Supplementary material

Identification of the structure and of microbial activities shaping pelagic iron-rich aggregates (iron snow)

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Materials and Methods

Geochemical analysis of lake water. Dissolved carbon dioxide was measured over the whole depth of the water column and methane was measured in water samples from depth of 3.6 m to 5.5 m in central basin and 3.8 m to 5.5 m in northern basin in May 2011. For these two analyses, 10 ml water samples were filled in 30 ml serum bottles, sealed tightly with rubber stoppers. Samples were treated with 0.1 ml of 2 M HCl and incubated for at least 30 min. The inner volume of serum bottle was calculated by mass differences between empty and water-filled (assumed density of 1 g/cm^3) bottle with rubber stopper and aluminium cap on. Five bottles were selected randomly and the mean value was used for later calculation. CO_2 and CH_4 in pre-treated samples were then measured in triplicates, with a gas chromatograph (HP 5890 series II, Hewlett-Packard Co., USA) with respective column and machine setting (9).

Metaproteomics analysis. The direct soil protein extraction method (SDS-TCA) was employed for total protein extraction (4) from iron snow samples. In brief, 11-22 g of thawed iron snow samples (equal to 0.15 to 0.4 g dry weight) were transferred to glass bottles and dispersed in alkaline-SDS buffer (1:2 sample to buffer ratio). Following vigorous vortexing for 2-3 min, the slurry was placed in boiling water bath for 15 min for effective cellular lyses and inactivation of the proteases. Partially cooled sediment was pelleted by centrifugation, the supernatant was transferred to a new tube and chilled 100% tricholoroacetic acid (TCA) was added to a final concentration of 25% and kept at -20 ℃ overnight. Samples were centrifuged at 14000 rpm for 20 min to obtain a tight protein pellet which was washed three times with 1 ml chilled acetone, air dried and solubilized in 6 M Guanidine buffer at 60 ℃ as described earlier (4). Proteins were

digested, peptides desalted and solvent exchanged as described earlier (15). Protein estimation was performed using the RC/DC protein estimation kit (Bio-Rad, USA) as per the manufacturer's protocol. BSA was used as standard for the assay. All chemicals were obtained from Sigma Chemical Co. (St. Louis, MO) unless mentioned otherwise. Modified sequencing grade trypsin (Promega, Madison, WI) was used for proteolysis. Formic acid (99%) was purchased from EM Science (Darmstadt, Germany, HPLC-grade water, acetonitrile and acetone were obtained from Burdick & Jackson (Muskegon, MI).

All LC-MS/MS measurements were made using hybrid LTQ XL/Orbitrap Velos mass spectrometer (ThermoFisher Scientific, Germany) interfaced with an Ultimate 3000 HPLC system (Dionex, USA) and operated in data dependent mode, regimented by Thermo Xcalibur software V2.1.0. Peptides were loaded onto a 5 cm SCX (Luna, Phenomenex, CA) in-house packed column and subjected to an offline wash with solvent A (5% acetonitrile, 95% HPLC-grade water, 0.1% formic acid) for 15 minutes to remove any lingering interferences followed by a gradient to 100% solvent B (70% acetonitrile, 30% HPLC-grade water, 0.1% formic acid) over 30 minutes. Following wash, the sample column was placed in step with C18 packed Picotip emitter (New Objective, USA) coupled to a Proxeon nanospray source (Odense, Denmark) placed facing the mass spectrometer. Peptides were analyzed via 24-hr MudPIT 2D-LC-MS/MS (11 salt-pulses of ammonium acetate) followed by a 100 minute gradient to 50% solvent B) in an operating in data-dependent mode. Full MS1 scans with 10 MS/MS per full scan were obtained using an Orbitrap mass analyzer set to 60K resolution. Rest of the instrument setup was similar to as described earlier (2, 15). Two replicate measurements were obtained for each sample.

In absence of an actual metagenomic sequence of iron snow from Lake 77, a database was generated by including sequenced microbial genomes from Integrated Microbial Genomes server (11) December 2010 version, including 114 bacteria full genomes, 9 bacterial plasmid sequences, 38 archaeal full genomes and 14 archaeal plasmid sequences (Table S3). The microbial genomes were selected based on the presence of genera reported from lake sediment, water and iron snow clone libraries and isolates (Lu *et al.*, 2010; Reiche *et al.*, 2011) in addition to published genome sequences of known acidophiles or microbes with Fe-cycling capacities (3, 11). Sequences for common contaminant such as trypsin, keratin, etc. were concatenated towards end of the assembled database. Peptide fragmentation spectra obtained for each sample was searched for database matches via SEQUEST v.27 (7). All the datasets and the database can be accessed at https://compbio.ornl.gov/mspipeline/Kuesel/. Output files were filtered using DTASelect (14) set to following filtering criteria for the SEQUEST searches: tryptic peptides only, delCN value of at least 0.08, and X correlation values of 1.8 (+1), 2.5 (+2), 3.5 (+3). Detection of at least two peptides per protein sequence was set as prerequisite for protein identification. The datasets were further evaluated using the Poisson regression model as described by Chourey *et al*. (5) wherein spectral counts of a protein was normalized to make it comparable across different datasets and p values generated were further adjusted using the Benjamini-Hochberg correction to obtain the q value (5). A q value of 0.05 (corresponding to 1% False Discovery Rate) was used to call out significant, differentially expressed proteins.

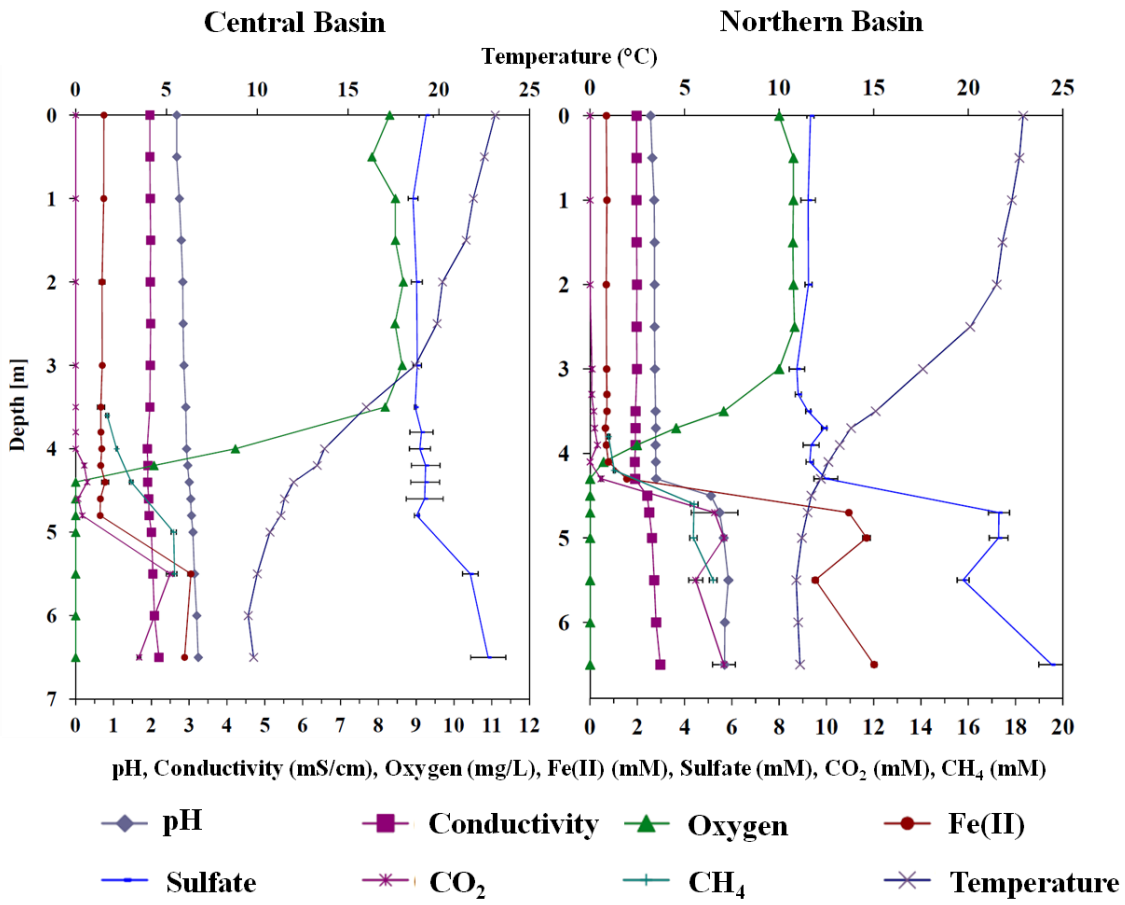

Fig. S1. Profiles of water geochemistry measured at the central basin and northern basin within the acidic lignite mine Lake 77 in May 2011. The central basin has a dimictic regime with an anoxic hypolimnion in summer and the northern basin has a continuous anoxic monimolimnion. A typical redoxcline was detected from water depth of 3.5 m to 4.8 m in central basin while the redoxcline started from around 3.6 m deep and extended to around 4.7 m in northern basin. The pH, conductivity, oxygen content and temperature were measured *in situ*, and the others were measured in water samples in laboratory.

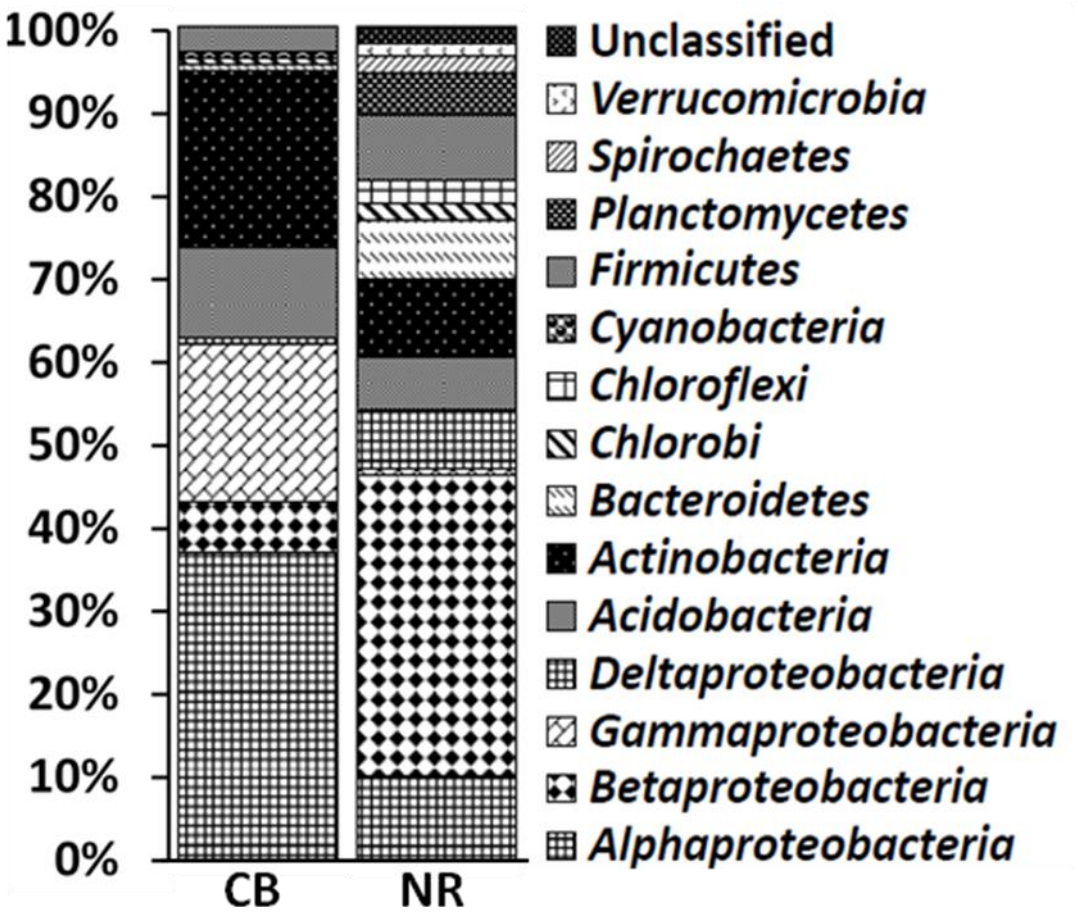

Fig. S2. Comparison of active bacteria phylogenetic lineages detected in cDNA-based 16S rRNA clone libraries derived from iron snow sampled from central basin bottom water column (CB) and northern basin redoxcline (NR). Calculations were based on the total number of clones associated with phylotypes of sequenced representatives at the phylum or class lever for *Proteobacteria*.

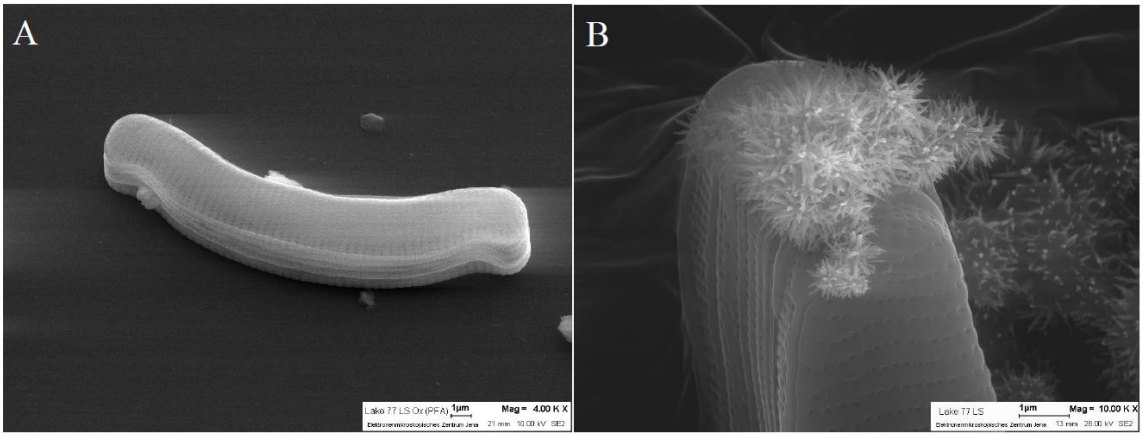

Fig. S3. SEM micrographs of one unicellular diatom from the acidic lignite mine Lake 77. It was ~ 22 µm in length (A, iron snow samples was washed previously using oxalate buffer), ~ 2 µm in width (B, non pre-treated sample) and morphologically close to *Eunotia* sp. It was found in close association with schwertmannite spheres and decorated by coral-like iron minerals on one terminal of the cell (B).

