Table S1 Proteins with predicted extracellular localization produced by soil bacterial community during growth in minimal medium supplemented with suberin, from 5 to 60 days

UniProt or UniRef accession number	Bacterial species	Putative function	Abundance (NSpC)				
			5 d	10 d	20 d	30 d	60 d
Amino acid metabolism							
A3KZ66 [a,b]	*Pseudomonas* spp.	Pvds-regulated endoprotease	-[c]	0.67	0.80	0.73	-
C3K3P0 [b]	*Pseudomonas* spp.	dihydroxy-acid dehydratase	0.03	-	-	-	-
C3K6V7 [b]	*Pseudomonas* spp.	protease	0.15	-	-	-	-
C3K907	*Pseudomonas fluorescens*	protease	0.08	-	-	-	-
E1T7C4	*Burkholderia* sp.	ArgE, acetylornithine deacetylase	-	0.04	-	-	-
F2LE35	*Burkholderia gladioli*	protease	-	0.12	-	-	-
J2YKE9	*Pseudomonas* sp.	dipeptidase	0.06	-	-	-	-
P34816	*Pseudomonas syringae*	tryptophan synthase	0.11	-	-	-	-
Carbohydrate metabolism							
A3ML77 [a,b]	*Burkholderia* spp.	enolase	-	0.11	-	-	-
C3K5I7	*Pseudomonas fluorescens*	malate:quinone oxidoreductase	0.03	-	-	-	-
C9ZE95	*Streptomyces scabiei*	xylanase A	-	-	0.08	-	-
UPI000289064F	*Pseudomonas* sp.	malic enzyme	0.29	0.09	-	-	-
Cell wall, membrane and envelope biogenesis							
A6BTB9 [a,b]	*Yersinia* spp.	peptidoglycan-associated lipoprotein	0.22	-	-	-	-
A8F2R2 [b]	*Rickettsia* spp.	peptidoglycan-associated lipoprotein	-	-	-	0.11	0.33
A9W4H1 [b]	*Methylobacterium* spp.	BamA	-	-	-	-	0.03
A9Z1A5	*Acinetobacter baumannii*	outer membrane protein A	0.19	-	-	-	-
B1FWC4 [b]	*Burkholderia* spp.	peptidoglycan-associated lipoprotein	-	0.53	-	-	-
B2JGA1 [b]	*Burkholderia* spp.	peptidoglycan-associated lipoprotein	-	0.61	-	-	-
C3JYS2 [b]	*Pseudomonas* spp.	TolB	0.13	0.04	-	-	-
C3K1L1	*Pseudomonas fluorescens*	BamB	0.20	-	-	-	-
C3K324	*Pseudomonas fluorescens*	LptD	0.05	-	-	-	-
C3KBX8 [b]	*Pseudomonas* spp.	OmpA family-lipoprotein	0.33	-	-	-	-
C3KDM6 [b]	*Pseudomonas* spp.	phosphatidylserine decarboxylase	0.06	-	-	-	-
E2XZ64	*Pseudomonas fluorescens*	SurA	0.06	-	-	-	-
G8M7G2	*Burkholderia* sp.	TolB	-	0.16	-	-	-
J0YEJ9 [b]	*Pseudomonas* spp.	peptidoglycan-associated lipoprotein	2.11	1.11	-	-	-
J2M1D5 [b]	*Pseudomonas* spp.	outer membrane protein H1	0.10	-	-	-	-
L7HFX4 [b]	*Pseudomonas* spp.	BamD	0.10	-	-	-	-
O85417	*Pseudomonas caricapapayae*	outer membrane lipoprotein I	-	-	-	0.56	-
UPI00028991C8	*Pseudomonas extremaustralis*	flagellin	0.78	-	-	-	-

Energy production and conversion							
B1FT18 [b]	*Burkholderia* spp.	PQQ-dependent dehydrogenase	-	0.12	-	-	-
B1FV46 [b]	*Burkholderia* spp.	malate dehydrogenase	-	0.34	-	-	-
C3K121 [b]	*Pseudomonas* spp.	phosphoenolpyruvate synthase	0.11	-	-	-	-
C3K1E7 [b]	*Pseudomonas* spp.	ATP synthase, gamma chain	0.13	-	-	-	-
C3K6M5 [b]	*Pseudomonas* spp.	succinate dehydrogenase flavoprotein subunit	0.09	-	-	-	-
C3KBL8	*Pseudomonas fluorescens*	aerobic glycerol-3-phosphate dehydrogenase	0.17	-	-	-	-
C3KCP3	*Pseudomonas fluorescens*	acetyltransferase	0.30	0.18	-	-	-
C3KE78	*Pseudomonas fluorescens*	azurin	0.31	-	-	-	-
I2BM47 [b]	*Pseudomonas* spp.	electron transfer flavoprotein, beta subunit	0.46	0.08	-	-	-
J1IL09 [b]	*Pseudomonas* spp.	UDP-glucose 6-dehydrogenase	0.08	-	-	-	-
Lipid metabolism and ketogenesis							
A9IIX3 [a,b]	*Bordetella* spp.	acetoacetyl-CoA reductase	-	0.19	-	-	-
C3JZ29 [b]	*Pseudomonas* spp.	glycerophosphoryl diester phosphodiesterase	0.07	-	-	-	-
C3K743 [b]	*Pseudomonas* spp.	3-hydroxydecanoyl-[acyl-carrier-protein] dehydratase	0.16	-	-	-	-
I4WGM2	*Rhodanobacter thiooxydans*	lipase	-	-	-	-	0.11
J0YBC2 [b]	*Pseudomonas* spp.	Yce1-like protein	-	0.14	-	-	-
Q1CWS1	*Myxococcus xanthus*	lipase	-	-	0.02	-	-
Replication, transcription, translation and DNA repair							
A2W9A3 [a,b]	*Burkholderia* spp.	elongation factor Ts	-	0.10	-	-	-
A4SUU7 [a,b]	*Polynucleobacter necessarius*	elongation factor Tu	-	0.35	-	-	-
A4VHN7 [a,b]	*Pseudomonas* spp.	50S ribosomal protein L16	0.27	-	-	-	-
A4VHP0 [a,b]	*Pseudomonas* spp.	50S ribosomal protein L14	0.15	-	-	-	-
A5VXR4 [b]	*Pseudomonas* spp.	30S ribosomal protein S5	0.61	0.17	-	-	-
A9ADK4 [a,b]	*Burkholderia* spp.	50S ribosomal protein L24	-	0.27	-	-	-
B2JHS8 [b]	*Burkholderia* spp.	LacI, transcriptional regulator	-	0.17	-	-	-
B2T724 [b]	*Burkholderia* spp.	50S ribosomal protein L17	-	0.13	-	-	-
B2T750 [b]	*Burkholderia* spp.	50S ribosomal protein L4	-	0.17	-	-	-
C1DKN6 [b]	*Pseudomonas* spp.	30S ribosomal protein S11	0.43	-	-	-	-
C3JXX2 [b]	*Pseudomonas* spp.	ATP-dependent RNA helicase	0.06	-	-	-	-
C3K2V7 [b]	*Pseudomonas* spp.	50S ribosomal protein L15	0.33	-	-	-	-
C3K3H0 [b]	*Pseudomonas* spp.	RNA helicase	0.03	-	-	-	-
C3KC10	*Pseudomonas fluorescens*	LemA, virulence regulator	0.22	-	-	-	-
C3KCS0	*Pseudomonas fluorescens*	50S ribosomal protein L25	0.18	-	-	-	-
C3KE70 [b]	*Pseudomonas* spp.	50S ribosomal protein L9	0.27	0.20	-	-	-
C5A9H1	*Burkholderia glumae*	30S ribosomal protein S14	-	0.50	-	-	-

E2XL76 [b]	*Pseudomonas* spp.	GTP-binding protein	0.08	-	-	-	-
E7PK79	*Pseudomonas syringae*	30S ribosomal protein S9	0.27	-	-	-	-
I2BR39	*Pseudomonas fluorescens*	ribosomal protein L25	0.33	-	-	-	-
K8R288	*Burkholderia* sp.	transcription accessory protein	-	0.08	-	-	-
Stress and defense mechanisms							
A0K6C2 [a,b]	*Burkholderia* spp.	FtsH, metalloprotease	-	0.04	-	-	-
C3K1W9 [b]	*Pseudomonas* spp.	thioredoxin reductase	0.21	-	-	-	-
C3K275	*Pseudomonas fluorescens*	DnaK	0.20	0.07	-	-	-
C3KB07 [b]	*Pseudomonas* spp.	peroxidase	0.08	-	-	-	-
C3KDG0 [b]	*Pseudomonas* spp.	RecA	0.21	-	-	-	-
E2XRC5	*Pseudomonas fluorescens*	thiol peroxidase	0.22	-	-	-	-
E2XY77	*Pseudomonas fluorescens*	hyperosmotically inducible periplasmic protein	0.71	-	-	-	-
E2XY89 [b]	*Pseudomonas* spp.	FtsH, metalloprotease	0.05	-	-	-	-
I2BQB7 [b]	*Pseudomonas* spp.	cold-shock DEAD box protein A	0.07	-	-	-	-
I4L9S5	*Pseudomonas synxantha*	DnaK	-	0.13	-	-	-
Transport, secretion and efflux							
A0K2W2 [a,b]	*Burkholderia* spp.	amino acid/amide ABC transporter	-	0.14	-	-	-
A1TUU8 [a,b]	*Acidovorax* spp.	monosaccharide ABC transporter	-	0.15	-	-	-
A1WC85 [a,b]	*Acidovorax* spp.	porin	-	-	-	0.17	0.25
A2VY88 [a,b]	*Burkholderia* spp.	cation/multidrug efflux pump	-	0.02	-	-	-
A5V8N4 [a]	*Sphingomonas wittichii*	TonB-dependent receptor	-	-	-	-	0.02
A8GAT7 [a]	*Serratia proteamaculans*	metal ABC transporter	0.16	-	-	-	-
A8GB28 [a,b]	*Serratia* spp.	amino acid transporter	0.09	-	-	-	-
A8GCJ4 [a]	*Serratia proteamaculans*	porin	0.34	-	-	-	-
A8GH34 [b]	*Serratia* spp.	cationic amino acid ABC transporter	0.11	-	-	-	-
A9VYY1 [b]	*Methylobacterium* spp.	porin	-	-	-	-	0.05
B0KQ05 [b]	*Pseudomonas* spp.	sulfate ABC transporter	0.24	-	-	-	-
B1FY32 [b]	*Burkholderia* spp.	OmpC family porin	-	0.18	-	-	0.15
B1G0N8	*Burkholderia graminis*	porin	-	-	-	-	0.19
B1GB98	*Burkholderia graminis*	porin	-	-	-	0.20	0.48
B1LV39	*Methylobacterium radiotolerans*	porin	-	-	-	-	0.10
B1ZFK7 [b]	*Methylobacterium* spp.	porin	-	-	0.30	-	-
B2JH03 [b]	*Burkholderia* spp.	monosaccharide-transporting ATPase	-	0.26	-	-	-
B2JK19 [b]	*Burkholderia* spp.	extracellular amino acid-binding receptor	-	1.50	-	-	-
B2JM60	*Burkholderia* spp.	porin	-	-	-	-	0.08
B2T4D9	*Burkholderia phytofirmans*	extracellular amino acid-binding protein	-	0.07	-	-	-

B2T6X5	*Burkholderia phytofirmans*	dipeptide-binding protein	-	0.07	-	-	-
B2U879	*Ralstonia pickettii*	OmpA/MotB domain protein	-	-	-	0.65	0.70
B2UDU1	*Ralstonia pickettii*	porin	-	0.08	0.11	1.08	1.03
B2UFC4[b]	*Ralstonia* spp.	porin	-	-	-	0.27	0.23
B5WCV4[b]	*Burkholderia* spp.	amino acid ligand-binding receptor	-	0.10	-	-	-
B5WIR3	*Burkholderia* sp.	cationic amino acid ABC transporter	-	0.29	-	-	-
B7S235	*unclassified Gammaproteobacteria*	TonB-dependent receptor	-	-	-	-	0.02
C3JXZ7[b]	*Pseudomonas* spp.	histidine-binding periplasmic protein	0.11	-	-	-	-
C3JYK8	*Pseudomonas fluorescens*	RND efflux transporter	-	0.17	-	-	-
C3JYX7[b]	*Pseudomonas* spp.	branched-chain amino acid ABC transporter	0.07	-	-	-	-
C3JZ77[b]	*Pseudomonas* spp.	maltose-binding protein	0.07	-	-	-	-
C3JZG0	*Pseudomonas fluorescens*	ferric siderophore receptor	0.03	-	-	-	-
C3K0T0	*Pseudomonas fluorescens*	porin A	3.14	0.14	-	-	-
C3K187[b]	*Pseudomonas* spp.	imelysin	0.13	-	-	-	-
C3K1B9	*Pseudomonas fluorescens*	metal ABC transporter	0.28	-	-	-	-
C3K1N2[b]	*Pseudomonas* spp.	SecD	0.04	-	-	-	-
C3K3C7[b]	*Pseudomonas* spp.	glycine betaine/L-proline ABC transporter	0.12	-	-	-	-
C3K3T8[b]	*Pseudomonas* spp.	putrescine ABC transporter	0.23	-	-	-	-
C3K3Z3[b]	*Pseudomonas* spp.	ABC transporter	0.07	-	-	-	-
C3K5B7	*Pseudomonas fluorescens*	porin	0.14	-	-	-	-
C3K5V1	*Pseudomonas fluorescens*	OprE3	0.40	-	-	-	-
C3K717[b]	*Pseudomonas* spp.	amino acid transporter	0.44	-	-	-	-
C3K7C1[b]	*Pseudomonas* spp.	SecB	0.22	-	-	-	-
C3K7I2	*Pseudomonas fluorescens*	TonB-dependent receptor	0.25	-	-	-	-
C3K8P0[b]	*Pseudomonas* spp.	nucleoside-binding protein	0.13	-	-	-	-
C3K8Z6	*Pseudomonas fluorescens*	branched amino acid ABC transporter	0.60	-	-	-	-
C3K914	*Pseudomonas fluorescens*	ABC transporter	0.31	-	-	-	-
C3KB06	*Pseudomonas fluorescens*	iron transporter	0.53	-	-	-	-
C3KBL7[b]	*Pseudomonas* spp.	glutamate/aspartate ABC transporter	0.27	0.15	-	-	-
C3KBT7[b]	*Pseudomonas* spp.	sulfate ABC transporter	0.16	-	-	-	-
C3KDU7[b]	*Pseudomonas* spp.	ABC transporter	0.38	-	-	-	-
C3KEB0	*Pseudomonas fluorescens*	amino acid ABC transporter	1.08	-	-	-	-
C3KEC2	*Pseudomonas fluorescens*	OmpA-like	0.62	-	-	-	-
D0S6Y6	*Acinetobacter calcoaceticus*	DcaP-like	0.53	0.53	0.43	0.17	-
D5H5Q2	*Salinibacter ruber*	TonB-dependent receptor	-	-	-	-	0.02
D8D960	*Comamonas testosteroni*	OmpA/MotB	-	-	0.61	0.43	-
D8G164	*Oscillatoria* sp.	TonB receptor	-	-	-	-	0.06

