

Clade A	S110359	1	-----ASTALPTGKALLNKVKELSHLPRRETAKACGYYSTSKGQVVRVNLTDYDAVLAARKVPLDPS	
	Cwat1519	1	MINNDRNLLIIEKRSKIDIRIMADTIDPNPTLTKGALLQEIKSLSDKPRRETARECGYYSVTKKQVVRVNLTDYDAVLAARKVPLDPS	
	Tery0216	1	MVEN-----TETPLTGKSLLOKVKELSDLPRETAKRGGYTLTKSDTRVNLTDYDALLAARKVPLDPS	
	Alr0946	1	MTET-----ATAPLTGKALLQKVKELSLTLPRREARAKCGGYSTVTKKNQVRVNLTDYDALLSARGIPLDPE	
	AM1_3666	1	MATDT-----ETPPLTGKALLQKVKELQHLSSREKAKRGGYYSITKKNQVRVNLTDYDALLSARGIPLDNP	
Clade B	Tery0493	1	-----MAKTTTEKNNTSEESNTQLTKGALLKKVKDLSSHSSKKEATAACGYYSVTKKQVVRVNLTDYDAVLAARKVPLDPS	
	T111150	1	-----MGKI-----KPLTGKALLQKVKELDGVSRKBAKACGYYSVTKKQVVRVNLTDYDAVLAARKVPLDPS	
	AM1_G0171	1	-----MAKKAALKKQKQKPLVTKGALLNKVKELSHLSSREKAKRGGYYSVTKKQVVRVNLTDYDAVLAARKVPLDPS	
	T112172	1	MGRKP-----VEPLTGAALLEKVKOLEHTSHSEKAKACGYYSVTKKQVVRVNLTDYDAVLAARKVPLDPS	
	AM1_4418	1	MAKKQKQKGTPLSGQALVEKVKOLELDSREKAKRGGYYSVTKKQVVRVNLTDYDAVLAARKVPLDPS	
	S110822	1	MAKSNA-----TKPLTGEALLEKVKOLELDPKEKAKRGGYYSVTKKQVVRVNLTDYDAVLAARKVPLDPS	
	Cwat2079	1	MTPD-----KPLTGKALLQKVKELDGLSREKAKRGGYYSVTKKQVVRVNLTDYDAVLAARKVPLDPS	
	All2080	1	MPKQKK-----IEPLTGEALLEKVKOLELNSREKAKRGGYYSVTKKQVVRVNLTDYDAVLAARKVPLDPS	
	Tery1859	1	MSKKN-----PDPLQGEDLLTKVKDLGNKTKEDKARACGYYSVTKKQVVRVNLTDYDAVLAARKVPLDPS	
	A. marina	AM1_A0352	1	MMPKRTKK-NKPLTGAALLLAKVSLDLSLTLREKAKACGYYSVTKKQVVRVNLTDYDAVLAARKVPLDPS
AM1_C0337		1	MPKTKKQSKPLTGAALLLTKVKALNDLTLREKAKACGYYSVTKKQVVRVNLTDYDAVLAARKVPLDPS	
AM1_G0136		1	-----MAFLNVAFLNAFLDABGMDLDAQ	
AM1_6174		1	-----MAFLNVAFLNAFLDABGMDLDAQ	
AM1_5314		1	MPRKKKSTPKPLKGAALITKVAQLGQATREKAKACGYYSVTKKQVVRVNLTDYDAVLAARKVPLDPS	
AM1_B0085		1	MPKLLKKVTKPLTGEKLLAKRRELGLDLSREKAKACGYYSVTKKQVVRVNLTDYDAVLAARKVPLDPS	
AM1_D0091		1	MPRKKKQ-----TKPLTGKDLVAKVKQLSDYTREREKAKACGYYSVTKKQVVRVNLTDYDAVLAARKVPLDPS	
AM1_F0178		1	MPRKKKQ-----AKPLTGKDLVAKVKQLSDYTREREKAKACGYYSVTKKQVVRVNLTDYDAVLAARKVPLDPS	
AM1_C0352		1	MPRKKKQ-----AKPLTGKDLVAKVKQLSDYTREREKAKACGYYSVTKKQVVRVNLTDYDAVLAARKVPLDPS	
AM1_4870		1	MPRKNKQ-----TKPLTGEALLLTKVKQLSDLTLREKAKACGYYSVTKKQVVRVNLTDYDAVLAARKVPLDPS	
AM1_E0162		1	MPRKRKQ-----SKPLTGAALLLTKVKALNDLTLREKAKACGYYSVTKKQVVRVNLTDYDAVLAARKVPLDPS	
Marine Clade B		Pmt0464	1	-----MLTGSDDLTKVKDLGQVSKSDLVACGYYSVTKKQVVRVNLTDYDAVLAARKVPLDPS
		SYNW1518	1	-----MLTGSDDLTKVKDLGQVSKSDLVACGYYSVTKKQVVRVNLTDYDAVLAARKVPLDPS
		Pro0575	1	-----MLTGSDDLTKVKDLGQVSKSDLVACGYYSVTKKQVVRVNLTDYDAVLAARKVPLDPS
		Pmm0573	1	-----MWIRFHE-----KNGSERLNFTAFYEALLEAKVNLGAT
	Pro1459	1	-----MLTGRDILLAKVRDLGQVSKSDLVACGYYSVTKKQVVRVNLTDYDAVLAARKVPLDPS	
S. elongatus	7942_1969	1	-----MTSITPLTKGALLTRKELGNASRSEATAKACGYYSITKTKGRERLNFTAFYEALLEAKVNLGAT	