Table S1 Primers used for qPCR detecting Fe-cycling bacteria groups in iron snow samples.

Target	Primer	Sequence (5'-3')	Amplicon length (bp)	Annealing temperature (°C)	AFC[a] temperature (°C)	Reference	Standard clone (acc. no.)
Bacteria	Uni-338F-RC	ACT CCT ACG GGA GGC AGC	571	57	78	(10)	HE604015
	Uni-907R	CCG TCA ATT CMT TTG AGT TT				(10)	
Acidimicrobium	Amf995	CTC TGC GGC TTT TCC CTC CAT G	110	53	79	(6)	HE604007
	Uni-907R-RC	AAA CTC AAA KGA ATT GAC GG				(10)	
Ferrovum	Ferrovum643F	ACA GAC TCT AGC TTG CCA GT	323	61	78	(8)	HE604015
	Uni-338F-RC	ACT CCT ACG GGA GGC AGC				(10)	
Albidiferax[b]	RdoR-RC	GAC CTG CAT TTG TGA CTG YA	312	57	78	(16), modified	HE604080
	Uni-907R	CCG TCA ATT CMT TTG AGT TT				(10)	
Geobacter	Geo561F	GCG TGT AGG CGG TTT BTT AA	297	56	78	(13), modified	JN885810[d]
	Geo858R	TCA ATA CCC GCA ACA CCT AG				(Lu *et al.*, 2010)	
Acidiphilium	ACD840	CGA CAC TGA AGT GCT AAG C	505	61	78	(1)	HE604018
	Uni-338F-RC	ACT CCT ACG GGA GGC AGC				(10)	
ApcA[c]	AphmCytoc-254F	ACA AGT TCC TGG CCA ATC C	104	58	83	This study	YP_001235217
	AphmCytoc-358R	TCT GCA GAT AGG CGA CCA C				This study	

[a] AFC: Amplification fluorescence collection.

[b] Previously known as *Rhodoferax ferrireducens* (12).

[c] *Acidiphilium* JF-5 cytochrome *c* class I gene.

[d] Reference for clone (Fabish *et al.*, unpublished)

Table S2. Genome database used for metaproteomics analysis.

Taxon_oid	Genome Name	Domain	Family	Genus
644736321	Acetobacter pasteurianus IFO 3283-01	Bacteria	Acetobacteraceae	Acetobacter
640048202	Acetobacter pasteurianus plasmid pAP12875	Plasmid:Bacteria		
641507351	Acetobacter pasteurianus plasmid pGR7	Plasmid:Bacteria		
647000200	Achromobacter piechaudii ATCC 43553	Bacteria	Alcaligenaceae	Achromobacter
644736322	Acidimicrobium ferrooxidans DSM 10331	Bacteria	Acidimicrobiaceae	Acidimicrobium
640427101	Acidiphilium cryptum JF-5	Bacteria	Acetobacteraceae	Acidiphilium
641210204	Acidiphilium multivorum JCM8867 plasmid pAM5	Plasmid:Bacteria		
645058727	Acidithiobacillus caldus ATCC 51756	Bacteria	Acidithiobacillaceae	Acidithiobacillus
640048203	Acidithiobacillus caldus F plasmid pTC-F14	Plasmid:Bacteria		
642914101	Acidithiobacillus caldus MNG plasmid pTcM1	Plasmid:Bacteria		
643348501	Acidithiobacillus ferrooxidans ATCC 23270	Bacteria	Acidithiobacillaceae	Acidithiobacillus
642555101	Acidithiobacillus ferrooxidans ATCC 53993	Bacteria	Acidithiobacillaceae	Acidithiobacillus
640048205	Acidithiobacillus ferrooxidans ATCC33020 plasmid pTF5	Plasmid:Bacteria		
640048204	Acidithiobacillus ferrooxidans MAL4-1 plasmid pTF4.1	Plasmid:Bacteria		
643692001	Acidobacterium capsulatum ATCC 51196	Bacteria	Acidobacteriaceae	Acidobacterium
639633001	Acidothermus cellulolyticus 11B	Bacteria	Acidothermaceae	Acidothermus
639633002	Acidovorax avenae citrulli AAC00-1	Bacteria	Comamonadaceae	Acidovorax
647000201	Acidovorax avenae subsp. avenae ATCC 19860	Bacteria	Comamonadaceae	Acidovorax
645058786	Acidovorax delafieldii 2AN	Bacteria	Comamonadaceae	Acidovorax
643348541	Acidovorax ebreus TPSY	Bacteria	Comamonadaceae	Acidovorax
639633003	Acidovorax sp. JS42	Bacteria	Comamonadaceae	Acidovorax
638341246	Agreia sp. PHSC20C1	Bacteria	Microbacteriaceae	unclassified
644736325	Alicyclobacillus acidocaldarius acidocaldarius 104-IA, DSM 446	Bacteria	Alicyclobacillaceae	Alicyclobacillus

642979336	Alicyclobacillus acidocaldarius LAA1	Bacteria	Alicyclobacillaceae	Alicyclobacillus
641736205	Alistipes putredinis DSM 17216	Bacteria	Rikenellaceae	Alistipes
646311904	Ammonifex degensii KC4	Bacteria	Thermoanaerobacteraceae	Ammonifex
641736271	Anaerotruncus colihominis DSM 17241	Bacteria	Ruminococcaceae	Anaerotruncus
643348508	Anoxybacillus flavithermus WK1	Bacteria	Bacillaceae	Anoxybacillus
637000012	Aromatoleum aromaticum EbN1	Bacteria	Rhodocyclaceae	Aromatoleum
639633005	Arthrobacter aurescens TC1	Bacteria	Micrococcaceae	Arthrobacter
643348509	Arthrobacter chlorophenolicus A6	Bacteria	Micrococcaceae	Arthrobacter
639633006	Arthrobacter sp. FB24	Bacteria	Micrococcaceae	Arthrobacter
639633007	Azoarcus sp. BH72	Bacteria	Rhodocyclaceae	Azoarcus
646311907	Azospirillum sp. B510	Bacteria	Rhodospirillaceae	Azospirillum
640753005	Bacillus amyloliquefaciens FZB42	Bacteria	Bacillaceae	Bacillus
643692005	Bacillus anthracis A0248	Bacteria	Bacillaceae	Bacillus
643692007	Bacillus cereus 03BB102	Bacteria	Bacillaceae	Bacillus
637000019	Bacillus clausii KSM-K16	Bacteria	Bacillaceae	Bacillus
640753007	Bacillus pumilus SAFR-032	Bacteria	Bacillaceae	Bacillus
646311909	Bacillus subtilis subsp. subtilis str. 168	Bacteria	Bacillaceae	Bacillus
646564510	Bacillus thuringiensis BMB171	Bacteria	Bacillaceae	Bacillus
646564511	Bacillus tusciae DSM 2912	Bacteria	Alicyclobacillaceae	unclassified
641228477	Bacillus weihenstephanensis KBAB4	Bacteria	Bacillaceae	Bacillus
641522606	Beijerinckia indica indica ATCC 9039	Bacteria	Beijerinckiaceae	Beijerinckia
641228479	Bordetella petrii	Bacteria	Alcaligenaceae	Bordetella
641522608	Burkholderia ambifaria MC40-6	Bacteria	Burkholderiaceae	Burkholderia
637000051	Burkholderia sp. 383	Bacteria	Burkholderiaceae	Burkholderia
637000053	Burkholderia xenovorans LB400	Bacteria	Burkholderiaceae	Burkholderia
644736333	Candidatus Accumulibacter phosphatis	Bacteria	C. Accumulibacter	C. Accumulibacter phosphatis
637000060	Carboxydothermus hydrogenoformans Z-2901	Bacteria	Thermoanaerobacteraceae	Carboxydothermus
642555120	Chlorobaculum parvum NCIB 8327	Bacteria	Chlorobiaceae	Chlorobaculum
637000073	Chlorobaculum tepidum TLS	Bacteria	Chlorobiaceae	Chlorobaculum
637000072	Chlorobium chlorochromatii CaD3	Bacteria	Chlorobiaceae	Chlorobium

638341060	Chlorobium ferrooxidans DSM 13031	Bacteria	Chlorobiaceae	Chlorobium
642555121	Chlorobium limicola DSM 245	Bacteria	Chlorobiaceae	Chlorobium
637000205	Chlorobium luteolum DSM 273	Bacteria	Chlorobiaceae	Pelodictyon
642555122	Chlorobium phaeobacteroides BS1	Bacteria	Chlorobiaceae	Chlorobium
639633020	Chlorobium phaeobacteroides DSM 266	Bacteria	Chlorobiaceae	Chlorobium
640427130	Chlorobium phaeovibrioides DSM 265	Bacteria	Chlorobiaceae	Chlorobium
642555123	Chloroherpeton thalassium ATCC 35110	Bacteria	Chlorobiaceae	Chloroherpeton
637000075	Chromohalobacter salexigens DSM 3043	Bacteria	Halomonadaceae	Chromohalobacter
646564522	Comamonas sp. CNB-1	Bacteria	Comamonadaceae	Comamonas
646311916	Comamonas testosteroni CNB-2	Bacteria	Comamonadaceae	Comamonas
637000230	Cupriavidus metallidurans CH34	Bacteria	Burkholderiaceae	Cupriavidus
637000088	Dechloromonas aromatica RCB	Bacteria	Rhodocyclaceae	Dechloromonas
641228489	Delftia acidovorans SPH-1	Bacteria	Comamonadaceae	Delftia
643348536	Desulfatibacillum alkenivorans AK-01	Bacteria	Desulfobacteraceae	Desulfatibacillum
643692021	Desulfobacterium autotrophicum HRM2, DSM 3382	Bacteria	Desulfobacteraceae	Desulfobacterium
641228490	Desulfococcus oleovorans Hxd3	Bacteria	Desulfobacteraceae	Desulfococcus
637000094	Desulfotalea psychrophila LSv54	Bacteria	Desulfobulbaceae	Desulfotalea
647000235	Desulfovibrio aespoeensis Aspo-2	Bacteria	Desulfovibrionaceae	Desulfovibrio
643348538	Desulfovibrio desulfuricans desulfuricans ATCC 27774	Bacteria	Desulfovibrionaceae	Desulfovibrio
637000095	Desulfovibrio desulfuricans G20	Bacteria	Desulfovibrionaceae	Desulfovibrio
644736352	Desulfovibrio magneticus RS-1	Bacteria	Desulfovibrionaceae	Desulfovibrio
642979316	Desulfovibrio piger ATCC 29098	Bacteria	Desulfovibrionaceae	Desulfovibrio
644736353	Desulfovibrio salexigens DSM 2638	Bacteria	Desulfovibrionaceae	Desulfovibrio
647000236	Desulfovibrio sp. FW1012B	Bacteria	Desulfovibrionaceae	Desulfovibrio
643348539	Desulfovibrio vulgaris Miyazaki F	Bacteria	Desulfovibrionaceae	Desulfovibrio
645058777	Desulfovibrio vulgaris RCH1	Bacteria	Desulfovibrionaceae	Desulfovibrio
639633022	Desulfovibrio vulgaris vulgaris DP4	Bacteria	Desulfovibrionaceae	Desulfovibrio
637000096	Desulfovibrio vulgaris vulgaris Hildenborough	Bacteria	Desulfovibrionaceae	Desulfovibrio
646564528	Desulfurivibrio alkaliphilus AHT2	Bacteria	Desulfobulbaceae	Desulfurivibrio

638341078	Desulfuromonas acetoxidans DSM 684	Bacteria	Desulfuromonadaceae	Desulfuromonas
644736368	Flavobacteriaceae bacterium 3519-10	Bacteria	unclassified	
645058854	Gallionella ferruginea ES-2	Bacteria	Gallionellaceae	Gallionella
642555129	Geobacter bemidjiensis Bem	Bacteria	Geobacteraceae	Geobacter
642555130	Geobacter lovleyi SZ	Bacteria	Geobacteraceae	Geobacter
637000119	Geobacter metallireducens GS-15	Bacteria	Geobacteraceae	Geobacter
643348554	Geobacter sp. FRC-32	Bacteria	Geobacteraceae	Geobacter
645058752	Geobacter sp. M18	Bacteria	Geobacteraceae	Geobacter
644736371	Geobacter sp. M21	Bacteria	Geobacteraceae	Geobacter
637000120	Geobacter sulfurreducens PCA	Bacteria	Geobacteraceae	Geobacter
640427115	Geobacter uraniumreducens Rf4	Bacteria	Geobacteraceae	Geobacter
642555132	Hydrogenobaculum sp. Y04AAS1	Bacteria	Aquificaceae	Hydrogenobaculum
641210332	Leptospirillum ferrooxidans ATCC 49879 plasmid p49879.1	Plasmid:Bacteria		
641210333	Leptospirillum ferrooxidans ATCC 49879 plasmid p49879.2	Plasmid:Bacteria		
641522635	Leptothrix cholodnii SP-6	Bacteria	unclassified	Genera incertae sedis
640963026	Limnobacter sp. MED105	Bacteria	Burkholderiaceae	Limnobacter
637000155	Magnetospirillum magneticum AMB-1	Bacteria	Rhodospirillaceae	Magnetospirillum
642555138	Methylacidiphilum infernorum V4	Bacteria	Methylacidiphilaceae	Methylacidiphilum
640069319	Methylibium petroleiphilum PM1	Bacteria	unclassified	Genera incertae sedis
643348565	Methylocella silvestris BL2	Bacteria	Beijerinckiaceae	Methylocella
644736390	Micrococcus luteus NCTC 2665	Bacteria	Micrococcaceae	Micrococcus
637000167	Moorella thermoacetica ATCC 39073	Bacteria	Thermoanaerobacteraceae	Moorella
637000204	Pelobacter carbinolicus DSM 2380	Bacteria	Pelobacteraceae	Pelobacter
639633050	Pelobacter propionicus DSM 2379	Bacteria	Pelobacteraceae	Pelobacter
642555146	Pelodictyon phaeoclathratiforme BU-1	Bacteria	Chlorobiaceae	Pelodictyon
642555149	Prosthecochloris aestuarii SK413, DSM 271	Bacteria	Chlorobiaceae	Prosthecochloris
640427136	Ralstonia eutropha H16	Bacteria	Burkholderiaceae	Cupriavidus
637000235	Rhodoferax ferrireducens T118	Bacteria	Comamonadaceae	Albidiferax
643348571	Rhodospirillum centenum SW	Bacteria	Rhodospirillaceae	Rhodospirillum

