

Table S1. OstA homologues in completely sequenced genomes.

Tr	16S	Gp_Abb	OstA ¹	Definition	Organism	Protein size	Recognized domain	GI#	TMS ²	SP ³	TMp ⁴	logP ⁵	Cat ⁶
1	1	G_Eca1	B	Organic solvent tolerance protein precursor	<i>Erwinia carotovora</i> subsp. <i>atroseptica</i> SCRI1043	787	A'C	49613303	0	Y	n7-17c24/25o	11	0
1	1	G_Ecoc1	B	Organic solvent tolerance protein precursor	<i>Escherichia coli</i> CFT073	784	AC	26245980	0	Y	n7-17c24/25o	11	1
1	1	G_Ecoe1	B	Organic solvent tolerance	<i>Escherichia coli</i> O157:H7 EDL933	784	AC	15799739	0	Y	n7-17c24/25o	11	1
1	1	G_Ecok1	B	Organic solvent tolerance	<i>Escherichia coli</i> K12	784	AC	1786239	0	Y	n7-17c24/25o	11	1
1	1	G_Ecool	B	Organic solvent tolerance protein	<i>Escherichia coli</i> O157:H7	784	AC	13359515	0	Y	n7-17c24/25o	11	1
1	1	G_Plu1	B	Organic solvent tolerance protein precursor	<i>Photorhabdus luminescens</i> subsp. <i>laumondii</i> TTO1	774	A'C	37524614	0	Y	n8-19c24/25o	11	1
1	1	G_Senc1	B	Organic solvent tolerance protein	<i>Salmonella enterica</i> subsp. <i>enterica</i> serovar Choleraesuis str. SC-B67	786	AC	62178658	0	Y	n7-17c24/25o	11	1
1	1	G_Senp1	B	Organic solvent tolerance protein precursor	<i>Salmonella enterica</i> subsp. <i>enterica</i> serovar Paratyphi A str. ATCC 9150	784	AC	56412364	0	Y	n7-17c24/25o	11	1
1	1	G_Sens1	B	Organic solvent tolerance protein precursor	<i>Salmonella enterica</i> subsp. <i>enterica</i> serovar Typhi str. CT18	784	AC	16759088	0	Y	n7-17c24/25o	11	1
1	1	G_Sent1	B	Organic solvent tolerance protein precursor	<i>Salmonella enterica</i> subsp. <i>enterica</i> serovar Typhi Ty2	784	AC	29140638	0	Y	n7-17c24/25o	11	1
1	1	G_Sfl1	B	Organic solvent tolerance protein	<i>Shigella flexneri</i> 2a str. 301	784	AC	24111500	0	Y	n7-17c24/25o	11	1
1	1	G_Sflt1	B	Organic solvent tolerance protein	<i>Shigella flexneri</i> 2a str. 2457T	784	AC	30061621	0	Y	n7-17c24/25o	11	1
1	1	G_Sso1	B	Organic solvent tolerance	<i>Shigella sonnei</i> Ss046	784	AC	74310673	0	Y	n7-17c24/25o	11	1
1	1	G_Sty1	B	Organic solvent tolerance protein	<i>Salmonella typhimurium</i> LT2	786	AC	16418590	0	Y	n7-17c24/25o	11	1
1	1	G_Ypeb1	B	Organic solvent tolerance protein precursor	<i>Yersinia pestis</i> biovar Medievalis str. 91001	780	AC	45438285	0	Y	n7-17c24/25o	5	1
1	1	G_Ypec1	B	Organic solvent tolerance protein precursor	<i>Yersinia pestis</i> CO92	780	AC	16120825	0	Y	n7-17c24/25o	5	1

1	1	G_Ypek1	B	Organic solvent tolerance protein	<i>Yersinia pestis</i> KIM	792	AC	22127554	0	Y	n19-29c36/37o	5	1
1	1	G_Yps1	B	Organic solvent tolerance	<i>Yersinia pseudotuberculosis</i> IP 32953	780	AC	51594987	0	Y	n7-17c24/25o	10	1
1	2	G_Cblf1	B	Organic solvent tolerance protein precursor	<i>Candidatus Blochmannia floridanus</i>	818	C	33519603	1	0	i22-46o	0	1
1	2	G_Cblp1	B	Organic solvent tolerance protein precursor	<i>Candidatus Blochmannia pennsylvanicus</i> str. BPEN	782	C	71891916	1	0	i7-27o	-1	0
1	2	G_Wgl1	L	Imp	<i>Wigglesworthia glossinidia</i> endosymbiont of <i>Glossina brevipalpis</i>	723	C'	25165972	1	0	i7-25o	0	3
1	3	G_Hdu1	B	Organic solvent tolerance protein	<i>Haemophilus ducreyi</i> 35000HP	779	AC	33152722	0	Y	n6-13c18/19o	-1	1
1	3	G_Hin1	B	Organic solvent tolerance protein	<i>Haemophilus influenzae</i> 86-028NP	782	AC	68057530	0	Y	n6-16c23/24o	9	1
1	3	G_Hinr1	B	Organic solvent tolerance protein	<i>Haemophilus influenzae</i> Rd KW20	782	AC	1573734	0	Y	n6-16c23/24o	9	1
1	3	G_Msu1	B	Imp protein	<i>Mannheimia succiniciproducens</i> MBEL55E	783	AC	52308464	0	Y	n7-17c24/25o	11	3
1	3	G_Pmu1	B	Unknown	<i>Pasteurella multocida</i> subsp. <i>multocida</i> str. Pm70	786	AC	12721996	0	Y	n13-24c28/29o	2	1
1	4	G_Ppr1	B	Hypothetical organic solvent tolerance protein	<i>Photobacterium profundum</i> SS9	788	A'C	54307619	0	Y	n7-18c23/24o	5	1
1	4	G_Vch1	B	Organic solvent tolerance protein	<i>Vibrio cholerae</i> O1 biovar eltor str. N16961	787	AC	15640473	0	Y	n12-23c28/29o	11	3
1	4	G_Vfi1	B	Organic solvent tolerance protein	<i>Vibrio fischeri</i> ES114	786	AC	59710896	0	Y	n8-19c24/25o	1	1
1	4	G_Vpa1	B	Organic solvent tolerance protein	<i>Vibrio parahaemolyticus</i> RIMD 2210633	781	AC	28897113	0	Y	n8-19c24/25o	5	3
1	4	G_Vvuc1	B	Organic solvent tolerance protein OstA	<i>Vibrio vulnificus</i> CMCP6	776	A'C	27360235	0	Y	n8-19c24/25o	4	3
1	4	G_Vvuy1	B	Organic solvent tolerance protein OstA	<i>Vibrio vulnificus</i> YJ016	776	A'C	37678665	0	Y	n8-19c24/25o	4	3
1	5	G_Cps1	B	Organic solvent tolerance protein	<i>Colwellia psychrerythraea</i> 34H	771	C	71279010	0	Y	n7-19c25/26o	-1	1
1	5	G_Ilo1	B	Organic solvent tolerance protein OstA	<i>Idiomarina loihiensis</i> L2TR	757	C	56461329	0	Y	n5-12c20/21o	4	1
1	5	G_Pha1	B	Organic solvent tolerance	<i>Pseudoalteromonas</i>	740	C	77361547	0	0	o	5	0

