Table S1. Proteins identified in the metaproteome of the Ace Lake 0.1 μm filters.

Gene ID: unique indentifier assigned to each predicted open reading frame in the metagenome.

Protein group identification (*): proteins that contain similar peptides that could not be differentiated by the mass spectral analysis were grouped. Only one gene number of that group is displayed.

Protein ambiguity groups ($_{a-z}$, $_{aa-pp}$) : proteins that have some shared peptides with one or more other proteins from the same sample depth are marked with the same subscript.

5 m - COG annotated proteins

Gene ID	Normalised spectral abundance	COG identifier	KO identifier	KEGG locus tag	COG description : KEGG description
167852195$_f$	0.02530	COG1653	K10232	AAur_0459	sugar-binding periplasmic proteins/domains : putative alpha-glucosides-binding ABC transporter (AglE)
167782381*	0.01724	COG1879	K02058	Ping_2790	periplasmic sugar-binding proteins : bifunctional carbohydrate binding and transport protein
167813321	0.01388	COG1629		GFO_2756	outer membrane receptor proteins, mostly Fe transport : TonB-dependent outer membrane receptor
167754347	0.01044	COG1879	K02058	CMM_0792	periplasmic sugar-binding proteins : putative sugar ABC transporter, solute-binding protein
167701754$_a$	0.00967	COG0834	K09969	SAR11_0953	ABC-type amino acid transport system, periplasmic component : yhdW
167792775	0.00630	COG1879	K10552	SMc02171	periplasmic sugar-binding proteins : fructose transport system substrate-binding protein
167932252$_d$	0.00537	COG0715	K02051	SAR11_0807	ABC-type nitrate/sulfonate/taurine/bicarbonate transport systems, periplasmic components
167759671	0.00493	COG0605		NEMVE_v1g231554	superoxide dismutase
167751919$_h$	0.00468	COG3740		ROP_69760	phage head maturation protease

167907426	0.00438	COG1638		SAR11_0266	dicarboxylate-binding periplasmic protein : TRAP dicarboxylate transporter - DctP subunit (mannitol/chloroaromatic compounds)
167711086	0.00425	COG0834	K02030	TM1040_0294	ABC-type amino acid transport system, periplasmic component : lysine-arginine-ornithine-binding periplasmic protein
167819184	0.00389	COG2113	K02002	SAR11_1302	ABC-type proline/glycine betaine transport systems, periplasmic components : opuAC
167680030	0.00346	COG0683	K01999	AAur_1271	ABC-type branched-chain amino acid transport systems, periplasmic component : braC
167865828[b]	0.00338	COG0834	K09969	HCH_05807	ABC-type amino acid transport system, periplasmic component
167684228[c]	0.00331	COG0459	K04077	SAR11_0162	chaperonin GroEL (HSP60 family)
167868594[d]	0.00311	COG0715	K02051	SAR11_0807	ABC-type nitrate/sulfonate/taurine/bicarbonate transport systems, periplasmic components
167785199[c]	0.00309	COG0459	K04077	CHU_1828	chaperonin GroEL (HSP60 family)
167819050	0.00304	COG2113	K02001	Plav_1066	ABC-type proline/glycine betaine transport systems, periplasmic components
167867034	0.00284	COG0687	K02055	SAR11_1336	spermidine/putrescine-binding periplasmic proteinp : potD;
167700934	0.00277	COG0450		SPO3383	peroxiredoxin : thiol-specific antioxidant protein
167816084[a]	0.00253	COG0834	K09969	SAR11_0953	ABC-type amino acid transport system, periplasmic component : yhdW
167714114	0.00179	COG0687	K02055	SAR11_1336	spermidine/putrescine-binding periplasmic protein : potD
167712994[b]	0.00175	COG0834	K09969	HCH_05807	ABC-type amino acid transport system, periplasmic component
167824568	0.00164	COG3181		Dshi_2450	uncharacterized BCR : hypothetical protein
167925495	0.00159	COG1653	K02027	Krad_1380	sugar-binding periplasmic proteins/domains

167695410[a]	0.00155	COG0834	K09969	SAR11_0953	ABC-type amino acid transport system, periplasmic component : yhdW
167695984*	0.00138	COG1879			periplasmic sugar-binding proteins
167703404	0.00134	COG1012	K00128	AAur_pTC20196	NAD-dependent aldehyde dehydrogenases
167718230	0.00125	COG0683	K01999	AAur_1271	ABC-type branched-chain amino acid transport systems, periplasmic component : braC
167735996	0.00103	COG0591		SAR11_0316	Na+/proline, Na+/panthothenate symporters and related permeases : yjcG
167739054	0.00101	COG1028	K00059	SH0230	dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases) : 3-oxoacyl-[acyl-carrier protein] reductase
167701096	0.00100	COG0776		KRH_03630	bacterial nucleoid DNA-binding protein : HU_IHF family transcriptional regulator
167817334	0.00098	COG0715		FRAAL1422	ABC-type nitrate/sulfonate/taurine/bicarbonate transport systems, periplasmic components
167703266[c]	0.00095	COG0459	K04077	Noca_3982	chaperonin GroEL (HSP60 family)
167768609	0.00095	COG3181		RD1_2202	uncharacterized BCR
167868532	0.00093	COG3181	K07795	HCH_01639	uncharacterized BCR : putative tricarboxylic transport membrane protein
167865516	0.00088	COG0747		CMM_2185	ABC-type dipeptide/oligopeptide/nickel transport systems, periplasmic components
167911715	0.00083	COG0776	K03530	Sala_0799	bacterial nucleoid DNA-binding protein : DNA-binding protein HU-beta
167736316	0.00082	COG0174	K01915	SAR11_0747	glutamine synthase : glnA
167916441	0.00079	COG1629		BF2044	outer membrane receptor proteins, mostly Fe transport : putative TonB-dependent outer membrane receptor protein
167920571	0.00078	COG0776	K03530	SAR11_0817	bacterial nucleoid DNA-binding protein : hupA

167703332	0.00066	COG1732	K05845	Strop_1633	periplasmic glycine betaine/choline-binding (lipo)protein of an ABC-type transport system (osmoprotectant binding protein)
167662373	0.00063	COG0834		Pden_1025	ABC-type amino acid transport system, periplasmic component : extracellular solute-binding protein, family 3
167890974	0.00062	COG1878		nfa12380	uncharacterized ACR, predicted metal-dependent hydrolases
167824660	0.00061	COG0683	K01999	SAR11_1361	ABC-type branched-chain amino acid transport systems, periplasmic component : livJ2; Leu/Ile/Val-binding protein precursor
167886240	0.00061	COG0335	K02884	CHU_0120	rplS; 50S ribosomal protein L19
167921445	0.00058	COG0811		GFO_0088	biopolymer transport proteins : exbB; ExbB-like MotA/TolQ/ExbB family
167776275$_{ee}$	0.00055	COG3740	K06904	BL0376	phage head maturation protease
167659892*$_{ee}$	0.00055	COG3740		ROP_69760	phage head maturation protease
167786475	0.00054	COG0098	K02988	Fjoh_0380	rpsE; 30S ribosomal protein S5
167693676*	0.00054	COG0776		Arth_3916	bacterial nucleoid DNA-binding protein
167818330	0.00048	COG0683		Rxyl_0363	ABC-type branched-chain amino acid transport systems, periplasmic component : extracellular ligand-binding receptor
167739596	0.00044	COG0545	K03772	BDI_2705	FKBP-type peptidyl-prolyl cis-trans isomerases 1
167808311$_{c}$	0.00044	COG0459	K04077	SAR11_0162	chaperonin GroEL (HSP60 family)
167706214	0.00044	COG0683		Tfu_1779	ABC-type branched-chain amino acid transport systems, periplasmic component
167866918	0.00044	COG2885	K03640	SAR11_0598	outer membrane protein and related peptidoglycan-associated (lipo)proteins : ompA; OmpA family

167807477	0.00042	COG0834		MSMEG_5368	ABC-type amino acid transport system, periplasmic component : ehuB; ectoine/hydroxyectoine ABC transporter solute-binding protein
167881416[e]	0.00040	COG0050	K02358	CHU_3175	GTPases - translation elongation factors : tufB, tuf
167765645[f]	0.00034	COG1653	K10232	Sare_3967	sugar-binding periplasmic proteins/domains
167730910	0.00033	COG3181		Dshi_2450	uncharacterized BCR
167725574	0.00032	COG0450	K03386	CHU_2724	peroxiredoxin : ahpC; alkyl hydroperoxide reductase, subunit C
167768817	0.00032	COG0740	K00288	CHU_1706	protease subunit of ATP-dependent Clp proteases : methylenetetrahydrofolate dehydrogenase (NADP+)
167886236	0.00031	COG0228	K02959	CHU_0117	rpsP; 30S ribosomal protein S16
167907528	0.00031	COG0591		SAR11_0316	Na+/proline, Na+/panthothenate symporters and related permeases : yjcG
167868396	0.00029	COG2358		PBPRA0389	predicted periplasmic binding protein : putative immunogenic protein
167718328	0.00027	COG1744	K07335	AAur_1253	surface lipoprotein : basic membrane protein A and related proteins
167769503[c]	0.00027	COG0459		CMS_2756	chaperonin GroEL (HSP60 family)
167818958	0.00026	COG1638		TM1040_0356	dicarboxylate-binding periplasmic protein : TRAP dicarboxylate transporter - DctP subunit
167702878	0.00025	COG1879		Krad_1186	periplasmic sugar-binding proteins : periplasmic binding protein/LacI transcriptional regulator
167665756	0.00025	COG0091	K02890	GFO_2834	rplV; 50S ribosomal protein L22
167730894	0.00023	COG1638		RD1_2185	dicarboxylate-binding periplasmic protein : dctP; C4-dicarboxylate-binding periplasmic protein, putative
167680092	0.00022	COG0094	K02931	Lxx20210	rplE; 50S ribosomal protein L5
167868548	0.00020	COG0834	K10018	SAR11_1210	ABC-type amino acid transport system, periplasmic component : octopine/nopaline transport system substrate-binding protein

167892279	0.00019	COG0834	K02030	Veis_2153	ABC-type amino acid transport system, periplasmic component
167817276	0.00018	COG0347	K04751	Acel_1565	nitrogen regulatory protein PII
167862242	0.00018	COG0087	K02906	BT_2727	rplC; 50S ribosomal protein L3
167933288	0.00018	COG1638		Dshi_3326	dicarboxylate-binding periplasmic protein : TRAP dicarboxylate transporter-DctP subunit
167713980*	0.00016	COG0330	K04088	SAR11_0008	membrane protease subunits, stomatin/prohibitin homologs : hflK
167867886	0.00016	COG3181		Csal_1767	uncharacterized BCR : uncharacterized protein UPF0065
167809873	0.00016	COG0539	K02945	CHU_1951	rpsA; 30S ribosomal protein S1
167713982	0.00015	COG0330	K04087	SAR11_0007	membrane protease subunits, stomatin/prohibitin homologs : hflC
167822210	0.00015	COG0776		SCO2950	bacterial nucleoid DNA-binding protein : hup, SCE59.09c; DNA-binding protein Hu (hs1)
167820450*	0.00015	COG1192		tlr0963	ATPases involved in chromosome partitioning : probable cell division inhibitor minD
167820614$_{g}$	0.00015	COG0174	K01915	Krad_3291	glutamine synthase
167714092	0.00014	COG0683	K01999	SAR11_1346	ABC-type branched-chain amino acid transport systems, periplasmic component : livJ
167817130	0.00014	COG0711	K02109	SCO5369	F0F1-type ATP synthase b subunit
167818902	0.00014	COG1638		SAR11_0864	dicarboxylate-binding periplasmic protein
167866078	0.00013	COG0605	K00518	Arth_2086	superoxide dismutase
167865698	0.00013	COG0740	K01358	AAur_2381	protease subunit of ATP-dependent Clp proteases
167817852	0.00013	COG0683		Noca_3017	ABC-type branched-chain amino acid transport systems, periplasmic component : extracellular ligand-binding receptor
167714042	0.00012	COG0683	K01999	SAR11_1361	ABC-type branched-chain amino acid transport systems, periplasmic component : livJ2; Leu/Ile/Val-binding protein precursor

167821000	0.00012	COG1732		MSMEG_2924	periplasmic glycine betaine/choline-binding (lipo)protein of an ABC-type transport system (osmoprotectant binding protein) : permease binding-protein component
167668848[g]	0.00011	COG0174	K01915	CMM_1636	glutamine synthase : glnA1
167748683*	0.00010	COG0834		PFL_3548	ABC-type amino acid transport system, periplasmic component
167718146	0.00010	COG0088	K02926	Lxx20320	rplD; 50S ribosomal protein L4
167862420	0.00010	COG1629		FP0112	outer membrane receptor proteins, mostly Fe transport : probable TonB-dependent outer membrane receptor precursor
167696080*	0.00010	COG1344	K02406	Csac_1680	flagellin and related hook-associated proteins
167735512	0.00010	COG0803	K09815	Smed_1697	ABC-type Mn/Zn transport system, periplasmic Mn/Zn-binding (lipo)protein (surface adhesin A)
167719882	0.00009	COG0096	K02994	SAR11_1103	rpsH; 30S ribosomal protein S8
167660431[h]	0.00009	COG3740	K06904	BL0376	phage head maturation protease
167718250	0.00009	COG2213	K02799	GK1948	phosphotransferase system, mannitol-specific IIBC component
167719862*	0.00008	COG0185	K02965	SAR11_1113	rpsS; 30S ribosomal protein S19
167702806	0.00008	COG0081	K02863	KRH_05860	rplA; 50S ribosomal protein L1
167719824*[e]	0.00008	COG0050	K02358	SAR11_1130	GTPases - translation elongation factors : tufB, tuf
167817466	0.00008	COG0404		mll1258	glycine cleavage system T protein (aminomethyltransferase) : sarcosine dehydrogenase
167868614	0.00008	COG2113	K02002	SAR11_0797	ABC-type proline/glycine betaine transport systems, periplasmic components : proX
167933120	0.00007	COG0803	K09815	Atu1521	ABC-type Mn/Zn transport system, periplasmic Mn/Zn-binding (lipo)protein (surface adhesin A) : znuA
167718168	0.00007	COG0094		CMS_0295	50S ribosomal protein L5
167868724	0.00007	COG0396	K09013	SAR11_0740	iron-regulated ABC transporter ATPase subunit SufC

167718156	0.00007	COG0092	K02982	Krad_0694	ribosomal protein S3
167719956	0.00006	COG0834	K02030	SAR11_1068	ABC-type amino acid transport system, periplasmic component : pheC; cyclohexadienyl dehydratase
167730882	0.00006	COG0004		SAR11_0818	ammonia permeases : amtB; ammonium transporter
167718138$_e$	0.00006	COG0050	K02358	Tfu_2648	GTPases - translation elongation factors: tuf
167718052	0.00006	COG1653	K02027	Krad_3469	sugar-binding periplasmic proteins/domains
167700960*	0.00006	COG3794		SMa1243	plastocyanin : Azu1 pseudoazurin (blue copper protein)
167868482	0.00005	COG0715			ABC-type nitrate/sulfonate/taurine/bicarbonate transport systems, periplasmic components
167868656	0.00005	COG0715	K02051	AZC_2351	ABC-type nitrate/sulfonate/taurine/bicarbonate transport systems, periplasmic components
167868494	0.00004	COG1638		SMa0157	dicarboxylate-binding periplasmic protein
167866460	0.00004	COG0687	K02055	SCO5667	spermidine/putrescine-binding periplasmic protein
167719840	0.00004	COG0085	K03043	SAR11_1123	DNA-directed RNA polymerase beta subunit/140 kD subunit (split gene in Mjan, Mthe, Aful) : rpoB
167816636	0.00004	COG0459	K04077	Krad_0736	chaperonin GroEL (HSP60 family)
167701680*	0.00004	COG3740	K06904	BL0376	phage head maturation protease
167717794*	0.00003	COG0195	K02600	SAR11_0388	phage head maturation protease
167717838	0.00003	COG0443	K04043	SAR11_0368	molecular chaperone : dnaK
167834314	0.00003	COG0443		CMS_2806	molecular chaperone : dnaK
167717784	0.00003	COG1185	K00962	SAR11_0392	polyribonucleotide nucleotidyltransferase (polynucleotide phosphorylase)
167818278	0.00003	COG1022		Noca_3113	long-chain acyl-CoA synthetases (AMP-forming) : AMP-dependent synthetase and ligase
167719850	0.00002	COG0480	K02355	SAR11_1119	translation elongation and release factors (GTPases) : fusA
167816480	0.00002	COG0086	K03046	Krad_0681	DNA-directed RNA polymerase beta' subunit/160 kD subunit (split gene in archaea and Syn)

167866408	0.00001	COG1185	K00962	Lxx09030	polyribonucleotide nucleotidyltransferase (polynucleotide phosphorylase)

5 m - KEGG and NR annotated proteins

Gene ID	normalised spectral abundance	NR identifier	KO identifier	KEGG / NR Locus tag	KEGG / NR description
167873078	0.03710	BAF91544			major capsid protein [uncultured Myoviridae]
167771989$_{i}$	0.02658			BTH_I0914	hypothetical protein
167723550$_{j}$	0.01559	YP_001648266		OsV5_190f	hypothetical protein [Ostreococcus virus OsV5]
167927818$_{j}$	0.01345	YP_001648266		OsV5_190f	hypothetical protein [Ostreococcus virus OsV5]
167933090	0.01298	YP_002590925			putative porin [Candidatus Pelagibacter sp. HTCC7211]
167711088	0.01230		K09969	PBPRA2185	putative amino acid ABC transporter, periplasmic amino acid-binding protein
167691398	0.01175			HM1_2880	phage major capsid protein, hk97 family
167922719$_{k}$	0.01174			Neut_1469	phage major capsid protein, HK97 family protein
167775105$_{l}$	0.01103	ABC95191			GP23-major capsid protein [Stenotrophomonas phage SMB14]
167687982$_{l}$	0.00968	NP_944113			gp23 major head protein [Aeromonas phage Aeh1]
167748599$_{m}$	0.00960			M6_Spy1138	phage prohead protease
167733772	0.00952			BBta_5785	putative phage major head protein
167925660	0.00923			SRU_2178	putative outer membrane protein, probably involved in nutrient binding
167796059$_{n}$	0.00853			APECO1_525	hypothetical protein
167883590	0.00820			PP_1567	phage major capsid protein, HK97 family
167666520$_{o}$	0.00818	BAF91544			major capsid protein [uncultured Myoviridae]
167664173*$_{p}$	0.00713			GDI3673	hypothetical protein
167667150$_{m}$	0.00687			LGAS_1485	predicted phage phi-C31 GP36 major capsid-like protein
167771337	0.00605	ABW90951			gp23 major capsid protein [uncultured Myoviridae]

167884290$_{l}$	0.00573	BAF91544			major capsid protein [uncultured Myoviridae]
167760139	0.00561			CHU_2679	probable outer membrane lipoprotein P61
167816468$_{q}$	0.00522			DR_A0099	hypothetical protein
167700634$_{j}$	0.00499	YP_001648266		OsV5_190f	hypothetical protein [Ostreococcus virus OsV5]
167687792$_{r}$	0.00498			Asuc_1240	phage major capsid protein, HK97 family
167842580$_{r}$	0.00453			BAV1464	major capsid protein
167700776	0.00447			Bpro_3745	hypothetical protein
167729766	0.00433	ZP_01224596		GB2207_03424	hypothetical protein [marine gamma proteobacterium HTCC2207]
167934698	0.00431			Swit_4452	hypothetical protein
167884738	0.00409			BBta_5785	putative phage major head protein
167669610$_{p}$	0.00397			GDI3673	hypothetical protein
167861688	0.00359			BDI_2874	putative outer membrane protein, probably involved in nutrient binding
167910063	0.00347			GDI3673	hypothetical protein
167893743*$_{s}$	0.00338	YP_001648158		OsV5_081f	hypothetical protein [Ostreococcus virus OsV5]
167888926$_{p}$	0.00326			GDI3673	hypothetical protein
167753643*	0.00324			Daci_1946	putative phage major head protein
167742624$_{p}$	0.00317			GDI3673	hypothetical protein
167908539$_{r}$	0.00304			BAV1464	major capsid protein
167675286*	0.00284			CKO_01864	hypothetical protein
167900893$_{n}$	0.00278			APECO1_525	hypothetical protein
167778265$_{p}$	0.00275			GDI3673	hypothetical protein
167786471	0.00267			mlr8524	phage major capsid protein, GP36
167735768	0.00265			FRAAL2681	hypothetical protein
167773951$_{t}$	0.00253			LGAS_1485	predicted phage phi-C31 GP36 major capsid-like protein
167841586$_{j}$	0.00250	A7U6E7			putative major capsid protein [Chrysochromulina ericina virus]

