Electronic Supplementary Information (ESI) for Molecular BioSystems

Genome-scale metabolic network analysis and drug targeting of multi-drug resistant pathogen *Acinetobacter baumannii* AYE

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Supplementary Table 1. Metabolic reactions of AbyMBEL891 with information on their genes and enzymes.

Supplementary Table 2. Metabolites participating in reactions of AbyMBEL891.

Supplementary Table 3. Biomass composition of *Acinetobacter baumannii*.

Supplementary Table 4. List of 246 essential reactions predicted under minimal medium with succinate as a sole carbon source.

Supplementary Table 5. List of 681 reactions considered for comparison of their essentiality in AbyMBEL891 with those from *Acinetobacter baylyi* ADP1.

Supplementary Table 6. List of 162 essential reactions predicted under arbitrary complex medium.

Supplementary Table 7. List of 211 essential metabolites predicted under arbitrary complex medium.

AbyMBEL891.sbml
Genome-scale metabolic model of *Acinetobacter baumannii* AYE, AbyMBEL891, is available as a separate file in the format of Systems Biology Markup Language (SBML) version 2.

Supplementary Table 1. Metabolic reactions of AbyMBEL891 with information on their genes and enzymes. Highlighed (yellow) reactions indicate that they are not assigned with genes.

No.	Metabolism	EC Number	ORF	Reaction	Enzyme
R001	Glycolysis/ Gluconeogenesis	5.1.3.3	ABAYE2829	GLC <-> bDGLC	aldose 1-epimerase
R002	Glycolysis/ Gluconeogenesis	5.3.1.9	ABAYE3801	G6P <-> bDG6P	glucose-6-phosphate isomerase
R003	Glycolysis/ Gluconeogenesis	5.3.1.9	ABAYE3801	G6P <-> F6P	glucose-6-phosphate isomerase
R004	Glycolysis/ Gluconeogenesis	5.3.1.9	ABAYE3801	bDG6P <-> F6P	glucose-6-phosphate isomerase
R005	Glycolysis/ Gluconeogenesis	5.4.2.2	ABAYE2928 OR ABAYE3800	G6P <-> G1P	phosphoglucomutase OR phosphomannomutase
R006	Glycolysis/ Gluconeogenesis	3.1.3.11	ABAYE0899	FDP -> F6P + PI	fructose-1,6-bisphosphatase
R007	Glycolysis/ Gluconeogenesis	4.1.2.13	ABAYE2088	FDP <-> G3P + DHAP	fructose-1,6-bisphosphate aldolase
R008	Glycolysis/ Gluconeogenesis	5.3.1.1	ABAYE3443	DHAP <-> G3P	triosephosphate isomerase
R009	Glycolysis/ Gluconeogenesis	1.2.1.12	ABAYE0958	G3P + PI + NAD <-> NADH + 13PDG	glyceraldehyde 3-phosphate dehydrogenase
R010	Glycolysis/ Gluconeogenesis	2.7.2.3	ABAYE2090	13PDG + ADP <-> 3PG + ATP	phosphoglycerate kinase
R011	Glycolysis/ Gluconeogenesis	5.4.2.1	ABAYE3537	3PG <-> 2PG	phosphoglycerate mutase
R012	Glycolysis/ Gluconeogenesis	4.2.1.11	ABAYE1669	2PG <-> PEP	enolase
R013	Glycolysis/ Gluconeogenesis	2.3.1.12	ABAYE0158 OR ABAYE1946	COA + ADLIPO -> DLIPO + ACCOA	pyruvate dehydrogenase E2 component (dihydrolipoamideacetyltransferase)
R014	Glycolysis/ Gluconeogenesis	1.8.1.4	ABAYE0505 OR ABAYE0782 OR ABAYE1945	DLIPO + NAD -> LIPO + NADH	dihydrolipoamide dehydrogenase
R015	Glycolysis/ Gluconeogenesis	6.2.1.1	ABAYE0179 OR ABAYE1413 OR ABAYE3766	ATP + AC + COA <-> AMP + PPI + ACCOA	acetyl-CoA synthetase
R016	Glycolysis/ Gluconeogenesis	1.2.1.3	ABAYE1028 OR ABAYE1460 OR ABAYE2333 OR ABAYE2837	ACAL + NAD -> NADH + AC	aldehyde dehydrogenase
R017	Glycolysis/ Gluconeogenesis	1.1.1.1	ABAYE0763 OR ABAYE1463 OR ABAYE1522 OR ABAYE1861 OR p2ABAYE0004 OR p3ABAYE0020 OR p3ABAYE0024	ACAL + NADH <-> ETH + NAD	alcohol dehydrogenase
R018	Glycolysis/ Gluconeogenesis	4.1.1.1	ABAYE1030	ACAL + THMPP <-> 2(HE)TPP	pyruvate decarboxylase/indolepyruvate decarboxylase
R019	TCA cycle	2.3.3.1	ABAYE0773	ACCOA + OA -> COA + CIT	citrate synthase
R020	TCA cycle	4.2.1.3	ABAYE1432 OR ABAYE3228 OR ABAYE3791	CIT <-> ICIT	aconitate hydratase
R021	TCA cycle	1.1.1.42	ABAYE0980 OR ABAYE0982	ICIT + NADP -> NADPH + AKG + CO2	isocitrate dehydrogenase
R022	TCA cycle	1.2.4.2	ABAYE0780	AKG + LIPO -> SDLIPO + CO2	2-oxoglutarate dehydrogenase E1 component
R023	TCA cycle	2.3.1.61	ABAYE0781	SDLIPO + COA -> DLIPO + SUCCOA	2-oxoglutarate dehydrogenase E2 component
R024	TCA cycle	6.2.1.5	ABAYE0783 AND ABAYE0784	ADP + PI + SUCCOA <-> ATP + SUCC + COA	succinyl-CoA synthetase
R025	TCA cycle	1.3.99.1	ABAYE0774 AND ABAYE0775 AND ABAYE0776 AND ABAYE0777	SUCC + FAD -> FUM + FADH2	succinate dehydrogenase
R026	TCA cycle	1.3.99.1	ABAYE0774 AND ABAYE0775 AND ABAYE0776 AND ABAYE0777	FUM + MKH2 -> SUCC + MK	fumarate reductase
R027	TCA cycle	1.3.99.1	ABAYE0774 AND ABAYE0775 AND ABAYE0776 AND ABAYE0777	FUM + DMKH2 -> SUCC + DMK	fumarate reductase
R028	TCA cycle	4.2.1.2	ABAYE1563 OR ABAYE3284	FUM <-> MAL	fumarate hydratase
R029	TCA cycle	1.1.1.37	ABAYE0465	MAL + NAD <-> NADH + OA	malate dehydrogenase
R030	Pentose phosphate pathway	5.1.3.1	ABAYE3114	RL5P <-> X5P	D-ribulose-5-phosphate 3-epimerase
R031	Pentose phosphate pathway	5.3.1.6	ABAYE1650	RL5P <-> R5P	ribose 5-phosphate isomerase A
R032	Pentose phosphate pathway	2.2.1.1	ABAYE2116 OR (ABAYE2823 AND ABAYE2824)	R5P + X5P <-> G3P + S7P	transketolase
R033	Pentose phosphate pathway	2.2.1.1	ABAYE2116 OR (ABAYE2823 AND ABAYE2824)	X5P + E4P <-> F6P + G3P	transketolase
R034	Pentose phosphate pathway	2.2.1.2	ABAYE1510	G3P + S7P <-> E4P + F6P	transaldolase
R035	Pentose phosphate pathway	4.1.2.4		DR5P -> G3P + ACAL	deoxyribose-phosphate aldolase
R036	Pentose phosphate pathway	5.4.2.7		DR1P <-> DR5P	phosphopentomutase
R037	Pentose phosphate pathway	4.1.2.14	ABAYE3280	KDPG -> PYR + G3P	bifunctional 4-hydroxy-2-oxoglutarate aldolase OR 2-dehydro-3-deoxyphosphogluconate aldolase
R038	Pentose phosphate pathway	2.7.1.12	ABAYE3278	GLUC + ATP -> D6PGC + ADP	gluconokinase
R039	Pentose phosphate pathway	4.2.1.12	ABAYE3281	D6PGC -> KDPG	phosphogluconate dehydratase
R040	Pentose phosphate pathway	5.4.2.2	ABAYE2928 OR ABAYE3800	R1P <-> R5P	phosphoglucomutase OR phosphomannomutase
R041	Pentose and glucuronate interconversions	1.1.1.22	ABAYE3802	UDPG + 2 NAD <-> UDPGLUC + 2 NADH	UDP-glucose 6-dehydrogenase
R042	Fructose and mannose metabolism	2.7.1.56	ABAYE1613	F1P + ATP -> FDP + ADP	fructose-1-phosphate kinase
R043	Fructose and mannose metabolism	4.1.2.13	ABAYE2088	F1P -> DHAP + T3	fructose-bisphosphate aldolase
R044	Fructose and mannose metabolism	5.3.1.8		MAN6P <-> F6P	phosphomannose isomerase
R045	Fructose and mannose metabolism	5.4.2.8	ABAYE2928 OR ABAYE3800	MAN6P <-> MAN1P	phosphomannomutase
R046	Fructose and mannose metabolism	2.7.7.13		GTP + MAN1P <-> PPI + GDPMAN	nucleoside-diphosphate-sugar pyrophosphorylase
R047	Fructose and mannose metabolism	1.1.1.-	ABAYE0043 OR ABAYE0109 OR ABAYE0479 OR ABAYE1356 OR ABAYE2589 OR ABAYE2607 OR ABAYE2613 OR ABAYE2618 OR ABAYE2845 OR ABAYE3187 OR ABAYE3378	S6P + NADP <-> SB1P + NADPH	alcohol dehydrogenase

No.	Metabolism	EC Number	ORF	Reaction	Enzyme
R048	Fructose and mannose metabolism	4.1.2.17	ABAYE3670	FUCP <-> DHAP + LACAL	aldolase class II
R049	Galactose metabolism	5.1.3.2	ABAYE1562 OR ABAYE3804	UDPG <-> UDPGAL	UDP-glucose 4-epimerase
R050	Galactose metabolism	2.7.7.9	ABAYE3803	G1P + UTP <-> UDPG + PPI	UTP-glucose-1-phosphate uridylyltransferase
R051	Ascorbate and aldarate metabolism	1.2.1.3	ABAYE1028 OR ABAYE1460 OR ABAYE2333 OR ABAYE2837	DGLUCL + NAD <-> DGLUCA + NADH	aldehyde dehydrogenase
R052	Starch and sucrose metabolism	3.2.1.93		TRE6P -> GLC + G6P	trehalose-6-phosphate hydrolase
R053	Starch and sucrose metabolism	2.4.1.15	ABAYE3007	UDPG + G6P <-> UDP + TRE6P	trehalose-6-phosphate synthase
R054	Starch and sucrose metabolism	3.1.3.12	ABAYE3006	TRE6P -> TRE + PI	trehalose-6-phosphate phophatase, biosynthetic
R055	Aminosugars metabolism	2.6.1.16	ABAYE0089	F6P + GLN -> GLU + GA6P	glucosamine-fructose-6-phosphate aminotransferase
R056	Aminosugars metabolism	5.4.2.10	ABAYE0167	GA6P <-> GA1P	phosphomannomutase
R057	Aminosugars metabolism	2.3.1.157	ABAYE0090	ACCOA + GA1P -> NAGA1P + COA	glucosamine-1-phosphate N-acetyltransferase
R058	Aminosugars metabolism	2.7.7.23	ABAYE0090	UTP + NAGA1P <-> UDPNAG + PPI	UDP-N-acetylglucosamine pyrophosphorylase
R059	Aminosugars metabolism	5.1.3.14	ABAYE0969	UDPNAG <-> NADMA + UDP	UDP-N-acetylglucosamine 2-epimerase
R060	Aminosugars metabolism	5.1.3.14	ABAYE0969	UDPNAG <-> UDPNADMA	UDP-N-acetylglucosamine 2-epimerase
R061	Aminosugars metabolism	1.1.1.-	ABAYE3815	UDPNADMA + 2 NAD -> UDPNADMAU + 2 NADH	UDP-N-acetyl-D-mannosaminuronate dehydrogenase
R062	Aminosugars metabolism	2.5.1.7	ABAYE3133	UDPNAG + PEP -> UDPNAGEP + PI	UDP-N-acetylglucosamine enolpyruvyl transferase
R063	Aminosugars metabolism	1.1.1.158	ABAYE1526	UDPNAGEP + NADPH -> UDPNAM + NADP	UDP-N-acetylenolpyruvoylglucosamine reductase
R064	Aminosugars metabolism	3.2.1.-	ABAYE2663	GLCAMN <-> GLCA + GLCAMN	bifunctional protein [includes: lytic murein transglycosylase C, membrane-bound
R065	Aminosugars metabolism	3.2.1.52	ABAYE3272	CHITB -> 2 NAGA	beta-N-acetyl-D-glucosaminidase
R066	Aminosugars metabolism	5.1.3.7	ABAYE3814	UDPNAG <-> UDPAGLACA	NAD-dependent epimerase/dehydratase
R067	Nucleotide sugars metabolism	5.1.3.2	ABAYE1562 OR ABAYE3804	DTDPGLU <-> DTDPGLAC	UDP-glucose 4-epimerase
R068	Nucleotide sugars metabolism	2.7.7.24		G1P + DTTP -> DTDPGLU + PPI	glucose-1-phosphate thymidylyltransferase
R069	Nucleotide sugars metabolism	4.2.1.46		DTDPGLU -> DTDP4O6DG	dTDP-glucose 4,6 dehydratase
R070	Nucleotide sugars metabolism	5.1.3.13		DTDP4O6DG -> DTDP4ORMNS	dTDP-4-deoxyrhamnose-3,5-epimerase
R071	Nucleotide sugars metabolism	1.1.1.133		DTDP4ORMNS + NADPH -> DTDPRMNS + NADP	dTDP-4-dehydrorhamnose reductase
R072	Pyruvate metabolism	2.7.9.2	ABAYE1391	ATP + PYR -> AMP + PEP + PI	phosphoenolpyruvate synthase
R073	Pyruvate metabolism	1.1.1.28	ABAYE3796	PYR + NADH <-> LAC + NAD	D-lactate dehydrogenase
R074	Pyruvate metabolism	2.3.1.8	ABAYE1138 OR ABAYE3283	ACCOA + PI <-> ACETYLP + COA	phosphate acetyltransferase
R075	Pyruvate metabolism	6.2.1.1	ABAYE0179 OR ABAYE1413 OR ABAYE3766	AAD + COA <-> AMP + ACCOA	acetyl-CoA synthase
R076	Pyruvate metabolism	6.2.1.1	ABAYE0179 OR ABAYE1413 OR ABAYE3766	ATP + AC <-> PPI + AAD	acetyl-CoA synthetase
R077	Pyruvate metabolism	2.7.2.1	ABAYE3282	ACETYLP + ADP <-> AC + ATP	acetate kinase
R078	Pyruvate metabolism	4.1.1.31	ABAYE0028	PEP + CO2 -> OA + PI	phosphoenolpyruvate carboxylase
R079	Pyruvate metabolism	1.1.1.38 OR 1.1.1.40	ABAYE3731 OR ABAYE1138	MAL + NAD <-> PYR + CO2 + NADH	malate dehydrogenase
R080	Pyruvate metabolism	1.1.1.38 OR 1.1.1.40	ABAYE3731 OR ABAYE1138	MAL + NADP <-> PYR + CO2 + NADPH	malate dehydrogenase
R081	Pyruvate metabolism	2.3.3.9	ABAYE2053	ACCOA + GLX -> MAL + COA	malate synthase
R082	Pyruvate metabolism	2.3.1.9	ABAYE0629 OR ABAYE0638 OR ABAYE1916 OR ABAYE2307	2 ACCOA -> COA + AACCOA	acetyl-CoA acetyltransferase
R083	Pyruvate metabolism	4.4.1.5	ABAYE1052	RGT + MTG <-> LTG	lactoylglutathione lyase
R084	Pyruvate metabolism	3.1.2.6	ABAYE1362 OR ABAYE1940	LTG -> RGT + LAC	hydroxyacylglutathione hydrolase GloB
R085	Pyruvate metabolism	1.1.2.3	ABAYE3797	SLAC + 2 FERIC <-> PYR + 2 FEROC	L-lactate dehydrogenase, FMN linked
R086	Pyruvate metabolism	1.1.99.16	ABAYE2869	MAL + FAD -> FADH2 + OA	malate dehydrogenase
R087	Pyruvate metabolism	1.2.1.3	ABAYE1028 OR ABAYE1460 OR ABAYE2333 OR ABAYE2837	ACAL + NADP <-> AC + NADPH	aldehyde dehydrogenase
R088	Pyruvate metabolism	1.2.4.1	ABAYE0157 OR (ABAYE1947 AND ABAYE1948)	2(HE)TPP + LIPO <-> ADLIPO + THMPP	pyruvate dehydrogenase subunit E1
R089	Pyruvate metabolism	2.3.3.13	ABAYE3292	IPPMAL + COA <-> ACCOA + OIVAL	2-isopropylmalate synthase
R090	Pyruvate metabolism	4.1.1.-	ABAYE1027	PYR + CO2 <-> HEDC	L-2,4-diaminobutyrate decarboxylase
R091	Pyruvate metabolism	4.1.1.32	ABAYE0818	GTP + OA <-> GDP + PEP + CO2	phosphoenolpyruvate carboxykinase [GTP] (PEP
R092	Pyruvate metabolism	4.1.1.32	ABAYE0818	ITP + OA <-> IDP + PEP + CO2	phosphoenolpyruvate carboxykinase [GTP] (PEP carboxykinase)
R093	Glyoxylate and dicarboxylate metabolism	4.1.3.1	ABAYE2783	ICIT -> SUCC + GLX	isocitrate lyase
R094	Glyoxylate and dicarboxylate metabolism	1.2.1.2	ABAYE0850	FORMATE + NAD -> CO2 + NADH	formate dehydrogenase
R095	Glyoxylate and dicarboxylate metabolism	1.2.1.21		GLAL + NAD -> NADH + GLYCOLATE	glycolaldehyde dehydrogenase
R096	Glyoxylate and dicarboxylate metabolism	3.1.3.18	ABAYE0081 OR ABAYE2988 OR ABAYE3373 OR ABAYE3498 OR ABAYE3835	2PPG -> GLYCOLATE + PI	phosphoglycolate phosphatase
R097	Glyoxylate and dicarboxylate metabolism	1.1.1.60	ABAYE1786	DGLYCERATE + NAD <-> HOPP + NADH	2-hydroxy-3-oxopropionate reductase OR tartronate semialdehyde reductase
R098	Glyoxylate and dicarboxylate metabolism	1.1.1.60	ABAYE1786	DGLYCERATE + NADP <-> HOPP + NADPH	2-hydroxy-3-oxopropionate reductase OR tartronate semialdehyde reductase
R099	Glyoxylate and dicarboxylate metabolism	1.1.1.93	ABAYE2964	MTTA + NAD <-> 2H3OSUCC + NADH	tartrate dehydrogenase/decarboxylase OR D-malate dehydrogenase [decarboxylating]
R100	Glyoxylate and dicarboxylate metabolism	1.1.1.93	ABAYE2964	TTA + NAD <-> 2H3OSUCC + NADH	tartrate dehydrogenase/decarboxylase OR D-malate dehydrogenase [decarboxylating]
R101	Glyoxylate and dicarboxylate metabolism	2.3.3.9	ABAYE2053	MAL + COA <-> ACCOA + GLX	malate synthase G
R102	Glyoxylate and dicarboxylate metabolism	5.3.1.22	ABAYE3188	HPYR <-> HOPP	hydroxypyruvate isomerase

No.	Metabolism	EC Number	ORF	Reaction	Enzyme
R103	Propanoate metabolism	4.2.1.17	ABAYE0482 OR ABAYE0915 OR ABAYE2065 OR ABAYE2290 OR ABAYE2304 OR ABAYE2311 OR ABAYE2369 OR ABAYE2370 OR ABAYE2628 OR ABAYE2852 OR ABAYE3186 OR ABAYE3763 OR ABAYE3764 OR ABAYE3470	3HPCOA <-> PPCOA	enoyl-CoA hydratase/isomerase OR 3-methylglutaconyl-CoA hydratase
R104	Propanoate metabolism	6.2.1.1	ABAYE0179 OR ABAYE1413 OR ABAYE3766	ATP + PROPANOATE <-> PPI + PPA	acetyl-CoA synthetase
R105	Propanoate metabolism	6.2.1.1	ABAYE0179 OR ABAYE1413 OR ABAYE3766	PPA + COA <-> AMP + PPACOA	propionyl-CoA synthetase
R106	Propanoate metabolism	2.7.2.1	ABAYE3282	PROPANOATE + ATP <-> PROPIONYLP + ADP	acetate kinase
R107	Propanoate metabolism	2.3.1.8	ABAYE1138 OR ABAYE3283	PPACOA + PI <-> PROPIONYLP + COA	phosphate acetyltransferase
R108	Propanoate metabolism	2.3.1.54		OBUT + COA <-> PPACOA + FORMATE	formate acetyltransferase
R109	Propanoate metabolism	1.2.1.3	ABAYE1028 OR ABAYE1460 OR ABAYE2333 OR ABAYE2837	2P1A + NAD -> PPN + NADH	aldehyde dehydrogenase
R110	Propanoate metabolism	2.3.3.5	ABAYE3792	2MCIT + COA <-> PPACOA + OA	2-methylcitrate synthase
R111	Propanoate metabolism	4.1.3.30	ABAYE3793	3HB123TC <-> PYR + SUCC	methylisocitrate lyase
R112	Propanoate metabolism	1.2.1.27	ABAYE1296 OR ABAYE3768	MMSA + COA + NAD -> PPACOA + CO2 + NADH	methylmalonate-semialdehyde dehydrogenase
R113	Propanoate metabolism	1.3.99.3	ABAYE0476 OR ABAYE2013	PPACOA + FAD <-> FADH2 + PPCOA	acyl-CoA dehydrogenase
R114	Propanoate metabolism	4.1.1.4	ABAYE1742	AAC -> ACTN + CO2	acetoacetate decarboxylase
R115	Propanoate metabolism	6.4.1.3	ABAYE0480	ATP + PPACOA + HCO3 <-> ADP + PI + MMALCOA	propionyl-CoA carboxylase
R116	Glycolysis/Gluconeogensis/Butanoate metabolism	2.2.1.6 OR 4.1.1.1 OR 1.2.4.1	(ABAYE2836 OR ABAYE3239 OR ABAYE3240) OR ABAYE1030 OR ABAYE0157 OR (ABAYE1947 AND ABAYE1948)	THMPP + PYR -> 2(HE)TPP + CO2	acetolactate synthase **OR** pyruvate dehydrogenase
R117	Butanoate metabolism	2.2.1.6	ABAYE2836 OR ABAYE3239 OR ABAYE3240	2(HE)TPP + PYR -> ACLAC + THMPP	acetolactate synthase
R118	Butanoate metabolism	1.1.1.35	ABAYE1411 OR ABAYE2460 OR ABAYE3470	3HBCOA + NAD <-> AACCOA + NADH	3-hydroxyacyl-CoA dehydrogenase
R119	Butanoate metabolism	5.1.2.3	ABAYE0628 OR ABAYE3470	3HBCOA <-> R3HBCOA	3-hydroxybutyryl-CoA epimerase
R120	Butanoate metabolism	4.2.1.17	ABAYE0482 OR ABAYE0915 OR ABAYE2065 OR ABAYE2290 OR ABAYE2304 OR ABAYE2311 OR ABAYE2369 OR ABAYE2370 OR ABAYE2628 OR ABAYE2852 OR ABAYE3186 OR ABAYE3470 OR ABAYE3763 OR ABAYE3764	3HBCOA <-> CCOA	enoyl-CoA hydratase/isomerase OR 3-methylglutaconyl-CoA hydratase
R121	Butanoate metabolism	1.1.1.-	ABAYE0043 OR ABAYE0109 OR ABAYE0479 OR ABAYE1356 OR ABAYE2589 OR ABAYE2607 OR ABAYE2613 OR ABAYE2618 OR ABAYE2845 OR ABAYE3187 OR ABAYE3378	1BOH + NAD <-> BUTANAL + NADH	alcohol dehydrogenase
R122	Butanoate metabolism	1.2.1.16	ABAYE0210 OR ABAYE2329 OR ABAYE2958	SUCCSA + NAD -> SUCC + NADH	succinate-semialdehyde dehydrogenase
R123	Butanoate metabolism	1.2.1.16	ABAYE0210 OR ABAYE2329 OR ABAYE2958	SUCCSA + NADP -> SUCC + NADPH	succinate-semialdehyde dehydrogenase
R124	Butanoate metabolism	2.6.1.19	ABAYE0209	GABA + AKG <-> SUCCSA + GLU	4-aminobutyrate aminotransferase
R125	Butanoate metabolism	4.1.3.4	ABAYE2292 OR ABAYE2344	3H3MGCOA -> ACCOA + AAC	hydroxymethylglutaryl-CoA lyase
R126	Butanoate metabolism	1.2.1.3	ABAYE1028 OR ABAYE1460 OR ABAYE2333 OR ABAYE2837	3B1A + NAD -> 3BUT + NADH	aldehyde dehydrogenase
R127	Butanoate metabolism	1.1.1.157	ABAYE2306 OR ABAYE2368	3HBCOA + NADP <-> AACCOA + NADPH	3-hydroxybutyryl-CoA dehydrogenase
R128	Butanoate metabolism	1.1.1.30	ABAYE1909	3HBUT + NAD <-> AAC + NADH	3-hydroxybutyrate dehydrogenase
R129	Butanoate metabolism	1.1.1.4	ABAYE1943	23BOH + NAD <-> ACT + NADH	(R,R)-butanediol dehydrogenase
R130	Butanoate metabolism	1.1.1.5	ABAYE1944	DAC + NADH -> ACT + NAD	acetoin dehydrogenase (DAC reductase)
R131	Butanoate metabolism	1.1.1.5	ABAYE1944	DAC + NADPH -> ACT + NADP	acetoin dehydrogenase (DAC reductase)
R132	Butanoate metabolism	1.1.1.83	ABAYE2964	RMAL + NAD -> PYR + CO2 + NADH	tartrate dehydrogenase/decarboxylase OR D-malate dehydrogenase [decarboxylating]
R133	Butanoate metabolism	2.8.3.5	ABAYE1913 AND ABAYE1914	SUCCOA + AAC <-> SUCC + AACCOA	acetoacetyl-CoA transferase
R134	Inositol metabolism	1.2.1.27	ABAYE1296 OR ABAYE3768	3OPP + COA + NAD -> ACCOA + CO2 + NADH	NAD-dependent aldehyde dehydrogenase

No.	Metabolism	EC Number	ORF	Reaction	Enzyme
R135	Oxidative phosphorylation	1.6.5.3 AND 1.6.99.3	(ABAYE3048 AND ABAYE3049 AND ABAYE3050 AND ABAYE3051 AND ABAYE3052 AND ABAYE3053 AND ABAYE3054 AND ABAYE3055 AND ABAYE3056 AND ABAYE3057 AND ABAYE3058 AND ABAYE3059 AND ABAYE3060) AND (ABAYE0977 OR ABAYE1736)	NADH + UQ -> NAD + UQH2	NADH dehydrogenase
R136	Oxidative phosphorylation	1.6.5.3 AND 1.6.99.3	(ABAYE3048 AND ABAYE3049 AND ABAYE3050 AND ABAYE3051 AND ABAYE3052 AND ABAYE3053 AND ABAYE3054 AND ABAYE3055 AND ABAYE3056 AND ABAYE3057 AND ABAYE3058 AND ABAYE3059 AND ABAYE3060) AND (ABAYE0977 OR ABAYE1736)	NADH + MK -> NAD + MKH2	NADH dehydrogenase
R137	Oxidative phosphorylation	1.6.5.3 AND 1.6.99.3	(ABAYE3048 AND ABAYE3049 AND ABAYE3050 AND ABAYE3051 AND ABAYE3052 AND ABAYE3053 AND ABAYE3054 AND ABAYE3055 AND ABAYE3056 AND ABAYE3057 AND ABAYE3058 AND ABAYE3059 AND ABAYE3060) AND (ABAYE0977 OR ABAYE1736)	NADH + DMK -> NAD + DMKH2	NADH dehydrogenase
R138	Oxidative phosphorylation	1.3.99.1	ABAYE0774 AND ABAYE0775 AND ABAYE0776 AND ABAYE0777	FADH2 + UQ -> FAD + UQH2	succinate dehydrogenase
R139	Oxidative phosphorylation	2.5.1.- AND 1.10.3.-	ABAYE1385 AND ABAYE1386 AND ABAYE1387 AND ABAYE1388 AND ABAYE1389 AND ((ABAYE1636 AND ABAYE1637) OR ABAYE2219 AND ABAYE2220))	UQH2 + 0.5 O2 -> UQ + 2 Hxt	cytochrome complexes
R140	Oxidative phosphorylation	3.6.1.1	ABAYE3675	PPI -> 2 PI	inorganic diphosphatase
R141	ATP synthesis	3.6.3.14	ABAYE3715 AND ABAYE3716 AND ABAYE3717 AND ABAYE3718 AND ABAYE3719 AND ABAYE3720 AND ABAYE3721 AND ABAYE3723	ADP + PI + 4 Hxt <-> ATP	ATP synthase
R142	Oxidative phosphorylation	2.7.4.1	ABAYE2803	ATP + PPI <-> ADP + PPPI	polyphosphate kinase
R143	Nitrogen metabolism	4.2.1.1	ABAYE0262 OR ABAYE2809	CO2 -> HCO3	carbonic anhydrase
R144	Nitrogen metabolism	1.7.99.4	ABAYE1546	NO3 + FEROC -> FERIC + NO2	nitrate reductase
R145	Nitrogen metabolism	1.7.1.4	ABAYE1544	NO2 + 3 NADH -> 3 NAD + NH3	nitrite reductase
R146	Nitrogen metabolism	1.7.1.4	ABAYE1544	NO2 + 3 NADPH -> 3 NADP + NH3	nitrite reductase
R147	Nitrogen metabolism	4.3.1.1	ABAYE1921	ASP <-> FUM + NH3	aspartate ammonia-lyase
R148	Nitrogen metabolism	1.13.11.32	ABAYE0966 OR ABAYE2310	O2 + 2 2NPRPN <-> 2 ACTN + 2 NO2	2-nitropropane dioxygenase
R149	Nitrogen metabolism	1.14.12.1	ABAYE1896 AND ABAYE1897	AN + O2 + NADH <-> CATECHOL + NH3 + CO2 + NAD	anthranilate dioxygenase
R150	Nitrogen metabolism	1.14.12.1	ABAYE1896 AND ABAYE1897	AN + O2 + NADPH <-> CATECHOL + NH3 + CO2 + NADP	anthranilate dioxygenase
R151	Nitrogen metabolism	1.4.1.13	ABAYE0298 AND ABAYE0299	2 GLU + NADP <-> GLN + AKG + NADPH	glutamate synthase
R152	Nitrogen metabolism	1.4.1.13	ABAYE0298 AND ABAYE0299	2 GLU + NAD <-> GLN + AKG + NADH	glutamate synthase
R153	Nitrogen metabolism	1.4.1.3 OR 1.4.1.4	ABAYE0351 OR ABAYE2764	GLU + NAD <-> AKG + NH3 + NADH	glutamate dehydrogenase (NAD(P)+) oxidoreductase protein
R154	Nitrogen metabolism	1.4.1.3 OR 1.4.1.4	ABAYE0351 OR ABAYE2764	GLU + NADP <-> AKG + NH3 + NADPH	glutamate dehydrogenase, NADP-specific
R155	Nitrogen metabolism	1.4.99.1	ABAYE1567 OR ABAYE3774	DALA + FAD <-> PYR + NH3 + FADH2	D-amino acid dehydrogenase
R156	Sulfur metabolism	2.7.7.4	ABAYE2790 AND ABAYE2791	SLF + ATP -> PPI + APS	sulfate adenylyltransferase
R157	Sulfur metabolism	2.7.1.25		APS + ATP -> ADP + PAPS	adenylylsulfate kinase
R158	Sulfur metabolism	1.8.4.8	ABAYE0709	PAPS + RTHIO -> OTHIO + H2SO3 + PAP	3'-phosphoadenosine 5'-phosphosulfate sulfotransferase (PAPS reductase)
R159	Sulfur metabolism	1.8.1.2	ABAYE0634 OR ABAYE0682	H2SO3 + 3 NADPH -> H2S + 3 NADP	sulfite reductase (NADPH)
R160	Sulfur metabolism	3.1.3.7		PAP -> PI + AMP	3',5'-bisphosphate nucleotidase
R161	Sulfur metabolism	1.8.1.2	ABAYE0634	SELT + 3 NADP -> SELD + 3 NADPH	sulfite reductase (NADPH)

