Supporting Information

Watanabe et al. 10.1073/pnas.1320599111

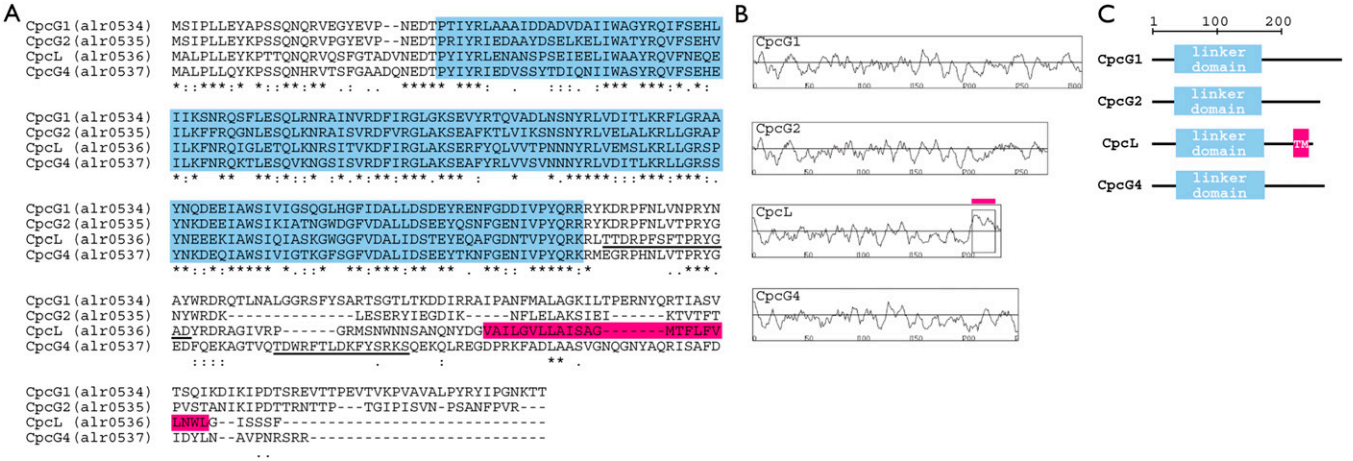

Fig. S1. Molecular characterization of CpcL and CpcG variants. (*A*) Sequence alignment, (*B*) hydropathy plots, and (*C*) domain architecture are shown for the four proteins. The hydrophobic segment specific to CpcL is highlighted in magenta. Linker domains are highlighted in blue. The underlined sequences indicate synthetic peptides that were used to generate antibodies.

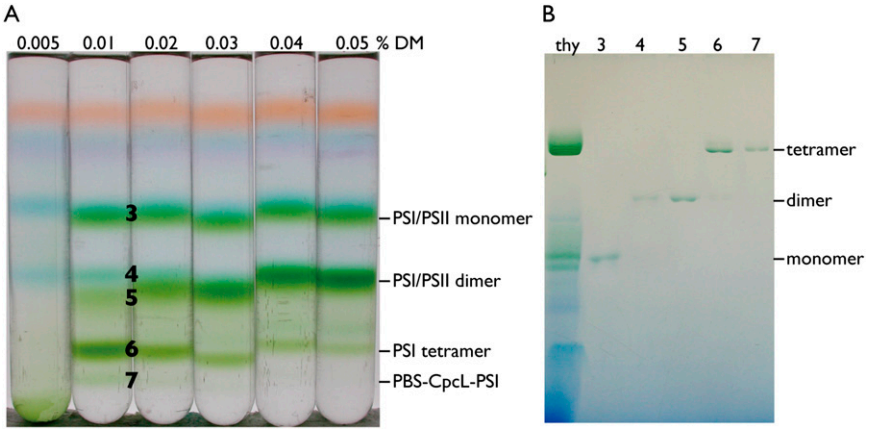

Fig. S2. Fractionation of *n*-dodecyl-β-D-maltoside (DM)-solubilized thylakoids by linear sucrose gradient centrifugation in the presence of a low-salt buffer. (*A*) Fractionation profile after centrifugation at 130,000 × *g* for 18 h at 4 °C. The sucrose gradient contained 0.005–0.05% DM. (*B*) Blue-native PAGE of the fractions. Fraction numbers correspond to those of 0.01% DM in *A*. Thylakoid (thy) was used as a marker.