167919545	0.00245			Pmen_3970	phage major capsid protein, HK97 family
167781901$_{u}$	0.00236	YP_214367			T4-like major capsid protein [Prochlorococcus phage P-SSM2]
167923659$_{p}$	0.00235			GDI3673	hypothetical protein
167852301$_{v}$	0.00230			MAB_1788	bacteriophage protein
167659301	0.00224			LGAS_1485	predicted phage phi-C31 GP36 major capsid-like protein
167861686	0.00223	YP_002789013			TonB dependent/ligand-gated channel [Polaribacter sp. MED152]
167712528$_{v}$	0.00215			MAB_1788	bacterial nucleoid DNA-binding protein
167678920*$_{w}$	0.00209	YP_001498525		AR158_C444L	hypothetical protein [Paramecium bursaria Chlorella virus AR158]
167849540$_{j}$	0.00201	YP_001648266		OsV5_190f	hypothetical protein [Ostreococcus virus OsV5]
167781903$_{u}$	0.00201	YP_214367			T4-like major capsid protein [Prochlorococcus phage P-SSM2]
167863158$_{j}$	0.00200	YP_001648266		OsV5_190f	hypothetical protein [Ostreococcus virus OsV5]
167663967*	0.00190			Swit_4461	hypothetical protein
167687108$_{u}$	0.00182	YP_214367			T4-like major capsid protein [Prochlorococcus phage P-SSM2]
167692622$_{i}$	0.00176			SG1188	hypothetical protein
167733858	0.00170	ZP_01017474			major capsid protein, HK97 family protein [Parvularcula bermudensis HTCC2503]
167852851$_{p}$	0.00167			GDI3673	hypothetical protein
167864542$_{k}$	0.00166			Neut_1469	phage major capsid protein, HK97 family protein
167803157	0.00165	ZP_01688540			lipoprotein, putative [Microscilla marina ATCC 23134]
167682644$_{j}$	0.00153	A7U6E7			putative major capsid protein [Chrysochromulina ericina virus]
167733004*$_{j}$	0.00150	A7U6F0			putative major capsid protein [Phaeocystis pouchetii virus]

167765429	0.00148			CHU_2610	gliding motility-related protein; possible GldN and/or GldO
167878228$_t$	0.00145			LGAS_1485	predicted phage phi-C31 GP36 major capsid-like protein
167775103	0.00145	YP_214669			gp23 [Prochlorococcus phage P-SSM4]
167702908	0.00143			mma_2202	hypothetical protein
167869946	0.00135	YP_195142			major capsid protein gp23 [Synechococcus phage S-PM2]
167834518	0.00128			Haur_0657	hypothetical protein
167807747	0.00122			Saro_0657	hypothetical protein
167816420	0.00121			APECO1_525	hypothetical protein
167809283$_k$	0.00119			Neut_1469	phage major capsid protein, HK97 family protein
167868514	0.00119			SAR11_1290	TRAP-type bacterial extracellular solute-binding protein
167750765	0.00118			Smed_1334	phage major capsid protein, HK97 family
167925457$_p$	0.00115			GDI3673	hypothetical protein
167782759	0.00113			Oter_1957	band 7 protein
167871794$_j$	0.00113	YP_001648266		OsV5_190f	hypothetical protein [Ostreococcus virus OsV5]
167756019	0.00112			CHU_0172	gldL; gliding motility-related protein
167670926$_x$	0.00112			BBta_5785	putative phage major head protein
167821362$_z$	0.00112			APECO1_525	hypothetical protein
167690910$_j$	0.00111	YP_001648266		OsV5_190f	hypothetical protein [Ostreococcus virus OsV5]
167685332$_j$	0.00110	YP_001648266		OsV5_190f	hypothetical protein [Ostreococcus virus OsV5]
167700460*	0.00110	YP_001648158		OsV5_081f	hypothetical protein [Ostreococcus virus OsV5]
167685474*$_{aa}$	0.00104	YP_001648182		OsV5_105r	hypothetical protein [Ostreococcus virus OsV5]
167734326bb	0.00103			amb4267	hypothetical protein
16775653$_q$	0.00101			Haur_0657	hypothetical protein
167733302$_p$	0.00101			GDI3673	hypothetical protein

167663981$_{p}$	0.00097			GDI3673	hypothetical protein
167763843	0.00096			Saro_0657	hypothetical protein
167768193$_{z}$	0.00096			CKO_01864	hypothetical protein
167719228$_{i}$	0.00095			SG1188	hypothetical protein
167844676	0.00091	ZP_03643684		BACCOPRO_02057	hypothetical protein [Bacteroides coprophilus DSM 18228]
167881504cc	0.00091			BSU26140	yqbE; hypothetical protein
167852559$_{oo}$	0.00090			HSM_0907	hypothetical protein
167804465*	0.00088	ZP_03724502		ObacDRAFT_9001	hypothetical protein [Opitutaceae bacterium TAV2]
167794165$_{p}$	0.00087			GDI3673	hypothetical protein
167734676	0.00085			Amet_4028	phage major capsid protein, HK97 family
167764813$_{u}$	0.00084	YP_214367			T4-like major capsid protein [Prochlorococcus phage P-SSM2]
167781783$_{p}$	0.00079			GDI3673	hypothetical protein
167759955	0.00077			Dgeo_0628	hypothetical protein
167733674	0.00076			Swit_4452	hypothetical protein
167878828	0.00075		K02027	SAV1394	ABC transporter solute-binding protein
167740142	0.00075	YP_002705257			gp34 [Stenotrophomonas sp. SKA14]
167834088	0.00074			Haur_0657	hypothetical protein
167821604$_{j}$	0.00072	YP_001648266		OsV5_190f	hypothetical protein [Ostreococcus virus OsV5]
167798697$_{p}$	0.00070			GDI3673	hypothetical protein
167823322$_{s}$	0.00070	YP_001648158		OsV5_081f	hypothetical protein [Ostreococcus virus OsV5]
167718758$_{j}$	0.00070	A7U6F0			putative major capsid protein [Phaeocystis pouchetii virus]
167713806	0.00069			SG1188	hypothetical protein
167778269dd	0.00068	YP_002276820		Gdia_2460	hypothetical protein [Gluconacetobacter diazotrophicus PAl 5]
167879936$_{s}$	0.00067	YP_001648158		OsV5_081f	hypothetical protein [Ostreococcus virus OsV5]
167701850	0.00064			M446_5960	hypothetical protein

167934792$_{p}$	0.00064			GDI3673	hypothetical protein
167874674	0.00063			GFO_0492	conserved hypothetical protein, secreted-possibly porin
167821292	0.00062			Oant_1504	peptidase U35 phage prohead HK97
167867556	0.00062			Rru_A2587	hypothetical protein
167901481	0.00061			Cthe_1719	phage major capsid protein, HK97 family
167824444	0.00059			Smed_5134	TRAP dicarboxylate transporter-DctP subunit
167696166*	0.00059			BTH_I0915	hypothetical protein
167936648	0.00056	EEI06235		XcelDRAFT_1815	hypothetical protein [Xylanimonas cellulosilytica DSM 15894]
167910361$_{j}$	0.00054	A7U6F0			putative major capsid protein [Phaeocystis pouchetii virus]
167675492*$_{p}$	0.00054			GDI3673	hypothetical protein
167801933$_{aa}$	0.00052	YP_001648182		OsV5_105r	hypothetical protein [Ostreococcus virus OsV5]
167725772cc	0.00051			BSU26140	yqbE; hypothetical protein
167820670	0.00050			gll0198	similar to bacteriorhodopsin
167832972$_{t}$	0.00050			LGAS_1485	predicted phage phi-C31 GP36 major capsid-like protein
167867536	0.00049			TM1040_0812	hypothetical protein
167783747	0.00048			Glov_2914	cell surface receptor IPT/TIG domain protein
167893945	0.00048			Oter_3420	hypothetical protein
167740708	0.00047		K03286	Pnap_1319	OmpA/MotB domain protein; OmpA-OmpF porin, OOP family
167772783	0.00047			RCIX1696	hypothetical protein
167734614$_{p}$	0.00047			GDI3673	hypothetical protein
167776587*	0.00046	YP_001648249		OsV5_172f	hypothetical protein [Ostreococcus virus OsV5]
167911245$_{s}$	0.00046	YP_001648315		OsV5_239r	hypothetical protein [Ostreococcus virus OsV5]
167867748$_{x}$	0.00044			Daci_1946	putative phage major head protein
167732694	0.00044			NMC0858	putative phage-related protein
167922873	0.00042			CHU_3230	hypothetical protein

167734178$_{p}$	0.00041			GDI3673	hypothetical protein
167873260	0.00041			Sare_3763	hypothetical protein
167685638*$_{w}$	0.00041	YP_001498525		AR158_C444L	hypothetical protein [Paramecium bursaria Chlorella virus AR158]
167901149	0.00040		K01358	azo1870	endopeptidase Clp; K01358 ATP-dependent Clp protease, protease subunit
167853099$_{i}$	0.00040			SG1188	hypothetical protein
167761349$_{x}$	0.00037			Daci_1946	putative phage major head protein
167776241	0.00037			mll0455	hypothetical protein
167824154	0.00036			SACE_4894	hydrolase, alpha/beta fold family
167843578$_{s}$	0.00035	YP_001648158		OsV5_081f	hypothetical protein [Ostreococcus virus OsV5]
167682808*	0.00035	YP_001648239		OsV5_162f	hypothetical protein [Ostreococcus virus OsV5]
167703228	0.00034			Dshi_0412	beta-Ig-H3/fasciclin
167918033$_{p}$	0.00034			GDI3673	hypothetical protein
167891224$_{p}$	0.00033			GDI3673	hypothetical protein
167867622	0.00033			Oant_1504	peptidase U35 phage prohead HK97
167732430$_{ff}$	0.00031	ZP_02092868		FAEPRAM212_03171	hypothetical protein [Faecalibacterium prausnitzii M21/2]
167684500$_{s}$	0.00031	YP_001648158		OsV5_081f	hypothetical protein [Ostreococcus virus OsV5]
167824164*	0.00030	YP_001648240		OsV5_163f	hypothetical protein [Ostreococcus virus OsV5]
167765431	0.00030			CHU_0173	gldM; gliding motility-related protein
167854137	0.00030	ZP_00743477		RBTH_08297	hypothetical protein [Bacillus thuringiensis serovar israelensis ATCC 35646]
167730288$_{k}$	0.00028			Neut_1469	phage major capsid protein, HK97 family protein
167685472*$_{gg}$	0.00027	YP_001648184		OsV5_107r	hypothetical protein [Ostreococcus virus OsV5]
167778267$_{p}$	0.00027			GDI3673	hypothetical protein
167919557	0.00027			PputW619_3936	hypothetical protein
167782645	0.00026			BBta_5785	putative phage major head protein

167908551	0.00026			CC_2781	hypothetical protein
16786723$_{p}$	0.00026			GDI3673	hypothetical protein
167896531	0.00026			BAV1464	major capsid protein
167821374	0.00025	YP_001919460		Mpop_5468	hypothetical protein [Methylobacterium populi BJ001]
167833472	0.00024			GDI3673	hypothetical protein
167733210	0.00024			Pmen_3970	phage major capsid protein, HK97 family
167713652*	0.00023			mlr8533	hypothetical protein
167935700$_{p}$	0.00023			GDI3673	hypothetical protein
167872214 hh	0.00023		K06907	Sfum_3815	phage tail sheath protein
167881636	0.00023			Rsph17025_0103	hypothetical protein
167791200$_{p}$	0.00023			GDI3673	hypothetical protein
167922981$_{p}$	0.00022			GDI3673	hypothetical protein
167824604	0.00022			Rsph17029_3578	uncharacterized protein UPF0065
167933608$_{ff}$	0.00022	ZP_02092868		FAEPRAM212_03171	hypothetical protein [Faecalibacterium prausnitzii M21/2]
167817058	0.00022		K00518	Sare_4077	superoxide dismutase
167823358*$_{gg}$	0.00021	YP_001648184		OsV5_107r	hypothetical protein [Ostreococcus virus OsV5]
167892855	0.00021	YP_001648184		OsV5_107r	hypothetical protein [Ostreococcus virus OsV5]
167840790	0.00021			Rsph17025_0437	hypothetical protein
167712150*$_{s}$	0.00021	YP_001648158		OsV5_081f	hypothetical protein [Ostreococcus virus OsV5]
167833160bb	0.00021			amb4267	hypothetical protein
167892985$_{j}$	0.00021	YP_001648266		OsV5_190f	hypothetical protein [Ostreococcus virus OsV5]
167696294$_{oo}$	0.00020			HS_1377	hypothetical protein
167759041	0.00019			PP_3877	hypothetical protein
167766087$_{s}$	0.00019	YP_001648153		OsV5_076f	hypothetical protein [Ostreococcus virus OsV5]

167919775	0.00019	YP_001294637		ORF044	hypothetical protein [Pseudomonas phage PA11]
167804453*	0.00017	ZP_03724505		ObacDRAFT_9004	hypothetical protein [Opitutaceae bacterium TAV2]
167833104	0.00017			Bcep1808_1173	hypothetical protein
167721370*	0.00016	YP_001648301		OsV5_225r	hypothetical protein [Ostreococcus virus OsV5]
167826943*	0.00016			Sare_3763	hypothetical protein
167865492	0.00015		K02027	Pput_3473	extracellular solute-binding protein, family 1; multiple sugar transport system substrate-binding protein
167685780*$_{j}$	0.00015	YP_001648266		OsV5_190f	hypothetical protein [Ostreococcus virus OsV5]
167910713	0.00014			Bd1641	hypothetical protein
167910061$_{p}$	0.00014			GDI3673	hypothetical protein
167833358$_{s}$	0.00013	YP_001648158		OsV5_081f	hypothetical protein [Ostreococcus virus OsV5]
167692314*$_{w}$	0.00012	YP_001498525		AR158_C444L	hypothetical protein [Paramecium bursaria Chlorella virus AR158]
167925393	0.00012			Oter_3421	hypothetical protein
167687436	0.00011		K01999	azo3443	conserved hypothetical ABC-type branched-chain amino acid transport systems, periplasmic component
167719658hh	0.00011		K06907	Dde_1889	hypothetical protein
167668360$_{s}$	0.00011	YP_001648158		OsV5_081f	hypothetical protein [Ostreococcus virus OsV5]
167735772	0.00010			FRAAL2683	hypothetical protein; putative mycobacteriophage protein (GP15) similarity
167702102	0.00010			Daci_1946	putative phage major head protein
167688622$_{p}$	0.00009			GDI3673	hypothetical protein
167782867$_{cc}$	0.00009			BSU26140	yqbE; hypothetical protein
167867386	0.00008			TM1040_1299	peptidase U35, phage prohead HK97
167789595	0.00008			APECO1_4044	hypothetical protein
167828425*$_{w}$	0.00007	YP_001498525		AR158_C444L	hypothetical protein [Paramecium bursaria Chlorella virus AR158]

167865490	0.00007		K02027	Rmet_2229	extracellular solute-binding protein, family 1; multiple sugar transport system substrate-binding protein
167840812	0.00006	ZP_01959135		BACCAC_00731	hypothetical protein [Bacteroides caccae ATCC 43185]
167706428	0.00005	YP_001648190		OsV5_113r	hypothetical protein [Ostreococcus virus OsV5]
167867920$_{p}$	0.00005			GDI3673	hypothetical protein
167842648*$_{s}$	0.00005	YP_001648315		OsV5_239r	hypothetical protein [Ostreococcus virus OsV5]
167869096$_{w}$	0.00005	YP_001498525		AR158_C444L	hypothetical protein [Paramecium bursaria Chlorella virus AR158]
167859444	0.00005	YP_001648151		OsV5_074f	hypothetical protein [Ostreococcus virus OsV5]
167871600	0.00005	YP_001648152		OsV5_075f	hypothetical protein [Ostreococcus virus OsV5]
167669608$_{p}$	0.00004			GDI3673	hypothetical protein
167678686$_{p}$	0.00004			GDI3673	hypothetical protein
167752119	0.00004	YP_001648152		OsV5_075f	hypothetical protein [Ostreococcus virus OsV5]
167825992$_{j}$	0.00003	A7U6E7			putative major capsid protein [Chrysochromulina ericina virus
167818634	0.00003			PputGB1_1751	hypothetical protein
167671778*	0.00003	YP_001648124		OsV5_047f	hypothetical protein [Ostreococcus virus OsV5]
167871626$_{s}$	0.00002	YP_001648158		OsV5_081f	hypothetical protein [Ostreococcus virus OsV5]
167753841	0.00002		K06907	Sfum_3815	phage tail sheath protein
167724632*	0.00002	YP_001648232		OsV5_155f	hypothetical protein [Ostreococcus virus OsV5]
167690816	0.00002	YP_001648190		OsV5_113r	hypothetical protein [Ostreococcus virus OsV5]
167742884*	0.00001			Dvul_0646	hypothetical protein
167875342$_{j}$	0.00001	YP_001648145		OsV5_068f	hypothetical protein [Ostreococcus virus OsV5]
5 m - Proteins with no annotation					
167699580*	0.01263				
167736790$_{ii}$	0.01043				
167796769	0.00914				
167722626$_{jj}$	0.00789				

167703824$_{pp}$	0.00714				
167753801	0.00626				
167854251	0.00577				
167744898*$_{o}$	0.00546				
167664175*$_{nn}$	0.00514				
167829145$_{pp}$	0.00433				
167779175$_{pp}$	0.00423				
167881060$_{pp}$	0.00419				
167887022$_{pp}$	0.00390				
167836216$_{jj}$	0.00369				
167688044$_{p}$	0.00353				
167697984$_{pp}$	0.00321				
167855765$_{jj}$	0.00318				
167764897$_{jj}$	0.00297				
167718436	0.00240				
167771817	0.00226				
167699330*	0.00220				
167891152$_{pp}$	0.00207				
167844558$_{pp}$	0.00197				
167801097$_{pp}$	0.00197				
167891908	0.00196				
167820168$_{ii}$	0.00192				
167688624	0.00182				
167746546$_{jj}$	0.00176				
167682238$_{p}$	0.00175				

167722606	0.00164				
167883488$_{pp}$	0.00157				
167839862$_{mm}$	0.00139				
167820406*	0.00139				
167858104	0.00138				
167806741$_{jj}$	0.00138				
167678192	0.00133				
167706644	0.00133				
167787801*$_{ll}$	0.00124				
167781039	0.00124				
167936638	0.00116				
167733554	0.00116				
167918031	0.00112				
167790652	0.00110				
167734428	0.00102				
167925455	0.00102				
167928078	0.00100				
167682970$_{o}$	0.00098				
167701282	0.00091				
167867140$_{o}$	0.00087				
167809975$_{jj}$	0.00087				
167750727	0.00082				
167883564$_{ll}$	0.00082				
167789467$_{pp}$	0.00080				
167669606	0.00078				
167733300	0.00076				
167750389$_{jj}$	0.00072				

167852849	0.00072				
167827017	0.00070				
167691436	0.00068				
167816466*	0.00067				
167678688	0.00063				
167796679	0.00062				
167761163	0.00059				
167916021$_{pp}$	0.00059				
167867918	0.00058				
167853885	0.00058				
167757667	0.00053				
167922983	0.00052				
167923663$_{nn}$	0.00051				
167922109	0.00051				
167661777	0.00051				
167936684	0.00050				
167867228	0.00050				
167791202	0.00049				
167819274	0.00046				
167765833*	0.00045				
167793451*	0.00045				
167732910	0.00043				
167890226	0.00043				
167718438	0.00042				
167688708	0.00041				
167699600$_{pp}$	0.00041				
167746630	0.00040				
167821290	0.00039				
167916161*	0.00038				

167700778	0.00037				
167701632$_{kk}$	0.00037				
167675494*	0.00036				
167711820	0.00034				
167663983	0.00033				
167689444*	0.00032				
167933464$_{nn}$	0.00032				
167891222	0.00032				
167852557	0.00031				
167843828	0.00031				
167843020	0.00031				
167677672	0.00030				
167776503*	0.00028				
167804815	0.00027				
167713808	0.00027				
167702310$_{dd}$	0.00026				
167913463$_{o}$	0.00025				
167881302	0.00025				
167907624$_{mm}$	0.00025				
167753609*	0.00024				
167829571	0.00024				
167921665	0.00024				
167920645	0.00023				
167714058	0.00022				
167677546*	0.00021				
167913465	0.00020				
167697624*	0.00020				
167912083$_{jj}$	0.00019				

167766043*	0.00018				
167678558*	0.00018				
167733556	0.00017				
167663383*	0.00016				
167905220*	0.00015				
167891594	0.00015				
167883594$_{ll}$	0.00015				
167879460	0.00014				
167919777	0.00014				
167884588$_{o}$	0.00014				
167822810	0.00013				
167713494	0.00012				
167841896*	0.00010				
167804467*	0.00010				
167925043$_{kk}$	0.00010				
167858106	0.00009				
167788223*	0.00009				
167878206	0.00008				
167764895$_{jj}$	0.00008				
167767179	0.00008				
167858640	0.00008				
167683530*	0.00007				
167918035	0.00006				
167766125*	0.00006				
167752051*	0.00005				
167890228	0.00004				
167685654*	0.00003				
167719670*	0.00002				
167879450	0.00002				