1	5	G_Son1	B	protein Organic solvent tolerance protein	<i>haloplanktis</i> TAC125 <i>Shewanella oneidensis</i> MR-1	765	C	24375135	0	Y	n6-13c18/19o	-1	1
1	6	G_Aad1	B	Organic solvent tolerance protein precursor	<i>Acinetobacter</i> sp. ADP1	819	C	50085461	0	Y	n13-23c31/32o	10	1
1	6	G_Cbu1	B	Organic solvent tolerance protein	<i>Coxiella burnetii</i> RSA 493	870	C	29655261	0	Y	n8-19c28/29o	1	1
1	6	G_Ftu1	B+P	Organic solvent tolerance protein	<i>Francisella tularensis</i> subsp. <i>tularensis</i> SCHU S4	868	C	56707609	0	Y	n9-20c24/25o	5	3
1	6	G_Ftu2	B+P	Organic solvent tolerance protein	<i>Francisella tularensis</i> subsp. <i>Tularensis</i> SCHU S4	721	C	56707855	0	0	o	4	3
1	6	G_Lpn1	B	Organic solvent tolerance protein	<i>Legionella pneumophila</i> subsp. <i>pneumophila</i> str. Philadelphia 1	889	A'C	52840552	2	0	o12-32i44-65o	2	1
1	6	G_Lpn11	B	Hypothetical protein lpl0350	<i>Legionella pneumophila</i> str. Lens	839	A'C	54293302	0	Y	n2-13c21/22o	6	1
1	6	G_Lpnp1	B	Hypothetical protein lpp0375	<i>Legionella pneumophila</i> str. Paris	839	A'C	54296346	0	Y	n2-13c21/22o	6	1
1	6	G_Mca1	B	Organic solvent tolerance protein, putative	<i>Methylococcus capsulatus</i> str. Bath	1091	C	53805076	0	Y	n3-10c15/16o	9	1
1	6	G_Noc1	B	Organic solvent tolerance protein	<i>Nitrosococcus oceani</i> ATCC 19707	738	C	77165201	0	Y	n8-21c26/27o	4	0
1	6	G_Pae1	B	Organic solvent tolerance protein OstA precursor	<i>Pseudomonas aeruginosa</i> PAO1	924	A'C	15595792	0	Y	n12-23c28/29o	11	1
1	6	G_Par1	B	Possible organic solvent tolerance protein	<i>Psychrobacter arcticus</i> 273-4	912	C	71066074	0	Y	n12-23c27/28o	10	3
1	6	G_Pflo1	B	Organic solvent tolerance protein	<i>Pseudomonas fluorescens</i> PfO-1	937	A'C	77461353	0	Y	n12-22c34/35o	11	3
1	6	G_Pflp1	B	Organic solvent tolerance protein, putative	<i>Pseudomonas fluorescens</i> Pf-5	962	A'C	70732934	0	Y	n29-40c50/51o	11	3
1	6	G_Psyb1	B	Organic solvent tolerance protein	<i>Pseudomonas syringae</i> pv. <i>syringae</i> B728a	926	A'C	66047851	0	Y	n12-22c34/35o	11	1
1	6	G_Psyp1	B	Organic solvent tolerance protein, putative	<i>Pseudomonas syringae</i> pv. <i>phaseolicola</i> 1448A	904	A'C	71735112	0	0	o	11	1
1	6	G_Psytl	B	Organic solvent tolerance protein, putative	<i>Pseudomonas syringae</i> pv. <i>tomato</i> str. DC3000	905	A'C	28867782	0	0	o	11	1
1	7	G_Xax1	B	Organic solvent tolerance precursor	<i>Xanthomonas axonopodis</i> pv. <i>citri</i> str. 306	817	C	21106997	0	Y	n11-22c26/27o	9	1

