

Identification of major zinc-binding proteins from a marine cyanobacterium: insight into metal uptake in oligotrophic environments

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Supplemental Information

Table S1: Growth medium used for culture of *Synechococcus* sp. WH8102

Table S2: Proteins identified in fractions with high Zn concentrations following 2D-LC separation of the *Synechococcus* sp. WH8102 proteome

Table S3: Genes for cyanobacterial porins (CBPs) and related porins from selected marine cyanobacterial genomes.

Figure S1: Potential metal-binding residues on CsoS1/CcmK1 from *Synechococcus* sp. WH8102

Figure S2: Model for CcmK2 from *Synechococcus* sp. WH8102, showing the same surface-exposed clusters of metal-binding residues as CcmK1.

Supplemental Information: Alignments for structural modelling

Table S1. Growth medium used for culture of *Synechococcus* sp. WH8102

	Chemical	Concentration (M)
Base media components (sterilized by autoclaving)	NaCl	4.20×10^{-1}
	Na ₂ SO ₄	2.88×10^{-2}
	KCl	9.39×10^{-3}
	NaHCO ₃	2.38×10^{-3}
	KBr	8.40×10^{-4}
	H ₃ BO ₃	4.85×10^{-4}
	NaF	7.14×10^{-5}
	MgCl ₂ ·6H ₂ O	5.46×10^{-2}
	CaCl ₂ ·2H ₂ O	1.05×10^{-2}
Additional nutrients and buffers (added by 0.22 µm filter sterilisation)	NaHPO ₄ ·H ₂ O	1.00×10^{-4}
	NaNO ₃	1.00×10^{-4}
	Na ₂ SiO ₃ ·9H ₂ O	1.00×10^{-4}
	EDTA pH 8.0	1.00×10^{-4}
	HEPES pH 8.0	2.00×10^{-3}
	FeCl ₃ ·6H ₂ O	1.00×10^{-6}
	MnCl ₂ ·4H ₂ O	1.21×10^{-7}
	CoCl ₂ ·6H ₂ O	5.03×10^{-8}
	Na ₂ MoO ₄ ·2H ₂ O	1.00×10^{-7}
	Na ₂ SeO ₃ ·5H ₂ O	1.00×10^{-8}
	NiCl ₂ ·6H ₂ O	1.00×10^{-8}
	SrCl ₂ ·6H ₂ O	6.38×10^{-5}
(ZnSO ₄ ·7H ₂ O	8.00×10^{-8}) ^{a)}	

^{a)} omitted in zinc-depleted medium

Table S2. Proteins identified in fractions with high Zn concentrations following 2D-LC separation of the *Synechococcus* sp. WH8102 proteome

Band No.	Mass (kDa)	Gene (<i>cluster</i>)^a	Protein name	No. matched peptides	Sequence coverage %	MOWSE score
1	17.9	<i>mpeA</i> ⁷⁹⁹⁴	C-phycoerythrin class 2 subunit alpha	7	63	74
2	20.5	<i>synw1753</i> ⁶⁶¹	Ribosome recycling factor	6	52	75
3	33.9	<i>pstS</i> ²³	ABC transporter – substrate binding protein (phosphate)	16	63	172
4	17.9	<i>mpeA</i> ⁷⁹⁹⁴	C-phycoerythrin class 2 subunit alpha	10	64	83

^aThis is the protein cluster number in the Cyanorak database which is publically accessible at <http://abims.sb-roscoff.fr/cyanorak/>.

Table S3. Genes for cyanobacterial porins (CBPs) and related porins from selected marine cyanobacterial genomes. Genes were retrieved through IMG (using Pfam (pfam04966; OprB) and TCDB (TC 1.B.23) annotations and BLAST searches), and Cyanorak (clusters 8 and 2231). ORFs translating into proteins with less than 300 residues were discarded. Genomic neighbourhoods were inspected up to ± 5 genes up/downstream of the porin gene. Gene products with a relationship to nutrient metabolism are listed in column 6; as far as possible, the related macro- or micronutrient is specified in column 7. As a rule, it is not straightforward to predict the specificity of proteins involved in metal homeostasis, but we have taken care to assign a specific metal only in the cases where this was unambiguously possible. For gene product abbreviation see footnotes at the end of the table.

