

Table S1.

Metabolic potentials of *Kocuria Polar* (first ten modules out of 932 analyzed from the genomic studies)

kegg_module	module_name	module_subcategory	module_definition	module_completeness	module_is_complete	kofam_hits_in_module
M00001	Glycolysis (Embden-Meyerhof pathway), glucose => pyruvate	Central carbohydrate metabolism	(K00844,K12407,K00845,K00886,K08074,K00918)(K01810,K06859,K13810,K15916)(K00850,K16370,K21071,K00918)(K01623,K01624,K11645,K16305,K16306) K01803 ((K00134,K00150) K00927,K11389)(K01834,K15633,K15634,K15635) K01689(K00873,K12406)	1	TRUE	K00134,K00134,K00845,K00873,K00873,K00886,K00886,K00886,K00927,K01624,K01624,K01689,K01803,K01834,K13810,K21071
M00002	Glycolysis, core module involving three-carbon compounds	Central carbohydrate metabolism	K01803 ((K00134,K00150) K00927,K11389)(K01834,K15633,K15634,K15635) K01689(K00873,K12406)	1	TRUE	K00134,K00134,K00873,K00873,K00927,K01689,K01803,K01834
M00003	Gluconeogenesis, oxaloacetate => fructose-6P	Central carbohydrate metabolism	(K01596,K01610) K01689 (K01834,K15633,K15634,K15635) K00927 (K00134,K00150) K01803 ((K01623,K01624,K11645) (K03841, K02446, K11532,K01086,K04041),K01622)	1	TRUE	K00134,K00134,K00927,K01596,K01624,K01624,K01689,K01803,K01834,K02446
M00004	Pentose phosphate pathway (Pentose phosphate cycle)	Central carbohydrate metabolism	(K13937,((K00036,K19243) (K01057,K07404))) K00033 K01783 (K01807,K01808) K00615 K00616 (K01810,K06859,K13810,K15916)	1	TRUE	K00033,K00033,K00036,K00036,K00036,K00615,K00616,K01057,K01783,K01808,K13810
M00005	PRPP biosynthesis, ribose 5P => PRPP	Central carbohydrate metabolism	K00948	1	TRUE	K00948
M00006	Pentose phosphate pathway, oxidative phase, glucose 6P => ribulose 5P	Central carbohydrate metabolism	(K13937,((K00036,K19243) (K01057,K07404))) K00033	1	TRUE	K00033,K00033,K00036,K00036,K00036,K01057
M00007	Pentose phosphate pathway, non-oxidative phase, fructose 6P => ribose 5P	Central carbohydrate metabolism	K00615 (K00616,K13810) K01783 (K01807,K01808)	1	TRUE	K00615,K00616,K01783,K01808,K13810
M00008	Entner-Doudoroff pathway, glucose-6P => glyceraldehyde-3P + pyruvate	Central carbohydrate metabolism	K00036 (K01057,K07404) K01690 K01625	0.5	FALSE	K00036,K00036,K00036,K01057
M00009	Citrate cycle (TCA cycle, Krebs cycle)	Central carbohydrate metabolism	(K01647,K05942) (K01681,K01682) (K00031,K00030)(K00164+K00658+K00382,K00174+K00175-K00177-K00176)(K01902+K01903,K01899+K01900,K18118)(K00234+K00235+K00236+K00237,K00239+K00240+K00241-(K00242,K18859,K18860),K00244+K00245+K00246,K00247)(K01676,K01679,K01677+K01678)(K00026,K00025,K00024,K00116)	0.875	TRUE	K00024,K00116,K00164,K00239,K00240,K00240,K00241,K00241,K00242,K00382,K00658,K01647,K01679,K01681,K01902,K01903
M00010	Citrate cycle, first carbon oxidation, oxaloacetate => 2-oxoglutarate	Central carbohydrate metabolism	(K01647,K05942) (K01681,K01682) (K00031,K00030)	0.66666667	FALSE	K01647,K01681

Table S1.

Metabolic potentials of *Kocuria polaris*

kegg_ module	module_name	module_subcategory	module_definition	module_completeness	module_is_complete	kofam_hits_in_module
M00001	Glycolysis (Embden-Meyerhof pathway), glucose => pyruvate	Central carbohydrate metabolism	(K00844,K12407,K00845,K00886,K08074,K00918) (K01810,K06859,K13810,K15916) (K00850,K16370,K21071,K00918) (K01623,K01624,K11645,K16305,K16306) K01803 ((K00134,K00150) K00927,K11389) (K01834,K15633,K15634,K15635) K01689 (K00873,K12406)	1	TRUE	K00134,K00134,K00845,K00873,K00873,K00886,K00886,K00886,K00927,K01624,K01624,K01689,K01803,K01834,K13810,K21071
M00002	Glycolysis, core module involving three-carbon compounds	Central carbohydrate metabolism	K01803 ((K00134,K00150) K00927,K11389) (K01834,K15633,K15634,K15635) K01689 (K00873,K12406)	1	TRUE	K00134,K00134,K00873,K00873,K00927,K01689,K01803,K01834
M00003	Gluconeogenesis, oxaloacetate => fructose-6P	Central carbohydrate metabolism	(K01596,K01610) K01689 (K01834,K15633,K15634,K15635) K00927 (K00134,K00150) K01803 ((K01623,K01624,K11645) (K03841,K02446,K11532,K01086,K04041),K01622)	1	TRUE	K00134,K00134,K00927,K01596,K01624,K01624,K01689,K01803,K01834,K02446
M00004	Pentose phosphate pathway (Pentose phosphate cycle)	Central carbohydrate metabolism	(K13937,((K00036,K19243) (K01057,K07404))) K00033 K01783 (K01807,K01808) K00615 K00616 (K01810,K06859,K13810,K15916)	1	TRUE	K00033,K00033,K00036,K00036,K00036,K00615,K00616,K01057,K01783,K01808,K13810
M00005	PRPP biosynthesis, ribose 5P => PRPP	Central carbohydrate metabolism	K00948	1	TRUE	K00948
M00006	Pentose phosphate pathway, oxidative phase, glucose	Central carbohydrate metabolism	(K13937,((K00036,K19243) (K01057,K07404))) K00033	1	TRUE	K00033,K00033,K00036,K00036,K00036,K01057

