

SUPP. MATERIALS

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Table S1. All oligonucleotides used in the manuscript are listed and explained.

Table S2. Summary of crystallographic information.

Tables S3-S5. Species and GenBank IDs of proteins used for hydrophobicity and conservation analysis of Tic22 (S4), BamB (S5) or ClpS (S6) are given

Supp. Figures

Figure S1. The phylogenetic distribution of the Tic22 family is shown.

Figure S2. Electron microscopy on wild type, AFS-I-*alr2269* and AFS-I-*tic22*.

Figure S3. The protein level of Tic22 in AFS-I-*alr2269*, AFS-I-*alr2270* and WT was determined.

Figure S4. The central cavity closed by the conserved septum is visualized.

Figure S5. The conservation of the Tic22 proteins is shown in the structural context.

Figure S6. The conservation and the hydrophobicity pockets of Tic22 is shown for the entire protein surface

Figure S7. Comparison of anaTic22 and synTic22.

Figure S8. The structural alignment between Tic22 and the structural homologue in *Thermus thermophilus*.

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Table S1: Primers used for the generation of constructs

Sequences of primers and restriction enzymes used for the cloning of the indicated constructs are given. f, forward primer, r, reverse primer.

Construct	Primer Sequence	f/r	Restriction site
panaTic22	TACGACATATGTTATCAGAACAACAAATCAAAGAAAAG	f	NdeI
	TGATCCTCGAGTTTTGCCCCAGGTCGGGAG	r	XhoI
pAFS-I- <i>alr0114</i>	GTAGCCTCGAGATGAAAGCATTGGTTCGCTG	f	XhoI
	ACATCAAGCTTGCAAATAACAGACGATTAGGGTC	r	HindIII
	GCTACAAGCTTGGAATTAAGGGGCAATGG	f	HindIII
	CAATCCTGCAGCTATTTGCCCCAGGTCGG	r	PstI
pAFS-PDGF- <i>alr0114</i>	TTCAGCTGCAGGGTATCCTCATTAATTTTCCGC	f	PstI
	CAGAAGACGTCGCCCCAGCGAACCAATGC	r	AatII
	TTGCTGACGTCAGTAAAGGAGAAGAATTTTCACTG	f	AatII
	CATAAGAATTCTTATTTGTATAGTTCATCCATGCC	r	EcoRI
pAFS-P _{petJ} - <i>all0114</i>	ATCGCTGCAGCCTCTGCCGATACC	f	PstI
	ATCGCTGCAGCCTCTGCCGATACC	r	Acc65I
	GGTACCCTTATGAAAGCATTGG	f	Acc65I
	CTCGAGGAATTCTATTTTGCCCC	r	XhoI
pAFS-P _{petJ} - <i>all0115</i>	ATCGCTGCAGCCTCTGCCGATACC	f	PstI
	ATCGCTGCAGCCTCTGCCGATACC	r	Acc65I
	GGTACCGGCATGACAAATCGACAGG	f	Acc65I
	CTCGAGTCATCACTGAATCTGTGCT	r	XhoI
pAFS-P _{petJ} - <i>all0114</i> _{D213R}	CCAAAACATCCCAAGGCGGTATTCAAGTTCTAGATATAGACGGTG	f	-
	CTAGAACTTGAATACGCGCCTTGGGATGTTTTGGCTTGAC	r	-
pAFS-P _{petJ} - <i>all0114</i> _{I219R}	TCAAGTTCTAGATCGAGACGGTGTACTACAGACATTACAAG	f	-
	CTGTAGTACACCGTCTCGATCTAGAAGTTGAATATCCGCCTTG	r	-
pAFS-P _{petJ} - <i>all0114</i> _{F136G}	CCCTAATCGTCTGTTATTTGCTGGTAAACCTGTAGATCAGGAAATTAAGGG	f	-
	CCTGATCTACAGGTTTACCAGCAAATAACAGACGATTAGGGTC	r	-
pAFS-P _{petJ} - <i>ssalr0114</i> - <i>AtTic22</i>	ATCGCTGCAGCCTCTGCCGATACC	f	PstI
	ATCGCTGCAGCCTCTGCCGATACC	r	Acc65I
	GGTACCCTTATGAAAGCATTGG	f	Acc65I
	TCTAGATCTTTGATTTGTTGTTCTG	r	XbaI
	TCTAGATCTTGTGCTAAAGCTCTC	f	XbaI
	CTCGAGGTTTTACTCTTTGATCAAATCC	r	XhoI

Table S2. Summary of crystallographic information

	anaTic22 SeMet Peak $\lambda=0.9798$	anaTic22 SeMet Inflection point $\lambda=0.9801$	anaTic22 SeMet Remote $\lambda=0.9760$	anaTic22 native
Data collection statistics				
space group	C2			C2
unit cell a, b, c (Å)	67.39, 110.86, 43.92			67.17, 111.19, 44.15
Unit cell α, γ, β	90.00°, 125.81°			90.00°, 125.36°
molecules in asymmetric unit	1			1
mosaicity (°)	0.29	0.30	0.31	0.75
solvent content (%)	39.9	39.9	39.9	40.6
average B (Å ²)	48	49	50	31
unique reflections	7882	7889	7882	19161
resolution (Å) / HR shell (Å)	30 – 2.62 / 2.71 – 2.62			36.01 - 1.95 / 1.98 - 1.95
R _{sym} (%) / HR shell (%) ^a	9.5 / 12.3	8.7 / 11.3	8.7 / 12.8	5.6 / 38.2
completeness (%) / HR shell (%)	100/100	100/100	100/100	99.5 / 99.9
<I> / <sigI> / HR shell	11.7 / 9.8	13.3 / 11.0	13.1 / 10.0	18.9 / 2.4
redundancy / HR shell	4.2 / 4.1	4.2 / 4.1	4.2 / 4.2	4.1 / 4.0
Refinement statistics				
amino acids (chain A)				31 – 256
total protein atoms (including double conformations)				1792
water				150
ligand atoms				
RMSD bonds (Å)				0.015
RMSD angles (°)				1.514
R _{free} (%) ^b				24.90
R _{work} (%) ^c				19.97
Ramachandran Plot statistics [†]				
most favored (residues / %)				177
additional favored (residues / %)				13
generously allowed (residues / %)				1
disallowed (residues / %)				0

^aR_{sym} = $\sum_h \sum_i |I(h) - \bar{I}(h)| / \sum_h \sum_i I(h)_i$, where $\bar{I}(h)$ is the mean intensity

^b5 % of the data were excluded to calculate R_{free}

^cR_{work} = $\sum_h |F_{obs}(h) - |F_{calc}(h)|| / \sum_h |F_{obs}(h)|$, where F_{obs}(h) and F_{calc}(h) are observed and calculated structure factors, respectively

Table S3: Species and GenBank IDs of proteins used for tree reconstruction (Figure S2) and hydrophobicity and conservation analysis of Tic22 (Figure 4)

GenBank ID	Organism	GenBank ID	Organism
225458599	Vitis vinifera	284929411	cyanobacterium UCYN-A
302142324	Vitis vinifera	16331677	Synechocystis sp. PCC 6803
A7NTV2_VITVI	Vitis vinifera	218247697	Cyanothece sp. PCC 8801
147834059	Vitis vinifera	257060966	Cyanothece sp. PCC 8802
224136756	Populus trichocarpa	257060965	Cyanothece sp. PCC 8802
224067266	Populus trichocarpa	218247698	Cyanothece sp. PCC 8801
255538318	Ricinus communis	172038586	Cyanothece sp. ATCC 51142
3769671	Pisum sativum	126657232	Cyanothece sp. CCY0110
15234162	Arabidopsis thaliana	67921947	Crocospaera watsonii WH 8501
297798602	Arabidopsis lyrata	158337449	Acaryochloris marina MBIC11017
194702742	Zea mays	220909750	Cyanothece sp. PCC 7425
226510510	Zea mays	22299571	Thermosynechococcus elongatus BP-1
242095102	Sorghum bicolor	119509582	Nodularia spumigena CCY9414
218197791	Oryza sativa Indica Group	17227610	Nostoc sp. PCC 7120
51091923	Oryza sativa Japonica Group	75907705	Anabaena variabilis ATCC 29413
222635191	Oryza sativa Japonica Group	298493042	Nostoc azollae' 0708
294461156	Picea sitchensis	282897450	Raphidiopsis brookii D9
302755278	Selaginella moellendorffii	218438434	Cyanothece sp. PCC 7424
302767048	Selaginella moellendorffii	196256226	Cyanothece sp. PCC 7822
168057172	Physcomitrella patens subsp. patens	86608446	Synechococcus sp. JA-2-3B'a(2-13)
168027187	Physcomitrella patens subsp. patens	86607397	Synechococcus sp. JA-3-3Ab
224065274	Populus trichocarpa	37523182	Gloeobacter violaceus PCC 7421
15229502	Arabidopsis thaliana	37521323	Gloeobacter violaceus PCC 7421
9293945	Arabidopsis thaliana	37521322	Gloeobacter violaceus PCC 7421
297831142	Arabidopsis lyrata subsp. lyrata	218438433	Cyanothece sp. PCC 7424
225463323	Vitis vinifera	196256227	Cyanothece sp. PCC 7822
242043704	Sorghum bicolor	170078206	Synechococcus sp. PCC 7002
219363709	Zea mays	254423739	Synechococcus sp. PCC 7335
125557998	Oryza sativa Indica Group	81300671	Synechococcus elongatus PCC 7942
115471591	Oryza sativa Japonica Group	162606048	Guillardia theta
125599875	Oryza sativa Japonica Group	160331815	Hemiselmis andersenii
302841733	Volvox carteri f. nagariensis	298711744	Ectocarpus siliculosus
186683988	Nostoc punctiforme PCC 73102	124506499	Plasmodium falciparum 3D7
300867728	Oscillatoria sp. PCC 6506	156095262	Plasmodium vivax Sal-1
113475327	Trichodesmium erythraeum IMS101	221056763	Plasmodium knowlesi strain H
254415151	Microcoleus chthonoplastes PCC 7420	221504814	Toxoplasma gondii VEG
119489126	Lyngbya sp. PCC 8106	237839889	Toxoplasma gondii ME49
119486658	Lyngbya sp. PCC 8106	221484621	Toxoplasma gondii GT1
284053639	Arthrospira platensis str. Paraca	122890336	Guillardia theta
291567204	Arthrospira platensis NIES-39	126667505	Marinobacter sp. ELB17
300945537	Arthrospira sp. PCC 8005	87124838	Synechococcus sp. RS9917
218438435	Cyanothece sp. PCC 7424	87123092	Synechococcus sp. RS9917
196256225	Cyanothece sp. PCC 7822	116074516	Synechococcus sp. RS9916
166366579	Microcystis aeruginosa NIES-843	219113187	Phaeodactylum tricornutum
159028709	Microcystis aeruginosa PCC 7806	223993307	Thalassiosira pseudonana CCMP1335
67925831	Crocospaera watsonii WH 8501	224002933	Thalassiosira pseudonana CCMP1335
172038585	Cyanothece sp. ATCC 51142	223993133	Thalassiosira pseudonana CCMP1335
126657231	Cyanothece sp. CCY0110	219115753	Phaeodactylum tricornutum CCAP 1055/1

GenBank ID	Organism	GenBank ID	Organism
223994511	Thalassiosira pseudonana CCMP1335	68075797	Plasmodium berghei strain ANKA
298715857	Ectocarpus siliculosus	70950842	Plasmodium chabaudi chabaudi
224011677	Thalassiosira pseudonana CCMP1335	83315316	Plasmodium yoelii yoelii str. 17XNL
219120571	Phaeodactylum tricornutum CCAP 1055/1	8809661	Arabidopsis thaliana
223999445	Thalassiosira pseudonana CCMP1335	297797241	Arabidopsis lyrata subsp. lyrata
71028066	Theileria parva strain Muguga	18424615	Arabidopsis thaliana
84996025	Theileria annulata strain Ankara	224134839	Populus trichocarpa
149072084	Rhodomonas salina	224077492	Populus trichocarpa
51210013	Gracilaria tenuistipitata var. liui	255545150	Ricinus communis
283794866	Cryptomonas paramecium	302143767	Vitis vinifera
11465684	Porphyra purpurea	225464627	Vitis vinifera
299890949	uncultured prymnesiophyte C19847	125569586	Oryza sativa Japonica Group
71842290	Emiliana huxleyi	125524979	Oryza sativa Indica Group
11465478	Cyanidium caldarium	13027350	Oryza sativa Japonica Group
2541891	Cyanidium caldarium	223947091	Zea mays
30468055	Cyanidioschyzon merolae strain 10D	238006828	Zea mays
2541881	Cyanidioschyzon merolae	242055909	Sorghum bicolor
156098011	Plasmodium vivax Sal-1	168023798	Physcomitrella patens subsp. patens
221053666	Plasmodium knowlesi strain H		

Table S4: Species and GenBank IDs of proteins used in hydrophobicity analysis of BamB (Figure 5)

