

**Supplementary Table 1** Key enzymes of surfactin biosynthesis module

EC	KEGG Orthology	Symbol	Name
Nonribosomal peptide synthetase (NRPS)			
	K15654	<i>srfAA</i>	surfactin family lipopeptide synthetase A
	K15655	<i>srfAB</i>	surfactin family lipopeptide synthetase B
	K15656	<i>srfAC</i>	surfactin family lipopeptide synthetase C
	K15657	<i>srfATE</i> , <i>srfAD</i> , <i>lchAD</i>	external thioesterase TE II
Surfactin Transcriptional factor			
	K02253	<i>comX</i>	competence protein ComX
	K02251	<i>comQ</i>	competence protein ComQ
EC:2.7.13.3	K07680	<i>comP</i>	two-component system, NarL family, sensor histidine kinase ComP
	K07691	<i>comA</i>	two-component system, NarL family, competent response regulator ComA
	K02252	<i>comS</i>	competence protein ComS
	K02250	<i>comK</i>	competence protein ComK
	K06352	<i>phrA</i>	phosphatase RapA regulator
	K06353	<i>phrC</i>	phosphatase RapC regulator
	K06354	<i>phrE</i>	phosphatase RapE regulator
	K06355	<i>phrF</i>	phosphatase RapF regulator
	K06356	<i>phrG</i>	phosphatase RapG regulator
	K06358	<i>phrK</i>	phosphatase RapK regulator
	K20389	<i>phrH</i>	phosphatase RapH inhibitor
EC:2.3.1.184	K22968	<i>sinI</i>	acyl homoserine lactone synthase
	K07699	<i>spo0A</i>	two-component system, response regulator, stage 0 sporulation protein A
EC:2.7.-.-	K06375	<i>spo0B</i>	stage 0 sporulation protein B (sporulation initiation phosphotransferase)
	K02490	<i>spo0F</i>	two-component system, response regulator, stage 0 sporulation protein F
EC:7.4.2.8	K03070	<i>secA</i>	preprotein translocase subunit SecA
	K03071	<i>secB</i>	preprotein translocase subunit SecB
	K03073	<i>secE</i>	preprotein translocase subunit SecE

---

	K03075	<i>secG</i>	preprotein translocase subunit SecG
	K03076	<i>secY</i>	preprotein translocase subunit SecY
EC:3.1.-.-	K06361	<i>rapC</i>	response regulator aspartate phosphatase C
EC:3.1.-.-	K06364	<i>rapF</i>	response regulator aspartate phosphatase F
EC:3.1.-.-	K06369	<i>rapK</i>	response regulator aspartate phosphatase K
	K15580	<i>oppA</i> , <i>mppA</i>	oligopeptide transport system substrate-binding protein
	K15581	<i>oppB</i>	oligopeptide transport system permease protein
	K15582	<i>oppC</i>	oligopeptide transport system permease protein
	K15583	<i>oppD</i>	oligopeptide transport system ATP- binding protein
	K07692	<i>degU</i>	two-component system, NarL family, response regulator DegU

---

**Supplementary Table 2** Key enzymes of branched chain amino acids module

EC	KEGG Orthology	Symbol	Name
Branched chain amino acids biosynthesis			
EC:2.2.1.6	K01652	<i>ilvB</i> , <i>ilvG</i> , <i>ilvI</i>	acetolactate synthase I/II/III large subunit
EC:2.2.1.6	K01653	<i>ilvH</i> , <i>ilvN</i>	acetolactate synthase I/III small subunit
EC:2.2.1.6	K11258	<i>ilvM</i>	acetolactate synthase II small subunit
EC:1.1.1.86	K00053	<i>ilvC</i>	ketol-acid reductoisomerase
EC:4.2.1.9	K01687	<i>ilvD</i>	dihydroxy-acid dehydratase
EC:2.6.1.42	K00826	<i>ilvE</i>	branched-chain amino acid aminotransferase
Branched chain amino acids degradation			
EC:1.2.4.4	K00166	<i>BCKDHA</i> , <i>bkdA1</i>	2-oxoisovalerate dehydrogenase E1 component alpha subunit
EC:1.2.4.4	K00167	<i>BCKDHB</i> , <i>bkdA2</i>	2-oxoisovalerate dehydrogenase E1 component beta subunit
EC:1.2.4.4	K11381	<i>bkdA</i>	2-oxoisovalerate dehydrogenase E1 component
EC:2.3.1.168	K09699	<i>DBT</i> , <i>bkdB</i>	2-oxoisovalerate dehydrogenase E2 component
EC:1.8.1.4	K00382	<i>DLD</i> , <i>lpd</i> , <i>pdhD</i>	dihydrolipoamide dehydrogenase
EC:1.3.8.4	K00253	<i>IVD</i> , <i>ivd</i>	isovaleryl-CoA dehydrogenase
EC:1.3.8.7	K00249	<i>ACADM</i> , <i>acd</i>	acyl-CoA dehydrogenase
EC:4.2.1.18	K05607	<i>AUH</i>	methylglutaconyl-CoA hydratase
EC:4.2.1.18	K13766	<i>liuC</i>	methylglutaconyl-CoA hydratase
EC:4.1.3.4	K01640	<i>HMGCL</i> , <i>hmgL</i>	hydroxymethylglutaryl-CoA lyase