	6P => ribulose 5P					
M00 007	Pentose phosphate pathway, non- oxidative phase, fructose 6P => ribose 5P	Central carbohy drate metabol ism	K00615 (K00616,K13810) K01783 (K01807,K01808)	1	TRUE	K00615,K00616,K01783,K01808,K13810
M00 008	Entner- Doudoroff pathway, glucose- 6P => glyceralde hyde-3P + pyruvate	Central carbohy drate metabol ism	K00036 (K01057,K07404) K01690 K01625	0.5	FALSE	K00036,K00036,K00036,K01057
M00 009	Citrate cycle (TCA cycle, Krebs cycle)	Central carbohy drate metabol ism	(K01647,K05942) (K01681,K01682) (K00031,K00030) (K00164+K00658+K00382,K00174+K00175-K00177- K00176) (K01902+K01903,K01899+K01900,K18118) (K00234+K00235+K00236+K00237,K00239+K00240+K0 0241- (K00242,K18859,K18860),K00244+K00245+K00246- K00247) (K01676,K01679,K01677+K01678) (K00026,K00025,K00024,K00116)	0.875	TRUE	K00024,K00116,K00164,K00239,K00240,K00240,K0 0241,K00241,K00242,K00382,K00658,K01647,K0167 9,K01681,K01902,K01903
M00 010	Citrate cycle, first carbon oxidation, oxaloaceta te => 2- oxoglutarate	Central carbohy drate metabol ism	(K01647,K05942) (K01681,K01682) (K00031,K00030)	0.66666 6667	FALSE	K01647,K01681
M00 011	Citrate cycle, second carbon oxidation, 2- oxoglutarate =>	Central carbohy drate metabol ism	(K00164+K00658+K00382,K00174+K00175-K00177- K00176) (K01902+K01903,K01899+K01900,K18118) (K00234+K00235+K00236+K00237,K00239+K00240+K0 0241- (K00242,K18859,K18860),K00244+K00245+K00246- K00247) (K01676,K01679,K01677+K01678) (K00026,K00025,K00024,K00116)	1	TRUE	K00024,K00116,K00164,K00239,K00240,K00240,K0 0241,K00241,K00242,K00382,K00658,K01679,K0190 2,K01903

	oxaloacetate					
M00012	Glyoxylate cycle	Other carbohydrate metabolism	K01647 (K01681,K01682) K01637 (K01638,K19282) (K00026,K00025,K00024)	1	TRUE	K00024,K01637,K01638,K01638,K01647,K01681
M00013	Malonate semialdehyde pathway, propanoyl-CoA => acetyl-CoA	Other carbohydrate metabolism	(K00248,K00232) (K07511,K14729) K05605 K23146 K00140	0.4	FALSE	K00140,K00140,K00232
M00014	Glucuronate pathway (uronate pathway)	Other carbohydrate metabolism	K00012 ((K12447 K16190),(K00699 (K01195,K14756))) K00002 K13247 -- K03331 (K05351,K00008) K00854	0.333333333	FALSE	K00008,K00012,K00854,K00854
M00015	Proline biosynthesis, glutamate => proline	Arginine and proline metabolism	((K00931 K00147),K12657) K00286	1	TRUE	K00147,K00286,K00931
M00016	Lysine biosynthesis, succinyl-DAP pathway, aspartate => lysine	Lysine metabolism	(K00928,K12524,K12525,K12526) K00133 K01714 K00215 K00674 (K00821,K14267) K01439 K01778 (K01586,K12526)	1	TRUE	K00133,K00215,K00674,K00821,K00928,K01439,K01586,K01586,K01714,K01714,K01714,K01778
M00017	Methionine biosynthesis, aspartate => homoserine => methionine	Cysteine and methionine metabolism	(K00928,K12524,K12525) K00133 (K00003,K12524,K12525) (K00651,K00641) K01739 (K01760,K14155) (K00548,K24042,K00549)	0.857142857	TRUE	K00003,K00133,K00549,K00549,K00549,K00549,K00641,K00928,K01739

M00 018	Threonine biosynthesis, aspartate => homoserine => threonine	Serine and threonine metabolism	(K00928,K12524,K12525,K12526) K00133 (K00003,K12524,K12525) (K00872,K02204,K02203) K01733	1	TRUE	K00003,K00133,K00872,K00928,K01733
M00 019	Valine/isoleucine biosynthesis, pyruvate => valine / 2-oxobutanoate => isoleucine	Branchd-chain amino acid metabolism	K01652+(K01653,K11258) K00053 K01687 K00826	1	TRUE	K00053,K00826,K01652,K01652,K01652,K01652,K01652,K01653,K01687,K01687
M00 020	Serine biosynthesis, glycerate-3P => serine	Serine and threonine metabolism	K00058 K00831 (K01079,K02203,K22305)	1	TRUE	K00058,K00058,K00058,K00831,K01079
M00 021	Cysteine biosynthesis, serine => cysteine	Cysteine and methionine metabolism	(K00640,K23304) (K01738,K13034,K17069)	1	TRUE	K00640,K00640,K00640,K01738
M00 022	Shikimate pathway, phosphoenolpyruvate + erythrose-4P => chorismate	Aromatic amino acid metabolism	(K01626,K03856,K13853) (((K01735,K13829) ((K03785,K03786) K00014,K13832)),K13830) ((K00891,K13829) (K00800,K24018),K13830) K01736	1	TRUE	K00014,K00014,K00800,K00891,K01626,K01735,K01736,K03786
M00 023	Tryptophan biosynthesis, chorismate	Aromatic amino acid metabolism	(((K01657+K01658,K13503,K13501,K01656) K00766),K13497) (((K01817,K24017) (K01656,K01609)),K13498,K13501) (K01695+(K01696,K06001),K01694)	1	TRUE	K00766,K01609,K01657,K01658,K01695,K01696,K24017

	e => tryptophan					
M00024	Phenylalanine biosynthesis, chorismate => phenylpyruvate => phenylalanine	Aromatic amino acid metabolism	((K01850,K04092,K14187,K04093,K04516,K06208,K06209) (K01713,K04518,K05359),K14170) (K00832,K00838)	0.666666667	FALSE	K04092,K04518
M00025	Tyrosine biosynthesis, chorismate => HPP => tyrosine	Aromatic amino acid metabolism	((((K01850,K04092,K14170,K04093,K04516,K06208,K06209) (K04517,K00211)),K14187) (K00832,K00838)	0.666666667	FALSE	K04092,K04517
M00026	Histidine biosynthesis, PRPP => histidine	Histidine metabolism	(K00765-K02502) (K01523 K01496,K11755,K14152) (K01814,K24017) (K02501+K02500,K01663) ((K01693 K00817 (K04486,K05602,K18649)),(K01089 K00817)) (K00013,K14152)	1	TRUE	K00013,K00765,K00817,K00817,K01496,K01523,K01693,K02500,K02501,K05602,K24017
M00027	GABA (gamma-Aminobutyrate) shunt	Other amino acid metabolism	K01580 (K13524,K07250,K00823,K16871) (K00135,K00139,K17761)	0.666666667	FALSE	K00135,K00135,K07250
M00028	Ornithine biosynthesis, glutamate => ornithine	Arginine and proline metabolism	(K00618,K00619,K14681,K14682,K00620,K22477,K22478) ((K00930,K22478) K00145,K12659) (K00818,K00821) (K01438,K14677,K00620)	1	TRUE	K00145,K00619,K00620,K00821,K00930,K01438,K22477
M00029	Urea cycle	Arginine and proline metabolism	K01948 K00611 K01940 (K01755,K14681) K01476	0.6	FALSE	K00611,K01755,K01940
M00032	Lysine degradation, lysine	Lysine metabolism	K14157 K14085 K00825 (K15791+K00658+K00382) K00252 (K07514,(K07515,K07511) K00022)	0.277777778	FALSE	K00252,K00252,K00252,K00252,K00382,K00658