GenBank ID	Organism	GenBank ID	Organism
311105362	<i>Achromobacter xylosoxidans</i> A8	253996244	<i>Methylothermobacter mobilis</i> JLW8
317403341	<i>Achromobacter xylosoxidans</i> C54	297538115	<i>Methylothermobacter versatilis</i> 301
262371081	<i>Acinetobacter johnsonii</i> SH046	334129945	<i>Methylothermobacter universalis</i> FAM5
262371653	<i>Acinetobacter junii</i> SH205	313201442	<i>Methylothermobacter</i> sp. MP688
262374929	<i>Acinetobacter lwoffii</i> SH145	149908866	<i>Moritella</i> sp. PE36
255321134	<i>Acinetobacter radioresistens</i> SK82	89095337	<i>Neptuniibacter caesariensis</i>
50083800	<i>Acinetobacter</i> sp. ADP1	88812664	<i>Nitrococcus mobilis</i> Nb-231
226954468	<i>Acinetobacter</i> sp. ATCC 27244	292492501	<i>Nitrosococcus halophilus</i> Nc4
260549070	<i>Acinetobacter</i> sp. RUH2624	254434401	<i>Nitrosococcus oceani</i> AFC27
330830065	<i>Aeromonas veronii</i> B565	30248178	<i>Nitrosomonas europaea</i> ATCC 19718
110834718	<i>Alcanivorax borkumensis</i> SK2	114332130	<i>Nitrosomonas eutropha</i> C91
254427070	<i>Alcanivorax</i> sp. DG881	325981900	<i>Nitrosomonas</i> sp. AL212
209694321	<i>Aliivibrio salmonicida</i> LFI1238	339483559	<i>Nitrosomonas</i> sp. Is79A3
114320410	<i>Alkalilimnicola ehrlichii</i> MLHE-1	82703489	<i>Nitrospira multiformis</i> ATCC 25196
288941005	<i>Allochromatium vinosum</i> DSM 180	87198966	<i>Novosphingobium aromaticivorans</i> DSM 12444
163797496	<i>alpha proteobacterium</i> BAL199	326386676	<i>Novosphingobium nitrogenifigens</i> DSM 19370
239997026	<i>Alteromonas macleodii</i> ATCC 27126	334140085	<i>Novosphingobium</i> sp. PP1Y
333892274	<i>Alteromonas</i> sp. SN2	83945265	<i>Oceanicaulis</i> sp. HTCC2633
284006777	<i>Arsenophonus nasoniae</i>	237745514	<i>Oxalobacter formigenes</i> HOxBSL
291571490	<i>Arthrospira platensis</i> NIES-39	237747712	<i>Oxalobacter formigenes</i> OXCC13
291571493	<i>Arthrospira platensis</i> NIES-39	329909336	<i>Oxalobacteraceae bacterium</i> IMCC9480
329850799	<i>Asticcacaulis biprosthecum</i> C19	317049133	<i>Pantoea</i> sp. At-9b
315499684	<i>Asticcacaulis excentricus</i> CB 48	154253925	<i>Parvibaculum lavamentivorans</i> DS-1
119897221	<i>Azoarcus</i> sp. BH72	227112683	<i>Pectobacterium carotovorum</i> subsp. <i>brasiliensis</i> PBR1692
288958551	<i>Azospirillum</i> sp. B510	269103272	<i>Photobacterium damsela</i> subsp. <i>damsela</i> CIP 102761
226946064	<i>Azotobacter vinelandii</i> DJ	330446668	<i>Photobacterium leiognathi</i> subsp. <i>mandapamensis</i> svers. 1.1.
162139366	<i>Baumannia cicadellincola</i> str. Hc (<i>Homalodisca coagulata</i>)	90410876	<i>Photobacterium profundum</i> 3TCK
153872645	<i>Beggiatoa</i> sp. PS	253988870	<i>Photorhabdus asymbiotica</i> subsp. <i>asymbiotica</i> ATCC 43949
94501122	<i>Bermanella marisrubri</i>	145589469	<i>Polynucleobacter necessarius</i> subsp. <i>asymbioticus</i> QLW-P1DMWA-1
187478831	<i>Bordetella avium</i> 197N	171463405	<i>Polynucleobacter necessarius</i> subsp. <i>necessarius</i> STIR1

GenBank ID	Organism	GenBank ID	Organism
33593200	<i>Bordetella pertussis</i> Tohama I	197285697	<i>Proteus mirabilis</i> HI4320
163856333	<i>Bordetella petrii</i> DSM 12804	212710612	<i>Providencia alcalifaciens</i> DSM 30120
238027074	<i>Burkholderia glumae</i> BGR1	183599735	<i>Providencia stuartii</i> ATCC 25827
161524639	<i>Burkholderia multivorans</i> ATCC 17616	109899428	<i>Pseudoalteromonas atlantica</i> T6c
167562552	<i>Burkholderia oklahomensis</i> EO147	332534676	<i>Pseudoalteromonas haloplanktis</i> ANT/505
186476175	<i>Burkholderia phymatum</i> STM815	162139936	<i>Pseudoalteromonas haloplanktis</i> TAC125
312796096	<i>Burkholderia rhizoxinica</i> HKI 454	88858477	<i>Pseudoalteromonas tunicata</i> D2
295676900	<i>Burkholderia</i> sp. CCGE1002	152987242	<i>Pseudomonas aeruginosa</i> PA7
91784204	<i>Burkholderia xenovorans</i> LB400	330807650	<i>Pseudomonas brassicacearum</i> subsp. <i>brassicacearum</i> NFM421
303257593	Burkholderiales bacterium 1_1_47	229592438	<i>Pseudomonas fluorescens</i> SBW25
257093698	Candidatus <i>Accumulibacter phosphatis</i> clade IIA str. UW-1	333901472	<i>Pseudomonas fulva</i> 12-X
238897952	Candidatus <i>Hamiltonella defensa</i> 5AT	330504676	<i>Pseudomonas mendocina</i> NK-01
339477884	Candidatus <i>Moranella endobia</i> PCIT	170723483	<i>Pseudomonas putida</i> W619
304414051	Candidatus <i>Regiella insecticola</i> LSR1	146283358	<i>Pseudomonas stutzeri</i> A1501
258545522	<i>Cardiobacterium hominis</i> ATCC 15826	301386120	<i>Pseudomonas syringae</i> pv. <i>tomato</i> Max13
167646459	<i>Caulobacter</i> sp. K31	319787002	<i>Pseudoxanthomonas suwonensis</i> 11-1
192361515	<i>Cellvibrio japonicus</i> Ueda107	119944926	<i>Psychromonas ingrahamii</i> 37
219850569	<i>Chloroflexus aggregans</i> DSM 9485	90408608	<i>Psychromonas</i> sp. CNPT3
163849340	<i>Chloroflexus aurantiacus</i> J-10-fl	332284651	<i>Pusillimonas</i> sp. T7-7
34498990	<i>Chromobacterium violaceum</i> ATCC 12472	322831769	<i>Rahnella</i> sp. Y9602
92114974	<i>Chromohalobacter salexigens</i> DSM 3043	113868335	<i>Ralstonia eutropha</i> H16
260425866	<i>Citricella</i> sp. SE45	73541771	<i>Ralstonia eutropha</i> JMP134
296284226	<i>Citromicrobium bathyomarinum</i> JL354	187928155	<i>Ralstonia pickettii</i> 12J
341615760	<i>Citromicrobium</i> sp. JLT1363	344171685	<i>Ralstonia syzygii</i> R24
340787108	<i>Collimonas fungivorans</i> Ter331	336317398	<i>Rheinheimera</i> sp. A13L
71279719	<i>Colwellia psychrerythraea</i> 34H	146278197	<i>Rhodobacter sphaeroides</i> ATCC 17025
88703669	<i>Congregibacter litoralis</i> KT71	126462123	<i>Rhodobacter sphaeroides</i> ATCC 17029
333954670	<i>Cronobacter sakazakii</i> E899	209964704	<i>Rhodospirillum centenum</i> SW
94311041	<i>Cupriavidus metallidurans</i> CH34	83594415	<i>Rhodospirillum rubrum</i> ATCC 11170
71908595	<i>Dechloromonas aromatica</i> RCB	160872141	<i>Rickettsiella grylli</i>
345130681	<i>Dechlorosoma suillum</i> PS	156742137	<i>Roseiflexus castenholzii</i> DSM 13941
242240152	<i>Dickeya dadantii</i> Ech703	90021084	<i>Saccharophagus degradans</i> 2-40

GenBank ID	Organism	GenBank ID	Organism
251788751	Dickeya zeae Ech1591	335420578	Salinisphaera shabanensis E1L3A
269140142	Edwardsiella tarda EIB202	194734846	Salmonella enterica subsp. enterica serovar
344225216	endosymbiont of Riftia pachyptila (vent Ph05)	293394878	Serratia odorifera DSM 4582
317490872	Enterobacteriaceae bacterium 9_2_54FAA	320539279	Serratia symbiotica str. Tucson
312173199	Erwinia amylovora ATCC BAA-2158	119775496	Shewanella amazonensis SB2B
300717948	Erwinia billingiae Eb661	91792617	Shewanella denitrificans OS217
319443752	Escherichia coli K-12	114562297	Shewanella frigidimarina NCIMB 400
315364663	Escherichia coli K-12	167623302	Shewanella halifaxensis HAW-EB4
308050454	Ferrimonas balearica DSM 9799	127512225	Shewanella loihica PV-4
118498116	Francisella novicida U112	212634302	Shewanella piezotolerans WP3
167627293	Francisella philomiragia subsp. philomiragia ATCC 25017	157374574	Shewanella sediminis HAW-EB3
302878617	Gallionella capsiferiformans ES-2	117919681	Shewanella sp. ANA-3
304311811	gamma proteobacterium HdN1	294140149	Shewanella violacea DSS12
90417494	gamma proteobacterium HTCC2207	170725904	Shewanella woodyi ATCC 51908
254449217	gamma proteobacterium HTCC5015	291613884	Sideroxydans lithotrophicus ES-1
329897034	gamma proteobacterium IMCC3088	85059735	Sodalis glossinidius str. 'morsitans'
254514002	gamma proteobacterium NOR5-3	294012484	Sphingobium japonicum UT26S
254281848	gamma proteobacterium NOR51-B	345136364	Sphingobium sp. SYK-6
221133871	Glaciecola sp. HTCC2999	332185241	Sphingomonas sp. S17
262274784	Grimontia hollisae CIP 101886	94495669	Sphingomonas sp. SKA58
83647147	Hahella chejuensis KCTC 2396	148556030	Sphingomonas wittichii RW1
257372971	Halomicrobium mukohataei DSM 12286	190574023	Stenotrophomonas maltophilia K279a
307543973	Halomonas elongata DSM 2581	323143787	Succinatimonas hippei YIT 12066
338997176	Halomonas sp. TD01	254786613	Teredinibacter turnerae T7901
121998565	Halorhodospira halophila SL1	237654044	Thauera sp. MZ1T
261856777	Halothiobacillus neapolitanus c2	289207922	Thioalkalivibrio sp. K90mix
300312254	Herbaspirillum seropedicae SmR1	220935214	Thioalkalivibrio sulfidophilus HL-EbGr7
134094494	Herminimonas arsenicoxydans	74316615	Thiobacillus denitrificans ATCC 25259
85712734	Idiomarina baltica OS145	344338107	Thiocapsa marina 5811
56461131	Idiomarina loihiensis L2TR	343919547	Thiorhodococcus drewsii AZ1
336451634	Idiomarina sp. A28L	237807665	Tolomonas auensis DSM 9187
152981826	Janthinobacterium sp. Marseille	255292049	uncultured bacterium

GenBank ID	Organism	GenBank ID	Organism
256823052	Kangiella koreensis DSM 16069	336124874	Vibrio anguillarum 775
152971373	Klebsiella pneumoniae subsp. pneumoniae MGH 78578	323491634	Vibrio brasiliensis LMG 20546
254499340	Legionella drancourtii LLAP12	312884307	Vibrio caribbenthicus ATCC BAA-2122
270156685	Legionella longbeachae D-4968	297581161	Vibrio cholerae RC385
52841772	Legionella pneumophila subsp. pneumophila str. Philadelphia 1	260776630	Vibrio coralliilyticus ATCC BAA-450
149926361	Limnobacter sp. MED105	260771393	Vibrio furnissii CIP 102972
144898966	Magnetospirillum gryphiswaldense MSR-1	343503631	Vibrio ichthyenteri ATCC 700023
114569753	Maricaulis maris MCS10	260773382	Vibrio metschnikovii CIP 69.14
344343053	Marichromatium purpuratum 984	343494443	Vibrio nigripulchritudo ATCC 27043
119505386	marine gamma proteobacterium HTCC2080	261252181	Vibrio orientalis CIP 102891 = ATCC 33934
119476374	marine gamma proteobacterium HTCC2143	254506709	Vibrio parahaemolyticus 16
311694387	Marinobacter adhaerens HP15	28897385	Vibrio parahaemolyticus RIMD 2210633
149375008	Marinobacter algicola DG893	149190087	Vibrio shilonii AK1
120554058	Marinobacter aquaeolei VT8	323499819	Vibrio sinaloensis DSM 21326
126668583	Marinobacter sp. ELB17	163802476	Vibrio sp. AND4
152995388	Marinomonas sp. MWYL1	342806779	Vibrio splendidus ATCC 33789
307353287	Methanoplanus petrolearius DSM 11571	343501752	Vibrio tubiashii ATCC 19109
91775968	Methylobacillus flagellatus KT	27363892	Vibrio vulnificus CMCP6
344942373	Methylobacter tundripaludum SV96	21231434	Xanthomonas campestris pv. campestris str. ATCC 33913
53802989	Methylococcus capsulatus str. Bath	290475996	Xenorhabdus bovienii SS-2004
334110080	Methylomicrobium album BG8	300724173	Xenorhabdus nematophila ATCC 19061
333985588	Methylomonas methanica MC09	182682230	Xylella fastidiosa M23
335043518	Methylophaga aminisulfidivorans MP	238797967	Yersinia mollaretii ATCC 43969
254492652	Methylophaga thiooxydans DMS010	260753035	Zymomonas mobilis subsp. mobilis NCIMB 11163

Table S5: Species and GenBank IDs of proteins used in hydrophobicity analysis of ClpS (Figure 5)

