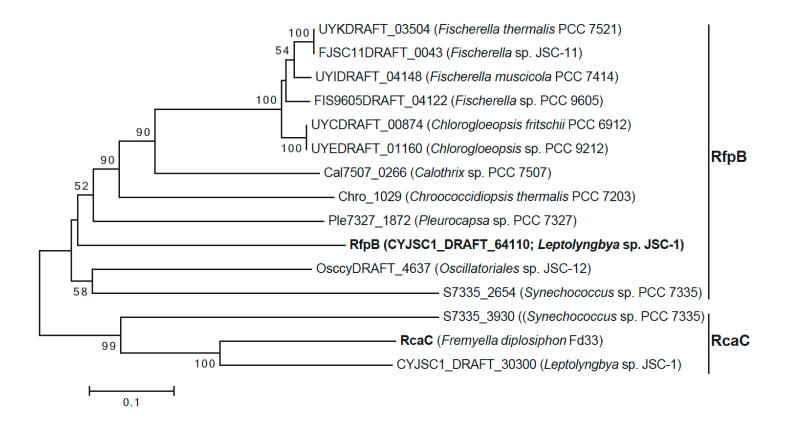
# **Supplementary Material**



**Figure S1.** Phylogenetic tree for RfpB sequences from strains with photosynthetic gene clusters similar to that in *Leptolyngbya* JSC-1. Sequences were aligned using the the MUSCLE module implemented in MEGA6, and a neighbor-joining tree was built from the resulting sequence alignment. Numbers at the nodes indicate the bootstrap support based upon 100 resamplings. A few RcaC sequences, the signal receiver/response regulator protein for CCA, were included as outgroup.

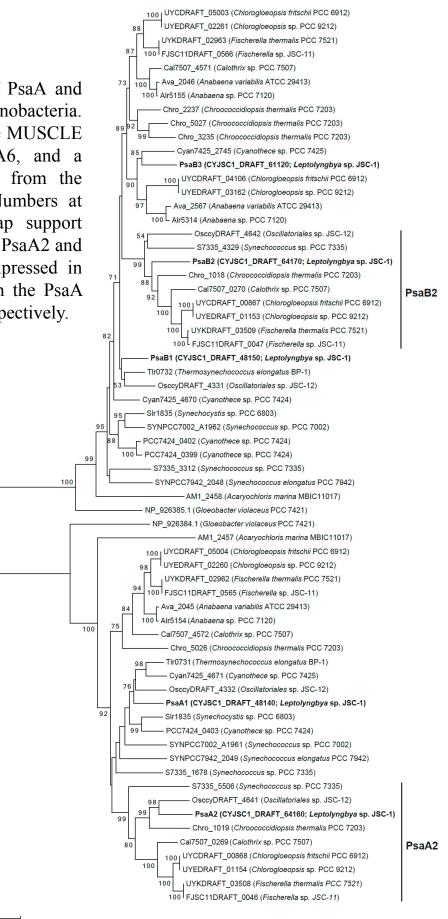
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<b>HRTLVEDDESXAALTUKVLTDEHTVIDVATGHIGKULVSERKYDLTIDVLLEDGIKECQURARGYTLVEFVALDDSSERTAGUNAG</b> Chro. 1029 MRLLVEDDECXAALENUGQURVVDATDGETWOLLGYTVDLILDVLENUGTISCUR, RURKYTVLLTAQOSSTRUKTGUNAG CYSCI, DART _ 4617 MRLLVEDDECXARLENUEGUNUDQURVVDATDGETWELVEFAYDLILUDVLENUEFSKORGTFULLTAXSSTDRTTGUNAG OSCOVDAT _ 4617 MRLLVEDDECXARLENUEFUNGEGUNUEFAYDLILUDVLENUEFSKORGTSULLTAVGSSTRUKTULTAVGSSTRUKTGUNAG VVCDAFT_6119 MRLLVEDDECXATLENUEGUNUDGUNUDGELGWELVEFAYDLILUDVLENUEFSKORGTSULLTAVGSSTRUKTULTAVGSSTRUKTGUNAG JVVCDRAFT_6414 MRLLVEDDECIANTENTLONHYVVDVANDGELGWELVEAFKVDLILUDVINENLDGIQLCQRLRSHWYQAVULTAVGSSTRUKTGUNAG JVVCDRAFT_6349 MRLLVEDDECIANTENTLONHYVVDVANDGELGWELVEAFKVDLILUDVINENLDGIQLCQRLRSHWYQAVULTAVGSSTRUKTGUNAG JVVCDRAFT_6349 MRLLVEDDECIANTENTLONHYVVDVANDGELGWELVEAFKVDLILUDVINENLDGIQLCQRLRSHWYQAVULTAVGSSTRUKTGUNAG JVVCDRAFT_6349 MRLLVEDDECIANTENTLONHYVVDVANDGELGWELVEAFKVDLILUDVINENLDGIQLCQRLRSHWYQAVULTAVGSSTRUKTGUNAG JVVCDRAFT_6349 MRLLVEDDECIANTENTLENGNYVTTUTEHKGLRLEVNSELTUFANKISLTEVENLDGIQLCQRLRSHWYQAVULTAVGSSTRUKTGUNAG JVVCDRAFT_6349 MRLLVEDDECIANTENTLENGNYVTVUTUANGELGUEVEAFKVDLILUDVINENLDGIQLCQRLRSHWYQAVULTAVGSSTRUKTUKGUNAG JVVCDRAFT_6349 KRULVERK-KKSLFPVLENDKUNALRAVGSSTVVTILTUGKSSTRUKGUNAGUNAGUNAGUNAGUNAGUNAGUNAGUNAGUNAGUNA

Figure S2. Cont.

Chro_1029 Ple7327_1872 CYJSC1_DRAFT_64110 OscovDRAFT_4637	PADVVILNLSLANTTAA SLDVVLLVFSLTNAAKD QPATFVVNLCLADNLAA LGGEPVLLLNLTAGEEK		AELTNRTPPIPVLLCTRGE ANLINQTPPTPVLFLTSSE RQLTHQLPPTSILLFTDQA ATYSQQAAPPLVLFIANQA ILCHY ILCHD ILCHD 	IRLSDRIELSRLGVHAFI INLTVRIEAARLCDRAFI IDLNLRVQFTQAGVHAVI INLNTRVKAARLGAHVFI	LRQPFNPEEVLAAVTRLQQT FQKLQLPERGLATMNKVLKQ LPKS-LVGQILSLAGQPAAQ LDKTELQSLVVQMTSNFSCQ
OSCCVDRAFT_64110 PSIPW	RPLAAQILEVVKQAKSHVC	TTTAKVMVVDDDPQILAGIRA VVDDVGE VLDDA VLDDA VLDDAIE VLDDAIE	LLEPWGLQLITLEEPRQFW		1PQINGIELCRAIRSEPRWQ 1PHFSGFELCRVVRNAPRWK
UYKDRAFT_03504 S7335_2654 HLPIV Chro_1029 KLPVL	710 720 FFTAHAEPHLQQAAFKAGG FLTAHTDDRTIQQVFTAGA FVSVHTDEDTVNQILRAGG FLTVHRDSETLRQMLEVGA	VLDDAIE 730 740 DNLIEKSLSDAQLLAHLEHQM NDCLSKSILGTELVTQIFNRL DDRISKSLIGPELVNRILNRL NALINKPIGESSALLPILTQI	GQMRLMQSIQ ERVHTLRSLTNANNPQLR KRAQVMRVMQ	۶P	

**Figure S2.** Sequence alignment for RfpB sequences from various strains containing photosynthetic gene clusters similar to that in *Leptolyngbya* JSC-1. Sequences were aligned using the MUSCLE module implemented in MEGA6. The red lines indicate the CheY-like signal-receiver domains at the N-terminus (residues 1 to 120) and C-terminus (residues 630 to 735). The green line indicates the DNA-binding, winged-helix domain (residues 128 to 233). The blue line indicates the histidine-containing phosphotransferase (HPT) domain (residues ~300 to 430).

**Figure S3.** Phylogenetic tree of PsaA and PsaB sequences from diverse cyanobacteria. Sequences were aligned using the MUSCLE module implemented in MEGA6, and a neighbor-joining tree was built from the resulting sequence alignment. Numbers at the nodes indicate the bootstrap support based upon 100 resamplings. The PsaA2 and PsaB2 sequences specifically expressed in FRL form distinctive clades with the PsaA and PsaB branches of the tree, respectively.