	7942_2255	1	-----MPKKAIP-----NOPLTGEALLLQVRELQDASKDQKARACGYYSVTKKQVVRVNLTDYDAVLAARKVPLDPS	
G. violaceus	Glr0411	1	-----MGAVAGKELLQILKONPGRSAKQLAEMAGYTTTTKQQRVKMMLAQSALVLEANNIRPV	
	Glr2814	1	-----MTPVSGKELLKLLKONPGRSAKQLAEMAGYTTTTKQQRVKMMLAQSALVLEANNIRPV	
	Glr0196	1	-----MAPLQGRDLLKLLIKENQKSAKQLAELAGYTTTTKSKQKRVKMLAQSALVLEANNIRPV	
Marine Clade A	Pro0439	1	-----MLVGEELDKARSLSKSEDEIARCGYYSVTKKQVVRVNLTDYDAVLAARKVPLDPS	
	Pmm0443	1	-----MLVGEELDKARSLSKSEDEIARCGYYSVTKKQVVRVNLTDYDAVLAARKVPLDPS	
	Pmt1344	1	-----MLVGEELDKARSLSKSEDEIARCGYYSVTKKQVVRVNLTDYDAVLAARKVPLDPS	
	SYNW1864	1	-----MLVGEELDKARSLSKSEDEIARCGYYSVTKKQVVRVNLTDYDAVLAARKVPLDPS	

S110359	66	-----GTKDGRGREPTFRVSVHKNQIVIGSTYTOEMGLKSGDEFETILGLYKH--IHLKQITD-----SDDEEEV-----128
Cwat1519	92	-----ATKDGRGREPTFRVSVHKNQIVIGSTYTOEMGLKSGDEFETILGLYKH--IHLKQVIG-----ADEEEA-----153
Tery0216	67	-----GNKDGRGREPTFRVSVHKNQIVIGATYETMGLKSGDEFETILGLYKH--IHLKQIDN-----EKDHTNGYDSEMEE--137
Alr0946	67	-----APKDGRGREPTFRVSVHKNQIVIGATYKAMGLKSGDEFETILGLYKH--IHLIQLGESDKKLSPLDIDDESDELDEEE--144
AM1_3666	68	-----GSKDGRGREPTFRVSVHKNQIVIGATYQAMGLKSGDEFETILGLYKH--IHLIQVDE-----DEVD-----127
Tery0493	77	-----DTKDGRGREPTFRVSVHKNQIVIGANYTDEMGLKSGDEFETILGLYKH--IHLRQNT-----EVENERQNEE-----144
T111150	65	-----EKEVNSQSGRGRSPSYRVKVNQIVIGANYTAMNPKPDEFETILGLYKH--IHLYLIDS-----EIDSEVNGAPRN--137
AM1_G0171	68	-----ANSDGRGREASRYRIKVNQIVIGSAYTEKMGLOTGDEFETILGRKH--IHLTQIT-----EDE-----125
T112172	67	-----SG-----RGGKRRGRSASRYRIVQANGNLLIGSAYTKOMNPKPDEFETILGRKH--IHLKQVSRNG-----QPIDDE-----133
AM1_4418	70	-----SQ-----NGNGRRGRNASYRISVQNGNLLIGSAYTKOMELAPGDEFETILGRKH--IHLKQIT-----DDED-----130
S110822	68	-----A-----SQGRRGRSASRYRISVQNGNLLIGSAYTKOMNPKPDEFETILGRKH--IHLKQVAD-----DEEE-----129
Cwat2079	65	-----A-----EGQRRGRSASRYRISVQNGNLLIGSAYTKOMGLKSGDEFETILGRKH--IHLKQVAGP-----NEDD-----126
All2080	68	-----P-----NANGRRGRSASRYRISVQNGNLLIGSAYTKOMNPKPDEFETILGRKH--IHLRQVVG-----EERELEIAEATA--137
Tery1859	68	-----Q-----NGNGRRGRSASRYRISVQNGNLLIGSAYTKOMDLPGDEFETILGRKH--IHLRQVGNV-----D-----VEEELEEMAIT--140
AM1_A0352	70	-----GK-----SNKR-----LGGKRLFRSIVQNGNLLIGSAYTKKMELOPGDEFETILGRKH--IHLKLMCEED-----129
AM1_C0337	70	-----VK-----RNKK-----MGGROPNFRSIVQNGKLLVSSAYTKKMELOPGDEFETILGRKH--IHLRLKTEED-----129
AM1_G0136	19	-----GE-----SNEQ-----LRGHNPSYRISVOTDEKLLIGSAYTKKMNLOPGDEFETILGRKH--IHLKVA-----75
AM1_6174	70	-----VI-----PHQK-----QSGRSPSYRISVQKNGQLLIGSAYSKOMELOPGDEFETILGRKH--IHLNKVI-----126
AM1_5314	70	-----PT-----SNGT-----GTSGRQPSYRISVQNGNLLIGSAYTKOMELSPGDMFEVTLGRKH--IHLTKVETDS-----130