11.5 m - COG annotated proteins					
Gene ID	**normalised spectral abundance**	**COG identifier**	**KO identifier**	**KEGG locus tag**	**COG description : KEGG description**
163207432	0.01734	COG0834	K09969	SAR11_0953	ABC-type amino acid transport system, periplasmic component : yhdW
163201696	0.01011	COG1879		MSMEG_1374	periplasmic sugar-binding proteins : ribose ABC transporter, periplasmic binding protein
163136433	0.00671	COG3409		Clos_2845	putative peptidoglycan-binding domain-containing protein
163539247	0.00629	COG1653		Noca_3914	sugar-binding periplasmic proteins/domains : extracellular solute-binding protein, family 1
163377029_a	0.00566	COG0050	K02358	amb3148	GTPases - translation elongation factors : tuf
163451248_b	0.00541	COG0715	K02051	SAR11_0807	ABC-type nitrate/sulfonate/taurine/bicarbonate transport systems, periplasmic components
163135049_c	0.00533	COG1638		SAR11_0266	dicarboxylate-binding periplasmic protein : TRAP dicarboxylate transporter - DctP subunit (mannitol/chloroaromatic compounds)
163451084	0.00531	COG2113	K02002	SAR11_1302	ABC-type proline/glycine betaine transport systems, periplasmic components : opuAC
163117735	0.00526	COG2113	K02001	Plav_1066	ABC-type proline/glycine betaine transport systems, periplasmic components
163198494_d	0.00415	COG0591		SAR11_0316	Na+/proline, Na+/panthothenate symporters and related permeases : yjcG
163416423*	0.00371	COG0776	K03530	SAR11_0817	bacterial nucleoid DNA-binding protein : hupA
163442042	0.00364	COG0687	K02055	SAR11_1336	spermidine/putrescine-binding periplasmic protein : potD
163208342_e	0.00356	COG0834	K09969	HCH_05807	ABC-type amino acid transport system, periplasmic component
163234668*	0.00338	COG0450		SPO3383	peroxiredoxin : thiol-specific antioxidant protein

163261506	0.00336	COG1638		SAR11_0864	dicarboxylate-binding periplasmic protein
163104605	0.00336	COG2213	K02799	GK1948	phosphotransferase system, mannitol-specific IIBC component
163357996[c]	0.00321	COG1638		SAR11_0266	dicarboxylate-binding periplasmic protein : TRAP dicarboxylate transporter - DctP subunit (mannitol/chloroaromatic compounds)
163381848[f]	0.00314	COG0459	K04077	SAR11_0162	chaperonin GroEL (HSP60 family)
163145053	0.00312	COG0683	K01999	SAR11_1361	ABC-type branched-chain amino acid transport systems, periplasmic component : livJ2; Leu/Ile/Val-binding protein precursor
163388714	0.00282	COG1638		RD1_2185	dicarboxylate-binding periplasmic proteind : DctP; C4-dicarboxylate-binding periplasmic protein, putative
163450920	0.00247	COG0683	K01999	SAR11_1361	ABC-type branched-chain amino acid transport systems, periplasmic component : livJ2; Leu/Ile/Val-binding protein precursor
163240441	0.00246	COG1653	K02027	PflO1_3630	sugar-binding periplasmic proteins/domains
163275955	0.00241	COG1638		TM1040_0356	dicarboxylate-binding periplasmic protein : TRAP dicarboxylate transporter - DctP subunit
163449626	0.00229	COG1638		Dshi_3326	dicarboxylate-binding periplasmic protein : TRAP dicarboxylate transporter, DctP subunit
163450966	0.00228	COG0687	K02055	SAR11_1336	spermidine/putrescine-binding periplasmic protein : potD
163174786	0.00223	COG2358		PBPRA0389	predicted periplasmic binding protein : putative immunogenic protein
163120641	0.00219	COG1879	K02058	CMM_0792	periplasmic sugar-binding proteins : putative sugar ABC transporter, solute-binding protein
163416343	0.00204	COG3181		Csal_1767	uncharacterized BCR
163441934	0.00198	COG2885	K03640	SAR11_0598	outer membrane protein and related peptidoglycan-associated (lipo)proteins : ompA; OmpA family

163320067	0.00176	COG2165	K02650	SAR11_0054	general secretory pathway proteins G and H and related periplasmic/secreted proteins : pilA; pilin (bacterial filament)
163274197[b]	0.00167	COG0715	K02051	SAR11_0807	ABC-type nitrate/sulfonate/taurine/bicarbonate transport systems, periplasmic components
163128105	0.00167	COG1012	K00128	AAur_pTC20196	NAD-dependent aldehyde dehydrogenases
163214443[e]	0.00161	COG0834	K09969	HCH_05807	ABC-type amino acid transport system, periplasmic component
163174178	0.00143	COG1879		RHA1_ro08504	periplasmic sugar-binding proteins : ABC sugar transporter, periplasmic substrate binding protein
163134937[d]	0.00138	COG0591		SAR11_0316	Na+/proline, Na+/panthothenate symporters and related permeases : yjcG
163451228	0.00132	COG2113	K02002	SAR11_0797	ABC-type proline/glycine betaine transport systems, periplasmic components : proX
163376697*	0.00129	COG0834	K10018	SAR11_1210	ABC-type amino acid transport system, periplasmic component : octopine/nopaline transport system substrate-binding protein
163104625	0.00119	COG0683	K01999	AAur_1271	ABC-type branched-chain amino acid transport systems, periplasmic component : braC;
163498557	0.00116	COG3181	K07795	Mmwyl1_1799	uncharacterized BCR : putative tricarboxylic transport membrane protein
163497259	0.00107	COG0747		CMM_2185	ABC-type dipeptide/oligopeptide/nickel transport systems, periplasmic components
163296806	0.00075	COG0834	K02030	SAR11_1068	ABC-type amino acid transport system, periplasmic componentp: pheC; cyclohexadienyl dehydratase; polar amino acid transport system substrate-binding protein
163277703	0.00071	COG0055	K02112	Acel_0653	F0F1-type ATP synthase beta subunit
163152101*[f]	0.00066	COG0459	K04077	SAR11_0162	chaperonin GroEL (HSP60 family)
163296936[a]	0.00055	COG0050	K02358	SAR11_1130	GTPases - translation elongation factors : tufB

163117667	0.00043	COG0174	K01915	SAR11_0747	glutamine synthase : glnA
163154554[a]	0.00042	COG0050	K02358	Tfu_2648	GTPases - translation elongation factors : tuf
163450946	0.00036	COG0683	K01999	SAR11_1346	ABC-type branched-chain amino acid transport systems, periplasmic component : livJ;
163208382	0.00035	COG0174	K01915	CMM_1636	glutamine synthase : glnA
163135037	0.00031	COG2133	K00540	Rsph17025_1771	glucose/sorbosone dehydrogenases
163150509	0.00028	COG0737		Haur_2906	5'-nucleotidase/2',3'-cyclic phosphodiesterase and related esterases
163195194	0.00028	COG0086	K03046	Lxx20630	DNA-directed RNA polymerase beta' subunit/160 kD subunit (split gene in archaea and Syn) : rpoC
163169240*	0.00027	COG0330	K04088	SAR11_0008	membrane protease subunits, stomatin/prohibitin homologs : hflK
163135897	0.00014	COG1185	K00962	SAR11_0392	polyribonucleotide nucleotidyltransferase (polynucleotide phosphorylase) : pnp; polynucleotide phosphorylase/polyadenylase

11.5 m KEGG and NR annotated proteins

Gene ID	normalised spectral abundance	NR identifier	KO identifier	KEGG / NR locus tag	KEGG / NR description
163498919[g]	0.04693	BAF91544			major capsid protein [uncultured Myoviridae]
163303017[h]	0.03153			GDI3673	hypothetical protein
163496543[i]	0.03095	YP_001648158			hypothetical protein [Ostreococcus virus OsV5]
163312513	0.02334	YP_002590925			putative porin [Candidatus Pelagibacter sp. HTCC7211]
163114028[g]	0.02078	YP_214669			gp23 [Prochlorococcus phage P-SSM4]
163447324[i]	0.01947	YP_001648266			hypothetical protein OsV5_190f [Ostreococcus virus OsV5]
163104039[j]	0.01469	YP_001498525		AR158_C444L	hypothetical protein [Paramecium bursaria Chlorella virus AR158]
163299338	0.01058			Sputw3181_2479	phage major capsid protein, HK97 family

163431599$_{i}$	0.01022	YP_001648266		OsV5_190f	hypothetical protein [Ostreococcus virus OsV5]
163486997$_{k}$	0.00971			SG1188	hypothetical protein
163200650	0.00948			mlr8524	phage major capsid protein, GP36
163146271*$_{l}$	0.00930			BBta_5785	putative phage major head protein
163466160	0.00921			BBta_5785	putative phage major head protein
163111996$_{h}$	0.00849			GDI3673	hypothetical protein
163277976	0.00767			Neut_1469	phage major capsid protein, HK97 family protein
163276037	0.00762			mma_2202	hypothetical protein
163114610$_{i}$	0.00717	A7U6E7			putative major capsid protein [Chrysochromulina ericina virus]
163191828	0.00696	ZP_03701413		Flav3CDRAFT_1333	hypothetical protein [Flavobacteria bacterium MS024-3C]
163121725*	0.00678	YP_001648124		OsV5_047f	hypothetical protein [Ostreococcus virus OsV5]
163383538*	0.00611			Neut_1469	phage major capsid protein, HK97 family protein
163125121$_{g}$	0.00600	YP_214669			gp23 [Prochlorococcus phage P-SSM4]
163161438	0.00539	ABW90951			gp23 major capsid protein [uncultured Myoviridae]
163404994$_{m}$	0.00493			Haur_0657	hypothetical protein
163115173*$_{n}$	0.00467	YP_001648182		OsV5_105r	hypothetical protein [Ostreococcus virus OsV5]
163253040	0.00435			Bpro_3745	hypothetical protein
163519031	0.00433	YP_002276820		Gdia_2460	hypothetical protein [Gluconacetobacter diazotrophicus PAl 5]
163228214$_{o}$	0.00413			Daci_1946	putative phage major head protein
163291274$_{h}$	0.00407			GDI3673	hypothetical protein
163206524*$_{i}$	0.00403	YP_001648266		OsV5_190f	hypothetical protein [Ostreococcus virus OsV5]
163514201	0.00400			MAB_1788	bacteriophage protein
163498539	0.00399			SAR11_1290	TRAP-type bacterial extracellular solute-binding protein
163432666	0.00396			Oter_3421	hypothetical protein
163480087	0.00392			APECO1_525	hypothetical protein
163187860	0.00390			GDI3673	hypothetical protein

163529078	0.00375			HM1_2880	phage major capsid protein, hk97 family
163526011$_i$	0.00371	A7U6E9			putative major capsid protein [Pyramimonas orientalis virus]
163180584	0.00369	BAE06835			hypothetical major capsid protein [Heterosigma akashiwo virus 01]
163459594$_i$	0.00364	BAE06835			hypothetical major capsid protein [Heterosigma akashiwo virus 01]
163503842$_h$	0.00357			GDI3673	hypothetical protein
163495193	0.00351			MAB_1788	bacteriophage protein
163385358$_p$	0.00324			GDI3673	hypothetical protein
163489449	0.00313			SG1188	hypothetical protein
163472957	0.00310			Asuc_1240	phage major capsid protein, HK97 family
163131623	0.00298	YP_195142			major capsid protein gp23 [Synechococcus phage S-PM2]
163118697$_i$	0.00289	A7U6F0			putative major capsid protein [Phaeocystis pouchetii virus]
163420549	0.00284			LGAS_1485	predicted phage phi-C31 GP36 major capsid-like protein
163142179	0.00279	ZP_03643684		BACCOPRO_02057	hypothetical protein [Bacteroides coprophilus DSM 18228]
163250350$_q$	0.00277	YP_214367			T4-like major capsid protein [Prochlorococcus phage P-SSM2]
163541257	0.00271			Swit_4452	hypothetical protein
163478791	0.00261			amb4267	hypothetical protein
163452556	0.00245			APECO1_525	hypothetical protein
163507581	0.00237			Cthe_2848	phage major capsid protein, HK97
163409546*	0.00234	YP_001648301		OsV5_225r	hypothetical protein [Ostreococcus virus OsV5]
163412911	0.00233	ZP_03724502		ObacDRAFT_9001	hypothetical protein [Opitutaceae bacterium TAV2]
163544869	0.00230			Smed_1334	phage major capsid protein, HK97 family
163323331	0.00222			LGAS_1485	predicted phage phi-C31 GP36 major capsid-like

					protein
163235228*	0.00221			BBta_5785	putative phage major head protein
163494515$_r$	0.00217			LGAS_1485	predicted phage phi-C31 GP36 major capsid-like protein
163372194	0.00216	ZP_01017474			major capsid protein, HK97 family protein [Parvularcula bermudensis HTCC2503]
163252031$_i$	0.00210	A7U6F0			putative major capsid protein [Phaeocystis pouchetii virus]
163390078$_p$	0.00210			GDI3673	hypothetical protein
163290252$_m$	0.00201			Haur_0657	hypothetical protein
163157042$_k$	0.00196			SG1188	hypothetical protein
163199564$_i$	0.00192	YP_001648266		OsV5_190f	hypothetical protein [Ostreococcus virus OsV5]
163490373$_h$	0.00191			GDI3673	hypothetical protein
163445182	0.00189			Acid_4111	hypothetical protein
163229276$_i$	0.00187	YP_001648266		OsV5_190f	hypothetical protein [Ostreococcus virus OsV5]
163485571$_i$	0.00185	YP_001648158		OsV5_081f	hypothetical protein [Ostreococcus virus OsV5]
163499762	0.00183			BBta_5785	putative phage major head protein
163227690$_i$	0.00181	YP_001648158		OsV5_081f	hypothetical protein [Ostreococcus virus OsV5]
163168692	0.00179			M446_5960	hypothetical protein
163109620*	0.00175	YP_001648249		OsV5_172f	hypothetical protein [Ostreococcus virus OsV5]
163105813	0.00173			APECO1_4044	hypothetical protein
163141843*$_i$	0.00172	YP_001648266		OsV5_190f	hypothetical protein [Ostreococcus virus OsV5]
163117897$_h$	0.00163			GDI3673	hypothetical protein
163173092	0.00163			Pmen_3970	phage major capsid protein, HK97 family
163491889	0.00161			CKO_01864	hypothetical protein
163453714$_h$	0.00159			GDI3673	hypothetical protein
163161098$_q$	0.00157	YP_214367			T4-like major capsid protein [Prochlorococcus phage P-SSM2]
163177212	0.00156			BBta_6597	putative peptidase S14, ClpP

163352152	0.00154			BDI_2873	putative outer membrane protein, probably involved in nutrient binding
163372026$_{i}$	0.00151	YP_001648266		OsV5_190f	hypothetical protein [Ostreococcus virus OsV5]
163287382$_{q}$	0.00151	YP_214367			T4-like major capsid protein [Prochlorococcus phage P-SSM2]
163379834$_{h}$	0.00151			GDI3673	hypothetical protein
163124973	0.00148			BAV1464	major capsid protein
163354170	0.00145	YP_001648190		OsV5_113r	hypothetical protein [Ostreococcus virus OsV5]
163115568*$_{s}$	0.00143	YP_001648153		OsV5_076f	hypothetical protein [Ostreococcus virus OsV5]
163410122$_{s}$	0.00140	YP_001648315		OsV5_239r	hypothetical protein [Ostreococcus virus OsV5]
163411861$_{r}$	0.00138			LGAS_1485	predicted phage phi-C31 GP36 major capsid-like protein
163220019	0.00132	ZP_00743477		RBTH_08297	hypothetical protein [Bacillus thuringiensis serovar israelensis ATCC 35646]
163134239*	0.00132	YP_001648234		OsV5_157f	hypothetical protein [Ostreococcus virus OsV5]
163174626*	0.00130		K06904	BL0376	hypothetical protein with similarity to putative maturation protease of prophage CP-9 33CE
163154474	0.00125			gll0198	similar to bacterioopsin
163467688$_{l}$	0.00115			Daci_1946	putative phage major head protein
163256412	0.00111	ZP_00743477		RBTH_08297	hypothetical protein [Bacillus thuringiensis serovar israelensis ATCC 35646]
163389410	0.00111			Oant_1504	peptidase U35 phage prohead HK97
163248889$_{i}$	0.00110	YP_001648266		OsV5_190f	hypothetical protein [Ostreococcus virus OsV5]
163415470$_{i}$	0.00104	A7U6F0			putative major capsid protein [Phaeocystis pouchetii virus]
163191410*	0.00100	YP_001648184		OsV5_107r	hypothetical protein [Ostreococcus virus OsV5]
163142589	0.00093			Pmen_3970	phage major capsid protein, HK97 family
163327003$_{t}$	0.00088		K06907	Dde_1889	hypothetical protein; K06907
163211634*$_{i}$	0.00086	YP_001648266		OsV5_190f	hypothetical protein [Ostreococcus virus OsV5]
163393172$_{i}$	0.00075	YP_001648266		OsV5_190f	hypothetical protein [Ostreococcus virus OsV5]

163161074$_t$	0.00073		K06907	Dde_1889	hypothetical protein; K06907
163141653*$_i$	0.00070	YP_001648158		OsV5_081f	hypothetical protein [Ostreococcus virus OsV5]
163110018	0.00068	YP_001294637		ORF044	hypothetical protein [Pseudomonas phage PA11]
163249021$_s$	0.00067	YP_001648315		OsV5_239r	hypothetical protein [Ostreococcus virus OsV5]
163445294*$_j$	0.00062	YP_001498525		AR158_C444L	hypothetical protein [Paramecium bursaria Chlorella virus AR158]
163507277	0.00058			CHLREDRAFT_186229	hypothetical protein
163298764$_i$	0.00058	YP_001648158		OsV5_081f	hypothetical protein [Ostreococcus virus OsV5]
163298596$_i$	0.00055	YP_001648266		OsV5_190f	hypothetical protein [Ostreococcus virus OsV5]
163335150	0.00053			BAV1464	major capsid protein
163327023*$_q$	0.00046	YP_214367			T4-like major capsid protein [Prochlorococcus phage P-SSM2]
163287366$_t$	0.00038		K06907	Sfum_3815	phage tail sheath protein; K06907
163475851$_o$	0.00028			ZMO0387	major head protein
163195236*$_s$	0.00027	YP_001648315		OsV5_239r	hypothetical protein [Ostreococcus virus OsV5]
163184761	0.00027	YP_001648134		OsV5_057f	hypothetical protein [Ostreococcus virus OsV5]
163109424*$_n$	0.00023	YP_001648182		OsV5_105r	hypothetical protein [Ostreococcus virus OsV5]
163368976	0.00020	YP_001648211		OsV5_134r	hypothetical protein [Ostreococcus virus OsV5]
163306940	0.00018	YP_001648185		OsV5_108r	hypothetical protein [Ostreococcus virus OsV5]
163162936*	0.00017	YP_001648263		OsV5_187r	hypothetical protein [Ostreococcus virus OsV5]
163151745$_s$	0.00017	YP_001648315		OsV5_239r	hypothetical protein [Ostreococcus virus OsV5]
11.5 m - Proteins with no annotation					
163171140	0.03385				
163345623$_u$	0.03193				
163279609	0.01466				
163534693	0.00797				
163109584	0.00788				
163251027	0.00668				
163250059$_u$	0.00668				

163386750$_u$	0.00650				
163254426	0.00638				
163129699	0.00610				
163113296*	0.00528				
163129983	0.00511				
163395912	0.00471				
163346783	0.00446				
163246177$_u$	0.00435				
163303354	0.00395				
163477113	0.00385				
163419181	0.00349				
163431790$_v$	0.00331				
163502200	0.00289				
163456165	0.00285				
163397872	0.00285				
163490375	0.00278				
163502202	0.00250				
163453476*	0.00247				
163503840	0.00234				
163187858	0.00225				
163224309$_v$	0.00211				
163117895	0.00204				
163285151$_w$	0.00191				
163511023$_u$	0.00182				
163156214	0.00160				
163311655	0.00157				
163286408$_w$	0.00138				
163254680	0.00138				
163439545*	0.00133				

163123675	0.00131				
163199154$_u$	0.00126				
163129981	0.00097				
163110772*	0.00096				
163211312	0.00094				
163207714	0.00092				
163342613	0.00074				
163217867*	0.00071				
163110016	0.00069				
163117805	0.00063				
163280533	0.00059				
163168938	0.00059				
163320197	0.00040				

12.7 m - COG annotated proteins

Gene ID	normalised spectral abundance	COG identifier	KO identifier	KEGG locus tag	COG description : KEGG description
165547755*	0.01035	COG0539	K02945	Cvib_1514	rpsA; 30S ribosomal protein S1
165526280	0.00768	COG0181	K01749	Cvib_1245	porphobilinogen deaminase : hydroxymethylbilane synthase
165511899	0.00756	COG0516	K00088	Cvib_1056	IMP dehydrogenase/GMP reductase
165562959	0.00530	COG1104	K04487	Cvib_0301	cysteine sulfinate desulfinase/cysteine desulfurase and related enzymes : aminotransferase, class V
165514395*	0.00452	COG0674	K00174	Cvib_1597	pyruvate:ferredoxin oxidoreductase and related 2-oxoacid:ferredoxin oxidoreductases, alpha subunit
165502373	0.00380	COG0129	K01687	Cvib_1169	dihydroxy-acid dehydratase
165514465*	0.00340	COG0054	K00794	Cvib_1632	riboflavin synthase beta-chain
165525758	0.00270	COG1862	K03210	Cvib_0223	preprotein translocase subunit YajC
165514421*	0.00243	COG0250	K02601	Cvib_1610	transcription antitermination protein NusG

