

ProMIT9313_02 1 -----MRIYCHQDQQAISMLCYIDEILESMDKQPRFGFVNFABTWNGLRAMGVTIGLSTELLTGQISLISQMLG----- 73
SynWH8102_06 1 -----MSDNARFGFVNFABTWNGLRAMGVTIGLSTELLTGQISLISQMLG----- 46
ProMED4_01 1 -----MNEEDNQPRFGFVNFABTWNGLRAMGVTIGLSTELLTGQISLISQMLG----- 48
ProSS120_04 1 -----MSPEDIEPRYGFVNFABTWNGLRAMGVTIGLSTELLTGQISLISQMLG----- 49
SynWH8102_01 1 -----MSDSASKTRDDWYQDAARAISSEFRNRAELNGLRAMGLTIGLSTELLTGQISLISQMLG----- 67
SynWH8102_05 1 -----MAGPHARRALGAETVRKSNPYQLKRGNGRSRVTVLRSIEIPMANSNDNWQFQTAARHILEQLKQAEFRNGRAAMLGVTIGLSTELLTGQISLISQMLG----- 118
Guillardia 1 MINIVLHNFNKIGKNIYGVKNLKTQYSTITDFISDDNNIPKIVLSEKIEISNREKLLKILAEKWKVLEKLEILNKIKFCSKYVSEFINCRFAMEFITTTCLLTELTKGSLISQMLGMLRVLGIIN----- 127
ProMED4_13 1 -----MKEEKPPLKNSDNPSTENLKEETNTNTSSDNEYSKWVDNQGDEVKDFGFGNSAELVNGRAAMIGFLMLLTELTKGSLISQMLG----- 88
ProSS120_06 1 -----MRMEDNLNQKNEEDRFDENLIGSRKEITGTSDAKWVDNDNEVTQVFGFENNAELVNGRAAMIGFLMLLTELTKGSLISQMLG----- 88
ProSS120_03 1 -----MFCNLKKAELVNGRLAMIGVTIGLSTELLTGQISLISQMLG----- 30
P-SSM2_06 1 -----MNQNPFTGNDSSIRTIRSMIDYSHQVWRMAERWNGRLAMIGVTIGLSTELLTGQISLISQMLG----- 52
ProMED4_20 1 -----MKKESKINKLTKKVVQKQELNLWKKGFTECAFVNGRMAIGLIGLITLIVIALISKFFSI----- 60
ProSS120_09 1 -----MNSQSTNKKKESTOSVEKSELNAWKHGFTECAFVNGRMAIGLIGLITLIVIALISKFFSI----- 60
ProMIT9313_01 1 -----MASEPLDNTSAPFVSEELNAWRHGFTECAFVNGRMAIGLIGLITLIVIALISKFFSI----- 67
SynWH8102_08 1 -----MAEQLEKTTGGVAFVGSDELNAWKHGFTECAFVNGRMAIGLIGLITLIVIALISKFFSI----- 59
AnabPCC7120_05 1 -----METRSTDLPKVATEYNGVDRNAFLFGVNPQSEHVNGLRAMIGFLAYLLWDLGYSVLRDVLHLIGY----- 67
AnabPCC7120_06 1 -----MQTRPSTDLPPVAPAYNGVDRNAFLFGVNPQSEHVNGLRAMIGFLAYLLWDLGYSVLRDVLHLIRY----- 67
AnabPCC7120_01 1 -----MELYPTDKTETAYNGKDRNAFLFGVNPQSEHVNGLRAMIGFLAYLLWDLGYSVLRDVLHLVAYNAG----- 67
AnabPCC7120_04 1 -----MTDTTKISASVVEDRNSWRWGFTECAFVNGRMAIGLIGLITLIVIALISKFFSI----- 59
AnabPCC7120_08 1 -----MGNHOSSEVNGRLAMIGFLAAITAEFFSGOGLHFWHIL----- 40
AnabPCC7120_07 1 -----MSGFKNPKSTVTSEFNVAFLFGTSESESNWGRFAMIGFLITLIVIALISKFFSI----- 59
SyncyPCC6803_C 1 -----MNNENSKFCPTAHANWNGRLAMIGFSSAITLIVIALISKFFSI----- 47
Cyanophora 1 -----MQEERNIWNWGFTECAFVNGRMAIGFLAALLTESLIGLITLIVIALISKFFSI----- 49
Arabidopsis 1 -----MSSSPLSSSLFHLPLSTLSTHCHGRQNLFCNRKQOPFVVRRAAKLPEGVIVRAQPKSPQAPLIGTQTAHWNRAACVIGLITLIVIALISKFFSI----- 110