D8JEE3 [b]	*Acinetobacter* spp.	porin	-	0.11	0.11	-	-
D8JLF9	*Acinetobacter* sp.	porin	0.39	0.43	0.43	-	-
D8NXA2	*Ralstonia solanacearum*	porin	-	-	-	0.72	0.74
E2T0T6	*Ralstonia* sp.	porin	-	-	0.05	0.44	0.51
E2XKC2	*Pseudomonas fluorescens*	type I secretion outer membrane protein	0.07	-	-	-	-
E2XKL7 [b]	*Pseudomonas* spp.	branched-chain amino acid ABC transporter	0.13	-	-	-	-
E2XLH2 [b]	*Pseudomonas* spp.	dipeptide ABC transporterer	0.05	-	-	-	-
E2XMS6 [b]	*Pseudomonas* spp.	OmpH	0.37	-	-	-	-
E2XN23	*Pseudomonas fluorescens*	type I secretion membrane fusion protein	0.12	-	-	-	-
E2XW23	*Pseudomonas fluorescens*	long-chain fatty acid transporter	0.04	-	-	-	-
E2Y0H8	*Pseudomonas fluorescens*	porin	0.29	-	-	-	-
E5C8U6 [b]	*Bacteroides* spp.	TonB-linked outer membrane protein	-	-	-	-	0.02
F0KK22	*Acinetobacter calcoaceticus*	porin D	0.13	0.15	0.06	-	-
F6KQ92	*Pseudomonas costantinii*	OprF	0.35	-	-	-	-
G3A5T6	*Ralstonia syzygii*	OmpA	-	-	-	0.54	0.63
G7Z7T4	*Azospirillum lipoferum*	OmaA	-	-	-	0.10	-
G8M678 [b]	*Burkholderia* spp.	extracellular solute-binding protein	-	0.43	-	-	-
G8M683 [b]	*Burkholderia* spp.	OmpC	-	0.13	-	-	-
G8M6G8	*Burkholderia* sp.	OmpA/MotB family protein	-	0.6	-	-	-
G8M893	*Burkholderia* sp.	porin	-	-	-	0.17	0.56
G8MAY7	*Burkholderia* sp.	porin	-	-	-	0.11	0.36
G8MB24 [b]	*Burkholderia* spp.	branched chain amino acid ABC transporter	-	0.07	-	-	-
G8TGU8	*Niastella koreensis*	TonB-dependent receptor G	-	-	-	-	0.02
H0E3A2 [a,b]	*Patulibacter* spp.	phosphate binding protein	-	1.49	1.08	0.08	-
H1KP99	*Methylobacterium extorquens*	porin	-	-	0.22	-	-
H1S518	*Cupriavidus basilensis*	HlyD	-	0.07	-	-	-
H1SI50	*Cupriavidus basilensis*	porin	-	-	-	-	0.18
H1Y2T7	*Mucilaginibacter paludis*	OmpA/MotB domain protein	-	-	-	0.06	0.10
I0KRP1	*Stenotrophomonas maltophilia*	TonB-dependent receptor	-	-	-	-	0.06
I2BKL0 [b]	*Pseudomonas* spp.	OprD	0.10	-	-	-	-
I2BLJ9	*Pseudomonas fluorescens*	porin	-	0.45	-	-	-
I2BPB1	*Pseudomonas fluorescens*	FpvA	0.09	-	-	-	-
I2BVR7	*Pseudomonas fluorescens*	OprD	0.38	-	-	-	-
I2BWR7	*Pseudomonas fluorescens*	TagQ	0.34	-	-	-	-
I2BWZ9	*Pseudomonas fluorescens*	NLPA family lipoprotein	0.39	-	-	-	-
I2IFR8 [b]	*Burkholderia* spp.	porin	-	-	-	-	0.48
I3AHW1	*Serratia plymuthica*	outer membrane protein A	0.29	-	-	-	-
I4K2Q7 [b]	*Pseudomonas* spp.	OprB	0.20	-	-	-	-

I4KG72 [b]	*Pseudomonas* spp.	amino acid ABC transporter	0.29	-	-	-	-
I4KV15	*Pseudomonas synxantha*	TonB-dependent receptor	0.15	-	-	-	-
I4MZT9	*Pseudomonas* sp.	LivK	0.43	-	-	-	-
I4VVL8 [b]	*Rhodanobacter* spp.	TonB-dependent receptor	-	-	-	0.03	0.06
I4W1F0	*Rhodanobacter spathiphylli*	TonB-dependent receptor	-	-	-	-	0.07
I4W299 [b]	*Rhodanobacter* spp.	PilQ	-	-	-	-	0.12
I5D4U3	*Burkholderia terrae*	OmpA/MotB domain-containing protein	-	0.43	-	-	0.52
J2SD86	*Flavobacterium* sp.	TonB-linked outer membrane protein,	-	-	-	-	0.02
J2T7G6	*Variovorax* sp.	porin	-	-	0.20	0.24	0.24
J2TZX3 [b]	*Pseudomonas* spp.	OprD family porin	-	-	0.06	-	-
J2Z2M0 [b]	*Pseudomonas* spp.	peptidoglycan-associated lipoprotein	0.24	0.19	0.08	-	-
J3CB80	*Variovorax* sp.	porin	-	0.10	0.05	0.20	0.25
J3CWR3	*Bradyrhizobium* sp.	porin	-	0.05	0.16	0.29	0.44
J3DTD1	*Pseudomonas putida*	OprD family porin	-	0.15	0.10	0.04	0.06
J3GVG6	*Pseudomonas* sp.	OprD family porin	-	0.13	0.04	-	-
K0HTW4	*Acidovorax* sp.	OmpA/MotB	-	-	-	0.32	-
K8P9Z0	*Afipia broomeae*	porin	-	-	-	-	0.24
K8R697	*Burkholderia* sp.	porin	-	-	-	-	0.15
K8R8N3	*Burkholderia* sp.	OmpC family porin	-	-	-	0.05	0.32
K8RAU9	*Burkholderia* sp.	OmpC family porin	-	0.13	0.10	0.15	0.53
K8RQJ6	*Burkholderia* sp.	porin	-	-	-	-	0.46
K9AC78	*Acinetobacter baumannii*	Omp38	0.39	0.58	0.45	0.08	-
K9ACC8	*Acinetobacter baumannii*	DcaP-like	0.15	0.38	0.21	-	-
K9CQK5	*Acinetobacter baumannii*	transporter, Ompp1/FadL/TodX family	-	0.09	0.06	-	-
L2EK35 [b]	*Cupriavidus* spp.	porin	-	-	-	0.43	0.96
L7H9X2	*Pseudomonas fluorescens*	branched-chain amino acid ABC transporter	0.35	-	-	-	-
L7HLG1	*Pseudomonas fluorescens*	porin	0.76	-	-	-	-
Q213J7	*Rhodopseudomonas palustris*	Omp2b	-	-	0.13	-	0.36
Q46WM6	*Ralstonia eutropha*	porin	-	-	-	-	0.33
Q4FCM8	*Acinetobacter* sp.	outer membrane protein A	0.16	-	-	-	-
Q5QQ59	*Pseudomonas fluorescens*	OprE3	0.49	-	-	-	-
Q6FE98	*Acinetobacter* sp.	porin	0.10	-	-	-	-
Q985C3	*Rhizobium loti*	porin	-	-	0.05	0.10	0.10
UPI0002885851	*Pseudomonas* sp.	LivK	0.63	-	-	-	-
UPI00028A1D9E	*Sphingomonas* sp.	TonB-dependent receptor	-	-	-	-	0.03
UPI00029AA93B	*Pseudomonas geniculata*	TonB-dependent receptor	-	-	-	-	0.05
Other functions							
A0KAZ1 [a,b]	*Burkholderia* spp.	cell division factor	-	0.10	-	-	-
A4VLW4 [a,b]	*Pseudomonas* spp.	adenylosuccinate lyase	0.06	-	-	-	-

A6VCJ6 [a]	*Pseudomonas aeruginosa*	polyribonucleotide nucleotidyltransferase	0.14	-	-	-	-
B2KBE7	*Elusimicrobium minutum*	Smc	-	-	-	0.03	-
C3K1M9 [b]	*Pseudomonas* spp.	inositol monophosphatase	0.13	-	-	-	-
C3K1U2	*Pseudomonas fluorescens*	aminotransferase	0.10	-	-	-	-
C3K5Y0 [b]	*Pseudomonas* spp.	NADP(H)-dependent aldo-keto reductase	0.08	-	-	-	-
C3KD06	*Pseudomonas fluorescens*	amidase	0.04	-	-	-	-
C3KEC6 [b]	*Pseudomonas* spp.	adenylate kinase	0.22	-	-	-	-
E2XPE0 [b]	*Pseudomonas* spp.	peptidyl-prolyl cis-trans isomerase	0.58	0.38	-	-	-
E2XX99	*Pseudomonas fluorescens*	iron-regulated protein	0.21	-	-	-	-
I2BTN8 [b]	*Pseudomonas* spp.	chromosome partitioning protein	0.20	-	-	-	-
I2BZ33 [b]	*Pseudomonas* spp.	YeaG	0.24	-	-	-	-
UPI00028A32F2	*Pseudomonas extremaustralis*	VacJ family lipoprotein	0.31	-	-	-	-
Function unknown							
A6UXA9 [a,b]	*Pseudomonas* spp.		0.08	-	-	-	-
A2VTE3 [a,b]	*Burkholderia* spp.		-	0.14	-	-	-
B7L1B2 [b]	*Methylobacterium* spp.		-	-	0.12	0.09	-
C3JYK6	*Pseudomonas fluorescens*		-	0.87	-	-	-
C3K3H1	*Pseudomonas fluorescens*		0.29	-	-	-	-
C3K3V2	*Pseudomonas fluorescens*		0.53	-	-	-	-
C3KBL3 [b]	*Pseudomonas* spp.		0.22	-	-	-	-
C3KED5	*Pseudomonas fluorescens*		0.35	-	-	-	-
C6WZ97	*Methylotenera mobilis*		0.19	0.14	0.17	0.12	0.10
D7DNB6	*Methylotenera* sp.		0.16	0.07	0.07	0.07	-
D8JLH9 [b]	*Acinetobacter* spp.		-	0.13	0.09	-	-
D8JYJ3	*Hyphomicrobium denitrificans*		-	-	-	-	0.06
E2XJW5	*Pseudomonas fluorescens*		0.10	-	-	-	-
E2XLQ8	*Pseudomonas fluorescens*		0.38	0.29	-	-	-
E2XUK8	*Pseudomonas fluorescens*		-	0.47	-	-	-
G4MGY8 [b]	*Burkholderia* spp.		-	0.59	-	-	-
I2BNE9 [b]	*Pseudomonas* spp.		0.11	-	-	-	-
I2BVK9	*Pseudomonas fluorescens*		-	0.60	-	-	-
I2BWV2 [b]	*Pseudomonas* spp.		0.44	0.13	-	-	-
J8V5Q9	*Pseudomonas putida*		-	0.11	0.33	-	-
UPI000288EA66	*Pseudomonas extremaustralis*		0.13	-	-	-	-
UPI000289F004	*Pseudomonas extremaustralis*		0.10	-	-	-	-

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[a] This protein could be assigned to more than one bacterial genus. The genus mentioned was arbitrarily chosen as it represented the most abundant genus at the sampling date.

[b] This protein could be assigned to more than one species of the genus mentioned.

[c] Protein not detected or protein identification not considered valid.

Table S2 Proteins produced by *Rhodanobacter thiooxidans* LCS2 during growth in minimal medium supplemented with suberin at day 5 and day 30

Uniprot accession number	Putative function	Abundance (NSpC[a])	
		5 days	30 days
Amino acid metabolism			
I4VHY4[b]	methylisocitrate lyase	0.16	0.23
I4VI38	cysteine synthase	-[c]	1.23
I4VNT3	isovaleryl-CoA dehydrogenase	0.07	-
I4VP75	glutamine synthetase	-	0.07
I4VUT5	pyrroline-5-carboxylate reductase	-	0.07
I4VWA7	Xaa-Pro aminopeptidase	0.04	-
I4W1V5	anthranilate phosphoribosyltransferase	-	0.04
I4W2U0	asparaginase	-	0.14
I4W3N8	HtpX, protease	-	0.05
I4W5U6	N-acetylornithine carbamoyltransferase	0.26	-
I4W668	aspartate-semialdehyde dehydrogenase	0.08	-
I4W6F3	histidine ammonia-lyase	-	0.04
I4W6N2	peptidyl-prolyl cis-trans isomerase	-	0.09
I4W9W4	cysteine synthase	3.41	7.35
I4WAC2	peptidyl-prolyl cis-trans isomerase	0.20	0.08
I4WAU6	3-dehydroquinate dehydratase	-	0.34
I4WAZ4	methylcrotonoyl-CoA carboxylase	0.03	-
I4WB23	4-hydroxy-tetrahydrodipicolinate synthase	0.08	0.13
I4WB48	methionine aminotransferase	0.04	0.40
I4WBE2	peptidase M28	0.04	-
I4WBP2	glycyl aminopeptidase	0.07	0.06
I4WBY8	arginine decarboxylase	0.03	0.04
I4WBY9	polyamine aminopropyl transferase	0.24	0.48
I4WC22	glutamine synthetase	0.13	-
I4WC30	Zn-dependent oligopeptidase	0.11	0.14
I4WC93	shikimate dehydrogenase	-	0.33
I4WCE3	branched-chain amino acid aminotransferase	-	0.09
I4WCR0	aminopeptidase N	0.10	-
I4WCU6	aromatic amino acid aminotransferase	0.34	0.58
I4WD72	peptidase M28	0.12	0.08
I4WD80	protease	0.17	0.63
I4WDN0	alanine dehydrogenase	-	0.07
I4WDQ1	leucine dehydrogenase	0.36	0.24
I4WDT5	ArgD, acetylornithine aminotransferase	0.22	0.40
I4WE81	arginase	0.03	-
I4WEE3	cysteine desulfurase	0.04	0.10