165526166	0.00209	COG0413	K00606	Cvib_0725	ketopantoate hydroxymethyltransferase : panB; 3-methyl-2-oxobutanoate hydroxymethyltransferase
165562961	0.00203	COG0031	K01738	Cvib_0300	cysteine synthase
165526282	0.00189	COG1587	K01719	Cvib_1246	uroporphyrinogen-III synthase
165514409*	0.00173	COG0086	K03046	Cvib_1604	DNA-directed RNA polymerase beta' subunit/160 kD subunit (split gene in archaea and Syn)
165514577*	0.00162	COG1778	K03270	Cvib_1694	uncharacterized proteins of HAD superfamily, CMP-Neu5Ac homologs : 3-deoxy-D-manno-octulosonate 8-phosphate phosphatase, YrbI family; (KDO 8-P phosphatase)
165514581*[a]	0.00158	COG0542		Cvib_1696	ATPases with chaperone activity, ATP-binding subunit : AAA-2 domain protein
165536856	0.00155	COG0157	K00767	Cvib_0335	nicotinate-nucleotide pyrophosphorylase [carboxylating]
165547841	0.00146	COG0493	K00266	Cvib_1478	NADPH-dependent glutamate synthase beta chain and related oxidoreductases
165514651*	0.00139	COG0797	K03642	Cvib_1727	lipoproteins : rare lipoprotein A
165525906	0.00137	COG0750	K01417	Cvib_0137	predicted membrane-associated Zn-dependent proteases 1
165501975*	0.00135	COG0740	K01358	Cvib_0441	protease subunit of ATP-dependent Clp proteases
165505943	0.00135	COG0543		Cvib_0839	2-polyprenylphenol hydroxylase and related flavodoxin oxidoreductases : oxidoreductase FAD/NAD(P)-binding domain protein
165526296	0.00133	COG0082	K01736	Cvib_1253	chorismate synthase
165547993	0.00132	COG0497	K03631	Cvib_1402	ATPases involved in DNA repair : DNA repair protein RecN
165547777	0.00126	COG0008	K01885	Cvib_1503	glutamyl-tRNA synthetase
165553075	0.00125	COG1158	K03628	Cvib_1537	transcription termination factor : Rho
165511737	0.00121	COG1726	K03615	Cvib_0797	Na+-transporting NADH:ubiquinone oxidoreductase alpha subunit : electron transport complex, RnfABCDGE type, C subunit

165526284	0.00118	COG0483	K01092	Cvib_1247	archaeal fructose-1,6-bisphosphatase and related enzymes of inositol monophosphatase family
165525808	0.00116	COG0331	K00645	Cvib_0199	(acyl-carrier-protein) S-malonyltransferase
165550953	0.00116	COG1022	K01897	Cvib_0930	long-chain acyl-CoA synthetases (AMP-forming) : AMP-dependent synthetase and ligase
165502369	0.00105	COG0440	K01653	Cvib_1171	acetolactate synthase, small subunit
165526250	0.00104	COG1522		Cvib_1231	transcriptional regulators : AsnC family
165525708	0.00102	COG0089	K02892	Cvib_0248	rplW; 50S ribosomal protein L23
165502825*	0.00102	COG0341	K03074	Cvib_0011	secF; preprotein translocase subunit SecF
165502225	0.00101	COG0557	K01147	Cvib_0574	Exoribonucleases : RNAse R; exoribonuclease II
165514389*	0.00101	COG0446		Cvib_1594	uncharacterized NAD(FAD)-dependent dehydrogenases : FAD-dependent pyridine nucleotide-disulphide oxidoreductase
165525802	0.00100	COG0333	K02911	Cvib_0202	rpmF; 50S ribosomal protein L32
165525664	0.00098	COG0100	K02948	Cvib_0271	30S ribosomal protein S11
165511903	0.00095	COG1240	K03404	Cvib_1058	Mg-chelatase subunit ChlI : protoporphyrin IX magnesium-chelatase
165514579*	0.00094	COG2877	K01627	Cvib_1695	3-Deoxy-D-manno-octulosonic acid (KDO) 8-phosphate synthase
165525806	0.00094	COG0332	K00648	Cvib_0200	3-oxoacyl-(acyl carrier protein) synthase III
165519368	0.00094	COG1192	K03496	Cvib_0388	ATPases involved in chromosome partitioning
165547931	0.00093	COG0217		Cvib_1432	uncharacterized ACR : hypothetical protein
165536866	0.00091	COG0468	K03553	Cvib_0340	RecA/RadA recombinase
165514413*	0.00086	COG0222	K02935	Cvib_1606	rplL; 50S ribosomal protein L7/L12
165547847	0.00086	COG0106	K01814	Cvib_1475	phosphoribosylformimino-5-aminoimidazole carboxamide ribotide isomerase
165525912	0.00085	COG0778		Cvib_0134	nitroreductase
165547827	0.00082	COG1136	K02003	Cvib_1485	ABC-type transport systems, involved in lipoprotein release, ATPase components

165547771	0.00080	COG0776	K05788	Cvib_1506	bacterial nucleoid DNA-binding protein : histone family protein DNA-binding protein; integration host factor subunit beta
165562901	0.00080	COG0003	K01551	Cvib_0328	predicted ATPase involved in chromosome partitioning : arsenite-activated ATPase ArsA
165530868	0.00079	COG2089	K01654	fnu:FN1684	sialic acid synthase : N-acetylneuraminate synthase
165562905	0.00078	COG0629	K03111	Cvib_0326	single-strand DNA-binding protein
165502829*	0.00077	COG0446	K00540	Cvib_0009	uncharacterized NAD(FAD)-dependent dehydrogenases : sulfide dehydrogenase (flavocytochrome), flavoprotein subunit
165511991	0.00076	COG1418	K06950	Cvib_1112	predicted HD superfamily hydrolase : hypothetical protein
165547765	0.00075	COG0503	K00759	Cvib_1509	adenine/guanine phosphoribosyltransferases and related PRPP-binding proteins
165515181	0.00075	COG0711	K02109	Cvib_1741	F0F1-type ATP synthase b subunit
165502313	0.00075	COG0209	K00525	Cvib_1199	ribonucleotide-diphosphate reductase subunit alpha
165525750[a]	0.00074	COG0542		Cvib_0227	ATPases with chaperone activity, ATP-binding subunit : AAA ATPase, central domain protein
165525840	0.00074	COG0360	K02990	Cvib_0181	rpsF; 30S ribosomal protein S6
165547781	0.00073	COG0723	K02636	Cvib_1501	Rieske Fe-S protein : plastoquinol--plastocyanin reductase; cytochrome b6-f complex iron-sulfur subunit
165548025	0.00073	COG0058	K00688	Cvib_1386	alpha-glucan phosphorylase
165511773	0.00072	COG0524		Cvib_0779	sugar kinases, ribokinase family : PfkB domain protein
165514433*	0.00071	COG0480	K02355	Cvib_1616	translation elongation and release factors (GTPases) : fusA; elongation factor G
165526086	0.00071	COG2089	K01654	Cvib_1025	sialic acid synthase : N-acetylneuraminate synthase
165502143	0.00070	COG3040	K03098	Cvib_0516	bacterial lipocalin
165547991	0.00070	COG0329	K01714	Cvib_1403	dihydrodipicolinate synthase/N-acetylneuraminate lyase

165536870	0.00069	COG0136	K00133	Cvib_0342	aspartate semialdehyde dehydrogenase
165502129	0.00067	COG0158	K03841	Cvib_0509	fructose-1,6-bisphosphatase
165525834	0.00067	COG0359	K02939	Cvib_0184	rplI; 50S ribosomal protein L9
165547783	0.00065	COG1290	K00412	Cvib_1500	cytochrome b subunit of the bc complex : cytochrome b/b6, N-terminal domain protein; ubiquinol-cytochrome c reductase
165553031	0.00065	COG0184	K02956	Cvib_1557	rpsO; 30S ribosomal protein S15
165502097	0.00065	COG0127	K01516	Cvib_0493	non-canonical purine NTP pyrophosphatase, RdgB/HAM1 family
165514535*	0.00064	COG0366		Cvib_1672	glycosidases : trehalose synthase
165536860	0.00064	COG0544	K03545	Cvib_0337	FKBP-type peptidyl-prolyl cis-trans isomerase (trigger factor)
165519356	0.00060	COG1410	K00548	Cvib_0382	methionine synthase I, cobalamin-binding domain : metH; 5-methyltetrahydrofolate--homocysteine methyltransferase
165525900	0.00058	COG0284	K01591	Cvib_0140	orotidine 5'-phosphate decarboxylase
165547983	0.00057	COG0674	K03737	Cvib_1407	pyruvate:ferredoxin oxidoreductase and related 2-oxoacid:ferredoxin oxidoreductases, alpha subunit
165547901	0.00057	COG3155		Cvib_1447	uncharacterized sigma cross-reacting protein 27A (ES1 or KNP-I alpha protein) : isoprenoid biosynthesis protein with amidotransferase-like domain
165562941	0.00057	COG2319		Cvib_0309	WD-40 repeat protein
165526078	0.00056	COG0589		Cvib_1021	universal stress protein UspA and related nucleotide-binding proteins
165516491	0.00056	COG0760		Cvib_1572	parvulin-like peptidyl-prolyl isomerase : PpiC-type peptidyl-prolyl cis-trans isomerase
165562981	0.00053	COG1043	K00677	Cvib_0290	acyl-[acyl carrier protein]--UDP-N-acetylglucosamine O-acyltransferase
165502845*	0.00052	COG0706	K03217	Cvib_1771	preprotein translocase subunit YidC

165525718	0.00051	COG0480	K02355	Cvib_0243	translation elongation and release factors (GTPases) : fusA; elongation factor G
165526290	0.00051	COG0511		Cvib_1250	biotin carboxyl carrier protein : biotin/lipoyl attachment domain-containing protein
165557791	0.00051	COG0074		Cvib_0866	succinyl-CoA synthetase alpha subunit : ATP citrate lyase subunit 2
165547973	0.00050	COG1493	K06023	Cvib_1412	serine kinase of the HPr protein, regulates carbohydrate metabolism
165502247	0.00050	COG0234	K04078	Plut_0541	groES; co-chaperonin GroES
165514671*	0.00050	COG0636	K02110	Plut_2097	F0F1-type ATP synthase c subunit/Archaeal/vacuolar-type H+-ATPase subunit K : ATP synthase F0, C subunit
165502267	0.00050	COG1077	K03569	Cvib_0595	HSP70 class molecular chaperones involved in cell morphogenesis : cell shape determining protein, MreB/Mrl family
165525868	0.00049	COG0188	K02469	Cvib_0172	DNA gyrase subunit A
165514647*	0.00048	COG0167	K00226	Cvib_1724	dihydroorotate dehydrogenase 2
165509259*	0.00046	COG0793	K03797	Cvib_0018	periplasmic protease : carboxyl-terminal protease
165548143	0.00046	COG0261	K02888	Cvib_1329	rplU; 50S ribosomal protein L21
165514553*	0.00045	COG0001	K01845	Cvib_1681	glutamate-1-semialdehyde 2,1-aminomutase
165525814	0.00044	COG0304	K09458	Cvib_0196	3-oxoacyl-[acyl-carrier-protein] synthase II
165547833	0.00043	COG2226	K03183	Cvib_1482	methylase involved in ubiquinone/menaquinone biosynthesis : demethylmenaquinone methyltransferase
165547919	0.00042	COG0036	K01783	Cvib_1438	ribulose-5-phosphate 3-epimerase
165525676	0.00042	COG1841	K02907	Cvib_0264	rpmD; 50S ribosomal protein L30
165502421	0.00042	COG0443	K04043	Cvib_1158	chaperone protein DnaK
165525692	0.00042	COG0093	K02874	Cvib_0256	rplN; 50S ribosomal protein L14
165525970	0.00042	COG1220	K03667	Cvib_0959	ATP-dependent protease, ATPase subunit : hslU
165525828	0.00041	COG0292	K02887	Cvib_0187	rplT; 50S ribosomal protein L20

165502239	0.00040	COG0596		Cvib_0581	predicted hydrolases or acyltransferases (alpha/beta hydrolase superfamily)
165525710	0.00039	COG0088	K02926	Cvib_0247	rplD; 50S ribosomal protein L4
165502125	0.00039	COG2838	K00031	Cvib_0507	monomeric isocitrate dehydrogenase
165526072	0.00039	COG1038	K01571	Cvib_1018	pyruvate carboxylase, C-terminal domain/subunit : biotin/lipoyl attachment domain-containing protein; oxaloacetate decarboxylase, alpha subunit
165562947	0.00038	COG0040	K00765	Cvib_0307	hisG; ATP phosphoribosyltransferase
165519380	0.00038	COG0447	K01661	Cvib_0394	dihydroxynaphthoic acid synthase
165514407*	0.00038	COG0439	K01961	Cvib_1603	acetyl-CoA carboxylase, biotin carboxylase
165547843	0.00038	COG0543	K00528	Cvib_1477	2-polyprenylphenol hydroxylase and related flavodoxin oxidoreductases : ferredoxin--NADP(+) reductase subunit alpha
165502249	0.00038	COG0459	K04077	Cvib_0586	chaperonin GroEL (HSP60 family)
165525978	0.00038	COG0190	K00288	Cvib_0963	methenyltetrahydrofolate cyclohydrolase (NADP+)
165548015	0.00037	COG0115	K00826	Cvib_1391	4-amino-4-deoxychorismate lyase : branched-chain amino acid aminotransferase
165526070	0.00037	COG1883	K01572	Cvib_1017	Na+-transporting methylmalonyl-CoA/oxaloacetate decarboxylase, beta subunit
165502323	0.00037	COG2406	K03594	Cvib_1194	uncharacterized ACR : ferritin, Dps family protein
165502157	0.00036	COG0182	K08963	Cvib_0532	translation initiation factor 2B subunit I family (IF-2BI); methylthioribose-1-phosphate isomerase
165502159	0.00036	COG0005	K03783	Cvib_0533	purine nucleoside phosphorylase
165526084	0.00035	COG0326	K04079	Cvib_1024	heat shock protein 90; molecular chaperone HtpG
165547741*	0.00034	COG1109	K01840	Cvib_1521	phosphoglucomutase
165547943	0.00033	COG0365	K01895	Cvib_1426	acyl-coenzyme A synthetases/AMP-(fatty) acid ligases : acetyl-coenzyme A synthetase
165547811	0.00033	COG1118	K02017	Cvib_1494	ABC-type sulfate/molybdate transport systems, ATPase component

165501997*	0.00032	COG0404	K00605	Cvib_0451	glycine cleavage system T protein (aminomethyltransferase)
165548139	0.00032	COG0039	K00026	Cvib_1331	malate dehydrogenase
165547815	0.00031	COG0725	K02020	Cvib_1492	ABC-type molybdate transport system, periplasmic component
165526254	0.00031	COG3349	K00514	Cvib_1233	uncharacterized ACR : zeta-carotene desaturase
165519338*	0.00031	COG1023	K00033	Cvib_0374	6-phosphogluconate dehydrogenase, family 2
165525774	0.00031	COG0315	K03637	Cvib_0215	moaC; bifunctional molybdenum cofactor biosynthesis protein C/molybdopterin-binding protein
165514597*	0.00031	COG0248		Cvib_1704	Ppx/GppA phosphatase
165505937	0.00030	COG1908		Cvib_0842	coenzyme F420-reducing hydrogenase, delta subunit : methyl-viologen-reducing hydrogenase, delta subunit
165505095	0.00030	COG1192		Cvib_0908	ATPases involved in chromosome partitioning : cobyrinic acid a,c-diamide synthase
165547897	0.00030	COG0178	K03701	Cvib_1449	excinuclease ABC subunit A
165553023	0.00030	COG0532	K02519	Cvib_1561	translation initiation factor 2 (GTPase) : infB
165553083	0.00029	COG3637		Cvib_1533	opacity protein and related surface antigens : porin
165562903	0.00029	COG0543	K02823	Cvib_0327	2-polyprenylphenol hydroxylase and related flavodoxin oxidoreductases : dihydroorotate oxidase B, electron transfer subunit
165547817	0.00029	COG0157	K03813	Cvib_1491	nicotinate-nucleotide pyrophosphorylase : ModD protein; molybdenum transport protein
165511803	0.00028	COG0152	K01923	Cvib_0763	phosphoribosylaminoimidazole-succinocarboxamide synthase
165502273	0.00028	COG1049	K01682	Cvib_0598	aconitase B: bifunctional aconitate hydratase 2/2-methylisocitrate dehydratase
165525716	0.00028	COG0050	K02358	Cvib_0244	GTPases - translation elongation factors : tuf
165505137*	0.00027	COG0724		Cvib_0890	RNA-binding proteins (RRM domain)
165511799	0.00027	COG0021	K00615	Cvib_0765	transketolase subunit A

165502001*	0.00027	COG0694	K07400	Cvib_0453	thioredoxin-like proteins and domains : nitrogen-fixing NifU domain protein
165525700	0.00027	COG0092	K02982	Cvib_0252	rpsC; 30S ribosomal protein S3
165548043	0.00027	COG0848		Cvib_1377	biopolymer transport protein ExbD/TolR
165502837*	0.00027	COG0426		Cvib_0005	uncharacterized flavoproteins : beta-lactamase domain protein
165502823*	0.00027	COG0760	K03771	Cvib_0012	parvulin-like peptidyl-prolyl isomerase : PpiC-type peptidyl-prolyl cis-trans isomerase
165525682	0.00026	COG0097	K02933	Cvib_0261	rplF; 50S ribosomal protein L6
165509275*	0.00026	COG0055	K02112	Cvib_0025	F0F1 ATP synthase subunit beta
165514365[a]	0.00026	COG0542	K03696	Cvib_1580	ATPases with chaperone activity, ATP-binding subunit : AAA-2 domain protein; ATP-dependent Clp protease
165525766	0.00026	COG3245		Cvib_0219	cytochrome c5
165514371*	0.00026	COG0451		Cvib_1582	nucleoside-diphosphate-sugar epimerases : NAD-dependent epimerase/dehydratase
165525810	0.00026	COG1028	K00059	Cvib_0198	dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases) : 3-oxoacyl-[acyl-carrier-protein] reductase
165502383	0.00025	COG0823	K03641	Cvib_1164	periplasmic component of the Tol biopolymer transport system : WD40 domain protein beta propeller; TolB protein
165557763	0.00025	COG0137	K01940	Cvib_0882	argininosuccinate synthase
165502177	0.00024	COG0591		Cvib_0542	Na+/proline, Na+/panthothenate symporters and related permeases
165525720	0.00024	COG0049	K02992	Cvib_0242	30S ribosomal protein S7
165553085	0.00024	COG0729	K07277	Cvib_1532	predicted outer membrane protein : surface antigen (D15)
165525770	0.00024	COG0345	K00286	Cvib_0217	pyrroline-5-carboxylate reductase
165514453*	0.00023	COG0527	K00928	Cvib_1626	aspartokinases
165509301*	0.00023	COG2920	K00396	Cvib_0038	sulfite reductase, gamma subunit : DsrC family

					protein
165514489*	0.00023	COG1538		Cvib_1644	outer membrane protein : outer membrane efflux protein
165562971	0.00022	COG0105	K00940	Cvib_0295	nucleoside diphosphate kinase
165562957	0.00022	COG0822	K04488	Cvib_0302	NifU homologs involved in Fe-S cluster formation
165501969*	0.00022	COG1752		Cvib_0421	predicted esterase of the alpha-beta hydrolase superfamily : surface antigen (D15)
165526170	0.00022	COG1832	K06929	Cvib_0723	predicted CoA-binding protein
165514455*	0.00021	COG0224	K02115	Cvib_1627	ATP synthase F1, gamma subunit
165562919	0.00021	COG1629	K02014	Plut_0256	outer membrane receptor proteins, mostly Fe transport : ferric siderophore receptor, putative, TonB receptor family
165550965	0.00020	COG0541	K03106	Cvib_0936	signal recognition particle GTPase : subunit FFH/SRP54 (SRP54)
165502821*	0.00020	COG0187	K02470	Cvib_0013	DNA gyrase subunit B
165509279*	0.00020	COG1274	K01596	Cvib_0027	phosphoenolpyruvate carboxykinase (GTP)
165514471*	0.00020	COG0407	K01599	Cvib_1635	uroporphyrinogen-III decarboxylase
165505923	0.00020	COG0653	K03070	Cvib_0853	preprotein translocase subunit SecA (ATPase, RNA helicase)
165526076	0.00020	COG1951	K01676	Cvib_1020	tartrate dehydratase alpha subunit/Fumarate hydratase class I, N-terminal domain
165547989	0.00020	COG0403	K00282	Cvib_1404	glycine cleavage system protein P (pyridoxal-binding), N-terminal domain : glycine dehydrogenase subunit 1
165550943	0.00020	COG0399		Cvib_0925	predicted pyridoxal phosphate-dependent enzyme apparently involved in regulation of cell wall biogenesis : DegT/DnrJ/EryC1/StrS aminotransferase
165519308*	0.00019	COG1233		Cvib_0356	phytoene dehydrogenase and related proteins : FAD dependent oxidoreductase
165525704	0.00019	COG0185	K02965	Cvib_0250	rpsS; 30S ribosomal protein S19

