

Table S2. Presence of PSHCP homologs in genomes.

Accession number	Locus Tag	Organism name	Length variation
YP_007045635.1	Cyagr_1114	<i>Cyanobium gracile</i> PCC 6307	62 a.a.
EDY37537.1	CPCC7001_416	<i>Cyanobium</i> sp. PCC 7001	MVPD+62 a.a.
YP_002048693.1	PCC_0022	<i>Paulinella chromatophora</i>	MSGVRVLHGAFKPSLAIS+ 62 a.a (89% identity)
YP_001008924.1	A9601_05291	<i>Prochlorococcus marinus</i> str. AS9601	62 a.a.+QK
EEE40790.1	P9202_1566	<i>Prochlorococcus marinus</i> str. MIT 9202	62 a.a.+QK
YP_001550360.1	P9211_04751	<i>Prochlorococcus marinus</i> str. MIT 9211	MSGVQVLHGAFDHPYSSFLVLR+62 a.a.
YP_001483756.1	P9215_05541	<i>Prochlorococcus marinus</i> str. MIT 9215	62 a.a.+QK
YP_001090723.1	P9301_04991	<i>Prochlorococcus marinus</i> str. MIT 9301	62 a.a.+QK
YP_001016697.1	P9303_06811	<i>Prochlorococcus marinus</i> str. MIT 9303	MSGVQVLHGASDGPSCSFLVPR+62 a.a.
YP_396971.1	PMT9312_0474	<i>Prochlorococcus marinus</i> str. MIT 9312	62 a.a.+QK
NP_895135.1	PMT1307	<i>Prochlorococcus marinus</i> str. MIT 9313	62 a.a.
YP_001010854.1	P9515_05381	<i>Prochlorococcus marinus</i> str. MIT 9515	62 a.a.
YP_001014357.1	NATL1_05301	<i>Prochlorococcus marinus</i> str. NATL1A	62 a.a.
YP_292998.1	PMN2A_1807	<i>Prochlorococcus marinus</i> str. NATL2A	62 a.a.
NP_874865.1	Pro0472	<i>Prochlorococcus marinus</i> subsp. marinus str. CCMP1375	62 a.a.
NP_892592.1	PMM0474	<i>Prochlorococcus marinus</i> subsp. pastoris str. CCMP1986	62 a.a.
ACT10292.1	n/a*	<i>Synechococcus</i> sp. ARC-11	62 a.a.
ACT10294.1	n/a*	<i>Synechococcus</i> sp. ARC-21	62 a.a.
EAU70123.1	BL107_10017	<i>Synechococcus</i> sp. BL107	62 a.a.
N/A**	contig08658	<i>Synechococcus</i> sp. CB0101	62 a.a.
N/A**	contig06975	<i>Synechococcus</i> sp. CB0205	62 a.a.
YP_731366.1	sync_2166	<i>Synechococcus</i> sp. CC9311	MSGVQVLHGASDDPLLAFLISS+62 a.a.
YP_380971.1	Syncc9605_0642	<i>Synechococcus</i> sp. CC9605	MFPSTFPVLS+62 a.a.
N/A**	Syn9616DRAFT_scaffold1.1	<i>Synechococcus</i> sp. CC9616	62 a.a.
YP_377719.1	Syncc9902_1717	<i>Synechococcus</i> sp. CC9902	62 a.a.
ACT10299.1	n/a*	<i>Synechococcus</i> sp. KD3a	62 a.a.
ACT10297.1	n/a*	<i>Synechococcus</i> sp. LS0504	62 a.a.
YP_001227921.1	SynRCC307_1665	<i>Synechococcus</i> sp. RCC307	62 a.a., R61→H61, P62→N62
EAU74499.1	RS9916_33367	<i>Synechococcus</i> sp. RS9916	62 a.a.
EAQ69597.1	RS9917_09186	<i>Synechococcus</i> sp. RS9917	62 a.a.
EAQ74693.1	WH5701_13905	<i>Synechococcus</i> sp. WH 5701	MSGVQVLHGALDAPSCSFLVPR+62 a.a.
YP_001225558.1	SynWH7803_1835	<i>Synechococcus</i> sp. WH 7803	62 a.a., I55→N55
EAR19986.1	WH7805_13738	<i>Synechococcus</i> sp. WH 7805	62 a.a.
N/A**	Syn8016_Contig50.1	<i>Synechococcus</i> sp. WH 8016	62 a.a.
NP_897916.1	SYNW1825	<i>Synechococcus</i> sp. WH 8102	62 a.a.
EEX07732.1	SH8109_2473	<i>Synechococcus</i> sp. WH 8109	62 a.a.

*Sequences are not from genome projects.

**Draft genome; BLAST search was performed at the IMG portal.