Porphyra 1 -----MKKNFVWFVGFDSAEVNGRMAIGFMAVITLIVIALISKFFSI----- 48
ProSS120_05 1 -----MTSNNPSELKSVSSKSESQENNDENTDVMQTFPATTPIPSFCNSGMAERVNGRMAIGFIALVITLIVIALISKFFSI----- 82
SynWH8102_02 1 -----MTSPSEPPATASVPETSAATSDVPAFCNSGMAERVNGRMAIGFIALVITLIVIALISKFFSI----- 66
ProMIT9313_04 1 -----MTSPKQNLPGDQLPSEQVAFEGSSEVQPPINSATTGDPPTFCNSGMAERVNGRMAIGFIALVITLIVIALISKFFSI----- 77
ProMED4_02 1 -----MTSNQEQNNQEMALEKTNSEBIKIEQSIIEIDRYEFGNSNYSPITNCRAMGLFALITLIVIALISKFFSI----- 88
SyncyPCC6803_D 1 -----MSEELQFNQTPVQEDPKFCENNYAELNCRAMGLFALITLIVIALISKFFSI----- 57
AnabPCC7120_03 1 -----MSQTPQVTPKLEBPKFGENYAEERLNGRAAMIGFLIMVIEYATNOCGLSLWELHK----- 56
ProMIT9313_03 1 -----MLEPTIIPQRKPRYCFHSHNKEKLNCRAMGLFIALVITLIVIALISKFFSI----- 50
SynWH8102_03 1 -----MLEPTIIPQRKPRYCFHSHNKEKLNCRAMGLFIALVITLIVIALISKFFSI----- 50
ProSS120_02 1 -----MIDPKIIPERKLPSPGHNHTENLNGRMAIGFIALVITLIVIALISKFFSI----- 50
ProMED4_03 1 -----MIKPDIVPKRKLPRYCFHFNKLNCRAMGLFIALVITLIVIALISKFFSI----- 50
SynWH8102_04 1 -----MAQTPSTDAPIRGATVITEDGRLNAFASERMOVVEAEOGWFHEBAEKLNGRMAIGFIALVITLIVIALISKFFSI----- 84
SynPCC7942_A 1 -----MRSGRVDFEFCRQNFATIEQVVAEADASNCEHEDRAEKLNGRMAIGFIALVITLIVIALISKFFSI----- 72
SyncyPCC6803_A 1 -----MTTRGFLDQDNRNLNFAIEPEVYVDSS-VQAGWTKYAEKNGRMAIGFASLITLIVIALISKFFSI----- 70
SyncyPCC6803_B 1 -----MTRGFLDQDNRNLNFAIEPEVYVDSS-VQAGWTKYAEKNGRMAIGFASLITLIVIALISKFFSI----- 70
AnabPCC7120_02 1 -----MRTNNAIVDDQGLMNFATIEPKVYVDEQDRTGTFYVAELVNGRMAIGFIALVITLIVIALISKFFSI----- 72
ProMED4_04 1 -----MTPBAERNGMAAMLGFVAAGVAVTTGQIIPGVF----- 35
P-SSP7_01 1 -----MKTLDLTLLENYAYEPIQLLPPKRLMSBBAERNGMAAMLGFVAAGVAVTTGQIIPGVF----- 63
ProMED4_12 1 -----MTPBAERNGMAAMLGFVAAGVAVTTGQIIPGVF----- 35
ProMED4_06 1 -----MTPBAERNGMAAMLGFVAAGVAVTTGQIIPGVF----- 35
ProMED4_16 1 -----MTPBAERNGMAAMLGFVAAGVAVTTGQIIPGVF----- 35
ProSS120_08 1 -----MTPBAERNGMAAMLGFVAAGVAVTTGQIIPGVF----- 35
ProSS120_11 1 -----MTPBAERNGMAAMLGFVAAGVAVTTGQIIPGVF----- 35
P-SSM2_03 1 -----MTPBAERNGMAAMLGFVAAGVAVTTGQIIPGVF----- 35
P-SSM4_01 1 -----MTPBAERNGMAAMLGFVAAGVAVTTGQIIPGVF----- 35
ProSS120_12 1 -----MTPBAERNGMAAMLGFVAAGVAVTTGQIIPGVF----- 35
ProMED4_08 1 -----MSPLAVFLILVSLTALLVASLTKQFQENLIYSNKNQMTNSNTKTKTIEKEKVVAEVNLNGRMAIGFIAAGVAVTTGQIIPGVF----- 86
ProMED4_18 1 -----MSPLAVFLILVSLTALLVASLTKQFQENLIYSNKNQMTNSNTKTKTIEKEKVVAEVNLNGRMAIGFIAAGVAVTTGQIIPGVF----- 86