I4WEG3	ornithine/acetylornithine aminotransferase	0.10	0.45
I4WEG6	proline iminopeptidase	-	0.13
I4WEG8	D-3-phosphoglycerate dehydrogenase	0.43	0.16
I4WEP6	dipeptidyl aminopeptidase/acylaminoacyl peptidase	-	0.03
I4WEZ1	nitrogen regulatory protein P-II	0.50	0.38
I4WFS5	protease	0.11	-
I4WFS8	leucine aminopeptidase	0.04	0.03
I4WG51	cystathionine beta-lyase/cystathionine gamma-synthase	0.10	0.10
I4WG78	GcvT, aminomethyltransferase	0.40	0.14
I4WG79	glycine cleavage system H protein	0.86	0.46
I4WGE0	maleylacetoacetate isomerase	-	0.08
I4WGE5	cysteine synthase	0.17	0.46
I4WGQ3	peptidase M28	-	0.09
I4WH07	peptidase S10 serine carboxypeptidase	-	0.02
I4WH24	peptidyl-dipeptidase	0.03	0.21
I4WHD2	bifunctional proline dehydrogenase/pyrroline-5-carboxylate dehydrogenase	0.14	0.11
I4WHD9	peptidyl-dipeptidase	0.07	0.52
I4WI88	4-hydroxy-tetrahydrodipicolinate reductase	0.08	0.04
I4WI91	carbamoyl-phosphate synthase	0.08	-
I4WI92	carbamoyl phosphate synthase	0.08	-
I4WIP0	3-phosphoshikimate 1-carboxyvinyltransferase	0.11	0.04
I4WIP2	phosphoserine aminotransferase	0.10	0.12
I4WIR5	glycine dehydrogenase	0.08	0.15
I4WIT5	D-amino acid dehydrogenase	0.07	0.14
I4WIU0	HflC	-	0.23
I4WIU1	protease	0.17	0.21
I4WIU5	peptidase	0.15	0.15
I4WIU6	peptidase S46	-	0.03
I4WIU8	L-threonine 3-dehydrogenase	0.09	-
I4WIV0	2-amino-3-ketobutyrate coenzyme A ligase	0.13	0.23
I4WIW2	aspartate aminotransferase	0.24	1.49
I4WIW4	peptidyl-prolyl cis-trans isomerase	-	0.17
I4WJA2	serine hydroxymethyltransferase	0.12	0.38
I4WJL2	protease	0.06	0.07
I4WJL5	X-Pro dipeptidyl-peptidase	-	0.03
I4WJU9	ProC, pyrroline-5-carboxylate reductase	0.18	-
I4WKD9	methylthioribose-1-phosphate isomerase	-	0.03
I4WKJ1	histidine ammonia-lyase	0.04	-
I4WL26	protease	0.20	0.16
I4WLF3	tryptophan synthase beta chain	0.01	-
I4WLH1	imidazoleglycerol-phosphate dehydratase	-	0.03
I4WLV4	aminotransferase	0.11	0.34

I4WM29	acetylornithine deacetylase	0.06	0.04
I4WM35	metalloendopeptidase	0.47	0.76
I4WM64	prepilin-type N-terminal cleavage	0.14	-
I4WM81	NAD-glutamate dehydrogenase	0.08	0.10
I4WM86	glutaryl-CoA dehydrogenase	0.27	0.36
I4WMC6	peptidyl-prolyl cis-trans isomerase	0.06	-
I4WMK5	kynureninase	-	0.15
I4WMM4	carbamoyl phosphate synthase	0.03	-
I4WN39	Xaa-Pro dipeptidase	0.05	0.22
I4WN55	peptidase S8/S53	0.02	0.17
I4WN66	Indole-3-glycerol phosphate synthase	0.21	0.29
I4WN78	dipeptidase	0.03	-
I4WPB8	HutI, imidazolonepropionase	0.06	0.03
I4WPC0	N-formimino-L-glutamate deiminase	-	0.03
I4WPD1	urocanate hydratase	0.06	0.31
I4WPH1	Xaa-Pro aminopeptidase	-	0.02
I4WPJ5	peptidyl-prolyl cis-trans isomerase	0.18	0.20
I4WPK6	peptidyl-prolyl cis-trans isomerase	0.85	0.44
I4WQ39	argininosuccinate synthase	0.17	0.10
I4WQ41	acetylornithine deacetylase	0.03	-
I4WQ42	acetylglutamate kinase	-	0.04
I4WQ44	argininosuccinate lyase	0.11	-
I4WQ91	metallopeptidase	0.02	0.23
I4WQ99	peptidyl-prolyl cis-trans isomerase	0.26	-
I4WQQ8	gamma-glutamyltranspeptidase	-	0.07
I4WRE3	TrpA, tryptophan synthase	0.17	-
I4WRG1	histidinol dehydrogenase	0.05	-
I4WRG9	enolase-phosphatase	0.10	0.98
I4WRS1	aminopeptidase	0.14	0.03
I4WRX3	gamma-glutamyltranspeptidase	0.08	-
I4WSM1	aminopeptidase	-	0.11
I4WSM4	threonine aldolase	-	0.25
I4WSY4	branched-chain amino acid aminotransferase	0.23	0.91
I4WSY6	methylenetetrahydrofolate reductase	-	0.08
I4WT46	peptidase M28	0.28	0.22
I4WTB2	metallopeptidase	0.05	0.07
I4WU28	2,3,4,5-tetrahydropyridine-2,6-dicarboxylate N-succinyltransferase	0.31	0.45
I4WVA0	peptidyl-prolyl cis-trans isomerase	0.36	-
I4WZ73	X-Pro dipeptidyl-peptidase	0.04	-
M4NC29	Zn-dependent peptidase	-	0.02
M4NEI4	ornithine carbamoyltransferase	-	0.14
Carbohydrate metabolism			

I4VKM3	inositol monophosphatase/fructose-1,6-bisphosphatase family protein	-	0.05
I4WAH6	phosphoglucomutase	0.08	0.10
I4WAH7	glucose-6-phosphate isomerase	0.04	0.16
I4WAH8	transaldolase	0.12	0.63
I4WBW6	ribokinase	-	0.18
I4WBX9	phosphomannomutase	0.02	0.09
I4WCH0	GDP-L-fucose synthase	0.07	-
I4WCI9	Fpb, fructose-1,6-bisphosphatase	0.09	0.11
I4WCL1	L-sorbosone dehydrogenase	0.08	0.13
I4WCP3	Glk PE, glucokinase	0.03	-
I4WDU0	6-phosphofructokinase	-	0.03
I4WEL7	2-dehydro-3-deoxy-6-phosphogalactonate aldolase	-	0.11
I4WEN5	6-phosphogluconate dehydrogenase-like protein	-	0.20
I4WEQ2	Entner-Doudoroff aldolase	0.45	0.75
I4WEQ3	phosphogluconate dehydratase	0.10	0.24
I4WEQ4	6-phosphogluconolactonase	0.44	0.42
I4WEQ5	glucose-6-phosphate 1-dehydrogenase	0.30	0.92
I4WF95	2,3-bisphosphoglycerate-dependent phosphoglycerate mutase	0.25	0.09
I4WGD0	glyceraldehyde-3-phosphate dehydrogenase	0.42	-
I4WGD2	Pyruvate kinase	0.48	0.62
I4WGD4	fructose-bisphosphate aldolase	0.33	0.49
I4WGD7	transketolase	0.11	0.75
I4WGD9	Pgk, phosphoglycerate kinase	0.13	0.21
I4WGM3	xylanase deacetylase	0.42	0.82
I4WH34	alpha,alpha-trehalase	0.05	-
I4WHZ0	phosphoketolase	-	0.06
I4WI35	propanediol utilization protein	0.29	-
I4WIU7	glycogen debranching enzyme	0.20	0.11
I4WM90	transketolase domain-containing protein	0.02	-
I4WN50	ribose-5-phosphate isomerase	0.35	0.52
I4WN86	glycoside hydrolase clan GH-D	-	0.01
I4WN98	ribulose-phosphate 3-epimerase	0.13	0.15
I4WPH4	enolase	0.33	1.17
I4WPK2	phosphoenolpyruvate synthase	0.13	0.08
I4WQC6	N-ethylammeline chlorohydrolase	0.09	0.25
I4WRP0	fructose-1,6-bisphosphatase	0.09	-
I4WRR0	cyclomaltodextrin glucanotransferase	0.20	0.38
I4WRR9	alpha-glucosidase	0.08	0.08
I4WU59	PEP phosphonomutase-like protein	-	0.07
M4NMT8	transaldolase	0.06	0.15
Cell wall, membrane and envelope biogenesis			
I4VNC9	glycosyl transferase family protein	-	0.09

I4VVG1	D-alanine--D-alanine ligase	0.08	-
I4VX44	LysM domain-containing protein	0.18	-
I4VZT9	C-terminal processing peptidase	0.05	-
I4W030	lipoprotein releasing system transmembrane protein LolC/E family	-	0.03
I4W2A0	pilus assembly protein	0.30	0.35
I4W2P0	membrane fusion protein	0.09	-
I4W6X0	UTP-glucose-1-phosphate uridylyltransferase	0.14	-
I4WAP1	BamD, outer membrane protein assembly factor	0.29	0.14
I4WAZ3	outer membrane protein	1.31	0.31
I4WB89	type 4 fimbrial biogenesis protein pily1-related protein	0.03	0.13
I4WC49	glycosyl transferase family protein	0.22	-
I4WCG1	glycosyl transferase family protein	0.06	0.05
I4WCH4	Class II pilin PilE	3.60	3.90
I4WDT8	UDP-N-acetylmuramate--L-alanine ligase	0.06	-
I4WDV8	glycosyltransferase	-	0.04
I4WEJ0	BamA .outer membrane protein assembly factor	0.09	0.23
I4WEJ4	lipid-A-disaccharide synthase	0.03	-
I4WEQ7	glucosamine-fructose-6-phosphate aminotransferase	0.11	-
I4WER7	lipid A 3-O-deacylase	0.19	-
I4WF26	Rhs family protein	-	0.01
I4WFA3	membrane fusion protein	-	0.08
I4WFN8	GlmU, bifunctional acetyl transferase/uridyl transferase	0.14	-
I4WFT7	D-alanyl-D-alanine carboxypeptidase	0.04	0.08
I4WG42	glucosamine--fructose-6-phosphate aminotransferase	-	0.13
I4WG67	aminotransferase	0.18	0.24
I4WGE3	OmpA/MotB domain-containing protein	-	0.07
I4WGE6	glucosamine--fructose-6-phosphate aminotransferase	0.15	-
I4WGM9	LysM domain-containing protein	0.79	0.51
I4WGP0	glycosyl/glycerophosphate transferase	-	0.09
I4WGU3	peptidoglycan-associated lipoprotein	3.39	6.24
I4WGU4	Tol-pal system protein	0.20	-
I4WH26	hemaglutitin	0.08	0.13
I4WI78	BamE, outer membrane protein assembly factor	-	0.15
I4WIC8	type IV pilus biogenesis/stability protein	0.05	0.12
I4WID1	BamB, outer membrane protein assembly factor	0.31	0.29
I4WIN9	3-deoxy-manno-octulosonate cytidylyltransferase	0.07	-
I4WIT4	alanine racemase	0.05	0.09
I4WIV2	peptidoglycan-associated protein	2.18	2.38
I4WJ11	capsular polysaccharide biosynthesis protein	0.04	0.04
I4WJS2	filamentous hemaglutin-like	0.77	0.29
I4WJT4	two-component system sensor histidine kinase-response regulator hybrid protein pill	0.05	0.05

I4WJT5	pilus biogenesis protein	0.22	0.17
I4WM62	Tfp pilus assembly protein FimT-like protein	-	0.08
I4WM66	PilY1, type 4 fimbrial biogenesis protein	0.03	0.03
I4WM67	PilE	-	0.09
I4WMA3	OmpA-like	-	0.54
I4WNG6	fimbrial assembly membrane protein	0.65	0.54
I4WNG7	fimbrial assembly membrane protein	0.29	0.40
I4WNG8	fimbrial assembly membrane protein	0.34	0.22
I4WNG9	penicillin-binding protein	-	0.02
I4WNH8	surface lipoprotein	0.03	0.13
I4WPA0	outer membrane lipoprotein	1.55	0.93
I4WPA1	outer membrane protein	1.06	0.24
I4WPB6	MsbA, lipid A export ATP-binding/permease protein	0.02	0.03
I4WPH3	2-dehydro-3-deoxyphosphooctonate aldolase	0.25	0.28
I4WPK7	UDP-glucose dehydrogenase	0.03	0.15
I4WQ35	outer membrane lipoprotein	1.21	0.61
I4WRC8	lytic murein transglycosylase	-	0.02
I4WRD8	FimV N-terminal domain-containing protein	0.43	0.13
I4WRZ3	flagellin domain-containing protein	-	0.29
I4WSL0	LPS-assembly protein LptD	0.08	0.05
I4WT16	UDP-N-acetylglucosamine--N-acetylmuramyl-(pentapeptide) pyrophosphoryl-undecaprenol N-acetylglucosamine transferase	0.12	0.05
I4WTB1	C-terminal processing peptidase	-	0.01
I4WUZ6	lytic murein transglycosylase	0.03	-
Energy production and conversion			
I4VKE0	isocitrate dehydrogenase	0.10	-
I4VM16	alcohol dehydrogenase	-	0.09
I4VXG5	succinyl-CoA ligase [ADP-forming] subunit alpha	0.28	-
I4W1D3	glyceraldehyde-3-phosphate dehydrogenase	-	0.19
I4W1F4	NADH:flavin oxidoreductase/NADH oxidase	-	0.02
I4W1R0	bifunctional malic enzyme oxidoreductase/phosphotransacetylase	-	0.02
I4W332	cytochrome c4	0.29	0.29
I4W6A9	high potential iron-sulfur protein	-	0.09
I4W788	isocitrate lyase	-	0.35
I4W7P8	rubrerythrin	-	0.33
I4W977	NADPH:quinone oxidoreductase	0.27	0.19
I4W9P0	fumarate hydratase class II	0.12	0.03
I4WAP4	succinyl-CoA ligase [ADP-forming] subunit beta	0.07	0.17
I4WB45	short-chain dehydrogenase	0.04	-
I4WB57	aconitate hydratase	0.22	0.61
I4WBN1	ubiquinol-cytochrome c reductase iron-sulfur subunit	0.52	0.34
I4WBN2	cytochrome b	-	0.04
I4WBN3	ubiquinol-cytochrome c reductase	0.39	0.26

