

OTUs

ICE

OTU	Env	P-value	Spearman r	Taxonomic affiliation
117288	POC	4,51E-05	-0,7451827	k__Bacteria; p__Proteobacteria; c__Gammaproteo
344542	Salinity	4,97E-05	-0,7424723	k__Bacteria; p__Proteobacteria; c__Gammaproteo
101074	Salinity	6,72E-05	-0,733945	k__Bacteria; p__Bacteroidetes; c__[Saprospirae]; o
251223	DOC	7,95E-05	-0,7290263	k__Bacteria; p__Proteobacteria; c__Gammaproteo
251223	POC	9,71E-05	-0,7230425	k__Bacteria; p__Proteobacteria; c__Gammaproteo
149844	PO4	0,000118315	-0,7169664	k__Bacteria; p__Proteobacteria; c__Gammaproteo
91093	POC	0,000122314	-0,715931	k__Bacteria; p__Verrucomicrobia; c__Opitutae; o__
149844	POC	0,000244534	-0,6933025	k__Bacteria; p__Proteobacteria; c__Gammaproteo
306210	Si	0,00024823	0,6927893	k__Bacteria; p__Proteobacteria; c__Gammaproteo
306210	Chla	0,000286513	0,6878302	k__Bacteria; p__Proteobacteria; c__Gammaproteo
114736	POC	0,000288212	-0,6876238	k__Bacteria; p__Proteobacteria; c__Alphaproteoba
181308	TotalBacte	0,00039661	-0,6762265	k__Bacteria; p__Proteobacteria; c__Gammaproteo
269609	Salinity	0,000399713	0,675942	k__Bacteria; p__Proteobacteria; c__Gammaproteo
258719	PO4	0,000502657	-0,6674411	k__Bacteria; p__Planctomycetes; c__Planctomycet
114736	Salinity	0,000534948	-0,6650846	k__Bacteria; p__Proteobacteria; c__Alphaproteoba
370222	DOC	0,000620605	-0,6593805	k__Bacteria; p__Proteobacteria; c__Gammaproteo
262570	Salinity	0,000626587	-0,659008	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; c
211827	TotalBacte	0,000701295	-0,6545963	k__Bacteria; p__Proteobacteria; c__Betaproteobac
117288	PO4	0,000712708	-0,6539583	k__Bacteria; p__Proteobacteria; c__Gammaproteo
219545	Salinity	0,000753172	0,6517648	k__Bacteria; p__Proteobacteria; c__Gammaproteo
211827	Chla	0,000764703	-0,6511583	k__Bacteria; p__Proteobacteria; c__Betaproteobac
140949	PO4	0,000858794	-0,6464826	k__Archaea; p__Crenarchaeota; c__Thaumarchaeo
251223	TN	0,000885125	-0,6452531	k__Bacteria; p__Proteobacteria; c__Gammaproteo
219545	Z	0,000910031	0,6441186	k__Bacteria; p__Proteobacteria; c__Gammaproteo
370222	POC	0,000937541	-0,642896	k__Bacteria; p__Proteobacteria; c__Gammaproteo
238441	TN	0,000995076	-0,6404352	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; c
278348	NO2.NO3	0,001008164	-0,6398925	k__Bacteria; p__Proteobacteria; c__Alphaproteoba
229855	Salinity	0,001017349	-0,6395152	k__Bacteria; p__Bacteroidetes; c__[Saprospirae]; o
316800	Salinity	0,001082538	-0,6369183	k__Bacteria; p__Proteobacteria; c__Alphaproteoba
149844	TN	0,001095748	-0,6364084	k__Bacteria; p__Proteobacteria; c__Gammaproteo
210698	POC	0,001274979	-0,6299636	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; c
77969	Salinity	0,001296457	-0,6292441	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; c
315661	NO2.NO3	0,001317792	-0,6285395	k__Bacteria; p__Proteobacteria; c__Gammaproteo
149844	Chla	0,001338985	-0,6278491	k__Bacteria; p__Proteobacteria; c__Gammaproteo
110844	Z	0,001356173	0,627296	k__Bacteria; p__Proteobacteria; c__Gammaproteo
238441	DOC	0,001365464	-0,6269995	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; c
139840	POC	0,001370152	-0,6268505	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; c
278348	Salinity	0,001380558	-0,6265214	k__Bacteria; p__Proteobacteria; c__Alphaproteoba
370222	TN	0,001384051	-0,6264114	k__Bacteria; p__Proteobacteria; c__Gammaproteo
240343	NO2.NO3	0,001471753	-0,6237245	k__Bacteria; p__Bacteroidetes; c__Cytophagia; o__
120983	Salinity	0,001488541	-0,6232258	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; c
158301	Salinity	0,001575249	0,6207238	k__Bacteria; p__Proteobacteria; c__Gammaproteo
315125	POC	0,001586171	-0,6204171	k__Bacteria; p__Proteobacteria; c__Alphaproteoba

238441	POC	0,001696968	-0,6174026	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; c
361772	POC	0,001739255	-0,6162961	k__Bacteria; p__Bacteroidetes; c__Sphingobacterii
367917	Si	0,001751015	0,6159924	k__Bacteria; p__Proteobacteria; c__Gammaproteo
258719	POC	0,001860321	-0,6132501	k__Bacteria; p__Planctomycetes; c__Planctomycet
211827	Si	0,001884889	-0,6126526	k__Bacteria; p__Proteobacteria; c__Betaproteobac
197435	Salinity	0,002127555	-0,6070814	k__Bacteria; p__Proteobacteria; c__Gammaproteo
258719	DOC	0,00215942	-0,6063905	k__Bacteria; p__Planctomycetes; c__Planctomycet
23581	Salinity	0,00216978	-0,6061677	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; c
254834	NO2.NO3	0,002277426	0,6136364	k__Bacteria; p__Proteobacteria; c__Gammaproteo
254834	Chla	2,47E-03	0,6096838	k__Bacteria; p__Proteobacteria; c__Gammaproteo
306210	TN	0,002684819	0,5960864	k__Bacteria; p__Proteobacteria; c__Gammaproteo
238441	Si	0,002856473	-0,5930903	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; c
117288	TN	0,003030073	-0,5902111	k__Bacteria; p__Proteobacteria; c__Gammaproteo
315661	Salinity	0,003070785	-0,5895561	k__Bacteria; p__Proteobacteria; c__Gammaproteo
240343	Z	0,003225837	-0,5871267	k__Bacteria; p__Bacteroidetes; c__Cytophagia; o__
23581	Z	0,0033065	-0,5859015	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; c
263093	PO4	0,003443707	-0,5838742	k__Bacteria; p__Bacteroidetes; c__[Saprospirae]; o
110844	NO2.NO3	0,003478205	0,5833752	k__Bacteria; p__Proteobacteria; c__Gammaproteo
149844	TotalBacte	0,003536933	-0,5825352	k__Bacteria; p__Proteobacteria; c__Gammaproteo
244663	NO2.NO3	0,003963995	-0,5767567	k__Bacteria; p__Bacteroidetes; c__[Saprospirae]; o
262570	NO2.NO3	0,003974633	-0,5766196	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; c
278348	PO4	0,0040004	-0,5762887	k__Bacteria; p__Proteobacteria; c__Alphaproteoba
140949	Chla	0,004103517	-0,5749823	k__Archaea; p__Crenarchaeota; c__Thaumarchaeo
140949	TN	0,004143289	-0,5744857	k__Archaea; p__Crenarchaeota; c__Thaumarchaeo
46499	POC	0,004165601	-0,5742089	k__Bacteria; p__Proteobacteria; c__Gammaproteo
141882	POC	0,00444259	-0,5708722	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; c
306798	POC	0,004492124	-0,570294	k__Bacteria; p__Bacteroidetes; c__[Saprospirae]; o
86963	Z	0,004505925	-0,5701338	k__Bacteria; p__Proteobacteria; c__Gammaproteo
315661	Z	0,004680713	-0,5681403	k__Bacteria; p__Proteobacteria; c__Gammaproteo
162915	DOC	0,004707053	-0,5678454	k__Bacteria; p__Proteobacteria; c__Gammaproteo
258719	Si	0,004756922	-0,5672906	k__Bacteria; p__Planctomycetes; c__Planctomycet
211827	PO4	0,004758699	-0,567271	k__Bacteria; p__Proteobacteria; c__Betaproteobac
363730	Chla	0,004822714	-0,5665662	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; c
93013	Si	0,004939677	-0,5731225	k__Bacteria; p__Proteobacteria; c__Gammaproteo
280778	POC	0,004957082	-0,565112	k__Bacteria; p__Bacteroidetes; c__Cytophagia; o__
370222	PO4	0,004970443	-0,5649692	k__Bacteria; p__Proteobacteria; c__Gammaproteo
278348	TN	0,004993418	-0,5647244	k__Bacteria; p__Proteobacteria; c__Alphaproteoba
287911	NO2.NO3	0,005058781	-0,5640331	k__Bacteria; p__Proteobacteria; c__Gammaproteo
113401	Salinity	0,005270697	-0,561842	k__Bacteria; p__Proteobacteria; c__Gammaproteo
111021	Salinity	0,005649459	-0,5581029	k__Bacteria; p__Proteobacteria; c__Alphaproteoba
149844	DOC	0,005942954	-0,5553469	k__Bacteria; p__Proteobacteria; c__Gammaproteo
141709	Z	0,006038133	0,5544775	k__Bacteria; p__Verrucomicrobia; c__Opitutae; o__
317414	POC	0,006092104	0,5612648	k__Bacteria; p__Proteobacteria; c__Gammaproteo
120983	Z	0,006098385	-0,553933	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; c
91093	DOC	0,006155275	-0,553423	k__Bacteria; p__Verrucomicrobia; c__Opitutae; o__
238441	PO4	0,006155275	-0,553423	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; c
167600	TotalBacte	0,006167185	-0,5533167	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; c

370222	Si	0,006375873	-0,5514819	k__Bacteria; p__Proteobacteria; c__Gammaproteo
46499	DOC	0,006490266	-0,5504972	k__Bacteria; p__Proteobacteria; c__Gammaproteo
162915	POC	0,006533763	-0,5501266	k__Bacteria; p__Proteobacteria; c__Gammaproteo
202680	Chla	0,006549624	0,5499919	k__Bacteria; p__Proteobacteria; c__Gammaproteo
211827	TN	0,006702765	-0,5487057	k__Bacteria; p__Proteobacteria; c__Betaproteobac
114736	PO4	0,006798721	-0,5479122	k__Bacteria; p__Proteobacteria; c__Alphaproteoba
149844	Si	0,006813046	-0,5477946	k__Bacteria; p__Proteobacteria; c__Gammaproteo
86963	POC	0,00695346	-0,546652	k__Bacteria; p__Proteobacteria; c__Gammaproteo
251223	Si	0,007031944	-0,5460217	k__Bacteria; p__Proteobacteria; c__Gammaproteo
270469	TN	0,007061793	0,5457836	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; c
117914	TN	0,007121697	-0,5453081	k__Archaea; p__Crenarchaeota; c__Thaumarchaeo
167824	POC	0,00716718	-0,5449493	k__Bacteria; p__Proteobacteria; c__Gammaproteo
47505	Salinity	0,00716937	-0,544932	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; c
254834	TotalBacte	0,007217128	0,5513834	k__Bacteria; p__Proteobacteria; c__Gammaproteo
192790	TN	0,007428443	-0,5429241	k__Bacteria; p__Proteobacteria; c__Alphaproteoba
242563	Z	0,007677014	-0,5410514	k__Bacteria; p__Verrucomicrobia; c__Verrucomicr
330941	NO2.NO3	0,007766306	-0,540391	k__Bacteria; p__Planctomycetes; c__Planctomycet
328766	POC	0,008012863	-0,5385995	k__Bacteria; p__Bacteroidetes; c__Sphingobacterii
91093	TN	0,008087262	-0,5380679	k__Bacteria; p__Verrucomicrobia; c__Opitutae; o__
251223	PO4	0,008161048	-0,5375447	k__Bacteria; p__Proteobacteria; c__Gammaproteo
226297	Z	0,008265346	0,5368117	k__Bacteria; p__Firmicutes; c__Bacilli; o__Lactobar
129034	Z	0,008416813	-0,5357608	k__Bacteria; p__Proteobacteria; c__Gammaproteo
372772	Salinity	0,008440981	-0,5355946	k__Bacteria; p__Proteobacteria; c__Gammaproteo
306210	TotalBacte	0,00880976	0,5331056	k__Bacteria; p__Proteobacteria; c__Gammaproteo
162915	TN	0,008915514	-0,5324078	k__Bacteria; p__Proteobacteria; c__Gammaproteo
249451	Salinity	0,008960993	-0,5321097	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; c
77969	Z	0,009323625	-0,5297773	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; c
110844	POC	0,009535029	0,5284518	k__Bacteria; p__Proteobacteria; c__Gammaproteo
23581	POC	0,009800265	-0,5268228	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; c
140949	POC	0,009800922	-0,5268188	k__Archaea; p__Crenarchaeota; c__Thaumarchaeo
139840	DOC	0,01000852	-0,525569	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; c
263093	POC	0,0100223	-0,5254868	k__Bacteria; p__Chloroflexi; c__SAR202; o__SAR20
271354	TotalBacte	0,0100223	-0,5254868	k__Bacteria; p__Bacteroidetes; c__[Saprospirae]; o
114736	TotalBacte	0,01003068	-0,5254369	k__Bacteria; p__Proteobacteria; c__Alphaproteoba
258719	TN	0,01026142	-0,524075	k__Bacteria; p__Planctomycetes; c__Planctomycet
247038	POC	0,01027151	-0,5240161	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; c
280778	TN	0,01074994	-0,521273	k__Bacteria; p__Bacteroidetes; c__Cytophagia; o__
117288	Salinity	0,01093837	-0,5202202	k__Bacteria; p__Proteobacteria; c__Gammaproteo
23581	NO2.NO3	0,01111346	-0,5192552	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; c
159330	NO2.NO3	0,01114272	-0,5190951	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; c
71505	DOC	0,01119944	-0,5187858	k__Bacteria; p__Proteobacteria; c__Alphaproteoba
250376	TotalBacte	0,01119944	-0,5187858	k__Bacteria; p__Proteobacteria; c__Alphaproteoba
345762	Si	0,01139803	0,5177131	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; c
141882	DOC	0,01150034	-0,5171665	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; c
79388	Salinity	0,01164614	-0,5163942	k__Bacteria; p__Bacteroidetes; c__[Saprospirae]; o
77969	NO2.NO3	0,01199129	-0,5145973	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; c
280778	DOC	0,01229456	-0,5130532	k__Bacteria; p__Bacteroidetes; c__Cytophagia; o__

278348	Chla	0,0123678	-0,5126849	k__Bacteria; p__Proteobacteria; c__Alphaproteoba
377816	Salinity	0,01274812	0,510801	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; c
280778	Z	0,01295993	-0,5097717	k__Bacteria; p__Bacteroidetes; c__Cytophagia; o__
278348	POC	0,01356554	-0,5069028	k__Bacteria; p__Proteobacteria; c__Alphaproteoba
171955	Si	0,01364718	0,5065241	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; c
271354	Chla	0,01375554	-0,5060243	k__Bacteria; p__Proteobacteria; c__Gammaproteo
167824	PO4	0,01375554	-0,5060243	k__Bacteria; p__Chloroflexi; c__SAR202; o__SAR20
219910	TotalBacte	0,01377857	-0,5059185	k__Bacteria; p__Proteobacteria; c__Gammaproteo
262570	PO4	0,01406205	-0,5046278	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; c
151752	POC	0,01443638	-0,5029557	k__Bacteria; p__Proteobacteria; c__Deltaproteoba
122717	Salinity	0,01457112	0,5023624	k__Bacteria; p__Proteobacteria; c__Gammaproteo
122887	Chla	0,01477045	-0,501493	k__Bacteria; p__Proteobacteria; c__Alphaproteoba
250376	PO4	0,01477045	-0,501493	k__Bacteria; p__Proteobacteria; c__Alphaproteoba
250376	POC	0,01477045	-0,501493	k__Bacteria; p__Planctomycetes; c__Phycisphaera
364329	Si	0,01526366	-0,4993821	k__Bacteria; p__Proteobacteria; c__Gammaproteo
364329	Salinity	0,01529346	0,4992563	k__Bacteria; p__Proteobacteria; c__Gammaproteo
181308	Si	0,01531345	-0,4991721	k__Bacteria; p__Proteobacteria; c__Gammaproteo
112372	Salinity	0,01576861	-0,4972778	k__Bacteria; p__Proteobacteria; c__Gammaproteo
306210	PO4	0,01622655	0,4954163	k__Bacteria; p__Proteobacteria; c__Gammaproteo
293057	POC	0,01634949	-0,4949238	k__Bacteria; p__Proteobacteria; c__Gammaproteo
224905	NO2.NO3	0,0164375	-0,4945731	k__Bacteria; p__Proteobacteria; c__Gammaproteo
240343	Salinity	0,01654364	-0,4941522	k__Bacteria; p__Bacteroidetes; c__Cytophagia; o__
139840	TN	0,01655947	-0,4940896	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; c
238441	Chla	0,01660191	-0,493922	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; c
322264	POC	0,01660638	0,4939044	k__Bacteria; p__GN02; c__BD1-5; o__BD1-5CL; f__
317414	Z	0,01669387	0,4935602	k__Bacteria; p__Proteobacteria; c__Gammaproteo
345762	Salinity	0,01669681	-0,4935486	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; c
159330	PO4	0,01671919	-0,4934608	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; c
46499	PO4	0,01671919	-0,4934608	k__Bacteria; p__Proteobacteria; c__Gammaproteo
270469	POC	0,01692477	0,4926586	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; c
163466	NO2.NO3	0,01708829	-0,4920262	k__Bacteria; p__Proteobacteria; c__Gammaproteo
117288	DOC	0,01756928	-0,490194	k__Bacteria; p__Proteobacteria; c__Gammaproteo
150331	TN	0,01785977	0,489107	k__Bacteria; p__Planctomycetes; c__Planctomycet
365604	Chla	0,01788598	0,4890096	k__Bacteria; p__Proteobacteria; c__Gammaproteo
123369	DOC	0,01788598	-0,4890096	k__Bacteria; p__Proteobacteria; c__Gammaproteo
123369	POC	0,01788598	-0,4890096	k__Bacteria; p__Proteobacteria; c__Gammaproteo
123369	TN	0,01788598	-0,4890096	k__Bacteria; p__Proteobacteria; c__Gammaproteo
123369	TotalBacte	0,01788598	-0,4890096	k__Bacteria; p__Proteobacteria; c__Gammaproteo
93490	DOC	0,01790566	-0,4889366	k__Bacteria; p__Proteobacteria; c__Gammaproteo
377714	POC	0,01793507	-0,4888276	k__Bacteria; p__Proteobacteria; c__Alphaproteoba
162915	Si	0,01801485	-0,4885326	k__Bacteria; p__Proteobacteria; c__Gammaproteo
278253	Chla	0,01802255	0,4885042	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; c
231646	DOC	0,01802255	-0,4885042	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; c
313037	DOC	0,01802255	-0,4885042	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; c
318602	DOC	0,01802255	-0,4885042	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; c
294599	DOC	0,01802255	-0,4885042	k__Bacteria; p__Proteobacteria; c__Gammaproteo
165350	NO2.NO3	0,01802255	-0,4885042	k__Bacteria; p__Fibrobacteres; c__Fibrobacteria; o

231646	POC	0,01802255	-0,4885042	k__Bacteria; p__Fibrobacteres; c__Fibrobacteria; o
313037	POC	0,01802255	-0,4885042	k__Bacteria; p__Fibrobacteres; c__Fibrobacteria; o
318602	POC	0,01802255	-0,4885042	k__Bacteria; p__Fibrobacteres; c__Fibrobacteria; o
294599	POC	0,01802255	-0,4885042	k__Bacteria; p__Proteobacteria; c__Gammaproteo
231646	TN	0,01802255	-0,4885042	k__Bacteria; p__Proteobacteria; c__Gammaproteo
313037	TN	0,01802255	-0,4885042	k__Bacteria; p__Proteobacteria; c__Gammaproteo
318602	TN	0,01802255	-0,4885042	k__Bacteria; p__Proteobacteria; c__Gammaproteo
294599	TN	0,01802255	-0,4885042	k__Bacteria; p__Proteobacteria; c__Gammaproteo
231646	TotalBacte	0,01802255	-0,4885042	k__Bacteria; p__Proteobacteria; c__Gammaproteo
313037	TotalBacte	0,01802255	-0,4885042	k__Bacteria; p__Proteobacteria; c__Gammaproteo
318602	TotalBacte	0,01802255	-0,4885042	k__Bacteria; p__Proteobacteria; c__Gammaproteo
294599	TotalBacte	0,01802255	-0,4885042	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; c
314117	Z	0,01802568	0,4884926	k__Bacteria; p__Proteobacteria; c__Gammaproteo
117914	NO2.NO3	0,01803497	-0,4884584	k__Archaea; p__Crenarchaeota; c__Thaumarchaeo
281332	Z	0,01804022	-0,488439	k__Bacteria; p__Proteobacteria; c__Gammaproteo
141882	Si	0,01807131	-0,4883245	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; c
196129	Salinity	0,01829255	0,487514	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; c
113232	DOC	0,01843703	-0,4869889	k__Bacteria; p__Proteobacteria; c__Gammaproteo
188066	PO4	0,01843703	-0,4869889	k__Bacteria; p__Proteobacteria; c__Gammaproteo
113232	POC	0,01843703	-0,4869889	k__Bacteria; p__Proteobacteria; c__Gammaproteo
113232	TN	0,01843703	-0,4869889	k__Bacteria; p__Proteobacteria; c__Gammaproteo
113232	TotalBacte	0,01843703	-0,4869889	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; c
140949	NO2.NO3	0,0185447	-0,4865998	k__Archaea; p__Crenarchaeota; c__Thaumarchaeo
167824	DOC	0,01855524	-0,4865618	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; c
380153	POC	0,01855524	-0,4865618	k__Bacteria; p__Proteobacteria; c__Gammaproteo
364867	POC	0,01855524	-0,4865618	k__Bacteria; p__Actinobacteria; c__Acidimicrobiia;
307260	Si	0,01855524	0,4865618	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; c
219545	NO2.NO3	0,01857523	0,4864899	k__Bacteria; p__Proteobacteria; c__Gammaproteo
250376	DOC	0,01922005	-0,4842001	k__Bacteria; p__Proteobacteria; c__Alphaproteoba
250376	TN	0,01922005	-0,4842001	k__Bacteria; p__Proteobacteria; c__Alphaproteoba
141113	Salinity	0,01951633	-0,4831688	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; c
200817	POC	0,01965587	-0,4826875	k__Bacteria;
315661	TN	0,01967967	-0,4826057	k__Bacteria; p__Proteobacteria; c__Gammaproteo
150331	Si	0,0197265	0,4824449	k__Bacteria; p__Planctomycetes; c__Planctomycet
315661	Chla	0,02005508	-0,4813256	k__Bacteria; p__Proteobacteria; c__Gammaproteo
93013	DOC	0,02098845	-0,4822134	k__Bacteria; p__Proteobacteria; c__Gammaproteo
101591	NO2.NO3	0,02106563	-0,4779733	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; c
315661	PO4	0,02181666	-0,475565	k__Bacteria; p__Proteobacteria; c__Gammaproteo
377714	TN	0,0221108	-0,47464	k__Bacteria; p__Proteobacteria; c__Alphaproteoba
117401	TN	0,02235574	0,4738772	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; c
210698	Salinity	0,02238928	-0,4737733	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; c
207850	DOC	0,02239449	-0,4737572	k__Bacteria; p__Proteobacteria; c__Gammaproteo
363730	POC	0,02241734	-0,4736865	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; c
363730	TotalBacte	0,02241734	-0,4736865	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; c
149844	NO2.NO3	0,02254957	-0,4732784	k__Bacteria; p__Proteobacteria; c__Gammaproteo
211827	POC	0,02261747	-0,4730696	k__Bacteria; p__Proteobacteria; c__Betaproteobac
150331	NO2.NO3	0,02263785	0,473007	k__Bacteria; p__Planctomycetes; c__Planctomycet

110844	Chla	0,02279079	0,4725389	k__Bacteria; p__Proteobacteria; c__Gammaproteo
315125	DOC	0,02294926	-0,4720565	k__Bacteria; p__Proteobacteria; c__Alphaproteoba
192790	NO2.NO3	0,0232483	-0,4711534	k__Bacteria; p__Proteobacteria; c__Alphaproteoba
364944	POC	0,02328607	-0,47104	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; c
367917	DOC	0,02344993	0,4705498	k__Bacteria; p__Proteobacteria; c__Gammaproteo
181308	TN	0,02346983	-0,4704904	k__Bacteria; p__Proteobacteria; c__Gammaproteo
114736	TN	0,02358096	-0,4701597	k__Bacteria; p__Proteobacteria; c__Alphaproteoba
224089	Si	0,02365999	0,4699253	k__Bacteria; p__Proteobacteria; c__Gammaproteo
270469	Si	0,02376852	0,4696044	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; c
125824	Si	0,02390876	-0,4691915	k__Bacteria; p__Proteobacteria; c__Gammaproteo
192790	DOC	0,02410384	-0,4686203	k__Bacteria; p__Proteobacteria; c__Alphaproteoba
310842	Z	0,02424773	-0,4682014	k__Archaea; p__Euryarchaeota; c__Thermoplasma
93013	TN	0,02440629	-0,4713439	k__Bacteria; p__Proteobacteria; c__Gammaproteo
263093	DOC	0,02462956	-0,4670994	k__Bacteria; p__Proteobacteria; c__Gammaproteo
226297	NO2.NO3	0,02462956	0,4670994	k__Bacteria; p__Firmicutes; c__Bacilli; o__Lactobac
271354	PO4	0,02462956	-0,4670994	k__Bacteria; p__Chloroflexi; c__SAR202; o__SAR20
271354	POC	0,02462956	-0,4670994	k__Bacteria; p__Chloroflexi; c__SAR202; o__SAR20
271354	Si	0,02462956	-0,4670994	k__Bacteria; p__Chloroflexi; c__SAR202; o__SAR20
167824	TN	0,02462956	-0,4670994	k__Bacteria; p__Bacteroidetes; c__[Saprospirae]; o
250376	Chla	0,02469661	-0,4669073	k__Bacteria; p__Proteobacteria; c__Alphaproteoba
123369	Chla	0,02474043	-0,4667819	k__Bacteria; p__Proteobacteria; c__Gammaproteo
123402	DOC	0,02474043	-0,4667819	k__Bacteria; p__Actinobacteria; c__Acidimicrobiia;
321377	DOC	0,02474043	-0,4667819	k__Bacteria; p__Actinobacteria; c__Acidimicrobiia;
123402	POC	0,02474043	-0,4667819	k__Bacteria; p__Actinobacteria; c__Acidimicrobiia;
321377	POC	0,02474043	-0,4667819	k__Bacteria; p__Proteobacteria; c__Gammaproteo
123402	TN	0,02474043	-0,4667819	k__Bacteria; p__Proteobacteria; c__Gammaproteo
321377	TN	0,02474043	-0,4667819	k__Bacteria; p__Proteobacteria; c__Gammaproteo
322468	TotalBacte	0,02474043	-0,4667819	k__Bacteria; p__Proteobacteria; c__Gammaproteo
101074	Z	0,02475752	-0,4667331	k__Bacteria; p__Bacteroidetes; c__[Saprospirae]; o
129034	Salinity	0,02522445	-0,4654094	k__Bacteria; p__Proteobacteria; c__Gammaproteo
197435	Z	0,02526461	-0,4652964	k__Bacteria; p__Proteobacteria; c__Gammaproteo
231646	Chla	0,02528395	-0,4652421	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; c
313037	Chla	0,02528395	-0,4652421	k__Bacteria; p__Proteobacteria; c__Alphaproteoba
318602	Chla	0,02528395	-0,4652421	k__Bacteria; p__Proteobacteria; c__Alphaproteoba
294599	Chla	0,02528395	-0,4652421	k__Bacteria; p__Proteobacteria; c__Alphaproteoba
267167	DOC	0,02528395	-0,4652421	k__Archaea; p__Euryarchaeota; c__Thermoplasma
97116	DOC	0,02528395	-0,4652421	k__Archaea; p__Euryarchaeota; c__Thermoplasma
102013	DOC	0,02528395	-0,4652421	k__Archaea; p__Euryarchaeota; c__Thermoplasma
150062	DOC	0,02528395	-0,4652421	k__Bacteria; p__Fibrobacteres; c__Fibrobacteria; o
267167	POC	0,02528395	-0,4652421	k__Bacteria; p__Proteobacteria; c__Gammaproteo
97116	POC	0,02528395	-0,4652421	k__Bacteria; p__Proteobacteria; c__Epsilonproteob
102013	POC	0,02528395	-0,4652421	k__Bacteria; p__Proteobacteria; c__Epsilonproteob
150062	POC	0,02528395	-0,4652421	k__Bacteria; p__Proteobacteria; c__Epsilonproteob
267167	TN	0,02528395	-0,4652421	k__Bacteria; p__Proteobacteria; c__Gammaproteo
97116	TN	0,02528395	-0,4652421	k__Bacteria; p__Proteobacteria; c__Deltaproteoba
102013	TN	0,02528395	-0,4652421	k__Bacteria; p__Proteobacteria; c__Deltaproteoba
150062	TN	0,02528395	-0,4652421	k__Bacteria; p__Proteobacteria; c__Deltaproteoba

324220	TotalBacte	0,02528395	-0,4652421	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; c
117401	Si	0,02553684	0,4645347	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; c
363730	PO4	0,0258907	-0,4635541	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; c
278641	TotalBacte	0,0258907	-0,4635541	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; c
258719	Chla	0,02608351	-0,4630244	k__Bacteria; p__Planctomycetes; c__Planctomycet
113232	Chla	0,02618729	-0,4627405	k__Bacteria; p__Proteobacteria; c__Betaproteobac
22543	DOC	0,02618729	-0,4627405	k__Bacteria; p__Proteobacteria; c__Betaproteobac
107378	DOC	0,02618729	-0,4627405	k__Bacteria; p__Proteobacteria; c__Betaproteobac
161507	DOC	0,02618729	-0,4627405	k__Bacteria; p__Proteobacteria; c__Gammaproteo
22543	POC	0,02618729	-0,4627405	k__Bacteria; p__Proteobacteria; c__Alphaproteoba
107378	POC	0,02618729	-0,4627405	k__Bacteria; p__Proteobacteria; c__Alphaproteoba
161507	POC	0,02618729	-0,4627405	k__Bacteria; p__Proteobacteria; c__Alphaproteoba
22543	TN	0,02618729	-0,4627405	k__Bacteria; p__Proteobacteria; c__Gammaproteo
107378	TN	0,02618729	-0,4627405	k__Bacteria; p__Proteobacteria; c__Gammaproteo
161507	TN	0,02618729	-0,4627405	k__Bacteria; p__Proteobacteria; c__Gammaproteo
151752	PO4	0,02626095	-0,4625396	k__Bacteria; p__Proteobacteria; c__Deltaproteoba
240343	TN	0,02640612	-0,462145	k__Bacteria; p__Bacteroidetes; c__Cytophagia; o__
190600	Salinity	0,02646815	0,4619768	k__Bacteria; p__Proteobacteria; c__Gammaproteo
202680	NO2.NO3	0,02667274	0,4614246	k__Bacteria; p__Proteobacteria; c__Gammaproteo
169677	Salinity	0,02719672	-0,4600256	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; c
203464	POC	0,02752164	-0,4591688	k__Bacteria; p__Verrucomicrobia; c__Opitutae; o__
192712	POC	0,02754258	-0,4591139	k__Bacteria; p__Proteobacteria; c__Gammaproteo
159330	Salinity	0,02758296	-0,459008	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; c
91369	Salinity	0,02760097	-0,4589609	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; c
326153	DOC	0,02799214	-0,4579424	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; c
326153	TotalBacte	0,02799214	-0,4579424	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; c
141113	DOC	0,02830779	0,4571288	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; c
240343	Chla	0,02848793	-0,4566677	k__Bacteria; p__Bacteroidetes; c__Cytophagia; o__
20442	PO4	0,02856542	-0,45647	k__Bacteria; p__Verrucomicrobia; c__Verrucomicro
367917	Salinity	0,02860567	-0,4563676	k__Bacteria; p__Proteobacteria; c__Gammaproteo
317932	Chla	0,02870863	0,4561059	k__Bacteria; p__Bacteroidetes;
151752	TotalBacte	0,02882798	-0,4558036	k__Bacteria; p__Proteobacteria; c__Deltaproteoba
315125	TN	0,02891968	-0,455572	k__Bacteria; p__Proteobacteria; c__Alphaproteoba
363730	DOC	0,02910305	-0,4551105	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; c
98948	TotalBacte	0,02920269	-0,4548608	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; c
223399	NO2.NO3	0,02923396	-0,4547825	k__Bacteria; p__Bacteroidetes; c__Cytophagia; o__
93013	Salinity	0,02940986	0,4543437	k__Bacteria; p__Proteobacteria; c__Gammaproteo
110844	Salinity	0,02943741	0,4542751	k__Bacteria; p__Proteobacteria; c__Gammaproteo
210698	TotalBacte	0,02965819	-0,4537276	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; c
98948	POC	0,02986298	-0,4532226	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; c
46499	Si	0,02991829	-0,4530867	k__Bacteria; p__Proteobacteria; c__Gammaproteo
278641	PO4	0,03012627	-0,4525775	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; c
115460	Salinity	0,03058464	-0,4514649	k__Bacteria; p__Proteobacteria; c__Gammaproteo
117914	DOC	0,03075394	-0,4510573	k__Archaea; p__Crenarchaeota; c__Thaumarchaeo
91093	PO4	0,03075458	-0,4510558	k__Bacteria; p__Verrucomicrobia; c__Opitutae; o__
190600	POC	0,03117567	-0,4500497	k__Bacteria; p__Proteobacteria; c__Gammaproteo
278641	POC	0,0311779	-0,4500444	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; c

162915	PO4	0,03131464	-0,44972	k__Bacteria; p__Proteobacteria; c__Gammaproteo
240569	POC	0,03135927	-0,4496144	k__Bacteria; p__Proteobacteria; c__Deltaproteoba
224905	Salinity	0,03151518	-0,4492464	k__Bacteria; p__Proteobacteria; c__Gammaproteo
125824	TN	0,0318741	-0,4484045	k__Bacteria; p__Proteobacteria; c__Gammaproteo
120983	NO2.NO3	0,03204485	-0,4480067	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; c
91093	Z	0,03208778	-0,4479069	k__Bacteria; p__Verrucomicrobia; c__Opitutae; o__
292848	Salinity	0,03215581	0,4477491	k__Bacteria; p__Proteobacteria; c__Gammaproteo
114726	POC	0,03218096	-0,4476908	k__Bacteria; p__Verrucomicrobia; c__Opitutae; o__
167824	NO2.NO3	0,03220422	-0,4476369	k__Bacteria; p__Proteobacteria; c__Gammaproteo
271354	TN	0,03220422	-0,4476369	k__Bacteria; p__Proteobacteria; c__Gammaproteo
263093	TN	0,03220422	-0,4476369	k__Bacteria; p__Chloroflexi; c__SAR202; o__SAR20
167824	TotalBacte	0,03220422	-0,4476369	k__Bacteria; p__Bacteroidetes; c__[Saprospirae]; o
117288	Chla	0,03233719	-0,4473295	k__Bacteria; p__Proteobacteria; c__Gammaproteo
377714	DOC	0,03280103	-0,4462648	k__Bacteria; p__Proteobacteria; c__Alphaproteoba
302992	TotalBacte	0,03280103	-0,4462648	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; c
272690	Si	0,03280613	-0,4462532	k__Bacteria; p__Planctomycetes; c__vadinHA49; o
46499	TN	0,03290083	-0,4460373	k__Bacteria; p__Proteobacteria; c__Gammaproteo
315661	POC	0,03314534	-0,4454822	k__Bacteria; p__Proteobacteria; c__Gammaproteo
270469	DOC	0,03333819	0,4450466	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; c
306798	DOC	0,03342906	-0,4448421	k__Bacteria; p__Bacteroidetes; c__[Saprospirae]; o
113232	Si	0,0335573	-0,4445542	k__Bacteria; p__Proteobacteria; c__Gammaproteo
364195	Z	0,03387208	-0,4438512	k__Bacteria; p__Proteobacteria; c__Gammaproteo
128241	Z	0,03412231	-0,4432961	k__Bacteria; p__Proteobacteria; c__Gammaproteo
380239	Z	0,03412231	-0,4432961	k__Archaea; p__Euryarchaeota; c__Thermoplasma
117401	TotalBacte	0,03437658	0,4427353	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; c
330571	POC	0,03465439	-0,4421262	k__Bacteria; p__Proteobacteria; c__Gammaproteo
101637	Chla	0,03472136	-0,44198	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; c
335627	DOC	0,03472136	-0,44198	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; c
101637	POC	0,03472136	-0,44198	k__Bacteria; p__Fibrobacteres; c__Fibrobacteria; o
231646	Si	0,03472136	-0,44198	k__Bacteria; p__Proteobacteria; c__Gammaproteo
313037	Si	0,03472136	-0,44198	k__Bacteria; p__Proteobacteria; c__Gammaproteo
318602	Si	0,03472136	-0,44198	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; c
294599	Si	0,03472136	-0,44198	k__Bacteria; p__SAR406; c__AB16; o__Arctic96B-7
374536	Si	0,03472136	-0,44198	k__Bacteria; p__SAR406; c__AB16; o__Arctic96B-7
322246	TN	0,03472136	-0,44198	k__Archaea; p__Crenarchaeota; c__Thaumarchaeo
81434	Z	0,03479268	-0,4418245	k__Bacteria; p__Proteobacteria; c__Betaproteobac
93490	Salinity	0,03510109	0,441155	k__Bacteria; p__Proteobacteria; c__Gammaproteo
188066	DOC	0,03539896	-0,4405128	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; c
188066	POC	0,03539896	-0,4405128	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; c
139656	Si	0,03539896	-0,4405128	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; c
188066	TN	0,03539896	-0,4405128	k__Bacteria; p__Proteobacteria; c__Gammaproteo
166246	NO2.NO3	0,0354058	-0,4404981	k__Bacteria; p__Proteobacteria; c__Alphaproteoba
151752	DOC	0,03559793	-0,4400862	k__Bacteria; p__Proteobacteria; c__Deltaproteoba
150331	Chla	0,0360417	0,4391415	k__Bacteria; p__Planctomycetes; c__Planctomycet
101074	NO2.NO3	0,03629103	-0,4386147	k__Bacteria; p__Bacteroidetes; c__[Saprospirae]; o
117288	NO2.NO3	0,03632805	-0,4385367	k__Bacteria; p__Proteobacteria; c__Gammaproteo
123369	Si	0,03634925	-0,4384921	k__Bacteria; p__Proteobacteria; c__Gammaproteo

210698	PO4	0,03641827	-0,438347	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; c
344542	NO2.NO3	0,03662234	-0,4379192	k__Bacteria; p__Proteobacteria; c__Gammaproteo
278348	TotalBacte	0,03681505	-0,4375168	k__Bacteria; p__Proteobacteria; c__Alphaproteoba
79388	NO2.NO3	0,03708415	-0,4369578	k__Bacteria; p__Bacteroidetes; c__[Saprospirae]; o
137355	POC	0,03728892	-0,4365346	k__Bacteria; p__Proteobacteria; c__Alphaproteoba
364329	POC	0,03777539	-0,4355364	k__Bacteria; p__Proteobacteria; c__Gammaproteo
117914	POC	0,03786736	-0,4353488	k__Archaea; p__Crenarchaeota; c__Thaumarchaeo
278641	Salinity	0,0381602	-0,434754	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; c
345762	DOC	0,03854026	0,4339872	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; c
94191	Salinity	0,03901253	0,4330428	k__Bacteria; p__Proteobacteria; c__Epsilonproteob
219924	Chla	0,03937621	0,4323215	k__Bacteria; p__Proteobacteria; c__Gammaproteo
291227	DOC	0,03946002	-0,4321561	k__Bacteria; p__Verrucomicrobia; c__Verrucomicro
291227	POC	0,03946002	-0,4321561	k__Bacteria; p__Verrucomicrobia; c__Verrucomicro
20442	Chla	0,03953859	-0,4320012	k__Bacteria; p__Verrucomicrobia; c__Verrucomicro
270469	PO4	0,03978616	0,4315148	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; c
278641	TN	0,03980984	-0,4314684	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; c
254834	Salinity	4,00E-02	0,4310821	k__Bacteria; p__Proteobacteria; c__Gammaproteo
213420	POC	0,04022591	-0,4306567	k__Bacteria; p__Verrucomicrobia; c__Verrucomicro
117914	PO4	0,04050666	-0,4301127	k__Archaea; p__Crenarchaeota; c__Thaumarchaeo
240343	PO4	0,04058264	-0,429966	k__Bacteria; p__Bacteroidetes; c__Cytophagia; o__
113401	Z	0,04151259	-0,4281874	k__Bacteria; p__Proteobacteria; c__Gammaproteo
307260	Chla	0,04151946	0,4281744	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; c
335078	POC	0,04151946	0,4281744	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; c
263093	Si	0,04151946	-0,4281744	k__Bacteria; p__Bacteroidetes; c__[Saprospirae]; o
263093	TotalBacte	0,04151946	-0,4281744	k__Bacteria; p__Bacteroidetes; c__[Saprospirae]; o
125824	DOC	0,04155214	-0,4281125	k__Bacteria; p__Proteobacteria; c__Gammaproteo
278348	DOC	0,04167507	-0,4278799	k__Bacteria; p__Proteobacteria; c__Alphaproteoba
328766	DOC	0,04253661	-0,4262648	k__Bacteria; p__Bacteroidetes; c__Sphingobacterii
364329	TotalBacte	0,04287476	-0,4256379	k__Bacteria; p__Proteobacteria; c__Gammaproteo
186510	Salinity	0,04289601	0,4255986	k__Bacteria; p__Proteobacteria; c__Deltaproteoba
140949	Si	0,04347552	-0,4245335	k__Archaea; p__Crenarchaeota; c__Thaumarchaeo
162915	Chla	0,04354453	-0,4244074	k__Bacteria; p__Proteobacteria; c__Gammaproteo
377714	Si	0,04358231	-0,4243385	k__Bacteria; p__Proteobacteria; c__Alphaproteoba
158301	NO2.NO3	0,04368401	0,4241531	k__Bacteria; p__Proteobacteria; c__Gammaproteo
306210	NO2.NO3	0,04376541	0,4240049	k__Bacteria; p__Proteobacteria; c__Gammaproteo
196129	TotalBacte	0,04406234	-0,4234663	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; c
139840	PO4	0,04436577	-0,4229188	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; c
322468	Chla	0,04469586	-0,4223265	k__Bacteria; p__Actinobacteria; c__Acidimicrobiia;
113232	PO4	0,04469586	-0,4223265	k__Bacteria; p__Proteobacteria; c__Gammaproteo
322468	TN	0,04469586	-0,4223265	k__Bacteria; p__Proteobacteria; c__Gammaproteo
123402	TotalBacte	0,04469586	-0,4223265	k__Bacteria; p__Proteobacteria; c__Gammaproteo
321377	TotalBacte	0,04469586	-0,4223265	k__Bacteria; p__Proteobacteria; c__Gammaproteo
110844	TN	0,04484011	0,4220687	k__Bacteria; p__Proteobacteria; c__Gammaproteo
219910	POC	0,04495263	-0,4218681	k__Bacteria; p__Proteobacteria; c__Gammaproteo
114736	NO2.NO3	0,04512342	-0,4215644	k__Bacteria; p__Proteobacteria; c__Alphaproteoba
89505	Salinity	0,04542256	-0,4210345	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; c
232438	Salinity	0,04542256	-0,4210345	k__Bacteria; p__Proteobacteria; c__Alphaproteoba

112981	Salinity	0,04542256	-0,4210345	k__Bacteria; p__Proteobacteria; c__Alphaproteoba
254834	TN	4,55E-02	0,4229249	k__Bacteria; p__Proteobacteria; c__Gammaproteo
141882	PO4	0,04589812	-0,4201977	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; c
20442	TN	0,04590329	-0,4201887	k__Bacteria; p__Verrucomicrobia; c__Verrucomicr
322246	Z	0,04603125	-0,4199647	k__Archaea; p__Crenarchaeota; c__Thaumarchaeo
307120	Salinity	0,04632989	-0,4194438	k__Bacteria; p__Verrucomicrobia; c__Verrucomicr
186416	Salinity	0,04632989	-0,4194438	k__Bacteria; p__Proteobacteria; c__Alphaproteoba
324220	Chla	0,04674864	-0,4187179	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; c
150051	DOC	0,04674864	0,4187179	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; c
101158	DOC	0,04674864	-0,4187179	k__Bacteria; p__Proteobacteria; c__Alphaproteoba
231646	PO4	0,04674864	-0,4187179	k__Bacteria; p__Bacteroidetes; c__Sphingobacterii
313037	PO4	0,04674864	-0,4187179	k__Archaea; p__Euryarchaeota; c__Thermoplasma
318602	PO4	0,04674864	-0,4187179	k__Bacteria; p__Fibrobacteres; c__Fibrobacteria; o
294599	PO4	0,04674864	-0,4187179	k__Bacteria; p__Proteobacteria; c__Gammaproteo
335627	POC	0,04674864	-0,4187179	k__Bacteria; p__Proteobacteria; c__Deltaproteoba
324220	Si	0,04674864	-0,4187179	k__Bacteria; p__Proteobacteria; c__Epsilonproteob
324220	TN	0,04674864	-0,4187179	k__Bacteria; p__Proteobacteria; c__Gammaproteo
267167	TotalBacte	0,04674864	-0,4187179	k__Bacteria; p__Proteobacteria; c__Deltaproteoba
97116	TotalBacte	0,04674864	-0,4187179	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; c
102013	TotalBacte	0,04674864	-0,4187179	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; c
150062	TotalBacte	0,04674864	-0,4187179	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; c
150331	PO4	0,04746378	0,4174898	k__Bacteria; p__Planctomycetes; c__Planctomycet
315125	TotalBacte	0,04798211	-0,4166086	k__Bacteria; p__Proteobacteria; c__Alphaproteoba
259896	NO2.NO3	0,04818247	0,4162699	k__Bacteria; p__Proteobacteria; c__Gammaproteo
269689	DOC	0,04818575	0,4162644	k__Bacteria; p__Proteobacteria; c__Gammaproteo
322468	Si	0,04818575	-0,4162644	k__Bacteria; p__Proteobacteria; c__Gammaproteo
326153	Si	0,04834342	-0,4159987	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; c
210698	NO2.NO3	0,04839201	-0,415917	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; c
143537	NO2.NO3	0,0485364	0,4156744	k__Bacteria; p__Proteobacteria; c__Alphaproteoba
278641	NO2.NO3	0,04868489	-0,4154256	k__Bacteria; p__Proteobacteria; c__Gammaproteo
287911	PO4	0,04868489	-0,4154256	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; c
186510	Z	0,04869719	0,415405	k__Bacteria; p__Proteobacteria; c__Deltaproteoba
122887	NO2.NO3	0,04892246	-0,4150287	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; c
107743	POC	0,04892246	-0,4150287	k__Bacteria; p__Planctomycetes; c__Phycisphaera
189443	TotalBacte	0,04892246	-0,4150287	k__Bacteria; p__Proteobacteria; c__Betaproteobac
123369	PO4	0,04939496	-0,4142437	k__Bacteria; p__Proteobacteria; c__Gammaproteo
188066	Si	0,04939496	-0,4142437	k__Bacteria; p__Proteobacteria; c__Betaproteobac
22543	TotalBacte	0,04939496	-0,4142437	k__Bacteria; p__Proteobacteria; c__Alphaproteoba
107378	TotalBacte	0,04939496	-0,4142437	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; c
161507	TotalBacte	0,04939496	-0,4142437	k__Bacteria; p__Proteobacteria; c__Gammaproteo
139840	Si	0,04952878	-0,4140224	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; c
207850	POC	0,04958121	-0,4139359	k__Bacteria; p__Proteobacteria; c__Gammaproteo

SW

OTU	Env	P-value	Spearman r	Taxonomic affiliation
101591	PO4	3,17852E-05	0,7665176	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; c

263093	Si	1,36E-04	0,7374581	k__Bacteria; p__Bacteroidetes; c__[Saprospirae]; o
304309	Z	0,000208483	-0,7109134	k__Bacteria; p__Proteobacteria; c__Alphaproteoba
51448	DOC	0,000232466	-0,7200852	k__Bacteria; p__Proteobacteria; c__Gammaproteo
281929	Si	0,000248633	0,7178021	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; c
325407	Z	0,00042828	-0,6856388	k__Bacteria; p__Proteobacteria; c__Alphaproteoba
251742	TotalBacte	0,000485903	-0,6809399	k__Bacteria; p__Planctomycetes; c__OM190; o__C
281929	PO4	0,000524495	0,6780539	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; c
71505	TN	0,000587566	0,6737074	k__Bacteria; p__Proteobacteria; c__Alphaproteoba
100891	Z	0,000616789	-0,671828	k__Bacteria; p__Proteobacteria; c__Gammaproteo
94744	Z	0,000847444	-0,6591956	k__Bacteria; p__Proteobacteria; c__Betaproteobac
210698	TotalBacte	0,000919568	-0,6558523	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; c
123402	TN	0,000962024	-0,6539876	k__Bacteria; p__Actinobacteria; c__Acidimicrobiia;
91369	NO2.NO3	0,001022261	-0,6514588	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; c
364944	PO4	0,001338875	-0,6399443	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; c
114736	DOC	0,001401556	-0,6507218	k__Bacteria; p__Proteobacteria; c__Alphaproteoba
117914	TN	0,001443501	0,6366493	k__Archaea; p__Crenarchaeota; c__Thaumarchaeo
92901	TotalProtis	0,001564022	-0,6330962	k__Bacteria; p__Verrucomicrobia; c__Verrucomicr
141882	Si	0,001602355	-0,6447638	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; c
308895	TotalBacte	0,001689239	-0,6296426	k__Bacteria; p__Proteobacteria; c__Alphaproteoba
197435	TotalProtis	0,001726932	-0,6286454	k__Bacteria; p__Proteobacteria; c__Gammaproteo
364329	TotalProtis	0,001747156	-0,628118	k__Bacteria; p__Proteobacteria; c__Gammaproteo
265656	POC	0,001876099	0,6510672	k__Bacteria; p__Proteobacteria; c__Alphaproteoba
249494	PO4	0,001915114	0,6239268	k__Bacteria; p__Bacteroidetes; c__Cytophagia; o__
202680	TotalBacte	0,002265584	0,6160973	k__Bacteria; p__Proteobacteria; c__Gammaproteo
163466	TotalBacte	0,002306315	-0,615255	k__Bacteria; p__Proteobacteria; c__Gammaproteo
159330	Salinity	0,002307145	-0,615238	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; c
317414	DOC	0,002424039	0,6255278	k__Bacteria; p__Proteobacteria; c__Gammaproteo
301703	Salinity	0,002681	0,6080447	k__Bacteria; p__Gemmatimonadetes; c__Gemm-2;
374536	NO2.NO3	0,002718163	0,6073767	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; c
36166	TotalProtis	0,002941009	0,6035252	k__Bacteria; p__Lentisphaerae; c__[Lentisphaeria];
93013	Si	0,002986605	0,6153348	k__Bacteria; p__Proteobacteria; c__Gammaproteo
270469	DOC	0,003043726	0,6143922	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; c
140949	TN	0,00309021	0,6010815	k__Archaea; p__Crenarchaeota; c__Thaumarchaeo
290192	DOC	0,003170973	-0,6123445	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; c
263093	PO4	0,003320711	0,5974943	k__Bacteria; p__Bacteroidetes; c__[Saprospirae]; o
101591	Si	0,003595652	0,6059735	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; c
131420	Z	0,003646598	-0,5927634	k__Bacteria; p__Proteobacteria; c__Alphaproteoba
327244	Salinity	0,003729522	0,5916164	k__Bacteria; p__Proteobacteria; c__Gammaproteo
101637	Chla	0,003800438	0,5906523	k__Bacteria; p__SAR406; c__AB16; o__Arctic96B-7
281929	NO2.NO3	0,003914856	0,5891281	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; c
91369	TN	0,004203121	-0,5854469	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; c
355505	NO2.NO3	0,004215716	0,5852909	k__Bacteria; p__Bacteroidetes;
322468	Chla	0,00444011	0,5825754	k__Bacteria; p__Proteobacteria; c__Gammaproteo
164602	NO2.NO3	0,004596463	-0,5807502	k__Bacteria; p__Proteobacteria; c__Gammaproteo
123402	NO2.NO3	0,004629735	-0,5803685	k__Bacteria; p__Actinobacteria; c__Acidimicrobiia;
40973	TotalBacte	0,004913067	-0,5772076	k__Bacteria;
292848	Chla	0,005127154	0,5749185	k__Bacteria; p__Proteobacteria; c__Gammaproteo

292701	TN	0,005323142	-0,5728916	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; c
115425	TotalBacte	0,005338716	-0,5727333	k__Bacteria; p__Proteobacteria; c__Deltaproteoba
292848	NO2.NO3	0,005352079	-0,5725977	k__Bacteria; p__Proteobacteria; c__Gammaproteo
261211	TN	0,00536178	-0,5724994	k__Bacteria; p__Proteobacteria; c__Gammaproteo
215143	Salinity	0,005376828	0,5723473	k__Bacteria; p__Proteobacteria; c__Gammaproteo
279636	DOC	0,005581353	0,5825981	k__Archaea; p__Crenarchaeota; c__Thaumarchaeo
335627	TotalBacte	0,005671652	-0,569436	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; c
60936	TN	0,005848675	-0,5677478	k__Bacteria; p__Chlamydiae; c__ChlamydiaePH; o_
252674	Salinity	0,005895544	0,567308	k__Bacteria; p__Proteobacteria; c__Gammaproteo
249494	NO2.NO3	0,006146703	0,5649993	k__Bacteria; p__Bacteroidetes; c__Cytophagia; o__
244663	Si	0,006237863	-0,5764023	k__Bacteria; p__Bacteroidetes; c__[Saprospirae]; o
141113	Si	0,006410608	0,574862	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; c
254095	TN	0,007032529	-0,5574356	k__Bacteria; p__Planctomycetes; c__Phycisphaera
224905	Si	0,007045766	0,5694776	k__Bacteria; p__Proteobacteria; c__Gammaproteo
271191	NO2.NO3	0,007224547	0,5559011	k__Bacteria; p__Planctomycetes; c__Planctomycet
364944	Si	0,007277474	-0,5676127	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; c
364944	NO2.NO3	0,007282805	-0,5554421	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; c
141882	TN	0,007389031	-0,5546131	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; c
81434	PO4	0,007453421	0,5541154	k__Bacteria; p__Proteobacteria; c__Betaproteobac
247038	TN	0,007499176	-0,5537639	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; c
117914	Si	0,007649302	0,5647197	k__Archaea; p__Crenarchaeota; c__Thaumarchaeo
247038	NO2.NO3	0,007821212	-0,5513386	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; c
95531	Z	0,008001585	-0,5500161	k__Bacteria; p__Proteobacteria; c__Gammaproteo
254095	Si	0,008035721	-0,5618332	k__Bacteria; p__Planctomycetes; c__Phycisphaera
130084	TotalBacte	0,008338723	-0,5476086	k__Bacteria; p__Proteobacteria; c__Gammaproteo
117401	Si	0,008509251	-0,5584475	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; c
173116	Salinity	0,008553996	0,546113	k__Bacteria; p__Proteobacteria; c__Alphaproteoba
245942	Chla	0,009465224	0,5401065	k__Bacteria; p__Proteobacteria; c__Gammaproteo
139421	TN	0,009664866	0,5388544	k__Bacteria; p__SAR406; c__AB16; o__Arctic96B-7
173116	TotalBacte	0,01005693	-0,5364562	k__Bacteria; p__Proteobacteria; c__Alphaproteoba
164602	Chla	0,01032808	0,5348421	k__Bacteria; p__Proteobacteria; c__Gammaproteo
126619	Si	0,01047156	-0,5458789	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; c
191808	TotalBacte	0,010741	-0,5324496	k__Bacteria; p__Actinobacteria; c__Acidimicrobiia;
310842	TotalBacte	0,01114002	0,5302082	k__Archaea; p__Euryarchaeota; c__Thermoplasma
123178	Z	0,0111655	-0,5300673	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; c
60936	NO2.NO3	0,01135656	-0,5290192	k__Bacteria; p__Chlamydiae; c__ChlamydiaePH; o_
181913	PO4	0,01145483	0,5284857	k__Bacteria; p__Planctomycetes; c__OM190; o__C
200364	POC	0,01174662	-0,5513109	k__Bacteria; p__Proteobacteria; c__Alphaproteoba
255572	Chla	0,01200174	-0,5255833	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; c
380153	TN	0,01206544	0,5252523	k__Bacteria; p__Actinobacteria; c__Acidimicrobiia;
306210	Si	0,01212887	0,5366856	k__Bacteria; p__Proteobacteria; c__Gammaproteo
23581	Si	0,01226132	-0,535996	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; c
357686	Chla	0,01230938	0,5239978	k__Bacteria; p__Proteobacteria; c__Gammaproteo
200114	TotalBacte	0,01239079	-0,5235837	k__Bacteria; p__Planctomycetes; c__Planctomycet
140949	Si	0,0124486	0,5350311	k__Archaea; p__Crenarchaeota; c__Thaumarchaeo
316800	TotalBacte	0,01254593	-0,5228006	k__Bacteria; p__Proteobacteria; c__Alphaproteoba
310842	Salinity	0,01275061	-0,5217794	k__Archaea; p__Euryarchaeota; c__Thermoplasma