**S4** 

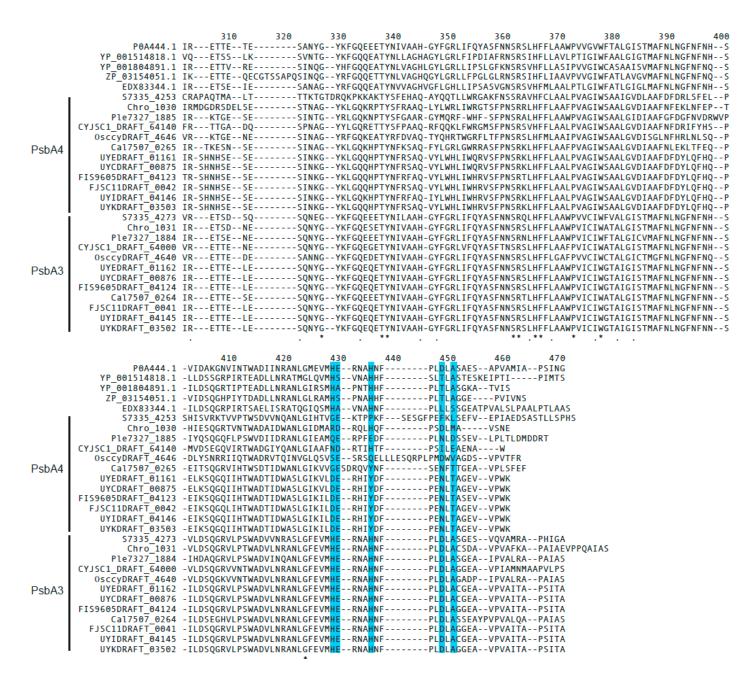
PsaB

PsaA

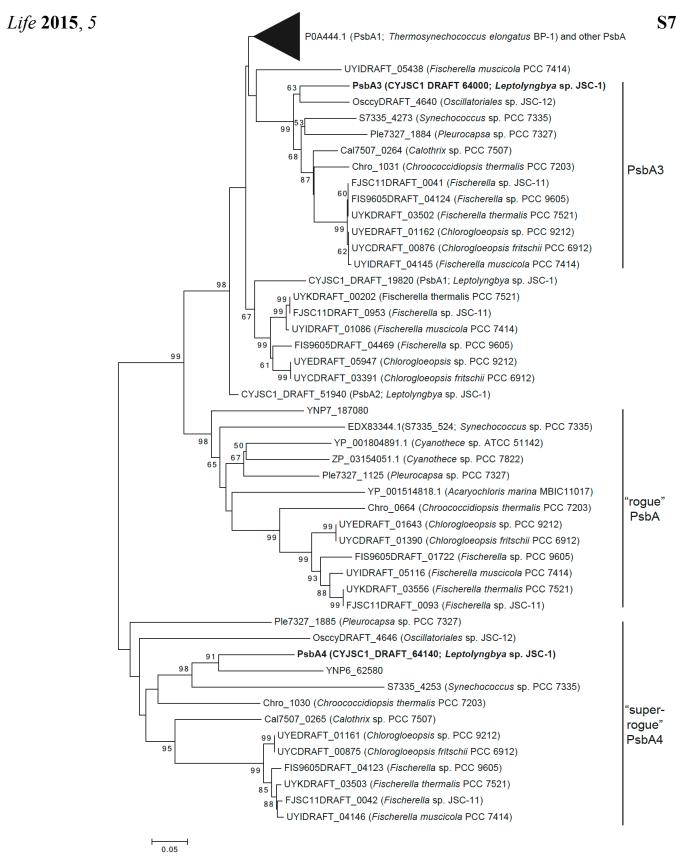
Lije <b>2</b> 0	15,5									60
		10	20	30	40	50	60	70	80	90 100
	P0A444.1 YP_001514818.1 YP_001804891.1 ZP_03154051.1 EDX83344.1								MTTTLQRRESAI MSTTFQTPSRLPTV MTNVFPRQKELDFG MSSVIQGRRELDIGI MSTSIRYRRGPSLSLSI	NLWERFCNWVTS SAWDQFCEWITS QLWSNFCEWITS DSWELFCQWITS DLWEQFCEWVTS
	\$7335_4253 Chro_1030	MIQTGFGRTS	SALEGFEQPFD	PAQAIDLESPL	TSTDTS			-VENTT	RNAGALWPSSQPL IPVTNELKKRQST	
	Ple7327_1885		MVQQEPT	LTPSIEVDSAI	ESPTE				-STTALNRRETLL/	AKWEEFCRWITS
	CYJSC1_DRAFT_64140 0sccyDRAFT_4646			MLIQFGRAS	SVAKS			-DQPDQ	ISIAEQPIQRPRI TITSPLSNRKTLS	SPWEQFCRWVTS
PsbA4		MQKIILLSAVLETVAJ	ENSYLIMQGS						TIATNILERWEEV	
	UYEDRAFT_01161 UYCDRAFT 00875								PTANKLSKRRKKVI PTANKLSKRRKKVI	
	FIS9605DRAFT_04123			MKLESDHVI	ATSDSS			-DYTSE	PTANKLSERRKKVI	NHWEKFCSWVTS
	FJSC11DRAFT_0042 UYIDRAFT_04146								PTANKLSERRKKVI PTANKLSERRKKVI	
	UYKDRAFT_03503								PTANKLSERRKKVI	
	\$7335_4273 Chro 1031								MTTVLQRQL NRVI	PAWERFCNWVTS
	Ple7327_1884			MPESLRSRKVL	NLPEFVEF	KFLL		-KKTLV	NSMTTTLQKREIPI	NLWEQFCQWVTS
	CYJSC1_DRAFT_64000 OsccyDRAFT_4640								MTTLLQRRGARVO MTTLLQQRKIASI	DQWERFCNWITS
PsbA3	UYEDRAFT_01162 UYCDRAFT_00876								MTTISTRPTSRFF MTTISTRPTSRFF	
	FIS9605DRAFT_04124								MTTISTRPTSRF	PTWDRFCNWVTS
	Cal7507_0264 FJSC11DRAFT 0041								MTTILQRQKGRSI MTTISTRPTSRFI	
	UYIDRAFT_04145 UYKDRAFT 03502								MTTISTRPTSRFI MTTISTRPTSRFI	
	• 01KDKAF1_03302								HITTSTRFTSKFT	TWORFCNWVTS
		110	120	130	140	150	160	170	180 1	90 200
		TDNRLYVGWFGVIMIF	TLLAATICFV	IAFIAAPPVDI	GIREPVS	GSLLYGNNII	TGAVVPSSNA	IGLHFY	PIWEAASLDEWLYNGGP	YQLIIFHFLLGA
									PLWEATSMDEWLYNGGP' PIWEAASIDEWLYNGGP'	
									PIWDAASIDEWLYNGGP' PLWEASSVAEWLYNGGP'	
	\$7335_4253	TENRIYIGWFGMLAIP	TLATAAIVEV	LAIIAAPAVDM	1 <mark>D</mark> GTGRMVS	GSLLDGNNLI	TAAVVPTSAA	IGLHFY	PIWEAASLDEWLINGGP	YQLIVLHFIIGI
									PLWEAASLDEWLYNGGP PIWAAASIDEWLYNGGP	
	CYJSC1_DRAFT_64140	TENRLYIGWFGVLLIP	TMLTAAITEV	VAIIAAPAVDI	NGTGEMIS	GSLLDGNNII	TAAVVPTSAA	IGLHFY	PIWEASSLKEWLTNGGP	YQLIVLHFLIGI
PsbA4									PIWAAASVDEWLYNGGP PIWEAASLDEWLYNGGP	
									PIWEAASIDEWLYNGGP PIWEAASIDEWLYNGGP	
	FIS9605DRAFT_04123	TENRLYIGWFGVLMIP	CILTATTVFI	IAIIAAPPVDM	1 <mark>D</mark> GIGAPIS	GSILSGNNII	TAAVVPTSAA	IGLHFY	PIWEAASLDEWLYNGGP	YQMIVLHFLIGI
									PIWEAASIDEWLYNGGP PIWEATSIDEWLYNGGP	
	UYKDRAFT_03503	TENRLYVGWFGVLMIP	CILTATTVFI	IAIIAAPPVDM	1 <mark>D</mark> GIGAPIS	GSILSGNNII	TAAVVPTSAA	IGLHFY	PIWEAVSIDEWLYNGGP	YQMIVLHFLIGI
	\$7335_4273 Chro_1031								PIWEAATLDEWLYNGGP PIWEAASMDEWLYNGGP	
	Ple7327_1884 CYJSC1_DRAFT_64000								PIWEAASMDEWLYNGGP PIWEAASMDEWLYNGGP	
	OsccyDRAFT_4640	TENRLYIGWFGVLMIP	PLLGVSICVFT	IAFIAAPPVDI	DGIREPVA	GSLLYGNNII	TAAVVPSSNA	IGLHFY	PIWEAASIDEWLYNGGP	YQMIGAHYIPAL
PsbA3									PIWEAASMDEWLYNGGP PIWEAASMDEWLYNGGP	
	FIS9605DRAFT_04124								PIWEAASMDEWLYNGGP PIWEAASMDEWLYNGGP	
	FJSC11DRAFT_0041	TENRLYIGWFGVLMIP	LLGVSICVFT	IAFIAAPPVDI	DGIREPVS	GSLLYGNNII	TAAVVPMSNA	IGLHFY	PIWEAASMDEWLYNGGP	YQMIGFHYIPAL
									PIWEAASMEEWLYNGGP PIWEAASMDEWLYNGGP	
	-			* . ** **					•.• • ••• ••••	
		210	220	230	240	250	260	270		90 300
									HPFHQLGVAGVFGGALF HPFHMLGVVGVFGGAFL	
	YP_001804891.1	WCYLGRLWELSYRLGM	IRPWISVAFSA	PVAAATSIFLV	/YPLGQGSF	S <mark>E</mark> GMPLGISG	TFHFMLAFQA	DHNILM	HPLHMLGVAGIFTGAVL/	AALHGSLVTSSL
	EDX83344.1	WAYLGRQWELSYRLGM	IRPWIAVAFSA	PVAAATAVLLV	/YPIGQGSF	S <mark>E</mark> GMPLGISG	TFHFMLTLQS	RHNVLM	HPLHMLGVAGIFGGALL HPFHMLGVAGIFGGALL	SALHGSLVTASL
									SPLHQMGVIGVLGGALL( SPFHVLGVIGVLGGAFL(	
	Ple7327_1885	ICYQDREWELSYRLGM	IRPWISLAFTA	PVAACISVFLV	/YPVGQGSF	S <mark>E</mark> GMPLGISG	TFNFMLRFQA	DHNILM	NPFHQIGVIGVLGGAFL/	AAMHGSLVTSTL
	CYJSC1_DRAFT_64140 OsccyDRAFT_4646								NPFHQLGVIGVFGGSFL SPLHQLGVVGVVGGAFC	
PsbA4	Ca17507_0265	ICYQDREWELSYRLGM	IRPWISLAFTA	PVAAAISVFLI	YPIGQGSF	S <mark>A</mark> GMPLGIAG	TFNFMFQFQA	DHNILM	SPLHQLGVIGVLGGAMM	SAMHGSLVTSTL
	UYCDRAFT_00875	IAYQDREWELSYRLGM	IRPWISLAFTA	PVAASVSVLLI	YPVGQGSL	S <mark>A</mark> GMPLGISG	TFHFMLQFQA	DHNILM	SPLHQLGVIGVLGGAFA/ SPLHQLGVIGVLGGAFA/	AAMHGSLVTSTL
	FIS9605DRAFT_04123 FJSC11DRAFT_0042								SPLHQLGVIGVLGGAFA/ NPLHQLGVIGVLGGAFA/	
	UYIDRAFT_04146	IAYQDREWELSYRLGM	IRPWISLAFTA	PVAASVSVLLI	YPVGQGSL	S <mark>A</mark> GMPLGISG	TFHFMLQFQA	DHNILM	NPLHQLGVIGVLGGAFA/	AAMHGSLVTSTL
									SPLHQLGVIGVLGGAFA/ HPFHMLGVAGVLGGSLF(	
									HPFHMLGVAGVLGGSLF( HPFHMLGVAGVFGGAFF(	
	CYJSC1_DRAFT_64000	CCYMGREWELSYRLGM	IRPWIAVAYSA	PLAATVSVFLI	YPIGQGSF	S <mark>D</mark> GLPMGISG	TFNFMFVFQA	EHNILM	HPFHMLGVAGVFGGSLF	CAMHGSLVTSSL
PsbA3									HPFHMLGVIGVFGGSLF( HPLHMIGVAGVLGGSLF(	
. 56/10	UYCDRAFT_00876	ACYMGREWELSYRLGM	IRPWIAVAYSA	PLAATTSVFLI	YPIGQGSF	S <mark>D</mark> GLPMGISG	TFNFMFVFQA	EHNILM	HPLHMIGVAGVLGGSLF	CAMHGSLVTSSL
		SCYMGREWELSYRLGM	IRPWICVAYSA	PLAATTSVFLI	YPIGQGSF	S <mark>D</mark> GLPMGISG	TENEMEVEQA	EHNILM	HPFHMLGVAGVLGGSLF	CAMHGSLVTSSL
									HPLHMIGVAGVLGGSLF( HPLHMIGVAGVLGGSLF(	
		ACYMGREWELSYRLGM	IRPWIAVAYSA	PLAATTSVFLI	<b>IVPIGQGSF</b>	SDGLPMGISG	TFNFMFVFQA	EHNILM	HPLHMIGVAGVLGGSLF	CAMHGSLVTSSL
			***	••••••			•••••••••••	••.•	* * .** *. *.	

Figure S4. Cont.