	=> saccharopine => acetoacetyl-CoA					
M00033	Ectoine biosynthesis, aspartate => ectoine	Serine and threonine metabolism	K00928 K00133 K00836 K06718 K06720	0.4	FALSE	K00133,K00928
M00034	Methionine salvage pathway	Cysteine and methionine metabolism	K00789 K01611 K00797 ((K01243,K01244) K00899,K00772) K08963 (K16054,K08964 (K09880,K08965 K08966)) K08967 (K00815,K08969,K23977,K00832,K00838)	0.333333333	FALSE	K00789,K00797,K01243
M00035	Methionine degradation	Cysteine and methionine metabolism	K00789 (K00558,K17398,K17399) K01251 (K01697,K10150)	0.25	FALSE	K00789
M00036	Leucine degradation, leucine => acetoacetate + acetyl-CoA	Branchd-chain amino acid metabolism	K00826 ((K00166+K00167,K11381)+K09699+K00382) (K00253,K00249) (K01968+K01969) (K05607,K13766) K01640	0.472222222	FALSE	K00249,K00249,K00382,K00826,K01969
M00038	Tryptophan metabolism, tryptophan => kynurenine => 2-aminomucionate	Aromatic amino acid metabolism	(K00453,K00463) (K01432,K14263,K07130) K00486 K01556 K00452 K03392 (K10217,K23234)	0.142857143	FALSE	K07130,K07130
M00039	Monolignol biosynthesis	Biosynthesis of phytoch	(K10775,K13064) K00487 K01904 K13065 K09754 K00588 K09753 K09755 K13066 (K00083,K22395)	0.1	FALSE	K00588

	is, phenylalanine/tyrosine => monolignol	emical compounds				
M00040	Tyrosine biosynthesis, chorismate => aroenate => tyrosine	Aromatic amino acid metabolism	(K01850,K04092,K14170) (K00832,K15849) (K00220,K24018,K15227)	0.33333333	FALSE	K04092
M00044	Tyrosine degradation, tyrosine => homogentisate	Aromatic amino acid metabolism	(K00815,K00838,K00832,K03334) K00457 K00451 K01800 (K01555,K16171)	0.6	FALSE	K00451,K00457,K01555
M00046	Pyrimidine degradation, uracil => beta-alanine, thymine => 3-aminoisobutanoate	Pyrimidine metabolism	(K00207,K17722+K17723) K01464 (K01431,K06016)	0.33333333	FALSE	K06016
M00048	Inosine monophosphate biosynthesis, PRPP + glutamine => IMP	Purine metabolism	K00764 (K01945,K11787,K11788,K13713) (K00601,K11175,K08289,K11787,K01492) (K01952,(K23269+K23264+K23265),(K23270+K23265)) (K01933,K11787,K11788 (K01587,K11808,K01589 K01588)) (K01923,K01587,K13713) K01756 (K00602,(K01492,K06863 K11176))	1	TRUE	K00602,K00764,K01588,K01589,K01756,K01923,K01933,K01945,K11175,K23264,K23265,K23269
M00049	Adenine ribonucleotide biosynthesis, IMP => ADP,ATP	Purine metabolism	K01939 K01756 (K00939,K18532,K18533,K00944) (K00940,K00873,K12406)	1	TRUE	K00873,K00873,K00939,K00940,K01756,K01939

M00050	Guanine ribonucleotide biosynthesis is IMP => GDP,GTP	Purine metabolism	K00088 K01951 K00942 (K00940,K18533,K00873,K12406)	1	TRUE	K00088,K00088,K00873,K00873,K00940,K00942,K01951,K01951
M00051	Uridine monophosphate biosynthesis, glutamine (+ PRPP) => UMP	Pyrimidine metabolism	(K11540,(K11541 K01465),((K01954,K01955+K01956) (K00609+K00610,K00608) K01465)) (K00226,K00254,K17828) (K13421,K00762 K01591)	0.91666667	TRUE	K00254,K00609,K00762,K01465,K01591,K01955,K01956
M00052	Pyrimidine ribonucleotide biosynthesis, UMP => UDP/UTP ,CDP/CTP	Pyrimidine metabolism	(K13800,K13809,K09903) (K00940,K18533) K01937	1	TRUE	K00940,K01937,K09903
M00053	Pyrimidine deoxyribonucleotide biosynthesis, CDP/CTP => dCDP/dCTP,dTDP/dTTP	Pyrimidine metabolism	(K00524,K00525+K00526,K10807+K10808) (K00940,K18533) (K00527,K21636) K01494 K01520 (K00560,K13998) K00943 K00940	0.875	TRUE	K00525,K00526,K00560,K00940,K00943,K01494,K01520
M00064	ADP-L-glycero-D-mannoheptose biosynthesis	Lipopolysaccharide metabolism	K03271 (K03272,K21344) K03273 (K03272,K21345) K03274	0.8	TRUE	K03271,K03272,K03273
M00082	Fatty acid biosynthesis	Fatty acid	(K11262,(K02160+K01961,K11263)+(K01962+K01963,K18472)) (K00665,K00667+K00668,K11533,(K00645 (K00648,K18473)))	0.83333333	TRUE	K00645,K00648,K02160,K11263

	is, initiation	metabolism				
M00083	Fatty acid biosynthesis, elongation	Fatty acid metabolism	K00665,(K00667 K00668),K11533,((K00647,K09458) K00059 (K02372,K01716,K16363) (K00208,K02371,K10780,K00209))	0.5	FALSE	K00059,K00059,K00059,K00059,K00059,K00059,K00059,K09458
M00086	beta-Oxidation, acyl-CoA synthesis	Fatty acid metabolism	K01897,K15013	1	TRUE	K01897,K01897,K01897
M00087	beta-Oxidation	Fatty acid metabolism	(K00232,K00249,K00255,K06445,K09479) (((K01692,K07511,K13767) (K00022,K07516))),K01825,K01782,K07514,K07515,K10527) (K00632,K07508,K07509,K07513)	0.75	TRUE	K00232,K00249,K00249,K00632,K01692,K01692,K01692,K01692,K01692
M00088	Ketone body biosynthesis, acetyl-CoA => acetoacetate/3-hydroxybutyrate/acetone	Lipid metabolism	K00626 K01641 K01640 K00019 K01574	0.4	FALSE	K00019,K00626,K00626,K00626,K00626,K00626
M00089	Triacylglycerol biosynthesis	Lipid metabolism	(K00629,K13506,K13507,K00630,K13508) (K00655,K13509,K13523,K19007,K13513,K13517,K13519,K14674,K22831) (K01080,K15728,K18693) (K11155,K11160,K14456,K22848,K22849)	0.25	FALSE	K00655,K00655,K00655,K00655
M00093	Phosphatidylethanolamine (PE) biosynthesis, PA => PS => PE	Lipid metabolism	K00981 (K00998,K17103) K01613	0.333333333	FALSE	K00981
M00095	C5 isoprenoid biosynthesis, mevalonate pathway	Terpenoid backbone biosynthesis	K00626 K01641 K00021 K00869 (K00938,K13273) K01597 K01823	0.285714286	FALSE	K00626,K00626,K00626,K00626,K00626,K01823
M00096	C5 isoprenoid biosynthesis	Terpenoid backbone	K01662 K00099 (K00991,K12506) K00919 (K01770,K12506) K03526 K03527 K01823	1	TRUE	K00099,K00919,K00991,K01662,K01770,K01823,K03526,K03527