637000241	Rhodospirillum rubrum ATCC 11170	Bacteria	Rhodospirillaceae	Rhodospirillum
640069329	Saccharopolyspora erythraea NRRL 2338	Bacteria	Pseudonocardiaceae	Saccharopolyspora
646564569	Sideroxydans lithotrophicus ES-1	Bacteria	Gallionellaceae	Sideroxydans
639633060	Solibacter usitatus Ellin6076	Bacteria	Solibacteraceae	Candidatus Solibacter
643692050	Sulfurihydrogenibium azorense Az-Fu1	Bacteria	Hydrogenothermaceae	Sulfurihydrogenibium
642555165	Sulfurihydrogenibium sp. YO3AOP1	Bacteria	Hydrogenothermaceae	Sulfurihydrogenibium
639633063	Syntrophobacter fumaroxidans MPOB	Bacteria	Syntrophobacteraceae	Syntrophobacter
637000317	Syntrophus aciditrophicus SB	Bacteria	Syntrophaceae	Syntrophus
643348581	Thermodesulfovibrio yellowstonii DSM 11347	Bacteria	Nitrospiraceae	Thermodesulfovibrio
637000324	Thiobacillus denitrificans ATCC 25259	Bacteria	Hydrogenophilaceae	Thiobacillus
646564585	Thiomonas intermedia K12	Bacteria	unclassified	Genera incertae sedis
644736413	Variovorax paradoxus S110	Bacteria	Comamonadaceae	Variovorax
638154502	Archaeoglobus fulgidus DSM 4304	Archaea		
646311906	Archaeoglobus profundus DSM 5631	Archaea		
646564534	Ferroglobus placidus DSM 10642	Archaea		
638341092	Ferroplasma acidarmanus Fer1	Archaea		
641522631	Halobacterium salinarum R1	Archaea		
638154504	Halobacterium sp. NRC-1	Archaea		
646564536	Haloferax volcanii DS2	Archaea		
644736372	Halomicrobium mukohataei DSM 12286	Archaea		
637000129	Haloquadratum walsbyi DSM 16790	Archaea		
644736373	Halorhabdus utahensis DSM 12940	Archaea		
643692025	Halorubrum lacusprofundi ATCC 49239	Archaea		
646311934	Haloterrigena turkmenica DSM 5511	Archaea		
640427120	Metallosphaera sedula DSM 5348	Archaea		
637000161	Methanococcoides burtonii DSM 6242	Archaea		
640753034	Methanococcus aeolicus Nankai-3	Archaea		
640069316	Methanococcus maripaludis C5	Archaea		
646564549	Methanococcus voltae A3	Archaea		
646564550	Methanohalophilus mahii DSM 5219	Archaea		

638154507	Methanopyrus kandleri AV19	Archaea		
638154508	Methanosarcina acetivorans C2A	Archaea		
637000162	Methanosarcina barkeri fusaro	Archaea		
638154509	Methanosarcina mazei Go1	Archaea		
637000163	Methanosphaera stadtmanae DSM 3091	Archaea		
638154510	Methanothermobacter thermautotrophicus Delta H	Archaea		
638154512	Picrophilus torridus DSM 9790	Archaea		
638154517	Sulfolobus acidocaldarius DSM 639	Archaea		
640048573	Sulfolobus islandicus HEN7H2 plasmid pHEN7	Plasmid:Archaea		
646311959	Sulfolobus islandicus L.D.8.5	Archaea		
643692044	Sulfolobus islandicus L.S.2.15	Archaea		
643692045	Sulfolobus islandicus M.14.25	Archaea		
643692046	Sulfolobus islandicus M.16.27	Archaea		
643692047	Sulfolobus islandicus M.16.4	Archaea		
640048574	Sulfolobus islandicus P1 plasmid pING1	Plasmid:Archaea		
641210467	Sulfolobus islandicus plasmid pARN3	Plasmid:Archaea		
641210468	Sulfolobus islandicus plasmid pARN4	Plasmid:Archaea		
641210469	Sulfolobus islandicus plasmid pHVE14	Plasmid:Archaea		
641210470	Sulfolobus islandicus plasmid pKEF9	Plasmid:Archaea		
642914220	Sulfolobus islandicus plasmid pSOG1	Plasmid:Archaea		
642914221	Sulfolobus islandicus plasmid pSOG2	Plasmid:Archaea		
642481274	Sulfolobus islandicus plasmid pXZ1	Plasmid:Archaea		
640048575	Sulfolobus islandicus REN1H1 plasmid pRN1	Plasmid:Archaea		
640048576	Sulfolobus islandicus REN1H1 plasmid pRN2	Plasmid:Archaea		
641507387	Sulfolobus islandicus Rey 15/4 plasmid pSSVx	Plasmid:Archaea		
643692048	Sulfolobus islandicus Y.G.57.14	Archaea		
643692049	Sulfolobus islandicus Y.N.15.51	Archaea		
646862347	Sulfolobus solfataricus 98/2	Archaea		
641210472	Sulfolobus solfataricus IT3 plasmid pIT3	Plasmid:Archaea		

638154518	Sulfolobus solfataricus P2	Archaea		
638154519	Sulfolobus tokodaii 7	Archaea		
638154520	Thermococcus kodakaraensis KOD1	Archaea		
638154521	Thermoplasma acidophilum DSM 1728	Archaea		
641210476	Thermoplasma acidophilum H0-122 plasmid pTA1	Plasmid:Archaea		

Table S3. Energy-dispersive X-ray spectroscopy analysis of iron snow in the Lake 77 obtained from sediment traps at central basin: central redoxcline (CR) and central bottom (CB); and northern basin: northern redoxcline (NR) and northern bottom (NB) on July 2010.

Elements	CB (Mass %)	CR (Mass %)	NR (Mass %)	NB (Mass %)	Schwertmannite ideal formula
Fe	63.4 ±1.8	59.7 ±1.6	53.8 ±1.4	61.3 ±1.7	58
O	31.6 ±3.4	34.9 ±3.6	41.9 ±4.3	34.7 ±3.6	37
S	5.1 ±0.2	5.4 ±0.2	4.2 ±0.2	4.0 ±0.2	4

Table S4. Statistical analysis of cDNA-based 16S rRNA gene clone libraries using ecological and molecular estimates of phylotype diversity.

Sample[a]	No. of clones	No. of phylotypes	Coverage (%)	ACE[b]	Chao1 ± SD	Diversity index	
						Shannon	Simpson's (1/D)
CB	131	43	88.6	85.9	95.1 ±30.6	3.17	16.86
NR	142	66	77.2	138.8	146.7 ±34.9	3.59	17.23

[a] CB and NR stand for the iron snow bacterial cDNA-based 16S rRNA gene clone libraries obtained from the central basin bottom or the northern basin redoxcline of Lake 77.

[b] ACE stands for abundance-based coverage estimator.

Table S5. cDNA 16S rRNA gene clone sequence information. CB strands for central basin bottom.

Sequence_id	Accession No.	NO. of clones	Phylum	Class	Family
CB-cDNA_clone1	HE604007	17	Actinobacteria	Actinobacteria	Acidimicrobiaceae
CB-cDNA_clone100	HE603991	1	Chlorobi	Chlorobia	Chlorobiaceae
CB-cDNA_clone112	HE603992	1	Acidobacteria	Acidobacteria_Gp1	unclassified
CB-cDNA_clone114	HE603993	2	Proteobacteria	Betaproteobacteria	Hydrogenophilaceae
CB-cDNA_clone121	HE603994	3	Proteobacteria	Alphaproteobacteria	Acetobacteraceae
CB-cDNA_clone128	HE603995	1	Actinobacteria	Actinobacteria	Acidimicrobiaceae
CB-cDNA_clone136	HE603996	1	Acidobacteria	Acidobacteria_Gp1	unclassified
CB-cDNA_clone138	HE603997	1	Proteobacteria	Alphaproteobacteria	Acetobacteraceae
CB-cDNA_clone15	HE604000	3	Actinobacteria	Actinobacteria	Acidimicrobiaceae
CB-cDNA_clone155	HE603998	2	Proteobacteria	Gammaproteobacteria	Pseudomonadaceae
CB-cDNA_clone159	HE603999	1	Proteobacteria	Gammaproteobacteria	Acidithiobacillaceae
CB-cDNA_clone16	HE604003	1	Proteobacteria	Gammaproteobacteria	Sinobacteraceae
CB-cDNA_clone162	HE604001	1	Actinobacteria	Actinobacteria	unclassified
CB-cDNA_clone164	HE604002	1	Proteobacteria	Gammaproteobacteria	Sinobacteraceae
CB-cDNA_clone172	HE604004	1	Proteobacteria	Alphaproteobacteria	Acetobacteraceae
CB-cDNA_clone179	HE604005	1	Proteobacteria	Alphaproteobacteria	Acetobacteraceae
CB-cDNA_clone18	HE604006	1	Proteobacteria	Gammaproteobacteria	Moraxellaceae
CB-cDNA_clone2	HE604011	17	Proteobacteria	Alphaproteobacteria	Acetobacteraceae
CB-cDNA_clone24	HE604008	2	Acidobacteria	Acidobacteria_Gp1	unclassified
CB-cDNA_clone25	HE604009	13	Proteobacteria	Gammaproteobacteria	Sinobacteraceae
CB-cDNA_clone29	HE604010	1	Proteobacteria	Alphaproteobacteria	Acetobacteraceae
CB-cDNA_clone39	HE604012	1	Proteobacteria	Betaproteobacteria	Hydrogenophilaceae
CB-cDNA_clone4	HE604013	4	Proteobacteria	Gammaproteobacteria	Pseudomonadaceae
CB-cDNA_clone5	HE604017	1	Proteobacteria	Gammaproteobacteria	Sinobacteraceae
CB-cDNA_clone52	HE604014	2	Firmicutes	Bacilli	Bacillaceae
CB-cDNA_clone54	HE604015	1	Proteobacteria	Betaproteobacteria	Rhodocyclaceae
CB-cDNA_clone56	HE604016	4	Actinobacteria	Actinobacteria	Iamiaceae

CB-cDNA_clone61	HE604018	1	Proteobacteria	Alphaproteobacteria	Acetobacteraceae
CB-cDNA_clone63	HE604019	1	Proteobacteria	Gammaproteobacteria	Pseudomonadaceae
CB-cDNA_clone67	HE604020	1	Proteobacteria	Alphaproteobacteria	Acetobacteraceae
CB-cDNA_clone7	HE604025	7	Acidobacteria	Acidobacteria_Gp1	unclassified
CB-cDNA_clone70	HE604021	1	Proteobacteria	Deltaproteobacteria	Geobacteraceae
CB-cDNA_clone75	HE604022	4	Proteobacteria	Betaproteobacteria	Nitrosomonadaceae
CB-cDNA_clone77	HE604023	2	Proteobacteria	Alphaproteobacteria	Acetobacteraceae
CB-cDNA_clone78	HE604024	1	Proteobacteria	Alphaproteobacteria	Acetobacteraceae
CB-cDNA_clone8	HE604030	5	Proteobacteria	Alphaproteobacteria	Acetobacteraceae
CB-cDNA_clone81	HE604026	1	Bacteroidetes	Bacteroidia	Porphyromonadaceae
CB-cDNA_clone83	HE604027	1	Actinobacteria	Actinobacteria	Acidimicrobiaceae
CB-cDNA_clone85	HE604028	1	Actinobacteria	Actinobacteria	Micrococcaceae
CB-cDNA_clone89	HE604029	2	Firmicutes	Clostridia	Thermoanaerobacteraceae
CB-cDNA_clone9	HE604033	14	Proteobacteria	Alphaproteobacteria	Acetobacteraceae
CB-cDNA_clone94	HE604031	1	Cyanobacteria	Cyanobacteria	Cryptomonadaceae
CB-cDNA_clone95	HE604032	3	Acidobacteria	Acidobacteria_Gp1	unclassified

Table S6. cDNA 16S rRNA gene clone sequence information. NR stands for northern basin redoxcline.

