: methionine−−−tRNA ligase
tRNA charging: lysine−−−tRNA ligase
tRNA charging: glycine−−−tRNA ligase
tRNA charging: leucine−−−tRNA ligase
tRNA charging: tryptophan−−−tRNA ligase
tRNA charging: tyrosine−−−tRNA ligase
tRNA charging: cysteine−−−tRNA ligase
tRNA charging: arginine−−−tRNA ligase
tRNA charging: phenylalanine−−−tRNA ligase
tRNA charging: serine−−−tRNA ligase
tRNA charging: histidine−−−tRNA ligase
tRNA charging: asparagine−−−tRNA ligase
tRNA charging: valine−−−tRNA ligase
tRNA charging: glutamate−−−tRNA ligase
tRNA charging: isoleucine−−−tRNA ligase
tRNA charging: proline−−−tRNA ligase
tRNA charging: threonine−−−tRNA ligase
tRNA charging: aspartate−−−tRNA ligase
UDP−N−acetyl−D−glucosamine biosynthesis I: phosphoglucosamine mutase
UDP−N−acetyl−D−glucosamine biosynthesis I: UDP−N−acetylglucosamine diphosphorylase
UDP−N−acetyl−D−glucosamine biosynthesis I: glucosamine−1−phosphate N−acetyltransferase
pyruvate fermentation to acetate and (S)−lactate I: L−lactate dehydrogenase
UDP−N−acetyl−D−glucosamine biosynthesis I: glutamine−−−fructose−6−phosphate transaminase (isomerizing)
UMP biosynthesis I: carbamoyl−phosphate synthase (glutamine−hydrolysing)
UMP biosynthesis I: orotidine−5'−phosphate decarboxylase
UMP biosynthesis I: dihydroorotase
UMP biosynthesis I: orotate phosphoribosyltransferase
UMP biosynthesis I: aspartate carbamoyltransferase
pyruvate fermentation to acetate and (S)−lactate I: phosphate acetyltransferase
pyruvate fermentation to acetate and (S)−lactate I: acetate kinase
UMP biosynthesis II: dihydroorotate dehydrogenase (fumarate)
6−hydroxymethyl−dihydropterin diphosphate biosynthesis I: GTP cyclohydrolase I
6−hydroxymethyl−dihydropterin diphosphate biosynthesis I: 2−amino−4−hydroxy−6−hydroxymethyldihydropteridine diphosphokinase
6−hydroxymethyl−dihydropterin diphosphate biosynthesis I: dihydroneopterin aldolase
CDP−diacylglycerol biosynthesis I: 1−acylglycerol−3−phosphate O−acyltransferase
CDP−diacylglycerol biosynthesis I: glycerol−3−phosphate dehydrogenase [NAD(P)+]
CDP−diacylglycerol biosynthesis I: phosphatidate cytidylyltransferase
mevalonate pathway I (eukaryotes and bacteria): mevalonate kinase
mevalonate pathway I (eukaryotes and bacteria): isopentenyl−diphosphate Delta−isomerase
mevalonate pathway I (eukaryotes and bacteria): phosphomevalonate kinase
mevalonate pathway I (eukaryotes and bacteria): acetyl−CoA C−acetyltransferase
mevalonate pathway I (eukaryotes and bacteria): diphosphomevalonate decarboxylase
mevalonate pathway I (eukaryotes and bacteria): hydroxymethylglutaryl−CoA synthase
UDP−N−acetyl−D−glucosamine biosynthesis I: glucose−6−phosphate isomerase
lactose and galactose degradation I: galactose−6−phosphate isomerase
lactose and galactose degradation I: 6−phospho−beta−galactosidase
lactose and galactose degradation I: tagatose−bisphosphate aldolase
lactose and galactose degradation I: tagatose−6−phosphate kinase
dTDP−&beta−L−rhamnose biosynthesis: dTDP−glucose 4,6−dehydratase
dTDP−&beta−L−rhamnose biosynthesis: dTDP−4−dehydrorhamnose reductase
dTDP−&beta−L−rhamnose biosynthesis: glucose−1−phosphate thymidylyltransferase
5−aminoimidazole ribonucleotide biosynthesis I: phosphoribosylformylglycinamidine cyclo−ligase
5−aminoimidazole ribonucleotide biosynthesis I: phosphoribosylamine−−−glycine ligase
5−aminoimidazole ribonucleotide biosynthesis I: phosphoribosylformylglycinamidine synthase