I4WBP6	sulfur oxidation protein, flavocytochrome C	0.03	0.06
I4WBR2	DsrE/DsrF-like family protein	0.40	0.24
I4WD44	aldehyde dehydrogenase	-	0.12
I4WD61	oxydoreductase	0.08	-
I4WDW2	NADH dehydrogenase/NAD(P)H nitroreductase	0.21	0.12
I4WDY5	dihydrolipoamide dehydrogenase	0.38	0.13
I4WDY6	dihydrolipoamide acetyltransferase	0.78	0.24
I4WE11	pyruvate dehydrogenase E1 component	0.39	0.30
I4WE12	bifunctional malic enzyme oxidoreductase/phosphotransacetylase	0.15	-
I4WE63	aconitate hydratase	-	0.04
I4WE70	pyruvate dehydrogenase E1 alpha subunit	0.09	1.25
I4WE71	pyruvate/2-oxoglutarate dehydrogenase complex, dehydrogenase component beta subunit	0.46	1.82
I4WEG7	FAD/FMN-dependent dehydrogenase	0.19	0.68
I4WEU1	sulfide-quinone reductase	0.45	0.41
I4WFA2	cytochrome c	0.53	0.22
I4WFB8	isocitrate dehydrogenase	0.34	1.24
I4WFD5	NADPH:quinone reductase	0.18	-
I4WFN1	ATP synthase subunit b	0.62	0.35
I4WFN2	AtpH, ATP synthase subunit delta	0.18	-
I4WFN3	ATP synthase subunit alpha	0.54	0.66
I4WFN4	ATP synthase gamma chain	0.15	0.13
I4WFN5	ATP synthase subunit beta	0.56	0.55
I4WG68	electron transfer flavoprotein alpha subunit	0.36	0.69
I4WG69	electron transfer flavoprotein subunit beta	0.65	0.44
I4WG74	electron transfer flavoprotein-ubiquinone oxidoreductase	0.05	0.03
I4WG85	glucose-methanol-choline oxidoreductase	0.09	-
I4WGC7	azurin	0.75	0.34
I4WH70	NAD(P) transhydrogenase	0.26	0.30
I4WH92	FAD-dependent pyridine nucleotide-disulfide oxidoreductase	0.34	0.83
I4WHD0	cytochrome c oxidase subunit 2	0.05	0.05
I4WHD3	aldehyde dehydrogenase	0.15	0.07
I4WI10	short chain dehydrogenase/reductase f	0.09	0.07
I4WIV5	citrate synthase	0.29	-
I4WIW1	malate dehydrogenase	0.30	0.56
I4WJ90	voltage-gated potassium channel beta subunit	-	0.11
I4WJ91	alcohol dehydrogenase superfamily protein	0.16	0.26
I4WJC7	rubrerythrin	0.83	-
I4WKC6	2-oxoglutarate dehydrogenase	0.15	0.22
I4WKC7	2-oxoglutarate dehydrogenase	0.43	0.34
I4WKC8	dihydrolipoyl dehydrogenase	0.54	0.33
I4WKE9	NADH-quinone oxidoreductase subunit N	-	0.05
I4WKF6	NADH dehydrogenase subunit G	0.08	0.04

I4WKF7	NADH-quinone oxidoreductase	0.07	-
I4WKG0	NADH-quinone oxidoreductase	0.13	-
I4WLR8	NADH-quinone oxidoreductase subunit C	-	0.15
I4WMA7	cytochrome c family protein	0.05	0.08
I4WML0	short-chain dehydrogenase	0.19	0.19
I4WNH1	citrate synthase	0.48	0.45
I4WP39	cytochrome c biogenesis protein	0.05	-
I4WPA7	succinate dehydrogenase	0.09	0.05
I4WPA8	succinate dehydrogenase	0.14	0.17
I4WQ25	FAD linked oxidase domain-containing protein	-	0.07
I4WRH2	high potential iron-sulfur protein	0.33	-
I4WSC0	NADP oxidoreductase	0.14	0.21
I4WSY9	phosphoenolpyruvate carboxylase	0.18	0.12
I4WU19	short-chain dehydrogenase	0.12	0.37
I4WU37	nitrous-oxide reductase	-	0.08
I4WUC8	NADPH dehydrogenase	0.11	0.24
I4WW98	pyruvate dehydrogenase	0.29	-
M4NS93	citrate synthase	-	0.47
M4NTL5	ATP synthase subunit delta	-	0.03
Lipid metabolism and ketogenesis			
I4VIC2	acyl carrier protein	-	1.44
I4VRU7	3-hydroxyacyl-CoA dehydrogenase	-	0.28
I4VV45	YdiF, acetate-CoA transferase	-	0.13
I4VY74	3-oxoacyl-ACP reductase	-	0.07
I4VZY3	acetoacetyl-CoA reductase	-	0.06
I4W091	acyl-CoA dehydrogenase domain-containing protein	0.04	-
I4WAL3	3-hydroxydecanoyl-[acyl-carrier-protein] dehydratase	-	0.08
I4WAL4	beta-ketoacyl-[ACP] synthase I	0.12	0.43
I4WAZ2	acetoacetyl-CoA thiolase	0.66	0.66
I4WB09	3-hydroxybutyryl-CoA dehydratase	0.13	-
I4WB55	long-chain fatty acyl-CoA ligase	-	0.07
I4WBU8	acetyl-coenzyme A synthetase	0.11	0.12
I4WBY7	3-hydroxybutyrate dehydrogenase	-	0.09
I4WBZ6	acetyl-CoA acetyltransferase	0.13	0.07
I4WCN8	GpsA, glycerol-3-phosphate dehydrogenase	0.13	0.07
I4WDA0	acyl-CoA dehydrogenase	0.04	0.25
I4WE25	fatty acid binding protein	0.15	0.09
I4WE72	branched-chain alpha-keto acid dehydrogenase subunit E2	0.38	0.22
I4WEJ2	FabZ, 3-hydroxyacyl-[acyl-carrier-protein] dehydratase	-	0.29
I4WEK0	acetyl-coenzyme A carboxylase carboxyl transferase	-	0.04
I4WFP4	fatty acyl-CoA synthetase	0.16	0.05
I4WGM2	lipase	0.14	0.09

I4WIC3	acetyl-CoA acetyltransferase	0.23	0.62
I4WIC4	3-hydroxyacyl-CoA dehydrogenase	0.20	0.94
I4WJC3	polyhydroxyalkanoate depolymerase	0.07	-
I4WKE0	poly(R)-hydroxyalkanoic acid synthase, class III, PhaC subunit	0.14	0.05
I4WKE1	poly(R)-hydroxyalkanoic acid synthase subunit	0.05	-
I4WKH0	3-oxoacyl-[acyl-carrier-protein] synthase	0.12	0.21
I4WKH1	acyl carrier protein	0.11	-
I4WKH2	3-ketoacyl-[acyl-carrier-protein] reductase	0.20	0.04
I4WKH3	malonyl-CoA-acyl carrier protein transacylase	0.14	0.31
I4WKH4	3-oxoacyl-[acyl-carrier-protein] synthase	0.16	0.13
I4WKP8	acyl-CoA dehydrogenase	-	0.04
I4WM78	acyl-CoA dehydrogenase domain-containing protein	-	0.12
I4WM94	acyl-CoA dehydrogenase	-	0.06
I4WM95	acyl-CoA dehydrogenase	-	0.03
I4WM96	acetoacetate decarboxylase	0.20	0.13
I4WMY1	phasin	1.86	5.43
I4WP46	trans-2-enoyl-CoA reductase	0.11	0.25
I4WPL0	enoyl-CoA hydratase	0.19	0.20
I4WPU1	acyl-CoA dehydrogenase	-	0.05
I4WR42	acyl carrier protein	0.10	0.35
I4WR77	enoyl-CoA hydratase	0.08	-
I4WSC3	lipase	0.08	0.20
I4WSG8	acyl-CoA dehydrogenase	0.37	1.02
I4WU86	acyl-CoA thiolesterase	-	0.16
I4WUC2	lipase	-	0.07
I4WUD4	acetoacetyl-CoA reductase	0.17	-
I4WZ09	YdiF, acetate CoA-transferase	0.13	-
M4NHA9	acyl-CoA dehydrogenase	-	0.36
Replication, transcription, translation and DNA repair			
G4FZ48	elongation factor Tu	1.83	1.03
I4VIS9	NusG, transcription termination/antitermination protein	-	0.10
I4VIT0	50S ribosomal protein L11	0.43	0.43
I4VIT2	50S ribosomal protein L10	0.42	-
I4VIT3	50S ribosomal protein L7/L12	-	0.08
I4VK78	methionine--tRNA ligase	0.04	-
I4VLN4	RNA polymerase sigma factor RpoD	0.04	0.03
I4VM70	30S ribosomal protein S10	0.42	0.25
I4VM75	30S ribosomal protein S19	-	0.30
I4VM80	30S ribosomal protein S17	0.45	-
I4VM82	50S ribosomal protein L24	0.59	0.50
I4VM90	50S ribosomal protein L15	-	0.13
I4VM95	DNA-directed RNA polymerase subunit alpha	-	0.42

I4VN96	30S ribosomal protein S6	-	0.22
I4VQ72	30S ribosomal protein S21	0.39	-
I4VS93	50S ribosomal protein L7/L12	0.31	-
I4VWM0	chromosome partition protein	-	0.01
I4VXT9	DNA topoisomerase 1	-	0.03
I4VZ43	30S ribosomal protein S11	0.64	0.14
I4VZ44	30S ribosomal protein S13	-	0.38
I4VZ46	50S ribosomal protein L15	0.37	-
I4VZ51	30S ribosomal protein S8	1.18	-
I4VZ55	50S ribosomal protein L14	0.50	0.77
I4VZ56	30S ribosomal protein S17	-	0.30
I4VZ58	50S ribosomal protein L16	0.17	-
I4VZ59	30S ribosomal protein S3	0.13	0.25
I4VZC9	30S ribosomal protein S2	-	0.40
I4W0F8	Crp/Fnr family transcriptional regulator	0.07	-
I4W1I1	amidase	0.09	-
I4W447	RecA	0.24	0.11
I4W664	N5-glutamine S-adenosyl-L-methionine-dependent methyltransferase	0.04	-
I4W6N1	nucleoid DNA-binding protein	7.00	2.85
I4WA42	serine--tRNA ligase	0.07	0.17
I4WAQ1	Fis family transcriptional regulator	0.18	0.05
I4WB47	transcriptional regulator	-	0.10
I4WBV8	DNA gyrase subunit B	0.03	0.03
I4WBW0	DNA polymerase III subunit beta	0.66	0.32
I4WBX1	tyrosine--tRNA ligase	0.09	0.04
I4WBY3	ArgS, arginine--tRNA ligase	0.02	-
I4WC48	chromosome partitioning protein	0.08	-
I4WC56	transcriptional regulator	0.12	0.08
I4WCN6	50S ribosomal protein L28	0.28	-
I4WCP9	Rho, transcription termination factor	0.17	0.11
I4WCU7	RdgC, recombination-associated protein	0.04	-
I4WD05	RhlB, ATP-dependent RNA helicase	0.02	-
I4WDR8	50S ribosomal protein L23	-	0.23
I4WEH2	phenylalanine--tRNA ligase beta subunit	0.08	-
I4WEH6	translation initiation factor IF-3	0.31	-
I4WEI2	30S ribosomal protein S2	0.66	-
I4WEI3	elongation factor Ts	0.24	0.15
I4WF04	NADPH-dependent 7-cyano-7-deazaguanine reductase	-	0.17
I4WFK0	Glycine--tRNA ligase beta subunit	0.04	0.02
I4WG27	50S ribosomal protein L25	0.15	-
I4WGB3	50S ribosomal protein L1	0.48	0.27
I4WGB4	50S ribosomal protein L10	0.34	0.26

I4WGF0	Mg-dependent DNase	0.07	0.25
I4WGM7	DNA topoisomerase 1	0.06	-
I4WGT1	aspartate--tRNA ligase	0.16	0.12
I4WHZ5	GreA/GreB family elongation factor	0.20	0.20
I4WI04	exodeoxyribonuclease I	-	0.03
I4WI69	ribonuclease E	0.12	0.04
I4WI93	GreA, transcription elongation factor	0.29	0.24
I4WI99	30S ribosomal protein S1	0.46	0.12
I4WIK9	lysine--tRNA ligase	0.10	-
I4WIR1	ribonuclease R	0.01	-
I4WIT6	regulatory protein	-	0.05
I4WIU3	Hfq, RNA-binding protein	0.41	-
I4WJD2	glutamine--tRNA ligase	0.04	-
I4WJK2	ValS, valine-tRNA ligase	0.06	-
I4WJK8	proline--tRNA ligase	0.06	0.16
I4WJK9	DNA-binding protein H-NS	3.21	0.71
I4WKB9	transcriptional regulator	0.73	0.27
I4WKC4	transcription factor	0.07	0.04
I4WKD8	DNA gyrase	0.05	0.03
I4WKE2	polyribonucleotide nucleotidyltransferase	0.45	1.07
I4WKE6	translation initiation factor IF-2	0.12	0.07
I4WKE7	NusA, transcription elongation factor	0.09	0.18
I4WKH5	50S ribosomal protein L32	0.43	-
I4WKI6	DNA polymerase III	0.02	0.06
I4WKJ2	histidine--tRNA ligase	-	0.05
I4WKR3	50S ribosomal protein L3	-	0.52
I4WKR6	50S ribosomal protein L2	-	0.20
I4WKR7	30S ribosomal protein S19	0.45	-
I4WKT0	30S ribosomal protein S5	0.58	0.31
I4WKT6	30S ribosomal protein S4	-	0.54
I4WKT7	DNA-directed RNA polymerase subunit alpha	0.92	-
I4WKT8	50S ribosomal protein L17	0.68	-
I4WKU7	ribonuclease G	0.02	-
I4WL10	elongation factor G	0.25	0.22
I4WL11	30S ribosomal protein S7	1.41	0.56
I4WL13	DNA-directed RNA polymerase subunit beta	0.40	0.18
I4WL14	DNA-directed RNA polymerase subunit beta	0.17	0.14
I4WL19	NusG, transcription termination/antitermination protein	0.52	-
I4WL23	elongation factor Tu	-	0.91
I4WL41	amidase	0.04	0.02
I4WL46	30S ribosomal protein S4	0.31	-
I4WL48	30S ribosomal protein S13	0.88	-

I4WL53	50S ribosomal protein L18	0.79	0.58
I4WL54	50S ribosomal protein L6	0.22	-
I4WL55	30S ribosomal protein S8	-	0.75
I4WL57	50S ribosomal protein L5	0.45	0.95
I4WL64	50S ribosomal protein L22	0.33	0.17
I4WL66	50S ribosomal protein L2	0.35	-
I4WL67	50S ribosomal protein L23	0.64	-
I4WL68	50S ribosomal protein L4	0.64	0.66
I4WL69	50S ribosomal protein L3	0.28	-
I4WM58	isoleucine--tRNA ligase	0.06	0.25
I4WMK9	elongation factor P	0.02	0.05
I4WN52	30S ribosomal protein S9	0.43	0.46
I4WN53	50S ribosomal protein L13	0.19	0.81
I4WN63	Crp, transcriptional regulator	0.11	-
I4WNH2	50S ribosomal protein L31 type B	0.15	-
I4WNH5	endoribonuclease	0.88	1.73
I4WNL3	50S ribosomal protein L17	-	0.53
I4WNP6	ribosome-recycling factor	-	0.02
I4WP50	MarR family transcriptional regulator	-	0.06
I4WP94	polyhydroxyalkonate synthesis repressor	0.21	-
I4WPI7	RNA-binding protein	0.23	-
I4WPL6	LepA, elongation factor	0.03	-
I4WPU8	single-stranded DNA-binding protein	0.19	1.42
I4WPX4	FusA, elongation factor G	-	0.07
I4WQ37	transcriptional regulator	-	0.07
I4WQA4	endoribonuclease	-	0.07
I4WQB0	asparagine--tRNA ligase	0.13	0.13
I4WQB2	30S ribosomal protein S6	0.56	-
I4WQB3	30S ribosomal protein S18	0.61	-
I4WQB4	50S ribosomal protein L9	1.16	0.56
I4WQB9	30S ribosomal protein S16	0.67	-
I4WQC2	50S ribosomal protein L19	0.75	0.32
I4WQD3	DksA, RNA polymerase-binding transcription factor	0.13	-
I4WQM0	leucine--tRNA ligase	0.05	0.05
I4WRF0	glutamate--tRNA ligase	0.16	0.05
I4WT09	ribosomal RNA small subunit methyltransferase	0.15	-
I4WT42	MarR family transcriptional regulator	0.32	0.06
I4WTM6	cysteine--tRNA ligase	0.04	-
I4WTZ3	Crp/Fnr family transcriptional regulator	-	0.04
I4WU00	metallo-beta-lactamase family protein, RNA-specific	0.02	0.04
I4WU53	regulatory protein	-	0.07
I4WUG6	alanine--tRNA ligase	0.07	0.04