	is, non-mevalonate pathway	ne biosynthesis				
M00097	beta-Carotene biosynthesis, GGAP => beta-carotene	Plant terpenoid biosynthesis	K02291 K02293 K15744 K00514 K09835 K06443	0.33333333	FALSE	K02291,K06443
M00098	Acylglycerol degradation	Lipid metabolism	(K01046,K12298,K16816,K13534,K14073,K14074,K14075,K14076,K22283,K14452,K22284,K14674,K14675,K17900) K01054	0.5	FALSE	K01046
M00113	Jasmonic acid biosynthesis	Lipid metabolism	K00454 K01723 K10525 K05894 K10526 K00232 K10527 K07513 --	0.11111111	FALSE	K00232
M00114	Ascorbate biosynthesis, plants, fructose-6P => ascorbate	Other carbohydrate metabolism	K01809 K17497 K00966 K10046 K14190 K10047 K17744 K00225	0.125	FALSE	K01809
M00115	NAD biosynthesis, aspartate => quinolinic acid => NAD	Cofactor and vitamin metabolism	(K00278,K06989) K03517 K00767 (K00969,K06210) (K01916,K01950)	1	TRUE	K00278,K00767,K00969,K01916,K01916,K03517
M00116	Menaquinone biosynthesis, chorismate (+ polyprenyl-PP) => menaquinol	Cofactor and vitamin metabolism	K02552 K02551 K08680 K02549 K01911 K01661 K19222 K02548 K03183	0.88888889	TRUE	K01661,K01911,K02548,K02549,K02551,K02552,K03183,K19222,K19222
M00117	Ubiquinone biosynthesis,	Cofactor and vitamin	(K03181,K18240) K03179 (K03182+K03186) K18800 K00568 K03185 K03183 K03184 K00568	0.11111111	FALSE	K03183

	prokaryotes, chorismate (+ polyprenyl-PP) => ubiquinol	metabolism				
M00119	Pantothenate biosynthesis, valine/L-aspartate => pantothenate	Cofactor and vitamin metabolism	K00826 K00606 K00077 K01579 (K01918,K13799)	0.8	TRUE	K00606,K00826,K01579,K01918
M00120	Coenzyme A biosynthesis, pantothenate => CoA	Cofactor and vitamin metabolism	(K00867,K03525,K01947,K09680) ((K01922,K21977) K01598,K13038) (K02318,(K00954,K02201) K00859)	1	TRUE	K00859,K00867,K00954,K13038
M00121	Heme biosynthesis, plants and bacteria, glutamate => heme	Cofactor and vitamin metabolism	K01885 K02492 K01845 K01698 K01749 (K01719,K13542,K13543) K01599 (K00228,K02495) (K00230,K00231,K08973) K01772	1	TRUE	K00230,K00231,K00231,K01599,K01698,K01719,K01719,K01719,K01749,K01772,K01845,K01885,K01885,K02492,K02495
M00122	Cobalamin biosynthesis, cobyrinate a,c- diamide => cobalamin	Cofactor and vitamin metabolism	(K00798,K19221) K02232 (K02225,K02227) K02231 K00768 (K02226,K22316) K02233	0.142857143	FALSE	K02226
M00124	Pyridoxal-P biosynthesis, erythrose-	Cofactor and vitamin metabolism	K03472 K03473 K00831 K00097 K03474 K00275	0.333333333	FALSE	K00275,K00831

	4P => pyridoxal-P					
M00125	Riboflavin biosynthesis, plants and bacteria, GTP => riboflavin/FMN/FA D	Cofactor and vitamin metabolism	(K01497,K14652) (K01498 K00082,K11752) (K22912,K20860,K20861,K20862,K21063,K21064) (K02858,K14652) K00794 K00793 (K20884 K22949,K11753)	1	TRUE	K00793,K00794,K01497,K02858,K11752,K11752,K11753,K21064,K21064
M00126	Tetrahydrofolate biosynthesis, GTP => THF	Cofactor and vitamin metabolism	(K01495,K09007,K22391) (K01077,K01113,(K08310,K19965)) ((K13939,(K13940,K01633 K00950) K00796),(K01633 K13941)) (K11754,K20457) (K00287,K13998)	0.857142857	TRUE	K00287,K00796,K00950,K01495,K01633,K11754,K22391
M00127	Thiamine biosynthesis, prokaryotes, AIR (+DXP/tyrosine) => TMP/TPP	Cofactor and vitamin metabolism	K03148+K03154 K03151 K03150 K03149 K03147 ((K00941 K00788),K14153,K21219) K00946	0.5625	FALSE	K00788,K00788,K00941,K00946,K03149,K03154
M00129	Ascorbate biosynthesis, animals, glucose-1P => ascorbate	Other carbohydrate metabolism	K00963 K00012 K00699 K01195 K00002 K01053 K00103	0.428571429	FALSE	K00012,K00963,K01053
M00131	Inositol phosphate metabolism, Ins(1,3,4,5)P4 => Ins(1,3,4)P3 => myo-inositol	Other carbohydrate metabolism	K01106 K01107 K01109 K01092	0.25	FALSE	K01092
M00133	Polyamine biosynthesis	Polyamine	(K01583,K01584,K01585,K02626) K01480 K01611 K00797	0.5	FALSE	K00797,K01480

	is, arginine => agmatine => putrescine => spermidine	biosynthesis				
M00135	GABA biosynthesis, eukaryotes, putrescine => GABA	Polyamine biosynthesis	K00657 K00274 (K00128,K14085,K00149) --	0.25	FALSE	K00274
M00140	C1-unit interconversion, prokaryotes	Cofactor and vitamin metabolism	K00600 (K01491,(K00300 K01500)) K01938	1	TRUE	K00600,K00600,K01491,K01500,K01938
M00141	C1-unit interconversion, eukaryotes	Cofactor and vitamin metabolism	K00600 (K00288,(K13403 K13402))	0.5	FALSE	K00600,K00600
M00149	Succinate dehydrogenase, prokaryotes	ATP synthesis	K00241+(K00242,K18859,K18860)+K00239+K00240	1	TRUE	K00239,K00240,K00240,K00241,K00241,K00242
M00151	Cytochrome bc1 complex respiratory unit	ATP synthesis	((K00412+K00413,K00410)+K00411),K03886+K03887+K03888,K03890+K03891+K03889	1	TRUE	K03889,K03890,K03891
M00154	Cytochrome c oxidase	ATP synthesis	(K02257+K02262+K02256+K02261+K02263+K02264+K02265+K02266+K02267+K02268+K02270-K02271+K02272-K02273+K02258+K02259+K02260)	0.13333333	FALSE	K02257,K02259
M00155	Cytochrome c oxidase, prokaryotes	ATP synthesis	K02275+(K02274+K02276,K15408)-K02277	1	TRUE	K02274,K02275,K02276