L−methionine biosynthesis III: 5−methyltetrahydropteroyltriglutamate−−−homocysteine S−methyltransferase
L−methionine biosynthesis III: O−acetylhomoserine aminocarboxypropyltransferase
L−methionine biosynthesis III: homoserine O−acetyltransferase
thiamine phosphate formation from pyrithiamine and oxythiamine (yeast): hydroxyethylthiazole kinase
pentose phosphate pathway (non−oxidative branch) I: transketolase
pentose phosphate pathway: 6−phosphogluconolactonase
NAD salvage pathway V (PNC V cycle): nicotinamidase
superpathway of thiamine diphosphate biosynthesis III (eukaryotes): phosphomethylpyrimidine synthase
sucrose biosynthesis II: UTP−monosaccharide−1−phosphate uridylyltransferase
superpathway of thiamine diphosphate biosynthesis III (eukaryotes): thiamine diphosphokinase
pentose phosphate pathway (non−oxidative branch) I: ribulose−phosphate 3−epimerase
pentose phosphate pathway (non−oxidative branch) I: ribose−5−phosphate isomerase
superpathway of L−isoleucine biosynthesis I: aspartate−semialdehyde dehydrogenase
superpathway of L−isoleucine biosynthesis I: aspartate transaminase
superpathway of L−isoleucine biosynthesis I: aspartate kinase
glycogen degradation II: glucokinase
thiamine phosphate formation from pyrithiamine and oxythiamine (yeast): thiamine phosphate synthase
superpathway of L−isoleucine biosynthesis I: homoserine dehydrogenase
NAD salvage pathway V (PNC V cycle): NAD+ synthase (glutamine−hydrolysing)
superpathway of L−isoleucine biosynthesis I: homoserine kinase
thiamine phosphate formation from pyrithiamine and oxythiamine (yeast): phosphooxymethylpyrimidine kinase
pentose phosphate pathway (non−oxidative branch) I: transaldolase
NAD salvage pathway V (PNC V cycle): nicotinate−nucleotide adenylyltransferase
pentose phosphate pathway: glucose−6−phosphate dehydrogenase (NADP+)
NAD salvage pathway V (PNC V cycle): nicotinate phosphoribosyltransferase
pentose phosphate pathway (non−oxidative branch) II: fructose−bisphosphate aldolase
pentose phosphate pathway: phosphogluconate dehydrogenase (NADP+−dependent, decarboxylating)
superpathway of L−isoleucine biosynthesis I: threonine synthase
pyruvate fermentation to isobutanol (engineered): alcohol dehydrogenase
glycogen biosynthesis I (from ADP−D−Glucose): phosphoglucomutase (alpha−D−glucose−1,6−bisphosphate−dependent)
sucrose degradation IV (sucrose phosphorylase): glucose−6−phosphate isomerase
sucrose degradation IV (sucrose phosphorylase): sucrose phosphorylase
sucrose degradation IV (sucrose phosphorylase): fructokinase
superpathway of branched chain amino acid biosynthesis: ketol−acid reductoisomerase (NADP+)
superpathway of branched chain amino acid biosynthesis: dihydroxy−acid dehydratase
superpathway of branched chain amino acid biosynthesis: acetolactate synthase
superpathway of branched chain amino acid biosynthesis: branched−chain−amino−acid transaminase
methylerythritol phosphate pathway I: 2−C−methyl−D−erythritol 2,4−cyclodiphosphate synthase
methylerythritol phosphate pathway I: 2−C−methyl−D−erythritol 4−phosphate cytidylyltransferase
methylerythritol phosphate pathway I: 4−(cytidine 5'−diphospho)−2−C−methyl−D−erythritol kinase
methylerythritol phosphate pathway I: 4−hydroxy−3−methylbut−2−en−1−yl diphosphate reductase
methylerythritol phosphate pathway I: 1−deoxy−D−xylulose−5−phosphate synthase