ProMED4_21 1 -----MAKIKSVEKEKIVAEKLNCRMAIGFIAAGVAVTTGQIIPGVF----- 44
ProMED4_05 1 -----MNSKRVKVLTKTVEKEKVVAEKLNCRMAIGFIAAGVAVTTGQIIPGVF----- 51
P-SSM4_03 1 -----MTTPKPIEKEKIVAEKLNCRMAIGFIAAGVAVTTGQIIPGVF----- 44
ProMED4_11 1 -----MKNNEPKLVEKEKIVAEKLNCRMAIGFIAAGVAVTTGQIIPGVF----- 46
ProMIT9313_08 1 -----MKKTPTNVRVENKQLTAERVNGRMAIGFIAAGVAVTTGQIIPGVF----- 47
ProMED4_10 1 -----MEFVKKFVTEKAEKNGRMAIGFIAAGVAVTTGQIIPGVF----- 42
ProMED4_07 1 -----MSNSSYTTESGGRONMFPSETRPYIDESVSYDQYFQNAEKVNGRMAIGFVALLGAVVTTGQIIPGVF----- 69
ProMED4_17 1 -----MSNSSYTTESGGRONMFPSETRPYIDESVSYDQYFQNAEKVNGRMAIGFVALLGAVVTTGQIIPGVF----- 68
ProMED4_14 1 -----MANSQVTTESGGRONMFPSETRPYIDESVSYDQYFQNAEKVNGRMAIGFVALLGAVVTTGQIIPGVF----- 69
ProSS120_07 1 -----MTSSAQAIITTESGRONMFPVBAQPOLVEN--YSGLIEDAKRNGRMAIGFIALGAVLTTGQIIPGVF----- 69
P-SSM2_01 1 -----MTSSSTTEKYVTEYKQNMFGAEVTPWVDENDNYEGYALNAEKVNGRMAIGFIALGAVLTTGQIIPGVF----- 72
ProMIT9313_09 1 -----MNEENAEVNGRMAIGFIALGAVLTTGQIIPGVF----- 35
ProMIT9313_06 1 -----MTSSTNVITEDGGRONMYASEER--MOIDPEYTAESKEAELNCRMAIGFIAAGVAVTTGQIIPGVF----- 67
P-SSM4_04 1 -----KTDLIEDVATQAEVNGRMAIGFIAAGVAVTTGQIIPGVF----- 68
ProSS120_10 1 -----MKTSTSTKVTESKVLAEKLNCRMAIGFIAAGVAVTTGQIIPGVF----- 47
P-SSM2_05 1 -----MTKQTKTEDKVDVFAEAKWNGRMAIGFIAAGVAVTTGQIIPGVF----- 47
P-SSM4_02 1 -----MDEKAEKLNCRMAIGFIAAGVAVTTGQIIPGVF----- 36
ProMIT9313_05 1 -----MPSDFLKEITINDCMFNKAEVNLNGRMAIGFIALGAVLTTGQIIPGVF----- 48
ProMIT9313_07 1 -----MTIADFMSNKAETVNGRMAIGFIALGAVLTTGQIIPGVF----- 41
ProSS120_13 1 -----MDQANVSLVDIAHGRFAMIGFIALGAVLTTGQIIPGVF----- 39
P-SSM2_04 1 -----MNNKQIFLRANGRAAMIGFIALGAVLTTGQIIPGVF----- 37
ProMED4_09 1 -----MNSKPNYQNAERTNCRMAIGFIALGAVLTTGQIIPGVF----- 42
ProMED4_19 1 -----MNSKPNYQNAERTNCRMAIGFIALGAVLTTGQIIPGVF----- 42
ProMED4_22 1 -----MSPLTGFTIVVIAITLQFTLYTIKRLQEPDLPNLFDSQKSPKMNRRKKSFKWNAELVNGRMAIGFIALGAVLTTGQIIPGVF----- 84
P-SSM2_02 1 -----MNYWKNAEVNGRMAIGFIAAGVAVTTGQIIPGVF----- 37
ProMED4_15 1 -----MIEKKGDNIRSENFYDPSNYLLDQNTPEETLPEEQIFNTKKEFWPNSYWFIAERVNGRMAIGFIAAGVAVTTGQIIPGVF----- 84
ProSS120_01 1 -----MNNYWTIAERVNGRMAIGFIALGAVLTTGQIIPGVF----- 39
SynWH8102_07 1 -----VFAAMTRPAFOYEQPERFGEISLTTARPWKKSALTEVERLNGRAAMVGFSAVLCGLITGQIIPGVF----- 77

Clustal Consen 1

AE--NGR-AMIGF TGQIIPGIF