202680	Salinity	0,01287009	-0,5211895	k__Bacteria; p__Proteobacteria; c__Gammaproteo
195358	TotalProtis	0,01288922	0,5210955	k__Bacteria; p__Proteobacteria; c__Gammaproteo
53737	Chla	0,01302726	0,5204203	k__Bacteria; p__Bacteroidetes; c__[Saprospirae]; o
192198	Z	0,01314708	-0,5198389	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; c
315125	Z	0,01334737	0,5188767	k__Bacteria; p__Proteobacteria; c__Alphaproteoba
232517	POC	0,01360286	-0,5418091	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; c
224905	TN	0,01365093	0,5174404	k__Bacteria; p__Proteobacteria; c__Gammaproteo
117401	TotalProtis	0,01381446	0,5166775	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; c
215368	TN	0,01404312	-0,5156229	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; c
101591	NO2.NO3	0,01407196	0,5154908	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; c
117914	NO2.NO3	0,01409697	0,5153766	k__Archaea; p__Crenarchaeota; c__Thaumarchaeo
138577	Z	0,01434814	0,5142377	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; c
178816	TotalBacte	0,01464662	0,5129051	k__Bacteria; p__Proteobacteria; c__Gammaproteo
242563	TotalBacte	0,01467064	-0,5127988	k__Bacteria; p__Verrucomicrobia; c__Verrucomicro
309485	Salinity	0,01473953	0,5124948	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; c
287911	Z	0,01474747	0,5124598	k__Bacteria; p__Proteobacteria; c__Gammaproteo
143882	PO4	0,01487523	0,5118993	k__Bacteria; p__Proteobacteria; c__Alphaproteoba
219117	Si	0,01533473	-0,5214747	k__Bacteria; p__Proteobacteria; c__Gammaproteo
126619	TN	0,01575273	-0,5081516	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; c
360749	DOC	0,0159095	-0,5190258	k__Bacteria; p__Proteobacteria; c__Gammaproteo
129439	TotalProtis	0,01596946	-0,5072521	k__Bacteria; p__Actinobacteria; c__Acidimicrobiia;
158301	Z	0,01628638	0,5059544	k__Bacteria; p__Proteobacteria; c__Gammaproteo
123205	TN	0,01650846	-0,5050572	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; c
315125	Si	0,01653835	-0,5164269	k__Bacteria; p__Proteobacteria; c__Alphaproteoba
93013	TN	0,016642	0,5045224	k__Bacteria; p__Proteobacteria; c__Gammaproteo
197435	Si	0,01686646	0,5151023	k__Bacteria; p__Proteobacteria; c__Gammaproteo
293057	NO2.NO3	0,0168874	0,5035486	k__Bacteria; p__Proteobacteria; c__Gammaproteo
170551	TotalBacte	0,01694307	0,5033293	k__Bacteria; p__Bacteroidetes; c__[Saprospirae]; o
269609	TotalBacte	0,01696736	-0,5032338	k__Bacteria; p__Proteobacteria; c__Gammaproteo
257198	TN	0,01722832	-0,5022146	k__Bacteria; p__Planctomycetes; c__Phycisphaera
54806	PO4	0,01727861	0,5020196	k__Bacteria; p__Proteobacteria; c__Deltaproteoba
53737	TN	0,01736337	-0,5016921	k__Bacteria; p__Bacteroidetes; c__[Saprospirae]; o
242341	Si	0,01748903	-0,5126451	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; c
244663	TotalBacte	0,01757007	-0,5008986	k__Bacteria; p__Bacteroidetes; c__[Saprospirae]; o
258719	POC	0,01764487	-0,524277	k__Bacteria; p__Planctomycetes; c__Planctomycet
40092	Si	0,01767913	-0,5119089	k__Bacteria; p__Bacteroidetes; c__[Saprospirae]; o
219117	PO4	0,01772711	-0,5003008	k__Bacteria; p__Proteobacteria; c__Gammaproteo
249494	TotalProtis	0,01775597	0,5001914	k__Bacteria; p__Bacteroidetes; c__Cytophagia; o__
123454	TotalProtis	0,01791946	0,4995744	k__Bacteria; p__Proteobacteria; c__Alphaproteoba
349003	Chla	0,01799445	0,4992929	k__Bacteria; p__Proteobacteria; c__Deltaproteoba
106286	PO4	0,01814611	-0,4987265	k__Bacteria; p__Proteobacteria; c__Gammaproteo
287800	TotalBacte	0,01822192	0,4984448	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; c
245447	NO2.NO3	0,01822192	-0,4984448	k__Bacteria; p__Actinobacteria; c__Thermoleophili
111553	NO2.NO3	0,01822192	0,4984448	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; c
287800	Si	0,01844388	0,5090097	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; c
153955	Salinity	0,01865307	-0,4968604	k__Bacteria; p__Bacteroidetes; c__[Saprospirae]; o
287774	TotalBacte	0,01868402	-0,4967478	k__Bacteria; p__Proteobacteria; c__Deltaproteoba

96187	Salinity	0,01868686	0,4967375	k__Bacteria; p__Proteobacteria; c__Alphaproteoba
219910	Si	0,01870644	-0,5080367	k__Bacteria; p__Proteobacteria; c__Gammaproteo
186510	Z	0,01872868	0,4965856	k__Bacteria; p__Proteobacteria; c__Deltaproteoba
91369	Si	0,01876249	-0,5078303	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; c
249451	Si	0,01893812	-0,5071871	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; c
349046	POC	0,01902228	-0,5190406	k__Bacteria; p__Proteobacteria; c__Betaproteobac
73128	Salinity	0,01904493	0,4954458	k__Bacteria; p__GN02; c__GN02PH; o__GN02PH; f
215143	TotalBacte	0,01923037	-0,4947846	k__Bacteria; p__Proteobacteria; c__Gammaproteo
143227	TotalBacte	0,01927837	-0,4946142	k__Bacteria; p__Proteobacteria; c__Deltaproteoba
23581	TotalBacte	0,01964521	-0,4933237	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; c
122887	TotalBacte	0,01966328	-0,4932606	k__Bacteria; p__Planctomycetes; c__Phycisphaera
233524	Chla	0,01983758	0,4926546	k__Bacteria; p__Proteobacteria; c__Gammaproteo
278253	NO2.NO3	0,02004684	0,4919328	k__Bacteria; p__Proteobacteria; c__Gammaproteo
178816	TN	0,02022722	0,4913154	k__Bacteria; p__Proteobacteria; c__Gammaproteo
242341	PO4	0,02068736	-0,4897603	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; c
141882	Chla	0,02096958	0,4888202	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; c
281929	TN	0,02122094	0,4879914	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; c
253059	DOC	0,02145772	-0,4984471	k__Bacteria; p__Proteobacteria; c__Alphaproteoba
170762	TN	0,02148593	0,4871262	k__Archaea; p__Euryarchaeota; c__Thermoplasma
245673	TotalProtis	0,02149858	-0,487085	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; c
267542	TotalProtis	0,02149858	-0,487085	k__Bacteria; p__Firmicutes; c__Bacilli; o__Bacillale
123205	Chla	0,02169717	0,4864425	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; c
145818	Salinity	0,02169928	0,4864357	k__Bacteria; p__Proteobacteria; c__Epsilonproteob
374536	TN	0,02182277	0,4860386	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; c
40092	NO2.NO3	0,02197685	-0,4855456	k__Bacteria; p__Bacteroidetes; c__[Saprospirae]; o
249494	Si	0,02206846	0,4964531	k__Bacteria; p__Bacteroidetes; c__Cytophagia; o__
244663	TN	0,0223946	-0,4842228	k__Bacteria; p__Bacteroidetes; c__[Saprospirae]; o
141113	TN	0,02245438	0,4840351	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; c
171955	Si	0,02254023	-0,4949428	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; c
313037	TotalBacte	0,02261815	-0,483523	k__Bacteria; p__Fibrobacteres; c__Fibrobacteria; o
26513	Si	0,02270752	-0,4944132	k__Bacteria; p__Bacteroidetes; c__Cytophagia; o__
214190	Salinity	0,02273578	-0,483157	k__Bacteria; p__Proteobacteria; c__Alphaproteoba
270032	TN	0,02275063	-0,4831109	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; c
270032	NO2.NO3	0,02279462	-0,4829745	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; c
335078	Chla	0,02288356	-0,4826993	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; c
139840	Si	0,02294745	-0,4936592	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; c
117401	TN	0,02317333	-0,4818087	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; c
124210	NO2.NO3	0,02325958	-0,4815454	k__Bacteria; p__Proteobacteria; c__Gammaproteo
238441	TotalProtis	0,02336286	0,481231	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; c
176376	TotalProtis	0,02336885	0,4812129	k__Bacteria; p__Proteobacteria; c__Deltaproteoba
181913	DOC	0,02343972	0,4921316	k__Bacteria; p__Planctomycetes; c__OM190; o__C
269689	Chla	0,02358342	0,4805635	k__Bacteria; p__Proteobacteria; c__Gammaproteo
51736	PO4	0,02361938	-0,4804551	k__Bacteria; p__Proteobacteria; c__Alphaproteoba
124210	PO4	0,0236228	-0,4804448	k__Bacteria; p__Proteobacteria; c__Gammaproteo
164602	TN	0,02365517	-0,4803474	k__Bacteria; p__Proteobacteria; c__Gammaproteo
238441	TN	0,02367807	-0,4802785	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; c
172942	TotalProtis	0,02377563	0,4799858	k__Bacteria; p__Proteobacteria; c__Alphaproteoba

283953	NO2.NO3	0,02408568	-0,4790617	k__Bacteria; p__Proteobacteria; c__Alphaproteoba
125541	Si	0,02410416	-0,4901097	k__Bacteria; p__Planctomycetes; c__Phycisphaera
374536	PO4	0,02412636	0,4789412	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; c
282725	Si	0,02414803	-0,4899777	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; c
321377	DOC	0,02415155	0,4899672	k__Bacteria; p__Proteobacteria; c__Gammaproteo
141113	TotalBacte	0,02465096	0,4774012	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; c
255372	Salinity	0,02492384	-0,4766105	k__Bacteria; p__SAR406; c__AB16; o__Arctic96B-7
107378	TN	0,02492952	-0,4765941	k__Bacteria; p__Proteobacteria; c__Alphaproteoba
130084	POC	0,02498833	-0,4993477	k__Bacteria; p__Proteobacteria; c__Gammaproteo
137355	TotalProtis	0,02529619	0,4755426	k__Bacteria; p__Proteobacteria; c__Alphaproteoba
281448	Z	0,02543946	-0,475135	k__Bacteria; p__Proteobacteria; c__Deltaproteoba
372772	Si	0,02556306	0,4858211	k__Bacteria; p__Proteobacteria; c__Gammaproteo
287800	TotalProtis	0,02563004	0,4745957	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; c
278485	TN	0,02568545	0,4744395	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; c
115460	Si	0,02573523	-0,485328	k__Bacteria; p__Proteobacteria; c__Gammaproteo
212589	Chla	0,02591682	-0,4737901	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; c
120820	Si	0,02593635	-0,4847551	k__Bacteria; p__Proteobacteria; c__Alphaproteoba
123454	TotalBacte	0,02601265	0,4735225	k__Bacteria; p__Proteobacteria; c__Alphaproteoba
79916	NO2.NO3	0,02601265	0,4735225	k__Bacteria; p__Proteobacteria; c__Deltaproteoba
141882	NO2.NO3	0,02620587	-0,4729854	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; c
123369	Salinity	0,02621339	-0,4729645	k__Bacteria; p__Proteobacteria; c__Gammaproteo
316870	PO4	0,02637584	0,4725154	k__Bacteria; p__Proteobacteria; c__Alphaproteoba
287800	DOC	0,02684158	0,4822197	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; c
245447	DOC	0,02684158	-0,4822197	k__Bacteria; p__Actinobacteria; c__Thermoleophili
281929	Salinity	0,02711178	0,4705081	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; c
114057	PO4	0,02721838	-0,470221	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; c
348543	TotalBacte	0,02724323	-0,4701542	k__Bacteria; p__Proteobacteria; c__Alphaproteoba
157089	TotalBacte	0,02739582	-0,469745	k__Bacteria; p__Proteobacteria; c__Alphaproteoba
106752	POC	0,02758971	-0,4919174	k__Bacteria; p__Proteobacteria; c__Deltaproteoba
149844	Si	0,027614	0,4801094	k__Bacteria; p__Proteobacteria; c__Gammaproteo
117123	PO4	0,02771683	0,46889	k__Bacteria; p__Bacteroidetes; c__[Saprospirae]; o
159330	TN	0,02773409	-0,4688443	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; c
170551	DOC	0,02786307	-0,4794388	k__Bacteria; p__Bacteroidetes; c__[Saprospirae]; o
107378	NO2.NO3	0,02808167	-0,4679279	k__Bacteria; p__Proteobacteria; c__Alphaproteoba
271191	PO4	0,02816868	0,4676999	k__Bacteria; p__Planctomycetes; c__Planctomycet
36289	TN	0,02842986	-0,4670188	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; c
363730	Salinity	0,02846568	0,4669258	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; c
335627	Salinity	0,02858451	0,4666179	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; c
102013	Z	0,02862912	-0,4665026	k__Bacteria; p__Proteobacteria; c__Epsilonproteob
315661	Si	0,0287333	-0,4771326	k__Bacteria; p__Proteobacteria; c__Gammaproteo
150331	Si	0,02919515	-0,475931	k__Bacteria; p__Planctomycetes; c__Planctomycet
218815	Chla	0,02934899	-0,464661	k__Bacteria; p__Proteobacteria; c__Gammaproteo
119576	TotalBacte	0,02935863	-0,4646366	k__Bacteria; p__Proteobacteria; c__Gammaproteo
206631	TN	0,02940085	-0,4645297	k__Bacteria; p__Verrucomicrobia; c__[Pedosphaer
165350	POC	0,02942421	0,487003	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; c
292701	NO2.NO3	0,02966872	-0,4638545	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; c
36289	NO2.NO3	0,03000165	-0,463022	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; c

292848	PO4	0,03021084	-0,4625027	k__Bacteria; p__Proteobacteria; c__Gammaproteo
167100	TotalProtis	0,03023912	-0,4624327	k__Bacteria; p__Proteobacteria; c__Gammaproteo
147164	PO4	0,03069072	-0,461322	k__Bacteria; p__Proteobacteria; c__Gammaproteo
162693	PO4	0,03069072	-0,461322	k__Bacteria; p__Proteobacteria; c__Alphaproteoba
323303	Z	0,03087591	0,4608702	k__Bacteria; p__Firmicutes; c__Bacilli; o__Lactoba
269689	TotalBacte	0,03129303	0,4598606	k__Bacteria; p__Proteobacteria; c__Gammaproteo
247038	Si	0,03130182	-0,470633	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; c
219924	TotalBacte	0,03148797	0,4593924	k__Bacteria; p__Proteobacteria; c__Gammaproteo
105938	DOC	0,03155736	0,4700097	k__Bacteria; p__Proteobacteria; c__Alphaproteoba
189443	Si	0,03172654	0,4695992	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; c
125824	TN	0,03172851	0,4588178	k__Bacteria; p__Proteobacteria; c__Gammaproteo
244955	TotalProtis	0,03194613	-0,4583009	k__Bacteria; p__Proteobacteria; c__Gammaproteo
75124	Salinity	0,03199897	0,4581758	k__Bacteria; p__Planctomycetes; c__Planctomycet
283225	Salinity	0,03235612	0,4573346	k__Bacteria; p__Proteobacteria; c__Alphaproteoba
269689	Z	0,03243803	0,4571427	k__Bacteria; p__Proteobacteria; c__Gammaproteo
245942	Salinity	0,03245051	0,4571135	k__Bacteria; p__Proteobacteria; c__Gammaproteo
289137	TN	0,0324656	-0,4570782	k__Bacteria; p__Proteobacteria; c__Alphaproteoba
35800	Si	0,03260523	-0,4674943	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; c
110844	DOC	0,03262413	-0,4674495	k__Bacteria; p__Proteobacteria; c__Gammaproteo
103649	Z	0,03264467	0,4566603	k__Bacteria; p__Planctomycetes; c__Phycisphaera
302992	TotalBacte	0,03265316	0,4566405	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; c
156587	Si	0,03271336	0,4672384	k__Bacteria; p__Verrucomicrobia; c__Verrucomicr
302439	NO2.NO3	0,03278908	0,4563246	k__Bacteria; p__Proteobacteria; c__Alphaproteoba
166246	Z	0,03286633	-0,4561455	k__Bacteria; p__Proteobacteria; c__Alphaproteoba
374536	Si	0,03298069	0,4666085	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; c
214190	TN	0,03330328	-0,4551387	k__Bacteria; p__Proteobacteria; c__Alphaproteoba
196129	Z	0,03355112	-0,4545723	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; c
292848	Si	0,0337459	-0,4648273	k__Bacteria; p__Proteobacteria; c__Gammaproteo
269689	TotalProtis	0,03385904	0,4538731	k__Bacteria; p__Proteobacteria; c__Gammaproteo
367917	TN	0,03406478	-0,4534087	k__Bacteria; p__Proteobacteria; c__Gammaproteo
96187	PO4	0,03410699	0,4533137	k__Bacteria; p__Proteobacteria; c__Alphaproteoba
181913	Si	0,03417942	0,4638323	k__Bacteria; p__Planctomycetes; c__OM190; o__C
233524	NO2.NO3	0,03500203	0,4513208	k__Bacteria; p__Proteobacteria; c__Gammaproteo
321056	POC	0,03524461	-0,4728537	k__Bacteria; p__Proteobacteria; c__Alphaproteoba
145818	TotalProtis	0,03549712	0,4502356	k__Bacteria; p__Proteobacteria; c__Epsilonproteob
373256	Z	0,03554653	-0,4501279	k__Bacteria; p__Proteobacteria; c__Deltaproteoba
219910	TN	0,03555625	-0,4501067	k__Bacteria; p__Proteobacteria; c__Gammaproteo
190600	Salinity	0,0355646	0,4500885	k__Bacteria; p__Proteobacteria; c__Gammaproteo
364867	POC	0,03559906	0,4720528	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; c
243995	TotalBacte	0,03591304	0,449333	k__Bacteria; p__Proteobacteria; c__Gammaproteo
297756	NO2.NO3	0,035936	0,4492834	k__Archaea; p__Crenarchaeota; c__Thaumarchaeo
47505	Si	0,03600993	-0,4597368	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; c
306210	NO2.NO3	0,0361347	0,4488554	k__Bacteria; p__Proteobacteria; c__Gammaproteo
161507	Chla	0,03613543	-0,4488538	k__Bacteria; p__Proteobacteria; c__Gammaproteo
232374	Chla	0,03613543	-0,4488538	k__Bacteria; p__Proteobacteria; c__Gammaproteo
287800	PO4	0,03613543	0,4488538	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; c
19266	Chla	0,03613543	-0,4488538	k__Bacteria; p__Proteobacteria; c__Alphaproteoba

245447	TN	0,03619447	-0,448727	k__Bacteria; p__Actinobacteria; c__Thermoleophili
150246	TotalBacte	0,03625352	-0,4486003	k__Bacteria; p__Planctomycetes; c__Planctomycet
317932	Salinity	0,0363295	0,4484375	k__Bacteria; p__Bacteroidetes;
227678	PO4	0,03646851	0,4481404	k__Bacteria; p__Proteobacteria; c__Deltaproteoba
302439	PO4	0,03661039	0,4478381	k__Bacteria; p__Proteobacteria; c__Alphaproteoba
380153	Z	0,03665756	-0,4477378	k__Bacteria; p__Actinobacteria; c__Acidimicrobiia;
117288	TN	0,03668559	-0,4476782	k__Bacteria; p__Proteobacteria; c__Gammaproteo
157611	POC	0,03692946	0,4691009	k__Bacteria; p__Proteobacteria; c__Deltaproteoba
114057	Si	0,03728742	-0,4569741	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; c
289137	Si	0,03749333	-0,4565357	k__Bacteria; p__Proteobacteria; c__Alphaproteoba
327255	TotalBacte	0,03756586	-0,4458257	k__Bacteria; p__Proteobacteria; c__Gammaproteo
53737	NO2.NO3	0,03756738	-0,4458226	k__Bacteria; p__Bacteroidetes; c__[Saprospirae]; o
164602	TotalProtis	0,03796396	0,4449991	k__Bacteria; p__Proteobacteria; c__Gammaproteo
273024	DOC	0,03801679	-0,4554298	k__Bacteria; p__Proteobacteria; c__Alphaproteoba
317616	DOC	0,03801679	0,4554298	k__Bacteria; p__Proteobacteria; c__Alphaproteoba
165325	Si	0,03801679	0,4554298	k__Bacteria; p__SAR406; c__AB16; o__Arctic96B-7
266771	DOC	0,03801679	0,4554298	k__Bacteria; p__Proteobacteria; c__Gammaproteo
132904	Si	0,03801679	-0,4554298	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; c
171955	PO4	0,03802886	-0,444865	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; c
60936	Si	0,03814868	-0,455153	k__Bacteria; p__Chlamydiae; c__ChlamydiaePH; o__
283390	POC	0,03864627	0,4654115	k__Bacteria; p__Planctomycetes; c__OM190; o__a
124210	Si	0,03865429	-0,4540988	k__Bacteria; p__Proteobacteria; c__Gammaproteo
117123	Si	0,03890211	0,453586	k__Bacteria; p__Bacteroidetes; c__[Saprospirae]; o
165350	Z	0,03892647	-0,4430283	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; c
263241	Si	0,03899002	-0,4534047	k__Bacteria; p__Actinobacteria; c__Acidimicrobiia;
152420	DOC	0,03906724	0,4532457	k__Bacteria; p__Proteobacteria; c__Alphaproteoba
141882	PO4	0,03923695	-0,4424007	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; c
304309	Chla	0,03933399	-0,4422053	k__Bacteria; p__Proteobacteria; c__Alphaproteoba
255097	Si	0,03938118	-0,4526019	k__Bacteria; p__Proteobacteria; c__Deltaproteoba
377761	POC	0,03981057	-0,4629811	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; c
103644	POC	0,03981057	0,4629811	k__Bacteria; p__Tenericutes; c__Mollicutes; o__An
126619	NO2.NO3	0,03996442	-0,4409453	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; c
81434	Si	0,0399839	0,451377	k__Bacteria; p__Proteobacteria; c__Betaproteobac
71453	DOC	0,04001014	-0,451324	k__Bacteria; p__Proteobacteria; c__Alphaproteoba
149844	TotalProtis	0,04006518	-0,4407453	k__Bacteria; p__Proteobacteria; c__Gammaproteo
317932	TotalBacte	0,04007259	-0,4407306	k__Bacteria; p__Bacteroidetes;
119060	DOC	0,04015207	-0,4510378	k__Bacteria; p__Planctomycetes; c__OM190; o__a
35800	TotalBacte	0,04032899	-0,4402237	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; c
140949	NO2.NO3	0,04048687	0,4399128	k__Archaea; p__Crenarchaeota; c__Thaumarchaeo
314117	DOC	0,04088134	0,4495794	k__Bacteria; p__Proteobacteria; c__Gammaproteo
219117	NO2.NO3	0,04091106	-0,4390821	k__Bacteria; p__Proteobacteria; c__Gammaproteo
143227	Si	0,0409382	-0,4494666	k__Bacteria; p__Proteobacteria; c__Deltaproteoba
51736	Si	0,0409382	-0,4494666	k__Bacteria; p__Proteobacteria; c__Alphaproteoba
75124	Z	0,04142209	-0,4380902	k__Bacteria; p__Planctomycetes; c__Planctomycet
289137	TotalProtis	0,0415678	0,4378092	k__Bacteria; p__Proteobacteria; c__Alphaproteoba
219910	Chla	0,04163497	0,4376799	k__Bacteria; p__Proteobacteria; c__Gammaproteo
169677	TotalProtis	0,04174937	0,43746	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; c

273861	Salinity	0,04180419	-0,4373548	k__Bacteria; p__Proteobacteria; c__Alphaproteoba
94441	Si	0,04180646	0,4477583	k__Bacteria; p__Proteobacteria; c__Deltaproteoba
241136	Chla	0,0421041	0,4367813	k__Bacteria; p__Proteobacteria; c__Alphaproteoba
146454	Z	0,04212983	-0,4367322	k__Bacteria; p__Proteobacteria; c__Alphaproteoba
321935	Chla	0,04217119	0,4366534	k__Bacteria; p__Proteobacteria; c__Epsilonproteob
60936	Chla	0,04220625	0,4365867	k__Bacteria; p__Chlamydiae; c__ChlamydiaePH; o__
255572	Z	0,04249989	-0,4360293	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; c
96187	TotalBacte	0,04253589	-0,4359611	k__Bacteria; p__Proteobacteria; c__Alphaproteoba
293057	TN	0,04256391	0,4359081	k__Bacteria; p__Proteobacteria; c__Gammaproteo
280778	TotalProtis	0,04270802	-0,435636	k__Bacteria; p__Bacteroidetes; c__Cytophagia; o__
287005	TotalBacte	0,04273854	0,4355784	k__Bacteria; p__Proteobacteria; c__Alphaproteoba
213026	TN	0,04293698	0,4352051	k__Bacteria; p__Proteobacteria; c__Gammaproteo
229855	DOC	0,04311289	0,4452391	k__Bacteria; p__Bacteroidetes; c__[Saprospirae]; o
302439	Si	0,04314616	0,4451757	k__Bacteria; p__Proteobacteria; c__Alphaproteoba
113401	TotalProtis	0,04319207	0,4347271	k__Bacteria; p__Proteobacteria; c__Gammaproteo
172942	Salinity	0,04322968	-0,4346568	k__Bacteria; p__Proteobacteria; c__Alphaproteoba
77969	TotalProtis	0,04323976	-0,434638	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; c
255097	NO2.NO3	0,04339125	-0,4343554	k__Bacteria; p__Proteobacteria; c__Deltaproteoba
186389	Si	0,04382623	-0,4438885	k__Bacteria; p__Proteobacteria; c__Gammaproteo
154682	Salinity	0,04419238	-0,4328736	k__Bacteria; p__Proteobacteria; c__Gammaproteo
374641	TotalProtis	0,04429706	0,4326816	k__Bacteria; p__Proteobacteria; c__Alphaproteoba
19223	Salinity	0,04471013	-0,4319271	k__Bacteria; p__Chlamydiae; c__Chlamydia; o__Cl
69077	POC	0,04488452	-0,4529906	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; c
82221	Salinity	0,04508314	0,4312505	k__Bacteria; p__Proteobacteria; c__Gammaproteo
307120	DOC	0,04518216	-0,4413674	k__Bacteria; p__Verrucomicrobia; c__Verrucomicr
307260	Z	0,04552444	0,4304555	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; c
129034	Salinity	0,04578155	-0,4299952	k__Bacteria; p__Proteobacteria; c__Gammaproteo
175258	Z	0,04623949	-0,4291801	k__Bacteria; p__Bacteroidetes; c__Cytophagia; o__
135679	PO4	0,04632177	-0,4290343	k__Bacteria; p__Proteobacteria; c__Gammaproteo
294599	TotalBacte	0,04648519	-0,4287454	k__Bacteria; p__Proteobacteria; c__Gammaproteo
181913	NO2.NO3	0,04677009	0,4282435	k__Bacteria; p__Planctomycetes; c__OM190; o__C
107992	Chla	0,04677681	-0,4282317	k__Bacteria; p__Proteobacteria; c__Gammaproteo
323303	TN	0,0468457	-0,4281108	k__Bacteria; p__Firmicutes; c__Bacilli; o__Lactoba
293250	Chla	0,04687645	0,4280568	k__Bacteria; p__Proteobacteria; c__Alphaproteoba
241961	NO2.NO3	0,04691462	0,4279899	k__Bacteria; p__Proteobacteria; c__Alphaproteoba
309108	Z	0,04694787	0,4279316	k__Archaea; p__Euryarchaeota; c__Thermoplasma
150062	NO2.NO3	0,04698993	-0,4278579	k__Bacteria; p__Proteobacteria; c__Deltaproteoba
189481	DOC	0,04701333	-0,438054	k__Bacteria; p__Proteobacteria; c__Alphaproteoba
364867	Salinity	0,04768428	-0,4266491	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; c
278253	PO4	0,04776042	0,4265173	k__Bacteria; p__Proteobacteria; c__Gammaproteo
94191	TotalBacte	0,04783639	-0,4263861	k__Bacteria; p__Proteobacteria; c__Epsilonproteob
224905	NO2.NO3	0,04788207	0,4263072	k__Bacteria; p__Proteobacteria; c__Gammaproteo
156587	PO4	0,04788695	0,4262988	k__Bacteria; p__Verrucomicrobia; c__Verrucomicr
330571	TotalBacte	0,04810276	-0,4259271	k__Bacteria; p__Proteobacteria; c__Gammaproteo
250185	Salinity	0,04824612	-0,4256808	k__Archaea; p__Crenarchaeota; c__Thaumarchaeo
330941	TotalBacte	0,04829274	0,4256009	k__Bacteria; p__Planctomycetes; c__Planctomycet
66007	Z	0,04857344	-0,4251208	k__Bacteria; p__Proteobacteria; c__Deltaproteoba

184270	Z	0,04857344	-0,4251208	k__Archaea; p__Crenarchaeota; c__Thaumarchaeo
75124	TotalBacte	0,04878059	-0,4247679	k__Bacteria; p__Planctomycetes; c__Planctomycet
364944	TN	0,04892731	-0,4245186	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; c
213922	DOC	0,04909471	-0,4344068	k__Bacteria; p__Bacteroidetes; c__Cytophagia; o__
242341	Chla	0,04925331	0,4239668	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; c
245447	Chla	0,04928252	0,4239175	k__Bacteria; p__Actinobacteria; c__Thermoleophili
138050	PO4	0,04928252	0,4239175	k__Bacteria; p__Planctomycetes; c__Planctomycet
263531	Chla	0,04928252	-0,4239175	k__Bacteria; p__Proteobacteria; c__Gammaproteo
105684	POC	0,04934919	0,4448959	k__Bacteria; p__Planctomycetes; c__Phycisphaerae
19266	TN	0,04935353	0,4237977	k__Bacteria; p__Proteobacteria; c__Alphaproteoba
359997	TotalBacte	0,04942456	0,4236781	k__Bacteria; p__Actinobacteria; c__Acidimicrobiia;
197113	TotalBacte	0,04942456	-0,4236781	k__Bacteria; p__Proteobacteria; c__Betaproteobac
48072	TotalBacte	0,04942456	-0,4236781	k__Bacteria; p__Proteobacteria; c__Gammaproteo
181308	POC	0,04974895	-0,4441989	k__Bacteria; p__Proteobacteria; c__Gammaproteo
380239	TotalProtis	0,04985934	-0,4229485	k__Archaea; p__Euryarchaeota; c__Thermoplasma

Functions

ICE

Env	P-value	Spearman r	Function	Level 1	Level 2	Level 3
Chla	0,000309	0,9856108	Aconitate hyc	Carbohydrates	Central car	Glyoxylate
NO2.NO3	0,000309	0,9856108	Arginine N-su	Amino Acids and Derivative	Arginine; u	Arginine an
Salinity	0,000309	-0,9856108	DNA gyrase s	Clustering-based subsystem -		DNA gyrase
NO2.NO3	0,000309	0,9856108	Guanosine-5'	Phosphorus Metabolism	-	Phosphate
DOC	0,000309	0,9856108	Isoquinoline	Clustering-based subsystem	Putative Is	CBSS-3142f
NO2.NO3	0,000309	-0,9856108	Pyruvate deh	Amino Acids and Derivative	Lysine, thre	Methionine
POC	0,002778		1 Carbamoyl-pl	Cell Division and Cell Cycle	-	Macromole
TN	0,002778		1 Phosphoribo	Nucleosides and Nucleotide	Purines	De Novo Pu
Si	0,005098	-0,9411239	2,4-dienoyl-C	Fatty Acids, Lipids, and Isop	Fatty acids	Fatty acid c
POC	0,005098	-0,9411239	2-amino-3-ke	Amino Acids and Derivative	Alanine, se	Glycine and
TN	0,005098	-0,9411239	4-hydroxy-3-r	Fatty Acids, Lipids, and Isop	Isoprenoid	Isoprenoid
TotalBacte	0,005098	-0,9411239	5-Enolpyruvy	Amino Acids and Derivative	Aromatic a	Chorismate
Chla	0,005098	-0,9411239	ATP synthase	Respiration	ATP syntha	F0F1-type /
PO4	0,005098	-0,9411239	ATP synthase	Respiration	ATP syntha	F0F1-type /
TotalBacte	0,005098	-0,9411239	ATP-depende	Clustering-based subsystem	Ribosomal	A Gram-po
NO2.NO3	0,005098	-0,9411239	ATP-depende	Protein Metabolism	Protein deg	Proteasom
Chla	0,005098	0,9411239	Cell division	Clustering-based subsystem -		Bacterial C
POC	0,005098	-0,9411239	Chemotaxis	Motility and Chemotaxis	-	Bacterial C
TN	0,005098	-0,9411239	Cold-shock D	RNA Metabolism	RNA proce	ATP-depen
NO2.NO3	0,005098	0,9411239	Cytochrome l	Miscellaneous	Plant-Prok	At1g54520
Z	0,005098	-0,9411239	Diaminobuty	Stress Response	Osmotic sti	Ectoine bio
POC	0,005098	-0,9411239	Ferredoxin-d	Amino Acids and Derivative	Glutamine, Glutamine,	
Z	0,005098	-0,9411239	Flavodoxin 1	Cofactors, Vitamins, Prosthe	Riboflavin, Flavodoxin	
Z	0,005098	-0,9411239	Galactokinase	Carbohydrates	-	Sugar utiliz
TN	0,005098	-0,9411239	Isocitrate de	Carbohydrates	Central car	TCA Cycle
NO2.NO3	0,005098	-0,9411239	LSU ribosom	Clustering-based subsystem -		LSU ribosor
Si	0,005098	-0,9411239	Methylmalon	Carbohydrates	Sugar alco	Inositol cat

TN	0,005098	-0,9411239	Molybdenum Cofactors, Vitamins, Prosthe	Folate and Molybdenu
Z	0,005098	-0,9411239	N-carbamoyl Amino Acids and Derivatives	Arginine; u Arginine an
TN	0,005098	-0,9411239	NfuA Fe-S prc	Miscellaneous Plant-Prok; Biotin biosy
TotalBacte	0,005098	-0,9411239	Oxaloacetate	Carbohydrates Central car Pyruvate m
NO2.NO3	0,005098	-0,9411239	Phenylacetat	Metabolism of Aromatic Coi - Phenylacet
Chla	0,005098	-0,9411239	Polyphosphat	Nucleosides and Nucleotide Purines Purine conv
PO4	0,005098	-0,9411239	Polyphosphat	Nucleosides and Nucleotide Purines Purine conv
TotalBacte	0,005098	-0,9411239	Pyruvate deh	Carbohydrates Central car Dehydroge
TN	0,005098	-0,9411239	SSU ribosom	Clustering-based subsystem - CBSS-1762
Salinity	0,005098	-0,9411239	Succinyl-CoA: Amino Acids and Derivatives	Branched-c Branched c
Z	0,005098	-0,9411239	Superoxide di	Stress Response Oxidative s Oxidative s
Z	0,005098	-0,9411239	Threonine de	Amino Acids and Derivatives Alanine, se Glycine anc
Si	0,005098	-0,9411239	Topoisomera	DNA Metabolism DNA replic; DNA topois
NO2.NO3	0,005098	-0,9411239	Transcription	Clustering-based subsystem - LSU ribosor
TN	0,005098	-0,9411239	tRNA-i(6)A37	Clustering-based subsystem - tRNA-meth
Z	0,007666	-0,9276337	2-isopropylm	Amino Acids and Derivatives Branched-c Branched-C
NO2.NO3	0,007666	-0,9276337	2-methylcitra	Carbohydrates Organic aci Methylcitra
POC	0,007666	0,9276337	2-oxoglutarat	Carbohydrates Central car Dehydroge
TotalBacte	0,007666	0,9276337	Acetolactate	Amino Acids and Derivatives Branched-c Branched-C
Z	0,007666	-0,9276337	Acetyl-coenz	Amino Acids and Derivatives Branched-c Ketoisovale
NO2.NO3	0,007666	0,9276337	Aconitate hyc	Carbohydrates Central car Glyoxylate
Chla	0,007666	0,9276337	Arginine N-su	Amino Acids and Derivatives Arginine; u Arginine an
Chla	0,007666	-0,9276337	Argininosucci	Amino Acids and Derivatives Arginine; u Arginine Bi
NO2.NO3	0,007666	-0,9276337	Argininosucci	Amino Acids and Derivatives Arginine; u Arginine Bi
DOC	0,007666	0,9276337	Coproporphy	Cofactors, Vitamins, Prosthe Tetrapyrrol Heme and !
POC	0,007666	-0,9276337	dTDP-glucose	Cell Wall and Capsule Capsular ar dTDP-rham
PO4	0,007666	-0,9276337	dTDP-glucose	Cell Wall and Capsule Capsular ar dTDP-rham
Si	0,007666	0,9276337	FKBP-type pe	Protein Metabolism Protein folk Peptidyl-pr
NO2.NO3	0,007666	-0,9276337	Glutathione s	Clustering-based subsystem - CBSS-3203
Chla	0,007666	0,9276337	Guanosine-5'	Phosphorus Metabolism - Phosphate
Chla	0,007666	-0,9276337	Holliday junct	DNA Metabolism DNA recomb RuvABC plu
NO2.NO3	0,007666	-0,9276337	Holliday junct	DNA Metabolism DNA recomb RuvABC plu
Chla	0,007666	-0,9276337	Nucleoside di	Nucleosides and Nucleotide Purines Purine conv
Si	0,007666	0,9276337	Pyruvate carl	Carbohydrates Central car Pyruvate m
DOC	0,007666	-0,9276337	Ribose-phosp	Carbohydrates Central car Pentose ph
Chla	0,007666	-0,9276337	S-adenosylm	Amino Acids and Derivatives Lysine, thr Methionine
NO2.NO3	0,007666	-0,9276337	S-adenosylm	Amino Acids and Derivatives Lysine, thr Methionine
DOC	0,007666	0,9276337	Single-strand	DNA Metabolism DNA repair DNA Repair
Chla	0,007666	-0,9276337	tRNA(Cytosin	Clustering-based subsystem Translation CBSS-3264
NO2.NO3	0,007666	-0,9276337	tRNA(Cytosin	Clustering-based subsystem Translation CBSS-3264
NO2.NO3	0,007666	-0,9276337	Tryptophan s	Amino Acids and Derivatives Aromatic a Chorismate
POC	0,007666	-0,9276337	Urease acces	Amino Acids and Derivatives Arginine; u Urea decon
TotalBacte	0,014889	-0,8986451	2-keto-3-deo	Amino Acids and Derivatives Aromatic a Chorismate
TotalBacte	0,014889	-0,8986451	Aspartate-ser	Amino Acids and Derivatives Lysine, thr Lysine Bios
NO2.NO3	0,014889	0,8986451	GTP pyropho	Clustering-based subsystem Probably G CBSS-1762
DOC	0,014889	0,8986451	Phosphoribo	Nucleosides and Nucleotide Purines De Novo Pl
Chla	0,016667	0,9428571	Cytochrome l	Photosynthesis Electron tr; Photosyste

Chla	0,016667	-0,9428571	Glycine dehyd	Amino Acids and Derivatives: Alanine, se Glycine and
Chla	0,016667	0,9428571	Oligopeptida	Protein Metabolism Protein deg Protein deg
NO2.NO3	0,016667	0,9428571	Oligopeptida	Protein Metabolism Protein deg Protein deg
NO2.NO3	0,016667	0,9428571	probable RuB	Carbohydrates CO2 fixatio CO2 uptake
Z	0,016667	0,9428571	Ribulose bisp	Carbohydrates CO2 fixatio Calvin-Bens
NO2.NO3	0,016667	-0,9428571	tRNA-guanine	RNA Metabolism RNA proce: Queuosine-
POC	0,020599	-0,8804063	1-hydroxy-2-r	Clustering-based subsystem Isoprenoid, CBSS-8333:
Chla	0,020599	-0,8804063	2,4-dienoyl-C	Fatty Acids, Lipids, and Isopr Fatty acids Fatty acid d
PO4	0,020599	-0,8804063	2,4-dienoyl-C	Fatty Acids, Lipids, and Isopr Fatty acids Fatty acid d
DOC	0,020599	0,8804063	2,4-dihydroxy	Amino Acids and Derivatives: Aromatic a Aromatic ai
POC	0,020599	-0,8804063	2-methylcitra	Carbohydrates Organic aci Methylcitra
Si	0,020599	-0,8804063	3-isopropylm	Amino Acids and Derivatives: Branched-c Branched-C
Z	0,020599	-0,8804063	4-alpha-gluca	Carbohydrates Di- and olig Maltose an
Chla	0,020599	-0,8804063	4-hydroxy-3-r	Fatty Acids, Lipids, and Isopr Isoprenoid: Isoprenoid
PO4	0,020599	-0,8804063	4-hydroxy-3-r	Fatty Acids, Lipids, and Isopr Isoprenoid: Isoprenoid
Salinity	0,020599	-0,8804063	5-Enolpyruvy	Amino Acids and Derivatives: Aromatic a Chorismate
DOC	0,020599	0,8804063	Argininosucci	Amino Acids and Derivatives: Arginine; u Arginine Bi
TotalBacte	0,020599	-0,8804063	Aspartate car	Clustering-based subsystem - CBSS-3203:
TN	0,020599	-0,8804063	ATP synthase	Respiration ATP syntha FOF1-type /
Si	0,020599	-0,8804063	ATP synthase	Respiration ATP syntha FOF1-type /
Salinity	0,020599	-0,8804063	ATP-depende	Clustering-based subsystem Ribosomal A Gram-po:
Z	0,020599	-0,8804063	ATP-depende	Protein Metabolism Protein deg Proteasom:
Salinity	0,020599	-0,8804063	ATP-depende	Protein Metabolism Protein deg Proteasom:
Si	0,020599	-0,8804063	ATP-depende	RNA Metabolism RNA proce: ATP-depen:
DOC	0,020599	0,8804063	Butyryl-CoA c	Amino Acids and Derivatives: Branched-c Isoleucine c
POC	0,020599	-0,8804063	C4-type zinc f	Clustering-based subsystem - CBSS-235.1
Z	0,020599	-0,8804063	Catalase (EC :	Carbohydrates CO2 fixatio Photorespi
DOC	0,020599	0,8804063	Chaperone pr	Protein Metabolism Protein folk Protein cha
Chla	0,020599	-0,8804063	Cold-shock DI	RNA Metabolism RNA proce: ATP-depen:
PO4	0,020599	-0,8804063	Cold-shock DI	RNA Metabolism RNA proce: ATP-depen:
DOC	0,020599	0,8804063	Cysteine synt	Amino Acids and Derivatives: Lysine, thr: Cysteine Bi
NO2.NO3	0,020599	-0,8804063	Diaminobutyr	Stress Response Osmotic sti Ectoine bio
POC	0,020599	-0,8804063	DNA polymer	Clustering-based subsystem - EC49-61
TN	0,020599	-0,8804063	DNA polymer	Clustering-based subsystem - CBSS-3506:
TN	0,020599	-0,8804063	Flagellar synt	Motility and Chemotaxis Flagellar m Flagellar m:
NO2.NO3	0,020599	-0,8804063	Flavodoxin 1	Cofactors, Vitamins, Prosthe Riboflavin, Flavodoxin
TotalBacte	0,020599	-0,8804063	Formate--tet:	Carbohydrates One-carbor One-carbor
NO2.NO3	0,020599	-0,8804063	Galactokinase	Carbohydrates - Sugar utiliz:
Z	0,020599	-0,8804063	GDP-mannos:	Cell Wall and Capsule Capsular ar Capsular he
Si	0,020599	-0,8804063	General secre	Membrane Transport Protein sec General Ser
Z	0,020599	-0,8804063	Glycyl-tRNA s	Protein Metabolism Protein bio tRNA amin:
DOC	0,020599	-0,8804063	HflK protein	Miscellaneous Plant-Prok: Scaffold pr
TotalBacte	0,020599	-0,8804063	Iron-sulfur cl	Amino Acids and Derivatives: Alanine, se Alanine bio
Chla	0,020599	-0,8804063	Isocitrate del	Carbohydrates Central car TCA Cycle
PO4	0,020599	-0,8804063	Isocitrate del	Carbohydrates Central car TCA Cycle
Z	0,020599	-0,8804063	LSU ribosom:	Clustering-based subsystem - LSU ribosor
Salinity	0,020599	-0,8804063	LSU ribosom:	Clustering-based subsystem - LSU ribosor

Chla	0,020599	-0,8804063	Methylmalon Carbohydrates	Sugar alcoh	Inositol cat
PO4	0,020599	-0,8804063	Methylmalon Carbohydrates	Sugar alcoh	Inositol cat
Chla	0,020599	-0,8804063	Molybdenum Cofactors, Vitamins, Prosthe	Folate and	Molybdenu
PO4	0,020599	-0,8804063	Molybdenum Cofactors, Vitamins, Prosthe	Folate and	Molybdenu
Z	0,020599	0,8804063	Na(+)-translo	Respiration	Electron dc Na(+)-trans
Salinity	0,020599	0,8804063	Na(+)-translo	Respiration	Electron dc Na(+)-trans
NO2.NO3	0,020599	0,8804063	Na(+)-translo	Respiration	Electron dc Na(+)-trans
TN	0,020599	-0,8804063	NAD(FAD)-uti	Miscellaneous	Plant-Prok: COG2509
NO2.NO3	0,020599	-0,8804063	N-carbamoyl	Amino Acids and Derivatives	Arginine; u Arginine an
Chla	0,020599	-0,8804063	NfuA Fe-S prc	Miscellaneous	Plant-Prok: Biotin biosy
PO4	0,020599	-0,8804063	NfuA Fe-S prc	Miscellaneous	Plant-Prok: Biotin biosy
DOC	0,020599	0,8804063	Nicotinate ph	Cofactors, Vitamins, Prosthe	NAD and N NAD and N.
DOC	0,020599	-0,8804063	Nucleoside-di	Clustering-based subsystem -	CBSS-2965
Salinity	0,020599	-0,8804063	Oxaloacetate	Carbohydrates	Central car Pyruvate m
Z	0,020599	-0,8804063	Peroxidase (E	Secondary Metabolism	Plant Horm Auxin degr:
Z	0,020599	-0,8804063	Phenylacetat	Metabolism of Aromatic Coi-	Phenylacet
Salinity	0,020599	-0,8804063	Phenylacetat	Metabolism of Aromatic Coi-	Phenylacet
Z	0,020599	-0,8804063	Phosphate A	Clustering-based subsystem	Phosphate PhoR-PhoB
TN	0,020599	-0,8804063	Polyphosphat	Nucleosides and Nucleotide	Purines Purine con
Si	0,020599	-0,8804063	Polyphosphat	Nucleosides and Nucleotide	Purines Purine con
Salinity	0,020599	-0,8804063	Pyruvate deh	Carbohydrates	Central car Dehydroge
TN	0,020599	-0,8804063	Rare lipoprot	Cell Wall and Capsule	- Peptidoglyc
Si	0,020599	-0,8804063	Ribonucleotic	Clustering-based subsystem -	Ribonucleo
TotalBacte	0,020599	-0,8804063	Ribonucleotic	Nucleosides and Nucleotide -	Ribonucleo
Chla	0,020599	-0,8804063	SSU ribosom	Clustering-based subsystem -	CBSS-1762
PO4	0,020599	-0,8804063	SSU ribosom	Clustering-based subsystem -	CBSS-1762
POC	0,020599	-0,8804063	Succinate de	Carbohydrates	Central car TCA Cycle
TotalBacte	0,020599	-0,8804063	Succinyl-CoA: Amino Acids and Derivatives	Branched-c	Branched c
NO2.NO3	0,020599	-0,8804063	Succinyl-CoA: Amino Acids and Derivatives	Branched-c	Branched c
NO2.NO3	0,020599	-0,8804063	Superoxide di	Stress Response	Oxidative s Oxidative s
NO2.NO3	0,020599	-0,8804063	Threonine de	Amino Acids and Derivatives	Alanine, se Glycine anc
Chla	0,020599	-0,8804063	Topoisomera	DNA Metabolism	DNA replic: DNA topo
PO4	0,020599	-0,8804063	Topoisomera	DNA Metabolism	DNA replic: DNA topo
Z	0,020599	-0,8804063	Transcription	Clustering-based subsystem -	LSU ribosor
Salinity	0,020599	-0,8804063	Transcription	Clustering-based subsystem -	LSU ribosor
DOC	0,020599	0,8804063	Translation el	Clustering-based subsystem -	CBSS-1762
Chla	0,020599	-0,8804063	tRNA-i(6)A37	Clustering-based subsystem -	tRNA-meth
PO4	0,020599	-0,8804063	tRNA-i(6)A37	Clustering-based subsystem -	tRNA-meth
DOC	0,020599	0,8804063	Tryptophan 2	Amino Acids and Derivatives	Aromatic a Aromatic ai
Z	0,020599	-0,8804063	Type cbb3 cy	Respiration	- Biogenesis
Z	0,020599	-0,8804063	Type I restrict	DNA Metabolism	- Restriction-
TN	0,020599	-0,8804063	Urea ABC tra	Amino Acids and Derivatives	Arginine; u Urea decon
Z	0,020599	-0,8804063	Valyl-tRNA sy	Protein Metabolism	Protein bio tRNA amin
POC	0,020599	-0,8804063	Xanthine deh	Clustering-based subsystem	Clustering- Putative di
Z	0,020599	0,8804063	Zinc-regulat	Membrane Transport	- Transport c
Salinity	0,020599	0,8804063	Zinc-regulat	Membrane Transport	- Transport c
NO2.NO3	0,020599	0,8804063	Zinc-regulat	Membrane Transport	- Transport c

Si	0,024377	0,8696566	Adenylosuccinyl-CoA Clustering-based subsystem	Clustering-based subsystem	CBSS-2627
POC	0,024377	0,8696566	Fumarate hydratase Carbohydrates	Central car TCA Cycle	
PO4	0,024377	-0,8696566	Isocitrate lyase Carbohydrates	Central car Glyoxylate	
Salinity	0,024377	-0,8696566	LSU ribosomal protein Metabolism	Protein bio Ribosome L	
Chla	0,024377	-0,8696566	Pyruvate dehydrogenase Amino Acids and Derivatives	Lysine, threonine Methionine	
Chla	0,033333	0,8857143	ATP synthase Respiration	ATP synthase FOF1-type I	
TotalBacter	0,033333	0,8857143	ATP synthase Respiration	ATP synthase FOF1-type I	
NO2.NO3	0,033333	0,8857143	ATP synthase Respiration	ATP synthase FOF1-type I	
DOC	0,033333	-0,8857143	Glycyl-tRNA synthetase Protein Metabolism	Protein bio tRNA aminoacyl	
Si	0,033333	-0,8857143	LSU ribosomal protein Metabolism	Protein bio Ribosome L	
Salinity	0,033333	-0,8857143	Methylcrotonyl-CoA Amino Acids and Derivatives	Branched-chain Branched-chain	
PO4	0,033333	0,8857143	Phosphoribosyl transferase Nucleosides and Nucleotides	Purines De Novo Purine	
POC	0,033333	-0,8857143	photosystem Photosynthesis	Electron transport Photosynthesis	
POC	0,033333	-0,8857143	Photosystem Photosynthesis	Electron transport Photosynthesis	
PO4	0,033333	-0,8857143	Photosystem Photosynthesis	Electron transport Photosynthesis	
Z	0,033333	0,8857143	probable RuBisCO Carbohydrates	CO2 fixation CO2 uptake	
Salinity	0,033333	0,8857143	probable RuBisCO Carbohydrates	CO2 fixation CO2 uptake	
NO2.NO3	0,033333	0,8857143	Ribulose biphosphate Carbohydrates	CO2 fixation Calvin-Benson	
TotalBacter	0,034109	-0,8451543	2,3-bisphosphoglycerate Carbohydrates	Central car Entner-Doudoroff	
TN	0,034109	-0,8451543	3-hydroxyacyl-CoA Metabolism of Aromatic Compounds	Phenylacetate	
NO2.NO3	0,034109	-0,8451543	3-hydroxyacyl-CoA Metabolism of Aromatic Compounds	Phenylacetate	
Salinity	0,034109	-0,8451543	3-isopropylmalate Amino Acids and Derivatives	Branched-chain Branched-chain	
Chla	0,034109	-0,8451543	3-isopropylmalate Amino Acids and Derivatives	Branched-chain Branched-chain	
PO4	0,034109	-0,8451543	3-isopropylmalate Amino Acids and Derivatives	Branched-chain Branched-chain	
Si	0,034109	-0,8451543	4-keto-6-deoxyglucose Protein Metabolism	Protein processing N-linked Glycosylation	
Salinity	0,034109	-0,8451543	5-oxoprolinate Stress Response	Oxidative stress Glutathione	
Chla	0,034109	-0,8451543	5-oxoprolinate Stress Response	Oxidative stress Glutathione	
PO4	0,034109	-0,8451543	5-oxoprolinate Stress Response	Oxidative stress Glutathione	
Si	0,034109	-0,8451543	Acetoin dehydrogenase Carbohydrates	Central car Dehydrogenation	
TotalBacter	0,034109	0,8451543	Acetyl-coenzyme A Fatty Acids, Lipids, and Isoprenoids	Fatty acids Fatty Acid Metabolism	
TotalBacter	0,034109	-0,8451543	Adenylylsulfate Amino Acids and Derivatives	Lysine, threonine Cysteine Biosynthesis	
TotalBacter	0,034109	-0,8451543	Aerobic cobalamin Cofactors, Vitamins, Prosthetic Groups	Tetrapyrrole Coenzyme B12	
Salinity	0,034109	-0,8451543	Agmatinase (HPLC) Amino Acids and Derivatives	Arginine; urea Arginine and	
Chla	0,034109	-0,8451543	Agmatinase (HPLC) Amino Acids and Derivatives	Arginine; urea Arginine and	
PO4	0,034109	-0,8451543	Agmatinase (HPLC) Amino Acids and Derivatives	Arginine; urea Arginine and	
TN	0,034109	-0,8451543	Aldehyde dehydrogenase Carbohydrates	Central car Methylglyoxal	
NO2.NO3	0,034109	-0,8451543	Aldehyde dehydrogenase Carbohydrates	Central car Methylglyoxal	
Z	0,034109	-0,8451543	Amidase cluster Nitrogen Metabolism	- Amidase cluster	
TotalBacter	0,034109	0,8451543	Aminomethylamine Amino Acids and Derivatives	Alanine, serine Glycine and	
TN	0,034109	-0,8451543	Anthranilate synthase Amino Acids and Derivatives	Aromatic amino acid Chorismate	
NO2.NO3	0,034109	-0,8451543	Anthranilate synthase Amino Acids and Derivatives	Aromatic amino acid Chorismate	
TotalBacter	0,034109	-0,8451543	Anthranilate synthase Amino Acids and Derivatives	Aromatic amino acid Chorismate	
Z	0,034109	-0,8451543	Anthranilate synthase Amino Acids and Derivatives	Aromatic amino acid Chorismate	
TN	0,034109	-0,8451543	ApaG protein Clustering-based subsystem	- EC49-61	
NO2.NO3	0,034109	-0,8451543	ApaG protein Clustering-based subsystem	- EC49-61	
TN	0,034109	-0,8451543	Arsenic resistance Virulence, Disease and Defense Resistance	Arsenic resistance	
NO2.NO3	0,034109	-0,8451543	Arsenic resistance Virulence, Disease and Defense Resistance	Arsenic resistance	