Sequence_id	Accession No.	NO. of clones	Phylum	Class	Family
NR-cDNA_clone110	HE604034	1	Proteobacteria	Betaproteobacteria	Comamonadaceae
NR-cDNA_clone104	HE604035	1	Acidobacteria	Acidobacteria_Gp3	unclassified
NR-cDNA_clone107	HE604036	1	Bacteroidetes	Bacteroidia	Bacteroidaceae
NR-cDNA_clone109	HE604037	1	Proteobacteria	Betaproteobacteria	Comamonadaceae
NR-cDNA_clone112	HE604038	1	Actinobacteria	Actinobacteria	Cellulomonadaceae
NR-cDNA_clone113	HE604039	1	Spirochaetes	Spirochaetes	Spirochaetaceae
NR-cDNA_clone116	HE604040	1	Planctomycetes	Planctomycetacia	Planctomycetaceae
NR-cDNA_clone118	HE604041	1	Proteobacteria	Alphaproteobacteria	Rhodospirillaceae
NR-cDNA_clone120	HE604042	1	Unclassified		
NR-cDNA_clone121	HE604043	2	Proteobacteria	Deltaproteobacteria	Geobacteraceae
NR-cDNA_clone125	HE604044	1	Proteobacteria	Betaproteobacteria	Comamonadaceae
NR-cDNA_clone126	HE604045	1	Chlorobi	Chlorobia	Chlorobiaceae
NR-cDNA_clone129	HE604046	3	Bacteroidetes	unclassified	unclassified
NR-cDNA_clone130	HE604047	1	Proteobacteria	Alphaproteobacteria	Acetobacteraceae
NR-cDNA_clone131	HE604048	1	Acidobacteria	Acidobacteria_Gp3	unclassified
NR-cDNA_clone134	HE604049	1	Actinobacteria	Actinobacteria	Cellulomonadaceae
NR-cDNA_clone135	HE604050	1	Planctomycetes	Planctomycetacia	Planctomycetaceae
NR-cDNA_clone137	HE604051	1	Firmicutes	Clostridia	Ruminococcaceae
NR-cDNA_clone140	HE604052	1	Actinobacteria	Actinobacteria	Rubrobacteraceae
NR-cDNA_clone143	HE604053	2	Proteobacteria	Deltaproteobacteria	Geobacteraceae
NR-cDNA_clone152	HE604054	3	Proteobacteria	Alphaproteobacteria	Acetobacteraceae
NR-cDNA_clone154	HE604055	2	Planctomycetes	Planctomycetacia	Planctomycetaceae
NR-cDNA_clone155	HE604056	1	Actinobacteria	Actinobacteria	Conexibacteraceae
NR-cDNA_clone163	HE604057	2	unclassified	unclassified	unclassified
NR-cDNA_clone164	HE604058	1	Proteobacteria	Betaproteobacteria	Comamonadaceae
NR-cDNA_clone168	HE604059	1	Bacteroidetes	Bacteroidia	Marinilabiaceae

NR-cDNA_clone16	HE604060	1	Firmicutes	Clostridia	Veillonellaceae
NR-cDNA_clone171	HE604061	1	Proteobacteria	Betaproteobacteria	Comamonadaceae
NR-cDNA_clone172	HE604062	1	Proteobacteria	Deltaproteobacteria	Desulfuromonadaceae
NR-cDNA_clone177	HE604063	3	Chloroflexi	Anaerolineae	Anaerolineaceae
NR-cDNA_clone178	HE604064	1	Spirochaetes	Spirochaetes	Spirochaetaceae
NR-cDNA_clone183	HE604065	2	Chlorobi	Chlorobia	Chlorobiaceae
NR-cDNA_clone185	HE604066	1	Bacteroidetes	Bacteroidia	Marinilabiaceae
NR-cDNA_clone186	HE604067	1	Proteobacteria	Alphaproteobacteria	Caulobacteraceae
NR-cDNA_clone188	HE604068	1	Bacteroidetes	incertae sedis	unclassified
NR-cDNA_clone195	HE604069	1	Bacteroidetes	Bacteroidia	Porphyromonadaceae
NR-cDNA_clone197	HE604070	1	Proteobacteria	Deltaproteobacteria	Desulfuromonadaceae
NR-cDNA_clone198	HE604071	1	Proteobacteria	Betaproteobacteria	Comamonadaceae
NR-cDNA_clone199	HE604072	1	Proteobacteria	Betaproteobacteria	Burkholderiales incertae sedis
NR-cDNA_clone205	HE604073	1	Chloroflexi	Anaerolineae	Anaerolineaceae
NR-cDNA_clone206	HE604074	1	Verrucomicrobia	Verrucomicrobiae	Rubritaleaceae
NR-cDNA_clone213	HE604075	1	Firmicutes	Clostridia	Veillonellaceae
NR-cDNA_clone215	HE604076	1	Proteobacteria	Betaproteobacteria	Burkholderiales incertae sedis
NR-cDNA_clone229	HE604077	1	Verrucomicrobia	Opitutae	Opitutaceae
NR-cDNA_clone233	HE604078	1	Proteobacteria	Betaproteobacteria	Rhodocyclaceae
NR-cDNA_clone237	HE604079	2	Bacteroidetes	unclassified	unclassified
NR-cDNA_clone27	HE604080	31	Proteobacteria	Betaproteobacteria	Comamonadaceae
NR-cDNA_clone2	HE604081	2	Planctomycetes	Planctomycetacia	Planctomycetaceae
NR-cDNA_clone30	HE604082	1	Spirochaetes	Spirochaetes	Spirochaetaceae
NR-cDNA_clone34	HE604083	1	Proteobacteria	Gammaproteobacteria	unclassified
NR-cDNA_clone36	HE604084	3	Firmicutes	Clostridia	Thermoanaerobacteraceae
NR-cDNA_clone37	HE604085	2	Proteobacteria	Deltaproteobacteria	Cystobacteraceae
NR-cDNA_clone3	HE604086	4	Proteobacteria	Alphaproteobacteria	Acetobacteraceae
NR-cDNA_clone47	HE604087	5	Actinobacteria	Actinobacteria	Streptomycetaceae
NR-cDNA_clone50	HE604088	2	Actinobacteria	Actinobacteria	Acidimicrobiaceae
NR-cDNA_clone54	HE604089	2	Proteobacteria	Deltaproteobacteria	Cystobacteraceae
NR-cDNA_clone59	HE604090	7	Acidobacteria	Acidobacteria_Gp3	unclassified

NR-cDNA_clone60	HE604091	1	Actinobacteria	Actinobacteria	unclassified
NR-cDNA_clone61	HE604092	1	Proteobacteria	Betaproteobacteria	Comamonadaceae
NR-cDNA_clone62	HE604093	2	Proteobacteria	Alphaproteobacteria	Acetobacteraceae
NR-cDNA_clone63	HE604094	5	Firmicutes	Clostridia	Veillonellaceae
NR-cDNA_clone8	HE604095	2	Proteobacteria	Alphaproteobacteria	Acetobacteraceae
NR-cDNA_clone90	HE604096	1	Planctomycetes	Planctomycetacia	Planctomycetaceae
NR-cDNA_clone98	HE604097	1	Actinobacteria	Actinobacteria	Conexibacteraceae
NR-cDNA_clone99	HE604098	10	Proteobacteria	Betaproteobacteria	Comamonadaceae

Table S7. Protein hits in northern basin using metaproteomics. The protein length and pI refer to the number of amino acids and isoelectric point of protein, respectively. The BH correction stands for Benjamini-Hochberg correction to obtain the q value.

Microbial strain	Protein description	Protein accession no.	Gene ID	Protein Length	Mol Wt (Da)	pI	Spectral Counts				p value	BH Correction (q value)
							NB1	NB2	NR1	NR2		
Acetobacter pasteurianus IFO 3283-01	heat shock protein GroES	YP_003188291	APA01_17860	123	13427	9.1	2				1.95E-02	3.45E-01
Acetobacter pasteurianus IFO 3283-01	heat shock protein GroEL	YP_003188292	APA01_17870	546	58135	5.7	5	3	2	4	9.39E-01	2.77E+00
Acidimicrobium ferrooxidans DSM 10331	microcompartments protein	YP_003108768	Afer_0126	107	10727	5.4			3	2	2.10E-03	2.74E-03
Acidimicrobium ferrooxidans DSM 10331	microcompartments protein	YP_003108766	Afer_0124	103	10328	5.1			3	2	2.88E-03	3.70E-03
Acidimicrobium ferrooxidans DSM 10331	microcompartments protein	YP_003108767	Afer_0125	103	10314	5.1			3	2	8.22E-03	1.07E-02
Acidiphilium cryptum JF-5	translation elongation factor Tu	YP_001235068	Acry_1948	395	42629	5.5				3	4.39E-07	8.94E-07
Acidiphilium cryptum JF-5	OmpA/MotB domain protein	YP_001233320	Acry_0173	364	38926	8.8				2	2.87E-06	4.89E-06
Acidiphilium cryptum JF-5	OmpA/MotB domain protein	YP_001233321	Acry_0174	361	38288	9.4				2	7.04E-06	1.21E-05
Acidiphilium cryptum JF-5	putative cold-shock DNA-binding domain protein	YP_001235951	Acry_2842	68	7488	8.6			8	3	9.36E-05	1.56E-04
Acidiphilium cryptum JF-5	protein of unknown function DUF796	YP_001236175	Acry_3068	161	17093	4.8				2	1.43E-04	2.46E-04
Acidiphilium cryptum JF-5	ribosomal protein L1	YP_001235075	Acry_1955	230	23961	9.6	2				2.47E-05	6.99E-04
Acidiphilium cryptum JF-5	Monosaccharide-transporting ATPase	YP_001235093	Acry_1973	369	38701	8.9	2	3	5	4	7.52E-05	1.94E-03
Acidiphilium cryptum JF-5	malate dehydrogenase	YP_001236171	Acry_3063	327	34474	6.2	2	3	6	6	1.01E-04	2.19E-03
Acidiphilium cryptum JF-5	Glycine hydroxymethyltransferase	YP_001235241	Acry_2123	432	45773	6.9			4		3.19E-03	4.47E-03
Acidiphilium cryptum JF-5	periplasmic binding protein/LacI transcriptional regulator	YP_001234974	Acry_1853	339	35251	9.7			5	7	4.56E-03	6.69E-03
Acidiphilium cryptum JF-5	cytochrome c, class I	YP_001235217	Acry_2099	123	12427	9.2			3	2	7.90E-03	9.89E-03
Acidiphilium cryptum JF-5	chaperonin GroEL	YP_001235613	Acry_2503	549	58230	5.5	19	9	15	15	8.14E-03	1.05E-02
Acidiphilium cryptum JF-5	OmpA/MotB domain protein	YP_001233507	Acry_0363	167	17206	8.6	14	13	26	17	1.02E-02	1.58E-02
Acidiphilium cryptum JF-5	phasin family protein	YP_001235948	Acry_2839	177	18665	8.3			5	2	1.45E-02	2.14E-02
Acidiphilium cryptum JF-5	histone family protein DNA-binding protein	YP_001234058	Acry_0920	87	9308	8.5				13	1.84E-02	4.33E-02
Acidiphilium cryptum JF-5	phasin family protein	YP_001233302	Acry_0155	157	17485	6.8	2				2.36E-03	9.54E-02
Acidiphilium cryptum JF-5	chaperonin Cpn10	YP_001235614	Acry_2504	104	11141	7.3	2				7.52E-03	1.77E-01
Acidiphilium cryptum JF-5	ribosomal protein L18	YP_001235050	Acry_1930	120	12976	10.5	2				8.08E-03	2.86E-01
Acidiphilium cryptum JF-5	flagellin domain protein	YP_001233255	Acry_0108	294	30157	8.3		3	3	5	4.19E-01	4.62E-01

Acidiphilium cryptum JF-5	ribosomal protein L10	YP_001235074	Acry_1954	174	18358	9.4		3			4.68E-01	5.10E-01
Acidiphilium cryptum JF-5	putative cold-shock DNA-binding domain protein	YP_001233151	Acry_0003	67	7155	9.6	6	2	3	2	7.90E-01	2.30E+00
Acidiphilium cryptum JF-5	ABC-type branched-chain amino acid transport systems periplasmic component-like protein	YP_001236039	Acry_2930	411	44456	8.6	3				9.63E-01	4.54E+00
Acidiphilium cryptum JF-5	ATP synthase F1, beta subunit	YP_001234805	Acry_1681	476	51197	5.0	2		5	5	6.17E-01	1.94E+01
Acidithiobacillus caldus ATCC 51756	carboxysome shell protein CsoS1	ZP_05293099	ACA_2773	102	10375	5.8			3	2	6.54E-03	8.15E-03
Acidithiobacillus caldus ATCC 51756	carboxysome shell protein CsoS1	ZP_05293098	ACA_2772	98	9949	5.9			3	2	1.64E-01	2.04E-01
Acidithiobacillus caldus ATCC 51756	carboxysome shell protein CsoS1	ZP_05293097	ACA_2771	98	9935	5.9			3	2	2.32E-01	2.84E-01
Acidithiobacillus caldus ATCC 51756	Heat shock protein 60 family chaperone GroEL	ZP_05291681	ACA_2307	549	58312	5.5	3				9.43E-01	4.52E+00
Acidithiobacillus ferrooxidans ATCC 23270	carboxysome shell peptide	YP_002426106	AFE_1684	100	10197	5.9			3	2	2.25E-06	2.84E-06
Acidithiobacillus ferrooxidans ATCC 23270	chaperonin, 60 kDa	YP_002425034	AFE_0542	551	58631	5.3			2		2.02E-05	2.06E-05
Acidithiobacillus ferrooxidans ATCC 23270	carboxysome shell peptide	YP_002426105	AFE_1683	112	11364	5.4			3	2	3.94E-03	4.96E-03
Acidithiobacillus ferrooxidans ATCC 53993	chaperonin GroEL	YP_002219156	Lferr_0698	551	58631	5.3			2		2.38E-05	2.43E-05
Acidithiobacillus ferrooxidans ATCC 53993	microcompartments protein	YP_002219821	Lferr_1381	112	11295	5.1			3	2	4.23E-05	5.36E-05
Acidithiobacillus ferrooxidans ATCC 53993	microcompartments protein	YP_002219822	Lferr_1382	98	9937	5.3			3	2	6.61E-03	8.46E-03
Acidovorax avenae citrulli AAC00-1	methyl-accepting chemotaxis sensory transducer	YP_972617	Aave_4303	528	54975	5.4				2	7.62E-06	1.28E-05
Acidovorax avenae citrulli AAC00-1	porin, Gram-negative type	YP_972658	Aave_4344	340	36479	9.0			2	3	5.85E-03	5.87E-03
Acidovorax avenae citrulli AAC00-1	DNA-directed RNA polymerase, beta' subunit	YP_972841	Aave_4530	1411	154757	7.0			2		7.12E-03	7.17E-03
Acidovorax avenae citrulli AAC00-1	porin, Gram-negative type	YP_972657	Aave_4343	329	35306	9.1			2	3	4.17E-01	4.17E-01
Acidovorax avenae citrulli AAC00-1	ubiquitin	YP_973019	Aave_4710	287	30111	5.9	4	2	5	4	8.35E-01	2.60E+00
Acidovorax avenae citrulli AAC00-1	chaperonin GroEL	YP_969317	Aave_0945	545	57008	5.2	3				7.96E-01	4.02E+00
Acidovorax avenae citrulli AAC00-1	OmpA/MotB domain protein	YP_971613	Aave_3279	219	22926	9.3	3				8.32E-01	4.13E+00
Acidovorax avenae citrulli AAC00-1	flagellin domain protein	YP_972715	Aave_4401	492	49324	5.9	2				7.56E-02	7.13E+00
Acidovorax avenae citrulli AAC00-1	flagellin domain protein	YP_972714	Aave_4400	492	49423	5.9	2				1.82E-01	2.57E+01
Acidovorax avenae subsp. avenae ATCC 19860	flagellin domain protein	ZP_06211442	AcavDRAFT_3188	492	49358	5.6	2				6.89E-06	3.90E-04
Acidovorax avenae subsp. avenae ATCC 19860	porin Gram-negative type	ZP_06212028	AcavDRAFT_3774	336	35964	9.1			2	3	3.57E-03	3.61E-03
Acidovorax avenae subsp. avenae ATCC 19860	flagellin domain protein	ZP_06211443	AcavDRAFT_3189	492	49292	5.9	2				5.75E-03	2.71E-01