# **S5**



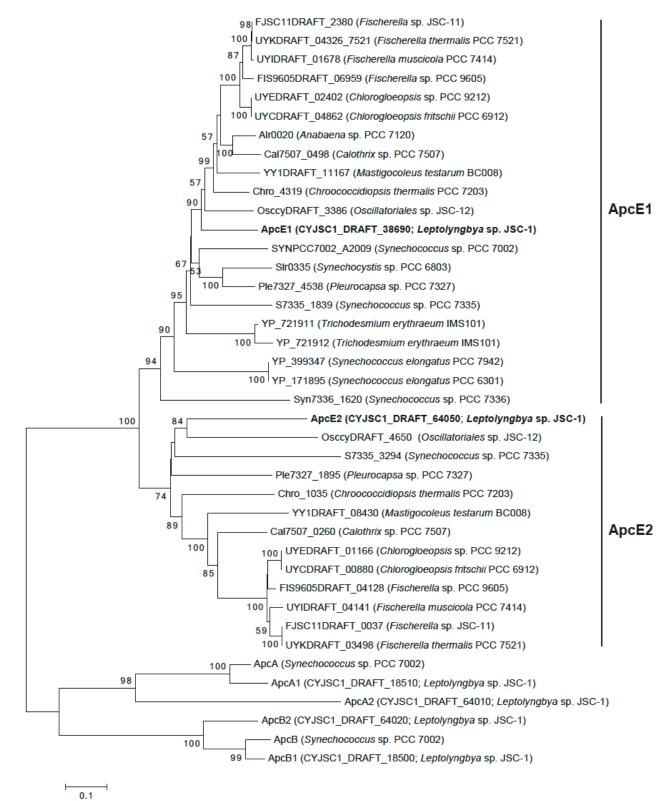
**Figure S4.** Sequence alignment for PsbA3 and PsbA4 sequences from various strains containing photosynthetic gene clusters similar to that in *Leptolyngbya* JSC-1. A few sequences from other strains are also included for comparison (also see Figure 5). Sequences were aligned using the MUSCLE module implemented in MEGA6. The residues shaded in blue are functionally important residues that provide ligands to important prosthetic groups for electron transfer (for details, see [41]). The D1 protein encoded by *psbA3* includes most of the highly conserved, functionally important residues for binding prosthetic groups, in particular the Mn<sub>4</sub> cluster of the oxygen-evolving complex.



**Figure S5.** Phylogenetic tree for PsbA1, PsbA3, "rogue" and "super-rogue" PsbA4 sequences. The included PsbA3 and PsbA4 sequences are found in the photosynthetic gene clusters that are similar to the 21-gene cluster found in *Leptolyngbya* JSC-1 [28]. Sequences were aligned using the MUSCLE module implemented in MEGA6. The designations of "rogue" PsbA and "Super-rogue" PsbA sequences are taken from the analysis of Murray [41]. For additional details, see main text.

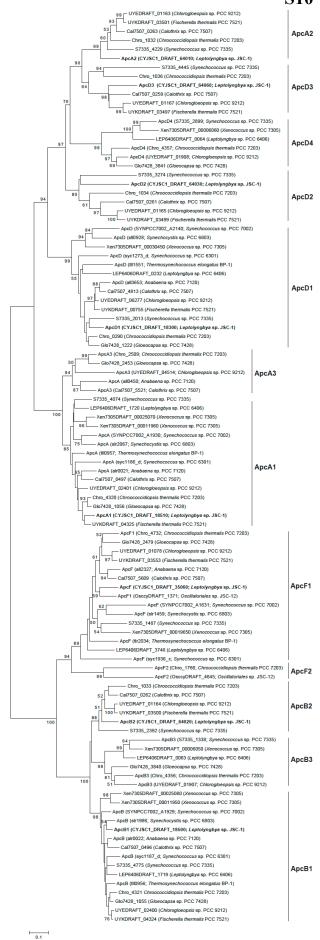
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	(7002)ADCA	DVVS	PGGN	AYGEEMTAT		RI TTYGVVAGD	VTPTEETGI VG	VREMYKSI G	<b>TPVDAVAOAVREM</b>	KAVATGMMS	GDDA		
ApcA		DVVS											
		VTPS											
	(7002)ApcB	DVTR	PGGN	MYTTRRYAA	LIRDLDYYL	RYATYAMLAGD	PSILDERVLNG	LKETYNSLG	/PVGSTVQAIQAM	KEVTAGLVG	ADAG		
ApcB	(JSC1)ApcB1	DITR	PGGN	MYTTRRYAA	CIRDLDYYL	RYATYAMLAGD	PSILDERVLNG	LKETYNSLG	<b>VPIAATVQAIQAI</b>	KEVTASLVG	ADAG		
	(JSC1)ApcB2	DITA	PGGN	MYTCRRYAA	CIRDLDYFL	RYATYAMLAGD	PSILDERILNG	LRETYNSLG	<b>/PIGATIRSVQAM</b>	KEATTDLVG	AEAG		
	(IMS101)YP 721911	FNNLAAGG-SGPI	PTGFRPIPVS	SKYGPANMTK	SLRDL SWFL	RYITYAIVAGD	YNILS-VNVRG	LKEIIEN-A	STAATIVAIQQM	RQASIKYF-	QDEEAKDIVAQ	YFDVVLTEF	RGSTPSNKQRQGQSS
	(7942)YP_399347	LGGAGAVRI	PSGFRPINVA	ARYGPRNMQK	<mark>S</mark> LRDMSWFL	RYITYAIVAGD	PNILV-VNVRG	LREIIEK-A	STPATLVALQDM	RATSAGYFR	NDPEAQQLVKD	YFDVLIREFE	EAPTPSLKQRQRFAE
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Abor	(7336)Syn7336_1620												
	(IMS101)YP_721912												
	(7002)SYNPCC7002_A2009												
													KAPTPSNKLRQRPSG
													QTQVPNDKLRQRPSI
	(7335) \$7335_1839												
	(7203) Chro_4319												
	(7327) Ple7327_4538												
	(JSC-1) CYJSC1_DRAFT_38690												
	(JSC-12) OsccyDRAFT_3386												
ApcE1	(7507) Ca17507_0498												
	(9212) UYEDRAFT_02402												
	(6912) UYCDRAFT_04862												
	(9605) FIS9605DRAFT_06959 (JSC-11) FJSC11DRAFT 2380		PPGFKPINVA				PNIIA-VNIKG	LKEIIEN-A	SGEATIVALUEL		KDSEAIDIVSQ		
	(7414) UYIDRAFT 01678												
	(7521) UYKDRAFT 04326												
	(BC008) YY1DRAFT 11167												
	(7335) \$7335 3294												
	(7203) Chro 1035												
	(7327) Ple7327 1895												
	(JSC-1) CYJSC1 DRAFT 64050												
	(JSC-12) OSCCYDRAFT 4650												
A	(7507) Cal7507 0260												
ApcE2	(9212) UYEDRAFT 01166												
	(6912) UYCDRAFT 00880	FTDREPL	PEGFRFINIS	SRYGPTRMKR	SMRDLAWFL	RYITFAIVAGD	TSILS-ANARG	LRGVIPE-D	T-DATVVALKEM	QRQSLSYFA	NDAEAQEIIKH	INFEVLISEYL	LVEKPPAQLRIGVSN
	(9605) FIS9605DRAFT_04128	FTDRDPL	PEGFRFINIS	SRYGPTRMKR	SMRDLAWFL	RYITFAIVAGD	TSILS-ANARG	LRGIIPE-D	T-DATVVALKEM	QRQSLSYFA	NDAEAQEIIKH	INFEVLISEYL	VEKPPAQLRIGVSN
	(JSC-11) FJSC11DRAFT 0037	FTDRDPL	PEGFRFINIS	SRYGPTRMKR	SMRDLAWFL	RYITYAIVAGD	TSILS-ANARG	LRGIIPE-D	T-DATVVALKEM	QRQSLNYFA	NDAEAQEIIKH	INFQVLISEYL	LVEKPPIELRIGVSD
	(7414) UYIDRAFT_04141												
	(7521) UYKDRAFT_03498												
	(BC008) YY1DRAFT_08430	FTDRDPL	PGGFRFINIS	SRYGPKRMKR	SMRDL SWFL	RYITYAIVAGD	PSILT-VNVRG	LRGVMPE-D	T-EATVVALKEM	RRISVSYLQ	DNTEATNVIKY	YFDVLISEYL	LEEKPPVKLRIGVSN
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**Figure S6.** Sequence alignment of a portion of the N-terminal, phycobiliproteins-like domains of ApcE1 and ApcE2 proteins (compared to the corresponding regions of selected ApcA and ApcB sequences). Sequences were aligned using the MUSCLE module implemented in MEGA6. The phycocyanobilin-binding cysteine residue in ApcA and ApcB is highlighted in yellow and red font. The corresponding residue is serine in all ApcE1 and ApcE2 sequences. The chromophore binding cysteine residue for ApcE1 sequences is shaded in green. In all ApcE2 sequences, cysteine does not occur at either position as shown by the yellow and blue shading. Because the chromophore binding pocket is still present (residues 180 to 230), it is probable that the phycocyanobilin associated with ApcE2 is non-covalently bound.



**Figure S7.** Phylogenetic tree for ApcE1 and ApcE2 sequences from strains with photosynthetic gene clusters similar to that in *Leptolyngbya* JSC-1 and from a few other selected strains with ApcE/ApcE1-like sequences. Sequences were aligned using the MUSCLE module implemented in MEGA6, and a neighborjoining tree was built from the resulting sequence alignment. Numbers at the nodes indicate the bootstrap support based upon 100 resamplings. Only the N-terminal phycobiliprotein-like domain and REP domains 1 and 2 were included in the analysis. For additional details, see main text.

Figure 8. Phylogenetic tree for ApcA, ApcB, ApcD, and ApcF sequences from strains with photosynthetic gene clusters similar to that in Leptolyngbya JSC-1 and from a few other selected strains. Sequences were aligned using the **MUSCLE** module implemented in MEGA6, and a neighbor-joining tree was built from the resulting sequence alignment. Numbers at the nodes indicate the bootstrap support based upon 100 resamplings. Seven clades of allophycocyanin alpha subunits (ApcA1, ApcA2, ApcA3, ApcD1, ApcD2, ApcD3 and ApcD4) were identified. ApcA1 and ApcD1 are replaced by ApcA2, ApcD2, and ApcD3 when cells are grown in FRL. Four clades of beta subunits (ApcB1, ApcB3 and ApcF) ApcB2, were identified. ApcB2 replaces ApcB1 when FaRLiP strains are grown in FRL. In most strains, the *apcF* gene is present as a single-copy gene and presumably the product of that gene is used with both ApcE2. However, ApcE1 and two FaRLiP organisms, Chr. thermalis PCC 7203 and Oscillatoria sp. JSC-12, have two ApcF genes, and in the latter organism, the apcF2 gene is localized in the FaRLiP gene cluster (see [28]). The functional roles of ApcA3, ApcB3, and ApcD4 are unknown. Additional details can be found in the main text.