165502209	0.00019	COG0493	K00266	Cvib_0559	NADPH-dependent glutamate synthase beta chain and related oxidoreductases : gltD
165548183	0.00019	COG0057	K00134	Cvib_1310	glyceraldehyde-3-phosphate dehydrogenase
165509303*	0.00018	COG2221	K00396	Cvib_0039	oxidoreductase related to nitrite reductase : sulfite reductase, dissimilatory-type alpha subunit
165502855*	0.00018	COG0126	K00927	Cvib_1766	pgk; phosphoglycerate kinase
165548189	0.00018	COG0399		Cvib_1298	predicted pyridoxal phosphate-dependent enzyme apparently involved in regulation of cell wall biogenesis : DegT/DnrJ/EryC1/StrS aminotransferase
165502083	0.00018	COG0723	K09879	Cvib_0486	Rieske Fe-S protein : isorenieratene synthase
165502241	0.00018	COG1959		Cvib_0582	predicted transcriptional regulator : transcriptional regulator, BadM/Rrf2 family
165505101	0.00018	COG1744	K07335	Cvib_0906	surface lipoprotein
165562997	0.00018	COG1348	K04037	Cvib_0283	nitrogenase subunit NifH (ATPase) : chlL, bchL; protochlorophyllide reductase iron-sulfur ATP-binding protein
165514479*	0.00017	COG0517		Plut_1996	CBS domains
165509257*	0.00017	COG2171	K00674	Cvib_0017	tetrahydrodipicolinate N-succinyltransferase : dapD; 2,3,4,5-tetrahydropyridine-2-carboxylate N-succinyltransferase
165525898	0.00017	COG0449	K00820	Cvib_0141	glucosamine 6-phosphate synthetase, contains amidotransferase and phosphosugar isomerase domains : glutamine--fructose-6-phosphate transaminase
165526040	0.00017	COG0226	K02040	Cvib_0998	phosphate binding protein; phosphate transport system substrate-binding protein
165526106	0.00017	COG0718	K09747	Cvib_1034	uncharacterized BCR : conserved hypothetical protein 103
165525660	0.00017	COG0202	K03040	Cvib_0273	DNA-directed RNA polymerase subunit alpha
165563007	0.00017	COG0218	K03978	Cvib_0278	yihA, ysxC, engB; GTPase EngB

165526124	0.00016	COG0589		Cvib_1041	universal stress protein UspA and related nucleotide-binding proteins
165526138	0.00016	COG1554		Cvib_1047	trehalose and maltose hydrolases (possible phosphorylases) : beta-phosphoglucomutase family hydrolase
165525892	0.00016	COG0724		Cvib_0162	RNA-binding proteins (RRM domain)
165514417*	0.00016	COG0081	K02863	Cvib_1608	rplA; 50S ribosomal protein L1
165550985	0.00016	COG0260	K01255	Cvib_0947	leucyl aminopeptidase
165514655*	0.00016	COG1899	K00809	Cvib_1729	deoxyhypusine synthase
165525670	0.00016	COG0024	K01265	Cvib_0267	methionine aminopeptidase : type I
165526140	0.00015	COG0809	K07568	Cvib_1048	S-adenosylmethionine:tRNA-ribosyltransferase-isomerase (queuine synthetase) : queuosine biosynthesis protein
165502015	0.00015	COG0264	K02357	Cvib_0459	elongation factor Ts : tsf
165514419*	0.00015	COG0080	K02867	Plut_1966	rplK; 50S ribosomal protein L11
165553033	0.00015	COG1561		Cvib_1556	uncharacterized stress-induced protein : hypothetical protein
165519394	0.00015	COG0372	K01647	Cvib_0401	citrate synthase
165548035	0.00015	COG0112	K00600	Cvib_1381	glycine hydroxymethyltransferase
165525666	0.00014	COG0099	K02952	Cvib_0270	rpsM; 30S ribosomal protein S13
165502377	0.00014	COG0811	K03562	Cvib_1167	biopolymer transport proteins : MotA/TolQ/ExbB proton channel
165519372	0.00014	COG0289	K00215	Cvib_0390	dihydrodipicolinate reductase
165526294	0.00014	COG0113	K01698	Cvib_1252	delta-aminolevulinic acid dehydratase
165553057	0.00014	COG0142	K00795	Cvib_1546	geranyltranstransferase
165511739	0.00014	COG1805	K03614	Cvib_0796	Na+-transporting NADH:ubiquinone oxidoreductase subunit 2 : electron transport complex, RnfABCDGE type, D subunit
165553087	0.00014	COG0020	K00806	Cvib_1531	undecaprenyl pyrophosphate synthetase
165502433	0.00013	COG0633	K08953	Cvib_1151	ferredoxin : chlorosome envelope protein J

165526246	0.00013	COG0174	K01915	Cvib_1230	glutamine synthetase, catalytic region
165502389	0.00013	COG1729		Cvib_1161	uncharacterized BCR : tetratricopeptide domain protein
165562927	0.00012	COG2265	K03428	Cvib_0317	SAM-dependent methyltransferases related to tRNA (uracil-5-)-methyltransferase : Mg-protoporphyrin IX methyl transferase
165511967	0.00012	COG1538		Cvib_1100	outer membrane protein : outer membrane efflux protein
165514411*	0.00012	COG0085	K03043	Cvib_1605	rpoB; DNA-directed RNA polymerase subunit beta
165502197	0.00012	COG0045	K01903	Cvib_0553	succinyl-CoA synthetase (ADP-forming) beta subunit
165525686	0.00012	COG0199	K02954	Plut_0194	rpsN; 30S ribosomal protein S14
165548039	0.00012	COG0811	K03561	Cvib_1379	biopolymer transport proteins : MotA/TolQ/ExbB proton channel
165509331*	0.00012	COG0007	K02302	Cvib_0053	uroporphyrinogen-III C-methyltransferase
165518169*	0.00012	COG2221	K00396	Cvib_0040	oxidoreductase related to nitrite reductase : sulfite reductase, dissimilatory-type beta subunit
165547929	0.00012	COG0077	K04518	Cvib_1433	prephenate dehydratase
165557761	0.00012	COG0165	K01755	Cvib_0883	argininosuccinate lyase
165511743	0.00012	COG1347	K03613	Cvib_0794	Na+-transporting NADH:ubiquinone oxidoreductase subunit 4 : SoxR-reducing system protein RsxE; electron transport complex protein RnfE
165511765	0.00012	COG0003	K01551	Cvib_0783	predicted ATPase involved in chromosome partitioning : arsenite-activated ATPase ArsA
165502673*	0.00011	COG1396		Plut_1890	predicted transcriptional regulators: XRE family
165505117	0.00011	COG0698	K01808	Cvib_0896	ribose 5-phosphate isomerase RpiB
165526204	0.00011	COG0019	K01586	Cvib_0705	diaminopimelate decarboxylase
165526060	0.00011	COG0526	K03671	Cvib_1012	thiol-disulfide isomerase and thioredoxins
165501979*	0.00010	COG0568	K03086	Cvib_0443	DNA-directed RNA polymerase sigma subunits (sigma70/sigma32) : RpoH
165525702	0.00010	COG0091	K02890	Cvib_0251	rplV; 50S ribosomal protein L22

165562969	0.00010	COG1225		Cvib_0296	peroxiredoxin
165548179	0.00010	COG0484	K03686	Cvib_1312	molecular chaperones (contain C-terminal Zn finger domain) : chaperone protein DnaJ
165526058	0.00010	COG0492	K00384	Cvib_1011	thioredoxin reductase
165514477*	0.00010	COG1053	K00239	Cvib_1638	succinate dehydrogenase/fumarate reductase, flavoprotein subunits
165514475*	0.00010	COG0479	K00240	Cvib_1637	succinate dehydrogenase/fumarate reductase Fe-S protein : succinate dehydrogenase subunit B
165514463*	0.00010	COG0204	K00655	Cvib_1631	1-acyl-sn-glycerol-3-phosphate acyltransferase
165512005	0.00010	COG0499	K01251	Cvib_1122	S-adenosyl-L-homocysteine hydrolase; adenosylhomocysteinase
165511973	0.00010	COG2077	K00435	Cvib_1103	peroxiredoxin : thiol peroxidase (atypical 2-Cys peroxiredoxin)
165519288*	0.00009	COG0031	K01697	Cvib_0346	cysteine synthase
165502065	0.00009	COG2177	K09811	Cvib_0478	cell division protein FtsX
165502349	0.00009	COG1610	K09117	Cvib_1181	uncharacterized ACR : GatB/YqeY domain protein
165502361	0.00009	COG0065	K01703	Cvib_1175	homoaconitate hydratase family protein; K01703 3-isopropylmalate/(R)-2-methylmalate dehydratase large subunit
165526160	0.00009	COG0047	K01952	Cvib_0728	phosphoribosylformylglycinamidine synthase I
165526016	0.00009	COG3118	K05838	Cvib_0982	thioredoxin domain-containing protein
165525690	0.00009	COG0198	K02895	Plut_0192	rplX; 50S ribosomal protein L24
165519322*	0.00009	COG2606		Cvib_0364	uncharacterized ACR : YbaK/prolyl-tRNA synthetase associated region
165502387	0.00009	COG2885		Cvib_1162	outer membrane protein and related peptidoglycan-associated (lipo)proteins : OmpA/MotB domain protein
165525762	0.00009	COG0075	K00839	Cvib_0221	serine-pyruvate aminotransferase/archaeal aspartate aminotransferase : aminotransferase, class V

165511763	0.00009	COG0722	K01626	Cvib_0784	3-Deoxy-D-arabino-heptulosonate 7-phosphate (DAHP) synthase : phospho-2-dehydro-3-heoxyheptonate aldolase; 3-deoxy-7-phosphoheptulonate synthase
165525764	0.00009	COG3245		Cvib_0220	cytochrome c5
165514427*	0.00009	COG0821	K03526	Cvib_1613	essential bacterial protein, involved in density-dependent regulation of peptidoglycan biosynthesis : 4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase
165525908	0.00009	COG0216	K02835	Cvib_0136	prfA; peptide chain release factor 1
165526270	0.00009	COG1217	K06207	Cvib_1242	predicted membrane GTPase involved in stress response : GTP-binding protein TypA
165526178	0.00008	COG0845	K02005	Cvib_0719	membrane-fusion protein : efflux transporter, RND family, MFP subunit; HlyD family secretion protein
165525656*	0.00008	COG0357	K03501	Cvib_0275	predicted S-adenosylmethionine-dependent methyltransferase involved in bacterial cell division: gidB; glucose-inhibited division protein B
165519392	0.00008	COG1432		Cvib_0400	uncharacterized ACR : hypothetical protein
165526108	0.00008	COG0021	K00615	Cvib_1035	transketolase subunit B
165502205	0.00008	COG0588	K01834	Cvib_0557	phosphoglycerate mutase 1
165548031	0.00008	COG0458	K01955	Cvib_1383	carbamoyl-phosphate synthase large subunit (split gene in MJ)
165509283*	0.00008	COG3360	K09165	Cvib_0029	uncharacterized ACR : protein of unknown function DUF1458; hypothetical protein
165514653*	0.00008	COG0176	K00616	Cvib_1728	putative translaldolase
165514561*	0.00008	COG0243	K08352	Cpha266_2562	anaerobic dehydrogenases, typically selenocysteine-containing : formate dehydrogenase; thiosulfate reductase
165525714	0.00008	COG0051	K02946	Cvib_0245	rpsJ, nusE; 30S ribosomal protein S10
165525826	0.00008	COG0290	K02520	Cvib_0189	infC; translation initiation factor IF-3

165509297*	0.00008	COG0425		Cvib_0036	predicted redox protein, regulator of disulfide bond formation : SirA family protein
165526206	0.00008	COG0267	K02913	Cvib_0704	rpmG; 50S ribosomal protein L33
165562999	0.00008	COG2710	K04039	Cvib_0282	nitrogenase molybdenum-iron protein, alpha and beta chains : light-independent protochlorophyllide reductase subunit B
165525658	0.00008	COG0203	K02879	Cvib_0274	rplQ; 50S ribosomal protein L17
165501991*	0.00008	COG1704	K03744	Cvib_0448	uncharacterized ACR : LemA family protein
165525684	0.00007	COG0096	K02994	Cvib_0260	rpsH; 30S ribosomal protein S8
165501995*	0.00007	COG3762	K08988	Cvib_0450	predicted membrane protein : protein of unknown function DUF477
165525960	0.00007	COG1979	K00001	Cvib_0955	uncharacterized oxidoreductases, Fe-dependent alcohol dehydrogenase family
165525712	0.00007	COG0087	K02906	Cvib_0246	rplC; 50S ribosomal protein L3
165519466	0.00007	COG0489	K03593	Cvib_0454	ATP-binding protein involved in chromosome partitioning : protein of unknown function DUF59
165536850*	0.00007	COG0003	K01551	Cvib_0332	predicted ATPase involved in chromosome partitioning : arsenite-activated ATPase ArsA
165511901[b]	0.00007	COG1429	K03403	Cvib_1057	cobalamin biosynthesis protein CobN and related Mg-chelatases : hydrogenobyrinic acid a,c-diamide cobaltochelatase
165553047	0.00007	COG2825	K06142	Cvib_1549	outer membrane protein : outer membrane chaperone Skp (OmpH)
165547985	0.00007	COG0566	K03218	Cvib_1406	rRNA methylases : RNA methyltransferase, TrmH family, group 3
165548057	0.00007	COG0635	K02495	Cvib_1370	coproporphyrinogen III oxidase and related Fe-S oxidoreductases
165525972	0.00007	COG0638	K01419	Cvib_0960	proteasome protease subunit : ATP-dependent HslUV protease, peptidase subunit HslV

165548053	0.00007	COG1252	K03885	Cvib_1373	NADH dehydrogenase, FAD-containing subunit : FAD-dependent pyridine nucleotide-disulphide oxidoreductase;
165502427	0.00007	COG1595	K03088	Cvib_1154	DNA-directed RNA polymerase specialized sigma subunits, sigma24 homologs : RpoE; RNA polymerase sigma-70 factor, ECF subfamily
165514401*	0.00006	COG0776	K03530	Plut_1957	bacterial nucleoid DNA-binding protein : histone-like DNA-binding protein; HU-beta
165502013*	0.00006	COG0052	K02967	Cvib_0458	rpsB; 30S ribosomal protein S2
165525904	0.00006	COG0743	K00099	Cvib_0138	1-deoxy-D-xylulose 5-phosphate reductoisomerase
165514571*	0.00006	COG0461	K00762	Cvib_1691	pyrE; orotate phosphoribosyltransferase
165502127	0.00006	COG1692	K09769	Cvib_0508	uncharacterized BCR : metallophosphoesterase
165502831*	0.00006	COG2863	K00540	Cvib_0008	cytochrome c553 : sulfide dehydrogenase (flavocytochrome), cytochrome c subunit
165512003	0.00006	COG0192	K00789	Cvib_1121	S-adenosylmethionine synthetase
165562939	0.00006	COG1278	K03704	Cvib_0310	cold shock proteins : cold-shock DNA-binding protein family (beta-ribbon, CspA family)
165502325	0.00006	COG1592		Cvib_1193	rubrerythrin
165514457*	0.00006	COG0056	K02111	Cvib_1628	F0F1 ATP synthase subunit alpha
165502099	0.00006	COG0854	K03474	Cvib_0494	pyridoxal phosphate biosynthetic protein PdxJ; pyridoxine 5-phosphate synthase
165562943	0.00006	COG2319		Cvib_0309	WD-40 repeat protein
165548049	0.00006	COG0160	K00818	Cvib_1374	PLP-dependent aminotransferases : acetylornithine and succinylornithine aminotransferase
165547915	0.00006	COG0458	K01955	Cvib_1440	carbamoyl-phosphate synthase large subunit (split gene in MJ)
165501985*	0.00006	COG0612		Cvib_0445	predicted Zn-dependent peptidases
165501959*	0.00006	COG1611	K06966	Cvib_0416	predicted Rossmann fold nucleotide-binding protein : conserved hypothetical protein 730

165511907	0.00006	COG1239	K03405	Cvib_1059	Mg-chelatase subunit ChlI : protoporphyrin IX magnesium-chelatase
165502365	0.00006	COG0473	K00052	Cvib_1173	isocitrate/isopropylmalate dehydrogenase
165547721*	0.00005	COG0154	K02433	Cvib_1530	aspartyl/glutamyl-tRNA(Asn/Gln) amidotransferase subunit A
165512001	0.00005	COG1209	K00973	Cvib_1120	dTDP-glucose pyrophosphorylase : 3 glucose-1-phosphate thymidylyltransferase
165526008	0.00005	COG0605	K04564	Cvib_0978	superoxide dismutase, Fe-Mn family
165525688	0.00005	COG0094	K02931	Cvib_0258	rplE; 50S ribosomal protein L5
165548233	0.00005	COG0149	K01803	Cvib_1275	triosephosphate isomerase
165525674	0.00005	COG0200	K02876	Cvib_0265	rplO; 50S ribosomal protein L15
165511945	0.00005	COG1143	K00338	Cvib_1088	formate hydrogenlyase subunit 6/NADH:ubiquinone oxidoreductase 23 kD subunit (chain I)
165511741	0.00005	COG2869		Cvib_0795	Na+-transporting NADH:ubiquinone oxidoreductase gamma subunit : electron transport complex, RnfABCDGE type, G subunit
165502243	0.00005	COG0178	K03701	Cvib_0583	excinuclease ABC subunit A
165526286	0.00005	COG0777	K01966	Cvib_1248	acetyl-CoA carboxylase beta subunit : propionyl-CoA carboxylase beta chain
165548017	0.00005	COG0205	K00850	Cvib_1390	6-phosphofructokinase
165502343	0.00005	COG2873	K01740	Cvib_1184	O-acetylhomoserine/O-acetylserine sulfhydrylase
165511795	0.00005	COG0436	K00812	Cvib_0768	PLP-dependent aminotransferases : aspartate aminotransferase
165514397*	0.00005	COG1013	K00175	Cvib_1598	pyruvate:ferredoxin oxidoreductase and related 2-oxoacid:ferredoxin oxidoreductases, beta subunit
165553021	0.00005	COG0195	K02600	Cvib_1562	nusA; transcription elongation factor NusA; N utilization substance protein A
165514415*	0.00005	COG0244	K02864	Cvib_1607	rplJ; 50S ribosomal protein L10

165525916	0.00005	COG0446		Cvib_0131	uncharacterized NAD(FAD)-dependent dehydrogenases : FAD-dependent pyridine nucleotide-disulphide oxidoreductase
165526186	0.00005	COG2885		Cvib_0715	outer membrane protein and related peptidoglycan-associated (lipo)proteins : OmpA/MotB domain protein
165514585*	0.00005	COG2062	K08296	Cvib_1698	phosphohistidine phosphatase SixA
165525698	0.00005	COG0197	K02878	Cvib_0253	rplP; 50S ribosomal protein L16
165501973*	0.00005	COG1351	K03465	Plut_0366	predicted alternative thymidylate synthase: thyX
165548141	0.00004	COG0211	K02899	Cvib_1330	rpmA; 50S ribosomal protein L27
165547947	0.00004	COG1185	K00962	Cvib_1424	polyribonucleotide nucleotidyltransferase (polynucleotide phosphorylase)
165502321	0.00004	COG0450	K03386	Cvib_1195	peroxiredoxin (alkyl hydroperoxide reductase subunit C)
165525706	0.00004	COG0090	K02886	Cvib_0249	rplB; 50S ribosomal protein L2
165562989	0.00004	COG0241	K05602	Cvib_0287	histidinol-phosphate phosphatase family protein
165502123	0.00004	COG0623	K00208	Cvib_0506	enoyl-[acyl-carrier-protein] reductase [NADH]
165502053	0.00004	COG1734		Cvib_0476	DnaK suppressor protein : transcriptional regulator, TraR/DksA family
165502207	0.00004	COG0069	K00284	Cvib_0558	glutamate synthase (NADH) large subunit; K00284 glutamate synthase (ferredoxin)
165514485*	0.00004	COG0841		Cvib_1642	cation/multidrug efflux pump : acriflavin resistance protein
165550957	0.00004	COG0335	K02884	Cvib_0932	rplS; 50S ribosomal protein L19
165547723*	0.00004	COG0074	K01902	Cvib_1529	succinyl-CoA synthetase (ADP-forming) alpha subunit
165502827*	0.00004	COG0342	K03072	Cvib_0010	secD; preprotein translocase subunit SecD
165547889	0.00004	COG1151	K00378	Cvib_1455	6Fe-6S prismane cluster-containing protein : hydroxylamine reductase
165501971*	0.00004	COG0777	K01963	Cvib_0422	acetyl-CoA carboxylase beta subunit : acetyl-coenzyme A carboxylase carboxyl transferase subunit alpha