Acidovorax avenae subsp. avenae ATCC 19860	chaperonin GroEL	ZP_06209478	AcavDRAFT_1224	545	57033	5.3	2				3.33E-02	2.36E+00
Acidovorax avenae subsp. avenae ATCC 19860	OmpA/MotB domain protein	ZP_06210205	AcavDRAFT_1951	219	22900	9.3	3				8.90E-01	4.34E+00
Acidovorax delafieldii 2AN	porin Gram-negative type	ZP_04762009	AcdelDRAFT_1240	347	35636	9.2			2	3	1.08E-05	1.09E-05
Acidovorax delafieldii 2AN	flagellin domain protein	ZP_04761711	AcdelDRAFT_0942	521	51748	5.4	2				1.27E-06	2.56E-05
Acidovorax delafieldii 2AN	OmpA/MotB domain protein	ZP_04762534	AcdelDRAFT_1765	212	22228	9.2	2				6.22E-03	1.17E-01
Acidovorax delafieldii 2AN	flagellin domain protein	ZP_04761710	AcdelDRAFT_0941	522	51977	6.0	3			4	9.62E-01	4.39E+00
Acidovorax sp. JS42	DNA-directed RNA polymerase, beta' subunit	YP_988079	Ajs_3896	1409	154585	7.0			2		2.48E-05	2.55E-05
Acidovorax sp. JS42	flagellin domain protein	YP_987997	Ajs_3814	278	29109	5.5				2	1.17E-03	2.04E-03
Acidovorax sp. JS42	chaperonin GroEL	YP_985019	Ajs_0699	546	57197	5.2	8	2	3	6	6.86E-01	1.67E+00
Acidovorax sp. JS42	OmpA/MotB domain protein	YP_986700	Ajs_2463	218	22763	9.3	3				9.73E-01	4.51E+00
Arthrobacter aurescens TC1	aldehyde dehydrogenase (NAD) family protein	YP_947158	AAur_1380	507	55034	5.4	2				5.00E-01	1.41E+02
Arthrobacter chlorophenolicus A6	extracellular solute-binding protein family 1	YP_002486822	Achl_0736	352	37322	5.2				2	1.13E-06	1.91E-06
Azoarcus sp. BH72	conserved hypothetical membrane protein	YP_931922	azo0418	280	31103	9.0	11	5	29	13	1.96E-02	3.52E-02
Azoarcus sp. BH72	chaperonin GroEL	YP_932478	azo0974	549	57885	5.2	2		4		1.97E-02	3.27E-01
Azoarcus sp. BH72	chaperonin GroEL	YP_933870	azo2366	547	56950	5.2	2		4		3.97E-01	5.91E+00
Azoarcus sp. BH72	cold-shock protein	YP_932638	azo1134	67	7315	7.2	2				4.05E-01	6.36E+00
Azoarcus sp. EbN1	DNA-directed RNA polymerase beta' subunit	YP_159177	ebA3819	1409	155259	7.0			2		2.48E-05	2.54E-05
Azoarcus sp. EbN1	elongation factor Tu	YP_159181	ebA3826	396	43204	5.6		2			2.38E-01	2.92E-01
Azoarcus sp. EbN1	elongation factor Tu	YP_159169	ebA3808	396	43204	5.6		2			4.26E-01	5.27E-01
Azoarcus sp. EbN1	chaperonin 60kD subunit	YP_157650	ebA1185	550	58039	5.2	2		4		4.03E-01	5.71E+00
Azoarcus sp. EbN1	putative cold-shock protein	YP_159566	ebC12	67	7287	7.2	2				5.86E-01	7.90E+00
Azospirillum sp. B510	protein-L-isoaspartate(D-aspartate) O-methyltransferase	YP_003448631	AZL_014490	217	24059	9.8			3		4.87E-03	6.38E-03
Azospirillum sp. B510	60 chaperonin GroEL	YP_003447528	AZL_003460	547	57681	5.1	9	2	3	6	6.95E-01	1.68E+00
Bacillus cereus 03BB102	hydrolase, haloacid dehalogenase-like family	YP_002751416	BCA_4164	268	30111	5.0				2	2.05E-03	3.57E-03
Beijerinckia indica indica ATCC 9039	chaperone protein DnaK	YP_001831275	Bind_0128	632	67609	5.1				2	3.58E-03	6.30E-03
Beijerinckia indica indica ATCC 9039	monofunctional biosynthetic peptidoglycan transglycosylase	YP_001831566	Bind_0424	236	26044	10.2				2	7.23E-03	1.29E-02
Bordetella petrii	flagellin	YP_001630704	Bpet2095	501	52096	4.3				2	1.81E-02	3.26E-02
Bordetella petrii	hypothetical protein	YP_001631060	Bpet2450	574	63164	6.4		2			3.88E-01	4.73E-01
Burkholderia ambifaria MC40-6	translation elongation factor Tu	YP_001806978	BamMC406_0261	396	43006	5.5			3		2.23E-08	2.94E-08
Burkholderia ambifaria MC40-6	translation elongation factor Tu	YP_001806991	BamMC406_0274	396	43006	5.5			3		2.58E-08	3.41E-08

Burkholderia ambifaria MC40-6	chaperonin GroEL	YP_001816085	BamMC406_6096	540	57105	5.3			5		5.89E-02	8.73E-02
Burkholderia sp. 383	DNA-directed RNA polymerase beta' subunit	YP_367686	Bcep18194_A3440	1414	156262	6.9			2		2.44E-05	2.52E-05
Burkholderia sp. 383	outer membrane protein (porin)	YP_372528	Bcep18194_B1770	363	38513	9.4			2	3	3.06E-05	3.18E-05
Burkholderia sp. 383	methyl-accepting chemotaxis sensory transducer	YP_372281	Bcep18194_B1523	539	56801	5.2			6		3.43E-03	5.51E-03
Burkholderia sp. 383	methyl-accepting chemotaxis sensory transducer	YP_367286	Bcep18194_C7598	552	58722	5.3			5		9.88E-02	1.47E-01
Burkholderia sp. 383	elongation factor Tu	YP_367678	Bcep18194_A3432	396	42934	5.6		2	3		4.22E-01	5.08E-01
Burkholderia sp. 383	elongation factor Tu	YP_367691	Bcep18194_A3445	396	42934	5.6		2	3		4.55E-01	5.43E-01
Burkholderia sp. 383	chaperonin GroEL	YP_368198	Bcep18194_A3955	546	57064	5.2	2				5.88E-01	7.57E+00
Burkholderia xenovorans LB400	DNA-directed RNA polymerase	YP_560678	Bxe_A0307	1412	156317	6.8			2		4.26E-05	4.44E-05
Burkholderia xenovorans LB400	methyl-accepting chemotaxis sensory transducer	YP_556284	Bxe_C1067	634	66910	5.3			5		2.76E-03	4.36E-03
Burkholderia xenovorans LB400	methyl-accepting chemotaxis sensory transducer	YP_552715	Bxe_B2628	515	55488	5.2			5		7.56E-03	1.17E-02
Burkholderia xenovorans LB400	methyl-accepting chemotaxis sensory transducer	YP_555860	Bxe_C0612	539	57466	5.4			5		7.78E-03	1.22E-02
Burkholderia xenovorans LB400	methyl-accepting chemotaxis sensory transducer	YP_556750	Bxe_A4301	587	62058	5.7			5		1.60E-01	2.40E-01
Burkholderia xenovorans LB400	methyl-accepting chemotaxis sensory transducer	YP_556971	Bxe_A4080	549	57335	5.0			5		2.47E-01	3.72E-01
Burkholderia xenovorans LB400	Translation elongation factor Tu	YP_560686	Bxe_A0299	396	43058	5.6		2			4.03E-01	4.74E-01
Burkholderia xenovorans LB400	Translation elongation factor Tu	YP_560673	Bxe_A0312	396	43058	5.6		2			4.76E-01	5.63E-01
Burkholderia xenovorans LB400	methyl-accepting chemotaxis sensory transducer	YP_557310	Bxe_A3731	515	54365	5.7			5		3.77E-01	5.71E-01
Burkholderia xenovorans LB400	60 kDa chaperonin (Cpn60), groEL	YP_558394	Bxe_A4544	540	57018	5.5			5		5.68E-01	8.64E-01
Burkholderia xenovorans LB400	60 kDa chaperonin (Cpn60), groEL	YP_558424	Bxe_A2609	540	57018	5.5			5		8.03E-01	1.23E+00
Burkholderia xenovorans LB400	methyl-accepting chemotaxis sensory transducer	YP_559602	Bxe_A1404	526	54978	5.8			5		9.19E-01	1.41E+00
Burkholderia xenovorans LB400	60 kDa chaperonin, GroEL	YP_557235	Bxe_A3815	546	57198	5.2	2				5.91E-01	7.27E+00
Candidatus Accumulibacter phosphatis clade IIA str. UW-1	hypothetical protein	YP_003165196	CAP2UW1_4617	280	31148	5.9			3	2	4.79E-08	6.37E-08
Carboxydothermus hydrogenoformans Z-2901	ATP synthase F1, beta subunit	YP_361338	CHY_2545	473	51635	5.3	3		8	5	7.84E-01	2.61E+00
Chlorobaculum parvum NCIB 8327	ATP synthase F1, beta subunit	YP_001997673	Cpar_0045	462	50149	5.1			7	5	5.55E-07	9.14E-07
Chlorobaculum parvum NCIB 8327	porphobilinogen deaminase	YP_001998354	Cpar_0737	312	34358	5.4				2	2.26E-03	4.24E-03
Chlorobaculum parvum NCIB 8327	translation elongation factor Tu	YP_001997802	Cpar_0175	393	42699	5.3				5	1.20E-01	2.63E-01
Chlorobaculum parvum NCIB 8327	integral membrane sensor hybrid histidine kinase	YP_001998415	Cpar_0799	681	77428	7.0	25				4.24E-01	4.45E-01