TN	0,034109	-0,8451543	Arsenical-resi	Virulence, Disease and Defe	Resistance	Arsenic resi
NO2.NO3	0,034109	-0,8451543	Arsenical-resi	Virulence, Disease and Defe	Resistance	Arsenic resi
Z	0,034109	-0,8451543	ATP phospho	Amino Acids and Derivatives	Histidine N	Histidine Bi
TotalBacte	0,034109	0,8451543	ATP synthase	Respiration	ATP syntha	FOF1-type /
Si	0,034109	-0,8451543	ATPase YjeE,	Cell Wall and Capsule	-	YjeE
Salinity	0,034109	-0,8451543	ATP-depende	RNA Metabolism	RNA proce	ATP-depen
Chla	0,034109	-0,8451543	ATP-depende	RNA Metabolism	RNA proce	ATP-depen
PO4	0,034109	-0,8451543	ATP-depende	RNA Metabolism	RNA proce	ATP-depen
Z	0,034109	-0,8451543	ATP-depende	RNA Metabolism	RNA proce	ATP-depen
Si	0,034109	-0,8451543	ATP-depende	RNA Metabolism	RNA proce	ATP-depen
Z	0,034109	-0,8451543	Beta-galactos	Carbohydrates	-	Sugar utiliz
TN	0,034109	-0,8451543	Biotin synthe	Cofactors, Vitamins, Prosthe	Biotin	Biotin biosy
NO2.NO3	0,034109	-0,8451543	Biotin synthe	Cofactors, Vitamins, Prosthe	Biotin	Biotin biosy
TN	0,034109	-0,8451543	Branched-ch	Membrane Transport	ABC transp	ABC transp
NO2.NO3	0,034109	-0,8451543	Branched-ch	Membrane Transport	ABC transp	ABC transp
Salinity	0,034109	-0,8451543	Carbamoyl-p	Cell Division and Cell Cycle	-	Macromole
Chla	0,034109	-0,8451543	Carbamoyl-p	Cell Division and Cell Cycle	-	Macromole
PO4	0,034109	-0,8451543	Carbamoyl-p	Cell Division and Cell Cycle	-	Macromole
Z	0,034109	-0,8451543	Cell division p	Cell Division and Cell Cycle	-	Bacterial Cy
POC	0,034109	-0,8451543	Chorismate r	Amino Acids and Derivatives	Aromatic a	Chorismate
Si	0,034109	-0,8451543	Clavamate	Miscellaneous	Plant-Prok	At4g17370
Z	0,034109	-0,8451543	CobW GTPase	Cofactors, Vitamins, Prosthe	Tetrapyrrol	Coenzyme
Z	0,034109	-0,8451543	Cobyric acid s	Cofactors, Vitamins, Prosthe	Tetrapyrrol	Cobalamin
TN	0,034109	-0,8451543	COG2363	Miscellaneous	Plant-Prok	COG2363
NO2.NO3	0,034109	-0,8451543	COG2363	Miscellaneous	Plant-Prok	COG2363
TN	0,034109	-0,8451543	Cold shock pr	Stress Response	Cold shock	Cold shock,
NO2.NO3	0,034109	-0,8451543	Cold shock pr	Stress Response	Cold shock	Cold shock,
Salinity	0,034109	-0,8451543	Conserved pr	Regulation and Cell signaling	Regulation A	conserved
Chla	0,034109	-0,8451543	Conserved pr	Regulation and Cell signaling	Regulation A	conserved
PO4	0,034109	-0,8451543	Conserved pr	Regulation and Cell signaling	Regulation A	conserved
TN	0,034109	-0,8451543	CTP synthase	Clustering-based subsystem	-	CTP syntha
NO2.NO3	0,034109	-0,8451543	CTP synthase	Clustering-based subsystem	-	CTP syntha
TotalBacte	0,034109	0,8451543	Cyclohexadie	Amino Acids and Derivatives	Aromatic a	Chorismate
Z	0,034109	-0,8451543	Cyclopropane	Clustering-based subsystem	-	CBSS-2913
TN	0,034109	-0,8451543	Cytochrome c	Protein Metabolism	Protein fol	Periplasmic
NO2.NO3	0,034109	-0,8451543	Cytochrome c	Protein Metabolism	Protein fol	Periplasmic
TotalBacte	0,034109	-0,8451543	Cytochrome c	Respiration	Electron ac	Terminal cy
Si	0,034109	-0,8451543	Deoxyribodip	Clustering-based subsystem	-	EC699-706
Z	0,034109	-0,8451543	D-erythrose-4	Cofactors, Vitamins, Prosthe	Pyridoxine	Pyridoxin (N
TN	0,034109	-0,8451543	Diaminopime	Amino Acids and Derivatives	Lysine, thr	Lysine Bios
NO2.NO3	0,034109	-0,8451543	Diaminopime	Amino Acids and Derivatives	Lysine, thr	Lysine Bios
Salinity	0,034109	-0,8451543	Diaminopime	Amino Acids and Derivatives	Lysine, thr	Lysine Bios
Chla	0,034109	-0,8451543	Diaminopime	Amino Acids and Derivatives	Lysine, thr	Lysine Bios
PO4	0,034109	-0,8451543	Diaminopime	Amino Acids and Derivatives	Lysine, thr	Lysine Bios
TotalBacte	0,034109	-0,8451543	Dimeric dUTP	Nucleosides and Nucleotide	Detoxificat	Houseclear
Salinity	0,034109	-0,8451543	Dipeptidyl ca	Protein Metabolism	Protein deg	Protein deg
Chla	0,034109	-0,8451543	Dipeptidyl ca	Protein Metabolism	Protein deg	Protein deg

PO4	0,034109	-0,8451543	Dipeptidyl car	Protein Metabolism	Protein deg	Protein deg
TN	0,034109	-0,8451543	DNA mismatc	DNA Metabolism	DNA repair	DNA repair
NO2.NO3	0,034109	-0,8451543	DNA mismatc	DNA Metabolism	DNA repair	DNA repair
TotalBacte	0,034109	0,8451543	DNA topoisor	Clustering-based subsystem -	Conserved	
Salinity	0,034109	-0,8451543	D-tyrosyl-tRN	Clustering-based subsystem	D-tyrosyl-tl	CBSS-3426:
Chla	0,034109	-0,8451543	D-tyrosyl-tRN	Clustering-based subsystem	D-tyrosyl-tl	CBSS-3426:
PO4	0,034109	-0,8451543	D-tyrosyl-tRN	Clustering-based subsystem	D-tyrosyl-tl	CBSS-3426:
TN	0,034109	-0,8451543	Electron tran	Respiration	Electron dc	Na(+)-trans
NO2.NO3	0,034109	-0,8451543	Electron tran	Respiration	Electron dc	Na(+)-trans
TotalBacte	0,034109	-0,8451543	Enoyl-[acyl-c	Cell Wall and Capsule	Cell wall of mycolic aci	
Si	0,034109	-0,8451543	ethylmalonyl-	Carbohydrates	One-carbor	Serine-glyo
TN	0,034109	-0,8451543	Ferric siderop	Iron acquisition and metabo -	Campyloba	
NO2.NO3	0,034109	-0,8451543	Ferric siderop	Iron acquisition and metabo -	Campyloba	
Z	0,034109	-0,8451543	Ferroxidase (I	Stress Response	Oxidative s	Oxidative s
Salinity	0,034109	-0,8451543	FIG000325: c	Clustering-based subsystem -	CBSS-3506:	
Chla	0,034109	-0,8451543	FIG000325: c	Clustering-based subsystem -	CBSS-3506:	
PO4	0,034109	-0,8451543	FIG000325: c	Clustering-based subsystem -	CBSS-3506:	
Z	0,034109	-0,8451543	FIG000506: P	Clustering-based subsystem -	Cluster con	
TotalBacte	0,034109	0,8451543	FIG000859: h	DNA Metabolism	DNA recomb	RuvABC plu
Si	0,034109	-0,8451543	Flagellar bios	Motility and Chemotaxis	Flagellar m	Flagellar m
TotalBacte	0,034109	0,8451543	Flagellar bios	Motility and Chemotaxis	Flagellar m	Flagellar m
Si	0,034109	-0,8451543	Flagellar moti	Motility and Chemotaxis	-	Bacterial Cl
TotalBacte	0,034109	-0,8451543	Flagellar P-rin	Motility and Chemotaxis	Flagellar m	Flagellum
POC	0,034109	-0,8451543	Flagellin	Motility and Chemotaxis	Flagellar m	Flagellar m
POC	0,034109	-0,8451543	Flagellin prot	Motility and Chemotaxis	Flagellar m	Flagellum
TN	0,034109	-0,8451543	Folate-depen	Cofactors, Vitamins, Prosthe	Folate and	YgfZ
NO2.NO3	0,034109	-0,8451543	Folate-depen	Cofactors, Vitamins, Prosthe	Folate and	YgfZ
POC	0,034109	-0,8451543	Fructose-6-ph	Carbohydrates	Central car	Pentose ph
DOC	0,034109	0,8451543	Fructose-bisp	Carbohydrates	Central car	Glycolysis a
TN	0,034109	0,8451543	Fructose-bisp	Carbohydrates	Central car	Glycolysis a
TotalBacte	0,034109	-0,8451543	Fumarate hyc	Carbohydrates	Central car	TCA Cycle
Si	0,034109	-0,8451543	Functional ro	Nitrogen Metabolism	-	Nitrosative
TotalBacte	0,034109	-0,8451543	Glucosamine-	Cell Wall and Capsule	-	UDP-N-acei
TN	0,034109	-0,8451543	Glucose-1-ph	Cell Wall and Capsule	Capsular ar	dTDP-rham
NO2.NO3	0,034109	-0,8451543	Glucose-1-ph	Cell Wall and Capsule	Capsular ar	dTDP-rham
TotalBacte	0,034109	0,8451543	Glutamate-1-	Clustering-based subsystem	Cytochrom	CBSS-1961:
Z	0,034109	-0,8451543	Glutamine an	Cofactors, Vitamins, Prosthe	NAD and N	NAD and N.
Salinity	0,034109	-0,8451543	Glutamyl-tRN	Cofactors, Vitamins, Prosthe	Tetrapyrrol	Heme and !
Chla	0,034109	-0,8451543	Glutamyl-tRN	Cofactors, Vitamins, Prosthe	Tetrapyrrol	Heme and !
PO4	0,034109	-0,8451543	Glutamyl-tRN	Cofactors, Vitamins, Prosthe	Tetrapyrrol	Heme and !
TN	0,034109	-0,8451543	Glycolate de	Carbohydrates	Central car	Glycolate, g
NO2.NO3	0,034109	-0,8451543	Glycolate de	Carbohydrates	Central car	Glycolate, g
TotalBacte	0,034109	0,8451543	GTP pyropho	Clustering-based subsystem	Nucleotidy	CBSS-2225:
TotalBacte	0,034109	0,8451543	GTP pyropho	Clustering-based subsystem	Nucleotidy	CBSS-2225:
Salinity	0,034109	-0,8451543	GTP-binding	Clustering-based subsystem -	CBSS-2906:	
Chla	0,034109	-0,8451543	GTP-binding	Clustering-based subsystem -	CBSS-2906:	
PO4	0,034109	-0,8451543	GTP-binding	Clustering-based subsystem -	CBSS-2906:	

Si	0,034109	-0,8451543	GTP-binding p	Clustering-based subsystem -	Bacterial Ce
TotalBacte	0,034109	-0,8451543	Guanine dear	Nucleosides and Nucleotide Purines	Purine conv
TotalBacte	0,034109	0,8451543	Guanosine-3'	Clustering-based subsystem Probably G	CBSS-1762!
Chla	0,034109	0,8451543	Heme O syntl	Clustering-based subsystem -	CBSS-3160!
NO2.NO3	0,034109	0,8451543	Heme O syntl	Clustering-based subsystem -	CBSS-3160!
Si	0,034109	-0,8451543	Histidinol-phc	Amino Acids and Derivative	Histidine V Histidine Bi
TotalBacte	0,034109	0,8451543	Histidinol-phc	Amino Acids and Derivative	Histidine V Histidine Bi
Z	0,034109	-0,8451543	HTH-type tra	Stress Response	Osmotic sti Choline anc
TN	0,034109	-0,8451543	Imidazole gly	Amino Acids and Derivative	Histidine V Histidine Bi
NO2.NO3	0,034109	-0,8451543	Imidazole gly	Amino Acids and Derivative	Histidine V Histidine Bi
Si	0,034109	-0,8451543	Imidazoleglyc	Amino Acids and Derivative	Histidine V Histidine Bi
TotalBacte	0,034109	0,8451543	IncF plasmid	Membrane Transport	Protein anc Conjugative
Z	0,034109	-0,8451543	Iron-binding f	Cofactors, Vitamins, Prosthe	Folate and YgfZ-Iron
TotalBacte	0,034109	0,8451543	Isoaspartyl di	Amino Acids and Derivative	Arginine; u Cyanophyci
TN	0,034109	-0,8451543	Lipid A biosyr	Cell Wall and Capsule	Gram-Neg: KDO2-Lipid
NO2.NO3	0,034109	-0,8451543	Lipid A biosyr	Cell Wall and Capsule	Gram-Neg: KDO2-Lipid
Si	0,034109	-0,8451543	Lipoate synth	Cofactors, Vitamins, Prosthe	Folate and YgfZ
Si	0,034109	-0,8451543	LSU ribosom	Clustering-based subsystem	Ribosomal A Gram-po:
Salinity	0,034109	-0,8451543	Magnesium a	Clustering-based subsystem -	CBSS-5678!
Chla	0,034109	-0,8451543	Magnesium a	Clustering-based subsystem -	CBSS-5678!
PO4	0,034109	-0,8451543	Magnesium a	Clustering-based subsystem -	CBSS-5678!
TN	0,034109	-0,8451543	Malate dehyc	Carbohydrates	Central car Glyoxylate
NO2.NO3	0,034109	-0,8451543	Malate dehyc	Carbohydrates	Central car Glyoxylate
Z	0,034109	-0,8451543	Metal-depen	Phosphorus Metabolism	- Alkylphosphl
Salinity	0,034109	-0,8451543	Methylmalon	Amino Acids and Derivative	Branched-c Branched c
Chla	0,034109	-0,8451543	Methylmalon	Amino Acids and Derivative	Branched-c Branched c
PO4	0,034109	-0,8451543	Methylmalon	Amino Acids and Derivative	Branched-c Branched c
Si	0,034109	-0,8451543	Methylmalon	Carbohydrates	One-carboi Serine-glyo
Z	0,034109	-0,8451543	Multicopper	Virulence, Disease and Defe	Resistance Copper hor
POC	0,034109	-0,8451543	NAD(P) transl	Phosphorus Metabolism	- Phosphate
Z	0,034109	-0,8451543	NAD-depend	Respiration	- Formate hy
Salinity	0,034109	-0,8451543	NADH-depen	Carbohydrates	Fermentati Acetone Bu
Chla	0,034109	-0,8451543	NADH-depen	Carbohydrates	Fermentati Acetone Bu
PO4	0,034109	-0,8451543	NADH-depen	Carbohydrates	Fermentati Acetone Bu
Si	0,034109	-0,8451543	NADH-ubiqui	Respiration	Electron dc Respiratory
TotalBacte	0,034109	0,8451543	NADP-depen	Carbohydrates	Central car Pyruvate m
TotalBacte	0,034109	0,8451543	NAD-specific	Amino Acids and Derivative	Proline anc Proline, 4-h
TotalBacte	0,034109	0,8451543	NAD-specific	Amino Acids and Derivative	Glutamine, Glutamate
TotalBacte	0,034109	-0,8451543	Nitrogenase (Nitrogen Metabolism	- Nitrogen fi
Z	0,034109	-0,8451543	Non-specific	Stress Response	Oxidative s Oxidative s
Salinity	0,034109	-0,8451543	Peptide chain	Clustering-based subsystem	Protein ex; CBSS-3931!
Chla	0,034109	-0,8451543	Peptide chain	Clustering-based subsystem	Protein ex; CBSS-3931!
PO4	0,034109	-0,8451543	Peptide chain	Clustering-based subsystem	Protein ex; CBSS-3931!
TotalBacte	0,034109	-0,8451543	Phenylacetic	Metabolism of Aromatic Coi-	Phenylacet
TN	0,034109	-0,8451543	Phosphate tr;	Phosphorus Metabolism	- High affinity
NO2.NO3	0,034109	-0,8451543	Phosphate tr;	Phosphorus Metabolism	- High affinity
TotalBacte	0,034109	0,8451543	Phosphoenol	Carbohydrates	Central car Pyruvate m

TotalBacte	0,034109	-0,8451543	Phosphoman Carbohydrates	Monosacch Mannose M
Z	0,034109	-0,8451543	Phosphonate Phosphorus Metabolism	- Alkylphosph
TotalBacte	0,034109	-0,8451543	Phosphoribos Clustering-based subsystem	- CBSS-2512
TN	0,034109	-0,8451543	Phytoene de Fatty Acids, Lipids, and Isoprenoid	Carotenoid
NO2.NO3	0,034109	-0,8451543	Phytoene de Fatty Acids, Lipids, and Isoprenoid	Carotenoid
TN	0,034109	-0,8451543	POSSIBLE LIN Cell Wall and Capsule	Cell wall of mycolic aci
NO2.NO3	0,034109	-0,8451543	POSSIBLE LIN Cell Wall and Capsule	Cell wall of mycolic aci
Z	0,034109	-0,8451543	Pre-mRNA sp RNA Metabolism	RNA proces Spliceosom
TotalBacte	0,034109	-0,8451543	Proline dehyd Amino Acids and Derivatives	Proline anc Proline, 4-h
Si	0,034109	-0,8451543	Proline/sodium Amino Acids and Derivatives	Proline anc Proline, 4-h
Si	0,034109	-0,8451543	Prolipoprotei Carbohydrates	Central car HPr kinase
TotalBacte	0,034109	-0,8451543	proteasome r Protein Metabolism	Protein deg Proteasom
Salinity	0,034109	-0,8451543	Protein of un Clustering-based subsystem	- Conserved
Chla	0,034109	-0,8451543	Protein of un Clustering-based subsystem	- Conserved
PO4	0,034109	-0,8451543	Protein of un Clustering-based subsystem	- Conserved
TotalBacte	0,034109	-0,8451543	Protein-L-isoz Clustering-based subsystem	- CBSS-2115
Salinity	0,034109	-0,8451543	Protoporphyr Cofactors, Vitamins, Prosthe	Tetrapyrrol Chlorophyll
Chla	0,034109	-0,8451543	Protoporphyr Cofactors, Vitamins, Prosthe	Tetrapyrrol Chlorophyll
PO4	0,034109	-0,8451543	Protoporphyr Cofactors, Vitamins, Prosthe	Tetrapyrrol Chlorophyll
TotalBacte	0,034109	-0,8451543	PrpF protein i Carbohydrates	Organic aci Methylcitra
TotalBacte	0,034109	0,8451543	Putative heat Miscellaneous	- ZZ gjo need
Salinity	0,034109	-0,8451543	Putative NAD Respiration	- Quinone ox
Chla	0,034109	-0,8451543	Putative NAD Respiration	- Quinone ox
PO4	0,034109	-0,8451543	Putative NAD Respiration	- Quinone ox
Z	0,034109	-0,8451543	Putative sens Regulation and Cell signaling	- Orphan reg
TN	0,034109	-0,8451543	Putative TEG Clustering-based subsystem	Translation CBSS-3264
NO2.NO3	0,034109	-0,8451543	Putative TEG Clustering-based subsystem	Translation CBSS-3264
TotalBacte	0,034109	-0,8451543	Pyridine nucle Nucleosides and Nucleotide	Pyrimidine Pyrimidine
TN	0,034109	-0,8451543	Pyridoxine 4- Cofactors, Vitamins, Prosthe	Pyridoxine Pyridoxin(V
NO2.NO3	0,034109	-0,8451543	Pyridoxine 4- Cofactors, Vitamins, Prosthe	Pyridoxine Pyridoxin(V
TotalBacte	0,034109	-0,8451543	Ribonuclease RNA Metabolism	RNA proces RNA proces
Salinity	0,034109	-0,8451543	Ribonuclease Clustering-based subsystem	- Conserved
Chla	0,034109	-0,8451543	Ribonuclease Clustering-based subsystem	- Conserved
PO4	0,034109	-0,8451543	Ribonuclease Clustering-based subsystem	- Conserved
TotalBacte	0,034109	0,8451543	Ribonuclease Cell Division and Cell Cycle	- Two cell div
TotalBacte	0,034109	-0,8451543	Ribonuclease RNA Metabolism	RNA proces tRNA proces
Si	0,034109	-0,8451543	Ribosomal lar RNA Metabolism	RNA proces RNA pseud
Z	0,034109	-0,8451543	Ribosomal RN Clustering-based subsystem	- Conserved
Salinity	0,034109	-0,8451543	Ribosomal RN Clustering-based subsystem	- CBSS-2698
Chla	0,034109	-0,8451543	Ribosomal RN Clustering-based subsystem	- CBSS-2698
PO4	0,034109	-0,8451543	Ribosomal RN Clustering-based subsystem	- CBSS-2698
Chla	0,034109	0,8451543	RNA polymer Cell Division and Cell Cycle	- Macromole
NO2.NO3	0,034109	0,8451543	RNA polymer Cell Division and Cell Cycle	- Macromole
TN	0,034109	-0,8451543	RNA polymer Clustering-based subsystem	- CBSS-2115
NO2.NO3	0,034109	-0,8451543	RNA polymer Clustering-based subsystem	- CBSS-2115
DOC	0,034109	0,8451543	RNA polymer Clustering-based subsystem	- Lipopolysac
TN	0,034109	0,8451543	RNA polymer Clustering-based subsystem	- Lipopolysac

TN	0,034109	-0,8451543	RND efflux sy	Virulence, Disease and Defe	Resistance	Multidrug e
NO2.NO3	0,034109	-0,8451543	RND efflux sy	Virulence, Disease and Defe	Resistance	Multidrug e
TN	0,034109	-0,8451543	Sigma-54 dep	Regulation and Cell signaling	Quorum se	Symbiotic c
NO2.NO3	0,034109	-0,8451543	Sigma-54 dep	Regulation and Cell signaling	Quorum se	Symbiotic c
TotalBacte	0,034109	0,8451543	Soluble pyridi	Phosphorus Metabolism	-	Phosphate
TN	0,034109	-0,8451543	SSU ribosom	Protein Metabolism	Protein bio	Ribosome S
NO2.NO3	0,034109	-0,8451543	SSU ribosom	Protein Metabolism	Protein bio	Ribosome S
TN	0,034109	-0,8451543	Transcription	Virulence, Disease and Defe	Resistance	BlaR1 Fami
NO2.NO3	0,034109	-0,8451543	Transcription	Virulence, Disease and Defe	Resistance	BlaR1 Fami
TotalBacte	0,034109	-0,8451543	Translation el	Protein Metabolism	Protein bio	Translation
Z	0,034109	-0,8451543	TRAP-type C4	Miscellaneous	Plant-Prok	At4g17370
Si	0,034109	-0,8451543	TRAP-type tr	Cell Wall and Capsule	Capsular ar	Sialic Acid M
POC	0,034109	-0,8451543	Trk system pc	Clustering-based subsystem	-	Bacterial RI
TotalBacte	0,034109	-0,8451543	tRNA-specific	RNA Metabolism	RNA proce	tRNA modifi
POC	0,034109	-0,8451543	Type I restrict	DNA Metabolism	-	Restriction-
Si	0,034109	-0,8451543	Tyrosyl-tRNA	Protein Metabolism	Protein bio	tRNA amin
Salinity	0,034109	-0,8451543	Ubiquinone/r	Cofactors, Vitamins, Prosthe	Quinone cc	Menaquin
Chla	0,034109	-0,8451543	Ubiquinone/r	Cofactors, Vitamins, Prosthe	Quinone cc	Menaquin
PO4	0,034109	-0,8451543	Ubiquinone/r	Cofactors, Vitamins, Prosthe	Quinone cc	Menaquin
POC	0,034109	-0,8451543	UDP-3-O-[3-h	Cell Wall and Capsule	Gram-Neg	KDO2-Lipid
TotalBacte	0,034109	-0,8451543	UDP-N-acetyl	Cell Wall and Capsule	-	Peptidoglyc
POC	0,034109	-0,8451543	UDP-N-acetyl	Cell Wall and Capsule	Capsular ar	CMP-N-ace
TotalBacte	0,034109	0,8451543	Uncharacteri	Cell Wall and Capsule	Gram-Neg	Lipopolysac
TotalBacte	0,034109	0,8451543	Uracil-DNA gl	DNA Metabolism	DNA repair	DNA Repair
TN	0,034109	-0,8451543	Voltage-gate	Potassium metabolism	-	Potassium I
NO2.NO3	0,034109	-0,8451543	Voltage-gate	Potassium metabolism	-	Potassium I
POC	0,034109	-0,8451543	Xylulose-5-ph	Carbohydrates	Central car	Pentose ph
NO2.NO3	0,036058	-0,840668	DNA gyrase s	Clustering-based subsystem	-	DNA gyrase
DOC	0,036058	-0,840668	DNA-directed	RNA Metabolism	Transcripti	RNA polym
Chla	0,036058	0,840668	FKBP-type pe	Protein Metabolism	Protein fol	Peptidyl-pr
PO4	0,036058	0,840668	FKBP-type pe	Protein Metabolism	Protein fol	Peptidyl-pr
TotalBacte	0,036058	-0,840668	Holliday junct	DNA Metabolism	DNA recor	RuvABC plu
TN	0,036058	-0,840668	IMP cyclohyd	Nucleosides and Nucleotide	Purines	De Novo Pu
TotalBacte	0,036058	-0,840668	Iron(III) dicit	Iron acquisition and metabo	-	Iron(III) dici
TotalBacte	0,036058	-0,840668	Phenylacetic	Metabolism of Aromatic Co	-	Phenylacet
TN	0,036058	-0,840668	Phosphoribo	Cofactors, Vitamins, Prosthe	Folate and	5-FCL-like p
Chla	0,036058	0,840668	Pyruvate car	Carbohydrates	Central car	Pyruvate m
PO4	0,036058	0,840668	Pyruvate car	Carbohydrates	Central car	Pyruvate m
POC	0,045837	-0,8196886	3-ketoacyl-Cc	Amino Acids and Derivative	Branched-c	Branched c
NO2.NO3	0,045837	-0,8196886	4-hydroxy-3-r	Fatty Acids, Lipids, and Isopr	Isoprenoid	Isoprenoid
DOC	0,045837	0,8196886	Aerobic glyce	Carbohydrates	Sugar alco	Glycerol an
TN	0,045837	0,8196886	Aerobic glyce	Carbohydrates	Sugar alco	Glycerol an
NO2.NO3	0,045837	0,8196886	Cell division	Clustering-based subsystem	-	Bacterial C
NO2.NO3	0,045837	-0,8196886	Cold-shock D	RNA Metabolism	RNA proce	ATP-depen
Chla	0,045837	0,8196886	Cytochrome l	Miscellaneous	Plant-Prok	At1g54520
Si	0,045837	-0,8196886	DNA ligase (E	Clustering-based subsystem	-	CBSS-3931
POC	0,045837	-0,8196886	Flagellar regu	Motility and Chemotaxis	Flagellar m	Flagellum

NO2.NO3	0,045837	-0,8196886 Isocitrate dehyd Carbohydrates	Central car TCA Cycle
NO2.NO3	0,045837	-0,8196886 Molybdenum Cofactors, Vitamins, Prosthe	Folate and Molybdenu
POC	0,045837	-0,8196886 NADH-ubiquin Respira	Electron dc Respiratory
NO2.NO3	0,045837	-0,8196886 NfuA Fe-S prc Miscellaneous	Plant-Prok Biotin biosy
Si	0,045837	-0,8196886 O-acetylhom Amino Acids and Derivative	Lysine, thre Methionine
Si	0,045837	-0,8196886 O-succinylhom Amino Acids and Derivative	Lysine, thre Methionine
NO2.NO3	0,045837	-0,8196886 SSU ribosoma Clustering-based subsystem -	CBSS-1762
Salinity	0,045837	-0,8196886 Succinate dehyd Carbohydrates	Central car TCA Cycle
PO4	0,045837	-0,8196886 Succinate dehyd Carbohydrates	Central car TCA Cycle
Chla	0,045837	-0,8196886 Succinyl-CoA: Amino Acids and Derivative	Branched-c Branched c
DOC	0,045837	0,8196886 tRNA (Guanin Protein Metabolism	Protein bio Ribosome l
TN	0,045837	0,8196886 tRNA (Guanin Protein Metabolism	Protein bio Ribosome l
NO2.NO3	0,045837	-0,8196886 tRNA-i(6)A37 Clustering-based subsystem -	tRNA-meth
TotalBacte	0,045837	0,8196886 Ubiquinol--cy Respira	Electron ac Ubiquinone
Salinity	0,045837	-0,8196886 Xanthine dehyd Clustering-based subsystem	Clustering- Putative di
PO4	0,045837	-0,8196886 Xanthine dehyd Clustering-based subsystem	Clustering- Putative di
NO2.NO3	0,049858	-0,8116794 2,3,4,5-tetra Amino Acids and Derivative	Lysine, thre Lysine Bios
Chla	0,049858	-0,8116794 2-keto-3-deo: Amino Acids and Derivative	Aromatic a Chorismate
NO2.NO3	0,049858	-0,8116794 2-keto-3-deo: Amino Acids and Derivative	Aromatic a Chorismate
Z	0,049858	-0,8116794 2-methylcitra Carbohydrates	Organic aci Methylcitra
DOC	0,049858	0,8116794 Acetate perm Carbohydrates	Central car Pyruvate m
PO4	0,049858	0,8116794 Aconitate hyc Carbohydrates	Central car Glyoxylate
Salinity	0,049858	0,8116794 Arginine N-su Amino Acids and Derivative	Arginine; u Arginine an
TN	0,049858	-0,8116794 Argininosucci Amino Acids and Derivative	Arginine; u Arginine Bi
Chla	0,049858	-0,8116794 Aspartate-ser Amino Acids and Derivative	Lysine, thre Lysine Bios
NO2.NO3	0,049858	-0,8116794 Aspartate-ser Amino Acids and Derivative	Lysine, thre Lysine Bios
Chla	0,049858	-0,8116794 CDP-diacylgly Fatty Acids, Lipids, and Isopr	Phospholip Glycerolipic
NO2.NO3	0,049858	-0,8116794 Dihydroxy-aci Amino Acids and Derivative	Branched-c Branched-C
Z	0,049858	-0,8116794 DNA gyrase s Clustering-based subsystem -	DNA gyrase
DOC	0,049858	-0,8116794 DNA-directed RNA Metabolism	Transcripti RNA polym
Si	0,049858	-0,8116794 dTDP-glucose Cell Wall and Capsule	Capsular ar dTDP-rham
Z	0,049858	-0,8116794 Glutathione s Clustering-based subsystem -	CBSS-3203
Z	0,049858	0,8116794 GTP pyropho: Clustering-based subsystem	Probably G CBSS-1762
Salinity	0,049858	0,8116794 Guanosine-5' Phosphorus Metabolism	- Phosphate
Salinity	0,049858	-0,8116794 Holliday junct DNA Metabolism	DNA recomb RuvABC plu
PO4	0,049858	-0,8116794 IMP cyclohyd Nucleosides and Nucleotide	Purines De Novo Pu
POC	0,049858	-0,8116794 Isocitrate lya: Carbohydrates	Central car Glyoxylate
NO2.NO3	0,049858	-0,8116794 LSU ribosoma Clustering-based subsystem -	LSU ribosor
Z	0,049858	-0,8116794 LSU ribosoma Protein Metabolism	Protein bio Ribosome l
Chla	0,049858	-0,8116794 LSU ribosoma Protein Metabolism	Protein bio Ribosome l
NO2.NO3	0,049858	-0,8116794 LSU ribosoma Protein Metabolism	Protein bio Ribosome l
NO2.NO3	0,049858	-0,8116794 Na(+)-translo Respira	Electron dc Na(+)-trans
Si	0,049858	-0,8116794 Nucleoside di Nucleosides and Nucleotide	Purines Purine conv
PO4	0,049858	-0,8116794 Phosphoribo: Cofactors, Vitamins, Prosthe	Folate and 5-FCL-like p
DOC	0,049858	-0,8116794 RNA polymer Clustering-based subsystem -	EC49-61
TN	0,049858	-0,8116794 S-adenosylm Amino Acids and Derivative	Lysine, thre Methionine
TN	0,049858	-0,8116794 tRNA(Cytosin Clustering-based subsystem	Translation CBSS-3264

Z	0,049858	-0,8116794	Tryptophan s	Amino Acids and Derivatives	Aromatic a Chorismate
DOC	0,049858	-0,8116794	Uncharacteri	Cell Wall and Capsule	Gram-Neg; Lipopolysac

SW

Env	P-value	Spearman r	Function	Level 1	Level 2	Level 3
TotalProtis	8,07E-06	-0,9627329	Betaine--hom	Amino Acids and Derivatives	Lysine, thr	Methionine
Salinity	1,19E-05	0,958851	Nitric oxide r	Nitrogen Metabolism	-	Denitrificat
Chla	3,96E-05	-9,44E-01	Rare lipoprot	Cell Wall and Capsule	-	Peptidoglyc
TN	3,96E-05	-9,44E-01	Vanillate O-d	Metabolism of Aromatic Co	Peripheral	Phenylprop
Z	0,000112	-9,27E-01	NAD-specific	Amino Acids and Derivatives	Proline anc	Proline, 4-h
Z	0,000112	-9,27E-01	NAD-specific	Amino Acids and Derivatives	Glutamine, Glutamate	
DOC	0,00013	0,9245067	S-formylgluta	Cofactors, Vitamins, Prosthe	Folate and	YgfZ
Si	0,00013	-0,9272727	Propionyl-Co	Carbohydrates	Organic aci	Propionyl-C
Chla	0,000169	-0,9191989	Proline imino	Amino Acids and Derivatives	Proline anc	Proline, 4-h
Salinity	0,00023	0,9125797	Salicylate hyd	Metabolism of Aromatic Co	Metabolism	Salicylate a
Si	0,00024	0,9115765	ATP synthase	Respiration	ATP syntha	F0F1-type /
Z	0,000248	-0,910808	Electron tran	Amino Acids and Derivatives	Branched-c	Branched c
POC	0,000307	0,9057793	Peptide chain	Clustering-based subsystem	-	LMPTP Ywl
Z	0,000352	-0,902439	Propionate--C	Carbohydrates	Organic aci	Methylcitra
TN	0,000359	0,9019084	LSU ribosom	Protein Metabolism	Protein bio	Ribosome L
Salinity	0,000368	-0,9013033	Oligopeptide	Membrane Transport	ABC transp	ABC transp
POC	0,000392	0,8997002	ATP synthase	Respiration	ATP syntha	F0F1-type /
POC	0,000392	0,8997002	Catalase (EC	Carbohydrates	CO2 fixatio	Photorespi
Z	0,000445	-0,8963415	Lipoate synth	Cofactors, Vitamins, Prosthe	Folate and	YgfZ
TN	0,000482	-0,8941867	Transcription	RNA Metabolism	Transcripti	Transcripti
TotalProtis	0,000511	0,892566	Peptide meth	Clustering-based subsystem	Carbohydr	Cluster Ytf
NO2.NO3	0,000567	0,8896375	Guanine dear	Nucleosides and Nucleotide	Purines	Purine conv
TN	0,000567	-0,8896375	tolB protein	Membrane Transport	-	Ton and To
NO2.NO3	0,000567	-0,8896375	ubiquinol cyt	Respiration	Electron ac	Ubiquinone
NO2.NO3	0,000602	0,8879337	Predicted nuc	Carbohydrates	Monosacch	Deoxyribos
TN	0,000608	-0,8876254	L-seryl-tRNA	Protein Metabolism	Selenoprot	Selenocyste
DOC	0,000649	0,8857162	Enoyl-CoA hy	Amino Acids and Derivatives	Branched-c	Branched c
POC	0,000736	-0,8819277	Excinuclease	DNA Metabolism	DNA repair	DNA repair
POC	0,000736	-0,8819277	SSU ribosom	Clustering-based subsystem	-	CBSS-3506
NO2.NO3	0,000742	-0,8816806	Pseudaminic	Cell Wall and Capsule	Capsular ar	Pseudamin
POC	0,000747	0,881463	3-isopropylm	Amino Acids and Derivatives	Branched-c	Branched-C
POC	0,000747	0,881463	Peroxidase (E	Secondary Metabolism	Plant Horm	Auxin degr
Salinity	0,000768	-0,8805866	NADH ubiqui	Respiration	Electron dc	Respiratory
Z	0,000782	-0,8800375	Preprotein tr	Membrane Transport	Protein tra	HtrA and Se
Z	0,000833	-0,8780488	Glycerol-3-ph	Carbohydrates	-	Sugar utiliz
Chla	0,000851	-0,8773667	ATP-depende	RNA Metabolism	RNA proce	ATP-depen
POC	0,000871	-0,8766301	Carbon mon	Clustering-based subsystem	-	CBSS-3142
Z	0,000871	-0,8766301	NAD-depend	Clustering-based subsystem	-	CBSS-2965
POC	0,000871	-0,8766301	N-succinyl-L,L	Amino Acids and Derivatives	Lysine, thr	Lysine Bios
Salinity	0,000872	-0,87661	Carbonic anh	Carbohydrates	CO2 fixatio	Carboxysor
NO2.NO3	0,00088	-0,9030303	GDP-mannos	Cell Wall and Capsule	Capsular ar	Capsular he

TN	0,000905	-0,875384	Lipoprotein r	Cell Wall and Capsule	Gram-Neg	Lipopolysac
Z	0,000917	-0,8749564	Methenyltet	Carbohydrates	One-carbo	One-carbo
Z	0,000917	-0,8749564	Methylenete	Carbohydrates	One-carbo	One-carbo
Z	0,000917	-0,8749564	Methylenete	Cofactors, Vitamins, Prosthe	Folate and 5-FCL-like p	
DOC	0,000945	0,8739696	dTDP-4-dehy	Cell Wall and Capsule	Capsular ar	Capsular he
DOC	0,00098	0,872786	Phosphoribo	Nucleosides and Nucleotide	Purines	De Novo Pu
NO2.NO3	0,00098	0,872786	RNA helicase,	Protein Metabolism	Protein bio	Nucleolar p
Salinity	0,000995	0,8722784	Sulfate adeny	Amino Acids and Derivatives	Lysine, thr	Cysteine Bi
Chla	0,001091	-0,8691745	Deoxyribose-	Carbohydrates	Monosacch	Deoxyribos
Chla	0,001091	-0,8691745	SSU ribosom	Phages, Prophages, Transpo	Pathogenic	Staphyloco
POC	0,001098	-0,8689582	Chromosome	Cell Division and Cell Cycle	-	Bacterial Cy
POC	0,001098	-0,8689582	Cytochrome l	Photosynthesis	Electron tr	Photosyste
POC	0,001098	-0,8689582	Cytosine dear	Amino Acids and Derivatives	-	Creatine an
POC	0,001098	-0,8689582	Various polyc	Stress Response	Detoxificat	Uptake of s
Z	0,001321	-0,8624734	(3R)-hydroxy	Fatty Acids, Lipids, and Isopr	Fatty acids	Fatty Acid E
POC	0,001324	-0,8624123	Uroporphyrin	Cofactors, Vitamins, Prosthe	Tetrapyrrol	Heme and '
NO2.NO3	0,00142	0,8598559	Crossover jun	DNA Metabolism	DNA recon	RuvABC plu
DOC	0,00142	0,8598559	Gamma-gluta	Amino Acids and Derivatives	Glutamine, Poly-gamm	
Chla	0,001547	-0,8566684	Fe-S-cluster-c	Respiration	Electron ac	Anaerobic r
NO2.NO3	0,001547	-0,8566684	Protein simil	RNA Metabolism	RNA proce	Polyadenyl
POC	0,001576	-0,8559886	Histidine amr	Amino Acids and Derivatives	Histidine M	Histidine Di
TotalProtis	0,0016	-0,8554211	D-mannose is	Carbohydrates	Monosacch	Mannose M
Z	0,001675	0,8536585	Lipid A export	Miscellaneous	-	ZZ gjo need
Z	0,001675	-0,8536585	Methylmalon	Amino Acids and Derivatives	Branched-c	Branched c
NO2.NO3	0,001791	-0,8510678	Aerobic cobal	Cofactors, Vitamins, Prosthe	Tetrapyrrol	Coenzyme
NO2.NO3	0,001791	-0,8510678	Aldehyde del	Carbohydrates	Central car	Methylglyo
NO2.NO3	0,001791	-0,8510678	Ribonucleotic	Clustering-based subsystem	-	Ribonucleo
Z	0,001875	-0,849267	Formyltetrah	Carbohydrates	One-carbo	One-carbo
Z	0,001877	-0,8492354	archaeosine t	RNA Metabolism	RNA proce	Queuosine-
POC	0,001877	-0,8492354	ATP-depende	DNA Metabolism	DNA repair	DNA repair
POC	0,001877	-0,8492354	Ferric siderop	Iron acquisition and metabo	-	Campyloba
Z	0,001877	-0,8492354	Minor pilin of	Membrane Transport	Protein anc	Vir-like typ
POC	0,001877	-0,8492354	Voltage-gate	Potassium metabolism	-	Potassium l
Chla	0,001988	-0,8469257	Cytosine/puri	Nucleosides and Nucleotide	Purines	Purine Utili
NO2.NO3	0,002002	-0,846658	Phenylacetat	Metabolism of Aromatic Co	-	Phenylacet
DOC	0,002002	0,846658	Thiamine-mo	Cofactors, Vitamins, Prosthe	-	Thiamin bic
Chla	0,002002	-0,846658	Ubiquinone/r	Cofactors, Vitamins, Prosthe	Quinone cc	Menaquinc
TN	0,002086	-0,8449887	Nitrogen regl	Nitrogen Metabolism	-	Ammonia a
POC	0,002086	0,8449887	Polyphosphat	Nucleosides and Nucleotide	Purines	Purine com
TotalBacte	0,002128	-0,8441623	Uncharacteri	Stress Response	Oxidative s	Glutaredox
Z	0,002183	0,8431128	Cytochrome c	Respiration	-	Biogenesis
POC	0,002183	-0,8431128	RNA-binding	RNA Metabolism	RNA proce	Polyadenyl
POC	0,002188	-0,8430191	Acetaldehyde	Metabolism of Aromatic Co	Metabolism	Central me
TotalProtis	0,002247	0,8419239	DNA repair e	DNA Metabolism	DNA repair	DNA repair
NO2.NO3	0,002322	0,8405541	LSU ribosom	Protein Metabolism	Protein bio	Ribosome l
NO2.NO3	0,002322	-0,8405541	V-type ATP sy	Respiration	ATP syntha	V-Type ATP
POC	0,002414	0,8389097	3-oxoacyl-[ac	Cell Wall and Capsule	Cell wall of mycolic aci	

Z	0,002414	0,8389097	Deoxyhypusine Secondary Metabolism	Plant Alkaloid alkaloid biosynthesis
TN	0,002414	0,8389097	Excinuclease DNA Metabolism	DNA repair DNA repair
Z	0,002414	0,8389097	Prolyl endopeptidase Protein Metabolism	Protein degradation Serine endopeptidase
Z	0,002505	-0,8373239	NAD-specific Amino Acids and Derivatives	Glutamine, Glutamate
POC	0,002552	-0,8365344	SSU ribosome Protein Metabolism	Protein biosynthesis Ribosome
Z	0,002552	-0,8365344	tRNA N6-threosine RNA Metabolism	RNA processing Methylthio
POC	0,002611	-0,835538	Maltose/maltotriose Carbohydrates	Di- and oligosaccharides Maltose and maltotriose
Chla	0,002681	0,8666667	DNA-directed Miscellaneous	Plant-Protocist At2g23840
DOC	0,002705	0,8339956	Glutamate formyltransferase Miscellaneous	Plant-Protocist Experiment
DOC	0,002705	0,8339956	Histidinol-phosphate Amino Acids and Derivatives	Histidine N Histidine Biosynthesis
DOC	0,002767	0,8330023	Phosphopantetheine Clustering-based subsystem	CBSS-2698
NO2.NO3	0,002778	0,8328306	Excinuclease DNA Metabolism	DNA repair DNA repair
NO2.NO3	0,002852	-0,8316562	DNA replication DNA Metabolism	DNA replication DNA replication
POC	0,002891	-0,8310518	Microsomal cytochrome Cofactors, Vitamins, Prosthetic	Quinone coenzyme Pyruvate
Z	0,002891	-0,8310518	Stage 0 sporulation Cell Division and Cell Cycle	Bacterial Cell Division
POC	0,002957	-0,8300496	Adenosine (5') Clustering-based subsystem	CBSS-2249
Z	0,002957	-0,8300496	Gene SCO449 Cofactors, Vitamins, Prosthetic	Quinone coenzyme Menaquinone
Z	0,003009	-0,8292683	DNA-directed RNA Metabolism	Transcription RNA polymerase
Z	0,003009	-0,8292683	Urea ABC transporter Amino Acids and Derivatives	Arginine; urea Urea degradation
TotalProtein	0,003009	-0,8292634	Spermidine synthase Amino Acids and Derivatives	Arginine; urea Polyamine
TotalProtein	0,003075	-0,8282832	LSU ribosome Clustering-based subsystem	CBSS-1762
NO2.NO3	0,00318	-0,8267515	NADH-ubiquinol Respiration	Electron transport Respiratory
Si	0,00322	0,8261744	Ferric iron ABC transporter Iron acquisition and metabolism	Campylobacter
Si	0,00322	0,8261744	Flagellar motor Motility and Chemotaxis	Bacterial Chemotaxis
Chla	0,00322	-0,8261744	Glycerol-3-phosphate Carbohydrates	Sugar alcohol Glycerol and
DOC	0,00322	0,8261744	Phosphatidylglycerol Fatty Acids, Lipids, and Isoprenoids	Phospholipid Glycerolipid
TN	0,00322	-0,8261744	Protein RtcB RNA Metabolism	RNA processing RNA 3'-terminal
Salinity	0,003323	-0,824713	Ammonium transporter Nitrogen Metabolism	Ammonia assimilation
Z	0,003328	-0,8246505	5-aminolevulinic acid Cofactors, Vitamins, Prosthetic	Tetrapyrrole Heme and
Z	0,003328	-0,8246505	NAD-reducing Respiration	Electron transport Hydrogenase
Z	0,003406	-0,8235648	4Fe-4S ferredoxin Sulfur Metabolism	Inorganic sulfur Inorganic Sulfur
Salinity	0,003497	0,8223258	ATP-dependent Clustering-based subsystem	ClpAS cluster
TN	0,003505	-0,8545455	ATP-dependent Clustering-based subsystem	CBSS-1762
POC	0,003534	-0,8218407	Flagellar synthase Motility and Chemotaxis	Flagellar motor Flagellar motor
DOC	0,003592	0,8210654	MiaB family protein Protein Metabolism	Protein processing Ribosomal
PO4	0,003592	0,8210654	RNA helicase, Protein Metabolism	Protein biosynthesis Nucleolar protein
DOC	0,003592	0,8210654	Sensor histidine kinase Regulation and Cell signaling	Global Two-component
Si	0,003724	0,8193465	NusA protein RNA Metabolism	Transcription Transcription
DOC	0,003724	0,8193465	Possible subunit Nucleosides and Nucleotide	Purines De Novo Purine
Si	0,003739	0,8191501	Gamma-aminobutyrate Amino Acids and Derivatives	Arginine; urea Putrescine
Chla	0,003739	-0,8191501	PrpF protein in Carbohydrates	Organic acid Methylcitrate
Chla	0,003739	-0,8191501	tRNA(Cytosine) Clustering-based subsystem	Translation CBSS-3264
Z	0,00379	0,8184964	AmpG permease Cell Wall and Capsule	Recycling of
Z	0,00379	-0,8184964	Aspartate carboxylase Clustering-based subsystem	CBSS-3203
Salinity	0,003815	0,8181828	Squalene hydroxylase Clustering-based subsystem	Carotenoid CBSS-3203
POC	0,003903	-0,8170801	Putative cytochrome Respiration	Biogenesis
TN	0,003989	0,8160123	LSU ribosome Protein Metabolism	Protein biosynthesis Ribosome

Z	0,004052	-0,815251	Phosphohept Cell Wall and Capsule	Capsular ar Capsular he
NO2.NO3	0,004106	-0,8145934	Lipoprotein r Cell Wall and Capsule	Gram-Neg; Lipopolysac
NO2.NO3	0,004249	-0,812897	HtrA protease Cell Wall and Capsule	Gram-Neg; Lipopolysac
DOC	0,004249	0,812897	tRNA (cytosin RNA Metabolism	RNA proce; RNA methy
TotalBacte	0,004259	-0,8127768	Heavy metal ; Virulence, Disease and Defe	Resistance Cobalt-zinc
TotalBacte	0,004259	-0,8127768	NADH-depen Carbohydrates	Fermentati Acetone Bu
TotalBacte	0,004259	-0,8127768	Replicative D Clustering-based subsystem	Clustering- CBSS-2627
Z	0,004297	-0,8123423	DNA polymer Clustering-based subsystem -	CBSS-3506
Z	0,004416	-0,8109756	TATA-box bin RNA Metabolism	Transcripti RNA polym
POC	0,004449	-0,8105953	2-ketoglutaric Carbohydrates	Monosaccl L-Arabinose
NO2.NO3	0,004459	-0,8424242	Prolyl-tRNA s Protein Metabolism	Protein bio tRNA aminc
Z	0,004582	-0,8090995	Ribose 1,5-bi Carbohydrates	CO2 fixatio Calvin-Bens
Z	0,004582	-0,8090995	Thiazole bios Cofactors, Vitamins, Prosthe	Thiamin bic
Salinity	0,004618	-0,8087036	DNA topoisor DNA Metabolism	DNA replic; DNA topois
NO2.NO3	0,004635	-0,8085144	Nitrogen regl Nitrogen Metabolism	- Ammonia a
POC	0,004669	-0,8081434	DNA ligase, p Phages, Prophages, Transpo	Phages, Prc Phage repli
POC	0,004669	-0,8081434	Glycerophos Carbohydrates	Sugar alcof Glycerol an
POC	0,004669	-0,8081434	Saccharopine Amino Acids and Derivatives	Lysine, thre Lysine bios
DOC	0,00467	0,8081352	Intracellular s Cell Division and Cell Cycle	- Intracellula
PO4	0,004807	-0,806644	Protein simila RNA Metabolism	RNA proce; Polyadenyl
Chla	0,004807	-0,806644	tRNA (cytosin RNA Metabolism	RNA proce; RNA methy
POC	0,004871	-0,8059635	Geranyl-CoA ; Fatty Acids, Lipids, and Isopr	Isoprenoid; Acyclic terp
POC	0,004871	-0,8059635	Maltose phos Carbohydrates	Di- and olig Maltose an
Si	0,004897	0,8056907	Biotin carbox Respiration	Sodium Ion Na+ transcl
Chla	0,004897	-0,8056907	Flagellin prot Motility and Chemotaxis	Flagellar m Flagellum
Z	0,004974	-0,804878	Adenylosucci Nucleosides and Nucleotide	Purines De Novo Pu
POC	0,004989	-0,804719	16S rRNA m Clustering-based subsystem -	Conserved
POC	0,004989	-0,804719	Gentisate 1,2 Metabolism of Aromatic Coi	Gentisare c
POC	0,005048	-0,8041105	Dihydrolipoar Amino Acids and Derivatives	Branched-c Branched c
POC	0,005048	-0,8041105	Sodium/gluta Amino Acids and Derivatives	Glutamine, Glutamate
TotalProtis	0,005064	0,8039424	2-aminoethyl Phosphorus Metabolism	- Phosphoen
TotalProtis	0,005084	-0,8037415	4-hydroxyphc Amino Acids and Derivatives	Aromatic a Aromatic ai
Si	0,005084	0,8037415	GTP-binding ; Protein Metabolism	Protein bio Universal G
Chla	0,005084	-0,8037415	Leucine-, isoc Carbohydrates	Central car Dehydroge
Chla	0,005084	-0,8037415	Ribosomal lar RNA Metabolism	RNA proce; RNA pseud
PO4	0,005211	-0,8024353	DNA-binding Regulation and Cell signaling	- The Chv reg
POC	0,005211	0,8024353	Leucyl-tRNA ; Protein Metabolism	Protein bio tRNA aminc
Salinity	0,005358	-0,8009692	Tol biopolym Membrane Transport	- Ton and To
TN	0,005416	0,8003909	Di-/tripeptide Membrane Transport	Uni- Sym- ; Proton-dep
POC	0,005426	-0,8002922	Indolepyruva Amino Acids and Derivatives	Aromatic a Aromatic ai
POC	0,005426	-0,8002922	Monoamine c Amino Acids and Derivatives	Alanine, se Glycine anc
POC	0,005426	-0,8002922	Similarity witl Stress Response	Oxidative s Glutathiony
POC	0,005426	-0,8002922	TonB-depend Cofactors, Vitamins, Prosthe	Folate and YgfZ-Iron
POC	0,005453	-0,8000341	cytochrome k Respiration	- Soluble cyti
Z	0,005453	-0,8000341	IMP cyclohyd Nucleosides and Nucleotide	Purines De Novo Pu
Z	0,005453	-0,8000341	Phosphoribos Cofactors, Vitamins, Prosthe	Folate and 5-FCL-like p
POC	0,005488	-0,7996914	Acetyl-CoA C- Metabolism of Aromatic Coi	Peripheral Benzoate c

Si	0,005573	0,7988628	2-C-methyl-D Clustering-based subsystem -	CBSS-21158
DOC	0,005573	0,7988628	Acriflavin resi Virulence, Disease and Defe Resistance	Multidrug F
Si	0,005573	0,7988628	Acriflavin resi Virulence, Disease and Defe Resistance	Multidrug F
Chla	0,005573	-0,7988628	Benzoylformæ Metabolism of Aromatic Coi	Peripheral Benzoate d
Si	0,005573	0,7988628	Cobalamin sy Cofactors, Vitamins, Prosthe	Tetrapyrrol Cobalamin
NO2.NO3	0,005573	-0,7988628	L-seryl-tRNA(Protein Metabolism	Selenoprot Selenocyste
Si	0,005573	0,7988628	Putative glutæ Sulfur Metabolism	Organic sul Utilization r
Chla	0,005573	-0,7988628	putative periç Protein Metabolism	Protein prc G3E family
TN	0,005573	-0,7988628	Succinate deç Respiration	Electron dc Succinate d
DOC	0,005573	0,7988628	Taurine-bindi Sulfur Metabolism	Organic sul Taurine Uti
Si	0,005573	0,7988628	Taurine-bindi Sulfur Metabolism	Organic sul Taurine Uti
DOC	0,005573	0,7988628	Uracil-DNA gl DNA Metabolism	DNA repair Uracil-DNA
Si	0,005573	0,7988628	Uracil-DNA gl DNA Metabolism	DNA repair Uracil-DNA
Chla	0,005677	-0,7978634	CDP-diacylgly Fatty Acids, Lipids, and Isopr	Phospholip Glycerolipic
Si	0,005677	-0,7978634	Flagellar moti Motility and Chemotaxis	- Bacterial Cl
Si	0,005677	-0,7978634	Glutamate-ar Clustering-based subsystem -	CBSS-31608
Chla	0,005677	-0,7978634	Hydroxymeth Amino Acids and Derivativeç	Branched-c Leucine Deç
TotalBacte	0,005677	-0,7978634	N-acetylgluco Carbohydrates	Aminosuga Chitin and I
Si	0,005677	-0,7978634	Para-aminobæ Amino Acids and Derivativeç	Aromatic a Chorismate
Si	0,005677	0,7978634	Ribosomal lar Clustering-based subsystem -	EC49-61
Chla	0,005677	-0,7978634	sulfur oxidatiç Sulfur Metabolism	- Sulfur oxidæ
Z	0,005702	-0,7976258	4-coumarate- Secondary Metabolism	Biosynthes Caffaic acid
Z	0,005702	0,7976258	ATP phospho Amino Acids and Derivativeç	Histidine V Histidine Bi
Z	0,005702	-0,7976258	Pyruvate kina Carbohydrates	Central car Entner-Dou
Z	0,005702	-0,7976258	SSU ribosomæ Protein Metabolism	Protein bio Ribosome S
Salinity	0,005776	0,7969258	Inner membr. Clustering-based subsystem -	CTP syntha
POC	0,005837	0,7963563	5-carboxymeç Amino Acids and Derivativeç	Aromatic a Aromatic ai
Si	0,005837	-0,7963563	Glutarate-ser Amino Acids and Derivativeç	Lysine, thrç Lysine degr
Chla	0,005961	-0,7952051	hydantoin rac Nucleosides and Nucleotide -	Hydantoin i
Chla	0,005961	-0,7952051	Uncharacteriç Clustering-based subsystem	Clustering- Putative diç
Salinity	0,005974	0,7950896	Assimilatory r Nitrogen Metabolism	- Nitrate and
Salinity	0,005974	0,7950896	sulfonate mo Sulfur Metabolism	Organic sul Alkanesulfc
POC	0,006044	-0,794446	Predicted ma Membrane Transport	- Transport c
Z	0,006044	-0,794446	Twin-arginine Clustering-based subsystem	proteosom Cluster-bas
Chla	0,006078	0,7941379	ABC-type sug Miscellaneous	Plant-Prokæ COG3533
NO2.NO3	0,006078	0,7941379	Di-/tripeptide Membrane Transport	Uni- Sym- æ Proton-dep
Si	0,006078	0,7941379	Maltose/malt Carbohydrates	Di- and olig Maltose an
PO4	0,006078	-0,7941379	Ribosomal lar Clustering-based subsystem	Fatty acid r COG1399
Z	0,006106	-0,79388	Crotonyl-CoA Carbohydrates	Central car Ethylmalon
Z	0,006106	-0,79388	GTP-binding ç Protein Metabolism	Protein bio Universal G
POC	0,00624	0,7926829	Cystathionine Amino Acids and Derivativeç	Alanine, se Glycine anc
Z	0,00624	-0,7926829	Thermosome Protein Metabolism	Protein folk Thermoson
TotalBacte	0,006313	-0,7920349	GTP cyclohyd Cofactors, Vitamins, Prosthe	Folate and methanopt
Chla	0,006313	-0,7920349	Heme biosyni Cofactors, Vitamins, Prosthe	Tetrapyrrol Heme biosy
Chla	0,006313	-0,7920349	Heme biosyni Cofactors, Vitamins, Prosthe	Tetrapyrrol Heme biosy
Chla	0,006313	-0,7920349	Riboflavin syr Cofactors, Vitamins, Prosthe	Riboflavin, riboflavin ti
TotalProtis	0,006325	-0,791933	Manganese-d Phosphorus Metabolism	- Phosphate