No.	Metabolism	EC Number	ORF	Reaction	Enzyme
R162	Fatty acid biosynthesis	6.4.1.2 AND 6.3.4.14	(ABAYE0614 OR ABAYE1537 OR ABAYE1538 OR ABAYE3153) AND (ABAYE1537 OR ABAYE2291 OR ABAYE2438)	ACCOA + ATP + HCO3 -> MALCOA + ADP + PI	acetyl-CoA carboxylase
R163	Fatty acid biosynthesis	2.3.1.39	ABAYE2227 OR ABAYE2993	MALCOA + ACP -> MALACP + COA	malonyl CoA-acyl carrier protein transacylase
R164	Fatty acid biosynthesis	2.3.1.180	ABAYE2562	ACCOA + ACP -> ACACP + COA	3-oxoacyl-[acyl-carrier-protein] synthase
R165	Fatty acid biosynthesis			PPACOA + ACP -> PPAACP + COA	malonyl CoA-acyl carrier protein transacylase
R166	Fatty acid biosynthesis (nonanoic acid; c9:0)	1.1.1.100 AND 1.3.1.9 AND 2.3.1.41 AND 2.3.1.180 AND 4.2.1.-	(ABAYE1514 OR ABAYE1706 OR ABAYE2246 OR ABAYE2992) AND ABAYE3250 AND ABAYE2951 AND ABAYE2562 AND ABAYE1586	PPAACP + 3 MALACP + 6 NADPH -> 6 NADP + C090ACP + 3 CO2 + 3 ACP	synthesis of nonanoyl-[acyl-carrier protein]
R167	Fatty acid biosynthesis (decanoic acid; c10:0)	1.1.1.100 AND 1.3.1.9 AND 2.3.1.41 AND 2.3.1.180 AND 4.2.1.-	(ABAYE1514 OR ABAYE1706 OR ABAYE2246 OR ABAYE2992) AND ABAYE3250 AND ABAYE2951 AND ABAYE2562 AND ABAYE1586	ACACP + 4 MALACP + 8 NADPH -> 8 NADP + C100ACP + 4 CO2 + 4 ACP	synthesis of decanoyl-[acyl-carrier protein]
R168	Fatty acid biosynthesis (undecanoic acid; c11:0)	1.1.1.100 AND 1.3.1.9 AND 2.3.1.41 AND 2.3.1.180 AND 4.2.1.-	(ABAYE1514 OR ABAYE1706 OR ABAYE2246 OR ABAYE2992) AND ABAYE3250 AND ABAYE2951 AND ABAYE2562 AND ABAYE1586	PPAACP + 4 MALACP + 8 NADPH -> 8 NADP + C110ACP + 4 CO2 + 4 ACP	synthesis of undecanoyl-[acyl-carrier protein]
R169	Fatty acid biosynthesis (dodecanoic acid; c12:0)	1.1.1.100 AND 1.3.1.9 AND 2.3.1.41 AND 2.3.1.180 AND 4.2.1.-	(ABAYE1514 OR ABAYE1706 OR ABAYE2246 OR ABAYE2992) AND ABAYE3250 AND ABAYE2951 AND ABAYE2562 AND ABAYE1586	ACACP + 5 MALACP + 10 NADPH -> 10 NADP + C120ACP + 5 CO2 + 5 ACP	synthesis of dodecanoyl-[acyl-carrier protein]
R170	Fatty acid biosynthesis (tridecanoic acid; c13:0)	1.1.1.100 AND 1.3.1.9 AND 2.3.1.41 AND 2.3.1.180 AND 4.2.1.-	(ABAYE1514 OR ABAYE1706 OR ABAYE2246 OR ABAYE2992) AND ABAYE3250 AND ABAYE2951 AND ABAYE2562 AND ABAYE1586	PPAACP + 5 MALACP + 10 NADPH -> 10 NADP + C130ACP + 5 CO2 + 5 ACP	synthesis of tridecanoyl-[acyl-carrier protein]
R171	Fatty acid biosynthesis (tetradecanoic acid; c14:0)	1.1.1.100 AND 1.3.1.9 AND	(ABAYE1514 OR ABAYE1706 OR	ACACP + 6 MALACP + 12 NADPH -> 12 NADP + C140ACP + 6 CO2 + 6 ACP	synthesis of tetradecanoyl-[acyl-carrier protein]
R172	Fatty acid biosynthesis (pentadecanoic acid; c15:0)	1.1.1.100 AND 1.3.1.9 AND 2.3.1.41 AND 2.3.1.180 AND 4.2.1.-	(ABAYE1514 OR ABAYE1706 OR ABAYE2246 OR ABAYE2992) AND ABAYE3250 AND ABAYE2951 AND ABAYE2562 AND ABAYE1586	PPAACP + 6 MALACP + 12 NADPH -> 12 NADP + C150ACP + 6 CO2 + 6 ACP	synthesis of pentadecanoyl-[acyl-carrier protein]
R173	Fatty acid biosynthesis (pentadecenoic acid; c15:1)	1.1.1.100 AND 1.3.1.9 AND 2.3.1.41 AND 2.3.1.180 AND 4.2.1.-	(ABAYE1514 OR ABAYE1706 OR ABAYE2246 OR ABAYE2992) AND ABAYE3250 AND ABAYE2951 AND ABAYE2562 AND ABAYE1586	PPAACP + 6 MALACP + 11 NADPH -> 11 NADP + C151ACP + 6 CO2 + 6 ACP	synthesis of pentadecenoyl-[acyl-carrier protein]
R174	Fatty acid biosynthesis (hexadecanoic acid; c16:0)	1.1.1.100 AND 1.3.1.9 AND 2.3.1.41 AND 2.3.1.180 AND 4.2.1.-	(ABAYE1514 OR ABAYE1706 OR ABAYE2246 OR ABAYE2992) AND ABAYE3250 AND ABAYE2951 AND ABAYE2562 AND ABAYE1586	ACACP + 7 MALACP + 14 NADPH -> 14 NADP + C160ACP + 7 CO2 + 7 ACP	synthesis of hexadecanoyl-[acyl-carrier protein]
R175	Fatty acid biosynthesis (hexadecenoic acid; c16:1)	1.1.1.100 AND 1.3.1.9 AND 2.3.1.41 AND 2.3.1.180 AND 4.2.1.-	(ABAYE1514 OR ABAYE1706 OR ABAYE2246 OR ABAYE2992) AND ABAYE3250 AND ABAYE2951 AND ABAYE2562 AND ABAYE1586	ACACP + 7 MALACP + 13 NADPH -> 13 NADP + C161ACP + 7 CO2 + 7 ACP	synthesis of hexadecenoyl-[acyl-carrier protein]
R176	Fatty acid biosynthesis (heptadecanoic acid; c17:0)	1.1.1.100 AND 1.3.1.9 AND 2.3.1.41 AND 2.3.1.180 AND 4.2.1.-	(ABAYE1514 OR ABAYE1706 OR ABAYE2246 OR ABAYE2992) AND ABAYE3250 AND ABAYE2951 AND ABAYE2562 AND ABAYE1586	PPAACP + 7 MALACP + 14 NADPH -> 14 NADP + C170ACP + 7 CO2 + 7 ACP	synthesis of heptadecanoyl-[acyl-carrier protein]
R177	Fatty acid biosynthesis (heptadecenoic acid; c17:1)	1.1.1.100 AND 1.3.1.9 AND 2.3.1.41 AND 2.3.1.180 AND 4.2.1.-	(ABAYE1514 OR ABAYE1706 OR ABAYE2246 OR ABAYE2992) AND ABAYE3250 AND ABAYE2951 AND ABAYE2562 AND ABAYE1586	PPAACP + 7 MALACP + 13 NADPH -> 13 NADP + C171ACP + 7 CO2 + 7 ACP	synthesis of heptadecenoyl-[acyl-carrier protein]

No.	Metabolism	EC Number	ORF	Reaction	Enzyme
R178	Fatty acid biosynthesis (octadecanoic acid; c18:0)	1.1.1.100 AND 1.3.1.9 AND 2.3.1.41 AND 2.3.1.180 AND 4.2.1.-	(ABAYE1514 OR ABAYE1706 OR ABAYE2246 OR ABAYE2992) AND ABAYE3250 AND ABAYE2951 AND ABAYE2562 AND ABAYE1586	ACACP + 8 MALACP + 16 NADPH -> 16 NADP + C180ACP + 8 CO2 + 8 ACP	synthesis of octadecanoyl-[acyl-carrier protein]
R179	Fatty acid biosynthesis (octadecenoic acid; c18:1)	1.1.1.100 AND 1.3.1.9 AND 2.3.1.41 AND 2.3.1.180 AND 4.2.1.-	(ABAYE1514 OR ABAYE1706 OR ABAYE2246 OR ABAYE2992) AND ABAYE3250 AND ABAYE2951 AND ABAYE2562 AND ABAYE1586	ACACP + 8 MALACP + 15 NADPH -> 15 NADP + C181ACP + 8 CO2 + 8 ACP	synthesis of octadecenoyl-[acyl-carrier protein]
R180	Fatty acid biosynthesis (nonadecanoic acid; c19:0)	1.1.1.100 AND 1.3.1.9 AND 2.3.1.41 AND 2.3.1.180 AND 4.2.1.-	(ABAYE1514 OR ABAYE1706 OR ABAYE2246 OR ABAYE2992) AND ABAYE3250 AND ABAYE2951 AND ABAYE2562 AND ABAYE1586	PPAACP + 8 MALACP + 16 NADPH -> 16 NADP + C190ACP + 8 CO2 + 8 ACP	synthesis of nonadecanoyl-[acyl-carrier protein]
R181	Fatty acid biosynthesis (nonadecenoic acid; c19:1)	1.1.1.100 AND 1.3.1.9 AND 2.3.1.41 AND 2.3.1.180 AND 4.2.1.-	(ABAYE1514 OR ABAYE1706 OR ABAYE2246 OR ABAYE2992) AND ABAYE3250 AND ABAYE2951 AND ABAYE2562 AND ABAYE1586	PPAACP + 8 MALACP + 15 NADPH -> 15 NADP + C191ACP + 8 CO2 + 8 ACP	synthesis of nonadecenoyl-[acyl-carrier protein]
R182	Fatty acid biosynthesis (eicosanoic acid; c20:0)	1.1.1.100 AND 1.3.1.9 AND 2.3.1.41 AND 2.3.1.180 AND 4.2.1.-	(ABAYE1514 OR ABAYE1706 OR ABAYE2246 OR ABAYE2992) AND ABAYE3250 AND ABAYE2951 AND ABAYE2562 AND ABAYE1586	ACACP + 9 MALACP + 18 NADPH -> 18 NADP + C200ACP + 9 CO2 + 9 ACP	synthesis of eicosanoyl-[acyl-carrier protein]
R183	Fatty acid metabolism (decanoic acid; c10:0)	6.2.1.3 AND 1.3.99.- AND 1.3.99.3 AND 1.3.99.13 AND 4.2.1.17 AND 1.1.1.35 AND 2.3.1.16 AND 2.3.1.9 AND 1.3.99.7	(ABAYE2630 OR ABAYE3678) AND ABAYE1145 AND (ABAYE0436 OR ABAYE1204 OR ABAYE2631) AND (ABAYE1411 OR ABAYE2460 OR ABAYE3470) AND (ABAYE0482 OR ABAYE0915 OR ABAYE2065 OR ABAYE2290 OR ABAYE2304 OR ABAYE2311 OR ABAYE2369 OR ABAYE2370 OR ABAYE2628 OR ABAYE2852 OR ABAYE3186 OR ABAYE3470 OR ABAYE3763 OR ABAYE3764) AND ABAYE3097 AND ABAYE3471	C100 + 5 COA + 4 FAD + 4 NAD + ATP -> 5 ACCOA + 4 FADH2 + 4 NADH + AMP + PPI	oxidation of decanoic acid
R184	Fatty acid metabolism (dodecanoic acid; c12:0)	6.2.1.3 AND 1.3.99.- AND 1.3.99.3 AND 1.3.99.13 AND 4.2.1.17 AND 1.1.1.35 AND 2.3.1.16 AND 2.3.1.9 AND 1.3.99.7	(ABAYE2630 OR ABAYE3678) AND ABAYE1145 AND (ABAYE0436 OR ABAYE1204 OR ABAYE2631) AND (ABAYE1411 OR ABAYE2460 OR ABAYE3470) AND (ABAYE0482 OR ABAYE0915 OR ABAYE2065 OR ABAYE2290 OR ABAYE2304 OR ABAYE2311 OR ABAYE2369 OR ABAYE2370 OR ABAYE2628 OR ABAYE2852 OR ABAYE3186 OR ABAYE3470 OR ABAYE3763 OR ABAYE3764) AND ABAYE3097 AND ABAYE3471	C120 + 6 COA + 5 FAD + 5 NAD + ATP -> 6 ACCOA + 5 FADH2 + 5 NADH + AMP + PPI	oxidation of dodecanoic acid

No.	Metabolism	EC Number	ORF	Reaction	Enzyme
R185	Fatty acid metabolism (tetradecanoic acid; c14:0)	6.2.1.3 AND 1.3.99.- AND 1.3.99.3 AND 1.3.99.13 AND 4.2.1.17 AND 1.1.1.35 AND 2.3.1.16 AND 2.3.1.9 AND 1.3.99.7	(ABAYE2630 OR ABAYE3678) AND ABAYE1145 AND (ABAYE0436 OR ABAYE1204 OR ABAYE2631) AND (ABAYE1411 OR ABAYE2460 OR ABAYE3470) AND (ABAYE0482 OR ABAYE0915 OR ABAYE2065 OR ABAYE2290 OR ABAYE2304 OR ABAYE2311 OR ABAYE2369 OR ABAYE2370 OR ABAYE2628 OR ABAYE2852 OR ABAYE3186 OR ABAYE3470 OR ABAYE3763 OR ABAYE3764) AND ABAYE3097 AND ABAYE3471	C140 + 7 COA + 6 FAD + 6 NAD + ATP -> 7 ACCOA + 6 FADH2 + 6 NADH + AMP + PPI	oxidation of tetradecanoic acid
R186	Fatty acid metabolism (pentadecanoic acid; c15:0)	6.2.1.3 AND 1.3.99.- AND 1.3.99.3 AND 1.3.99.13 AND 4.2.1.17 AND 1.1.1.35 AND 2.3.1.16 AND 2.3.1.9 AND 1.3.99.7	(ABAYE2630 OR ABAYE3678) AND ABAYE1145 AND (ABAYE0436 OR ABAYE1204 OR ABAYE2631) AND (ABAYE1411 OR ABAYE2460 OR ABAYE3470) AND (ABAYE0482 OR ABAYE0915 OR ABAYE2065 OR ABAYE2290 OR ABAYE2304 OR ABAYE2311 OR ABAYE2369 OR ABAYE2370 OR ABAYE2628 OR ABAYE2852 OR ABAYE3186 OR ABAYE3470 OR ABAYE3763 OR ABAYE3764) AND ABAYE3097 AND ABAYE3471	C150 + 7 COA + 6 FAD + 6 NAD + ATP -> 6 ACCOA + PPACOA + 6 FADH2 + 6 NADH + AMP + PPI	oxidation of pentadecanoic acid
R187	Fatty acid metabolism (hexadecanoic acid; c16:0)	6.2.1.3 AND 1.3.99.- AND 1.3.99.3 AND 1.3.99.13 AND 4.2.1.17 AND 1.1.1.35 AND 2.3.1.16 AND 2.3.1.9 AND 1.3.99.7	(ABAYE2630 OR ABAYE3678) AND ABAYE1145 AND (ABAYE0436 OR ABAYE1204 OR ABAYE2631) AND (ABAYE1411 OR ABAYE2460 OR ABAYE3470) AND (ABAYE0482 OR ABAYE0915 OR ABAYE2065 OR ABAYE2290 OR ABAYE2304 OR ABAYE2311 OR ABAYE2369 OR ABAYE2370 OR ABAYE2628 OR ABAYE2852 OR ABAYE3186 OR ABAYE3470 OR ABAYE3763 OR ABAYE3764) AND ABAYE3097 AND ABAYE3471	C160 + 8 COA + 7 FAD + 7 NAD + ATP -> 8 ACCOA + 7 FADH2 + 7 NADH + AMP + PPI	oxidation of hexadecanoic acid
R188	Fatty acid metabolism (hexadecenoic acid; c16:1)	6.2.1.3 AND 1.3.99.- AND 1.3.99.3 AND 1.3.99.13 AND 4.2.1.17 AND 1.1.1.35 AND 2.3.1.16 AND 2.3.1.9 AND 1.3.99.7	(ABAYE2630 OR ABAYE3678) AND ABAYE1145 AND (ABAYE0436 OR ABAYE1204 OR ABAYE2631) AND (ABAYE1411 OR ABAYE2460 OR ABAYE3470) AND (ABAYE0482 OR ABAYE0915 OR ABAYE2065 OR ABAYE2290 OR ABAYE2304 OR ABAYE2311 OR ABAYE2369 OR ABAYE2370 OR ABAYE2628 OR ABAYE2852 OR ABAYE3186 OR ABAYE3470 OR ABAYE3763 OR ABAYE3764) AND ABAYE3097 AND ABAYE3471	C161 + 8 COA + 7 FAD + 7 NAD + ATP -> 8 ACCOA + 7 FADH2 + 7 NADH + AMP + PPI	oxidation of hexadecenoic acid

No.	Metabolism	EC Number	ORF	Reaction	Enzyme
R189	Fatty acid metabolism (heptadecanoic acid; c17:0)	6.2.1.3 AND 1.3.99.- AND 1.3.99.3 AND 1.3.99.13 AND 4.2.1.17 AND 1.1.1.35 AND 2.3.1.16 AND 2.3.1.9 AND 1.3.99.7	(ABAYE2630 OR ABAYE3678) AND ABAYE1145 AND (ABAYE0436 OR ABAYE1204 OR ABAYE2631) AND (ABAYE1411 OR ABAYE2460 OR ABAYE3470) AND (ABAYE0482 OR ABAYE0915 OR ABAYE2065 OR ABAYE2290 OR ABAYE2304 OR ABAYE2311 OR ABAYE2369 OR ABAYE2370 OR ABAYE2628 OR ABAYE2852 OR ABAYE3186 OR ABAYE3470 OR ABAYE3763 OR ABAYE3764) AND ABAYE3097 AND ABAYE3471	C170 + 8 COA + 7 FAD + 7 NAD + ATP -> 7 ACCOA + PPACOA + 7 FADH2 + 7 NADH + AMP + PPI	oxidation of heptadecanoic acid
R190	Fatty acid metabolism (heptadecenoic acid; c17:1)	6.2.1.3 AND 1.3.99.- AND 1.3.99.3 AND 1.3.99.13 AND 4.2.1.17 AND 1.1.1.35 AND 2.3.1.16 AND 2.3.1.9 AND 1.3.99.7	(ABAYE2630 OR ABAYE3678) AND ABAYE1145 AND (ABAYE0436 OR ABAYE1204 OR ABAYE2631) AND (ABAYE1411 OR ABAYE2460 OR ABAYE3470) AND (ABAYE0482 OR ABAYE0915 OR ABAYE2065 OR ABAYE2290 OR ABAYE2304 OR ABAYE2311 OR ABAYE2369 OR ABAYE2370 OR ABAYE2628 OR ABAYE2852 OR ABAYE3186 OR ABAYE3470 OR ABAYE3763 OR ABAYE3764) AND ABAYE3097 AND ABAYE3471	C171 + 8 COA + 7 FAD + 7 NAD + ATP -> 7 ACCOA + PPACOA + 7 FADH2 + 7 NADH + AMP + PPI	oxidation of heptadecenoic acid
R191	Fatty acid metabolism (octadecanoic acid; c18:0)	6.2.1.3 AND 1.3.99.- AND 1.3.99.3 AND 1.3.99.13 AND 4.2.1.17 AND 1.1.1.35 AND 2.3.1.16 AND 2.3.1.9 AND 1.3.99.7	(ABAYE2630 OR ABAYE3678) AND ABAYE1145 AND (ABAYE0436 OR ABAYE1204 OR ABAYE2631) AND (ABAYE1411 OR ABAYE2460 OR ABAYE3470) AND (ABAYE0482 OR ABAYE0915 OR ABAYE2065 OR ABAYE2290 OR ABAYE2304 OR ABAYE2311 OR ABAYE2369 OR ABAYE2370 OR ABAYE2628 OR ABAYE2852 OR ABAYE3186 OR ABAYE3470 OR ABAYE3763 OR ABAYE3764) AND ABAYE3097 AND ABAYE3471	C180 + 9 COA + 8 FAD + 8 NAD + ATP -> 9 ACCOA + 8 FADH2 + 8 NADH + AMP + PPI	oxidation of octadecanoic acid
R192	Fatty acid metabolism (octadecenoic acid; c18:1)	6.2.1.3 AND 1.3.99.- AND 1.3.99.3 AND 1.3.99.13 AND 4.2.1.17 AND 1.1.1.35 AND 2.3.1.16 AND 2.3.1.9 AND 1.3.99.7	(ABAYE2630 OR ABAYE3678) AND ABAYE1145 AND (ABAYE0436 OR ABAYE1204 OR ABAYE2631) AND (ABAYE1411 OR ABAYE2460 OR ABAYE3470) AND (ABAYE0482 OR ABAYE0915 OR ABAYE2065 OR ABAYE2290 OR ABAYE2304 OR ABAYE2311 OR ABAYE2369 OR ABAYE2370 OR ABAYE2628 OR ABAYE2852 OR ABAYE3186 OR ABAYE3470 OR ABAYE3763 OR ABAYE3764) AND ABAYE3097 AND ABAYE3471	C181 + 9 COA + 8 FAD + 8 NAD + ATP -> 9 ACCOA + 8 FADH2 + 8 NADH + AMP + PPI	oxidation of octadecenoic acid
R193	Fatty acid metabolism	1.14.15.3	ABAYE2014	C120ACP + O2 + RRBRDX <-> C120OH + ORBRDX + ACP	terminal alkane-1-monooxygenase
R194	Fatty acid metabolism	1.14.15.3	ABAYE2014	C120ACP + O2 + FADH2 <-> C120OH + FAD + ACP	terminal alkane-1-monooxygenase