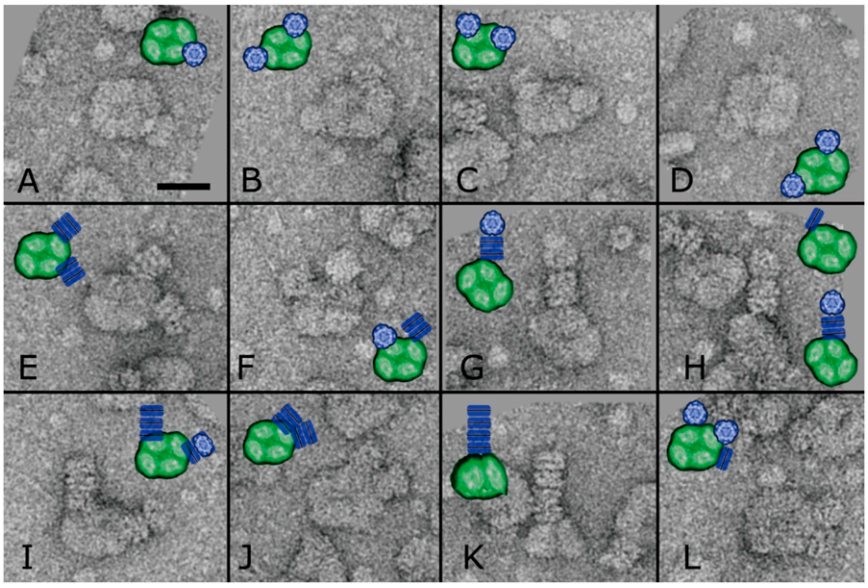

Fig. S3. Representative examples of EM projections of negatively stained phycobilisome (PBS)–CpcL–photosystem I (PSI) supercomplex and fragments of these complexes. (*A–D*) Projection maps showing PSI tetramers in an almost nontilted situation with one to two vertically positioned phycocyanin (PC) rods attached at the periphery. Models at 70% scaling illustrate positions of the PC hexamers of the CpcL–PBS rods (blue) on the tetramers (green). (*E* and F) Projection maps of tetramers with two rods, each composed of two PC hexamers, which have fallen over. (*G* and *H*) Projection maps of tetramers in the top-view position with disintegrated rods made of three PC/PEC hexamers. The first two hexamers are in a side-on position, the last (*Upper*) hexamer lays in a face-on position. (*I* and *J*) Projection maps of tetramers showing part of the PBS rods in a position intermediate to the face-on and side-on position. (*K*) Map of a tetramer in side-view position with a PBS rod consisting of four PC/PEC hexamers attached. (*L*) Rare case of a projection of a tetramer with three PBS rods attached. (Scale bar = 200 Å.)

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     Anabaena 7120  MALPLLEYKPTTQNQRVQSFGTADVNEDTPYIYRLENANSPSEIEELIWAAYRQVFNEQEILKFNRQIGLETQLKNRSITVKDFIRGLAKSERFYQLVVT  100
Anabaena variabilis MALPLLEYKPTTQNQRVQSFGTADVNEDTPYIYRLEDANSPSEIEELIWAAYRQVFNEQEILKFNRQIGLETQLKNRSITVKDFIRGLAKSERFYQLVVT  100
  Fischerella JSC11 MALPIHTYKPTTQNQRVCSFGTADLNEDSPYIYRLEDTNSSGEIAELIWAAYRQVFNEQEILQFNRQIALETQLKNRSITVRDFIRGLAKSGRFYQLVVA  100