Strain	No of CBPs	Locus tags	SLH domain present ?	Cyanorak cluster ^{a)}	nutrient-related gene products in genomic neighbourhood	Nutrient
Syn. WH8102	4	SYNW2128	yes	8	HupE; CbiG/CobJ ^{b)}	Co (Ni)
		SYNW2223	yes	8	-	-
		SYNW2224	yes	8	-	-
		SYNW2227	yes	8	-	-
Syn. BL107	5	BL107_05009	yes	8	-	-
		BL107_05014	yes	8	-	-
		BL107_12315	yes	8	-	-
		BL107_08309	yes	8	-	-
		BL107_08384	yes	8	PFBP ^{c)}	Fe
Syn. RCC307	3	SynRCC307_0264	yes	8	-	-
		SynRCC307_0265	yes	8	-	-
		SynRCC307_0582	no	2231	-	-
Syn. RS9916	4	RS9916_28359	yes	8	ABC/PBP ^{d)}	Mn?
		RS9916_28664	yes	8	PFBP	Fe
		RS9916_35737	yes	8	-	-
		RS9916_35742	yes	8	-	-
Syn. RS9917	7	RS9917_01931	no	4836	PhoH ^{e)}	-
		RS9917_07245	yes	8	-	-
		RS9917_07250	yes	8	-	-
		RS9917_07255	yes	8	-	P
		RS9917_09246	no	2231	-	-
		RS9917_11001	yes	8	ZnuA ^{f)}	Zn
		RS9917_12245	no	8	"chromate"	?
Syn. WH7803	6	SynWH7803_0993	yes	8	ZnuA	Zn
		SynWH7803_1178	(yes)	8	"chromate"	?
		SynWH7803_1779	yes	8	-	-
		SynWH7803_1822	no	2231	-	-
		SynWH7803_2235	yes	8	-	-
		SynWH7803_2236	yes	8	-	-

Syn. WH7805	5	WH7805_01492	yes	8	ZnuA	Zn
		WH7805_01867	yes	8	PFBP	Fe
		WH7805_03077	yes	8	ZnuA (or MntC)	Zn/Mn?
		WH7805_11218	yes	8	-	-
		WH7805_11223	yes	8	-	-
		WH7805_13798	no	2231	-	-
Syn. WH8109	4	SH8109_0798	yes	-	-	-
		SH8109_0800	yes	-	-	-
		SH8109_2131	yes	-	PFBP	Fe
		SH8109_2153	yes	-	PFBP, HupE/UreJ	Fe, Co/Ni?
Syn. WH8016	6	Syn8016_0522	yes	-	PstS ⁹⁾	P
		Syn8016_0544	yes	-	PFBP	Fe
		Syn8016_2122	yes	-	PstS	P
		Syn8016_2429	yes	-	-	-
		Syn8016_2430	yes	-	-	-
		Syn8016_1277	no	-	PhoH	P
		WH5701_00705	yes	8	-	-
Syn. WH5701	3	WH5701_00710	yes	8	-	-
		WH5701_11554	yes	8	ZnuA	Zn
		Syncc9902_0323	yes	8	-	-
Syn. CC9902	4	Syncc9902_0324	yes	8	-	-
		Syncc9902_1999	yes	8	PFBP	Fe
		Syncc9902_2012	yes	8	HupE/UreJ	Co/Ni?
		Syncc9605_0833	yes	8	-	-
Syn. CC9605	6	Syncc9605_1095	yes	8	various ABC/PBPs	P, As, Cr
		Syncc9605_1575	yes	8	PFBP	Fe
		Syncc9605_1591	yes	8	HupE/UreJ	Co/Ni?
		Syncc9605_2366	yes	8	cysteine synthase	S?
		Syncc9605_2367	yes	8	-	-
		sync_0678	yes	8	FeoB, ferritin	Fe
Syn. CC9311	6	sync_1500	yes	8	ZnuA	Zn
		sync_1501	yes	8	Fe-regul. protein A	Fe
		sync_1542	yes	8	PFBP	Fe
		sync_2579	yes	8	-	-
		sync_2581	yes	8	-	-
		sync_2059	no	2231	-	-
		Syn9616DRAFT_1973	yes	-	-	-
Syn. CC9616	6	Syn9616DRAFT_1974	no?	-	-	-
		Syn9616DRAFT_1976	yes	-	-	-
		Syn9616DRAFT_1978	yes	-	-	-
		Syn9616DRAFT_2699	yes	-	PstS	P
		Syn9616DRAFT_2714	yes	-	PFBP	Fe