No.	Metabolism	EC Number	ORF	Reaction	Enzyme
R195	Fatty acid metabolism	1.14.15.3	ABAYE2014	C140ACP + O2 + RRBRDX <-> C140OH + ORBRDX + ACP	terminal alkane-1-monooxygenase
R196	Fatty acid metabolism	1.14.15.3	ABAYE2014	C140ACP + O2 + FADH2 <-> C140OH + FAD + ACP	terminal alkane-1-monooxygenase
R197	Fatty acid metabolism	1.1.1.1	ABAYE0763 OR ABAYE1463 OR ABAYE1522 OR ABAYE1861 OR p2ABAYE0004 OR p3ABAYE0020 OR p3ABAYE0024	CH3OR + NAD <-> RCHO + NADH	alcohol dehydrogenase
R198	Fatty acid metabolism	1.14.15.3	ABAYE2014	RH + RRBRDX + O2 <-> ORBRDX + CH3OR	terminal alkane-1-monooxygenase
R199	Fatty acid metabolism	1.18.1.1 OR 1.18.1.3	(ABAYE1067 OR ABAYE2799) OR ABAYE2843	RRBRDX + NAD <-> ORBRDX + NADH	rubredoxin-NAD(+) reductase OR ferredoxin reductase component (dioxygenase)
R200	Fatty acid metabolism	1.18.1.3	ABAYE2843	RRBRDX + NADP <-> ORBRDX + NADPH	ferredoxin reductase component (dioxygenase)
R201	Fatty acid metabolism	1.2.1.3	ABAYE1028 OR ABAYE1460 OR ABAYE2333 OR ABAYE2837	RCHO + NAD <-> 0.015 C100 + 0.048 C120 + 0.003 C140 + 0.003 C150 + 0.281 C160 + 0.192 C161 + 0.017 C170 + 0.016 C171 + 0.008 C180 + 0.375 C181 + 0.041 C120OH + NADH	aldehyde dehydrogenase
R202	Fatty acid metabolism	5.3.3.8	ABAYE3470	C121COA <-> C122COA	fatty oxidation complex alpha subunit
R203	Biosynthesis of steroids	2.2.1.7	ABAYE0381	PYR + G3P -> DX5P + CO2	1-deoxy-D-xylulose-5-phosphate synthase
R204	Biosynthesis of steroids	1.1.1.267	ABAYE1581	DX5P + NADPH -> MDE4P + NADP	1-deoxy-D-xylulose-5-phosphate reductoisomerase
R205	Biosynthesis of steroids	2.7.7.60	ABAYE1672	MDE4P + CTP -> CDPMDE + PPI	4-diphosphocytidyl-2-methyl-D-erythritol synthase
R206	Biosynthesis of steroids	4.6.1.12	ABAYE1569	2PCDPMDE -> MDECPP + CMP	2-C-methyl-D-erythritol 2,4-cyclodiphosphate synthase
R207	Biosynthesis of steroids	1.17.4.3	ABAYE3263	MDECPP + NADH -> NAD + HMB4PP	4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase
R208	Biosynthesis of steroids	1.17.1.2	ABAYE0313	HMB4PP + NADH -> NAD + IPP	4-hydroxy-3-methylbut-2-enyl diphosphate reductase
R209	Biosynthesis of steroids	2.5.1.10	ABAYE0722	DMPP + IPP -> GPP + PPI	geranylgeranyl pyrophosphate synthase
R210	Biosynthesis of steroids	2.5.1.10	ABAYE0722	GPP + IPP -> FPP + PPI	geranylgeranyl pyrophosphate synthase
R211	Biosynthesis of steroids			GGPP + IPP -> PPPP + PPI	dimethylallyltranstransferase
R212	Biosynthesis of steroids			HEPPP + IPP -> OPP + PPI	trans-hexaprenyltranstransferase
R213	Glycerolipid metabolism	2.7.1.31	ABAYE0849	3PG + ADP <-> DGLYCERATE + ATP	glycerate kinase
R214	Glycerolipid metabolism	1.2.1.3	ABAYE1028 OR ABAYE1460 OR ABAYE2333 OR ABAYE2837	NADH + DGLYCERATE <-> T3 + NAD	aldehyde dehydrogenase
R215	Glycerolipid metabolism	2.7.1.30	ABAYE0816	GL + ATP -> GL3P + ADP	glycerol kinase
R216	Glycerolipid metabolism	3.1.1.3	ABAYE0325 OR ABAYE2810	DGR -> AGL + 0.015 C100 + 0.048 C120 + 0.003 C140 + 0.003 C150 + 0.281 C160 + 0.192 C161 + 0.017 C170 + 0.016 C171 + 0.008 C180 + 0.375 C181 + 0.041 C120OH	triacylglycerol lipase
R217	Glycerolipid metabolism	3.1.1.3	ABAYE0325 OR ABAYE2810	TGL -> DGR + 0.015 C100 + 0.048 C120 + 0.003 C140 + 0.003 C150 + 0.281 C160 + 0.192 C161 + 0.017 C170 + 0.016 C171 + 0.008 C180 + 0.375 C181 + 0.041 C120OH	triacylglycerol lipase
R218	Glycerolipid metabolism	2.3.1.15	ABAYE0397	GL3P + ACCOA -> AGL3P + COA	glycerol-3-phosphate acyltransferase
R219	Glycerolipid metabolism	2.3.1.20	ABAYE0708	TGL + COA -> DGR + 0.015 C100 + 0.048 C120 + 0.003 C140 + 0.003 C150 + 0.281 C160 + 0.192 C161 + 0.017 C170 + 0.016 C171 + 0.008 C180 + 0.375 C181 + 0.041 C120OH	bifunctional protein [wax ester synthase / acyl-CoA:diacylglycerol acyltransferase]
R220	Glycerophospholipid metabolism	1.1.1.94	ABAYE1223	DHAP + NADH -> GL3P + NAD	glycerol-3-phosphate dehydrogenase
R221	Glycerophospholipid metabolism	1.1.1.94	ABAYE1223	DHAP + NADPH -> GL3P + NADP	glycerol-3-phosphate dehydrogenase
R222	Glycerophospholipid metabolism	1.1.99.5	ABAYE0817	DHAP + UQH2 <-> GL3P + UQ	glycerol-3-phosphate dehydrogenase
R223	Glycerophospholipid metabolism	1.1.99.5	ABAYE0817	DHAP + MKH2 <-> GL3P + MK	glycerol-3-phosphate dehydrogenase
R224	Glycerophospholipid metabolism	1.1.99.5	ABAYE0817	DHAP + DMKH2 <-> GL3P + DMK	glycerol-3-phosphate dehydrogenase
R225	Glycerophospholipid metabolism	2.3.1.-	ABAYE0497 OR ABAYE0625 OR ABAYE1513 OR ABAYE1675 OR ABAYE1715 OR ABAYE1811 OR ABAYE2153 OR ABAYE2367 OR ABAYE2457 OR ABAYE2483 OR ABAYE3572 OR ABAYE3588 OR ABAYE3697 OR ABAYE3807	GL3P + ACOA -> 2AGL3P + COA	acetyltransferase
R226	Glycerophospholipid metabolism	2.3.1.15	ABAYE0397	GL3P + 0.015 C100ACP + 0.048 C120ACP + 0.003 C140ACP + 0.003 C150ACP + 0.281 C160ACP + 0.192 C161ACP + 0.017 C170ACP + 0.016 C171ACP + 0.008 C180ACP + 0.375 C181ACP + 0.041 C120OH -> AGL3P + 0.958 ACP	glycerol-3-phosphate O-acyltransferase
R227	Glycerophospholipid metabolism	2.3.1.51		AGL3P + 0.015 C100ACP + 0.048 C120ACP + 0.003 C140ACP + 0.003 C150ACP + 0.281 C160ACP + 0.192 C161ACP + 0.017 C170ACP + 0.016 C171ACP + 0.008 C180ACP + 0.375 C181ACP + 0.041 C120OH -> PA + 0.958 ACP	1-acylglycerol-3-phosphate O-acyltransferase
R228	Glycerophospholipid metabolism	2.7.1.107	ABAYE0824	DGR + ATP -> ADP + PA	diacylglycerol kinase
R229	Glycerophospholipid metabolism	3.1.1.32	ABAYE1646	PC -> 2AG3PC + 0.015 C100 + 0.048 C120 + 0.003 C140 + 0.003 C150 + 0.281 C160 + 0.192 C161 + 0.017 C170 + 0.016 C171 + 0.008 C180 + 0.375 C181 + 0.041 C120OH	phospholipase
R230	Glycerophospholipid metabolism	3.1.4.46	ABAYE0604 OR ABAYE0826	G3PC -> CHOLINE + GL3P	glycerophosphoryl diester phosphodiesterase
R231	Glycerophospholipid metabolism	2.7.7.41	ABAYE1580	PA + CTP <-> CDPDG + PPI	phosphatidate cytidylyltransferase
R232	Glycerophospholipid metabolism	2.7.8.8	ABAYE0470	CDPDG + SER <-> CMP + PS	phosphatidylserine synthase
R233	Glycerophospholipid metabolism	3.1.1.32	ABAYE1646	PS -> 2AG3PS + 0.015 C100 + 0.048 C120 + 0.003 C140 + 0.003 C150 + 0.281 C160 + 0.192 C161 + 0.017 C170 + 0.016 C171 + 0.008 C180 + 0.375 C181 + 0.041 C120OH	phospholipase
R234	Glycerophospholipid metabolism	4.1.1.65	ABAYE0104	PS -> PE + CO2	phosphatidylserine decarboxylase
R235	Glycerophospholipid metabolism	3.1.1.32	ABAYE1646	PE -> 2AG3PE + 0.015 C100 + 0.048 C120 + 0.003 C140 + 0.003 C150 + 0.281 C160 + 0.192 C161 + 0.017 C170 + 0.016 C171 + 0.008 C180 + 0.375 C181 + 0.041 C120OH	phospholipase
R236	Glycerophospholipid metabolism	3.1.4.46	ABAYE0604 OR ABAYE0826	G3PE -> ETHA + GL3P	glycerophosphoryl diester phosphodiesterase

No.	Metabolism	EC Number	ORF	Reaction	Enzyme
R237	Glycerophospholipid metabolism	2.7.8.5	ABAYE3463	CDPDG + GL3P <-> CMP + PGP	CDP-diacylglycerol--glycerol-3-phosphate 3-phosphatidyltransferase
R238	Glycerophospholipid metabolism	3.1.3.27	ABAYE0091 OR ABAYE0749 OR ABAYE3269	PGP -> PI + PG	phosphatidylglycerophosphatase
R239	Glycerophospholipid metabolism	2.7.8.-		CDPDG + PG -> CMP + CL	cardiolipin synthase
R240	Glycerophospholipid metabolism	3.1.4.3	ABAYE1520 OR ABAYE3825	PC <-> DGR + CHOLINEP	phospholipase C precursor (phosphatidylcholine cholinephosphohydrolase) (phosphatidylcholine-hydrolyzing phospholipase C)
R241	Glycerophospholipid metabolism	3.1.4.3	ABAYE1520 OR ABAYE3825	PE <-> DGR + ETHAP	phospholipase C precursor (phosphatidylcholine cholinephosphohydrolase) (phosphatidylcholine-hydrolyzing phospholipase C)
R242	Glycerophospholipid metabolism	3.1.4.3	ABAYE1520 OR ABAYE3825	PG <-> DGR + GL3P	phospholipase C precursor (phosphatidylcholine cholinephosphohydrolase) (phosphatidylcholine-hydrolyzing phospholipase C)
R243	Glycerophospholipid metabolism	4.3.1.7	ABAYE1457 AND ABAYE1458	ETHA <-> ACAL + NH3	ethanolamine ammonia-lyase
R244	Purine metabolism	2.7.6.1	ABAYE1789 OR ABAYE2981	R5P + ATP <-> PRPP + AMP	ribose-phosphate pyrophosphokinase
R245	Purine metabolism (De novo)	2.4.2.14	ABAYE1280	PRPP + GLN -> PRAM + PPI + GLU	amidophosphoribosyltransferase
R246	Purine metabolism (De novo)	6.3.4.13	ABAYE1366	PRAM + ATP + GLY <-> GAR + ADP + PI	phosphoribosylamine-glycine ligase
R247	Purine metabolism (De novo)	2.1.2.2	ABAYE0888 OR ABAYE2179	GAR + FTHF -> FGAR + THF	phosphoribosylglycinamide formyltransferase
R248	Purine metabolism (De novo)	6.3.5.3	ABAYE0912	FGAR + ATP + GLN -> FGAM + GLU + ADP + PI	phosphoribosylformylglycinamidine synthase
R249	Purine metabolism (De novo)	6.3.3.1	ABAYE0889	FGAM + ATP -> AIR + ADP + PI	phosphoribosylformylglycinamidine cyclo-ligase
R250	Purine metabolism (De novo)	4.1.1.21	ABAYE3871 AND ABAYE3872	AIR + CO2 + ATP -> CAIR + ADP + PI	phosphoribosylaminoimidazole carboxylase
R251	Purine metabolism (De novo)	6.3.2.6	ABAYE0056	CAIR + ATP + ASP <-> SAICAR + ADP + PI	phosphoribosylaminoimidazole-succinocarboxamide synthase
R252	Purine metabolism (De novo)	4.3.2.2	ABAYE1039	SAICAR <-> AICAR + FUM	adenylosuccinate lyase
R253	Purine metabolism (De novo)	2.1.2.3	ABAYE1367	AICAR + FTHF <-> PRFICA + THF	phosphoribosylaminoimidazolecarboxamide formyltransferase
R254	Purine metabolism (De novo)	3.5.4.10	ABAYE1367	PRFICA <-> IMP	phosphoribosylaminoimidazolecarboxamide formyltransferase; IMP cyclohydrolase
R255	Purine metabolism (De novo)	6.3.4.4	ABAYE2592	IMP + GTP + ASP -> ASUC + GDP + PI	adenylosuccinate synthase
R256	Purine metabolism (De novo)	4.3.2.2	ABAYE1039	ASUC <-> FUM + AMP	adenylosuccinate lyase
R257	Purine metabolism (De novo)	1.1.1.205	ABAYE0166	IMP + NAD -> XMP + NADH	IMP dehydrogenase
R258	Purine metabolism (De novo)	6.3.5.2	ABAYE1456 OR ABAYE3740	XMP + ATP + GLN -> GMP + GLU + AMP + PPI	GMP synthetase
R259	Purine metabolism	3.5.4.4	ABAYE2601 OR ABAYE3101	ADN -> INS + NH3	adenosine deaminase
R260	Purine metabolism	3.5.4.4	ABAYE2601 OR ABAYE3101	DA <-> DIN + NH3	adenosine deaminase
R261	Purine metabolism	3.1.3.5	ABAYE1047 OR ABAYE1886	IMP -> INS + PI	5'-nucleotidase
R262	Purine metabolism	3.1.3.5	ABAYE1047 OR ABAYE1886	AMP -> ADN + PI	5'-nucleotidase
R263	Purine metabolism	3.1.3.5	ABAYE1047 OR ABAYE1886	XMP -> XTSINE + PI	5'-nucleotidase
R264	Purine metabolism	3.1.3.5	ABAYE1047 OR ABAYE1886	GMP -> GSN + PI	5'-nucleotidase
R265	Purine metabolism	3.1.3.5	ABAYE1047 OR ABAYE1886	DAMP <-> DA + PI	5'-nucleotidase
R266	Purine metabolism	3.1.3.5	ABAYE1047 OR ABAYE1886	DGMP <-> DG + PI	5'-nucleotidase
R267	Purine metabolism	2.7.4.8	ABAYE0312	DGMP + ATP <-> DGDP + ADP	guanylate kinase
R268	Purine metabolism	2.7.4.6	ABAYE3267	IDP + ATP <-> ITP + ADP	nucleoside-diphosphate kinase
R269	Purine metabolism	2.7.4.6	ABAYE3267	ATP + DIDP <-> ADP + DITP	nucleoside-diphosphate kinase
R270	Purine metabolism	2.4.2.8	ABAYE3887	HYXN + PRPP -> PPI + IMP	hypoxanthine phosphoribosyltransferase
R271	Purine metabolism	2.4.2.8	ABAYE3887	XAN + PRPP -> PPI + XMP	hypoxanthine phosphoribosyltransferase
R272	Purine metabolism	2.4.2.8	ABAYE3887	AMP + PPI <-> AD + PRPP	hypoxanthine phosphoribosyltransferase
R273	Purine metabolism	3.1.5.1	ABAYE0911	DGTP -> DG + PPPI	dGTP triphosphohydrolase
R274	Purine metabolism	2.7.6.5	ABAYE3181	ATP + GTP -> pppGpp + AMP	GTP pyrophosphokinase
R275	Purine metabolism	3.1.7.2	ABAYE0310	ppGpp <-> GDP + PPI	guanosine-3',5'-bis(diphosphate) 3'-pyrophosphohydrolase
R276	Purine metabolism	2.7.4.3	ABAYE2767	ATP + AMP <-> 2 ADP	adenylate kinase
R277	Purine metabolism	1.17.4.1	ABAYE3065 AND ABAYE3067	ADP + RTHIO -> DADP + OTHIO	ribonucleoside-diphosphate reductase
R278	Purine metabolism	2.7.4.6	ABAYE3267	DADP + ATP <-> DATP + ADP	nucleoside-diphosphate kinase
R279	Purine metabolism	2.7.4.8	ABAYE0312	GMP + ATP <-> GDP + ADP	guanylate kinase
R280	Purine metabolism	2.7.4.6	ABAYE3267	GDP + ATP <-> GTP + ADP	nucleoside-diphosphate kinase
R281	Purine metabolism	1.17.4.1	ABAYE3065 AND ABAYE3067	GDP + RTHIO -> DGDP + OTHIO	ribonucleoside-diphosphate reductase
R282	Purine metabolism	2.7.4.6	ABAYE3267	DGDP + ATP <-> DGTP + ADP	nucleoside-diphosphate kinase
R283	Purine metabolism	3.6.1.13	ABAYE3519	ARIB -> AMP + R5P	ADPribose ribophosphohydrolase
R284	Purine metabolism	2.7.4.3	ABAYE2767	ATP + DAMP <-> ADP + DADP	adenylate kinase
R285	Purine metabolism	3.6.1.41	ABAYE0491	ApppA -> 2 ADP	bis(5'-nucleosyl)-tetraphosphatase
R286	Purine metabolism	1.17.1.4	ABAYE1114 AND ABAYE1115	HYXN + NAD <-> XAN + NADH	xanthine dehydrogenase
R287	Purine metabolism	1.17.1.4	ABAYE1114 AND ABAYE1115	XAN + NAD <-> URT + NADH	xanthine dehydrogenase
R288	Purine metabolism	3.5.3.19	ABAYE0127	UDGLYCOLATE <-> GLX + 2 NH3 + CO2	ureidoglycolate amidohydrolase(decarboxylating)
R289	Purine metabolism	3.5.3.4	ABAYE0128	ALLNT <-> UDGLYCOLATE + UREA	allantoicase
R290	Purine metabolism	3.5.4.3	ABAYE2396 OR ABAYE3885	GN <-> XAN + NH3	guanine deaminase
R291	Purine metabolism	3.6.1.11	ABAYE3154	pppGpp -> ppGpp + PI	exopolyphosphatase (exopolypase)
R292	Purine metabolism	3.6.1.15	ABAYE3296	ATP <-> ADP + PI	hypothetical protein
R293	Purine metabolism	3.6.1.19	ABAYE3179	DITP -> DIMP + PPI	nucleoside-triphosphate pyrophosphatase
R294	Purine metabolism	3.6.1.19	ABAYE3179	GTP -> GMP + PPI	nucleoside-triphosphate pyrophosphatase
R295	Purine metabolism	3.6.1.19	ABAYE3179	ITP -> IMP + PPI	nucleoside-triphosphate pyrophosphatase
R296	Purine metabolism	3.6.1.19	ABAYE3179	XTP -> XMP + PPI	nucleoside-triphosphate pyrophosphatase
R297	Purine metabolism	3.6.1.19	ABAYE3179	DGTP -> DGMP + PPI	nucleoside-triphosphate pyrophosphatase
R298	Purine metabolism	4.1.1.-	ABAYE1027	5AI + CO2 <-> 5A4ICA	L-2,4-diaminobutyrate decarboxylase
R299	Pyrimidine metabolism (De novo)	2.1.3.2	ABAYE2578	CAP + ASP -> CAASP + PI	aspartate carbamoyltransferase
R300	Pyrimidine metabolism (De novo)	3.5.2.3	ABAYE2577 OR ABAYE2646	CAASP <-> DOROA	dihydroorotase
R301	Pyrimidine metabolism (De novo)	1.3.3.1	ABAYE1278	DOROA + UQ <-> UQH2 + OROA	dihydroorotate oxidase
R302	Pyrimidine metabolism (De novo)	1.3.3.1	ABAYE1278	DOROA + MK <-> MKH2 + OROA	dihydroorotate oxidase
R303	Pyrimidine metabolism (De novo)	2.4.2.10	ABAYE0144	OROA + PRPP <-> PPI + OMP	orotate phosphoribosyltransferase

No.	Metabolism	EC Number	ORF	Reaction	Enzyme
R304	Pyrimidine metabolism (De novo)	4.1.1.23	ABAYE2058	OMP -> CO2 + UMP	orotidine-5'-phosphate decarboxylase
R305	Pyrimidine metabolism (De novo)	2.7.4.6	ABAYE3267	UDP + ATP <-> UTP + ADP	nucleoside-diphosphate kinase
R306	Pyrimidine metabolism (De novo)	6.3.4.2	ABAYE1667	UTP + GLN + ATP -> GLU + CTP + ADP + PI	CTP synthase
R307	Pyrimidine metabolism	6.3.4.2	ABAYE1667	ATP + UTP + NH3 -> ADP + PI + CTP	CTP synthase
R308	Pyrimidine metabolism	2.7.4.6	ABAYE3267	CDP + ATP <-> CTP + ADP	nucleoside-diphosphate kinase
R309	Pyrimidine metabolism	1.17.4.1	ABAYE3065 AND ABAYE3067	CDP + RTHIO -> DCDP + OTHIO	ribonucleoside-diphosphate reductase
R310	Pyrimidine metabolism	2.7.4.6	ABAYE3267	DCDP + ATP <-> DCTP + ADP	nucleoside-diphosphate kinase
R311	Pyrimidine metabolism	2.7.4.9	ABAYE0933	DTMP + ATP <-> DTDP + ADP	thymidylate kinase
R312	Pyrimidine metabolism	2.7.4.6	ABAYE3267	DTDP + ATP <-> DTTP + ADP	nucleoside-diphosphate kinase
R313	Pyrimidine metabolism	2.7.4.14	ABAYE2062	CMP + ATP <-> ADP + CDP	cytidylate kinase
R314	Pyrimidine metabolism	1.8.1.9	ABAYE2940 OR ABAYE3661	OTHIO + NADPH -> RTHIO + NADP	thioredoxin reductase
R315	Pyrimidine metabolism	2.7.4.14	ABAYE2062	DCMP + ATP <-> ADP + DCDP	cytidylate kinase
R316	Pyrimidine metabolism	2.4.2.9	ABAYE3047	URA + PRPP <-> UMP + PPI	uracil phosphoribosyltransferase
R317	Pyrimidine metabolism	4.2.1.70	ABAYE1445	URA + R5P <-> PURI5P	pseudouridylate synthase
R318	Pyrimidine metabolism	2.1.1.45	ABAYE3314	DUMP + METTHF -> DHF + DTMP	thymidylate synthase
R319	Pyrimidine metabolism	2.4.2.1 OR 2.4.2.4		DU + PI -> URA + DR1P	purine-nucleoside phosphorylase **OR** thymidine phosphorylase
R320	Pyrimidine metabolism	2.4.2.4		DT + PI -> TM + DR1P	thymidine phosphorylase
R321	Pyrimidine metabolism	2.7.4.6	ABAYE3267	DUDP + ATP <-> DUTP + ADP	nucleoside-diphosphate kinase
R322	Pyrimidine metabolism	1.17.4.1	ABAYE3065 AND ABAYE3067	UDP + RTHIO -> OTHIO + DUDP	ribonucleoside-diphosphate reductase
R323	Pyrimidine metabolism	2.7.4.9	ABAYE0933	ATP + DUMP <-> ADP + DUDP	thymidylate kinase
R324	Pyrimidine metabolism	3.1.3.5	ABAYE1047 OR ABAYE1886	UMP -> URI + PI	5'-nucleotidase
R325	Pyrimidine metabolism	3.1.3.5	ABAYE1047 OR ABAYE1886	CMP -> CYTD + PI	5'-nucleotidase
R326	Pyrimidine metabolism	3.1.3.5	ABAYE1047 OR ABAYE1886	DCMP -> DC + PI	5'-nucleotidase
R327	Pyrimidine metabolism	3.1.3.5	ABAYE1047 OR ABAYE1886	DTMP -> DT + PI	5'-nucleotidase
R328	Pyrimidine metabolism	3.5.4.1		5MC <-> TM + NH3	cytosine deaminase
R329	Pyrimidine metabolism	3.5.4.1		CT -> URA + NH3	cytosine deaminase
R330	Pyrimidine metabolism	3.5.4.5		DC -> DU + NH3	cytidine deaminase
R331	Pyrimidine metabolism	2.7.4.14 OR 2.7.4.22	ABAYE2062 OR ABAYE1577	ATP + UMP <-> ADP + UDP	cytidylate kinase OR uridylate kinase
R332	Pyrimidine metabolism	3.5.4.13	ABAYE3025	CTP -> UTP + NH3	deoxycytidine triphosphate deaminase
R333	Pyrimidine metabolism	3.5.4.13	ABAYE3025	DCTP -> DUTP + NH3	deoxycytidine triphosphate deaminase
R334	Pyrimidine metabolism	3.6.1.19	ABAYE3179	UTP -> UMP + PPI	nucleoside-triphosphate pyrophosphatase
R335	Pyrimidine metabolism	3.6.1.19 OR 3.6.1.23	ABAYE3179 OR ABAYE2929	DUTP -> DUMP + PPI	nucleoside-triphosphate pyrophosphatase OR deoxyuridine 5'-triphosphate nucleotidohydrolase
R336	Glutamate metabolism	6.3.1.2	ABAYE1126 OR ABAYE1425	GLU + NH3 + ATP -> GLN + ADP + PI	glutamine synthetase
R337	Glutamate metabolism	1.4.1.13 OR 1.4.1.14	ABAYE0298 AND ABAYE0299	GLN + AKG + NADPH -> 2 GLU + NADP	glutamate synthase
R338	Glutamate metabolism	6.3.5.5	ABAYE0800 AND ABAYE0801	GLN + 2 ATP + HCO3 -> GLU + CAP + 2 ADP + PI	carbamoyl-phosphate synthase
R339	Glutamate metabolism	6.1.1.17	ABAYE0277	TRNAGLU + GLU + ATP -> GLUTRNAGLU + PPI + AMP	glutamyl-tRNA synthetase
R340	Glutamate metabolism	6.1.1.18	ABAYE1455	ATP + GLN + TRNAGLN -> AMP + PPI + GTRNA	glutaminyl-tRNA synthetase
R341	Glutamate metabolism	3.5.1.2 OR 3.5.1.38	ABAYE2832 OR ABAYE2188	GLN -> GLU + NH3	glutaminase OR glutaminase-asparaginase
R342	Glutamate metabolism	6.3.5.7	ABAYE0697 AND ABAYE0698 AND ABAYE0699	GTRNA + GLU + PI + ADP <-> GLUTRNAGLN + GLN + ATP	aspartyl/glutamyl-tRNA(Asn/Gln) amidotransferase
R343	Alanine and aspartate metabolism	2.6.1.1	ABAYE0951	OA + GLU <-> ASP + AKG	aspartate aminotransferase
R344	Alanine and aspartate metabolism	6.1.1.12	ABAYE0588	ATP + ASP + TRNAASP -> AMP + PPI + ASPTRNAASP	aspartyl-tRNA synthetase
R345	Alanine and aspartate metabolism	6.1.1.7	ABAYE2595	ATP + ALA + TRNAALA <-> AMP + PPI + ALATRNA	alanyl-tRNA synthetase
R346	Alanine and aspartate metabolism	6.3.5.4		ASP + ATP + GLN -> GLU + ASN + AMP + PPI	asparagine synthase
R347	Alanine and aspartate metabolism	3.5.1.1 OR 3.5.1.38	ABAYE3351 OR ABAYE2188	ASN -> ASP + NH3	L-asparaginase I OR glutaminase-asparaginase
R348	Alanine and aspartate metabolism	3.4.13.3	ABAYE1209	CNS -> bALA + HIS	aminoacyl-histidine dipeptidase (peptidase D)
R349	Alanine and aspartate metabolism	1.4.3.16	ABAYE0935	ASP + O2 -> OA + NH3 + H2O2	L-aspartate oxidase
R350	Alanine and aspartate metabolism	5.1.1.13	ABAYE1354	ASP <-> DASP	aspartate/glutamate racemase
R351	Alanine and aspartate metabolism	6.3.5.6	ABAYE0697 AND ABAYE0698 AND ABAYE0699	ASNTRNAASN + GLU + PI + ADP <-> ASPTRNAASN + GLN + ATP	aspartyl/glutamyl-tRNA(Asn/Gln) amidotransferase
R352	Glycine, serine and threonine metabolism	2.7.2.4	ABAYE2596	ASP + ATP -> ADP + BASP	aspartate kinase
R353	Glycine, serine and threonine metabolism	1.2.1.11	ABAYE3348	BASP + NADPH -> NADP + PI + ASPSA	aspartate-semialdehyde dehydrogenase
R354	Glycine, serine and threonine metabolism	1.1.1.3	ABAYE1937 OR ABAYE3530	ASPSA + NADH <-> NAD + HSER	homoserine dehydrogenase
R355	Glycine, serine and threonine metabolism	1.1.1.3	ABAYE1937 OR ABAYE3530	ASPSA + NADPH <-> NADP + HSER	homoserine dehydrogenase
R356	Glycine, serine and threonine metabolism	2.7.1.39	ABAYE0244	HSER + ATP -> ADP + PHSER	homoserine kinase
R357	Glycine, serine and threonine metabolism	4.2.3.1	ABAYE3531	PHSER -> THR + PI	threonine synthase
R358	Glycine, serine and threonine metabolism	1.1.1.95	ABAYE0332	3PG + NAD -> NADH + PHP	D-3-phosphoglycerate dehydrogenase
R359	Glycine, serine and threonine metabolism	2.6.1.52	ABAYE0877	PHP + GLU -> AKG + 3PSER	phosphoserine aminotransferase
R360	Glycine, serine and threonine metabolism	3.1.3.3	ABAYE0098	3PSER -> PI + SER	phosphoserine phosphatase
R361	Glycine, serine and threonine metabolism	2.1.2.1	ABAYE1171	THF + SER <-> GLY + METTHF	serine hydroxymethyltransferase