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     Anabaena 7120  PNNNYRLVEMSLKRLLGRSPYNEEEKIAWSIQIASKGWGGFVDALIDSTEYEQAFGDNTVPYQRKRLTTDRPFSFTPRYGADYRDRAGIVRPGRMSN--W  198
Anabaena variabilis PNNNYRLVEMSLKRLLGRSPYNEEEKIAWSIQIASKGWGGFVDALIDSTEYEQAFGDNAVPYQRKRLTTDRPFSFTPRYGADYRDRAGIVRPGRMSN--W  198
  Fischerella JSC11 ANNNYRLVEICLKRLLGRAPYNQEEEIAWSIQIATRGWSGFVDALIDSEEYEQAFGDNTVPYQRKRMSTDRPFSFTPRYGEDYRDRAGIVQTSWIHHTEW  200

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     Anabaena 7120  N-----NSANQNYDGVAILGVLLAISAGMTFLFVLNWLGISSSF   237
Anabaena variabilis N-----NSANQNYDGMAILGVLLAISTGLTFLFVLNWLGISSSF   237
  Fischerella JSC11 YGFLAPSPYPKQVDWRTISAVIIGLSGIIAFLLLLNWFVNSSAF   244
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Fig. S4. Sequence alignment of CpcL species. The hydrophobic segment is highlighted in magenta. Linker domains are highlighted in blue. *Anabaena variabilis*, CP000117.1; *Fischerella* sp. JSC-11, AGIZ00000000. *, identical residues; :, conserved residues; ., similar residues.

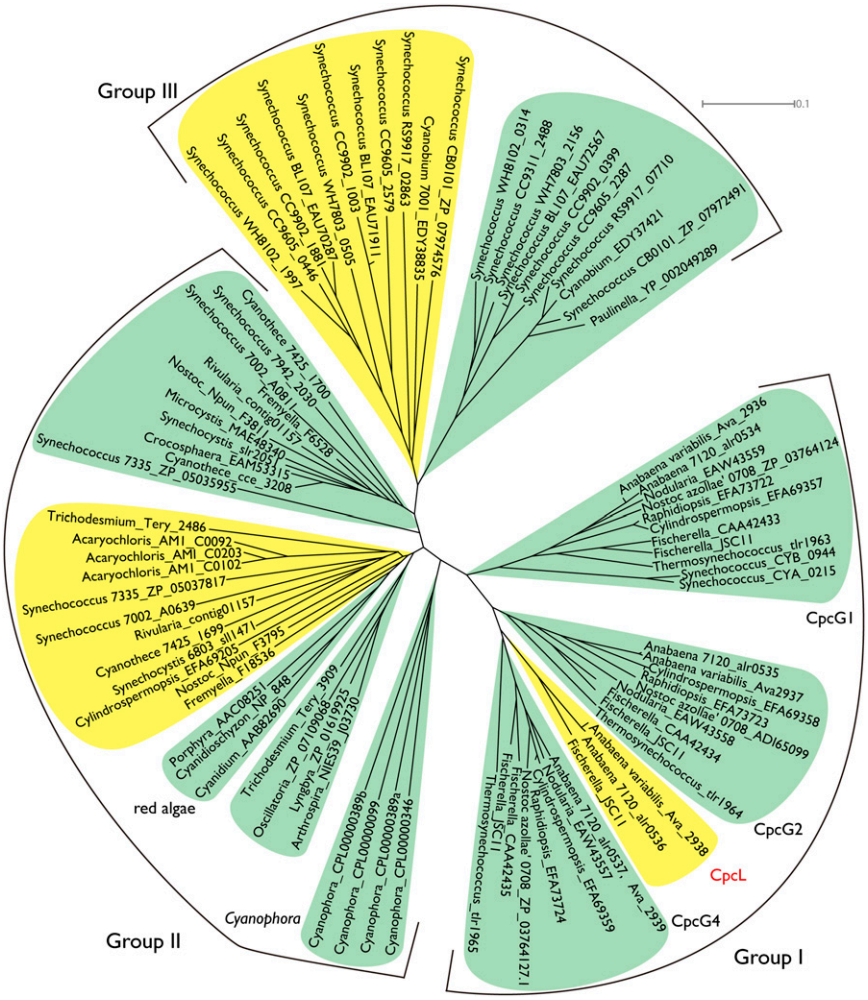

Fig. S5. Phylogenetic tree of linker domains of members of the CpcG/CpcL superfamily. The tree was inferred using the neighbor-joining method with ClustalX (http://www.clustal.org/). Tree stability was evaluated by bootstrap analysis with 1,000 replicates. CpcL and CpcG are highlighted in yellow and green, respectively.