Syn. 7002	4	SYNPCC7002_G0011	yes	-	ABC/PBP; Cation-transp. ATPase	N/S/C ? M?
		SYNPCC7002_A0782	yes	-	-	-
		SYNPCC7002_A1034	yes	-	-	-
		SYNPCC7002_A2813	yes	-	-	-
Proch. CCMP1375 (SS120)	2	pro0737	yes	8	-	-
		pro1269	yes	8	PFBP	Fe
Proch. CCMP1986 (MED4)	3	pmm0709	yes	2330	PstS	P
		pmm1119	no	2330	HupE; sulfotransferase	Ni/Co?; S?
		pmm1121	no	2330	HupE; sulfotransferase	Ni/Co?; S?
Proch. CC9202	4	P9202_362	no	-	sulfotransferase	S?
		P9202_799	no	-	-	-
		P9202_943	no	-	PFBP	Fe
		P9202_1395	no	-	sulfotransferase	-
Proch. MIT 9301	4	P9301_12261	no	-	-	-
		P9301_12271	no	-	-	-
		P9301_12401	yes	-	PstS	P
		P9301_13641	no	-	PFBP	Fe
Proch. MIT 9303	4	P9303_11091	yes	-	ZnuA	Zn
		P9303_14071	yes	-	-	-
		P9303_26321	yes	-	cysteine synthase	S?
		P9303_19511	no	-	PhoH	P?
Proch. MIT 9211	3	P9211_12581	yes	-	PFBP	Fe
		P9211_12591	yes	-	PFBP	Fe
		P9211_08291	yes	-	-	-
Proch. MIT 9312	6	PMT9312_0721	yes	-	PstS	P
		PMT9312_1130	no	-	-	-
		PMT9312_1131	no	-	-	-
		PMT9312_1264	no	-	PFBP	Fe
		PMT9312_1512	no	-	-	-
		PMT9312_1515	no	-	-	-
Proch. MIT 9313	4	PMT0284	yes	8	PFBP	Fe
		PMT0802	yes	8	-	-
		PMT0998	yes	8	PhoB, PstS	P
		PMT1979	yes	8	cysteine synthase	S?
Proch. MIT 9215	3	P9215_12551	no	-	sulfotransferase	S?
		P9215_12571	no	-	sulfotransferase	S?
		P9215_13761	no	-	PFBP	Fe
Proch. MIT 9515	3	P9515_12111	no	-	PstS	P
		P9515_12121	no	-	PstS	P
		P9515_13341	no	-	PFBP	Fe

Proch. NATL1A	5	NATL1_11511	no	-	PstS	P
		NATL1_04791	no	-	PFBP	Fe
		NATL1_16211	no	-	ZnuA	Zn
		NATL1_18981	no	-	urease assembly	Ni
		NATL1_19301	no	-		
Proch. NATL2A	5	PMN2A_0440	no	-	PstS	P
		PMN2A_0777	no	-	PFBP	Fe
		PMN2A_1028	no	-	ZnuA	Zn
		PMN2A_1057	no	-	urease assembly	Ni
		PMN2A_1757	no	-	-	-
Proch. AS9601	3	A9601_12251	no	-	sulfotransferase	S?
		A9601_12271	no	-	sulfotransferase	S?
		A9601_13551	no	-	PFBP	Fe
Trichodesmium erythraeum IMS 101	4	Tery_0838	yes	-	-	-
		Tery_1234	yes	-	cysteine synthase	S?
		Tery_4465	yes	-	-	-
		Tery_4466	yes	-	-	-
Crocospaera watsonii WH8501	3	CWat_WH8501_draft2_00022400	yes	-	-	-
		CWat_WH8501_draft2_00051630	yes	-	PhoU ^{h)}	P
		CWat_WH8501_draft2_00053510	yes	-	PFBP	Fe

a) This column refers to the Cyanorak database, accessible at <http://abims.sb-roscoff.fr/cyanorak/>. if no entry is given, then the genome is not included in the database

b) HupE: Hydrogenase/urease accessory protein; CbiG/CobJ: bifunctional cbiH protein and precorrin-3B C17-methyl-transferase. Probably both proteins involved in cobalamin biosynthesis

c) PFBP: ABC-type Fe³⁺ transport system, periplasmic component (COG1840), variously annotated as afuA, futA1, idiA

d) ABC/PBP: ABC-type transport system; periplasmic component, with uncertain specificity

e) PhoH: Phosphate starvation-inducible protein (cytoplasmic), predicted ATPase

f) ZnuA: Periplasmic binding protein for Zn²⁺; not consistently annotated in genomes; for annotation here, we used criteria developed previously (Blindauer, Chem. Biodiv. 2008).