TotalProtis	0,006377	-0,7914706 Fumarate hyc	Carbohydrates	Central car	TCA Cycle
NO2.NO3	0,006377	-0,7914706 N-succinyl-L,L	Amino Acids and Derivatives	Arginine; u	Arginine Bi
TN	0,006377	-0,7914706 Predicted nuc	Carbohydrates	Monosacch	Deoxyribos
TN	0,006377	0,7914706 YgjD/Kae1/Qi	Cell Division and Cell Cycle	-	Macromole
POC	0,006415	-0,791141 COG2047: Un	RNA Metabolism	RNA proce	Queuosine-
Z	0,006415	-0,791141 Malate synth	Carbohydrates	Central car	Glyoxylate
POC	0,006415	-0,791141 Phosphate st	Clustering-based subsystem	-	CBSS-5678
Salinity	0,00648	0,7905758 DNA repair pr	DNA Metabolism	DNA repair	DNA repair
NO2.NO3	0,006514	-0,7902772 Altronate hyc	Carbohydrates	Monosacch	D-Galactur
Si	0,006514	0,7902772 Branched-ch	Amino Acids and Derivatives	Branched-c	Branched c
POC	0,006514	0,7902772 Thioredoxin	Miscellaneous	Plant-Prok	DOE COG2
TotalProtis	0,006685	0,7888199 Phosphoman	Carbohydrates	Monosacch	Mannose M
NO2.NO3	0,006811	0,8181818 Translation el	Protein Metabolism	Protein bio	Translation
Z	0,006814	-0,7877259 Delta-1-pyrro	Amino Acids and Derivatives	Arginine; u	Arginine an
TotalProtis	0,006814	-0,7877259 L-arabonate c	Carbohydrates	Monosacch	L-Arabinos
TotalProtis	0,006814	-0,7877259 Uracil-xanthir	Nucleosides and Nucleotide	Purines	Purine Utili
Z	0,007105	0,7853335 Arginine-tRN	Protein Metabolism	Protein deg	Protein deg
Si	0,00712	0,7852071 Glutaminase	Amino Acids and Derivatives	Glutamine, Glutamine,	
Chla	0,00712	0,7852071 Phenylacetat	Metabolism of Aromatic Co	-	Phenylacet
Si	0,00712	0,7852071 prolyl oligope	Miscellaneous	Plant-Prok	Synechocys
Salinity	0,00714	0,7850505 Cysteine synt	Amino Acids and Derivatives	Lysine, thr	Cysteine Bi
Z	0,007188	-0,7846563 NADPH-depe	RNA Metabolism	RNA proce	Queuosine-
POC	0,007188	-0,7846563 YciL protein	Miscellaneous	-	Broadly dis
POC	0,007245	0,7841982 Protein expor	Clustering-based subsystem	Protein ex	CBSS-3931
Salinity	0,007331	0,783514 Copper resist	Virulence, Disease and Defe	Resistance	Copper hor
Salinity	0,007331	0,783514 SSU ribosom	Protein Metabolism	Protein bio	Ribosome S
DOC	0,007488	0,7822749 3-hydroxyacy	Amino Acids and Derivatives	Branched-c	Isoleucine c
DOC	0,007488	0,7822749 Phosphoribo	Amino Acids and Derivatives	Histidine M	Histidine Bi
TotalBacte	0,007488	-0,7822749 Similar to N-t	Miscellaneous	Plant-Prok	Competenc
Si	0,007571	0,7816317 Peptidyl-proh	Protein Metabolism	Protein fol	Peptidyl-pr
NO2.NO3	0,007571	-0,7816317 Similarity to	Miscellaneous	Plant-Prok	At4g17370
PO4	0,007571	-0,7816317 Similarity to	Miscellaneous	Plant-Prok	At4g17370
Z	0,007579	-0,7815718 Beta-ketoadi	Metabolism of Aromatic Co	Metabolism	Protocatecl
Salinity	0,007617	-0,7812733 L-asparaginas	Amino Acids and Derivatives	Glutamine, Glutamine,	
Z	0,007669	-0,7808751 Sporulation ir	Cell Division and Cell Cycle	-	Bacterial Cy
Salinity	0,00779	-0,779945 Flagellar mot	Motility and Chemotaxis	-	Bacterial Cl
Salinity	0,00779	-0,779945 Glutamate-ar	Clustering-based subsystem	-	CBSS-3160
Salinity	0,00779	-0,779945 Para-aminob	Amino Acids and Derivatives	Aromatic a	Chorismate
NO2.NO3	0,007889	-0,7791998 DNA mismatc	DNA Metabolism	DNA repair	DNA repair
TotalProtis	0,007889	0,7791998 Pyruvate carl	Carbohydrates	Central car	Pyruvate m
TN	0,007889	-0,7791998 ubiquinol cy	Respiration	Electron ac	Ubiquinone
Salinity	0,007939	-0,77882 ATP synthase	Respiration	ATP syntha	F0F1-type /
Salinity	0,007939	-0,77882 DNA topoisor	DNA Metabolism	DNA replic	DNA topois
TotalProtis	0,007966	0,7786214 Predicted L-r	Carbohydrates	Monosacch	L-rhamnose
NO2.NO3	0,007998	0,7783792 5-nucleotidas	Clustering-based subsystem	-	CBSS-2115
DOC	0,007998	0,7783792 delta 1-pyrro	Cofactors, Vitamins, Prosthe	Folate and	Methanopt
PO4	0,008033	-0,7781191 Aerobic cobal	Cofactors, Vitamins, Prosthe	Tetrapyrro	Coenzyme

POC	0,008033	0,7781191	Potassium up Clustering-based subsystem -	Cluster co-ε
TN	0,008033	-0,7781191	Ribonucleotic Clustering-based subsystem -	Ribonucleo
Z	0,008084	0,7777391	Na ⁺ /H ⁺ anti Membrane Transport	Uni- Sym- z NhaA, NhaI
POC	0,00814	-0,7773243	Glucosamine- Carbohydrates	Aminosuga Chitin and I
POC	0,00814	-0,7773243	Taurine trans Sulfur Metabolism	Organic sul Taurine Uti
Chla	0,008236	0,8060606	Citrate synth Carbohydrates	Central car Glyoxylate
DOC	0,008236	-0,8060606	Transketolase Carbohydrates	- Sugar utiliz
Z	0,008402	-0,7754177	LSU ribosoma Miscellaneous	Plant-Prok: COG0523
POC	0,008402	-0,7754177	Pyrimidine A Nucleosides and Nucleotide	Pyrimidine: Pyrimidine
TotalProtis	0,008577	-0,7741648	Inner membr Miscellaneous	- YbbK
Si	0,00888	-0,77204	2-keto-3-deo: Amino Acids and Derivatives	Aromatic a Chorismate
TN	0,00888	-0,77204	Cell division p Cell Division and Cell Cycle	- Bacterial C
Z	0,00888	-0,77204	Isocitrate lya Carbohydrates	Central car Glyoxylate
POC	0,00888	0,77204	SSU ribosoma Protein Metabolism	Protein bio Ribosome S
Z	0,008931	-0,7716867	LSU ribosoma Protein Metabolism	Protein bio Ribosome L
POC	0,009122	-0,7703748	Acetoacetyl-C Carbohydrates	Central car Ethylmalon
POC	0,009122	-0,7703748	Carotenoid ci Fatty Acids, Lipids, and Isop	Isoprenoid: Carotenoid
POC	0,009122	-0,7703748	LSU ribosoma Protein Metabolism	Protein bio Ribosome L
POC	0,009122	-0,7703748	Mr7403 prot Clustering-based subsystem -	CBSS-2906:
POC	0,009122	-0,7703748	Putative TEG Clustering-based subsystem	Translation CBSS-3264:
POC	0,009122	-0,7703748	ThiI/Pfpl fam Clustering-based subsystem -	CBSS-1762:
Si	0,009274	0,7693447	Biosynthetic / Amino Acids and Derivatives	Aromatic a Phenylalani
TotalBacte	0,009274	-0,7693447	Cytochrome b Respiration	- Cytochrom
DOC	0,009274	0,7693447	DNA-directed RNA Metabolism	Transcripti RNA polym
Si	0,009274	0,7693447	DNA-directed RNA Metabolism	Transcripti RNA polym
TotalBacte	0,009274	-0,7693447	Flagellar regu Motility and Chemotaxis	Flagellar m Flagellum
DOC	0,009274	0,7693447	Glutathione r Stress Response	Oxidative s Glutathione
Si	0,009274	0,7693447	Glutathione r Stress Response	Oxidative s Glutathione
DOC	0,009274	0,7693447	Ribonucleotic Nucleosides and Nucleotide -	Ribonucleo
TotalProtis	0,009286	0,7692635	ATP-depende Protein Metabolism	Protein deg Proteasom
Z	0,009286	-0,7692635	Methylisocitr Carbohydrates	Organic aci Methylcitra
Chla	0,009307	-0,7691256	Glutamate fo Amino Acids and Derivatives	Histidine V Histidine D
TN	0,009307	-0,7691256	HtrA protease Cell Wall and Capsule	Gram-Neg: Lipopolysac
TN	0,009307	0,7691256	Predicted nuc Carbohydrates	Monosacch Deoxyribos
POC	0,009426	-0,7683309	ATP phospho Amino Acids and Derivatives	Histidine V Histidine Bi
Salinity	0,009454	-0,7681426	Methylthioric Amino Acids and Derivatives	Lysine, thre Methionine
TN	0,00947	0,7680368	Acetylamino Amino Acids and Derivatives	Lysine, thre Lysine bios
Si	0,00947	0,7680368	Ferritin-like p Miscellaneous	Plant-Prok: Iron-sulfur
DOC	0,00947	0,7680368	Glutamate As Amino Acids and Derivatives	Glutamine, Glutamate
DOC	0,00947	0,7680368	N-acetylgalac Carbohydrates	Aminosuga N-Acetyl-G
Si	0,00947	0,7680368	Nucleoside tr Dormancy and Sporulation	- Sporulation
TotalBacte	0,00947	0,7680368	Oligopeptide Membrane Transport	ABC transp ABC transp
DOC	0,00947	0,7680368	Succinyl-CoA Carbohydrates	Central car TCA Cycle
POC	0,00962	-0,7670513	Aspartokinas Amino Acids and Derivatives	Lysine, thre Lysine Bios
POC	0,00962	-0,7670513	Phosphate st: Phosphorus Metabolism	- P uptake (c
POC	0,00962	-0,7670513	Phosphate st: Clustering-based subsystem -	CBSS-5678:
Z	0,00962	-0,7670513	TRAP-type C4 Miscellaneous	Plant-Prok: At4g17370

TotalProtis	0,009638	0,7669289	ATP-depende Protein Metabolism	Protein deg Proteasom
TN	0,009638	-0,7669289	Phenylacetat Metabolism of Aromatic Co	Phenylacet
NO2.NO3	0,009638	-0,7669289	tolB protein f Membrane Transport	- Ton and To
Salinity	0,009726	0,7663589	RNA polymer RNA Metabolism	Transcripti Transcriptic
POC	0,009787	0,765961	NAD-depend Carbohydrates	Central car Entner-Dou
DOC	0,009844	-0,7939394	Glycyl-tRNA s Protein Metabolism	Protein bio tRNA aminc
NO2.NO3	0,009844	-0,7939394	Omega-amin Carbohydrates	Central car Pyruvate Al
DOC	0,009979	0,7647234	carbon mono Clustering-based subsystem	- CBSS-3142f
Chla	0,009979	-0,7647234	Cytochrome c Respiration	- Biogenesis
PO4	0,009979	-0,7647234	Eukaryotic tr Protein Metabolism	Protein bio Translation
Si	0,009979	0,7647234	Flagellar bios Motility and Chemotaxis	Flagellar m Flagellum
Chla	0,009979	-0,7647234	Mesaconyl-C Carbohydrates	Central car Ethylmalon
Chla	0,009979	-0,7647234	Nitrate ABC tr Nitrogen Metabolism	- Nitrate and
DOC	0,009979	0,7647234	Phosphonoac Phosphorus Metabolism	- Phosphona
TotalBacte	0,009979	-0,7647234	Ribosomal lar RNA Metabolism	RNA proce RNA pseud
TotalProtis	0,010097	0,7639752	LSU ribosom Protein Metabolism	Protein bio Ribosome L
POC	0,010152	-0,763627	Alpha-glucosi Membrane Transport	ABC transp Periplasmic
POC	0,010152	-0,763627	UPF0129 pro Respiration	- Methanoge
POC	0,010234	-0,7631094	ABC-type pol Clustering-based subsystem	Translation CBSS-3264
POC	0,010234	-0,7631094	Glutamate--c Cofactors, Vitamins, Prosthe	Folate and YgfZ
Z	0,010234	-0,7631094	Phospholipas Miscellaneous	Plant-Prok At2g23840
DOC	0,010272	0,7628726	Fe-S-cluster-c Respiration	Electron ac Anaerobic r
TotalProtis	0,010344	0,7624216	Nucleotide su Clustering-based subsystem	- CBSS-2965f
Z	0,010381	-0,7621951	Succinyl-CoA Carbohydrates	Central car TCA Cycle
Z	0,010403	-0,7620588	Integration h DNA Metabolism	- DNA structi
POC	0,010951	-0,7587172	6-pyruvoyl te Cofactors, Vitamins, Prosthe	Folate and Methanopt
DOC	0,011089	0,7578955	Ferric iron AB Iron acquisition and metabo	- Campyloba
DOC	0,011089	0,7578955	Flagellar moti Motility and Chemotaxis	- Bacterial Cl
Z	0,011249	-0,7569553	ABC-type mul Clustering-based subsystem	Cytochrom CBSS-1961f
Z	0,011249	-0,7569553	GTP pyropho Clustering-based subsystem	Probably G CBSS-1762f
Z	0,011249	-0,7569553	Sulfite oxidas Sulfur Metabolism	- Sulfur oxidz
POC	0,011279	-0,7567783	Glycolate del Carbohydrates	Central car Glycolate, g
POC	0,011279	-0,7567783	Inositol trans Carbohydrates	Sugar alcof Inositol cat
POC	0,011279	-0,7567783	Probable corr Cell Wall and Capsule	Gram-Neg Lipopolysac
NO2.NO3	0,011306	0,7566195	3-dehydroqui Amino Acids and Derivative	Aromatic a Chorismate
TotalBacte	0,011306	0,7566195	Na+/H+ antip Membrane Transport	Uni- Sym- z NhaA, NhaI
TotalBacte	0,011306	-0,7566195	Phosphoribo Cofactors, Vitamins, Prosthe	Folate and YgfZ
Chla	0,011341	-0,7564146	DNA-directed RNA Metabolism	Transcripti RNA polym
TotalBacte	0,011341	-0,7564146	Ferredoxin--N Sulfur Metabolism	Inorganic s Inorganic S
Chla	0,011341	-0,7564146	Heme biosyn Cofactors, Vitamins, Prosthe	Tetrapyrrol Heme biosy
Chla	0,011341	-0,7564146	Heme biosyn Cofactors, Vitamins, Prosthe	Tetrapyrrol Heme biosy
PO4	0,011341	-0,7564146	Translation el Protein Metabolism	Protein bio Translation
Z	0,011396	-0,7560976	DNA-directed RNA Metabolism	Transcripti RNA polym
Z	0,011396	-0,7560976	LSU ribosom Protein Metabolism	Protein bio Ribosome L
POC	0,011513	-0,755416	Alternative cy Respiration	Electron ac Terminal cy
POC	0,011513	-0,755416	Functional ro Nitrogen Metabolism	- Nitrosative
POC	0,011513	-0,755416	Integral mem Clustering-based subsystem	- CBSS-630.2

POC	0,011513	-0,755416	Leucine-resp	Amino Acids and Derivatives	Branched-c	Branched-C
Z	0,011513	-0,755416	RNA polymer	RNA Metabolism	Transcripti	Transcripti
POC	0,011513	-0,755416	TcuA: flavopr	Carbohydrates	Organic aci	Tricarballyl
POC	0,011513	-0,755416	tRNA pseudo	RNA Metabolism	RNA proce	rRNA modii
POC	0,011513	-0,755416	V-type ATP sy	Miscellaneous	Plant-Prok	lojap
TN	0,011645	-0,754658	Homoserine	(Amino Acids and Derivatives)	Lysine, thr	Methionine
NO2.NO3	0,011651	0,7818182	Membrane al	Protein Metabolism	Protein deg	Aminocept
NO2.NO3	0,011651	-0,7818182	Pyruvate,pho	Carbohydrates	Central car	Glycolysis a
TN	0,011795	-0,7538029	Carbamoyl-pl	Cell Division and Cell Cycle	-	Macromole
NO2.NO3	0,011795	-0,7538029	Carbamoyl-pl	Cell Division and Cell Cycle	-	Macromole
POC	0,011795	0,7538029	Transcription	RNA Metabolism	Transcripti	Transcripti
POC	0,011874	-0,753354	Oxidoreducta	Miscellaneous	Plant-Prok	At4g17370
PO4	0,011915	-0,7531234	Collagen alph	Protein Metabolism	Protein bio	Nucleolar p
TotalBacte	0,011915	0,7531234	Cytochrome c	Respiration	Electron ac	Terminal cy
Chla	0,011915	-0,7531234	DNA-binding	RNA Metabolism	RNA proce	tRNA modii
PO4	0,011915	-0,7531234	Inner membr	Clustering-based subsystem	-	Cluster witl
Si	0,011915	0,7531234	Membrane-b	Cell Wall and Capsule	-	Murein Hyc
NO2.NO3	0,011915	0,7531234	Metal-depen	Phosphorus Metabolism	-	Alkylphospl
NO2.NO3	0,011915	-0,7531234	Metallo-beta	Clustering-based subsystem	-	Bacterial RI
TotalBacte	0,011915	-0,7531234	Nicotinate-nu	Cofactors, Vitamins, Prosthe	NAD and N	NAD and N.
TotalBacte	0,011915	0,7531234	N-methylhyd	Amino Acids and Derivatives	-	Creatine an
DOC	0,011915	0,7531234	Protein YicC	Clustering-based subsystem	-	CBSS-3230
NO2.NO3	0,011915	0,7531234	Protein-expo	Membrane Transport	Protein tra	HtrA and Se
DOC	0,011915	0,7531234	Pyridine nucl	Nucleosides and Nucleotide	Pyrimidine	Pyrimidine
PO4	0,011915	-0,7531234	SSU ribosom	Protein Metabolism	Protein bio	Ribosome S
Salinity	0,01203	0,7524758	NADPH-depe	Carbohydrates	Central car	Methylglyo
POC	0,012074	-0,7522324	Dihydroorota	Cofactors, Vitamins, Prosthe	Folate and	YgfZ
DOC	0,012283	0,7510676	3-oxoadipate	Metabolism of Aromatic Co	Metabolism	Catechol br
DOC	0,012283	0,7510676	Clavamate	Miscellaneous	Plant-Prok	At4g17370
Si	0,012283	0,7510676	Cyanophycin	Amino Acids and Derivatives	Arginine; u	Cyanophyci
Chla	0,012283	-0,7510676	General secre	Membrane Transport	Protein sec	General Ser
DOC	0,012283	0,7510676	Hemoprotein	Cofactors, Vitamins, Prosthe	Tetrapyrrol	Heme and !
NO2.NO3	0,012283	-0,7510676	N-acetylgluco	Cell Wall and Capsule	-	Peptidoglyc
DOC	0,012283	0,7510676	Phosphonate	Membrane Transport	ABC transp	ABC transp
DOC	0,012283	0,7510676	Pup ligase Pa	Clustering-based subsystem	proteosom	Cluster-bas
Chla	0,012283	-0,7510676	Queuosine bi	Cofactors, Vitamins, Prosthe	Folate and	Methanopt
DOC	0,012283	0,7510676	Rubredoxin-N	Stress Response	Oxidative s	Rubrrerythri
DOC	0,012283	-0,7510676	Succinate de	Respiration	Electron dc	Succinate d
Z	0,012332	-0,7508012	Ribosomal pr	Protein Metabolism	Protein prc	Ribosomal
Z	0,012332	-0,7508012	tRNA-(ms[2])	RNA Metabolism	RNA proce	tRNA modii
Si	0,012411	0,7503665	tRNA (cytosin	RNA Metabolism	RNA proce	RNA methy
Z	0,012478	0,75	Peptide meth	Carbohydrates	-	Unknown c
Z	0,012567	-0,7495147	Chromosome	Cell Division and Cell Cycle	-	Bacterial Cy
Z	0,012567	-0,7495147	Ribonuclease	RNA Metabolism	RNA proce	tRNA proce
POC	0,012567	-0,7495147	Trehalose ph	Carbohydrates	Di- and olig	Trehalose E
DOC	0,0129	0,7477238	Branched-ch	Amino Acids and Derivatives	Branched-c	Branched c
POC	0,0129	0,7477238	NADH-ubiqui	Respiration	Electron dc	Respiratory

POC	0,0129	0,7477238	Pyruvate deh	Carbohydrates	Central car	Dehydroge
POC	0,0129	0,7477238	Translation el	Protein Metabolism	Protein bio	Translation
TotalProtis	0,012975	0,7473241	Aconitate hyc	Carbohydrates	Central car	TCA Cycle
TotalProtis	0,012975	-0,7473241	FIG000875: T	Miscellaneous	Plant-Prok	COG3760
TotalProtis	0,012975	-0,7473241	intein-contair	Protein Metabolism	Protein prc	Inteins
TotalProtis	0,012975	-0,7473241	Legionaminic	Cell Wall and Capsule	Capsular ar	Legionamir
TotalProtis	0,012975	-0,7473241	Mannose-1-p	Carbohydrates	Monosacct	Mannose N
TotalProtis	0,012975	-0,7473241	NG,NG-dimet	Stress Response	-	Dimethylar
TotalProtis	0,012975	-0,7473241	Periplasmic b	Carbohydrates	Di- and olig	Beta-Gluco
TotalProtis	0,012975	-0,7473241	RNA binding r	RNA Metabolism	RNA proce	rRNA modii
TotalProtis	0,012975	-0,7473241	Xylose ABC tr	Carbohydrates	Monosacct	Xylose utili
Salinity	0,013042	0,7469705	Methylmalon	Carbohydrates	Sugar alcof	Inositol cat
TotalProtis	0,013042	-0,7469701	3-hydroxybut	Carbohydrates	Fermentati	Acetyl-CoA
TotalProtis	0,013042	0,7469701	DNA polymer	Clustering-based subsystem	-	DNA replica
TotalProtis	0,013128	-0,746516	Respiratory n	Nitrogen Metabolism	-	Nitrate and
Z	0,013154	0,7463786	Lipid A export	Cell Wall and Capsule	Gram-Neg	KDO2-Lipid
Z	0,013154	-0,7463786	Uncharacteri	Stress Response	Oxidative s	Glutaredox
POC	0,013274	-0,7457477	Acetoacetyl-C	Amino Acids and Derivative	Branched-c	HMG CoA S
POC	0,013274	-0,7457477	ATP-depende	Clustering-based subsystem	Ribosomal	A Gram-po
Z	0,013274	-0,7457477	Plasmid replic	DNA Metabolism	DNA replic	Plasmid rep
Z	0,013274	-0,7457477	putative metI	Phages, Prophages, Transpo	Phages, Prc	r1t-like stre
POC	0,013274	-0,7457477	Ribosomal R	Clustering-based subsystem	-	Conserved
Salinity	0,013475	-0,7447035	ABC transpor	Miscellaneous	Plant-Prok	COG3533
Chla	0,013565	-0,7442397	Eukaryotic tr	Protein Metabolism	Protein bio	Translation
TotalBacte	0,013565	-0,7442397	Propionate c	Carbohydrates	Organic aci	Methylcitra
Chla	0,013565	-0,7442397	Thymidylate I	Clustering-based subsystem	-	CBSS-3931
DOC	0,013589	0,7441134	L-alanine-DL-	Cell Wall and Capsule	-	Recycling o
TN	0,013589	-0,7441134	Pseudaminic	Cell Wall and Capsule	Capsular ar	Pseudamin
Z	0,01363	-0,7439024	Ferric uptake	Iron acquisition and metabo	-	Campyloba
Z	0,01363	-0,7439024	Ferric uptake	Clustering-based subsystem	-	Bacterial RI
POC	0,01363	-0,7439024	Imidazole gly	Amino Acids and Derivative	Histidine M	Histidine Bi
Chla	0,013672	0,769697	Argininosucci	Amino Acids and Derivative	Arginine; u	Arginine Bi
NO2.NO3	0,013672	-0,769697	Cysteine synt	Amino Acids and Derivative	Lysine, thr	Cysteine Bi
NO2.NO3	0,013672	-0,769697	Enolase (EC 4	Carbohydrates	Central car	Entner-Dou
DOC	0,013672	-0,769697	MoxR-like AT	Clustering-based subsystem	-	Aerotolera
PO4	0,013672	0,769697	Translation el	Protein Metabolism	Protein bio	Translation
DOC	0,013712	0,7434844	3-ketoacyl-Cc	Amino Acids and Derivative	Branched-c	Branched c
DOC	0,013712	0,7434844	Chaperone pr	Protein Metabolism	Protein fol	Protein cha
TN	0,013712	0,7434844	Formate deh	Respiration	-	Formate hy
DOC	0,013712	0,7434844	Glycerol-3-ph	Carbohydrates	Sugar alcof	Glycerol an
NO2.NO3	0,013712	-0,7434844	Hydantoinase	Nucleosides and Nucleotide	-	Hydantoin i
TN	0,013712	0,7434844	Putative form	Respiration	-	Formate hy
Z	0,013759	-0,7432426	Coupling prot	Membrane Transport	Protein anc	pVir Plasm
Z	0,013759	-0,7432426	Gamma-amin	Amino Acids and Derivative	Arginine; u	Putrescine
POC	0,013791	-0,743081	Nitrogenase (Nitrogen Metabolism	-	Nitrogen fi
TotalBacte	0,013928	-0,7423872	Beta-ketoadi	Metabolism of Aromatic Co	Metabolism	Protocatecl
Chla	0,013928	-0,7423872	Electron tran	Respiration	Electron dc	Na(+)-trans

Salinity	0,014022	0,7419115	Periplasmic tl Miscellaneous	Plant-Prok: At2g23840
TN	0,014075	-0,7416448	Aldehyde de Carbohydrates	Central car Methylglyo
Salinity	0,014245	-0,7407972	Acetyl-coenz Fatty Acids, Lipids, and Isopr	Fatty acids Fatty Acid E
POC	0,014313	-0,7404573	DNA polymer DNA Metabolism	DNA repair DNA repair
POC	0,014313	-0,7404573	Glycerol-3-ph Carbohydrates	- Sugar utiliz
POC	0,014313	-0,7404573	Histidinol-phc Amino Acids and Derivatives	Histidine M Histidine Bi
POC	0,014313	-0,7404573	Predicted sial Cell Wall and Capsule	Capsular ar Sialic Acid M
Z	0,014384	-0,7401065	Orotate phos Cofactors, Vitamins, Prosthe	Folate and YgfZ
TotalProtis	0,014486	0,7396039	Ethanolamin Carbohydrates	Sugar alcoh Ethanolami
TotalProtis	0,014492	0,7395738	N-acetyl-L-L-c Amino Acids and Derivatives	Lysine, thr Lysine Bios
Z	0,014555	0,7392629	Dihydrodipic Amino Acids and Derivatives	Lysine, thr Lysine Bios
TotalProtis	0,014583	0,7391304	5-deoxy-gluc Carbohydrates	Sugar alcoh Inositol cat
TotalProtis	0,014583	0,7391304	Ribose ABC tr Motility and Chemotaxis	- Bacterial Cl
Z	0,014713	-0,738493	Lactoylglutatl Carbohydrates	Central car Methylglyo
Z	0,014713	-0,738493	tRNA (Guanin Protein Metabolism	Protein bio Ribosome k
Z	0,014713	-0,738493	tRNA-i(6)A37 Clustering-based subsystem	- tRNA-meth
TotalBacte	0,014771	0,7382101	2-Oxobutyra Amino Acids and Derivatives	Lysine, thr Methionine
TotalBacte	0,014771	0,7382101	ATP-depende Protein Metabolism	Protein deg Proteasom
TotalBacte	0,014771	0,7382101	Carbon monoclustering-based subsystem	- CBSS-3142
Si	0,014771	0,7382101	Deoxyribodip DNA Metabolism	DNA repair DNA repair
TotalBacte	0,014771	-0,7382101	Hypothetical Virulence, Disease and Defe	Resistance Cobalt-zinc
TotalBacte	0,014771	0,7382101	LL-diaminopir Amino Acids and Derivatives	Lysine, thr Lysine Bios
TotalBacte	0,014771	0,7382101	Predicted L-rh Carbohydrates	Monosaccl L-rhamnose
TotalBacte	0,014771	0,7382101	Predicted bet Carbohydrates	Di- and olig Beta-Gluc
NO2.NO3	0,014771	-0,7382101	Predicted cok Cofactors, Vitamins, Prosthe	Tetrapyrrol Coenzyme
NO2.NO3	0,014771	-0,7382101	proteasome r Protein Metabolism	Protein deg Proteasom
TotalBacte	0,014771	0,7382101	Pyruvate:ferr Carbohydrates	Central car Pyruvate:fe
Chla	0,014771	-0,7382101	STRUCTURAL Clustering-based subsystem	Biosynthes CBSS-2585
NO2.NO3	0,014771	-0,7382101	Sulfite reduct Respiration	Electron ac Anaerobic r
TN	0,014771	-0,7382101	Thermostabl Protein Metabolism	Protein deg Metallocarl
Chla	0,014771	-0,7382101	tmRNA-bindir Miscellaneous	Plant-Prok: Competenc
TotalBacte	0,014771	0,7382101	Transcription Carbohydrates	Monosaccl Fructose ut
TotalBacte	0,014771	0,7382101	transcription: Sulfur Metabolism	- Sulfur oxid
TN	0,014844	-0,7378604	Sensor histidi Regulation and Cell signaling	- The Chv reg
Z	0,014855	-0,7378049	3-oxoacyl-[ac Fatty Acids, Lipids, and Isopr	Fatty acids Fatty Acid E
Z	0,014855	-0,7378049	Acetyl-CoA ac Amino Acids and Derivatives	Lysine, thr Lysine ferm
DOC	0,014937	-0,7374118	Protein RtcB RNA Metabolism	RNA proce: RNA 3'-terr
POC	0,015028	-0,7369705	Maleylaceto Cofactors, Vitamins, Prosthe	Folate and Pterin carbi
POC	0,015323	0,7355657	Aspartyl-tRNA/ Protein Metabolism	Protein bio tRNA amin
POC	0,015323	0,7355657	Methylcroto Amino Acids and Derivatives	Branched-c Branched c
PO4	0,015921	-0,7575758	Enolase (EC 4 Carbohydrates	Central car Entner-Dou
Chla	0,015921	0,7575758	Glutamate sy Amino Acids and Derivatives	Glutamine, Glutamine,
TN	0,015921	-0,7575758	Lipopolysaccl Cell Wall and Capsule	Gram-Neg: KDO2-Lipid
DOC	0,015921	-0,7575758	Scaffold prot Miscellaneous	Plant-Prok: Iron-sulfur
DOC	0,015921	0,7575758	tungsten-con Respiration	- Formate hy
Z	0,015921	-0,7327782	Predicted red Nucleosides and Nucleotide	Pyrimidine: Pyrimidine
TotalProtis	0,016016	0,7323389	Serine-pyruv Carbohydrates	One-carboi Serine-glyo

Si	0,016177	0,7316073	Adenylylsulfa	Respiration	Electron ac Anaerobic r
Si	0,016177	0,7316073	Phosphogluc	Carbohydrates	Central car Entner-Dou
Si	0,016177	-0,7316073	photosystem	Photosynthesis	Electron tr: Photosyste
Chla	0,016177	-0,7316073	Sulfur oxidati	Sulfur Metabolism	- Sulfur oxid
Z	0,016377	-0,7306984	Acetyl-CoA C-	Metabolism of Aromatic Co	Peripheral Benzoate c
Z	0,016377	-0,7306984	D-Lactate del	Carbohydrates	Organic aci Lactate util
TotalBacte	0,016402	-0,730584	ABC-type tun	Membrane Transport	ABC transp ABC transp
Chla	0,016402	0,730584	L-seryl-tRNA(Protein Metabolism	Selenoprot Selenocyste
PO4	0,016402	0,730584	Spermidine P	Amino Acids and Derivatives	Arginine; u Polyamine
Chla	0,016409	-0,7305542	Aspartate am	Amino Acids and Derivatives	Glutamine, Glutamine,
Chla	0,016409	-0,7305542	Chaperone pr	Protein Metabolism	Protein folk Protein cha
Si	0,016409	0,7305542	Enoyl-CoA hy	Amino Acids and Derivatives	Branched-c Branched c
TotalBacte	0,016409	0,7305542	Glutamate 5-	Amino Acids and Derivatives	Proline anc Proline Syn
Chla	0,016409	-0,7305542	Glycerol-3-ph	Carbohydrates	Sugar alcof Glycerol an
Chla	0,016409	-0,7305542	Pyruvate carl	Carbohydrates	Central car Pyruvate m
DOC	0,016409	0,7305542	SOS-response	DNA Metabolism	DNA repair DNA repair,
Salinity	0,016476	0,7302507	Cobalt-preco	Cofactors, Vitamins, Prosthe	Tetrapyrrol Coenzyme
TotalProtis	0,016506	-0,7301163	Aconitate hyc	Carbohydrates	Central car Glyoxylate
TotalProtis	0,016506	0,7301163	ATP-depende	RNA Metabolism	RNA proce: ATP-depen
TotalProtis	0,016506	-0,7301163	Dihydrolipoar	Carbohydrates	Central car Dehydroge
TN	0,016506	-0,7301163	DNA mismatc	DNA Metabolism	DNA repair DNA repair,
NO2.NO3	0,016506	-0,7301163	Predicted nuc	Carbohydrates	Monosaccl Deoxyribos
DOC	0,016506	0,7301163	Succinylargini	Amino Acids and Derivatives	Arginine; u Arginine an
DOC	0,016647	-0,7294867	Aldehyde del	Carbohydrates	Central car Methylglyo
POC	0,016647	0,7294867	Aspartyl-tRN	Miscellaneous	Plant-Prok: At5g37530
DOC	0,016647	-0,7294867	Lipoprotein r	Cell Wall and Capsule	Gram-Neg: Lipopolysac
POC	0,016647	0,7294867	Thiamin bios	Cofactors, Vitamins, Prosthe	- Thiamin bic
POC	0,016647	0,7294867	Urease alpha	Amino Acids and Derivatives	Arginine; u Urea decon
POC	0,01667	-0,7293836	5-keto-2-deo	Carbohydrates	Sugar alcof Inositol cat
POC	0,01667	-0,7293836	Capsular poly	Cell Wall and Capsule	Capsular ar Capsular Pc
POC	0,01667	-0,7293836	LSU ribosom	Protein Metabolism	Protein bio Ribosome L
TotalProtis	0,017277	-0,7267081	Helicase PriA	Clustering-based subsystem -	Conserved
TotalProtis	0,017329	0,726484	Cell division p	Clustering-based subsystem -	Bacterial C
POC	0,017373	-0,7262934	MII7752 prot	Clustering-based subsystem	Probably G CBSS-1762
TotalProtis	0,017492	0,7257795	3,7-dideoxy-L	Amino Acids and Derivatives	Aromatic a Chorismate
TotalProtis	0,017492	0,7257795	DNA/RNA-bin	Miscellaneous	Plant-Prok: At1g69340
POC	0,017557	0,7254986	NG,NG-dimet	Stress Response	- Dimethylar
POC	0,017557	-0,7254986	Protein of un	Clustering-based subsystem -	Conserved
POC	0,017557	-0,7254986	Protocatechu	Metabolism of Aromatic Co	Metabolism Protocated
POC	0,017557	-0,7254986	Transcription	Carbohydrates	Monosaccl L-rhamnose
POC	0,017557	-0,7254986	Type cbb3 cy	Respiration	- Biogenesis
Chla	0,017591	-0,7253543	Cobalt-preco	Cofactors, Vitamins, Prosthe	Tetrapyrrol Cobalamin
Salinity	0,017772	-0,7245771	ATP-depende	DNA Metabolism	DNA repair DNA repair,
DOC	0,017965	0,7237561	B12 binding d	Carbohydrates	Organic aci Propionyl-C
NO2.NO3	0,017965	-0,7237561	Organic solve	Clustering-based subsystem -	EC49-61
NO2.NO3	0,017965	-0,7237561	Outer membr	Cell Wall and Capsule	Gram-Neg: Lipopolysac
NO2.NO3	0,017965	-0,7237561	Two-compon	Cell Wall and Capsule	Gram-Neg: Major Oute

Si	0,017965	0,7237561	Xanthine-gua Nucleosides and Nucleotide: Purines	Purine conv
DOC	0,018074	0,7232967	Chemotaxis p Motility and Chemotaxis	- Bacterial Cl
TotalBacte	0,018074	0,7232967	COG1272: ProCofactors, Vitamins, Prosthe	Folate and YgfZ-Iron
NO2.NO3	0,018074	-0,7232967	Proton/glutar Miscellaneous	- ZZ gjo need
DOC	0,018074	0,7232967	Resolvase/int Phages, Prophages, Transpo	Transposat Tn552
PO4	0,018074	0,7232967	Ribosomal lar Clustering-based subsystem	- EC49-61
NO2.NO3	0,018074	-0,7232967	Tetraacyldisa Cell Wall and Capsule	Gram-Neg: KDO2-Lipid
POC	0,018255	-0,722535	glutamyl-Q-tf Miscellaneous	Plant-Prok: At2g23840
Salinity	0,018317	-0,7222773	Octanoate-[a Cofactors, Vitamins, Prosthe	Lipoic acid Lipoic acid
Si	0,018414	0,7454545	Adenosylhom Amino Acids and Derivative	Lysine, thre Methionine
NO2.NO3	0,018414	-0,7454545	Aerobic cobal Cofactors, Vitamins, Prosthe	Tetrapyrrol Coenzyme
NO2.NO3	0,018414	-0,7454545	ATP-depende Clustering-based subsystem	- CBSS-1762
Chla	0,018414	0,7454545	Digeranylger: Fatty Acids, Lipids, and Isopr	Isoprenoid: Archaeal lip
Chla	0,018414	0,7454545	HNH endonuc Miscellaneous	Plant-Prok: At2g23840
NO2.NO3	0,018414	-0,7454545	NADH-ubiqui Respiration	Electron dc Respiratory
TotalProtis	0,018468	0,7216491	Heme O syntl Clustering-based subsystem	- CBSS-3160
Salinity	0,018598	0,7211103	LSU ribosoma Miscellaneous	Plant-Prok: COG0523
Salinity	0,018598	0,7211103	Muconate cy Metabolism of Aromatic Co	Metabolism Catechol br
POC	0,01886	-0,7200307	Glucose-6-ph Carbohydrates	- Sugar utiliz
POC	0,01886	0,7200307	Helicase PriA Clustering-based subsystem	- Conserved
Z	0,01886	-0,7200307	Isocitrate de Carbohydrates	Central car TCA Cycle
Z	0,018915	-0,7198086	Cob(I)alamin Cofactors, Vitamins, Prosthe	Tetrapyrrol Cobalamin
Z	0,018915	-0,7198086	Cold shock pr Stress Response	Cold shock Cold shock,
Z	0,018987	0,7195122	2-keto-3-deo: Amino Acids and Derivative	Aromatic a Chorismate
DOC	0,019088	0,7191012	Di-/tripeptide Membrane Transport	Uni- Sym- : Proton-dep
TotalBacte	0,019088	-0,7191012	Endonucleas Cell Division and Cell Cycle	- Control of c
Si	0,019088	0,7191012	Stage 0 sporu Cell Division and Cell Cycle	- Bacterial Cy
TotalProtis	0,019146	-0,7188673	Aspartate 1-d Cofactors, Vitamins, Prosthe	Coenzyme Coenzyme
TotalProtis	0,019146	-0,7188673	Magnesium a Clustering-based subsystem	- CBSS-5678
POC	0,019322	-0,7181542	Cyclohexadie Amino Acids and Derivative	Aromatic a Phenylalani
Z	0,019322	-0,7181542	Xylulose kina Carbohydrates	- Sugar utiliz
Chla	0,019399	0,7178454	DNA mismatc DNA Metabolism	DNA repair DNA repair
DOC	0,019399	-0,7178454	ubiquinol cyt Respiration	Electron ac Ubiquinone
PO4	0,019454	-0,7176241	Carbonic anhy Miscellaneous	Plant-Prok: At5g04520
PO4	0,019454	-0,7176241	Cobalt-preco Cofactors, Vitamins, Prosthe	Tetrapyrrol Coenzyme
TotalBacte	0,019454	0,7176241	Peptidyl-prol Protein Metabolism	Protein fol Peptidyl-pr
Chla	0,019454	-0,7176241	Phosphoribo Amino Acids and Derivative	Histidine M Histidine Bi
TN	0,019454	0,7176241	RNA polymer Clustering-based subsystem	- CBSS-2115
NO2.NO3	0,019454	0,7176241	RNA polymer Clustering-based subsystem	- CBSS-2115
POC	0,019528	0,7173285	Argininosucci Amino Acids and Derivative	Arginine; u Arginine Bi
POC	0,019528	0,7173285	NAD-depend Carbohydrates	Central car Pyruvate m
TN	0,019528	-0,7173285	NADH-ubiqui Respiration	Electron dc Respiratory
NO2.NO3	0,019528	-0,7173285	Succinyl-CoA Carbohydrates	Central car TCA Cycle
Si	0,019528	0,7173285	UDP-N-acetyl Cell Wall and Capsule	- Peptidoglyc
TN	0,019629	0,7169282	Arsenate red Respiration	Electron ac Anaerobic r
Si	0,019629	-0,7169282	Hydroxymeth Amino Acids and Derivative	Branched-c Ketoisovale
Si	0,019629	0,7169282	Phosphatidyl Fatty Acids, Lipids, and Isopr	Phospholip Glycerolipic

Si	0,019629	-0,7169282	Phosphoserin Amino Acids and Derivatives	Alanine, se Glycine and
Salinity	0,019733	-0,7165144	3-hydroxyiso Amino Acids and Derivatives	Branched-c Branched c
Salinity	0,019733	0,7165144	YciO family	Miscellaneous Plant-Prok: YrdC-YciO-5
POC	0,019942	-0,7156863	Enoyl-[acyl-c	Fatty Acids, Lipids, and Isop Fatty acids Polyunsatu
POC	0,019942	-0,7156863	L-asparaginas Amino Acids and Derivatives	Glutamine, Glutamine,
Salinity	0,019959	0,7156201	Monofunctio	Cell Wall and Capsule - Peptidoglyc
TotalProtis	0,020036	0,7153188	Phenylacetat	Metabolism of Aromatic Coi - Phenylacet
Salinity	0,020277	0,7143757	Probable acyl Amino Acids and Derivatives	Branched-c Isoleucine c
Salinity	0,020392	0,7139306	LSU ribosom	Protein Metabolism Protein bio Ribosome L
TotalProtis	0,020405	-0,7138766	Ribosome rec	Clustering-based subsystem - CBSS-1762
Z	0,020525	-0,7134146	Translation el	Protein Metabolism Protein bio Translation
POC	0,020548	-0,7133239	Arginine/orni Amino Acids and Derivatives	Arginine; u Arginine an
Z	0,020548	-0,7133239	Biosynthetic / Amino Acids and Derivatives	Aromatic a Phenylalani
POC	0,020548	-0,7133239	DNA-directed RNA Metabolism	Transcripti RNA polym
POC	0,020548	-0,7133239	NAD synthet	Cofactors, Vitamins, Prosthe NAD and N NAD and N.
POC	0,020548	-0,7133239	PF00070 fam	Miscellaneous Plant-Prok: COG0398
POC	0,020548	-0,7133239	Pseudouridin Nucleosides and Nucleotide	- Pseudourid
DOC	0,020672	-0,7128482	DNA replicati	DNA Metabolism DNA replic: DNA replic:
TotalProtis	0,020905	0,7119551	Rhodanese d	Miscellaneous Plant-Prok: Single-Rhoc
POC	0,020924	-0,7118821	Carboxyl-tern	Clustering-based subsystem - CBSS-2249
POC	0,020924	-0,7118821	Iron-sulfur cl	Miscellaneous Plant-Prok: Scaffold pr
POC	0,021091	0,7112495	Adenylosuccin	Clustering-based subsystem Clustering- CBSS-2627
Si	0,021091	-0,7112495	GMP synthas	Nucleosides and Nucleotide: Purines Purine conv
Si	0,021091	-0,7112495	Lipid A export	Miscellaneous - ZZ gjo need
NO2.NO3	0,021166	-0,7333333	Glycyl-tRNA s	Protein Metabolism Protein bio tRNA amin
TN	0,021166	-0,7333333	Isocitrate de	Carbohydrates Central car TCA Cycle
TN	0,021166	-0,7333333	Omega-amin	Carbohydrates Central car Pyruvate Al
TN	0,021166	-0,7333333	Sulfate adeny	Amino Acids and Derivatives: Lysine, thr Cysteine Bi
DOC	0,021166	-0,7333333	V-type ATP sy	Respiration ATP synth V-Type ATP
DOC	0,021396	0,7101003	Alcohol dehy	Carbohydrates - Sugar utiliz:
DOC	0,021396	0,7101003	Aldehyde de	Clustering-based subsystem Methylami CBSS-2650
DOC	0,021396	0,7101003	Allantoicase (Nitrogen Metabolism - Allantoin U
DOC	0,021396	0,7101003	Anaerobic de	Respiration Electron ac Anaerobic r
TotalBacte	0,021396	0,7101003	Dna binding r	Regulation and Cell signaling - Global Two
DOC	0,021396	0,7101003	Glucose-6-ph	Carbohydrates Central car Glycolysis a
DOC	0,021396	0,7101003	ISPsy4, trans	Phages, Prophages, Transpo Transposat CBSS-2031
NO2.NO3	0,021396	-0,7101003	Membrane-b	Cell Wall and Capsule - Murein Hyc
Chla	0,021396	-0,7101003	Membrane-b	Cell Wall and Capsule - Murein Hyc
DOC	0,021396	0,7101003	Respiratory n	Nitrogen Metabolism - Nitrate and
DOC	0,021396	0,7101003	S-adenosyl-L-	Clustering-based subsystem - CBSS-2913
DOC	0,021396	0,7101003	Transcription	Regulation and Cell signaling - Orphan reg
NO2.NO3	0,021396	-0,7101003	tRNA-specific	RNA Metabolism RNA proce: tRNA modii
TotalProtis	0,02161	0,7092994	Endonucleas	Clustering-based subsystem - EC699-706
TotalProtis	0,02161	0,7092994	Phosphate:ac	Clustering-based subsystem Fatty acid r COG1399
TotalProtis	0,021693	0,7089886	DNA-directed RNA Metabolism	Transcripti RNA polym
Salinity	0,022021	0,7077761	SSU ribosom	Protein Metabolism Protein bio Ribosome 5
Z	0,022036	-0,7077225	Ferredoxin--s	Sulfur Metabolism Inorganic s Inorganic S

Z	0,022146	-0,7073171 Homoserine (Amino Acids and Derivatives: Lysine, thr	Methionine
Z	0,022277	-0,7068391 Galactonate (Carbohydrates	Monosacch D-galacton
Z	0,022277	-0,7068391 Methylated-E Clustering-based subsystem -	CBSS-3931
Z	0,022277	-0,7068391 Nitrate ABC tr Nitrogen Metabolism	- Nitrate and
Z	0,022277	-0,7068391 RND efflux sy Virulence, Disease and Defe	Resistance Multidrug e
TN	0,022344	-0,7065951 Adenylate kin Nucleosides and Nucleotide: Purines	Purine con
PO4	0,022344	-0,7065951 DNA replicati DNA Metabolism	DNA replic: DNA replica
TotalBacte	0,022344	-0,7065951 GDP-L-fucose Cell Wall and Capsule	Capsular ar Capsular he
Si	0,022344	-0,7065951 N-acetyl-gam Amino Acids and Derivatives: Lysine, thr	Lysine bios
POC	0,022616	-0,70561 L-fuconate de Carbohydrates	Monosacch L-fucose ut
TN	0,022626	0,7055746 Guanine dear Nucleosides and Nucleotide: Purines	Purine con
NO2.NO3	0,022626	0,7055746 NAD(FAD)-uti Miscellaneous	Plant-Prok: COG2509
DOC	0,022626	-0,7055746 Phosphogluc Clustering-based subsystem Chromosor	SeqA and C
Chla	0,022626	-0,7055746 Succinylargini Amino Acids and Derivatives: Arginine; u	Arginine an
Chla	0,022626	0,7055746 V-type ATP sy Respiration	ATP syntha V-Type ATP
Z	0,02267	-0,7054133 archaeosine t RNA Metabolism	RNA proce: tRNA modifi
POC	0,022738	0,7051704 Acetyl-coenz Amino Acids and Derivatives: Branched-c	Ketoisovale
TN	0,022738	0,7051704 Betaine alde Miscellaneous	Plant-Prok: Niacin-Chol
Chla	0,022738	-0,7051704 Branched-ch Amino Acids and Derivatives: Branched-c	Branched c
PO4	0,022738	0,7051704 Serine--pyruv Carbohydrates	One-carboi Serine-glyo
POC	0,022738	0,7051704 TRAP-type C4 Clustering-based subsystem Tricarboxyl	CBSS-4933
Si	0,02287	0,7046939 Galactonate (Carbohydrates	Monosacch D-galacton
NO2.NO3	0,02287	-0,7046939 Glucose-met Respiration	Electron dc Respiratory
TotalBacte	0,02287	-0,7046939 Putative stor Clustering-based subsystem Probably Yl	CBSS-3160
Si	0,02287	0,7046939 S-formylgluta Cofactors, Vitamins, Prosthe	Folate and YgfZ
NO2.NO3	0,02287	-0,7046939 Shwachman-I Clustering-based subsystem Proteasom	Proteasom
Si	0,02287	-0,7046939 Tol biopolym Membrane Transport	- Ton and To
Salinity	0,02305	0,7040533 HflK protein Miscellaneous	Plant-Prok: Scaffold pro
Salinity	0,023133	-0,7037573 tRNA (5-met Miscellaneous	Plant-Prok: At5g37530
DOC	0,02327	0,7032724 2-C-methyl-D Clustering-based subsystem -	CBSS-2115
PO4	0,02327	-0,7032724 Aspartate 1-d Cofactors, Vitamins, Prosthe	Coenzyme Coenzyme
DOC	0,02327	0,7032724 Cobalamin sy Cofactors, Vitamins, Prosthe	Tetrapyrrol Cobalamin
DOC	0,02327	-0,7032724 L-seryl-tRNA(Protein Metabolism	Selenoprot Selenocyste
PO4	0,02327	-0,7032724 Magnesium a Clustering-based subsystem -	CBSS-5678
NO2.NO3	0,02327	0,7032724 Phosphate tr Phosphorus Metabolism	- High affinity
DOC	0,02327	0,7032724 Putative glut Sulfur Metabolism	Organic sul Utilization (
TN	0,02327	0,7032724 Queuosine Bi Miscellaneous	Plant-Prok: Experiment
NO2.NO3	0,02327	-0,7032724 Succinate de Respiration	Electron dc Succinate d
POC	0,023408	-0,7027819 2-dehydro-3- Carbohydrates	Monosacch D-galactara
POC	0,023408	0,7027819 acyl-acyl carri Virulence, Disease and Defe	- C jejuni coli
POC	0,023408	0,7027819 ATP synthase Respiration	ATP syntha FOF1-type /
POC	0,023408	-0,7027819 ATP-depende RNA Metabolism	RNA proce: ATP-depend
POC	0,023408	-0,7027819 Benzoate trar Metabolism of Aromatic Coi-	Benzoate tr
POC	0,023408	-0,7027819 carbon mono Clustering-based subsystem -	CBSS-3142
POC	0,023408	-0,7027819 Cytochrome (Protein Metabolism	Protein fol Periplasmic
POC	0,023408	-0,7027819 Homolog of f Carbohydrates	Monosacch Hexose Phc
POC	0,023408	-0,7027819 Intramembra Clustering-based subsystem Isoprenoid, CBSS-8333:	

POC	0,023408	-0,7027819 isobutyryl-Co	Carbohydrates	One-carbon	Serine-glyc
POC	0,023408	0,7027819 Phenylacetat	Metabolism of Aromatic Co	-	Phenylacet
POC	0,023408	-0,7027819 PTS system, f	Carbohydrates	-	Sugar utiliz
POC	0,023408	-0,7027819 Thiol peroxid	Clustering-based subsystem	-	CBSS-2573:
POC	0,023408	-0,7027819 TldD family p	Protein Metabolism	Protein deg	Putative Tlc
POC	0,023408	-0,7027819 UDP-glucose: Cell Wall and Capsule		Gram-Neg	LOS core ol
POC	0,023408	-0,7027819 Uracil perme	Nucleosides and Nucleotide	Pyrimidine: De Novo Py	
POC	0,023408	-0,7027819 Valine--pyruv	Amino Acids and Derivatives	Alanine, se	Alanine bio
Salinity	0,023491	0,7024894 Carnitine rac	Fatty Acids, Lipids, and Isop	Fatty acids	Carnitine M
Salinity	0,023491	0,7024894 Carnitiny-Co	Fatty Acids, Lipids, and Isop	Fatty acids	Carnitine M
Z	0,023496	-0,702474 Alpha-1,2-ma	Carbohydrates	Monosacch	Mannose M
POC	0,023496	-0,702474 Aspartyl-tRN	Miscellaneous	Plant-Prok	At3g21300
POC	0,023496	-0,702474 Glutamyl-tRN	Miscellaneous	Plant-Prok	At3g21300
TotalProtis	0,023622	0,7020318 acyl-CoA synt	Cell Wall and Capsule	Cell wall of mycolic aci	
TotalProtis	0,023622	0,7020318 Biosynthetic	Amino Acids and Derivatives	Aromatic a	Phenylalani
TotalProtis	0,023622	0,7020318 Coenzyme F	Respiration	Electron dc	Coenzyme I
TotalProtis	0,023622	0,7020318 Cyclomaltode	Carbohydrates	Polysaccha	Alpha-Amyl
TotalProtis	0,023622	0,7020318 SSU ribosom	Protein Metabolism	Protein bio	Ribosome S
TotalProtis	0,02367	0,7018634 Epi-inositol h	Carbohydrates	Sugar alcoh	Inositol cat
TotalProtis	0,02367	0,7018634 Naphthoate s	Cofactors, Vitamins, Prosthe	Quinone cc	Menaquinoc
Salinity	0,023739	0,7016215 2-methylcitra	Carbohydrates	Organic aci	Methylcitra
Z	0,023754	-0,7015684 3-polyprenyl-	Cofactors, Vitamins, Prosthe	Quinone cc	Menaquinoc
TotalProtis	0,023754	-0,7015684 ATP-depende	Protein Metabolism	Protein deg	Proteasom
POC	0,023854	-0,7012195 Septum site-c	Cell Division and Cell Cycle	-	Bacterial Cy
Salinity	0,024012	0,7006707 Phosphoribo	Nucleosides and Nucleotide	Purines	De Novo Pu
Chla	0,024019	0,700649 2-keto-3-deo	Amino Acids and Derivatives	Aromatic a	Chorismate
NO2.NO3	0,024019	0,700649 ABC transpor	Amino Acids and Derivatives	Arginine; u	Polyamine
TotalBacte	0,024019	-0,700649 ABC-type tun	Membrane Transport	ABC transp	ABC transp
TotalBacte	0,024019	-0,700649 Alkylated DN	DNA Metabolism	DNA repair	DNA repair
TotalBacte	0,024019	-0,700649 Allophanate	Amino Acids and Derivatives	Arginine; u	Urea carbo
TotalBacte	0,024019	-0,700649 BarA sensory	Membrane Transport	Protein sec	Type III sec
TotalBacte	0,024019	-0,700649 BatE	Clustering-based subsystem	-	Aerotolera
TotalBacte	0,024019	-0,700649 Benzoate trar	Metabolism of Aromatic Co	Peripheral	Benzoate d
DOC	0,024019	0,700649 Capsular poly	Cell Wall and Capsule	Capsular ar	Capsular Pc
TotalBacte	0,024019	-0,700649 Capsular poly	Cell Wall and Capsule	Capsular ar	Exopolysac
DOC	0,024019	-0,700649 Cell division p	Cell Division and Cell Cycle	-	Bacterial Cy
NO2.NO3	0,024019	-0,700649 Cell division p	Cell Division and Cell Cycle	-	Bacterial Cy
DOC	0,024019	0,700649 conserved pr	Miscellaneous	Plant-Prok	DOE COG2
TotalBacte	0,024019	-0,700649 DamX, an inn	Clustering-based subsystem	-	Shikimate k
Chla	0,024019	0,700649 D-galactonat	Carbohydrates	Monosacch	D-galacton
TotalBacte	0,024019	-0,700649 diguanylate c	Stress Response	-	Bacterial he
PO4	0,024019	0,700649 Dihydroneop	Clustering-based subsystem	-	CBSS-235.1
Si	0,024019	0,700649 Dihydroneop	Clustering-based subsystem	-	CBSS-235.1
DOC	0,024019	0,700649 DNA helicase	Phages, Prophages, Transpo	Phages, Prc	Phage repli
PO4	0,024019	0,700649 DNA recombi	Clustering-based subsystem	-	DNA replica
Si	0,024019	0,700649 DNA recombi	Clustering-based subsystem	-	DNA replica
Chla	0,024019	0,700649 DNA topoisor	Phages, Prophages, Transpo	Phages, Prc	Phage repli