Table S1. N-terminal amino acid sequencing showing the determined sequences

Subunit	Amino acid sequence
PsaC	M**SHTVKIYDTCIGCTQ**CVRACPTDVLEMVPWDGCKAAQVASSPRTEDCVGCKRCETACPTDFLSIRVYLGAETTRSMGLAY
PsaD	M**AETLSGKTPL**FAGSTGGLLTKAVEEEKYAITWTSPKAQVFELPTGGAATMHEGENLLYIARKEYGIALGGQLRKFKITNYKIYRILPSGETTFIHPAD GVFPEKVNAGREKVRFNARSIGENPNPSQVKFSGKATYDA
PsaE	M**VQRGSKVRIL**RPESYWFQDVGTVASVDQSGIKYPVIVRFDKVNYAGINTNNFAVDELIEVEAPKAKAKK
PsaF	MRRLFALILVICLSFSFAPPAKA**LGADLTPCAENPAFQALA**KNARNTTADPQSGQKRFERYSQALCGPEGYPHLIVDGRLDRAGDFLIPSILFLYI AGWIGWVGRAYLQAIKKDSDTEQKEIQLDLGIALPIIATGFAWPAAAVKELLSGELTAKDSEITVSPR
PsaI	MATAFLPSILA**DASFLSSIFV**PVIGWVVPIATFSFLFLYIEREDVA
PsaJ	M**ADKADQSSYL**IKFISTAPVAATIWLTITAGILIEFNRFFPDLLFHPLP
PsaK	MLTSTLLA**AATTPLEWS**PTVGIIMVIANVIAITFGRQTIKYPSAEPALPSAKFFGGFGAPALLATTAFGHILGVGLVLGLHNLGRI
PsaL*	M<u>**AQAVDASKNLPSDPRNREVVFPAGRDP**</u>QWGNLETPVNASPLVKWFINNLPAYRPGLTPFRRGLEVGMAHGYFLFGPFAKLGPLRDAANANLAGLL GAIGLVVLFTLALSLYANSNPPTALASVTVPNPPDAFQSKEGWNNFASAFLIGGIGGAVVAYFLTSNLALIQGLVG
PsaX	M**AKAKISPVAN**TGAKPPYTFRTGWALLLLAVNFLVAAYYFHIIQ
PecC	M**SSSVAERLAIRDAIG**NKVELRQNWSEDDLQKVFRAAYEQIFGRQGIYASQKFTSAEALLRNGKISVRQFVEILAKSEFYKECFFYKNSQVRLIELNY KHLLGRAPYDQSEIADHVDIYAARGYDADIDAYIYSSEYENAFGNSIVPYYRGFQSIPGMKTVGFNRICELYRGRGNSDNAQMGRTNSRLR TKVSLNLPNGILPPTSAGTNFVSAAPTLISSATKGDNRMFVIEAIAGGLNTNVAVRRSRQVYTVSYERLSATYQEIHKRGGKIVKISQV
CpcA	M**VKTPITEAIA**AADTQGRFLGNTELQSARGRYERAAASLEAARGLTSNAQRLIDGATQAVYQKFPYTTQTPGPQFAADSRGKSKCARDVGH YLRIITYSLVAGGTGPLDEYLIAGLAEINSTFDLSPSWYVEALKHIKANHGLSGQAANEANTYIDYAINALS
CpcB	M**TLDVFTKVVSQADSRGEFLS**NEQLDALANVVKEGNKRLDVVNRITSNASAIVTNAARALFEEQPQLIAPGGNAYTNRRMAACLRDMEIILRYV TYAILAGDASVLDDRCLNGLRETYQALGTPGSSVAVGVQKMKDAAVGIANDPNGITKGDCSQLISEVASYFDRAAAAVG