g) PstS: ABC transporter periplasmic component, phosphate-binding protein

h) PhoU: phosphate transport system regulatory protein

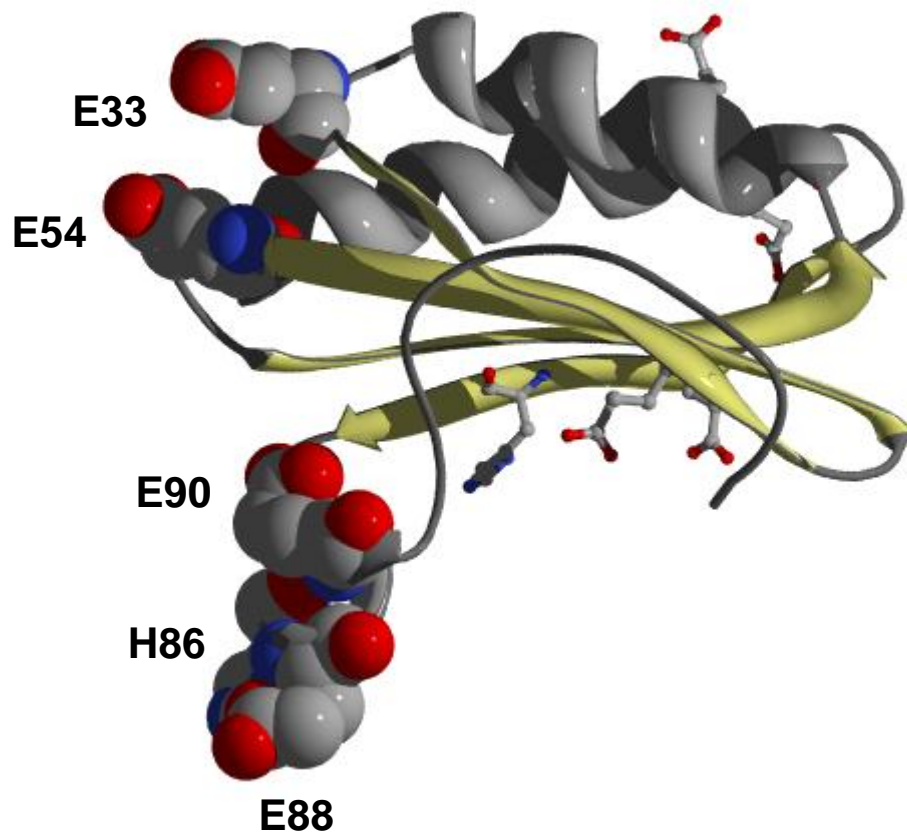


Figure S1. Potential metal-binding residues on CsoS1/CcmK1 from *Synechococcus* sp. WH8102. Five residues that are in sufficiently close proximity to each other are shown in space-filling mode, isolated residues with metal affinity (Asp, Glu, His) as ball-and stick models. The model is based on pdb 2EWH (CsoS1 from *Halothiobacillus neapolitanus*) and was generated using Modeller v. 9.7.¹ The five residues highlighted in space-filling mode are conserved in the second domain of CcmK2 (SYNW1712) (see Figure S2).