#### **S10**

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Ар	57335 4074 Chro 4320 CA1 CYJSC1 DRAFT 18510 Ca17507 0497 UYEDRAFT 052401 UYKDRAFT 04325 S7335_4229	MSIVTKSIVNADAEARYLSPGELDRIKSFVTSGERRLRIAQALTDNRERIVKQAGDQLFQKRPDVVSPGGNAYGQEMTATCLRDLDYYLRLITYGVVAGD MSIVTKSIVNADAEARYLSPGELDRIKSFVTSGERRLRIAQVLTDSRERIVKQAGDQLFQKRPDVVSPGGNAYGQELTATCLRDLDYYLRLITYGVVSGD MSIVTKAIVNADAEARYLSPGELDRIKSFVSGGERRLRIAQVLTDNRERIVKQAGDQLFQKRPDVVSPGGNAYGQELTATCLRDLDYYLRLVTYGIVAGD MSIVTKSIVNADAEARYLSPGELDRIKSFVSGGERRLRIAQVLTDNRERIVKQAGDQLFQKRPDVVSPGGNAYGQEMTATCLRDLDYYLRLVTYGVVAGD MSIVTKAIVNADAEARYLSPGELDRIKSFVSGGERRLRIAQVLTDNRERIVKQAGDQLFQKRPDVVSPGGNAYGQEMTATCLRDLDYYLRLVTYGVVAGD MSIVTKAIVNADAEARYLSPGELDRIKSFVSGGERRLRIAQVLTDNRERIVKQAGDQLFQKRPDVSPGGNAYGQEMTATCLRDLDYYLRLVTYGVVAGD MSIVTKAIVNADAEARYLSPGELDRIKSFVSGGERRLRIAQVLTDNRERIVKQAGDQLFQKRPDVSPGGNAYGQEMTATCLRDLDYYLRLTYGVVAGD MSIVTKAIVNADAEARYLSPGELDRIKSFVSGFRRLRIAQVLTDNRERIVKQAGDQLFQKRPDVSPGGNAYGQEMTATCLRDLDYYLRLTYGVVAGD
Ар	CA2 CYJSC1 DRAFT 64010 Ca17507 0263 UYEDRAFT 01163 UYKDRAFT_03501 Chro 2509	MSVVTELILNADSESRYPVPKEMRIFQDFLRSGEQRIRIAATLAENEQRIVQNASAKFWERCPVTPSNSGNPRKTASCQRDQGWYIRLVAYSVLAGS MSIVTELILNADSESRYPAPKELRVFQEFLKSGDQRIRIAKILSQNEQQIVQNGSLKFWERCPNTPSNSGNERKTASCQRDQGWYVRLVAYSILAGS MSVVTELILNADSESRYPAPKELRIFQDFVKTGDQRIRIAKILSDNEQIVQRGSQRFWERCPNTPSNSGNERKTASCQRDQGWYVRLVAYSVLAGS MSVVTELILNADSESRYPAPKELRIFQDFLRTGDQRIRIAKILAENEQLIVQRGSQKFWERCPNTPSNSGNERKTASCQRDQGWYVRLVAYSVLAGS
Ар	CA17507-5521 UYKDRAFT 04521 (7002)ApcD \$7335-2013	MSLILKSILNADTEARYLTPGELEPIKSFVKNGERRLRLVQALTENRERIVKQSGTQLFQKRPDVVSPGGNAYGQEMTATCLRDIDYYLRLITYSIVAGD MSIITKMIVNADAEVRYLSPGELDQIKIFIKSSEHRLHLVQILTQSRDRIIKQAGNQLFQRRPSLISPGGNAYGQMTATCLRDMDYYLRLITYSVAAGD MSVVSQVILRADDELRYPSSGELSGINNFLATGAVRIRIAEALADMEKKIVDQAQKQLFSIHPEYRTSGGNAATTKQYNQCLRDYGWYLRLVTYGILAGD
Ар	Chro_0290 cD1 CYJSC1 DRAFT T8300 Ca17507_4813 UYEDRAFT_06277 UYKDRAFT_06277 S7335_3274	MSVVSQVILKADDELRYPSAGELENIKNFLQTGIQRMRIAATLAENEKKIVQEASKLUKQKRPDFIAPGGNAYGERQRALCLROYGMYLRLITYGVLAGD MSVVTQVILNADEELRYPSSGELKSIQNFLQTGSQRMRIAATLAENEKKIVQEASKELWKKRPDFIAPGGNAYGERQRSLCIRDYGWYLRLISYGVLAGD MTVISQVIFKADDELRYPSSGELKSIQNFLQTGIQRTRIAATLAENEKKIVQEATKQLWQKRPDFIAPGGNAYGERQRSLCIRDFGWYLRLITYGVLAGD MTVISQVILKADDELRYPSSGELKSIKDFLQTGEQRVRIANTLAENEKKIVQEATKQLWQKRPDFIAPGGNAYGERQRSLCIRDFGWYLRLITYGVLAGD MTVVSQVILKADDELRYPSSGELKSIKDFLQTGEQRVRIANTLAENEKKIVQEATKQLWQKRPDFIAPGGNAYGERQRSLCIRDFGWYLRLITYGVLAGD MTVVSQVILKADDELRYPSSGELKSIKDFLQTGEQRVRIASTLAENEKKIVQEATKQLWQKRPDFISPGGNAYGERQRSLCIRDFGWYLRLITYGVLAGD MSVISQVIATADREVRYLSKGELDAINRFFNNGPQRLRIVSILNSNAEEIVEKGARRFWQRCPITPSNSDNQUFQASCLRDQAWFIRLISYAVAVGD
Ар	Chro 1034 CVJSC1_DRAFT_64030 CZJSC1_DRAFT_64030 CA17507_0261 UYEDRAFT_61165 UYKDRAFT_03499 S7335_4445 Chro 1036	MSIITNVIATADREARYLNVEELNAVQNFYAAGRDRLRLAATLAANEQRIVEQATQRFWQRCPVTPSNSGNPTFQSSCMRDQSWYVRLVTYAIVLGD MSIITKSIASADREARYLSPGELNAIRDFYEGGFYRMRIAITLTENEQKIVEKASLKFWERCHDTPSNSGNRIYRSSCLRDQSWYIRLITYSIVLQD MSIIIKSIVNADREARYLNAGELRAIQEFYENGVSRLNFAVTLTENEKKIVEKASLKFWERCPNTPSNSGNRMYRNSCLRDQSWYIRLITYAUVVGD MSIIIKSIVNADREARYLNAGELSAIQEFYESGVSRLNLAMTLTENEQKIVEKASLKFWERCPNTPSNSGSRMYRNSCLRDQSWYIRLITYAVVVGD MSIVADREARYLNAGELESAIQEFYESGVSRLNLAMTLTENEQKIVEKASLKFWERCPNTPSNSGSPRKTEAAQRDMSWYIRLITYAUVVGD
Ар	CYJSC1_DRAFT_64060 Ca17507_0259 UYEDRAFT_03497 UYKDRAFT_03497 S7335_2899	MSLVKQVIQNADEELRYPTPGEIRMIQNFCQTGERRIQIAQKLAAAEQDLVQKGSQRFWKRCPVTPSNSGNPRKTASCQRDQGWYIRLVAYCVLAGS MSLVKQVILNADEELRYPTPAEIRMIQNFCHSGEKRIRIATTLAKNQNRLVEKASDKFWKRCPITPSNSGNMRKTASCQRDQGWYIRLVAYCVLAGS MSLVKQVIENADEQMRYPTPGEIRMIQNFCHSGDKRIRIATVLASNQNRLVEKASQKFWKRCPITPSNSGNMRKTASCQRDQGWYIRLVAYCVLAGS MSLVKQVIENADEQMRYPSPGEIRMIQNFCHSGDKRIRIATVLASNQNRLVEKASQKFWKRCPVTPSNSGNMRKTASCQRDQGWYIRLVAYCVLAGS
Ар	Chro <sup>-</sup> 4357 UYEDRAFT_01908 Xen7305DRAFT_00006060 LEP6406DRAFT_0064 Glo7428_3841	MSLVAQVIAQSDEADRELSRTELDKLQDFFKTGETRLKVAQILSKMEQKIVQEGSQRFWKV <mark>IP</mark> NTPSNSGDPKKTALCQRDQAWYLRLITYAVLAGN MSIVAQVIAQSDDAARFLSRTELDKLDNFFKSGETRLRVAQILAQNEQNIVEEGSRRFWKI <mark>V</mark> PNTPSNSGDPKKTALCQRDQSWYLRLITYAVLAGN MSIVAKVIAQSDRSDRFPSTAEITQLQDFFNNSSVRISTAQKLSENQQKIVEGSKRFWAQ <mark>C</mark> PNTPSNSGDATKTALCQRDQGWYIRLVSYCVLAGN MSIVAKVIAQSDEASRFLSSAELTKLQDFFGNGTVRISASQKLASNQQKIVDEGSKRFWAQCPNTPSNSGDSQKTMLCQRDQGWYIRLVSYCVLAGN
	(7002)ApcA	
Ар	57335_4074 Chro_4320 CA1 CYJSC1_DRAFT_8510 Ca17507_0497 UYEDRAFT_02401 UYKDRAFT_04325 S7335_4229	VTPIEEIGLVGVREMYKSLGTPVDAVAQAVREMKAVATGMMSGDDAAEAGAYFDYVIGAME VAPIEEIGLVGAREMYNSLGTSIPAMADSIRCMKSVAGSMMSGDDALEAASYFDYVIGGAQ VTPIEEIGIVGVREMYKSLGTPIDAVAEGVRAMKNVATSMLSGDDAEAGSYFDYLVGAMQ VTPIEEIGIVGVREMYKSLGTPIDAVAEGVRAMKSVATSLLSGDDAAEAGTYFDYVIGALQ VTPIEEIGVIGARELYKSLGTPIDAVAEGVRAMKSVATSLLSADDASEAGSYFDYLVGALL VTPIEEIGVVGVREMYKSLGTPIDAVAAGVASMKNVAASLLSADDASEAGAYFDYLVGALA VTPIEEIGVVGVREMYKSLGTPIDAVAAGVASMKNVAASLLSGDDAAEAGYFDYLVGALA VTPIEEIGVVGVREMYKSLGTPIDAVAAGVASMKNVAASLLSGDAAEAGAYFDYLVGALS ERPLEDIGTVGIKEMYNNLEIPIRNIAECMRCLKEEAMAVLSDEDAAEAGYFDYLVGALS
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Ар	CA1 CYJSC1_DRAFT_8510 CA1 CYJSC1_DRAFT_8510 Ca17507_0497 UYEDRAFT_62401 UYKDRAFT_62401 UYKDRAFT_64202 CA2 CYJSC1_DRAFT_6101 CA2 CYJSC1_DRAFT_6101 CA3 UYKDRAFT_01163 UYKDRAFT_0163 UYKDRAFT_6101 CA17507_5521 CA3 UYKDRAFT_64521 C7002)ApcD S7335_2013 Chro_0290 CYJSC1_DRAFT_8800 Ca17507_4813 UYKDRAFT_66277 UYKDRAFT_60275 S7335_3274	VTPIEEIGLVGVREMYKSLGTPUDAVAQAVREMKAVATGMMSGDDALEAGAYFDYVIGGME VAPIEEIGLVGVREMYKSLGTPIDAVAEGVRAMKAVATSMMSGDDALEAGAYFDYVIGGLQ VTPIEEIGIVGVREMYKSLGTPIDAVAEGVRAMKSVATSILSGDDALEAGSYFDYLVGAMQ VTPIEEIGIVGVREMYKSLGTPIDAVAEGVRAMKSVATSILSGDDALEAGSYFDYLVGAMQ VTPIEEIGIVGVREMYKSLGTPIDAVAEGVRAMKSVATSLLSGDDALEAGSYFDYLVGALL VTPIEEIGIVGVREMYKSLGTPIDAVAAGVSAMKNVAASLLSGDDALEAGSYFDYLVGALL VTPIEEIGIVGVREMYKSLGTPIDAVAAGVSAMKNVAASLLSADDASEAGAYFDYLVGALL VTPIEEIGIVGVREMYKSLGTPIDAVAAGVSAMKNVAASLLSADDASEAGAYFDYLVGALL VTPIEEIGIVGVREMYKSLGTPIDAVAAGVSAMKNVAASLLSADDASEAGAYFDYLVGALL VTPIEEIGVVGREMYKSLGTPIDAVAAGVSAMKNVAASLLSADDASEAGAYFDYLVGALS ERPLEDIGTVGIKEMYNNLEIPLRNIVECHRCLKEEAASLDSEDAQEVAAYFDLIIQSLS EKPLEEIGTIGIKEMYNNLEIPLRNIVECHRCLKEEAASLMSEEDAVEVGPYFDYIIRALS EKPLEEIGTIGIKEMYNNLEIPLRNIVECHRCLKEEAISLMSEEDAVEVGPYFDYIIRALS EKPLEEIGTVGIKEMYNNLEIPLRNIVEAMRCVKDEAISLMSEEDAVEVGPYFDYIIRALS EKPLEEIGTVGIKEMYNNLEIPLRNIVEAMRCKEEAISLMSEEDAVEVGPYFDYIIRALS EKPLEEIGTVGIKEMYNNLEIPLRNIVEAMRCKEAISLMSEEDAVEVGPYFDYIIRALS ATPIEEIGVGIGKMYNNLEIPLRNIVEAMRCKEAISLMSEEDAVEVGPYFDYIIRALS ATPIEEIGVGIKEMYNNLEIPLRNIVEAMRCKEAISLMSEEDAVEVGPYFDYIIRALS ATPIEEIGVGIKMEMYNLEJPLRNIVEAMRCKKEAISLMSEEDAVEVGPYFDYIIRALS ATPIEEIGVGIKMEMYNLEJPLRNIVEAMRCKKEAISLMSEDAVEVGPYFDYIIRALS ATPIEEIGVGIKMEMYNLEJPLRNIVEAMRCKKEAISLMSEEDAVEVGPYFDYIIGAMQ ATPIQEIGVIGARMMYRSLGTPIEAVAESIRAMKNITISMHSGEDALSGVGFYDVLIGAMQ ATPIQEIGVIGARMMYRSLGTPIEAVAESIRAMKNITSMHSGEDALSGDAVFDYTDIIALS KEPIEKIGLIGVREMYNSLGVPVPMVEAIRCLKNASLSLMSEDAVEVGPYFDYIIGAMS KEPIEKIGLIGVREMYNSLGVPVPMVEAIRCLKNASLSLMSEDAAVEVPTPYTDYIIQAMS KEPIEKIGLIGVREMYNSLGVPVPMEAIRCLKNASLSLMSEDAAVEVPTPYTDYIIQAMS KEPIEKIGLIGVREMYNSLGVPVPGWVESIRCLKNASLSLLSAEEAAEAAPYFDYIIQAMS KEPIEKIGLIGVREMYNSLGVPVPGWVESIRCLKNASLSLLSAEEAAEAAPYFDYIIQAMS KEPIEKIGLIGVREMYNSLGVPVPGWVEAINCLKKASLDLLNADDSAEAAPYFDYIIQAMS KEPIEKIGLIGVREMYNSLGVPVPGWVEAINCLKKASLDLLNADDSAEAAPYFDYIIQAMS VDPLEASGVRGVREMYLSLEVPLRSVALCMRSLKEVTLAMLSRDAAEAPYFDYIIQAMS