CpcC	M**AITTAASRLGTEPF**SDAPKVELRPKASREEVESVIRAVYRHVLGNDYILASERLVSAESLLRDGNLTVREFVRSVAKSELYKKKFFY NSFQTRLIELNYKHLLGRAPYDESEVVYHLDLYQNKGYDAEIDSYIDSWEYQSNFGDNVVPYYRGFETQVGQKTAGFNRIFRLYRGYANSD RAQVEGTKSRLARELASNKASTIVGPSGTNDSWGFRASADVAPKKNLGNAVGEGDRVYRLEVTGIRSPGYPSVRR SSTVFIVPYERLSDKIQQVHKQGGKIVSVTSA
CpcD	M**FGQTTLGAGSVSSS**ASRVFRYEVVGLRQSSETDKNKYNIRNSGSVFITVPYSRMNEEYQRITRLGGKIVKIEQLVSAEA
CpcG1	M**SIPLLEYAPSSQN**QRVEGYEVPNEDTPTIYRLAAAIDDADVDAIIWAGYRQIFSEHLIIKSNRQSFLESQLRNRAINVRDFIRGLG KSEVYRTQVADLNSNYRLVDITLKRFLGRAAYNQDEEIAWSIVIGSQGLHGFIDALLDSDEYRENFGDDIVPYQRRRYKDRPFNLVNPRYNAY WRDRQTLNALGGRSFYSARTSGTLTKDDIRRAIPANFMALAGKILTPERNYQRTIASVTSQIKDIKIPDTSREVTTPEVTVKPVAVALPYRYIPGNKTT
CpcG2	M**SIPLLEYKPSSQNQ**RVPGYEVPNEDTPRIYRIEDAAYDSELKELIWATYRQVFSEHVILKFFRQGNLESQLKNRAISVRDFVRGLAK SEAFKTLVIKSNSNYRLVELALKRLLGRAPYNKDEEIAWSIKIATNGWDGFVDALLDSEEYQSNFGENIVPYQRRRYKDRPFNLVTPRYGNYW RDKLESERYIEGDIKNFLELAKSIEIKTVTFTPVSTANIKIPDTTRNTTPTGIPISVNPSANFPVR
CpcG4	M**ALPLLQYKPSSQN**HRVTSFGAADQNEDTPYIYRIEDVSSYTDIQNIIWASYRQVFSEHEILKFNRQKTLESQVKNGSISVRDFIRGLAKSEAF YRLVVSVNNNYRLVDITLKRLLGRSSYNKDEQIAWSIVIGTKGFSGFVDALIDSEEYTKNFGENIVPYQRKRMEGRPHNLVTPRY GEDFQEKAGTVQTDWRFTLDKFYSRKSQEKQLREGDPRKFADLAASVGNQGNYAQRISAFDIDYLNAVPNRSRR
CpcL	M**ALPLLEYKPTTQNQR**VQSFGTADVNEDTPYIYRLENANSPSEIEELIWAAYRQVFNEQEILKFNRQIGLETQLKNRSITVKDFIRGLAKSERFYQLVV TPNNNYRLVEMSLKRLLGRSPYNEEEKIAWSIQIASKGWGGFVDALIDSTEYEQAFGDNTVPYQRKRLTTDRPFSFTPRYGADYRDRAGIVRP GRMSNWNNSANQNYDGVAILGVLLAISAGMTFLFVLNWLGISSSF
ApcC	M**SRLFKITALVPSLSRTRTQR**ELQNTYFTKLVPYENWFREQQRIQKAGGKIIKVELATGKQGTNAGLQ

Determined sequences are in boldface.
*Three distinct N-terminal sequences are underlined.