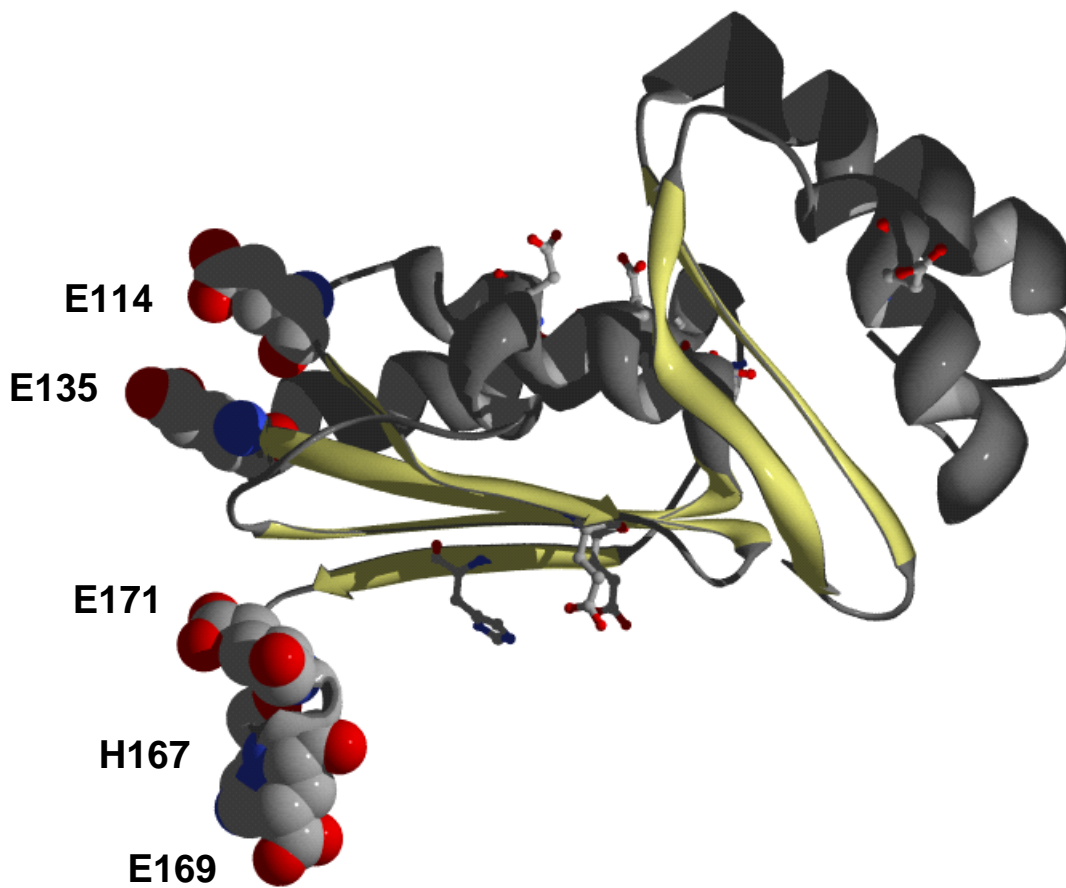


Figure S2. Model for CcmK2 from *Synechococcus* sp. WH8102, showing the same surface-exposed clusters of metal-binding residues as CcmK1. The N-terminal domain is almost devoid of potential metal-binding residues. The model was generated by Phyre², using pdb 3NWG (a PduT homolog from a novel bacterial microcompartment from *Desulfitobacterium hafniense*) as template.

Supplemental Information: Alignments for structural modelling

1. CcmK1 (SYNW1719)

Potential metal-binding residues (C,H, E, D) in the target sequence are highlighted in colour

1 d2ewhal Probab=100.00 E-value=2.8e-34 Score=191.88 Aligned_columns=92 Identities=88%

```
Q ccmk1_ 7 GIALGMIETRGLVPAIEAADAMTKAAEVRLIGREFVGGYVTVLVRETGAVNAAVRAGADACERVGDGLVAAHIIARFH 86 (103)
T d2ewhal 1 GIALGMIETRGLVPAIEAADAMTKAAEVRLVGRQFVGGYVTVLVRETGAVNAAVRAGADACERVGDGLVAAHIIARVH 80 (92)
```

```
Q ccmk1_ 87 REVEPALGNGNF 98 (103)
T d2ewhal 81 SEVENILPKAPQ 92 (92)
```

2. CcmK2 (SYNW1712)

Potential metal-binding residues (C,H, E, D) in the target sequence are highlighted in colour