methylerythritol phosphate pathway I: (E)−4−hydroxy−3−methylbut−2−enyl−diphosphate synthase (flavodoxin)
methylerythritol phosphate pathway I: 1−deoxy−D−xylulose−5−phosphate reductoisomerase
L−histidine biosynthesis: phosphoribosyl−AMP cyclohydrolase
L−histidine biosynthesis: imidazoleglycerol−phosphate dehydratase
L−histidine biosynthesis: phosphoribosyl−ATP diphosphatase
L−histidine biosynthesis: ATP phosphoribosyltransferase
L−histidine biosynthesis: imidazole glycerol−phosphate synthase
L−histidine biosynthesis: 1−(5−phosphoribosyl)−5−[(5−phosphoribosylamino)methylideneamino]imidazole−4−carboxamide isomerase
L−histidine biosynthesis: histidinol−phosphate transaminase
L−arginine biosynthesis I (via L−ornithine): carbamoyl−phosphate synthase (glutamine−hydrolysing)
L−arginine biosynthesis I (via L−ornithine): acetylglutamate kinase
L−arginine biosynthesis I (via L−ornithine): ornithine carbamoyltransferase
L−arginine biosynthesis I (via L−ornithine): N−acetyl−gamma−glutamyl−phosphate reductase
L−arginine biosynthesis I (via L−ornithine): amino−acid N−acetyltransferase
L−arginine biosynthesis I (via L−ornithine): acetylornithine transaminase
L−arginine biosynthesis I (via L−ornithine): argininosuccinate synthase
L−arginine biosynthesis I (via L−ornithine): argininosuccinate lyase
L−arginine biosynthesis II (acetyl cycle): glutamate N−acetyltransferase
superpathway of branched chain amino acid biosynthesis: 2−isopropylmalate synthase
S−adenosyl−L−methionine salvage I: methionine adenosyltransferase
S−adenosyl−L−methionine salvage I: adenosylhomocysteine nucleosidase
S−adenosyl−L−methionine salvage I: S−ribosylhomocysteine lyase
guanosine ribonucleotides de novo biosynthesis: IMP dehydrogenase
guanosine ribonucleotides de novo biosynthesis: GMP synthase (glutamine−hydrolysing)
guanosine ribonucleotides de novo biosynthesis: guanylate kinase
inosine−5'−phosphate biosynthesis I: adenylosuccinate lyase
5−aminoimidazole ribonucleotide biosynthesis I: amidophosphoribosyltransferase
inosine−5'−phosphate biosynthesis I: 5−(carboxyamino)imidazole ribonucleotide synthase
inosine−5'−phosphate biosynthesis I: phosphoribosylaminoimidazolesuccinocarboxamide synthase
inosine−5'−phosphate biosynthesis I: 5−(carboxyamino)imidazole ribonucleotide mutase
inosine−5'−phosphate biosynthesis I: IMP cyclohydrolase
inosine−5'−phosphate biosynthesis I: phosphoribosylaminoimidazolecarboxamide formyltransferase
chorismate biosynthesis I: 3−deoxy−7−phosphoheptulonate synthase
chorismate biosynthesis I: 3−dehydroquinate dehydratase
chorismate biosynthesis I: 3−phosphoshikimate 1−carboxyvinyltransferase
chorismate biosynthesis I: chorismate synthase
chorismate biosynthesis I: shikimate kinase
chorismate biosynthesis I: 3−dehydroquinate synthase
glycogen degradation II: glycogen phosphorylase
glycogen degradation II: 4−alpha−glucanotransferase
UMP biosynthesis I: dihydroorotate dehydrogenase (quinone)
peptidoglycan biosynthesis I (meso−diaminopimelate containing): UDP−N−acetylmuramoyl−L−alanyl−D−glutamate−−−2,6−diaminopimelate ligase
superpathway of L−lysine, L−threonine and L−methionine biosynthesis II: homoserine dehydrogenase
superpathway of L−lysine, L−threonine and L−methionine biosynthesis II: threonine synthase
L−lysine biosynthesis II: aspartate kinase
L−lysine biosynthesis II: N−acetyldiaminopimelate deacetylase