GenBank ID	Organism	GenBank ID	Organism
B0CF44	<i>Acaryochloris marina</i> (strain MBIC 11017)	D3PRX9	<i>Meiothermus ruber</i> (strain ATCC 49081)
B0C861	<i>Acaryochloris marina</i> (strain MBIC 11017)	C1XR29	<i>Meiothermus silvanus</i> DSM 9946
C7RNB3	<i>Accumulibacter phosphatis</i> (strain UW-1)	C8SEG7	<i>Mesorhizobium opportunistum</i> WSM2075
C7K4L6	<i>Acetobacter pasteurianus</i>	Q11IK7	<i>Mesorhizobium</i> sp. (strain BNC1)
C7M265	<i>Acidimicrobium ferrooxidans</i> (strain DSM 10331)	Q11GF3	<i>Mesorhizobium</i> sp. (strain BNC1)
A5G1K4	<i>Acidiphilium cryptum</i> (strain JF-5)	B3E050	<i>Methylacidiphilum inferorum</i> (isolate V4)
A5G2E8	<i>Acidiphilium cryptum</i> (strain JF-5)	A2SIM8	<i>Methylibium petroleiphilum</i> (strain PM1)
C6NSV8	<i>Acidithiobacillus caldus</i> ATCC 51756	Q1H408	<i>Methylobacillus flagellatus</i> (strain KT / ATCC 51484)
B7J540	<i>Acidithiobacillus ferrooxidans</i> (strain ATCC 23270)	B1ZAW5	<i>Methylobacterium populi</i> (strain ATCC BAA-705)
A0LVK3	<i>Acidothermus cellulolyticus</i> (strain ATCC 43068 / 11B)	B1LXN3	<i>Methylobacterium radiotolerans</i> (strain ATCC 27329)
A1TS63	<i>Acidovorax citrullii</i> (strain AAC00-1)	B0UEH9	<i>Methylobacterium</i> sp. (strain 4-46)
C5T196	<i>Acidovorax delafieldii</i> 2AN	B8EPD1	<i>Methylocella silvestris</i> (strain BL2)
A1W6Z3	<i>Acidovorax</i> sp. (strain JS42)	Q607H2	<i>Methylococcus capsulatus</i> (strain ATCC 33009)
B0VQK1	<i>Acinetobacter baumannii</i> (strain SDF)	C6WYC4	<i>Methylotenera mobilis</i> (strain JLW8)
D0SE13	<i>Acinetobacter johnsonii</i> SH046	C6X9T7	<i>Methylorvus</i> sp. (strain SIP3-4)
D0SIG8	<i>Acinetobacter junii</i> SH205	A5DGJ3	<i>Meyerozyma guilliermondii</i> (strain ATCC 6260)
D0SVE3	<i>Acinetobacter lwoffii</i> SH145	C5CA92	<i>Micrococcus luteus</i> (strain ATCC 4698)
D0T1K6	<i>Acinetobacter radioresistens</i> SH164	B4VR76	<i>Microcoleus chthonoplastes</i> PCC 7420
C0W0S7	<i>Actinomyces coleocanis</i> DSM 15436	A8YNY8	<i>Microcystis aeruginosa</i> PCC 7806
A7B8X1	<i>Actinomyces odontolyticus</i> ATCC 17982	D3CAR9	<i>Micromonospora</i> sp. L5
C0W2H3	<i>Actinomyces urogenitalis</i> DSM 15434	A1ZHK3	<i>Microscilla marina</i> ATCC 23134
C6WNP2	<i>Actinosynnema mirum</i> (strain ATCC 29888)	C2BRJ4	<i>Mobiluncus curtisii</i> ATCC 43063
C6WMJ9	<i>Actinosynnema mirum</i> (strain ATCC 29888 / DSM 43827 / NBRC 14064)	C2KQY4	<i>Mobiluncus mulieris</i> ATCC 35243
Q16WN2	<i>Aedes aegypti</i>	A9V1Y2	<i>Monosiga brevicollis</i>
A0KJD6	<i>Aeromonas hydrophila</i> subsp. <i>hydrophila</i> (strain ATCC 7966)	A6FC31	<i>Moritella</i> sp. PE36
B9J797	<i>Agrobacterium radiobacter</i> (strain K84 / ATCC BAA-868)	Q6WKZ8	<i>Mus musculus</i> (Mouse)
Q8UFN4	<i>Agrobacterium tumefaciens</i> (strain C58 / ATCC 33970)	Q2M411	<i>Mus musculus</i> (Mouse)
Q8UD95	<i>Agrobacterium tumefaciens</i> (strain C58 / ATCC 33970)	B1MLY4	<i>Mycobacterium abscessus</i> (strain ATCC 19977 / DSM 44196)
B9JX42	<i>Agrobacterium vitis</i> (strain S4 / ATCC BAA-846)	A0QCZ8	<i>Mycobacterium avium</i> (strain 104)
B9JZ42	<i>Agrobacterium vitis</i> (strain S4 / ATCC BAA-846)	P53423	<i>Mycobacterium leprae</i>
C0NSF8	<i>Ajellomyces capsulata</i> (strain G186AR)	A0R1X7	<i>Mycobacterium smegmatis</i> (strain ATCC 700084 / mc(2)155)
C5GTB0	<i>Ajellomyces dermatitidis</i> (strain ER-3 / ATCC MYA-2586)	A3Q388	<i>Mycobacterium</i> sp. (strain JLS)
C5JLN9	<i>Ajellomyces dermatitidis</i> (strain SLH14081)	A2VHM2	<i>Mycobacterium tuberculosis</i> C

GenBank ID	Organism	GenBank ID	Organism
Q0VQ16	<i>Alcanivorax borkumensis</i> (strain SK2 / ATCC 700651 / DSM 11573)	A1TD23	<i>Mycobacterium vanbaalenii</i> (strain DSM 7251 / PYR-1)
A3I246	<i>Algoriphagus</i> sp. PR1	Q1CZL3	<i>Myxococcus xanthus</i> (strain DK 1622)
B6EIX3	<i>Aliivibrio salmonicida</i> (strain LFI1238)	C8XFX3	<i>Nakamurella multipartita</i> (strain ATCC 700099)
Q0A8P0	<i>Alkalilimnicola ehrlichei</i> (strain MLHE-1)	B9L8R5	<i>Nautilia profundicola</i> (strain ATCC BAA-1463 / DSM 18972 / AmH)
D3RVX6	<i>Allochromatium vinosum</i> (strain ATCC 17899)	C7YKE0	<i>Nectria haematococca</i> (strain 77-13-4)
A8U362	alpha proteobacterium BAL199	D4DP95	<i>Neisseria elongata</i> subsp. <i>glycolytica</i> ATCC 29315
D0RNQ7	alpha proteobacterium HIMB114	C5TIN3	<i>Neisseria flavescens</i> SK114
A0Y1L2	Alteromonadales bacterium TW-7	A9M3Y5	<i>Neisseria meningitidis</i> serogroup C (strain 053442)
B4S1R5	<i>Alteromonas macleodii</i> (strain DSM 17117 / Deep ecotype)	C6M0Z0	<i>Neisseria sicca</i> ATCC 29256
Q3M980	<i>Anabaena variabilis</i> (strain ATCC 29413 / PCC 7937)	Q2BNI6	<i>Neptuniibacter caesariensis</i>
A7H8K1	<i>Anaeromyxobacter</i> sp. (strain Fw109-5)	Q7SGT6	<i>Neurospora crassa</i> (strain ATCC 24698)
B4UEC7	<i>Anaeromyxobacter</i> sp. (strain K)	A6Q1Y4	<i>Nitratiruptor</i> sp. (strain SB155-2)
Q7QEV6	<i>Anopheles gambiae</i>	Q1QKP0	<i>Nitrobacter hamburgensis</i> (strain X14 / DSM 10229)
Q9SX29	<i>Arabidopsis thaliana</i>	Q1QQ45	<i>Nitrobacter hamburgensis</i> (strain X14 / DSM 10229)
A8EW20	<i>Arcobacter butzleri</i> (strain RM4018)	Q3SRY4	<i>Nitrobacter winogradskyi</i> (strain Nb-255 / ATCC 25391)
Q5P201	<i>Aromatoleum aromaticum</i> (strain EbN1)	Q3SUZ4	<i>Nitrobacter winogradskyi</i> (strain Nb-255 / ATCC 25391)
A1R7T3	<i>Arthrobacter aurescens</i> (strain TC1)	A4BTH7	<i>Nitrococcus mobilis</i> Nb-231
B8HAW8	<i>Arthrobacter chlorophenolicus</i> (strain A6)	Q3J8G4	<i>Nitrosococcus oceani</i> (strain ATCC 19707 / NCIMB 11848)
A0JY44	<i>Arthrobacter</i> sp. (strain FB24)	Q82TY3	<i>Nitrosomonas europaea</i>
D4AUI0	<i>Arthroderma benhamiae</i> (strain ATCC MYA-4681 / CBS 112371)	Q0AEG2	<i>Nitrosomonas eutropha</i> (strain C91)
C5G122	<i>Arthroderma otae</i> (strain ATCC MYA-4605 / CBS 113480)	C6MBC4	<i>Nitrosomonas</i> sp. AL212
B5VXX9	<i>Arthrospira maxima</i> CS-328	Q2Y6T2	<i>Nitrosospora multififormis</i> (strain ATCC 25196 / NCIMB 11849)
B5W610	<i>Arthrospira maxima</i> CS-328	Q5Z0W0	<i>Nocardia farcinica</i>
Q75F74	<i>Ashbya gossypii</i> (strain ATCC 10895 / CBS 109.51 / FGSC 9923 / NRRL Y-1056) (Ye)	A0ZEM1	<i>Nodularia spumigena</i> CCY9414
C5SJR0	<i>Asticcacaulis excentricus</i> CB 48	B9YSP8	<i>Nostoc azollae</i> 0708
A1K4J5	<i>Azoarcus</i> sp. (strain BH72)	B2J5C3	<i>Nostoc punctiforme</i> (strain ATCC 29133 / PCC 73102)
A8HYA7	<i>Azorhizobium caulinodans</i> (strain ATCC 43989 / DSM 5975 / ORS 571)	B2J7K9	<i>Nostoc punctiforme</i> (strain ATCC 29133 / PCC 73102)
D3NSE6	<i>Azospirillum</i> sp. (strain B510)	Q8YP75	<i>Nostoc</i> sp. (strain PCC 7120)
C1DKZ8	<i>Azotobacter vinelandii</i> (strain DJ / ATCC BAA-1303)	Q2GB27	<i>Novosphingobium aromaticivorans</i> (strain DSM 12444)
A7AWT0	<i>Babesia bovis</i>	A9DW31	<i>Oceanibulbus indolifex</i> HEL-45
B3C5G9	<i>Bacteroides intestinalis</i> DSM 17393	A3UJU7	<i>Oceanicaulis</i> sp. HTCC2633
B5CXJ2	<i>Bacteroides plebeius</i> DSM 17135	A3TVK3	<i>Oceanicola batsensis</i> HTCC2597
C6ZB35	<i>Bacteroides</i> sp. 4_3_47FAA	A3TXJ2	<i>Oceanicola batsensis</i> HTCC2597
A7V170	<i>Bacteroides uniformis</i> ATCC 8492	Q2CDM6	<i>Oceanicola granulosus</i> HTCC2516

