

Table S1. Core proteins described as having a general functional characterization or no functional characterization.

Protein	Organism	Approximate DNA Coordinates	Locus Tag*	Gene Associated Description
prot31 (Unknown Function)	<i>Arthrobacter sp.</i> FB24	2676632...2678221 (-)	Arth_2389	GTP1/OBG subdomain PFAM
	<i>C. crescentus</i> CB15	331907...332971 (-)	CC0315	GTP-binding protein CgtA
	<i>D. radiodurans</i> R1	86474...87790 (-)	DR0084	GTP-binding protein Obg
	<i>D. desulfuricans</i> G20	2696935...2698218 (-)	Dde_2690	GTP-binding protein, GTP1/OBG family
	<i>D. vulgaris</i> Hilldenborough	1018596...1019696 (+)	DVU0929	GTP-binding protein, GTP1/OBG family
	<i>G. metallireducens</i> GS-15	3597639...3598655 (+)	Gmet_3197	GTP-binding protein, GTP1/OBG family
	<i>G. sulfurreducens</i> PCA	3519000...3520016 (-)	GSU3213	GTP-binding protein, GTP1/OBG family
	<i>P. fluorescens</i> PfO-1	5477922...5479145 (-)	Pfl_4858	GTP-binding protein, GTP1/Obg family
	<i>P. ubique</i> HTC1062	221539...222522 (+)	SAR11_0222	GTP-binding protein
	<i>R. sphaeroides</i> 2.4.1	17904...18932 (+)	RSP3822	ATP/GTP-binding site motif A (P-loop):GTP1/OBG family
	<i>S. oneidensis</i> MR-1	3805701...3806867 (-)	SO3649	GTP-binding protein, GTP1/Obg family
	<i>S. typhi</i> TY2	3310236...3311408 (-)	t3218	Probable GTP-binding protein
	<i>S. typhimurium</i> LT2	3470219...3471391	STM3301	Putative GTP-binding protein
	<i>Synechocystis sp.</i> PCC6803	397037...398143 (+)	slr1090	GTP-binding protein
	<i>Y. enterocolitica</i>	489388...490560 (+)	YE0421	Putative GTP-binding factor
	<i>Y. pestis</i> KIM	758194...759366 (+)	y0675	Putative GTP-binding factor
	<i>Y. pseudotuberculosis</i> YPIII	551563...552735 (+)	YPTB0467	Putative GTP-binding protein
prot36 (Unknown Function)	<i>Arthrobacter sp.</i> FB24	2671314...2671715 (-)	Arth_2383	Iojap-related protein TIGR
	<i>C. crescentus</i> CB15	3676177...3676518 (+)	CC3432	Iojap-related protein
	<i>D. radiodurans</i> R1	2588246...2588596 (-)	DR2580	conserved hypothetical protein
	<i>D. desulfuricans</i> G20	1813661...1814056 (+)	Dde_1756	Iojap-related protein
	<i>D. vulgaris</i> Hilldenborough	1702850...1703254 (+)	DVU1618	Iojap-related protein
	<i>G. metallireducens</i> GS-15	3601811...3602206 (+)	Gmet_3201	Iojap-related protein
	<i>G. sulfurreducens</i> PCA	3515275...3515670 (-)	GSU3209	Iojap-related protein
	<i>P. fluorescens</i> PfO-1	5600475...5600969 (-)	Pfl_4972	Hypothetical protein
	<i>P. ubique</i> HTC1062	225411...225761 (+)	SAR11_0226	Iojap-related protein
	<i>R. sphaeroides</i> 2.4.1	2616422...2616742 (+)	RSP0865	Iojap protein family
	<i>S. oneidensis</i> MR-1	1213093...1213422 (-)	SO1170	Iojap domain protein
	<i>S. typhi</i> TY2	2291579...2291896 (+)	t2225	Conserved hypothetical protein (ybeB)
	<i>S. typhimurium</i> LT2	704426...704743 (-)	STM0642	Homolog of plant Iojap protein (ybeB)
	<i>Synechocystis sp.</i> PCC6803	1245395...1245859 (+)	slr1886	Hypothetical protein
	<i>Y. enterocolitica</i> **	3271557...3271874 (+)	YE3000	Hypothetical protein