1 c3nwgA_ Probab=100.00 E-value=0 Score=262.89 Aligned_columns=159 Identities=23%

```
Q ccmk2_ 13 TRSSAAANKTVDVNPVATPATPAASTAATPATPPAPSTTRRSTTTTTRSAASGSAGGGSVA-----KPVSNTAPA 83 (183)
T c3nwgA_ 10 VNSIARGIEAADAXLKAAQVDLLEAKPVCPGKYIVLICGDVAAVQSSVTAGKTXAAHSVLDDFILPNVHPQVLTAISAT 89 (180)
```

```
Q ccmk2_ 84 SPVQGIALGMIETRGMVPAIEAADAMTKAEVSLICREYVGG--GYVTVMVRETGAVNAAVRAGADACERVGDLVAAH 161 (183)
T c3nwgA_ 90 PLTLIKALGIIETFSIASLIVAADTAAKTGVDLVEIRIGXIGGKSFVLTGDVASVESSVAGVXLASERGX--LVDKV 168 (180)
```

```
Q ccmk2_ 162 IIARFHQEVEP 172 (183)
T c3nwgA_ 169 VIPSPHDHLKR 179 (180)
```

3. ZnuA (SYNW2481)

The three Zn-binding His residues are highlighted

8 c2ov3A_ Probab=100.00 E-value=0 Score=435.59 Aligned_columns=258 Identities=24%

```
Q synw2481_znua_ 31 KKISIMTSFLPITLFARAVAGECGDVKALIPTNIGPHDFQSTPKDILSIGKADIFFINGL 90 (302)
T c2ov3A_ 1 DAMDITVSIPPQYFLEKIGGDLVRVSVLVPGNNDPHTYEPKQQLAALSEAEAYVLIGL 60 (260)
```

```
Q synw2481_znua_ 91 GMETFLDRLISSASTTLSVVDTSIGIKTISTDISNADSDPNHIWLDPIRAISQVETIK 150 (302)
T c2ov3A_ 61 GFEQPWLEKLKA--NANMKLIDSAQGITPLEMP--GRLMVADPHIWLSPTLVKRQATTIA 117 (260)
```

```
Q synw2481_znua_ 151 DALAELNPACEVTLNASAYVDDLLALHAEILSKLEPYQGKSFIAYHDFAPYFAERYQL 210 (302)
T c2ov3A_ 118 KELAELDPDNRDQEANLAAFLAELERLNQELGQILQPLQRKFIVFHPSWAYFARDYNL 177 (260)
```

```
Q synw2481_znua_ 211 KAEYLVDLDPINSPVDLQRVSNLVRDSDLKALLTEPQDGNNSFNSLARDLNIKIALFNP 270 (302)
T c2ov3A_ 178 VQIPI--EVEGQEPSAQELKQLIDTAKENNLTMVFGETQFSTKSEAIAAEIGAGVELLDP 236 (260)
```

```
Q synw2481_znua_ 271 IETISRDFVYDESLYFDLMRDNLSNLLSLGG 302 (302)
T c2ov3A_ 237 L-----AADWSSNLKAVAQKIANANSA 258 (260)
```

4. CynA (SYNW2487)

The three metal-binding Cys residues are highlighted. No template was identified for the first 196 residues.

3 c3un6A_ Probab=100.00 E-value=0 Score=324.79 Aligned_columns=289 Identities=17%

```
Q SYNW2487_ 197 KTNLKIGFIPITCATPIIMSEP--MGFYKSNGLKCKVVKMPSWGAVRDSAIAGELDAYHMLAPMPISMTLGLGTSPFSVKL 275
T c3un6A_ 1 QQVIKIGYLPITHSANLXTKKLSQYNHPKYKLELVKFNNWPDLXDALNSGRIDGASTLIELAXKSK----QKGSNIKA 76
```

```
Q SYNW2487_ 276 ASIENINGQAITVANRHKDKVKSAADMKGFVFGVPFPYSMHNLLRYLAKGVDPDKDVQIRPVPPDSVAQMVAGDID 355
T c3un6A_ 77 VALGHHEGNVIXQKG--XHLNEFNNGDDYHFGIPHRYSTHYLLELRKQLKIKPG--HFSYHEXSPAEXPAALSEHRIT 154
```

```
Q SYNW2487_ 356 AYLMPDPFNQRAVFEGVGFIHLLTKDLVWGHPCCAFAAGEPWINKHPNTFKAINKSIIEAANYATNPTNRSEIAKYISGR 435
T c3un6A_ 155 GYSVAEPFGALGEKLGKGKTLKHGDDVIPDAYCCVLVLRGELLDQHKDVAQAFVQDYKKSGFKXN---DRKQSVDIX--T 229
```

```
Q SYNW2487_ 436 AFLNQPTKVVEAVLTGKFDDGLGNKNVPDRIDFKPYPWQSFSHWIQSQLVRWDLGGAADAIKAGDFNANSAAIFLTNEA 515
T c3un6A_ 230 HHFQSRDVLTQSAAWTS-----YGDLTIKPSGYQEITL--VKQHHLFNPAY----DDFVEPSLY 285
```

```
Q SYNW2487_ 516 QSLER 520 (559)
T c3un6A_ 286 KEASR 290 (291)
```