Ар Ар Ар	CA1 CYJSC1_DRAFT_6240 CYJSC1_DRAFT_6240 CYJSC1_DRAFT_6240 UYKDRAFT_02497 UYKDRAFT_02497 Chro_1032 CA2 CYJSC1_DRAFT_64010 Ca17507 0263 UYEDRAFT_61163 UYKDRAFT_03561 CA3 UYKDRAFT_03561 CA3 CYJSC1_DRAFT_64210 C7335_2013 Chro_0290 CD1 CYJSC1_DRAFT_64030 CA17507_4813 UYKDRAFT_06755 S7335_3274 Chro_1034 CYJSC1_DRAFT_64030 CA17507_0261 UYKDRAFT_0155 S7335_3274 Chro_1034 CYJSC1_DRAFT_64030 CA17507_0261 UYEDRAFT_61165 UYKDRAFT_0335 445	VTPIEEIGLVGVREMYKSLGTPUDAVAQAVREMKAVATGMMSGDDALEAGAYFDYVIGGNU VAPIEEIGLVGVREMYKSLGTPIEAVAEGVRAMKSVATSMMSGDDALEAGAYFDYVIGGUQ VTPIEEIGIVGVREMYKSLGTPIEAVAEGVRAMKSVATSMMSGDDALEAGAYFDYVIGGAUQ VTPIEEIGIVGVREMYKSLGTPIDAVAEGVRAMKSVATSMMSGDDALEAGAYFDYVVGAALU VTPIEEIGIVGVREMYKSLGTPIDAVAEGVRAMKSVATSLLSGDDALEAGAYFDYVGAALA VTPIEEIGIVGVREMYKSLGTPIDAVAAGVSAMKNVAASLLSGDDALEAGAYFDYVGAALA VTPIEEIGIVGVREMYKSLGTPIDAVAAGVSAMKNVAASLLSADDASEAGAYFDYVGAALA VTPIEEIGIVGVREMYKSLGTPIDAVAAGVSAMKNVAASLLSADDASEAGAYFDYVGAALA VTPIEEIGVVGVREMYKSLGTPIDAVAAGVSAMKNVAASLLSGDDAVEAVAYFDLIIQSLS EKPLEDITVGIKEMYNNLEIPLRNIVECMRCLKEEAAUSLDSDDAQEVAAYFDLIIQSLS EKPLEEIGTVGIKEMYNNLEIPLRNIVECMRCLKEEAAUSLDSDDAQEVAAYFDVIRALS EKPLEEIGTIGIKEMYNNLEIPLRNIVECMRCLKEEAISLMSEDDAVEVAPYFDYIRALS EKPLEEIGTIGIKEMYNNLEIPLRNIVECMRCLKEEAISLMSEDDAVEVAPYFDYIRALS EKPLEEIGTVGIKEMYNNLEIPLRNIVEAMRCKEEAISLMSEDDAVEVAPYFDYIRALS EKPLEEIGTVGIKEMYNNLEIPLRNIVEAMRCKEEAISLMSEDDAVEVGPYFDYIIRALS EKPLEEIGTVGIKEMYNNLEIPLRNIVEAMRCKEAISLMSEDDAVEVGPYFDYIIRALS ATPIEEIGVIGVRGMYRSLGTPIEAVESVRAMKNITSTMMSGEDAGEVGAYFDVILGAMQ ATPIQEIGVIGAREMYRSLGTPIEAVESVRAMKNITSTMMSGEDAGEVGAYFDVILGAMQ ATPIQEIGVIGVRGMYRSLGTPIEAVESVRAMKNITSMMSGEDAGEVGAYFDVILGAMQ KDPIERIGLIGVKEMYNALGVPVPGMVDAIRCLKDAALGVLDSEEAAIAPYFDFITQAMS KEPIESIGLIGVREMYNALGVPVPGMVEAINCLKDAALGVLDSEEAAIAPYFDFITQAMS KEPIESIGLIGVREMYNALGVPVPGMVEAIRCLKDAALGVLDSEARIAAPYFDFITQAMS KEPIEKIGLIGVREMYNSLGVPVPGMVEAIRCLKNASLLLAEDAAAEATPYFDYIIQAMS KEPIEKIGLIGVREMYNSLGVPVPGMVEAINCLKKASLDLLNADDAAEAAPYFDYIIQAMS KEPIEKIGLIGVREMYNSLGVPVPGMVEAINCLKKASLDLLNADDAAEAAPYFDYIIQAMS KEPIEKIGLIGVREMYNSLGVPVPGMVEAINCLKKASLDLLNADDAAEAAPYFDYIIQAMS KEPIEKIGLIGVREMYNSLGVPVPGMVEAINCLKKASLDLLNADDAAEAAPYFDYIIQAMS KEPIEKIGLIGVREMYNSLGVPVPGMVEAINCLKKASLDLLNADDAAEAAPYFDYIIQAMS KEPIEKIGLIGVREMYNSLGVPVPGMVEAINCLKKASLDLLNADDAAEAAPYFDYIIQAMS KEPIEKIGLIGVREMYNSLGVPVPGMVEAINCLKKASLDLLNADDAAEAAPYFDYIIQAMS KEPIEKIGLIGVREMYNSLGVPVPGMVEAINCLKKASLDLLNADDAAEAAPYFDYIIQAMS KEPIEKIGLIGVREMYNSLGVPVFGMVEAINCLKKASLDLLNADDAAEAAPYFDYIIQGLMP VEPLAAIGTIGQUEMYNSLEIPLNUVECIRCLKEVSLDIFTEDAAEVTPYFDVLIQGLMP VEPLAAIGTIGVSEE
Ар Ар Ар	CA1 CYJSC1_DRAFT_18510 CA17507_0497 UYEDRAFT_02401 UYKDRAFT_02401 UYKDRAFT_02401 UYKDRAFT_04325 S7335_4229 Chro_1032 CA2 CYJSC1_DRAFT_64010 Ca17507_0263 UYEDRAFT_0163 UYKDRAFT_03501 CA3 UYKDRAFT_04521 UYKDRAFT_04521 CYJSC1_DRAFT_18300 Ca17507_2531 Chro_0290 CD1 CYJSC1_DRAFT_64030 Ca17507_0261 UYEDRAFT_06755 S7335_327445 CD2 CJSC1_DRAFT_64030 Ca17507_0261 UYEDRAFT_01655 UYKDRAFT_03499 S7335_4445 Chro_1036 CYJSC1_DRAFT_64030 Ca17507_0251 UYEDRAFT_03499 S7335_4445 Chro_1036 CYJSC1_DRAFT_64060 Ca17507_0251 UYEDRAFT_64050 CA17507_0251 UYEDRAFT_64050 CA17507_0251 UYEDRAFT_64050 CA17507_0251 UYEDRAFT_64050 CA17507_0251 UYEDRAFT_64050 CA17507_0251 UYEDRAFT_64050 CA17507_0251 UYEDRAFT_64050 CA17507_0251 UYEDRAFT_64050 CA17507_0251 UYEDRAFT_64050 CA17507_0251 UYEDRAFT_64050 CA17507_0251 UYEDRAFT_64050 CA17507_0251 UYEDRAFT_64050 CA17507_0251 UYEDRAFT_64050 CA17507_0251 UYEDRAFT_64050 CA17507_0251 UYEDRAFT_64050 CA17507_0251 CA17507_05521	VTPIEEIGLVGVREMYKSLGTPUDAVAQAVREMKAVATGMMSGDDALEAGAYFDYVIGGNU VAPIEEIGLVGVREMYKSLGTPIDAVAEGVRAMKSVATSMMSGDDALEAGAYFDYVIGGU VTPIEEIGIVGVREMYKSLGTPIDAVAEGVRAMKSVATSMMSGDDALEAGAYFDYVVGANQ VTPIEEIGIVGVREMYKSLGTPIDAVAEGVRAMKSVATSMMSGDDALEAGAYFDYVVGALL VTPIEEIGIVGVREMYKSLGTPIDAVAEGVRAMKSVATSLLSGDDALEAGAYFDYVVGALL VTPIEEIGIVGVREMYKSLGTPIDAVAAGVSAMKNVAASLLSADDASEAGAYFDYVGAALA VTPIEEIGIVGVREMYKSLGTPIDAVAAGVSAMKNVAASLLSADDASEAGAYFDYVGAALA VTPIEEIGIVGVREMYKSLGTPIDAVAAGVSAMKNVAASLLSADDASEAGAYFDYVGAALA VTPIEEIGIVGVREMYKSLGTPIDAVAAGVSAMKNVAASLLSADDASEAGAYFDYVGAALA VTPIEEIGVVGREMYKSLGTPIDAVAAGVSAMKNVAASLLSADDASEAGAYFDVVGAALA VTPIEEIGVGVREMYKSLGTPIDAVAAGVSAMKNVAASLLSADDASEAGAYFDVVGAALS ERPLEDIGTVGIKEMYNNLEIPLRNIVECHRCLKEEAAVSNUSDEDAQEVAAYFDVIIGSLS EKPLEEIGTIGIKEMYNNLEIPLRNIVECHRCLKEEAAVSNUSDEDAQEVAAYFDVIIGSLS EKPLEEIGTIGIKEMYNNLEIPLRNIVEARGKKEEAISLMSEDDAVEVAPYFDVIIRALS EKPLEEIGTVGIKEMYNNLEIPLRNIVEARGKKEEAISLMSEDDAVEVAPYFDVIIRALS EKPLEEIGTVGIKEMYNNLEIPLRNIVEARGKKEEAISLMSEDDAVEVGPYFDVIIRALS EKPLEEIGTVGIKEMYNNLEIPLRNIVEARGKKEEASMMSEDDAVEVGPYFDVIIRALS ATPIEEIGVGKMEMYNNLEIPLRNIVEARGKKEEASMMSEDDAVEVGPYFDVIIRALS ATPIEEIGVGKMEMYNNLEJPLRNIVEARGKKEEASMMSEDDAVEVGPYFDVIIRALS ATPIEEIGVGKMEMYNNLEJPLRNIVEARGKKEASMMSEDDAVEVGPYFDVIIRALS ATPIEEIGVGKMEMYNNLEJPLRNIVEARGKKKEASMMSEDDAVEVGPYFDVIIRALS ATPIEEIGVGKMEMYNLEJPLRNIVEARGKKKEASMMSEDDAVEVGPYFDVIIRALS ATPIEEIGVGKMEMYNNLEJPLRNIVEARGKKKEASMMSEDDAVEVGPYFDVIIRALS ATPIEEIGVGKMEMYNNLEJPLRNVECHKEASSMMSEDDAVEVGPYFDVIIAGANG KEPIEKIGLIGVREMYNSLGPVPGMVEAINGKKKASSLULSAEDAVEVGYFDVIIAGANG KEPIEKIGLIGVREMYNSLGPVPGMVEAINGKKASSLULTADATAMYFDFIJQAMS KEPIEKIGLIGVREMYNSLGVPVGMVEAINGKKASSLULSAEAAAAPYFDVIIQAMS KEPIEKIGLIGVREMYNSLGVPVPGMVEAINGKKASSLULADADEAAPYFDVIIQAMS KEPIEKIGLIGVREMYNSLGVPVPGMVEAINGLKKASSLULADADSAEAAPYFDVIIQAMS KEPIEKIGLIGVREMYNSLGVPVPGMVEAINGLKKASSLULADADSAEAAPYFDVIIQAMS KEPIEKIGLIGVREMYNSLGVPVPGMVEAINGLKKASLULLADDAVEVAPYFDVIIQAMS KEPIEKIGLIGVREMYNSLGVPVPGMVEAINGLKKASLULLADDAVEVAPYFDVIIQAMS VEPLAAIGTIGVKEMYSLEIPPLNUVECIRGLKEVSLULTULLSREDAAEVPYFDVIIQAMS VEPLAAIGTIGVKEMYSLGPPLANLVAIRGKVENSLUCHVEANSL