superpathway of N−acetylglucosamine, N−acetylmannosamine and N−acetylneuraminate degradation: N−acylglucosamine−6−phosphate 2−epimerase
superpathway of N−acetylglucosamine, N−acetylmannosamine and N−acetylneuraminate degradation: N−acetylneuraminate lyase
L−lysine biosynthesis II: diaminopimelate epimerase
L−lysine biosynthesis II: aspartate−semialdehyde dehydrogenase
L−lysine biosynthesis II: 4−hydroxy−tetrahydrodipicolinate synthase
fatty acid biosynthesis initiation (mitochondria): acetyl−CoA carboxylase
L−lysine biosynthesis II: 4−hydroxy−tetrahydrodipicolinate reductase
L−lysine biosynthesis II: diaminopimelate decarboxylase
superpathway of N−acetylglucosamine, N−acetylmannosamine and N−acetylneuraminate degradation: glucosamine−6−phosphate deaminase
superpathway of L−lysine, L−threonine and L−methionine biosynthesis II: homoserine kinase
fatty acid biosynthesis initiation (mitochondria): [acyl−carrier−protein] S−malonyltransferase
superpathway of N−acetylglucosamine, N−acetylmannosamine and N−acetylneuraminate degradation: N−acetylglucosamine−6−phosphate deacetylase
fatty acid biosynthesis initiation (mitochondria): beta−ketoacyl−[acyl−carrier−protein] synthase II
folate transformations II (plants): dihydrofolate reductase
folate transformations II (plants): thymidylate synthase
folate transformations II (plants): methenyltetrahydrofolate cyclohydrolase
folate transformations II (plants): methylenetetrahydrofolate dehydrogenase (NADP+)
folate transformations II (plants): glycine hydroxymethyltransferase
folate transformations II (plants): formate−−−tetrahydrofolate ligase
folate transformations II (plants): 5−formyltetrahydrofolate cyclo−ligase
superpathway of coenzyme A biosynthesis III (mammals): pantothenate kinase
acetylene degradation (anaerobic): phosphate acetyltransferase
acetylene degradation (anaerobic): acetate kinase
sucrose degradation IV (sucrose phosphorylase): phosphoglucomutase (alpha−D−glucose−1,6−bisphosphate−dependent)
acetylene degradation (anaerobic): acetaldehyde dehydrogenase (acetylating)
acetylene degradation (anaerobic): alcohol dehydrogenase
superpathway of L−threonine biosynthesis: aspartate kinase
superpathway of L−threonine biosynthesis: aspartate−semialdehyde dehydrogenase
superpathway of L−threonine biosynthesis: homoserine dehydrogenase
superpathway of L−threonine biosynthesis: threonine synthase
superpathway of L−threonine biosynthesis: homoserine kinase
superpathway of L−alanine biosynthesis: alanine racemase
superpathway of L−alanine biosynthesis: cysteine desulfurase
superpathway of L−alanine biosynthesis: alanine transaminase
peptidoglycan maturation (meso−diaminopimelate containing): serine−type D−Ala−D−Ala carboxypeptidase
5−aminoimidazole ribonucleotide biosynthesis II: phosphoribosylformylglycinamidine cyclo−ligase
5−aminoimidazole ribonucleotide biosynthesis II: phosphoribosylamine−−−glycine ligase
sucrose biosynthesis II: glucose−6−phosphate isomerase
glycogen degradation II: phosphoglucomutase (alpha−D−glucose−1,6−bisphosphate−dependent)
5−aminoimidazole ribonucleotide biosynthesis II: phosphoribosylformylglycinamidine synthase
UDP−N−acetylmuramoyl−pentapeptide biosynthesis II (lysine−containing): UDP−N−acetylmuramoyl−L−alanyl−D−glutamate−−−L−lysine ligase
superpathway of L−alanine biosynthesis: branched−chain−amino−acid transaminase