5. FutA/IdiA (SYNW1797)

```

1 c2pt1A_ Probab=100.00 E-value=0 Score=301.97 Aligned_columns=313 Identities=40%
Q FutA_ 35 TSQIGVYSGRHYNSDKDLYERFTEATGIQVKLLEAKDDALIERLNTEGDDSPADVLILAD 94 (347)
T c2pt1A_ 1 QQEINLYSSRHYNTDNELYAKFTAETGIKVNLIIEGKADELLERIKSEGANSFADVLLTVD 60 (317)

Q FutA_ 95 VARLDRAAGMNLFQTVSDSDALNQAVPRDLRDSEGRWFGLTRRLRAPMFNADRNVNAEQVSS 154 (347)
T c2pt1A_ 61 LARLWRAEEDGIFQPVQSEILETNVPEYLRSPDGMWFGFTKRARVIMYNKGVKPEELST 120 (317)

Q FutA_ 155 YGALADPSLKGKLCRLNRRSVYNQSLVAFMLDEQQAATEDWIKGIVNNLAEPVSSDTP 214 (347)
T c2pt1A_ 121 YEELADPKWGRVIRSSSNEYNSQLVASLVVADGEESTLAWAKGFVSNFAREPQGNDA 180 (317)

Q FutA_ 215 MIRAVAQQCGVALANSYYLGRMQAGDKGEADRSLSGKVTVRWPD---PVHVNITGGGV 271 (347)
T c2pt1A_ 181 QIEAVSSGEADLTLANITYMGRLESEDPQAQKAIENGVGFPPNQEGRGTHVNVSGVGVV 240 (317)

Q FutA_ 272 RASRNPEAAQRLLLEFLSSDQAQGGYAAANHEHYPL-KGIGEDPVLQAWGPFNQAKVSAERL 330 (347)
T c2pt1A_ 241 KTAPNREGAVKVFIEFLVSEPAQAFLAQNYYEYVPLAGVPLNKSVASFGFEKSDTSLDKL 300 (317)

Q FutA_ 331 GELNAQALELMAANGWQ 347 (347)
T c2pt1A_ 301 GPALAPATKIMNEAGWK 317 (317)

```

6. CBP (SYNW2224)

Sequence of SYNW2224, colour-coded according to alignment with templates used for structural modelling by Phyre² (yellow: 3PYW, red: 3SWF, cyan: 4GF4). Signal peptide is shown in grey.

```

>tr|Q7U448|Q7U448_SYNPX Possible porin OS=Synechococcus sp. (strain WH8102)
GN=som PE=4 SV=1

```

```

MKLFQQLLVAPAAALGLLASGANAAADLNINGVSDYAASEEQVTSITQFSDVYPTDWAYQAL
ANLIERYGCVAGYPNGTFAGNRAMTRYEAAAALLNACLDRITEVTDDELRRRIKKEFETELAV
IRGRVDGLEARVGEIAATQFSITTTKLGKATFVTGAINSEDDADKSVYDALSFSDLRRLG
LKTSFTGKDLLFTRLRGGNMKDGSAFSGGLRKLKLDVSGMSGNTMEIDRLYYRFPVAKGLTA
IAGPLARNTESLGMKPTAYKVKTLNMFGGHWGTPGVYNKETGGLVGLIWKQKQVAKGPKPF
TAAVNYVADAGEAENS DPTAGGMFGSNSRANTTAQIGYGSKKWGLAFGYRYGQCKAGFGT
GFYKAQDCVKGTDVYSNNFAFNGFWKPAETGLIPIISAGYGFSSLEGS DVETLASWVMVF
QWDKIADTSHKLVGFGAPQYVVSQKGD DPAPELAFEASLKLKVAKKVSVIPAVFYLPE
QSQGVDDASQWGGVVQTVFKF