M00157	F-type ATPase, prokaryotes and chloroplasts	ATP synthesis	K02111+K02112+K02113+K02114+K02115+K02108+K02109+K02110	1	TRUE	K02108,K02109,K02110,K02111,K02112,K02113,K02114,K02115
M00162	Cytochrome b6f complex	ATP synthesis	K02635+K02637+K02634+K02636+K02642+K02643+K03689+K02640	0.125	FALSE	K02636
M00165	Reductive pentose phosphate cycle (Calvin cycle)	Carbon fixation	K00855 (K01601-K01602) K00927 (K05298,K00150,K00134) (K01623,K01624) (K03841,K02446,K11532,K01086) K00615 (K01623,K01624) (K01100,K11532,K01086) K00615 (K01807,K01808)	0.727272727	FALSE	K00134,K00134,K00615,K00927,K01624,K01624,K01808,K02446
M00166	Reductive pentose phosphate cycle, ribulose-5P => glyceraldehyde-3P	Carbon fixation	K00855 (K01601-K01602) K00927 (K05298,K00150,K00134)	0.5	FALSE	K00134,K00134,K00927
M00167	Reductive pentose phosphate cycle, glyceraldehyde-3P => ribulose-5P	Carbon fixation	(K01623,K01624) (K03841,K02446,K11532,K01086) K00615 (K01623,K01624) (K01100,K11532,K01086) K00615 (K01807,K01808)	0.857142857	TRUE	K00615,K01624,K01624,K01808,K02446
M00168	CAM (Crassulacean acid metabolism), dark	Carbon fixation	K01595 (K00025,K00026,K00024)	1	TRUE	K00024,K01595
M00170	C4-dicarboxylic acid cycle, phosphoenolpyruvate	Carbon fixation	K01595 K14454 K14455 K01610	0.25	FALSE	K01595

	carboxykinase type					
M00171	C4-dicarboxylic acid cycle, NAD - malic enzyme type	Carbon fixation	K01595 K14454 K14455 (K00025,K00026) K00028 (K00814,K14272) K01006	0.142857143	FALSE	K01595
M00172	C4-dicarboxylic acid cycle, NADP - malic enzyme type	Carbon fixation	K01595 K00051 K00029 K01006	0.25	FALSE	K01595
M00173	Reductive citrate cycle (Arnon-Buchanan cycle)	Carbon fixation	(K00169+K00170+K00171+K00172,K03737) ((K01007,K01006) K01595,K01959+K01960,K01958) K00024 (K01676,K01679,K01677+K01678) (K00239+K00240-K00241-K00242,K00244+K00245-K00246-K00247,K18556+K18557+K18558+K18559+K18560) (K01902+K01903) (K00174+K00175-K00177-K00176) K00031 (K01681,K01682) (K15230+K15231,K15232+K15233 K15234)	0.636363636	FALSE	K00024,K00239,K00240,K00240,K00241,K00241,K00242,K01007,K01007,K01595,K01679,K01681,K01902,K01903,K01958,K01958
M00176	Assimilatory sulfate reduction, sulfate => H2S	Sulfur metabolism	(K13811,K00958+K00860,K00955+K00957,K00956+K00957+K00860) K00390 (K00380+K00381,K00392)	0.888888889	TRUE	K00390,K00392,K00956,K00957
M00307	Pyruvate oxidation, pyruvate => acetyl-CoA	Central carbohydrate metabolism	((K00163,K00161+K00162)+K00627+K00382-K13997),K00169+K00170+K00171+(K00172,K00189),K03737	1	TRUE	K00161,K00162,K00162,K00163,K00163,K00382,K00627
M00308	Semi-phosphorylative Entner-Doudoroff pathway, gluconate	Central carbohydrate metabolism	K05308 K00874 K01625 (K00134 K00927,K00131,K18978)	0.4	FALSE	K00134,K00134,K00927

	=> glycerate-3P					
M00344	Formaldehyde assimilation, xylulose monophosphate pathway	Methanometabolism	K17100 K00863 K01624 K03841	0.25	FALSE	K01624,K01624
M00345	Formaldehyde assimilation, ribulose monophosphate pathway	Methanometabolism	((K08093,K13812) K08094),K13831) (K00850,K16370) K01624	0.333333333	FALSE	K01624,K01624
M00346	Formaldehyde assimilation, serine pathway	Methanometabolism	K00600 K00830 K00018 K11529 K01689 K01595 K00024 K08692+K14067 K08691	0.555555556	FALSE	K00024,K00600,K00600,K00830,K01595,K01689
M00357	Methanogenesis, acetate => methane	Methanometabolism	((K00925 K00625),K01895) (K00193+K00197+K00194) (K00577+K00578+K00579+K00580+K00581-K00582-K00583+K00584) (K00399+K00401+K00402) (K22480+K22481+K22482,K03388+K03389+K03390,K08264+K08265,K03388+K03389+K03390+K14127+(K14126+K14128,K22516+K00125))	0.2	FALSE	K00925,K01895,K01895
M00364	C10-C20 isoprenoid biosynthesis, bacteria	Terpenoid backbone biosynthesis	K01823 (K00795,K13789,K13787)	1	TRUE	K01823,K13787,K13787
M00365	C10-C20 isoprenoid biosynthesis, archaea	Terpenoid backbone biosynthesis	K01823 K13787	1	TRUE	K01823,K13787,K13787
M00366	C10-C20 isoprenoid	Terpenoid	K01823 K14066 K00787 K13789	0.25	FALSE	K01823

	biosynthesis, plants	backbone biosynthesis				
M00367	C10-C20 isoprenoid biosynthesis, non-plant eukaryotes	Terpenoid backbone biosynthesis	K01823 K00787 K00804	0.333333333	FALSE	K01823
M00368	Ethylene biosynthesis, methionine => ethylene	Cysteine and methionine metabolism	K00789 (K01762,K20772) K05933	0.333333333	FALSE	K00789
M00373	Ethylmalonyl pathway	Other carbohydrate metabolism	K00626 K00023 K17865 K14446 K14447 K14448 K14449 K08691 K14451 K01965+K01966 K05606 K01847	0.125	FALSE	K00626,K00626,K00626,K00626,K00626,K01966
M00374	Dicarboxylate-hydroxybutyrate cycle	Carbon fixation	(K00169+K00170+K00171+K00172) K01007 K01595 K00024 (K01677+K01678) (K00239+K00240-K00241-K18860) (K01902+K01903) (K15038,K15017) K14465 (K14467,K18861) K14534 K15016 K00626	0.461538462	FALSE	K00024,K00239,K00240,K00240,K00241,K00241,K00626,K00626,K00626,K00626,K00626,K01007,K01007,K01595,K01902,K01903
M00375	Hydroxypropionate-hydroxybutyrate cycle	Carbon fixation	(K01964+K15037+K15036) K15017 K15039 K15018 K15019 K15020 K05606 (K01848+K01849) (K15038,K15017) K14465 (K14466,K18861) K14534 K15016 K00626	0.071428571	FALSE	K00626,K00626,K00626,K00626,K00626
M00376	3-Hydroxypropionate bi-cycle	Carbon fixation	(K02160+K01961+K01962+K01963) K14468 K14469 K15052 K05606 (K01847,K01848+K01849) (K14471+K14472) (K00239+K00240+K00241) K01679 K08691 K14449 K14470 K09709	0.173076923	FALSE	K00239,K00240,K00240,K00241,K00241,K01679,K02160
M00377	Reductive acetyl-CoA pathway (Wood-Ljungdahl pathway)	Carbon fixation	K00198 K05299-K15022 K01938 K01491 K00297 K15023 K14138+K00197+K00194	0.428571429	FALSE	K00297,K01491,K01938