GenBank ID	Organism	GenBank ID	Organism
A1USD4	<i>Bartonella bacilliformis</i> (strain ATCC 35685 / KC583)	C4WK63	<i>Ochrobactrum intermedium</i> LMG 3301
Q6G5D4	<i>Bartonella henselae</i> (Rochalimaea henselae)	B5J1S5	<i>Octadecabacter antarcticus</i> 307
Q6FZM5	<i>Bartonella quintana</i> (Rochalimaea quintana)	B6JFT1	<i>Oligotropha carboxidovorans</i> (strain ATCC 49405 / DSM 1227 / OM5)
A9ISI4	<i>Bartonella tribocorum</i> (strain CIP 105476 / IBS 506)	C0AEU1	<i>Opiritaceae bacterium</i> TAV2
Q6MNG7	<i>Bdellovibrio bacteriovorus</i>	B1ZW63	<i>Opiritutus terrae</i> (strain DSM 11246 / PB90-1)
A7BUX7	<i>Beggiatoa</i> sp. PS	A2WWP3	<i>Oryza sativa</i> subsp. indica (Rice)
A7BKX4	<i>Beggiatoa</i> sp. SS	Q6ZAA3	<i>Oryza sativa</i> subsp. japonica (Rice)
B2IC44	<i>Beijerinckia indica</i> subsp. indica (strain ATCC 9039 / DSM 1715 / NCIB 8712)	C3X5C8	<i>Oxalobacter formigenes</i> HOxBL5
Q1N4N1	<i>Bermanella marisrubri</i>	C3XBK3	<i>Oxalobacter formigenes</i> OXCC13
B6BW15	beta proteobacterium KB13	C8Q7Q4	<i>Pantoea</i> sp. At-9b.
C5BY86	<i>Beutenbergia cavernae</i> (strain ATCC BAA-8 / DSM 12333 / NBRC 16432)	C1GRI7	<i>Paracoccidioides brasiliensis</i> (strain ATCC MYA-826 / Pb01)
A3ZYE4	<i>Blastopirellula marina</i> DSM 3645	A1B2V9	<i>Paracoccus denitrificans</i> (strain Pd 1222)
A4A1M8	<i>Blastopirellula marina</i> DSM 3645	A7HWX2	<i>Parvibaculum lavamentivorans</i> (strain DS-1 / DSM 13023 / NCIMB 13966)
Q2KZI1	<i>Bordetella avium</i> (strain 197N)	A3VTI9	<i>Parvularcula bermudensis</i> HTCC2503
Q7W7E8	<i>Bordetella parapertussis</i>	A6EAS7	<i>Pedobacter</i> sp. BAL39
A6S1L2	<i>Botryotinia fuckeliana</i> (strain B05.10) (Noble rot fungus) (<i>Botrytis cinerea</i>)	B9XH82	<i>Pedosphaera parvula</i> Ellin514
C7ME10	<i>Brachybacterium faecium</i> (strain ATCC 43885 / DSM 4810 / NCIB 9860)	Q3A2A7	<i>Pelobacter carbinolicus</i> (strain DSM 2380 / Gra Bd 1)
Q89RX6	<i>Bradyrhizobium japonicum</i>	Q3B6X1	<i>Pelodictyon luteolum</i> (strain DSM 273)
A5EKV5	<i>Bradyrhizobium</i> sp. (strain BTAi1 / ATCC BAA-1182)	B4SAN3	<i>Pelodictyon phaeoclathratiforme</i> (strain DSM 5477 / BU-1)
A5EEP3	<i>Bradyrhizobium</i> sp. (strain BTAi1 / ATCC BAA-1182)	C5LR49	<i>Perkinsus marinus</i> (strain ATCC 50983 / TXsc)
C3XRV1	<i>Branchiostoma floridae</i> (Florida lancelet) (<i>Amphioxus</i>)	C0QRD5	<i>Persephonella marina</i> (strain DSM 14350 / EX-H1)
D0XNL3	<i>Brevundimonas subvibrioides</i> ATCC 15264	A9EI43	<i>Phaeobacter gallaeciensis</i> 2.10
C7LCC1	<i>Brucella microti</i> (strain CCM 4915)	B7G1Y3	<i>Phaeodactylum tricorutum</i> (strain CCAP 1055/1)
A8PEX3	<i>Brugia malayi</i> (Filarial nematode worm)	B5Y4P7	<i>Phaeodactylum tricorutum</i> (strain CCAP 1055/1)
B2JDY3	<i>Burkholderia phymatum</i> (strain DSM 17167 / STM815)	B7FSL9	<i>Phaeodactylum tricorutum</i> (strain CCAP 1055/1)
D4MS43	butyrate-producing bacterium SM4/1	B7G3L2	<i>Phaeodactylum tricorutum</i> (strain CCAP 1055/1)
A8XEC1	<i>Caenorhabditis briggsae</i>	Q0UYK0	<i>Phaeosphaeria nodorum</i> (strain SN15 / ATCC MYA-4574)
P91133	<i>Caenorhabditis elegans</i>	B4R947	<i>Phenylobacterium zucineum</i> (strain HLK1)
Q4HGQ1	<i>Campylobacter coli</i> RM2228	B6S340	<i>Philodina roseola</i>
A0RNV2	<i>Campylobacter fetus</i> subsp. fetus (strain 82-40)	Q1Z142	<i>Photobacterium profundum</i> 3TCK
C8PIY9	<i>Campylobacter gracilis</i> RM3268	Q2C5M0	<i>Photobacterium</i> sp. SKA34
A712C8	<i>Campylobacter hominis</i> (strain ATCC BAA-381 / CH001A)	C7BQY5	<i>Photorhabdus asymbiotica</i> subsp. asymbiotica (strain ATCC 43949)
A3ZBJ2	<i>Campylobacter jejuni</i> subsp. jejuni HB93-13	A1IW46	<i>Physcomitrella patens</i>
B9KCU5	<i>Campylobacter lari</i> (strain RM2100 / D67 / ATCC BAA-1060)	A9SM76	<i>Physcomitrella patens</i> subsp. patens

GenBank ID	Organism	GenBank ID	Organism
B9D3L8	Campylobacter rectus RM3267	D0MZT0	Phytophthora infestans (strain T30-4)
C6RD16	Campylobacter showae RM3277	C4QVD7	Pichia pastoris (strain GS115 / ATCC 20864)
Q4HSE0	Campylobacter upsaliensis RM3195	C4R851	Pichia pastoris (strain GS115 / ATCC 20864)
B6BMD4	Campylobacteriales bacterium GD 1	D2R4L2	Pirellula staleyi (strain ATCC 27377 / DSM 6068 / ICPB 4128)
C4YHF5	Candida albicans (strain WO-1)	Q4Y4T9	Plasmodium chabaudi
B9WFZ2	Candida dubliniensis (strain CD36)	Q8IEB2	Plasmodium falciparum (isolate 3D7)
Q6FRD9	Candida glabrata (strain ATCC 2001)	B3LC14	Plasmodium knowlesi (strain H)
C5M2Q0	Candida tropicalis (strain ATCC MYA-3404 / T1)	A5JZI8	Plasmodium vivax (strain Salvador I)
B6BP63	Candidatus Pelagibacter sp. HTCC7211	Q7RHW1	Plasmodium yoelii yoelii
D2MLG5	Candidatus Poribacteria sp. WGA-A3	A6G681	Plesiocystis pacifica SIR-1
C2M3W6	Capnocytophaga gingivalis ATCC 33624	B2A9Y4	Podospora anserina (strain S)
C7M443	Capnocytophaga ochracea (strain ATCC 27872)	A4C351	Polaribacter irgensii 23-P
C8ND08	Cardiobacterium hominis ATCC 15826	A2U3V0	Polaribacter sp. MED152
C7QA15	Catenulispora acidiphila (strain DSM 44928)	A1VNL5	Polaromonas naphthalenivorans (strain CJ2)
Q9A5I0	Caulobacter crescentus	Q129D7	Polaromonas sp. (strain JS666 / ATCC BAA-500)
C1RJ77	Cellulomonas flavigena DSM 20109	A4SZP8	Polynucleobacter sp. (strain QLW-P1DMWA-1)
B3PL55	Cellvibrio japonicus (strain Ueda107)	B9HWL2	Populus trichocarpa
Q0E5Q6	Celosia cristata	A9PHW1	Populus trichocarpa
Q2HD17	Chaetomium globosum (strain ATCC 6205)	B9HVL2	Populus trichocarpa
C7PM80	Chitinophaga pinensis (strain ATCC 43595)	D1PH54	Prevotella copri DSM 18205
A8IQY8	Chlamydomonas reinhardtii	D3IE92	Prevotella sp. oral taxon 299 str. F0039
A8JGV8	Chlamydomonas reinhardtii	D3IKB5	Prevotella sp. oral taxon 317 str. F0108
B3QRF9	Chlorobaculum parvum (strain NCIB 8327)	C9PUC5	Prevotella sp. oral taxon 472 str. F0295
Q3AP10	Chlorobium chlorochromatii (strain CaD3)	A9BCJ0	Prochlorococcus marinus (strain MIT 9211)
Q0YQL7	Chlorobium ferrooxidans DSM 13031	A9BC83	Prochlorococcus marinus (strain MIT 9211)
B3EDQ4	Chlorobium limicola (strain DSM 245)	A8G6Z9	Prochlorococcus marinus (strain MIT 9215)
B3EJK6	Chlorobium phaeobacteroides (strain BS1)	A8G4W6	Prochlorococcus marinus (strain MIT 9215)
A1BCI9	Chlorobium phaeobacteroides (strain DSM 266)	A2C9Y6	Prochlorococcus marinus (strain MIT 9303)
Q8KAC6	Chlorobium tepidum	Q31AU5	Prochlorococcus marinus (strain MIT 9312)
B9LKT3	Chloroflexus aurantiacus (strain ATCC 29364 / DSM 637 / Y-400-fl)	Q7V4Z2	Prochlorococcus marinus (strain MIT 9313)
B3QRW3	Chloroherpeton thalassium (strain ATCC 35110 / GB-78)	A2C4T6	Prochlorococcus marinus (strain NATL1A)
Q7NRW1	Chromobacterium violaceum	A2C393	Prochlorococcus marinus (strain NATL1A)
Q1QUS0	Chromohalobacter salexigens (strain DSM 3043)	Q7VA15	Prochlorococcus marinus (strain SARG)
C0YS07	Chryseobacterium gleum ATCC 35910	Q7UZZ4	Prochlorococcus marinus subsp. pastoris (strain CCMP1986 / MED4)

GenBank ID	Organism	GenBank ID	Organism
B4DBP2	<i>Chthoniobacter flavus</i> Ellin428	D3ME74	<i>Propionibacterium acnes</i> J165
D0D3M6	<i>Citricella</i> sp. SE45	B4S981	<i>Prosthecochloris aestuarii</i> (strain DSM 271 / SK 413)
A5CQG1	<i>Clavibacter michiganensis</i> subsp. <i>michiganensis</i> (strain NCPPB 382)	A4SC42	<i>Prosthecochloris vibrioformis</i> (strain DSM 265)
C4YA51	<i>Clavospora lusitaniae</i> (strain ATCC 42720)	B4EV82	<i>Proteus mirabilis</i> (strain HI4320)
Q97I31	<i>Clostridium acetobutylicum</i>	D1P046	<i>Providencia rustigianii</i> DSM 4541
A6M0Y3	<i>Clostridium beijerinckii</i> (strain ATCC 51743 / NCIMB 8052)	B2Q440	<i>Providencia stuartii</i> ATCC 25827
C4IJM3	<i>Clostridium butyricum</i> E4 str. BoNT E BL5262	Q15T97	<i>Pseudoalteromonas atlantica</i> (strain T6c / ATCC BAA-1087)
C6Q0C7	<i>Clostridium carboxidivorans</i> P7	A4CC50	<i>Pseudoalteromonas tunicata</i> D2
D3AB39	<i>Clostridium hathewayi</i> DSM 13479	Q02NB3	<i>Pseudomonas aeruginosa</i> (strain UCBPP-PA14)
B9E3N2	<i>Clostridium kluyveri</i> (strain NBRC 12016)	Q1IBD9	<i>Pseudomonas entomophila</i> (strain L48)
C1I7V9	<i>Clostridium</i> sp. 7_2_43FAA	Q3KA75	<i>Pseudomonas fluorescens</i> (strain Pf0-1)
D1NJ64	<i>Clostridium thermocellum</i> JW20	A4XUY4	<i>Pseudomonas mendocina</i> (strain ymp)
C5PH89	<i>Coccidioides posadasii</i> (strain C735)	A4VLV7	<i>Pseudomonas stutzeri</i> (strain A1501)
Q480C4	<i>Colwellia psychrerythraea</i> (strain 34H / ATCC BAA-681)	B6RA22	<i>Pseudovibrio</i> sp. JE062
D3F5Q7	<i>Conexibacter woesei</i> (strain DSM 14684)	Q4FRL1	<i>Psychrobacter arcticus</i> (strain DSM 17307 / 273-4)
A4A3B7	<i>Congregibacter litoralis</i> KT71	A5WUFU6	<i>Psychrobacter</i> sp. (strain PRwf-1)
C3PIP1	<i>Corynebacterium aurimucosum</i> (strain ATCC 700975)	Q1VZV8	<i>Psychroflexus torquis</i> ATCC 700755
Q6NFN0	<i>Corynebacterium diphtheriae</i>	A1SSX9	<i>Psychromonas ingrahamii</i> (strain 37)
Q8FMT9	<i>Corynebacterium efficiens</i>	Q1ZEG9	<i>Psychromonas</i> sp. CNPT3
C8NSV6	<i>Corynebacterium genitalium</i> ATCC 33030	B5SHF8	<i>Ralstonia solanacearum</i> IPO1609
C2GJP0	<i>Corynebacterium glucuronolyticum</i> ATCC 51866	A4BDP9	<i>Reinekea blandensis</i> MED297
C8RVS8	<i>Corynebacterium jeikeium</i> ATCC 43734	A9WNP2	<i>Renibacterium salmoninarum</i> (strain ATCC 33209)
C0XR95	<i>Corynebacterium lipophiloflavum</i> DSM 44291	B3PV12	<i>Rhizobium etli</i> (strain CIAT 652)
C0E3M7	<i>Corynebacterium matruchotii</i> ATCC 33806	C6AWZ0	<i>Rhizobium leguminosarum</i> bv. <i>trifolii</i> (strain WSM1325)
C2CLJ7	<i>Corynebacterium striatum</i> ATCC 6940	Q1MDL3	<i>Rhizobium leguminosarum</i> bv. <i>viciae</i> (strain 3841)
C6R809	<i>Corynebacterium tuberculostearicum</i> SK141	Q98HS2	<i>Rhizobium loti</i> (strain MAFF303099) (<i>Mesorhizobium loti</i>)
B1VGX5	<i>Corynebacterium urealyticum</i> (strain ATCC 43042)	C3MFM8	<i>Rhizobium</i> sp. (strain NGR234)
A3UB67	<i>Croceibacter atlanticus</i> (strain ATCC BAA-628)	C8RWL8	<i>Rhodobacter</i> sp. SW2
Q4BZR4	<i>Crocospaera watsonii</i> WH 8501	A4WPY6	<i>Rhodobacter sphaeroides</i> (strain ATCC 17025 / ATH 2.4.3)
C9YFK9	<i>Curvibacter</i> putative symbiont of <i>Hydra magnipapillata</i>	A3JNU8	<i>Rhodobacteraceae</i> bacterium HTCC2150
D3EQD2	<i>Cyanobacterium</i> UCYN-A	B9NR55	<i>Rhodobacteraceae</i> bacterium KLH11
D3ENI8	<i>Cyanobacterium</i> UCYN-A	Q0FA33	<i>Rhodobacterales</i> bacterium HTCC2255
B5IPW7	<i>Cyanobium</i> sp. PCC 7001	B6BBF4	<i>Rhodobacterales</i> bacterium Y41
B1X012	<i>Cyanothece</i> sp. (strain ATCC 51142)	C3JU49	<i>Rhodococcus erythropolis</i> SK121