```

```

2 c3pywA_ Probab=98.98 E-value=7.8e-10 Score=91.31 Aligned_columns=52 Identities=33%

```

```

Q Synw2224_inten 46 QFSDVYPTDWAYQALANLIERYGCVAGYPNGTFAGNRAMTRYEAAAALLNACLDRITEVTDDELRRRIKKEFETELAV 98 (501)
T c3pywA_ 2 TFPDVPADHWGIDSINYLVEK-GAVKGNKGMFEPGKELTRAEATMMAQILN 53 (178)

```

```

4 c3swfA_ Probab=93.40 E-value=0.2 Score=30.19 Aligned_columns=50 Identities=22%

```

```

Q Synw2224_inten 92 LLNACLDRIT---EVTDE-LRRLIKEFETELAVIRGRVDGLEARVGEIAATQFS 141 (501)
T c3swfA_ 1 GLEEKVTRMESSVDLLQTRFARILAEYESMQQKQRLTKVEKFLKPLIDTEFS 54 (56)

```

```

Q Synw2224_inten 92 LLNACLDRIT---EVTDE-LRRLIKEFETELAVIRGRVDGLEARVGEIAATQFS 141 (501)
T c3swfA_ 1 GLEEKVTRMESSVDLLQTRFARILAEYESMQQKQRLTKVEKFLKPLIDTEFS 54 (56)

```

```

1 c4gf4A_ Probab=99.19 E-value=1.1e-06 Score=68.53 Aligned_columns=276 Identities=16%

```

```

Q Synw2224_inten 134 ELAATQFSTTTKLGKATFVTGAINSEDDADKSVYDALSFSDLRRLGLKTSF-----TGK 188 (501)
T c4gf4A_ 18 ELLDKGYDFTLDYVGEVAGNLDK-----TARYSDQFALGAHLDLQKILGW 63 (299)

```

```

Q Synw2224_inten 189 DLLFTRLRGGNMKDGSAFSGGLRKLKLDVSGMSGNTMEIDRLYYRFPVA-KGLTAIAGPLAR 247 (501)
T c4gf4A_ 64 HDAEFKLAITERSGRNLSNDRFSSVQEVWGRGQTWRLTQXWIKQKYFDGALDVKFGFRFGE 123 (299)

```

```

Q Synw2224_inten 248 NTESLGMKPTAYKVKTLNMFGGHWGTPGVYNKETGGLVGLIWKQKQVAKGPKFTAANVYV 307 (501)
T c4gf4A_ 124 GEDFNSNWPVSQW-----ALRVKYN-----TPAFFVQV--- 152 (299)

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Q Synw2224_inten 308 ADAGEAENS DPTAGGMFGSNSRANTTAQIGYGSKKWGLAFGYRYGQCKAGFGTGFYKAQD 367 (501)
T c4gf4A_ 153 -----GAFEQTKGAIXPXEAVWSPKVNGLPGEYRLGYYYSTSKHGWWVV-- 196 (299)

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Q Synw2224_inten 368 CVKGTDVYSNNFAFNGFWKPAETGLIPSIAGYGFSSLEGSDEVETLASWVGFQWDKIAD 427 (501)
T c4gf4A_      197 -----AQQQVTAHGGD---VNRGLSLFANFTVHDKVDNYQQVGLVYKGAFDAR 241 (299)

Q Synw2224_inten 428 TSHKLAVGFGAPQYVVSQKGDPPDAPELAFEASLKLKVAKKVSVIPAVFYLPQSQGVDD 487 (501)
T c4gf4A_      242 PKDDIGFGVARIHV-----NQRTEYNAELYGFHVTNWLTVRPNLQYIKS----- 286 (299)

Q Synw2224_inten 488 ASQWGGVVQTVFKF 501 (501)
T c4gf4A_      287 -NALVAGXKXQSSF 299 (299)

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1. N. Eswar, D. Eramian, B. Webb, M.-Y. Shen and A. Sali, in *Methods in Molecular Biology*, eds. B. Kobe, M. Guss and T. Huber, Humana Press Inc, 999 Riverview Dr, Ste 208, Totowa, Nj 07512-1165 USA, Editon edn., 2008, vol. 426, pp. 145-159.