No.	Metabolism	EC Number	ORF	Reaction	Enzyme
R362	Glycine, serine and threonine metabolism	1.8.1.4	ABAYE0505 OR ABAYE0782 OR ABAYE1945	DHLIPOYLPROTEIN + NAD -> NADH + LIPOYLPROTEIN	dihydrolipoamide dehydrogenase
R363	Glycine, serine and threonine metabolism	4.3.1.17 OR 4.3.1.19	ABAYE2377 OR (ABAYE0691 OR ABAYE1083 OR ABAYE1649)	SER <-> PYR + NH3	L-serine ammonia-lyase
R364	Glycine, serine and threonine metabolism	4.3.1.19	ABAYE0691 OR ABAYE1083 OR ABAYE1649	THR -> OBUT + NH3	threonine dehydratase
R365	Glycine, serine and threonine metabolism	6.1.1.3	ABAYE3169	ATP + THR + TRNATHR -> AMP + PPI + THRTRNATHR	threonyl-tRNA synthetase
R366	Glycine, serine and threonine metabolism	6.1.1.11	ABAYE0757	ATP + SER + TRNASER -> AMP + PPI + SERTRNASER	seryl-tRNA synthetase
R367	Glycine, serine and threonine metabolism	6.1.1.14	ABAYE0367 AND ABAYE0368	ATP + GLY + TRNAGLY -> AMP + PPI + GLYTRNAGLY	glycyl-tRNA synthetase
R368	Glycine, serine and threonine metabolism	2.6.1.76	ABAYE1026	GLU + ASPSA -> AKG + 24DAB	glutamate decarboxylase
R369	Glycine, serine and threonine metabolism	1.1.99.1	ABAYE2868	BAL + FAD -> FADH2 + BETAINE	choline dehydrogenase
R370	Glycine, serine and threonine metabolism	1.2.1.8	ABAYE1066 OR ABAYE2867	BAL + NAD -> BETAINE + NADH	NAD-dependent aldehyde dehydrogenase
R371	Glycine, serine and threonine metabolism	1.1.1.-	ABAYE0043 OR ABAYE0109 OR ABAYE0479 OR ABAYE1356 OR ABAYE2589 OR ABAYE2607 OR ABAYE2613 OR ABAYE2618 OR ABAYE2845 OR ABAYE3187 OR ABAYE3378	MTG + NADPH -> HAC + NADP	alcohol dehydrogenase
R372	Glycine, serine and threonine metabolism	1.4.3.21	ABAYE1710	AACTN + O2 <-> MTG + NH3 + H2O2	copper amine oxidase precursor (tyramine oxidase) (2-phenylethylamine oxidase)
R373	Glycine, serine and threonine metabolism	4.3.1.18	ABAYE2819	DSER <-> PYR + NH3	D-serine deaminase (dehydratase)
R374	Methionine metabolism	4.4.1.8	ABAYE0405	LLCT -> HCYS + PYR + NH3	cystathionine beta-lyase, PLP-dependent
R375	Methionine metabolism	2.1.1.13	ABAYE2822	HCYS + MTHF <-> THF + MET	methionine synthase I
R376	Methionine metabolism	2.1.1.14	ABAYE3079	5MTGLU + HCYS -> TGLU + MET	5-methyltetrahydropteroyltriglutamate-homocysteine methyltransferase
R377	Methionine metabolism	6.1.1.10	ABAYE3031	ATP + MET + TRNAMET -> AMP + PPI + METTRNA	methionyl-tRNA synthetase
R378	Methionine metabolism	2.1.2.9	ABAYE0022	METTRNA + FTHF -> THF + FMETTRNA	methionyl-tRNA formyltransferase
R379	Methionine metabolism	2.5.1.6	ABAYE2118	MET + ATP -> PPI + PI + SAM	S-adenosylmethionine synthetase
R380	Methionine metabolism	3.2.2.9	ABAYE3028 OR ABAYE3846	SAH <-> SRLH + AD	S-adenosylhomocysteine nucleosidase
R381	Methionine metabolism	2.1.1.37	ABAYE0084	SAM + CT <-> SAH + 5MC	cytosine-specific methyltransferase
R382	Methionine metabolism	2.3.1.31	ABAYE3293	ACCOA + HSER <-> COA + OAHSER	homoserine O-acetyltransferase
R383	Methionine metabolism	2.5.1.-	ABAYE1970	OSLHSER + H2S <-> HCYS + SUCC	O-succinylhomoserine sulfhydrylase
R384	Methionine metabolism	2.5.1.49	ABAYE0264	OAHSER + H2S <-> HCYS + AC	homocysteine synthase
R385	Methionine metabolism	2.5.1.49	ABAYE0264	OAHSER + HO3S2 + RTHIO <-> HCYS + H2SO3 + OTHIO + AC	homocysteine synthase
R386	Cysteine metabolism	4.4.1.8	ABAYE0405	H2S + PYR + NH3 -> CYS	cystathionine beta-lyase
R387	Cysteine metabolism	4.4.1.8	ABAYE0405	CYST -> PYR + NH3 + TCYS	cystathionine beta-lyase
R388	Cysteine metabolism	2.3.1.30	ABAYE2191 OR ABAYE2248	SER + ACCOA <-> COA + ASER	serine acetyltransferase
R389	Cysteine metabolism	2.5.1.47	ABAYE3184 OR ABAYE3696	ASER + H2S -> CYS + AC	cysteine synthase
R390	Cysteine metabolism	2.5.1.47 OR 2.5.1.49	ABAYE3184 OR ABAYE3696 OR ABAYE0264	ASER + HO3S2 + RTHIO -> CYS + H2SO3 + OTHIO + AC	cysteine synthase
R391	Cysteine metabolism	2.5.1.47	ABAYE3184 OR ABAYE3696	ASER + HO3S2 -> SSLCYS + AC	cysteine synthase
R392	Cysteine metabolism	2.6.1.1	ABAYE0951	CYSTEATE + AKG <-> 3SPYR + GLU	aspartate aminotransferase
R393	Cysteine metabolism	2.6.1.1	ABAYE0951	3SLALA + AKG -> 3SFPYR + GLU	aspartate aminotransferase
R394	Cysteine metabolism	2.6.1.1	ABAYE0951	MPYR + GLU -> CYS + AKG	aspartate aminotransferase
R395	Cysteine metabolism	4.3.1.17	ABAYE2377	SER -> 2AA	L-serine dehydratase
R396	Cysteine metabolism	6.1.1.16	ABAYE2493	ATP + CYS + TRNACYS -> AMP + PPI + CYSTRNACYS	cysteinyl-tRNA synthetase
R397	Cysteine metabolism	4.4.1.15	ABAYE3037	DCYS <-> H2S + NH3 + PYR	D-cysteine desulfhydrase
R398	Valine, leucine and isoleucine degradation	1.1.1.31	ABAYE3767	HIBUT + NAD -> 3OPP + NADH	3-hydroxyisobutyrate dehydrogenase
R399	Valine, leucine and isoleucine degradation	1.3.99.3 OR 1.3.99.10	(ABAYE0476 OR ABAYE2013) OR ABAYE2288	3MBCOA + FAD <-> 3MCCOA + FADH2	acyl-CoA dehydrogenase
R400	Valine, leucine and isoleucine degradation	4.2.1.17	ABAYE0482 OR ABAYE0915 OR ABAYE2065 OR ABAYE2290 OR ABAYE2304 OR ABAYE2311 OR ABAYE2369 OR ABAYE2370 OR ABAYE2628 OR ABAYE2852 OR ABAYE3186 OR ABAYE3763 OR ABAYE3764	3HIVCOA <-> 3MCCOA	enoyl-CoA hydratase
R401	Valine, leucine and isoleucine degradation	4.2.1.17	ABAYE0482 OR ABAYE0915 OR ABAYE2065 OR ABAYE2290 OR ABAYE2304 OR ABAYE2311 OR ABAYE2369 OR ABAYE2370 OR ABAYE2628 OR ABAYE2852 OR ABAYE3186 OR ABAYE3763 OR ABAYE3764	2MP2ECOA -> 3HIBCOA	enoyl-CoA hydratase

No.	Metabolism	EC Number	ORF	Reaction	Enzyme
R402	Valine, leucine and isoleucine degradation	4.2.1.17	ABAYE0482 OR ABAYE0915 OR ABAYE2065 OR ABAYE2290 OR ABAYE2304 OR ABAYE2311 OR ABAYE2369 OR ABAYE2370 OR ABAYE2628 OR ABAYE2852 OR ABAYE3186 OR ABAYE3763 OR ABAYE3764	3H2MBCOA -> 2MB2ECOA	enoyl-CoA hydratase
R403	Valine, leucine and isoleucine degradation	6.4.1.4	ABAYE0483	ATP + 3MCCOA + HCO3 -> ADP + PI + 3MGCOA	3-methylcrotonyl-CoA carboxylase
R404	Valine, leucine and isoleucine degradation	1.1.1.35	ABAYE1411 OR ABAYE2460 OR ABAYE3470	HIBUT + NAD <-> MMSA + NADH	3-hydroxyacyl-CoA dehydrogenase
R405	Valine, leucine and isoleucine degradation	1.1.1.35	ABAYE1411 OR ABAYE2460 OR ABAYE3470	3H2MBCOA + NAD <-> 2MAACCOA + NADH	3-hydroxyacyl-CoA dehydrogenase
R406	Valine, leucine and isoleucine degradation	1.2.1.3	ABAYE1028 OR ABAYE1460 OR ABAYE2333 OR ABAYE2837	MMSA + NAD -> MM + NADH	aldehyde dehydrogenase
R407	Valine, leucine and isoleucine degradation	2.3.1.16	ABAYE3471	COA + 2MAACCOA -> PPACOA + ACCOA	acetyl-CoA acyltransferase
R408	Valine, leucine and isoleucine degradation	1.3.99.3	ABAYE0476 OR ABAYE2013	2MPPACOA + FAD <-> 2MP2ECOA + FADH2	acyl-CoA dehydrogenase
R409	Valine, leucine and isoleucine degradation	1.3.99.3	ABAYE0476 OR ABAYE2013	2MBCOA + FAD <-> 2MB2ECOA + FADH2	acyl-CoA dehydrogenase
R410	Valine, leucine and isoleucine degradation	2.6.1.18	ABAYE1295	ALA + MMSA <-> PYR + AIBUT	omega-amino acid--pyruvate aminotransferase (omega-APT) (beta-alanine--pyruvate aminotransferase)
R411	Valine, leucine and isoleucine degradation	2.6.1.42	ABAYE0577	ILE + AKG <-> 3MOP + GLU	branched-chain amino acid transferase
R412	Valine, leucine and isoleucine degradation	2.6.1.42	ABAYE0577	LEU + AKG <-> 4MOP + GLU	branched-chain amino acid transferase
R413	Valine, leucine and isoleucine biosynthesis	1.1.1.86	ABAYE3238	ACLAC + NADPH -> NADP + DHMVA	acetohydroxy acid isomeroreductase
R414	Valine, leucine and isoleucine biosynthesis	4.2.1.9	ABAYE0023 OR ABAYE1724 OR ABAYE1781	DHMVA -> OIVAL	dihydroxy-acid dehydratase OR 6-phosphogluconate dehydratase
R415	Valine, leucine and isoleucine biosynthesis	2.6.1.42	ABAYE0577	OIVAL + GLU <-> AKG + VAL	branched-chain amino acid aminotransferase
R416	Valine, leucine and isoleucine biosynthesis	2.2.1.6	ABAYE2836 OR (ABAYE3239 AND ABAYE3240)	OBUT + 2(HE)TPP -> ABUT + THMPP	acetolactate synthase
R417	Valine, leucine and isoleucine biosynthesis	1.1.1.86	ABAYE3238	ABUT + NADPH -> NADP + DHMP	ketol-acid reductoisomerase
R418	Valine, leucine and isoleucine biosynthesis	4.2.1.9	ABAYE0023 OR ABAYE1724 OR ABAYE1781	DHMP -> 3MOP	dihydroxy-acid dehydratase
R419	Valine, leucine and isoleucine biosynthesis	2.6.1.42	ABAYE0577	3MOP + GLU <-> AKG + ILE	branched-chain amino acid aminotransferase
R420	Valine, leucine and isoleucine biosynthesis	2.3.3.13	ABAYE3292	ACCOA + OIVAL -> COA + IPPMAL	isopropylmalate synthase
R421	Valine, leucine and isoleucine biosynthesis	4.2.1.33	ABAYE3359 AND ABAYE3360	IPPMAL <-> CBHCAP	3-isopropylmalate dehydratase
R422	Valine, leucine and isoleucine biosynthesis	1.1.1.85	ABAYE3357	CBHCAP + NAD -> NADH + OICAP	isopropylmalate dehydrogenase
R423	Valine, leucine and isoleucine biosynthesis			OICAP -> 4MOP + CO2	spontaneous
R424	Valine, leucine and isoleucine biosynthesis	2.6.1.42	ABAYE0577	4MOP + GLU <-> AKG + LEU	branched-chain amino acid aminotransferase
R425	Valine, leucine and isoleucine biosynthesis	6.1.1.4	ABAYE3244	ATP + LEU + TRNALEU -> AMP + PPI + LEUTRNA	leucyl-tRNA synthetase
R426	Valine, leucine and isoleucine biosynthesis	6.1.1.9	ABAYE0740	ATP + VAL + TRNAVAL -> AMP + PPI + VALTRNAVAL	valyl-tRNA synthetase
R427	Valine, leucine and isoleucine biosynthesis	6.1.1.5	ABAYE3852	ATP + ILE + TRNAILE -> AMP + PPI + ILETRNAILE	isoleucyl-tRNA synthetase
R428	Lysine biosynthesis	4.2.1.52	ABAYE0058 OR ABAYE2388 OR ABAYE2878 OR ABAYE3671	ASPSA + PYR -> DHDP	dihydrodipicolinate synthase
R429	Lysine biosynthesis	1.3.1.26	ABAYE0036	DHDP + NADPH -> NADP + TDHDP	dihydrodipicolinate reductase
R430	Lysine biosynthesis	1.3.1.26	ABAYE0036	DHDP + NADH -> NAD + TDHDP	dihydrodipicolinate reductase
R431	Lysine biosynthesis	2.3.1.117	ABAYE0923	TDHDP + SUCCOA -> SAOPIM + COA	2,3,4,5-tetrahydropyridine-2,6-carboxylate N-succinyltransferase
R432	Lysine biosynthesis	2.6.1.17	ABAYE2181	SAOPIM + GLU -> SDAPIM + AKG	succinyldiaminopimelate transaminase
R433	Lysine biosynthesis	3.5.1.18	ABAYE0676	SDAPIM -> DAPIM + SUCC	succinyl-diaminopimelate desuccinylase
R434	Lysine biosynthesis	5.1.1.7	ABAYE0861	DAPIM <-> MDAPIM	diaminopimelate epimerase
R435	Lysine biosynthesis	4.1.1.20	ABAYE0860	MDAPIM -> LYS + CO2	diaminopimelate decarboxylase
R436	Lysine biosynthesis	6.1.1.6	ABAYE0854 OR ABAYE2794	ATP + LYS + TRNALYS -> AMP + PPI + LYSTRNA	lysyl-tRNA synthetase
R437	Lysine biosynthesis	1.1.1.3	ABAYE1937 OR ABAYE3530	HSER + NAD <-> ASPSA + NADH	homoserine dehydrogenase
R438	Lysine biosynthesis	1.1.1.3	ABAYE1937 OR ABAYE3530	HSER + NADP <-> ASPSA + NADPH	homoserine dehydrogenase
R439	Lysine biosynthesis	1.2.1.11	ABAYE3348	ASPSA + PI + NADP <-> BASP + NADPH	aspartate-semialdehyde dehydrogenase
R440	Lysine degradation	1.2.4.2	ABAYE0780	2OAD + LIPO -> SGDHL + CO2	2-oxoglutarate dehydrogenase E1 component
R441	Lysine degradation	2.3.1.61	ABAYE0781	GLUTCOA + DLIPO <-> COA + SGDHL	2-oxoglutarate dehydrogenase E2 component
R442	Lysine degradation	1.14.13.59	ABAYE1094	LYS + O2 + NADPH <-> NHLYS + NADP	acinetobactin siderophore biosynthesis protein OR lysine N6-hydroxylase
R443	Lysine degradation	1.2.1.3	ABAYE1028 OR ABAYE1460 OR ABAYE2333 OR ABAYE2837	4TMABT + NAD <-> 4TMABTO + NADH	aldehyde dehydrogenase
R444	Lysine degradation	1.3.99.7	ABAYE3097	GLUTCOA <-> CCOA + CO2	glutaryl-CoA dehydrogenase
R445	Arginine and proline metabolism	2.3.1.109	ABAYE0353	SUCCOA + ARG -> COA + N2SUCCARG	arginine succinyltransferase
R446	Arginine and proline metabolism	6.1.1.19	ABAYE3732	ATP + ARG + TRNAARG <-> AMP + PPI + ARGTRNAARG	arginyl-tRNA synthetase
R447	Arginine and proline metabolism	1.5.1.12	ABAYE2108	P5C + NAD -> NADH + GLU	bifunctional proline dehydrogenase OR delta-1-pyrroline-5-carboxylate dehydrogenase

No.	Metabolism	EC Number	ORF	Reaction	Enzyme
R448	Arginine and proline metabolism	1.5.1.12	ABAYE2108	P5C + NADP -> NADPH + GLU	bifunctional proline dehydrogenase OR delta-1-pyrroline-5-carboxylate dehydrogenase
R449	Arginine and proline metabolism	1.5.1.12	ABAYE2108	GLUGSAL + NAD -> NADH + GLU	1-pyrroline-5-carboxylate dehydrogenase
R450	Arginine and proline metabolism	1.5.99.8	ABAYE2108	PRO + FAD -> P5C + FADH2	proline dehydrogenase
R451	Arginine and proline metabolism	6.1.1.15	ABAYE0663	ATP + PRO + TRNAPRO -> AMP + PPI + PROTRNAPRO	prolyl-tRNA synthetase
R452	Arginine and proline metabolism	1.5.1.2	ABAYE2533 OR ABAYE3151	L1P3H5C + NADH -> 4HPRO + NAD	pyrroline-5-carboxylate reductase
R453	Arginine and proline metabolism	1.5.1.2	ABAYE2533 OR ABAYE3151	L1P3H5C + NADPH -> 4HPRO + NADP	pyrroline-5-carboxylate reductase
R454	Arginine and proline metabolism	1.5.1.12	ABAYE2108	L1P3H5C + NAD -> E4HGLU + NADH	1-pyrroline-5-carboxylate dehydrogenase
R455	Arginine and proline metabolism	1.5.1.12	ABAYE2108	L1P3H5C + NADP -> E4HGLU + NADPH	1-pyrroline-5-carboxylate dehydrogenase
R456	Arginine and proline metabolism	1.5.1.12 OR 1.5.99.8	ABAYE2108	E4HGLU + NAD <-> 4HGLUSA + NADH	1-pyrroline-5-carboxylate dehydrogenase
R457	Arginine and proline metabolism	2.6.1.1	ABAYE0951	E4HGLU + AKG -> HYDROXYAKG + GLU	aspartate aminotransferase
R458	Arginine and proline metabolism	4.1.2.14	ABAYE3280	HYDROXYAKG <-> PYR + GLX	4-hydroxy-2-oxoglutarate aldolase
R459	Arginine and proline metabolism	1.2.1.71	ABAYE0354	N2SUCCGLU5SA + NAD -> N2SUCCGLU + NADH	succinylglutamic semialdehyde dehydrogenase
R460	Arginine and proline metabolism	2.6.1.81	ABAYE0352	SORN + AKG -> N2SUCCGLU5SA + GLU	succinylornithine transaminase
R461	Arginine and proline metabolism	3.5.1.96	ABAYE0356	N2SUCCGLU -> GLU + SUCC	succinylglutamate desuccinylase
R462	Arginine and proline metabolism	3.5.3.23	ABAYE0355	N2SUCCARG -> SORN + CO2 + 2 NH3	succinylarginine dihydrolase
R463	Arginine and proline metabolism	3.5.3.3	p3ABAYE0029	CRTN <-> SCSN + UREA	creatinase (Creatine amidinohydrolase)
R464	Arginine and proline metabolism	5.1.1.4	ABAYE2385	PRO <-> DPRO	proline racemase
R465	Histidine metabolism	2.4.2.17	ABAYE2593 OR ABAYE3132	PRPP + ATP -> PPI + PRBATP	ATP phosphoribosyltransferase
R466	Histidine metabolism	3.6.1.31	ABAYE3428	PRBATP -> PPI + PRBAMP	phosphoribosyl-ATP pyrophosphohydrolase
R467	Histidine metabolism	3.5.4.19	ABAYE3428	PRBAMP -> PRFP	phosphoribosyl-AMP cyclohydrolase
R468	Histidine metabolism	5.3.1.16	ABAYE0250	PRFP -> PRLP	phosphoribosylformimino-5-aminoimidazole carboxamide ribotide isomerase
R469	Histidine metabolism	2.4.2.- OR 4.1.3.-	ABAYE0243 OR ABAYE0253	PRLP + GLN -> GLU + AICAR + DIMGP	imidazole glycerol phosphate synthase OR glutamine amidotransferase
R470	Histidine metabolism	4.2.1.19	ABAYE0254	DIMGP -> IMACP	imidazoleglycerol-phosphate dehydratase
R471	Histidine metabolism	2.6.1.9	ABAYE3130	IMACP + GLU -> AKG + HISOLP	histidinol-phosphate aminotransferase
R472	Histidine metabolism	3.1.3.15		HISOLP -> PI + HISOL	histidinol-phosphatase
R473	Histidine metabolism	1.1.1.23	ABAYE3131	HISOL + 2 NAD -> HIS + 2 NADH	histidinol dehydrogenase
R474	Histidine metabolism	2.1.1.-	ABAYE0624 OR ABAYE2481 OR ABAYE2566 OR ABAYE2771 OR ABAYE2871	HIS + SAM -> NMHIS + SAH	N6-adenine-specific methylase
R475	Histidine metabolism	6.1.1.21	ABAYE3262	ATP + HIS + TRNAHIS -> AMP + PPI + HISTRNAHIS	histidyl-tRNA synthetase
R476	Histidine metabolism	4.3.1.3	ABAYE0076	HIS -> UC + NH3	histidine ammonia-lyase
R477	Histidine metabolism	4.2.1.49	ABAYE0075	UC -> 4I5P	urocanate hydratase
R478	Histidine metabolism	3.5.2.7	ABAYE0078	4I5P -> NFGLU	imidazolonepropionase
R479	Histidine metabolism	3.5.3.8	ABAYE0079	NFGLU -> GLU + FA	formiminoglutamase
R480	Histidine metabolism	1.2.1.3	ABAYE1028 OR ABAYE1460 OR ABAYE2333 OR ABAYE2837	I4AA + NAD -> I4AC + NADH	aldehyde dehydrogenase
R481	Histidine metabolism	1.14.13.-	ABAYE0129 OR ABAYE0435 OR ABAYE2606 OR ABAYE2614	2 H5P <-> O2 + 2 4I5P	flavin-binding family monooxygenase
R482	Histidine metabolism	4.1.1.22	ABAYE1098	HIS <-> HIEA + CO2	histidine decarboxylase
R483	Tyrosine metabolism	5.3.3.10	ABAYE1465	5CM2HM -> 5C2O3E	5-carboxymethyl-2-hydroxymuconate isomerase
R484	Tyrosine metabolism	2.6.1.1	ABAYE0951	AKG + TYR <-> 4HPP + GLU	aspartate aminotransferase
R485	Tyrosine metabolism	1.13.11.27	ABAYE0064	4HPP + O2 -> HOMOGEN + CO2	4-hydroxyphenylpyruvate dioxygenase
R486	Tyrosine metabolism	5.2.1.2	ABAYE0067	4MAAC -> 4FAAC	maleylacetoacetate isomerase
R487	Tyrosine metabolism	1.1.1.1	ABAYE0763 OR ABAYE1463 OR ABAYE1522 OR ABAYE1861 OR p2ABAYE0004 OR p3ABAYE0020 OR p3ABAYE0024	34DHPEG + NAD <-> 34DHMA + NADH	alcohol dehydrogenase
R488	Tyrosine metabolism	1.14.13.-	ABAYE0129 OR ABAYE0435 OR ABAYE2606 OR ABAYE2614	TRM + O2 + NADH <-> DPM + NAD	flavin-binding family monooxygenase
R489	Tyrosine metabolism	1.14.13.-	ABAYE0129 OR ABAYE0435 OR ABAYE2606 OR ABAYE2614	4HPACALO + NADPH + O2 <-> 4HMN + NADP	flavin-binding family monooxygenase
R490	Tyrosine metabolism	1.14.13.3	ABAYE3078	3HPA + O2 + NADH <-> 34DHPA + NAD	flavoprotein oxidoreductase
R491	Tyrosine metabolism	1.14.13.3	ABAYE3078	4HPA + O2 + NADH <-> 34DHPA + NAD	flavoprotein oxidoreductase
R492	Tyrosine metabolism	1.4.3.21	ABAYE1710	TRM + O2 <-> 4HPACAL + NH3 + H2O2	copper amine oxidase precursor (tyramine oxidase) (2-phenylethylamine oxidase)
R493	Tyrosine metabolism	1.4.3.21	ABAYE1710	DPM + O2 <-> DHPACAL + NH3 + H2O2	copper amine oxidase precursor (tyramine oxidase) (2-phenylethylamine oxidase)
R494	Tyrosine metabolism	2.1.1.-	ABAYE0624 OR ABAYE2481 OR ABAYE2566 OR ABAYE2771 OR ABAYE2871	MTRM + SAM <-> HDN + SAH	O-methyltransferase protein
R495	Tyrosine metabolism	2.3.1.-	ABAYE0497 OR ABAYE0625 OR ABAYE1513 OR ABAYE1675 OR ABAYE1715 OR ABAYE1811 OR ABAYE2153 OR ABAYE2367 OR ABAYE2457 OR ABAYE2483 OR ABAYE3572 OR ABAYE3588 OR ABAYE3697 OR ABAYE3807	4HPACOA + GLY <-> 4HPAGLY + COA	acyltransferase OR acetyl transferase OR acyl-CoA thiolase OR beta-ketoadipyl CoA thiolase OR GCN5-related N-acetyltransferase
R496	Tyrosine metabolism	2.6.1.9 OR 2.6.1.57	ABAYE3130 OR ABAYE3795	TYR + AKG <-> 4HPP + GLU	histidinol-phosphate aminotransferase OR tyrosine aminotransferase
R497	Tyrosine metabolism	3.7.1.2	ABAYE0068	AAC + FUM <-> 4FAAC	fumarylacetoacetase (fumarylacetoacetate hydrolase)
R498	Tyrosine metabolism	4.1.1.-	ABAYE1027	HOMOGEN + O2 + NADPH <-> GENAL + CO2 + NADP	L-2,4-diaminobutyrate decarboxylase

No.	Metabolism	EC Number	ORF	Reaction	Enzyme
R499	Tyrosine metabolism	4.1.1.-	ABAYE1027	DHI + CO2 <-> CDHDHI	L-2,4-diaminobutyrate decarboxylase
R500	Tyrosine metabolism	4.1.1.-	ABAYE1027	DPCHR <-> DHI + CO2	L-2,4-diaminobutyrate decarboxylase
R501	Phenylalanine metabolism	2.6.1.1 OR 2.6.1.9 OR 2.6.1.57	ABAYE0951 OR ABAYE3130 OR ABAYE3795	PHE + AKG <-> PHPYR + GLU	aspartate aminotransferase
R502	Phenylalanine metabolism	1.13.11.27	ABAYE0064	PHPYR + O2 -> 2HPA + CO2	4-hydroxyphenylpyruvate dioxygenase
R503	Phenylalanine metabolism	1.4.99.1	ABAYE1567 OR ABAYE3774	DPHE + FAD -> PHPYR + FADH2 + NH3	D-amino-acid dehydrogenase
R504	Phenylalanine metabolism	1.11.1.7	ABAYE0619	PHE <-> PAA	antioxidant protein
R505	Phenylalanine metabolism	1.14.13.-	ABAYE0129 OR ABAYE0435 OR ABAYE2606 OR ABAYE2614	2HPA <-> DHPA	flavin-binding family monooxygenase
R506	Phenylalanine metabolism	1.2.1.39	ABAYE1712	PACAL + NAD <-> PLA + NADH	phenylacetaldehyde dehydrogenase
R507	Phenylalanine metabolism	1.4.3.21	ABAYE1710	PEA + O2 <-> PACAL + NH3 + H2O2	copper amine oxidase precursor (tyramine oxidase) (2-phenylethylamine oxidase)
R508	Phenylalanine metabolism	2.3.1.-	ABAYE0497 OR ABAYE0625 OR ABAYE1513 OR ABAYE1675 OR ABAYE1715 OR ABAYE1811 OR ABAYE2153 OR ABAYE2367 OR ABAYE2457 OR ABAYE2483 OR ABAYE3572 OR ABAYE3588 OR ABAYE3697 OR ABAYE3807	PACOA + GLY <-> PACGLY + COA	acyltransferase OR acetyl transferase OR acyl-CoA thiolase OR beta-ketoadipyl CoA thiolase OR GCN5-related N-acetyltransferase
R509	Phenylalanine metabolism	3.5.1.32	ABAYE3086	HIPPRT <-> BZ + GLY	hydrolase
R510	Phenylalanine metabolism	3.5.1.4	ABAYE1700 OR ABAYE2422	PAA <-> PLA + NH3	amidase
R511	Phenylalanine metabolism	6.2.1.30	ABAYE2366	ATP + PLA + COA <-> AMP + PPI + PACOA	phenylacetate-coenzyme A ligase (phenylacetyl-CoA ligase)
R512	Tryptophan metabolism	6.1.1.2	ABAYE0788	ATP + TRP + TRNATRP -> AMP + PPI + TRPTRNATRP	tryptophanyl-tRNA synthetase
R513	Tryptophan metabolism	1.2.1.3	ABAYE1028 OR ABAYE1460 OR ABAYE2333 OR ABAYE2837	5HIAA + NAD -> 5HIAC + NADH	aldehyde dehydrogenase
R514	Tryptophan metabolism	1.2.1.3	ABAYE1028 OR ABAYE1460 OR ABAYE2333 OR ABAYE2837	I3AA + NAD -> I3AC + NADH	aldehyde dehydrogenase
R515	Tryptophan metabolism	1.11.1.6	ABAYE2270 OR ABAYE2342 OR ABAYE3366	2 3HAN + 2 O2 -> CVN + 2 H2O2	catalase
R516	Tryptophan metabolism	1.2.4.2	ABAYE0780	2OAD + COA + NAD -> GLUTCOA + CO2 + NADH	2-oxoglutarate dehydrogenase E1 component
R517	Tryptophan metabolism	2.1.1.-	ABAYE0624 OR ABAYE2481 OR ABAYE2566 OR ABAYE2771 OR ABAYE2871	AEIOH + MTHF <-> MOT + THF	methyltransferase
R518	Tryptophan metabolism	3.5.1.4	ABAYE1700 OR ABAYE2422	I3AAM <-> I3AC + NH3	amidase
R519	Tryptophan metabolism	3.7.1.3	ABAYE1599	FKYN <-> FAN + ALA	L-kynurenine hydrolase
R520	Tryptophan metabolism	3.7.1.3	ABAYE1599	KYN <-> AN + ALA	L-kynurenine hydrolase
R521	Tryptophan metabolism	3.7.1.3	ABAYE1599	HKYN <-> 3HAN + ALA	L-kynurenine hydrolase
R522	Tryptophan metabolism	4.1.1.74	ABAYE1030	IPYR <-> I3AA + CO2	pyruvate decarboxylase OR indolepyruvate decarboxylase
R523	Phenylalanine, tyrosine and tryptophan biosynthesis	2.5.1.54	ABAYE1658 OR ABAYE1989	E4P + PEP -> PI + 3DDAH7P	3-deoxy-D-arabino-heptulosonate 7-phosphate synthase
R524	Phenylalanine, tyrosine and tryptophan biosynthesis	4.2.3.4	ABAYE0296	3DDAH7P -> DQT + PI	3-dehydroquinate synthetase
R525	Phenylalanine, tyrosine and tryptophan biosynthesis	4.2.1.10	ABAYE1539 OR ABAYE1682	DQT <-> DHSK	3-dehydroquinate dehydratase II OR catabolic 3-dehydroquinate dehydratase (3-dehydroquinase)
R526	Phenylalanine, tyrosine and tryptophan biosynthesis	1.1.1.25	ABAYE0377	DHSK + NADPH -> SME + NADP	shikimate 5-dehydrogenase
R527	Phenylalanine, tyrosine and tryptophan biosynthesis	2.7.1.71	ABAYE0295	SME + ATP -> ADP + SME3P	shikimate kinase
R528	Phenylalanine, tyrosine and tryptophan biosynthesis	2.5.1.19	ABAYE1207	SME3P + PEP -> 3PSME + PI	3-phosphoshikimate 1-carboxyvinyltransferase
R529	Phenylalanine, tyrosine and tryptophan biosynthesis	4.2.3.5	ABAYE1953	3PSME -> PI + CHOR	chorismate synthase
R530	Phenylalanine, tyrosine and tryptophan biosynthesis	4.1.3.27	ABAYE1123 OR ABAYE3497	CHOR + GLN -> GLU + PYR + AN	anthranilate synthase
R531	Phenylalanine, tyrosine and tryptophan biosynthesis	4.1.3.27	ABAYE1123 OR ABAYE3497	CHOR + NH3 -> AN + PYR	anthranilate synthase
R532	Phenylalanine, tyrosine and tryptophan biosynthesis	2.4.2.18	ABAYE1119	AN + PRPP -> PPI + NPRAN	anthranilate phosphoribosyltransferase
R533	Phenylalanine, tyrosine and tryptophan biosynthesis	5.3.1.24	ABAYE0607	NPRAN -> CPAD5P	phosphoribosylanthranilate isomerase
R534	Phenylalanine, tyrosine and tryptophan biosynthesis	4.1.1.48	ABAYE1118	CPAD5P -> CO2 + IGP	indole-3-glycerol phosphate synthase
R535	Phenylalanine, tyrosine and tryptophan biosynthesis	4.2.1.20	ABAYE0608 OR ABAYE0613 OR ABAYE1955	IGP + SER -> G3P + TRP	tryptophan synthase
R536	Phenylalanine, tyrosine and tryptophan biosynthesis	4.2.1.20	ABAYE0608 OR ABAYE1955	SER + INDOLE -> TRP	tryptophan synthase
R537	Phenylalanine, tyrosine and tryptophan biosynthesis	4.2.1.20	ABAYE0613	INDOLE + G3P <-> IGP	tryptophan synthase
R538	Phenylalanine, tyrosine and tryptophan biosynthesis	5.4.99.5	ABAYE1206 OR ABAYE1477	CHOR <-> PHEN	chorismate mutase
R539	Phenylalanine, tyrosine and tryptophan biosynthesis	4.2.1.51	ABAYE1206	PHEN -> CO2 + PHPYR	prephenate dehydratase
R540	Phenylalanine, tyrosine and tryptophan biosynthesis	6.1.1.20	ABAYE3159 AND ABAYE3160	ATP + PHE + TRNAPHE -> AMP + PPI + PHETRNAPHE	phenylalanyl-tRNA synthetase
R541	Phenylalanine, tyrosine and tryptophan biosynthesis	1.3.1.12	ABAYE1207	PHEN + NAD -> 4HPP + CO2 + NADH	prephenate dehydrogenase
R542	Phenylalanine, tyrosine and tryptophan biosynthesis	2.6.1.1 OR 2.6.1.9 OR 2.6.1.57	ABAYE0951 OR ABAYE3130 OR ABAYE3795	4HPP + GLU -> AKG + TYR	histidinol-phosphate aminotransferase