GenBank ID	Organism	GenBank ID	Organism
B7KAW6	Cyanothece sp. (strain PCC 7424)	C1AVW7	Rhodococcus opacus (strain B4)
B7KA84	Cyanothece sp. (strain PCC 7424)	Q21UT1	Rhodoferax ferrireducens (strain DSM 15236 / ATCC BAA-621 / T118)
B8HQQ4	Cyanothece sp. (strain PCC 7425)	D2LHX3	Rhodomicrobium vannielii ATCC 17100
B8HUH2	Cyanothece sp. (strain PCC 7425)	Q7UJ48	Rhodopirellula baltica (strain SH1)
B8HXL0	Cyanothece sp. (strain PCC 7425)	Q6NAI2	Rhodopseudomonas palustris (strain ATCC BAA-98 / CGA009)
B7JWS7	Cyanothece sp. (strain PCC 8801)	Q211R9	Rhodopseudomonas palustris (strain BisB18)
C7QN96	Cyanothece sp. (strain PCC 8802)	Q21A80	Rhodopseudomonas palustris (strain BisB18)
Q11W93	Cytophaga hutchinsonii (strain ATCC 33406 / NCIMB 9469)	Q21XG0	Rhodopseudomonas palustris (strain HaA2)
A2RV49	Danio rerio	Q2J0T6	Rhodopseudomonas palustris (strain HaA2)
Q6BHH4	Debaryomyces hansenii (strain ATCC 36239)	D2M6I8	Rhodopseudomonas palustris DX-1
Q47BF7	Dechloromonas aromatica (strain RCB)	B6INJ3	Rhodospirillum centenum (strain ATCC 51521 / SW)
C1D1J8	Deinococcus deserti (strain VCD115 / DSM 17065 / LMG 22923)	Q2RSI5	Rhodospirillum rubrum (strain ATCC 11170 / NCIB 8255)
Q11YB5	Deinococcus geothermalis (strain DSM 11300)	D0MKG3	Rhodothermus marinus (strain ATCC 43812 / DSM 4252 / R-10)
Q9RWS9	Deinococcus radiodurans	A4CM82	Robiginitalea biformata (strain ATCC BAA-864 / HTCC2501 / KCTC 12146)
A9BWB8	Delftia acidovorans (strain DSM 14801 / SPH-1)	A5UVH1	Roseiflexus sp. (strain RS-1)
Q1NYG9	delta proteobacterium MLMS-1	A9HDA6	Roseobacter litoralis Och 149
B8FGA3	Desulfatibacillum alkenivorans (strain AK-01)	A6FP19	Roseobacter sp. AzwK-3b
C0QI24	Desulfobacterium autotrophicum (strain ATCC 43914)	A3XCA7	Roseobacter sp. MED193
A8ZW52	Desulfococcus oleovorans (strain DSM 6200 / Hxd3)	A4EZI6	Roseobacter sp. SK209-2-6
C8X2K8	Desulfohalobium retbaense (strain DSM 5692)	A3SLI5	Roseovarius nubinihibens ISM
C7LNU7	Desulfomicrobium baculatum (strain DSM 4028 / VKM B-1378)	A6DVP3	Roseovarius sp. TM1035
C0GLA3	Desulfonatronospira thiodismutans ASO3-1	D2NTX5	Rothia mucilaginosa (strain DY-18)
Q6APV7	Desulfotalea psychrophila	Q1AX97	Rubrobacter xylanophilus (strain DSM 9941 / NBRC 16129)
D1UAC6	Desulfovibrio aespoensis Aspo-2	Q1AUC8	Rubrobacter xylanophilus (strain DSM 9941 / NBRC 16129)
B8J0Q5	Desulfovibrio desulfuricans (strain ATCC 27774 / DSM 6949)	A1AXG8	Ruthia magnifica subsp. Calyptogena magnifica
Q30ZJ9	Desulfovibrio desulfuricans (strain G20)	C7MWD2	Saccharomonospora viridis (strain ATCC 15386)
C4XT60	Desulfovibrio magneticus (strain ATCC 700980 / DSM 13731 / RS-1)	C7MWC9	Saccharomonospora viridis (strain ATCC 15386)
B6WT25	Desulfovibrio piger ATCC 29098	A6ZUJ5	Saccharomyces cerevisiae (strain YJM789)
C6BTW1	Desulfovibrio salexigens (strain ATCC 14822)	Q21K33	Saccharophagus degradans (strain 2-40 / ATCC 43961 / DSM 17024)
D2L0R1	Desulfovibrio sp. FW1012B	A4F902	Saccharopolyspora erythraea (strain NRRL 23338)
B8DJU4	Desulfovibrio vulgaris (strain Miyazaki F / DSM 19637)	A3K8H7	Sagittula stellata E-37
C5TW41	Desulfovibrio vulgaris RCH1	Q2S3Y5	Salinibacter ruber (strain DSM 13855 / M31)
D3C236	Desulfurispirillum indicum S5	A8M4H4	Salinispora arenicola (strain CNS-205)
C8QZIO	Desulfurivibrio alkaliphilus AHT2	D1BK05	Sanguibacter keddieii (strain ATCC 51767)

GenBank ID	Organism	GenBank ID	Organism
Q1JY16	Desulfuromonas acetoxidans DSM 684	A3GGK8	Scheffersomyces stipitis (strain ATCC 58785)
A5EV84	Dichelobacter nodosus (strain VCS1703A)	C1M0R4	Schistosoma mansoni (Blood fluke)
D2C1L3	Dickeya dadantii (strain Ech586)	B6K064	Schizosaccharomyces japonicus (strain yFS275 / FY16936)
A2TW75	Dokdonia donghaensis MED134	B6K7B1	Schizosaccharomyces japonicus (strain yFS275 / FY16936)
B3N0B2	Drosophila ananassae (Fruit fly)	O13731	Schizosaccharomyces pombe (strain 972 / ATCC 24843)
B3NWA6	Drosophila erecta (Fruit fly)	A1S7A6	Shewanella amazonensis (strain ATCC BAA-1098 / SB2B)
B4JN26	Drosophila grimshawi (Fruit fly)	Q12N59	Shewanella denitrificans (strain OS217 / ATCC BAA-1090 / DSM 15013)
B4L4X4	Drosophila mojavensis (Fruit fly)	Q081G4	Shewanella frigidimarina (strain NCIMB 400)
B4HA29	Drosophila persimilis (Fruit fly)	B8CLI1	Shewanella piezotolerans (strain WP3 / JCM 13877)
B4IEW0	Drosophila sechellia (Fruit fly)	A8FUH3	Shewanella sediminis (strain HAW-EB3)
B4M1M7	Drosophila virilis (Fruit fly)	Q0HJP4	Shewanella sp. (strain MR-4)
B4NCA8	Drosophila willistoni (Fruit fly)	C6P7C7	Sideroxydans lithotrophicus ES-1
C6W4L8	Dyadobacter fermentans (strain ATCC 700827 / DSM 18053 / NS114)	D0CUL2	Silicibacter lacuscaerulensis ITI-1157
D4F757	Edwardsiella tarda ATCC 23685	Q5LMA7	Silicibacter pomeroyi (strain ATCC 700808 / DSM 15171 / DSS-3)
C0DTJ4	Eikenella corrodens ATCC 23834	Q1GDK0	Silicibacter sp. (strain TM1040)
Q5B6A7	Emericella nidulans (Aspergillus nidulans)	A6U8I7	Sinorhizobium medicae (strain WSM419)
C8PUE9	Enhydrobacter aerosaccus SK60	A6UBR7	Sinorhizobium medicae (strain WSM419)
A7MEQ8	Enterobacter sakazakii (strain ATCC BAA-894)	Q2NTZ9	Sodalis glossinidius (strain morsitans)
D4I9N7	Erwinia amylovora (strain ATCC 49946 / CCPPB 0273 / Ea273 / 27-3)	Q029R9	Solibacter usitatus (strain Ellin6076)
Q6D3T7	Erwinia carotovora subsp. atroseptica	A9F361	Sorangium cellulosum (strain So ce56)
Q2N862	Erythrobacter litoralis (strain HTCC2594)	A9ENU4	Sorangium cellulosum (strain So ce56)
A3WE92	Erythrobacter sp. NAP1	D1ZH87	Sordaria macrospora (strain ATCC MYA-333)
A5PCY2	Erythrobacter sp. SD-21	C5PPN8	Sphingobacterium spiritivorum ATCC 33861
B7NM96	Escherichia coli O7:K1 (strain IA139 / ExPEC)	Q1NF75	Sphingomonas sp. SKA58
A3J6P3	Flavobacteria bacterium BAL38	A5V4L2	Sphingomonas wittichii (strain RW1 / DSM 6014)
C0BKF5	Flavobacteria bacterium MS024-2A	Q1GVU8	Sphingopyxis alaskensis (strain DSM 13593)
C6X4E7	Flavobacteriaceae bacterium (strain 3519-10)	D2QP41	Spirosoma linguale (strain ATCC 33905)
A8UHM8	Flavobacteriales bacterium ALC-1	D3PZ93	Stackebrandtia nassauensis (strain DSM 44728)
A5FE48	Flavobacterium johnsoniae (strain ATCC 17061)	B4SIN7	Stenotrophomonas maltophilia (strain R551-3)
A6H073	Flavobacterium psychrophilum (strain JIP02/86 / ATCC 49511)	Q08XV1	Stigmatella aurantiaca (strain DW4/3-1)
Q2JEP4	Frankia sp. (strain Ccl3)	D1WV64	Streptomyces cf. griseus XylebKG-1
A8L772	Frankia sp. (strain EAN1pec)	B5GSN2	Streptomyces clavuligerus ATCC 27064
D1VKS8	Frankia sp. Eul1c	B5HGA3	Streptomyces pristinaespiralis ATCC 25486
D3M8G8	Frankia symbiont of Datisca glomerata	C9Z164	Streptomyces scabies (strain 87.22)

GenBank ID	Organism	GenBank ID	Organism
Q0G6C3	Fulvimarina pelagi HTCC2506	B5GJ13	Streptomyces sp. SPB74
Q0FZ47	Fulvimarina pelagi HTCC2506	B5HNV9	Streptomyces sviceps ATCC 29083
C5V7D1	Gallionella capsiferriformans ES-2	D2AT38	Streptosporangium roseum (strain ATCC 12428)
Q1YTJ4	gamma proteobacterium HTCC2207	A3STC4	Sulfitobacter sp. NAS-14.1
B8KGE5	gamma proteobacterium NOR5-3	Q30TE2	Sulfurimonas denitrificans (strain ATCC 33889 / DSM 1251)
B8KRL2	gamma proteobacterium NOR51-B	D1B3H2	Sulfurospirillum deleyianum (strain ATCC 51133 / DSM 6946 / 5175)
D2SBE1	Geodermatophilus obscurus (strain ATCC 25078)	A6QBZ8	Sulfurovum sp. (strain NBC37-1)
Q7NML9	Gloeobacter violaceus	Q31QE7	Synechococcus elongatus (strain PCC 7942)
Q7NIE5	Gloeobacter violaceus	Q5N387	Synechococcus sp. (strain ATCC 27144 / PCC 6301 / SAUG 1402/1) (
Q7NHK4	Gloeobacter violaceus	B1XJ94	Synechococcus sp. (strain ATCC 27264 / PCC 7002 / PR-6)
A9H4B8	Gluconacetobacter diazotrophicus (strain ATCC 49037)	B1XI77	Synechococcus sp. (strain ATCC 27264 / PCC 7002 / PR-6)
Q5FTB0	Gluconobacter oxydans	Q01D69	Synechococcus sp. (strain CC9311)
C6T1Z0	Glycine max	Q01A93	Synechococcus sp. (strain CC9311)
C6SY21	Glycine max	Q3AUR5	Synechococcus sp. (strain CC9902)
D0L9M6	Gordonia bronchialis (strain ATCC 25592)	Q2JHL4	Synechococcus sp. (strain JA-2-3B'a(2-13))
A0LYH3	Gramella forsetii (strain KT0803)	Q2JUQ6	Synechococcus sp. (strain JA-3-3Ab)
Q0BRK5	Granulibacter bethesdensis (strain ATCC BAA-1260 / CGDNIH1)	A5GW24	Synechococcus sp. (strain RCC307)
D0I6W9	Grimontia hollisae CIP 101886	A5GTV2	Synechococcus sp. (strain RCC307)
Q5K279	Guillardia theta (Cryptomonas phi)	A4CST5	Synechococcus sp. (strain WH7805)
D0LVD1	Haliangium ochraceum (strain DSM 14365 / JCM 11303 / SMP-2)	A4CUN7	Synechococcus sp. (strain WH7805)
A1WVV6	Halorhodospira halophila (strain DSM 244 / SL1)	Q7U4C2	Synechococcus sp. (strain WH8102)
D0L1L0	Halothiobacillus neapolitanus (strain ATCC 23641 / c2)	Q7U6N4	Synechococcus sp. (strain WH8102)
C4K3S2	Hamiltonella defensa subsp. Acyrthosiphon pisum (strain 5AT)	Q067H2	Synechococcus sp. BL107
Q17ZL8	Helicobacter acinonychis (strain Sheeba)	B4WIM3	Synechococcus sp. PCC 7335
C3XFH6	Helicobacter bilis ATCC 43879	Q05T34	Synechococcus sp. RS9916
C5ZY75	Helicobacter canadensis MIT 98-5491	A3Z8Q6	Synechococcus sp. RS9917
Q7VFW0	Helicobacter hepaticus	A3Z6Y0	Synechococcus sp. RS9917
D3UJ94	Helicobacter mustelae (strain ATCC 43772)	A3YX68	Synechococcus sp. WH 5701
C5EYX6	Helicobacter pullorum MIT 98-5489	A3YZS7	Synechococcus sp. WH 5701
B9XWS9	Helicobacter pylori 98-10	D0CL44	Synechococcus sp. WH 8109
Q9ZN32	Helicobacter pylori J99	D0CJA5	Synechococcus sp. WH 8109
C3XMM0	Helicobacter winghamensis ATCC BAA-430	P74335	Synechocystis sp. (PCC 6803)
A9B6X2	Herpetosiphon aurantiacus (strain ATCC 23779 / DSM 785)	P73634	Synechocystis sp. (PCC 6803)
C6XL87	Hirschia baltica (strain ATCC 49814 / DSM 5838 / IFAM 1418)	Q2LQK8	Syntrophus aciditrophicus (strain SB)