165526020	0.00004	COG0277		Cvib_0987	FAD linked oxidase domain protein
165526194	0.00004	COG1825	K02897	Cvib_0711	50S ribosomal protein L25/general stress protein Ctc
165512009	0.00004	COG0596		Cvib_1124	predicted hydrolases or acyltransferases (alpha/beta hydrolase superfamily)
165525836	0.00004	COG0238	K02963	Cvib_0183	rpsR; 30S ribosomal protein S18
165525680	0.00003	COG0256	K02881	Cvib_0262	rplR; 50S ribosomal protein L18
165547963	0.00003	COG0780	K06879	Cvib_1417	enzyme related to GTP cyclohydrolase I : 7-cyano-7-deazaguanine reductase
165514617*	0.00003	COG0550	K03168	Cvib_1714	topoisomerase IA
165525894	0.00003	COG1090	K07071	Cvib_0161	predicted nucleoside-diphosphate sugar epimerases (SulA family) : domain of unknown function DUF1731
165525944	0.00003	COG0376	K03782	cpb:Cphamn1_0152	catalase/peroxidase HPI
165553059	0.00003	COG1304	K01823	Cvib_1545	L-lactate dehydrogenase (FMN-dependent) and related alpha-hydroxy acid dehydrogenases : isopentenyl pyrophosphate isomerase
165502021	0.00003	COG3347		Cvib_0462	uncharacterized ACR : short chain dehydrogenase
165502163	0.00003	COG0652	K03767	Cvib_0535	peptidyl-prolyl cis-trans isomerase (rotamase) - cyclophilin family
165526224	0.00003	COG0451	K01795	Cvib_1219	nucleoside-diphosphate-sugar epimerases : NAD-dependent epimerase/dehydratase
165548235	0.00003	COG0422	K03147	Cvib_1273	thiamine biosynthesis protein ThiC
165553035	0.00003	COG0194	K00942	Cvib_1555	gmk; guanylate kinase
165550983	0.00003	COG1004	K00012	Cvib_0945	Predicted UDP-glucose 6-dehydrogenase
165519410	0.00003	COG0254	K02909	Plut_0349	rpmE; 50S ribosomal protein L31
165519370	0.00003	COG1475	K03497	Cvib_0389	predicted transcriptional regulators : chromosome segregation DNA-binding protein; ParB family
165505127	0.00003	COG0191	K01624	Cvib_0892	fructose-bisphosphate aldolase
165514563*	0.00003	COG0437	K04014	Cpha266_2563	Fe-S-cluster-containing hydrogenase components 1 : 4Fe-4S ferredoxin, iron-sulfur binding domain protein; formate-dependent nitrite reductase, Fe-S

					protein
165562929	0.00003	COG1032	K04035	Cvib_0316	Fe-S oxidoreductases family 2 : magnesium-protoporphyrin IX monomethyl ester anaerobic oxidative cyclase
165562921	0.00003	COG1629	K02014	CT1953	outer membrane receptor proteins, mostly Fe transport : ferric siderophore receptor, putative, TonB receptor family
165519408	0.00003	COG0233	K02838	Cvib_0408	ribosome recycling factor
165526146	0.00003	COG1032		Cvib_1051	Fe-S oxidoreductases family 2 : radical SAM domain protein
165519340*	0.00003	COG0364	K00036	Cvib_0375	glucose-6-phosphate 1-dehydrogenase
165502423	0.00003	COG0640	K03892	Cvib_1156	predicted transcriptional regulators : ArsR family
165562991	0.00003	COG0297	K00703	Cvib_0286	glycogen/starch synthase, ADP-glucose type
165501977*	0.00003	COG0525	K01873	Cvib_0442	valS; valyl-tRNA synthetase
165515179	0.00003	COG0712	K02113	Cvib_1740	F0F1-type ATP synthase delta subunit (mitochondrial oligomycin sensitivity protein)
165509255*	0.00003	COG1530	K08301	Cvib_0016	ribonucleases G and E : Rne/Rng family
165526126	0.00002	COG0330		Plut_1305	membrane protease subunits, stomatin/prohibitin homologs : band 7 protein
165563005	0.00002	COG0104	K01939	Cvib_0279	adenylosuccinate synthetase
165502333	0.00002	COG0513	K05592	Cvib_1189	superfamily II DNA and RNA helicases : DEAD/DEAH box helicase domain protein
165514511*	0.00002	COG0702		Cvib_1655	predicted nucleoside-diphosphate-sugar epimerases : NAD-dependent epimerase/dehydratase
165511735	0.00002	COG2878		Cvib_0798	predicted alternative beta subunit of Na+-transporting NADH:ubiquinone oxidoreductase : ferredoxin
165548065	0.00002	COG1509	K01843	Cvib_1367	L-lysine 2,3-aminomutase

165502839*	0.00002	COG0592	K02338	Cvib_0002	DNA polymerase sliding clamp subunit (PCNA homolog) : DNA polymerase III, beta subunit
165502087	0.00002	COG1463		Cvib_0488	permease component of an ABC-transporter : mammalian cell entry related domain protein
165525662	0.00002	COG0522	K02986	Cvib_0272	rpsD; 30S ribosomal protein S4
165519336*	0.00002	COG1028		Cvib_0372	dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases)
165525742	0.00002	COG0536	K03979	Cvib_0231	predicted GTPase : obgE, yhbZ, obg, cgtA; GTPase ObgE
165557789	0.00002	COG0045		Cvib_0867	succinyl-CoA synthetase beta subunit : ATP citrate lyase subunit 1
165502295	0.00002	COG1945	K02626	Cvib_1209	uncharacterized ACR : pyruvoyl-dependent arginine decarboxylase
165562923[b]	0.00002	COG1429	K06050	Cvib_0320	cobalamin biosynthesis protein CobN and related Mg-chelatases : hydrogenobyrinic acid a,c-diamide cobaltochelatase
165525722	0.00002	COG0048	K02950	Cvib_0241	rpsL; 30S ribosomal protein S12
165525678	0.00002	COG0098	K02988	Cvib_0263	rpsE; 30S ribosomal protein S5
165502367	0.00002	COG0059	K00053	Cvib_1172	ketol-acid reductoisomerase
165514527*	0.00002	COG0330		Cvib_1667	membrane protease subunits, stomatin/prohibitin homologs : SPFH domain, band 7 family protein
165502009*	0.00002	COG0102	K02871	Cvib_0456	rplM; 50S ribosomal protein L13
165505071	0.00002	COG0589		Cvib_0918	universal stress protein UspA and related nucleotide-binding proteins
165525694	0.00002	COG0186	K02961	Cvib_0255	rpsQ; 30S ribosomal protein S17
165547949	0.00002	COG0414	K01918	Cvib_1423	pantothenate synthetase; pantoate--beta-alanine ligase
165548085	0.00002	COG2873	K01740	cch:Cag_1257	O-acetylhomoserine/O-acetylserine sulfhydrylase
165502203	0.00001	COG2070		Cvib_0556	dioxygenases related to 2-nitropropane dioxygenase
165550995	0.00001	COG0563	K00939	Cvib_0952	adenylate kinase and related kinases

165525902	0.00001	COG0465	K03798	Cvib_0139	ATP-dependent Zn proteases : FtsH; cell division protease
165509287*	0.00001	COG0243		Plut_0027	anaerobic dehydrogenases, typically selenocysteine-containing : molybdenum enzyme related to thiosulfate reductase and polysulfide reductase, large subunit
165526192	0.00001	COG0462	K00948	Cvib_0712	phosphoribosylpyrophosphate synthetase : ribose-phosphate pyrophosphokinase
165502889*	0.00001	COG0206	K03531	Cvib_1749	cell division protein FtsZ
165509325*	0.00001	COG0437		Cvib_0050	Fe-S-cluster-containing hydrogenase components 1 : 4Fe-4S ferredoxin, iron-sulfur binding domain protein
165525812	0.00001	COG0236	K02078	Cvib_0197	acyl carrier protein
165502351	0.00001	COG0300	K00059	Cvib_1180	short-chain dehydrogenase/reductase SDR
165502011*	0.00001	COG0103	K02996	Cvib_0457	rpsI; 30S ribosomal protein S9
165514403*	0.00001	COG0231	K02356	Cvib_1601	translation elongation factor P (EF-P)
165553067	0.00001	COG0268	K02968	Cvib_1540	rpsT; 30S ribosomal protein S20
165519310*	0.00001	COG0668		Cvib_0357	small-conductance mechanosensitive channel
165511815	0.00001	COG3808	K01507	Cvib_0758	inorganic pyrophosphatase : hppA; membrane-bound proton-translocating pyrophosphatase
165502023	0.00001	COG1830	K08321	Cvib_0463	DhnA-type fructose-1,6-bisphosphate aldolase and related enzymes
165514567*	0.00001	COG0446	K00540	Cpha266_2569	uncharacterized NAD(FAD)-dependent dehydrogenases : sulfide-quinone reductase
165502077	0.00001	COG0138	K01492	Cvib_0483	phosphoribosylaminoimidazolecarboxamide formyltransferase / IMP cyclohydrolase
165514431*	0.00001	COG0148	K01689	Cvib_1615	enolase
165525838	0.00000	COG0629	K03111	Plut_0115	single-strand DNA-binding protein
165502007*	0.00000	COG1160	K03977	Cvib_0455	predicted GTPases: engA, yfgK, yphC; GTP-binding protein EngA
165526038	0.00000	COG0226	K02040	Cvib_0997	phosphate binding protein; phosphate transport system substrate-binding protein

12.7 m - KEGG and NR annotated proteins

Gene ID	normalised spectral abundance	NR identifier	KO identifier	KEGG / NR locus tag	KEGG / NR description
165547733*	0.01965			Cvib_1525	hypothetical protein
165512927	0.01028			Cpha266_2650	hypothetical protein
165511987	0.00235		K03075	Cvib_1110	secG; preprotein translocase subunit SecG
165514495*	0.00209		K08946	Cvib_1647	chlorosome envelope protein B
165512925	0.00200		K08252	Cpha266_2649	lipopolysaccharide biosynthesis; receptor protein-tyrosine kinase
165571674	0.00148			dac:Daci_1946	putative phage major head protein
165563017	0.00148			ava:Ava_1043	methyltransferase FkbM
165502419	0.00139		K08943	Cvib_1159	photosystem P840 reaction center protein PscD
165519328*	0.00133		K08946	Cvib_0367	chlorosome envelope protein B
165547761*	0.00123			Cvib_1511	hypothetical protein
165525930	0.00094			Cvib_0125	hypothetical protein
165525844	0.00090			Cvib_0179	hypothetical protein
165526256	0.00077		K08951	Cvib_1234	chlorosome envelope protein H
165552335*	0.00074		K08947	Cvib_0329	chlorosome envelope protein C
165526330	0.00072			cpb:Cphamn1_2160	CRISPR-associated protein, CSE2 family
165547799	0.00067			Cvib_1499	alpha amylase, catalytic region
165512931*	0.00063			cch:Cag_0645	hypothetical protein
165547879	0.00057			Cvib_1459	cytochrome c, putative
165502219	0.00057			amr:AM1_B0391	hypothetical protein
165526074	0.00052			Cvib_1019	sodium pump decarboxylase, gamma subunit
165514639*	0.00052			Cvib_1720	hypothetical protein
165562993	0.00049			Cvib_0285	hypothetical protein
165548153	0.00048		K08944	Cvib_1325	bacteriochlorophyll A protein
165531268$_c$	0.00047			bvi:Bcep1808_1173	hypothetical protein
165526332	0.00047			cpb:Cphamn1_2161	CRISPR-associated protein, CSE3 family

165502381	0.00046			Cvib_1165	TonB-like protein
165511855	0.00037			Cvib_0746	hypothetical protein
165514665*	0.00035		K05807	Cvib_1734	putative lipoprotein
165548239	0.00034			Plut_0883	hypothetical protein
165501961	0.00034			Cvib_0417	hypothetical protein
165550963	0.00034		K02959	Plut_0966	rpsP; 30S ribosomal protein S16
165505939	0.00033			Cvib_0841	4Fe-4S ferredoxin, iron-sulfur binding domain protein
165519418$_d$	0.00032			Cvib_0413	hypothetical protein
165547769	0.00029			Cvib_1507	hypothetical protein
165519030*	0.00027			cbf:CLI_2438	hypothetical protein
165525752	0.00027			Cvib_0226	hypothetical protein
165511809	0.00026			Cvib_0760	cytochrome c family protein
165514873*	0.00024			Cvib_1579	hypothetical protein
165550993	0.00024			Cvib_0951	hypothetical protein
165514437*	0.00024		K08941	Cvib_1618	4Fe-4S ferredoxin, iron-sulfur binding domain protein; photosystem P840 reaction center iron-sulfur protein
165547729	0.00023			Cvib_1527	hypothetical protein
165502893	0.00022			Cvib_1747	O-methyltransferase, family 2
165547803	0.00022			Cvib_1498	hypothetical protein
165514537*	0.00020			Cvib_1673	alpha amylase, catalytic region
165525748	0.00016			Cvib_0228	hypothetical protein
165502181	0.00015			Cpha266_0714	hypothetical protein
165526208	0.00015		K07164	Cvib_0703	protein of unknown function DUF164
165502165	0.00014			Cvib_0536	TPR repeat-containing protein
165526334	0.00013			cte:CT1975	hypothetical protein
165547961	0.00013		K08942	Cvib_1418	photosystem P840 reaction center cytochrome c-551
165502029	0.00012			Cvib_0466	hypothetical protein
165505111	0.00011			Cvib_0901	hypothetical protein
165557793	0.00011			Cvib_0865	chlorosome envelope protein B

165548243	0.00011			cpb:Cphamn1_0811	hypothetical protein
165562965	0.00011			Cvib_0298	hypothetical protein
165551017	0.00010	ZP_01060966		MED217_12439	hypothetical protein
165548069	0.00010			Cvib_1365	GCN5-related N-acetyltransferase
165548181	0.00010			Cvib_1311	hypothetical protein
165514447*	0.00009			Cvib_1623	cytochrome c, class I
165513587	0.00007			Cvib_0828	hypothetical protein
165509309*	0.00007			Cvib_0042	hypothetical protein
165502185	0.00006			Cpha266_0718	hypothetical protein
165548171	0.00006			Cvib_1316	hypothetical protein
165502237	0.00006			Cvib_0580	hypothetical protein
165570114[c]	0.00005			bvi:Bcep1808_1173	hypothetical protein
165532404*	0.00004		K08945	Cvib_0330	bacteriochlorophyll C binding protein; chlorosome envelope protein A
165514439*	0.00004		K08940	Cvib_1619	photosystem P840 reaction center, large subunit
165505087	0.00004			Cvib_0912	hypothetical protein
165526028	0.00004			Cvib_0992	phosphate uptake regulator, PhoU
165547971	0.00004			Cvib_1413	hypothetical protein
165511805	0.00003			Cvib_0762	hypothetical protein
165525848	0.00003			Cvib_0177	hypothetical protein
165548087	0.00003			Cvib_1356	MOSC domain containing protein
165519298*	0.00003			Cvib_0351	hypothetical protein
165508719	0.00003			xft:PD0972	hypothetical protein
165562895	0.00003			Cvib_0331	hypothetical protein
165509277*	0.00002			Cvib_0026	redoxin domain protein
165523112	0.00002			pmn:PMN2A_1227	hypothetical protein
165553037	0.00001			Plut_1772	hypothetical protein
165548159	0.00001			Cvib_1322	sporulation domain protein
165525928[d]	0.00001			Cvib_0126	hypothetical protein
12.7 m - Proteins with no annotation					

165502275	0.00389				
165497987	0.00265				
165499977*	0.00077				
165506645$_{e}$	0.00072				
165563289$_{e}$	0.00049				
165566413$_{e}$	0.00035				
165563289	0.00012				
165503831	0.00006				
165525058$_{e}$	0.00006				
165519980*	0.00005				
165549781$_{e}$	0.00005				
165509979*	0.00002				

14 m - COG annotated proteins

Gene ID	**normalised spectral abundance**	**COG identifier**	**KO identifier**	**KEGG locus tag**	**COG description : KEGG description**
166198186	0.06300	COG0149	K01803	Cvib_1275	triosephosphate isomerase
166137511	0.04782	COG0157	K03813	Cvib_1491	nicotinate-nucleotide pyrophosphorylase : ModD protein; molybdenum transport protein
166198448	0.04506	COG0776	K03530	Plut_1957	bacterial nucleoid DNA-binding protein : histone-like DNA-binding protein; HU-beta
166172204	0.03837	COG0329	K01714	Cvib_1403	dihydrodipicolinate synthase/N-acetylneuraminate lyase
166126920	0.03524	COG0526	K03671	Cvib_1012	thiol-disulfide isomerase and thioredoxins
166145532$_{a}$	0.03313	COG0459	K04077	Cvib_0586	chaperonin GroEL (HSP60 family)
166124688	0.03285	COG1899	K00809	Cvib_1729	deoxyhypusine synthase
166179415	0.02422	COG2406	K03594	Cvib_1194	uncharacterized ACR : ferritin, Dps family protein
166074810	0.02266	COG2165			general secretory pathway proteins G and H and related periplasmic/secreted proteins

166188979	0.01945	COG0459	K04077	Cvib_0586	chaperonin GroEL (HSP60 family)
166184768	0.01314	COG1629	K02014	CT1953	outer membrane receptor proteins, mostly Fe transport : ferric siderophore receptor, putative, TonB receptor family
166090652	0.01164	COG1629	K02014	CT1953	outer membrane receptor proteins, mostly Fe transport : ferric siderophore receptor, putative, TonB receptor family
166103931	0.01162	COG2885		Cvib_0715	outer membrane protein and related peptidoglycan-associated (lipo)proteins : OmpA/MotB domain protein
166147146	0.01120	COG0522	K02986	Cvib_0272	rpsD; 30S ribosomal protein S4; K02986 small subunit ribosomal protein S4
166118837	0.01040	COG0605	K04564	Cvib_0978	superoxide dismutase : Fe-Mn family
166147056	0.01018	COG0045		Cvib_0867	succinyl-CoA synthetase beta subunit : ATP citrate lyase subunit 1
166109428	0.00951	COG1704	K03744	Cvib_0448	uncharacterized ACR : LemA family protein
166140297	0.00925	COG2165			general secretory pathway proteins G and H and related periplasmic/secreted proteins
166105505	0.00911	COG0723	K02636	Cvib_1501	rieske Fe-S protein : plastoquinol--plastocyanin reductase; cytochrome b6-f complex iron-sulfur subunit
166164770	0.00908	COG0284	K01591	Cvib_0140	orotidine 5'-phosphate decarboxylase
166118277	0.00863	COG0080	K02867	Plut_1966	rplK; 50S ribosomal protein L11
166129078	0.00843	COG0055	K02112	Cvib_0025	F0F1-type ATP synthase beta subunit
166150726	0.00842	COG0054	K00794	Cvib_1632	riboflavin synthase beta-chain : 6,7-dimethyl-8-ribityllumazine synthase
166160341	0.00833	COG2165		MXAN_5783	general secretory pathway proteins G and H and related periplasmic/secreted proteins : pilA; pilin
166090624	0.00817	COG0446	K00540	Cvib_0009	uncharacterized NAD(FAD)-dependent dehydrogenases : sulfide dehydrogenase (flavocytochrome), flavoprotein subunit

166091252	0.00741	COG0181	K01749	Cvib_1245	porphobilinogen deaminase : hydroxymethylbilane synthase
166159279	0.00737	COG0074		Cvib_0866	succinyl-CoA synthetase alpha subunit : ATP citrate lyase subunit 2
166131402	0.00732	COG0776	K05788	Cvib_1506	bacterial nucleoid DNA-binding protein : histone family protein DNA-binding protein; integration host factor subunit beta
166196008	0.00715	COG0056	K02111	Cvib_1628	F0F1-type ATP synthase alpha subunit
166145114	0.00711	COG0050	K02358	Cvib_0244	GTPases - translation elongation factors : tuf
166114564	0.00664	COG0056	K02111	Cvib_1628	F0F1-type ATP synthase alpha subunit
166136070	0.00664	COG2838	K00031	Cvib_0507	monomeric isocitrate dehydrogenase
166175476	0.00652	COG0724		Cvib_0890	RNA-binding proteins (RRM domain) : RNP-1 like RNA-binding protein
166136072	0.00648	COG0623	K00208	Cvib_0506	enoyl-[acyl-carrier-protein] reductase (NADH)
166076054	0.00647	COG0633	K08953	Cvib_1151	ferredoxin : chlorosome envelope protein J
166097866[a]	0.00589	COG0459	K04077	Acid345_1097	chaperonin GroEL (HSP60 family)
166097888	0.00584	COG0191	K01624	Cvib_0892	fructose/tagatose bisphosphate aldolase
166157335	0.00575	COG0450	K03386	Cvib_1195	peroxiredoxin
166112774	0.00570	COG0191	K01624	Cvib_0892	fructose/tagatose bisphosphate aldolase
166114562	0.00568	COG0224	K02115	Cvib_1627	F0F1-type ATP synthase gamma subunit
166073786	0.00553	COG0045	K01903	Cvib_0553	succinyl-CoA synthetase beta subunit
166094904	0.00543	COG0330		Cvib_1667	membrane protease subunits, stomatin/prohibitin homologs : SPFH domain, band 7 family protein
166105507	0.00538	COG1290	K00412	Cvib_1500	cytochrome b subunit of the bc complex : ubiquinol-cytochrome c reductase cytochrome b subunit
166073832	0.00525	COG0359	K02939	Cvib_0184	rplI; 50S ribosomal protein L9
166145084	0.00522	COG0094	K02931	Cvib_0258	rplE; 50S ribosomal protein L5
166107961	0.00493	COG0674	K03737	Cvib_1407	pyruvate:ferredoxin oxidoreductase and related 2-oxoacid:ferredoxin oxidoreductases, alpha subunit
166118279	0.00485	COG0081	K02863	Cvib_1608	rplA; 50S ribosomal protein L1