prof325 (Hypothetical Protein)	<i>Y. pestis</i> KIM**	1324183...1324500 (-)	y1180	Hypothetical protein
	<i>Y. pseudotuberculosis</i> YPIII	1316981...1317298 (-)	YPTB1099	Conserved hypothetical protein
	<i>Arthrobacter</i> sp. FB24	2513295...2514071 (-)	Arth_2234	Conserved hypothetical protein
	<i>C. crescentus</i> CB15	3658975...3659691 (-)	CC3415	Conserved hypothetical protein
	<i>D. radiodurans</i> R1	1535576...1536304 (-)	DR1520	Conserved hypothetical protein
	<i>D. desulfuricans</i> G20	2040355...2041071 (+)	Dde_1997	Conserved hypothetical protein
	<i>D. vulgaris</i> Hilldenborough	1764117...1764866 (+)	DVU1685	Conserved hypothetical protein
	<i>G. metallireducens</i> GS-15	3800542...3801733 (+)	Gmet_3387	Conserved hypothetical protein
	<i>G. sulfurreducens</i> PCA	477066...477848 (-)	GSU0446	Conserved hypothetical protein
	<i>P. fluorescens</i> PfO-1	5951311...5952030 (+)	Pfl_5288	Hypothetical protein
	<i>P. ubique</i> HTC1062**	143525...144226 (-)	SAR11_0136	Conserved hypothetical protein
	<i>R. sphaeroides</i> 2.4.1	2765413...2766186 (-)	RSP1007	Conserved hypothetical protein
	<i>S. oneidensis</i> MR-1	850577...851308 (-)	S0832	Conserved hypothetical proteins
	<i>S. typhi</i> TY2	3097369...3098100 (+)	t3006	Conserved hypothetical protein
	<i>S. typhimurium</i> LT2	3256140...3256919 (+)	STM3094	Putative cytoplasmic protein (yggJ)
	<i>Synechocystis</i> sp. PCC6803	108290...109201 (+)	slr0722	Hypothetical protein
	<i>Y. enterocolitica</i>	3740817...3741548 (+)	YE426	Hypothetical protein
	<i>Y. pestis</i> KIM**	3654517...3655248 (+)	y3320	Hypothetical protein
	<i>Y. pseudotuberculosis</i> YPIII	3772297...3773028 (+)	YPTB3206	Conserved hypothetical protein
	prof330 (Unknown Function)	<i>Arthrobacter</i> sp. FB24	2519298...2521151 (-)	Arth_2240
<i>C. crescentus</i> CB15		1165328...1167274 (-)	CC1034	GTP-binding protein LepA
<i>D. radiodurans</i> R1		1153825...1155645 (-)	DR1145	GTP-binding elongation factor family protein LepA
<i>D. desulfuricans</i> G20		2802606...2804411 (-)	Dde_2817	Small GTP-binding protein domain:GTP-binding protein
<i>D. vulgaris</i> Hilldenborough		782190...783995 (+)	DVU0703	GTP-binding protein LepA
<i>G. metallireducens</i> GS-15		1980477...1982366 (+)	Gmet_1766	GTP-binding protein LepA
<i>G. sulfurreducens</i> PCA		1377368...1379170 (+)	GSU1266	GTP-binding protein LepA
<i>P. fluorescens</i> PfO-1		1153445...1155241 (+)	Pfl_0992	GTP-binding protein lepA
<i>P. ubique</i> HTC1062		438405...440213 (+)	SAR11_0444	GTP-Binding protein lepA
<i>R. sphaeroides</i> 2.4.1		681644...683443 (-)	RSP2088	GTP-binding elongation factor
<i>S. oneidensis</i> MR-1		1402041...1403831 (+)	SO1346	GTP-binding protein (LepA)
<i>S. typhi</i> TY2		312191...313990 (+)	t0274	GTP-binding protein LepA
<i>S. typhimurium</i> LT2		2726772...2728571 (-)	STM2583	GTP-binding elongation factor (lepA)
<i>Synechocystis</i> sp. PCC6803		3564838...3566649 (+)	slr0604	GTP-binding protein
<i>Y. enterocolitica</i>		1134410...1136209 (+)	YE1015	GTP-binding elongation factor (lepA)
<i>Y. pestis</i> KIM		1438342...1440141 (+)	y1295	GTP-binding elongation factor (lepA)