1	7	G_Xca1	B	Organic solvent tolerance precursor	<i>Xanthomonas campestris</i> pv. <i>campestris</i> str. 8004	809	C	66769739	0	Y	n12-18c22/23o	9	1
1	7	G_Xcaa1	B	Organic solvent tolerance precursor	<i>Xanthomonas campestris</i> pv. <i>campestris</i> str. ATCC 33913	809	C	21230268	0	Y	n7-18c22/23o	9	1
1	7	G_Xfa1	B	Organic solvent tolerance precursor	<i>Xylella fastidiosa</i> 9a5c	792	C	15837439	0	Y	n7-18c22/23o	5	3
1	7	G_Xfat1	B	Organic solvent tolerance precursor	<i>Xylella fastidiosa</i> Temecula1	792	C	28199705	0	Y	n7-18c22/23o	9	3
1	7	G_Xor1	B	Organic solvent tolerance precursor	<i>Xanthomonas oryzae</i> pv. <i>oryzae</i> KACC10331	832	C	58583368	0	Y	n26-37c41/42o	10	1
1	8	B_Aeb1	B	Organic solvent tolerance transmembrane protein	<i>Azoarcus</i> sp. EbN1	787	C	56476035	0	0	o	1	0
1	8	B_Bbr1	B	Putative outer membrane (permeability) protein	<i>Bordetella bronchiseptica</i> RB50	790	A'C	33603076	0	Y	n7-15c20/21o	9	1
1	8	B_Bma1	L	Organic solvent tolerance protein, putative	<i>Burkholderia mallei</i> ATCC 23344	787	C	52428438	0	Y	n22-33c39/40o	11	1
1	8	B_Bpa1	B	Putative outer membrane (permeability) protein	<i>Bordetella parapertussis</i> 12822	790	A'C	33598181	0	Y	n7-15c20/21o	9	1
1	8	B_Bpe1	B	Putative outer membrane (permeability) protein	<i>Bordetella pertussis</i> Tohama I	790	A'C	33594221	0	Y	n7-15c20/21o	9	1
1	8	B_Bps1	B	Hypothetical protein BPSL0658	<i>Burkholderia pseudomallei</i> K96243	787	C	53718301	0	Y	n22-33c39/40o	11	1
1	8	B_Cvi1	B	Organic solvent tolerance protein	<i>Chromobacterium violaceum</i> ATCC 12472	753	C	34499684	0	Y	n9-19c26/27o	11	1
1	8	B_Dar1	B	Organic solvent tolerance protein	<i>Dechloromonas aromatica</i> RCB	849	C	71909271	0	Y	n9-20c25/26o	-2	0
1	8	B_Neu1	B	Putative organic solvent tolerance transmembrane protein	<i>Nitrosomonas europaea</i> ATCC 19718	723	C	30248885	0	Y	n6-17c23/24o	-1	0
1	8	B_Ngo1	B	OstA	<i>Neisseria gonorrhoeae</i> FA 1090	801	C	59802036	0	Y	n10-19c24/25o	11	1
1	8	B_Nmem1	B	Putative organic solvent tolerance protein	<i>Neisseria meningitidis</i> MC58	758	C	7225505	0	0	o	11	1
1	8	B_Nmez1	B	Putative solvent tolerance protein	<i>Neisseria meningitidis</i> Z2491	802	C	7380826	0	Y	n10-20c25/26o	11	1
1	8	B_Reu1	B	Organic solvent tolerance protein	<i>Ralstonia eutropha</i> JMP134	810	AC	73540203	0	0	o	9	1

1	8	B_Rso1	B	PROBABLE ORGANIC SOLVENT TOLERANCE TRANSMEMBRANE PROTEIN	<i>Ralstonia solanacearum</i> GMI1000	811	C	17545234	0	Y	n29-40c48/49o	5	0
1	8	B_Thde1	B	Organic solvent tolerance transmembrane protein	<i>Thiobacillus denitrificans</i> ATCC 25259	728	C	74318355	0	Y	n3-14c19/20o	5	1
1	9	A_Atu1	B	Organic solvent tolerance protein	<i>Agrobacterium tumefaciens</i> str. C58	793	C	17935013	0	Y	n15-26c34/35o	11	1
1	9	A_Bab1	B	Organic solvent tolerance, hypothetical	<i>Brucella abortus biovar 1</i> str. 9-941	792	A'C	62289647	0	Y	n15-30c36/37o	11	1
1	9	A_Bhe1	B	Expressed protein	<i>Bartonella henselae</i> str. Houston-1	789	A'C	49475337	0	Y	n22-33c37/38o	-1	1
1	9	A_Bja1	B+P	Hypothetical protein bli4105	<i>Bradyrhizobium japonicum</i> USDA 110	850	C	27379216	2	0	o12-31i52-72o	11	3
1	9	A_Bja2	B+P	Hypothetical protein blr1955	<i>Bradyrhizobium japonicum</i> USDA 110	817	C	27377066	1	0	i20-41o	11	3
1	9	A_Bme1	B	ORGANIC SOLVENT TOLERANCE PROTEIN	<i>Brucella melitensis</i> 16M	797	C	17983250	0	Y	n20-35c41/42o	11	1
1	9	A_Bqu1	B	Hypothetical protein	<i>Bartonella quintana</i> str. Toulouse	790	A'C	49239603	0	Y	n22-33c38/39o	-1	1
1	9	A_Bsu1	B	Organic solvent tolerance, putative	<i>Brucella suis</i> 1330	792	A'C	23347485	0	Y	n15-30c36/37o	11	1
1	9	A_Ccr1	B	Hypothetical protein CC1689	<i>Caulobacter crescentus</i> CB15	809	C	16125934	0	Y	n24-35c43/44o	11	
1	9	A_Cpe1	L	Organic solvent tolerance-like protein	<i>Candidatus Pelagibacter ubique</i> HTCC1062	814	C'	71083416	0	Y	n5-16c24/25o	-2	1
1	9	A_Gox1	B	Organic solvent tolerance protein	<i>Gluconobacter oxydans</i> 621H	752	C	58038775	0	0	o	11	1
1	9	A_Mlo1	B	Hypothetical protein mll7864	<i>Mesorhizobium loti</i> MAFF303099	808	C	13476524	0	Y	n19-30c37/38o	11	1
1	9	A_Nwi1	B	Organic solvent tolerance protein	<i>Nitrobacter winogradskyi</i> Nb-255	829	C	75675871	0	Y	n34-45c57/58o	9	1
1	9	A_Rco1	B	Organic solvent tolerance protein homolog	<i>Rickettsia conorii</i> str. Malish 7	713	C	15892947	0	Y	n5-16c20/21o	-3	1
1	9	A_Rfe1	B	Organic solvent tolerance protein homolog	<i>Rickettsia felis</i> URRWXCal2	713	C	67004179	0	Y	n5-16c20/21o	-3	1
1	9	A_Rpa1	B	Organic solvent tolerance protein homolog	<i>Rhodopseudomonas palustris</i> CGA009	837	C	39936126	0	Y	n25-40c53/54o	11	1
1	9	A_Rpr1	B	Hypothetical protein	<i>Rickettsia prowazekii</i> str.	711	C	15604517	0	Y	n3-14c18/19o	-3	1