peptidoglycan biosynthesis II (staphylococci): lipid II:glycine glycyltransferase
S−adenosyl−L−methionine salvage I: 5−methyltetrahydropteroyltriglutamate−−−homocysteine S−methyltransferase
peptidoglycan biosynthesis III (mycobacteria): peptidoglycan glycosyltransferase
Bifidobacterium shunt: ribulose−phosphate 3−epimerase
Bifidobacterium shunt: glucokinase
Bifidobacterium shunt: fructose−6−phosphate phosphoketolase
Bifidobacterium shunt: ribose−5−phosphate isomerase
Bifidobacterium shunt: phosphoglycerate kinase
Bifidobacterium shunt: phosphopyruvate hydratase
Bifidobacterium shunt: transaldolase
Bifidobacterium shunt: pyruvate kinase
pyrimidine deoxyribonucleosides salvage: thymidine kinase
pyrimidine deoxyribonucleosides salvage: cytidine deaminase
pyrimidine deoxyribonucleotide phosphorylation: nucleoside−diphosphate kinase
glycolysis I (from glucose 6−phosphate): glyceraldehyde−3−phosphate dehydrogenase (phosphorylating)
glycolysis I (from glucose 6−phosphate): triose−phosphate isomerase
glycolysis I (from glucose 6−phosphate): phosphopyruvate hydratase
glycolysis I (from glucose 6−phosphate): phosphoglycerate kinase
glycolysis I (from glucose 6−phosphate): fructose−bisphosphate aldolase
glycolysis I (from glucose 6−phosphate): pyruvate kinase
glycolysis I (from glucose 6−phosphate): 6−phosphofructokinase
glycolysis I (from glucose 6−phosphate): phosphoglycerate mutase (2,3−diphosphoglycerate−dependent)
glycolysis I (from glucose 6−phosphate): glucose−6−phosphate isomerase
superpathway of pyrimidine nucleobases salvage: UMP kinase
pyrimidine deoxyribonucleotide phosphorylation: (d)CMP kinase
pyrimidine deoxyribonucleotide phosphorylation: dTMP kinase
superpathway of pyrimidine nucleobases salvage: uracil phosphoribosyltransferase
glycolysis I (from glucose 6−phosphate): pyruvate, water dikinase
superpathway of pyrimidine nucleobases salvage: CTP synthase (glutamine hydrolysing)
CDP−diacylglycerol biosynthesis III: acyl phosphate:glycerol−3−phosphate acyltransferase
CDP−diacylglycerol biosynthesis III: glycerol−3−phosphate dehydrogenase [NAD(P)+]
CDP−diacylglycerol biosynthesis III: phosphate acyltransferase
CDP−diacylglycerol biosynthesis III: phosphatidate cytidylyltransferase
stachyose degradation: UDP−glucose−−−hexose−1−phosphate uridylyltransferase
stachyose degradation: galactokinase
stachyose degradation: UTP−−−glucose−1−phosphate uridylyltransferase
stachyose degradation: alpha−galactosidase
O−antigen building blocks biosynthesis (E. coli): glucose−6−phosphate isomerase
O−antigen building blocks biosynthesis (E. coli): UDP−galactopyranose mutase
O−antigen building blocks biosynthesis (E. coli): UDP−N−acetylglucosamine diphosphorylase
O−antigen building blocks biosynthesis (E. coli): glucosamine−1−phosphate N−acetyltransferase
O−antigen building blocks biosynthesis (E. coli): phosphoglucosamine mutase
O−antigen building blocks biosynthesis (E. coli): glutamine−−−fructose−6−phosphate transaminase (isomerizing)
L−lysine biosynthesis I: aspartate kinase
L−lysine biosynthesis I: diaminopimelate decarboxylase
L−lysine biosynthesis I: 4−hydroxy−tetrahydrodipicolinate reductase
L−lysine biosynthesis I: 4−hydroxy−tetrahydrodipicolinate synthase
L−lysine biosynthesis I: aspartate−semialdehyde dehydrogenase
GDP−mannose biosynthesis: mannose−6−phosphate isomerase
glycogen degradation II: glucan 1,4−alpha−glucosidase