GenBank ID	Organism	GenBank ID	Organism
A9DCU1	Hoeflea phototrophica DFL-43	A3F514	Taenia asiatica
C6QH28	Hyphomicrobium denitrificans ATCC 51888	C5BIJ4	Teredinibacter turnerae (strain ATCC 39867 / T7901)
Q0C3E2	Hyphomonas neptunium (strain ATCC 15444)	Q4RM05	Tetraodon nigroviridis
A3WQW6	Idiomarina baltica OS145	C7DBQ6	Thalassiosira sp. R2A62
Q5R0C3	Idiomarina loihiensis (strain ATCC BAA-735 /)	B8BU43	Thalassiosira pseudonana
A3TFZ3	Janibacter sp. HTCC2649	B8C287	Thalassiosira pseudonana
Q28KG0	Jannaschia sp. (strain CCS1)	B8C9R8	Thalassiosira pseudonana
A6T108	Janthinobacterium sp. (strain Marseille)	B8LC11	Thalassiosira pseudonana
C7R2H4	Jonesia denitrificans (strain ATCC 14870)	B8LC42	Thalassiosira pseudonana
C7RC85	Kangiella koreensis (strain DSM 16069 / KCTC 12182 / SW-125)	B5YMJ3	Thalassiosira pseudonana
A6WEJ0	Kineococcus radiotolerans (strain ATCC BAA-149)	B8CBQ7	Thalassiosira pseudonana
C4GH53	Kingella oralis ATCC 51147	Q4N751	Theileria parva
D3RLA9	Klebsiella variicola (strain At-22)	D1CBX2	Thermobaculum terrenum (strain ATCC BAA-798 / YNP1)
O60014	Kluyveromyces lactis (strain ATCC 8585)	Q47MB7	Thermobifida fusca (strain YX)
B2GM04	Kocuria rhizophila (strain ATCC 9341 / DSM 348 / NBRC 103217 / DC2201)	B5YGC3	Thermodesulfovibrio yellowstonii (strain ATCC 51303)
A9EB50	Kordia algicida OT-1	D1AD95	Thermomonospora curvata (strain ATCC 19995)
D2PPG8	Kribbella flavida (strain DSM 17836 / JCM 10339 / NBRC 14399)	Q8DMB0	Thermosynechococcus elongatus (strain BP-1)
C7NGK6	Kytococcus sedentarius (strain ATCC 14392)	Q8DJY3	Thermosynechococcus elongatus (strain BP-1)
A0NW83	Labrenzia aggregata IAM 12614	B8GSL6	Thioalkalivibrio sp. (strain HL-EbGR7)
A0NYC6	Labrenzia aggregata IAM 12614	D3S9R7	Thioalkalivibrio sp. (strain K90mix)
B9R273	Labrenzia alexandrii DFL-11	Q3SJH2	Thiobacillus denitrificans (strain ATCC 25259)
C5DCJ9	Lachancea thermotolerans (strain ATCC 56472)	Q31GL7	Thiomicrospira crunogena (strain XCL-2)
C1DBG4	Laribacter hongkongensis (strain HLHK9)	C4L948	Tolomonas auensis (strain DSM 9187 / TA4)
Q1MQQ6	Lawsonia intracellularis (strain PHE/MN1-00)	B9Q249	Toxoplasma gondii
A3XJM5	Leeuwenhoekiiella blandensis (strain CECT 7118)	Q1JTH4	Toxoplasma gondii
C6MZI8	Legionella drancourtii LLAP12	Q73KU4	Treponema denticola (strain ATCC 35405 / CIP 103919 / DSM 14222)
D3HJ48	Legionella longbeachae serogroup 1 (strain NSW150)	D1ZZM2	Tribolium castaneum
Q5ZXB5	Legionella pneumophila subsp. pneumophila	Q116U1	Trichodesmium erythraeum (strain IMS101)
Q6AEN2	Leifsonia xyli subsp. xyli (strain CTCB07)	Q10Y18	Trichodesmium erythraeum (strain IMS101)
A6DNS4	Lentisphaera araneosa HTCC2155	B3RZ22	Trichoplax adhaerens
A6BL23	Leptolyngbya valderiana BDU 20041	C2AS57	Tsukamurella paurometabola DSM 20162
B0S9H9	Leptospira biflexa serovar Patoc (strain Patoc 1 / Ames)	A3RGX2	uncultured bacterium
B0SFH1	Leptospira biflexa serovar Patoc (strain Patoc 1 /)	Q2YZM2	uncultured epsilon proteobacterium
B0SL07	Leptospira biflexa serovar Patoc (strain Patoc 1)	D1KCM6	uncultured SUP05 cluster bacterium

GenBank ID	Organism	GenBank ID	Organism
Q8F4D8	<i>Leptospira interrogans</i> serogroup Icterohaemorrhagiae serovar Lai	A6ENG7	unidentified eubacterium SCB49
Q8F2Y0	<i>Leptospira interrogans</i> serogroup Icterohaemorrhagiae serovar Lai	Q4PIJ6	<i>Ustilago maydis</i> (strain 521 / FGSC 9021)
B1XY29	<i>Leptothrix cholodnii</i> (strain ATCC 51168)	A7TFK8	<i>Vanderwaltozyma polyspora</i> (strain ATCC 22028)
C6XH92	<i>Liberibacter asiaticus</i> (strain psy62)	C5CLL8	<i>Variovorax paradoxus</i> (strain S110)
A6GTR2	<i>Limnobacter</i> sp. MED105	A1WRC7	<i>Verminephrobacter eiseniae</i> (strain EF01-2)
A5E3N6	<i>Lodderomyces elongisporus</i> (strain ATCC 11503)	B5JJB9	Verrucomicrobiae bacterium DG1235
A5E3N7	<i>Lodderomyces elongisporus</i> (strain ATCC 11503)	A7N1L5	<i>Vibrio harveyi</i> (strain ATCC BAA-1116)
A3V765	<i>Loktanella vestfoldensis</i> SKA53	D0GX99	<i>Vibrio mimicus</i> MB451
B9Z1Y7	<i>Lutiella nitroferum</i> 2002	C9QJL5	<i>Vibrio orientalis</i> CIP 102891 = ATCC 33934
A0YUC9	<i>Lyngbya</i> sp. (strain PCC 8106)	B7VM32	<i>Vibrio splendidus</i> (strain LGP32)
A4RQ90	<i>Magnaporthe oryzae</i> (strain 70-15 / ATCC MYA-4617 / FGSC 8958)	A5ASY4	<i>Vitis vinifera</i>
A0L8H6	<i>Magnetococcus</i> sp. (strain MC-1)	A5AM53	<i>Vitis vinifera</i>
A4TY92	<i>Magnetospirillum gryphiswaldense</i>	Q7MSL3	<i>Wolinella succinogenes</i>
Q2W899	<i>Magnetospirillum magneticum</i> (strain AMB-1 / ATCC 700264)	A7IP12	<i>Xanthobacter autotrophicus</i> (strain ATCC BAA-1158 / Py2)
Q1YI54	Manganese-oxidizing bacterium (strain SI85-9A1)	B0RT34	<i>Xanthomonas campestris</i> pv. <i>campestris</i> (strain B100)
A4AVV2	<i>Maribacter</i> sp. (strain HTCC2170)	Q3BTY4	<i>Xanthomonas campestris</i> pv. <i>vesicatoria</i> (strain 85-10)
Q0AQ60	<i>Maricaulis maris</i> (strain MCS10)	Q498F1	<i>Xenopus laevis</i> (African clawed frog)
A0Z1Z8	marine gamma proteobacterium HTCC2080	D3UZL1	<i>Xenorhabdus bovienii</i> (strain SS-2004)
A0YBV0	marine gamma proteobacterium HTCC2143	D3VBG5	<i>Xenorhabdus nematophila</i> (strain ATCC 19061)
B7RUZ6	marine gamma proteobacterium HTCC2148	D1BZD3	<i>Xylanimonas cellulosilytica</i> (strain DSM 15894)
A1U1H1	<i>Marinobacter aquaeolei</i> (strain ATCC)	Q3R219	<i>Xylella fastidiosa</i> subsp. <i>sandyi</i> Ann-1
A3JG01	<i>Marinobacter</i> sp. ELB17	C4HDU5	<i>Yersinia pestis</i> biovar <i>Orientalis</i> str. PEXU2
A6W0D8	<i>Marinomonas</i> sp. (strain MWYL1)	B6U7Z5	<i>Zea mays</i>
A3YG97	<i>Marinomonas</i> sp. MED121	C5DRS0	<i>Zygosaccharomyces rouxii</i> (strain ATCC 2623)
Q0EXS1	<i>Mariprofundus ferrooxydans</i> PV-1	Q5NLR1	<i>Zymomonas mobilis</i>
A3VET3	<i>Maritimibacter alkaliphilus</i> HTCC2654		

Supp. Figures

FIGURE S1. **Phylogeny of the Tic22 family.**

Homologues of Tic22 were collected by PSI-BLAST from GenBank (Table S5) and redundant sequences were removed with CD-Hit (Li, W., and Godzik, A. (2006) *Bioinformatics* 22, 1658-1659) leaving 133 sequences. A multiple sequence alignment (MSA) was constructed with MAFFT v6.811b (Kato, K., and Toh, H. (2010) *Bioinformatics* 26, 1899-1900). All columns containing more than 5 gaps were removed from the MSA leaving 124 non-redundant sequences and a maximum likelihood phylogeny was reconstructed with RAxML v7.0.4 using gamma-distributed rate heterogeneity and the WAG model (Whelan, S., and Goldman, N. (2001) *Mol. Biol. Evol.* 18, 691–699; Stamatakis, A. (2006) *Bioinformatics*. 22, 2688–2690). A bootstrap analysis was performed on 1,000 trees with RAxML's rapid bootstrap algorithm using CAT approximation (Stamatakis, A. *et al.* (2008) *Syst. Biol.* 57, 758-771). Clades were collapsed with the software MEGA (Tamura, K. *et al.* (2007) *Mol. Biol. Evol.* 24, 1596-1599) in order to make the tree more accessible to the reader. Only a single proteobacterial sequence with similarity to Tic22 could be found in *Marinobacter*, which is closely related to a cyanobacterial sequence from *Synechococcus*. Whether this is a genomic contamination or a result of horizontal gene transfer remains to be investigated.

FIGURE S2. **Analysis of the ultrastructure of the outer membrane of wild-type, AFS-I-*alr2269* and AFS-I-*tic22*.**

Cells of the indicated strains were analysed by electron microscopy as described in materials and methods.

FIGURE S3. **Analysis of protein level of Tic22 in AFS-I-*alr2269* and AFS-I-*alr2270*.**

Cells of the indicated strains were subjected to immunodecoration at different dilutions and the dilution factor with respect to the wild-type sample is indicated. The samples were immunodecorated with α ATP antibodies for loading control and α anaTic22 antibodies to estimate the protein abundance in the mutants.

FIGURE S4. **The deep central pocket of Tic22.**

A, Surface representation rotated by 90° with respect to (Figure 5B) as indicated by the arrow with an added transparent molecular surface. The helices α 1 and α 3 from both domains point at each other with their N-termini. B, A cut through the surface to visualize the pockets (indicated by arrowheads) is shown. On the right a zoom of the upper pocket (top) and the septum between the two pockets (bottom) is shown. Blue color highlights conserved residues. C, The same views as in (B), but the secondary structure elements and the outer

surface are colored as in Figure 5A to highlight, which secondary structure elements contribute to the pockets. *D*, The amino acid network separating the two pockets is shown. *E*, Tic22 is shown in a surface representation oriented as in Fig. 5B. For each residue in the crystal structure of Tic22 the mean hydrophobicity of amino acids was assigned. Sidechain atoms of residues with an assigned mean hydrophobicity of >-0.4 (glycine) were colored ranging from yellow (low hydrophobicity) to green (high hydrophobicity), while all positions with a mean hydrophobicity of <-0.4 are colored grey. *F*, Tic22 is shown in a surface representation oriented as in Fig. 5B. For each position in the crystal structure of Tic22 the conservation of amino acid properties was calculated from the corresponding columns of the in here created multiple sequence alignment of all non redundant, cyanobacterial Tic22 sequences from GenBank. Positions with at least 80% conservation of amino acid properties are color-coded as follows: magenta (N, Q; large, polar), violet (C, S, T; small, polar), blue (H, K, R; positively charged), red (D, E; negatively charged), yellow (F, W, Y; aromatic), light green (A, V; small, hydrophobic), green (I, L, M; large, hydrophobic), dark violet (G; tiny), orange (P). All other positions are colored in grey.

FIGURE S5. Tic22 conservation.

A, Conserved residues are shown in the context of the anaTic22 structure. The degree of conservation is color-coded and increases from light blue ($>70\%$) to dark blue (100%). Residue conservation was calculated from the multiple sequence alignment of all available cyanobacterial and plant Tic22 sequences (133), which were filtered with cd-hit to a maximal sequence identity of 90% leaving 110 sequences in the set. *B*, This column diagram contains the detailed conservation information shown in 'A' only for $>70\%$ conservation. The upper panel shows the degree of conservation for each type of amino acid, the lower panel shows the conservation of amino acids grouped by their physicochemical properties.

FIGURE S6. Conserved hydrophobic pockets of anaTic22.

The molecular surface of the structure of anaTic22 is shown. The structure is rotated by 180° around the y-axis relative to Fig. 5B. Bound solvent molecules are shown as sticks. *A*, The average hydrophobicity of each column in the multiple sequence alignment of cyanobacterial Tic22 proteins aligning to anaTic22 is shown. Hydrophobicity is color coded from 4.5 (=Ile, dark green) to -0.4 (=Gly, yellow), positions more hydrophilic (<-0.4) are colored in grey. *B*, The sequence conservation ($>70\%$) of cyanobacterial proteins filtered to a maximal sequence identity of 90% with cd-hit is mapped onto the surface of anaTic22 (darkness of blue indicates strength of conservation).