1	9	A_Rsp1	B	RP674 Putative organic solvent tolerance protein	Madrid E <i>Rhodobacter sphaeroides</i> 2.4.1	714	C'	77463459	0	Y	n6-17c21/22o	5	0
1	9	A_Rty1	B	Probable organic solvent tolerance protein OstA	<i>Rickettsia typhi</i> str. Wilmington	711	C	51473853	0	Y	n3-14c18/19o	-3	1
1	9	A_Sme1	B	Hypothetical protein SMc00582	<i>Sinorhizobium meliloti</i> 1021	781	C	15964905	0	Y	n14-27c35/36o	5	1
1	9	A_Spo1	B	Organic solvent tolerance protein, putative	<i>Silicibacter pomeroyi</i> DSS-3	718	C'	56679043	0	Y	n4-15c23/24o	5	0
1	9	A_Zmo1	B	Organic solvent tolerance protein	<i>Zymomonas mobilis</i> subsp. <i>mobilis</i> ZM4	763	A'C	56543781	0	Y	n3-10c15/16o	4	0
1	10	D_Bba1	L	Organic solvent tolerance protein	<i>Bdellovibrio bacteriovorus</i> HD100	803	C'	42523581	0	Y	n6-17c25/26o	1	3
1	10	D_Dps1	B	Related to organic solvent tolerance protein (OstA)	<i>Desulfotalea psychrophila</i> LSv54	932	C'	50877899	0	Y	n24-34c41/42o	-4	
1	10	D_Dvu1	L	Organic solvent tolerance protein, putative	<i>Desulfovibrio vulgaris</i> subsp. <i>vulgaris</i> str. Hildenborough	764	C'	46579367	0	Y	n2-9c21/22o	-1	1
1	10	D_Gsu1	B	Organic solvent tolerance protein, putative	<i>Geobacter sulfurreducens</i> PCA	628	C'	39997463	0	0	o	2	1
1	10	D_Pca1	B	Organic solvent tolerance protein, putative	<i>Pelobacter carbinolicus</i> DSM 2380	701	C'	77918353	0	Y	n10-21c28/29o	-3	1
1	11	E_Cjen1	B	Putative periplasmic protein	<i>Campylobacter jejuni</i> subsp. <i>jejuni</i> NCTC 11168	682	A'C	6968685	0	Y	n5-15c20/21o	5	3
1	11	E_Cjer1	B	Organic solvent tolerance protein, putative	<i>Campylobacter jejuni</i> RM1221	682	C	57238126	0	Y	n5-15c20/21o	5	3
1	11	E_Hhe1	B	Organic solvent tolerance protein	<i>Helicobacter hepaticus</i> ATCC 51449	710	C'	32262144	0	0	o	4	3
1	11	E_Hpy1	B	Conserved hypothetical secreted protein	<i>Helicobacter pylori</i> 26695	660	C	2314377	0	Y	n5-13c18/19o	4	3
1	11	E_Hpyj1	B	Putative role in outer membrane permeability	<i>Helicobacter pylori</i> J99	766	C	15612203	0	Y	n18-26c31/32o	1	3
1	11	E_Wsu1	B	OUTER MEMBRANE PERMEABILITY PROTEIN	<i>Wolinella succinogenes</i> DSM 1740	700	C	34557286	0	Y	n2-12c17/18o	-1	3
1	14	S_Linc1	L	Outer membrane protein, porin superfamily	<i>Leptospira interrogans</i> serovar Copenhageni str. Fiocruz L1-130	991	C'	45657333	0	Y	n5-16c20/21o	5	1
1	14	S_Lin11	L	Hypothetical protein	<i>Leptospira interrogans</i>	991	C'	24215210	0	Y	n5-16c20/21o	5	1

1	15	S_Bbu1	L	LA2510 Hypothetical protein BB0838	serovar Lai str. 56601 <i>Borrelia burgdorferi</i> B31	1146	C'	15595183	0	Y	n13-24c29/30o	-2	1
1	15	S_Bga1	L	Hypothetical protein BG0863	<i>Borrelia garinii</i> Pbi	1133	C'	51573660	0	Y	n2-13c18/19o	0	1
1	15	S_Tde1	L	Hypothetical protein TDE1011	<i>Treponema denticola</i> ATCC 35405	1073	C'	42526522	0	Y	n4-15c22/23o	-3	1
1	15	S_Tpa1	L	Hypothetical protein TP0515	<i>Treponema pallidum</i> subsp. <i>pallidum</i> str. Nichols	991	C	15639506	0	Y	n7-15c19/20o	-3	
1	16	O_Bfm1	L	Conserved hypothetical exported protein	<i>Bacteroides fragilis</i> NCTC 9343	912	C'	60494493	0	Y	n8-19c27/28o	11	3
1	16	O_Bfry1	L	Hypothetical protein BF3817	<i>Bacteroides fragilis</i> YCH46	912	C'	53715101	0	Y	n8-19c27/28o	11	3
1	16	O_Bth1	L	Conserved hypothetical protein	<i>Bacteroides</i> <i>thetaiotaomicron</i> VPI-5482	902	C'	29339443	0	Y	n8-19c27/28o	5	3
1	16	O_Pgi1	L	Hypothetical protein PG1405	<i>Porphyromonas gingivalis</i> W83	951	C'	34541085	0	Y	n13-24c29/30o	1	3
1	16	R_Cte1	L(P?)	Hypothetical protein CT0523	<i>Chlorobium tepidum</i> TLS	963	C'	21673358	0	0	o	5	3
1	12a	Q_Aae1	B	Organic solvent tolerance protein	<i>Aquifex aeolicus</i> VF5	653	C	15606281	0	Y	n2-10c15/16o	-2	1
1	12b	I_Tth1	L(B?)	Hypothetical protein TTC0028	<i>Thermus thermophilus</i> HB27	824	C'	46198336	0	Y	n4-12c16/17o	-2	
1	12b	I_Tthh1	L(B?)	Hypothetical protein TTHA0396	<i>Thermus thermophilus</i> HB8	824	C'	55980365	0	Y	n4-12c16/17o	-2	1
1	N	H_Psp1	L	Hypothetical protein	<i>Parachlamydia</i> sp. UWE25	720	C'	46399882	0	Y	n6-16c21/22o	-3	
1	N	P_Rba1	L	Hypothetical protein- transmembrane prediction	<i>Rhodopirellula baltica</i> SH 1	1120	C'	32445093	0	0	o	1	
2	1	G_Eca2	B	Putative exported protein	<i>Erwinia carotovora</i> subsp. <i>atroseptica</i> SCR11043	190	A	49609776	0	Y	n12-23c27/28o	6	
2	1	G_Ecoc2	B	Protein yhbN precursor	<i>Escherichia coli</i> CFT073	192	A	26249786	0	Y	n19-30c34/35o	-1	
2	1	G_Ecoe2	B	Hypothetical protein Z4563	<i>Escherichia coli</i> O157:H7 EDL933	185	A	15803740	0	Y	n12-23c27/28o	0	
2	1	G_Ecok2	B	Putative transport protein (ABC superfamily, peri_bind)	<i>Escherichia coli</i> K12	185	A	16131090	0	Y	n12-23c27/28o	0	
2	1	G_Ecoo2	B	Hypothetical protein ECs4079	<i>Escherichia coli</i> O157:H7	185	A	15833333	0	Y	n12-22c27/28o	0	