chitin degradation II (Vibrio): beta−N−acetylhexosaminidase
Bifidobacterium shunt: L−lactate dehydrogenase
Bifidobacterium shunt: glyceraldehyde−3−phosphate dehydrogenase (phosphorylating)
sucrose degradation III (sucrose invertase): beta−fructofuranosidase
GDP−mannose biosynthesis: phosphomannomutase
L−lysine biosynthesis I: succinyl−diaminopimelate desuccinylase
Bifidobacterium shunt: acetate kinase
superpathway of L−serine and glycine biosynthesis I: phosphoserine transaminase
chitin degradation II (Vibrio): chitinase
superpathway of L−serine and glycine biosynthesis I: phosphoserine phosphatase
folate transformations II (plants): methylenetetrahydrofolate reductase [NAD(P)H]
L−lysine biosynthesis I: 2,3,4,5−tetrahydropyridine−2,6−dicarboxylate N−succinyltransferase
L−methionine biosynthesis II: cystathionine gamma−synthase
L−lysine biosynthesis I: diaminopimelate epimerase
L−methionine biosynthesis II: homoserine kinase
glycogen biosynthesis I (from ADP−D−Glucose): 1,4−alpha−glucan branching enzyme
glycogen biosynthesis I (from ADP−D−Glucose): glucose−1−phosphate adenylyltransferase
glycogen biosynthesis I (from ADP−D−Glucose): starch synthase (glycosyl−transferring)
sucrose biosynthesis II: glycogen phosphorylase
sucrose biosynthesis II: 4−alpha−glucanotransferase
phosphopantothenate biosynthesis I: 2−dehydropantoate 2−reductase
L−arginine degradation XIII (reductive Stickland reaction): pyrroline−5−carboxylate reductase
phosphopantothenate biosynthesis I: pantoate−−−beta−alanine ligase (AMP−forming)
L−arginine degradation XIII (reductive Stickland reaction): arginine deiminase
L−arginine degradation XIII (reductive Stickland reaction): ornithine carbamoyltransferase
5−aminoimidazole ribonucleotide biosynthesis I: phosphoribosylglycinamide formyltransferase 1
dTDP−&beta−L−rhamnose biosynthesis: dTDP−4−dehydrorhamnose 3,5−epimerase
chorismate biosynthesis I: shikimate dehydrogenase (NADP+)
glycolysis IV: triose−phosphate isomerase
superpathway of L−aspartate and L−asparagine biosynthesis: aspartate transaminase
glycolysis IV: 6−phosphofructokinase
cis−vaccenate biosynthesis: enoyl−[acyl−carrier−protein] reductase (NADH)
cis−vaccenate biosynthesis: 3−oxoacyl−[acyl−carrier−protein] reductase
preQ0 biosynthesis: GTP cyclohydrolase I
glycolysis IV: pyruvate kinase
glycolysis IV: phosphoglycerate mutase (2,3−diphosphoglycerate−independent)
cis−vaccenate biosynthesis: 3−hydroxyacyl−[acyl−carrier−protein] dehydratase
glycolysis IV: phosphopyruvate hydratase
glycolysis IV: phosphoglycerate kinase
glycolysis IV: fructose−bisphosphate aldolase
L−isoleucine biosynthesis I (from threonine): acetolactate synthase
L−isoleucine biosynthesis I (from threonine): branched−chain−amino−acid transaminase
L−isoleucine biosynthesis I (from threonine): ketol−acid reductoisomerase (NADP+)
L−isoleucine biosynthesis I (from threonine): dihydroxy−acid dehydratase
5−aminoimidazole ribonucleotide biosynthesis II: amidophosphoribosyltransferase
sucrose biosynthesis II: UTP−−−glucose−1−phosphate uridylyltransferase
superpathway of aromatic amino acid biosynthesis: prephenate dehydratase
&gamma−glutamyl cycle: glutamate−−−cysteine ligase
superpathway of aromatic amino acid biosynthesis: chorismate mutase
L−lysine biosynthesis I: succinyldiaminopimelate transaminase