I4WYD0	poly(A) polymerase I	-	0.10
M4NEI0	DksA, RNA polymerase-binding protein	0.13	0.02
Stress and defense mechanisms			
I4VQY6	hemolysin D	-	0.02
I4VYT9	anaerobically induced outer membrane transmembrane protein	-	0.38
I4VZV3	thioredoxin	-	0.42
I4W2P1	ariflavin resistance protein D	-	0.02
I4W6N0	Lon protease	0.02	-
I4W949	cold shock protein	1.63	1.25
I4WAB5	AhpD, alkyl hydroperoxide reductaseS	0.04	0.54
I4WAV1	10 kDa chaperonin	3.60	16.30
I4WAV2	60 kDa chaperonin	3.14	2.01
I4WB26	PhoH family protein, phosphate starvation inducible protein	0.11	0.07
I4WB63	GTP-binding protein TypA/BipA	0.04	-
I4WBN4	stringent starvation protein	0.17	-
I4WBS7	ATP-dependent protease ATPase subunit HslU	0.46	0.26
I4WC57	salt-induced outer membrane protein	0.38	0.48
I4WDA1	OsmC-like protein	-	0.07
I4WDM9	thioredoxin reductase	0.13	0.07
I4WE54	anaerobically induced outer membrane protein	0.63	1.69
I4WEF2	aminoglycoside phosphotransferase	-	0.01
I4WEG4	PsiF repeat family protein	0.33	-
I4WEU5	acriflavin resistance protein	0.03	0.05
I4WEZ6	CRISPR-associated protein Csd2 family	-	0.06
I4WFB4	CRISPR-associated protein	-	0.12
I4WG36	thiol-disulfide isomerase-like thioredoxin	0.24	0.18
I4WG89	chaperonin	-	0.08
I4WGC1	anaerobically induced outer membrane protein	0.04	0.52
I4WGS4	chaperone	0.12	0.06
I4WI84	GrpE, chaperone	0.21	0.79
I4WI86	DnaK, chaperone	0.54	0.88
I4WIA8	beta-lactamase	0.11	-
I4WIQ0	HflD, high frequency lysogenization protein	0.11	-
I4WIV8	alkyl hydroperoxide reductase	1.55	2.60
I4WJB1	carbon starvation protein	-	0.02
I4WJR0	superoxide dismutase	0.76	5.60
I4WKI2	starvation-inducible outer membrane lipoprotein	1.05	1.02
I4WMA1	starvation-inducible lipoprotein	0.19	-
I4WPF1	activator of Hsp90 ATPase 1 family protein	-	0.44
I4WQL5	thioredoxin	0.19	0.27
I4WRQ8	AhpD, alkyl hydroperoxide reductase	0.23	-
I4WSK9	SurA, chaperone	0.41	1.25

I4WUA1	thioredoxin	0.22	0.13
I4WUC5	cold shock protein	0.38	-
I4WUC6	cold shock protein	2.69	-
I4WUD7	HtpG, chaperone protein	0.31	0.22
I4WUF3	catalase	0.31	0.82
I4WYA6	competence/damage-inducible protein CinA-like	-	0.12
Transport, secretion and efflux			
I4VLQ8	bacterioferritin	0.19	-
I4VNB1	YajC, preprotein translocase subunit	-	0.38
I4VRS1	sortase system response regulator	0.08	0.10
I4VUA8	ExbB, biopolymer transport protein	-	0.31
I4VUA9	TonB family protein	0.65	-
I4VVG8	translocase subunit SecA	0.05	0.03
I4VYG3	FtsY, signal recognition particle receptor	-	0.06
I4VYN0	TolQ protein	0.14	0.16
I4VYN5	YbgF, Tol-pal system protein	-	0.05
I4W0B9	FtsY, signal recognition particle receptor	0.07	-
I4W1W5	Oar protein	-	0.02
I4W345	outer membrane receptor protein	0.03	-
I4W9D2	twin arginine-targeting protein translocase	-	0.36
I4WAP8	TonB-dependent receptor	0.03	0.15
I4WBA3	bacterioferritin	-	0.36
I4WBV4	ExbD1, biopolymer transport protein	0.03	0.30
I4WBV5	ExbB, biopolymer transport protein	1.25	-
I4WBW4	YidC, insertase	0.04	-
I4WBX8	ABC transporter	0.19	-
I4WC41	TonB dependent receptor protein	-	0.02
I4WDN2	LolA, outer-membrane lipoprotein carrier protein	0.31	0.52
I4WDU8	bacterioferritin	0.14	-
I4WDV1	TolC family type I secretion outer membrane protein	0.63	0.81
I4WDW0	Na$^+$/proline symporter	0.06	0.05
I4WE23	TonB-dependent outer membrane receptor protein	0.67	1.61
I4WEF4	SecF, protein-export membrane protein	-	0.06
I4WEF5	SecD, translocase	0.04	0.09
I4WEQ9	TonB-dependent receptor	0.33	0.34
I4WEU4	RND family efflux transporter	0.29	0.18
I4WEX9	TonB-dependent receptor	0.35	0.33
I4WFK2	ferrienterochelin and colicin receptor	1.44	1.75
I4WFT1	cobalamin receptor protein	0.19	0.29
I4WG81	TonB protein	0.30	0.14
I4WGD3	TonB family protein	0.06	0.13
I4WGD5	OmpB-like	2.90	3.24

I4WGD6	autotransorter	-	0.13
I4WGS8	ferric enterobactin receptor	0.04	0.14
I4WGU0	TolR protein	-	0.09
I4WGU2	TolB	0.36	0.26
I4WH55	TonB-dependent siderophore receptor	0.11	0.17
I4WH99	sodium ABC transporter ATP-binding protein	-	0.07
I4WHB0	ABC transporter ATP-binding protein	-	0.06
I4WHD4	long chain fatty acid transport protein	0.12	0.25
I4WIQ1	porin	0.13	0.26
I4WIQ3	PstS, phosphate-binding protein	0.74	0.76
I4WIQ6	PstB, phosphate import ATP-binding protein	-	0,05
I4WIQ7	PhoU, phosphate-specific transport system accessory protein	0.54	-
I4WIX0	TonB-dependent receptor	0.07	0.04
I4WJ71	TonB-dependent receptor	0.14	0.20
I4WJJ4	preprotein translocase	0.21	-
I4WJQ5	TonB-dependent outer membrane receptor	0.13	0.24
I4WJU6	TonB dependent receptor protein	0.23	0.34
I4WL02	outer membrane efflux protein	-	0.04
I4WM79	hydrophobe/amphiphile efflux-1 (HAE1) family transporter	0.05	0.05
I4WM80	multidrug resistance protein	0.23	0.12
I4WNG4	type IV pilus secretin	0.34	0.05
I4WNI0	ABC transporter auxiliary protein	0.76	0.70
I4WNI1	ABC transporter periplasmic protein	0.10	0.05
I4WNI3	ABC transporter	0.03	0.12
I4WP57	ABC transporter permease	-	0.02
I4WP96	efflux pump membrane protein	0.05	0.05
I4WPE6	RNA signal recognition particle 4.5S RNA	-	0.19
I4WPJ0	trigger factor	-	0.05
I4WPL7	signal peptidase	-	0.05
I4WPX5	TonB-dependent receptor	0.03	0.04
I4WQ75	TonB-dependent receptor protein	0.08	0.08
I4WR37	hemolysin D	0.32	0.11
I4WRP8	sugar transporter	-	0.07
I4WRR8	outer membrane protein	0.20	0.26
I4WSA6	ferritin	0.50	0.21
I4WSX0	ABC-type transporter	0.11	0.08
I4WSX8	Fe^{2+}-dicitrate sensor	0.08	0.11
I4WT49	RND family efflux transporter	0.07	-
I4WTY3	TonB-dependent outer membrane receptor	0.12	0.07
I4WU14	efflux pump membrane fusion protein	0.09	0.04
I4WU70	polyketide cyclase/dehydrase and lipid transport	0.73	1.13
I4WUB7	metal ion ABC transporter substrate-binding protein	0.90	0.66
I4WUE7	TonB-dependent siderophore receptor	0.08	0.12

I4WWB0	outer membrane cobalamin receptor protein	0.33	-
I4WZB9	ABC transporter ATP-binding protein	0.09	-
Other functions			
I4VJ32	serine/threonine phosphatase with Cache sensor	-	0.01
I4VJL1	dTDP-glucose 4.6-dehydratase	-	0.05
I4VKW0	Cell division protein	0.10	-
I4VP03	MoxR-like ATPase	-	0.06
I4VPB8	modulator of FtsH protease	0.29	-
I4VPN3	cell division protein	-	0.04
I4VPP0	partition protein	-	0.11
I4VQ36	FtsE, cell division ATP-binding protein	0.04	-
I4VQR5	MreB, rod shape-determining protein	-	0.11
I4VTQ2	AMP nucleosidase	-	0.09
I4VV38	response regulator consisting of a CheY-like receiver domain and a Fis-type HTH domain protein	0.18	-
I4VV66	PilH, two-component system response regulatory protein	0.18	-
I4VV67	response regulator receiver protein	0.42	-
I4VXH1	two-component system response regulator protein	0.12	0.06
I4VZJ1	response regulator receiver domain-containing protein	-	0.27
I4W0C6	NTP pyrophosphohydrolase	-	0.07
I4W2S6	ribose-phosphate pyrophosphokinase	0.12	-
I4W459	sulfate adenylyltransferase subunit 2	-	0.04
I4W782	protein kinase	-	0.02
I4W8Y5	amidohydrolase	-	0.11
I4W9N8	glutathione S-transferase	-	0.02
I4W9N9	adenylosuccinate lyase	-	0.21
I4W9T6	methyltransferase	-	0.16
I4WAH3	HemC, porphobilinogen deaminase	0.16	-
I4WAT9	PurH, bifunctional purine biosynthesis protein	0.09	0.04
I4WAZ7	ObgE, GTPase	0.04	-
I4WB46	metal-dependent amidohydrolase	0.10	0.11
I4WB49	amidohydrolase	-	0.08
I4WBQ6	5'-nucleotidase domain-containing protein	0.03	-
I4WBV2	PdxJ, pyridoxine 5'-phosphate synthase	0.15	-
I4WBZ2	partition protein	0.17	-
I4WCC3	alkaline phosphatase	-	0.03
I4WCC6	5'-nucleotidase domain-containing protein	0.08	0.04
I4WCF1	thymidylate synthase	0.08	0.23
I4WCF2	dihydrofolate reductase	0.28	-
I4WCL9	Amidohydrolase	-	0.04
I4WCM6	thymidine kinase	-	0.09
I4WCP1	haloacid dehalogenase-like hydrolase	-	0.20

I4WCP5	delta-aminolevulinic acid dehydratase	0.06	0.49
I4WCP7	dihydroorotase	0.12	0.39
I4WCP8	glutamate--cysteine ligase	0.04	0.17
I4WD04	thioredoxin	0.17	-
I4WD67	methyltransferase	0.09	-
I4WD71	metallo carboxipeptidase	0.04	-
I4WDN1	FtsK, DNA segregation ATPase	-	0.02
I4WDT2	thiamine-phosphate synthase	0.11	-
I4WDT3	HemL, glutamate-1-semialdehyde 2.1-aminomutase	0.10	0.12
I4WDT9	Adk, adenylate kinase	1.53	1.18
I4WDU5	inorganic pyrophosphatase	0.08	0.50
I4WDV0	L-isoaspartate carboxylmethyltransferase	-	0.13
I4WDW1	lipid/polyisoprenoid binding protein	2.76	1.19
I4WE19	aspartyl/asparaginyl beta-hydroxylase	0.02	-
I4WE39	NAD-dependent epimerase/dehydratase	0.11	0.48
I4WE90	response regulator with CheY-like receiver domain	0.69	0.29
I4WEG5	uracil phosphoribosyltransferase	0.09	-
I4WEI4	uridylate kinase	0.08	0.12
I4WF02	glutathione S-transferase	0.21	-
I4WF09	MreB, rod shape-determining protein	0.25	-
I4WF36	UbiB, kinase	0.02	-
I4WF93	oxygen-dependent coproporphyrinogen-III oxidase	-	0.22
I4WF97	N-acyl-L-amino acid amidohydrolase	-	0.04
I4WFD4	amidohydrolase	0.02	0.02
I4WG63	acetyl transferase	-	0.03
I4WG75	amidase	-	0.03
I4WG76	sulfate adenylyltransferase	0.17	-
I4WG77	bifunctional sulfate adenylyltransferase /adenylylsulfate kinase protein	0.24	0.10
I4WG87	signal transduction protein	0.20	0.10
I4WGC2	formylglycine-generating sulfatase family protein	0.39	0.29
I4WGC3	SCO1 /SenC family protein	0.36	-
I4WGC5	thiol peroxidase	0.21	0.29
I4WGP6	glutamine cyclotransferase	0.14	0.24
I4WGV1	laccase-domain protein	0.36	-
I4WH93	RmuC domain-containing protein	0.05	0.03
I4WH94	GTP cyclohydrolase	0.33	0.04
I4WHH6	uroporphyrin-III C-methyltransferase	0.28	-
I4WIB5	pirin	0.10	0.34
I4WIC6	nucleoside diphosphate kinase	0.63	1.53
I4WID0	GTP binding protein	0.19	0.13
I4WID4	inosine-5'-monophosphate dehydrogenase	-	0.10
I4WID5	GMP synthase	0.05	-