2	1	G_Plu2	B	Hypothetical protein plu4039	<i>Photorhabdus luminescens</i> subsp. <i>laumondii</i> TTO1	177	A	37527891	0	Y	n8-19c23/24o	-3
2	1	G_Senc2	B	Putative ABC superfamily (bind_prot) transport protein	<i>Salmonella enterica</i> subsp. <i>enterica</i> serovar Choleraesuis str. SC-B67	191	A	62181826	0	Y	n19-30c34/35o	-1
2	1	G_Senp2	B	Hypothetical protein SPA3185	<i>Salmonella enterica</i> subsp. <i>enterica</i> serovar Paratyphi A str. ATCC 9150	172	A	56415247	0	Y	n2-11c15/16o	-1
2	1	G_Sens2	B	Hypothetical protein STY3497	<i>Salmonella enterica</i> subsp. <i>enterica</i> serovar Typhi str. CT18	172	A	16762080	0	Y	n2-11c15/16o	-1
2	1	G_Sent2	B	Hypothetical protein t3235	<i>Salmonella enterica</i> subsp. <i>enterica</i> serovar Typhi Ty2	172	A	29143569	0	Y	n2-11c15/16o	-1
2	1	G_Sfl2	B	Hypothetical protein SF3240	<i>Shigella flexneri</i> 2a str. 301	185	A	56480284	0	Y	n12-23c27/28o	0
2	1	G_Sflt2	B	Hypothetical protein S3458	<i>Shigella flexneri</i> 2a str. 2457T	185	A	30064538	0	Y	n12-23c27/28o	0
2	1	G_Sso2	B	Hypothetical protein SSO_3348	<i>Shigella sonnei</i> Ss046	185	A	74313737	0	Y	n12-23c27/28o	0
2	1	G_Sty2	B	Putative ABC superfamily transport protein	<i>Salmonella typhimurium</i> LT2	184	A	16421875	0	Y	n12-23c27/28o	-1
2	1	G_Ypeb2	B	Hypothetical protein YP3835	<i>Yersinia pestis</i> biovar <i>Medievalis</i> str. 91001	188	A	45443566	0	Y	n17-28c32/33o	-1
2	1	G_Ypec2	B	Hypothetical protein YPO3580	<i>Yersinia pestis</i> CO92	181	A	16123724	0	Y	n10-21c25/26o	-1
2	1	G_Ypek2	B	Hypothetical protein y0152	<i>Yersinia pestis</i> KIM	188	A	22124072	0	Y	n17-28c32/33o	-1
2	1	G_Yps2	B	Hypothetical protein YPTB3524	<i>Yersinia pseudotuberculosis</i> IP 32953	181	A	51597816	0	Y	n10-21c25/26o	-1
2	2	G_Cblf2	B	Hypothetical protein Bfl043	<i>Candidatus Blochmannia floridanus</i>	168	A	33519525	1	0	i9-28o	0
2	2	G_Cblp2	B	Putative transport protein (ABC superfamily, peri_bind)	<i>Candidatus Blochmannia pennsylvanicus</i> str. BPEN	169	A	71891835	0	Y	n11-22c27/28o	-1
2	3	G_Hdu2	B	Hypothetical protein HD0587	<i>Haemophilus ducreyi</i> 35000HP	167	A	33151776	0	Y	n7-18c22/23o	2
2	3	G_Hin2	B	Conserved hypothetical protein	<i>Haemophilus influenzae</i> 86-028NP	172	A	68057897	0	Y	n8-18c23/24o	0
2	3	G_Hinr2	B	Hypothetical protein	<i>Haemophilus influenzae</i> Rd	172	A	16273644	0	Y	n8-18c23/24o	0

2	3	G_Msu2	B	HI1149m Unknown	KW20 <i>Mannheimia succiniciproducens</i> MBEL55E	171	A	52307822	0	Y	n8-19c23/24o	4
2	3	G_Pmu2	B	Unknown	<i>Pasteurella multocida</i> subsp. <i>multocida</i> str. Pm70	170	A	12720391	0	Y	n7-18c22/23o	0
2	4	G_Ppr2	B	Hypothetical protein yhbN precursor	<i>Photobacterium profundum</i> SS9	165	A	54310341	0	Y	n6-14c22/23o	-2
2	4	G_Vch2	B	Conserved hypothetical protein	<i>Vibrio cholerae</i> O1 biovar elton str. N16961	179	A	9657110	0	Y	n21-29c35/36o	-1
2	4	G_Vfi2	B	Hypothetical protein VF0389	<i>Vibrio fischeri</i> ES114	165	A	59710996	0	Y	n3-14c22/23o	-1
2	4	G_Vpa2	B	Putative ABC superfamily transport protein	<i>Vibrio parahaemolyticus</i> RIMD 2210633	164	A	28899442	0	Y	n4-15c20/21o	2
2	4	G_Vvuc2	B	Conserved hypothetical protein	<i>Vibrio vulnificus</i> CMCP6	153	A	27360265	0	0	o	6
2	4	G_Vvuy2	B	Hypothetical protein VV0450	<i>Vibrio vulnificus</i> YJ016	169	A	37678634	0	Y	n9-20c25/26o	4
2	5	G_Cps2	B	OstA family protein	<i>Colwellia psychrerythraea</i> 34H	201	A	71277840	0	Y	n10-22c27/28o	0
2	5	G_Ilo2	B	Uncharacterized conserved membrane protein	<i>Idiomarina loihiensis</i> L2TR	180	A	56459509	0	Y	n6-16c22/23o	0
2	5	G_Pha2	B	Conserved protein of unknown function; putative transport protein (ABC superfamily, periplasmic binding component)	<i>Pseudoalteromonas haloplanktis</i> TAC125	181	A	77361464	0	Y	n7-17c22/23o	2
2	5	G_Son2	B	Hypothetical protein SO3959	<i>Shewanella oneidensis</i> MR- 1	183	A	24375446	0	Y	n6-13c21/22o	5
2	6	G_Aad2	B	Conserved hypothetical protein; putative transport protein (ABC superfamily, peri_bind)	<i>Acinetobacter</i> sp. ADP1	158	A	50084656	0	0	o	4
2	6	G_Cbu2	B	Hypothetical protein CBU_0747	<i>Coxiella burnetii</i> RSA 493	173	A	29654081	0	Y	n15-26c31/32o	0
2	6	G_Lpn2	B	Hypothetical protein lpg0837	<i>Legionella pneumophila</i> subsp. <i>pneumophila</i> str. Philadelphia 1	169	A	52841073	0	Y	n8-18c23/24o	-1
2	6	G_Lpn12	B	Hypothetical protein	<i>Legionella pneumophila</i> str.	169	A	54293812	0	Y	n9-19c23/24o	-1