Chlorobaculum parvum NCIB 8327	chaperone protein DnaK	YP_001998265	Cpar_0645	638	69083	5.1	2				6.38E-01	5.64E+00
Chlorobaculum tepidum TLS	translation elongation factor TU	NP_663065	CT2191	393	42899	5.5			6	6	1.79E-03	2.90E-03
Chlorobaculum tepidum TLS	porphobilinogen deaminase	NP_662313	CT1427	312	34394	6.4				2	2.65E-03	5.06E-03
Chlorobaculum tepidum TLS	ATP synthase subunit B	NP_663108	CT2234	462	50125	5.1	3		8	6	8.27E-01	3.16E+00
Chlorobaculum tepidum TLS	DnaK protein	NP_661540	CT0643	633	68388	5.3	2				6.47E-01	5.08E+00
Chlorobaculum tepidum TLS	chaperonin, 60 kDa	NP_661430	CT0530	545	58080	5.3	2				6.44E-01	5.21E+00
Chlorobium chlorochromatii CaD3	Porphobilinogen deaminase	YP_379813	Cag_1515	313	34640	6.6				2	9.91E-03	1.80E-02
Chlorobium chlorochromatii CaD3	Chaperonin Cpn60/TCP-1	YP_379609	Cag_1306	547	58079	5.1	4			2	8.29E-01	2.55E+00
Chlorobium chlorochromatii CaD3	Glutamate-1-semialdehyde-2,1-aminomutase	YP_380259	Cag_1968	431	46154	5.6	2			3	5.90E-01	6.43E+00
Chlorobium chlorochromatii CaD3	ATP synthase subunit B	YP_380305	Cag_2014	462	50242	5.2	2	2	4	6	5.90E-01	6.68E+00
Chlorobium clathratiforme BU-1	ATP synthase F1, beta subunit	YP_002017022	Ppha_0048	462	50363	5.2				4	1.93E-05	4.07E-05
Chlorobium clathratiforme BU-1	porphobilinogen deaminase	YP_002017854	Ppha_0950	313	34678	7.2				2	1.53E-03	2.79E-03
Chlorobium clathratiforme BU-1	glutamate-1-semialdehyde-2,1-aminomutase	YP_002019566	Ppha_2800	431	46146	5.6				2	1.60E-03	2.93E-03
Chlorobium clathratiforme BU-1	translation elongation factor Tu	YP_002017237	Ppha_0287	393	42943	5.6				5	9.97E-02	2.17E-01
Chlorobium clathratiforme BU-1	gas vesicle protein GVPa	YP_002018669	Ppha_1821	68	7216	4.9	10	7	23	8	1.77E-01	4.06E-01
Chlorobium clathratiforme BU-1	gas vesicle protein GVPa	YP_002018668	Ppha_1820	68	7216	4.9	10	7	23	8	3.03E-01	7.09E-01
Chlorobium clathratiforme BU-1	gas vesicle protein GVPa	YP_002018667	Ppha_1819	68	7216	4.9	10	7	23	8	3.86E-01	9.19E-01
Chlorobium clathratiforme BU-1	gas vesicle protein GVPa	YP_002018666	Ppha_1818	68	7216	4.9	10	7	23	8	5.66E-01	1.36E+00
Chlorobium clathratiforme BU-1	phosphate binding protein	YP_002018625	Ppha_1776	290	30865	9.7	4		11		8.55E-01	2.55E+00
Chlorobium clathratiforme BU-1	3-oxoacyl-(acyl-carrier-protein) reductase	YP_002017151	Ppha_0197	245	25749	5.5	4				8.68E-01	2.64E+00
Chlorobium clathratiforme BU-1	bacteriochlorophyll C binding protein	YP_002019351	Ppha_2572	80	8289	5.9	4				9.28E-01	2.79E+00
Chlorobium clathratiforme BU-1	chaperone protein DnaK	YP_002018976	Ppha_2156	640	69918	5.2	3		2		9.83E-01	4.28E+00
Chlorobium ferrooxidans DSM 13031	ribosomal protein L29	ZP_01386373	CferDRAFT_0652	68	7944	9.6			4		1.00E-05	1.41E-05
Chlorobium ferrooxidans DSM 13031	porphobilinogen deaminase	ZP_01386964	CferDRAFT_0191	313	34548	7.2				2	1.65E-03	3.04E-03
Chlorobium ferrooxidans DSM 13031	Bacteriochlorophyll C binding protein	ZP_01386130	CferDRAFT_1054	80	8302	8.6			13		3.70E-03	6.20E-03
Chlorobium ferrooxidans DSM 13031	Histone-like bacterial DNA-binding protein	ZP_01385964	CferDRAFT_1283	91	9604	9.4	10		44	32	5.12E-03	1.15E-02
Chlorobium ferrooxidans DSM 13031	Phosphate binding protein	ZP_01386251	CferDRAFT_0849	306	32543	9.6	19	7	31	23	9.22E-03	1.18E-02

Chlorobium ferrooxidans DSM 13031	Cold-shock protein, DNA-binding	ZP_01386437	CferDRAFT_0712	69	7505	7.4	11	5	11	6	1.24E-01	2.18E-01
Chlorobium ferrooxidans DSM 13031	ribosomal protein L21	ZP_01386030	CferDRAFT_1140	96	10963	10.0		2	2		4.50E-01	5.19E-01
Chlorobium ferrooxidans DSM 13031	ATP synthase F1, beta subunit	ZP_01386566	CferDRAFT_0519	462	50309	5.1	4		9	8	6.52E-01	1.68E+00
Chlorobium ferrooxidans DSM 13031	conserved hypothetical protein	ZP_01385077	CferDRAFT_1941	365	39646	7.2	4	2	5	8	6.86E-01	1.78E+00
Chlorobium ferrooxidans DSM 13031	Pyruvate flavodoxin/ferredoxin oxidoreductase-like	ZP_01385961	CferDRAFT_1280	626	67552	6.2	4			2	7.08E-01	1.85E+00
Chlorobium ferrooxidans DSM 13031	3-oxoacyl-(acyl-carrier-protein) reductase	ZP_01386932	CferDRAFT_0216	245	25647	6.7	4				7.04E-01	1.92E+00
Chlorobium ferrooxidans DSM 13031	Chaperone DnaK	ZP_01386796	CferDRAFT_0385	638	69823	5.2	3		2		7.92E-01	2.70E+00
Chlorobium ferrooxidans DSM 13031	Aspartate-semialdehyde dehydrogenase, USG-1 related	ZP_01386118	CferDRAFT_1042	340	37462	5.6	3			5	9.81E-01	4.14E+00
Chlorobium ferrooxidans DSM 13031	Uncharacterised conserved protein UCP025560	ZP_01386627	CferDRAFT_0580	113	12175	9.7	3				9.99E-01	4.29E+00
Chlorobium ferrooxidans DSM 13031	TonB-dependent receptor:TonB-dependent receptor, plug	ZP_01386528	CferDRAFT_0640	805	88267	7.2	3	2	7	3	9.81E-01	4.34E+00
Chlorobium ferrooxidans DSM 13031	Ribosomal protein L22/L17	ZP_01386370	CferDRAFT_0649	90	10097	10.8	2		2		6.16E-01	6.22E+00
Chlorobium ferrooxidans DSM 13031	Plastoquinol--plastocyanin reductase	ZP_01386076	CferDRAFT_1000	181	18898	8.9	2				6.08E-01	6.37E+00
Chlorobium ferrooxidans DSM 13031	ribosomal protein L7/L12	ZP_01385970	CferDRAFT_1289	124	12759	4.8	2				6.01E-01	7.08E+00
Chlorobium limicola DSM 245	ATP synthase F1, beta subunit	YP_001942116	Clim_0029	462	50296	5.1				4	2.42E-05	5.16E-05
Chlorobium limicola DSM 245	porphobilinogen deaminase	YP_001942951	Clim_0893	313	34533	6.5			2	2	6.99E-05	7.30E-05
Chlorobium limicola DSM 245	translation elongation factor Tu	YP_001944234	Clim_2231	393	43141	5.6	11		6	6	3.63E-03	5.81E-03
Chlorobium limicola DSM 245	chaperone protein DnaK	YP_001942820	Clim_0761	639	69167	5.1	2				6.24E-01	5.89E+00
Chlorobium limicola DSM 245	Polyribonucleotide nucleotidyltransferase	YP_001942665	Clim_0599	736	80188	5.5	2	2			6.22E-01	6.07E+00
Chlorobium luteolum DSM 273	Porphobilinogen deaminase	YP_375329	Plut_1427	313	34607	6.8				2	1.72E-03	3.20E-03
Chlorobium luteolum DSM 273	gas vesicle synthesis protein GvpA	YP_374607	Plut_0686	68	7233	4.9	10	7	23	8	2.82E-02	6.54E-02
Chlorobium luteolum DSM 273	gas vesicle synthesis protein GvpA	YP_374609	Plut_0688	68	7200	4.9	10	7	23	8	5.89E-02	1.33E-01
Chlorobium luteolum DSM 273	Heat shock protein Hsp70	YP_374547	Plut_0621	637	68887	5.1			2		4.03E-01	4.24E-01
Chlorobium luteolum DSM 273	gas vesicle synthesis protein GvpA	YP_374610	Plut_0689	68	7200	4.9	10	7	23	8	2.47E-01	5.29E-01
Chlorobium luteolum DSM 273	ATP synthase subunit B	YP_373956	Plut_0021	482	52334	5.1	3		8	6	8.26E-01	2.92E+00
Chlorobium luteolum DSM 273	Chaperonin Cpn60/TCP-1	YP_374469	Plut_0542	547	58249	5.1	3		2	2	9.28E-01	3.60E+00
Chlorobium luteolum DSM 273	Ribosomal protein L7/L12	YP_375848	Plut_1963	123	12667	4.7	2				6.35E-01	5.80E+00
Chlorobium phaeobacteroides BS1	glutamate-1-semialdehyde-2,1-aminomutase	YP_001958656	Cphamn1_0202	431	46503	5.2				2	2.12E-03	4.00E-03

Chlorobium phaeobacteroides DSM 266	ATP synthase F1, beta subunit	YP_910543	Cpha266_0049	462	50339	5.1				3	1.04E-06	2.13E-06
Chlorobium phaeobacteroides DSM 266	glutamate-1-semialdehyde-2,1-aminomutase	YP_912969	Cpha266_2557	431	46315	5.9				3	1.06E-06	2.18E-06
Chlorobium phaeobacteroides DSM 266	translation elongation factor Tu	YP_912837	Cpha266_2425	393	43289	5.6	11		6	6	2.28E-03	3.58E-03
Chlorobium phaeobacteroides DSM 266	porphobilinogen deaminase	YP_912237	Cpha266_1796	313	34891	6.8				2	2.18E-03	4.15E-03
Chlorobium phaeobacteroides DSM 266	chaperone protein DnaK	YP_911339	Cpha266_0864	640	69142	5.2	2				6.42E-01	5.34E+00
Chlorobium phaeobacteroides DSM 266	Polyribonucleotide nucleotidyltransferase	YP_911032	Cpha266_0552	732	79495	5.4	2				6.40E-01	5.48E+00
Comamonas testosteroni CNB-2	gram-negative type outer membrane porin protein	YP_003279907	CtCNB1_3865	345	35902	9.5			2	3	2.98E-01	3.17E-01
Comamonas testosteroni CNB-2	gram-negative type outer membrane porin protein	YP_003279658	CtCNB1_3616	349	36819	9.4			2	3	4.16E-01	4.41E-01
Comamonas testosteroni CNB-2	gram-negative type outer membrane porin protein	YP_003276683	CtCNB1_0641	361	36951	9.5			2	3	4.43E-01	4.68E-01
Comamonas testosteroni CNB-2	chaperonin GroEL	YP_003276685	CtCNB1_0643	547	57045	5.1	7	2	2	6	6.59E-01	1.65E+00
Dechloromonas aromatica RCB	DNA-directed RNA polymerase beta' subunit	YP_283542	Daro_0313	1403	155039	6.8			2		7.37E-03	7.96E-03
Dechloromonas aromatica RCB	Chaperonin Cpn60/TCP-1	YP_283653	Daro_0426	550	57850	5.3	2				6.47E-01	4.95E+00
Delftia acidovorans SPH-1	porin, gram-negative type	YP_001562753	Daci_1725	348	36818	9.5			2	3	6.13E-03	6.55E-03
Delftia acidovorans SPH-1	porin, gram-negative type	YP_001566967	Daci_5954	327	35284	9.0			2	3	6.67E-03	7.15E-03
Delftia acidovorans SPH-1	chaperonin GroEL	YP_001566674	Daci_5661	547	57159	5.1	7	2	2	6	6.53E-01	1.62E+00
Delftia acidovorans SPH-1	translation elongation factor Tu	YP_001561534	Daci_0503	396	43025	5.7	3		5		8.56E-01	3.46E+00
Delftia acidovorans SPH-1	translation elongation factor Tu	YP_001561420	Daci_0389	396	43095	5.7	3		5		8.58E-01	3.52E+00
Desulfatibacillum alkenivorans AK-01	protein of unknown function DUF364	YP_002433255	Dalk_4102	262	28158	7.4			2		7.21E-03	7.76E-03
Desulfatibacillum alkenivorans AK-01	methyl-viologen-reducing hydrogenase delta subunit	YP_002431430	Dalk_2269	807	87599	6.4	3				8.80E-01	3.46E+00
Desulfotalea psychrophila LSv54	chaperonin GroEL	YP_063926	DP0190	518	55647	5.6	2				6.50E-01	4.71E+00
Desulfovibrio aespoeensis Aspo-2	ATP synthase F1, beta subunit	ZP_06232055	DaesDRAFT_1401	465	49908	5.0			3	4	2.41E-07	3.22E-07
Desulfovibrio aespoeensis Aspo-2	protein of unknown function DUF201	ZP_06232787	DaesDRAFT_2134	337	36290	6.6	6			3	6.93E-01	1.75E+00
Desulfovibrio desulfuricans G20	ATP synthase F1, beta subunit	YP_387481	Dde_0985	470	50824	4.9	5	3	10	8	7.05E-01	2.01E+00
Desulfovibrio salexigens DSM 2638	hypothetical protein	YP_002991847	Desal_2252	293	33670	6.2			2		6.41E-03	6.96E-03
Desulfovibrio vulgaris vulgaris DP4	ATP synthase F1, beta subunit	YP_967638	Dvul_2195	470	50742	5.1	3		8	5	8.60E-01	3.12E+00
Desulfovibrio vulgaris vulgaris Hildenborough	ATP synthase subunit B	YP_009996	DVU0775	470	50742	5.1	3		8	5	7.86E-01	2.71E+00
Desulfuromonas acetoxidans DSM 684	chaperonin GroEL	ZP_01313307	Dace_1148	545	57890	4.8			4		1.91E-06	2.70E-06
Desulfuromonas acetoxidans DSM 684	ATP synthase F1, beta subunit	ZP_01312711	Dace_1461	468	50804	4.8	3	3	4	5	9.79E-01	4.40E+00