I4WIK5	ZipA, cell division protein	0.08	-
I4WIM0	TraB, pheromone shutdown-related protein	0.03	-
I4WIN6	histone-like protein	3.65	1.50
I4WIT8	adenylosuccinate synthetase	0.24	0.21
I4WIV3	2-methylcitrate dehydratase	0.16	0.32
I4WJ80	acetylornithine aminotransferase	-	0.19
I4WJ85	Parathion hydrolase	0.03	-
I4WJ96	6,7-dimethyl-8-ribityllumazine synthase	0.22	-
I4WJ97	L.D-carboxypeptidase A	0.06	0.21
I4WJ98	3,4-dihydroxy-2-butanone 4-phosphate synthase	0.06	0.10
I4WJA5	orotidine 5'-phosphate decarboxylase	-	0.05
I4WJB8	phosphoribosylformylglycinamidine synthase	-	0.02
I4WJQ4	Rossmann fold nucleotide-binding protein	-	0.07
I4WJR1	N5-carboxyaminoimidazole ribonucleotide synthase	0.11	-
I4WJR2	N5-carboxyaminoimidazole ribonucleotide mutase	0.28	-
I4WJS9	adenosylmethionine-8-amino-7-oxononanoate aminotransferase	-	0.04
I4WJT2	chemotaxis-related protein	0.25	0.03
I4WJT6	chemotaxis signal transduction protein pili	-	0.10
I4WJT9	glutathione synthetase	0.08	-
I4WJU3	aspartate carbamoyltransferase	0.13	0.01
I4WJU7	twitching motility protein	-	0.02
I4WJU8	twitching motility protein	0.28	0.09
I4WKD1	response regulator receiver protein	0.54	0.12
I4WKD2	DnaJ-class molecular chaperone	0.11	-
I4WKH9	MoxR-like ATPase	0.04	-
I4WKI3	diadenosine tetraphosphate hydrolase	-	0.38
I4WMK7	2-amino-3-carboxymuconate-6-semialdehyde decarboxylase	-	0.05
I4WNA1	phosphoribosylaminoimidazole-succinocarboxamide synthase	0.14	0.03
I4WNG3	MoxR-like ATPase	0.11	-
I4WNH3	inosine-uridine nucleoside N-ribohydrolase	-	0.12
I4WNV0	sulfatase-modifying factor protein	0.05	-
I4WP91	2-polyprenyl-6-methoxyphenol hydroxylase-like oxidoreductase	0.04	-
I4WPE1	3-demethylubiquinone-9 3-methyltransferase	-	0.26
I4WPF7	glutathione S-transferase	-	0.10
I4WPG0	penicillin acylase	-	0.02
I4WPG1	succinate-CoA transferase	0.04	0.04
I4WPG2	3-demethylubiquinone-9 3-methyltransferase	-	0.33
I4WPH2	PyrG, CTP synthase	0.10	-
I4WPJ1	ATP-dependent Clp protease	0.24	0.87
I4WPM8	hypoxanthine-guanine phosphoribosyltransferase	0.12	0.10
I4WPM9	S-methyl-5'-thioinosine phosphorylase	-	0.11
I4WPV1	geranylgeranyl pyrophosphate synthase	0.06	0.15

I4WPV4	polyisoprenoid-binding protein	-	0.08
I4WPW4	polyisoprenoid-binding protein	0.05	0.05
I4WQ95	S-formylglutathione hydrolase	-	0.07
I4WQC3	PAS/PAC sensor-containing diguanylate cyclase/phosphodiesterase	0.07	0.07
I4WQC8	UbiG, ubiquinone biosynthesis O-methyltransferase	0.08	-
I4WQL8	PqiB family protein	0.05	0.03
I4WRC2	carboxymethylenebutenolidase	0.25	-
I4WRC7	ATPase	0.05	0.04
I4WRK0	bifunctional folylpolyglutamate synthase/dihydrofolate synthase	0.03	-
I4WRN4	isoprenoid biosynthesis protein	0.18	0.14
I4WSD6	nucleotide-binding protein	0.03	-
I4WSL8	GTP binding protein	0.04	-
I4WSY2	response regulator with CheY-like receiver domain	0.36	0.26
I4WSY8	adenosylhomocysteinase	-	0.03
I4WSZ6	S-adenosylmethionine synthase	0.14	0.28
I4WT06	LppC family lipoprotein	0.13	0.16
I4WT08	MraZ, transcriptional regulator	0.24	0.12
I4WU93	acetyl transferase	0.23	-
I4WUC9	pirin	0.23	0.11
I4WV01	phosphoglycerol transferase family protein, alkaline phosphatase superfamily	-	0.04
I4WV06	pteridine reductase	-	0.11
I4WVE3	disulfide isomerase	0.24	0.53
I4WVE4	thiol:disulfide interchange protein	0.17	0.19
I4WVX6	(p)ppGpp synthetase	-	0.01
I4WXN8	inosine-5'-monophosphate dehydrogenase	0.07	-
I4WYH0	N5-carboxyaminoimidazole ribonucleotide synthase	-	0.04
M4NDJ5	heme biosynthesis enzyme	-	0.05
Function unknown			
I4VQ20		-	0.19
I4VSJ4		0.04	-
I4VV34		-	0.35
I4W9G3		-	0.06
I4W9L9		0.21	-
I4WAA1		0.81	0.23
I4WB04		0.08	0.05
I4WB10		0.21	0.44
I4WB40		0.10	-
I4WBM4		-	0.02
I4WBS3		0.25	0.32
I4WBT2		0.06	0.06
I4WBV7		0.72	0.44

I4WC23	-	0.50
I4WC53	-	0.07
I4WCF0	0.09	-
I4WD84	0.11	0.13
I4WDU6	0.28	0.20
I4WDZ3	0.11	-
I4WDZ5	0.09	0.19
I4WE01	0.09	-
I4WE02	0.15	-
I4WE09	0.15	-
I4WE16	0.17	0.12
I4WEN9	-	0.14
I4WEU3	0.57	2.33
I4WEX6	0.01	0.01
I4WF92	-	0.09
I4WF94	0.45	0.02
I4WFK9	0.14	-
I4WFL9	0.02	0.01
I4WFM7	5.89	9.61
I4WG57	-	0.03
I4WG83	0.26	-
I4WG92	0.13	0.03
I4WGK8	0.05	0.45
I4WGK9	1.02	0.17
I4WH42	-	0.16
I4WH59	0.08	0.03
I4WHT8	0.06	0.16
I4WJA7	-	0.06
I4WJS3	0.28	0.36
I4WJU4	0.15	0.10
I4WM37	0.10	-
I4WMC4	-	0.14
I4WMK6	0.50	0.67
I4WN45	0.15	-
I4WN49	0.21	-
I4WNI6	-	0.14
I4WNX0	-	0.01
I4WPE8	0.15	0.14
I4WPL8	0.21	-
I4WPM4	0.25	-
I4WQL9	0.08	0.13
I4WQS0	0.08	-
I4WRB7	0.59	0.35

I4WRC0	0.38	0.26
I4WRF9	0.64	0.14
I4WRK1	-	0.06
I4WRN7	-	0.02
I4WRW1	-	0.04
I4WRX1	0.69	1.28
I4WSB0	0.14	0.08
I4WSB4	-	0.11
I4WSM6	0.01	0.01
I4WSW9	0.07	-
I4WU94	0.19	-
I4WUA7	0.28	-
I4WUC4	0.44	0.16
I4WUE0	0.28	-
I4WYZ8	0.39	-

[a] Data are the mean of two replicates.

[b] Proteins in bold characters have a predicted intracellular localization.

[c] Protein not detected or protein identification not considered valid.

Table S3 Proteins produced by *Myxococcus xanthus* DK 1622 during growth in minimal medium supplemented with suberin at day 5 and day 25

Uniprot accession number	Putative function	Abundance (NSpC[a])	
		5 days	25 days
Amino acid metabolism			
Q1D8A6	penicillin acylase	0.18	0.11
Q1D5W7	peptidase	0.27	0.03
Q1D4C2[b]	Glu/Leu/Phe/Val dehydrogenase	0.36	0.04
Q1D7P1	peptidase	0.24	-[c]
PNP	Glu/Leu/Phe/Val dehydrogenase	0.28	-
Q1D9F6	peptidase	0.30	-
Q1DBU7	peptidase	0.29	0.14
Q1D215	aminotransferase	0.22	0.22
Q1DAS8	prolyl endopeptidase	0.22	0.04
Q1DAR8	Xaa-Pro aminopeptidase	0.19	0.04
Q1CXD4	peptidase	0.18	0.23
Q1DAQ9	Cys/Met metabolism PLP-dependent enzyme	0.19	0.11
Q1DBU8	peptidase	0.22	0.08
Q1D7X2	glycine dehydrogenase	0.16	0.05
Q1CY03	peptidase	0.15	-
Q!CZK0	pptidase	0.13	-
Q1DD17	peptidase	0.27	0.20
Q1DC00	cysteine synthase	0.29	0.39
Q1CZV8	4-hydroxy-tetrahydrodipicolinate synthase	0.21	-
Q1D6Z0	aspartate aminotransferase	0.12	-
Q1D7L0	peptidase	0.15	-
Q1D4A7	urocanate hydratase	0.24	-
Q1D827	branched-chain amino acid aminotransferase	0.13	-
Q1CWK6	peptidase	0.26	-
Q1CZV3	peptidase	0.19	0.07
GLYA	serine hydroxymethyltransferase	0.18	-
Q1D3P1	2-oxoisovalerate dehydrogenase	0.19	0.24
Q1D9S1	aminopeptidase	0.10	0.10
Q1DER8	serine protease	0.16	0.05
METK	S-adenosylmethionine synthase	0.11	-
Q1D5T1	peptidase	0.11	-
Q1DEW1	peptidase	0.18	-
Q1D3P0	2-oxoisovalerate dehydrogenase	0.10	-
HUTH	histidine ammonia-lyase	0.08	-
Q1CWF2	peptidase	0.09	-
Q1D6F2	peptidyl-dipeptidase	0.14	-
Q1DDV0	glutamine synthetase	0.10	0.07
Q1DAV7	peptidase	0.13	0.02
Q1DFN7	peptidase	0.15	0.21

SAHH	adenosylhomocysteinase	0.12	-
Q1DDP8	peptidase.	0.11	-
Q1CZZ5	1-pyrroline-5-carboxylate dehydrogenase	0.12	-
Q1D2E3	peptidase	0.13	-
Q1D4V2	alanine dehydrogenase	0.11	-
Q1D2K4	aminopeptidase	0.07	-
Q1CZD2	zinc metalloprotease	0.10	-
Q1CYE6	arginine N-succinyltransferase	0.05	-
CARB	carbamoyl-phosphate synthase	0.09	-
HSLU	ATP-dependent protease	0.10	0.17
Q1CYQ0	fumarylacetoacetate hydrolase	0.13	0.13
Q1DBS1	chymotrypsin	0.10	-
F8CLH1	aspartate-semialdehyde dehydrogenase	0.03	-
Q1D9N1	peptidase	0.05	-
Q1DEY9	dipeptidyl peptidase	0.05	-
Q1DAK3	peptidase	0.08	-
ASTB	N-succinylarginine dihydrolase	0.06	-
Q1DA13	peptidase	0.06	-
Q1DAQ3	cystathionine beta-synthase	0.06	-
Q1D625	peptidase	0.05	-
Q1D624	peptidase	0.05	-
Q1DG40	peptidase	0.06	-
Q1D459	L-erytro-3,5-diaminohexanoate dehydrogenase	0.02	-
Q1DD72	peptidase	0.02	-
Q1D4R7	peptidase	0.07	-
Q1D6K7	chorismate synthase	0.15	-
Q1CY62	protease	0.04	-
Q1D3A8	L-lysine 2,3-aminomutase	0.04	-
Q1CW90	metallopeptidase	0.04	-
Q1CY13	peptidase	0.03	0.09
Q1CYP7	serine protease	0.02	-
Q1DCI3	gamma-glutamyltranspeptidase	0.05	-
Q1DBP3	deoxyhypusine synthase family protein	0.03	-
Q1DDS8	protease	0.03	-
Q1D013	glutamate dehydrogenase	0.03	-
A0A0H4WWS1	sarcosine oxidase	0.02	-
Q1DA16	peptidyl-dipeptidase	0.03	-
Q1D3D3	dihydrodipicolinate reductase	0.05	-
DAPB	4-hydroxy-tetrahydrodipicolinate reductase	0.04	-
Q1DDD9	Glu/Leu/Phe/Val dehydrogenase	0.02	-
Q1D1D4	peptidase	0.03	0.10
Q1DCD4	L-allo-threonine aldolase	0.02	-
HGD	homogentisate 1,2-dioxygenase	-	0.13
Q1D188	peptidase	-	0.04
Q1D6G9	peptidase	-	0.09

Q1D7W5	aspartate-semialdehyde dehydrogenase	-	0.03
Q1CYR4	serine protease	-	0.06
Q1DFN6	aminotransferase	-	0.03
Q1D8P6	peptidase	-	0.03
Q1DE55	peptidase	-	0.02
Q1CZR8	peptidase	-	0.04
Q1D8L5	protease	-	0.07
PAND	aspartate 1-decarboxylase	-	0.08
SERC	phosphoserine aminotransferase	-	0.11
Q1DEW6	peptidase		
Carbohydrate metabolism			
Q1DCV2	phosphoenolpyruvate carboxykinase	0.22	-
Q1D5Z8	fructose-bisphosphate aldolase	0.34	0.06
Q1D8J1	glyceraldehyde-3-phosphate dehydrogenase	0.28	0.43
Q1CVV7	transketolase	0.13	-
ENO	enolase	0.23	0.05
TAL	transaldolase	0.29	-
Q1DDQ9	glucose-6-phosphate 1-dehydrogenase	0.17	-
TPIS	triosephosphate isomerase	0.26	0.09
Q1CY18	gluconolaconase	0.12	0.11
Q1D1J6	GDP-mannose 4,6-dehydratase	0.11	-
Q1DDR1	6-phosphogluconate dehydrogenase	0.10	-
G6PI	glucose-6-phosphate isomerase	0.09	0.16
Q1D0G8	phosphoglucomutase/phosphomannomutase	0.04	-
Q1CXL1	glucose/sorbosone dydrogenase	0.08	0.04
Q1D6M2	UDP-glucose 4-epimerase	0.07	-
Q1D8J0	phosphoglycerate kinase	0.06	-
Q1D6L5	pyruvate kinase	0.05	-
Q1CYU9	pyruvate kinase	0.03	-
Q1DCE1	UTP-glucose-1-phosphate uridylyltransferase	0.05	-
Q1D3S1	chitinase	0.05	-
Q1DDR0	6-phosphogluconolactonase	0.04	-
GLGA	glycogen synthase	0.02	-
Cell wall, membrane and envelope biogenesis			
Q1DDQ0	lipoprotein	0.17	0.17
Q1CVX7	lipoprotein	0.23	0.03
Q1CZE8	outer membrane protein	0.23	0.13
MLPA	lipoprotein MlpA	0.20	0.20
Q1D8U6	lipoprotein	0.15	0.14
Q1D0K1	lipoprotein	0.50	0.28
Q1DD51	lipoprotein	0.10	-
Q1D8L4	lipoprotein	0.26	0.17
Q1CXU8	lipoprotein	0.12	0.08
Q1CYZ9	Kelch motif/HYR domain protein	0.09	0.06
Q1CWA7	outer membrane protein	0.26	-
Q1DFL0	cell surface protein	0.23	0.20