No.	Metabolism	EC Number	ORF	Reaction	Enzyme
R543	Phenylalanine, tyrosine and tryptophan biosynthesis	6.1.1.1	ABAYE0014	ATP + TYR + TRNATYR -> AMP + PPI + TRYTRNATYR	tyrosyl-tRNA synthetase
R544	Phenylalanine, tyrosine and tryptophan biosynthesis	4.2.1.51	ABAYE1206	AG -> PHE + CO2	prephenate dehydratase
R545	Phenylalanine, tyrosine and tryptophan biosynthesis	1.1.99.25	ABAYE1685	QNT + PQQ <-> PQQH2 + DQT	quinate/shikimate dehydrogenase
R546	Phenylalanine, tyrosine and tryptophan biosynthesis	1.1.99.25	ABAYE1685	SME + PQQ <-> DHSK + PQQH2	quinate/shikimate dehydrogenase
R547	Phenylalanine, tyrosine and tryptophan biosynthesis	4.2.1.- (QuiC)	ABAYE1683	DHSK <-> 34DHB	3-dehydroshikimate dehydratase OR DHS dehydratase)
R548	Urea cycle and metabolism of amino groups	2.7.2.11	ABAYE0962	GLU + ATP -> ADP + GLUP	glutamate 5-kinase
R549	Urea cycle and metabolism of amino groups	1.2.1.41	ABAYE3276	GLUP + NADPH -> NADP + PI + GLUGSAL	gamma-glutamyl phosphate reductase
R550	Urea cycle and metabolism of amino groups			GLUGSAL <-> P5C	spontaneous
R551	Urea cycle and metabolism of amino groups	1.5.1.2	ABAYE2533 OR ABAYE3151	P5C + NADPH <-> PRO + NADP	pyrroline-5-carboxylate reductase
R552	Urea cycle and metabolism of amino groups	1.5.1.2	ABAYE2533 OR ABAYE3151	PRO + NAD <-> P5C + NADH	pyrroline-5-carboxylate reductase
R553	Urea cycle and metabolism of amino groups	2.3.1.1	ABAYE3105 OR ABAYE3839	GLU + ACCOA -> COA + NAGLU	amino-acid N-acetyltransferase
R554	Urea cycle and metabolism of amino groups	2.7.2.8	ABAYE2927	NAGLU + ATP -> ADP + NAGLUP	acetylglutamate kinase
R555	Urea cycle and metabolism of amino groups	1.2.1.38	ABAYE1653	NAGLUP + NADPH -> NADP + PI + NAGLUS	N-acetyl-gamma-glutamyl-phosphate reductase
R556	Urea cycle and metabolism of amino groups	2.6.1.11	ABAYE1625	NAGLUS + GLU -> AKG + NAORN	acetylornithine aminotransferase
R557	Urea cycle and metabolism of amino groups	2.3.1.35	ABAYE3105	NAORN + GLU <-> ORN + NAGLU	bifunctional ornithine acetyltransferase/N-acetylglutamate synthase
R558	Urea cycle and metabolism of amino groups	2.1.3.3	ABAYE1571	ORN + CAP <-> CITR + PI	ornithine carbamoyltransferase
R559	Urea cycle and metabolism of amino groups	6.3.4.5	ABAYE2641	CITR + ASP + ATP <-> AMP + PPI + ARGSUCC	argininosuccinate synthase
R560	Urea cycle and metabolism of amino groups	4.3.2.1	ABAYE3511	ARGSUCC <-> FUM + ARG	argininosuccinate lyase
R561	Urea cycle and metabolism of amino groups	1.2.1.3	ABAYE1028 OR ABAYE1460 OR ABAYE2333 OR ABAYE2837	N4AAB + NAD <-> 4AABUT + NADH	aldehyde dehydrogenase
R562	Urea cycle and metabolism of amino groups	1.2.1.3	ABAYE1028 OR ABAYE1460 OR ABAYE2333 OR ABAYE2837	4AB + NADP <-> GABA + NADPH	aldehyde dehydrogenase
R563	Urea cycle and metabolism of amino groups	3.2.2.9	ABAYE3028 OR ABAYE3846	5MTA <-> AD + 5MDR	5'-methylthioadenosine/S-adenosylhomocysteine nucleosidase
R564	Urea cycle and metabolism of amino groups	3.4.13.3	ABAYE1209	HCNS <-> GABA + HIS	aminoacyl-histidine dipeptidase
R565	Urea cycle and metabolism of amino groups	3.5.1.4	ABAYE1700 OR ABAYE2422	4GBTA <-> 4GBTR + NH3	amidase
R566	Urea cycle and metabolism of amino groups	3.5.1.5	ABAYE2776 AND ABAYE2777 AND ABAYE2778	UREA <-> CO2 + 2 NH3	urease
R567	Urea cycle and metabolism of amino groups	3.5.1.54	ABAYE2439	U1C <-> 2 CO2 + 2 NH3	allophanate hydrolase
R568	beta-Alanine metabolism	1.2.1.3	ABAYE1028 OR ABAYE1460 OR ABAYE2333 OR ABAYE2837	bAPA + NAD -> bALA + NADH	aldehyde dehydrogenase (NAD+)
R569	beta-Alanine metabolism	1.4.3.21	ABAYE1710	13DAP + O2 <-> 3AP + NH3 + H2O2	copper amine oxidase precursor (tyramine oxidase) (2-phenylethylamine oxidase)
R570	beta-Alanine metabolism	2.6.1.18	ABAYE1295	ALA + 3OPP <-> PYR + bALA	omega-amino acid--pyruvate aminotransferase (omega-APT) (beta-alanine--pyruvate aminotransferase)
R571	beta-Alanine metabolism	2.6.1.19	ABAYE0209	bALA + AKG <-> OPP + GLU	4-aminobutyrate aminotransferase, PLP-dependent
R572	beta-Alanine metabolism	4.1.1.11	ABAYE2984	ASP -> bALA + CO2	aspartate 1-decarboxylase precursor
R573	Taurine and hypotaurine metabolism	1.14.11.17	ABAYE2209	TR + AKG + O2 -> H2SO3 + AAA + SUCC + CO2	taurine dioxygenase
R574	Taurine and hypotaurine metabolism	2.3.2.2	ABAYE2905	5GLUPEPT + TR -> PEPTIDE + GLUTR	gamma-glutamyltranspeptidase precursor
R575	Aminophosphonate metabolism	2.6.1.37	ABAYE2318	(2AE)P + PYR <-> PPAC + ALA	2-aminoethylphosphonate-pyruvate transaminase
R576	Aminophosphonate metabolism	2.1.1.-	ABAYE0624 OR ABAYE2481 OR ABAYE2566 OR ABAYE2771 OR ABAYE2871	MCB + PPAC -> 2HPP + VB12	N6-adenine-specific methylase
R577	Aminophosphonate metabolism	2.7.8.-	ABAYE1103 OR ABAYE3258 OR ABAYE3750	CMPAEP + NAS <-> NASAEP + CMP	4'-phosphopantetheinyl transferase
R578	Aminophosphonate metabolism	3.11.1.1	ABAYE2317	PPAC <-> ACAL + PI	phosphonoacetaldehyde phosphonohydrolase (phosphonatase)
R579	Selenoamino acid metabolism	4.4.1.8	ABAYE0405	SLLCT -> SHCYS + NH3 + PYR	cystathionine beta-lyase
R580	Selenoamino acid metabolism			SHCYS -> SMET	
R581	Selenoamino acid metabolism	6.1.1.10	ABAYE3031	ATP + SMET + TRNAMET -> AMP + PPI + SMETTRNAMET	methionyl-tRNA synthetase
R582	Selenoamino acid metabolism	2.5.1.6	ABAYE2118	ATP + SMET -> PI + PPI + SeASMET	S-adenosylmethionine synthetase
R583	Selenoamino acid metabolism	2.5.1.47	ABAYE3184 OR ABAYE3696	ASER + SELD -> SCYS + AC	cysteine synthase
R584	Selenoamino acid metabolism	2.7.7.4	ABAYE2790 AND ABAYE2791	ATP + SELNT <-> PPI + ASELNT	sulfate adenylyltransferase
R585	Selenoamino acid metabolism	2.3.2.2	ABAYE2905	5GLUPEPT + MSCYS -> PEPTIDE + GGLUMSCYS	gamma-glutamyltranspeptidase precursor
R586	Selenoamino acid metabolism	3.3.1.1	ABAYE1142	SASHCYS <-> ADN + SHCYS	S-adenosyl-L-homocysteine hydrolase
R587	Selenoamino acid metabolism	4.4.1.16	ABAYE2250	SCYS + FADH2 <-> SELD + ALA + FAD	cysteine desulfurase 1 OR selenocysteine lyase
R588	Cyanoamino acid metabolism	2.3.2.2	ABAYE2905	CALA + GLU -> GLUBCALA	gamma-glutamyltranspeptidase precursor
R589	Cyanoamino acid metabolism	2.3.2.2	ABAYE2905	APN + GLU -> GAPN	gamma-glutamyltranspeptidase precursor
R590	D-Glutamine and D-glutamate metabolism	3.5.1.2 OR 3.5.1.38	ABAYE2832 OR ABAYE2188	DGLN -> DGLU + NH3	glutaminase OR glutaminase-asparaginase
R591	D-Glutamine and D-glutamate metabolism	5.1.1.3	ABAYE0082 OR ABAYE3395	DGLU <-> GLU	glutamate racemase
R592	D-Alanine metabolism	5.1.1.1	ABAYE1380 OR ABAYE3773	ALA <-> DALA	alanine racemase
R593	D-Alanine metabolism	6.3.2.4	ABAYE0150	2 DALA + ATP -> ALAALA + ADP + PI	D-alanine-D-alanine ligase

No.	Metabolism	EC Number	ORF	Reaction	Enzyme
R594	Glutathione metabolism	3.4.11.1 OR 3.4.11.2 OR 3.4.13.3	ABAYE3540 OR ABAYE1469 OR ABAYE1209	CYSGLY -> CYS + GLY	aminopeptidase A (EC:3.4.11.1) OR membrane alanyl aminopeptidase OR aminoacyl-histidine dipeptidase (peptidase D) (EC:3.4.13.3)
R595	Glutathione metabolism	1.11.1.9	ABAYE2184 OR ABAYE3713	H2O2 + 2 RGT <-> OGT	glutathione peroxidase
R596	Glutathione metabolism	2.3.2.2	ABAYE2905	RGT -> CYSGLY + GLU	gamma-glutamyltranspeptidase precursor
R597	Glutathione metabolism	6.3.2.2	ABAYE0116	ATP + GLU + CYS <-> ADP + PI + GCYS	gamma-glutamate-cysteine ligase
R598	Glutathione metabolism	6.3.2.3	ABAYE0147	ATP + GCYS + GLY <-> ADP + PI + RGT	glutathione synthetase
R599	Lipopolysaccharide biosynthesis	2.3.1.129	ABAYE1587	C140ACP + UDPNAG -> ACP + UDPG2AA	UDP-N-acetylglucosamine acyltransferase
R600	Lipopolysaccharide biosynthesis	3.5.1.-	ABAYE0154	UDPG2AA -> UDPG2A + AC	UDP-3-O-[3-hydroxymyristoyl] N-acetylglucosamine deacetylase
R601	Lipopolysaccharide biosynthesis	2.3.1.-	ABAYE1585	UDPG2A + C140ACP -> ACP + UDPG23A	UDP-3-O-[3-hydroxymyristoyl] glucosamine N-acyltransferase
R602	Lipopolysaccharide biosynthesis	3.6.1.-	ABAYE1453	UDPG23A -> UMP + LIPX	UDP-2,3-diacylglucosamine hydrolase
R603	Lipopolysaccharide biosynthesis	2.4.1.182	ABAYE1983	LIPX + UDPG23A -> UDP + DISAC1P	lipid-A-disaccharide synthase
R604	Lipopolysaccharide biosynthesis	2.7.1.130	ABAYE2077	DISAC1P + ATP -> ADP + LIPIV	tetraacyldisaccharide 4'-kinase
R605	Lipopolysaccharide biosynthesis	2.-.-.-	ABAYE0175	LIPIV + CMPKDO -> KDOLIPIV + CMP	3-deoxy-D-manno-octulosonic-acid transferase
R606	Lipopolysaccharide biosynthesis	2.-.-.-	ABAYE0175	KDOLIPIV + CMPKDO -> K2LIPIV + CMP	3-deoxy-D-manno-octulosonic-acid transferase
R607	Lipopolysaccharide biosynthesis	2.3.1.-	ABAYE0885 OR ABAYE3343	C140ACP + LK2LIPIV -> K2LIPA + ACP	lipid A biosynthesis (KDO)2-(lauroyl)-lipid iva acyltransferase
R608	Lipopolysaccharide biosynthesis	5.3.1.13		RL5P <-> A5P	D-arabinose 5-phosphate isomerase
R609	Lipopolysaccharide biosynthesis	2.5.1.55	ABAYE1668	PEP + A5P -> KDOP + PI	2-dehydro-3-deoxyphosphooctonate aldolase (KDO 8-P synthase)
R610	Lipopolysaccharide biosynthesis	3.1.3.45	ABAYE2491	KDOP -> KDO + PI	3-deoxy-D-manno-octulosonate 8-phosphate phosphatase
R611	Lipopolysaccharide biosynthesis	2.7.7.38	ABAYE2076	KDO + CTP -> PPI + CMPKDO	3-deoxy-manno-octulosonate cytidylyltransferase
R612	Peptidoglycan biosynthesis	6.3.2.8	ABAYE0149	UDPNAM + ALA + ATP -> ADP + PI + UDPNAMA	UDP-N-acetylmuramate--alanine ligase
R613	Peptidoglycan biosynthesis	6.3.2.9	ABAYE3524	UDPNAMA + DGLU + ATP -> UDPNAMAG + ADP + PI	UDP-N-acetylmuramoylalanine--D-glutamate ligase
R614	Peptidoglycan biosynthesis	6.3.2.13	ABAYE0283	UDPNAMAG + MDAPIM + ATP -> UDPMNLADGMD + ADP + PI	UDP-N-acetylmuramoylalanyl-D-glutamate--2,6-diaminopimelate ligase
R615	Peptidoglycan biosynthesis	6.3.2.10	ABAYE0284	UDPMNLADGMD + ALAALA + ATP -> UDPMNLADGMDDADA + ADP + PI	UDP-N-acetylmuramoyl-tripeptide--D-alanyl-D-alanine ligase
R616	Peptidoglycan biosynthesis	2.7.8.13	ABAYE0285	UDPMNLADGMDDADA + UDCP -> UPPMNLADGMDDADA + UMP	phospho-N-acetylmuramoyl-pentapeptide-transferase
R617	Peptidoglycan biosynthesis	2.4.1.227	ABAYE0148	UPPMNLADGMDDADA + UDPNAG -> UPPMN(GN)LADGMDDADA + UDP	UDP-N-acetylglucosamine--N acetylmuramyl-(pentapeptide) pyrophosphoryl-undecaprenol N-acetylglucosamine transferase
R618	Peptidoglycan biosynthesis	6.3.1.2	ABAYE1126 OR ABAYE1425	UPPMN(GN)LADGMDDADA + ATP + NH3 -> UPPMN(GN)LADGNMDDADA + ADP + PI	glutamine synthetase
R619	Peptidoglycan biosynthesis	2.3.2.10		5 GLY + UPPMN(GN)LADGNMDDADA -> UPPMN(GN)LADGNMD(G)5DADA	L-Alanyl-tRNA:UDP-N-acetylmuramoyl-L-alanyl-D-glutamyl-L-lysyl-D-alanyl-D-alanine N6-alanyltransferase
R620	Peptidoglycan biosynthesis			UPPMN(GN)LADGNMD(G)5DADA -> UDCPP + PPEPTIDO	
R621	Peptidoglycan biosynthesis	2.6.1.21		PPEPTIDO + DALA -> 0.9208 PEPTIDO + 0.8 DALAxt	D-Alanine:2-oxoglutarate aminotransferase
R622	Peptidoglycan biosynthesis	3.6.1.27	ABAYE0716	UDCPP -> UDCP + PI	undecaprenyl-diphosphatase
R623	Thiamine metabolism	thiC	ABAYE3518	AIR -> AHM	thiamine biosynthesis protein ThiC
R624	Thiamine metabolism	2.7.1.49	ABAYE2989	AHM + ATP -> AHMP + ADP	hydroxymethylpyrimidine kinase
R625	Thiamine metabolism	2.7.4.7	ABAYE2989	AHMP + ATP -> AHMPP + ADP	phosphomethylpyrimidine kinase
R626	Thiamine metabolism	2.5.1.3	ABAYE1010	THZP + AHMPP -> THMP + PPI	thiamine-phosphate pyrophosphorylase
R627	Thiamine metabolism	2.7.4.16	ABAYE0093	THMP + ATP <-> THMPP + ADP	thiamine-monophosphate kinase
R628	Thiamine metabolism	1.4.3.19	ABAYE2910	GLY <-> IGLY	D-amino acid oxidase
R629	Thiamine metabolism	2.7.1.50	ABAYE1466	ATP + THZ <-> ADP + MPET	hydroxyethylthiazole kinase
R630	Thiamine metabolism	3.5.99.2	ABAYE0200	THIAMIN <-> AHM + THZ	TenA family transcriptional activator
R631	Thiamine metabolism	3.6.1.15	ABAYE3296	THMPP <-> THMP + PI	nucleoside-triphosphatase
R632	Riboflavin metabolism	3.5.4.25	ABAYE0096 OR ABAYE0379	GTP -> D6RP5P + FORMATE + PPI	GTP cyclohydrolase II
R633	Riboflavin metabolism	3.5.4.26	ABAYE3546	D6RP5P -> A6RP5P + NH3	diaminohydroxyphosphoribosylaminopyrimidine deaminase
R634	Riboflavin metabolism	1.1.1.193	ABAYE3546	A6RP5P + NADPH -> A6RP5P2 + NADP	5-amino-6-(5-phosphoribosylamino)uracil reductase
R635	Riboflavin metabolism	3.1.3-		A6RP5P2 -> A6RP + PI	phosphatase
R636	Riboflavin metabolism	RIBB	ABAYE0096 OR ABAYE2987	RL5P -> DB4P + FORMATE	3,4-dihydroxy-2-butanone 4-phosphate synthase
R637	Riboflavin metabolism	RIBH	ABAYE0095	DB4P + A6RP -> D8RL + PI	riboflavin synthase
R638	Riboflavin metabolism	2.5.1.9	ABAYE3544	2 D8RL -> RIBFLAV + A6RP	riboflavin synthase
R639	Riboflavin metabolism	2.7.1.26	ABAYE3851	RIBFLAV + ATP -> FMN + ADP	riboflavin kinase
R640	Riboflavin metabolism	2.7.7.2	ABAYE3851	FMN + ATP -> FAD + PPI	FMN adenylyltransferase
R641	Riboflavin metabolism	2.4.2.21	ABAYE1993	NACN + DMB -> NAC + N1(5PADR)DMB	nicotinate-nucleotide--dimethylbenzimidazole phosphoribosyltransferase
R642	Vitamin B6 metabolism	1.2.1.72	ABAYE2594	E4P + NAD <-> ER4P + NADH	D-erythrose 4-phosphate dehydrogenase
R643	Vitamin B6 metabolism	1.1.1.290	ABAYE0853	ER4P + NAD <-> OHB + NADH	erythronate-4-phosphate dehydrogenase
R644	Vitamin B6 metabolism	2.6.1.52	ABAYE0877	OHB + GLU <-> PHT + AKG	phosphoserine aminotransferase
R645	Vitamin B6 metabolism	4.2.3.1	ABAYE3531	PHT -> 4HLT + PI	threonine synthase
R646	Vitamin B6 metabolism	1.1.1.262	ABAYE0489	PHT + NAD -> 3A2OP + NADH + CO2	4-hydroxythreonine-4-phosphate dehydrogenase
R647	Vitamin B6 metabolism	2.6.99.2	ABAYE0945	3A2OP + DX5P -> P5P + PI	pyridoxine 5-phosphate synthase
R648	Vitamin B6 metabolism	1.4.3.5	ABAYE0168	P5P + O2 -> PL5P + H2O2	pyridoxamine 5'-phosphate oxidase
R649	Vitamin B6 metabolism	3.1.3.-		PL5P -> PL + PI	phosphatase
R650	Vitamin B6 metabolism	1.4.3.5	ABAYE0168	PDLA5P + O2 -> PL5P + NH3 + H2O2	pyridoxamine 5'-phosphate oxidase
R651	Vitamin B6 metabolism	1.4.3.5	ABAYE0168	PYRDX + O2 <-> PL + H2O2	pyridoxamine 5'-phosphate oxidase
R652	Vitamin B6 metabolism	1.4.3.5	ABAYE0168	PL + O2 + NH3 <-> PDLA + H2O2	pyridoxamine 5'-phosphate oxidase
R653	Nicotinate and nicotinamide metabolism	1.4.3.16	ABAYE0935	ASP + FUM -> IASP + SUCC	L-aspartate oxidase
R654	Nicotinate and nicotinamide metabolism	1.4.3.16	ABAYE0935	ASP + O2 -> IASP + H2O2	L-aspartate oxidase
R655	Nicotinate and nicotinamide metabolism	NadA	ABAYE3104	IASP + DHAP -> QA + PI	quinolinate synthase
R656	Nicotinate and nicotinamide metabolism	2.4.2.19	ABAYE3823	QA + PRPP -> NACN + CO2 + PPI	nicotinate-nucleotide pyrophosphorylase (carboxylating)
R657	Nicotinate and nicotinamide metabolism	3.1.3.5	ABAYE1047 OR ABAYE1886	NACN -> NACD + PI	5'-nucleotidase
R658	Nicotinate and nicotinamide metabolism	3.1.3.5	ABAYE1047 OR ABAYE1886	NAMN -> NAMD + PI	5'-nucleotidase
R659	Nicotinate and nicotinamide metabolism	2.4.2.11	ABAYE0102	NAC + PRPP -> NACN + PPI	nicotinate phosphoribosyltransferase
R660	Nicotinate and nicotinamide metabolism	2.7.7.1 OR 2.7.7.18	ABAYE0916 OR ABAYE0916	ATP + NAMN <-> PPI + NAD	nicotinamide/nicotinate-nucleotide adenylyltransferase
R661	Nicotinate and nicotinamide metabolism	2.7.7.1 OR 2.7.7.18	ABAYE0916 OR ABAYE0916	NACN + ATP -> PPI + NAAD	nicotinate-nucleotide adenylyltransferase
R662	Nicotinate and nicotinamide metabolism	6.3.5.1	ABAYE2955	NAAD + ATP + GLN -> NAD + AMP + PPI + GLU	glutamine-dependent NAD(+) synthetase

No.	Metabolism	EC Number	ORF	Reaction	Enzyme
R663	Nicotinate and nicotinamide metabolism	3.5.1.19	ABAYE0059	NAM -> NAC + NH3	nicotinamidase
R664	Nicotinate and nicotinamide metabolism	1.6.1.2	ABAYE3191 AND ABAYE3192 AND ABAYE3193	NADP + NADH -> NADPH + NAD	NAD(P) transhydrogenase
R665	Nicotinate and nicotinamide metabolism	2.7.1.23	ABAYE1199	NAD + ATP -> NADP + ADP	NAD kinase
R666	Nicotinate and nicotinamide metabolism	1.6.1.1	ABAYE1147	NADPH + NAD <-> NADP + NADH	NAD(P) transhydrogenase
R667	Nicotinate and nicotinamide metabolism	1.4.1.21	ABAYE2838	ASP + NAD <-> IASP + NADH	L-aspartate dehydrogenase
R668	Nicotinate and nicotinamide metabolism	1.4.1.21	ABAYE2838	ASP + NADP <-> IASP + NADPH	L-aspartate dehydrogenase
R669	Nicotinate and nicotinamide metabolism	3.6.1.22	ABAYE2666	NAD <-> AMP + NAMN	NUDIX family NADH pyrophosphatase
R670	Nicotinate and nicotinamide metabolism	3.6.1.22	ABAYE2666	NAAD <-> AMP + NACN	NUDIX family NADH pyrophosphatase
R671	Pantothenate and CoA biosynthesis	2.2.1.6	ABAYE2836 OR (ABAYE3239 AND ABAYE3240)	2 PYR -> ACLAC + CO2	acetolactate synthase
R672	Pantothenate and CoA biosynthesis	2.1.2.11	ABAYE3175	OIVAL + METTHF -> DHPANT + THF	3-methyl-2-oxobutanoate hydroxymethyltransferase
R673	Pantothenate and CoA biosynthesis	1.1.1.169		DHPANT + NADPH -> NADP + PANT	2-dehydropantoate 2-reductase
R674	Pantothenate and CoA biosynthesis	6.3.2.1	ABAYE3174	PANT + bALA + ATP -> AMP + PPI + PNTO	pantoate-beta-alanine ligase
R675	Pantothenate and CoA biosynthesis	2.7.1.33	ABAYE3016	PNTO + ATP -> ADP + 4PPNTO	pantothenate kinase
R676	Pantothenate and CoA biosynthesis	2.7.1.33	ABAYE3016	ATP + N(P)CYS -> ADP + 4PPNCYS	pantothenate kinase
R677	Pantothenate and CoA biosynthesis	2.7.1.33	ABAYE3016	ATP + PTT -> ADP + 4PPNTE	pantothenate kinase
R678	Pantothenate and CoA biosynthesis	6.3.2.5	ABAYE0524	4PPNTO + CTP + CYS -> CMP + PPI + 4PPNCYS	phosphopantothenate-cysteine ligase
R679	Pantothenate and CoA biosynthesis	4.1.1.36	ABAYE0524	4PPNCYS -> CO2 + 4PPNTE	phosphopantothenoylcysteine decarboxylase
R680	Pantothenate and CoA biosynthesis	2.7.7.3	ABAYE2969	4PPNTE + ATP -> PPI + DPCOA	pantetheine-phosphate adenylyltransferase
R681	Pantothenate and CoA biosynthesis	2.7.1.24	ABAYE3447	DPCOA + ATP -> ADP + COA	dephospho-CoA kinase
R682	Biotin metabolism	2.3.1.47	ABAYE3003	ALA + CHCOA <-> CO2 + COA + AONA	8-amino-7-oxononanoate synthase
R683	Biotin metabolism	2.6.1.62	ABAYE3004	SAM + AONA <-> SAMOB + DANNA	adenosylmethionine-8-amino-7-oxononanoateaminotransferase
R684	Biotin metabolism	6.3.3.3	ABAYE3001	CO2 + DANNA + ATP <-> DTB + PI + ADP	dethiobiotin synthetase
R685	Biotin metabolism	2.8.1.6	ABAYE2129	DTB + S -> BT	biotin synthase
R686	Biotin metabolism	6.3.4.15	ABAYE3015	ATP + BT -> PPI + B5AMP	biotin-[acetyl-CoA-carboxylase] ligase
R687	Biotin metabolism	6.3.4.15	ABAYE3015	B5AMP + A[C] -> AMP + H[C]	biotin-[acetyl-CoA-carboxylase] ligase
R688	Folate biosynthesis	3.5.4.16	ABAYE1113	GTP -> FORMATE + AHTD	GTP cyclohydrolase I
R689	Folate biosynthesis	3.6.1.-	ABAYE3429	AHTD -> DHP + PPI + PI	recG-like helicase
R690	Folate biosynthesis	4.1.2.25	ABAYE1417	DHP -> AHHMP + GLAL	dihydroneopterin aldolase
R691	Folate biosynthesis	2.7.6.3	ABAYE1418 OR ABAYE3176	AHHMP + ATP -> AMP + AHHMD	2-amino-4-hydroxy-6-hydroxymethyldihydropteridine pyrophosphokinase
R692	Folate biosynthesis	2.6.1.85	ABAYE3129	CHOR + GLN -> ADCHOR + GLU	para-aminobenzoate synthase
R693	Folate biosynthesis	4.1.3.38	ABAYE0931	ADCHOR -> PYR + PABA	4-amino-4-deoxychorismate lyase
R694	Folate biosynthesis	2.5.1.15	ABAYE0807 OR ABAYE3568 OR ABAYE3612 OR ABAYE3616	PABA + AHHMD -> PPI + DHPT	dihydropteroate synthase
R695	Folate biosynthesis	2.5.1.15	ABAYE0807 OR ABAYE3568 OR ABAYE3612 OR ABAYE3616	PABA + AHHMP -> DHPT	dihydropteroate synthase
R696	Folate biosynthesis	6.3.2.12 OR 6.3.2.17	ABAYE0615	DHPT + ATP + GLU -> ADP + PI + DHF	dihydrofolate synthase
R697	Folate biosynthesis	1.5.1.3	ABAYE3315 OR ABAYE3614 OR ABAYE3644	DHF + NADPH -> NADP + THF	dihydrofolate reductase
R698	Folate biosynthesis	1.5.1.3	ABAYE3315 OR ABAYE3614 OR ABAYE3644	DHF + NADH -> NAD + THF	dihydrofolate reductase
R699	Folate biosynthesis	1.5.1.3	ABAYE3315 OR ABAYE3614 OR ABAYE3644	DHF + NAD <-> FL + NADH	dihydrofolate reductase
R700	Folate biosynthesis	1.5.1.3	ABAYE3315 OR ABAYE3614 OR ABAYE3644	DHF + NADP <-> FL + NADPH	dihydrofolate reductase
R701	Folate biosynthesis	1.5.1.3	ABAYE3315 OR ABAYE3614 OR ABAYE3644	FL + NADH -> THF + NAD	dihydrofolate reductase
R702	Folate biosynthesis	1.5.1.3	ABAYE3315 OR ABAYE3614 OR ABAYE3644	FL + NADPH -> THF + NADP	dihydrofolate reductase
R703	Folate biosynthesis	6.3.2.17	ABAYE0615	THF + ATP + GLU <-> ADP + PI + THFG	folylpolyglutamate synthase
R704	Folate biosynthesis	4.2.3.12	ABAYE2067	AHTD -> PYTHP + PPPI	6-pyruvoyl tetrahydrobiopterin synthase
R705	Folate biosynthesis	3.1.3.1	ABAYE0811	AHTD <-> DHP + 3 PI	alkaline phosphatase D precursor
R706	One carbon pool by folate	2.1.2.2	ABAYE0888 OR ABAYE2179	GAR + METHF -> FGAR + THF	phosphoribosylglycinamide formyltransferase
R707	One carbon pool by folate	3.5.4.9	ABAYE0812	METHF -> FTHF	bifunctional protein [includes: 5,10-methylene-tetrahydrofolate dehydrogenase; 5,10-methylene-tetrahydrofolate cyclohydrolase]
R708	One carbon pool by folate	1.5.1.5	ABAYE0812	METTHF + NADP <-> METHF + NADPH	bifunctional protein [includes: 5,10-methylene-tetrahydrofolate dehydrogenase; 5,10-methylene-tetrahydrofolate cyclohydrolase]
R709	One carbon pool by folate	3.5.4.9	ABAYE0812	METHF <-> FTHF	bifunctional protein [includes: 5,10-methylene-tetrahydrofolate dehydrogenase; 5,10-methylene-tetrahydrofolate cyclohydrolase]
R710	One carbon pool by folate	1.5.1.20	ABAYE1141 OR ABAYE1792	METTHF + NADPH -> MTHF + NADP	methylenetetrahydrofolate reductase
R711	One carbon pool by folate	1.5.1.20	ABAYE1141 OR ABAYE1792	METTHF + FADH2 <-> MTHF + FAD	methylenetetrahydrofolate reductase