FIGURE S7. Comparison of anaTic22 and synTic22.

A, The amino acid sequences of slr0194 and alr0114 have been aligned by T-Coffee (Notredame, C., Higgins, D.G., and Heringa, J. (2000) *J. Mol. Biol.* **302**, 205-217.) and the result is shown in Clustal format. The sequences were analysed with SignalP 4.0 (Petersen, T.N., Brunak, S., von Heijne, G., and Nielsen, H. (2011) *Nature Methods*, **8**, 785-786.) and the most predicted cleavage site is indicated. Please note the prediction for slr0194 have been below treshhold. B, Indicated amounts of thylakoids were subjected to BN-PAGE followed by Coomassie Blu staing as described in (Ladig, R., *et al.* (2011) *Plant J.* 67, 181-194.). Complexes are assigned as: photosystem I, PS-I; photosystem II, PS-II; ATP synthase, ATP; phycobilisomes, PB; and Cyt-b6/f complex, Cyt; according to (Ladig, R., *et al.* (2011) *Plant J.* 67, 181-194.).

FIGURE S8. A structural homologue in *Thermus thermophilus*.

The protein TTHA0547 was crystallized in a structural genomics approach (pdb: 2z0r). Its fold is alike the structure of each of the two domains of Tic22. Shown is a structure-based sequence alignment of the two domains of *anaTic22* and of TTHA0547. Secondary structure elements are indicated underneath.

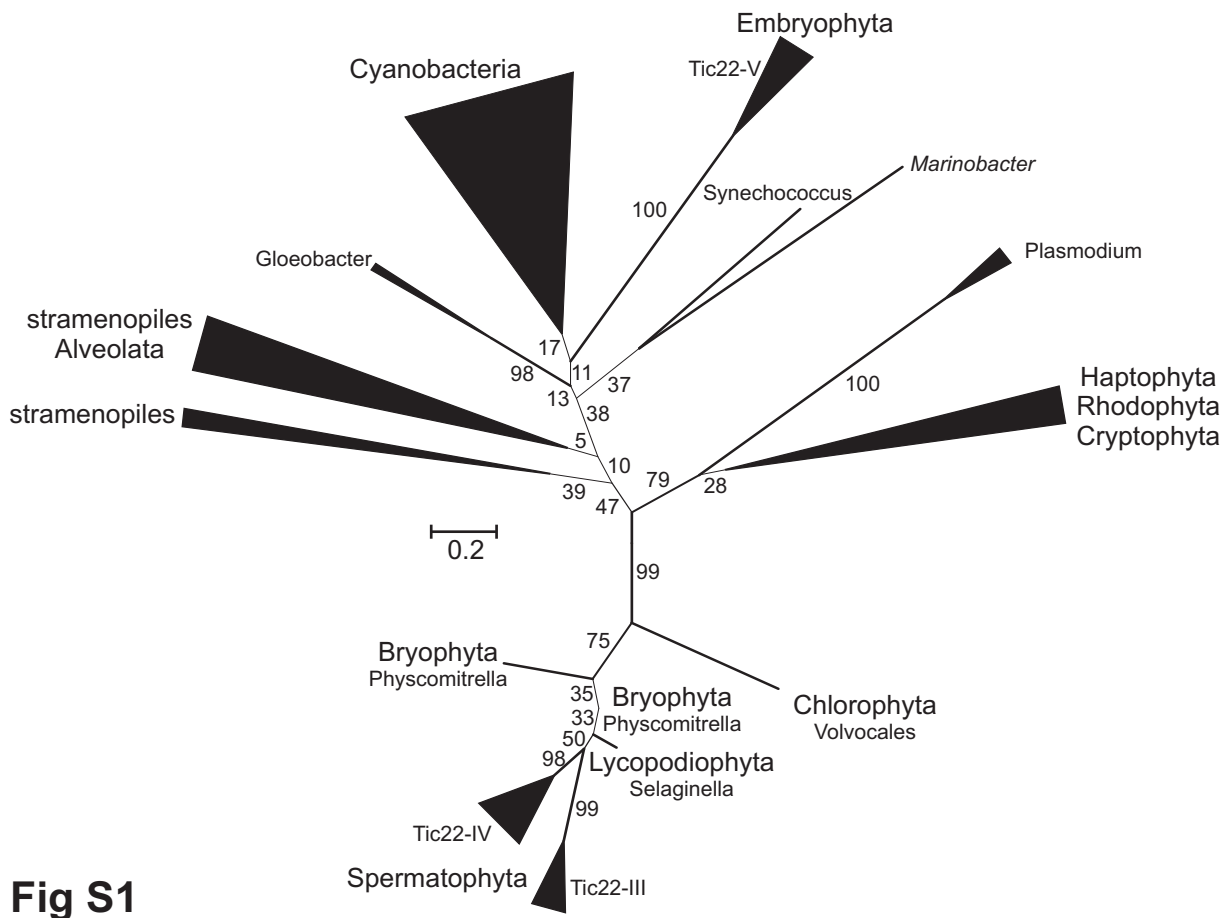
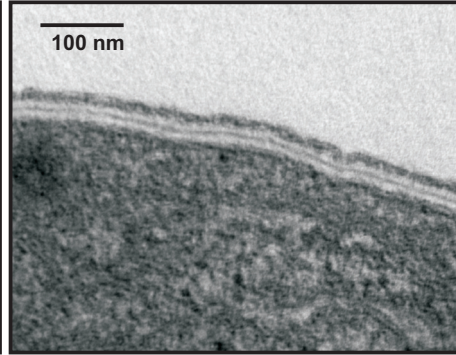
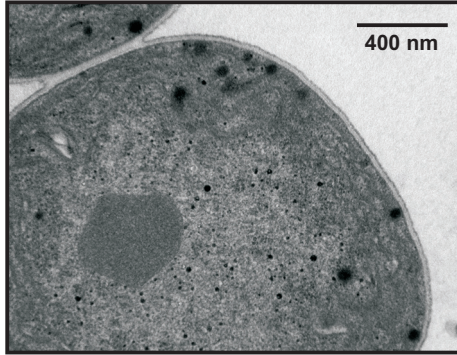
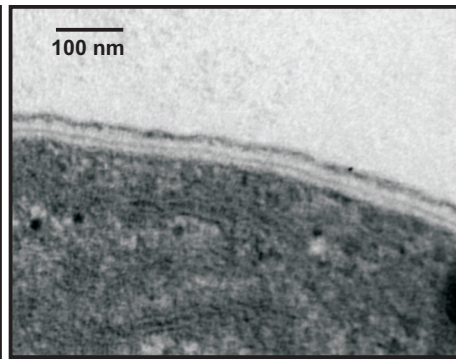
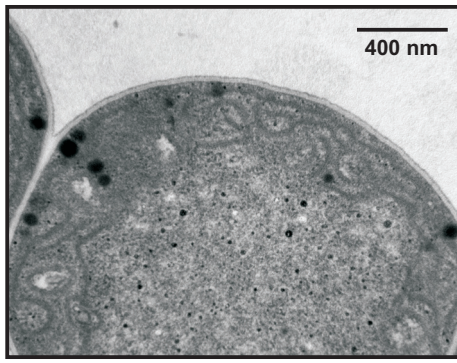
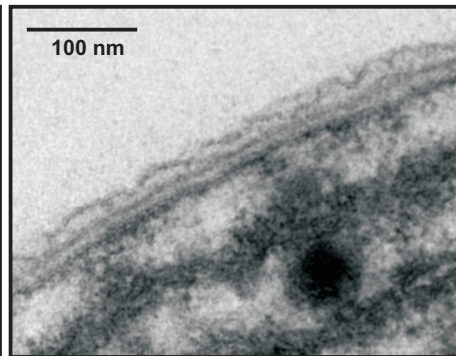
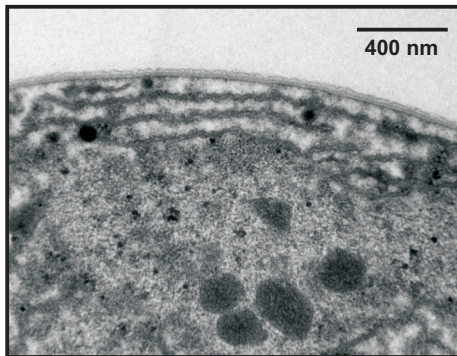
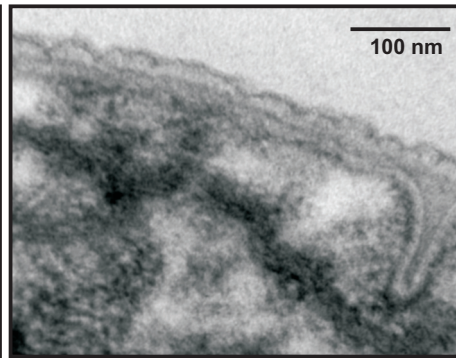
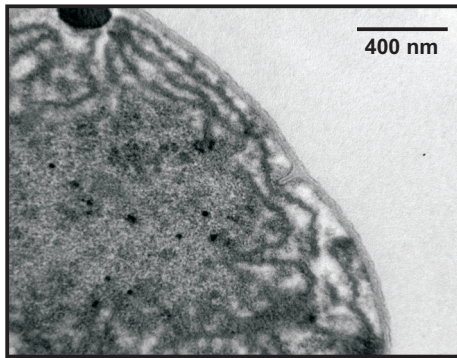


Fig S1

Anabaena sp. PCC 7120



AFS-I-*alr*2269



AFS-I-*tic*22

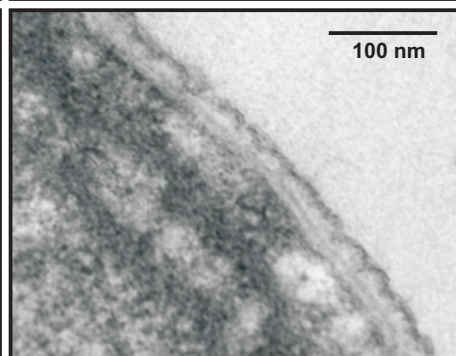
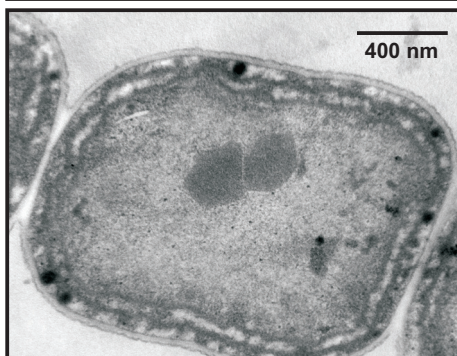
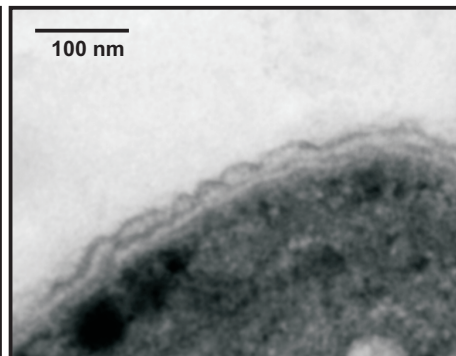
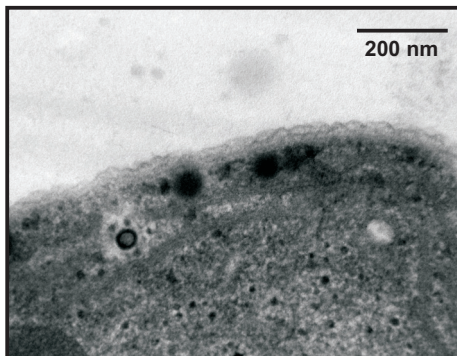