166102730	0.00462	COG0776	K03530	ECA1151	bacterial nucleoid DNA-binding protein : hupB, hopD; transcriptional regulator HU subunit beta
166081105	0.00459	COG0674	K00174	Cvib_1597	pyruvate:ferredoxin oxidoreductase and related 2-oxoacid:ferredoxin oxidoreductases, alpha subunit : 2-oxoglutarate ferredoxin oxidoreductase, alpha subunit
166176327$_b$	0.00459	COG0050	K02358	Cvib_0244	GTPases - translation elongation factors : tuf
166154349	0.00458	COG0776	K03530	Maqu_1837	bacterial nucleoid DNA-binding protein : DNA-binding protein HU-beta
166147144	0.00453	COG0522	K02986	Cvib_0272	rpsD; 30S ribosomal protein S4
166171164	0.00439	COG1038	K01571	Cvib_1018	pyruvate carboxylase, C-terminal domain/subunit : biotin/lipoyl attachment domain-containing protein; oxaloacetate decarboxylase, alpha subunit
166161092	0.00429	COG0074	K01902	Cvib_1529	succinyl-CoA synthetase alpha subunit
166169642	0.00428	COG0003	K01551	Cvib_0783	predicted ATPase involved in chromosome partitioning : arsenite-activated ATPase ArsA
166129916	0.00422	COG1185	K00962	Cvib_1424	polyribonucleotide nucleotidyltransferase (polynucleotide phosphorylase)
166145082	0.00408	COG0094	K02931	Cvib_0258	rplE; 50S ribosomal protein L5
166129918	0.00407	COG1185	K00962	Cvib_1424	polyribonucleotide nucleotidyltransferase (polynucleotide phosphorylase)
166175528	0.00404	COG0261	K02888	Cvib_1329	rplU; 50S ribosomal protein L21
166116994	0.00393	COG1274	K01596	Cvib_0027	phosphoenolpyruvate carboxykinase (GTP)
166102162	0.00393	COG0330		Plut_1305	membrane protease subunits, stomatin/prohibitin homologs : band 7 protein
166112188	0.00388	COG1049	K01682	Cvib_0598	aconitase B : bifunctional aconitate hydratase 2/2-methylisocitrate dehydratase
166098678	0.00381	COG0443	K04043	Cvib_1158	molecular chaperone : DnaK
166168134	0.00358	COG0052	K02967	Cvib_0458	rpsB; 30S ribosomal protein S2; K02967 small subunit ribosomal protein S2

166074098	0.00356	COG0233	K02838	Cvib_0408	ribosome recycling factor
166169194	0.00350	COG0001	K01845	Cvib_1681	glutamate-1-semialdehyde 2,1-aminomutase
166125344	0.00346	COG0174	K01915	Cvib_1230	glutamine synthetase
166137459	0.00346	COG0335	K02884	Cvib_0932	rplS; 50S ribosomal protein L19
166118281	0.00345	COG0244	K02864	Cvib_1607	rplJ; 50S ribosomal protein L10
166145072	0.00342	COG0098	K02988	Cvib_0263	rpsE; 30S ribosomal protein S5
166166464$_c$	0.00335	COG0057	K00134	Cvib_1310	glyceraldehyde-3-phosphate dehydrogenase/erythrose-4-phosphate dehydrogenase
166077950	0.00311	COG0039	K00026	Cvib_1331	malate/lactate dehydrogenases
166175692	0.00303	COG1378		NEQ098	predicted transcriptional regulators : hypothetical protein
166145074	0.00301	COG0256	K02881	Cvib_0262	rplR; 50S ribosomal protein L18
166145070	0.00294	COG0200	K02876	Cvib_0265	rplO; 50S ribosomal protein L15
166145094	0.00270	COG0197	K02878	Cvib_0253	rplP; 50S ribosomal protein L16
166188981	0.00259	COG0234	K04078	Plut_0541	Co-chaperonin GroES (HSP10)
166193190	0.00256	COG1049	K01682	Cvib_0598	aconitase B : bifunctional aconitate hydratase 2/2-methylisocitrate dehydratase
166170748	0.00252	COG0115	K00826	Cvib_1391	branched-chain amino acid aminotransferase/4-amino-4-deoxychorismate lyase
166166696	0.00245	COG0085	K03043	Cvib_1605	DNA-directed RNA polymerase beta subunit/140 kD subunit (split gene in Mjan, Mthe, Aful)
166177107	0.00243	COG0652	K03767	Cvib_0535	peptidyl-prolyl cis-trans isomerase (rotamase) - cyclophilin family
166185496	0.00241	COG0588	K01834	Cvib_0557	phosphoglycerate mutase 1
166083171	0.00234	COG0192	K00789	Cvib_1121	S-adenosylmethionine synthetase
166086944	0.00222	COG1014	K03737	Cvib_1407	pyruvate:ferredoxin oxidoreductase and related 2-oxoacid:ferredoxin oxidoreductases, gamma subunit
166154673	0.00220	COG0629	K03111	Cvib_0326	single-strand binding protein

166176323	0.00216	COG0480	K02355	Cvib_0243	translation elongation and release factors (GTPases) : fusA; elongation factor G
166136530	0.00213	COG0711	K02109	Cvib_1741	F0F1-type ATP synthase b subunit
166176321	0.00213	COG0049	K02992	Cvib_0242	30S ribosomal protein S7
166145098	0.00203	COG0091	K02890	Cvib_0251	rplV; 50S ribosomal protein L22
166090169[a]	0.00200	COG0459	K04077	Oter_2054	chaperonin GroEL (HSP60 family)
166087916	0.00197	COG0462	K00948	Cvib_0712	phosphoribosylpyrophosphate synthetase
166177021	0.00192	COG0001	K01845	Cvib_1681	glutamate-1-semialdehyde 2,1-aminomutase
166152385	0.00189	COG0086	K03046	Cvib_1604	DNA-directed RNA polymerase beta' subunit/160 kD subunit (split gene in archaea and Syn)
166145088	0.00188	COG0093	K02874	Cvib_0256	rplN; 50S ribosomal protein L14
166190942	0.00188	COG0085	K03043	Cvib_1605	DNA-directed RNA polymerase beta subunit/140 kD subunit (split gene in Mjan, Mthe, Aful)
166118275	0.00187	COG0250	K02601	Cvib_1610	transcription antitermination protein NusG
166145096	0.00183	COG0092	K02982	Cvib_0252	rpsC; 30S ribosomal protein S3
166091362	0.00181	COG2319		Cvib_0309	WD-40 repeat protein
166124685	0.00181	COG0176	K00616	Cvib_1728	translaldolase
166135982	0.00177	COG0126	K00927	Cvib_1766	pgk; phosphoglycerate kinase
166164640	0.00175	COG1729		Cvib_1161	uncharacterized BCR : tetratricopeptide domain protein
166087918	0.00167	COG1825	K02897	Cvib_0711	50S ribosomal protein L25/general stress protein Ctc
166189760	0.00167	COG0148	K01689	Cvib_1615	enolase
166102164	0.00157	COG0589		Cvib_1041	universal stress protein UspA and related nucleotide-binding proteins
166154669	0.00154	COG0003	K01551	Cvib_0328	predicted ATPase involved in chromosome partitioning : arsenite-activated ATPase ArsA
166131420	0.00154	COG1611	K06966	Cvib_0416	predicted Rossmann fold nucleotide-binding protein : conserved hypothetical protein 730
166103031	0.00153	COG0724		Cag_1551	RNA-binding proteins (RRM domain) : RNP-1 (RNA recognition motif)

166145110	0.00150	COG0087	K02906	Cvib_0246	rplC; 50S ribosomal protein L3
166143572	0.00147	COG0103	K02996	Cvib_0457	rpsI; 30S ribosomal protein S9
166081107	0.00142	COG1013	K00175	Cvib_1598	pyruvate:ferredoxin oxidoreductase and related 2-oxoacid:ferredoxin oxidoreductases, beta subunit : 2-oxoglutarate ferredoxin oxidoreductase subunit beta
166119893	0.00140	COG0113	K01698	Cvib_1252	delta-aminolevulinic acid dehydratase : porphobilinogen synthase
166145108	0.00135	COG0088	K02926	Cvib_0247	rplD; 50S ribosomal protein L4
166091020	0.00135	COG0112	K00600	Cvib_1381	glycine hydroxymethyltransferase
166125448	0.00133	COG1239	K03405	Cvib_1059	Mg-chelatase subunit ChlI
166079276	0.00131	COG0499	K01251	Cvib_1122	S-adenosyl-L-homocysteine hydrolase
166145076	0.00128	COG0097	K02933	Cvib_0261	rplF; 50S ribosomal protein L6
166145078	0.00127	COG0096	K02994	Cvib_0260	rpsH; 30S ribosomal protein S8
166102716	0.00125	COG0446	K00540	Cpha266_2569	uncharacterized NAD(FAD)-dependent dehydrogenases : sulfide-quinone reductase
166176319	0.00124	COG0048	K02950	Cvib_0241	rpsL; 30S ribosomal protein S12
166079074	0.00122	COG1049	K01682	Cvib_0598	aconitase B : bifunctional aconitate hydratase 2/2-methylisocitrate dehydratase
166111074	0.00118	COG0539	K02945	Cvib_1514	rpsA; 30S ribosomal protein S1
166136657	0.00118	COG1360	K02557	Pcar_1973	flagellar motor protein : chemotaxis protein MotB
166124033	0.00118	COG0158	K03841	Cvib_0509	fructose-1,6-bisphosphatase
166176325	0.00117	COG0480	K02355	Plut_0177	translation elongation and release factors (GTPases) : fusA; elongation factor G
166137753	0.00115	COG1778	K03270	Cvib_1694	uncharacterized proteins of HAD superfamily, CMP-Neu5Ac homologs : 3-deoxy-D-manno-octulosonate 8-phosphate phosphatase, YrbI family
166125498	0.00112	COG0377	K00331	Cvib_1092	NADH:ubiquinone oxidoreductase 20 kD subunit and related Fe-S oxidoreductases
166144212	0.00110	COG2101	K03120	AF0373	transcription initiation factor TFIID (TATA-binding protein)

166171940	0.00110	COG0100	K02948	Cvib_0271	30S ribosomal protein S11
166195033	0.00109	COG0809	K07568	Cvib_1048	S-adenosylmethionine:tRNA-ribosyltransferase-isomerase (queuine synthetase)
166186408	0.00109	COG0365	K01895	Plut_1637	acyl-coenzyme A synthetases/AMP-(fatty) acid ligases
166177113	0.00106	COG0005	K03783	Cvib_0533	purine nucleoside phosphorylase
166154527	0.00105	COG0413	K00606	Cvib_0725	ketopantoate hydroxymethyltransferase : panB; 3-methyl-2-oxobutanoate hydroxymethyltransferase
166150004	0.00105	COG1028		Cvib_0372	dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases)
166187454	0.00104	COG0059	K00053	Cvib_1172	ketol-acid reductoisomerase
166112410*	0.00100	COG0086	K03046	HM1_1371	DNA-directed RNA polymerase beta' subunit/160 kD subunit (split gene in archaea and Syn)
166118285	0.00099	COG0085	K03043	Cvib_1605	DNA-directed RNA polymerase beta subunit/140 kD subunit (split gene in Mjan, Mthe, Aful)
166147142	0.00098	COG0202	K03040	Cvib_0273	DNA-directed RNA polymerase alpha subunit/40 kD subunit
166091254	0.00097	COG1587	K01719	Cvib_1246	uroporphyrinogen-III synthase
166123058	0.00096	COG1028	K00059	Cvib_1180	dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases): 3-oxoacyl-[acyl-carrier protein] reductase
166083688	0.00096	COG0330	K04088	Pcar_2262	membrane protease subunits, stomatin/prohibitin homologsh: HflK
166081389	0.00095	COG0241	K05602	Cvib_0287	histidinol phosphatase and related phosphatases
166104095	0.00094	COG1837	K06960	CAC1756	predicted RNA-binding protein (KH domain)
166137513	0.00094	COG0725	K02020	Cvib_1492	ABC-type molybdate transport system, periplasmic component
166073556	0.00093	COG0592	K02338	Cvib_0002	DNA polymerase sliding clamp subunit (PCNA homolog)
166085896	0.00092	COG0086	K03046	Cvib_1604	DNA-directed RNA polymerase beta' subunit/160 kD subunit (split gene in archaea and Syn)

166171160	0.00092	COG0511	K01571	Cvib_1018	biotin carboxyl carrier protein : oxaloacetate decarboxylase, alpha subunit
166143662	0.00089	COG0289	K00215	Cvib_0390	dihydrodipicolinate reductase
166128308	0.00082	COG2873	K01740	Cag_1257	O-acetylhomoserine/O-acetylserine sulfhydrylase
166096460	0.00082	COG1561		Cvib_1556	uncharacterized stress-induced protein
166174470	0.00080	COG3040	K03098	Cvib_0516	bacterial lipocalin : Blc
166142836	0.00079	COG0480	K02355	Cvib_1616	translation elongation and release factors (GTPases) : fusA; elongation factor G
166198126	0.00078	COG0326	K04079	Cvib_1024	molecular chaperone, HSP90 family : HtpG
166187456	0.00077	COG0440	K01653	Cvib_1171	acetolactate synthase, small subunit
166195031	0.00076	COG1554		Cvib_1047	trehalose and maltose hydrolases (possible phosphorylases) : beta-phosphoglucomutase family hydrolase
166112772	0.00076	COG0191	K01624	Cvib_0892	fructose/tagatose bisphosphate aldolase
166167622	0.00075	COG0499	K01251	Cvib_1122	S-adenosyl-L-homocysteine hydrolase
166163472	0.00074	COG3637		Cvib_1533	opacity protein and related surface antigens : porin, opacity type
166186410	0.00070	COG0365	K01895	Cvib_1426	acyl-coenzyme A synthetases/AMP-(fatty) acid ligases
166137755	0.00069	COG2877	K01627	Cvib_1695	3-Deoxy-D-manno-octulosonic acid (KDO) 8-phosphate synthase : 2-dehydro-3-deoxyphosphooctonate aldolase
166109758	0.00069	COG2171	K00674	Cvib_0017	tetrahydrodipicolinate N-succinyltransferase : dapD; 2,3,4,5-tetrahydropyridine-2-carboxylate N-succinyltransferase
166164026	0.00068	COG3808	K01507	Cvib_0758	inorganic pyrophosphatase : hppA
166139077	0.00068	COG1837	K06960	Bcer98_2495	predicted RNA-binding protein (KH domain)
166087626[c]	0.00067	COG0057	K00134	Bcer98_3682	glyceraldehyde-3-phosphate dehydrogenase/erythrose-4-phosphate dehydrogenase
166134708	0.00066	COG0760		Cvib_1572	parvulin-like peptidyl-prolyl isomerase : PpiC-type peptidyl-prolyl cis-trans isomerase

166150020	0.00066	COG2606		Cvib_0364	uncharacterized ACR : YbaK/prolyl-tRNA synthetase associated region
166179493	0.00066	COG0058	K00688	Cvib_1386	alpha-glucan phosphorylase; starch phosphorylase
166164028	0.00063	COG3808	K01507	Plut_1202	inorganic pyrophosphatase : hppA
166083948	0.00063	COG0173	K01876	Cvib_1052	aspS; aspartyl-tRNA synthetase
166090630	0.00063	COG1252	K03885	Cvib_1373	NADH dehydrogenase, FAD-containing subunit : FAD-dependent pyridine nucleotide-disulphide oxidoreductase
166150732	0.00063	COG0407	K01599	Cvib_1635	uroporphyrinogen-III decarboxylase
166134876	0.00060	COG0195	K02600	Cvib_1562	transcription elongation factor NusA : N utilization substance protein A
166151470[b]	0.00057	COG0050	K02358	Nwi_1362	GTPases - translation elongation factors : tuf
166180979	0.00056	COG3245		Cvib_0219	cytochrome c5
166110008	0.00055	COG1429	K03403	Cvib_1057	cobalamin biosynthesis protein CobN and related Mg-chelatases : hydrogenobyrinic acid a,c-diamide cobaltochelatase
166093481	0.00054	COG0260	K01255	Cvib_0947	leucyl aminopeptidase
166084291	0.00053	COG3360	K09165	Cvib_0029	uncharacterized ACR : protein of unknown function DUF1458
166134544	0.00053	COG2920	K00396	Cvib_0038	sulfite reductase, gamma subunit : DsrC family protein
166183160	0.00052	COG1077	K03569	Cvib_0595	HSP70 class molecular chaperones involved in cell morphogenesis: MreB/Mrl family
166079969	0.00052	COG0539	K02945	Cvib_1514	rpsA; 30S ribosomal protein S1
166074910	0.00051	COG0003	K01551	Cvib_0332	predicted ATPase involved in chromosome partitioning : arsenite-activated ATPase ArsA
166078208	0.00049	COG1032	K04035	Cvib_0316	Fe-S oxidoreductases family 2 : magnesium-protoporphyrin IX monomethyl ester anaerobic oxidative cyclase
166148744	0.00048	COG0217		Cvib_1432	uncharacterized ACR : hypothetical protein

166164642	0.00047	COG2885		Cvib_1162	outer membrane protein and related peptidoglycan-associated (lipo)proteins : OmpA/MotB domain protein
166124690	0.00046	COG1899	K00809	Cvib_1729	deoxyhypusine synthase
166074701	0.00046	COG0360	K02990	Cvib_0181	rpsF; 30S ribosomal protein S6
166078272	0.00044	COG0811	K03562	Cvib_1167	biopolymer transport proteins : MotA/TolQ/ExbB proton channel
166160978	0.00044	COG2077	K00435	Cvib_1103	Peroxiredoxin : thiol peroxidase (atypical 2-Cys peroxiredoxin)
166089421	0.00042	COG0330		SYN_00180	membrane protease subunits, stomatin/prohibitin homologs : bacterial HflC protein
166184106	0.00041	COG1351	K03465	Plut_0366	predicted alternative thymidylate synthase : thyX
166146666	0.00040	COG1538		Plut_2001	outer membrane protein : LipD protein, putative
166107875[b]	0.00039	COG0050	K02358	Pcar_0699	GTPases - translation elongation factors : tufA, tuf
166185036	0.00038	COG0436	K00812	Cvib_0768	PLP-dependent aminotransferases : aspartate aminotransferase
166085075	0.00038	COG0694	K07400	Cvib_0453	thioredoxin-like proteins and domains : nitrogen-fixing NifU domain protein
166166220	0.00038	COG0330	K04087	Pcar_2263	membrane protease subunits, stomatin/prohibitin homologsh: HflC protein
166156045	0.00037	COG3155		Cvib_1447	uncharacterized sigma cross-reacting protein 27A (ES1 or KNP-I alpha protein) : isoprenoid biosynthesis protein with amidotransferase-like domain
166197986	0.00034	COG0342	K03072	Cvib_0010	preprotein translocase subunit SecD
166147140	0.00034	COG0203	K02879	Cvib_0274	rplQ; 50S ribosomal protein L17
166073820	0.00033	COG0188	K02469	Cvib_0172	DNA gyrase (topoisomerase II) A subunit
166181669	0.00033	COG0082	K01736	Cvib_1253	chorismate synthase
166159821	0.00033	COG2884	K09812	Cvib_1198	predicted ATPase involved in cell division : FtsE
166145122	0.00031	COG3347		Cvib_0462	uncharacterized ACR : short chain dehydrogenase
166081203	0.00030	COG0468	K03553	Cvib_0340	RecA/RadA recombinase