	<i>Y. pseudotuberculosis</i> YPIII	3422285...3424084 (-)	YPTB1099	Putative GTP-binding elongation factor (lepA)
prof371 (Hypothetical Protein)	<i>Arthrobacter</i> sp. FB24	2593536...2594291 (-)	Arth_2304	Protein of unknown function DUF28
	<i>C. crescentus</i> CB15	3504459...3505214 (-)	CC3243	Conserved hypothetical protein
	<i>D. radiodurans</i> R1	2550845...2551579 (-)	DR2548	Conserved hypothetical protein
	<i>D. desulfuricans</i> G20	2342035...2342781 (-)	Dde_2325	Protein of unknown function DUF28
	<i>D. vulgaris</i> Hilddenborough	2352787...2353530 (-)	DVU2259	Conserved hypothetical protein
	<i>G. metallireducens</i> GS-15	817626...818369 (+)	Gmet_0743	Hypothetical protein
	<i>G. sulfurreducens</i> PCA	1163086...1163829 (+)	GSU1074	Conserved hypothetical protein
	<i>P. fluorescens</i> PfO-1	4969166...4969912 (-)	Pfl_4410	Hypothetical UPF0082 protein
	<i>P. ubique</i> HTC1062	578863...579588 (+)	SAR11_0592	Domain of unknown function DUF28
	<i>R. sphaeroides</i> 2.4.1	2393628...2394374 (-)	RSP0655	Conserved hypothetical
	<i>S. oneidensis</i> MR-1	2540604...2541350 (-)	SO2432	Expressed protein of unknown function DUF28
	<i>S. typhi</i> TY2	1066996...1067736 (+)	t0978	Conserved hypothetical protein (yebC)
	<i>S. typhimurium</i> LT2	1993786...1994526 (-)	STM1899	Putative cytoplasmic protein (yebC)
	<i>Synechocystis</i> sp. PCC6803**	22572036...2257964 (+)	slr0989	Hypothetical protein
	<i>Y. enterocolitica</i>	2583739...2584482 (-)	YE2395	Hypothetical protein
	<i>Y. pestis</i> KIM	2484824...2485579 (-)	y2255	Hypothetical protein
	<i>Y. pseudotuberculosis</i> YPIII	2402812...2403555	YPTB2038	Conserved hypothetical protein
prof738 (Hypothetical Protein)	<i>Arthrobacter</i> sp. FB24	2809834...2810412 (+)	Arth_2509	Putative methyltransferase
	<i>C. crescentus</i> CB15	243490...244056 (-)	CC0227	Conserved hypothetical protein
	<i>D. radiodurans</i> R1	655597...656157 (-)	DR0643	N-6 adenine-specific DNA restriction methylase, Putative
	<i>D. desulfuricans</i> G20	1834501...1835070 (+)	Dde_1782	Conserved hypothetical protein
	<i>D. vulgaris</i> Hilddenborough	1599751...1600323 (+)	DVU1531	Methyltransferase, Putative
	<i>G. metallireducens</i> GS-15	1974741...1975307 (-)	Gmet_1760	Hypothetical protein
	<i>G. sulfurreducens</i> PCA	1345954...1346517 (-)	GSU1244	Methyltransferase, Putative
	<i>P. fluorescens</i> PfO-1	6000676...6001284 (+)	Pfl_5340	Methyltransferase, Putative
	<i>P. ubique</i> HTC1062	157024...157590 (+)	SAR11_0154	N6-adenine-specific methylase
	<i>R. sphaeroides</i> 2.4.1	2651080...2651634 (+)	RSP0901	N-6 Adenine-specific DNA methylase
	<i>S. oneidensis</i> MR-1	4782794...4783441 (+)	SO4587	Putative methylase involved in ubiquinone biosynthesis
	<i>S. typhi</i> TY2	4089701...4090297 (-)	t3950	Conserved hypothetical protein
	<i>S. typhimurium</i> LT2	3740347...3740943 (+)	STM3572	Putative methyltransferase
	<i>Synechocystis</i> sp. PCC6803**	2385351...2385911 (+)	slr0383	Hypothetical protein
	<i>Y. enterocolitica</i> **	259672...260226 (-)	YE0224	Hypothetical protein
	<i>Y. pestis</i> KIM**	463268...463930 (-)	y0415	Hypothetical protein