M00432	Leucine biosynthesis, 2-oxoisovalerate => 2-oxoisocaproate	Branch d-chain amino acid metabolism	K01649 (K01702,K01703+K01704) K00052	1	TRUE	K00052,K01649,K01703,K01704
M00525	Lysine biosynthesis, acetyl-DAP pathway, aspartate => lysine	Lysine metabolism	K00928 K00133 K01714 K00215 K05822 K00841 K05823 K01778 K01586	0.666666667	FALSE	K00133,K00215,K00928,K01586,K01586,K01714,K01714,K01714,K01778
M00526	Lysine biosynthesis, DAP dehydrogenase pathway, aspartate => lysine	Lysine metabolism	(K00928,K12524,K12525,K12526) K00133 K01714 K00215 K03340 (K01586,K12526)	0.833333333	TRUE	K00133,K00215,K00928,K01586,K01586,K01714,K01714,K01714
M00527	Lysine biosynthesis, DAP aminotransferase pathway, aspartate => lysine	Lysine metabolism	(K00928,K12524,K12525,K12526) K00133 K01714 K00215 K10206 K01778 (K01586,K12526)	0.857142857	TRUE	K00133,K00215,K00928,K01586,K01586,K01714,K01714,K01714,K01778
M00529	Denitrification, nitrate => nitrogen	Nitrogen metabolism	(K00370+K00371+K00374,K02567+K02568) (K00368,K15864) (K04561+K02305) K00376	0.5	FALSE	K00368,K00370,K00371,K00374
M00530	Dissimilatory nitrate reduction, nitrate => ammonia	Nitrogen metabolism	(K00370+K00371+K00374,K02567+K02568) (K00362+K00363,K03385+K15876)	1	TRUE	K00362,K00363,K00370,K00371,K00374
M00531	Assimilatory nitrate reduction,	Nitrogen metabolism	(K00367,K10534,K00372-K00360) (K00366,K17877)	0.5	FALSE	K00367,K00372

	nitrate => ammonia					
M00532	Photorespiration	Other carbohydrate metabolism	(K01601-K01602) K19269 K11517 K03781 K14272 K00600 K00830 (K15893,K15919) K15918 K00281+K00605+K00382+K02437	0.4	FALSE	K00281,K00281,K00382,K00600,K00600,K00605,K00830,K02437,K02437,K03781,K03781
M00533	Homoproteocatechuate degradation, homoproteocatechuate => 2-oxohept-3-enedioate	Aromatic amino acid metabolism	K00455 K00151 K01826 K05921	0.25	FALSE	K05921
M00535	Isoleucine biosynthesis, pyruvate => 2-oxobutanoate	Branchd-chain amino acid metabolism	K09011 K01703+K01704 K00052	0.666666667	FALSE	K00052,K01703,K01704
M00537	Xylene degradation, xylene => methylbenzoate	Aromatic degradation	K15757+K15758 K00055 K00141	0.666666667	FALSE	K00055,K00141
M00538	Toluene degradation, toluene => benzoate	Aromatic degradation	K15760+K15761-K15762+K15763+K15764-K15765 K00055 K00141	0.666666667	FALSE	K00055,K00141
M00545	Trans-cinnamate degradation, trans-cinnamate => acetyl-CoA	Aromatic degradation	((K05708+K05709+K05710+K00529) K05711),K05712) K05713 K05714 K02554 K01666 K04073	0.166666667	FALSE	K00529,K05710,K05710,K05712

M00546	Purine degradation, xanthine => urea	Purine metabolism	(K00106,K00087+K13479+K13480,K13481+K13482,K11177+K11178+K13483) (K00365,K16838,K16839,K22879) (K13484,K07127 (K13485,K16838,K16840)) (K01466,K16842) K01477	0.833333333	TRUE	K00365,K01466,K07127,K13481,K13482,K16840
M00549	Nucleotide sugar biosynthesis, glucose => UDP-glucose	Other carbohydrate metabolism	(K00844,K00845,K12407,K00886) (K01835,K15779,K15778) (K00963,K12447)	1	TRUE	K00845,K00886,K00886,K00886,K00963,K01835
M00550	Ascorbate degradation, ascorbate => D-xylulose-5P	Other carbohydrate metabolism	K02821+K02822+K03475 K03476 K03078 K03079 K03077	0.533333333	FALSE	K02821,K03077,K03079,K03475
M00551	Benzoate degradation, benzoate => catechol / methylbenzoate => methylcatechol	Aromatic degradation	K05549+K05550+K05784 K05783	1	TRUE	K05549,K05550,K05783,K05784
M00552	D-galactonate degradation, De Ley-Doudoroff pathway, D-galactonate => glycerate-3P	Other carbohydrate metabolism	K01684 K00883 K01631 K00134 K00927	0.4	FALSE	K00134,K00134,K00927
M00554	Nucleotide sugar biosynthesis	Other carbohydrate	K00849 K00965	1	TRUE	K00849,K00849,K00965,K00965

	is, galactose => UDP- galactose	metabol ism				
M00 555	Betaine biosynthes is, choline => betaine	Serine and threonin e metabol ism	(K17755,((K00108,K11440,K00499) (K00130,K14085)))	1	TRUE	K00108,K00130,K17755
M00 565	Trehalose biosynthes is, D- glucose 1P => trehalose	Other carbohy drate metabol ism	K00975 K00703 (K00700,K16149) K01214 K06044 K01236	0.83333 3333	TRUE	K00700,K00975,K00975,K01214,K01236,K06044
M00 568	Catechol ortho- cleavage, catechol => 3- oxoadipat e	Aromati cs degrada tion	K03381 K01856 K03464 (K01055,K14727)	0.75	TRUE	K01055,K01055,K01055,K03381,K03464
M00 569	Catechol meta- cleavage, catechol => acetyl- CoA / 4- methylcat echol => propanoyl -CoA	Aromati cs degrada tion	(K00446,K07104) ((K10217 K01821 K01617),K10216) (K18364,K02554) (K18365,K01666) (K18366,K04073)	0.28571 4286	FALSE	K01821,K07104
M00 570	Isoleucine biosynthes is, threonine => 2- oxobutano ate => isoleucine	Branche d-chain amino acid metabol ism	(K17989,K01754) K01652+(K01653,K11258) K00053 K01687 K00826	1	TRUE	K00053,K00826,K01652,K01652,K01652,K01652,K01652,K01653,K01687,K01687,K01754
M00 572	Pimeloyl- ACP biosynthes	Cofacto r and vitamin	K02169 (K00647,K09458) K00059 K02372 K00208 (K02170,K09789,K19560,K19561)	0.33333 3333	FALSE	K00059,K00059,K00059,K00059,K00059,K00059,K0059,K09458

	is, BioC-BioH pathway, malonyl-ACP => pimeloyl-ACP	metabolism				
M00579	Phosphate acetyltransferase- acetate kinase pathway, acetyl-CoA => acetate	Carbon fixation	(K00625,K13788,K15024) K00925	1	TRUE	K00925,K13788
M00609	Cysteine biosynthesis, methionine => cysteine	Cysteine and methionine metabolism	K00789 K17462 K01243 K07173 K17216 K17217	0.333333333	FALSE	K00789,K01243
M00611	Oxygenic photosynthesis in plants and cyanobacteria	Metabolic capacity	(M00161,M00163) M00165	0.363636364	FALSE	K00134,K00134,K00615,K00927,K01624,K01624,K01808,K02446
M00612	Anoxygenic photosynthesis in purple bacteria	Metabolic capacity	M00597 M00165	0.363636364	FALSE	K00134,K00134,K00615,K00927,K01624,K01624,K01808,K02446
M00613	Anoxygenic photosynthesis in green nonsulfur bacteria	Metabolic capacity	M00597 M00376	0.086538462	FALSE	K00239,K00240,K00240,K00241,K00241,K00242,K01679,K01966,K02160
M00614	Anoxygenic photosynthesis	Metabolic capacity	M00598 M00173	0.318181818	FALSE	K00024,K00239,K00240,K00240,K00241,K00241,K00242,K01007,K01007,K01595,K01679,K01681,K01902,K01903,K01958,K01958