**Figure S9.** Sequence alignment of ApcA and ApcD allophycocyanin subunits. ApcA1 is the major allophycocyanin alpha subunit produced in WL, GL, and RL, and ApcA2 (ApcD5) is specifically produced when cells are grown in FRL. ApcD1 is the allophycocyanin-B alpha subunit produced in WL, GL, and RL, and ApcD2 and ApcD3 are subunits produced in cells grown in FRL. Sequences were aligned using the MUSCLE module implemented in MEGA6. Yellow shading indicates conserved cysteine residues. The conserved cysteine residue at position 81 typically forms a covalent thioether bond to phycocyanobilin. Additional details can be found in the main text.

	(7002)ApcB	MQDAITSVINSADVQGKYLDGSAMDKLKAYFTTGALRVRAASTISANAAAIVKEAVAKSL-LYSDVTRPGGNMYTTRRYAACIRDLDYYLRYATYA	MLA
	\$7335 4775	MQDAITAVINASDVQGKYLDSSSMDKLKAYFQTGELRVRAATSISANAAEIVKEAVAKSL-LYSDITRPGGNMYTTRRYAA <mark>C</mark> IRDLDYYLRYSTYA	MLA
	Chro 4321		
ApcB1	CYJSC1 DRAFT 18500		
npeb l		MAQDAITAVINSADVQGKYLDTAAIEKLKGYFSSGDLRVRAAGTISANAAVIVKEAVAKSL-LYSDITRPGGNMYTTRRYAA <mark>C</mark> IRDLDYYLRYATYA	
	UYEDRAFT 02400		
	UYKDRAFT 04324		
	\$7335 2392		
	Chro 1033		
AuroDa			
ApcB2			
	Ca17507_0262		
	UYEDRAFT_01164		
	UYKDRAFT_03500		
	\$7335_1338		
	Chro_4356		MLA
ApcB3	3 UYEDRAFT_01907	MQDTITSLINPADLRGKYLDNTELDKLRKYFQSGELRVKAAATISENAANIVSQAVANSL-LYGDIT <mark>C</mark> PGGNMYPTRRYAA <mark>C</mark> LRDLTLFLRYATYA	MLA
	Xen7305DRAFT_00006050	MQDTITSLINPADEKGQYLEGQELDQLKKYFQSGSLRVKAADQIGSAAASIITESVAKSL-LYGDIT <mark>L</mark> PGGNMYPTRRYAA <mark>C</mark> LRDLTYFLRYAVYA	MLA
	LEP6406DRAFT 0063	MODTITATINPADEQGIYLEGEQLDALKAYFQSGTLRVKAASQIGDSAASIISETVAKSL-LYGDIT <mark>C</mark> PGGNMYPTRRYAA <mark>C</mark> LRDLTYFLRYATYA	MLA
	Glo7428 3840	MQDTITSLINPADQRGKYLETEELEKLRRYFQSGELRVKAASAISNNAANIIREAVANSL-LYGDIT <mark>C</mark> PGGNMYPTRRYAA <mark>C</mark> IRDLTLFLRYATYA	MLA
	(7002)ApcF		
	\$7335 1487		
	Chro 4732		
	CYISC1 DRAFT 35060		
ApcF1	OsccyDRAFT 1371		
	Ca17507 5609		
	UYEDRAFT 02400		
	UYKDRAFT 04324		
	Chro 1766	······································	
ApcF2			
	OsccyDRAFT_4645	MQDTLTRVINRYDVTDRFLDNAAIATLTEFLETGSLRVQVVAVINANAVEIVRESARQLFEELPYLIQPGGNAYTTRRHSM <mark>Y</mark> LRDMDYFLRYSSYA	LLI
		110 120 120 140 150 160	
	(7002) 40		
		GDPSILDERVLNGLKETYNSLGVPVGSTVQAIQAMKEVTAGLVGADAGREMGVYFDYICSGLS	
	\$7335_4775	GDPSILDERVLNGLKETYNSLGVPVGSTVQAIQAMKEVTAGLVGADAGREMGVYFDYICSGLS GDPSILDERVLNGLKETYNSLGVPVGATVQAIQAIKEVTASLVGADAGKEMGVYLDYICSGLS	
	\$7335_4775 Chro_4321	GDPSILDERVLNGLKETYNSLGVPVGSTVQAIQAMKEVTAGLVGADAGREMGVYFDYICSGLS GDPSILDERVLNGLKETYNSLGVPVGATVQAIQAIKEVTASLVGADAGKEMGVYLDYICSGLS GDPSILDERVLNGLKETYNSLGVPVGATVQAIQAMKEVTASLTGPDAGKEMGVYFDYICSGLS	
ApcB1	S7335_4775 Chro_4321 CYJSC1_DRAFT_18500	GDPSILDERVLNGLKETYNSLGVPVGSTVQAIQAMKEVTAGLVGADAGREMGVYFDYICSGLS GDPSILDERVLNGLKETYNSLGVPVGATVQAIQAIKEVTASLVGADAGKEMGVYFDYICSGLS GDPSILDERVLNGLKETYNSLGVPVGATVQAIQAMKEVTASLTGPDAGKEMGVYFDYICSGLS GDPSILDERVLNGLKETYNSLGVPIAATVQAIQAIKEVTASLVGADAGKEMGVYLDYICSGLS	
ApcB1	\$7335_4775 Chro_4321 CYJSC1_DRAFT_18500 Ca17507_0496	GDPSILDERVLNGLKETYNSLGVPVGSTVQAIQAMKEVTAGLVGADAGREMGVYFDYICSGLS GDPSILDERVLNGLKETYNSLGVPVGATVQAIQAIKEVTASLVGADAGKEMGVYLDYICSGLS GDPSILDERVLNGLKETYNSLGVPVGATVQAIQAMKEVTASLTGPDAGKEMGVYLDYICSGLS GDPSILDERVLNGLKETYNSLGVPIAATVQAIQAIKEVTASLVGADAGKEMGVYLDYICSGLS GDASILDERVLNGLKETYNSLGVPVGATVQAIQAIKEVTAGLVGSDAGREIGVYLDYICSGLS	
ApcB1	57335_4775 Chro_4321 CYJSC1_DRAFT_18500 Ca17507_0496 UYEDRAFT_02400	GDPSILDERVLNGLKETYNSLGVPVGSTVQAIQAMKEVTAGLVGADAGREMGVYFDYICSGLS GDPSILDERVLNGLKETYNSLGVPVGATVQAIQAIKEVTASLVGADAGKEMGVYLDYICSGLS GDPSILDERVLNGLKETYNSLGVPVGATVQAIQAMKEVTASLTGADAGKEMGVYFDYICSGLS GDPSILDERVLNGLKETYNSLGVPVGATVQAIQAIKEVTASLVGADAGKEMGVYLDYICSGLS GDASILDERVLNGLKETYNSLGVPVGATVQAIQAIKEVTASLVGPDAGKEMGVYFDYISSGLS GDPSILDERVLNGLKETYNSLGVPIGATVQAIQAMKEVTASLVGPDAGKEMGVYFDYISSGLS	
ApcB1	57335_4775 Chro_4321 CYJSC1_DRAFT_8500 Ca17507_0496 UYEDRAFT_02400 UYKDRAFT_04324	GDPSILDERVLNGLKETYNSLGVPVGSTVQAIQAMKEVTAGLVGADAGREMGVYFDYICSGLS GDPSILDERVLNGLKETYNSLGVPVGATVQAIQAIKEVTASLVGADAGKEMGVYLDYICSGLS GDPSILDERVLNGLKETYNSLGVPVGATVQAIQAMKEVTASLTGPDAGKEMGVYLDYICSGLS GDPSILDERVLNGLKETYNSLGVPVGATVQAIQAIKEVTASLVGADAGKEMGVYLDYICSGLS GDPSILDERVLNGLKETYNSLGVPVGATVQAIQAIKEVTASLVGSDAGREIGVYLDYISSGLS GDPSILDERVLNGLKETYNSLGVPVGATVQAIQAIKEVTASLVGPDAGKEMGVYLDYISSGLS GDPSILDERVLNGLKETYNSLGVPIGATVQAIQAIKAVTASLVGPDAGKEMGVYLDYISSGLS GDPSILDERVLNGLKETYNSLGVPIGATVQAIQAIKEVTASLVGPDAGKEMGVYLDYISSGLS	
ApcB1	57335_4775 Chro_4321 CYJSC1_DRAFT_18500 Ca17507_0496 UYEDRAFT_02400 UYKDRAFT_04324 S7335_2392	GDPSILDERVLNGLKETYNSLGVPVGSTVQAIQAMKEVTAGLVGADAGREMGVYFDYICSGLS GDPSILDERVLNGLKETYNSLGVPVGATVQAIQAIKEVTASLVGADAGKEMGVYLDYICSGLS GDPSILDERVLNGLKETYNSLGVPVGATVQAIQAIKEVTASLTGPDAGKEMGVYLDYICSGLS GDPSILDERVLNGLKETYNSLGVPIAATVQAIQAIKEVTASLVGADAGKEMGVYLDYICSGLS GDASILDERVLNGLKETYNSLGVPIGATVQAIQAIKEVTASLVGSDAGREIGVYLDYISSGLS GDPSILDERVLNGLKETYNSLGVPIGATVQAIQAMKEVTASLVGPDAGKEMGVYLDYISSGLS GDPSILDERVLNGLKETYNSLGVPIGATVQAIQAMKEVTASLVGPDAGKEMGVYLDYISSGLS GDPSILDERVLNGLKETYNSLGVPIGATVQAIQAMKEVTASLVGPDAGKEMGVYLDYISSGLS GDPSILDERVLNGLKETYNSLGVPIGATVQAIQAMKEVTASLVGPDAGKEMGVYLDYISSGLS GDPSILDERVLNGLKETYNSLGVPIGATVQAIQAMKEVXNDHLGAEAGKEVGYYPDHICSGLS	
