

Spinach 1 MAATTTTMMGMATTFVFKPQAPPMAALPSNTGRSLFGLKT-GSRGGR-MTMAAYKVTLEVTPTGN--VEFCPPDDVYILDAAEAEAGIDLPSYCRAGSCSS 96
 SynWH8102_1 1 -----MASYKVTLE---GG--SIFECDDVYILDAAEAEAGIDLPSYCRAGACST 44
 SynPCC7002 1 -----MATYKVTLLTPDGE--VSYDAPDDEYILDAAGDAGYDLPAASCRAGACST 47
 SynPCC6803_1 1 -----MASYKVTLLTPDGE--SIFECDDVYILDAAEAEAGIDLPSYCRAGACST 47
 Arabidopsis 1 MASTALSSAIVSTSFLLRQQTPISLRSLPANTQSLFGLKSSSTARGGVMTAMATYKVKHETPEGE--QEVCEDEYVYILDAAEAEAGIDLPSYCRAGSCSS 98
 Chlamydomonas 1 -----MAMAMRSTFAARVGAKEPAVRGAPASRMSCMAYKVTLEKTPSG--DKTIECPADTYILDAAEAEAGIDLPSYCRAGACSS 76
 AnaPCC7120_1 1 -----MASYKVTLLNKKODITTEIIEEETITLDGAENGIELPFSCHSKSCSS 49
 AnaPCC7120_2 1 -----MATYKVTLLNEAEGTKHEIEVDPDEYILDAAEAEAGIDLPSYCRAGACST 49
 ProSS120_1 1 -----MASYKVTLVSESEGLNQTIEVPDDQYILDAAEAEAGIDLPSYCRAGACST 49
 ProMED4_1 1 -----MASYKVTLLVSESEGLNSTIEVPDDQYILDAAEAEAGIDLPSYCRAGACST 49
 SynWH8102_2 1 -----MASYKVTLVSESEGLNKTIEVPDDQYILDAAEAEAGIDLPSYCRAGACST 49
 ProMIT9313_1 1 -----MASYKVTLLVSESEGLNKTIEVPDDQYILDAAEAEAGIDLPSYCRAGACST 49
 Cyanothece 1 -----MATYKVTLLNECEGINATIDVPEDEYILDAAEAEAGIDLPSYCRAGACST 49
 Cyanophora 1 -----MAVYKVTLLICEEQGLDITTECPDDEYILDAAEAEAGIDLPSYCRAGACST 49
 Syn elongatus 1 -----MATYKVTLLVRPDGS--ETITDVPDEYILDAAEAEAGIDLPSYCRAGACST 48
 P-SSM2 1 -----MAYSTITRSPDGA--EEVVOCEDEYILDAAEAEAGIDLPSYCRAGACSA 47
 SynPCC6803_2 1 -----MGLIYSWNLVNPATGSDVTEVAEDELILEAAENQGLDLPYCRAGACSA 50
 SynWH8102_3 1 -----MGTSHRITLHWRQEQRTITLHDVPEGEYILDAAEAEAGIDLPSYCRAGACST 50
 ProMIT9313_2 1 -----MTSLHKITLHHRQAGRTITFDVDPGEYILDAAEAEAGIDLPSYCRAGACST 50
 ProSS120_2 1 -----MHSKRTIVRLRDNRIISKETPEGSEILRKEEEDGVLFPSCRNGCCCT 49
 ProMED4_2 1 -----MKKTKVITITNKETGKIYQENISDQYILKEPEKKGIRLPFSCRNGCCCT 50
 SynPCC6803_3 1 -----MSRSHRVLHHRQNEKDYSVIYDRIYHQADQGFELPFSCRNGACSA 50
 AnaPCC7120_3 1 -----MSEHTVYKVRDRATGQYTLKVPEDRYILDAAEAEAGIDLPSYCRAGACT 50
 SynWH8102_4 1 -----MSEVATYTVRAEPEGTHSFSRADQTVLNAABAAGVTLFPSSCCSGVCTT 50
 ProMED4_3 1 -----MSEYNIKVLEKKTYVFLCPEDQITLSAAKANGIDLPSYCRAGACSA 47
 SynPCC6803_4 1 -----MVNTYTAIEIQHGGQTYTISVPEDKTVLGAADDEGICLFTSCGAGVCTT 48
 AnaPCC7120_4 1 -----MSKTYTVEILHQKTHLQVPEKDTILSVADEQGLDLPSSCHAGVCTT 48
 Clustal Consen 1 :: * : * * : * : 9

Spinach 97 CAGKLTGSLNDDQ--SFLDDDDQIDEGVLTCAAYPVSQVITIEH--KEEELTA----- 147