	hesis in green sulfur bacteria					
M00615	Nitrate assimilation	Metabolic capacity	(K02575,K15576+K15577+K15578-K15579) M00531	0.75	TRUE	K00367,K00372,K02575,K02575
M00616	Sulfate-sulfur assimilation	Metabolic capacity	(K02048,K23163)+K02046+K02047+K02045 M00176	0.44444444	FALSE	K00390,K00392,K00956,K00957
M00617	Methanogen	Metabolic capacity	M00567,M00357,M00356,M00563	0.2	FALSE	K00925,K01895,K01895,K13788
M00618	Acetogen	Metabolic capacity	M00377 M00579	0.714285714	FALSE	K00297,K00925,K01491,K01938,K13788
M00620	Incomplete reductive citrate cycle, acetyl-CoA => oxoglutarate	Carbon fixation	(K00169+K00170+K00171+K00172) (K01959+K01960) K00024 (K01677+K01678) (K18209+K18210) (K01902+K01903) (K00174+K00175+K00176+K00177)	0.285714286	FALSE	K00024,K01902,K01903
M00627	beta-Lactam resistance, Bla system	Drug resistance	K02172 K02171 (K18766,K17836)	0.333333333	FALSE	K17836
M00632	Galactose degradation, Leloir pathway, galactose => alpha-D-glucose-1P	Other carbohydrate metabolism	K01785 K00849 K00965 K01784	1	TRUE	K00849,K00849,K00965,K00965,K01784,K01784,K01785,K01785
M00651	Vancomycin resistance,	Drug resistance	(K18345 K18344 K07260 K18346),(K18351 K18352 K18354 K18353) (K18347 K15739 K08641)	0.142857143	FALSE	K07260,K07260

	D-Ala-D-Lac type					
M00714	Multidrug resistance, efflux pump QacA	Drug resistance	K18938 K08167	0.5	FALSE	K08167,K08167
M00725	Cationic antimicrobial peptide (CAMP) resistance, dltABCD operon	Drug resistance	K19077 K19078 K03367+K03739+K14188+K03740	0.083333333	FALSE	K03367
M00740	Methylaspartate cycle	Other carbohydrate metabolism	K01647 K01681 K00031 K00261 K19268+K01846 K04835 K19280 K14449 K19281 K19282 K00024	0.272727273	FALSE	K00024,K01647,K01681
M00741	Propanoyl-CoA metabolism, propanoyl-CoA => succinyl-CoA	Other carbohydrate metabolism	(K01965+K01966,K11263+(K18472,K19312+K22568),K01964+K15036+K15037) K05606 (K01847,K01848+K01849)	0.166666667	FALSE	K01966,K11263
M00778	Type II polyketide backbone biosynthesis, acyl-CoA + malonyl-CoA => polyketide	Type II polyketide biosynthesis	K05551+K05552+K05553 -K12420 ((K05554,K14249,K15884,K15885) (K05555,K14250),K15886)	0.333333333	FALSE	K05555,K05555
M00804	Complete nitrification, comammox, ammonia	Nitrogen metabolism	K10944+K10945+K10946 K10535 K00370+K00371	0.333333333	FALSE	K00370,K00371

	=> nitrite => nitrate					
M00835	Pyocyanine biosynthesis, chorismate => pyocyanine	Biosynthesis of other bacterial compounds	K13063 K20261 K06998 K20260 K20262 K21103 K20940	0.285714286	FALSE	K06998,K20940
M00840	Tetrahydrofolate biosynthesis, mediated by ribA and trpF, GTP => THF	Cofactor and vitamin metabolism	K14652 K22100 -- K01633 K13941 K22099 K00287	0.285714286	FALSE	K00287,K01633
M00841	Tetrahydrofolate biosynthesis, mediated by PTPS, GTP => THF	Cofactor and vitamin metabolism	K01495 K22101 K13941 K11754 K13998	0.4	FALSE	K01495,K11754
M00842	Tetrahydrobiopterin biosynthesis, GTP => BH4	Cofactor and vitamin metabolism	K01495 K01737 K00072	0.666666667	FALSE	K01495,K01737
M00843	L-threo-Tetrahydrobiopterin biosynthesis, GTP => L-threo-BH4	Cofactor and vitamin metabolism	K01495 K01737 K17745	0.666666667	FALSE	K01495,K01737
M00844	Arginine biosynthesis, ornithine	Arginine and proline metabolism	K00611 K01940 (K01755,K14681)	1	TRUE	K00611,K01755,K01940

	=> arginine					
M00 845	Arginine biosynthesis, glutamate => acetylcitrulline => arginine	Arginine and proline metabolism	K22478 K00145 K00821 K09065 K01438 K01940 K01755	0.714285714	FALSE	K00145,K00821,K01438,K01755,K01940
M00 846	Siroheme biosynthesis, glutamyl-tRNA => siroheme	Cofactor and vitamin metabolism	K02492 K01845 K01698 K01749 (K01719,K13542,K13543) (K02302,(K00589,K02303,K02496,K13542,K13543)+K02304-K03794)	0.916666667	TRUE	K01698,K01719,K01719,K01719,K01749,K01845,K02303,K02492
M00 848	Aurachin biosynthesis, anthranilate => aurachin A	Biosynthesis of other antibiotics	K09460 K02078+K14245+K14246+K22798 K22799 K22800 K21272 K21271 K22801 K22802	0.03125	FALSE	K02078
M00 849	C5 isoprenoid biosynthesis, mevalonate pathway, archaea	Terpenoid backbone biosynthesis	K00626 K01641 (K00021,K00054) ((K00869 K17942),(K18689 K18690 K22813)) K06981 K01823	0.285714286	FALSE	K00626,K00626,K00626,K00626,K00626,K01823
M00 854	Glycogen biosynthesis, glucose-1P => glycogen/starch	Other carbohydrate metabolism	(K00963 (K00693+K00750,K16150,K16153,K13679,K20812)),(K00975 (K00703,K13679,K20812)) (K00700,K16149)	0.666666667	FALSE	K00700,K00963,K00975,K00975
M00 855	Glycogen degradation, glycogen => glucose-6P	Other carbohydrate metabolism	(K00688,K16153) (K01196,((K00705,K22451) (K02438,K01200))) (K15779,K01835,K15778)	0.75	TRUE	K00688,K00705,K01835