PO4	0,024019	-0,700649	DnaJ-class mc Protein Metabolism	Protein folk Protein cha
TotalBacte	0,024019	0,700649	Endonuclease Clustering-based subsystem -	EC699-706
DOC	0,024019	0,700649	Error-prone r DNA Metabolism	DNA repair DNA repair,
DOC	0,024019	0,700649	Erythritol phc Carbohydrates	Sugar alcof Erythritol u
DOC	0,024019	0,700649	FIG001590: P Clustering-based subsystem -	CBSS-8762f
Chla	0,024019	0,700649	FIG022199: F. Fatty Acids, Lipids, and Isopr	Fatty acids Phospholip
DOC	0,024019	0,700649	FKBP-type pe Potassium metabolism	- Potassium l
TotalBacte	0,024019	-0,700649	Flagellar moti Motility and Chemotaxis	Flagellar m Flagellar m
DOC	0,024019	0,700649	Flagellar moti Motility and Chemotaxis	- Bacterial Cl
DOC	0,024019	0,700649	High-affinity l Membrane Transport	ABC transp ABC transp
Chla	0,024019	0,700649	Hydrogenase Respiration	- Formate hy
Chla	0,024019	0,700649	Lipid A biosyr Cell Wall and Capsule	Gram-Negz KDO2-Lipid
Chla	0,024019	0,700649	LSU ribosoma Protein Metabolism	Protein bio Ribosome l
DOC	0,024019	0,700649	Membrane pi Clustering-based subsystem -	CBSS-5678f
DOC	0,024019	0,700649	Methyl-direct Clustering-based subsystem -	Shikimate k
DOC	0,024019	0,700649	Negative tran Regulation and Cell signaling	Regulation Streptococi
DOC	0,024019	0,700649	N-methylhyd; Amino Acids and Derivatives -	Creatine an
Chla	0,024019	0,700649	Phenazine bic Secondary Metabolism	Bacterial cy Phenazine l
DOC	0,024019	0,700649	Phenylacetal; Metabolism of Aromatic Coi-	Aromatic A
TotalBacte	0,024019	-0,700649	Phosphatase, Phosphorus Metabolism	- Phosphate
TotalBacte	0,024019	0,700649	Phosphate:ac Clustering-based subsystem	Fatty acid r COG1399
DOC	0,024019	0,700649	Phytoene/sqi Miscellaneous	Plant-Prokz At2g23840
DOC	0,024019	0,700649	Probable VAN Metabolism of Aromatic Coi	Peripheral Phenylprop
TotalBacte	0,024019	-0,700649	Protein of avi Clustering-based subsystem -	USS-DB-7
DOC	0,024019	0,700649	Putative glutz Sulfur Metabolism	Organic sul Utilization r
DOC	0,024019	0,700649	Putative NAD Respiration	- Quinone ox
DOC	0,024019	0,700649	Putative oxid; Amino Acids and Derivatives	Arginine; u Putrescine
DOC	0,024019	0,700649	Putative phos DNA Metabolism	DNA repair 2-phosphog
DOC	0,024019	0,700649	Putative sodi; Miscellaneous	Plant-Prokz At5g38900
PO4	0,024019	0,700649	RecD-like DN; DNA Metabolism	DNA repair DNA repair,
Si	0,024019	0,700649	RecD-like DN; DNA Metabolism	DNA repair DNA repair,
DOC	0,024019	0,700649	Ribulokinase Carbohydrates	Monosaccl L-Arabinose
DOC	0,024019	0,700649	RNA polymer Clustering-based subsystem	Putative as CBSS-3160f
PO4	0,024019	-0,700649	Sarcosine oxir Clustering-based subsystem	Methylami Glutamate-
DOC	0,024019	0,700649	Similar to rib; Protein Metabolism	Protein bio Ribosome l
TotalBacte	0,024019	-0,700649	Structure-spe Protein Metabolism	Protein bio tRNA aminc
TotalBacte	0,024019	-0,700649	Structure-spe Protein Metabolism	Protein bio tRNA aminc
DOC	0,024019	0,700649	TonB-depend Iron acquisition and metabo-	Iron acquisi
Chla	0,024019	0,700649	TPR repeat cc Membrane Transport	- Ton and To
Chla	0,024019	0,700649	Transport ATI Respiration	Electron ac Terminal cy
TotalBacte	0,024019	-0,700649	Uncharacteri; Cell Wall and Capsule	Gram-Negz Lipopolysac
Chla	0,024019	0,700649	Uronate isom Carbohydrates	Monosaccl D-Galacturc
DOC	0,024019	0,700649	Xanthosine/ir Stress Response	Heat shock Heat shock
POC	0,024104	-0,7003543	Glutathione-r Potassium metabolism	- Glutathione
POC	0,024104	-0,7003543	Phenylacetic Metabolism of Aromatic Coi-	Phenylacet
POC	0,024104	-0,7003543	RNA polymer Cell Wall and Capsule	Capsular ar Alginate m
DOC	0,024107	0,700342	Cell division p Cell Division and Cell Cycle	- Bacterial Cy

DOC	0,024107	-0,700342	Pseudaminic	Cell Wall and Capsule	Capsular ar	Pseudamin
NO2.NO3	0,024195	-0,721212	Adenine dea	Nucleosides and Nucleotide	Purines	Purine con
TN	0,024195	-0,721212	Cysteine synt	Amino Acids and Derivatives	Lysine, thr	Cysteine Bi
Chla	0,024195	0,721212	Excinnuclease	DNA Metabolism	DNA repair	DNA repair
DOC	0,024195	-0,721212	NADH-ubiqui	Respiration	Electron dc	Respiratory
Si	0,024195	-0,721212	Pyruvate deh	Carbohydrates	Central car	Dehydroge
Chla	0,024195	0,721212	Ubiquinol--cy	Respiration	Electron ac	Ubiquinone
POC	0,024471	0,6990914	2-oxoglutarat	Carbohydrates	Central car	Dehydroge
Chla	0,024471	-0,6990914	3'-to-5' exoril	RNA Metabolism	RNA proces	RNA proces
NO2.NO3	0,024471	-0,6990914	Alkyl hydrope	Stress Response	Oxidative s	Oxidative s
NO2.NO3	0,024471	0,6990914	Glucosamine-	Cell Wall and Capsule	-	UDP-N-acei
Z	0,024625	-0,6985646	Predicted tra	Amino Acids and Derivatives	Branched-c	Branched c
Salinity	0,024844	-0,6978227	Beta-galactos	Carbohydrates	-	Sugar utiliz
Salinity	0,024844	0,6978227	Trk system pc	Clustering-based subsystem	-	Bacterial RI
Chla	0,025253	-0,6964445	Cell division p	Cell Division and Cell Cycle	-	Bacterial Cy
TotalBacte	0,025253	0,6964445	Iron-sulfur cl	Amino Acids and Derivatives	Alanine, se	Alanine bio
PO4	0,025253	0,6964445	NusA protein	RNA Metabolism	Transcripti	Transcripti
Si	0,025253	0,6964445	Spermidine P	Amino Acids and Derivatives	Arginine; u	Polyamine
Si	0,025253	0,6964445	Transcription	Clustering-based subsystem	Methylami	CBSS-2650
TotalProtis	0,025288	0,6963281	Photosystem	Photosynthesis	Electron tr	Photosyste
POC	0,025512	-0,6955811	LSU ribosom	Protein Metabolism	Protein bio	Ribosome L
POC	0,025512	-0,6955811	Menaquinon	Cofactors, Vitamins, Prosthe	Quinone cc	Menaquinc
POC	0,025512	-0,6955811	Pantoate kin	Cofactors, Vitamins, Prosthe	Coenzyme	Coenzyme
POC	0,025512	-0,6955811	Phage prohe	Phages, Prophages, Transpo	Phages, Pr	Phage caps
Z	0,025512	-0,6955811	Queuosine Bi	Cofactors, Vitamins, Prosthe	Folate and	YgfZ
Z	0,025562	-0,6954142	DNA polymer	DNA Metabolism	DNA replic	DNA-replic
Z	0,025562	0,6954142	Fumarylacetc	Cofactors, Vitamins, Prosthe	Folate and	Pterin carbi
Z	0,025562	0,6954142	Segregation a	Cell Division and Cell Cycle	-	Two cell div
POC	0,025562	-0,6954142	Sulfite reduct	Sulfur Metabolism	-	Sulfate redi
Salinity	0,025589	-0,6953257	Penicillin-bin	Cell Wall and Capsule	-	Peptidoglyc
Z	0,02565	-0,695122	Glutamine sy	Amino Acids and Derivatives	Glutamine, Glutamine	
Z	0,02565	-0,695122	Isoleucyl-tRN	Clustering-based subsystem	Cell Divisio	Cell Divisio
NO2.NO3	0,025964	-0,694089	Alpha-galactc	Carbohydrates	-	Sugar utiliz
Chla	0,025964	-0,694089	Dihydroorota	Clustering-based subsystem	Hypothetic	Hypothetic
Salinity	0,026008	-0,6939443	lojap protein	Clustering-based subsystem	-	CBSS-3162
Salinity	0,026008	-0,6939443	Protein gp47,	Phages, Prophages, Transpo	Phages, Pr	Listeria phi
Salinity	0,026008	-0,6939443	Type III restri	DNA Metabolism	-	Restriction-
POC	0,026031	-0,6938696	6-phosphoglu	Carbohydrates	-	Sugar utiliz
POC	0,026031	-0,6938696	carbon mono	Clustering-based subsystem	-	CBSS-3142
Z	0,026031	-0,6938696	Chromate tra	Virulence, Disease and Defe	Resistance	Resistance
POC	0,026031	0,6938696	Inner membr	Cell Wall and Capsule	Gram-Neg	Lipopolysac
Z	0,026031	-0,6938696	V-type ATP sy	Respiration	ATP syntha	V-Type ATP
POC	0,026031	-0,6938696	Xanthine deh	Clustering-based subsystem	Clustering-	Putative di
PO4	0,026153	-0,6934701	Alanine racen	Amino Acids and Derivatives	Alanine, se	Alanine bio
DOC	0,026153	0,6934701	Capsular poly	Cell Wall and Capsule	Capsular ar	Exopolysac
NO2.NO3	0,026153	-0,6934701	COG2106 Me	RNA Metabolism	RNA proces	rRNA modifi
NO2.NO3	0,026153	-0,6934701	Exodeoxyribo	DNA Metabolism	DNA repair	DNA repair

PO4	0,026153	0,6934701	Ferritin-like p Miscellaneous	Plant-Prok: Iron-sulfur
DOC	0,026153	0,6934701	Formaldehyd Cofactors, Vitamins, Prosthe	Folate and YgfZ
DOC	0,026153	0,6934701	Formate hydr Respiration	- Formate hy
DOC	0,026153	0,6934701	Fructose ABC Carbohydrates	Monosaccl Fructose ut
Chla	0,026153	-0,6934701	Glutaredoxin- Stress Response	Oxidative s Glutaredox
TotalBacte	0,026153	0,6934701	Hexuronate t Carbohydrates	Monosaccl D-Galactur
Chla	0,026153	-0,6934701	IncF plasmid t Clustering-based subsystem -	Conjugative
NO2.NO3	0,026153	0,6934701	L-2-keto-3-de Carbohydrates	Monosaccl L-Arabinose
Chla	0,026153	-0,6934701	Lipid carrier : Clustering-based subsystem -	CBSS-2965
Si	0,026153	0,6934701	LSU ribosom: Protein Metabolism	Protein bio Ribosome l
Chla	0,026153	-0,6934701	Membrane-b Cell Wall and Capsule	- Murein Hyc
DOC	0,026153	0,6934701	Methionine A Amino Acids and Derivatives	Lysine, thr: Methionine
TN	0,026153	0,6934701	Periplasmic a Cofactors, Vitamins, Prosthe	- Molybdopt
DOC	0,026153	0,6934701	Phosphoribo: Cofactors, Vitamins, Prosthe	Folate and 5-FCL-like p
Chla	0,026153	0,6934701	Predicted col Cofactors, Vitamins, Prosthe	Tetrapyrrol Coenzyme
DOC	0,026153	0,6934701	Predicted ma Carbohydrates	Monosaccl Mannose M
Chla	0,026153	0,6934701	proteasome r Protein Metabolism	Protein deg Proteasom
Chla	0,026153	-0,6934701	Protein ImpG Clustering-based subsystem -	USS-DB-7
DOC	0,026153	0,6934701	Protein YidD Clustering-based subsystem -	RNA modifi
TotalBacte	0,026153	-0,6934701	Pyrimidine-n: Carbohydrates	Monosaccl Deoxyribos
PO4	0,026153	-0,6934701	Ribonucleotic Nucleosides and Nucleotide-	- Ribonucleo
Chla	0,026153	0,6934701	Sulfite reduct Respiration	Electron ac Anaerobic r
DOC	0,026153	0,6934701	Sulfur oxidati Sulfur Metabolism	- Sulfur oxid:
Si	0,026203	-0,6933037	AmpG perme Cell Wall and Capsule	- Recycling o
Chla	0,026203	-0,6933037	Crotonyl-CoA Carbohydrates	Central car Ethylmalon
TN	0,026203	-0,6933037	Cysteine des: Amino Acids and Derivatives	: Alanine, se Alanine bio
NO2.NO3	0,026203	-0,6933037	Cysteine des: Amino Acids and Derivatives	: Alanine, se Alanine bio
TotalProtis	0,026203	-0,6933037	Cytochrome c Respiration	Electron ac Terminal cy
Si	0,026203	0,6933037	Electron tran: Respiration	Electron dc Na(+)-trans
NO2.NO3	0,026203	0,6933037	Tryptophan s: Amino Acids and Derivatives	: Aromatic a Chorismate
POC	0,026276	-0,6930659	4-hydroxythr: Clustering-based subsystem -	EC49-61
POC	0,026276	-0,6930659	Succinate del Respiration	Electron dc Succinate d
POC	0,026293	0,6930123	Excinuclease : DNA Metabolism	DNA repair DNA repair
NO2.NO3	0,026293	-0,6930123	Imidazole gly: Amino Acids and Derivatives	: Histidine M Histidine Bi
Z	0,026293	0,6930123	Peptide chain Clustering-based subsystem -	LMPTP Ywl
PO4	0,026293	-0,6930123	Succinyl-CoA Carbohydrates	Central car TCA Cycle
TotalProtis	0,026671	0,6917858	ABC transpor Virulence, Disease and Defe	Bacteriocin Bacitracin S
TotalProtis	0,026671	0,6917858	Gluconate pe Carbohydrates	Monosaccl D-gluconat
TotalProtis	0,026671	0,6917858	Glutathione S Stress Response	Oxidative s Glutathione
TotalProtis	0,026671	0,6917858	Inositol oxyge Carbohydrates	Sugar alcof Inositol cat
TotalProtis	0,026671	0,6917858	Maltose O-ac Carbohydrates	Di- and olig Maltose an
TotalProtis	0,026671	0,6917858	Outer memb: Membrane Transport	- Ton and To
TotalProtis	0,026671	0,6917858	Probable poly Cell Wall and Capsule	Capsular ar Alginate m
TotalProtis	0,026671	0,6917858	Protein Yail Clustering-based subsystem -	CBSS-562.2
TotalProtis	0,026671	0,6917858	Similar to cop Clustering-based subsystem -	CBSS-630.2
TotalProtis	0,026671	0,6917858	Soluble lytic r Miscellaneous	Plant-Prok: COG0451
TotalProtis	0,026671	0,6917858	SSU ribosom: Protein Metabolism	Protein bio Ribosome S

NO2.NO3	0,026678	-0,6917638	Aminotransferase Sulfur Metabolism	Organic sulfur DMSP breakdown
TN	0,026678	-0,6917638	Benzoate 1,2-Metabolism of Aromatic Compounds	Peripheral Benzoate degradation
TN	0,026678	0,6917638	Crossover junction DNA Metabolism	DNA recombination RuvABC plus
PO4	0,026678	0,6917638	Crossover junction DNA Metabolism	DNA recombination RuvABC plus
DOC	0,026678	0,6917638	DNA primase DNA Metabolism	DNA replication DNA replication
Si	0,026678	0,6917638	DNA-directed RNA Metabolism	Transcription RNA polymerase
TotalBacteria	0,026678	-0,6917638	Glucose ABC Transporter Carbohydrates	Central carbon Peripheral carbon
Chla	0,026678	0,6917638	Glucose-methyl Respiration	Electron donor Respiratory
PO4	0,026678	-0,6917638	Putrescine transporter Amino Acids and Derivatives	Arginine; urea Polyamine
POC	0,026693	-0,6917159	Malonate transporter Carbohydrates	Organic acids Malonate degradation
TotalProteins	0,02723	-0,6899978	tRNA (guanine) Miscellaneous	Plant-Protists YggW
Chla	0,02735	-0,6896166	Acetoacetyl-CoA Carbohydrates	Fermentation Acetyl-CoA
NO2.NO3	0,02735	-0,6896166	Acetoin dehydrogenase Carbohydrates	Central carbon Dehydrogenase
TN	0,02735	-0,6896166	Cobalt-precipitation Cofactors, Vitamins, Prosthetic	Tetrapyrrole Cobalamin
TN	0,02735	0,6896166	Glutamate N- Amino Acids and Derivatives	Arginine; urea Arginine biosynthesis
NO2.NO3	0,02735	-0,6896166	Protein RtcB RNA Metabolism	RNA processing RNA 3'-terminal
NO2.NO3	0,02735	0,6896166	Response regulator Virulence, Disease and Defense	Resistance Zinc resistance
DOC	0,02735	0,6896166	Spermidine P Amino Acids and Derivatives	Arginine; urea Polyamine
PO4	0,02735	0,6896166	Two-component Regulation and Cell signaling	Orphan regulator
TN	0,02735	-0,6896166	Vanillate O-decarboxylation Metabolism of Aromatic Compounds	Peripheral Phenylpropanoid
TotalProteins	0,027405	0,689441	Inositol transporter Carbohydrates	Sugar alcohol Inositol catabolism
Salinity	0,027431	0,6893588	Replication factor DNA Metabolism	DNA replication DNA replication
Salinity	0,027446	0,6893123	Homogentisate Cofactors, Vitamins, Prosthetic	Folate and Pterin catabolism
Salinity	0,027446	-0,6893123	Pyruvate dehydrogenase Carbohydrates	Central carbon Dehydrogenase
Salinity	0,027446	0,6893123	SSU ribosomal Protein Metabolism	Protein biosynthesis Ribosome
POC	0,027463	-0,6892601	Glycerol-3-phosphate Carbohydrates	- Sugar utilization
Z	0,027463	-0,6892601	Guanosine-3' Clustering-based subsystem	Probably G CBSS-1762
DOC	0,027514	-0,7090909	Acetate permease Carbohydrates	Central carbon Pyruvate metabolism
Chla	0,027514	0,7090909	ATP-dependent Protein Metabolism	Protein degradation Proteolysis
DOC	0,027514	-0,7090909	Glycine dehydrogenase Amino Acids and Derivatives	Alanine, serine Glycine and
Chla	0,027514	0,7090909	LSU ribosomal Clustering-based subsystem	- LSU ribosome
Si	0,027514	-0,7090909	MoxR-like ATP Clustering-based subsystem	- Aerotolerance
Si	0,027514	-0,7090909	Transketolase Carbohydrates	- Sugar utilization
NO2.NO3	0,027514	-0,7090909	Xylonate dehydrogenase Carbohydrates	Monosaccharide Xylose utilization
Salinity	0,02752	-0,6890776	DNA-directed RNA Metabolism	Transcription RNA polymerase
Z	0,027537	-0,6890244	GTP-binding protein Protein Metabolism	Protein biosynthesis Universal G
Salinity	0,027553	-0,6889757	Xaa-Pro amine Clustering-based subsystem	- CBSS-8762
TotalBacteria	0,027916	-0,6878359	GMP reductase Nucleosides and Nucleotide	Purines Purine conversion
NO2.NO3	0,027916	-0,6878359	Vanillate O-decarboxylation Metabolism of Aromatic Compounds	Peripheral Phenylpropanoid
POC	0,02806	-0,6873848	2-methylacrylate Carbohydrates	Organic acids 2-methylcitrate
POC	0,02806	-0,6873848	DNA polymerase DNA Metabolism	DNA repair DNA repair
POC	0,02806	-0,6873848	TRAP-type C4 Miscellaneous	Plant-Protists At4g17370
POC	0,02806	-0,6873848	Uronate isomerase Carbohydrates	- Sugar utilization
TotalProteins	0,028115	0,6872146	4-hydroxybenzoate Membrane Transport	- Ton and Ton
TotalProteins	0,028115	-0,6872146	Possible hypoxanthine Clustering-based subsystem	Clustering-based Putative di
TotalProteins	0,028115	-0,6872146	Replication factor DNA Metabolism	DNA replication DNA replication
TotalProteins	0,028205	0,6869343	Alpha-amylase Carbohydrates	Di- and oligo Maltose and

DOC	0,028206	0,6869333	Excinuclease	DNA Metabolism	DNA repair	DNA repair
Z	0,028206	-0,6869333	Sulfate adeny	Sulfur Metabolism	Inorganic s	Inorganic S
Z	0,028251	-0,6867938	Maltose/malt	Carbohydrates	Di- and olig	Maltose an
POC	0,028251	-0,6867938	Sporulation ir	Cell Division and Cell Cycle	-	Bacterial Cy
Salinity	0,028364	-0,6864415	Adenine-spec	Clustering-based subsystem	-	CBSS-2573:
Salinity	0,028364	-0,6864415	Ribonuclease	Clustering-based subsystem	-	CBSS-2284:
Z	0,028515	-0,6859756	NADH-ubiqui	Respiration	Electron dc	Respiratory
POC	0,028693	-0,6854293	(S)-2-hydroxy	Carbohydrates	Central car	Glycolate, g
POC	0,028693	-0,6854293	1-deoxy-D-xy	Clustering-based subsystem	Isoprenoid,	CBSS-8333:
Z	0,028693	-0,6854293	Arsenical pun	Virulence, Disease and Defe	Resistance	Arsenic resi
POC	0,028693	-0,6854293	BatB	Clustering-based subsystem	-	Aerotolera
POC	0,028693	-0,6854293	CDP-glycerol	Cell Wall and Capsule	Gram-Posit	Teichoic an
Z	0,028693	-0,6854293	Cell division p	Cell Division and Cell Cycle	-	Bacterial Cy
Z	0,028693	-0,6854293	DNA methyl t	Phages, Prophages, Transpo	Phages, Prc	Phage DNA
Z	0,028693	-0,6854293	DNA-directed	RNA Metabolism	Transcripti	RNA polym
POC	0,028693	-0,6854293	D-xylose prot	Carbohydrates	Monosacch	Xylose utili:
POC	0,028693	-0,6854293	Electron tran	Respiration	Electron dc	Na(+)-trans
POC	0,028693	-0,6854293	FIG003620: P	Clustering-based subsystem	alpha-prot	CBSS-5259:
Z	0,028693	-0,6854293	Glutamine sy	Amino Acids and Derivative	Glutamine, Glutamine,	
POC	0,028693	-0,6854293	Glutamine-de	Amino Acids and Derivative	Lysine, thr	Methionine
POC	0,028693	-0,6854293	Glycyl-tRNA s	Protein Metabolism	Protein bio	tRNA amin
POC	0,028693	-0,6854293	Hydroxypyruv	Carbohydrates	Organic aci	Glycerate n
Z	0,028693	-0,6854293	LSU ribosom	Protein Metabolism	Protein bio	Ribosome L
Z	0,028693	-0,6854293	Metal-depen	Clustering-based subsystem	-	CBSS-5678:
POC	0,028693	-0,6854293	N-acetylmura	Cell Wall and Capsule	-	Recycling o
POC	0,028693	-0,6854293	NAD-depend	Carbohydrates	Central car	Pyruvate m
Z	0,028693	-0,6854293	Phage lysin	Phages, Prophages, Transpo	Phages, Prc	Phage entr
POC	0,028693	-0,6854293	PlcB, ORFX, O	Clustering-based subsystem	Methylami	CBSS-2650:
POC	0,028693	-0,6854293	Polysaccharid	Cell Wall and Capsule	Capsular ar	Capsular Pc
POC	0,028693	-0,6854293	S-nitrosomyc	Stress Response	Oxidative s	Glutathione
POC	0,028693	-0,6854293	Sodium/glyci	Amino Acids and Derivative	Alanine, se	Glycine cle:
Z	0,028693	-0,6854293	SSU ribosom	Protein Metabolism	Protein bio	Ribosome S
Z	0,028693	-0,6854293	Sulfite reduct	Respiration	Electron ac	Anaerobic r
Z	0,028693	-0,6854293	thioredoxin S	Sulfur Metabolism	-	Sulfur oxid:
POC	0,028693	-0,6854293	Thiosulfate r	Respiration	Electron ac	Anaerobic r
POC	0,028693	-0,6854293	Transcription	RNA Metabolism	Transcripti	RNA polym
POC	0,028693	-0,6854293	Transcription	Cell Wall and Capsule	Gram-Neg	Lipid A mo
POC	0,028693	-0,6854293	Translation el	Protein Metabolism	Protein bio	Translation
POC	0,028693	-0,6854293	Tricarboxylat	Membrane Transport	-	Tricarboxyl
Z	0,028693	0,6854293	UDP-N-acetyl	Cell Wall and Capsule	-	Peptidoglyc
POC	0,028693	-0,6854293	Uncharacteri	Iron acquisition and metabo	-	Encapsulati
POC	0,028693	-0,6854293	Universal stre	Stress Response	-	Universal si
POC	0,028693	-0,6854293	VgrG protein	Clustering-based subsystem	-	USS-DB-7
POC	0,028693	-0,6854293	Xylan oligosa	Carbohydrates	-	Sugar utiliz:
TotalProtis	0,029061	0,6843064	NADH:ubiqui	Respiration	Electron dc	Respiratory
TotalProtis	0,029061	0,6843064	Phosphoribul	Carbohydrates	CO2 fixatio	Calvin-Bens
TN	0,029377	0,6833491	2,3-dihydroxy	Metabolism of Aromatic Co	Peripheral	Biphenyl De

PO4	0,029377	-0,6833491	2-hydroxy-6-oxo-2-oxobutyrat	Metabolism of Aromatic Compounds	carbazol de
DOC	0,029377	-0,6833491	2-keto-3-deoxy-6-phosphogluconate	Amino Acids and Derivatives	Aromatic a Chorismate
NO2.NO3	0,029377	-0,6833491	2-keto-3-deoxy-6-phosphogluconate	Amino Acids and Derivatives	Aromatic a Chorismate
PO4	0,029377	-0,6833491	2-Oxobutyrat	Amino Acids and Derivatives	Lysine, threonine Methionine
Chla	0,029377	-0,6833491	4-keto-6-deoxy-6-phosphogluconate	Protein Metabolism	Protein precursor N-linked Glycosylation
PO4	0,029377	-0,6833491	5-methylthioadenosine	Amino Acids and Derivatives	Lysine, threonine Methionine
TotalBacte	0,029377	0,6833491	ABC transporter	Virulence, Disease and Defense	Bacteriocin Bacitracin S
PO4	0,029377	0,6833491	ADP-L-glycerol	Cell Wall and Capsule	Gram-Negative LOS core oligosaccharide
Si	0,029377	0,6833491	ADP-L-glycerol	Cell Wall and Capsule	Gram-Negative LOS core oligosaccharide
TN	0,029377	0,6833491	Asp-X dipeptide	Protein Metabolism	Protein degradation Protein degradation
Chla	0,029377	-0,6833491	ATP-dependent	DNA Metabolism	DNA repair DNA Repair
PO4	0,029377	0,6833491	capsular polysaccharide	Cell Wall and Capsule	Capsular antigen Rhamnose
Si	0,029377	0,6833491	capsular polysaccharide	Cell Wall and Capsule	Capsular antigen Rhamnose
PO4	0,029377	0,6833491	Capsular polysaccharide	Cell Wall and Capsule	Capsular antigen Serotype determinant
Si	0,029377	0,6833491	Capsular polysaccharide	Cell Wall and Capsule	Capsular antigen Serotype determinant
DOC	0,029377	0,6833491	Carbamoyl-phosphate	Nucleosides and Nucleotides	Pyrimidine: De Novo Pyrimidine biosynthesis
PO4	0,029377	0,6833491	CDP-6-deoxy-6-phosphogluconate	Miscellaneous	Plant-Protokoll: COG0451
Si	0,029377	0,6833491	CDP-6-deoxy-6-phosphogluconate	Miscellaneous	Plant-Protokoll: COG0451
Chla	0,029377	0,6833491	Cell division protein	Cell Division and Cell Cycle	- Bacterial Cytodivision
DOC	0,029377	0,6833491	COG2110, Methylglutathione	Miscellaneous	Plant-Protokoll: At1g69340
Chla	0,029377	-0,6833491	Cold shock protein	Stress Response	Cold shock Cold shock,
TN	0,029377	0,6833491	Dethiobiotin	Cofactors, Vitamins, Prosthetic Cofactors	Biotin Biotin biosynthesis
DOC	0,029377	-0,6833491	D-galactonate	Carbohydrates	Monosaccharide D-galactonate
NO2.NO3	0,029377	-0,6833491	D-galactonate	Carbohydrates	Monosaccharide D-galactonate
DOC	0,029377	0,6833491	Dihydrofolate	Cofactors, Vitamins, Prosthetic Cofactors	Folate and Folate Biosynthesis
DOC	0,029377	0,6833491	DNA polymerase	Clustering-based subsystem	- CBSS-2284: DNA polymerase
DOC	0,029377	-0,6833491	DNA topoisomerase	Phages, Prophages, Transposons	Phages, Prophages, PRC Phage replication
NO2.NO3	0,029377	-0,6833491	DNA topoisomerase	Phages, Prophages, Transposons	Phages, Prophages, PRC Phage replication
TN	0,029377	-0,6833491	Endonuclease	DNA Metabolism	DNA repair DNA repair,
TN	0,029377	-0,6833491	Feruloyl-CoA	Metabolism of Aromatic Compounds	Peripheral Phenylpropanoid
TotalBacte	0,029377	-0,6833491	FIG004453: p	Clustering-based subsystem	- CBSS-2810: FIG004453: p
PO4	0,029377	0,6833491	FIG004454: R	Miscellaneous	Plant-Protokoll: At4g10620
Si	0,029377	0,6833491	FIG004454: R	Miscellaneous	Plant-Protokoll: At4g10620
DOC	0,029377	-0,6833491	FIG022199: F	Fatty Acids, Lipids, and Isoprenoids	Fatty acids Phospholipid
NO2.NO3	0,029377	-0,6833491	FIG022199: F	Fatty Acids, Lipids, and Isoprenoids	Fatty acids Phospholipid
DOC	0,029377	0,6833491	Folypolyglutamate	Cofactors, Vitamins, Prosthetic Cofactors	Folate and Folate Biosynthesis
TN	0,029377	0,6833491	Glucarate dehydrogenase	Carbohydrates	Monosaccharide D-galactaric acid
TotalBacte	0,029377	0,6833491	Gluconate phosphatase	Carbohydrates	Monosaccharide D-gluconate
TotalBacte	0,029377	0,6833491	Glutathione S-transferase	Stress Response	Oxidative stress Glutathione
TN	0,029377	0,6833491	Glycine oxidase	Cofactors, Vitamins, Prosthetic Cofactors	- Thiamin biosynthesis
DOC	0,029377	0,6833491	HTH-type transcription factor	Amino Acids and Derivatives	Alanine, serine Alanine biosynthesis
PO4	0,029377	-0,6833491	Hydantoinase	Nucleosides and Nucleotides	- Hydantoinase
DOC	0,029377	-0,6833491	Hydrogenase	Respiration	- Formate hydrogenase
NO2.NO3	0,029377	-0,6833491	Hydrogenase	Respiration	- Formate hydrogenase
TotalBacte	0,029377	-0,6833491	Inner membrane protein	Membrane Transport	Protein anchor pVir Plasmid
TotalBacte	0,029377	0,6833491	Inositol oxygenase	Carbohydrates	Sugar alcohol Inositol catabolism
Si	0,029377	-0,6833491	Iojap protein	Clustering-based subsystem	- CBSS-3162: Iojap protein

TN	0,029377	0,6833491	Isoaspartyl ar Protein Metabolism	Protein deç Omega pep
PO4	0,029377	-0,6833491	Isohexenylglu Fatty Acids, Lipids, and Isopr	Isoprenoid: Acyclic terp
PO4	0,029377	-0,6833491	Isopentenyl p Fatty Acids, Lipids, and Isopr	Isoprenoid: Archaeal lip
PO4	0,029377	0,6833491	Light-indeper Cofactors, Vitamins, Prosthe	Tetrapyrrol Chlorophyll
Si	0,029377	0,6833491	Light-indeper Cofactors, Vitamins, Prosthe	Tetrapyrrol Chlorophyll
DOC	0,029377	-0,6833491	Lipid A biosyr Cell Wall and Capsule	Gram-Neg: KDO2-Lipid
NO2.NO3	0,029377	-0,6833491	Lipid A biosyr Cell Wall and Capsule	Gram-Neg: KDO2-Lipid
TotalBacte	0,029377	-0,6833491	LSU m3Psi19: Miscellaneous	Plant-Prok: lojap
TN	0,029377	0,6833491	LSU ribosom: Protein Metabolism	Protein bio Ribosome L
DOC	0,029377	-0,6833491	LSU ribosom: Protein Metabolism	Protein bio Ribosome L
NO2.NO3	0,029377	-0,6833491	LSU ribosom: Protein Metabolism	Protein bio Ribosome L
PO4	0,029377	0,6833491	LSU ribosom: Clustering-based subsystem	Fatty acid r COG1399
Si	0,029377	0,6833491	LSU ribosom: Clustering-based subsystem	Fatty acid r COG1399
TotalBacte	0,029377	0,6833491	Maltose O-ac Carbohydrates	Di- and olig Maltose an
DOC	0,029377	0,6833491	Mannonate d Carbohydrates	- Sugar utiliz:
Chla	0,029377	-0,6833491	Methionyl-tR Clustering-based subsystem	- Conserved
PO4	0,029377	0,6833491	NADH-ubiqui: Respiration	Electron dc Respiratory
Si	0,029377	0,6833491	NADH-ubiqui: Respiration	Electron dc Respiratory
PO4	0,029377	0,6833491	NAD-reducinç Respiration	Electron dc Hydrogena:
Si	0,029377	0,6833491	NAD-reducinç Respiration	Electron dc Hydrogena:
Chla	0,029377	-0,6833491	Niacin transp: Cofactors, Vitamins, Prosthe	NAD and N NAD and N.
PO4	0,029377	-0,6833491	Nitrite transp Nitrogen Metabolism	- Nitrate and
PO4	0,029377	0,6833491	N-Ribosylnicc Cofactors, Vitamins, Prosthe	NAD and N NAD and N.
Si	0,029377	0,6833491	N-Ribosylnicc Cofactors, Vitamins, Prosthe	NAD and N NAD and N.
TotalBacte	0,029377	0,6833491	Outer membr: Membrane Transport	- Ton and To
PO4	0,029377	-0,6833491	Periplasmic cl Amino Acids and Derivative:	Aromatic a Chorismate
DOC	0,029377	0,6833491	Perosamine s Cell Wall and Capsule	Gram-Neg: Perosamine
DOC	0,029377	-0,6833491	Phenazine bic Secondary Metabolism	Bacterial cy Phenazine l
NO2.NO3	0,029377	-0,6833491	Phenazine bic Secondary Metabolism	Bacterial cy Phenazine l
PO4	0,029377	0,6833491	Phenylacetic Metabolism of Aromatic Coi-	Phenylacet:
Si	0,029377	0,6833491	Phenylacetic Metabolism of Aromatic Coi-	Phenylacet:
DOC	0,029377	0,6833491	Poly(A) polyn RNA Metabolism	RNA proce: Polyadenyl:
TotalBacte	0,029377	-0,6833491	Predicted ma Carbohydrates	Di- and olig Maltose an
TotalBacte	0,029377	-0,6833491	Predicted sigr Clustering-based subsystem	DNA polym CBSS-3426:
PO4	0,029377	-0,6833491	Probable carl Clustering-based subsystem	- CBSS-3931:
Chla	0,029377	-0,6833491	probable cytc Respiration	Electron ac Terminal cy
TotalBacte	0,029377	0,6833491	Probable poly Cell Wall and Capsule	Capsular ar Alginate m:
PO4	0,029377	-0,6833491	Protein expor Clustering-based subsystem	- Glutaredox
Si	0,029377	-0,6833491	Protein gp47, Phages, Prophages, Transpo	Phages, Prc Listeria phi:
TotalBacte	0,029377	0,6833491	Protein Yail Clustering-based subsystem	- CBSS-562.2
PO4	0,029377	0,6833491	Putative Dim: Miscellaneous	Plant-Prok: Niacin-Chol
Si	0,029377	0,6833491	Putative Dim: Miscellaneous	Plant-Prok: Niacin-Chol
PO4	0,029377	0,6833491	Putative pern Miscellaneous	- ZZ gjo need
Si	0,029377	0,6833491	Putative pern Miscellaneous	- ZZ gjo need
Chla	0,029377	-0,6833491	Putative pred DNA Metabolism	- Restriction-
PO4	0,029377	-0,6833491	rRNA biogene RNA Metabolism	RNA proce: Ribosome t
PO4	0,029377	-0,6833491	rRNA small sl Clustering-based subsystem	- CBSS-1604:

TotalBacte	0,029377	-0,6833491	Serine/threor	Clustering-based subsystem -	Conserved
Chla	0,029377	-0,6833491	Signal peptid	Stress Response	Heat shock Heat shock
TotalBacte	0,029377	0,6833491	Similar to cop	Clustering-based subsystem -	CBSS-630.2
PO4	0,029377	-0,6833491	Sodium-depe	Membrane Transport	Uni- Sym- ε NhaA, NhaI
TotalBacte	0,029377	0,6833491	Soluble lytic r	Miscellaneous	Plant-Prok; COG0451
TotalBacte	0,029377	0,6833491	SSU ribosomε	Protein Metabolism	Protein bio Ribosome ε
TN	0,029377	-0,6833491	Succinate del	Respiration	Electron dc Succinate d
TotalBacte	0,029377	-0,6833491	T7-like phage	Phages, Prophages, Transpo	Phages, Prc T7-like pha
PO4	0,029377	-0,6833491	Thiol:disulfidε	Respiration	- Biogenesis
PO4	0,029377	-0,6833491	TldD family p	Clustering-based subsystem -	CBSS-3162
DOC	0,029377	-0,6833491	TPR repeat cc	Membrane Transport	- Ton and To
NO2.NO3	0,029377	-0,6833491	TPR repeat cc	Membrane Transport	- Ton and To
PO4	0,029377	-0,6833491	Transcription	Carbohydrates	Fermentati Acetoin, bu
DOC	0,029377	-0,6833491	Transport ATI	Respiration	Electron ac Terminal cy
NO2.NO3	0,029377	-0,6833491	Transport ATI	Respiration	Electron ac Terminal cy
PO4	0,029377	-0,6833491	tRNA pseudo	RNA Metabolism	RNA proce: RNA pseud
Si	0,029377	-0,6833491	Type III restri	DNA Metabolism	- Restriction-
DOC	0,029377	0,6833491	Tyrosine reco	Clustering-based subsystem	Hypothetic CBSS-3238
PO4	0,029377	0,6833491	UDP-GlcNAC-:	Cell Wall and Capsule	Capsular ar Pseudamin
Si	0,029377	0,6833491	UDP-GlcNAC-:	Cell Wall and Capsule	Capsular ar Pseudamin
TotalBacte	0,029377	-0,6833491	Uncharacteri	Cell Wall and Capsule	Gram-Negε Lipopolysac
PO4	0,029377	0,6833491	Uncharacteri	Clustering-based subsystem -	CBSS-3142
Si	0,029377	0,6833491	Uncharacteri	Clustering-based subsystem -	CBSS-3142
TotalBacte	0,029377	-0,6833491	Uncharacteri	Clustering-based subsystem -	USS-DB-7
PO4	0,029377	0,6833491	Unspecified n	Clustering-based subsystem	Monosaccl Unspecified
Si	0,029377	0,6833491	Unspecified n	Clustering-based subsystem	Monosaccl Unspecified
PO4	0,029377	0,6833491	Unspecified n	Clustering-based subsystem	Monosaccl Unspecified
Si	0,029377	0,6833491	Unspecified n	Clustering-based subsystem	Monosaccl Unspecified
DOC	0,029377	0,6833491	Urea carboxy	Amino Acids and Derivative	Arginine; u Urea decon
DOC	0,029377	-0,6833491	Uronate isom	Carbohydrates	Monosaccl D-Galactur
NO2.NO3	0,029377	-0,6833491	Uronate isom	Carbohydrates	Monosaccl D-Galactur
PO4	0,029377	0,6833491	YgfY COG293	Cofactors, Vitamins, Prosthe	Folate and YgfZ
Si	0,029377	0,6833491	YgfY COG293	Cofactors, Vitamins, Prosthe	Folate and YgfZ
Z	0,029457	0,683106	Arabinose 5-γ	Cell Wall and Capsule	Gram-Negε KDO2-Lipid
TotalProtis	0,029457	0,683106	Taurine trans	Sulfur Metabolism	Organic sul Taurine Uti
POC	0,029517	-0,6829268	Glutamine an	Amino Acids and Derivative	Glutamine, Glutamine,
Si	0,029563	-0,6827887	Phenylpropio	Metabolism of Aromatic Co	Peripheral Phenylprop
Salinity	0,029617	0,6826257	Protein similε	RNA Metabolism	RNA proce: Polyadenyl
NO2.NO3	0,029966	-0,6815829	Chaperone pr	Protein Metabolism	Protein folk Protein cha
Si	0,029966	-0,6815829	Formiminogl	Amino Acids and Derivative	Histidine M Histidine D
NO2.NO3	0,029966	0,6815829	Ribonuclease	Clustering-based subsystem	Fatty acid r COG1399
POC	0,030013	-0,6814429	N-Acetyl-D-gl	Carbohydrates	Aminosuga Chitin and I
Si	0,030151	0,6810329	Dihydrolipoar	Amino Acids and Derivative	Branched-c Isoleucine c
DOC	0,030151	-0,6810329	H4MPT-deper	Cofactors, Vitamins, Prosthe	Folate and 5-FCL-like p
NO2.NO3	0,030151	-0,6810329	H4MPT-deper	Cofactors, Vitamins, Prosthe	Folate and 5-FCL-like p
DOC	0,030151	-0,6810329	Homoserine (Amino Acids and Derivative	Lysine, thre Methionine
TotalProtis	0,030151	-0,6810329	Oxaloacetate	Carbohydrates	Central car Pyruvate m

Chla	0,030151	-0,6810329	Pyrimidine A Nucleosides and Nucleotide	Pyrimidine	Pyrimidine
DOC	0,030151	0,6810329	Pyrimidine A Nucleosides and Nucleotide	Pyrimidine	Pyrimidine
POC	0,030196	-0,6809001	Acetoacetate	Carbohydrates	Fermentati Acetone Bu
POC	0,030196	-0,6809001	Glycine betai	Miscellaneous	Plant-Prok Niacin-Chol
POC	0,030196	-0,6809001	Leucine dehy	Amino Acids and Derivative	Branched-c Branched c
Z	0,030211	0,6808542	Acetate perm	Carbohydrates	Central car Pyruvate m
TN	0,030211	-0,6808542	Cold-shock D	RNA Metabolism	RNA proce ATP-depen
POC	0,030211	0,6808542	Nucleoside di	Nucleosides and Nucleotide	Purines Purine conv
Z	0,03029	-0,6806224	BatA (Bacter	Clustering-based subsystem -	Aerotolera
Z	0,03029	-0,6806224	Cytochrome c	Clustering-based subsystem	Cytochrom CBSS-1961
Z	0,03029	-0,6806224	D-glycerate 3	Carbohydrates	CO2 fixatio Photorespi
POC	0,03029	-0,6806224	FIG006126: D	Clustering-based subsystem -	CBSS-3162
Z	0,03029	-0,6806224	histone acety	RNA Metabolism	RNA proce mcm5s2U l
POC	0,03029	-0,6806224	Hydroxymeth	Amino Acids and Derivative	Branched-c Branched c
Z	0,03029	-0,6806224	Nucleoside p	Carbohydrates	Monosacch Deoxyribos
Z	0,03029	-0,6806224	Predicted iro	Clustering-based subsystem -	Conserved
Z	0,03029	-0,6806224	Predicted L-r	Carbohydrates	Monosacch L-rhamnose
Z	0,03029	-0,6806224	Replication fa	DNA Metabolism	DNA replic DNA replica
Z	0,03029	-0,6806224	SAM-depend	Clustering-based subsystem -	Glutaredox
POC	0,03029	-0,6806224	Thiamin ABC	Cofactors, Vitamins, Prosthe	Thiamin bic
POC	0,03029	-0,6806224	Urease acces	Amino Acids and Derivative	Arginine; u Urea decon
POC	0,030324	0,6805217	Iron binding	Amino Acids and Derivative	Alanine, se Alanine bio
NO2.NO3	0,030899	-0,6788336	L-allo-threoni	Amino Acids and Derivative	Lysine, thr Threonine c
NO2.NO3	0,030899	-0,6788336	L-allo-threoni	Amino Acids and Derivative	Lysine, thr Threonine c
TN	0,030899	-0,6788336	Lycopene bet	Fatty Acids, Lipids, and Isop	Isoprenoid Carotenoid
Si	0,030899	-0,6788336	Methylthior	Amino Acids and Derivative	Lysine, thr Methionine
Chla	0,030899	-0,6788336	N-acetyl-lysin	Amino Acids and Derivative	Lysine, thr Lysine bios
NO2.NO3	0,030899	-0,6788336	N-methylhyd	Amino Acids and Derivative	- Creatine an
Si	0,030899	0,6788336	Phosphoribos	Amino Acids and Derivative	Histidine N Histidine Bi
NO2.NO3	0,030899	-0,6788336	Phosphoribul	Carbohydrates	CO2 fixatio Calvin-Bens
PO4	0,030899	-0,6788336	Recombinatic	DNA Metabolism	DNA repair DNA repair
PO4	0,030899	0,6788336	Site-specific r	Phages, Prophages, Transpo	Phages, Pr Phage integ
Chla	0,030899	-0,6788336	SSU ribosom	Protein Metabolism	Protein bio Ribosome S
Chla	0,030994	-0,6785567	2-dehydro-3-	Carbohydrates	Monosacch D-galacton
Chla	0,030994	-0,6785567	Alginate lyase	Cell Wall and Capsule	Capsular ar Alginate me
DOC	0,030994	0,6785567	Arylsulfatase	Clustering-based subsystem	Sulfatases Sulfatases a
NO2.NO3	0,030994	-0,6785567	ATPase with c	Membrane Transport	Protein sec Widesprea
Si	0,030994	0,6785567	Bacillosamine	Cell Wall and Capsule	Capsular ar Legionamir
PO4	0,030994	0,6785567	Deoxyribodip	DNA Metabolism	DNA repair DNA repair
DOC	0,030994	0,6785567	DNA topoisor	Clustering-based subsystem -	Conjugative
Chla	0,030994	-0,6785567	Ferritin-like p	Miscellaneous	Plant-Prok Iron-sulfur
TotalBacte	0,030994	0,6785567	Flagellar basa	Motility and Chemotaxis	Flagellar m Flagellum
NO2.NO3	0,030994	0,6785567	Gluconolacto	Carbohydrates	Central car Entner-Dou
DOC	0,030994	-0,6785567	Glucose ABC	Carbohydrates	Central car Peripheral
Si	0,030994	0,6785567	Glutamate As	Amino Acids and Derivative	Glutamine, Glutamate
Si	0,030994	0,6785567	Guanylate kir	Clustering-based subsystem -	CBSS-3230
Si	0,030994	0,6785567	L-fuco-beta-p	Carbohydrates	Monosacch L-fucose ut

DOC	0,030994	0,6785567	LSU ribosome	Protein Metabolism	Protein bio	Ribosome L
DOC	0,030994	0,6785567	Menaquinone	Cofactors, Vitamins, Prosthe	Quinone cc	Menaquin
Chla	0,030994	0,6785567	Metallo-beta	Clustering-based subsystem	-	Bacterial RI
TN	0,030994	-0,6785567	Molybdenum	Cofactors, Vitamins, Prosthe	Folate and	Molybdenu
NO2.NO3	0,030994	-0,6785567	Molybdenum	Cofactors, Vitamins, Prosthe	Folate and	Molybdenu
PO4	0,030994	-0,6785567	N-acetylgluco	Carbohydrates	Aminosuga	Chitin and I
PO4	0,030994	0,6785567	Nucleoside tr	Dormancy and Sporulation	-	Sporulation
DOC	0,030994	0,6785567	Pantoate kin	Cofactors, Vitamins, Prosthe	Coenzyme	Coenzyme .
DOC	0,030994	0,6785567	Phage prohe	Phages, Prophages, Transpo	Phages, Prc	Phage caps
TotalBacte	0,030994	-0,6785567	Phenylacetic	Metabolism of Aromatic Coi	-	Phenylacet
TotalBacte	0,030994	-0,6785567	Possible pyrir	Nucleosides and Nucleotide	Pyrimidine	Novel non-
NO2.NO3	0,030994	-0,6785567	Predicted ATf	Membrane Transport	Protein sec	Widesprea
TN	0,030994	-0,6785567	Putative iron	Miscellaneous	Plant-Prok	Iron-sulfur
DOC	0,030994	0,6785567	Quinone oxid	Miscellaneous	-	ZZ gjo need
Si	0,030994	0,6785567	Succinyl-CoA	Carbohydrates	Central car	TCA Cycle
DOC	0,030994	0,6785567	transcription	Stress Response	Oxidative s	Oxidative s
PO4	0,030994	-0,6785567	Uroporphyrin	Cofactors, Vitamins, Prosthe	Tetrapyrro	Coenzyme
TN	0,031141	-0,6969697	Glutamate-1-	Clustering-based subsystem	Cytochrom	CBSS-1961
TN	0,031141	-0,6969697	Peptide chain	Protein Metabolism	Protein bio	Translation
TN	0,031141	-0,6969697	Pyruvate,pho	Carbohydrates	Central car	Glycolysis a
DOC	0,031141	-0,6969697	RecA protein	Clustering-based subsystem	Two relate	CBSS-2573
Si	0,031141	-0,6969697	Scaffold prot	Miscellaneous	Plant-Prok	Iron-sulfur
NO2.NO3	0,031141	-0,6969697	Valyl-tRNA sy	Protein Metabolism	Protein bio	tRNA amin
TotalProtis	0,031395	-0,6773942	Zinc ABC tran	Membrane Transport	-	Transport c
POC	0,031398	-0,6773856	Chaperone pr	Protein Metabolism	Protein fol	Protein cha
TotalProtis	0,031415	0,6773373	TldE/PmbA p	Cell Wall and Capsule	Gram-Neg	Lipopolysac
TotalProtis	0,031415	0,6773373	UTP--glucose	Cell Wall and Capsule	Capsular ar	Streptococ
TotalProtis	0,031525	0,6770186	Branched-ch	Membrane Transport	ABC transp	ABC transp
POC	0,031549	-0,6769519	Branched-ch	Amino Acids and Derivatives	Branched-c	Branched c
Z	0,031549	-0,6769519	Ribose 5-pho	Carbohydrates	Central car	Pentose ph
Z	0,031591	-0,6768293	GTP-binding	Clustering-based subsystem	-	CBSS-235.1
Salinity	0,031801	0,6762281	Carbon mon	Clustering-based subsystem	-	CBSS-3142
TotalBacte	0,031895	0,6759609	2-keto-4-pen	Metabolism of Aromatic Coi	-	Benzoate tr
TotalBacte	0,031895	-0,6759609	Flagellar bios	Motility and Chemotaxis	Flagellar m	Flagellum
PO4	0,031895	0,6759609	General secre	Membrane Transport	Protein sec	General Ser
DOC	0,031895	0,6759609	Glutaminase	Amino Acids and Derivatives	Glutamine, Glutamine,	
Chla	0,031895	-0,6759609	Long-chain-fa	Cofactors, Vitamins, Prosthe	Biotin	Biotin biosy
DOC	0,031895	0,6759609	prolyl oligope	Miscellaneous	Plant-Prok	Synechocys
TN	0,031895	-0,6759609	Proteasome s	Clustering-based subsystem	proteosom	Cluster-bas
TotalBacte	0,031895	-0,6759609	Selenocysteir	Protein Metabolism	Selenoprot	Selenocyste
DOC	0,031895	0,6759609	Two-compon	Regulation and Cell signaling	-	Orphan reg
Si	0,032116	0,6753298	Fe-S-cluster-c	Respiration	Electron ac	Anaerobic r
DOC	0,032116	0,6753298	Sulfur oxidati	Sulfur Metabolism	-	Sulfur oxid
POC	0,032312	0,6747752	Amidophosph	Cofactors, Vitamins, Prosthe	Folate and	YgfZ
Si	0,032312	-0,6747752	RNA polymer	Phages, Prophages, Transpo	Phages, Prc	Phage regu
NO2.NO3	0,032312	-0,6747752	Transcription	RNA Metabolism	Transcripti	RNA polym
POC	0,032439	-0,6744153	L-allo-threoni	Amino Acids and Derivatives	Lysine, thr	Threonine r

POC	0,032439	-0,6744153	L-allo-threoni Amino Acids and Derivatives	Lysine, thre Threonine (
Z	0,032498	0,6742496	probable iron Clustering-based subsystem -	CBSS-3162
TotalProtis	0,032542	0,6741248	Dipeptide tra Membrane Transport	ABC transp ABC transp
Salinity	0,03261	0,6739331	membrane c- Respiration	Electron ac Terminal cy
Salinity	0,03261	0,6739331	Pyruvate:ferr Carbohydrates	Central car Pyruvate:fe
Z	0,032892	0,673143	Nucleotide su Clustering-based subsystem -	CBSS-2965
Salinity	0,032983	0,6728908	Ribosome rec Clustering-based subsystem -	CBSS-1762
TotalProtis	0,033362	0,6718368	Acyl-CoA synt Miscellaneous	Plant-Prok: At1g52510
TotalProtis	0,033362	0,6718368	D-arabino-3-1 Carbohydrates	One-carbor Formaldehy
POC	0,033739	-0,6707978	4-hydroxypro Amino Acids and Derivatives	Proline anc Proline, 4-h
TotalProtis	0,033854	0,670482	Pre-mRNA sp RNA Metabolism	RNA proce: Spliceosom
Salinity	0,034102	0,6698041	Succinyl-CoA Carbohydrates	Central car TCA Cycle
DOC	0,034348	0,669133	5-Enolpyruvy Amino Acids and Derivatives	Aromatic a Chorismate
Si	0,034348	0,669133	ABC-type Fe3 Clustering-based subsystem	Molybdopt CBSS-2697
DOC	0,034348	0,669133	ATP-depende Clustering-based subsystem -	CBSS-3931
PO4	0,034348	0,669133	Biotin carbox Respiration	Sodium Ion Na+ translo
NO2.NO3	0,034348	-0,669133	Biotin carbox Amino Acids and Derivatives	Branched-c HMG CoA S
NO2.NO3	0,034348	-0,669133	CTP-depende Cofactors, Vitamins, Prosthe	Riboflavin, riboflavin tr
Chla	0,034348	-0,669133	DMSP demeth Sulfur Metabolism	Organic sul DMSP brea
NO2.NO3	0,034348	-0,669133	DNA-binding Cofactors, Vitamins, Prosthe	Riboflavin, Riboflavin,
PO4	0,034348	-0,669133	Flagellar basa Motility and Chemotaxis	Flagellar m Flagellum
Chla	0,034348	-0,669133	Glutaminase Amino Acids and Derivatives	Glutamine, Glutamine,
DOC	0,034348	-0,669133	Lipoprotein N Clustering-based subsystem -	CBSS-2115
Si	0,034348	0,669133	Molybdenum Clustering-based subsystem	Molybdopt CBSS-2697
Chla	0,034348	-0,669133	prolyl oligope Miscellaneous	Plant-Prok: Synechocys
DOC	0,034348	0,669133	Putative sucro Carbohydrates	Di- and olig Maltose an
Chla	0,034348	-0,669133	Urea carboxy Amino Acids and Derivatives	Arginine; u Urea carbo
Chla	0,034369	-0,6690768	Isocitrate dehydro Carbohydrates	Central car Glyoxylate
DOC	0,034369	0,6690768	Peptidyl-proly Protein Metabolism	Protein fold Peptidyl-pr
TotalBacte	0,034369	-0,6690768	Ribose 1,5-bis Carbohydrates	CO2 fixatio Calvin-Bens
TotalBacte	0,034369	-0,6690768	Thiazole bios Cofactors, Vitamins, Prosthe	Thiamin bic
Chla	0,034485	0,668762	Cysteine desulf Amino Acids and Derivatives	Alanine, ser Alanine bio
NO2.NO3	0,034485	-0,668762	Glutaminyl-tRNA Protein Metabolism	Protein bio tRNA amin
NO2.NO3	0,034485	0,668762	Methylcroton Amino Acids and Derivatives	Branched-c Branched c
NO2.NO3	0,034485	-0,668762	Phosphoglucose Clustering-based subsystem	Chromosom SeqA and C
DOC	0,034485	0,668762	Predicted nucle Carbohydrates	Monosacchar Deoxyribos
Si	0,034485	0,668762	tRNA-i(6)A37 Clustering-based subsystem -	tRNA-meth
Z	0,03451	0,6686961	Argininosuccin Amino Acids and Derivatives	Arginine; u Arginine Bic
TN	0,03451	0,6686961	F420-depende Carbohydrates	One-carbor Methanoge
Chla	0,03451	0,6686961	NADH-ubiquinol Respiration	Electron dc Respiratory
TN	0,03451	-0,6686961	Phosphate AE Clustering-based subsystem	Phosphate PhoR-PhoB
PO4	0,03451	-0,6686961	Phosphoribos Nucleosides and Nucleotide	Purines De Novo Pu
POC	0,03451	0,6686961	V-type ATP synth Respiration	ATP synthase V-Type ATP
Z	0,034793	-0,6679305	Cytochrome b Respiration	- Cytochrome
Z	0,034793	-0,6679305	D-Lactate dehydro Carbohydrates	Central car Glycolate, g
Z	0,034793	-0,6679305	Glutathione re Potassium metabolism	- Glutathione
POC	0,034793	-0,6679305	NADPH-dehydro RNA Metabolism	RNA proce: Queuosine-