2	6	G_Lpnp2	B	lpl0868 Hypothetical protein lpp0899	Lens <i>Legionella pneumophila</i> str. Paris	169	A	54296858	0	Y	n9-19c23/24o	-1
2	6	G_Mca2	B	Hypothetical protein MCA0743	<i>Methylococcus capsulatus</i> str. Bath	177	A	53804951	0	Y	n13-23c29/30o	-3
2	6	G_Noc2	B	OstA-like protein	<i>Nitrosococcus oceani</i> ATCC 19707	275	AS	77166243	0	Y	n5-16c28/29o	-2
2	6	G_Pae2	B	Hypothetical protein PA4460	<i>Pseudomonas aeruginosa</i> PAO1	175	A	15599656	0	Y	n6-17c24/25o	7
2	6	G_Par2	B	Possible OstA-like protein	<i>Psychrobacter arcticus</i> 273-4	189	A	71065485	0	Y	n25-36c40/41o	11
2	6	G_Pflo2	B	OstA-like protein	<i>Pseudomonas fluorescens</i> PfO-1	181	A	77457086	0	Y	n6-17c22/23o	4
2	6	G_Pflp2	B	OstA family protein	<i>Pseudomonas fluorescens</i> Pf-5	181	A	70728299	0	Y	n6-17c22/23o	7
2	6	G_Ppu1	S(FS ⁷)	Hypothetical protein PP0954	<i>Pseudomonas putida</i> KT2440	174	A	26987690	0	Y	n6-17c24/25o	7
2	6	G_Psyb2	B	OstA-like protein	<i>Pseudomonas syringae</i> pv. <i>syringae</i> B728a	182	A	66047372	0	Y	n6-17c22/23o	7
2	6	G_Psyp2	B	OstA family protein	<i>Pseudomonas syringae</i> pv. <i>phaseolicola</i> 1448A	182	A	71734892	0	Y	n6-17c22/23o	7
2	6	G_Psy2	B	OstA family protein	<i>Pseudomonas syringae</i> pv. <i>tomato</i> str. DC3000	182	A	28871586	0	Y	n6-17c22/23o	7
2	7	G_Xax2	B	Conserved hypothetical protein	<i>Xanthomonas axonopodis</i> pv. <i>citri</i> str. 306	186	A	21109278	0	Y	n9-16c22/23o	0
2	7	G_Xca2	B	Hypothetical protein XC_1313	<i>Xanthomonas campestris</i> pv. <i>campestris</i> str. 8004	178	A	66767640	0	Y	n9-16c22/23o	0
2	7	G_Xcaa2	B	Hypothetical protein XCC2800	<i>Xanthomonas campestris</i> pv. <i>campestris</i> str. ATCC 33913	178	A	21232231	0	Y	n9-16c22/23o	0
2	7	G_Xfa2	B	Hypothetical protein XF1410	<i>Xylella fastidiosa</i> 9a5c	176	A	15838011	0	Y	n7-18c23/24o	-1
2	7	G_Xfat2	B	Hypothetical protein PD0639	<i>Xylella fastidiosa</i> Temecula1	176	A	28198547	0	Y	n7-18c23/24o	2
2	7	G_Xor2	B	Hypothetical protein XOO1286	<i>Xanthomonas oryzae</i> pv. <i>oryzae</i> KACC10331	182	A	58580909	0	Y	n9-16c22/23o	0
2	8	B_Aeb2	B	OstA-like family protein	<i>Azoarcus</i> sp. EbN1	190	A	56476150	0	Y	n4-17c25/26o	-1
2	8	B_Bbr2	B	Hypothetical protein BB4504	<i>Bordetella bronchiseptica</i> RB50	206	A	33603478	0	Y	n13-24c29/30o	-1