M00861	beta-Oxidation, peroxisome, VLCFA	Fatty acid metabolism	K00232 K12405 (K07513,K08764)	0.33333333	FALSE	K00232
M00868	Heme biosynthesis, animals and fungi, glycine => heme	Cofactor and vitamin metabolism	K00643 K01698 K01749 K01719 K01599 K00228 K00231 K01772	0.75	TRUE	K00231,K00231,K01599,K01698,K01719,K01719,K01719,K01749,K01772
M00872	O-glycan biosynthesis, mannose type (core M3)	Glycan biosynthesis	K00728 K18207 K09654 K17547 K21031 K19872 K19873 K21052 K21032 K09668	0.1	FALSE	K00728
M00873	Fatty acid biosynthesis is in mitochondria, animals	Fatty acid metabolism	K18660 K03955+K00645 K09458 K11539+K13370 K22540 K07512	0.25	FALSE	K00645,K09458
M00874	Fatty acid biosynthesis is in mitochondria, fungi	Fatty acid metabolism	K11262 K03955+K00645 K09458 K00059 K22541 K07512	0.41666667	FALSE	K00059,K00059,K00059,K00059,K00059,K00059,K00645,K09458
M00875	Staphyloferrin B biosynthesis, L-serine => staphyloferrin B	Biosynthesis of other bacterial compounds	K23371 K21949 K21721 K23372 K23373 K23374 K23375	0.285714286	FALSE	K21721,K21949
M00878	Phenylacetate degradation, phenylacetate => acetyl-CoA/succinyl-CoA	Aromatic degradation	K01912 K02609+K02610+K02611+K02612+K02613 K15866 K02618 K02615 K01692 K00074	0.714285714	FALSE	K00074,K01692,K01692,K01692,K01692,K01692,K01912,K01912,K01912,K02609,K02610,K02611,K02612,K02613,K02618

M00880	Molybdenum cofactor biosynthesis, GTP => molybdenum cofactor	Cofactor and vitamin metabolism	((K03639 K03637),K20967) (K03635,K21142) (((K03831,K03638) K03750),K15376)	0.8	TRUE	K03635,K03637,K03639,K03639,K03750,K03750
M00881	Lipoic acid biosynthesis, plants and bacteria, octanoyl-ACP => dihydrolipoyl-E2/H	Cofactor and vitamin metabolism	K03801 K03644	1	TRUE	K03644,K03801
M00882	Lipoic acid biosynthesis, eukaryotes, octanoyl-ACP => dihydrolipoyl-H	Cofactor and vitamin metabolism	K23735 K03644	0.5	FALSE	K03644
M00883	Lipoic acid biosynthesis, animals and bacteria, octanoyl-ACP => dihydrolipoyl-H => dihydrolipoyl-E2	Cofactor and vitamin metabolism	(K23735,K23734) K03644 (K10105,K16869)	0.666666667	FALSE	K03644,K16869
M00884	Lipoic acid biosynthesis	Cofactor and vitamin	K23750 K03644	0.5	FALSE	K03644

	is, octanoyl- CoA => dihydrolip oyl-E2	metabol ism				
M00 892	UDP-N- acetyl-D- glucosami ne biosynthes is, eukaryote s, glucose => UDP- GlcNAc	Other carbohy drate metabol ism	(K00844,K12407,K00845) K01810 K00820 K00621 K01836 K00972	0.33333 3333	FALSE	K00820,K00845
M00 895	Thiamine biosynthes is, prokaryot es, AIR (+ DXP/glyci ne) => TMP/TPP	Cofacto r and vitamin metabol ism	K03148+K03154 K03151 K03153 K03149 K10810 K03147 K00941 K00788 K00946	0.61111 1111	FALSE	K00788,K00788,K00941,K00946,K03149,K03153,K0 3154
M00 896	Thiamine biosynthes is, archaea, AIR (+ NAD+) => TMP/TPP	Cofacto r and vitamin metabol ism	K22699 K03147 (K00941 (K00788,K21220),K21219) K00946	0.6	FALSE	K00788,K00788,K00941,K00946
M00 899	Thiamine salvage pathway, HMP/HE T => TMP	Cofacto r and vitamin metabol ism	K00878 ((K00941 K00788),K14153,K21219)	1	TRUE	K00788,K00788,K00878,K00941
M00 909	UDP-N- acetyl-D- glucosami ne biosynthes is, prokaryot es,	Other carbohy drate metabol ism	K00845 (K01810,K13810,K15916) K00820 K03431 K04042	1	TRUE	K00820,K00845,K03431,K04042,K13810

	glucose => UDP- GlcNAc					
M00 911	Riboflavin biosynthes is, fungi, GTP => riboflavin/ FMN/FA D	Cofacto r and vitamin metabol ism	K01497 K14654 K14655 -- K02858 K00794 K00793 K00861 K00953	0.44444 4444	FALSE	K00793,K00794,K01497,K02858
M00 912	NAD biosynthes is, tryptopha n => quinolinat e => NAD	Cofacto r and vitamin metabol ism	(K00453,K00463) (K01432,K14263,K07130) K00486 K01556 K00452 K00767 (K00969,K06210) (K01916,K01950)	0.5	FALSE	K00767,K00969,K01916,K01916,K07130,K07130
M00 913	Pantothen ate biosynthes is, 2- oxoisoval erate/sper mine => pantothen ate	Cofacto r and vitamin metabol ism	K00606 K00077 K13367 K00128 K01918	0.4	FALSE	K00606,K01918
M00 914	Coenzyme A biosynthes is, archaea, 2- oxoisoval erate => 4- phosphop antoate => CoA	Cofacto r and vitamin metabol ism	K00606 K00077 K06982 K09722 K13038 K02201 K09735	0.28571 4286	FALSE	K00606,K13038
M00 916	Pyridoxal- P biosynthes is, R5P + glyceralde hyde-3P +	Cofacto r and vitamin metabol ism	K06215+K08681	1	TRUE	K06215,K08681

	glutamine => pyridoxal- P					
M00 918	Aerobactin biosynthesis, lysine => aerobactin	Biosynthesis of other bacterial compounds	K03897 K03896 K03894 K03895	0.25	FALSE	K03897
M00 919	Ectoine degradation, ectoine => aspartate	Serine and threonine metabolism	K15783 K15784 K15785 K15786	0.25	FALSE	K15783
M00 921	Cyclooctatin biosynthesis, dimethylallyl-PP + isopentenyl-PP => cyclooctatin	Biosynthesis of other bacterial compounds	K13787 K18686 K22997 K22998	0.25	FALSE	K13787,K13787
M00 924	Cobalamin biosynthesis, anaerobic, uroporphyrinogen III => sirohydrochlorin => cobyrinate a,c- diamide	Cofactor and vitamin metabolism	(K02302,(K02303,K13542) K02304) (K02190,K03795,K22011) K03394 (K05934,K13541,K21479) K05936 (K02189,K13541) K02188 K05895 (K02191 K03399,K00595) K06042 K02224	0.16666 6667	FALSE	K02303,K03795
M00 925	Cobalamin biosynthesis,	Cofactor and vitamin	(K02303,K13542) (K03394,K13540) K02229 (K05934,K13540,K13541) K05936 K02228 K05895 K00595 K06042 K02224 K02230+K09882+K09883	0.09090 9091	FALSE	K02303

	aerobic, uroporphyrinogen III => precorrin 2 => cobyrinate a,c- diamide	metabol ism				
M00 926	Heme biosynthesis, bacteria, glutamyl- tRNA => coproporphyrin III => heme	Cofactor and vitamin metabol ism	K02492 K01845 K01698 K01749 (K01719,K13542) K01599 K00231 K01772 K00435	1	TRUE	K00231,K00231,K00435,K01599,K01698,K01719,K01719,K01719,K01749,K01772,K01845,K02492
M00 932	Phylloquinone biosynthesis, chorismate (+ phytyl-PP) => phylloquinol	Cofactor and vitamin metabol ism	(K02552 K02551 K08680 K02549,K14759) (K01911,K14760) K01661 (K19222,K12073) K23094 K17872 K23095	0.6	FALSE	K01661,K01911,K02549,K02551,K02552,K19222,K19222