DOC	0,035092	-0,6848485	Dihydropyrim Nucleosides and Nucleotide	Pyrimidine	Novel non-
Chla	0,035092	0,6848485	GDP-mannos	Cell Wall and Capsule	Capsular ar Capsular he
NO2.NO3	0,035092	-0,6848485	L-proline glyc	Stress Response	Osmotic sti Choline and
TN	0,035092	-0,6848485	Pyrophospha	Phosphorus Metabolism	- Phosphate
Chla	0,035552	-0,6659034	3-hydroxyacy	Amino Acids and Derivatives	Branched-c Isoleucine c
Si	0,035552	0,6659034	Alpha-glucosi	Membrane Transport	ABC transp Periplasmic
TotalBacte	0,035552	0,6659034	Cold shock pr	Stress Response	Cold shock Cold shock,
NO2.NO3	0,035552	0,6659034	D-2-hydroxyg	Miscellaneous	Plant-Prok: COG0277
NO2.NO3	0,035552	0,6659034	GTP-binding f	Miscellaneous	- ZZ gjo need
Chla	0,035552	-0,6659034	Histidinol-phc	Amino Acids and Derivatives	Histidine N Histidine Bi
DOC	0,035552	0,6659034	Molybdopte	Clustering-based subsystem	Molybdopt CBSS-2697
NO2.NO3	0,035552	0,6659034	Na(+)-translo	Respiration	Electron dc Na(+)-trans
NO2.NO3	0,035552	-0,6659034	NAD kinase (f	Clustering-based subsystem	Nucleotidy CBSS-2225
TN	0,035552	-0,6659034	Phage prohe	Phages, Prophages, Transpo	Phages, Prc Phage caps
TotalBacte	0,035552	-0,6659034	Phosphate tr	Phosphorus Metabolism	- Phosphate
Chla	0,035552	-0,6659034	UDP-N-acetyl	Cell Wall and Capsule	Capsular ar Legionamir
POC	0,035643	0,6656636	4-hydroxyber	Cofactors, Vitamins, Prosthe	Quinone cc Menaquin
POC	0,035643	-0,6656636	Capsular poly	Cell Wall and Capsule	Capsular ar Exopolysac
POC	0,035643	-0,6656636	Formaldehyd	Cofactors, Vitamins, Prosthe	Folate and YgfZ
POC	0,035643	-0,6656636	Formate hydr	Respiration	- Formate hy
POC	0,035643	-0,6656636	Fructose ABC	Carbohydrates	Monosaccl Fructose ut
POC	0,035643	-0,6656636	Fumarylacetc	Cofactors, Vitamins, Prosthe	Folate and Pterin carbi
POC	0,035643	-0,6656636	Homocystein	Amino Acids and Derivatives	Lysine, thr Methionine
POC	0,035643	-0,6656636	Methionine A	Amino Acids and Derivatives	Lysine, thr Methionine
POC	0,035643	-0,6656636	Phosphoribo	Cofactors, Vitamins, Prosthe	Folate and 5-FCL-like p
POC	0,035643	-0,6656636	Predicted ma	Carbohydrates	Monosaccl Mannose N
Z	0,035643	-0,6656636	Protein-N(5)-	Miscellaneous	Plant-Prok: YrdC-YciO-S
POC	0,035643	-0,6656636	Ribosylnicotir	Cofactors, Vitamins, Prosthe	NAD and N NAD and N.
POC	0,035643	-0,6656636	SSU ribosom	Clustering-based subsystem	- KH domain
POC	0,035643	-0,6656636	Sulfur oxidati	Sulfur Metabolism	- Sulfur oxid
TotalProtis	0,036017	-0,6646768	Gluconate de	Carbohydrates	Central car Entner-Dou
Z	0,03603	-0,6646437	Branched-ch	Amino Acids and Derivatives	Branched-c Branched c
Z	0,03603	-0,6646437	Glycine cleav	Amino Acids and Derivatives	Alanine, se Glycine and
POC	0,03603	-0,6646437	Phytoene de	Fatty Acids, Lipids, and Isopr	Isoprenoid: Carotenoid
POC	0,03603	-0,6646437	Rhodanese d	Miscellaneous	Plant-Prok: Single-Rhoc
TotalProtis	0,03603	0,6646437	Succinyl-CoA:	Amino Acids and Derivatives	Branched-c Branched c
Z	0,036033	-0,6646341	Alanyl-tRNA s	Clustering-based subsystem	- CBSS-2810
Z	0,036033	-0,6646341	Iron-sulfur cl	Clustering-based subsystem	Cytochrom CBSS-1961
Z	0,036033	-0,6646341	Phage major	Phages, Prophages, Transpo	Phages, Prc Phage caps
TotalProtis	0,036048	0,6645963	TRAP-type un	Clustering-based subsystem	Tricarboxyl CBSS-4933
Z	0,036152	-0,6643212	5-keto-2-deo	Carbohydrates	Sugar alcof Inositol cat
Z	0,036152	-0,6643212	Alpha-glucosi	Membrane Transport	ABC transp Periplasmic
Z	0,036152	-0,6643212	Capsular poly	Cell Wall and Capsule	Capsular ar Capsular Pc
Z	0,036152	-0,6643212	UPF0129 pro	Respiration	- Methanoge
DOC	0,036412	0,6636434	Allophanate f	Amino Acids and Derivatives	Arginine; u Urea carbo
DOC	0,036412	0,6636434	BarA-associat	Membrane Transport	Protein sec Type III sec
Chla	0,036412	-0,6636434	Beta-mannos	Carbohydrates	Monosaccl Mannose N

TN	0,036412	-0,6636434	COG0009 Sua Clustering-based subsystem -	LMPTP Ywl
Chla	0,036412	-0,6636434	Glutaredoxin Phages, Prophages, Transpo Phages, Prc Phage DNA	
DOC	0,036412	0,6636434	low-specificit Amino Acids and Derivative: Lysine, thr Threonine (
TotalBacte	0,036412	-0,6636434	Low-specificit Amino Acids and Derivative: Alanine, se Glycine Bio	
PO4	0,036412	0,6636434	Membrane-b Cell Wall and Capsule -	Murein Hyc
NO2.NO3	0,036412	0,6636434	putative Cyto Respiration	Electron ac Terminal cy
DOC	0,036412	0,6636434	Putative oxid Respiration -	Quinone ox
Si	0,036412	-0,6636434	RNA 3'-termir RNA Metabolism	RNA proce: RNA 3'-terr
PO4	0,036412	-0,6636434	Sulfopyruvat Cofactors, Vitamins, Prosthe Coenzyme coenzyme I	
TotalBacte	0,036412	-0,6636434	Superoxide di Stress Response	Oxidative s Regulation
Si	0,036412	0,6636434	Transcription Clustering-based subsystem -	CBSS-2913:
Si	0,036412	0,6636434	Tryptophan 2 Amino Acids and Derivative: Aromatic a Aromatic ai	
Salinity	0,036438	0,6635757	3-oxoadipate Metabolism of Aromatic Coi Metabolism Catechol br	
TotalProtis	0,03644	0,6635698	Heme A synt Respiration -	Biogenesis
TotalProtis	0,03644	-0,6635698	Phage integr Phages, Prophages, Transpo Phages, Prc Phage integr	
Salinity	0,036621	-0,6630975	Biotin carbox Clustering-based subsystem -	Allophanat
Salinity	0,036621	-0,6630975	Enoyl-CoA hy Carbohydrates	Central car Dehydroge
TN	0,036727	0,6628237	3-dehydroqui Amino Acids and Derivative: Aromatic a Chorismate	
TotalBacte	0,036727	-0,6628237	Biosynthetic : Amino Acids and Derivative: Arginine; u Arginine an	
Chla	0,036727	0,6628237	Pseudaminic Cell Wall and Capsule	Capsular ar Pseudamin
DOC	0,036727	-0,6628237	Similarity to Miscellaneous	Plant-Prok: At4g17370
NO2.NO3	0,036727	-0,6628237	Transcription RNA Metabolism	Transcripti Transcriptic
Chla	0,036727	-0,6628237	Xylulose kina: Carbohydrates	- Sugar utiliz:
POC	0,036806	0,662617	Dihydropyrim Nucleosides and Nucleotide -	Hydantoin i
Z	0,036806	0,662617	DNA-directed Miscellaneous	Plant-Prok: At2g23840
Si	0,036806	-0,662617	photosystem Photosynthesis	Electron tr: Photosyste
POC	0,036806	0,662617	Succinate de Carbohydrates	Central car TCA Cycle
Chla	0,036927	-0,6623051	DNA-directed Clustering-based subsystem	Probably G CBSS-1762:
Chla	0,036927	0,6623051	Ethanolamine Carbohydrates	Sugar alco Ethanolami
TN	0,036927	-0,6623051	Fructose-1,6- Carbohydrates	Central car Glycolysis a
Si	0,036927	0,6623051	Oxidoreducta Miscellaneous	Plant-Prok: At4g17370
Si	0,036927	0,6623051	Predicted ma Membrane Transport	- Transport c
POC	0,03716	-0,6617054	Cys regulon ti Amino Acids and Derivative: Lysine, thr Cysteine Bi	
POC	0,03716	-0,6617054	Membrane p Miscellaneous	- YbbK
POC	0,037261	-0,6614458	1-pyrroline-4- Amino Acids and Derivative: Proline anc Proline, 4-h	
POC	0,037261	-0,6614458	Phosphonate Membrane Transport	ABC transp ABC transp
TotalProtis	0,037421	-0,661035	Putrescine tr: Amino Acids and Derivative: Arginine; u Polyamine	
TotalProtis	0,037421	-0,661035	Translation el Protein Metabolism	Protein bio Translation
POC	0,037475	-0,6608969	4-hydroxyber Metabolism of Aromatic Coi -	Benzoate ti
POC	0,037475	-0,6608969	Signal peptid: Virulence, Disease and Defe Adhesion	Streptococi
POC	0,037475	-0,6608969	Signal peptid: Clustering-based subsystem	Probably G CBSS-1762:
POC	0,037475	-0,6608969	Various polyc Stress Response	Detoxificat Uptake of s
Salinity	0,037654	0,6604393	FIG000859: h DNA Metabolism	DNA recor RuvABC plu
Salinity	0,038337	-0,6587065	Arginine N-su Amino Acids and Derivative: Arginine; u Arginine an	
POC	0,038392	-0,6585694	Branched-ch Membrane Transport	ABC transp ABC transp
POC	0,038405	-0,6585366	2-amino-3-ke Amino Acids and Derivative: Alanine, se Glycine anc	
Z	0,038405	-0,6585366	Gamma-gluta Amino Acids and Derivative: Proline anc Proline Syn	

POC	0,038423	-0,6584896	Exodeoxyribo DNA Metabolism	DNA repair DNA Repair
POC	0,038423	0,6584896	Nucleoside-di Clustering-based subsystem -	CBSS-2965
POC	0,038829	-0,6574726	COG2833: un Miscellaneous	Plant-Prok: At5g04520
Salinity	0,038928	-0,6572257	Protein secre Miscellaneous	- ZZ gjo need
TotalProtis	0,039156	0,6566576	DNA topoisor DNA Metabolism	DNA replic: DNA topo
TotalProtis	0,039156	0,6566576	Rubredoxin Stress Response	Oxidative s Rubrerythri
Si	0,039191	0,6565707	Methenyltetr Carbohydrates	One-carbor One-carbor
Si	0,039191	0,6565707	Methylenetet Carbohydrates	One-carbor One-carbor
Si	0,039191	0,6565707	Methylenetet Cofactors, Vitamins, Prosthe	Folate and 5-FCL-like p
TN	0,039191	0,6565707	Outer membr Membrane Transport	- Ton and To
PO4	0,039204	0,656538	Anthranilate : Amino Acids and Derivatives	Aromatic a Chorismate
Z	0,039204	0,656538	ATP-depende Protein Metabolism	Protein deg Proteolysis
PO4	0,039204	0,656538	Glutathione s Clustering-based subsystem -	CBSS-3203
Z	0,039204	0,656538	Methylsuccin Carbohydrates	Central car Ethylmalon
POC	0,039204	0,656538	RNA polymer RNA Metabolism	Transcripti Transcriptic
TN	0,039223	0,6564911	Cytochrome l Respiration	- Cytochrom
Si	0,039223	0,6564911	DNA polymer Clustering-based subsystem -	CBSS-3506
NO2.NO3	0,039223	-0,6564911	L-pipecolate (Amino Acids and Derivatives	Lysine, thr Lysine degr
NO2.NO3	0,039223	-0,6564911	Na+/H+ antip Miscellaneous	- ZZ gjo need
Si	0,039223	-0,6564911	Naphthoate s Cofactors, Vitamins, Prosthe	Quinone cc Menaquin
NO2.NO3	0,039223	-0,6564911	Probable exo: Clustering-based subsystem	Proteasom Proteasom
TotalBacte	0,039223	-0,6564911	tRNA-(ms[2]) RNA Metabolism	RNA proces: tRNA modif
TotalProtis	0,039223	-0,6564911	Tryptophan s Amino Acids and Derivatives	Aromatic a Chorismate
PO4	0,039223	0,6564911	Urea ABC tra: Amino Acids and Derivatives	Arginine; u Urea decon
TN	0,039381	-0,6727273	1-hydroxy-2-r Clustering-based subsystem	Isoprenoid, CBSS-8333
Chla	0,039381	0,6727273	Aconitate hyc Carbohydrates	Central car Glyoxylate
TN	0,039381	-0,6727273	Chaperone pr Protein Metabolism	Protein fol: Protein cha
PO4	0,039381	0,6727273	DNA gyrase s Clustering-based subsystem -	DNA gyrase
NO2.NO3	0,039381	-0,6727273	DNA-directed RNA Metabolism	Transcripti RNA polym
PO4	0,039381	0,6727273	L-alanine:glyc Carbohydrates	Central car Pyruvate Al
Chla	0,039381	0,6727273	LSU ribosom: Protein Metabolism	Protein bio Ribosome l
NO2.NO3	0,039381	0,6727273	Phenylacetat: Metabolism of Aromatic Co	- Phenylacet
DOC	0,039381	-0,6727273	Pyruvate deh Amino Acids and Derivatives	Lysine, thr Methionine
Chla	0,039633	-0,6554772	2-C-methyl-D Clustering-based subsystem -	CBSS-2115
Chla	0,039633	-0,6554772	DNA-binding DNA Metabolism	- DNA structi
Si	0,039633	0,6554772	General secre Membrane Transport	Protein sec General Ser
DOC	0,039633	0,6554772	glutamyl-Q-tf Miscellaneous	Plant-Prok: At2g23840
DOC	0,039633	0,6554772	Glycolate deh Carbohydrates	Central car Glycolate, g
DOC	0,039633	0,6554772	Inositol trans Carbohydrates	Sugar alcof Inositol cat
NO2.NO3	0,039633	-0,6554772	Predicted 2-k Amino Acids and Derivatives	Aromatic a Aromatic al
DOC	0,039633	0,6554772	Probable corr Cell Wall and Capsule	Gram-Neg: Lipopolysac
Chla	0,039633	-0,6554772	Putative glut: Sulfur Metabolism	Organic sul Utilization (
Chla	0,039633	-0,6554772	Spermidine P Amino Acids and Derivatives	Arginine; u Polyamine
Chla	0,039633	-0,6554772	Two-compon Regulation and Cell signaling	- Orphan reg
Z	0,039651	-0,6554333	ATP phospho Amino Acids and Derivatives	Histidine M Histidine Bi
Z	0,039651	-0,6554333	Pup ligase Pa: Clustering-based subsystem	proteosom Cluster-bas
Salinity	0,03973	-0,6552396	Phenylpropio Metabolism of Aromatic Co	Peripheral Phenylprop

Z	0,039843	-0,654961	Acetoacetyl-C Amino Acids and Derivative	Branched-c HMG CoA S
POC	0,039843	-0,654961	Cytochrome c Clustering-based subsystem	Cytochrom CBSS-1961f
Z	0,039843	-0,654961	Ribosomal R Clustering-based subsystem -	Conserved
POC	0,039843	-0,654961	Xylose ABC tr Carbohydrates	Monosaccl Xylose utili
Salinity	0,040215	-0,6540507	Beta-caroten Fatty Acids, Lipids, and Isop	Isoprenoid: Carotenoid
POC	0,040216	-0,6540482	archaeosine t RNA Metabolism	RNA proces tRNA modifi
DOC	0,040658	0,6529733	3-hydroxyacy Amino Acids and Derivative	Branched-c Branched c
Chla	0,040658	-0,6529733	Aminopeptid Clustering-based subsystem -	CBSS-1762f
Si	0,040658	-0,6529733	Dihydrodipic Amino Acids and Derivative	Lysine, thr Lysine Bios
Si	0,040658	0,6529733	DNA primase DNA Metabolism	DNA replic DNA replica
TotalBacte	0,040658	-0,6529733	DNA repair ar DNA Metabolism	DNA recomb DNA recomb
NO2.NO3	0,040658	0,6529733	Formate dehy Respiration	- Formate hy
Chla	0,040658	-0,6529733	Glutathione r Stress Response	Oxidative s Glutathione
Si	0,040658	0,6529733	Histidinol-ph Amino Acids and Derivative	Histidine N Histidine Bi
TN	0,040658	-0,6529733	Indolepyruva Amino Acids and Derivative	Aromatic a Aromatic ai
Si	0,040658	-0,6529733	L-asparaginas Amino Acids and Derivative	Glutamine, Glutamine,
DOC	0,040658	-0,6529733	Lycopene bet Fatty Acids, Lipids, and Isop	Isoprenoid: Carotenoid
Chla	0,040658	-0,6529733	MiaB family p Protein Metabolism	Protein prc Ribosomal
Si	0,040658	0,6529733	MiaB family p Protein Metabolism	Protein prc Ribosomal
NO2.NO3	0,040658	0,6529733	Putative form Respiration	- Formate hy
Chla	0,040658	-0,6529733	Ribonucleotic Nucleosides and Nucleotide	- Ribonucleo
DOC	0,040658	0,6529733	RNA polymer Clustering-based subsystem -	CBSS-2115f
Z	0,040879	-0,652439	4-hydroxyph Amino Acids and Derivative	Metabolism of Aromatic Coi
Z	0,040879	-0,652439	SSU ribosom Protein Metabolism	Protein bio Ribosome S
Z	0,040922	-0,6523355	Autoinducer : Regulation and Cell signaling	Quorum se Autoinduce
Z	0,040922	-0,6523355	Phosphoribo Nucleosides and Nucleotide	Purines De Novo Pl
POC	0,040922	-0,6523355	Probable exo Clustering-based subsystem	Proteasom Proteasom
Z	0,040938	-0,6522973	Glutathione S Clustering-based subsystem -	Conserved
TotalProtis	0,040989	-0,6521739	Choline dehy Miscellaneous	Plant-Prok Niacin-Chol
TotalProtis	0,040989	0,6521739	Uracil-DNA gl DNA Metabolism	DNA repair DNA Repair
Salinity	0,041156	-0,6517727	5-carboxyme Amino Acids and Derivative	Aromatic a Aromatic ai
Salinity	0,041156	0,6517727	Phosphoenol Carbohydrates	Sugar alcoh Mannitol U
Salinity	0,041156	0,6517727	SSU ribosom Protein Metabolism	Protein bio Nucleolar p
Z	0,041602	-0,6507049	ammonium/r Nitrogen Metabolism	- Ammonia a
POC	0,041602	-0,6507049	Bacterial sug Clustering-based subsystem	Biosynthes CBSS-3766f
POC	0,041602	-0,6507049	Benzoate trar Metabolism of Aromatic Coi	- Benzoate tr
POC	0,041602	-0,6507049	Dihydrolipoar Carbohydrates	Central car Dehydroge
POC	0,041602	-0,6507049	Glutamate de Stress Response	Acid stress Acid resista
POC	0,041602	-0,6507049	Malate:quino Carbohydrates	Central car TCA Cycle
POC	0,041602	-0,6507049	Nudix-like ND Nucleosides and Nucleotide	Detoxificat Nudix prote
POC	0,041602	-0,6507049	Oligopeptide Membrane Transport	ABC transp ABC transp
POC	0,041602	-0,6507049	Phosphatidyl Miscellaneous	- ZZ gjo need
POC	0,041602	-0,6507049	response reg Phosphorus Metabolism	- Phosphate
POC	0,041602	-0,6507049	Shufflon-spec Membrane Transport	Protein anc Type 4 conj
Z	0,041602	-0,6507049	Spore matura Dormancy and Sporulation	- Spore Core
POC	0,041602	-0,6507049	Sulfite reduct Amino Acids and Derivative	Lysine, thr Cysteine Bi
Z	0,041602	-0,6507049	Threonine de Amino Acids and Derivative	Lysine, thr Threonine c

Z	0,041602	-0,6507049	Transcription Virulence, Disease and Defe Resistance	Multidrug F
POC	0,041602	-0,6507049	UDP-3-O-[3-h Cell Wall and Capsule	Gram-Neg: KDO2-Lipid
Z	0,041636	-0,6506239	Enoyl-[acyl-c: Fatty Acids, Lipids, and Isopr	Fatty acids Polyunsatu
Z	0,041636	-0,6506239	Glucosamine- Carbohydrates	Aminosuga Chitin and I
Z	0,041636	-0,6506239	L-asparaginas Amino Acids and Derivatives	Glutamine, Glutamine,
NO2.NO3	0,041705	0,6504589	tRNA (5-meth	Miscellaneous Plant-Prok: At5g37530
DOC	0,041765	0,6503176	Dihydroorota Clustering-based subsystem	Hypothetic Hypothetic
TN	0,041765	-0,6503176	Uracil-DNA gl DNA Metabolism	DNA repair Uracil-DNA
TotalProtis	0,042006	0,6497454	FIG042796: H Clustering-based subsystem -	EC699-706
Z	0,042253	-0,6491612	Arsenic resist Virulence, Disease and Defe Resistance	Arsenic resi
POC	0,042253	-0,6491612	Chromosome Cell Division and Cell Cycle -	Bacterial Cy
Z	0,042253	-0,6491612	Peptidyl-proly Protein Metabolism	Protein fol: Peptidyl-pr
Z	0,042253	-0,6491612	Translation in Protein Metabolism	Protein bio Translation
NO2.NO3	0,042436	-0,6487301	ATP-depende RNA Metabolism	RNA proce: ATP-depen
Chla	0,042436	0,6487301	COG2106 Me RNA Metabolism	RNA proce: rRNA modifi
TN	0,042436	-0,6487301	Exodeoxyribo DNA Metabolism	DNA repair DNA repair
DOC	0,042436	0,6487301	FIG006126: D Clustering-based subsystem -	CBSS-3162
PO4	0,042436	0,6487301	Gluconolacto Carbohydrates	Central car Entner-Dou
DOC	0,042436	0,6487301	Hydroxymeth Amino Acids and Derivatives	Branched-c Branched c
DOC	0,042436	0,6487301	hypothetical Protein Metabolism	Protein bio Ribosome k
TotalBacte	0,042436	0,6487301	LSU ribosom: Protein Metabolism	Protein bio Ribosome L
DOC	0,042436	-0,6487301	membrane c- Respiration	Electron ac Terminal cy
PO4	0,042436	-0,6487301	Nicotinate-nu Cofactors, Vitamins, Prosthe	NAD and N NAD and N.
Chla	0,042436	-0,6487301	Nucleoside tr Dormancy and Sporulation -	Sporulation
TotalBacte	0,042436	0,6487301	Predicted RN: RNA Metabolism	RNA proce: tRNA modifi
TotalBacte	0,042436	0,6487301	Ribosomal RN Clustering-based subsystem -	Conserved
DOC	0,042436	0,6487301	Thiamin ABC Cofactors, Vitamins, Prosthe -	Thiamin bic
NO2.NO3	0,042436	-0,6487301	UPF0246 pro: Miscellaneous	- YaaA
NO2.NO3	0,04247	-0,6486493	Ketoglutarate Amino Acids and Derivatives	Proline anc Proline, 4-h
POC	0,042544	-0,6484762	DMSP breakd Sulfur Metabolism	Organic sul DMSP brea
Salinity	0,042756	-0,6479782	Anthranilate : Amino Acids and Derivatives	Aromatic a Chorismate
Salinity	0,043507	0,6462303	Malate dehyc Carbohydrates	Central car Glyoxylate
Z	0,043528	-0,6461814	Archaeal DNA DNA Metabolism	DNA replic: DNA replic:
POC	0,043596	-0,6460252	Aspartate am Amino Acids and Derivatives	Glutamine, Aspartate a
Z	0,043596	-0,6460252	Ferredoxin, 2 Amino Acids and Derivatives	Alanine, se Alanine bio
POC	0,043596	-0,6460252	Lysine biosyn Amino Acids and Derivatives	Lysine, thr: Lysine bios
TotalProtis	0,043743	0,645686	Aspartate am Amino Acids and Derivatives	Glutamine, Aspartate a
NO2.NO3	0,044027	-0,6606061	1-hydroxy-2-r Clustering-based subsystem	Isoprenoid, CBSS-8333:
NO2.NO3	0,044027	-0,6606061	ATP-depende Protein Metabolism	Protein deg: Proteasom
NO2.NO3	0,044027	-0,6606061	Lipopolysaccl Cell Wall and Capsule	Gram-Neg: KDO2-Lipid
DOC	0,044027	-0,6606061	NADH-ubiqui: Respiration	Electron dc Respiratory
PO4	0,044027	-0,6606061	Omega-amin: Carbohydrates	Central car Pyruvate Al
Chla	0,044027	0,6606061	photosystem Photosynthesis	Electron tr: Photosyste
Chla	0,044027	0,6606061	Pyruvate deh Amino Acids and Derivatives	Lysine, thr: Methionine
Si	0,044027	-0,6606061	RNA polymer RNA Metabolism	Transcripti: Transcripti
Chla	0,044027	0,6606061	Scaffold prot: Miscellaneous	Plant-Prok: Iron-sulfur
DOC	0,044027	-0,6606061	Thiamin biosy Cofactors, Vitamins, Prosthe -	Thiamin bic

Chla	0,044027	0,6606061 Translation el Miscellaneous	Plant-Prok: lojap
TotalBacte	0,044027	0,6606061 Urocanate hy Amino Acids and Derivative	Histidine N Histidine D
DOC	0,044027	-0,6606061 V-type ATP sy Respiration	ATP synth V-Type ATP
Salinity	0,044111	0,644839 Cystathionine Amino Acids and Derivative	Lysine, thr Methionine
POC	0,044312	0,6443799 2,3,4,5-tetra Amino Acids and Derivative	Lysine, thr Lysine Bios
DOC	0,044312	-0,6443799 Aerobic cobal Cofactors, Vitamins, Prosthe	Tetrapyrrol Coenzyme
TN	0,044312	-0,6443799 Aerobic cobal Cofactors, Vitamins, Prosthe	Tetrapyrrol Coenzyme
NO2.NO3	0,044312	-0,6443799 Cold-shock D RNA Metabolism	RNA proces ATP-depen
Z	0,044312	0,6443799 Iron-sulfur cl Clustering-based subsystem Cytochrom	CBSS-1961f
TotalBacte	0,044381	-0,6442203 3-polyprenyl- Cofactors, Vitamins, Prosthe	Quinone cc Menaquino
Si	0,044381	0,6442203 5-carboxyme Amino Acids and Derivative	Aromatic a Aromatic a
TotalBacte	0,044381	-0,6442203 ATPase, AFG1 Protein Metabolism	Protein deg Proteolysis
Si	0,044381	0,6442203 Delta-1-pyrro Amino Acids and Derivative	Arginine; u Arginine an
TotalProtis	0,044381	0,6442203 DNA-directed RNA Metabolism	Transcripti RNA polym
NO2.NO3	0,044381	0,6442203 GTP pyropho Clustering-based subsystem Nucleotidy	CBSS-2225
NO2.NO3	0,044381	0,6442203 GTP pyropho Clustering-based subsystem Probably G	CBSS-1762
TotalProtis	0,044381	0,6442203 Histidinol de Amino Acids and Derivative	Histidine N Histidine Bi
NO2.NO3	0,044381	-0,6442203 Homoserine (Amino Acids and Derivative	Lysine, thr Methionine
TotalProtis	0,044381	0,6442203 LSU ribosoma Clustering-based subsystem -	LSU ribosom
TotalProtis	0,044381	-0,6442203 LSU ribosoma Protein Metabolism	Protein bio Ribosome L
TotalProtis	0,044381	-0,6442203 Malate synth Carbohydrates	Central car Glyoxylate
TotalBacte	0,04445	-0,6440646 D-malic enzyr Carbohydrates	Central car Pyruvate m
Si	0,04445	-0,6440646 Ornithine dec Amino Acids and Derivative	Arginine; u Arginine an
Chla	0,04445	0,6440646 Peptide meth Clustering-based subsystem Carbohydr	Cluster Ytf
PO4	0,04445	-0,6440646 Pseudaminic Cell Wall and Capsule	Capsular ar Pseudamin
Si	0,04445	0,6440646 SSU ribosoma Protein Metabolism	Protein bio Ribosome S
TotalBacte	0,04445	-0,6440646 Tartrate deca Carbohydrates	Organic aci Glycerate n
TotalBacte	0,04445	-0,6440646 Tartrate dehy Clustering-based subsystem Choline bit	CBSS-3446
POC	0,044577	-0,6437752 Glutathione S Miscellaneous	Plant-Prok: At3g50560
Z	0,044577	-0,6437752 Indoleacetam Amino Acids and Derivative	Aromatic a Aromatic a
Salinity	0,044634	0,6436439 Acetyl-coenz Fatty Acids, Lipids, and Isopr	Fatty acids Fatty Acid E
Salinity	0,044634	0,6436439 Biotin carbox Fatty Acids, Lipids, and Isopr	Fatty acids Fatty Acid E
Salinity	0,044634	0,6436439 Biotin carbox Fatty Acids, Lipids, and Isopr	Fatty acids Fatty Acid E
Salinity	0,044634	-0,6436439 D-glycerate tr Carbohydrates	Monosacch D-galactara
Salinity	0,044634	0,6436439 IncF plasmid (Clustering-based subsystem -	Conjugative
Salinity	0,044634	-0,6436439 Microbial coll Amino Acids and Derivative	Proline anc Proline, 4-h
Salinity	0,044634	0,6436439 Putative tran RNA Metabolism	Transcripti Transcriptic
Salinity	0,044741	-0,6434015 1,4-alpha-glu Carbohydrates	Di- and olig Trehalose E
Salinity	0,044741	-0,6434015 Arsenical-resi Virulence, Disease and Defe	Resistance Arsenic resi
Z	0,044967	-0,6428891 Isoquinoline Clustering-based subsystem Putative Is	CBSS-3142f
Z	0,044967	-0,6428891 L-alanine-DL- Cell Wall and Capsule	- Recycling o
POC	0,044967	-0,6428891 SSU ribosoma Protein Metabolism	Protein bio Ribosome S
Salinity	0,04535	0,6420242 L-arabonate c Carbohydrates	Monosacch L-Arabinose
Z	0,045365	-0,6419915 Cytochrome c Respiration	Electron ac Terminal cy
TotalBacte	0,04544	-0,6418214 Copper resist Virulence, Disease and Defe	Resistance Copper hor
NO2.NO3	0,04544	-0,6418214 Cystathionine Amino Acids and Derivative	Lysine, thr Methionine
TotalBacte	0,04544	-0,6418214 FKBP-type pe Protein Metabolism	Protein folk Peptidyl-pr

NO2.NO3	0,04544	0,6418214	Peptidyl-prolyl Protein Metabolism	Protein fold	Peptidyl-pr
TotalBacte	0,04544	0,6418214	Stringent star Stress Response	-	Carbon Sta
Salinity	0,045473	-0,6417477	Naphthoate s Cofactors, Vitamins, Prosthe	Quinone cc	Menaquinc
TotalProtis	0,04552	0,6416419	ATP-depende Protein Metabolism	Protein deg	Proteasom
Salinity	0,04565	0,6413506	Cell division c DNA Metabolism	DNA replic	DNA replica
Salinity	0,04565	-0,6413506	Cytochrome c Clustering-based subsystem	-	CBSS-3160
Salinity	0,04565	0,6413506	Origin of repl DNA Metabolism	DNA replic	DNA replica
POC	0,046098	-0,6403509	Phosphonoac Phosphorus Metabolism	-	Phosphona
NO2.NO3	0,046236	0,6400431	Adenosine de Nucleosides and Nucleotide	Purines	Purine conv
PO4	0,046236	-0,6400431	Alcohol dehyd Carbohydrates	Fermentati	Acetone Bu
TotalBacte	0,046236	-0,6400431	Aromatic-L-ar Amino Acids and Derivatives	Aromatic a	Aromatic ai
Chla	0,046236	0,6400431	ATP phospho Amino Acids and Derivatives	Histidine N	Histidine Bi
Si	0,046236	0,6400431	Branched-cha Membrane Transport	ABC transp	ABC transp
TotalBacte	0,046236	-0,6400431	D-Lactate de Carbohydrates	Central car	Glycolate, g
PO4	0,046236	-0,6400431	LSU ribosoma Clustering-based subsystem	Proteasom	Proteasom
Si	0,046236	0,6400431	Molybdopter Clustering-based subsystem	Molybdopt	CBSS-2697
TotalBacte	0,046236	-0,6400431	PhnI protein Phosphorus Metabolism	-	Alkylphospl
NO2.NO3	0,046236	-0,6400431	tRNA cytosine RNA Metabolism	RNA proce	tRNA modif
POC	0,046243	-0,6400273	Possible ster Miscellaneous	Plant-Prok	COG0398
POC	0,046367	-0,6397531	N-succinyl-L,L Amino Acids and Derivatives	Lysine, thr	Lysine Bios
TotalProtis	0,046367	-0,6397516	Serine acetyl Amino Acids and Derivatives	Lysine, thr	Cysteine Bi
TotalProtis	0,046546	0,6393558	Urea ABC tra Amino Acids and Derivatives	Arginine; u	Urea decon
Z	0,047024	0,6383008	2',3'-cyclic-nu Nucleosides and Nucleotide	Purines	Purine conv
TN	0,047024	-0,6383008	Alkyl hydrope Stress Response	Oxidative s	Oxidative s
Z	0,047024	0,6383008	ATP synthase Respiration	ATP syntha	F0F1-type /
Chla	0,047248	0,6378115	Protein simila RNA Metabolism	RNA proce	Polyadenyl
Salinity	0,047694	0,6368362	Electron tran Respiration	Electron dc	Na(+)-trans
Salinity	0,047694	0,6368362	Glucose-met Respiration	Electron dc	Respiratory
POC	0,047795	-0,6366171	Ribonucleotic Nucleosides and Nucleotide	-	Ribonucleo
Z	0,048197	0,6357462	Manganese A Membrane Transport	-	Transport c
Si	0,048546	0,6349935	ATP-depende DNA Metabolism	DNA repair	DNA repair
DOC	0,048546	0,6349935	DMSP demeth Sulfur Metabolism	Organic sul	DMSP brea
TN	0,048546	-0,6349935	L-Aspartate d Cofactors, Vitamins, Prosthe	NAD and N	NAD and N
PO4	0,048546	-0,6349935	Phage integr Phages, Prophages, Transpo	Phages, Prc	Phage integ
TotalProtis	0,04861	0,6348554	Kynureninase Amino Acids and Derivatives	Aromatic a	Tryptophar
TotalProtis	0,04861	0,6348554	Pyrimidine o Nucleosides and Nucleotide	Pyrimidine	De Novo Py
TotalProtis	0,04861	0,6348554	tRNA cytosine RNA Metabolism	RNA proce	tRNA modif
Z	0,048941	-0,6341463	Dimethylglyci Amino Acids and Derivatives	-	Creatine an
Z	0,048941	-0,6341463	Inorganic pyr Miscellaneous	Plant-Prok	lojap
Z	0,048941	-0,6341463	Ribonucleotic Clustering-based subsystem	-	Ribonucleo
Si	0,049043	0,6484848	Aconitate hyc Carbohydrates	Central car	Glyoxylate
DOC	0,049043	-0,6484848	Argininosucci Amino Acids and Derivatives	Arginine; u	Arginine Bi
NO2.NO3	0,049043	-0,6484848	ATP-depende Protein Metabolism	Protein deg	Proteolysis
Chla	0,049043	0,6484848	Glycyl-tRNA s Protein Metabolism	Protein bio	tRNA amin
DOC	0,049043	-0,6484848	Iron-sulfur cl Clustering-based subsystem	Cytochrom	CBSS-1961
Chla	0,049043	0,6484848	MoxR-like AT Clustering-based subsystem	-	Aerotolera
TN	0,049043	-0,6484848	NAD-depend Respiration	-	Formate hy

DOC	0,049043	-0,6484848	Pyrophosphat Phosphorus Metabolism	-	Phosphate
Si	0,049043	0,6484848	tungsten-con Respiration	-	Formate hy
Salinity	0,049046	-0,6339212	Iron-sulfur cl Amino Acids and Derivatives	Alanine, se	Alanine bio
POC	0,049069	-0,6338732	Butyryl-CoA c Amino Acids and Derivatives	Branched-c	Isoleucine c
TotalProtis	0,049069	0,6338732	RNA polymer Phages, Prophages, Transpo Phages, Prc	Phage regu	
Chla	0,049095	0,6338167	Biphenyl-2,3- Metabolism of Aromatic Coi	Peripheral	Biphenyl Di
DOC	0,049095	-0,6338167	Lysine-arginir Amino Acids and Derivatives	Arginine; u	Arginine an
DOC	0,049095	-0,6338167	Mannose-6-p Carbohydrates	-	Sugar utiliz
TN	0,049095	-0,6338167	Oligopeptide Membrane Transport	ABC transp	ABC transp
DOC	0,049095	-0,6338167	omega-3 poly Fatty Acids, Lipids, and Isopr	Fatty acids	Polyunsatu
DOC	0,049095	-0,6338167	UPF0434 proi Miscellaneous	-	Broadly dis
POC	0,049243	-0,6335022	FIG003879: P Clustering-based subsystem	TldD cluste	CBSS-354.1
POC	0,049243	-0,6335022	Possible fuco Carbohydrates	Monosaccl	L-fucose ut
Z	0,049253	-0,633481	Adenylylsulfa Respiration	Electron ac	Anaerobic r
PO4	0,049846	-0,6322218	Aldehyde del Carbohydrates	Central car	Methylglyo
DOC	0,049846	-0,6322218	Carbamoyl-pl Cell Division and Cell Cycle	-	Macromole
NO2.NO3	0,049846	-0,6322218	Glutamate sy Amino Acids and Derivatives	Glutamine, Glutamine,	
Si	0,049846	0,6322218	Glutamine sy Amino Acids and Derivatives	Glutamine, Glutamine :	
POC	0,049846	0,6322218	LSU ribosoma Protein Metabolism	Protein bio	Ribosome l
Z	0,049846	0,6322218	Phosphoenol Carbohydrates	Central car	Pyruvate m
POC	0,049846	0,6322218	Propionyl-Co Carbohydrates	One-carboi	Serine-glyo
Z	0,049846	0,6322218	Urocanate hy Amino Acids and Derivatives	Histidine N	Histidine Di
NO2.NO3	0,049975	-0,6319494	Chromosome Cell Division and Cell Cycle	-	Two cell div
TotalProtis	0,049975	0,6319494	Dihydrolipoar Carbohydrates	Central car	Dehydroge
DOC	0,049975	-0,6319494	Dipeptide tra Membrane Transport	ABC transp	ABC transp
PO4	0,049975	-0,6319494	Glycine dehy Amino Acids and Derivatives	Alanine, se	Glycine anc
TN	0,049975	-0,6319494	L-pipecolate c Amino Acids and Derivatives	Lysine, thr	Lysine degr
PO4	0,049975	0,6319494	Methylcroto Amino Acids and Derivatives	Branched-c	Branched c
NO2.NO3	0,049975	0,6319494	Nucleoside-di Clustering-based subsystem	-	CBSS-2965
Chla	0,049975	-0,6319494	Predicted nuc Carbohydrates	Monosaccl	Deoxyribos
Si	0,049975	0,6319494	Pyrimidine A Nucleosides and Nucleotide	Pyrimidine	Pyrimidine
TotalBacte	0,049975	-0,6319494	Rubisco activ Carbohydrates	CO2 fixatio	CO2 uptake
PO4	0,049975	0,6319494	sugar ABC tra Miscellaneous	Plant-Prok	COG3533
TN	0,049975	-0,6319494	V-type ATP sy Respiration	ATP syntha	V-Type ATP
NO2.NO3	0,049975	0,6319494	YgjD/Kae1/Qi Cell Division and Cell Cycle	-	Macromole

bacteria; o__Oceanospirillales; f__Halomonadaceae; g__Candidatus Portiera;
 bacteria; o__Alteromonadales; f__Alteromonadaceae; g__Glaciecola;
 c__[Saprospirales]; f__Saprospiraceae; g__Lewinella;
 bacteria; o__GammaproteobacteriaCL; f__GammaproteobacteriaCL; g__GammaproteobacteriaCL;
 bacteria; o__GammaproteobacteriaCL; f__GammaproteobacteriaCL; g__GammaproteobacteriaCL;
 bacteria; o__Alteromonadales; f__Colwelliaceae; g__ColwelliaceaeFA;
 c__Puniceicoccales; f__Puniceicoccaceae; g__Coralimargarita;
 bacteria; o__Alteromonadales; f__Colwelliaceae; g__ColwelliaceaeFA;
 bacteria; o__Alteromonadales; f__Alteromonadaceae; g__Glaciecola;
 bacteria; o__Alteromonadales; f__Alteromonadaceae; g__Glaciecola;
 bacteria; o__Rhodobacterales; f__Rhodobacteraceae; g__Octadecabacter;
 bacteria; o__Alteromonadales; f__Psychromonadaceae; g__PsychromonadaceaeFA;
 bacteria; o__Alteromonadales; f__Alteromonadaceae; g__Candidatus Endobugula;
 bacteria; o__Pirellulales; f__Pirellulaceae; g__PirellulaceaeFA;
 bacteria; o__Rhodobacterales; f__Rhodobacteraceae; g__Octadecabacter;
 bacteria; o__Vibrionales; f__Pseudoalteromonadaceae; g__Pseudoalteromonas;
 c__Flavobacteriales; f__Flavobacteriaceae; g__Maribacter;
 bacteria; o__Methylophilales; f__Methylophilaceae; g__MethylophilaceaeFA;
 bacteria; o__Oceanospirillales; f__Halomonadaceae; g__Candidatus Portiera;
 bacteria; o__Alteromonadales; f__Colwelliaceae; g__ColwelliaceaeFA;
 bacteria; o__Methylophilales; f__Methylophilaceae; g__MethylophilaceaeFA;
 bacteria; o__Cenarchaeales; f__Cenarchaeaceae; g__Nitrosopumilus;
 bacteria; o__GammaproteobacteriaCL; f__GammaproteobacteriaCL; g__GammaproteobacteriaCL;
 bacteria; o__Alteromonadales; f__Colwelliaceae; g__ColwelliaceaeFA;
 bacteria; o__Vibrionales; f__Pseudoalteromonadaceae; g__Pseudoalteromonas;
 c__Flavobacteriales; f__Cryomorphaceae; g__Crocinitomix;
 bacteria; o__Sphingomonadales; f__Erythrobacteraceae; g__Erythrobacter;
 c__[Saprospirales]; f__Saprospiraceae; g__Lewinella;
 bacteria; o__Rhodobacterales; f__Rhodobacteraceae;
 bacteria; o__Alteromonadales; f__Colwelliaceae; g__ColwelliaceaeFA;
 c__Flavobacteriales; f__FlavobacterialesOR; g__FlavobacterialesOR;
 c__Flavobacteriales; f__Flavobacteriaceae; g__FlavobacteriaceaeFA;
 bacteria; o__Pseudomonadales; f__Pseudomonadaceae; g__Pseudomonas;
 bacteria; o__Alteromonadales; f__Colwelliaceae; g__ColwelliaceaeFA;
 bacteria; o__Alteromonadales; f__Alteromonadaceae;
 c__Flavobacteriales; f__Cryomorphaceae; g__Crocinitomix;
 c__Flavobacteriales; f__FlavobacterialesOR; g__FlavobacterialesOR;
 bacteria; o__Sphingomonadales; f__Erythrobacteraceae; g__Erythrobacter;
 bacteria; o__Vibrionales; f__Pseudoalteromonadaceae; g__Pseudoalteromonas;
 c__Cytophagales; f__Flammeovirgaceae; g__Flexibacter;
 c__Flavobacteriales; f__Flavobacteriaceae; g__FlavobacteriaceaeFA;
 bacteria; o__Oceanospirillales; f__Oceanospirillaceae; g__Amphritea;
 bacteria; o__Rhodospirillales; f__Rhodospirillaceae; g__RhodospirillaceaeFA;

o__Flavobacteriales; f__Cryomorphaceae; g__Crocinitomix;
 a; o__Sphingobacteriales; f__NS11-12; g__NS11-12FA;
 bacteria; o__Alteromonadales; f__Alteromonadaceae; g__Candidatus Endobugula;
 ia; o__Pirellulales; f__Pirellulaceae; g__PirellulaceaeFA;
 bacteria; o__Methylophilales; f__Methylophilaceae; g__MethylophilaceaeFA;
 bacteria; o__Alteromonadales; f__Alteromonadaceae; g__Candidatus Endobugula;
 ia; o__Pirellulales; f__Pirellulaceae; g__PirellulaceaeFA;
 o__Flavobacteriales; f__FlavobacterialesOR; g__FlavobacterialesOR;
 bacteria; o__Alteromonadales; f__Alteromonadaceae; g__AlteromonadaceaeFA;
 bacteria; o__Alteromonadales; f__Alteromonadaceae; g__AlteromonadaceaeFA;
 bacteria; o__Alteromonadales; f__Alteromonadaceae; g__Glaciecola;
 o__Flavobacteriales; f__Cryomorphaceae; g__Crocinitomix;
 bacteria; o__Oceanospirillales; f__Halomonadaceae; g__Candidatus Portiera;
 bacteria; o__Pseudomonadales; f__Pseudomonadaceae; g__Pseudomonas;
 Cytophagales; f__Flammeovirgaceae; g__Flexibacter;
 o__Flavobacteriales; f__FlavobacterialesOR; g__FlavobacterialesOR;
 [Saprospirales]; f__Saprospiraceae; g__Lewinella;
 bacteria; o__Alteromonadales; f__Alteromonadaceae;
 bacteria; o__Alteromonadales; f__Colwelliaceae; g__ColwelliaceaeFA;
 [Saprospirales]; f__Saprospiraceae; g__SaprospiraceaeFA;
 o__Flavobacteriales; f__Flavobacteriaceae; g__Maribacter;
 bacteria; o__Sphingomonadales; f__Erythrobacteraceae; g__Erythrobacter;
 ta; o__Cenarchaeales; f__Cenarchaeaceae; g__Nitrosopumilus;
 ta; o__Cenarchaeales; f__Cenarchaeaceae; g__Nitrosopumilus;
 bacteria; o__Oceanospirillales; f__Saccharospirillaceae; g__SaccharospirillaceaeFA;
 o__Flavobacteriales; f__FlavobacterialesOR; g__FlavobacterialesOR;
 [Saprospirales]; f__Saprospiraceae; g__Saprospira;
 bacteria; o__Thiohalorhabdales; f__ThiohalorhabdalesOR; g__ThiohalorhabdalesOR;
 bacteria; o__Pseudomonadales; f__Pseudomonadaceae; g__Pseudomonas;
 bacteria; o__Oceanospirillales; f__OceanospirillalesOR; g__OceanospirillalesOR;
 ia; o__Pirellulales; f__Pirellulaceae; g__PirellulaceaeFA;
 bacteria; o__Methylophilales; f__Methylophilaceae; g__MethylophilaceaeFA;
 o__Flavobacteriales; f__NS9; g__NS9FA;
 bacteria; o__Alteromonadales; f__Colwelliaceae; g__ColwelliaceaeFA;
 Cytophagales; f__Flammeovirgaceae; g__Reichenbachella;
 bacteria; o__Vibrionales; f__Pseudoalteromonadaceae; g__Pseudoalteromonas;
 bacteria; o__Sphingomonadales; f__Erythrobacteraceae; g__Erythrobacter;
 bacteria; o__Alteromonadales; f__HTCC2188; g__HTCC;
 bacteria; o__Alteromonadales; f__OM60; g__OM60FA;
 bacteria; o__Rhodobacterales; f__Rhodobacteraceae; g__RhodobacteraceaeFA;
 bacteria; o__Alteromonadales; f__Colwelliaceae; g__ColwelliaceaeFA;
 Opitutales; f__Opitutaceae; g__Opitutus;
 bacteria; o__Alteromonadales; f__Alteromonadaceae; g__Alteromonas;
 o__Flavobacteriales; f__Flavobacteriaceae; g__FlavobacteriaceaeFA;
 Puniceococcales; f__Puniceococcaceae; g__Coraliomargarita;
 o__Flavobacteriales; f__Cryomorphaceae; g__Crocinitomix;
 o__Flavobacteriales; f__FlavobacterialesOR; g__FlavobacterialesOR;

bacteria; o__Vibrionales; f__Pseudoalteromonadaceae; g__Pseudoalteromonas;
 bacteria; o__Oceanospirillales; f__Saccharospirillaceae; g__SaccharospirillaceaeFA;
 bacteria; o__Oceanospirillales; f__OceanospirillalesOR; g__OceanospirillalesOR;
 bacteria; o__Alteromonadales; f__AlteromonadalesOR; g__AlteromonadalesOR;
 bacteria; o__Methylophilales; f__Methylophilaceae; g__MethylophilaceaeFA;
 bacteria; o__Rhodobacterales; f__Rhodobacteraceae; g__Octadecabacter;
 bacteria; o__Alteromonadales; f__Colwelliaceae; g__ColwelliaceaeFA;
 bacteria; o__Thiohalorhabdales; f__ThiohalorhabdalesOR; g__ThiohalorhabdalesOR;
 bacteria; o__GammaproteobacteriaCL; f__GammaproteobacteriaCL; g__GammaproteobacteriaCL;
 o__Flavobacteriales; f__Flavobacteriaceae; g__Polaribacter;
 bacteria; o__Cenarchaeales; f__Cenarchaeaceae; g__Nitrosopumilus;
 bacteria; o__Alteromonadales; f__Alteromonadaceae; g__Marinobacter;
 o__Flavobacteriales; f__Flavobacteriaceae; g__Tenacibaculum;
 bacteria; o__Alteromonadales; f__Alteromonadaceae; g__AlteromonadaceaeFA;
 bacteria; o__Rhodobacterales; f__Rhodobacteraceae; g__Phaeobacter;
 bacteria; o__Verrucomicrobiales; f__Verrucomicrobiaceae; g__Persicirhabdus;
 bacteria; o__Pirellulales; f__Pirellulaceae; g__PirellulaceaeFA;
 bacteria; o__Sphingobacteriales; f__SphingobacterialesOR; g__SphingobacterialesOR;
 bacteria; o__Puniceococcales; f__Puniceococcaceae; g__Coralimargarita;
 bacteria; o__GammaproteobacteriaCL; f__GammaproteobacteriaCL; g__GammaproteobacteriaCL;
 o__Carnobacteriales; f__Carnobacteriaceae; g__Carnobacterium;
 bacteria; o__Alteromonadales; f__Alteromonadaceae; g__Candidatus Endobugula;
 bacteria; o__Oceanospirillales; f__Oceanospirillaceae; g__Oleispira;
 bacteria; o__Alteromonadales; f__Alteromonadaceae; g__Glaciecola;
 bacteria; o__Oceanospirillales; f__OceanospirillalesOR; g__OceanospirillalesOR;
 o__Flavobacteriales; f__Flavobacteriaceae; g__Formosa;
 o__Flavobacteriales; f__Flavobacteriaceae; g__FlavobacteriaceaeFA;
 bacteria; o__Alteromonadales; f__Alteromonadaceae;
 o__Flavobacteriales; f__FlavobacterialesOR; g__FlavobacterialesOR;
 bacteria; o__Cenarchaeales; f__Cenarchaeaceae; g__Nitrosopumilus;
 o__Flavobacteriales; f__FlavobacterialesOR; g__FlavobacterialesOR;
 o__SAR202CL; f__SAR202CL; g__SAR202CL;
 o__[Saprospirales]; f__Saprospiraceae; g__Lewinella;
 bacteria; o__Rhodobacterales; f__Rhodobacteraceae; g__Octadecabacter;
 bacteria; o__Pirellulales; f__Pirellulaceae; g__PirellulaceaeFA;
 o__Flavobacteriales; f__Flavobacteriaceae; g__FlavobacteriaceaeFA;
 o__Cytophagales; f__Flammeovirgaceae; g__Reichenbachiella;
 bacteria; o__Oceanospirillales; f__Halomonadaceae; g__Candidatus Portiera;
 o__Flavobacteriales; f__FlavobacterialesOR; g__FlavobacterialesOR;
 o__Flavobacteriales; f__Flavobacteriaceae; g__Ulvibacter;
 bacteria; o__Rickettsiales; f__RickettsialesOR; g__RickettsialesOR;
 bacteria; o__AlphaproteobacteriaCL; f__AlphaproteobacteriaCL; g__AlphaproteobacteriaCL;
 o__Flavobacteriales; f__Flavobacteriaceae; g__Winogradskyella;
 o__Flavobacteriales; f__FlavobacterialesOR; g__FlavobacterialesOR;
 o__[Saprospirales]; f__Saprospiraceae; g__SaprospiraceaeFA;
 o__Flavobacteriales; f__Flavobacteriaceae; g__FlavobacteriaceaeFA;
 o__Cytophagales; f__Flammeovirgaceae; g__Reichenbachiella;

icteria; o__Sphingomonadales; f__Erythrobacteraceae; g__Erythrobacter;
 o__Flavobacteriales; f__FlavobacterialesOR; g__FlavobacterialesOR;
 _Cytophagales; f__Flammeovirgaceae; g__Reichenbachella;
 icteria; o__Sphingomonadales; f__Erythrobacteraceae; g__Erythrobacter;
 o__Flavobacteriales; f__Flavobacteriaceae; g__Psychroserpens;
 bacteria; o__Alteromonadales; f__Alteromonadaceae; g__Marinobacter;
 12CL; f__SAR202CL; g__SAR202CL;
 bacteria; o__Oceanospirillales; f__OceanospirillalesOR; g__OceanospirillalesOR;
 o__Flavobacteriales; f__Flavobacteriaceae; g__Maribacter;
 cteria; o__Desulfobacterales; f__Nitrospinae; g__Nitrospina;
 bacteria; o__Alteromonadales; f__Colwelliaceae; g__ColwelliaceaeFA;
 icteria; o__AlphaproteobacteriaCL; f__AlphaproteobacteriaCL; g__AlphaproteobacteriaCL;
 icteria; o__AlphaproteobacteriaCL; f__AlphaproteobacteriaCL; g__AlphaproteobacteriaCL;
 e; o__Phycisphaerales; f__PhycisphaeralesOR; g__PhycisphaeralesOR;
 bacteria; o__Oceanospirillales; f__Oceanospirillaceae; g__OceanospirillaceaeFA;
 bacteria; o__Oceanospirillales; f__Oceanospirillaceae; g__OceanospirillaceaeFA;
 bacteria; o__Alteromonadales; f__Psychromonadaceae; g__PsychromonadaceaeFA;
 bacteria; o__Thiohalorhabdales; f__ThiohalorhabdalesOR; g__ThiohalorhabdalesOR;
 bacteria; o__Alteromonadales; f__Alteromonadaceae; g__Glaciecola;
 bacteria; o__Alteromonadales; f__Alteromonadaceae; g__Candidatus Endobugula;
 bacteria; o__Vibrionales; f__Pseudoalteromonadaceae; g__Pseudoalteromonas;
 _Cytophagales; f__Flammeovirgaceae; g__Flexibacter;
 o__Flavobacteriales; f__FlavobacterialesOR; g__FlavobacterialesOR;
 o__Flavobacteriales; f__Cryomorphaceae; g__Crocinitomix;
 BD1-5CL; g__BD1-5CL;
 bacteria; o__Alteromonadales; f__Alteromonadaceae; g__Alteromonas;
 o__Flavobacteriales; f__Flavobacteriaceae; g__Winogradskyella;
 o__Flavobacteriales; f__Flavobacteriaceae; g__Ulvibacter;
 bacteria; o__Oceanospirillales; f__Saccharospirillaceae; g__SaccharospirillaceaeFA;
 o__Flavobacteriales; f__Flavobacteriaceae; g__Polaribacter;
 bacteria; o__Alteromonadales; f__Colwelliaceae; g__Colwellia;
 bacteria; o__Oceanospirillales; f__Halomonadaceae; g__Candidatus Portiera;
 ia; o__Pirellulales; f__Pirellulaceae; g__PirellulaceaeFA;
 bacteria; o__Oceanospirillales; f__Oceanospirillaceae; g__OceanospirillaceaeFA;
 bacteria; o__Oceanospirillales; f__Oceanospirillaceae; g__OceanospirillaceaeFA;
 bacteria; o__Oceanospirillales; f__Oceanospirillaceae; g__OceanospirillaceaeFA;
 bacteria; o__Oceanospirillales; f__Oceanospirillaceae; g__OceanospirillaceaeFA;
 bacteria; o__Alteromonadales; f__Alteromonadaceae; g__AlteromonadaceaeFA;
 bacteria; o__Alteromonadales; f__Alteromonadaceae; g__Candidatus Endobugula;
 icteria; o__Rickettsiales; f__RickettsialesOR; g__RickettsialesOR;
 bacteria; o__Oceanospirillales; f__OceanospirillalesOR; g__OceanospirillalesOR;
 o__Flavobacteriales; f__Flavobacteriaceae; g__FlavobacteriaceaeFA;
 o__Flavobacteriales; f__Flavobacteriaceae; g__FlavobacteriaceaeFA;
 o__Flavobacteriales; f__Flavobacteriaceae; g__FlavobacteriaceaeFA;
 o__Flavobacteriales; f__Flavobacteriaceae; g__FlavobacteriaceaeFA;
 bacteria; o__Alteromonadales; f__Alteromonadaceae; g__Glaciecola;
 __Fibrobacterales; f__FibrobacteralesOR; g__FibrobacteralesOR;