AM1_B0085	69	-----SP-----NNGNNGSRKASRYRISVQNGNLLIGSAYTKOMELSPGDEFETILGRKH--IHLTKVA-----125
AM1_D0091	69	-----SP-----NNGNNGSRKASRYRISVQNGNLLIGSAYTKOMELSPGDEFETILGRKH--IHLTKVA-----125
AM1_F0178	69	-----SP-----NNGNNGSRKASRYRISVQNGNLLIGSAYTKOMELSPGDEFETILGRKH--IHLTKVA-----125
AM1_C0352	69	-----SS-----NSGSGVGRRASRYRISVQNGNLLIGSAYTKOMELSPGDEFETILGRKH--IHLTKVA-----125
AM1_4870	69	-----SA-----DGDGRGRKASRYRISVQNGNLLIGSAYTKOMELSPGDEFETILGRKH--IHLTKVA-----125
AM1_E0162	69	-----SSSGNNGRRGRKASRYRISVQNGNLLIGSAYTKELDVKPGDEFETILGRKH--IHLNKVAEPS-----130
Pmt0464	60	-----GV-----AGIGKGGKRLSYVATVQNGNLLIGKAYTALLDKPGDEFETILGRKO--IHLVPPAGSD-----EDD-----123
SYNW1518	60	-----GI-----GCVGKGGKRLSYVATVQNGNLLIGKAYTALLDKPGDEFETILGRKO--IHLVPPAGSD-----EDD-----123
Pro0575	60	-----GV-----AGIGKGGKRLSYIATVQNGNLLIGKAYTALLDKPGDEFETILGRKO--IHLVPPAGSD-----EDD-----123
Pmm0573	35	-----GV-----AGIGKGGKRLSYIATVQNGNLLIGKAYTALLDKPGDEFETILGRKO--IHLVPPAGSD-----EDD-----123
Pro1459	60	-----SA-----AGIGKGGKRLSYVATVQNGNLLIGKAYTALLDKPGDEFETILGRKO--IHLVPPAGSD-----EDD-----123
SYNW2103	59	-----GG-----AGIGKGGKRLSYIATVQNGNLLIGKAYTALLDKPGDEFETILGRKO--IHLVPPAGSD-----EDD-----123
7942_1969	64	-----AA-----PRKGRHPSYTRVQNGNLLIGSAYTRQMLTPGDEFETILGRKO--IHLVPPAGSD-----EDD-----123
7942_2255	69	-----LK-----LGRGRTGRSPFRSIVQNGNLLIGSAYTRQMLTPGDEFETILGRKO--IHLVPPAGSD-----EDD-----123
Glr0411	62	-----EE-----EQTNVGRGRKASYRIQVQNGNLLIGSAYTRQMLTPGDEFETILGRKO--IHLVPPAGSD-----EDD-----123
Glr2814	62	-----QE-----VETVRGRKASYRIQVQNGNLLIGSAYTRQMLTPGDEFETILGRKO--IHLVPPAGSD-----EDD-----123
Glr0196	62	-----HE-----GEGVRGRKASYRIQVQNGNLLIGSAYTRQMLTPGDEFETILGRKO--IHLVPPAGSD-----EDD-----123
Pro0439	56	-----GP-----GRPNRNRSSRQAEFFKTRVHNGNLLIGHAYTKKMLGEPGDEFETILGRKO--IHLVPPAGSD-----EDD-----123
Pmm0443	56	-----AA-----GRAGNRSSRQAEFFKTRVHNGNLLIGHAYTKKMLGEPGDEFETILGRKO--IHLVPPAGSD-----EDD-----123
Pmt1344	54	-----SS-----SGGSAASRQAEFFRTRVHNGNLLIGHAYTRRLGEPGDEFETILGRKO--IHLVPPAGSD-----EDD-----123
SYNW1864	60	-----TT-----NSGCGGSRQAEFFRTRVHNGNLLIGHAYTRRLGEPGDEFETILGRKO--IHLVPPAGSD-----EDD-----123



Fig. S1. Multiple sequence alignment of cyAbrBs from 12 cyanobacterial genomes. The sequences were aligned using the CLUSTALW program (ver. 1.83) at the DNA Database of Japan (DDBJ) (<http://clustalw.ddbj.nig.ac.jp/top-j.html>) and formatted using the BOXSHADE (ver. 3.21) program (http://www.ch.embnet.org/software/BOX_form.html). The predicted secondary structure of the AbrB-like DNA-binding domain (Coles et al. 2005) is shown below the sequences.