Desulfuromonas acetoxidans DSM 684	Chaperone DnaK	ZP_01313919	Dace_0265	636	68116	4.7	2		3	3	6.44E-01	4.80E+00
Diaphorobacter sp. TPSY	porin Gram-negative type	YP_002552141	Dtpsy_0661	362	37887	9.0			2	3	4.49E-01	4.91E-01
Diaphorobacter sp. TPSY	chaperonin GroEL	YP_002552157	Dtpsy_0677	546	57199	5.2	7	2	2	6	6.61E-01	1.63E+00
Diaphorobacter sp. TPSY	OmpA/MotB domain protein	YP_002552861	Dtpsy_1397	218	22763	9.3	3				8.57E-01	3.19E+00
Diaphorobacter sp. TPSY	flagellin domain protein	YP_002554520	Dtpsy_3087	493	50280	5.4	2				6.53E-01	4.62E+00
Flavobacteriaceae bacterium 3519-10	Heat shock protein 60 family chaperone GroEL	YP_003094795	FIC_00260	541	57414	5.0	5	2	2	4	6.85E-01	1.94E+00
Gallionella ferruginea ES-2	cold-shock DNA-binding domain protein	ZP_04831683	GalfDRAFT_2127	67	7199	5.9	3			2	8.47E-01	3.53E+00
Geobacter bemidjiensis Bem	ATP synthase F1, beta subunit	YP_002140738	Gbem_3950	470	51057	5.0	4		8	6	6.72E-01	1.71E+00
Geobacter lovleyi SZ	cold-shock DNA-binding domain protein	YP_001952860	Glov_2627	66	7196	5.3			2		4.67E-01	5.12E-01
Geobacter lovleyi SZ	ATP synthase F1, beta subunit	YP_001953396	Glov_3170	471	51139	5.1	4		8	6	6.66E-01	1.76E+00
Geobacter metallireducens GS-15	Resolvase-like	YP_385231	Gmet_2281	216	23741	10.1				3	6.53E-06	1.36E-05
Geobacter metallireducens GS-15	Excinuclease ABC, A subunit	YP_383102	Gmet_0128	937	104116	6.9				2	2.84E-03	5.47E-03
Geobacter metallireducens GS-15	Chaperone DnaK	YP_386462	Gmet_3532	638	68479	5.1				2	3.36E-03	6.52E-03
Geobacter metallireducens GS-15	chaperonin GroEL	YP_383004	Gmet_0029	546	58015	5.2			2		4.23E-01	4.68E-01
Geobacter metallireducens GS-15	ATP synthase subunit B	YP_386343	Gmet_3406	470	51033	5.1	5	3	10	8	6.78E-01	1.86E+00
Geobacter sp. FRC-32	cold-shock DNA-binding domain protein	YP_002538748	Geob_3304	66	7227	5.3			2		3.96E-01	4.40E-01
Geobacter sulfurreducens PCA	cold-shock domain family protein	NP_951268	GSU0207	66	7208	5.9			2		5.59E-03	6.26E-03
Geobacter sulfurreducens PCA	60 kDa chaperonin	NP_954380	GSU3340	544	58149	5.3			2		6.52E-03	7.32E-03
Geobacter sulfurreducens PCA	chaperone protein dnaK	NP_951095	GSU0033	636	68468	5.1				2	3.87E-03	7.56E-03
Geobacter sulfurreducens PCA	cold-shock domain family protein	NP_951252	GSU0191	66	7188	5.3			2		2.23E-01	2.48E-01
Geobacter sulfurreducens PCA	ATP synthase subunit B	NP_951175	GSU0113	470	50973	5.1	5	3	10	8	6.73E-01	1.81E+00
Geobacter uraniumreducens Rf4	hypothetical protein	YP_001230223	Gura_1451	138	14500	10.4	3				8.77E-01	3.06E+00
Haloterrigena turkmenica DSM 5511	Glycine hydroxymethyltransferase	YP_003405642	Htur_4145	416	44858	4.5			2		6.58E-03	7.42E-03
Leptothrix cholodnii SP-6	translation elongation factor Tu	YP_001792893	Lcho_3874	396	42881	5.9			3		5.76E-06	7.76E-06
Leptothrix cholodnii SP-6	translation elongation factor Tu	YP_001792883	Lcho_3864	396	42881	5.9			3		6.08E-06	8.15E-06
Leptothrix cholodnii SP-6	chaperonin GroEL	YP_001789523	Lcho_0483	549	57310	5.2	2				6.55E-01	4.52E+00
Magnetospirillum magneticum AMB-1	F0F1-type ATP synthase, beta subunit	YP_423502	amb4139	474	50655	5.2	4	2	11	9	6.89E-01	1.91E+00
Magnetospirillum magneticum AMB-1	amb0203 Chaperonin GroEL	YP_419566	amb0203	552	57846	5.3	4		2	3	6.85E-01	1.92E+00

Magnetospirillum magneticum AMB-1	hypothetical protein	YP_420427	amb1064	521	56848	9.1	2		7		6.53E-01	4.30E+00
Methylibium petroleiphilum PM1	flagellin-related hook-associated protein	YP_001022055	Mpe_A2866	404	42037	4.7	3			5	7.92E-01	2.52E+00
Methylibium petroleiphilum PM1	putative phosphate-binding periplasmic (pbp) ABC transporter protein	YP_001020469	Mpe_A1272	346	36673	9.0	2				6.60E-01	4.24E+00
Methylibium petroleiphilum PM1	putative chaperonin	YP_001019625	Mpe_A0428	548	57391	5.3	2				6.56E-01	4.42E+00
Methylocella silvestris BL2	integral membrane sensor signal transduction histidine kinase	YP_002361662	Msil_1335	518	55277	6.6			2		7.14E-03	8.08E-03
Methylocella silvestris BL2	cytochrome c oxidase, subunit II	YP_002361568	Msil_1237	303	33346	7.2	2	2			6.76E-01	4.16E+00
Methylocella silvestris BL2	ATP synthase F1, beta subunit	YP_002360684	Msil_0343	483	51344	5.0	2				6.63E-01	4.17E+00
Moorella thermoacetica ATCC 39073	Flagellin-like	YP_429621	Moth_0760	380	40019	8.7				4	1.61E-01	3.48E-01
Moorella thermoacetica ATCC 39073	ATP synthase F1, beta subunit	YP_431203	Moth_2378	462	50451	5.1	3			4	7.72E-01	2.48E+00
Pelobacter carbinolicus DSM 2380	60 kDa chaperonin	YP_358175	Pcar_2770	551	58460	5.1			4		4.75E-06	6.75E-06
Pelobacter propionicus DSM 2379	ATP synthase F1, beta subunit	YP_900295	Ppro_0606	471	51118	5.1	3		8	5	7.76E-01	2.53E+00
Pelobacter propionicus DSM 2379	ATP synthase F1, beta subunit	YP_901180	Ppro_1507	471	51132	5.1	3		8	5	7.75E-01	2.61E+00
Prosthecochloris aestuarii SK413, DSM 271	porphobilinogen deaminase	YP_002016206	Paes_1539	312	34687	6.3				2	1.46E-08	2.86E-08
Prosthecochloris vibrioformis DSM 265	translation elongation factor Tu	YP_001129768	Cvib_0244	393	43015	5.3				5	1.88E-02	4.15E-02
Prosthecochloris vibrioformis DSM 265	ribosomal protein L7/L12	YP_001131118	Cvib_1606	123	12429	4.7	2				6.77E-01	3.99E+00
Prosthecochloris vibrioformis DSM 265	chaperone protein DnaK	YP_001130672	Cvib_1158	635	68685	5.1	2				6.78E-01	4.08E+00
Ralstonia eutropha H16	translation elongation factor EF-1alpha (EF-TU,GTPase)	YP_727927	H16_A3491	396	43046	5.7			3		9.52E-06	1.29E-05
Ralstonia eutropha H16	translation elongation factor EF-TU (GTPase)	YP_727940	H16_A3505	396	43046	5.7			3		1.54E-05	2.10E-05
Ralstonia eutropha H16	Flagellin	YP_841872	H16_B2360	435	44823	5.3			2	2	7.38E-03	8.39E-03
Ralstonia eutropha H16	ABC-type transporter, periplasmic component: PhoT family	YP_726901	H16_A2444	343	36181	9.3	2				7.94E-01	4.59E+00
Ralstonia metallidurans CH34	translation elongation factor Tu	YP_585482	Rmet_3341	396	43088	5.6			3		1.71E-05	2.35E-05
Ralstonia metallidurans CH34	translation elongation factor Tu	YP_585465	Rmet_3324	396	43088	5.6			3		2.11E-05	2.89E-05
Ralstonia metallidurans CH34	chaperonin GroEL	YP_582771	Rmet_0616	547	57378	5.2			4		6.16E-05	8.89E-05
Ralstonia metallidurans CH34	porin, Gram-negative type	YP_581783	Rmet_5974	355	37720	9.4			2	3	7.66E-03	8.77E-03
Ralstonia metallidurans CH34	porin, Gram-negative type	YP_587632	Rmet_5504	379	40739	9.3			2	3	2.15E-01	2.57E-01
Ralstonia metallidurans CH34	porin, Gram-negative type	YP_587246	Rmet_5118	355	37809	9.4			2	3	2.18E-01	2.58E-01

Ralstonia metallidurans CH34	porin, Gram-negative type	YP_586965	Rmet_4834	353	36246	9.2			2	3	2.29E-01	2.67E-01
Ralstonia metallidurans CH34	porin, Gram-negative type	YP_587416	Rmet_5288	386	41052	8.8			2	3	2.34E-01	2.78E-01
Ralstonia metallidurans CH34	DNA-directed RNA polymerase, subunit beta-prime	YP_585474	Rmet_3333	1413	155726	7.0			2		2.38E-01	2.78E-01
Ralstonia metallidurans CH34	porin, Gram-negative type	YP_585375	Rmet_3234	401	41950	9.0			2	3	2.94E-01	3.41E-01
Ralstonia metallidurans CH34	Periplasmic phosphate binding protein	YP_584333	Rmet_2185	343	36292	9.2	2				7.77E-01	4.31E+00
Rhodoferax ferrireducens T118	ribosomal protein L7/L12	YP_524828	Rfer_3593	123	12635	5.0				2	2.97E-08	5.92E-08
Rhodoferax ferrireducens T118	Phasin	YP_523395	Rfer_2140	180	18731	5.6			6	3	8.52E-08	1.39E-07
Rhodoferax ferrireducens T118	extracellular solute-binding protein, family 1	YP_524902	Rfer_3671	577	63825	8.5				2	7.70E-08	1.55E-07
Rhodoferax ferrireducens T118	chaperonin GroEL	YP_524251	Rfer_3009	544	57703	5.4			4		4.19E-05	6.02E-05
Rhodoferax ferrireducens T118	malate dehydrogenase	YP_523063	Rfer_1803	328	35077	7.0			6		2.11E-03	3.43E-03
Rhodoferax ferrireducens T118	protein of unknown function DUF150	YP_523387	Rfer_2132	204	22118	5.8			2		6.23E-03	7.11E-03
Rhodoferax ferrireducens T118	ribosomal protein L29	YP_525018	Rfer_3787	68	7668	10.4				7	3.74E-03	8.54E-03
Rhodoferax ferrireducens T118	DNA-directed RNA polymerase, subunit beta-prime	YP_524826	Rfer_3591	1405	154592	7.3			2		8.12E-03	9.34E-03
Rhodoferax ferrireducens T118	ribosomal protein S16	YP_522666	Rfer_1402	83	9319	11.4				6	1.03E-01	2.29E-01
Rhodoferax ferrireducens T118	Periplasmic phosphate binding protein	YP_521865	Rfer_0583	347	36680	9.3	5	3	21	10	6.46E-01	1.73E+00
Rhodoferax ferrireducens T118	translation elongation factor Tu	YP_525028	Rfer_3797	396	42977	6.0	3	2			7.91E-01	2.60E+00
Rhodoferax ferrireducens T118	RNA-binding region RNP-1	YP_525452	Rfer_4234	140	13554	9.4	3	2			8.37E-01	2.63E+00
Rhodoferax ferrireducens T118	flagellin-like	YP_521912	Rfer_0630	472	46171	5.8	3		3	7	8.22E-01	2.94E+00
Rhodoferax ferrireducens T118	flagellin-like	YP_521913	Rfer_0631	471	46121	7.0	3		3	4	8.57E-01	3.23E+00
Rhodoferax ferrireducens T118	chaperonin GroEL	YP_522403	Rfer_1131	552	57628	5.4	3				8.61E-01	3.43E+00
Rhodoferax ferrireducens T118	translation elongation factor Tu	YP_524834	Rfer_3599	396	42991	6.0	3	2			9.57E-01	3.52E+00
Rhodoferax ferrireducens T118	OmpA/MotB	YP_522835	Rfer_1572	212	22309	9.3	2				7.83E-01	4.43E+00
Rhodospirillum centenum SW	electron transfer flavoprotein, alpha subunit	YP_002300260	RC1_4109	313	31620	5.3				2	1.81E-08	3.57E-08
Rhodospirillum centenum SW	ATP synthase F1, beta subunit	YP_002298441	RC1_2241	484	51674	5.1			4	5	1.16E-05	1.65E-05
Rhodospirillum centenum SW	chaperonin GroL, putative	YP_002298788	RC1_2595	546	57761	5.2				3	1.74E-05	3.64E-05
Rhodospirillum rubrum ATCC 11170	GlpX	YP_427496	Rru_A2409	335	34105	5.3				2	3.65E-07	7.38E-07
Rhodospirillum rubrum ATCC 11170	Glycine hydroxymethyltransferase	YP_426230	Rru_A1142	434	45849	7.8			4		8.97E-05	1.30E-04

Rhodospirillum rubrum ATCC 11170	ATP synthase F1, beta subunit	YP_426314	Rru_A1226	474	50853	5.1	2	2	5	7	7.73E-01	4.05E+00
Syntrophobacter fumaroxidans MPOB	ATP synthase F1, beta subunit	YP_846695	Sfum_2582	469	50613	5.0			7	4	1.30E-06	2.16E-06
Syntrophus aciditrophicus SB	chaperonin GroEL	YP_460096	SYN_00027	544	58645	5.1			5		8.00E-03	1.27E-02
Thiobacillus denitrificans ATCC 25259	Carboxysome structural peptide CsoS1B	YP_316402	Tbd_2644	124	12445	4.9			3	2	1.99E-04	2.74E-04
Thiobacillus denitrificans ATCC 25259	carboxysome shell protein CsoS1A	YP_316403	Tbd_2645	101	10142	5.3			3	2	4.75E-04	6.59E-04
Thiobacillus denitrificans ATCC 25259	carboxysome shell protein, CsoS1C	YP_316404	Tbd_2646	99	9996	5.9			3	2	1.25E-03	1.74E-03
Thiobacillus denitrificans ATCC 25259	flagellin FliC	YP_315348	Tbd_1590	609	59537	5.0			2	3	3.83E-01	4.63E-01
Thiobacillus denitrificans ATCC 25259	DNA-directed RNA polymerase beta' subunit	YP_314157	Tbd_0399	1398	153692	7.1			2		3.86E-01	4.69E-01
Thiobacillus denitrificans ATCC 25259	chaperonin GroEL (Hsp60, Cpn10)	YP_313849	Tbd_0091	547	57562	5.2	2		4		7.72E-01	4.20E+00
Thiomonas intermedia K12	chaperonin GroEL	YP_003642376	Tint_0646	546	57615	5.3	2				7.94E-01	4.08E+00
Thiomonas intermedia K12	Holliday junction DNA helicase RuvB	YP_003641962	Tint_0220	352	38258	5.5	2				7.90E-01	4.22E+00
Variovorax paradoxus S110	transcriptional regulator, LysR family	YP_002947316	Vapar_5454	305	32747	7.9			4	3	2.91E-04	4.24E-04
Variovorax paradoxus S110	flagellin domain protein	YP_002946045	Vapar_4166	412	42248	5.0	4		7	7	6.80E-01	1.96E+00
Total: 283 proteins												

Table S8. Protein hits in central basin using metaproteomics. The protein length and pI refer to the number of amino acids and isoelectric point of protein, respectively. The BH correction stands for Benjamini-Hochberg correction to obtain the q value.