Fig S2

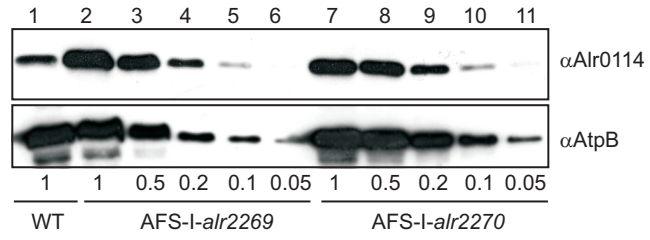


Fig S3

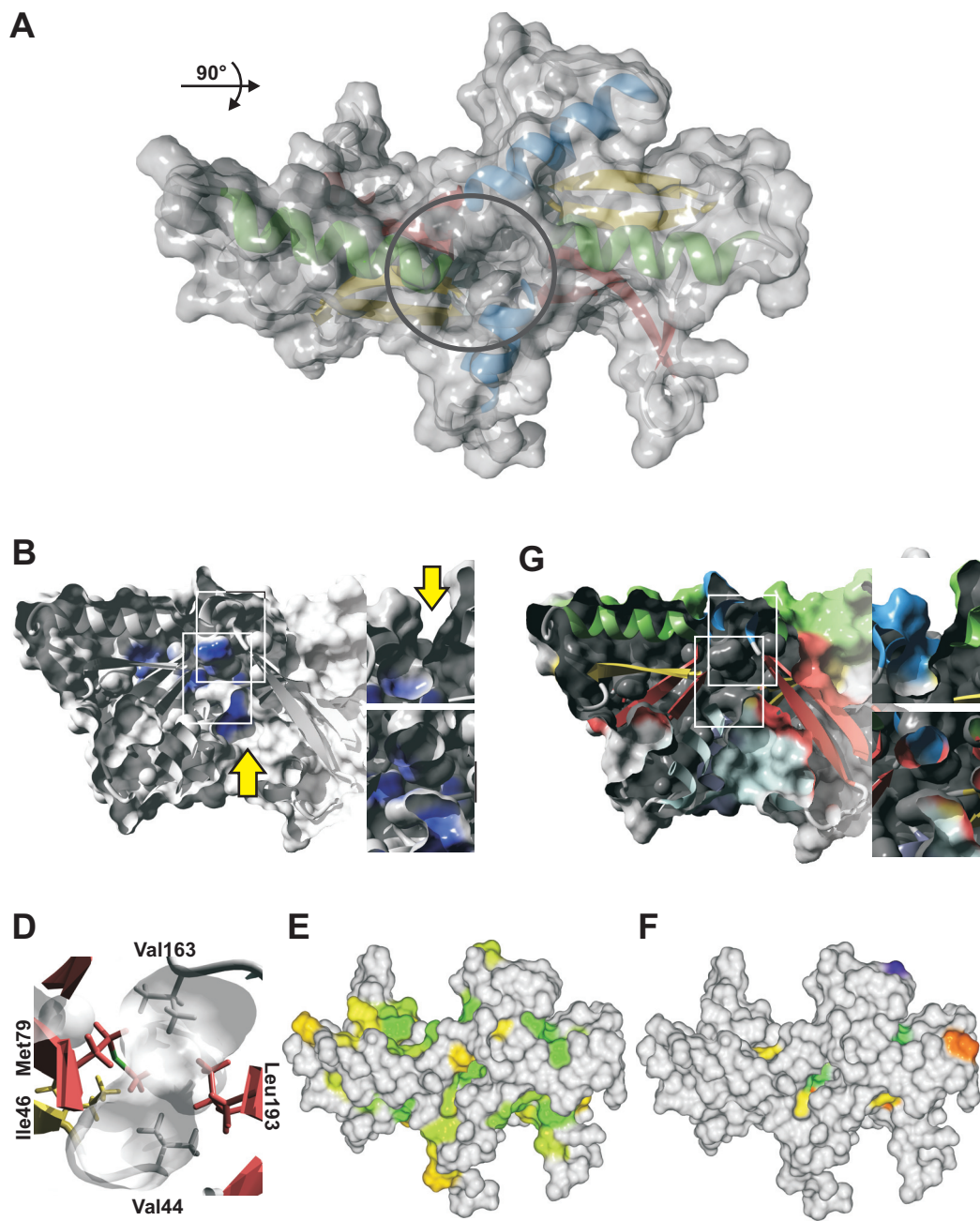


Fig S4

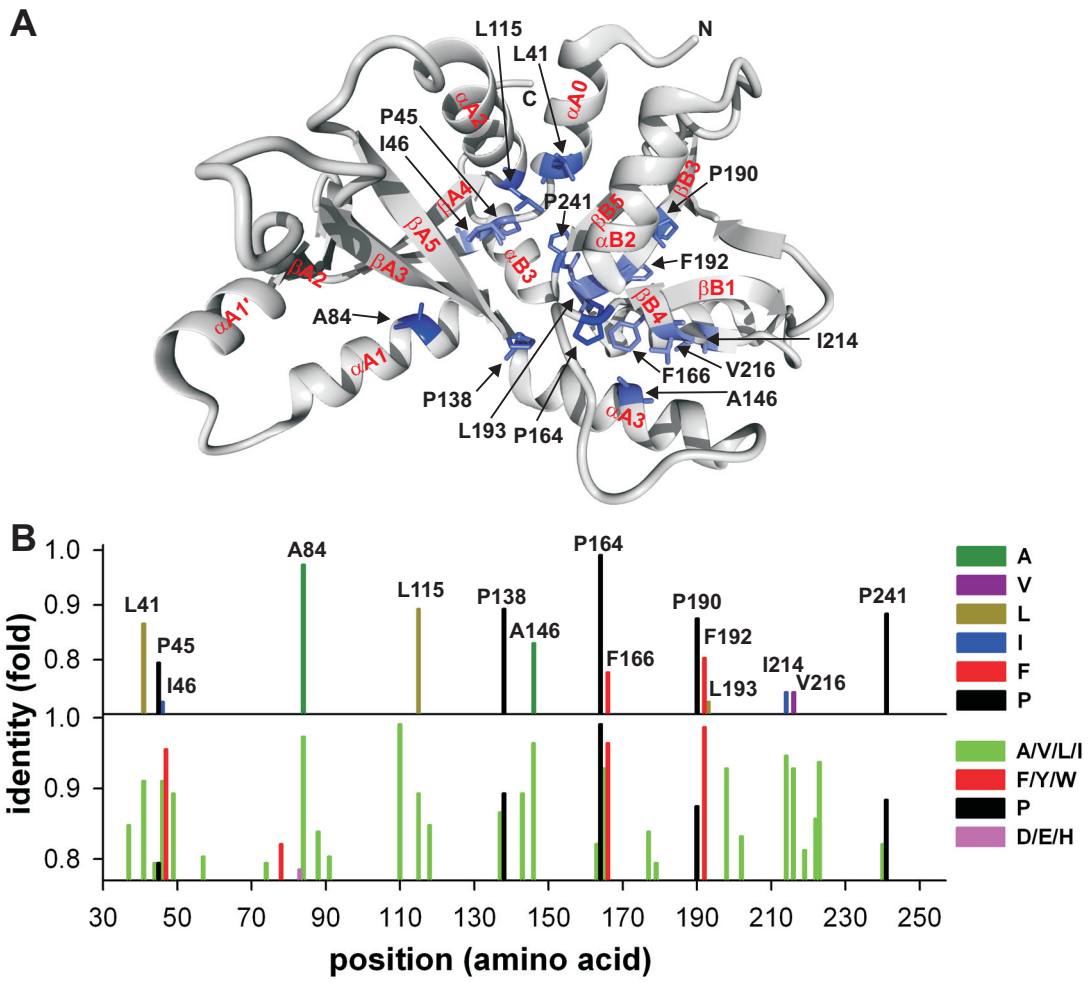


Fig S5

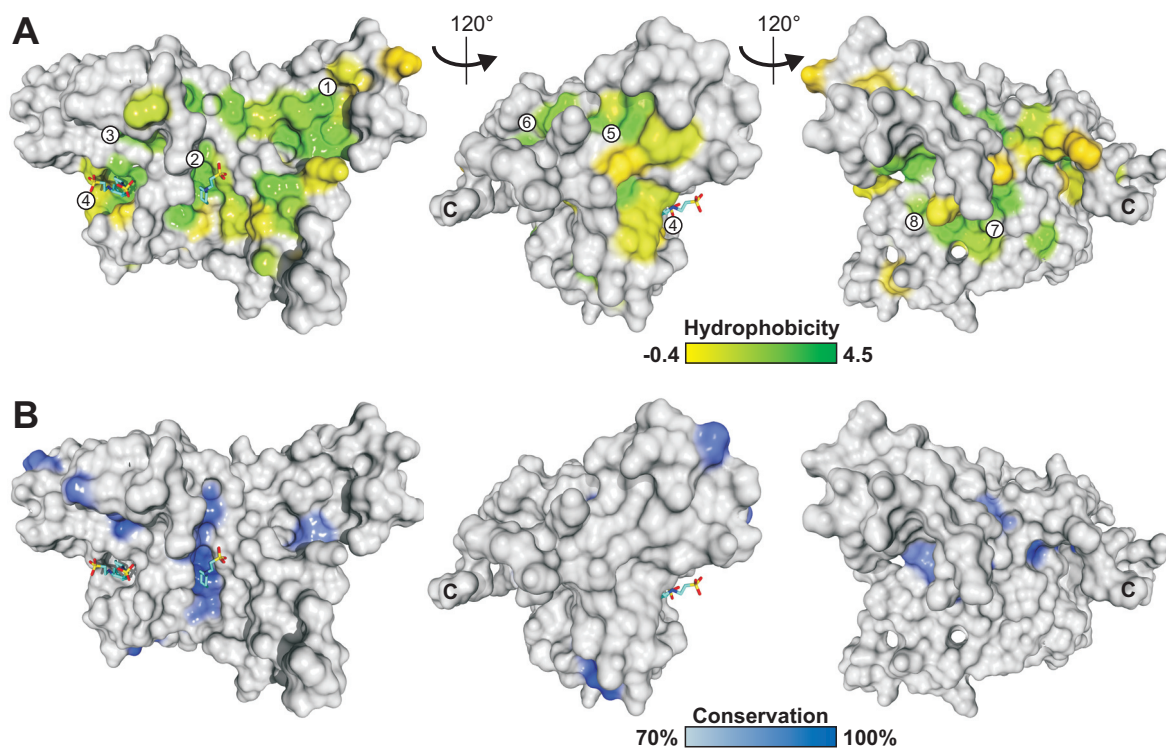


Fig. S6

A

```

slr0924    MPWLQTFSFRRSPFSLARRHLKMKIIVKIKSIFLLSLLFEATATMKSLLR
alr0114    -----MKALVR
                                                **:*:

```

```

slr0924    IGATLGLIGTTAIGTWLGTTLQALALPTEEVVKILQGVPVFTIVDAQQGAP
alr0114    WGATLGLVGSTLLGTLNLSLPAIALSEQQIKEKLDVPIYLVLTNEKGLP
    *****:*. * :*. * :* *:* . :: : *:*:*: :. : * *

```

```

slr0924    LVAVG-----NDNEKVTGVFISQQEANGFLQELKKQKP-----DVGS
alr0114    LSRPLPNAPNGQKAGGSITGAYMSRQEAQAFINELRNAKNKDPKMQEIVK
    *      : . .:*:*:*:*:*:*:*:*: *      :. .

```

```

slr0924    QVSVQPVSLGEVVKIAQANANQTDPLGFAYVPIPAQVQAAQQMPNSEYQ-
alr0114    SLQVTAVPLGVVYQQQLQQTKKDPNRLLFQAFKPVVDQEIKGAMDLLRQSGQQ
    :.* *.** : : * . ::. : * ** : * : :.* :. . . *

```

```

slr0924    ----GGVPLFVARGGEDQGYLTIQ--QENEQIIPFFLEASQIQMVERFK
alr0114    VNQFKSVPMFAVRFAPDQGYVPIKVGTVGNEQVPLFLSKQDAQGLLGQVK
    .**:*.* . *****:*: ***:*.** . : * :. :.*

```

```

slr0924    QEQPAMADSIDVIDVIAMENVISTLQTSDDAMLKQIRIVPTQEAIQFIRSL
alr0114    PKHPK-ADI---QVLDDIGVLQTLQDKNDTWLNQVVLVPSPESEYIRTL
    :.* ** :* :. :.*:* . :* :* :* :* :* :* :* :* :*

```

```

slr0924    SA-----QQPK
alr0114    PKPPNTPAAPNRNNNSRPGAK
    .

```

B

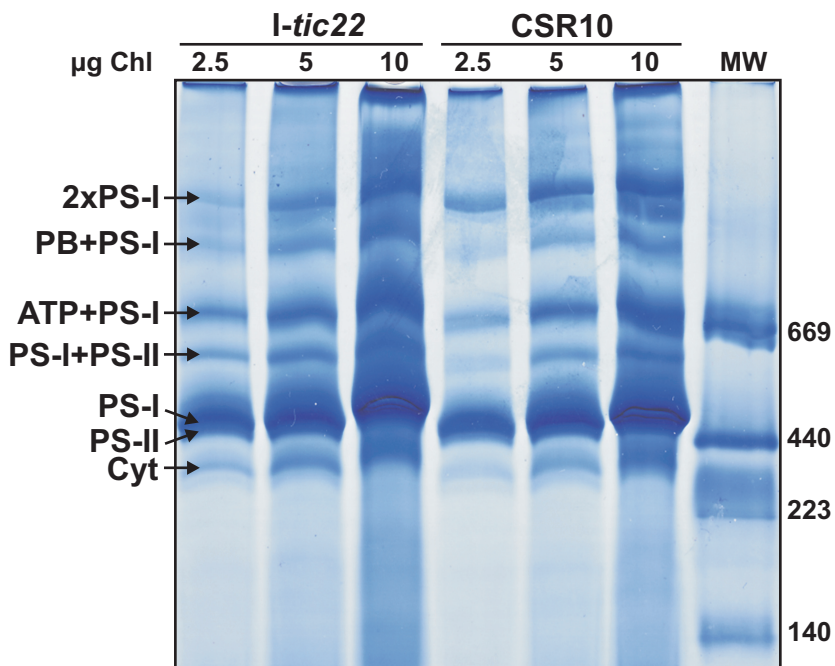


Fig. S7

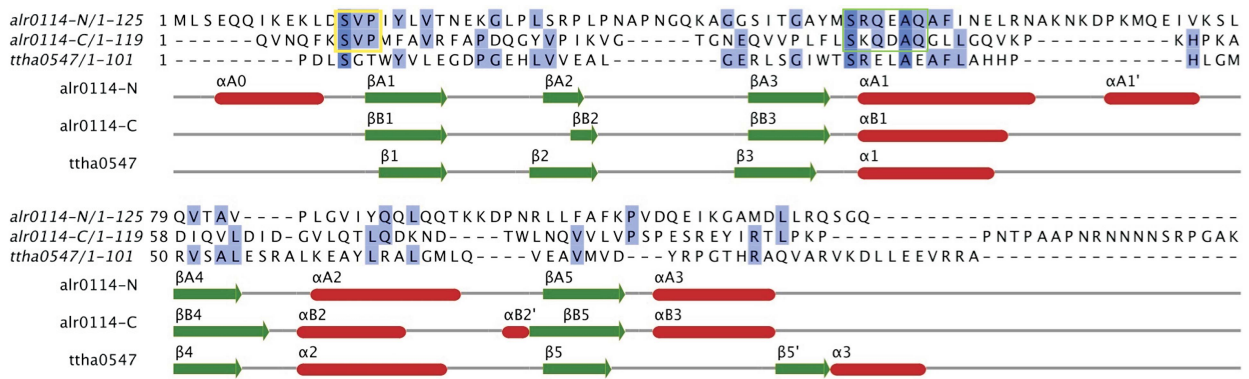


Fig S8