__Fibrobacterales; f__FibrobacteralesOR; g__FibrobacteralesOR;
 __Fibrobacterales; f__FibrobacteralesOR; g__FibrobacteralesOR;
 __Fibrobacterales; f__FibrobacteralesOR; g__FibrobacteralesOR;
 bacteria; o__Legionellales; f__Francisellaceae; g__FrancisellaceaeFA;
 bacteria; o__Legionellales; f__Francisellaceae; g__FrancisellaceaeFA;
 bacteria; o__Legionellales; f__Francisellaceae; g__FrancisellaceaeFA;
 bacteria; o__Legionellales; f__Francisellaceae; g__FrancisellaceaeFA;
 bacteria; o__Thiotrichales; f__Piscirickettsiaceae; g__PiscirickettsiaceaeFA;
 bacteria; o__Thiotrichales; f__Piscirickettsiaceae; g__PiscirickettsiaceaeFA;
 bacteria; o__Thiotrichales; f__Piscirickettsiaceae; g__PiscirickettsiaceaeFA;
 bacteria; o__Thiotrichales; f__Piscirickettsiaceae; g__PiscirickettsiaceaeFA;
 c__Flavobacteriales; f__Flavobacteriaceae; g__FlavobacteriaceaeFA;
 bacteria; o__Alteromonadales; f__Colwelliaceae; g__ColwelliaceaeFA;
 ta; o__Cenarchaeales; f__Cenarchaeaceae; g__Nitrosopumilus;
 bacteria; o__Pseudomonadales; f__Moraxellaceae; g__Perlucidibaca;
 c__Flavobacteriales; f__FlavobacterialesOR; g__FlavobacterialesOR;
 c__Flavobacteriales; f__Cryomorphaceae; g__CryomorphaceaeFA;
 bacteria; o__Alteromonadales; f__Colwelliaceae; g__ColwelliaceaeFA;
 bacteria; o__Alteromonadales; f__Colwelliaceae; g__ColwelliaceaeFA;
 bacteria; o__Alteromonadales; f__Colwelliaceae; g__ColwelliaceaeFA;
 bacteria; o__Alteromonadales; f__Colwelliaceae; g__ColwelliaceaeFA;
 c__Flavobacteriales; f__Flavobacteriaceae; g__FlavobacteriaceaeFA;
 ta; o__Cenarchaeales; f__Cenarchaeaceae; g__Nitrosopumilus;
 c__Flavobacteriales; f__Flavobacteriaceae; g__Polaribacter;
 bacteria; o__Alteromonadales; f__Alteromonadaceae; g__Marinobacter;
 o__Acidimicrobiales; f__TK06; g__TK06FA;
 c__Flavobacteriales; f__FlavobacterialesOR; g__FlavobacterialesOR;
 bacteria; o__Alteromonadales; f__Colwelliaceae; g__ColwelliaceaeFA;
 icteria; o__AlphaproteobacteriaCL; f__AlphaproteobacteriaCL; g__AlphaproteobacteriaCL;
 icteria; o__AlphaproteobacteriaCL; f__AlphaproteobacteriaCL; g__AlphaproteobacteriaCL;
 c__Flavobacteriales; f__Flavobacteriaceae; g__Polaribacter;

bacteria; o__Pseudomonadales; f__Pseudomonadaceae; g__Pseudomonas;
 ia; o__Pirellulales; f__Pirellulaceae; g__PirellulaceaeFA;
 bacteria; o__Pseudomonadales; f__Pseudomonadaceae; g__Pseudomonas;
 bacteria; o__Alteromonadales; f__Colwelliaceae; g__ColwelliaceaeFA;
 c__Flavobacteriales; f__Flavobacteriaceae; g__Polaribacter;
 bacteria; o__Pseudomonadales; f__Pseudomonadaceae; g__Pseudomonas;
 icteria; o__Rickettsiales; f__RickettsialesOR; g__RickettsialesOR;
 c__Flavobacteriales; f__Flavobacteriaceae; g__Ulvibacter;
 c__Flavobacteriales; f__FlavobacterialesOR; g__FlavobacterialesOR;
 bacteria; o__GammaproteobacteriaCL; f__GammaproteobacteriaCL; g__GammaproteobacteriaCL;
 c__Flavobacteriales; f__NS9; g__NS9FA;
 c__Flavobacteriales; f__NS9; g__NS9FA;
 bacteria; o__Alteromonadales; f__Colwelliaceae; g__ColwelliaceaeFA;
 icteria; o__Methylophilales; f__Methylophilaceae; g__MethylophilaceaeFA;
 ia; o__Pirellulales; f__Pirellulaceae; g__PirellulaceaeFA;

bacteria; o__Alteromonadales; f__Alteromonadaceae;
 icteria; o__Rhodospirillales; f__Rhodospirillaceae; g__RhodospirillaceaeFA;
 icteria; o__Rhodobacterales; f__Rhodobacteraceae; g__Phaeobacter;
 o__Flavobacteriales; f__Cryomorphaceae; g__Crocinitomix;
 bacteria; o__Alteromonadales; f__Alteromonadaceae; g__Candidatus Endobugula;
 bacteria; o__Alteromonadales; f__Psychromonadaceae; g__PsychromonadaceaeFA;
 icteria; o__Rhodobacterales; f__Rhodobacteraceae; g__Octadecabacter;
 bacteria; o__Alteromonadales; f__Alteromonadaceae; g__Glaciecola;
 o__Flavobacteriales; f__Flavobacteriaceae; g__Polaribacter;
 bacteria; o__Alteromonadales; f__Colwelliaceae; g__ColwelliaceaeFA;
 icteria; o__Rhodobacterales; f__Rhodobacteraceae; g__Phaeobacter;
 ta; o__E2; f__Marine group II; g__Marine group IIFA;
 bacteria; o__Alteromonadales; f__Colwelliaceae; g__ColwelliaceaeFA;
 bacteria; o__Alteromonadales; f__Alteromonadaceae; g__Marinobacter;
 cillales; f__Carnobacteriaceae; g__Carnobacterium;
 I2CL; f__SAR202CL; g__SAR202CL;
 I2CL; f__SAR202CL; g__SAR202CL;
 I2CL; f__SAR202CL; g__SAR202CL;
 [Saprospirales]; f__Saprospiraceae; g__Lewinella;
 icteria; o__AlphaproteobacteriaCL; f__AlphaproteobacteriaCL; g__AlphaproteobacteriaCL;
 bacteria; o__Oceanospirillales; f__Oceanospirillaceae; g__OceanospirillaceaeFA;
 o__Acidimicrobiales; f__SC3-41; g__SC3-41FA;
 o__Acidimicrobiales; f__SC3-41; g__SC3-41FA;
 o__Acidimicrobiales; f__SC3-41; g__SC3-41FA;
 bacteria; o__Oceanospirillales; f__Halomonadaceae; g__Candidatus Portiera;
 bacteria; o__Oceanospirillales; f__OceanospirillalesOR; g__OceanospirillalesOR;
 bacteria; o__Oceanospirillales; f__OceanospirillalesOR; g__OceanospirillalesOR;
 bacteria; o__Oceanospirillales; f__OceanospirillalesOR; g__OceanospirillalesOR;
 [Saprospirales]; f__Saprospiraceae; g__Lewinella;
 bacteria; o__Alteromonadales; f__Alteromonadaceae; g__Candidatus Endobugula;
 bacteria; o__Alteromonadales; f__Alteromonadaceae; g__Candidatus Endobugula;
 o__Flavobacteriales; f__Flavobacteriaceae; g__FlavobacteriaceaeFA;
 icteria; o__Rickettsiales; f__RickettsialesOR; g__RickettsialesOR;
 icteria; o__Rickettsiales; f__RickettsialesOR; g__RickettsialesOR;
 icteria; o__Rickettsiales; f__RickettsialesOR; g__RickettsialesOR;
 ta; o__E2; f__Marine group II; g__Marine group IIFA;
 ta; o__E2; f__Marine group II; g__Marine group IIFA;
 ta; o__E2; f__Marine group II; g__Marine group IIFA;
 __Fibrobacterales; f__FibrobacteralesOR; g__FibrobacteralesOR;
 bacteria; o__Legionellales; f__Francisellaceae; g__FrancisellaceaeFA;
 acteria; o__Campylobacterales; f__Campylobacteraceae; g__Arcobacter;
 acteria; o__Campylobacterales; f__Campylobacteraceae; g__Arcobacter;
 acteria; o__Campylobacterales; f__Campylobacteraceae; g__Arcobacter;
 bacteria; o__Thiotrichales; f__Piscirickettsiaceae; g__PiscirickettsiaceaeFA;
 cteria; o__Myxococcales; f__OM27; g__OM27FA;
 cteria; o__Myxococcales; f__OM27; g__OM27FA;
 cteria; o__Myxococcales; f__OM27; g__OM27FA;

o__Flavobacteriales; f__Cryomorphaceae; g__Fluviicola;
 o__Flavobacteriales; f__Flavobacteriaceae; g__Ulvibacter;
 o__Flavobacteriales; f__NS9; g__NS9FA;
 o__Flavobacteriales; f__FlavobacterialesOR; g__FlavobacterialesOR;
 ia; o__Pirellulales; f__Pirellulaceae; g__PirellulaceaeFA;
 tertia; o__Methylophilales; f__Methylophilaceae; g__Methylostenobacter;
 tertia; o__Methylophilales; f__Methylophilaceae; g__Methylostenobacter;
 tertia; o__Methylophilales; f__Methylophilaceae; g__Methylostenobacter;
 bacteria; o__Alteromonadales; f__Colwelliaceae; g__ColwelliaceaeFA;
 icteria; o__Rhodospirillales; f__Rhodospirillaceae; g__RhodospirillaceaeFA;
 icteria; o__Rhodospirillales; f__Rhodospirillaceae; g__RhodospirillaceaeFA;
 icteria; o__Rhodospirillales; f__Rhodospirillaceae; g__RhodospirillaceaeFA;
 bacteria; o__Alteromonadales; f__HTCC2188; g__HTCC;
 bacteria; o__Alteromonadales; f__HTCC2188; g__HTCC;
 bacteria; o__Alteromonadales; f__HTCC2188; g__HTCC;
 cteria; o__Desulfobacterales; f__Nitrospiraceae; g__Nitrospina;
 _Cytophagales; f__Flammeovirgaceae; g__Flexibacter;
 bacteria; o__Oceanospirillales; f__Halomonadaceae; g__Candidatus Portiera;
 bacteria; o__Alteromonadales; f__AlteromonadalesOR; g__AlteromonadalesOR;
 o__Flavobacteriales; f__Flavobacteriaceae; g__Psychroserpens;
 _Puniceicoccales; f__Puniceicoccaceae; g__Coralimargarita;
 bacteria; o__Oceanospirillales; f__Oceanospirillaceae; g__OceanospirillaceaeFA;
 o__Flavobacteriales; f__Flavobacteriaceae; g__Ulvibacter;
 o__Flavobacteriales; f__Flavobacteriaceae; g__FlavobacteriaceaeFA;
 o__Flavobacteriales; f__NS9; g__NS9FA;
 o__Flavobacteriales; f__NS9; g__NS9FA;
 o__Flavobacteriales; f__Flavobacteriaceae; g__Polaribacter;
 _Cytophagales; f__Flammeovirgaceae; g__Flexibacter;
 obiae; o__Verrucomicrobiales; f__Verrucomicrobiaceae; g__Rubritalea;
 bacteria; o__Alteromonadales; f__Alteromonadaceae; g__Candidatus Endobugula;

cteria; o__Desulfobacterales; f__Nitrospiraceae; g__Nitrospina;
 icteria; o__Rhodospirillales; f__Rhodospirillaceae; g__RhodospirillaceaeFA;
 o__Flavobacteriales; f__NS9; g__NS9FA;
 o__Flavobacteriales; f__NS9; g__NS9FA;
 _Cytophagales; f__Flammeovirgaceae; g__Roseivirga;
 bacteria; o__Alteromonadales; f__Colwelliaceae; g__ColwelliaceaeFA;
 bacteria; o__Alteromonadales; f__Alteromonadaceae;
 o__Flavobacteriales; f__FlavobacterialesOR; g__FlavobacterialesOR;
 o__Flavobacteriales; f__NS9; g__NS9FA;
 bacteria; o__Oceanospirillales; f__Saccharospirillaceae; g__SaccharospirillaceaeFA;
 o__Flavobacteriales; f__FlavobacterialesOR; g__FlavobacterialesOR;
 bacteria; o__GammaproteobacteriaCL; f__GammaproteobacteriaCL; g__GammaproteobacteriaCL;
 ta; o__Cenarchaeales; f__Cenarchaeaceae; g__Nitrosopumilus;
 _Puniceicoccales; f__Puniceicoccaceae; g__Coralimargarita;
 bacteria; o__Oceanospirillales; f__Halomonadaceae; g__Candidatus Portiera;
 o__Flavobacteriales; f__FlavobacterialesOR; g__FlavobacterialesOR;

bacteria; o__Oceanospirillales; f__OceanospirillalesOR; g__OceanospirillalesOR;
 cteria; o__NB1-j; f__JTB38; g__JTB38FA;
 bacteria; o__Vibrionales; f__Pseudoalteromonadaceae; g__Pseudoalteromonas;
 bacteria; o__Alteromonadales; f__Colwelliaceae; g__ColwelliaceaeFA;
 o__Flavobacteriales; f__Flavobacteriaceae; g__FlavobacteriaceaeFA;
 _Puniceococcales; f__Puniceicoccaceae; g__Coralimargarita;
 bacteria; o__Alteromonadales; f__Colwelliaceae; g__ColwelliaceaeFA;
 _Puniceococcales; f__Puniceicoccaceae; g__Coralimargarita;
 bacteria; o__Alteromonadales; f__Alteromonadaceae; g__Marinobacter;
 bacteria; o__Alteromonadales; f__Alteromonadaceae; g__Marinobacter;
 I2CL; f__SAR202CL; g__SAR202CL;
 _[Saprospirales]; f__Saprospiraceae; g__Lewinella;
 bacteria; o__Oceanospirillales; f__Halomonadaceae; g__Candidatus Portiera;
 icteria; o__Rickettsiales; f__RickettsialesOR; g__RickettsialesOR;
 o__Flavobacteriales; f__Cryomorphaceae; g__CryomorphaceaeFA;
 __vadinHA49CL; f__vadinHA49CL; g__vadinHA49CL;
 bacteria; o__Oceanospirillales; f__Saccharospirillaceae; g__SaccharospirillaceaeFA;
 bacteria; o__Pseudomonadales; f__Pseudomonadaceae; g__Pseudomonas;
 o__Flavobacteriales; f__Flavobacteriaceae; g__Polaribacter;
 _[Saprospirales]; f__Saprospiraceae; g__Saprospira;
 bacteria; o__Alteromonadales; f__Colwelliaceae; g__ColwelliaceaeFA;
 bacteria; o__Oceanospirillales; f__SUP05; g__SUP05FA;
 bacteria; o__Pseudomonadales; f__Moraxellaceae; g__Psychrobacter;
 ta; o__E2; f__Marine group II; g__Marine group IIFA;
 o__Flavobacteriales; f__Flavobacteriaceae; g__Ulvibacter;
 bacteria; o__Oceanospirillales; f__Halomonadaceae; g__Candidatus Portiera;
 o__Flavobacteriales; f__Flavobacteriaceae; g__FlavobacteriaceaeFA;
 o__Flavobacteriales; f__Flavobacteriaceae; g__FlavobacteriaceaeFA;
 __Fibrobacterales; f__FibrobacteralesOR; g__FibrobacteralesOR;
 bacteria; o__Legionellales; f__Francisellaceae; g__FrancisellaceaeFA;
 bacteria; o__Thiotrichales; f__Piscirickettsiaceae; g__PiscirickettsiaceaeFA;
 o__Flavobacteriales; f__Flavobacteriaceae; g__FlavobacteriaceaeFA;
 ; f__A714017; g__SGSH944;
 ; f__A714017; g__SGSH944;
 ita; o__Cenarchaeales; f__Cenarchaeaceae; g__CenarchaeaceaeFA;
 ertia; o__Burkholderiales; f__Comamonadaceae; g__Curvibacter;
 bacteria; o__Alteromonadales; f__Alteromonadaceae; g__Candidatus Endobugula;
 o__Flavobacteriales; f__Flavobacteriaceae; g__FlavobacteriaceaeFA;
 o__Flavobacteriales; f__Flavobacteriaceae; g__FlavobacteriaceaeFA;
 o__Flavobacteriales; f__Flavobacteriaceae; g__FlavobacteriaceaeFA;
 bacteria; o__Alteromonadales; f__Colwelliaceae; g__ColwelliaceaeFA;
 icteria; o__AlphaproteobacteriaCL; f__AlphaproteobacteriaCL; g__AlphaproteobacteriaCL;
 cteria; o__Desulfobacterales; f__Nitrospinae; g__Nitrospina;
 ia; o__Pirellulales; f__Pirellulaceae; g__PirellulaceaeFA;
 _[Saprospirales]; f__Saprospiraceae; g__Lewinella;
 bacteria; o__Oceanospirillales; f__Halomonadaceae; g__Candidatus Portiera;
 bacteria; o__Oceanospirillales; f__Oceanospirillaceae; g__OceanospirillaceaeFA;

o__Flavobacteriales; f__FlavobacterialesOR; g__FlavobacterialesOR;
 bacteria; o__Alteromonadales; f__Alteromonadaceae; g__Glaciecola;
 icteria; o__Sphingomonadales; f__Erythrobacteraceae; g__Erythrobacter;
 i__[Saprospirales]; f__Saprospiraceae; g__SaprospiraceaeFA;
 icteria; o__Rickettsiales; f__RickettsialesOR; g__RickettsialesOR;
 bacteria; o__Oceanospirillales; f__Oceanospirillaceae; g__OceanospirillaceaeFA;
 ita; o__Cenarchaeales; f__Cenarchaeaceae; g__Nitrosopumilus;
 o__Flavobacteriales; f__FlavobacterialesOR; g__FlavobacterialesOR;
 o__Flavobacteriales; f__Flavobacteriaceae; g__Winogradskyella;
 bacteria; o__Campylobacterales; f__Campylobacteraceae; g__Arcobacter;
 bacteria; o__Alteromonadales; f__Alteromonadaceae; g__AlteromonadaceaeFA;
 obiae; o__Verrucomicrobiales; f__Verrucomicrobiaceae; g__VerrucomicrobiaceaeFA;
 obiae; o__Verrucomicrobiales; f__Verrucomicrobiaceae; g__VerrucomicrobiaceaeFA;
 obiae; o__Verrucomicrobiales; f__Verrucomicrobiaceae; g__Rubritalea;
 o__Flavobacteriales; f__Flavobacteriaceae; g__Polaribacter;
 o__Flavobacteriales; f__FlavobacterialesOR; g__FlavobacterialesOR;
 bacteria; o__Alteromonadales; f__Alteromonadaceae; g__AlteromonadaceaeFA;
 obiae; o__Verrucomicrobiales; f__Verrucomicrobiaceae; g__Rubritalea;
 ita; o__Cenarchaeales; f__Cenarchaeaceae; g__Nitrosopumilus;
 _Cytophagales; f__Flammeovirgaceae; g__Flexibacter;
 bacteria; o__Alteromonadales; f__OM60; g__OM60FA;
 o__Flavobacteriales; f__Flavobacteriaceae; g__Polaribacter;
 o__Flavobacteriales; f__Flavobacteriaceae; g__Polaribacter;
 i__[Saprospirales]; f__Saprospiraceae; g__Lewinella;
 i__[Saprospirales]; f__Saprospiraceae; g__Lewinella;
 bacteria; o__Alteromonadales; f__Colwelliaceae; g__ColwelliaceaeFA;
 icteria; o__Sphingomonadales; f__Erythrobacteraceae; g__Erythrobacter;
 a; o__Sphingobacteriales; f__SphingobacterialesOR; g__SphingobacterialesOR;
 bacteria; o__Oceanospirillales; f__Oceanospirillaceae; g__OceanospirillaceaeFA;
 cteria; o__NB1-j; f__JTB38; g__JTB38FA;
 ita; o__Cenarchaeales; f__Cenarchaeaceae; g__Nitrosopumilus;
 bacteria; o__Oceanospirillales; f__OceanospirillalesOR; g__OceanospirillalesOR;
 icteria; o__Rickettsiales; f__RickettsialesOR; g__RickettsialesOR;
 bacteria; o__Oceanospirillales; f__Oceanospirillaceae; g__Amphritea;
 bacteria; o__Alteromonadales; f__Alteromonadaceae; g__Glaciecola;
 o__Flavobacteriales; f__Cryomorphaceae; g__CryomorphaceaeFA;
 o__Flavobacteriales; f__FlavobacterialesOR; g__FlavobacterialesOR;
 o__Acidimicrobiales; f__SC3-41; g__SC3-41FA;
 bacteria; o__Oceanospirillales; f__Halomonadaceae; g__Candidatus Portiera;
 bacteria; o__Oceanospirillales; f__Halomonadaceae; g__Candidatus Portiera;
 bacteria; o__Alteromonadales; f__Colwelliaceae; g__ColwelliaceaeFA;
 bacteria; o__Oceanospirillales; f__OceanospirillalesOR; g__OceanospirillalesOR;
 bacteria; o__Alteromonadales; f__Alteromonadaceae;
 bacteria; o__Oceanospirillales; f__OceanospirillalesOR; g__OceanospirillalesOR;
 icteria; o__Rhodobacterales; f__Rhodobacteraceae; g__Octadecabacter;
 o__Flavobacteriales; f__Cryomorphaceae; g__Owenweeksia;
 icteria; o__Rhodobacterales; f__Rhodobacteraceae;

acteria; o__Rhodobacterales; f__Rhodobacteraceae; g__RhodobacteraceaeFA;
bacteria; o__Alteromonadales; f__Alteromonadaceae; g__AlteromonadaceaeFA;
o__Flavobacteriales; f__FlavobacterialesOR; g__FlavobacterialesOR;
obiae; o__Verrucomicrobiales; f__Verrucomicrobiaceae; g__Rubritalea;
ta; o__Cenarchaeales; f__Cenarchaeaceae; g__CenarchaeaceaeFA;
obiae; o__Verrucomicrobiales; f__Verrucomicrobiaceae; g__VerrucomicrobiaceaeFA;
acteria; o__Rhodobacterales; f__Rhodobacteraceae; g__Octadecabacter;
o__Flavobacteriales; f__Flavobacteriaceae; g__FlavobacteriaceaeFA;
o__Flavobacteriales; f__Flavobacteriaceae; g__FlavobacteriaceaeFA;
acteria; o__Rickettsiales; f__RickettsialesOR; g__RickettsialesOR;
a; o__Sphingobacteriales; f__SphingobacterialesOR; g__SphingobacterialesOR;
ta; o__E2; f__Marine group II; g__Marine group IIFA;
__Fibrobacterales; f__FibrobacteralesOR; g__FibrobacteralesOR;
bacteria; o__Legionellales; f__Francisellaceae; g__FrancisellaceaeFA;
acteria; o__Sva0853; f__JTB36; g__JTB36FA;
acteria; o__Campylobacterales; f__Campylobacteraceae; g__Arcobacter;
bacteria; o__Thiotrichales; f__Piscirickettsiaceae; g__PiscirickettsiaceaeFA;
acteria; o__Myxococcales; f__OM27; g__OM27FA;
o__Flavobacteriales; f__Cryomorphaceae; g__Fluviicola;
o__Flavobacteriales; f__Cryomorphaceae; g__Fluviicola;
o__Flavobacteriales; f__Cryomorphaceae; g__Fluviicola;
ia; o__Pirellulales; f__Pirellulaceae; g__PirellulaceaeFA;
acteria; o__Rhodospirillales; f__Rhodospirillaceae; g__RhodospirillaceaeFA;
bacteria; o__Alteromonadales; f__Alteromonadaceae; g__Candidatus Endobugula;
bacteria; o__Oceanospirillales; f__Halomonadaceae; g__Candidatus Portiera;
bacteria; o__Alteromonadales; f__Alteromonadaceae; g__AlteromonadaceaeFA;
o__Flavobacteriales; f__NS9; g__NS9FA;
o__Flavobacteriales; f__FlavobacterialesOR; g__FlavobacterialesOR;
acteria; o__Rhodobacterales; f__Rhodobacteraceae; g__Paracoccus;
bacteria; o__Alteromonadales; f__HTCC2188; g__HTCC;
o__Flavobacteriales; f__FlavobacterialesOR; g__FlavobacterialesOR;
acteria; o__NB1-j; f__JTB38; g__JTB38FA;
o__Flavobacteriales; f__FlavobacterialesOR; g__FlavobacterialesOR;
e; o__Phycisphaerales; f__PhycisphaeralesOR; g__PhycisphaeralesOR;
acteria; o__Burkholderiales; f__Comamonadaceae; g__Methylibium;
bacteria; o__Oceanospirillales; f__Oceanospirillaceae; g__OceanospirillaceaeFA;
acteria; o__Methylophilales; f__Methylophilaceae; g__Methylophilales;
acteria; o__Rhodospirillales; f__Rhodospirillaceae; g__RhodospirillaceaeFA;
o__Flavobacteriales; f__Flavobacteriaceae; g__FlavobacteriaceaeFA;
bacteria; o__Alteromonadales; f__HTCC2188; g__HTCC;
o__Flavobacteriales; f__FlavobacterialesOR; g__FlavobacterialesOR;
bacteria; o__GammaproteobacteriaCL; f__GammaproteobacteriaCL; g__GammaproteobacteriaCL;

o__Flavobacteriales; f__Flavobacteriaceae; g__Polaribacter;

o__[Saprospirales]; f__Saprospiraceae; g__Lewinella;
 bacteria; o__Rickettsiales; f__RickettsialesOR; g__RickettsialesOR;
 bacteria; o__Alteromonadales; f__AlteromonadalesOR; g__AlteromonadalesOR;
 o__Flavobacteriales; f__Flavobacteriaceae; g__FlavobacteriaceaeFA;
 bacteria; o__Rhodobacterales; f__Rhodobacteraceae; g__Loktanella;
 OM190CL; f__OM190CL; g__OM190CL;
 o__Flavobacteriales; f__Flavobacteriaceae; g__FlavobacteriaceaeFA;
 bacteria; o__Rickettsiales; f__RickettsialesOR; g__RickettsialesOR;
 bacteria; o__Alteromonadales; f__Idiomarinaceae; g__Idiomarina;
 bacteria; o__Burkholderiales; f__Comamonadaceae; g__Schlegelella;
 o__Flavobacteriales; f__FlavobacterialesOR; g__FlavobacterialesOR;
 o__Acidimicrobiales; f__SC3-41; g__SC3-41FA;
 o__Flavobacteriales; f__Flavobacteriaceae; g__FlavobacteriaceaeFA;
 o__Flavobacteriales; f__Cryomorphaceae; g__Crocinitomix;
 bacteria; o__Rhodobacterales; f__Rhodobacteraceae; g__Octadecabacter;
 ita; o__Cenarchaeales; f__Cenarchaeaceae; g__Nitrosopumilus;
 obiae; o__Verrucomicrobiales; f__Verrucomicrobiaceae; g__Rubritalea;
 o__Flavobacteriales; f__FlavobacterialesOR; g__FlavobacterialesOR;
 bacteria; o__AlphaproteobacteriaCL; f__AlphaproteobacteriaCL; g__AlphaproteobacteriaCL;
 bacteria; o__Alteromonadales; f__Alteromonadaceae; g__Candidatus Endobugula;
 bacteria; o__Oceanospirillales; f__Oceanospirillaceae; g__OceanospirillaceaeFA;
 bacteria; o__Sphingomonadales; f__Sphingomonadaceae; g__Sphingobium;
 _Cytophagales; f__Flammeovirgaceae; g__FlammeovirgaceaeFA;
 bacteria; o__Alteromonadales; f__AlteromonadalesOR; g__AlteromonadalesOR;
 bacteria; o__Alteromonadales; f__Colwelliaceae; g__Colwellia;
 o__Flavobacteriales; f__Flavobacteriaceae; g__Ulvibacter;
 bacteria; o__Alteromonadales; f__Alteromonadaceae; g__Alteromonas;
 ; o__Gemm-2CL; f__Gemm-2CL; g__Gemm-2CL;
 o__Flavobacteriales; f__Flavobacteriaceae; g__FlavobacteriaceaeFA;
 ; o__Lentisphaerales; f__Lentisphaeraceae; g__Lentisphaera;
 bacteria; o__Alteromonadales; f__Colwelliaceae; g__ColwelliaceaeFA;
 o__Flavobacteriales; f__Flavobacteriaceae; g__Polaribacter;
 ita; o__Cenarchaeales; f__Cenarchaeaceae; g__Nitrosopumilus;
 o__Flavobacteriales; f__Flavobacteriaceae; g__FlavobacteriaceaeFA;
 o__[Saprospirales]; f__Saprospiraceae; g__Lewinella;
 o__Flavobacteriales; f__Flavobacteriaceae; g__Polaribacter;
 bacteria; o__Rhizobiales; f__Bradyrhizobiaceae; g__Bradyrhizobium;
 bacteria; o__Alteromonadales; f__Alteromonadaceae; g__Candidatus Endobugula;
 ; f__A714017; g__SGSH944;
 o__Flavobacteriales; f__Flavobacteriaceae; g__FlavobacteriaceaeFA;
 o__Flavobacteriales; f__Flavobacteriaceae; g__FlavobacteriaceaeFA;

 bacteria; o__Oceanospirillales; f__Halomonadaceae; g__Candidatus Portiera;
 bacteria; o__Oceanospirillales; f__Halomonadaceae; g__Halomonas;
 o__Acidimicrobiales; f__SC3-41; g__SC3-41FA;

 bacteria; o__Alteromonadales; f__Colwelliaceae; g__ColwelliaceaeFA;

o__Flavobacteriales; f__Flavobacteriaceae; g__Polaribacter;
 cteria; o__PB19; f__PB19OR; g__PB19OR;
 bacteria; o__Alteromonadales; f__Colwelliaceae; g__ColwelliaceaeFA;
 bacteria; o__Alteromonadales; f__Shewanellaceae; g__Shewanella;
 bacteria; o__Alteromonadales; f__Colwelliaceae; g__ColwelliaceaeFA;
 ta; o__Cenarchaeales; f__Cenarchaeaceae; g__Nitrosopumilus;
 o__Flavobacteriales; f__Flavobacteriaceae; g__FlavobacteriaceaeFA;
 __ChlamydiaePH; f__ChlamydiaePH; g__ChlamydiaePH;
 bacteria; o__Thiotrichales; f__Thiotrichaceae; g__Cocleimonas;
 __Cytophagales; f__Flammeovirgaceae; g__FlammeovirgaceaeFA;
 __[Saprospirales]; f__Saprospiraceae; g__SaprospiraceaeFA;
 o__Flavobacteriales; f__Flavobacteriaceae; g__Polaribacter;
 e; o__Phycisphaerales; f__PhycisphaeralesOR; g__PhycisphaeralesOR;
 bacteria; o__Vibrionales; f__Pseudoalteromonadaceae; g__Pseudoalteromonas;
 ia; o__Pirellulales; f__Pirellulaceae; g__PirellulaceaeFA;
 o__Flavobacteriales; f__Cryomorphaceae; g__Crocinitomix;
 o__Flavobacteriales; f__Cryomorphaceae; g__Crocinitomix;
 o__Flavobacteriales; f__FlavobacterialesOR; g__FlavobacterialesOR;
 bacteria; o__Burkholderiales; f__Comamonadaceae; g__Curvibacter;
 o__Flavobacteriales; f__Flavobacteriaceae; g__FlavobacteriaceaeFA;
 ta; o__Cenarchaeales; f__Cenarchaeaceae; g__Nitrosopumilus;
 o__Flavobacteriales; f__Flavobacteriaceae; g__FlavobacteriaceaeFA;
 bacteria; o__Thiotrichales; f__Piscirickettsiaceae; g__PiscirickettsiaceaeFA;
 e; o__Phycisphaerales; f__PhycisphaeralesOR; g__PhycisphaeralesOR;
 bacteria; o__Alteromonadales; f__Shewanellaceae; g__Shewanella;
 o__Flavobacteriales; f__Flavobacteriaceae; g__Ulvibacter;
 bacteria; o__Rickettsiales; f__RickettsialesOR; g__RickettsialesOR;
 bacteria; o__Alteromonadales; f__Alteromonadaceae; g__AlteromonadaceaeFA;
 ; f__A714017; g__SargSea-WGS;
 bacteria; o__Rickettsiales; f__RickettsialesOR; g__RickettsialesOR;
 bacteria; o__Oceanospirillales; f__Halomonadaceae; g__Halomonas;
 o__Flavobacteriales; f__Flavobacteriaceae; g__Polaribacter;
 o__Acidimicrobiales; f__OCS155; g__OCS155FA;
 ta; o__E2; f__Marine group II; g__Marine group IIFA;
 o__Flavobacteriales; f__FlavobacterialesOR; g__FlavobacterialesOR;
 __ChlamydiaePH; f__ChlamydiaePH; g__ChlamydiaePH;
 OM190CL; f__OM190CL; g__OM190CL;
 bacteria; o__Rickettsiales; f__RickettsialesOR; g__RickettsialesOR;
 o__Flavobacteriales; f__Flavobacteriaceae; g__FlavobacteriaceaeFA;
 o__Acidimicrobiales; f__TK06; g__TK06FA;
 bacteria; o__Alteromonadales; f__Alteromonadaceae; g__Glaciecola;
 o__Flavobacteriales; f__FlavobacterialesOR; g__FlavobacterialesOR;
 bacteria; o__[Marinicellales]; f__[Marinicellaceae]; g__Marinicella;
 ia; o__Pirellulales; f__Pirellulaceae; g__PirellulaceaeFA;
 ta; o__Cenarchaeales; f__Cenarchaeaceae; g__Nitrosopumilus;
 bacteria; o__Rhodobacterales; f__Rhodobacteraceae;
 ta; o__E2; f__Marine group II; g__Marine group IIFA;

bacteria; o__Alteromonadales; f__AlteromonadalesOR; g__AlteromonadalesOR;
 bacteria; o__Alteromonadales; f__HTCC2188; g__HTCC;
 f__[Saprospirales]; f__Saprospiraceae; g__SaprospiraceaeFA;
 o__Flavobacteriales; f__Flavobacteriaceae; g__Flavobacterium;
 bacteria; o__Rhodospirillales; f__Rhodospirillaceae; g__RhodospirillaceaeFA;
 o__Flavobacteriales; f__Flavobacteriaceae; g__FlavobacteriaceaeFA;
 bacteria; o__Vibrionales; f__Pseudoalteromonadaceae; g__Pseudoalteromonas;
 o__Flavobacteriales; f__Flavobacteriaceae; g__Ulvibacter;
 o__Flavobacteriales; f__Flavobacteriaceae; g__Polaribacter;
 o__Flavobacteriales; f__Flavobacteriaceae; g__Polaribacter;
 bacteria; o__Cenarchaeales; f__Cenarchaeaceae; g__Nitrosopumilus;
 o__Flavobacteriales; f__Flavobacteriaceae; g__Ulvibacter;
 bacteria; o__Alteromonadales; f__Alteromonadaceae; g__AlteromonadaceaeFA;
 bacteria; o__Verrucomicrobiales; f__Verrucomicrobiaceae; g__Persicirhabdus;
 o__Flavobacteriales; f__Flavobacteriaceae; g__FlavobacteriaceaeFA;
 bacteria; o__Alteromonadales; f__HTCC2188; g__HTCC;
 bacteria; o__Rhizobiales; f__Rhizobiaceae; g__Mycoplana;
 bacteria; o__Alteromonadales; f__Psychromonadaceae; g__Psychromonas;
 o__Flavobacteriales; f__Flavobacteriaceae; g__Polaribacter;
 bacteria; o__Alteromonadales; f__Alteromonadaceae; g__Candidatus Endobugula;
 o__Acidimicrobiales; f__TK06; g__TK06FA;
 bacteria; o__Oceanospirillales; f__Oceanospirillaceae; g__Amphritea;
 o__Flavobacteriales; f__Flavobacteriaceae; g__FlavobacteriaceaeFA;
 bacteria; o__Rhodospirillales; f__Rhodospirillaceae; g__RhodospirillaceaeFA;
 bacteria; o__Alteromonadales; f__Colwelliaceae; g__ColwelliaceaeFA;
 bacteria; o__Alteromonadales; f__Alteromonadaceae; g__Candidatus Endobugula;
 bacteria; o__Alteromonadales; f__Alteromonadaceae; g__Candidatus Endobugula;
 f__[Saprospirales]; f__Saprospiraceae; g__SaprospiraceaeFA;
 bacteria; o__Alteromonadales; f__Alteromonadaceae; g__Candidatus Endobugula;
 bacteria; o__Phycisphaerales; f__Phycisphaeraceae; g__PhycisphaeraceaeFA;
 bacteria; o__Sva0853; f__SAR324; g__SAR324FA;
 f__[Saprospirales]; f__Saprospiraceae; g__SaprospiraceaeFA;
 o__Flavobacteriales; f__NS9; g__NS9FA;
 f__[Saprospirales]; f__Saprospiraceae; g__SaprospiraceaeFA;
 bacteria; o__Pirellulales; f__Pirellulaceae; g__PirellulaceaeFA;
 f__[Saprospirales]; f__Saprospiraceae; g__SaprospiraceaeFA;
 bacteria; o__Alteromonadales; f__Psychromonadaceae; g__Psychromonas;
 bacteria; o__Cytophagales; f__Flammeovirgaceae; g__FlammeovirgaceaeFA;
 bacteria; o__Rhodospirillales; f__Rhodospirillaceae; g__Nisaea;
 bacteria; o__Desulfobacterales; f__Nitrospinaceae; g__Nitrospina;
 bacteria; o__Legionellales; f__Coxiellaceae; g__CoxiellaceaeFA;
 o__Flavobacteriales; f__Cryomorphaceae; g__CryomorphaceaeFA;
 bacteria; o__Solirubrobacterales; f__SolirubrobacteralesOR; g__SolirubrobacteralesOR;
 o__Flavobacteriales; f__Flavobacteriaceae; g__FlavobacteriaceaeFA;
 o__Flavobacteriales; f__Cryomorphaceae; g__CryomorphaceaeFA;
 f__[Saprospirales]; f__Saprospiraceae; g__SaprospiraceaeFA;
 bacteria; o__NB1-j; f__JTB38; g__JTB38FA;

icteria; o__Sphingomonadales; f__Erythrobacteraceae; g__ErythrobacteraceaeFA;
 bacteria; o__Oceanospirillales; f__OceanospirillalesOR; g__OceanospirillalesOR;
 cteria; o__NB1-j; f__JTB38; g__JTB38FA;
 o__Flavobacteriales; f__Flavobacteriaceae; g__FlavobacteriaceaeFA;
 o__Flavobacteriales; f__Flavobacteriaceae; g__Formosa;
 cteria; o__Burkholderiales; f__Comamonadaceae; g__RS62;
 __GN02PH; g__GN02PH;
 bacteria; o__Alteromonadales; f__Colwelliaceae; g__ColwelliaceaeFA;
 cteria; o__Bdellovibrionales; f__Bacteriovoracaceae; g__BacteriovoracaceaeFA;
 o__Flavobacteriales; f__FlavobacterialesOR; g__FlavobacterialesOR;
 e; o__Phycisphaerales; f__PhycisphaeralesOR; g__PhycisphaeralesOR;
 bacteria; o__Alteromonadales; f__Shewanellaceae; g__Shewanella;
 bacteria; o__Alteromonadales; f__Alteromonadaceae; g__Glaciecola;
 bacteria; o__Alteromonadales; f__Alteromonadaceae; g__AlteromonadaceaeFA;
 o__Flavobacteriales; f__NS9; g__NS9FA;
 o__Flavobacteriales; f__FlavobacterialesOR; g__FlavobacterialesOR;
 o__Flavobacteriales; f__Flavobacteriaceae; g__FlavobacteriaceaeFA;
 icteria; o__Sphingomonadales; f__Sphingomonadaceae; g__Blastomonas;
 ta; o__E2; f__Marine group III; g__Marine group IIIFA;
 o__Flavobacteriales; f__Cryomorphaceae; g__Crocinitomix;
 s; f__Paenibacillaceae; g__Paenibacillus;
 o__Flavobacteriales; f__Flavobacteriaceae; g__FlavobacteriaceaeFA;
 oacteria; o__Campylobacteriales; f__Campylobacteraceae; g__Arcobacter;
 o__Flavobacteriales; f__Flavobacteriaceae; g__FlavobacteriaceaeFA;
 __[Saprospirales]; f__Saprospiraceae; g__SaprospiraceaeFA;
 __Cytophagales; f__Flammeovirgaceae; g__FlammeovirgaceaeFA;
 __[Saprospirales]; f__Saprospiraceae; g__SaprospiraceaeFA;
 o__Flavobacteriales; f__Flavobacteriaceae; g__Polaribacter;
 o__Flavobacteriales; f__Flavobacteriaceae; g__Psychroserpens;
 __Fibrobacterales; f__FibrobacteralesOR; g__FibrobacteralesOR;
 __Cytophagales; f__[Amoebophilaceae]; g__SC3-56;
 icteria; o__Rhodospirillales; f__Rhodospirillaceae; g__RhodospirillaceaeFA;
 o__Flavobacteriales; f__Flavobacteriaceae; g__FlavobacteriaceaeFA;
 o__Flavobacteriales; f__Flavobacteriaceae; g__FlavobacteriaceaeFA;
 o__Flavobacteriales; f__Flavobacteriaceae; g__Polaribacter;
 o__Flavobacteriales; f__FlavobacterialesOR; g__FlavobacterialesOR;
 o__Flavobacteriales; f__Flavobacteriaceae; g__Ulvibacter;
 bacteria; o__Alteromonadales; f__Alteromonadaceae; g__HTCC2207;
 o__Flavobacteriales; f__Cryomorphaceae; g__Crocinitomix;
 cteria; o__Desulfobacterales; f__Nitrospinaceae; g__Nitrospina;
 OM190CL; f__OM190CL; g__OM190CL;
 bacteria; o__Alteromonadales; f__Alteromonadaceae; g__AlteromonadaceaeFA;
 icteria; o__Rickettsiales; f__RickettsialesOR; g__RickettsialesOR;
 bacteria; o__Alteromonadales; f__Alteromonadaceae; g__HTCC2207;
 bacteria; o__Oceanospirillales; f__Halomonadaceae; g__Halomonas;
 o__Flavobacteriales; f__Cryomorphaceae; g__Crocinitomix;
 icteria; o__Sphingomonadales; f__Sphingomonadaceae; g__Novosphingobium;

icteria; o__Sphingomonadales; f__Sphingomonadaceae; g__Sphingomonas;
 e; o__Phycisphaerales; f__PhycisphaeralesOR; g__PhycisphaeralesOR;
 o__Flavobacteriales; f__Flavobacteriaceae; g__FlavobacteriaceaeFA;
 o__Flavobacteriales; f__Cryomorphaceae; g__CryomorphaceaeFA;
 bacteria; o__Oceanospirillales; f__OceanospirillalesOR; g__OceanospirillalesOR;
 o__Flavobacteriales; f__Flavobacteriaceae; g__Polaribacter;
 ; f__A714017; g__SGSH944;
 icteria; o__Rhodospirillales; f__Rhodospirillaceae; g__RhodospirillaceaeFA;
 bacteria; o__Alteromonadales; f__Shewanellaceae; g__Shewanella;
 icteria; o__Rickettsiales; f__RickettsialesOR; g__RickettsialesOR;
 cteria; o__Myxococcales; f__OM27; g__OM27FA;
 bacteria; o__Oceanospirillales; f__Oceanospirillaceae; g__Oleispira;
 o__Flavobacteriales; f__Cryomorphaceae; g__CryomorphaceaeFA;
 o__Flavobacteriales; f__Cryomorphaceae; g__Cryomorpha;
 bacteria; o__GammaproteobacteriaCL; f__GammaproteobacteriaCL; g__GammaproteobacteriaCL;
 o__Flavobacteriales; f__Cryomorphaceae; g__CryomorphaceaeFA;
 icteria; o__Rhizobiales; f__Methylobacteriaceae; g__MethylobacteriaceaeFA;
 icteria; o__Rhodospirillales; f__Rhodospirillaceae; g__Nisaea;
 cteria; o__GMD14H09; f__GMD14H09OR; g__GMD14H09OR;
 o__Flavobacteriales; f__FlavobacterialesOR; g__FlavobacterialesOR;
 bacteria; o__Oceanospirillales; f__Oceanospirillaceae; g__OceanospirillaceaeFA;
 icteria; o__Rhodobacterales; f__Rhodobacteraceae; g__Loktanelia;
 o__Flavobacteriales; f__Cryomorphaceae; g__CryomorphaceaeFA;
 ia; o__Solirubrobacterales; f__SolirubrobacteralesOR; g__SolirubrobacteralesOR;
 o__Flavobacteriales; f__Flavobacteriaceae; g__FlavobacteriaceaeFA;
 o__Flavobacteriales; f__Flavobacteriaceae; g__Winogradskyella;
 icteria; o__Rhodospirillales; f__Rhodospirillaceae; g__RhodospirillaceaeFA;
 icteria; o__Rickettsiales; f__RickettsialesOR; g__RickettsialesOR;
 cteria; o__Myxococcales; f__MyxococcalesOR; g__MyxococcalesOR;
 bacteria; o__Alteromonadales; f__Colwelliaceae; g__ColwelliaceaeFA;
 f__[Saprospirales]; f__Saprospiraceae; g__SaprospiraceaeFA;
 o__Flavobacteriales; f__Flavobacteriaceae; g__Ulvibacter;
 f__[Saprospirales]; f__Saprospiraceae; g__SaprospiraceaeFA;
 icteria; o__Rhodospirillales; f__Rhodospirillaceae; g__RhodospirillaceaeFA;
 ia; o__Pirellulales; f__Pirellulaceae; g__PirellulaceaeFA;
 o__Flavobacteriales; f__Flavobacteriaceae; g__Polaribacter;
 o__Flavobacteriales; f__NS9; g__NS9FA;
 o__Flavobacteriales; f__Flavobacteriaceae; g__FlavobacteriaceaeFA;
 bacteria; o__Campylobacterales; f__Campylobacteraceae; g__Arcobacter;
 bacteria; o__Pseudomonadales; f__Pseudomonadaceae; g__Pseudomonas;
 ia; o__Pirellulales; f__Pirellulaceae; g__PirellulaceaeFA;
 bacteria; o__Alteromonadales; f__Alteromonadaceae;
 bacteria; o__Alteromonadales; f__Alteromonadaceae; g__Candidatus Endobugula;
 ae]; o__[Pedosphaerae]CL; f__[Pedosphaerae]CL; g__[Pedosphaerae]CL;
 o__Flavobacteriales; f__Flavobacteriaceae; g__FlavobacteriaceaeFA;
 o__Flavobacteriales; f__Flavobacteriaceae; g__Polaribacter;
 o__Flavobacteriales; f__Flavobacteriaceae; g__Polaribacter;

bacteria; o__Alteromonadales; f__Colwelliaceae; g__ColwelliaceaeFA;
 bacteria; o__Legionellales; f__Francisellaceae; g__FrancisellaceaeFA;
 bacteria; o__Oceanospirillales; f__Oceanospirillaceae; g__OceanospirillaceaeFA;
 bacteria; o__AlphaproteobacteriaCL; f__AlphaproteobacteriaCL; g__AlphaproteobacteriaCL;
 cilliales; f__LactobacillalesOR; g__LactobacillalesOR;
 bacteria; o__Alteromonadales; f__Alteromonadaceae; g__AlteromonadaceaeFA;
 o__Flavobacteriales; f__Flavobacteriaceae; g__FlavobacteriaceaeFA;
 bacteria; o__Alteromonadales; f__Alteromonadaceae; g__AlteromonadaceaeFA;
 bacteria; o__Rickettsiales; f__RickettsialesOR; g__RickettsialesOR;
 o__Flavobacteriales; f__FlavobacterialesOR; g__FlavobacterialesOR;
 bacteria; o__Alteromonadales; f__Colwelliaceae; g__ColwelliaceaeFA;
 bacteria; o__Alteromonadales; f__Alteromonadaceae; g__BD2-13;
 ia; o__Planctomycetales; f__Planctomycetaceae; g__Planctomyces;
 bacteria; o__Rickettsiales; f__Rickettsiaceae; g__RickettsiaceaeFA;
 bacteria; o__Alteromonadales; f__Alteromonadaceae; g__AlteromonadaceaeFA;
 bacteria; o__Alteromonadales; f__Alteromonadaceae; g__AlteromonadaceaeFA;
 bacteria; o__Sphingomonadales; f__Sphingomonadaceae; g__Sphingomonas;
 o__Flavobacteriales; f__Flavobacteriaceae; g__Flavobacterium;
 bacteria; o__Alteromonadales; f__Alteromonadaceae;
 e; o__Phycisphaerales; f__PhycisphaeralesOR; g__PhycisphaeralesOR;
 o__Flavobacteriales; f__Cryomorphaceae; g__CryomorphaceaeFA;
 obiae; o__Verrucomicrobiales; f__Verrucomicrobiaceae; g__Verrucomicrobium;
 bacteria; o__Rhodospirillales; f__Rhodospirillaceae; g__RhodospirillaceaeFA;
 bacteria; o__AlphaproteobacteriaCL; f__AlphaproteobacteriaCL; g__AlphaproteobacteriaCL;
 o__Flavobacteriales; f__Flavobacteriaceae; g__FlavobacteriaceaeFA;
 bacteria; o__Rhodospirillales; f__Rhodospirillaceae; g__RhodospirillaceaeFA;
 o__Flavobacteriales; f__Cryomorphaceae; g__CryomorphaceaeFA;
 bacteria; o__Alteromonadales; f__Colwelliaceae; g__ColwelliaceaeFA;
 bacteria; o__Alteromonadales; f__Alteromonadaceae; g__AlteromonadaceaeFA;
 bacteria; o__Alteromonadales; f__Alteromonadaceae; g__Candidatus Endobugula;
 bacteria; o__Sphingomonadales; f__Erythrobacteraceae; g__ErythrobacteraceaeFA;
 OM190CL; f__OM190CL; g__OM190CL;
 bacteria; o__Alteromonadales; f__Shewanellaceae; g__Shewanella;
 bacteria; o__Rhizobiales; f__Rhizobiaceae; g__Mycoplana;
 bacteria; o__Campylobacteriales; f__Campylobacteraceae; g__Arcobacter;
 bacteria; o__PB19; f__PB19OR; g__PB19OR;
 bacteria; o__Oceanospirillales; f__OceanospirillalesOR; g__OceanospirillalesOR;
 bacteria; o__Oceanospirillales; f__Halomonadaceae; g__Candidatus Portiera;
 o__Flavobacteriales; f__FlavobacterialesOR; g__FlavobacterialesOR;
 bacteria; o__Oceanospirillales; f__Oceanospirillaceae; g__OceanospirillaceaeFA;
 ta; o__Cenarchaeales; f__Cenarchaeaceae; g__Nitrosopumilus;
 o__Flavobacteriales; f__Flavobacteriaceae; g__Tenacibaculum;
 bacteria; o__Alteromonadales; f__Alteromonadaceae; g__Glaciecola;
 bacteria; o__Alteromonadales; f__HTCC2188; g__HTCC;
 bacteria; o__Thiotrichales; f__Piscirickettsiaceae; g__PiscirickettsiaceaeFA;
 o__Flavobacteriales; f__Cryomorphaceae; g__CryomorphaceaeFA;
 bacteria; o__Rhodospirillales; f__Rhodospirillaceae; g__RhodospirillaceaeFA;

ia; o__Solirubrobacterales; f__SolirubrobacteralesOR; g__SolirubrobacteralesOR;
ia; o__Pirellulales; f__Pirellulaceae; g__PirellulaceaeFA;

cteria; o__Myxococcales; f__OM27; g__OM27FA;
acteria; o__Rhodospirillales; f__Rhodospirillaceae; g__RhodospirillaceaeFA;
o__Acidimicrobiales; f__TK06; g__TK06FA;
bacteria; o__Oceanospirillales; f__Halomonadaceae; g__Candidatus Portiera;
cteria; o__Sva0853; f__SAR324; g__SAR324FA;
o__Flavobacteriales; f__Flavobacteriaceae; g__Winogradskyella;
acteria; o__Sphingomonadales; f__Sphingomonadaceae; g__Sphingomonas;
bacteria; o__Thiohalorhabdales; f__ThiohalorhabdalesOR; g__ThiohalorhabdalesOR;
__[Saprospirales]; f__Saprospiraceae; g__SaprospiraceaeFA;
bacteria; o__Oceanospirillales; f__Halomonadaceae; g__Halomonas;
acteria; o__AlphaproteobacteriaCL; f__AlphaproteobacteriaCL; g__AlphaproteobacteriaCL;
acteria; o__AlphaproteobacteriaCL; f__AlphaproteobacteriaCL; g__AlphaproteobacteriaCL;
; f__A714017; g__SGSH944;
bacteria; o__Xanthomonadales; f__Xanthomonadaceae; g__XanthomonadaceaeFA;
o__Flavobacteriales; f__Flavobacteriaceae; g__FlavobacteriaceaeFA;
o__Flavobacteriales; f__Flavobacteriaceae; g__Psychroserpens;
__ChlamydiaePH; f__ChlamydiaePH; g__ChlamydiaePH;
gg27; f__agg27OR; g__agg27OR;
bacteria; o__Alteromonadales; f__Alteromonadaceae; g__HTCC2207;
__[Saprospirales]; f__Saprospiraceae; g__SaprospiraceaeFA;
o__Flavobacteriales; f__Flavobacteriaceae; g__FlavobacteriaceaeFA;
o__Acidimicrobiales; f__ZA3409c; g__ZA3409cFA;
acteria; o__Rickettsiales; f__Rickettsiaceae; g__RickettsiaceaeFA;
o__Flavobacteriales; f__FlavobacterialesOR; g__FlavobacterialesOR;
acteria; o__Rickettsiales; f__RickettsialesOR; g__RickettsialesOR;
cteria; o__Myxococcales; f__OM27; g__OM27FA;
o__Flavobacteriales; f__FlavobacterialesOR; g__FlavobacterialesOR;
aeroplasmatales; f__Anaeroplasmataceae; g__AnaeroplasmataceaeFA;
o__Flavobacteriales; f__Flavobacteriaceae; g__Polaribacter;
acteria; o__Burkholderiales; f__Comamonadaceae; g__Curvibacter;
acteria; o__Rickettsiales; f__RickettsialesOR; g__RickettsialesOR;
bacteria; o__Alteromonadales; f__Colwelliaceae; g__ColwelliaceaeFA;

gg27; f__agg27OR; g__agg27OR;
o__Flavobacteriales; f__Flavobacteriaceae; g__Flavobacterium;
ta; o__Cenarchaeales; f__Cenarchaeaceae; g__Nitrosopumilus;
bacteria; o__Alteromonadales; f__Colwelliaceae; g__ColwelliaceaeFA;
bacteria; o__Alteromonadales; f__Psychromonadaceae; g__Psychromonas;
cteria; o__Bdellovibrionales; f__Bacteriovoracaceae; g__BacteriovoracaceaeFA;
acteria; o__Rickettsiales; f__RickettsialesOR; g__RickettsialesOR;
ia; o__Planctomycetales; f__Planctomycetaceae; g__Planctomyces;
acteria; o__Sphingomonadales; f__Sphingomonadaceae; g__Sphingomonas;
bacteria; o__Oceanospirillales; f__OceanospirillalesOR; g__OceanospirillalesOR;
o__Flavobacteriales; f__Flavobacteriaceae; g__Psychroserpens;