prof774 (Unknown Function)	<i>Y. pseudotuberculosis</i> YPIII	262318...262980 (-)	YPTB0220	Conserved hypothetical protein
	<i>Arthrobacter</i> sp. FB24	2896748..2897452 (-)	Arth_2580	Ham1-like protein TIGR
	<i>C. crescentus</i> CB15	156966...157550 (-)	CC0146	Ham1 family protein
	<i>D. radiodurans</i> R1	179684...180286 (+)	DR0179	Conserved hypothetical protein
	<i>D. desulfuricans</i> G20	511225...511854 (-)	Dde_0504	Ham1-like protein
	<i>D. vulgaris</i> Hilldenborough	3307131...3307754 (+)	DVU3154	HAM1 family protein
	<i>G. metallireducens</i> GS-15	2090602...2091192 (-)	Gmet_1875	HAM1-like protein
	<i>G. sulfurreducens</i> PCA	1960195...1960794 (-)	GSU1794	HAM1 protein
	<i>P. fluorescens</i> PfO-1	5487966...5988562 (+)	Pfl_5326	HAM1 protein homolog
	<i>P. ubique</i> HTC1062	361572...362174 (+)	SAR11_0370	HAM1 protein homolog
	<i>R. sphaeroides</i> 2.4.1	2994982...2995593 (+)	RSP1222	Putative Ham1p_like, Ham1 family
	<i>S. oneidensis</i> MR-1	3500363...3500980 (+)	SO3358	Non-canonical purine NTP pyrophosphatase, rdgB/HAM1
	<i>S. typhi</i> TY2	3103707...3104300 (+)	t3015	Conserved hypothetical protein
	<i>S. typhimurium</i> LT2	3262528...3263121 (+)	STM3103	Putative Xanthosine triphosphate pyrophosphatase
	<i>Synechocystis</i> sp. PCC6803	2151606...2152190 (+)	slr0402	Hypothetical protein
	<i>Y. enterocolitica</i>	3750245...3750838 (+)	YE3437	Putative ribosomal protein
	<i>Y. pestis</i> KIM	3663573...3664244 (+)	y3331	Putative ribosomal protein
<i>Y. pseudotuberculosis</i> YPIII	3781431...3782024 (+)	YPTB3217	Possible Xanthosine triphosphate pyrophosphatase	
prof901 (Regulatory Function)	<i>Arthrobacter</i> sp. FB24	3165359..3167287 (-)	Arth_2817	Small GTP-binding protein domain:GTP-binding protein (TypA_BipA)
	<i>C. crescentus</i> CB15	811916...813748 (-)	CC0741	elongation factor Tu family protein
	<i>D. radiodurans</i> R1	1206001...1207782 (-)	DR1198	GTP-binding elongation factor family protein TypA/BipA
	<i>D. desulfuricans</i> G20	1551395...1553239 (-)	Dde_1533	Small GTP-binding protein domain:GTP-binding protein TypA
	<i>D. vulgaris</i> Hilldenborough	2323364...2325205 (+)	DVU2231	GTP-binding protein TypA
	<i>G. metallireducens</i> GS-15	3397598...3399394 (+)	Gmet_3013	GTP-binding protein
	<i>G. sulfurreducens</i> PCA	533056...534852 (+)	GSU0500	GTP-binding protein TypA
	<i>P. fluorescens</i> PfO-1	391491...393311 (+)	Pfl_0347	GTP-binding protein TypA/BipA
	<i>P. ubique</i> HTC1062	168376...170202 (+)	SAR11_0165	GTP-binding protein, TypA
	<i>R. sphaeroides</i> 2.4.1	2178615...2180435 (+)	RSP0448	EF-Tu; elongation factor Tu
	<i>S. oneidensis</i> MR-1	4600874...4602685 (-)	SO4408	virulence regulator BipA
	<i>S. typhi</i> TY2	3711782...3713605 (-)	t3613	GTP-binding elongation factor family protein (typA)
	<i>S. typhimurium</i> LT2	4217384...4219207 (+)	STM4009	GTP-binding protein (typA)
	<i>Synechocystis</i> sp. PCC6803	204604...206397 (+)	slr1105	GTP-binding protein TypA/BipA
	<i>Y. enterocolitica</i>	38529...40352 (+)	YE0029	Putative GTP-binding factor
	<i>Y. pestis</i> KIM	4221887...4223710 (-)	y3803	Putative GTP-binding factor

prot902 (Hypothetical Protein)