Q1CZ46	secretion system protein	0.32	-
Q1CY27	cell surface protein	0.08	0.06
Q1CY79	lipoprotein	0.32	-
Q1D364	outer membrane lipoprotein	0.12	0.08
Q1D6V9	lipoprotein	0.18	0.04
Q1CXU6	lipoprotein	0.14	0.10
Q1D9N0	cell surface protein lipoprotein	0.18	0.08
Q1CWM1	lipoprotein	0.18	-
Q1D0H4	lipoprotein	0.17	-
Q1DCM4	lipoprotein	0.11	0.11
Q1DE07	chemotaxis protein MotB	0.22	-
Q1D8J2	N-acetylmuramoyl-L-alanine amidase	0.05	0.02
Q1CY59	stomatin-like domain-containing protein	0.14	-
Q1D5A9	stomatin-like domain-containing protein	0.16	-
Q1D813	LysM domain protein	0.12	-
Q1D9B4	outer membrane protein	0.13	0.05
Q1CWS3	chemotaxis protein MotB	0.16	-
Q1CWB1	lipoprotein	0.03	0.03
Q1D1K7	outer membrane protein	0.15	-
Q1D3C1	outer membrane protein	0.13	0.07
Q1DDE9	lipoprotein	0.12	-
Q1CXN6	lipoprotein	0.18	0.18
Q1D049	Ig-like domain protein	0.02	0.01
Q1D805	membrane protein	0.05	-
Q1CVX8	lipoprotein	0.13	-
Q1DEJ6	lipoprotein	0.05	0.02
Q1D227	Tol-pal system protein YbgF	0.11	-
Q1D729	L-seryl-tRNA(Sec) selenium transferase	0.07	-
Q1DC33	lipoprotein	0.13	-
Q1D638	lipoprotein	0.11	-
Q1D917	outer membrane protein	0.13	0.11
Q1D3F5	pilus assembly protein	0.14	-
Q1D122	lipoprotein	0.18	0.16
Q1DE38	lipoprotein	0.06	-
Q1D139	outer membrane protein	0.09	0.07
Q1DDT8	outer membrane protein	0.09	0.11
Q1CYN2	lipoprotein	0.13	0.08
Q1DDJ2	type IV pilus assembly protein	0.02	-
Q1DA87	lipoprotein	0.05	-
Q1DCK1	pilus assembly protein	0.02	0.01
Q1D0G9	outer membrane protein	0.06	-
Q1DAK4	OmpA domain protein	0.03	-
Q306N4	type IV secretion protein PilO	0.07	-
Q1DFQ7	lipoprotein	0.16	-
Q1D1X6	OmpA domain protein	0.05	-
Q1D218	OmpA family protein	0.12	-

Q1D811	MotA/TolQ/ExbB proton channel protein	0.05	-
Q1D383	BamA	0.02	-
Q1D0S5	UDP-N-acetylmuramyl-tripeptide synthetase	0.05	-
Q1DD080	pilus assembly protein PilM	0.04	-
Q1D427	outermmebrane protein	0.09	-
Q1CYZ8	OmpA domain protein	0.04	-
Q1D314	surface cell protein	0.01	0.02
Q1D991	lipoprotein	0.03	-
Q1D2C6	OmpA domain protein	0.03	0.10
Q1D1M7	collagen triple helix repeat protein	0.05	0.09
Q1CWC6	lipoprotein	0.06	0.04
Q1D3M7	membrane protein	0.07	-
Q1D1J2	lipoprotein	0.08	-
Q1D8L3	lipoprotein	0.04	0.04
Q1DAX3	lipoprotein	0.05	-
Q1DAE0	lipoprotein	0.01	0.02
Q1D6F4	lipoprotein	0.05	-
Q1DE67	lipoprotein	0.02	0.03
Q1D0I5	lipoprotein	0.02	-
Q1D191	cell surface protein	-	0.21
Q1CVK5	Ig domain protein	-	0.04
Q1D8Z4	outer membrane lipoprotein	-	0.06
Q1D0T6	OmpA domain protein	-	0.01
Q1D9T7	lipoprotein	-	0.04
Q1DE25	lipoprotein	-	0.07
Q1D271	Ig domain protein	-	0.02
Q1D7R7	lipoprotein	-	0.01
Q1D646	lipoprotein	-	0.03
Q1D7R8	lipoprotein	-	0.02
Q1D303	type IV secretion system protein	-	0.06
Q1CXP7	lipoprotein	-	0.02
Q1CXB9	lipoprotein	-	0.07
A0A0H4WXC7	outer membrane protein assembly factor	-	0.02
Q1D9P7	Omp A domain protein	-	0.06
Energy production and conversion			
ATPB	ATP synthase	0.43	0.11
Q1D4M9	dihydrolipoyl dehydrogenase	0.38	0.09
Q1CZF9	molybdopterin oxidoreductase	0.20	0.07
ATPA	ATP synthase	0.38	0.11
Q1D6L0	citrate synthase	0.27	0.14
Q1D8Y7	pyruvate dehydrogenase	0.34	0.04
Q1D8Y8	pyruvate dehydrogenase	0.26	-
MDH	malate dehydrogenase	0.32	0.09
Q1D6J1	succinate dehydrogenase	0.22	0.04
Q1DCK3	aconitate hydratase	0.14	0.02

Q1CYR1	isocitrate dehydrogenase	0.31	0.08
Q1CZK3	2-oxoglutarate dehydrogenase	0.10	0.01
Q846U1	adventurous gliding motility protein	0.21	-
SUCC	succinyl-CoA ligase	0.29	-
Q1D8Y6	pyruvate dehydrogenase	0.16	-
Q1D4N1	alpha keto acid dehydrogenase	0.26	-
ATPG	ATP synthase	0.26	-
Q1D1C4	cytochrome c	0.12	0.07
Q1CZK2	2-oxoglutarate dehydrogenase	0.15	-
Q1CZX3	pyruvate dehydrogenase	0.14	-
Q1D4Q0	CyaE	0.12	-
Q1CZF6	cytochrome c family protein	0.20	-
Q1D6I8	succinyl-CoA ligase	0.18	-
Q1D6J0	succinate dehydrogenase	0.16	-
ATPD	ATP synthase	0.25	-
NUOD	NADH-quinone oxidoreductase	0.10	-
Q1D2C8	aldehyde dehydrogenase	0.06	-
Q1D856	NADH-quinone oxidoreductase	0.16	-
NUOI	NADH-quinone oxidoreductase	0.12	-
Q1D8S8	NADH dehydrogenase I	0.06	-
Q1CWX3	aldehyde dehydrogenase	0.04	-
Q1DA35	2-nitropropane dioxygenase	0.07	0.12
NUOB	NADH-quinone oxidoreductase	0.05	-
Q1CZG0	cytochrome c	0.12	-
Q1DDC7	NADH dehydrogenase	0.14	-
Q1D5X3	PQQ enzyme repeat domain protein	0.07	-
Q1CW00	short chain dehydrogenase	0.05	-
Q1DDC8	NADH dehydrogenase	0.05	-
ATPF	ATP synthase	0.12	-
Q1DDE1	succinate dehydrogenase	0.06	-
Q1CZF2	cytochrome c	0.03	-
Q1D6Y7	oxidoreductase	-	0.04
Lipid metabolism and ketogenesis			
Q1CWS1	lipase	0.31	0.21
Q1D4F3	patatin-like phospholipase	0.35	0.13
Q1CYB4	acetyl co-enzyme A carboxylase carboxyltransferase	0.37	0.16
Q1D030	acetyl-coenzyme A synthetase	0.19	0.06
Q1D5V0	acetyl-CoA acetyltransferase	0.33	0.10
Q1D9B8	long-chain-fatty-acid--CoA ligase	0.20	-
Q1D233	3-hydroxyacyl-CoA dehydrogenase	0.17	-
Q1D5Y2	carboxyl transferase domain protein	0.19	-
Q1D009	YceI-like family protein	0.27	0.14
Q1D3D6	acyl-CoA dehydrogenase	0.13	0.12
BKT	beta-ketothiolase	0.17	-
Q1D5U4	acyl-CoA dehydrogenase	0.10	-
Q1D984	acetyl-coenzyme A synthetase	0.06	-

Q1DDA0	propionyl-CoA carboxylase	0.07	0.02
Q1DFT0	3-oxoacyl-[acyl-carrier protein] reductase	0.21	-
Q1D0B9	acetyl-CoA carboxylase. biotin carboxylase	0.10	-
Q1D340	malonyl CoA-acyl carrier protein transacylase	0.11	-
Q1D5U1	3-hydroxyacyl-CoA dehydrogenase	0.18	-
Q1D5U2	enoyl CoA dehydratase	0.13	-
Q1D4E4	acyl-CoA dehydrogenase	0.07	-
Q1D0T9	acetyl CoA carboxylase	0.03	-
Q1D555	acetyl-coenzyme A carboxylase carboxyl transferase	0.06	-
Q1D234	acetyl-CoA acetyltransferase	0.05	-
Q1CZK4	enoyl-[acyl-carrier-protein]	0.07	-
Q1DDA2	propionyl-CoA carboxylase	0.04	-
Q1D343	3-oxoacyl-[acyl-carrier-protein] synthase	0.07	-
Q1D964	acyl-CoA hydrolase	0.08	-
Q1CYM5	medium-chain fatty acid-CoA ligase	0.03	-
A0A0H4WWQ8	acyl-CoA dehydrogenase	0.02	-
Q1D5Y4	3-hydroxybutyryl-CoA dehydratase	0.05	-
Q1D8V2	acetyl-coenzyme A carboxylase carboxyl transferase	0.05	-
Q1D5Y1	acyl-CoA dehydrogenase	0.04	-
Q1D5W1	patatin-like phospholipase family protein	0.01	-
Q1D5V2	3-oxoacid CoA-transferase family	0.07	-
Q1D855	long-chain-fatty-acid--CoA ligase	0.02	-
Q1D566	acyltransferase	0.02	-
Q1CZW5	acyl-CoA dehydrogenase	0.02	0.02
Q1D003	beta-ketothiolase	-	0.13
Replication, transcription, translation and DNA repair			
EFTU1	elongation factor Tu	0.62	-
RPOB	DNA-directed RNA polymerase	0.14	-
Q1CYZ6	cyclic nucleotide-binding domain protein	0.26	-
Q1DAM8	transcription termination/antitermination protein NusA	0.27	-
RPOC	DNA-directed RNA polymerase	0.10	-
RPOA	DNA-directed RNA polymerase	0.22	-
Q1DC39	DNA topoisomerase	0.36	-
Q1CYZ5	cyclic nucleotide-binding domain protein	0.15	-
Q1D015	ATP-dependent helicase	0.10	-
AGLZ	adventurous-gliding motility protein	0.06	-
TPS	development-specific protein	0.21	-
EFTS	elongation factor	0.25	-
Q1D9U0	glutamine--tRNA ligase	0.12	-
Q1D8J8	OB-fold nucleic acid binding domain protein	0.11	-
Q1DDC0	response regulator receiver domain protein (CheY-like)	0.11	-
SYP	proline--tRNA ligase	0.10	-
L7UF14	ribonuclease	0.03	-
SYM	methionine--tRNA ligase	0.06	-
SYT	threonine--tRNA ligase	0.07	-

Q1CWL9	5'-nucleotidase	0.06	-
Q1D5U8	SSU ribosomal protein S1p	0.07	-
IF2	translation initiation factor IF-2	0.04	-
Q1D1Z2	exodeoxyribonuclease III	0.10	-
RS2	30S ribosomal protein	0.12	-
Q1D0I2	PspA/IM30 family protein	0.14	-
EFG1	elongation factor G 1	0.04	-
Q1DCG4	transcriptional regulator	0.08	-
Q1DEC3	signal transduction protein	0.04	-
Q1DFW6	methyl-accepting chemotaxis protein	0.06	-
SYS	serine--tRNA ligase	0.02	-
Q1D7Q3	DNA-binding protein FruA	0.12	-
Q1CZ22	isoleucine--tRNA ligase	0.03	-
SYA	alanine--tRNA ligase	0.04	-
RL9	50S ribosomal protein L9	0.13	-
SYN	asparagine--tRNA ligase	0.05	-
TIG	trigger factor	0.05	-
Q1D293	50S ribosomal protein L25	0.13	-
Q1D5D5	tRNA pseudouridine synthase	0.03	-
SYGB	glycine--tRNA ligase	0.03	-
IF3	translation initiation factor IF-3	0.07	-
Q1D1I5	phosphohistidine phosphatase SixA	0.14	-
Q1D7R1	DNA polymerase I	0.02	-
RL10	50S ribosomal protein L10	0.08	-
Q1DGB6	exoribonuclease	0.04	-
RRF	ribosome-recycling factor	0.10	-
Q1D4V8	gliding motility regulatory protein	0.02	-
Q1DFR3	transcriptional regulator	0.19	-
Q1D3Z2	valine--tRNA ligase	0.01	-
Q1D5P9	tryptophanyl-tRNA synthetase	0.05	-
Q1D3Z1	response regulator	0.04	-
Q1D3C3	aspartyl-tRNA synthetase	0.01	-
RL2	50S ribosomal protein L2	0.05	-
Q1DEC4	histidine kinase/response regulator	0.01	-
Q1DAU4	30S ribosomal protein S9	0.10	-
Q1D3G7	histidine kinase/response regulator	0.02	-
Q1D8Z3	5'-nucleotidase family protein	0.02	0.02
Q1D668	methyl accepting chemotaxis protein	0.03	-
Q1D087	translation elongation factor	0.05	-
Q1D0P8	transcription termination factor Rho	0.02	-
EFTU2	elongation factor Tu 2	-	0.23
Q1DDE2	single-stranded DNA-binding protein	-	0.11
Stress and defense mechanisms			
CH602	chaperonin	0.49	0.11
Q1D7G6	DSBA-like thioredoxin domain protein	0.47	0.16
CH601	chaperonin	0.47	0.19