ApcB1	\$7335_4775 Chro 4321 CYJSC1_DRAFT_18500 Ca17507_0496 UYEDRAFT_02400 UYEDRAFT_04324 \$7335_2392 Chro_1033	GDPSILDERVLNGLKETYNSLGVPVGSTVQAIQAMKEVTAGLVGADAGREMGVYFDYICSGLS GDPSILDERVLNGLKETYNSLGVPVGATVQAIQAIKEVTASLVGADAGREMGVYLDYICSGLS GDPSILDERVLNGLKETYNSLGVPVGATVQAIQAMKEVTASLVGADAGKEMGVYLDYICSGLS GDPSILDERVLNGLKETYNSLGVPIAATVQAIQAIKEVTASLVGSDAGREIGVYLDYICSGLS GDPSILDERVLNGLKETYNSLGVPIGATVQAIQAIKEVTASLVGSDAGREIGVYLDYICSGLS GDPSILDERVLNGLKETYNSLGVPIGATVQAIQAMKEVTASLVGSDAGREIGVYLDYISSGLS GDPSILDERVLNGLKETYNSLGVPIGATVQAIQAMKEVTASLVGPDAGKEMGVYLDYISSGLS GDPSILDERVLNGLKETYNSLGVPIGATVQAIQAMKEVTASLVGPDAGKEMGVYLDYISSGLS GDSILDERVLNGLKETYNSLGVPIGATVQAIQAMKEVTASLVGPDAGKEMGVYLDYISSGLS GDSILDERVLNGLKETYNSLGVPIGATVQAIQAMKEVTASLVGAEAGKEVGYYDMICSGLS GDSILDERVLNGLKETYNSLGVPIGATIRAVQAMKEVVNDMLGAEAGKEVGYYDHICSGLS GDSILDERVLNGLKETYNSLGVPIGATIRAVQAMKEVVNDMLGAEAGKEVGYYDHICSGLS	
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ApcB2	\$7335_4775 Chro_4321 CYJSC1_DRAFT_18500 Ca17507_0496 UYEDRAFT_042400 UYEDRAFT_042400 UYEDRAFT_04324 S7335_2392 Chro_1033 CYJSC1_DRAFT_64020 Ca17507_0262 UYEDRAFT_01164 UYKDRAFT_03500 S7335_1338 Chro_4356 UYEDRAFT_01907 Xen7305DRAFT_00006050	GDPSILDERVLNGLKETYNSLGVPVGSTVQAIQAMKEVTAGLVGADAGREMGVYFDYICSGLS GDPSILDERVLNGLKETYNSLGVPVGATVQAIQAIKEVTASLVGADAGKEMGVYLDYICSGLS GDPSILDERVLNGLKETYNSLGVPVGATVQAIQAMKEVTASLVGADAGKEMGVYLDYICSGLS GDPSILDERVLNGLKETYNSLGVPVGATVQAIQAIKEVTASLVGADAGKEMGVYLDYISSGLS GDPSILDERVLNGLKETYNSLGVPVGATVQAIQAIKEVTASLVGFDAGKEMGVYLDYISSGLS GDPSILDERVLNGLKETYNSLGVPVGATVQAIQAIKEVTASLVGFDAGKEMGVYLDYISSGLS GDPSILDERVLNGLKETYNSLGVPVGATVQAIQAMKEVTASLVGFDAGKEMGVYLDYISSGLS GDPSILDERVLNGLKETYNSLGVPVGATIRAVQAMKEVTASLVGFDAGKEMGVYLDYISSGLS GDPSILDERVLNGLKETYNSLGVPVGATIRAVQAMKEVTASLVGFDAGKEMGVYFDHISGLS GDPSILDERVLNGLKETYNSLGVPVGATIRAVQAMKEVTASLVGADAGREMGVYFDHISGLS GDPSILDERVLNGLKETYNSLGVPVGATIRSVQAMKEVTSLVGAEAGKEMGVYFDHIAGLS GDPSILDERILNGLRETYNSLGVPIGATIRSVQAMKEVTSIVGAEAGKEMGVYFDYIASGLS GDPSILDERILNGLRETYNSLGVPIGATIRSVQAKKEVTSIVGAEAGKEMGVYFDYIASGLS GDPSILDERILNGLRETYNSLGVPIGATIRAVQAMKEVTNSIVGAEAGKEMGVYFDYIASGLS GDPSILDERILNGLRETYNSLGVPIGATIRAVQAMKEVTNSIVGAEAGKEMGVYFDYIASGLS GDPSILDERILNGLRETYNSLGVPIGATIRAVQAMKEVTNSIVGAEAGKEMGVYFDYIASGLS DDASIIDERILNGLRETYNSLGVPIGATIRAVQAMKEVTNSIVGAEAGKEMGVYFDYIASGLS DDASIIDERILNGLKTYSLGVPIGATIRAVQAMKEVTNSIVGAEAGKEMGVYFDYIASGLS DDASIIDERILNGLKDTYSSLGVPVEPTIQAIEAMKDVVSERVGTEAGQEVGKYLDHIIAGLR DDPSILDERVLDGLKETYNSLGVPIQFTQQAIQALKEVTTRUVGAEAGEWGYFDVIASGLS DDASUIDERVLDGLKETYNSLGVPIQFTQQAIQAKKEVTNSIGAEAGEWGKYLDHIIAGLR DDPSILDERVLDGLKETYNSLGVPIQFTQQAIQAKKEVTNSIGAEAGEWGKYLDHIIAGLS DDASUIDERVLDGLKETYNSLGVPIQFTQQAIQAKKEVTRVGAEAGEWGRHLDHICSGLSQ DDASVLDERVLDGLKETYNSLGVPIDFTIQAIEAMKDVVSERVGAEAGEWGRHLDHICSGLSQ DDASVLDERVLDGLKETYNSLGVPIDFTIQAIEAMKEVTRVGAEAGEWGRHLDHICSGLSQ DDASVLDERVLDGLKETYNSLGVPIDFTIQAVQAMKEVTRVGAEAGEWGRHLDHICSGLSQ DDASVLDERVLDGLKETYNSLGVPIDFTIQAVQAMKEVTRVGAEAGEWGRHLDHICNGLS	
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ApcB2	S7335_4775 Chro_4321 CYJSC1_DRAFT_18500 Ca17507_0496 UYEDRAFT_042400 UYEDRAFT_042400 UYEDRAFT_04324 S7335_2392 Chro_1033 CYJSC1_DRAFT_64020 Ca17507_0262 UYEDRAFT_01907 S7335_1338 Chro_4356 UYEDRAFT_01907 Xen7305DRAFT_00060650 LEP6406DRAFT_0063 G107428_3840 (7002)Apcf	GDPSILDERVLNGLKETYNSLGVPVGSTVQAIQAMKEVTAGLVGADAGREMGVYFDYICSGLS GDPSILDERVLNGLKETYNSLGVPVGATVQAIQAIKEVTASLVGADAGKEMGVYLDYICSGLS GDPSILDERVLNGLKETYNSLGVPVGATVQAIQAIKEVTASLVGADAGKEMGVYLDYICSGLS GDPSILDERVLNGLKETYNSLGVPVGATVQAIQAIKEVTASLVGADAGKEMGVYLDYISSGLS GDPSILDERVLNGLKETYNSLGVPVGATVQAIQAIKEVTASLVGFDAGKEMGVYLDYISSGLS GDPSILDERVLNGLKETYNSLGVPVGATVQAIQAIKEVTASLVGFDAGKEMGVYLDYISSGLS GDPSILDERVLNGLKETYNSLGVPVGATVQAIQAIKEVTASLVGFDAGKEMGVYLDYISSGLS GDPSILDERVLNGLKETYNSLGVPVGATIRAVQAMKEVTASLVGFDAGKEMGVYLDYISSGLS GDPSILDERVLNGLKETYNSLGVPVGATIRAVQAMKEVTASLVGFDAGKEMGVYFDHISGLS GDPSILDERVLNGLKETYNSLGVPVGATIRAVQAMKEVTASLVGADAGREMGVYFDHISGLS GDPSILDERVLNGLKETYNSLGVPVGATIRAVQAMKEVTVSLVGAAGKEMGVYFDHIAGLS GDPSILDERILNGLRETYNSLGVPVGATIRSVQAKEVTSIVGAAGKEMGVYFDYIASGLS GDPSILDERILNGLRETYNSLGVPVGATIRSVQAKKEVTSIVGAAGKEMGVYFDYIASGLS GDPSILDERILNGLRETYNSLGVPVGATIRSVQAKKEVTSIVGAEAGKEMGVYFDYIASGLS GDPSILDERILNGLRETYNSLGVPVGATIRSVQAKKEVTSIVGAEAGKEMGVYFDYIASGLS DDSILDERILNGLRETYNSLGVPVGATIRSVQAKKEVTSIVGAEAGKEMGVYFDYIASGLS DDSILDERILNGLRETYNSLGVPVGATIRSVQAKKEVTSIVGAEAGKEMGVYFDYIASGLS DDSILDERILNGLRETYNSLGVPVEPTIQAIEAMKEVTNSIVGAEAGKEMGVYFDIASGLS DDSILDERILNGLRETYNSLGVPVEPTIQAIQAMKEVTTRVGAEAGKEMGVYFDIASGLS DDSILDERVLNGLKETYSSLGVPVEPTIQAIQAMKEVTTRVGAEAGQEVGKYLDHIIAGLR DDPSILERVLFGLKETFSTLGVPIQPTIQAIQAKEVTTRVGAEAGQEVGRHLDHISGLSQ DDSSULDERVLNGLKETYNSLGVPVEPTIQAVQAMKEVTTRVGAEAGQEVGYLDHIIAGLS DDPSILDERVLNGLKETYSSLGVPVEATIQAVQAMKEVTTRVGAEAGEQMDVLDHIIAGLS DDPSILDERVLNGLKETYSSLGVPVEATIQAVQAMKEVTTRVGAEAGEQMDVLDHIIAGLS ADPSILDERVLNGLKETYSSLGVPVEATIQAVQAMKEVTTRVGAEAGEMDVYLDHIIAGLS ADPSILDERVLNGLKETYSSLGVPVEATIQAVQAMKEVTTRVGAEAGGEIGMYFDHITNGLS GDMVLNERVLQGLKETYNSLGVPIAPTVGGIQFLKDAIXEMAAAAGAATAATIDEPFDHTRKLSEVDL	