<i>Y. pseudotuberculosis</i> YPIII	34478...36301 (+)	YPTB0025	Putative GTPase (bipA)
<i>Arthrobacter</i> sp. FB24	3185803...3186909 (-)	Arth_2831	GTP-binding protein YchF
<i>C. crescentus</i> CB15	499915...501015 (-)	CC0479	GTP-binding protein, YchF family
<i>D. radiodurans</i> R1	1391767...1392864 (+)	DR1386	conserved hypothetical protein
<i>D. desulfuricans</i> G20	1752704...1753804 (-)	Dde_1698	Conserved hypothetical protein
<i>D. vulgaris</i> Hilldenborough	1503735...1504835 (-)	DVU1429	GTP-binding protein
<i>G. metallireducens</i> GS-15	3223418...3224512 (-)	Gmet_2845	GTP-binding protein
<i>G. sulfurreducens</i> PCA	700226...701320 (+)	GSU0664	GTP binding protein YchF
<i>P. fluorescens</i> PfO-1	5359504...5360604 (+)	Pfl_4756	GTP-binding protein YchF
<i>P. ubique</i> HTC1062	109411...110484 (+)	SAR11_0097	Predicted GTPase, Probable translation factor
<i>R. sphaeroides</i> 2.4.1	2577892...2578989 (+)	RSP0832	Putative GTP-binding protein
<i>S. oneidensis</i> MR-1	1228241...1229332 (+)	SO1185	GTPase/translation factor
<i>S. typhi</i> TY2	1176621...1177712 (-)	t1092	Putative ATP/GTP-binding protein
<i>S. typhimurium</i> LT2	1881818...1882909 (+)	STM1784	Putative GTP-binding protein
<i>Synechocystis</i> sp. PCC6803	1520009...1521100 (-)	sll0245	Probable GTP binding protein
<i>Y. enterocolitica</i>	2629139...2630230 (+)	YE2439	Putative GTP-binding protein
<i>Y. pestis</i> KIM	2533619...2534710 (+)	y2298	Putative GTP-binding protein
<i>Y. pseudotuberculosis</i> YPIII	2354015...2355106 (-)	YPTB3217	Conserved hypothetical protein

prot1177 (Hypothetical Protein)

<i>Arthrobacter</i> sp. FB24	1311164...1312177 (+)	Arth_1206	Protein of unknown function UPF0011 TIGR
<i>C. crescentus</i> CB15	154912...155784 (-)	CC0144	Tetrapyrrole methylase family protein
<i>D. radiodurans</i> R1	650694...651653 (-)	DR0636	Conserved hypothetical protein
<i>D. desulfuricans</i> G20	1122376...1123209 (-)	Dde_1092	Protein of unknown function UPF0011
<i>D. vulgaris</i> Hilldenborough	922377...923204 (-)	DVU0832	Tetrapyrrole methylase family protein
<i>G. metallireducens</i> GS-15	3246398...3247246 (-)	Gmet_2861	Hypothetical protein
<i>G. sulfurreducens</i> PCA	683565...684425 (+)	GSU0653	Tetrapyrrole methylase family protein
<i>P. fluorescens</i> PfO-1	1348994...1347876 (-)	Pfl_4683	Decarboxylase family protein
<i>P. ubique</i> HTC1062	363342...364205 (+)	SAR11_0372	Possible methylase or methyltransferase
<i>R. sphaeroides</i> 2.4.1	401856...402743 (+)	RSP1813	Conserved hypothetical protein
<i>S. oneidensis</i> MR-1	306578...307423 (+)	SO0301	Methyltransferase
<i>S. typhi</i> TY2	3275053...3275916 (-)	t3183	Conserved hypothetical protein
<i>S. typhimurium</i> LT2	3432400...3433263 (-)	STM3263	Putative methyltransferase
<i>Synechocystis</i> sp. PCC6803	1691493...1692332 (-)	sll0818	Tetrapyrrole methylase family protein
<i>Y. enterocolitica</i>	4067751...4068650 (-)	YE3726	Hypothetical protein
<i>Y. pestis</i> KIM**	125918...126817 (-)	y0117	Hypothetical protein
<i>Y. pseudotuberculosis</i> YPIII	41575324...4158423 (-)	YPTB3492	Possible tetrapyrrole methylase family protein

*<http://img.jgi.doe.gov/cgi-bin/pub/main.cgi>; **Not observed