2	8	B_Bpa2	B	Hypothetical protein BPP4031	<i>Bordetella parapertussis</i> 12822	206	A	33598533	0	Y	n13-24c29/30o	-1
2	8	B_Bpe2	B	Hypothetical protein BP0698	<i>Bordetella pertussis</i> Tohama I	206	A	33591886	0	Y	n13-24c29/30o	-1
2	8	B_Bps2	B	OstA-like protein	<i>Burkholderia pseudomallei</i> K96243	221	A	52208588	0	Y	n21-31c39/40o	2
2	8	B_Cvi2	B	Hypothetical protein CV3330	<i>Chromobacterium violaceum</i> ATCC 12472	186	A	34498785	0	Y	n7-17c22/23o	-1
2	8	B_Dar2	B	OstA-like protein	<i>Dechloromonas aromatica</i> RCB	200	A	71909033	0	Y	n5-16c20/21o	-3
2	8	B_Neu2	B	Putative signal peptide protein	<i>Nitrosomonas europaea</i> ATCC 19718	205	A	30248095	1	0	o24-43i	-3
2	8	B_Ngo2	B	Hypothetical protein NGO1606	<i>Neisseria gonorrhoeae</i> FA 1090	176	A	59801934	0	Y	n8-17c22/23o	4
2	8	B_Nmem2	B	Hypothetical protein NMB0355	<i>Neisseria meningitidis</i> MC58	176	A	15676270	0	Y	n8-17c22/23o	6
2	8	B_Nmez2	B	Putative outer membrane hypothetical protein	<i>Neisseria meningitidis</i> Z2491	176	A	7380753	0	Y	n8-17c22/23o	6
2	8	B_Reu2	B	OstA-like protein	<i>Ralstonia eutropha</i> JMP134	213	A	73540063	0	Y	n16-27c34/35o	1
2	8	B_Rso2	B	PUTATIVE SIGNAL PEPTIDE PROTEIN	<i>Ralstonia solanacearum</i> GMI1000	191	A	17545129	0	Y	n12-22c28/29o	-1
2	8	B_Thde2	B	OstA-like family protein	<i>Thiobacillus denitrificans</i> ATCC 25259	177	A	74316553	0	Y	n8-18c23/24o	-1
2	9	A_Atu2	B	AGR_C_585p	<i>Agrobacterium tumefaciens</i> str. C58	196	A	15155240	0	Y	n25-36c41/42o	4
2	9	A_Bab2	B	Hypothetical protein BruAb1_0152	<i>Brucella abortus</i> biovar 1 str. 9-941	204	A	62289132	0	Y	n7-18c25/26o	1
2	9	A_Bhe2	B	Hypothetical protein BH00160	<i>Bartonella henselae</i> str. Houston-1	192	A	49474847	0	Y	n3-14c19/20o	-3
2	9	A_Bme2	B	Hypothetical periplasmic protein	<i>Brucella melitensis</i> 16M	172	A	17983824	0	0	o	1
2	9	A_Bqu2	B	Hypothetical protein	<i>Bartonella quintana</i> str. Toulouse	192	A	49239205	0	0	o	-3
2	9	A_Bsu2	B	Conserved hypothetical protein	<i>Brucella suis</i> 1330	204	A	23346935	0	Y	n7-18c25/26o	1
2	9	A_Ccr2	B	Hypothetical protein CC3601	<i>Caulobacter crescentus</i> CB15	189	A	16127831	0	Y	n9-20c28/29o	4
2	9	A_Gox2	B	Hypothetical protein	<i>Gluconobacter oxydans</i>	266	A'	58040275	0	0	o	4

2	9	A_Mlo2	B	GOX1844 Hypothetical protein mll3198	621H <i>Mesorhizobium loti</i> MAFF303099	199	A	13472790	0	Y	n9-21c26/27o	2
2	9	A_Nwi2	B	OstA-like protein	<i>Nitrobacter winogradskyi</i> Nb-255	227	A	75674372	0	Y	n19-31c39/40o	8
2	9	A_Rco2	B	Hypothetical protein RC0659	<i>Rickettsia conorii</i> str. Malish 7	194	A'	15892582	1	0	i55-75o	-2
2	9	A_Rfe2	B	Hypothetical protein RF_0718	<i>Rickettsia felis</i> URRWXCal2	145	A'	67459110	1	0	i6-25o	-1
2	9	A_Rpa2	B	Hypothetical protein RPA0048	<i>Rhodopseudomonas</i> <i>palustris</i> CGA009	221	A	39933128	0	Y	n14-24c36/37o	7
2	9	A_Rpr2	B	Hypothetical protein RP507	<i>Rickettsia prowazekii</i> str. Madrid E	145	A'	15604367	1	0	i6-26o	-1
2	9	A_Rsp2	B	OstA-like protein	<i>Rhodobacter sphaeroides</i> 2.4.1	163	A	77464736	0	Y	n3-14c22/23o	2
2	9	A_Rty2	B	Rickettsial conserved hypothetical protein	<i>Rickettsia typhi</i> str. Wilmington	143	A'	51473689	1	0	i6-26o	-1
2	9	A_Sme2	B	HYPOTHETICAL TRANSMEMBRANE PROTEIN	<i>Sinorhizobium meliloti</i> 1021	186	A	15964136	0	Y	n13-24c31/32o	8
2	9	A_Spo2	B	Conserved hypothetical protein	<i>Silicibacter pomeroyi</i> DSS- 3	163	A	56676744	0	Y	n6-17c22/23o	7
2	9	A_Zmo2	B	Conserved hypothetical protein	<i>Zymomonas mobilis</i> subsp. <i>mobilis</i> ZM4	198	A	56542746	0	Y	n16-27c35/36o	-2
2	10	D_Dps2	B	Hypothetical protein DP0440	<i>Desulfotalea psychrophila</i> LSv54	166	A	51244292	0	Y	n8-17c23/24o	2
2	10	D_Gsu2	B	Conserved hypothetical protein	<i>Geobacter sulfurreducens</i> PCA	167	A	39983875	0	Y	n4-15c20/21o	5
2	10	D_Pca2	B	Hypothetical protein Pear_1940	<i>Pelobacter carbinolicus</i> DSM 2380	166	A	77919536	0	Y	n7-18c25/26o	4
2	11	E_Cjen2	B	Hypothetical protein Cj0649	<i>Campylobacter jejuni</i> subsp. <i>jejuni</i> NCTC 11168	153	A	15792009	0	Y	n5-13c18/19o	-3
2	11	E_Cjer2	B	OstA family protein	<i>Campylobacter jejuni</i> RM1221	153	A	57236962	0	Y	n5-13c18/19o	-3
2	11	E_Hhe2	B	Hypothetical protein HH1328	<i>Helicobacter hepaticus</i> ATCC 51449	156	A	32266827	0	Y	n4-11c16/17o	-2
2	11	E_Hpy2	B	Hypothetical protein HP1568	<i>Helicobacter pylori</i> 26695	183	A	15646175	0	Y	n3-14c19/20o	-2
2	11	E_Hpyj2	B	Hypothetical protein	<i>Helicobacter pylori</i> J99	185	A	15612541	0	Y	n3-14c19/20o	-2