Microbial strain	Protein description	Protein accession no.	Gene ID	Protein Length	Mol Wt (Da)	pI	Spectral Counts				p value	BH Correction (q value)
							CB1	CB2	CR1	CR2		
Acetobacter pasteurianus IFO 3283-01	heat shock protein GroES	YP_003188291	APA01_17860	123	13427	9.1			4	5	1.41E-01	1.54E-01
Acetobacter pasteurianus IFO 3283-01	heat shock protein GroEL	YP_003188292	APA01_17870	546	58135	5.7			2		5.00E-01	1.67E+00
Acidiphilium cryptum JF-5	ribosomal protein L10	YP_001235074	Acry_1954	174	18358	9.4			6	2	3.94E-01	4.37E-01
Acidiphilium cryptum JF-5	cytochrome c, class I	YP_001235217	Acry_2099	123	12427	9.2				2	5.00E-01	8.33E-01
Acidiphilium cryptum JF-5	putative cold-shock DNA-binding domain protein	YP_001235951	Acry_2842	68	7488	8.6				2	5.00E-01	8.14E-01
Acidiphilium cryptum JF-5	malate dehydrogenase	YP_001236171	Acry_3063	327	34474	6.2				2	5.00E-01	7.95E-01
Acidiphilium cryptum JF-5	ribosomal protein L1	YP_001235075	Acry_1955	230	23961	9.6				2	5.00E-01	8.97E-01
Acidiphilium cryptum JF-5	phasin family protein	YP_001233302	Acry_0155	157	17485	6.8				3	5.00E-01	9.46E-01
Acidiphilium cryptum JF-5	chaperonin Cpn10	YP_001235614	Acry_2504	104	11141	7.3			2		5.00E-01	1.40E+00
Acidiphilium cryptum JF-5	TonB-dependent receptor	YP_001220344	Acry_3609	819	89893	9.3	3				5.00E-01	1.94E+00
Acidiphilium cryptum JF-5	ATP synthase F1, beta subunit	YP_001234805	Acry_1681	476	51197	5.0		2		3	5.14E-01	3.27E+00
Acidiphilium cryptum JF-5	Monosaccharide-transporting ATPase	YP_001235093	Acry_1973	369	38701	8.9		3		3	5.21E-01	7.29E+00
Acidiphilium cryptum JF-5	chaperonin GroEL	YP_001235613	Acry_2503	549	58230	5.5	6	5	9	12	6.37E-01	1.11E+01
Acidiphilium cryptum JF-5	OmpA/MotB domain protein	YP_001233507	Acry_0363	167	17206	8.6	4		5	6	8.07E-01	2.82E+01
Acidothermus cellulolyticus 11B	ATP synthase F1, beta subunit	YP_872412	Acel_0653	490	53544	5.0				2	5.00E-01	8.53E-01
Acidovorax avenae citrulli AAC00-1	ubiquitin	YP_973019	Aave_4710	287	30111	5.9				3	5.00E-01	1.03E+00
Acidovorax delafieldii 2AN	pseudouridine synthase, RluA family	ZP_04761874	AcdelDRAFT_1105	336	37258	10.1	2				5.00E-01	2.69E+00
Acidovorax sp. JS42	chaperonin GroEL	YP_985019	Ajs_0699	546	57197	5.2			2		5.00E-01	1.59E+00
Anoxybacillus flavithermus WK1	Stage IV sporulation protein A	YP_002315450	Aflv_1089	508	57439	4.9	2				5.00E-01	2.50E+00
Azoarcus sp. BH72	conserved hypothetical membrane protein	YP_931922	azo0418	280	31103	9.0	10	11	7	14	9.35E-01	6.54E+01
Azospirillum sp. B510	large subunit ribosomal protein L7/L12	YP_003447753	AZL_005710	125	12884	4.9				3	5.00E-01	1.00E+00
Azospirillum sp. B510	chaperonin GroEL	YP_003447528	AZL_003460	547	57681	5.1	2	3	2	5	7.22E-01	1.68E+01
Burkholderia ambifaria MC40-6	parB-like partition protein	YP_001806815	BamMC406_0097	297	32099	7.6		2			4.92E-01	5.94E-01

Burkholderia sp. 383	ParB-like partition protein	YP_367524	Bcep18194_A3278	305	33059	8.3		2			4.92E-01	5.74E-01
Burkholderia xenovorans LB400	Transcriptional regulator, LysR family	YP_558941	Bxe_A2079	303	33074	6.9			2		5.00E-01	1.52E+00
Carboxydothermus hydrogenoformans Z-2901	ATP synthase F1, beta subunit	YP_361338	CHY_2545	473	51635	5.3		2		3	5.14E-01	5.99E+00
Chlorobium chlorochromatii CaD3	glycosyl transferase	YP_379771	Cag_1472	363	40670	9.3			5		5.00E-01	1.13E+00
Chlorobium clathratiforme BU-1	gas vesicle protein GVPa	YP_002018666	Ppha_1818	68	7216	4.9		3			4.95E-01	6.93E-01
Chlorobium clathratiforme BU-1	gas vesicle protein GVPa	YP_002018667	Ppha_1819	68	7216	4.9		3			4.95E-01	6.79E-01
Chlorobium clathratiforme BU-1	gas vesicle protein GVPa	YP_002018668	Ppha_1820	68	7216	4.9		3			4.95E-01	6.66E-01
Chlorobium clathratiforme BU-1	gas vesicle protein GVPa	YP_002018669	Ppha_1821	68	7216	4.9		3			4.95E-01	6.54E-01
Chlorobium luteolum DSM 273	gas vesicle synthesis protein GvpA	YP_374607	Plut_0686	68	7233	4.9		3			4.95E-01	6.42E-01
Chlorobium luteolum DSM 273	gas vesicle synthesis protein GvpA	YP_374609	Plut_0688	68	7200	4.9		3			4.95E-01	6.30E-01
Chlorobium luteolum DSM 273	gas vesicle synthesis protein GvpA	YP_374610	Plut_0689	68	7200	4.9		3			4.95E-01	6.19E-01
Chromohalobacter salexigens DSM 3043	Chaperone DnaK	YP_575137	Csal_3094	644	68798	4.7				2	5.00E-01	8.75E-01
Comamonas testosteroni CNB-2	chaperonin GroEL	YP_003276685	CtCNB1_0643	547	57045	5.1			2		5.00E-01	1.35E+00
Delftia acidovorans SPH-1	chaperonin GroEL	YP_001566674	Daci_5661	547	57159	5.1			2		5.00E-01	1.30E+00
Desulfovibrio aespoeensis Aspo-2	protein of unknown function DUF201	ZP_06232787	DaesDRAFT_2134	337	36290	6.6	4				5.00E-01	1.21E+00
Desulfovibrio desulfuricans G20	ATP synthase F1, beta subunit	YP_387481	Dde_0985	470	50824	4.9		2	2	4	3.65E-03	3.65E-03
Desulfovibrio salexigens DSM 2638	MscS Mechanosensitive ion channel	YP_002990657	Desal_1054	834	95142	9.7	3				5.00E-01	1.84E+00
Desulfuromonas acetoxidans DSM 684	ATP synthase F1, beta subunit	ZP_01312711	Dace_1461	468	50804	4.8		2		3	5.14E-01	5.14E+00
Diaphorobacter sp. TPSY	chaperonin GroEL	YP_002552157	Dtpsy_0677	546	57199	5.2			2		5.00E-01	1.46E+00
Ferroplasma acidarmanus Fer1	NADH-quinone oxidoreductase, chain I	ZP_00610230	FaciDRAFT_0352	165	19026	7.9		12			4.99E-01	7.12E-01
Flavobacteriaceae bacterium 3519-10	Heat shock protein 60 family chaperone GroEL	YP_003094795	FIC_00260	541	57414	5.0			2		5.00E-01	1.25E+00
Geobacter bemidjiensis Bem	ATP synthase F1, beta subunit	YP_002140738	Gbem_3950	470	51057	5.0		3	2	5	6.80E-02	7.11E-02
Geobacter lovleyi SZ	ATP synthase F1, beta subunit	YP_001953396	Glov_3170	471	51139	5.1		3	2	5	6.80E-02	7.22E-02
Geobacter metallireducens GS-15	ATP synthase subunit B	YP_386343	Gmet_3406	470	51033	5.1		3	2	5	6.80E-02	7.00E-02
Geobacter metallireducens GS-15	Translation elongation factor Tu	YP_383578	Gmet_0611	396	43207	5.3		2			4.92E-01	5.65E-01
Geobacter metallireducens GS-15	Translation elongation factor Tu	YP_383591	Gmet_0624	396	43207	5.3		2			4.92E-01	5.56E-01
Geobacter sp. M18	conserved hypothetical protein	ZP_05313199	GM18DRAFT_3858	574	64128	6.4	2				5.00E-01	2.33E+00
Geobacter sulfurreducens PCA	ATP synthase subunit B	NP_951175	GSU0113	470	50973	5.1		3	2	5	6.80E-02	6.90E-02

Geobacter uraniumreducens Rf4	ATP synthase F1, beta subunit	YP_001232979	Gura_4263	470	50848	5.0		2		3	5.14E-01	4.49E+00
Hydrogenobaculum sp. Y04AAS1	putative lipoprotein	YP_002121812	HY04AAS1_1148	308	36763	9.4	3				5.00E-01	1.75E+00
Magnetospirillum magneticum AMB-1	F0F1-type ATP synthase, beta subunit	YP_423502	amb4139	474	50655	5.2		2	2	3	8.37E-02	9.01E-02
Magnetospirillum magneticum AMB-1	Chaperonin GroEL	YP_419566	amb0203	552	57846	5.3				4	5.00E-01	1.06E+00
Magnetospirillum magneticum AMB-1	hypothetical protein	YP_420427	amb1064	521	56848	9.1				4	5.00E-01	1.09E+00
Methanococcus maripaludis C5	UDP-glucose/GDP-mannose dehydrogenase	YP_001097824	MmarC5_1312	437	48489	5.6		3			4.95E-01	6.08E-01
Methylocella silvestris BL2	cytochrome c oxidase, subunit II	YP_002361568	Msil_1237	303	33346	7.2				3	5.00E-01	9.72E-01
Moorella thermoacetica ATCC 39073	ATP synthase F1, beta subunit	YP_431203	Moth_2378	462	50451	5.1		2		3	5.14E-01	3.00E+00
Pelobacter propionicus DSM 2379	ATP synthase F1, beta subunit	YP_900295	Ppro_0606	471	51118	5.1		2		3	5.14E-01	4.00E+00
Pelobacter propionicus DSM 2379	ATP synthase F1, beta subunit	YP_901180	Ppro_1507	471	51132	5.1		2		3	5.14E-01	3.60E+00
Ralstonia metallidurans CH34	DNA repair protein RecO	YP_584562	Rmet_2416	298	33106	9.3	4				5.00E-01	1.17E+00
Rhodospirillum centenum SW	hypothetical protein	YP_002296704	RC1_0452	194	20045	7.3	2				5.00E-01	2.19E+00
Rhodospirillum rubrum ATCC 11170	Heat shock protein Hsp70	YP_428636	Rru_A3555	639	68734	5.2				2	5.00E-01	7.78E-01
Rhodospirillum rubrum ATCC 11170	Ribosomal protein L7/L12	YP_427780	Rru_A2696	123	12873	4.9				3	5.00E-01	9.21E-01
Sulfolobus acidocaldarius DSM 639	conserved protein	AAY79634	Saci_0215	204	23806	9.0	2				5.00E-01	2.06E+00
Sulfolobus islandicus L.S.2.15	protein of unknown function DUF1156	YP_002831737	LS215_1063	931	107208	7.5		15			4.99E-01	7.43E-01
Sulfolobus islandicus Y.G.57.14	protein of unknown function DUF1156	YP_002836780	YG5714_0563	931	107155	6.1		15			4.99E-01	7.28E-01
Sulfolobus tokodaii 7	ST0218a hypothetical protein	ST0218a	hypothetical	86	10113	8.4		2			4.92E-01	5.84E-01
Thiomonas intermedia K12	globin	YP_003643170	Tint_1458	162	18528	7.7		18			4.99E-01	7.60E-01
Total: 70 proteins												

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