superpathway of aromatic amino acid biosynthesis: indole−3−glycerol−phosphate synthase
superpathway of aromatic amino acid biosynthesis: anthranilate phosphoribosyltransferase
&gamma−glutamyl cycle: cytosol nonspecific dipeptidase
UDP−N−acetylmuramoyl−pentapeptide biosynthesis II (lysine−containing): UDP−N−acetylglucosamine 1−carboxyvinyltransferase
UDP−N−acetylmuramoyl−pentapeptide biosynthesis II (lysine−containing): D−alanine−−−D−alanine ligase
UDP−N−acetylmuramoyl−pentapeptide biosynthesis II (lysine−containing): UDP−N−acetylmuramate−−−L−alanine ligase
UDP−N−acetylmuramoyl−pentapeptide biosynthesis II (lysine−containing): UDP−N−acetylmuramate dehydrogenase
UDP−N−acetylmuramoyl−pentapeptide biosynthesis II (lysine−containing): UDP−N−acetylmuramoyl−L−alanine−−−D−glutamate ligase
UDP−N−acetylmuramoyl−pentapeptide biosynthesis II (lysine−containing): glutamate racemase
UDP−N−acetylmuramoyl−pentapeptide biosynthesis II (lysine−containing): UDP−N−acetylmuramoyl−tripeptide−−−D−alanyl−D−alanine ligase
stachyose degradation: UDP−glucose 4−epimerase
D−galactose degradation I (Leloir pathway): UDP−glucose 4−epimerase
D−galactose degradation I (Leloir pathway): UDP−glucose−−−hexose−1−phosphate uridylyltransferase
D−galactose degradation I (Leloir pathway): galactokinase
CMP−3−deoxy−D−manno−octulosonate biosynthesis: 3−deoxy−manno−octulosonate cytidylyltransferase
4−amino−2−methyl−5−diphosphomethylpyrimidine biosynthesis II: pyridoxal kinase
CMP−3−deoxy−D−manno−octulosonate biosynthesis: arabinose−5−phosphate isomerase
CMP−3−deoxy−D−manno−octulosonate biosynthesis: 3−deoxy−8−phosphooctulonate synthase
CMP−3−deoxy−D−manno−octulosonate biosynthesis: 3−deoxy−manno−octulosonate−8−phosphatase
4−amino−2−methyl−5−diphosphomethylpyrimidine biosynthesis II: pyridoxal 5'−phosphate synthase
4−amino−2−methyl−5−diphosphomethylpyrimidine biosynthesis II: phosphooxymethylpyrimidine kinase
NAD de novo biosynthesis I (from aspartate): L−aspartate oxidase
NAD de novo biosynthesis I (from aspartate): quinolinate synthase
NAD de novo biosynthesis I (from aspartate): nicotinate−nucleotide diphosphorylase (carboxylating)
UDP−N−acetylmuramoyl−pentapeptide biosynthesis I (meso−diaminopimelate containing): UDP−N−acetylmuramoyl−L−alanine−−−D−glutamate ligase
UDP−N−acetylmuramoyl−pentapeptide biosynthesis I (meso−diaminopimelate containing): UDP−N−acetylmuramate−−−L−alanine ligase
UDP−N−acetylmuramoyl−pentapeptide biosynthesis I (meso−diaminopimelate containing): D−alanine−−−D−alanine ligase
UDP−N−acetylmuramoyl−pentapeptide biosynthesis I (meso−diaminopimelate containing): glutamate racemase
UDP−N−acetylmuramoyl−pentapeptide biosynthesis I (meso−diaminopimelate containing): UDP−N−acetylmuramoyl−L−alanyl−D−glutamate−−−2,6−diaminopimelate ligase
UDP−N−acetylmuramoyl−pentapeptide biosynthesis I (meso−diaminopimelate containing): UDP−N−acetylglucosamine 1−carboxyvinyltransferase
L−histidine degradation III: glutamate formimidoyltransferase
tRNA charging: glutamine−−−tRNA ligase
glycolysis III (from glucose): glucokinase
L−lysine biosynthesis III: diaminopimelate decarboxylase
chorismate biosynthesis from 3−dehydroquinate: 3−phosphoshikimate 1−carboxyvinyltransferase
chorismate biosynthesis from 3−dehydroquinate: chorismate synthase
chorismate biosynthesis from 3−dehydroquinate: 3−dehydroquinate dehydratase
glycolysis III (from glucose): phosphopyruvate hydratase