ApcB2	S7335_4775 Chro_4321 CYJSC1_DRAFT_18500 Ca17507_0496 UYEDRAFT_042400 UYKDRAFT_04324 S7335_2392 Chro_1033 CYJSC1_DRAFT_04020 Ca17507_0262 UYEDRAFT_01164 UYKDRAFT_03500 S7335_1338 Chro_4356 UYEDRAFT_01907 Xen7305DRAFT_000606500 LEP6406DRAFT_0063 Glo7428_3840 (7002)ApcF S7335_1487	GDPSILDERVLNGLKETYNSLGVPVGSTVQAIQAMKEVTAGLVGADAGREMGVYFDYICSGLS GDPSILDERVLNGLKETYNSLGVPVGATVQAIQAIKEVTASLVGADAGKEMGVYFDYICSGLS GDPSILDERVLNGLKETYNSLGVPVGATVQAIQAIKEVTASLVGADAGKEMGVYLDYICSGLS GDPSILDERVLNGLKETYNSLGVPIGATVQAIQAIKEVTASLVGADAGKEMGVYLDYICSGLS GDPSILDERVLNGLKETYNSLGVPIGATVQAIQAMKEVTASLVGADAGKEMGVYLDYICSGLS GDPSILDERVLNGLKETYNSLGVPIGATVQAIQAMKEVTASLVGADAGKEMGVYLDYICSGLS GDPSILDERVLNGLKETYNSLGVPIGATVQAIQAMKEVTASLVGADAGKEMGVYLDYICSGLS GDPSILDERVLNGLKETYNSLGVPIGATVQAIQAMKEVTASLVGADAGKEMGVYLDYICSGLS GDPSILDERVLNGLKETYNSLGVPIGATIRAVQAMKEVTASLVGADAGKEMGVYLDYICSGLS GDSILDERILNGLKETYNSLGVPIGATIRAVQAMKEVTNSLVGADAGKEMGVYLDYICSGLS GDSILDERILNGLKETYNSLGVPIGATIRAVQAMKEVTNSLVGADAGKEMGVYFDHIAGLS GDSILDERILNGLRETYNSLGVPIGATIRSVQAMKEVTSLVGADAGKEMGVYFDYICAGLS GDPSILDERILNGLRETYNSLGVPIGATIRSVQAMKEVTSLVGADAGKEMGVYFDYIASGLS GDPSILDERILNGLRETYNSLGVPIGATIRSVQAMKEVTNSIVGAEAGKEMGVYFDYIASGLS GDPSILDERILNGLRETYNSLGVPIGATIRSVQAMKEVTNSIVGAEAGKEMGVYFDYIASGLS GDPSILDERILNGLRETYNSLGVPIGATIRAVQAMKEVTNSIVGAEAGKEMGVYFDYIASGLS DDASILDERILNGLRETYNSLGVPIGATIRAVQAMKEVTNSIVGAEAGKEMGVYFDYIASGLS DDASILDERILNGLRETYNSLGVPIGATIRAVQAMKEVTNSIVGAEAGKEMGVYFDYIASGLS DDSILDERILNGLKDTYSSLGVPVETIQAIQAKKEVTNSIVGAEAGEVGKYLDHIIAGLR DDPSILDERILNGLKETYSLGVPVETIQAIQAMKEVTNSWIGAEAGEVGKYLDHIIAGLS DDSILDERVLGLKETYSLGVPVETIQAIQAMKEVTRVGAEAGEQGEMLDHICSGLSQ DDASVLDERVLNGLKETYSSLGVPVETIQAVQAMKEVTRVGAEAGEQMGVLDHIIAGLS DDPSILDERVLNGLKETYSSLGVPVETIQAVQAMKEVTRVGAEAGEMDVYLDHIIAGLS DDPSILDERVLNGLKETYSSLGVPVETIQAVQAMKEVTTRVGAEAGEMDVYLDHIIAGLS ADPSILDERVLNGLKETYNSLGVPLATIQAVQAMKEVTTRVGAEAGEMDVYLDHIIAGLS DDPSILDERVLNGLKETYNSLGVPLATIQAVQAMKEVTTRVGAEAGEMDVYLDHIIAGLS ADPSILDERVLNGLKETYNSLGVPLATIQAVQAMKEVTTRVGAEAGEMDVYLDHIIAGLS ADPSILDERVLQGLRETYNSLGVPLATIQAVQAMKEVTTRVGAEAGEMDVYLDHIIAGLS ADPSILDERVLQGLRETYNSLGVPLATIQAVQAMKEVTTRVGAEAGEMDVYLDHIIAGLS ADDVLNERVLQGLRETYNSLGVPLATIQAUQAMKEVTTRVGAEAGEMDVYLDHIIAGLS ADDVLNERVLQGLRETYNSLGVPLATIQAUQAMKEVTTRVGAEAGEMDVYLDHIIAGLS ADDVLNERVLQGLRETYNSLGVPLATIQAUQAMKEVTRRV	
ApcB2	\$7335_4775 Chro_4321 CYJSC1_DRAFT_18500 Cal7507_0496 UYEDRAFT_02400 UYKDRAFT_04324 \$7335_2392 Chro_1033 CYJSC1_DRAFT_64020 Cal7507_0262 UYEDRAFT_01164 UYKDRAFT_01500 \$7335_1338 Chro_4356 UYEDRAFT_01907 Xen7305DRAFT_00006050 LEP6406DRAFT_00063 Gl07428_3840 (7002)ApcF \$7335_1487 Chro_4732	GDPSILDERVLNGLKETYNSLGVPVGSTVQAIQAMKEVTAGLVGADAGREMGVYFDYICSGLS GDPSILDERVLNGLKETYNSLGVPVGATVQAIQAIXEVTASLVGADAGKEMGVYLDVICSGLS GDPSILDERVLNGLKETYNSLGVPVGATVQAIQAMKEVTASLVGADAGKEMGVYLDVICSGLS GDPSILDERVLNGLKETYNSLGVPVGATVQAIQAIXEVTASLVGADAGKEMGVYLDVICSGLS GDPSILDERVLNGLKETYNSLGVPVGATVQAIQAIXEVTASLVGADAGKEMGVYLDVISSGLS GDPSILDERVLNGLKETYNSLGVPVGATVQAIQAMKEVTASLVGADAGKEMGVYLDVISSGLS GDPSILDERVLNGLKETYNSLGVPVGATVQAIQAMKEVTASLVGADAGKEMGVYLDVISSGLS GDPSILDERVLNGLKETYNSLGVPVGATIAAVQAMKEVTASLVGADAGKEMGVYLDVISSGLS GDPSILDERVLNGLKETYNSLGVPVGATIRAVQAMKEVTASLVGADAGKEMGVYLDVICSGLS GDPSILDERVLNGLKETYNSLGVPVGATIRAVQAMKEVTASLVGADAGKEMGVYFDHICSGLS GDPSILDERILNGLRETYNSLGVPVGATIRAVQAMKEVTASLVGADAGKEMGVYFDVICAGLS GDPSILDERILNGLRETYNSLGVPVGATIRSVQAKEVTSIVGADAGKEMGVYFDVICAGLS GDPSILDERILNGLRETYNSLGVPVGATIRSVQAKEVTSIVGADAGKEMGVYFDVICAGLS GDPSILDERILNGLRETYNSLGVPVGATIRSVQAKEVTSIVGADAGKEMGVYFDVIASGLS GDPSILDERILNGLRETYNSLGVPVGATIRSVQAKEVTNSMIGADAGKEMGVYFDVIASGLS GDPSILDERILNGLRETYNSLGVPVGATIAAVQAMKEVTNSMIGADAGKEMGVYFDVIASGLS GDPSILDERILNGLRETYNSLGVPVGATIAAVQAMKEVTNSMIGADAGKEMGVYFDVIASGLS DDPSILERVFVSLGVPVGATIQAVQAMKEVTNSMIGADAGKEMGVYFDVIASGLS DDPSILDERVLGLKTYNSLGVPVEPTIQAIEAMKEVVTQVGAEAGQEVGTHLDHICSGLSQ DDASVLDERVLDGLKETYNSLGVPVDRTIQAVQAMKEVTRVGAEAGQEVGRHLDHICSGLSQ DDASVLDERVLDGLKETYNSLGVPVDRTIQAVQAMKEVTRVGAEAGQEVGRHLDHICSGLSQ DDASVLDERVLDGLKETYNSLGVPVDRTIQAVQAMKEVTRV+GAEAGGEMGVYFDVIASGLS GDMDVLDERVLQGLRETYNSLGVPIAPTVRGIQFLXAMKEVTRLVGAEAGGEMGVYFDHIAGLS ADPSILDERVLNGLKETYNSLGVPIAPTVRGIQFLXAMKEVTRLVGAEAGGEMGVYFDHIAGLS ADPSILDERVLNGLKETYNSLGVPIAPTVRGIQFLXAMKEVXTRRVGAEAGGEMGVYFDHIAGLS ADPSILDERVLNGLKETYNSLGVPIAPTVRGIQFLXAMKEVXTRRVGAEAGGEMGVYFDHIAGLS GDMDVLNERVLQGLRETYNSLGVPIAPTVRGIQFLXAMKEVXAXAGVAFXFIDEPFDHMTRELSEVDL GNNDVLMERVLQGLRETYNSLGVPIAPTVRGIQMKKVKRAXAAGAVAFAGVENTAFIDEPFDHMTRELSEXDL	
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**Figure S10.** Sequence alignment of ApcB and ApcF subunits of allophycocyanin. ApcB1 is the major allophycocyanin beta subunit produced in WL, GL, or RL, and ApcB2 is the beta subunit of allophycocyanin produced in FRL. In most cyanobacteria, ApcF is a single-copy gene, the product of which apparently functions with both ApcE1 and ApcE2 subunits. Sequences were aligned using the MUSCLE module implemented in MEGA6. Yellow shading indicates conserved cysteine residues. The conserved cysteine residue at position 83 typically forms a covalent thioether bond to phycocyanobilin. Additional details can be found in the main text.