 SynWH8102_1 45 CAGKVLSGSVDQDDQ--SFLDDDDQIGGGFALLCVSYPTSDCSIKAN--AEDDL----- 93
 SynPCC7002 48 CAGKIYSGTVDQSEEQ--SFLDDDDQIEAGVVLTCVAYPTSDVTIETH--KEEELY----- 97
 SynPCC6803_1 48 CAGKITAGSVDQSDQ--SFLDDDDQIEAGVVLTCVAYPTSDCTIETH--KEEELY----- 97
 Arabidopsis 99 CAGKVVSGSIDQSDQ--SFLDDDDQMSSEGVVLTCAVYPTSDVVIETH--KEEAIM----- 148
 Chlamydomonas 77 CAGKVAAGTVDQSDQ--SFLDDDDQMGNGFVLTCAVYPTSDCTIOTH--QEEELY----- 126
 AnaPCC7120_1 50 CAGKVVSGSVDQSDQ--SFLDDDDQMGKGFALLCVTYPRSNCTIKTH--QEPYLA----- 99
 AnaPCC7120_2 50 CAGKLVSGTVDQSDQ--SFLDDDDQIEAGVVLTCVAYPTSDVVIOTH--KEEELY----- 99
 ProSS120_1 50 CAGKITSGSVDQSDQ--SFLDDDDQIEAGFVLTCAVYPTSDVTITTH--AEEELY----- 99
 ProMED4_1 50 CAGKITSGTVDQSDQ--SFLDDDDQIEAGFVLTCAVYPTSDVTITTH--AEEELY----- 99
 SynWH8102_2 50 CAGKITAGTVDQSDQ--SFLDDDDQIEAGFVLTCAVYPTSDCTIKTH--AEEELY----- 99
 ProMIT9313_1 50 CAGKLTGGSVDQSDQ--SFLDDDDQIEAGFVLTCAVYPTSDCTIKTH--AEEELY----- 99
 Cyanothece 50 CAGKLVGTVDQSDQ--SFLDDDDQVAGFVLTCAVYPTSDCTIETH--QEEELY----- 99
 Cyanophora 50 CAGKVVSGTVDQSDQ--SFLDDDDQVLAAGVLTCAVYPTSDCTIKTH--QEEELY----- 99
 Syn elongatus 49 CAGKLVGEGVDQSDQ--SFLDDDDQIEKGFVLTCAVYPTSDCTIKTN--QEEELY----- 98
 P-SSM2 48 CAGKLVGEGVNNDEEQ--SFLDDDDQIEKGFVLTCAVYPTSDCTIKTE--QEDNLD----- 97
 SynPCC6803_2 51 CAGRLLEGTVHEHDKGSDFLKPEELAAAGVLLCAAYATSDCKILTH--QEEALFG----- 103
 SynWH8102_3 51 CAVRVKQGQLDQREA--MGLSHELRQCGYLLCVARAIGFLEAETQ--DEDEVYDLOFGRHFRGKVTAGLPLDEE-- 122
 ProMIT9313_2 51 CAVRIISGEMDQTAG--IGLSKEMRDKGYGLLCAVARATSELEVETQ--DEDEVYEMQFGKDLGSIKSKAGSPFDL-- 121
 ProSS120_2 50 CAVRIISGTHDQHDG--IGLSKOMQENGYGLLCAKAVITGFADLETQ--DEDEVYELQFGRYLGSIKNRTPGNPFDM-- 120
 ProMED4_2 51 CAVKILSGKLDQPEA--MGLVSDLLKDKGYALLCVAVIETIEVETT--YYDEVYDLOFGYFGKGRKTRKAPWFEED 124
 SynPCC6803_3 51 CAVRVVSGQIHOPEA--MGLSPDLRQGYALLCVVYQSDLEVETQ--DEDEVYELQFGRYFAGRVRGLPLDED-- 122
 AnaPCC7120_3 51 CAVRVVSGDIYOPEA--VGLSLELRQGYALLCVVYARSLEVETQ--DEDEVYELQFGRYFAKGRVKAGLPLDEE-- 122
 SynWH8102_4 51 CAAVITSDGVEQEDA--MGLVKELOQQGYALLCVAVPRADLTAKAG--QEDALYEAQFGQYQK----- 109
 ProMED4_3 48 CASMVLDSVQEDA--MGLNDDLKQKGFALLCVAVYKSDLHETIIGDEVEDNLYNNOFGKYQI----- 108
 SynPCC6803_4 49 CAALITEGTAEADG--MGLVSAELQAGGYALLCVAVYPRDLKITE--REDEVYQROFGQGG----- 106
 AnaPCC7120_4 49 CAGQIITGTVDQSDG--MGLVSPLELQQGYALLCVAVYPRDLKITE--REDEVYQROFGK----- 104
 Clustal Consen 10 * : * : : * * * : : : 19