

## Accession numbers

Sequences were obtained from NCBI and the *Cyanidioschyzon merolae* Genome Project with the exception of cpcT from *Synechococcus* sp. PCC 7002, which was downloaded from [10].

*Synechocystis* sp. PCC 6803: Slr1649 [GenBank:NP\_441787], slr1648

[GenBank:BA000022], ssr2754 [GenBank:BA000022], ssr2755 [Genbank:]; *Crocospaera*

*watsonii*: CwatDRAFT\_4238 [GenBank:ZP\_00515713], CwatDRAFT\_0664

[GenBank:ZP\_00518424], CwatDRAFT\_5720 [GenBank:ZP\_00514725],

CwatDRAFT\_4297 [GenBank:AADV02000007], CwatDRAFT\_5719 (cpeS)

[GenBank:ZP\_00514726], CwatDRAFT\_5721 (cpeR) [GenBank:ZP\_00514724],

CwatDRAFT\_0663 (cpeA) [GenBank:ZP\_00518423], CwatDRAFT\_0665 (cpeY)

[GenBank:ZP\_00518425]; *Nostoc punctiformes* PCC 73102: Npun02004130

[GenBank:ZP\_00109088], Npun02004123 [GenBank:ZP\_00109082], Npun02007740

[GenBank:ZP\_00106171], Npun02004134 [GenBank:ZP\_00345510], Npun02004129 (thrC)

[GenBank:ZP\_00109087], Npun02004122 (cpeS) [GenBank:ZP\_00109081], Npun02004124

(cpeR) [GenBank:ZP\_00109083]; *Anabaena* sp. PCC 7120: all5339 [GenBank:NP\_489379],

alr0647 [GenBank:BAB72605]; *Anabaena variabilis*: Ava\_2579 [GenBank:YP\_323089],

Ava\_4579 [GenBank:YP\_325071]; *Thermosynechococcus elongates* BP-1; tlr2156

[GenBank:NP\_682946], tlr2154 [GenBank:BAC09706], tlr2155 (hemD)

[GenBank:NP\_682945]; *Synechococcus elongates* PCC 6301: syc0738\_d

[GenBank:YP\_171448], syc0764\_d [GenBank:YP\_171474], syc0740\_d (ruvC)

[GenBank:Q5N440], syc0739\_d [GenBank:BAD78929]; *Synechococcus* sp. CC9311:

sync\_0487 [GenBank:ABI46022], sync\_0509 [Genbank: ABI47049], sync\_0484

[Genbank:ABI45763], sync\_0485 (cpcF) [Genbank:ABI45480], sync\_0486 (cpcE)

[Genbank:ABI47764], sync\_0488 (cpcA) [Genbank:ABI45378], sync\_0489 (cpcB)

[Genbank:ABI47294], sync\_0490 (pebB) [Genbank:ABI46568], sync\_0510 (cpeS)