166160944	0.00029	COG0226	K02040	Cvib_0998	ABC-type phosphate transport system, periplasmic component
166171936	0.00029	COG0024	K01265	Cvib_0267	methionine aminopeptidase
166177115	0.00028	COG0182	K08963	Cvib_0532	translation initiation factor eIF-2B alpha subunit : methylthioribose-1-phosphate isomerase
166121954	0.00027	COG1239	K03404	Cvib_1058	Mg-chelatase subunit ChlI
166114512	0.00027	COG0729	K07277	Cvib_1532	predicted outer membrane protein : surface antigen (D15)
166123620[a]	0.00026	COG0459	K04077	MXAN_4895	chaperonin GroEL (HSP60 family)
166160942	0.00025	COG0226	K02040	Cvib_0997	ABC-type phosphate transport system, periplasmic component
166080265	0.00024	COG2878		Cvib_0798	predicted alternative beta subunit of Na+-transporting NADH:ubiquinone oxidoreductase : ferredoxin
166184114	0.00023	COG0568	K03086	Cvib_0443	DNA-directed RNA polymerase sigma subunits (sigma70/sigma32)
166163480	0.00023	COG1158	K03628	Cvib_1537	transcription termination factor: Rho
166132366	0.00023	COG1233		Cvib_0356	phytoene dehydrogenase and related proteins : FAD dependent oxidoreductase
166116816	0.00021	COG0542	K03696	Cvib_1580	ATPases with chaperone activity, ATP-binding subunit : ATP-dependent Clp protease ATP-binding subunit ClpC
166128316	0.00020	COG1629		Cvib_1353	outer membrane receptor proteins, mostly Fe transport : TonB receptor family
166163448	0.00020	COG0635	K02495	Cvib_1370	coproporphyrinogen III oxidase and related Fe-S oxidoreductases
166159573	0.00019	COG1151	K00378	Cvib_1455	6Fe-6S prismane cluster-containing protein : hydroxylamine reductase
166163870	0.00017	COG0209	K00525	Cvib_1199	ribonucleotide-diphosphate reductase subunit alpha
166135202	0.00013	COG0544	K03545	Cvib_0337	FKBP-type peptidyl-prolyl cis-trans isomerase (trigger factor)

166164774	0.00012	COG0743	K00099	Cvib_0138	1-deoxy-D-xylulose 5-phosphate reductoisomerase
166180975	0.00012	COG0075	K00839	Cvib_0221	serine-pyruvate aminotransferase/archaeal aspartate aminotransferase
166078200	0.00011	COG1429	K06050	Cvib_0320	cobalamin biosynthesis protein CobN and related Mg-chelatases : hydrogenobyrinic acid a,c-diamide cobaltochelatase
166185488	0.00010	COG0069	K00284	Cvib_0558	glutamate synthase domain 2

14 m - KEGG and NR annotated proteins

Gene ID	normalised spectral abundance	NR identifier	KO identifier	KEGG / NR locus tag	KEGG/NR description
166154667	0.12890		K08947	Cvib_0329	chlorosome envelope protein C
166116826	0.07870		K08944	Cvib_1325	bacteriochlorophyll A protein
166103043	0.07473			Cpha266_0714	hypothetical protein
166154665	0.04995		K08945	Cvib_0330	bacteriochlorophyll C binding protein
166084321	0.01855		K08951	Cvib_1234	chlorosome envelope protein H
166197596	0.01757			Cvib_0837	hypothetical protein
166078646	0.01703		K06142	Cvib_1549	outer membrane chaperone Skp (OmpH)
166183346	0.01613			CKO_01864	hypothetical protein
166103041	0.01438			Cpha266_0714	hypothetical protein
166128026	0.01374		K08943	Cvib_1159	photosystem P840 reaction center protein PscD; K08943 photosystem P840 reaction center protein PscD
166178625	0.01011			Plut_1996	CBS
166169946	0.00965			Psyr_2789	hypothetical protein
166128030	0.00924		K08943	Cvib_1159	photosystem P840 reaction center protein PscD
166105997	0.00871	ZP_02034709		BACCAP_00296	hypothetical protein [Bacteroides capillosus ATCC 29799]
166112572	0.00846			Daci_1946	putative phage major head protein
166160856	0.00694	ZP_03762235		CLOSTASPAR_06273	hypothetical protein [Clostridium asparagiforme DSM 15981]

166112574[d]	0.00672			Daci_1946	putative phage major head protein
166114838	0.00665			Cvib_0125	hypothetical protein
166191606	0.00636		K08940	Cvib_1619	photosystem P840 reaction center, large subunit; K08940 photosystem P840 reaction center large subunit
166147050	0.00612			Plut_1061	citrate lyase, subunit 1
166145430[e]	0.00533			Haur_0657	hypothetical protein
166076418	0.00499			Daci_1946	putative phage major head protein
166198192[e]	0.00493			Haur_0657	hypothetical protein
166177839	0.00469			Bcep1808_1173	hypothetical protein
166150012	0.00390		K08946	Cvib_0367	chlorosome envelope protein B;
166199138	0.00360		K08942	Cvib_1418	photosystem P840 reaction center cytochrome c-551
166145106	0.00354		K02926	Cvib_0247	rplD; 50S ribosomal protein L4
166115656	0.00353			Cag_0645	hypothetical protein
166171962	0.00347			BC1894	phage protein
166191394	0.00334			Cvib_0413	hypothetical protein
166075542	0.00331			Cvib_1747	O-methyltransferase, family 2
166195894	0.00312			CKL_1862	hypothetical protein
166194857	0.00290		K08941	Cvib_1618	4Fe-4S ferredoxin, iron-sulfur binding domain protein; photosystem P840 reaction center iron-sulfur protein
166111558	0.00220			Cvib_1311	hypothetical protein
166177105	0.00197			Cvib_0536	TPR repeat-containing protein
166147988[d]	0.00160			Daci_1946	putative phage major head protein
166143915	0.00156			GDI3673	hypothetical protein
166114744	0.00144			Cvib_0488	mammalian cell entry related domain protein
166136528	0.00134		K05807	Cvib_1734	putative lipoprotein
166189288	0.00132		K08946	Cvib_1647	chlorosome envelope protein B
166153135	0.00118			Cvib_1720	hypothetical protein
166115588	0.00099			Aave_2895	hypothetical protein

166126712	0.00099			Cphamn1_2160	CRISPR-associated protein, CSE2 family
166127542	0.00096			Cphamn1_0811	hypothetical protein
166085087	0.00091			Swit_4452	hypothetical protein
166129356	0.00081			Cvib_0992	phosphate uptake regulator, PhoU
166195535	0.00080			Cthe_1719	phage major capsid protein, HK97 family
166080497	0.00077			NEQ258	hypothetical protein
166126708	0.00075			CT1975	hypothetical protein
166148084	0.00075			Cvib_0912	hypothetical protein
166093483	0.00074		K01255	Cvib_0947	leucyl aminopeptidase
166170746	0.00073		K00850	Cvib_1390	6-phosphofructokinase
166140451	0.00071			amb4267	hypothetical protein
166097432	0.00047			GbCGDNIH1_1574	hypothetical protein
166135078	0.00039			Cvib_1499	alpha amylase, catalytic region
166091036	0.00024			Cvib_0951	hypothetical protein
14 m - Proteins with no annotation					
166113938	0.28150				
166170056[f]	0.23381				
166104559	0.21346				
166166078	0.11573				
166119911[g]	0.10078				
166141831	0.09127				
166155401	0.06411				
166178565[f]	0.05428				
166161827	0.05400				
166123502	0.04548				
166117935	0.04149				
166175637	0.03938				
166162109	0.03622				
166120729	0.02777				
166089615	0.02167				

166089117[h]	0.02020				
166122468[f]	0.01992				
166196000	0.01976				
166181749[k]	0.01745				
166122470[g]	0.01725				
166177993	0.01674				
166183514[i]	0.01619				
166106257	0.01486				
166168914	0.01399				
166098369	0.01350				
166184074	0.01201				
166118161	0.01166				
166098372	0.01130				
166152065	0.01097				
166142782	0.01080				
166094970	0.01010				
166198840	0.00950				
166086220	0.00949				
166147768	0.00898				
166083420	0.00834				
166197698	0.00829				
166128790	0.00815				
166198884	0.00771				
166185832	0.00744				
166115262[j]	0.00733				
166178177	0.00673				
166178731	0.00648				
166198482	0.00636				
166133494	0.00557				

166115313	0.00555				
166130570	0.00540				
166112498	0.00516				
166160740	0.00453				
166184588	0.00451				
166073347	0.00441				
166078332	0.00433				
166189276[i]	0.00432				
166098374	0.00416				
166165646	0.00377				
166141123	0.00348				
166133904	0.00341				
166197188	0.00341				
166098366	0.00332				
166161640	0.00304				
166150071	0.00276				
166185272	0.00270				
166173254[k]	0.00243				
166142790	0.00238				
166115308	0.00236				
166166040	0.00235				
166194855	0.00231				
166181319	0.00213				
166115336	0.00206				
166082335	0.00195				
166166084	0.00187				
166097710	0.00163				
166195563	0.00154				
166184076	0.00149				
166118309	0.00144				

166161638	0.00126				
166115340[j]	0.00118				
166160259	0.00108				
166199068	0.00102				
166077062	0.00085				
166116936	0.00077				
166095512	0.00076				
166186728	0.00071				
166110378[g]	0.00062				
166155981[h]	0.00056				
166132092	0.00056				
166176653	0.00051				
166102418	0.00048				
166176585	0.00040				
166128640	0.00035				
166135852	0.00023				

18 m - COG annotated proteins

Gene ID	normalised spectral abundance	COG identifier	KO identifier	KEGG locus tag	COG description : KEGG description
186212528[a]	0.05178	COG1378		NEQ098	predicted transcriptional regulators : hypothetical protein
186260184[a]	0.01990	COG1378		NEQ098	predicted transcriptional regulators : hypothetical protein
186323634	0.00815	COG1629			outer membrane receptor proteins, mostly Fe transport
186330135	0.00354	COG2165			general secretory pathway proteins G and H and related periplasmic/secreted proteins
186203427	0.00268	COG0459	K04077	Cvib_0586	chaperonin GroEL (HSP60 family)

186325396	0.00029	COG0330	K04088	MXAN_3171	membrane protease subunits, stomatin/prohibitin homologs : HflK
186302986	0.00014	COG1629	K02014	CT1953	outer membrane receptor proteins, mostly Fe transport : ferric siderophore receptor, putative, TonB receptor family

18 m - KEGG and NR annotated proteins

Gene ID	**normalised spectral abundance**	**NR identifier**	**KO identifier**	**KEGG / NR locus tag**	**KEGG / NR description**
186250193	0.03535			SAK_0748	prophage LambdaSa04, major capsid protein, HK97 family
186108954	0.01496	ZP_02186589		BAL199_17233	hypothetical protein [alpha proteobacterium BAL199]
186340319	0.01172	YP_002433801		Dalk_4655	hypothetical protein [Desulfatibacillum alkenivorans AK-01]
186120387	0.01077	ZP_02034709		BACCAP_00296	hypothetical protein [Bacteroides capillosus ATCC 29799]
186267822	0.00917			amb4267	hypothetical protein
186322918	0.00767	ZP_02186589		BAL199_17233	hypothetical protein [alpha proteobacterium BAL199]
186104395	0.00674		K08944	Cvib_1325	bacteriochlorophyll A protein
186171273	0.00587	ZP_03013728		BACINT_01287	hypothetical protein [Bacteroides intestinalis DSM 17393]
186216762	0.00511	YP_001648266			hypothetical protein OsV5_190f [Ostreococcus virus OsV5]
186188521	0.00474	AAU84208		GZ37D1_55	hypothetical protein [uncultured archaeon GZfos37D1]
186193139	0.00263			Cthe_1719	phage major capsid protein, HK97 family
186096477	0.00240			Cthe_1719	phage major capsid protein, HK97 family
186213938	0.00211			Nwi_1542	phage major capsid protein, HK97
186288435	0.00189			Bcep1808_1173	hypothetical protein
186186444	0.00140	YP_002765714		RER_22670	hypothetical protein [Rhodococcus erythropolis PR4]
186201365	0.00119	ABW90952			gp23 major capsid protein [uncultured Myoviridae]

186179269	0.00109			HSM_0907	hypothetical protein
186355884	0.00077			Aave_2365	hypothetical protein
186166939	0.00060	EEH89810			conserved hypothetical protein [Acidaminococcus sp. D21]
186255081	0.00050			BCE_0400	phage major capsid protein, HK97 family
18 m - Proteins with no annotation					
186096775	0.00241				
186097423	0.00916				
186098091	0.00174				
186111007	0.00078				
186111572	0.00059				
186115457	0.00104				
186115570*	0.00011				
186115576	0.00019				
186123594	0.00212				
186125293	0.00370				
186127924	0.00058				
186131984	0.00104				
186132934	0.00114				
186132940	0.00646				
186133174	0.02253				
186133182	0.00132				
186133258	0.00558				
186133464	0.04461				
186133598[b]	0.00897				
186133600[c]	0.02301				
186133668	0.00039				
186133988	0.00027				
186135915	0.00096				
186144849	0.00090				

186146871	0.00261				
186150520	0.03110				
186150522	0.01653				
186152236	0.00251				
186157988	0.00347				
186166888	0.00138				
186172010	0.00060				
186174298	0.00457				
186180639[b]	0.01514				
186180725[b]	0.00639				
186185958	0.00054				
186187134	0.00088				
186188427	0.00024				
186188638	0.00083				
186195344	0.00123				
186196955	0.01096				
186204438	0.00232				
186211626	0.00145				
186213126[d]	0.00737				
186218287	0.00057				
186221108[c]	0.00454				
186221116[b]	0.00898				
186221121	0.00041				
186225633[d]	0.03121				
186226973	0.00110				
186234910	0.00076				
186235104	0.00646				
186239503	0.00082				
186243868[c]	0.00678				

186243873*[b]	0.00555				
186247349	0.01576				
186251752	0.00149				
186255283	0.00020				
186263169	0.00052				
186289901	0.00120				
186296333	0.00288				
186296791	0.00187				
186303307	0.00035				
186305449	0.00032				
186308018	0.00041				
186308756	0.01295				
186321445	0.00459				
186321482[c]	0.04544				
186331727	0.00234				
186334026	0.00196				
186335225	0.00205				
186335471	0.00241				
186344860	0.00118				
186346285	0.01518				
186348107	0.00077				

23 m - COG annotated proteins

Gene ID	**normalised spectral abundance**	**COG identifier**	**KO identifier**	**KEGG locus tag**	**COG description : KEGG description**
184741277	0.017726037	COG0776		SYN_02859	bacterial nucleoid DNA-binding protein : DNA-binding protein HU
184609007	0.016332251	COG1450		Oter_2851	general secretory pathway protein D : type II and III secretion system protein

184630330	0.012087941	COG1837	K06960	CLL_A1247	predicted RNA-binding protein (KH domain) : hypothetical protein
184814744	0.007732722	COG3409			putative peptidoglycan-binding domain-containing protein
184723188	0.006645902	COG1653		Noca_3914	sugar-binding periplasmic proteins/domains : extracellular solute-binding protein, family 1
184729342	0.005151336	COG0459	K04077	Oter_2054	chaperonin GroEL (HSP60 family)
184751721	0.002038819	COG0776	K03530	azo0315	bacterial nucleoid DNA-binding protein : hupB
184834728	0.001993522	COG0683		SYN_00789	ABC-type branched-chain amino acid transport systems, periplasmic component
184819943	0.001917474	COG0776	K03530	Plut_1957	bacterial nucleoid DNA-binding protein : histone-like DNA-binding protein; HU-beta

23 m - KEGG and NR annotated proteins

Gene ID	normalised spectral abundance	NR identifier	KO identifier	KEGG / NR locus tag	KEGG / NR description
184829089	0.047540673			Smed_1892	hypothetical protein
184693861[a]	0.021620642	A7U6E7			putative major capsid protein [Chrysochromulina ericina virus]
184663677[a]	0.021221744	A7U6E7			putative major capsid protein [Chrysochromulina ericina virus]
184759346	0.020715407	YP_001648266		OsV5_190f	hypothetical protein [Ostreococcus virus OsV5]
184796349	0.019224766	ZP_03706494		CLOSTMETH_01228	hypothetical protein [Clostridium methylpentosum DSM 5476]
184674523[a]	0.01878926	A7U6E7			putative major capsid protein [Chrysochromulina ericina virus]
184727907	0.012780957	ZP_03013728		BACINT_01287	hypothetical protein [Bacteroides intestinalis DSM 17393]
184858354	0.012445286			Bcep1808_1173	hypothetical protein
184615458[b]	0.00783673	YP_002299293		RC1_3116	hypothetical protein [Rhodospirillum centenum SW]

184717784[a]	0.007606148	A7U6F0			putative major capsid protein [Phaeocystis pouchetii virus]
184783470[b]	0.00670957			amb4267	hypothetical protein
184677323*	0.006347478			plu3036	hypothetical protein
184765239*	0.005953867	AAU84208		GZ37D1_55	hypothetical protein [uncultured archaeon GZfos37D1]
184728060*	0.004522581			amb4267	hypothetical protein
184610116	0.004189109			Bd3266	cell wall surface anchor family protein
184609428	0.004101986	ZP_02421392		EUBSIR_00216	hypothetical protein [Eubacterium siraeum DSM 15702]
184762189[a]	0.003388765	A7U6E7			putative major capsid protein [Chrysochromulina ericina virus]
184616650*	0.003326858		K08945	Cvib_0330	bacteriochlorophyll C binding protein; chlorosome envelope protein A
184654290	0.003293628			Plut_0689	gas vesicle synthesis protein GvpA
184683542	0.003248441			Daci_1946	putative phage major head protein
184717084	0.002738548	AAU84208			hypothetical protein [uncultured archaeon GZfos37D1]
184761703	0.002499009			Fjoh_3203	Ig domain protein, group 2 domain protein
184619854	0.002486002	ACO64625			predicted protein [Micromonas sp. RCC299]
184806079	0.002155187			BTH_I0914	hypothetical protein
184598462	0.002025957			Cthe_1719	phage major capsid protein, HK97 family
184636514	0.001569903			PTH_2189	hypothetical protein
184699280	0.001564149			HSM_0907	hypothetical protein
184785344	0.001502137			nfa430	putative phage head
184622093	0.001315815		K08946	Cvib_1647	chlorosome envelope protein B
184698829	0.00124255		K08947	Cvib_0329	chlorosome envelope protein C
184699260	0.001048672		K08946	Cvib_0367	chlorosome envelope protein B
184602186	0.000904386			NT01CX_0836	phage capsid family protein, putative
184619542	0.000843609	ZP_03544057		CtesDRAFT_PD3290	hypothetical protein [Comamonas testosteroni KF-1]

184693284	0.000537906		K06142	Cvib_1549	outer membrane chaperone Skp (OmpH)
184853817	0.000476227			Cvib_1511	hypothetical protein
23 m - Proteins with no annotation					
184639659	0.043948442				
184736526$_{c}$	0.041039357				
184780301	0.034503992				
184816235	0.032095179				
184703327	0.028114494				
184757685	0.022912986				
184749374	0.022013987				
184768326	0.021859704				
184855542	0.021374309				
184647188	0.021260105				
184857022$_{d}$	0.019565025				
184844109$_{e}$	0.019406682				
184673540	0.016879013				
184673891	0.015992274				
184752115	0.014966957				
184830016	0.014369697				
184689526	0.014288459				
184830014$_{c}$	0.013541019				
184736969	0.012498216				
184794003	0.012175049				
184716841*$_{h}$	0.011673087				
184614058$_{e}$	0.011632278				
184843043	0.011452762				
184606136	0.010996161				
184701852	0.009831345				
184689528$_{d}$	0.009574146				

184818291	0.009186212				
184717128	0.009020845				
184634342	0.00885126				
184632228$_f$	0.008173806				
184609952*	0.008108204				
184743077$_h$	0.007954013				
184744668$_f$	0.007008787				
184693008	0.006893361				
184699860	0.00671353				
184644432*	0.006647				
184624307	0.006630331				
184717134$_h$	0.00629088				
184687320*	0.006087825				
184609995$_f$	0.005980399				
184606128	0.00593924				
184798514	0.005508034				
184820885	0.005452628				
184774274	0.005257476				
184634936$_d$	0.005138151				
184807615	0.004891909				
184717137$_f$	0.004760532				
184634670	0.004374106				
184699106$_g$	0.004352547				
184694334	0.004323657				
184701357$_g$	0.004288858				
184668292$_f$	0.00420732				
184616142	0.004153614				
184705566*$_i$	0.004036009				
184656354	0.003894939				

184699180	0.003299837				
184792136	0.003269076				
184803016	0.0031682				
184676233	0.003135831				
184634894	0.002503929				
184655451	0.002407637				
184694448$_i$	0.002080588				
184616145	0.001982117				
184693324	0.001959088				
184708522	0.001890434				
184651766	0.001881649				
184654540	0.00153123				
184705454$_f$	0.001429528				
184705654	0.001336639				
184805593	0.001324748				
184716621	0.001323209				
184743075$_f$	0.001221543				
184814882	0.001166233				
184792312	0.001093715				
184829092	0.000840101				
184716837$_f$	0.000762877				
184796632	0.000411936				
184845751	0.000200619				
184730970*	0.000186184				
184613774*	0.000170922				