2	11	E_Wsu2	B	jhp1476 Hypothetical protein WS2067	<i>Wolinella succinogenes</i> DSM 1740	181	A	34558351	0	Y	n2-15c20/21o	-4
2	12	I_Dra1	S(B?)	Hypothetical protein	<i>Deinococcus radiodurans</i> R1	303	A'	6460132	0	Y	n4-15c21/22o	4
2	12	Q_Aae2	B	Hypothetical protein aq_2173	<i>Aquifex aeolicus</i> VF5	144	A	15607109	0	Y	n5-15c20/21o	-3
2	13	C_Ava1	S(B?)	Hypothetical protein Ava_1639	<i>Anabaena variabilis</i> ATCC 29413	165	A	75907861	0	Y	n15-26c30/31o	1
2	13	C_Gvi1	S(B?)	Hypothetical protein glr3263	<i>Gloeobacter violaceus</i> PCC 7421	148	A'	37522832	0	Y	n2-13c21/22o	-3
2	13	C_Nsp1	S(B?)	alr4067	<i>Nostoc</i> sp. PCC 7120	165	A	17133202	0	Y	n15-26c30/31o	1
2	13	C_Pma1	S(B?)	Hypothetical protein PMT0573	<i>Prochlorococcus marinus</i> str. MIT 9313	145	A'	33862846	0	Y	n5-16c25/26o	11
2	13	C_Pmap1	S(B?)	Hypothetical protein PMM1406	<i>Prochlorococcus marinus</i> subsp. <i>pastoris</i> str. CCMP1986	123	A'	33861962	0	Y	n4-14c19/20o	0
2	13	C_Sel1	S(B?)	Hypothetical protein syc1006_d	<i>Synechococcus elongatus</i> PCC 6301	146	A	56751015	0	Y	n14-25c43/44o	-2
2	13	C_Sosp1	S(B?)	Conserved hypothetical protein	<i>Synechococcus</i> sp. WH 8102	150	A'	33632815	0	Y	n20-31c39/40o	4
2	13	C_Sysp1	S(B?)	Hypothetical protein slr0250	<i>Synechocystis</i> sp. PCC 6803	178	A	16329308	0	Y	n25-36c48/49o	2
2	13	C_Tel1	S(B?)	Hypothetical protein tll1572	<i>Thermosynechococcus</i> <i>elongatus</i> BP-1	148	A	22299115	0	Y	n12-22c34/35o	-2

¹Organisms containing OstA homologues: B indicates the presence of both large (L) and small (S) proteins; B+P, large, small, and an additional large OstA paralogue; L, large only; S, small only; FS, an authentic frame shift of the gene encoding the large OstA.

²The number of predicted transmembrane segments by Phobius (<http://phobius.cgb.ki.se/index.html>).

³Y/N, indicates whether a signal peptide was predicted or not (<http://phobius.cgb.ki.se/index.html>).

⁴Predicted topology of the protein (<http://phobius.cgb.ki.se/index.html>).

⁵The log of the probability of having a beta-barrel transmembrane (BBTM) protein; >6, BBTM protein, <-6, Non-BBTM protein (<http://www.bioinformatics.leeds.ac.uk/betaBarrel/>).

⁶The proteins are predicted to be integral beta-barrel outer membrane proteins by BOMP (<http://www.bioinfo.no/tools/bomp>). If not predicted, there is no listing in the table. The classification is from 0 to 5; 0 means that the predictor did not find the protein to be a beta-barrel integral outer membrane protein, but there were integral outer membrane homologues; 1 to 5: integral outer membrane proteins, 1 is the least reliable prediction, and 5 is the most reliable.

Table S2. Bacteria with a recognizable small OstA homologues as well as sequence divergent large OstA homologues.

Organismal type	GI# ¹	Protein size	Notes
<i>Anabaena variabilis</i> ATCC 29413	75909211	885	Pfam: potential match OstA 106 aas
<i>Deinococcus radiodurans</i> R1	15805600	971	CDD: no putative conserved domains have been detected; distantly related; similar to OstA_C of I_Tth1 46198336
<i>Gloeobacter violaceus</i> PCC 7421	37523201	649	CDD: Imp N part 80 aas
<i>Nostoc</i> sp. PCC 7120	17228773	865	Pfam: potential match OstA 106 aas
<i>Prochlorococcus marinus</i> str. MIT 9313	33864108	1027	CDD: Imp N part 78 aas
<i>Prochlorococcus marinus</i> subsp. <i>pastoris</i> str. CCMP1986	33860812	678	CDD: Imp N part 140 aas
<i>Pseudomonas putida</i> KT2440			Authentic frame shift mutation (GI#26986745)
<i>Synechococcus elongatus</i> PCC 6301	56752394	730	CDD: Imp N part 80 aas
<i>Synechococcus</i> sp. WH 8102	33864801	931	CDD: Imp N part 94 aas
<i>Synechocystis</i> sp. PCC 6803	16331286	803	CDD: Imp N part 81 aas
<i>Thermosynechococcus elongatus</i> BP-1	22298619	577	CDD: Imp N part 77 aas

¹The large OstA homologues included in this table are not listed in Table S1. The GI numbers provided are for these large OstA proteins.

Table S3. Bacteria with recognizable large OstA homologues but no recognizable small OstA homologues.

Organismal type
<i>Bacteroides fragilis</i> NCTC 9343
<i>Bacteroides fragilis</i> YCH46
<i>Bacteroides thetaiotaomicron</i> VPI-5482
<i>Bdellovibrio bacteriovorus</i> HD100
<i>Borrelia burgdorferi</i> B31
<i>Borrelia garinii</i> PBI
<i>Burkholderia mallei</i> ATCC 23344
<i>Candidatus Pelagibacter ubique</i> HTCC1062
<i>Desulfovibrio vulgaris</i> subsp. <i>vulgaris</i> str. Hildenborough
<i>Leptospira interrogans</i> serovar Copenhageni str. Fiocruz L1-130
<i>Leptospira interrogans</i> serovar Lai str. 56601
<i>Parachlamydia</i> sp. UWE25
<i>Porphyromonas gingivalis</i> W83
<i>Rhodopirellula baltica</i> SH 1
<i>Treponema denticola</i> ATCC 35405
<i>Treponema pallidum</i> subsp. <i>Pallidum</i> str. Nichols
<i>Wigglesworthia glossinidia</i> endosymbiont of <i>Glossina brevipalpis</i>
<i>Chlorobium tepidum</i> TLS
<i>Thermus thermophilus</i> HB27 ¹
<i>Thermus thermophilus</i> HB8 ¹

¹A small (309 aas) sequence divergent L-OstA was found in each strain of *T. thermophilus*. These two proteins (GI#s 46199043 and 55981069, respectively) have a 90 residue partial OstA-C domain.