[Genbank:ABI45963], sync\_0511 (cpeD-1) [Genbank:ABI47671], sync\_0512

[Genbank:ABI45417], sync\_0513 (cpeC) [Genbank:ABI45980]; *Synechococcus elongatus* PCC 7942: synpcc7942\_0772 [Genbank:ABB56804], synpcc7942\_0800 [Genbank:ABB56832], synpcc7942\_0799 [Genbank: ABB56831], synpcc7942\_0798 (ruvC) [Genbank:ABB56830]; *Synechococcus* sp. CC9605: syncc9605\_0440 (cpeT) [Genbank: ABB34216], syncc9605\_0419 [Genbank:ABB34195], syncc9605\_0439 (cpeR) [Genbank:ABB34215], syncc9605\_0441 (cpeS) [Genbank:ABB34217], syncc9605\_0421 (cpcB) [Genbank: ABB34197], syncc9605\_0420 (cpcA) [Genbank:ABB34196], syncc9605\_0418 (PBS lyase HEAT-like repeat) [Genbank:ABB34194]; *Synechococcus* sp. CC9902: Syncc9902\_1910 [GenBank:ABB26867], Syncc9902\_1887 [GenBank:ABB26844], Syncc9902\_1908 (cpcB) [GenBank:ABB26865], Syncc9902\_1909 (cpcA) [GenBank:ABB26866], Syncc9902\_1911 (phycocyanobilin lyase alpha subunit) [GenBank:ABB26868], Syncc9902\_1912 (PBS lyase HEAT-like repeat) [GenBank:ABB26869] Syncc9902\_1886 (CpeS) [Genbank:ABB26843]; *Synechococcus* sp. WH8102: SYNW2024 [GenBank:NP\_898115], SYNW2003 [GenBank:NP\_898094], SYNW2022 (rpcB) [GenBank:NP\_898113], SYNW2023 (rpcA) [GenBank:NP\_898114], SYNW2025 (putative phycocyanobilin lyase alpha and betafusion protein) [GenBank:NP\_898116], SYNW1999 (cpeC) [Genbank:NP\_898090], SYNW2000 (mpeD) [Genbank: NP\_898091], SYMW2001 (cpeE) [Genbank: NP\_898092], SYMW2002 (cpeS) [Genbank: NP\_898093], SYNW2004 (cpeR) [Genbank: NP\_898095]; *Trichodesmium erythraeum* IMS101: TeryDRAFT\_1163 [GenBank:ZP\_00674796], TeryDRAFT\_1416 [GenBank:ZP\_00674575], TeryDRAFT\_1162 (cpyX) [GenBank:ZP\_00674794], TeryDRAFT\_1258 (cyp) [GenBank:ZP\_00674795], TeryDRAFT\_1164 (transposase) [GenBank:ZP\_00674797], TeryDRAFT\_1417 (cpeF) [GenBank:ZP\_00674576], TeryDRAFT\_1415 (cpeZ) [GenBank:ZP\_00674574]; *Calothrix* PCC 7601.: cpeT [GenBank:AAK11648], CpeS [GenBank:AF334109], CpeR [GenBank:AAK11649]; *Gloeobacter violaceus* PCC 7421: glr1182 [GenBank:BAC89123], cpeT

[GenBank:BAC89134], glr1538 [GenBank:BAC89479], glr1181 (apcD)  
[GenBank:NP\_924127], glr1183 (cpcB) [GenBank:NP\_926163], glr1191 (ycf58)  
[GenBank:NP\_926164], glr1192 (cpeS) [GenBank:NP\_924138]; *Prochlorococcus marinus*  
MIT9313: PMT1678 [GenBank:NP\_895505], PMT1677 (cpeS) [GenBank:NP\_895504];  
*Prochlorococcus marinus* NATL2A: PMN2A\_1676 [GenBank:YP\_292867], PMN2A\_1677  
(cpeS) [GenBank:YP\_292868]; *Prochlorococcus marinus* CCMP1375: Pro0342  
[GenBank:CAB52704], Pro0343 (cpeS) [GenBank:Pro0343]; *Prochlorococcus marinus*  
MIT9211: P9211\_07167 [GenBank:ZP\_01005965], P9211\_07162 [GenBank:ZP\_01005964];  
*Prochlorococcus marinus* SS120: pro0342 (cpeT) [GenBank:NP\_874736], pro0343 (cpeS)  
[GenBank:NP\_874737], pro0344 [GenBank:NP\_874738], pro0345 (ppeC)  
[GenBank:NP\_874739], pro0346 (pucC) [GenBank:NP\_874740], pro0347  
[GenBank:NP\_874741]; *Guillardia theta*: orf222 [GenBank:NP\_113341]; *Cyanidioschyzon*  
*merolae*: CMK263C; Bacteriophage S-PM2: ORF216 [GenBank:CAF34280]; *Oryza sativa*:  
LOC\_Os11g32160 [GenBank:ABA93997]; *Arabidopsis thaliana*: AT5G51020  
[GenBank:NP\_199915]