icteria; o__Rhodobacterales; f__Rhodobacteraceae; g__Phaeobacter;
 cteria; o__Myxococcales; f__OM27; g__OM27FA;
 icteria; o__Rhodobacterales; f__Rhodobacteraceae; g__Octadecabacter;
 icteria; o__Sphingomonadales; f__Sphingomonadaceae; g__Sphingopyxis;
 oacteria; o__Campylobacterales; f__Campylobacteraceae; g__Arcobacter;
 __ChlamydiaePH; f__ChlamydiaePH; g__ChlamydiaePH;
 o__Flavobacteriales; f__Flavobacteriaceae; g__FlavobacteriaceaeFA;
 icteria; o__Sphingomonadales; f__Erythrobacteraceae; g__ErythrobacteraceaeFA;
 bacteria; o__Alteromonadales; f__Alteromonadaceae; g__Candidatus Endobugula;
 __Cytophagales; f__Flammeovirgaceae; g__Reichenbachella;
 icteria; o__Sphingomonadales; f__Sphingomonadaceae; g__SphingomonadaceaeFA;
 bacteria; o__Oceanospirillales; f__Oceanospirillaceae; g__OceanospirillaceaeFA;
 __[Saprospirales]; f__Saprospiraceae; g__Lewinella;
 icteria; o__Rhodospirillales; f__Rhodospirillaceae; g__RhodospirillaceaeFA;
 bacteria; o__Alteromonadales; f__OM60; g__OM60FA;
 icteria; o__Sphingomonadales; f__Sphingomonadaceae; g__Novosphingobium;
 o__Flavobacteriales; f__Flavobacteriaceae; g__FlavobacteriaceaeFA;
 cteria; o__Myxococcales; f__OM27; g__OM27FA;
 bacteria;
 bacteria; o__Legionellales; f__Francisellaceae; g__FrancisellaceaeFA;
 icteria; o__AlphaproteobacteriaCL; f__AlphaproteobacteriaCL; g__AlphaproteobacteriaCL;
 hlamydiales; f__ChlamydialesOR; g__ChlamydialesOR;
 o__Flavobacteriales; f__Cryomorphaceae; g__Fluviicola;
 bacteria; o__Oceanospirillales; f__Halomonadaceae; g__Candidatus Portiera;
 obiae; o__Verrucomicrobiales; f__Verrucomicrobiaceae; g__VerrucomicrobiaceaeFA;
 o__Flavobacteriales; f__Flavobacteriaceae; g__Polaribacter;
 bacteria; o__Alteromonadales; f__Alteromonadaceae; g__Candidatus Endobugula;
 __Cytophagales; f__Flammeovirgaceae; g__JTB248;
 bacteria; o__Alteromonadales; f__Alteromonadaceae; g__Glaciecola;
 bacteria; o__Thiotrichales; f__Piscirickettsiaceae; g__PiscirickettsiaceaeFA;
 OM190CL; f__OM190CL; g__OM190CL;
 bacteria; o__Chromatiales; f__ChromatialesOR; g__ChromatialesOR;
 illales; f__LactobacillalesOR; g__LactobacillalesOR;
 icteria; o__Rickettsiales; f__Rickettsiaceae; g__RickettsiaceaeFA;
 icteria; o__Rickettsiales; f__RickettsialesOR; g__RickettsialesOR;
 ta; o__E2; f__Marine group II; g__Marine group IIFA;
 cteria; o__Myxococcales; f__OM27; g__OM27FA;
 icteria; o__Sphingomonadales; f__SphingomonadalesOR; g__SphingomonadalesOR;
 o__Flavobacteriales; f__FlavobacterialesOR; g__FlavobacterialesOR;
 bacteria; o__Alteromonadales; f__Alteromonadaceae; g__Glaciecola;
 oacteria; o__Campylobacterales; f__Campylobacteraceae; g__Arcobacter;
 bacteria; o__Vibrionales; f__Pseudoalteromonadaceae; g__Pseudoalteromonas;
 obiae; o__Verrucomicrobiales; f__Verrucomicrobiaceae; g__Verrucomicrobium;
 bacteria; o__Oceanospirillales; f__Halomonadaceae; g__Candidatus Portiera;
 ta; o__Cenarchaeales; f__Cenarchaeaceae; g__Nitrosopumilus;
 ia; o__Pirellulales; f__Pirellulaceae; g__PirellulaceaeFA;
 cteria; o__DeltaproteobacteriaCL; f__DeltaproteobacteriaCL; g__DeltaproteobacteriaCL;

ta; o__Cenarchaeales; f__Cenarchaeaceae; g__Nitrosopumilus;
 ia; o__Planctomycetales; f__Planctomycetaceae; g__Planctomyces;
 o__Flavobacteriales; f__Cryomorphaceae; g__Crocinitomix;
 _Cytophagales; f__Flammeovirgaceae; g__FlammeovirgaceaeFA;
 o__Flavobacteriales; f__NS9; g__NS9FA;
 ia; o__Solirubrobacterales; f__SolirubrobacteralesOR; g__SolirubrobacteralesOR;
 ia; o__Pirellulales; f__Pirellulaceae; g__PirellulaceaeFA;
 bacteria; o__Legionellales; f__LegionellalesOR; g__LegionellalesOR;
 e; o__Phycisphaerales; f__PhycisphaeralesOR; g__PhycisphaeralesOR;
 icteria; o__Rhodospirillales; f__Rhodospirillaceae; g__RhodospirillaceaeFA;
 o__Acidimicrobiales; f__C111; g__C111FA;
 icteria; o__Burkholderiales; f__Oxalobacteraceae; g__Oxalobacter;
 bacteria;
 bacteria; o__Alteromonadales; f__Psychromonadaceae; g__PsychromonadaceaeFA;
 ta; o__E2; f__Marine group II; g__Marine group IIFA;

bypass

id Ornithine Degradation

e subunits

metabolism

57.3.peg.390

e Degradation

ecular synthesis operon

urine Biosynthesis

degradation regulons

l Serine Utilization

Biosynthesis

e Synthesis

ATP synthase

ATP synthase

sitive cluster that relates ribosomal protein L28P to a set of uncharacterized proteins

e bacterial

ell Division

remotaxis

dent RNA helicases, bacterial

synthesis and regulation

Glutamate, Aspartate and Asparagine Biosynthesis

ation in Thermotogales

nal proteins cluster

abolism

im cofactor biosynthesis
id Ornithine Degradation
ynthesis Experimental
etabolism I: anaplerotic reactions, PEP
yl-CoA catabolic pathway (core)
versions
versions
nase complexes
9.4.peg.1996B
hain amino acid degradation regulons
tress
d Serine Utilization
omerases, Type II, ATP-dependent
nal proteins cluster
ylthiotransferase containing cluster
Chain Amino Acid Biosynthesis
ite cycle
nase complexes
Chain Amino Acid Biosynthesis
erate oxidoreductase
bypass
id Ornithine Degradation
osynthesis extended
osynthesis extended
Siroheme Biosynthesis
nose synthesis
nose synthesis
olyl cis-trans isomerase
72.3.peg.6046
metabolism
is a hypothetical
is a hypothetical
versions
etabolism I: anaplerotic reactions, PEP
osphate pathway
 Biosynthesis
 Biosynthesis
 Base Excision
42.4.peg.1852
42.4.peg.1852
: Intermediate for synthesis of Tryptophan, PAPA antibiotics, PABA, 3-hydroxyanthranilate and more.
nposition
 Synthesis
ynthesis DAP Pathway
9.4.peg.1292
rine Biosynthesis
m II

l Serine Utilization

gradation

gradation

e, carboxysome

ion cycle

-Archaeosine Biosynthesis

1.1.peg.3039

legradation regulons

legradation regulons

mino acid degradation

ite cycle

Chain Amino Acid Biosynthesis

d Maltodextrin Utilization

Biosynthesis

Biosynthesis

l Synthesis

osynthesis extended

72.3.peg.6046

ATP synthase

ATP synthase

sitive cluster that relates ribosomal protein L28P to a set of uncharacterized proteins

e bacterial

e bacterial

dent RNA helicases, bacterial

degradation

.peg.567

ration (oxidative C2 cycle)

perones

dent RNA helicases, bacterial

dent RNA helicases, bacterial

osynthesis

synthesis and regulation

38.3.peg.1509

otility

r metabolism by tetrahydropterines

ation in Thermotogales

ptose biosynthesis

cretion Pathway

acylation, Gly

oteins for [4Fe-4S] cluster assembly (MRP family)

synthesis

nal proteins cluster

nal proteins cluster

abolism
abolism
im cofactor biosynthesis
im cofactor biosynthesis
:locating NADH-quinone oxidoreductase and rnf-like group of electron transport complexes
:locating NADH-quinone oxidoreductase and rnf-like group of electron transport complexes
:locating NADH-quinone oxidoreductase and rnf-like group of electron transport complexes

id Ornithine Degradation
ynthesis Experimental
ynthesis Experimental
ADP cofactor biosynthesis global
91.1.peg.2330
etabolism I: anaplerotic reactions, PEP
adation
yl-CoA catabolic pathway (core)
yl-CoA catabolic pathway (core)
two-component regulatory system
versions
versions
nase complexes
can Biosynthesis
tide reductase cluster
tide reduction
99.4.peg.1996B
99.4.peg.1996B

hain amino acid degradation regulons
hain amino acid degradation regulons
tress
d Serine Utilization
omerases, Type II, ATP-dependent
omerases, Type II, ATP-dependent
nal proteins cluster
nal proteins cluster
99.4.peg.1996B
ylthiotransferase containing cluster
ylthiotransferase containing cluster
mino acid degradation
of cbb3-type cytochrome c oxidases
-Modification System
nposition
acylation, Val
aminopropionate ammonia-lyase cluster
of Zinc
of Zinc
of Zinc

19.3.peg.410

bypass

.SU bacterial

ε Degradation

ATP synthase

ATP synthase

ATP synthase

acylation, Gly

.SU bacterial

chain amino acid degradation regulons

urine Biosynthesis

m I

m II

m II

ε, carboxysome

ε, carboxysome

son cycle

idoroff Pathway

yl-CoA catabolic pathway (core)

yl-CoA catabolic pathway (core)

chain Amino Acid Biosynthesis

chain Amino Acid Biosynthesis

chain Amino Acid Biosynthesis

ycosylation in Bacteria

ε: Biosynthesis and gamma-glutamyl cycle

ε: Biosynthesis and gamma-glutamyl cycle

ε: Biosynthesis and gamma-glutamyl cycle

nase complexes

Biosynthesis FASII

osynthesis

B12 biosynthesis

id Ornithine Degradation

id Ornithine Degradation

id Ornithine Degradation

xal Metabolism

xal Metabolism

ustered with urea and nitrile hydratase functions

d Serine Utilization

ε: Intermediate for synthesis of Tryptophan, PAPA antibiotics, PABA, 3-hydroxyanthranilate and more.

ε: Intermediate for synthesis of Tryptophan, PAPA antibiotics, PABA, 3-hydroxyanthranilate and more.

ε: Intermediate for synthesis of Tryptophan, PAPA antibiotics, PABA, 3-hydroxyanthranilate and more.

ε: Intermediate for synthesis of Tryptophan, PAPA antibiotics, PABA, 3-hydroxyanthranilate and more.

istance

istance

istance
istance
osynthesis
ATP synthase

dent RNA helicases, bacterial
dent RNA helicases, bacterial
dent RNA helicases, bacterial
dent RNA helicases, bacterial
dent RNA helicases, bacterial
ation in Thermotogales
ynthesis
ynthesis
orter branched-chain amino acid (TC 3.A.1.4.1)
orter branched-chain amino acid (TC 3.A.1.4.1)
ecular synthesis operon
ecular synthesis operon
ecular synthesis operon
ytoskeleton
ynthesis

B12 biosynthesis
synthesis

. CspA family of proteins
. CspA family of proteins
d operon linked to TyrR and possibly involved in virulence
d operon linked to TyrR and possibly involved in virulence
d operon linked to TyrR and possibly involved in virulence
se (EC 6.3.4.2) cluster
se (EC 6.3.4.2) cluster
ynthesis
31.3.peg.3674
: disulfide interchange
: disulfide interchange
rochrome d ubiquinol oxidases

itamin B6) Biosynthesis
ynthesis DAP Pathway
ynthesis DAP Pathway
ynthesis DAP Pathway
ynthesis DAP Pathway
ynthesis DAP Pathway
ing nucleoside triphosphate pyrophosphatases
gradation
gradation

gradation
, bacterial MutL-MutS system
, bacterial MutL-MutS system
gene cluster associated with Met-tRNA formyltransferase
10.3.peg.283
10.3.peg.283
10.3.peg.283
locating NADH-quinone oxidoreductase and rnf-like group of electron transport complexes
locating NADH-quinone oxidoreductase and rnf-like group of electron transport complexes
d synthesis
xylate cycle
cter Iron Metabolism
cter Iron Metabolism
tress
38.3.peg.1509
38.3.peg.1509
38.3.peg.1509
taining CofD-like protein and co-occurring with DNA repair
is a hypothetical
otility
otility
remotaxis

otility

osphate pathway
ind Gluconeogenesis
ind Gluconeogenesis

stress
tymuramate from Fructose-6-phosphate Biosynthesis
nose synthesis
nose synthesis
54.1.peg.461
ADP cofactor biosynthesis global
Siroheme Biosynthesis
Siroheme Biosynthesis
Siroheme Biosynthesis
glyoxylate interconversions
glyoxylate interconversions
23.1.peg.1311
23.1.peg.1311
33.1.peg.1906
33.1.peg.1906
33.1.peg.1906

all Division

versions

9.4.peg.1292

57.3.peg.563

57.3.peg.563

osynthesis

osynthesis

l Betaine Uptake and Betaine Biosynthesis

osynthesis

osynthesis

osynthesis

transfer

in Metabolism

A biosynthesis

A biosynthesis

sitive cluster that relates ribosomal protein L28P to a set of uncharacterized proteins

0.10.peg.1536

0.10.peg.1536

0.10.peg.1536

bypass

bypass

honate utilization

hain amino acid degradation regulons

hain amino acid degradation regulons

hain amino acid degradation regulons

xylate cycle

neostasis

metabolism

ydrogenase

itanol Ethanol Synthesis

itanol Ethanol Synthesis

itanol Ethanol Synthesis

r Complex I

etabolism I: anaplerotic reactions, PEP

ydroxyproline uptake and utilization

dehydrogenases

ation

tress

21.3.peg.2760

21.3.peg.2760

21.3.peg.2760

yl-CoA catabolic pathway (core)

y phosphate transporter and control of PHO regulon

y phosphate transporter and control of PHO regulon

etabolism I: anaplerotic reactions, PEP

Metabolism
hionate utilization
21.1.peg.1863
s
s
d synthesis
d synthesis
ie
hydroxyproline uptake and utilization
hydroxyproline uptake and utilization
and hprK operon in Gram-positive organisms
e eukaryotic
gene cluster associated with Met-tRNA formyltransferase
gene cluster associated with Met-tRNA formyltransferase
gene cluster associated with Met-tRNA formyltransferase
36.1.peg.3133
l Biosynthesis
l Biosynthesis
l Biosynthesis
ate cycle
l homes
idoreductase family
idoreductase family
idoreductase family
ulatory proteins
42.4.peg.1852
42.4.peg.1852
utilization
itamin B6) Degradation Pathway
itamin B6) Degradation Pathway
ssing and degradation, bacterial
gene cluster associated with Met-tRNA formyltransferase
gene cluster associated with Met-tRNA formyltransferase
gene cluster associated with Met-tRNA formyltransferase
ision clusters relating to chromosome partitioning
ssing
ouridine syntheses
gene cluster associated with Met-tRNA formyltransferase
01.1.peg.1715
01.1.peg.1715
01.1.peg.1715
ecular synthesis operon
ecular synthesis operon
36.1.peg.3133
36.1.peg.3133
charide assembly cluster
charide assembly cluster

efflux pump in Campylobacter jejuni (CmeABC operon)
efflux pump in Campylobacter jejuni (CmeABC operon)
colonization and sigma-dependent biofilm formation gene cluster
colonization and sigma-dependent biofilm formation gene cluster
metabolism
SU bacterial
SU bacterial
ly Regulatory Sensor-transducer Disambiguation
ly Regulatory Sensor-transducer Disambiguation
elongation factors bacterial

Metabolism
NA-metabolizing Zn-dependent hydrolases
fication Bacteria
-Modification System
acylation, Tyr
one and Phylloquinone Biosynthesis
one and Phylloquinone Biosynthesis
one and Phylloquinone Biosynthesis
A biosynthesis
can Biosynthesis
tylneuraminate Biosynthesis
saccharide assembly
r Base Excision
homeostasis
homeostasis
osphate pathway
e subunits
erase chloroplast
olyl cis-trans isomerase
olyl cis-trans isomerase
is a hypothetical
urine Biosynthesis
itrate transport system Fec
yl-CoA catabolic pathway (core)
rotein
etabolism I: anaplerotic reactions, PEP
etabolism I: anaplerotic reactions, PEP
hain amino acid degradation regulons
Biosynthesis
d Glycerol-3-phosphate Uptake and Utilization
d Glycerol-3-phosphate Uptake and Utilization
ell Division
dent RNA helicases, bacterial

im cofactor biosynthesis

Complex I

ynthesis Experimental

Biosynthesis

Biosynthesis

99.4.peg.1996B

hain amino acid degradation regulons

ogenesis bacterial

ogenesis bacterial

ylthiotransferase containing cluster

Menaquinone-cytochrome c reductase complexes

aminopropionate ammonia-lyase cluster

aminopropionate ammonia-lyase cluster

ynthesis DAP Pathway

Synthesis

Synthesis

ate cycle

etabolism II: acetyl-CoA, acetogenesis from pyruvate

bypass

id Ornithine Degradation

osynthesis extended

ynthesis DAP Pathway

ynthesis DAP Pathway

d and Glycerophospholipid Metabolism in Bacteria

Chain Amino Acid Biosynthesis

subunits

erase chloroplast

nose synthesis

72.3.peg.6046

99.4.peg.1292

metabolism

is a hypothetical

urine Biosynthesis

bypass

nal proteins cluster

.SU bacterial

.SU chloroplast

.SU chloroplast

olocating NADH-quinone oxidoreductase and rnf-like group of electron transport complexes

versions

rotein

Biosynthesis

42.4.peg.1852

Intermediate for synthesis of Tryptophan, PABA antibiotics, PABA, 3-hydroxyanthranilate and more.
carbohydrate assembly

Biosynthesis

ion

can Biosynthesis

anoid compound degradation

hydroxyproline uptake and utilization

dehydrogenases

CoA to Succinyl-CoA Module

hydroxyproline uptake and utilization

nd gentisate catabolism

ATP synthase

chain amino acid degradation regulons

E cluster

ate cycle

.SU bacterial

order oligopeptide (TC 3.A.1.5.1)

ATP synthase

ration (oxidative C2 cycle)

on factors bacterial

and putative sugar transporter

versions

I transport systems

Menquinone-cytochrome c reductase complexes

e and Deoxynucleoside Catabolism

aine metabolism

chain amino acid degradation regulons

, UvrABC system

38.3.peg.1509

ic Acid Biosynthesis

Chain Amino Acid Biosynthesis

adation

r Complex I

ec secretion

ation in Thermotogales

dent RNA helicases, bacterial

59.3.peg.1840

31.1.peg.2330

ynthesis DAP Pathway

ne

ptose biosynthesis

carbohydrate assembly
1 metabolism by tetrahydropterines
1 metabolism by tetrahydropterines
protein
ribose biosynthesis
urine Biosynthesis
protein complex
osynthesis
e and Deoxynucleoside Catabolism
ccal pathogenicity islands SaPI
cytoskeleton
m II
id Creatinine Degradation
selenate and selenite
biosynthesis FASII
Siroheme Biosynthesis
is a hypothetical
a-glutamate biosynthesis
respiratory reductases
ation specificity factor
egradation
Metabolism
l homes
hain amino acid degradation regulons
B12 biosynthesis
xal Metabolism
tide reductase cluster
1 metabolism by tetrahydropterines
-Archaeosine Biosynthesis
, bacterial UvrD and related helicases
cter Iron Metabolism
e 4 secretion system
homeostasis
zation
yl-CoA catabolic pathway (core)
osynthesis
one and Phylloquinone Biosynthesis
assimilation
versions
ins
of c-type cytochromes
ation bacterial
ta-cleavage pathway of aromatic compound degradation
, bacterial
SU bacterial
' synthase
d synthesis

ynthesis from L-lysine
, UvrABC system
eptidase (EC 3.4.21.-)
dehydrogenases
SU bacterial
transferases
d Maltodextrin Utilization

tal - Histidine Degradation
osynthesis
01.1.peg.1715
, UvrABC system
ation, archaeal
oline Quinone biosynthesis
toskeleton
11.1.peg.435
one Biosynthesis via Futasoline -- gjo
erase archaeal
nposition
Metabolism
79.3.peg.868
r Complex I
cter Iron Metabolism
remotaxis
d Glycerol-3-phosphate Uptake and Utilization
d and Glycerophospholipid Metabolism in Bacteria
ninal phosphate cyclase
ssimilation
Siroheme Biosynthesis
ses
ulfur Assimilation
er
09.4.peg.1996B
otility
protein S12p Asp methylthiotransferase
rotein complex
-component Regulator PrrBA in Proteobacteria
on elongation factors, archaeal
rine Biosynthesis
utilization pathways
ite cycle
42.4.peg.1852
f Peptidoglycan Amino Acids
72.3.peg.6046
38.3.peg.3759
of c-type cytochromes
.SU bacterial

aptose biosynthesis
scharide assembly
scharide assembly
lation
-cadmium resistance
itanol Ethanol Synthesis
19.3.peg.410
38.3.peg.1509
erase archaeal initiation factors
e utilization
acylation, Pro
son cycle
ssynthesis
omerases, Type I, ATP-independent
ssimilation
cation
d Glycerol-3-phosphate Uptake and Utilization
ynthesis AAA pathway 2
r septation in Enterobacteria
ation specificity factor
lation
enes utilization
d Maltodextrin Utilization
cating decarboxylases and related biotin-dependent enzymes

urine Biosynthesis
gene cluster associated with Met-tRNA formyltransferase
legradation
hain amino acid degradation regulons
and Aspartate uptake in Bacteria
olpyruvate phosphomutase
mino acid degradation
iTPases
nase complexes
ouridine syntheses
gulatory system of Alphaproteobacteria
acylation, Leu
l transport systems
endent Peptide Transporters
mino acid interconversions with aryl acids
l Serine Utilization
ylspermidine and Trypanothione

ochromes and functionally related electron carriers
urine Biosynthesis
rotein
atabolism

36.1.peg.3133

Resistance Efflux Pumps

Resistance Efflux Pumps

degradation

synthesis

serine metabolism

of glutathione as a sulphur source

of P-loop GTPases (metallocenter biosynthesis)

dehydrogenase

glycosylation

glycosylation

glycosylase

glycosylase

and Glycerophospholipid Metabolism in Bacteria

chemotaxis

57.3.peg.3521

degradation and HMG-CoA Metabolism

N-acetylglucosamine utilization

is: Intermediate for synthesis of Tryptophan, PABA antibiotics, PABA, 3-hydroxyanthranilate and more.

ation

l derivatives

osynthesis

idoroff Pathway

isSU eukaryotic and archaeal

se (EC 6.3.4.2) cluster

mino acid degradation

adation

metabolism

aminopropionate ammonia-lyase cluster

l nitrite ammonification

onate assimilation

of Manganese

ed Subsystem Grouping Hypotheticals - perhaps Proteosome Related

pendent Peptide Transporters

d Maltodextrin Utilization

yl-CoA pathway of C2 assimilation

iTPases

d Serine Utilization

ne, archaeal

erin biosynthesis

ynthesis orphans

ynthesis orphans

o FAD

metabolism

osynthesis extended
 e and Deoxynucleoside Catabolism
 ecular synthesis operon
 -Archaeosine Biosynthesis
 bypass
 0.10.peg.1536
 , bacterial
 onate and D-Glucuronate Utilization
 hain amino acid degradation regulons
 016
 Metabolism
 elongation factor G family
 id Ornithine Degradation
 e utilization
 zation
 gradation
 Glutamate, Aspartate and Asparagine Biosynthesis
 yl-CoA catabolic pathway (core)
 stis experimental
 osynthesis
 -Archaeosine Biosynthesis
 tributed proteins not in subsystems
 21.3.peg.2760
 neostasis
 ISU eukaryotic and archaeal
 degradation
 osynthesis
 e or DNA damage-inducible protein CinA and related protein families
 oyl cis-trans isomerase

huate branch of beta-ketoadipate pathway
 Glutamate, Aspartate and Asparagine Biosynthesis
 /toskeleton
 nemotaxis
 57.3.peg.3521
 :: Intermediate for synthesis of Tryptophan, PABA antibiotics, PABA, 3-hydroxyanthranilate and more.
 , bacterial MutL-MutS system
 etabolism I: anaplerotic reactions, PEP
 e Menaquinone-cytochrome c reductase complexes
 ATP synthase
 isomerases, Type II, ATP-dependent
 e utilization
 36.1.peg.3133
 erin biosynthesis2
 B12 biosynthesis

expressed with butyrate metabolism cluster
tude reductase cluster
D and Sodium-dependent phosphate transporters
N-acetylglucosamine utilization
lization
bypass
ation in Thermotogales

utilization

‡ Synthesis
/toskeleton
bypass
‡SU bacterial
‡SU eukaryotic and archaeal
yl-CoA pathway of C2 assimilation
s
‡SU eukaryotic and archaeal
33.1.peg.1906
42.4.peg.1852
30.1.peg.1561
ine and Tyrosine Branches from Chorismate
e B6-F complex
erase archaeal
erase archaeal

‡: Redox cycle
‡: Redox cycle
tude reduction
e bacterial
ite cycle
egradation
‡charide assembly
e and Deoxynucleoside Catabolism
osynthesis
‡ Salvage
ynthesis AAA pathway 2
cluster assembly
and Aspartate uptake in Bacteria
alactosamine and Galactosamine Utilization
‡ Cluster
orter oligopeptide (TC 3.A.1.5.1)

ynthesis DAP Pathway
yanobacteria)
‡.10.peg.1536

e bacterial
yl-CoA catabolic pathway (core)
l transport systems
on initiation, bacterial sigma factors
idoroff Pathway
acylation, Gly
lanine Serine Interconversions
59.3.peg.1840
of c-type cytochromes
initiation factors eukaryotic and archaeal

yl-CoA pathway of C2 assimilation
l nitrite ammonification
te metabolism
ouridine syntheses
.SU bacterial
:-Binding-Protein-Dependent Transport System for α-Glucosides
genesis strays
42.4.peg.1852

respiratory reductases
91.1.peg.2330

ural proteins, bacterial
erin biosynthesis2
cter Iron Metabolism
remotaxis
54.1.peg.1690
99.4.peg.1292
ation
glyoxylate interconversions
abolism
scharide assembly
s Synthesis
D and Sodium-dependent phosphate transporters

erase archaeal
ulfur Assimilation
ynthesis orphans
ynthesis orphans
elongation factors bacterial
erase archaeal
.SU bacterial
rtochrome C oxidases
stress
.peg.3360

Chain Amino Acid Biosynthesis
on initiation, bacterial sigma factors
ate Utilization
fication Archaea

e Biosynthesis
idases (EC 3.4.11.-)
ind Gluconeogenesis
ecular synthesis operon
ecular synthesis operon
on factors bacterial

rotein complex
rtochrome d ubiquinol oxidases
fication Archaea
n second YidC in Bacilli
drolases
honate utilization
VA-metabolizing Zn-dependent hydrolases
ADP cofactor biosynthesis global
id Creatinine Degradation
97.3.peg.2594
ec secretion
utilization
SU eukaryotic and archaeal
xal Metabolism

anch of beta-ketoadipate pathway

in Metabolism
cretion Pathway
Siroheme Biosynthesis
can Biosynthesis
orter alkylphosphonate (TC 3.A.1.9.1)
ed Subsystem Grouping Hypotheticals - perhaps Proteosome Related
erin biosynthesis2
in
lehydrogenase
protein S12p Asp methylthiotransferase
fication Bacteria
lation
arbohydrate utilization (cluster Ydj)
toskeleton
ssing
biosynthesis
hain amino acid degradation regulons
r Complex I

nase complexes
elongation factors eukaryotic and archaeal

ic Acid Biosynthesis

Metabolism

ginine metabolism

side Metabolism

fication Bacteria

zation

abolism

fermentation to Butyrate

ation cluster 1

l nitrite ammonification

A biosynthesis

ins

ynthesis

sitive cluster that relates ribosomal protein L28P to a set of uncharacterized proteins

lication

eptococcal phages

gene cluster associated with Met-tRNA formyltransferase

initiation factors eukaryotic and archaeal

ate cycle

33.3.peg.2787

f Peptidoglycan Amino Acids

ic Acid Biosynthesis

cter Iron Metabolism

VA-metabolizing Zn-dependent hydrolases

osynthesis

osynthesis extended

osynthesis

idoroff Pathway

nce operon in Bacteroides and potentially orthologous operons in other organisms

elongation factor G family

hain amino acid degradation regulons

perones

rdrogenase

d Glycerol-3-phosphate Uptake and Utilization

metabolism

rdrogenase

d of Campylobacter

utilization pathways

cation

huate branch of beta-ketoadipate pathway

ilocalizing NADH-quinone oxidoreductase and rnf-like group of electron transport complexes

xal Metabolism
 Biosynthesis FASII
 , bacterial
 ation in Thermotogales
 osynthesis
 Metabolism

 ine utilization
 ynthesis DAP Pathway
 ynthesis DAP Pathway
 abolism
 remotaxis
 xal Metabolism
 iogenesis bacterial
 ylthiotransferase containing cluster
 Degradation
 e bacterial
 59.3.peg.1840
 , bacterial photolyase
 -cadmium resistance
 ynthesis DAP Pathway
 e utilization
 side Metabolism
 B12 biosynthesis
 e eukaryotic
 rredoxin oxidoreductase
 94.1.peg.3339
 respiratory reductases
 boxypeptidases (EC 3.4.17.-)
 e or DNA damage-inducible protein CinA and related protein families
 ilization
 ation
 gulatory system of Alphaproteobacteria
 Biosynthesis FASII
 ientation
 ninal phosphate cyclase
 inolamine dehydratase
 cacylation, Asp and Asn
 hain amino acid degradation regulons
 idoroff Pathway
 Glutamate, Aspartate and Asparagine Biosynthesis
 A biosynthesis
 cluster assembly
 drogenase
 utilization
 xylate cycle

respiratory reductases
 idoroff Pathway
 m I
 ation
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 ization
 orte tungstate (TC 3.A.1.6.2)
 eine metabolism
 Metabolism
 Glutamate, Aspartate and Asparagine Biosynthesis
 iperones
 hain amino acid degradation regulons
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 d Glycerol-3-phosphate Uptake and Utilization
 etabolism I: anaplerotic reactions, PEP
 , bacterial
 B12 biosynthesis
 bypass
 dent RNA helicases, bacterial
 nase complexes
 , bacterial MutL-MutS system
 e and Deoxynucleoside Catabolism
 id Ornithine Degradation
 xal Metabolism

 ccharide assembly
 osynthesis
 nposition
 abolism
 polysaccharides Biosynthesis and Assembly
 .SU eukaryotic and archaeal
 gene cluster associated with Met-tRNA formyltransferase
 ell Division
 9.4.peg.1292
 : Synthesis
 At2g40600
 ginine metabolism
 gene cluster associated with Met-tRNA formyltransferase
 huate branch of beta-ketoadipate pathway
 e utilization
 of cbb3-type cytochrome c oxidases
 synthesis
 , bacterial RecFOR pathway
 CoA to Succinyl-CoA Module

 ccharide assembly
 er Membrane Proteins

versions
chemotaxis

homes

A biosynthesis

metabolism
Biosynthesis
B12 biosynthesis
1994.peg.1996B
oids

Complex I
1973.peg.563

branch of beta-ketoadipate pathway
ation in Thermotogales
gene cluster associated with Met-tRNA formyltransferase

synthesis
CspA family of proteins
Synthesis
pendent Peptide Transporters
cell elongation - division cycle in Bacilli
cytoskeleton
A Biosynthesis
2010.peg.1536
ine and Tyrosine Branches from Chorismate
ation in Thermotogales
, bacterial MutL-MutS system
Menaquinone-cytochrome c reductase complexes
AT1G06240
B12 biosynthesis
olyl cis-trans isomerase
osynthesis
1996.1.peg.3133
1996.1.peg.3133
osynthesis extended
metabolism I: anaplerotic reactions, PEP
Complex I

can Biosynthesis
respiratory reductases
rate oxidoreductase
d and Glycerophospholipid Metabolism in Bacteria

l Serine Utilization
hain amino acid degradation regulons
ua5 protein family
rated Fatty Acids synthesis
Glutamate, Aspartate and Asparagine Biosynthesis
an Biosynthesis
yl-CoA catabolic pathway (core)
degradation
SU bacterial
9.4.peg.1996B
elongation factor G family
d Ornithine Degradation
ine and Tyrosine Branches from Chorismate
erase II
ADP cofactor biosynthesis global

line catabolism
ation, archaeal
danese-domain proteins
11.1.peg.435
oteins for [4Fe-4S] cluster assembly (MRP family)
19.3.peg.410
versions
l homes
acylation, Gly

lanine Serine Interconversions
osynthesis
' synthase
ation in Thermotogales
72.7.peg.546
tilization
respiratory reductases
-component Regulator PrrBA in Proteobacteria
ind Gluconeogenesis
22.12.peg.188
drolases
drolases
l nitrite ammonification
31.3.peg.3674
ulatory proteins
fication Bacteria

erase chloroplast
SU bacterial
ulfur Assimilation

Biosynthesis
ate catabolism
24.3.peg.2657
l nitrite ammonification
efflux pump in *Campylobacter jejuni* (CmeABC operon)
versions
ation, archaeal
eptose biosynthesis
ynthesis AAA pathway 2
ilization
versions

o-occurring Genes
id Ornithine Degradation
' synthase
fication Archaea
erate oxidoreductase
line transport and metabolism
hain amino acid degradation regulons
xylate cycle
3.1.peg.459
ate catabolism
r dehydrogenases 1
57.3.peg.659

e subunit alpha archaeal cluster
l transport systems
oteins for [4Fe-4S] cluster assembly (MRP family)

36.1.peg.3133
A Biosynthesis
synthesis
eine metabolism
0.10.peg.1536
y phosphate transporter and control of PHO regulon
of glutathione as a sulphur source
tal-PTPS
lehydrogenase
ite, D-glucarate and D-glycerate catabolism
onization of chick caeca
ATP synthase
dent RNA helicases, bacterial
ransport and degradation cluster
59.3.peg.1840
: disulfide interchange
osphate Uptake System
1.1.peg.3039

xylate cycle
yl-CoA catabolic pathway (core)
ation in Thermotogales
14.1.peg.752
dE-TldD proteolytic complex
igosaccharide biosynthesis
rimidine Synthesis
synthesis
Metabolism in Microorganisms
Metabolism in Microorganisms
Metabolism

d synthesis
ine and Tyrosine Branches from Chorismate
F420-H2 dehydrogenase (methanophenazine)
lase locus in Streptococcus
SU chloroplast
abolism
one and Phylloquinone Biosynthesis
ite cycle
one Biosynthesis via Futasine -- gjo
e bacterial
toskeleton
urine Biosynthesis
:: Intermediate for synthesis of Tryptophan, PABA antibiotics, PABA, 3-hydroxyanthranilate and more.
Metabolism
orter tungstate (TC 3.A.1.6.2)
, bacterial
xylase and Allophanate hydrolase cluster
retion system orphans
nce operon in Bacteroides and potentially orthologous operons in other organisms
egradation
olysaccharide (CPS) of Campylobacter
charide Biosynthesis
toskeleton
toskeleton
016
kinase containing cluster
ate catabolism
emoglobins
.peg.567
.peg.567
cation
ation cluster 1
ation cluster 1
cation

perones

, bacterial UmuCD system

tilization

5.3.peg.3639

id and Fatty acid biosynthesis related cluster

homeostasis

otility

remotaxis

orter branched-chain amino acid (TC 3.A.1.4.1)

rdrogenase

A biosynthesis

.SU chloroplast

0.10.peg.1536

kinase containing cluster

cus pyogenes virulence regulators

id Creatinine Degradation

biosynthesis

min Catabolism

metabolism

anoid compound degradation

of glutathione as a sulphur source

idoreductase family

utilization pathways

glycolate salvage

, bacterial RecBCD pathway

, bacterial RecBCD pathway

utilization

57.3.peg.1308

mediated methylamine utilization pathway

riogenesis bacterial

acylation, Met

acylation, Met

ition in Vibrio

I transport systems

rochrome d ubiquinol oxidases

charide assembly

onate and D-Glucuronate Utilization

dnaK gene cluster extended

regulated potassium-efflux system and associated functions

yl-CoA catabolic pathway (core)

etabolism

toskeleton

ic Acid Biosynthesis

versions

osynthesis

, UvrABC system

r Complex I

nase complexes

± Menaquinone-cytochrome c reductase complexes

nase complexes

ssing and degradation, bacterial

tress

tylmuramate from Fructose-6-phosphate Biosynthesis

hain amino acid degradation regulons

ation in Thermotogales

VA-metabolizing Zn-dependent hydrolases

/toskeleton

synthesis

on elongation factors, archaeal

Metabolism

72.7.peg.546

m II

.SU eukaryotic and archaeal

one Biosynthesis via Futasine -- gjo

A Biosynthesis

id proteins

ation

inolamine dehydratase

/ision clusters relating to chromosome partitioning

uction-associated complexes

can Biosynthesis

synthetases

n Cluster

ation in Thermotogales

al Related to Dihydroorotate dehydrogenase

79.3.peg.746

-A118-like prophages

-Modification System

ation in Thermotogales

59.3.peg.1840

to chromium compounds

charide assembly

' synthase

aminopropionate ammonia-lyase cluster

synthesis

charide Biosynthesis

fication Archaea

, bacterial

cluster assembly

hydrogenase

utilization

ins

onate and D-Glucuronate Utilization

transfer related cluster

utilization

11.1.peg.2330

SU eukaryotic and archaeal

rolases

Biosynthesis

erin cytosine dinucleotide

rotein

B12 biosynthesis

Metabolism

e eukaryotic

ication cluster

e and Deoxynucleoside Catabolism

tide reduction

respiratory reductases

ation

f Peptidoglycan Amino Acids

yl-CoA pathway of C2 assimilation

synthesis

synthesis

rochrome C oxidases

locating NADH-quinone oxidoreductase and rnf-like group of electron transport complexes

:: Intermediate for synthesis of Tryptophan, PAPA antibiotics, PABA, 3-hydroxyanthranilate and more.

lehydrogenase

, UvrABC system

osynthesis

E cluster

stress Response

e and ketogluconates metabolism

: Non-redox reactions

abolism

d Maltodextrin Utilization

l transport systems

etabolism

.peg.5158 SK3 including

.peg.3360

SU chloroplast

kdown
egradation
is a hypothetical
is a hypothetical
ation, archaeal
erase archaeal
Glucose Catabolism Pathways
r dehydrogenases 1
Metabolism
lecarboxylase

fermentation to Butyrate
nase complexes
synthesis
osynthesis extended
ninal phosphate cyclase
nce
Metabolism
ulatory proteins
anoid compound degradation
abolism
ation, archaeal
inolamine dehydratase
nase complexes
SU bacterial
ation in Thermotogales
9.4.peg.1292
etabolism II: acetyl-CoA, acetogenesis from pyruvate
in bacteria, ATP-dependent
d Serine Utilization
nal proteins cluster
nce operon in Bacteroides and potentially orthologous operons in other organisms
ation in Thermotogales
zation
erase archaeal
iTPases
5.3.peg.3639
versions
anoid compound degradation
rate to 2-methylaconitate metabolism cluster
, bacterial

ation in Thermotogales
l transport systems
aminopropionate ammonia-lyase cluster
ation, archaeal
d Maltodextrin Utilization

, UvrABC system
 sulfur Assimilation
 d Maltodextrin Utilization
 /toskeleton
 14.1.peg.752
 10.1.peg.134
 / Complex I
 glyoxylate interconversions
 1.1.peg.3039
 instance
 nce operon in Bacteroides and potentially orthologous operons in other organisms
 d lipoteichoic acids biosynthesis
 /toskeleton
 . synthesis
 erase archaeal
 zation
 locating NADH-quinone oxidoreductase and rnf-like group of electron transport complexes
 3.3.peg.2843
 Glutamate, Aspartate and Asparagine Biosynthesis
 e Salvage
 acylation, Gly
 netabolism
 .SU bacterial
 0.10.peg.1536
 f Peptidoglycan Amino Acids
 etabolism II: acetyl-CoA, acetogenesis from pyruvate
 y and exit
 72.7.peg.546
 polysaccharides Biosynthesis and Assembly
 e analogs: mycothiol
 avage system
 iSU eukaryotic and archaeal
 respiratory reductases
 ation
 respiratory reductases
 erase II initiation factors
 difications
 elongation factors eukaryotic and archaeal
 ate transport system
 can Biosynthesis
 ing protein for DyP-type peroxidase and ferritin-like protein oligomers
 tress protein family

 ation in Thermotogales
 / Complex I
 son cycle
 egradation

egradation cluster

Intermediate for synthesis of Tryptophan, PABA antibiotics, PABA, 3-hydroxyanthranilate and more.

Intermediate for synthesis of Tryptophan, PABA antibiotics, PABA, 3-hydroxyanthranilate and more.

Degradation

ycosylation in Bacteria

Salvage

stress Response

igosaccharide biosynthesis

igosaccharide biosynthesis

egradation

Base Excision

containing glycans

containing glycans

etermining Capsular polysaccharide biosynthesis in Staphylococcus

etermining Capsular polysaccharide biosynthesis in Staphylococcus

rimidine Synthesis

toskeleton

At2g40600

CspA family of proteins

ynthesis

ate catabolism

ate catabolism

ynthesis

10.1.peg.134

cation

cation

, bacterial

anoid compound degradation

30.3.peg.464

At3g57180 At3g47450

At3g57180 At3g47450

id and Fatty acid biosynthesis related cluster

id and Fatty acid biosynthesis related cluster

ynthesis

ite, D-glucarate and D-glycerate catabolism

e and ketogluconates metabolism

Non-redox reactions

ynthesis

ynthesis

metabolism

drogenase

drogenase

d of Campylobacter

abolism

79.3.peg.746

ntidases (EC 3.4.19.-)

enes utilization

oids

l Biosynthesis

l Biosynthesis

A biosynthesis

A biosynthesis

.SU bacterial

.SU chloroplast

.SU chloroplast

d Maltodextrin Utilization

ation in Thermotogales

gene cluster associated with Met-tRNA formyltransferase

r Complex I

r Complex I

ses

ses

ADP cofactor biosynthesis global

l nitrite ammonification

ADP cofactor biosynthesis global

ADP cofactor biosynthesis global

l transport systems

l Synthesis

l Synthesis Vibrio

biosynthesis

biosynthesis

yl-CoA catabolic pathway (core)

yl-CoA catabolic pathway (core)

ation bacterial

d Maltodextrin Utilization

10.3.peg.1536

24.3.peg.2657

rtochrome C oxidases

etabolism

in 3 containing cluster

-A118-like prophages

.peg.5158 SK3 including

line transport and metabolism

line transport and metabolism

l homes

l homes

-Modification System

ogenesis archaeal

32.1.peg.550

gene cluster associated with Met-tRNA formyltransferase
dnaK gene cluster extended
.peg.3360
D and Sodium-dependent phosphate transporters

3SU chloroplast
lehydrogenase
ge core proteins
of c-type cytochromes
73.3.peg.448
I transport systems
I transport systems
itanediol metabolism
rtochrome d ubiquinol oxidases
rtochrome d ubiquinol oxidases
ouridine syntheses
-Modification System
50.3.peg.3269
ic Acid Biosynthesis
ic Acid Biosynthesis
ccharide assembly
59.3.peg.1840
59.3.peg.1840

l monosaccharide transport cluster
l monosaccharide transport cluster
l monosaccharide transport cluster
l monosaccharide transport cluster
nposition
onate and D-Glucuronate Utilization
onate and D-Glucuronate Utilization

A biosynthesis
lization
Glutamate, Aspartate and Asparagine Biosynthesis
anoid compound degradation
ation specificity factor
iperones
egradation

N-acetylglucosamine utilization
degradation
rotein
rotein
e Biosynthesis
etabolism I: anaplerotic reactions, PEP

utilization
 utilization
 Ethanol Ethanol Synthesis
 line transport and metabolism
 main amino acid degradation regulons
 metabolism II: acetyl-CoA, acetogenesis from pyruvate
 dent RNA helicases, bacterial
 versions
 nce operon in Bacteroides and potentially orthologous operons in other organisms
 54.1.peg.461
 ration (oxidative C2 cycle)
 73.3.peg.2378
 iosynthesis in tRNA
 main amino acid degradation regulons
 e and Deoxynucleoside Catabolism
 cluster around acetyltransferase YpeA in Enterobacteria
 e utilization
 ation, archaeal
 in 3 containing cluster 2
 osynthesis
 nposition
 synthesis
 degradation
 degradation
 s
 e Salvage
 ynthesis AAA pathway 2
 id Creatinine Degradation
 osynthesis
 son cycle
 , bacterial RecFOR pathway
 gration and excision
 sSU chloroplast
 ate catabolism
 etabolism
 and sulfatase modifying factor 1
 d colonization island
 ic Acid Biosynthesis
 , bacterial photolyase
 e transfer related cluster
 cluster assembly

 idoroff Pathway
 Glucose Catabolism Pathways
 and Aspartate uptake in Bacteria
 97.3.peg.2594
 ilization temp

.SU eukaryotic and archaeal
one Biosynthesis via Futasine -- gjo
NA-metabolizing Zn-dependent hydrolases
im cofactor biosynthesis
im cofactor biosynthesis
N-acetylglucosamine utilization
Cluster
A Biosynthesis
id proteins
yl-CoA catabolic pathway (core)
oxidative pathway of Uracil catabolism
d colonization island
cluster assembly
l homes

tress
B12 biosynthesis
54.1.peg.461
termination factors bacterial
ind Gluconeogenesis
14.1.peg.676
cluster assembly
acylation, Val
of Zinc
iperones
saccharide-related cluster in Alphaproteobacteria
cal Hyaluronic Acid Capsule
order branched-chain amino acid (TC 3.A.1.4.1)
hain amino acid degradation regulons
osphate pathway
.peg.567
59.3.peg.1840
ransport and degradation cluster

cretion Pathway
Glutamate, Aspartate and Asparagine Biosynthesis
ynthesis
stis experimental
ed Subsystem Grouping Hypotheticals - perhaps Proteosome Related
eine metabolism
ulatory proteins
respiratory reductases
ation

lation of gene expression
erase archaeal initiation factors
degradation

degradation

73.3.peg.922

orter dipeptide (TC 3.A.1.5.2)

rtochrome C oxidases

rreredoxin oxidoreductase

31.1.peg.2330

39.4.peg.1996B

AT4G12830 (COG0596)

yde assimilation: Ribulose monophosphate pathway

ydroxyproline uptake and utilization

ie

! Synthesis

39.3.peg.2220

21.3.peg.1913

icating decarboxylases and related biotin-dependent enzymes

ynthesis

o FAD

kdown

FMN and FAD metabolism

Glutamate, Aspartate and Asparagine Biosynthesis

36.1.peg.3133

39.3.peg.2220

itis experimental

d Maltodextrin Utilization

xylase and Allophanate hydrolase cluster

bypass

olyl cis-trans isomerase

ion cycle

osynthesis

synthesis

acylation, Glu and Gln

hain amino acid degradation regulons

o-occurring Genes

e and Deoxynucleoside Catabolism

ylthiotransferase containing cluster

osynthesis extended

genesis

/ Complex I

two-component regulatory system

urine Biosynthesis

' synthase

e B6-F complex

glyoxylate interconversions

3-regulated potassium-efflux system and associated functions

-Archaeosine Biosynthesis

oxidative pathway of Uracil catabolism
eptose biosynthesis
d Betaine Uptake and Betaine Biosynthesis
metabolism
degradation
:-Binding-Protein-Dependent Transport System for α-Glucosides
CspA family of proteins

l homes
osynthesis
99.3.peg.2220
locating NADH-quinone oxidoreductase and rnf-like group of electron transport complexes
23.1.peg.1311
id proteins
metabolism
ic Acid Biosynthesis
one Biosynthesis via Futasine -- gjo
charide Biosynthesis

ydrogenase
ilization
inolamine dehydratase
e Biosynthesis
e Biosynthesis
rotein
Metabolism
ua5 protein family
ADP cofactor biosynthesis global
RNA binding protein YlqC
ation
idoroff Pathway
hain amino acid degradation regulons
d Serine Utilization
s
danese-domain proteins
hain amino acid degradation regulons
90.3.peg.464
54.1.peg.1690
id proteins
3.1.peg.459
abolism
:-Binding-Protein-Dependent Transport System for α-Glucosides
olysaccharides Biosynthesis and Assembly
genesis strays
xylase and Allophanate hydrolase cluster
retion system orphans
Metabolism

E cluster
 . synthesis
 degradation
 synthesis
 diolases
 cytochrome d ubiquinol oxidases
 xidoreductase family
 ninal phosphate cyclase
 M biosynthesis
 of Oxidative Stress Response
 31.3.peg.3674
 amino acid degradation
 ranch of beta-ketoadipate pathway
 of cytochrome c oxidases
 gration and excision
 e hydrolase 2 and Biotin carboxylase cluster
 nase complexes
 e Synthesis
 id Ornithine Degradation
 ic Acid Biosynthesis

on factors bacterial
 ation in Thermotogales
 metabolism

m l

39.4.peg.1292
 ine utilization
 ind Gluconeogenesis, including Archaeal enzymes

of Manganese
 osynthesis

ydroxyproline uptake and utilization
 order alkylphosphonate (TC 3.A.1.9.1)
 Metabolism
 elongation factors bacterial
 ransport and degradation cluster
 cus pyogenes recombinatorial zone
 39.4.peg.1292
 ielenate and selenite
 is a hypothetical
 id Ornithine Degradation
 order branched-chain amino acid (TC 3.A.1.4.1)
 l Serine Utilization
 thesis

- Base Excision
- 1.1.peg.2330
- AT1G06240
- homes
- omerases, Type I, ATP-independent
- in
- metabolism by tetrahydropterines
- metabolism by tetrahydropterines
- rotein
- transport systems
- Intermediate for synthesis of Tryptophan, PABA antibiotics, PABA, 3-hydroxyanthranilate and more.
- in bacteria, ATP-dependent
- 72.3.peg.6046
- yl-CoA pathway of C2 assimilation
- on initiation, bacterial sigma factors
- e B6-F complex
- 38.3.peg.1509
- adation
- homes
- one and Phylloquinone Biosynthesis
- e subunit alpha archaeal cluster
- fication Bacteria
- Intermediate for synthesis of Tryptophan, PABA antibiotics, PABA, 3-hydroxyanthranilate and more.
- nposition
- 1.1.peg.3039
- bypass
- perones
- subunits
- erase archaeal
- lanine Serine Interconversions
- .SU bacterial
- yl-CoA catabolic pathway (core)
- Degradation
- 36.1.peg.3133
- ural proteins, bacterial
- cretion Pathway
- glyoxylate interconversions
- abolism
- mino acid degradation
- charide assembly
- of glutathione as a sulphur source
- Metabolism
- ulatory proteins
- osynthesis
- ed Subsystem Grouping Hypotheticals - perhaps Proteosome Related
- anoid compound degradation

ynthesis

54.1.peg.461

gene cluster associated with Met-tRNA formyltransferase

zation

s

fication Archaea

hain amino acid degradation regulons

30.1.peg.1561

ynthesis DAP Pathway

ation, archaeal

ibination, archaeal

ydrogenase

e: Redox cycle

osynthesis

mino acid interconversions with aryl acids

Glutamate, Aspartate and Asparagine Biosynthesis

s

protein S12p Asp methylthiotransferase

protein S12p Asp methylthiotransferase

ydrogenase

tide reduction

36.1.peg.3133

min Catabolism

ISU bacterial

er 2 (AI-2) transport and processing (IsrACDBFGE operon)

urine Biosynthesis

e subunit alpha archaeal cluster

cluster in Enterobacteriaceae downstream from YqjA, a DedA family protein

line transport and metabolism

r Base Excision

mino acid degradation

tilization

rotein complex

ssimilation

36.6.peg.291

ransport and degradation cluster

nase complexes

ince mechanisms

eins (nucleoside triphosphate hydrolases)

orter oligopeptide (TC 3.A.1.5.1)

l homes

metabolism

jugative transfer system, IncI1 type

Dehydration

osynthesis

degradation

Resistance Efflux Pumps

Ala biosynthesis

regulated Fatty Acids synthesis

N-acetylglucosamine utilization

Glutamate, Aspartate and Asparagine Biosynthesis

Ala Related to Dihydroorotate dehydrogenase

glycosylase

Resistance

Proteome

Prolyl cis-trans isomerase

Initiation factors bacterial

Dent RNA helicases, bacterial

Protein Archaea

, bacterial

73.3.peg.2378

Idoroff Pathway

Chain amino acid degradation regulons

Oxidogenesis bacterial

ASU bacterial

Proteome C oxidases

ADP cofactor biosynthesis global

Protein Cluster

Protein Archaea

Gene cluster associated with Met-tRNA formyltransferase

Oxidogenesis

Hydroxyproline uptake and utilization

Protein

Protein: Intermediate for synthesis of Tryptophan, PABA antibiotics, PABA, 3-hydroxyanthranilate and more.

Protein

Protein, archaeal

Protein transferase

Protein synthesis

Protein synthesis AAA pathway 2

Protein transferase

1.1.peg.3039

Protein bacterial

Ala biosynthesis

Protein Complex I

Alanine Serine Interconversions

Protein I

Protein Degradation

Protein initiation, bacterial sigma factors

Protein cluster assembly

Oxidogenesis

egradation
' synthase
e Biosynthesis
ynthesis DAP Pathway
B12 biosynthesis
B12 biosynthesis
dent RNA helicases, bacterial
54.1.peg.1690
one Biosynthesis via Futalosine -- gjo
mino acid degradation
in bacteria, ATP-dependent
id Ornithine Degradation
erase bacterial
23.1.peg.1311
99.4.peg.1292
osynthesis
e Biosynthesis
nal proteins cluster
.SU bacterial
bypass
etabolism I: anaplerotic reactions, PEP
id Ornithine Degradation
and putative sugar transporter
ic Acid Biosynthesis
SU bacterial
netabolism
10.3.peg.2335

mino acid degradation
3iosynthesis FASI
3iosynthesis FASI
3iosynthesis FASI
ite, D-glucarate and D-glycerate catabolism
e transfer related cluster
ydroxyproline uptake and utilization
on elongation factors, archaeal
3iosynthesis
istance
57.3.peg.390
f Peptidoglycan Amino Acids
SU bacterial
e utilization
rtochrome C oxidases
neostasis
e Biosynthesis
olyl cis-trans isomerase

olyl cis-trans isomerase
rvation
one and Phylloquinone Biosynthesis
e bacterial
ation, archaeal
57.3.peg.563
ation, archaeal
te metabolism
versions
itanol Ethanol Synthesis
mino acid degradation
osynthesis
orter branched-chain amino acid (TC 3.A.1.4.1)
glyoxylate interconversions
e subunit alpha archaeal cluster
99.3.peg.2220
honate utilization
fication Archaea

ynthesis DAP Pathway
osynthesis
nposition
versions
tress
ATP synthase
ation specificity factor
olocating NADH-quinone oxidoreductase and rnf-like group of electron transport complexes
r dehydrogenases 1
tide reduction
of Manganese
, bacterial UvrD and related helicases
kdown
ADP cofactor biosynthesis global
gration and excision
catabolism
rimidine Synthesis
fication Archaea
id Creatinine Degradation

tide reductase cluster
bypass
osynthesis extended
in bacteria, ATP-dependent
acylation, Gly
54.1.peg.1690
nce operon in Bacteroides and potentially orthologous operons in other organisms
ydrogenase

metabolism
hydrogenase
synthesis
degradation
lation of gene expression
egradation
id Ornithine Degradation
ation in Thermotogales
orter oligopeptide (TC 3.A.1.5.1)
rated Fatty Acids synthesis
tributed proteins not in subsystems
.peg.2917
ilization
respiratory reductases
xal Metabolism
ecular synthesis operon
Glutamate, Aspartate and Asparagine Biosynthesis
synthetases
.SU bacterial
etabolism I: anaplerotic reactions, PEP
xylate cycle
egradation
ision clusters relating to chromosome partitioning
nase complexes
orter dipeptide (TC 3.A.1.5.2)
d Serine Utilization
adation
hain amino acid degradation regulons
01.1.peg.2330
e and Deoxynucleoside Catabolism
utilization
e, carboxysome

' synthase
ecular synthesis operon