

**Table S2.** Primers used in this study.

<b>Primers</b>	<b>Sequence</b>
PN-up	5'- TTA <del>CT</del> CGAGACTACCTACGCATCATCACCTA -3'
PC-up	5'- CAGGAATTC <del>AACT</del> ATTGACTTTGAGCCAATAG -3'
PN-down	5'- ACTGCGGCCGCTAACATTGGGTGGAGA -3'
PC-down	5'- TACGAGCTCAGCAGTCTGCACATAC -3'
PN-G1	5'- CGGGAATTCAGTTTCATAAGAAAAGGTGAAAG -3'
PC-G1	5'- CAGACTAGTAGTTGTCAGTTGTCAGTCAACAG -3'
PN-G2	5'- GTAGAATTCCTGTTGACTGACA <del>ACT</del> GACA <del>ACT</del> -3'
PC-G2	5'- GCGACTAGTGAAGTAGGTCGGCAACTTA -3'
PN-G3E	5'- GCGGAATTCTAAGTTGCCGACCTACTTC -3'
PN-G3X	5'- GCGTCTAGATAAGTTGCCGACCTACTTC -3'
PC-G3	5'- ACAACTAGTCCGCATTAGGTTCAGAAGCTA -3'
PN-G4E	5'- GTGGAATTCAGTAAAGCATGAAGGAGGAT -3'
PN-G4X	5'- GTGTCTAGAAGTAAAGCATGAAGGAGGAT -3'
PC-G4	5'- GTCACTAGTAAAAACA <del>ACT</del> GGGTCTAGTCTC -3'
PN-EmS	5'- TCAACTAGTGCGTGCTATAATTATACTA -3'
PN-EmE	5'- CGAGAATTCATCGAATAAATACCTGTGA -3'
PC-Em	5'- TATGCGGCCGCTGAGTGAGCTGATACC -3'
PN-Fup	5'- CGCGAGATCTGATTACCTGGGAATAGC -3'
PC-Fup	5'- TATAGGATCCAATTTGGTTGCACTACG -3'
PN-Fdown	5'- TATAGTCGACAATTAAGCGAGCGGGAT -3'
PC-Fdown	5'- CACACTCGAGAGGACTTAGCAGAGGTT -3'

## Supplemental References:

- 1 Kelley LA, Sternberg MJ. Protein structure prediction on the Web: a case study using the Phyre server. *Nature protocols* 2009; **4**:363-371.
- 2 Reuter W, Wiegand G, Huber R, Than ME. Structural analysis at 2.2 Å of orthorhombic crystals presents the asymmetry of the allophycocyanin-linker complex, APLC7.8, from phycobilisomes of *Mastigocladus laminosus*. *Proceedings of the National Academy of Sciences of the United States of America* 1999; **96**:1363-1368.
- 3 Nield J, Rizkallah PJ, Barber J, Chayen NE. The 1.45 Å three-dimensional structure of C-phycocyanin from the thermophilic cyanobacterium *Synechococcus elongatus*. *Journal of structural biology* 2003; **141**:149-155.
- 4 Gao X, Zhang N, Wei TD *et al.* Crystal structure of the N-terminal domain of linker L(R) and the assembly of cyanobacterial phycobilisome rods. *Molecular microbiology* 2011; **82**:698-705.
- 5 Umena Y, Kawakami K, Shen JR, Kamiya N. Crystal structure of oxygen-evolving photosystem II at a resolution of 1.9 Å. *Nature* 2011; **473**:55-60.