chorismate biosynthesis from 3−dehydroquinate: shikimate dehydrogenase (NADP+)
guanosine nucleotides degradation III: guanine deaminase
UDP−N−acetylmuramoyl−pentapeptide biosynthesis I (meso−diaminopimelate containing): UDP−N−acetylmuramate dehydrogenase
gondoate biosynthesis (anaerobic): 3−oxoacyl−[acyl−carrier−protein] reductase
glycolysis III (from glucose): 6−phosphofructokinase
glycolysis III (from glucose): phosphoglycerate kinase
glycolysis III (from glucose): pyruvate kinase
gondoate biosynthesis (anaerobic): 3−hydroxyacyl−[acyl−carrier−protein] dehydratase
GDP−mannose biosynthesis: mannose−1−phosphate guanylyltransferase
glycolysis III (from glucose): phosphoglycerate mutase (2,3−diphosphoglycerate−independent)
glycolysis III (from glucose): triose−phosphate isomerase
glycolysis III (from glucose): fructose−bisphosphate aldolase
gondoate biosynthesis (anaerobic): enoyl−[acyl−carrier−protein] reductase (NADH)
glycolysis III (from glucose): glucose−6−phosphate isomerase
preQ0 biosynthesis: 7−cyano−7−deazaguanine synthase
preQ0 biosynthesis: 7−carboxy−7−deazaguanine synthase
queuosine biosynthesis I (de novo): preQ1 synthase
queuosine biosynthesis I (de novo): tRNA−guanosine34 preQ1 transglycosylase
L−lysine biosynthesis III: aspartate−semialdehyde dehydrogenase
superpathway of L−aspartate and L−asparagine biosynthesis: aspartate ammonia−lyase
L−lysine biosynthesis III: 4−hydroxy−tetrahydrodipicolinate synthase
glycolysis IV: diphosphate−−−fructose−6−phosphate 1−phosphotransferase
NAD de novo biosynthesis I (from aspartate): NAD+ synthase (glutamine−hydrolysing)
adenine and adenosine salvage III: hypoxanthine phosphoribosyltransferase
L−lysine biosynthesis III: aspartate kinase
superpathway of L−aspartate and L−asparagine biosynthesis: aspartate−−−ammonia ligase
queuosine biosynthesis I (de novo): S−adenosylmethionine:tRNA ribosyltransferase−isomerase
L−histidine degradation I: urocanate hydratase
L−histidine degradation I: histidine ammonia−lyase
L−histidine degradation I: imidazolonepropionase
inosine 5'−phosphate degradation: 5'−nucleotidase
NAD de novo biosynthesis I (from aspartate): nicotinate−nucleotide adenylyltransferase
inosine 5'−phosphate degradation: IMP dehydrogenase
lipid IVA biosynthesis (E. coli): acyl−[acyl−carrier−protein]−−−UDP−N−acetylglucosamine O−acyltransferase
inosine 5'−phosphate degradation: purine−nucleoside phosphorylase
lipid IVA biosynthesis (E. coli): UDP−2,3−diacylglucosamine diphosphatase
lipid IVA biosynthesis (E. coli): lipid−A−disaccharide synthase
superpathway of L−aspartate and L−asparagine biosynthesis: asparaginase
lipid IVA biosynthesis (E. coli): UDP−3−O−acyl−N−acetylglucosamine deacetylase
L−lysine biosynthesis III: 4−hydroxy−tetrahydrodipicolinate reductase
cis−vaccenate biosynthesis: beta−ketoacyl−[acyl−carrier−protein] synthase II
lipid IVA biosynthesis (E. coli): tetraacyldisaccharide 4'−kinase
L−lysine biosynthesis III: diaminopimelate dehydrogenase
Lactobacillus gasseri
Lactobacillus iners
Lactobacillus crispatus
Lactobacillus jensenii
Bifidobacterium bifidum
Bifidobacterium dentium
Gardnerella vaginalis
Atopobium vaginae
Prevotella timonensis
Bifidobacterium longum
Prevotella bivia
Alloscardovia omnicolens
Anaerococcus tetradius
Peptoniphilus lacrimalis
Prevotella buccalis
Aerococcus christensenii
Dialister micraerophilus
Lactobacillus vaginalis