No.	Metabolism	EC Number	ORF	Reaction	Enzyme
R712	One carbon pool by folate	2.1.1.45	ABAYE3314	DUMP + METTHF <-> DHF + DTMP	thymidylate synthase
R713	One carbon pool by folate	3.5.1.10	ABAYE3322	FTHF <-> FORMATE + THF	formyltetrahydrofolate deformylase
R714	One carbon pool by folate	1.5.1.3	ABAYE3315 OR ABAYE3614 OR ABAYE3644	THF + NAD <-> DHF + NADH	dihydrofolate reductase
R715	One carbon pool by folate	1.5.1.3	ABAYE3315 OR ABAYE3614 OR ABAYE3644	THF + NADP <-> DHF + NADPH	dihydrofolate reductase
R716	Porphyrin and chlorophyll metabolism	1.2.1.70	ABAYE2976	GTRNA + NADPH -> GSA + NADP	glutamyl-tRNA reductase
R717	Porphyrin and chlorophyll metabolism	5.4.3.8	ABAYE1011	GSA -> ALAV	glutamate-1-semialdehyde aminotransferase
R718	Porphyrin and chlorophyll metabolism	4.2.1.24	ABAYE2909	2 ALAV -> PBG	porphobilinogen synthase
R719	Porphyrin and chlorophyll metabolism	2.5.1.61	ABAYE3508	4 PBG -> HMB + 4 NH3	hydroxymethylbilane synthase
R720	Porphyrin and chlorophyll metabolism	4.2.1.75	ABAYE3507	HMB -> UPRG	uroporphyrinogen-III synthase
R721	Porphyrin and chlorophyll metabolism	2.1.1.107	ABAYE0758	2 SAM + UPRG -> 2 SAH + PC2	uroporphyrin-III C-methyltransferase
R722	Porphyrin and chlorophyll metabolism	1.3.1.76	ABAYE0758	PC2 + NAD -> NADH + SHCL	precorrin-2 dehydrogenase
R723	Porphyrin and chlorophyll metabolism	4.99.1.4	ABAYE0758	SHCL -> SHEME	sirohydrochlorin ferrochelatase
R724	Porphyrin and chlorophyll metabolism	4.1.1.37	ABAYE1106	UPRG -> 4 CO2 + CPP	uroporphyrinogen decarboxylase
R725	Porphyrin and chlorophyll metabolism	1.3.99.22	ABAYE0674 OR ABAYE3379	CPP + 2 SAM -> PPHG + 2 CO2 + 2 MET + 2 DA	oxygen-independent coproporphyrinogen III oxidase
R726	Porphyrin and chlorophyll metabolism	1.3.3.3	ABAYE0378	CPP + O2 -> PPHG + 2 CO2	coproporphyrinogen III oxidase
R727	Porphyrin and chlorophyll metabolism	4.99.1.1	ABAYE3393	PPIX -> PTH	ferrochelatase
R728	Porphyrin and chlorophyll metabolism	2.5.1.17	ABAYE0605	C(I)DA + ATP -> ACDA + PPI + PI	cob(I)alamin adenosyltransferase
R729	Porphyrin and chlorophyll metabolism	2.7.1.156	ABAYE1994	ADCBA + ATP -> ADCBAP + ADP	adenosylcobinamide kinase
R730	Porphyrin and chlorophyll metabolism	2.7.1.156	ABAYE1994	ADCBA + GTP -> ADCBAP + GDP	adenosylcobinamide kinase
R731	Porphyrin and chlorophyll metabolism	2.7.1.156	ABAYE1994	ADCBAP + GTP -> AGDPCBA + PPI	adenosylcobinamide-phosphate guanylyltransferase
R732	Porphyrin and chlorophyll metabolism	2.7.8.26	ABAYE1990	AGDPCBA + ARBZ -> CBCO + GMP	adenosylcobinamide-GDP ribazoletransferase
R733	Porphyrin and chlorophyll metabolism	2.5.1.17	ABAYE0605	ATP + CBA <-> PPPI + ADCBA	cob(I)alamin adenosyltransferase
R734	Porphyrin and chlorophyll metabolism	2.5.1.17	ABAYE0605	ATP + C(I)A <-> PPPI + CBCO	cob(I)alamin adenosyltransferase
R735	Porphyrin and chlorophyll metabolism	4.1.1.37	ABAYE1106	UPRGI <-> CPPI + 4 CO2	uroporphyrinogen decarboxylase
R736	Porphyrin and chlorophyll metabolism	2.5.1.-	ABAYE1385	PTH <-> HEMEO	protoheme IX farnesyltransferase
R737	Ubiquinone biosynthesis	5.4.4.2	ABAYE1104	CHOR <-> ICHOR	menaquinone-specific isochorismate synthase
R738	Ubiquinone biosynthesis	4.1.3.40	ABAYE1127	CHOR <-> 4HB + PYR	chorismate--pyruvate lyase
R739	Ubiquinone biosynthesis	2.5.1.-	ABAYE1128	OPP + 4HB -> 3OP4HB + PPI	4-hydroxybenzoate octaprenyltransferase
R740	Ubiquinone biosynthesis	UbiB	ABAYE3426	2OPP + O2 + NADPH -> 2OP6HP + NADP	ubiquinone biosynthesis protein
R741	Ubiquinone biosynthesis	2.1.1.64	ABAYE3834	2OP6HP + SAM -> 2OP6MP + SAH	3-demethylubiquinone-9 3-methyltransferase
R742	Ubiquinone biosynthesis	1.14.13.-	ABAYE2678	2OP6MP + O2 + NADPH -> 2OP6M14BQ + NADP	2-octaprenyl-6-methoxyphynol hydroxylase
R743	Ubiquinone biosynthesis	2.1.1.-	ABAYE3424	2OP6M14BQ + SAM -> 2OP3M6M14BQ + SAH	2-octaprenyl-6-methoxy-1,4-benzoquinone methylase
R744	Ubiquinone biosynthesis	2.1.1.64	ABAYE3834	2OP3M5H6M14BQ + SAM -> UQ + SAH	3-demethylubiquinone-9 3-methyltransferase
R745	Ubiquinone biosynthesis	2.5.1.64		ICHOR + AKG -> SHCHC + PYR + CO2	2-succinyl-6-hydroxy-2,4-cyclohexadiene-1-carboxylate synthase
R746	Ubiquinone biosynthesis	4.2.1.-		SHCHC -> OSB	O-succinylbenzoate-CoA synthase
R747	Ubiquinone biosynthesis	6.2.1.26		OSB + ATP + COA -> AMP + PPI + OSBCOA	O-succinylbenzoic acid--CoA ligase
R748	Ubiquinone biosynthesis	4.1.3.36		OSBCOA -> DHN + COA	dihydroxynaphthoic acid synthase
R749	Ubiquinone biosynthesis	2.5.1.-	ABAYE1128	DHN + OPP -> PPI + CO2 + DMK	4-hydroxybenzoate octaprenyltransferase
R750	Ubiquinone biosynthesis	2.1.1.-	ABAYE3424	DMK + SAM -> MKH2 + SAH	menaquinone biosynthesis methyltransferase
R751	Ubiquinone biosynthesis	2.1.1.-	ABAYE3424	2P14NQ + SAM -> PQ + SAH	menaquinone biosynthesis methyltransferase
R752	Ubiquinone biosynthesis	1.14.13.-	ABAYE1427	2HP3M6M14B + O2 + NADPH <-> 2HP3M5H6M14B + NADP	ubiquinone biosynthesis protein
R753	Protein			0.488 ALA + 0.281 ARG + 0.229 ASN + 0.229 ASP + 0.087 CYS + 0.25 GLU + 0.25 GLN + 0.582 GLY + 0.09 HIS + 0.276 ILE + 0.428 LEU + 0.326 LYS + 0.146 MET + 0.176 PHE + 0.21 PRO + 0.205 SER + 0.241 THR + 0.054 TRP + 0.131 TYR + 0.402 VAL + 40 ATP -> 40 ADP + 40 PI + PROTEIN	
R754	DNA	2.7.7.7		0.987 DATP + 0.631 DGTP + 0.631 DCTP + 0.987 DTTP + 4.4 ATP -> 4.4 ADP + 4.4 PI + 3.237 PPI + DNA	
R755	RNA	2.7.7.6		2.045 ATP + 0.920 GTP + 0.686 CTP + 0.689 UTP -> 1.25 ADP + 1.25 PI + 3.091 PPI + RNA	
R756	Phospholipid			0.168 CL + 0.548 PE + 0.302 PG + 0.12 2AG3PE -> PHOSPHOLIPID	
R757	Lipids			0.058 C100ACP + 0.185 C120ACP + 0.013 C140ACP + 0.012 C150ACP + 1.082 C160ACP + 0.74 C161ACP + 0.067 C170ACP + 0.06 C171ACP + 0.032 C180ACP + 1.443 C181ACP + 0.157 C120OH -> LIPID + 3.692 ACP	
R758	Lipopolysaccharide biosynthesis			0.182 KDO + 0.821 bDGLC + 0.656 UDPGAL + 0.018 DTDPRMNS + 0.365 UDPNAG + 0.255 UDPAGLACA + 0.037 C120ACP + 0.014 C160ACP + 0.079 C120OH + 0.009 C180ACP + 0.008 C181ACP + 0.071 C140OH -> LPS + 1.276 UDP + 0.018 DTDP + 0.068 ACP	
R759				2.794 DTDPRMNS + 2.117 bDGLC + 0.265 GDPMAN -> EXOPOLYS + 2.794 DTDP + 0.265 UDP	
R760	Cofactors and vitamins (CAV)			0.163 COA + 0.159 FAD + 0.274 FMN + 0.405 MK + 0.188 NAD + 0.168 NADP + 0.739 PYRDX + 0.281 THF -> CAV	
R761	Biomass			0.6 PROTEIN + 0.03 DNA + 0.19 RNA + 0.04 PHOSPHOLIPID + 0.02 LIPID + 0.005 LPS + 0.027 PEPTIDO + 0.038 EXOPOLYS + 0.03 CAV + 46 ATP -> BIOMASS + 46 ADP + 46 PI	

No.	Metabolism	EC Number	ORF	Reaction	Enzyme
R762	Maintenance			ATP -> ADP + PI	
R763	IMAL_transport	3.6.1.-		IMALxt + ATP <-> IMAL + PI + ADP	
R764	FRU_transport	2.7.1.69		FRUxt + PEP -> F1P + PYR	
R765	GLC_transport			GLCxt + ATP -> GLC + ADP + PI	
R766	GLUC_transport			GLUCxt + Hxt -> GLUC	
R767	MLT_transport			MLTxt + ATP -> MLT + ADP + PI	
R768	MNT_transport			MNTxt + ATP -> MNT + ADP + PI	
R769	NAGA_transport			NAGAxt + ATP -> NAGA + ADP + PI	
R770	SUC_transport			SUCxt + ATP -> SUC + ADP + PI	
R771	TRE_transport			TRExt + ATP -> TRE + ADP + PI	
R772	2PG_transport			2PGxt + ATP -> 2PG + ADP + PI	
R773	3PG_transport			3PGxt + ATP -> 3PG + ADP + PI	
R774	AC_transport			AC <-> ACxt + Hxt	
R775	AKG_transport			AKGxt + Hxt -> AKG	
R776	AKG_transport			AKGxt + Naxt -> AKG + Na	
R777	CIT_transport			CITxt <-> CIT	
R778	FORMATE_transport			FORMATE -> FORMATExt	
R779	FUM_transport			FUMxt + Hxt -> FUM	
R780	FUM_transport			FUMxt + Naxt -> FUM + Na	
R781	FUM_transport			FUMxt + SUCC <-> FUM + SUCCxt	
R782	ICIT_transport			ICITxt + Naxt -> ICIT + Na	
R783	MAL_transport			MALxt + Hxt -> MAL	
R784	MAL_transport			MALxt + Naxt -> MAL + Na	
R785	MAL_transport			MALxt + SUCC <-> MAL + SUCCxt	
R786	SLAC_transport			SLACxt + Hxt -> SLAC	
R787	SUCC_transport			SUCCxt + Hxt -> SUCC	
R788	SUCC_transport			SUCCxt + Naxt -> SUCC + Na	
R789	GLYCOLATE_transport			GLYCOLATExt <-> GLYCOLATE	
R790	ATP_transport			ATP <-> Hxt + ADP + PI	
R791	CO2_transport			CO2xt <-> CO2	
R792	Na_transport			Naxt <-> Na + Hxt	
R793	NH3_transport			NH3xt <-> NH3	
R794	NO2_transport			NO2 -> NO2xt	
R795	NO3_transport			NO3xt + ATP -> NO3 + ADP + PI	
R796	O2_transport			O2xt <-> O2	
R797	PI_transport			PIxt + Hxt <-> PI	
R798	PI_transport			PIxt + ATP -> 2 PI + ADP	
R799	SLF_transport			SLFxt + Hxt -> SLF	
R800	SLF_transport			SLFxt + ATP -> SLF + ADP + PI	
R801	ALA_transport			ALA + Hxt <-> ALAxt	
R802	ALA_transport			ALAxt + ATP -> ALA + ADP + PI	
R803	ALA_transport			ALAxt + Hxt -> ALA	
R804	ALA_transport			ALAxt + Naxt -> ALA + Na	
R805	ARG_transport			ARG + Hxt <-> ARGxt	
R806	ARG_transport			ARGxt + ATP -> ARG + ADP + PI	
R807	ARG_transport			ARGxt + Hxt -> ARG	
R808	ASN_transport			ASN + Hxt <-> ASNxt	
R809	ASN_transport			ASNxt + ATP -> ASN + ADP + PI	
R810	ASN_transport			ASNxt + Hxt -> ASN	
R811	ASP_transport			ASP + Hxt <-> ASPxt	
R812	ASP_transport			ASPxt + ATP -> ASP + ADP + PI	
R813	ASP_transport			ASPxt + Hxt -> ASP	
R814	CYS_transport			CYS + Hxt <-> CYSxt	
R815	CYS_transport			CYSxt + ATP -> CYS + ADP + PI	
R816	CYS_transport			CYSxt + Hxt -> CYS	
R817	DALA_transport			DALAxt + Hxt -> DALA	
R818	DGLU_transport			DGLUxt + Hxt -> DGLU	
R819	GLN_transport			GLN + Hxt <-> GLNxt	
R820	GLN_transport			GLNxt + ATP -> GLN + ADP + PI	
R821	GLN_transport			GLNxt + Hxt -> GLN	
R822	GLU_transport			GLU + Hxt <-> GLUxt	
R823	GLU_transport			GLUxt + ATP -> GLU + ADP + PI	
R824	GLU_transport			GLUxt + Hxt -> GLU	
R825	GLU_transport			GLUxt + Naxt -> GLU + Na	
R826	GLY_transport			GLY + Hxt <-> GLYxt	
R827	GLY_transport			GLYxt + ATP -> GLY + ADP + PI	
R828	GLY_transport			GLYxt + Hxt -> GLY	
R829	GLY_transport			GLYxt + Naxt -> GLY + Na	
R830	HIS_transport			HIS + Hxt <-> HISxt	
R831	HIS_transport			HISxt + ATP -> HIS + ADP + PI	
R832	HIS_transport			HISxt + Hxt -> HIS	
R833	ILE_transport			ILE + Hxt <-> ILExt	
R834	ILE_transport			ILExt + ATP -> ILE + ADP + PI	
R835	ILE_transport			ILExt + Hxt -> ILE	
R836	LEU_transport			LEU + Hxt <-> LEUxt	
R837	LEU_transport			LEUxt + ATP -> LEU + ADP + PI	
R838	LEU_transport			LEUxt + Hxt -> LEU	
R839	LYS_transport			LYS + Hxt <-> LYSxt	
R840	LYS_transport			LYS + Hxt -> LYSxt	
R841	LYS_transport			LYSxt + ATP -> LYS + ADP + PI	
R842	LYS_transport			LYSxt + Hxt -> LYS	
R843	MET_transport			MET + Hxt <-> METxt	
R844	MET_transport			METxt + ATP -> MET + ADP + PI	
R845	MET_transport			METxt + Hxt -> MET	
R846	PHE_transport			PHE + Hxt <-> PHExt	
R847	PHE_transport			PHExt + ATP -> PHE + ADP + PI	
R848	PHE_transport			PHExt + Hxt -> PHE	
R849	PRO_transport			PRO + Hxt <-> PROxt	
R850	PRO_transport			PROxt + ATP -> PRO + ADP + PI	
R851	PRO_transport			PROxt + Hxt -> PRO	
R852	PRO_transport			PROxt + Naxt -> PRO + Na	
R853	SER_transport			SER + Hxt <-> SERxt	
R854	SER_transport			SERxt + ATP -> SER + ADP + PI	
R855	SER_transport			SERxt + Hxt -> SER	
R856	THR_transport			THR + Hxt <-> THRxt	
R857	THR_transport			THRxt + ATP -> THR + ADP + PI	
R858	THR_transport			THRxt + Hxt -> THR	
R859	TRP_transport			TRP + Hxt <-> TRPxt	
R860	TRP_transport			TRPxt + ATP -> TRP + ADP + PI	
R861	TRP_transport			TRPxt + Hxt -> TRP	
R862	TYR_transport			TYR + Hxt <-> TYRxt	
R863	TYR_transport			TYRxt + ATP -> TYR + ADP + PI	
R864	TYR_transport			TYRxt + Hxt -> TYR	
R865	VAL_transport			VAL + Hxt <-> VALxt	

No.	Metabolism	EC Number	ORF	Reaction	Enzyme
R866	VAL_transport			VALxt + ATP -> VAL + ADP + PI	
R867	VAL_transport			VALxt + Hxt -> VAL	
R868	DSER_transport			DSERxt + Hxt -> DSER	
R869	ARG_transport			ARGxt + ORN <-> ARG + ORNxt	
R870	HSER_transport			HSER + Hxt <-> HSERxt	
R871	ORN_transport			ORNxt + ATP -> ORN + ADP + PI	
R872	PTRC_transport			PTRCxt + ATP -> PTRC + ADP + PI	
R873	SPRMD_transport			SPRMDxt + ATP -> SPRMD + ADP + PI	
R874	UREA_transport			UREAxt + ATP -> UREA + ADP + PI	
R875	CHOLINE_transport			CHOLINExt + Hxt -> CHOLINE	
R876	ADN_transport			ADNxt + Hxt -> ADN	
R877	CYTD_transport			CYTDxt + Hxt -> CYTD	
R878	DA_transport			DAxt + Hxt -> DA	
R879	DC_transport			DCxt + Hxt -> DC	
R880	DG_transport			DGxt + Hxt -> DG	
R881	DT_transport			DTxt + Hxt -> DT	
R882	DU_transport			DUxt + Hxt -> DU	
R883	GSN_transport			GSNxt + Hxt -> GSN	
R884	URI_transport			URIxt + Hxt -> URI	
R885	CT_transport			CTxt + Hxt -> CT	
R886	XAN_transport			XANxt + Hxt -> XAN	
R887	URA_transport			URAxt + Hxt -> URA	
R888	TR_transport			TRxt + ATP -> TR + ADP + PI	
R889	ETHA_transport			ETHAxt + Hxt -> ETHA	
R890	BETAINE_transport			BETAINExt + Hxt -> BETAINE	
R891	BZ_transport			BZxt + Hxt -> BZ	

Supplementary Table 2. Metabolites participating in reactions of AbyMBEL891.

Metabolite abbreviations	Metabolite names
(2AE)P	(2-Aminoethyl)phosphonate
13DAP	1,3-Diaminopropane; Trimethylenediamine; 1,3-Propanediamine; Propane-1,3-diamine
13PDG	3-Phospho-D-glyceroyl phosphate
1BOH	1-Butanol
2(HE)TPP	2-(alpha-Hydroxyethyl)thiamine diphosphate
23BOH	(R,R)-Butane-2,3-diol; (R,R)-2,3-Butanediol; (R,R)-2,3-Butylene glycol
24DAB	L-2,4-Diaminobutanoate
2AA	2-Aminoacrylate
2AG3PC	2-Acyl-sn-glycero-3-phosphocholine
2AG3PE	2-Acyl-sn-glycero-3-phosphoethanolamine; L-1-Lysophosphatidylethanolamine
2AG3PS	2-Acyl-sn-glycero-3-phosphoserine
2AGL3P	2-Acyl-sn-glycerol 3-phosphate
2H3OSUCC	2-Hydroxy-3-oxosuccinate; Oxaloglycolate
2HP3M5H6M14B	2-Hexaprenyl-3-methyl-5-hydroxy-6-methoxy-1,4-benzoquinone
2HP3M6M14B	2-Hexaprenyl-3-methyl-6-methoxy-1,4-benzoquinone
2HPA	2-Hydroxyphenylacetate
2HPP	2-Hydroxypropylphosphonate
2MAACCOA	2-Methylacetoacetyl-CoA
2MB2ECOA	2-Methylbut-2-enoyl-CoA
2MBCOA	(S)-2-Methylbutanoyl-CoA
2MCIT	2-Methylcitrate
2MP2ECOA	2-Methylprop-2-enoyl-CoA
2MPPACOA	2-Methylpropanoyl-CoA
2NPRPN	2-Nitropropane
2OAD	2-Oxoadipate
2OP3M5H6M14BQ	2-Octaprenyl-3-methyl-5-hydroxy-6-methoxy-1,4-benzoquinone
2OP3M6M14BQ	2-Octaprenyl-3-methyl-6-methoxy-1,4-benzoquinone
2OP6HP	2-Octaprenyl-6-hydroxyphenol
2OP6M14BQ	2-Octaprenyl-6-methoxy-1,4-benzoquinone
2OP6MP	2-Octaprenyl-6-methoxyphenol
2OPP	2-Octaprenylphenol
2P14NQ	2-Phytyl-1,4-naphthoquinone
2P1A	2-Propyn-1-al
2PCDPMDE	2-Phospho-4-(cytidine 5'-diphospho)-2-C-methyl-D-erythritol
2PG	2-Phospho-D-glycerate
2PPG	2-Phosphoglycolate
34DHB	3,4-Dihydroxybenzoate; 3,4-Dihydroxybenzoic acid;; Protocatechuate; Protocatechuic acid
34DHMA	3,4-Dihydroxymandelaldehyde
34DHPA	3,4-Dihydroxyphenylacetate
34DHPEG	3,4-Dihydroxyphenylethyleneglycol
3A2OP	3-Amino-2-oxopropyl phosphate
3AP	3-Aminopropanal; beta-Aminopropion aldehyde
3B1A	3-Butyn-1-al
3BUT	3-Butynoate
3DDAH7P	2-Dehydro-3-deoxy-D-arabino-heptonate 7-phosphate
3H2MBCOA	(2S,3S)-3-Hydroxy-2-methylbutanoyl-CoA
3H3MGCOA	(S)-3-Hydroxy-3-methylglutaryl-CoA
3HAN	3-Hydroxyanthranilate
3HB123TC	(2S,3R)-3-Hydroxybutane-1,2,3-tricarboxylate
3HBCOA	(S)-3-Hydroxybutanoyl-CoA
3HBUT	(R)-3-Hydroxybutanoate; (R)-3-Hydroxybutyric acid
3HIBCOA	(S)-3-Hydroxyisobutyryl-CoA
3HIVCOA	3-Hydroxyisovaleryl-CoA
3HPA	3-Hydroxyphenylacetate
3HPCOA	3-Hydroxypropionyl-CoA
3MBCOA	3-Methylbutanoyl-CoA
3MCCOA	3-Methylcrotonyl-CoA
3MGCOA	3-Methylglutaconyl-CoA
3MOP	(S)-3-Methyl-2-oxopentanoic acid; (S)-3-Methyl-2-oxopentanoate; (3S)-3-Methyl-2-oxopentanoic acid; (3S)-3-Methyl-2-oxopentanoate
3OP4HB	3-Octaprenyl-4-hydroxybenzoate
3OPP	3-Oxopropanoate; Malonate semialdehyde
3PG	3-Phospho-D-glycerate
3PSER	3-Phosphoserine
3PSME	5-O-(1-Carboxyvinyl)-3-phosphoshikimate
3SFPYR	3-Sulfinylpyruvate
3SLALA	3-Sulfino-L-alanine
3SPYR	3-Sulfopyruvate
4AABUT	4-Acetamidobutanoate
4AB	4-Aminobutanal
4FAAC	4-Fumarylacetoacetate
4GBTA	4-Guanidinobutanamide
4GBTR	4-Guanidinobutanoate; 4-Guanidinobutyric acid
4HB	4-Hydroxybenzoate
4HGLUSA	L-4-Hydroxyglutamate semialdehyde
4HLT	4-Hydroxy-L-threonine
4HMN	4-Hydroxymandelonitrile
4HPA	4-Hydroxyphenylacetate
4HPACAL	4-Hydroxyphenylacetaldehyde; 2-(4-Hydroxyphenyl)acetaldehyde
4HPACALO	(Z)-4-Hydroxyphenylacetaldehyde-oxime
4HPACOA	4-Hydroxyphenylacetyl-CoA
4HPAGLY	4-Hydroxyphenylacetylglycine
4HPP	3-(4-Hydroxyphenyl)pyruvate
4HPRO	trans-4-Hydroxy-L-proline
4I5P	4-Imidazolone-5-propanoate
4MAAC	4-Maleylacetoacetate
4MOP	4-Methyl-2-oxopentanoate
4PPNCYS	(R)-4'-Phosphopantothenoyl-L-cysteine
4PPNTE	Pantetheine 4'-phosphate
4PPNTO	D-4'-Phosphopantothenate
4TMABT	4-Trimethylammoniobutanal
4TMABTO	4-Trimethylammoniobutanoate
5A4ICA	5-Amino-4-imidazole carboxylate
5AI	5-Aminoimidazole; Aminoimidazole; 4-Aminoimidazole
5C2O3E	5-Carboxy-2-oxohept-3-enedioate
5CM2HM	5-Carboxymethyl-2-hydroxymuconate
5GLUPEPT	(5-L-Glutamyl)-peptide
5HIAA	5-Hydroxyindoleacetaldehyde
5HIAC	5-Hydroxyindoleacetate
5MC	DNA 5-methylcytosine; DNA containing 5-methylcytosine; 5-Methylcytosine (in DNA)
5MDR	5-Methylthio-D-ribose