**Supplementary Table 3** Key enzymes of branched chain fatty acids biosynthesis module

EC	KEGG Orthology	Symbol	Name
Fatty acid biosynthesis, initiation			
EC:6.4.1.2 6.3.4.14 2.1.3.15	K11262	<i>ACACA</i>	acetyl-CoA carboxylase/biotin carboxylase 1
	K02160	<i>accB, bccP</i>	acetyl-CoA carboxylase biotin carboxyl carrier protein
EC:6.4.1.2 6.3.4.14	K01961	<i>accC</i>	acetyl-CoA carboxylase, biotin carboxylase subunit
EC:6.4.1.2 2.1.3.15	K01962	<i>accA</i>	acetyl-CoA carboxylase carboxyl transferase subunit alpha
EC:6.4.1.2 2.1.3.15	K01963	<i>accD</i>	acetyl-CoA carboxylase carboxyl transferase subunit beta
EC:6.4.1.2 6.4.1.3 6.3.4.14	K11263	<i>bccA, pccA</i>	acetyl-CoA/propionyl-CoA carboxylase, biotin carboxylase, biotin carboxyl carrier protein
EC:6.4.1.2 6.4.1.3 2.1.3.15	K18472	<i>accD6</i>	acetyl-CoA/propionyl-CoA carboxylase carboxyl transferase subunit
EC:2.3.1.-	K11533	<i>fas</i>	fatty acid synthase
EC:2.3.1.39	K00645	<i>fabD, MCAI, MCTI</i>	[acyl-carrier-protein] S-malonyltransferase
EC:2.3.1.180	K00648	<i>fabH</i>	3-oxoacyl-[acyl-carrier-protein] synthase III
EC:2.3.1.180	K18473	<i>fabY</i>	acetoacetyl-[acyl-carrier-protein] synthase
Fatty acid biosynthesis, elongation			
EC:2.3.1.-	K11533	<i>fas</i>	fatty acid synthase
EC:2.3.1.41	K00647	<i>fabB</i>	3-oxoacyl-[acyl-carrier-protein] synthase I
EC:2.3.1.179	K09458	<i>fabF, OXSM, CEMI</i>	3-oxoacyl-[acyl-carrier-protein] synthase II
EC:1.1.1.100	K00059	<i>fabG, OARI</i>	3-oxoacyl-[acyl-carrier-protein] reductase
EC:4.2.1.59	K02372	<i>fabZ</i>	3-hydroxyacyl-[acyl-carrier-protein] dehydratase
EC:4.2.1.59 5.3.3.14	K01716	<i>fabA</i>	3-hydroxyacyl-[acyl-carrier-protein] dehydratase/trans-2-decenoyl-[acyl-carrier protein] isomerase