Q1DC07	alkyl hydroperoxide reductase	0.62	0.14
Q1D2K1	thioredoxin domain-containing protein	0.41	0.08
Q1D7I0	chaperone protein DnaK	0.21	0.03
Q1D6H4	encapsulating protein for peroxidase	0.23	0.20
Q1D2Y6	superoxide dismutase	0.23	0.16
Q1D024	superoxide dismutase	0.20	-
Q1D5A0	Lon protease	0.05	-
B8QZT3	chaperone HtpG	0.03	-
F8CP79	DSBA-like thioredoxin	0.03	-
A0A0F7E2A3	chaperonin	0.18	-
Q1D2Z9	chaperone ClpB	0.02	-
Q1D902	thioredoxin	0.25	0.13
Q1D0R6	chaperone	0.09	-
Q1DC09	Dps family protein	0.11	-
Q1CWM0	glutathione peroxidase	0.10	-
Q1D1X3	thioredoxin domain-containing protein	0.04	-
Q1CWQ0	peptide methionine sulfoxide reductase	0.06	-
Q1D8R6	OsmC/Ohr family protein	0.07	-
Q1D819	HtrA protease/chaperone protein	0.02	-
Q1CWL7	S-formylglutathione hydrolase	-	0.10
Transport, secretion and efflux			
Q1DCB6	TonB-dependent receptor	0.40	0.27
Q1CX48	TonB-dependent receptor	0.45	-
Q1CWS0	long fatty acid chain transporter	0.35	0.20
Q1D031	porin	0.24	0.14
Q1D365	TonB-dependent receptor	0.22	0.18
Q1DBN3	TonB family protein	0.18	-
Q1D2E5	TonB dependent receptor	0.23	0.05
Q1D9E0	secretion pathway protein	0.18	0.04
Q1D2D8	efflux transporter	0.30	0.27
Q1D304	type V1 secretion protein	0.22	0.08
Q1DCQ0	TonB dependent receptor	0.16	-
Q1CYB8	MotA/TolQ/ExbB proton channel family protein	0.22	0.16
Q1DCG9	PBS lyase HEAT-like repeat protein	0.13	-
Q1D4S2	outer membrane efflux protein	0.17	0.13
Q1CX94	MotA/TolQ/ExbB proton channel protein	0.23	0.12
Q1DE39	TonB family protein	0.10	0.03
Q1CVN2	efflux protein	0.18	0.05
Q1DCB8	MotA/TolQ/ExbB proton channel protein	0.21	-
A176_005531	Oar protein	0.01	-
Q1CXU1	branched chain amino acid ABC transporter	0.19	0.21
Q1DDZ2	apolipoprotein-containing domain	0.10	-
Q1D4F4	arsenical pump-driving ATPase	0.13	-
Q1D697	iron-chelator utilization protein	0.17	0.13

Q1DB13	porin	0.11	0.08
Q1D3P6	TonB dependent receptor	0.05	-
Q1CVZ3	porin	0.12	0.10
Q1DEY6	TonB-dependent receptor	0.05	0.02
SECA	translocase SecA	0.04	-
Q1D9H3	signal peptide peptidase SppA	0.06	-
Q1DFV8	efflux pump	0.05	-
Q1DEU2	phosphate-selective porin	0.08	-
Q1DCV4	ABC transporter	0.08	0.08
Q1DE87	iron ABC transporter	0.09	-
Q1DEU5	ABC transporter	0.04	-
Q1D5I8	efflux transporter	0.08	0.02
Q1D099	twitching motility protein	0.09	-
Q1D2U8	TonB domain protein	0.05	-
Q1DD62	amino acid transporter	0.07	0.04
Q1DFZ8	WD domain G-beta repeat/PBS lyase HEAT-like repeat protein	0.01	-
Q1DEV0	ABC transporter	0.03	-
Q1CWK2	cysteine-rich secretory protein	0.14	-
TOLB	TolB	0.07	-
Q1DEG8	ferric siderophore ABC transporter	0.06	-
Q1D696	siderophore biosynthesis aminotransferase	0.05	0.03
Q1DCP7	hemin ABC transporter	0.05	-
Q1DCC0	ExbD/TolR transport protein	0.11	-
Q1D7R4	protein transporter	0.04	-
Q1CZ64	efflux transporter	0.05	-
Q1CYB7	transport energizing protein	0.17	-
Q1D3B5	preprotein translocase YajC	0.17	-
Q1D521	ABC transporter	0.05	-
Q1DCB7	TonB	0.08	-
Q1D8I1	Nit/TauT transport system	0.05	-
Q1CVG1	insertase YidC	0.02	-
Q1D3Z8	polyketide cyclase/dehydrase and lipid transport	0.09	-
Q1CY23	TonB-dependent receptor	0.02	-
Q1D5Z6	phospholipid transport system	0.07	-
Q1D1X8	PBS lyase HEAT repeat-like domain protein	0.03	-
A0A0H4WT21	arsenical pump-driving ATPase	0.01	-
Q1D9M3	ABC transporter	0.04	-
Q1CVX9	TonB-dependent receptor	0.01	-
Q1D0D3	MotA/TolQ/ExbB proton channel protein	0.04	-
Other functions			
Q1CWK0	peptidyl-prolyl cis-trans isomerase	0.52	0.31
Q1D9I3	5'-nucleotidase family protein	0.31	0.12
Q1D3W0	phage tail sheath protein	0.20	0.30
Q1DF51	myo-inositol-1-phosphate synthase	0.28	-

Q1DCH7	alkaline phosphatase	0.17	0.14
Q1D0E3	aspartyl beta-hydroxylase	0.22	0.08
Q1DEX1	NAD dependent epimerase/dehydratase	0.18	-
Q1CVJ5	bactofilin	0.63	-
NDK	nucleoside diphosphate kinase	0.66	-
Q1D4V7	frizzy aggregation protein	0.24	0.07
Q1DD37	peptidyl-prolyl cis-trans isomerase	0.23	-
Q1D4E5	phosphodiesterase/nucleotide pyrophosphatase family protein	0.19	-
Q1DCD9	glutathione S-transferase	0.28	0.09
Q1DC52	adenosine deaminase	0.19	-
GLPK	glycerol kinase	0.17	-
Q1D458	feruloyl esterase	0.15	0.19
Q1D5W4	iInosine-5'-monophosphate dehydrogenase	0.11	0.05
CGLB	CglB	0.11	0.05
PURA	adenylosuccinate synthetase	0.12	-
Q1DA41	B12 binding domain/ArgK/methylmalonyl-CoA mutase family protein	0.05	-
Q1D440	methyl transferase	0.09	-
Q1CVR5	vegetative protein	0.21	-
Q1D1J7	phytase	0.11	-
Y1394	beta lactamase	0.14	-
Q1CYB9	oxidoreductase	0.14	-
Q1D6F6	metallophosphoesterase	0.12	0.03
Q1DDZ8	glutathione S-transferase	0.22	-
Q1D5X7	peptidyl-prolyl cis-trans isomerase	0.19	-
Q1DFJ0	oxidoreductase	0.14	-
Q1D7G7	dihydrofolate reductase	0.21	0.29
Q1D3H2	bactofilin	0.16	0.06
Q1DG65	amidohydrolase	0.01	-
Q1D4E8	polyketide synthase	0.02	-
L7U7N0	serine-threonine protein kinase	0.05	-
PYRF	orotidine 5'-phosphate decarboxylase	0.10	-
Q1CWR7	oxidoreductase	0.07	-
Q1DCF0	NAD-dependent epimerase/dehydratase	0.13	-
PYRG	CTP synthase	0.05	-
Q1D418	serine/threonine protein kinase	0.03	-
PYRB	aspartate carbamoyltransferase	0.09	-
Q1D2U6	adventurous gliding motility protein AglT	0.06	-
Q1DG46	amidohydrolase	0.04	-
DEOD	purine nucleoside phosphorylase	0.13	0.13
PUR4	phosphoribosylformylglycinamidine synthase	0.03	-
Q1CYZ7	terpene synthase	0.04	-
Q1CVY7	oxidoreductase	0.07	-
Q1D4M7	DofB	0.15	-
Q1CXA7	peptidyl-prolyl cis-trans isomerase	0.23	-

Q1D3V9	phage tail protein	0.16	0.38
Q1D025	methyl transferase	0.03	-
Q1CVM7	glycosyl transferase	0.04	-
Q1DA70	pirin family protein	0.05	-
Q1D2V2	adventurous gliding motility protein AgmX	0.04	-
Q1D0H5	pyrimidine-nucleoside phosphorylase	0.07	-
Q1D669	biotin synthase	0.10	-
Q1D7X4	aminomethyltransferase	0.06	-
Q1D3H8	L-aspartate oxidase	0.04	-
Q1CXJ4	coproporphyrinogen oxidase	0.06	-
Q1DDY8	glutathione S transferase	0.06	-
Q1D806	adventurous gliding motility protein AglU	0.04	-
Q1D689	2,3-dihydro-2,3-dihydroxybenzoate dehydrogenase	0.06	-
Q1CZT4	acetyltransferase	0.15	-
Q1D4E6	FAD-binding domain protein	0.03	-
A0A0H4XGT4	quorum sensing signal AsgA	0.05	-
Q1D4A1	bifunctional NAD(P)H-hydrate repair enzyme	0.03	-
Q1D9Y5	glutathione-disulfide reductase	0.03	0.05
A0A0H4WUN0	peptidyl-prolyl cis-trans isomerase PpiA	0.02	-
Q1D6L8	dihydroorotase	0.03	-
Q1D2F6	decarboxylase family protein	0.03	0.08
PSD	phosphatidylserine decarboxylase	0.06	-
Q1CWP9	myxobacterial hemagglutinin	0.04	0.05
Q1D1B9	choloylglycine hydrolase family protein	0.05	-
Q1D965	HesB/YadR/YfhF family protein	0.18	-
Q1CYQ7	glycine cleavage system T protein	0.04	-
Q1DEX3	aminotransferase	0.03	-
Q1D0V7	Inorganic pyrophosphatase	0.06	-
Q1D4F6	polyketide synthase	0.01	-
Q1CXC7	late embryogenesis abundant-like protein	0.07	-
Q1CVW0	vegetative protein	0.05	-
Q1D5D1	pyridine nucleotide-disulphide oxidoreductase	0.03	-
Q1D7W4	ferrodoxin	0.17	-
F8CEV8	pseudouridine synthase	0.02	-
Q1D910	peptidylprolyl isomerase	0.03	-
MGLA	gliding motility protein MglA	0.07	-
Q1DDR3	AMP-binding protein	0.02	-
Q1D7M7	xanthine dehydrogenase	0.01	0.03
Q1D559	glutathione S-transferase	0.04	-
Q1D161	male sterility protein-like protein	0.03	-
Q1D7K0	oxidoreductase	0.03	-
Q1DFD3	endonuclease/exonuclease/phosphatase family protein	-	0.12
DESS	development-specific protein S	-	0.16
Q1DDX6	amidohydrolase	-	0.01

Q1CWL6	S-(hydroxymethyl)glutathione dehydrogenase	-	0.04
Q1D3U9	phage tail protein	-	0.02
Q1D6W6	3,4-dihydroxy-2-butanone 4-phosphate synthase/GTP cyclohydrolase II	-	0.02
PNP	polyribonucleotide nucleotidyltransferase	-	0.03
Function unknown			
Q1DBN2		0.28	-
Q1D2V4		0.18	0.21
Q1D5E0		0.23	-
Q1D8Z5		0.27	0.28
Q1D2R6		0.33	0.12
Q1D2U5		0.17	-
Q1CVR0		0.18	0.14
Q1D1M5		0.22	0.19
Q1CZV5		0.13	0.03
Q1D2E4		0.23	0.16
Q1D9N6		0.09	0.06
Q1CXK5		0.29	0.13
Q1CZI8		0.22	-
Q1CXW5		0.14	-
Q1D077		0.33	0.27
Q1D9B3		0.13	-
Q1D840		0.05	-
Q1D6H7		0.19	0.21
Q1D5W5		0.35	-
Q1D3G6		0.15	0.04
Q1D2V0		0.14	0.05
Q1D7L1		0.06	-
Q1D2U9		0.18	0.09
Q1D4F5		0.38	0.19
Q1D959		0.13	0.08
Q1DEA6		0.10	-
Q1D0J9		0.29	0.21
Q1D5R1		0.13	0.10
Q1D9C8		0.23	-
Q1CX67		0.10	-
Q1CW98		0.23	0.13
Q1D0K0		0.16	0.18
Q1D4U1		0.15	-
Q1DBT9		0.07	0.02
Q1DDR7		0.04	0.03
Q1DEJ3		0.29	0.29
Q1D4F9		0.05	-
Q1V0D2		0.13	-
Q1CYL8		0.08	-
Q1CX74		0.24	-

Q1D3V0	0.07	0.08
Q1DFZ6	0.05	-
Q1DC42	0.07	-
Q1D6G2	0.08	0.01
Q1D9T8	0.08	0.09
Q1DEJ8	0.08	0.03
Q1D9B5	0.07	0.07
Q1CWJ8	0.05	-
Q1D4R8	0.06	-
Q1DA21	0.24	-
Q1DFS2	0.08	-
Q1D9J1	0.10	-
Q1D1K3	0.05	-
Q1D904	0.25	-
Q1D0U7	0.08	-
Q1D3U7	0.06	0.11
Q1D8D6	0.02	0.04
Q1DET2	0.09	-
Q1DCJ4	0.13	0.11
Q1DBX9	0.07	-
Q1DDY7	0.12	-
Q1DEJ9	0.04	-
Q1D9M7	0.05	0.08
Q1D5D6	0.06	-
Q1D3A5	0.09	-
Q1DF90	0.13	-
Q1D0E8	0.08	-
Q1D450	0.14	0.09
Q1D2W3	0.05	0.08
Q1D9I8	0.06	-
Q1CVW3	0.12	-
Q1CYX4	0.02	0.05
Q1CZ57	0.05	-
Q1CWY2	0.07	-
Q1DCE2	0.08	-
Q1CXT3	0.07	-
Q1D1Q5	0.06	-
Q1D3U8	0.06	0.06
Q1DDX9	0.11	-
Q1CZ58	0.04	-
Q1CZF4	0.12	-
Q1D615	0.08	-
Q1DEF2	0.11	-
Q1D2J1	0.06	-
Q1D100	0.06	-
Q1DCA5	0.12	-

Q1D417	0.03	-
Q1DBU4	0.08	-
Q1CZ63	0.02	-
Q1D4R1	0.02	-
Q1DFH8	0.06	-
Q1D4H9	0.08	-
Q1DD93	0.02	-
Q1CYW3	0.03	-
Q1D1C2	0.03	-
Q1DB38	0.08	-
Q1D4U3	0.02	-
Q1CVK8	0.14	0.23
Q1D2D5	0.09	-
Q1D6J5	0.05	-
Q1D992	0.05	-
Q1DAD6	0.05	-
Q1CZF7	0.05	-
Q1D8H6	0.08	-
Q1D8C0	0.02	-
Q1CZ50	0.01	-
Q1D1D7	0.02	-
Q1D680	-	0.12
Q1D3V8	-	0.06
Q1CXB7	-	0.11
Q1DA09	-	0.07
Q1DDQ6	-	0.03
Q1CX13	-	0.06
Q1CVF7	-	0.01

[a] Data are the mean of two replicates.

[b] Proteins in bold characters have a predicted intracellular localization.

[c] Protein not detected or protein identification not considered valid.