Metabolite abbreviations	**Metabolite names**
5MTA	5'-Methylthioadenosine
5MTGLU	5-Methyltetrahydropteroyltri-L-glutamate
A[C]	Apo-[carboxylase]
A5P	D-Arabinose 5-phosphate
A6RP	5-Amino-6-ribitylamino-2,4 (1H, 3H)-pyrimidinedione; 4-(1-D-Ribitylamino)-5-amino-2,6-dihydroxypyrimidine; 4-(1-D-Ribitylamino)-5-aminouracil
A6RP5P	5-Amino-6-(5'-phosphoribosylamino)uracil
A6RP5P2	5-Amino-6-(5'-phosphoribitylamino)uracil
AAA	Aminoacetaldehyde
AAC	Acetoacetate
AACCOA	Acetoacetyl-CoA
AACTN	Aminoacetone; 1-Amino-2-propanone
AAD	Acetyl adenylate
ABUT	(S)-2-Aceto-2-hydroxybutanoate
AC	Acetate
ACACP	Acetyl-[acyl-carrier protein]
ACAL	Acetaldehyde
ACCOA	Acetyl-CoA
ACDA	Adenosyl cobyrinate a,c diamide
ACETYLP	Acetyl phosphate
ACLAC	2-Acetolactate
ACOA	Acyl-CoA
ACP	Acyl-carrier protein
ACT	(R)-Acetoin; (R)-2-Acetoin; (R)-3-Hydroxy-2-butanone; (R)-Dimethylketol; (R)-3-Hydroxybutan-2-one
ACTN	Acetone; Dimethyl ketone; 2-Propanone
AD	Adenine
ADCBA	Adenosyl cobinamide
ADCBAP	Adenosyl cobinamide phosphate
ADCHOR	4-amino-4-deoxychorismate
ADLIPO	6-S-Acetyldihydrolipoamide; [Dihydrolipoyllysine-residue acetyltransferase] S-acetyldihydrolipoyllysine; S-Acetyldihydrolipoamide-E
ADN	Adenosine
ADP	ADP
AEIOH	3-(2-Aminoethyl)-1H-indol-5-ol; Serotonin; 5-Hydroxytryptamine; Enteramine
AG	L-Arogenate
AGDPCBA	Adenosine-GDP-cobinamide
AGL	Acylglycerol
AGL3P	1-Acyl-sn-glycerol 3-phosphate
AHHMD	2-Amino-7,8-dihydro-4-hydroxy-6-(diphosphooxymethyl)pteridine
AHHMP	2-Amino-4-hydroxy-6-hydroxymethyl-7,8-dihydropteridine
AHM	4-Amino-5-hydroxymethyl-2-methylpyrimidine
AHMP	4-Amino-5-hydroxymethyl-2-methylpyrimidine-phosphate
AHMPP	4-Amino-5-hydroxymethyl-2-methylpyrimidine-pyrophosphate
AHTD	2-Amino-4-hydroxy-6-(erythro-1,2,3-trihydroxypropyl)dihydropteridine triphosphate; 6-(L-erythro-1,2-Dihydroxypropyl 3-triphosphate)-7,8-dihydropterin; 6-[(1S,2R)-1,2-Dihydroxy-3-triphosphooxypropyl]-7,8-dihydropterin; 7,8-Dihydroneopterin 3'-triphosphate
AIBUT	L-3-Amino-isobutanoate; (S)-3-Amino-isobutyrate; L-3-Amino-isobutyrate; (S)-3-Amino-isobutanoate; (S)-3-Amino-2-methylpropanoate
AICAR	1-(5'-Phosphoribosyl)-5-amino-4-imidazolecarboxamide
AIR	Aminoimidazole ribotide
AKG	2-Oxoglutarate
ALA	L-Alanine
ALAALA	D-alanyl-D-alanine
ALATRNA	L-Alanyl-tRNA
ALAV	D-Aminolevulinate
ALLNT	Allantoate; Allantoic acid
AMP	AMP
AN	Anthranilate
AONA	8-amino-7-oxononanoate
APN	beta-Aminopropionitrile; 3-Aminopropiononitrile
ApppppA	P1,P4-Bis(5'-adenosyl) tetraphosphate
APS	Adenylylsulfate; Adenylyl sulfate; Adenosine 5'-phosphosulfate; APS; 5'-Adenylyl sulfate
ARBZ	alpha-Ribazole; N1-(alpha-D-ribosyl)-5,6-dimethylbenzimidazole
ARG	L-Arginine
ARGSUCC	N-(L-Arginino)succinate
ARGTRNAARG	L-Arginyl-tRNA(Arg)
ARIB	ADPribose
ASELNT	Adenylylselenate
ASER	O-Acetyl-L-serine
ASN	L-Asparagine
ASNTRNAASN	L-Asparaginyl-tRNA(Asn)
ASP	L-Aspartate
ASPSA	L-Aspartate 4-semialdehyde
ASPTRNAASN	L-Aspartyl-tRNA(Asn)
ASPTRNAASP	L-Aspartyl-tRNA(Asp)
ASUC	N6-(1,2-Dicarboxyethyl)-AMP
ATP	ATP
B5AMP	Biotinyl-5'-AMP
BAL	Betaine aldehyde
bALA	beta-Alanine
bAPA	beta-Aminopropion aldehyde
BASP	4-Phospho-L-aspartate
bDG6P	beta-D-Glucose 6-phosphate
bDGLC	beta-D-Glucose
BETAINE	Betaine; Glycine betaine
BT	Biotin
BUTANAL	Butanal
BZ	Benzoate; Benzoic acid; Benzenecarboxylic acid; Phenylformic acid; Dracylic acid
C(I)A	Cob(I)alamin; Cbl; Vitamin B12s
C(I)DA	Cob(I)yrinate a,c diamide
C090ACP	Nonanoyl-[acyl-carrier protein]
C100	Decanoic acid
C100ACP	Decanoyl-[acyl-carrier protein]
C110ACP	Undecanoyl-[acyl-carrier protein]
C120	Dodecanoic acid
C120ACP	Dodecanoyl-[acyl-carrier protein]
C120OH	beta-hydroxy dodecanoic acid
C121COA	cis,cis-3,6-Dodecadienoyl-CoA
C122COA	trans,cis-Lauro-2,6-dienoyl-CoA
C130ACP	Tridecanoyl-[acyl-carrier protein]
C140	Tetradecanoic acid
C140ACP	Tetradecanoyl-[acyl-carrier protein]

Metabolite abbreviations	Metabolite names
C140OH	beta-hydroxy tetradecanoic acid
C150	Pentadecanoic acid
C150ACP	Pentadecanoyl-[acyl-carrier protein]
C151ACP	Pentadecenoyl-[acyl-carrier protein]
C160	Hexadecanoic acid
C160ACP	Hexadecanoyl-[acyl-carrier protein]
C161	Hexadecenoic acid
C161ACP	Hexadecenoyl-[acyl-carrier protein]
C170	Heptadecanoic acid
C170ACP	Heptadecanoyl-[acyl-carrier protein]
C171	Heptadecenoic acid
C171ACP	Heptadecenoyl-[acyl-carrier protein]
C180	Octadecanoic acid
C180ACP	Octadecanoyl-[acyl-carrier protein]
C181	Octadecenoic acid
C181ACP	Octadecenoyl-[acyl-carrier protein]
C190ACP	Nonadecanoyl-[acyl-carrier protein]
C191ACP	Nonadecenoyl-[acyl-carrier protein]
C200ACP	Eicosanoyl-[acyl-carrier protein]
CAASP	N-Carbamoyl-L-aspartate
CAIR	1-(5-Phospho-D-ribosyl)-5-amino-4-imidazolecarboxylate
CALA	3-Cyano-L-alanine; L-3-Cyanoalanine; L-beta-Cyanoalanine
CAP	Carbamoyl phosphate
CATECHOL	Catechol; 1,2-Benzenediol; o-Benzenediol; 1,2-Dihydroxybenzene; Brenzcatechin; Pyrocatechol
CAV	Cofactors and vitamins
CBA	Cobinamide
CBCO	Cobamide coenzyme
CBHCAP	3-Isopropylmalate
CCOA	Crotonoyl-CoA
CDHDHI	2-Carboxy-2,3-dihydro-5,6-dihydroxyindole
CDP	CDP
CDPDG	CDP-diacylglycerol
CDPMDE	4-(Cytidine 5'-diphospho)-2-C-methyl-D-erythritol
CH3OR	Primary alcohol
CHCOA	6-carboxyhexanoyl-CoA; Pimeloyl-CoA
CHITB	Chitobiose
CHOLINE	Choline
CHOLINEP	Choline phosphate; Phosphorylcholine; Phosphocholine; O-Phosphocholine
CHOR	Chorismate
CIT	Citrate
CITR	L-Citrulline
CL	Cardiolipin (biomass component)
CMP	CMP
CMPAEP	CMP-2-aminoethylphosphonate; CMPciliatine
CMPKDO	CMP-2-keto-3-deoxyoctanoate
CNS	Carnosine
CO2	CO2
COA	CoA; coenzyme A
CPAD5P	1-(2-Carboxyphenylamino)-1-deoxy-D-ribulose 5-phosphate
CPP	Coproporphyrinogen III
CPPI	Coproporphyrinogen I
CRTN	Creatine; alpha-Methylguanidino acetic acid; Methylglycocyamine
CT	DNA cytosine; Cytosine (in DNA)
CTP	CTP
CVN	Cinnavalininate
CYS	L-Cysteine
CYSGLY	Cys-Gly; L-Cysteinylglycine
CYST	L-Cystine
CYSTEATE	L-Cysteate
CYSTRNACYS	L-Cysteinyl-tRNA(Cys)
CYTD	Cytidine
D6PGC	6-Phospho-D-gluconate
D6RP5P	2,5-Diamino-6-hydroxy-4-(5'-phosphoribosylamino)-pyrimidine
D8RL	6,7-Dimethyl-8-(1-D-ribityl)lumazine
DA	Deoxyadenosine
DAC	Diacetyl; Biacetyl; Dimethylglyoxal; 2,3-Butanedione
DADP	dADP
DALA	D-alanine
DAMP	dAMP
DANNA	7,8-Diaminononanoate
DAPIM	L,L-2,6-Diaminopimelate
DASP	D-Aspartate
DATP	dATP
DB4P	L-3,4-Dihydroxy-2-butanone 4-phosphate
DC	Deoxycytidine
DCDP	dCDP
DCMP	dCMP
DCTP	dCTP
DCYS	D-Cysteine; D-Amino-3-mercaptopropionic acid
DG	Deoxyguanosine
DGDP	dGDP
DGLN	D-Glutamine
DGLU	D-Glutamate
DGLUCA	D-Glucarate
DGLUCL	D-Glucuronolactone
DGLYCERATE	D-glycerate
DGMP	dGMP
DGR	1,2-Diacyl-sn-glycerol; 1,2-Diacylglycerol
DGTP	dGTP
DHAP	Glycerone phosphate
DHDP	2,3-Dihydrodipicolinate
DHF	Dihydrofolate
DHI	5,6-Dihydroxyindole
DHLIPOYLPROTEIN	Dihydrolipoylprotein
DHMP	(R)-2,3-dihydroxy-3-methylpentanoate
DHMVA	(R)-2,3-dihydroxy-3-methylbutanoate
DHN	1,4-dihydroxy-2-naphthoate
DHP	2-Amino-4-hydroxy-6-(D-erythro-1,2,3-trihydroxypropyl)-7,8-dihydropteridine
DHPA	2,6-Dihydroxyphenylacetate
DHPACAL	3,4-Dihydroxyphenylacetaldehyde; Protocatechuatealdehyde
DHPANT	2-Dehydropantoate
DHPT	Dihydropteroate
DHSK	3-Dehydroshikimate

Metabolite abbreviations	**Metabolite names**
DIDP	dIDP
DIMGP	D-erythro-1-(Imidazol-4-yl)glycerol 3-phosphate
DIMP	2'-Deoxyinosine 5'-phosphate; dIMP
DIN	Deoxyinosine
DISAC1P	2,3-bis(3-hydroxytetradecanoyl)-D-glucosaminyl-1,6-beta-D-2,3-bis(3-hydroxytetradecanoyl)-beta-D-glucosaminyl 1-phosphate or dissacharide 1-P
DITP	dITP
DLIPO	Enzyme N6-(dihydrolipoyl)lysine; Dihydrolipoamide-E
DMB	Dimethylbenzimidazole
DMK	2-Demethylmenaquinone
DMKH2	2-Demethylmenaquinol
DMPP	Dimethylallyl diphosphate
DNA	DNA (biomass component)
DOROA	(S)-Dihydroorotate
DPCHR	L-Dopachrome; 2-L-Carboxy-2,3-dihydroindole-5,6-quinone
DPCOA	Dephospho-CoA
DPHE	D-Phenylalanine
DPM	Dopamine; 4-(2-Aminoethyl)-1,2-benzenediol; 4-(2-Aminoethyl)benzene-1,2-diol; 3,4-Dihydroxyphenethylamine; 2-(3,4-Dihydroxyphenyl)ethylamine
DPRO	D-Proline
DQT	3-Dehydroquinate
DR1P	2-Deoxy-D-ribose 1-phosphate
DR5P	2-Deoxy-D-ribose 5-phosphate
DSER	D-Serine
DT	Thymidine
DTB	Dethiobiotin
DTDP	dTDP
DTDP4O6DG	4,6-Dideoxy-4-oxo-dTDP-D-glucose; dTDP-4-oxo-6-deoxy-D-glucose; dTDP-4-dehydro-6-deoxy-D-glucose; dTDP-4-dehydro-6-deoxy-alpha-D-glucose; dTDP-4-oxo-6-deoxy-alpha-D-glucose; dTDP-4-dehydro-6-deoxy-alpha-D-galactose; dTDP-4-dehydro-6-deoxy-D-galactose
DTDP4ORMNS	dTDP-4-dehydro-6-deoxy-L-mannose; dTDP-4-oxo-6-deoxy-L-mannose; dTDP-4-oxo-L-rhamnose
DTDPGLAC	dTDPgalactose
DTDPGLU	dTDP-glucose; dTDP-D-glucose; dTDP-alpha-D-glucose
DTDPRMNS	dTDP-6-deoxy-L-mannose; dTDP-L-rhamnose
DTMP	dTMP
DTTP	dTTP
DU	Deoxyuridine
DUDP	dUDP
DUMP	dUMP
DUTP	dUTP
DX5P	1-Deoxy-D-xylulose 5-phosphate
E4HGLU	L-erythro-4-Hydroxyglutamate
E4P	D-Erythrose 4-phosphate
ER4P	4-Phospho-D-erythronate; 4-Phosphoerythronate
ETH	Ethanol
ETHA	Ethanolamine
ETHAP	Ethanolamine phosphate; O-Phosphorylethanolamine; Phosphoethanolamine; O-Phosphoethanolamine
EXOPOLYS	Exopolysaccharide
F1P	D-Fructose 1-phosphate
F6P	beta-D-Fructose 6-phosphate
FA	Formamide
FAD	Flavin adenine dinucleotide; FAD
FADH2	FADH2
FAN	Formylanthranilate; N-Formylanthranilate; 2-(Formylamino)-benzoic acid
FDP	beta-D-Fructose 1,6-bisphosphate
FERIC	Ferricytochrome c
FEROC	Ferrocytochrome c
FGAM	2-(Formamido)-N1-(5'-phosphoribosyl)acetamidine
FGAR	5'-Phosphoribosyl-N-formylglycinamide
FKYN	L-Formylkynurenine; N-Formyl-L-kynurenine; N-Formylkynurenine
FL	Folate
FMETTRNA	N-Formylmethionyl-tRNA
FMN	FMN; Riboflavin-5-phosphate; Flavin mononucleotide
FORMATE	Formate
FPP	trans,trans-Farnesyl diphosphate
FTHF	10-Formyltetrahydrofolate
FUCP	L-Fuculose 1-phosphate
FUM	Fumarate
G1P	D-Glucose 1-phosphate
G3P	D-Glyceraldehyde 3-phosphate; (2R)-2-Hydroxy-3-(phosphonooxy)-propanal
G3PC	sn-glycero-3-Phosphocholine
G3PE	sn-glycero-3-Phosphoethanolamine
G6P	alpha-D-Glucose 6-phosphate
GA1P	D-Glucosamine 1-phosphate
GA6P	D-Glucosamine 6-phosphate
GABA	4-Aminobutanoate
GAPN	gamma-Glutamyl-beta-aminopropiononitrile; gamma-Glutamyl-3-aminopropiononitrile
GAR	5'-Phosphoribosylglycinamide
GCYS	gamma-L-Glutamyl-L-cysteine
GDP	GDP
GDPMAN	GDP-mannose
GENAL	Gentisate aldehyde
GGLUMSCYS	gamma-Glutamyl-Se-methylselenocysteine
GGPP	Geranylgeranyl diphosphate
GL	Glycerol
GL3P	sn-Glycerol 3-phosphate
GLAL	Glycolaldehyde
GLC	alpha-D-Glucose
GLCA	D-Glucosamine; Chitosamine; 2-Amino-2-deoxy-D-glucose
GLCAMN	D-Glucosaminide
GLN	L-Glutamine
GLU	L-Glutamate
GLUBCALA	gamma-Glutamyl-beta-cyanoalanine
GLUC	D-Gluconate
GLUGSAL	L-Glutamate 5-semialdehyde
GLUP	alpha-D-Glutamyl phosphate
GLUTCOA	Glutaryl-CoA
GLUTR	5-L-Glutamyl-taurine
GLUTRNAGLN	L-Glutamyl-tRNA(Gln)
GLUTRNAGLU	L-Glutamyl-tRNA(Glu)
GLX	Glyoxylate

Metabolite abbreviations	Metabolite names
GLY	Glycine
GLYCOLATE	Glycolate
GLYTRNAGLY	Glycyl-tRNA(Gly)
GMP	GMP
GN	Guanine
GPP	Geranyl diphosphate
GSA	Glutamate-1-semialdehyde
GSN	Guanosine
GTP	GTP
GTRNA	Glutaminyl-tRNA
H[C]	Holo-[carboxylase]
H2O2	H2O2
H2S	Hydrogen sulfide
H2SO3	Sulfite
H5P	Hydantoin-5-propionate; Hydantoin-propionate
HAC	Hydroxyacetone
HCNS	Homocarnosine
HCO3	HCO3
HCYS	L-Homocysteine
HDN	Hordenine; 4-[2-(Dimethylamino)ethyl]phenol
HEDC	2-Hydroxyethylenedicarboxylate; enol-Oxaloacetate; enol-Oxaloacetic acid; 2-Hydroxybut-2-enedioic acid
HEMEO	Heme O
HEPPP	all-trans-Heptaprenyl diphosphate
HIBUT	(S)-3-Hydroxyisobutyrate
HIEA	1H-Imidazole-4-ethanamine; Histamine; 2-(4-Imidazolyl)ethylamine
HIPPRT	Hippurate; Hippuric acid; N-Benzoylglycine; Benzoylaminoacetic acid
HIS	L-Histidine
HISOL	L-Histidinol
HISOLP	L-Histidinol phosphate
HISTRNAHIS	L-Histidyl-tRNA(His)
HKYN	3-Hydroxy-L-kynurenine
HMB	Hydroxymethylbilane
HMB4PP	1-Hydroxy-2-methyl-2-butenyl 4-diphosphate
HO3S2	Thiosulfate
HOMOGEN	Homogentisate
HOPP	2-Hydroxy-3-oxopropanoate; Tartronate semialdehyde
HPYR	Hydroxypyruvate; Hydroxypyruvic acid; 3-Hydroxypyruvate; 3-Hydroxypyruvic acid
HSER	L-Homoserine
Hxt	External proton
HYDROXYAKG	D-4-Hydroxy-2-oxoglutarate
HYXN	Hypoxanthine
I3AA	Indole-3-acetaldehyde
I3AAM	Indole-3-acetamide
I3AC	Indole-3-acetate
I4AA	Imidazole-4-acetaldehyde
I4AC	Imidazole-4-acetate
IASP	Iminoaspartate
ICHOR	Isochorismate
ICIT	Isocitrate
IDP	IDP
IGLY	Iminoglycine; Iminoacetic acid
IGP	Indoleglycerol phosphate
ILE	L-Isoleucine
ILETRNAILE	L-Isoleucyl-tRNA(Ile)
IMACP	3-(Imidazol-4-yl)-2-oxopropyl phosphate
IMAL	Isomaltose
IMP	IMP
INDOLE	Indole
INS	Inosine
IPP	Isopentenyl diphosphate
IPPMAL	2-Isopropylmalate; (2S)-2-Isopropylmalate; 3-Carboxy-3-hydroxy-4-methylpentanoate; 3-Carboxy-3-hydroxy-isocaproate; 3-Carboxy-3-hydroxyisocaproate; 2-Hydroxy-2-isopropylbutanedioate; 3-Hydroxy-4-methyl-3-carboxypentanoate
IPYR	Indolepyruvate; Indolepyruvic acid; (Indol-3-yl)pyruvate; Indole-3-pyruvate; 3-(Indol-3-yl)pyruvate
ITP	ITP
K2LIPA	KDO2-lipid (A); Di[3-deoxy-D-manno-octulosonyl]-lipid A
K2LIPIV	KDO2-lipid IV(A); Di[3-deoxy-D-manno-octulosonyl]-lipid IV(A);
KDO	2-Dehydro-3-deoxy-D-octonate
KDOLIPIV	KDO-lipid IV(A)
KDOP	2-Dehydro-3-deoxy-D-octonate 8-phosphate
KDPG	2-Dehydro-3-deoxy-6-phospho-D-gluconate
KYN	L-Kynurenine; 3-Anthraniloyl-L-alanine
L1P3H5C	L-1-Pyrroline-3-hydroxy-5-carboxylate
LAC	(R)-Lactate, D-Lactate
LACAL	(S)-Lactaldehyde; L-Lactaldehyde; L-2-Hydroxypropionaldehyde
LEU	L-Leucine
LEUTRNA	L-Leucyl-tRNA
LIPID	Lipids other than phospholipid
LIPIV	Lipid IV(A)
LIPO	Enzyme N6-(lipoyl)lysine; Lipoamide-E
LIPOYLPROTEIN	Lipoylprotein
LIPX	Lipid X
LK2LIPIV	Lauroyl-KDO2-lipid IV(A)
LLCT	L-Cystathionine
LPS	Lippolysaccharide
LTG	(R)-S-Lactoylglutathione
LYS	L-Lysine
LYSTRNA	L-Lysyl-tRNA
MAL	(S)-Malate
MALACP	Malonyl-[acyl-carrier protein]
MALCOA	Malonyl-CoA
MAN1P	alpha-D-Mannose 1-phosphate
MAN6P	D-Mannose 6-phosphate
MCB	Methylcobalamin
MDAPIM	meso-2,6-Diaminoheptanedioate; meso-2,6-Diaminopimelate; meso-2,6-Diaminopimelic acid; meso-Diaminoheptanedioate
MDE4P	2-C-Methyl-D-erythritol 4-phosphate
MDECPP	2-C-Methyl-D-erythritol 2,4-cyclodiphosphate
MET	L-Methionine
METHF	5,10-Methenyltetrahydrofolate
METTHF	5,10-Methylenetetrahydrofolate
METTRNA	L-Methionyl-tRNA

Metabolite abbreviations	**Metabolite names**
MK	menaquinone
MKH2	menaquinol
MLT	Maltose
MM	Methylmalonate
MMALCOA	(S)-Methylmalonyl-CoA; (S)-Methylmalonyl-coenzyme A; (2S)-Methylmalonyl-CoA; D-Methylmalonyl-CoA
MMSA	(S)-Methylmalonate semialdehyde
MNT	D-Mannitol
MOT	5-Methoxytryptamine; 5-MeOT
MPET	4-Methyl-5-(2-phosphoethyl)-thiazole; 4-Methyl-5-(2-phosphono-oxyethyl)-thiazole
MPYR	Mercaptopyruvate
MSCYS	Se-Methylselenocysteine
MTG	Methylglyoxal
MTHF	5-Methyltetrahydrofolate
MTRM	N-Methyltyramine
MTTA	meso-Tartaric acid; meso-Tartrate
N(P)CYS	N-((R)-Pantothenoyl)-L-cysteine
N1(5PADR)DMB	N1-(5-Phospho-alpha-D-ribosyl)-5,6-dimethylbenzimidazole
N2SUCCARG	N2-Succinyl-L-arginine
N2SUCCGLU	N-Succinyl-L-glutamate; (2S)-2-(3-Carboxypropanoylamino)pentanedioic acid
N2SUCCGLU5SA	N-Succinyl-L-glutamate 5-semialdehyde; (2S)-2-(3-Carboxypropanoylamino)-5-oxopentanoic acid
N4AAB	N4-Acetylaminobutanal
Na	Sodium
NAAD	Deamino-NAD+; Deamido-NAD+; Deamido-NAD
NAC	Nicotinate
NACD	Nicotinate D-ribonucleoside
NACN	Nicotinate D-ribonucleotide
NAD	NAD+; Nicotinamide adenine dinucleotide
NADH	NADH
NADMA	N-Acetyl-D-mannosamine
NADP	NADP+; Nicotinamide adenine dinucleotide phosphate
NADPH	NADPH
NAGA	N-Acetyl-D-glucosamine
NAGA1P	N-Acetyl-D-glucosamine 1-phosphate
NAGLU	N-Acetyl-L-glutamate
NAGLUP	N-Acetyl-L-glutamate 5-phosphate
NAGLUS	N-Acetyl-L-glutamate 5-semialdehyde
NAM	Nicotinamide
NAMD	N-Ribosylnicotinamide
NAMN	Nicotinamide D-ribonucleotide
NAORN	N2-Acetyl-L-ornithine
NAS	N-Acylsphingosine; Ceramide
NASAEP	Ceramide 2-aminoethylphosphonate; Ceramide ciliatine
NFGLU	N-Formimino-L-glutamate
NH3	NH3
NHLYS	N6-Hydroxy-L-lysine
NMHIS	N(pi)-Methyl-L-Histidine
NO2	Nitrite
NO3	Nitrate
NPRAN	N-(5-Phospho-D-ribosyl)anthranilate
O2	Oxygen
OA	Oxaloacetate
OAHSER	O-Acetyl-L-homoserine
OBUT	2-Oxobutanoate
OGT	Oxidized glutathione; Glutathione disulfide; Oxiglutatione
OHB	3-Hydroxy-4-phospho-hydroxy-alpha-ketobutyrate
OICAP	3-Carboxy-4-methyl-2-oxopentanoate
OIVAL	3-Methyl-2-oxobutanoic acid
OMP	Orotidine 5'-phosphate
OPP	all-trans-Octaprenyl diphosphate
ORBRDX	Oxidized rubredoxin
ORN	L-Ornithine
OROA	Orotate
OSB	O-succinylbenzoate
OSBCOA	O-succinylbenzoate-CoA
OSLHSER	O-Succinyl-L-homoserine
OTHIO	Thioredoxin disulfide; Oxidized thioredoxin; Thioredoxin sulfide
P5C	(S)-1-Pyrroline-5-carboxylate
P5P	Pyridoxine 5'-phosphate; Pyridoxine phosphate
PA	Phosphatidate; 1,2-Diacyl-sn-glycerol 3-phosphate
PAA	2-Phenylacetamide
PABA	4-Aminobenzoate
PACAL	Phenylacetaldehyde; alpha-Tolualdehyde
PACGLY	Phenylacetylglycine
PACOA	Phenylacetyl-CoA
PANT	(R)-pantoate
PAP	Adenosine 3',5'-bisphosphate
PAPS	3'-Phosphoadenylyl sulfate
PBG	Porphobilinogen
PC	Phosphatidylcholine
PC2	Percorrin 2
PDLA	Pyridoxamine
PDLA5P	Pyridoxamine-5-phosphate
PE	Phosphatidylethanolamine
PEA	Phenethylamine; 2-Phenylethylamine; beta-Phenylethylamine; Phenylethylamine
PEP	Phosphoenolpyruvate
PEPTIDE	Peptide
PEPTIDO	Peptidoglycan (biomass component)
PG	Phosphatidylglycerol
PGP	Phosphatidylglycerophosphate
PHE	L-Phenylalanine
PHEN	Prephenate
PHETRNAPHE	L-Phenylalanyl-tRNA(Phe)
PHOSPHOLIPID	Phospholipids (biomass component)
PHP	3-Phosphonooxypyruvate
PHPYR	Phenylpyruvate
PHSER	O-Phospho-L-homoserine
PHT	O-Phospho-4-hydroxy-L-threonine
PI	Orthophosphate
PL	Pyridoxal
PL5P	Pyridoxal 5'-phosphate
PLA	Phenylacetic acid; Benzylformic acid; Phenylacetate; Benzeneacetiic acid
PNTO	(R)-Pantothenate; Pantothenate