EC:3.5.1.108 4.2.1.59	K16363	<i>lpxC-fabZ</i>	UDP-3-O-[3- hydroxymyristoyl] N- acetylglucosamine deacetylase/3-hydroxyacyl- [acyl-carrier-protein] dehydratase
EC:1.3.1.9 1.3.1.10	K00208	<i>fabI</i>	enoyl-[acyl-carrier protein] reductase I
EC:1.3.1.9	K02371	<i>fabK</i>	enoyl-[acyl-carrier protein] reductase II
EC:1.3.1.104	K10780	<i>fabL</i>	enoyl-[acyl-carrier protein] reductase III
EC:1.3.1.9 1.3.1.44	K00209	<i>fabV, ter</i>	enoyl-[acyl-carrier protein] reductase/trans-2-enoyl-CoA reductase (NAD <sup>+</sup> )
Fatty acid biosynthesis, termination			
EC:6.2.1.3	K01897	<i>ACSL, fadD</i>	long-chain acyl-CoA synthetase
EC:6.2.1.3	K15013	<i>ACSBG</i>	long-chain-fatty-acid-CoA ligase ACSBG

6

**Supplementary Table 4** Key enzymes of central carbohydrate biosynthesis module

EC	KEGG Orthology	Symbol	Name
Glycolysis			
EC:2.7.1.1	K00844	<i>HK</i>	hexokinase
EC:2.7.1.2	K12407	<i>GCK</i>	glucokinase
EC:2.7.1.2	K00845	<i>glk</i>	glucokinase
EC:2.7.1.63	K00886	<i>ppgK</i>	polyphosphate glucokinase
EC:2.7.1.147	K08074	<i>ADPGK</i>	ADP-dependent glucokinase
EC:2.7.1.146 2.7.1.147	K00918	<i>pfkC</i>	ADP-dependent phosphofructokinase/glucokinase
EC:2.7.1.146 2.7.1.147	K01810	<i>GPI, pgi</i>	glucose-6-phosphate isomerase
EC:2.2.1.2 5.3.1.9	K13810	<i>tal-pgi</i>	transaldolase/glucose-6-phosphate isomerase
EC:5.3.1.9 5.3.1.8	K15916	<i>pgi-pmi</i>	glucose/mannose-6-phosphate isomerase
EC:2.7.1.11	K00850	<i>pfkA, PFK</i>	6-phosphofructokinase 1
EC:2.7.1.11	K16370	<i>pfkB</i>	6-phosphofructokinase 2
EC:2.7.1.11 2.7.1.90	K21071	<i>pfk, pfp</i>	ATP-dependent phosphofructokinase/diphosphate- dependent phosphofructokinase
EC:2.7.1.146 2.7.1.147	K00918	<i>pfkC</i>	ADP-dependent phosphofructokinase/glucokinase
EC:4.1.2.13	K01623	<i>ALDO</i>	fructose-bisphosphate aldolase, class I
EC:4.1.2.13	K01624	<i>FBA, fbaA</i>	fructose-bisphosphate aldolase, class II
EC:4.1.2.13	K11645	<i>fbaB</i>	fructose-bisphosphate aldolase, class I
EC:5.3.1.1	K01803	<i>TPI, tpiA</i>	triosephosphate isomerase (TIM)
EC:1.2.1.12	K00134	<i>GAPDH, gapA</i>	glyceraldehyde 3-phosphate dehydrogenase
EC:1.2.1.59	K00150	<i>gap2</i>	glyceraldehyde-3-phosphate dehydrogenase (NAD(P))
EC:2.7.2.3	K00927	<i>PGK, pgk</i>	phosphoglycerate kinase
EC:1.2.7.6	K11389	<i>gapor</i>	glyceraldehyde-3-phosphate dehydrogenase (ferredoxin)
EC:5.4.2.11	K01834	<i>PGAM, gpmA, gpmI, gpmB, apgM</i>	2,3-bisphosphoglycerate-dependent phosphoglycerate mutase
EC:4.2.1.11	K01689	<i>ENO, eno</i>	enolase
EC:2.7.1.40	K00873	<i>PK, pyk</i>	pyruvate kinase
EC:2.7.1.40	K12406	<i>PKLR</i>	pyruvate kinase isozymes R/L
Citrate cycle			
EC:2.3.3.1	K01647	<i>CS, gltA</i>	citrate synthase
EC:4.2.1.3	K01681	<i>ACO, acnA</i>	aconitate hydratase

EC:4.2.1.3			aconitate hydratase 2/2-
4.2.1.99	K01682	<i>acnB</i>	methylisocitrate dehydratase
EC:1.1.1.42	K00031	<i>IDH1, IDH2, icd</i>	isocitrate dehydrogenase
EC:1.1.1.41	K00030	<i>IDH3</i>	isocitrate dehydrogenase (NAD <sup>+</sup> )

---

8