Metabolite abbreviations	Metabolite names
PPA	Propinol adenylate
PPAACP	Propanoyl-[acyl-carrier protein]; Propionyl-[acyl-carrier protein]
PPAC	Phosphonoacetaldehyde
PPACOA	Propanoyl-CoA; Propionyl-CoA
PPCOA	Propenoyl-CoA; Acryloyl-CoA
PPEPTIDO	Peptidoglycan precursor
ppGpp	Guanosine 3',5'-bis(diphosphate)
PPHG	Protoporphyrinogen IX
PPI	Pyrophosphate; Diphosphate
PPIX	Protoporphyrin IX
PPN	Propynoate
pppGpp	Guanosine 3'-diphosphate 5'-triphosphate
PPPI	Triphosphate
PPPP	all-trans-Pentaprenyl diphosphate
PQ	Phylloquinone
PQQ	Pyrrolo-quinoline quinone; Pyrroloquinoline-quinone; Pyrroloquinoline quinone; 4,5-Dioxo-4,5-dihydro-1H-pyrrolo[2,3-f]quinoline-2,7,9-tricarboxylate
PQQH2	Reduced pyrroloquinoline-quinone
PRAM	5-Phosphoribosylamine
PRBAMP	N1-(5-Phospho-D-ribosyl)-AMP
PRBATP	N1-(5-Phospho-D-ribosyl)-ATP
PRFICA	1-(5'-Phosphoribosyl)-5-formamido-4-imidazolecarboxamide
PRFP	5-(5-Phospho-D-ribosylaminoformimino)-1-(5-phosphoribosyl)-imidazole-4-carboxamide
PRLP	N-(5'-Phospho-D-1'-ribulosylformimino)-5-amino-1-(5''-phospho-D-ribosyl)-4-imidazolecarboxamide
PRO	L-Proline
PROPANOATE	Propanoate
PROPIONYLP	Propanoyl phosphate
PROTEIN	Proteins
PROTRNAPRO	L-Prolyl-tRNA(Pro)
PRPP	5-Phospho-alpha-D-ribose 1-diphosphate
PS	Phosphatidylserine
PTH	Heme; Haem; Protoheme; Heme B; Protoheme IX
PTRC	Putrescine
PTT	Pantetheine
PURI5P	Pseudouridine 5'-phosphate
PYR	Pyruvate
PYRDX	Pyridoxine
PYTHP	6-Pyruvoyltetrahydropterin
QA	Quinolinate; Pyridine-2,3-dicarboxylate
QNT	Quinate; Quinic acid; Kinic acid; Chinic acid; L-Quinic acid; L-Quinate; (-)-Quinic acid
R1P	D-Ribose 1-phosphate; alpha-D-Ribose 1-phosphate; Ribose 1-phosphate
R3HBCOA	(R)-3-Hydroxybutanoyl-CoA
R5P	D-Ribose 5-phosphate
RCHO	Aldehyde
RGT	Glutathione
RH	Alkane
RIBFLAV	Riboflavin
RL5P	D-Ribulose 5-phosphate
RMAL	(R)-Malate; D-Malate; D-Malic acid
RNA	RNA
RRBRDX	Reduced rubredoxin
RTHIO	Thioredoxin
S	Sulfur
S6P	Sorbitol 6-phosphate
S7P	Sedoheptulose 7-phosphate
SAH	S-Adenosyl-L-homocysteine
SAICAR	1-(5'-Phosphoribosyl)-5-amino-4-(N-succinocarboxamide)-imidazole
SAM	S-Adenosyl-L-methionine
SAMOB	S-adenosyl-4-methylthio-2-oxobutanoate
SAOPIM	N-Succinyl-2-amino-6-oxopimelate
SASHCYS	Se-Adenosylselenohomocysteine
SB1P	Sorbose 1-phosphate
SCSN	Sarcosine; N-Methylglycine
SCYS	Selenocysteine
SDAPIM	N-Succinyl-L-2,6-diaminopimelate
SDLIPO	S-Succinyldihydrolipoamide
SeASMET	Se-Adenosylselenomethionine
SELD	Selenide
SELNT	Selenate
SELT	Selenite
SER	L-Serine
SERTRNASER	L-Seryl-tRNA(Ser)
SGDHL	S-Glutaryldihydrolipoamide
SHCHC	2-succinyl-6-hydroxy-2,4-cyclohexadiene-1-carboxylate
SHCL	Sirohydrochlorin
SHCYS	Selenohomocysteine
SHEME	Siroheme
SLAC	(S)-Lactate
SLF	Sulfate
SLLCT	Selenocystathionine
SME	Shikimate
SME3P	Shikimate 3-phosphate
SMET	Selenomethionine
SMETTRNAMET	Selenomethionyl-tRNA(Met)
SORN	N2-Succinyl-L-ornithine; (2S)-5-Amino-2-(3-carboxypropanoylamino)pentanoic acid
SPRMD	Spermidine
SRLH	S-Ribosyl-L-homocysteine
SSLCYS	S-Sulfo-L-cysteine
SUC	Sucrose
SUCC	Succinate
SUCCOA	Succinyl-CoA
SUCCSA	Succinate semialdehyde
T3	D-Glyceraldehyde
TCYS	Thiocysteine
TDHDP	2,3,4,5-Tetrahydrodipicolinate
TGL	Triacylglycerol
TGLU	Tetrahydropteroyltri-L-glutamate
THF	Tetrahydrofolate
THFG	Tetrahydrofolyl-[Glu](n)
THIAMIN	Thiamin
THMP	Thiamin monophosphate

Metabolite abbreviations	Metabolite names
THMPP	Thiamin diphosphate
THR	L-Threonine
THRTRNATHR	L-Threonyl-tRNA(Thr)
THZ	5-(2-Hydroxyethyl)-4-methylthiazole; 4-Methyl-5-(2'-hydroxyethyl)-thiazole; 4-Methyl-5-(2-hydroxyethyl)-thiazole
THZP	4-Methyl-5-(beta-hydroxyethyl)thiazole phosphate
TM	Thymine
TR	Taurine
TRE	alpha,alpha-Trehalose
TRE6P	alpha,alpha'-Trehalose 6-phosphate
TRM	Tyramine; 2-(p-Hydroxyphenyl)ethylamine
TRNAALA	tRNA(Ala)
TRNAARG	tRNA(Arg)
TRNAASP	tRNA(Asp)
TRNACYS	tRNA(Cys)
TRNAGLN	tRNA(Gln)
TRNAGLU	tRNA(Glu)
TRNAGLY	tRNA(Gly)
TRNAHIS	tRNA(His)
TRNAILE	tRNA(Ile)
TRNALEU	tRNA(Leu)
TRNALYS	tRNA(Lys)
TRNAMET	tRNA(Met)
TRNAPHE	tRNA(Phe)
TRNAPRO	tRNA(Pro)
TRNASER	tRNA(Ser)
TRNATHR	tRNA(Thr)
TRNATRP	tRNA(Trp)
TRNATYR	tRNA(Tyr)
TRNAVAL	tRNA(Val)
TRP	L-Tryptophan
TRPTRNATRP	L-Tryptophanyl-tRNA(Trp)
TRYTRNATYR	L-Tyrosyl-tRNA(Tyr)
TTA	(R,R)-Tartaric acid; (R,R)-Tartrate; L-Tartaric acid; Tartaric acid; Tartrate; 2,3-Dihydroxybutanedioic acid; (2R,3R)-Tartaric acid; (+)-Tartaric acid
TYR	L-Tyrosine
U1C	Urea-1-carboxylate; Allophanate; Allophanic acid
UC	Urocanate
UDCP	Undecaprenyl phosphate
UDCPP	Undecaprenyl diphosphate
UDGLYCOLATE	(-)-Ureidoglycolate; (S)-Ureidoglycolate
UDP	UDP
UDPAGLACA	UDP-N-acetyl-D-galactosamine
UDPG	UDP-glucose
UDPG23A	UDP-2,3-bis(3-hydroxytetradecanoyl)glucosamine
UDPG2A	UDP-3-O-(3-hydroxytetradecanoyl)glucosamine
UDPG2AA	UDP-3-O-(3-hydroxytetradecanoyl)-N-acetylglucosamine
UDPGAL	UDP-D-galactose
UDPGLUC	UDP-glucuronate
UDPMNLADGMD	UDP-N-acetylmuramoyl-L-alanyl-D-gamma-glutamyl-meso-2,6-diaminopimelate
UDPMNLADGMDDADA	UDP-N-acetylmuramoyl-L-alanyl-D-glutamyl-6-carboxy-L-lysyl-D-alanyl-D-alanine
UDPNADMA	UDP-N-acetyl-D-mannosamine
UDPNADMAU	UDP-N-acetyl-D-mannosaminouronate
UDPNAG	UDP-N-acetyl-D-glucosamine
UDPNAGEP	UDP-N-acetyl-3-(1-carboxyvinyl)-D-glucosamine
UDPNAM	UDP-N-acetylmuramate
UDPNAMA	UDP-N-acetylmuramoyl-L-alanine
UDPNAMAG	UDP-N-acetylmuramoyl-L-alanyl-D-glutamate
UMP	UMP
UPPMN(GN)LADGMDDADA	Undecaprenyl-diphospho-N-acetylmuramoyl-(N-acetylglucosamine)-L-alanyl-D-glutamyl-meso-2,6-diaminopimeloyl-D-alanyl-D-alanine
UPPMN(GN)LADGNMD(G)5DA	Undecaprenyl-diphospho-N-acetylmuramoyl-(N-acetylglucosamine)-L-alanyl-D-glutaminyl-meso-2,6-diaminopimeloyl-(glycyl)5-D-alanyl-D-alanine
UPPMN(GN)LADGNMDDADA	Undecaprenyl-diphospho-N-acetylmuramoyl-(N-acetylglucosamine)-L-alanyl-D-glutaminyl-meso-2,6-diaminopimeloyl-D-alanyl-D-alanine
UPPMNLADGMDDADA	Undecaprenyl-diphospho-N-acetylmuramoyl-L-alanyl-D-glutamyl-meso-2,6-diaminopimeloyl-D-alanyl-D-alanine
UPRG	Uroporphyrinogen III
UPRGI	Uroporphyrinogen I
UQ	Ubiquinone
UQH2	Ubiquinol
URA	Uracil
UREA	Urea
URI	Uridine
URT	Urate; Uric acid
UTP	UTP
VAL	L-Valine
VALTRNAVAL	L-Valyl-tRNA(Val)
VB12	Vitamin B12
X5P	D-Xylulose 5-phosphate
XAN	Xanthine
XMP	Xanthosine 5'-phosphate
XTP	XTP
XTSINE	Xanthosine
BIOMASS	Cell biomass
FRUxt	External D-fructose

Supplementary Table 3. Biomass composition of *Acinetobacter baumannii*. Abbreviations are shown in parenthesis next to each macromolecule.

Supplementary Table 3A. Macromolecular composition. Macromolecular composition of *A. baumannii* AYE was adopted from various sources, including its close species, *A. calcoaceticus*, *A. baylyi*, and other *Acinetobacter* species as well as *Escherichia coli*.

Component	Composition (g/g DCW)	References and comments
Protein (PROTEIN)	0.600	1
DNA (DNA)	0.030	2
RNA (RNA)	0.190	2
Phospholipids (PHOSPHOLIPID)	0.040	3
Fatty acids (LIPID)	0.020	1
Lipopolysaccharide (LPS)	0.005	4
Peptidoglycan (PEPTIDO)	0.027	4
Exopolysaccharide (EXOPOLYS)	0.038	5
Cofactors and vitamins (CAV)	0.030	-
Ash	0.019	Not included in the model
Sum	1.000	

Supplementary Table 3B. Amino acid composition. Amino acid composition was adopted from that of *E. coli* [6], based on the idea that amino acid composition does not affect enzyme and metabolite essentiality.

Amino acids	mmol/g protein
Alanine (ALA)	0.488
Arginine (ARG)	0.281
Asparagine (ASN)	0.229
Aspartate (ASP)	0.229
Cystein (CYS)	0.087
Glutamate (GLU)	0.250
Glutamine (GLN)	0.250
Glycine (GLY)	0.582
Histidine (HIS)	0.090
Isoleucine (ILE)	0.276
Leucine (LEU)	0.428
Lysine (LYS)	0.326
Methionine (MET)	0.146
Phenylalanine (PHE)	0.176
Proline (PRO)	0.210
Serine (SER)	0.205
Threonine (THR)	0.241
Tryptophan (TRP)	0.054
Tyrosine (TYR)	0.131
Valine (VAL)	0.402

Supplementary Table 3C. DNA composition. DNA composition was determined from the genomic sequence of *A. baumannii* AYE at Genome database of NCBI (http://www.ncbi.nlm.nih.gov/). GC content of *A. baumannii* AYE is 39% [7].

Nucleotide	mol/mol, DNA	MW, g/mol	mmol/g DNA
dAMP	0.305	313.2065	0.987
dGMP	0.195	329.2059	0.631
dCMP	0.195	289.1818	0.631
dTMP	0.305	304.1932	0.987

Supplementary Table 3D. RNA composition. It was assumed that mRNA makes up 5% and rRNA 80% of the total RNA. The rest was assumed to be tRNA [8].

Nucleotide	mol/mol RNA			MW, g/mol	mol/mol RNA	mmol/g RNA
	5% mRNA	80% rRNA	15% tRNA			
AMP	0.305	0.265	0.198	329.206	0.257	0.795
GMP	0.195	0.303	0.305	345.205	0.298	0.920
CMP	0.195	0.214	0.274	305.181	0.222	0.686
UMP	0.305	0.218	0.223	306.166	0.223	0.689

Supplementary Table 3E. Phospholipid composition [9].

Component	MW, g/mol, general structure	No. fatty acids	MW, g/mol, total phospholipids	mmol/g phospholipids
Cardiolipin (CL)[a]	508.219	4	1547.174	0.168
Phosphatidylethanolamine (PE)	269.146	2	788.623	0.548
Phosphatidylglycerol (PG)	300.157	2	819.634	0.302
L-1-Lysophosphatidylethanolamine (2AG3PE)	242.144	1	501.882	0.120

[a] Lysocardiolipin was also treated as cardiolipin as its molecular information was not available.

Supplementary Table 3F. Composition of fatty acids (LIPID) [10].

Fatty acid	g/g total fatty acids	MW, g/mol	mmol/g LIPID	mol/mol LIPID
C10:0 (C100ACP)	0.010	172.265	0.058	0.015
C12:0 (C120ACP	0.037	200.318	0.185	0.048
C14:0 (C140ACP)	0.003	228.371	0.013	0.003
C15:0 (C150ACP)	0.003	242.398	0.012	0.003
C16:0 (C160ACP)	0.276	256.424	1.082	0.281
C16:1 (C161ACP)[a]	0.188	254.408	0.740	0.192
C17:0 (C170ACP)	0.018	270.451	0.067	0.017
C17:1 (C171ACP)	0.016	268.435	0.060	0.016
C18:0 (C180ACP)	0.009	284.477	0.032	0.008
C18:1 (C181ACP)[b]	0.406	282.461	1.443	0.375
2-OH C12:0OH (C120OH)[c]	0.034	217.327	0.157	0.041

[a] C16:1(9t), C16:1(7c) and C16:1(9c) in Yamahira et al. (2008) are combined together.

[b] C18:1(9t) and C18:1(9c) in Yamahira et al. (2008) are combined together.

[c] 2-OH C12:0 and 3-OH C12:0 in Yamahira et al. (2008) are combined together.

Supplementary Table 3G. Lipopolysaccharide (LPS) composition [4, 11]. Metabolites included in AbyMBEL891 that closely resemble LPS components were selected for LPS formation: beta-D-glucose for glucose, UDP-N-acetyl-D-glucosamine for glucosamine, UDP-D-galactose for galactose and UDP-N-acetyl-D-galactosamine for galactosamine [11].

Component	Molar ratio	MW, g/mol	mmol/g LPS
2-Dehydro-3-deoxy-D-octonate (KDO)	1.0	238.192	0.182
beta-D-Glucose (bDGLC)[a]	4.5	180.156	0.821
UDP-D-galactose (UDPGAL)[a]	3.6	566.302	0.656
dTDP-L-rhamnose (DTDPRMNS)	0.1	548.330	0.018
UDP-N-acetyl-D-glucosamine (UDPNAG)[b]	2.0	607.354	0.365
UDP-N-acetyl-D-galactosamine (UDPAGLACA)[b]	1.4	607.354	0.255
Dodecanoic acid (C120ACP)[c]	0.2	199.308	0.037
Hexadecanoic acid (C160ACP)[c]	0.1	255.414	0.014
beta-hydroxy dodecanoic acid (C120OH)[c]	0.4	216.317	0.079
Octadecanoic acid (C180ACP)[c]	0.1	283.467	0.009
Octadecenoic acid (C181ACP)[c]	0.0	281.451	0.008
beta-hydroxy tetradecanoic acid (C140OH)[c]	0.4	245.218	0.071

[a] These two molecules account for hexoses of LPS in Thorne et al. (1973).

[b] These two molecules account for hexosamines of LPS in Thorne et al. (1973).

[c] These fatty acids account for total fatty acids of LPS in Thorne et al. (1973).

Supplementary Table 3H. Exopolysaccharide (EXOPOLYS) composition [5]. Similar to LPS formation, metabolites included in AbyMBEL891 that closely resemble EXOPOLYS components were selected for its formation: dTDP-L-rhamnose for rhamnose, beta-D-Glucose for glucose and GDP-mannose for mannose.

Component	Relative sugar composition (%, w/w)	MW, g/mol	mmol/g EXOPOLYS
dTDP-L-rhamnose (DTDPRMNS)	0.459	164.157	2.794
beta-D-Glucose (bDGLC)	0.381	180.156	2.117
GDP-mannose (GDPMAN)	0.160	603.325	0.265

Supplementary Table 3I. Cofactors and vitamins (CAV) incorporated in the biomass. Cofactors and vitamins are assumed to be the same ratio (w/w).

Molecule	MW, g/mol	g/g CAV	mmol/g CAV
Coenzyme A (COA)	767.535	0.125	0.163
Flavin adenine dinucleotide (FAD)	785.550	0.125	0.159
Flavin mononucleotide (FMN)	456.344	0.125	0.274
Menaquinone (MK)	308.414	0.125	0.405
NAD	664.433	0.125	0.188
NADP	744.413	0.125	0.168
Pyridoxine (PYRDX)	169.178	0.125	0.739
Tetrahydrofolate (THF)	445.430	0.125	0.281

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Supplementary Table 4. List of 246 essential reactions predicted under minimal medium with succinate as a sole carbon source. Information of each reaction is available in Supplementary Table 1.

Reaction number of essential enzymes
R001, R005, R006, R007, R008, R009, R010, R011, R012, R019, R020, R021, R025, R030, R031, R033, R035, R036, R044, R045, R046, R049, R050, R052, R053, R055, R056, R057, R058, R062, R063, R066, R068, R069, R070, R071, R095, R108, R143, R156, R157, R158, R159, R160, R162, R163, R164, R165, R167, R169, R171, R172, R174, R175, R176, R177, R178, R179, R183, R184, R185, R186, R187, R188, R189, R190, R191, R192, R203, R227, R231, R232, R234, R235, R237, R238, R239, R244, R245, R246, R248, R249, R250, R251, R252, R253, R254, R255, R256, R257, R258, R277, R278, R279, R281, R282, R299, R300, R303, R304, R305, R309, R310, R311, R312, R313, R314, R316, R320, R327, R328, R329, R331, R338, R346, R352, R356, R357, R361, R364, R375, R381, R382, R384, R413, R414, R415, R416, R417, R418, R421, R422, R423, R428, R431, R432, R433, R434, R435, R465, R466, R467, R468, R469, R470, R471, R472, R473, R501, R523, R524, R525, R526, R527, R528, R529, R532, R533, R534, R538, R539, R541, R548, R549, R550, R554, R555, R556, R557, R558, R559, R560, R571, R572, R591, R593, R608, R609, R610, R612, R613, R614, R615, R616, R617, R618, R619, R620, R621, R622, R632, R633, R634, R635, R636, R637, R638, R639, R640, R642, R643, R644, R646, R647, R648, R649, R651, R655, R656, R662, R665, R672, R673, R674, R675, R678, R679, R680, R681, R688, R690, R692, R693, R696, R708, R737, R745, R746, R747, R748, R749, R750, R753, R754, R755, R756, R757, R758, R759, R760, R761, R789, R791, R793, R796, R826

Supplementary Table 5. List of 681 reactions considered for comparison of their essentiality in AbyMBEL891 with those from *Acinetobacter baylyi* ADP1, which ultimately gave simulation-based prediction consistency of 72%. If essentiality of a reaction, either essential or non-essential, from AbyMBEL891 and ADP1 is the same, then they were considered consistent. This simulation was conducted under minimal medium with succinate as a sole carbon source. Information of each reaction is available in Supplementary Table 1.

Reaction number of essential enzymes considered for comparative study
R001, R002, R003, R004, R005, R006, R007, R008, R009, R010, R012, R013, R014, R015, R017, R018, R019, R020, R021, R022, R023, R024, R028, R030, R031, R034, R037, R038, R039, R040, R043, R044, R045, R047, R048, R049, R050, R053, R054, R056, R057, R058, R062, R063, R065, R066, R067, R068, R069, R070, R071, R072, R073, R074, R075, R076, R077, R078, R081, R082, R083, R084, R085, R088, R089, R090, R091, R092, R093, R094, R096, R097, R098, R101, R102, R103, R104, R106, R107, R110, R111, R112, R113, R115, R118, R119, R120, R121, R122, R123, R124, R125, R128, R129, R130, R131, R133, R135, R136, R137, R139, R140, R141, R142, R143, R144, R145, R146, R147, R148, R149, R150, R153, R154, R155, R156, R159, R160, R161, R162, R193, R194, R195, R196, R197, R198, R199, R200, R202, R203, R204, R208, R213, R215, R218, R219, R220, R221, R222, R223, R224, R225, R226, R228, R229, R230, R232, R233, R234, R235, R236, R237, R238, R240, R241, R242, R244, R245, R246, R247, R248, R249, R251, R252, R253, R254, R255, R256, R257, R258, R259, R260, R261, R262, R263, R264, R265, R266, R267, R268, R269, R273, R274, R275, R276, R277, R278, R279, R280, R281, R282, R284, R285, R286, R287, R289, R291, R298, R299, R303, R304, R305, R306, R307, R308, R309, R310, R312, R313, R314, R315, R316, R317, R318, R321, R322, R324, R325, R326, R327, R328, R329, R331, R332, R333, R338, R339, R340, R341, R342, R343, R344, R345, R347, R348, R349, R350, R351, R352, R353, R354, R355, R356, R357, R358, R359, R361, R362, R364, R365, R366, R367, R369, R371, R372, R373, R374, R375, R376, R377, R378, R380, R382, R384, R385, R386, R387, R388, R389, R390, R391, R392, R393, R394, R396, R397, R398, R399, R400, R401, R402, R404, R405, R407, R408, R409, R411, R412, R413, R414, R415, R418, R419, R420, R421, R422, R424, R425, R426, R427, R428, R429, R430, R431, R433, R434, R435, R436, R437, R438, R439, R440, R441, R444, R445, R446, R447, R448, R449, R450, R451, R452, R453, R454, R455, R456, R457, R458, R459, R460, R461, R462, R465, R467, R468, R469, R470, R471, R473, R475, R476, R481, R483, R484, R487, R488, R489, R490, R491, R492, R493, R494, R495, R497, R498, R499, R500, R501, R503, R504, R505, R507, R508, R509, R510, R512, R515, R516, R517, R518, R522, R523, R524, R525, R526, R527, R529, R530, R531, R533, R534, R535, R536, R537, R538, R539, R540, R542, R543, R544, R545, R546, R547, R549, R551, R552, R553, R554, R555, R556, R557, R558, R559, R560, R563, R564, R565, R566, R567, R569, R571, R572, R574, R577, R579, R581, R583, R584, R585, R586, R587, R588, R589, R590, R591, R592, R593, R594, R595, R596, R597, R598, R602, R603, R604, R605, R606, R607, R608, R609, R610, R611, R612, R613, R614, R615, R616, R617, R622, R623, R624, R625, R628, R629, R630, R632, R633, R634, R635, R636, R637, R638, R639, R640, R642, R643, R644, R645, R646, R648, R649, R650, R651, R652, R653, R654, R655, R656, R657, R658, R659, R660, R662, R663, R664, R665, R666, R667, R668, R669, R670, R672, R674, R675, R676, R677, R679, R680, R681, R682, R683, R684, R686, R687, R688, R689, R690, R692, R693, R694, R695, R696, R697, R698, R699, R700, R701, R702, R703, R704, R705, R706, R710, R711, R712, R714, R715,

R717, R718, R720, R721, R722, R723, R724, R727, R728, R733, R734, R735, R736, R737, R738, R739, R740, R741, R742, R743, R744, R749, R750, R751, R752, R763, R764, R765, R766, R767, R768, R769, R770, R771, R772, R773, R774, R775, R776, R777, R778, R779, R780, R781, R782, R783, R784, R785, R786, R787, R788, R789, R790, R791, R792, R793, R794, R795, R796, R797, R798, R799, R800, R801, R802, R803, R804, R805, R806, R807, R808, R809, R810, R811, R812, R813, R814, R815, R816, R817, R818, R819, R820, R821, R822, R823, R824, R825, R826, R827, R828, R829, R830, R831, R832, R833, R834, R835, R836, R837, R838, R839, R840, R841, R842, R843, R844, R845, R846, R847, R848, R849, R850, R851, R852, R853, R854, R855, R856, R857, R858, R859, R860, R861, R862, R863, R864, R865, R866, R867, R868, R869, R870, R871, R872, R873, R874, R875, R876, R877, R878, R879, R880, R881, R882, R883, R884, R885, R886, R887, R888, R889, R890, R891

Supplementary Table 6. List of 162 essential reactions predicted under arbitrary complex medium.

Reaction number of essential enzymes
R001, R005, R006, R030, R031, R033, R035, R036, R044, R045, R046, R049, R050, R055, R056, R057, R058, R062, R063, R066, R068, R069, R070, R071, R095, R108, R143, R162, R163, R164, R165, R167, R169, R171, R172, R174, R175, R176, R177, R178, R179, R183, R184, R185, R186, R187, R188, R189, R190, R191, R192, R203, R227, R231, R232, R234, R235, R237, R238, R239, R244, R255, R256, R258, R278, R279, R282, R305, R309, R310, R311, R312, R313, R314, R316, R320, R328, R329, R331, R364, R381, R428, R431, R432, R433, R434, R523, R524, R525, R526, R527, R528, R529, R571, R572, R593, R608, R609, R610, R612, R613, R614, R615, R616, R617, R618, R619, R620, R621, R622, R632, R633, R634, R635, R636, R637, R638, R639, R640, R642, R643, R644, R646, R647, R648, R649, R651, R655, R656, R662, R665, R672, R673, R674, R675, R678, R679, R680, R681, R688, R690, R692, R693, R696, R737, R745, R746, R747, R748, R749, R750, R753, R754, R755, R756, R757, R758, R759, R760, R761, R789, R796

Supplementary Table 7. List of 211 essential metabolites predicted under arbitrary complex medium. Full name of each essential metabolite is available in Supplementary Table 2.

Filtering criteria	**Essential metabolites**
Final 9 candidates selected from filtering framework	AHHMP, DGLU, DHDP, DHP, DHSK, DX5P, DQT, KDO, PABA
Association with enzymes homologous to human proteome (13 essential metabolites removed)	ASPSA, C120OH, C140OH, C171ACP, CHOR, DMK, MDAPIM, MK, MKH2, OPP, PHT, PPAACP, SME
Presence in human metabolism (75 essential metabolites removed)	ACACP, ACCOA, ACP, AHTD, ARG, ASN, ASP, bALA, bDGLC, C100ACP, C120ACP, C140ACP, C150ACP, C160ACP, C161ACP, C170ACP, C180ACP, C181ACP, CDPDG, CYS, DADP, DALA, DCDP, DCTP, DGDP, DGTP, DHAP, DHF, DTDP, DTDPGLU, DTDPRMNS, DTMP, DTTP, DUMP, E4P, F6P, FDP, FMN, G1P, G3P, G6P, GL3P, GLC, GLY, HCO3, HIS, ILE, LEU, LYS, MALACP, MET, NAAD, NACN, OBUT, OIVAL, PE, PEP, PG, PHE, PL, PPACOA, PRO, PRPP, PS, R5P, RL5P, SER, SUCCOA, THR, TRP, TYR, UDPG, UDPNAG, VAL, XMP
Association with less than 3 reactions or 2 consuming reactions (82 essential metabolites removed)	2AG3PE, 3A2OP, 3DDAH7P, 3PSME, 4PPNCYS, 4PPNTE, 4PPNTO, 5MC, A5P, A6RP, A6RP5P, A6RP5P2, ADCHOR, AGL3P, ALAALA, ASUC, CAV, CL, D6RP5P, D8RL, DAPIM, DATP, DB4P, DHN, DHPANT, DHPT, DNA, DPCOA, DT, DTDP4O6DG, DTDP4ORMNS, ER4P, EXOPOLYS, GA1P, GA6P, GDPMAN, IASP, ICHOR, KDOP, LIPID, LPS, MALCOA, MAN1P, MAN6P, NAGA1P, OHB, OSB, OSBCOA, P5P, PA, PANT, PEPTIDO, PGP, PHOSPHOLIPID, PL5P, PNTO, PPEPTIDO, PROTEIN, PYRDX, QA, RIBFLAV, RNA, SAOPIM, SDAPIM, SHCHC, SME3P, TDHDP, TM, UDCP, UDCPP, UDPAGLACA, UDPGAL, UDPMNLADGMD, UDPMNLADGMDDADA, UDPNAGEP, UDPNAM, UDPNAMA, UDPNAMAG, UPPMN(GN)LADGMDDADA, UPPMN(GN)LADGNMD(G)5DADA, UPPMN(GN)LADGNMDDADA, UPPMNLADGMDDADA
Currency metabolites (32 essential metabolites removed)	ADP, AKG, ALA, AMP, ATP, CDP, CO2, COA, CTP, FAD, GDP, GLN, GLU, GMP, GTP, H2O2, IMP, METTHF, NAD, NADP, NADPH, NH3, O2, OTHIO, PI, PYR, RTHIO, SAM, THF, UDP, UMP, UTP