FIGURE S3

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                        10        20        30        40        50        60
T. elongatus      MTNLPEHQSSPTEQSSAEVKKIPTMIEGFDDISHGGLPQGRTTLVSGTSGTGKTLFAVQF
Synechococcus     -MTSAEMTSPNNNSEHQAIAKMRTMIEGFDDISHGGLPIGRSTLVSGTSGTGKTLFSIQF
Synechocystis     MNLPIVNERNRPDVPRKGVQKIRTVIEGFDEITHGGLPIGRTTLVSGTSGTGKTLLAVQF
WH 8102           -----MQFPPASGSTQMQVQKLPTGIEGFDDVCQGGLPIGRSTLISGTSGTGKTVFSLHF
A.variabilis      --MSEKEQPEQQNTSGNGVEKIRTMIEGFDDISHGGLPVGRTTLVSGTSGTGKTLLSLQF
Anabaena          --MSEKEQQEQQNTSGNGVEKIRTMIEGFDDISHGGLPVGRTTLVSGTSGTGKTLLSLQF
Prochlorococcus   -----MKDKKISKSIKMQVQKIPTGIEGFDDVCRGGLPAARSTLVSGTSGTGKTVFSLQY

                        70        80        90       100       110       120
T. elongatus      LYNGITIFNEPGIFVTFEESPQDIIKNALSFGWNLQSLIDQGKLFILDASPDPDGQEVAG
Synechococcus     LYNGIIEFDEPGVFVTFEETPQDIIKNARSFGWDLAKLVDEGKLFILDASPDPEGQEVVG
Synechocystis     LYQGIHHFDYPGLFITFEESPSDIIENAYSFGWDLQQLIDDGKLFILDASPDPEGQEVVG
WH 8102           LHNGIKHFDEPGIFVTFEESPLDILRNAASFGWNLQEMVEQDKLFILDASPDPDGQDVAG
A.variabilis      LFNGISFFDEPGVFVTFEESPSDIIKNAHIFGWNLQRLINEGKLFILDASPDPEGQDIVG
Anabaena          LFNGISFFDEPGVFVTFEESPSDIIKNAHIFGWNLQRLINEGKLFILDASPDPEGQDIVG
Prochlorococcus   LHHGICNFDEPGIFITFEESPLDIIRNAASFGWDLQKLIDQNKLFILDASPDPDGQDVAG

                       130       140       150       160       170       180
T. elongatus      DFDLSALIERIQYAIRKYKATRVSIDSVTAVFQQYDAASVVRREIFRLAFRLKQLGVTTI
Synechococcus     GFDLSALIERINYAIQKYRARRVSIDSVTSVFQQYDASSVVRRELFRLVARLKQIGATTV
Synechocystis     TFDLSALIERIQYAVRKYKAKLVSIDSVTAVFQQYDAASVVRREIFRLVARLKQLQVTSI
WH 8102           SFDLSGLIERINYAIRKYKAKRVAIDSITAVFQQYDAVFVVRREIFRLIARLKEIGVTTV
A.variabilis      NFDLSALIERLQYAIRKYKAKRVSIDSITAVFQQYEAVGVVRREIFRLVARLKQLNVTTI
Anabaena          NFDLSALIERLQYAIRKYKAKRVSIDSITAVFQQYEAVGVVRREIFRLVARLKQLNVTTI
Prochlorococcus   NFDLSGLIERISYAIRKYKAKRVAIDSITAVFQQYDAIYVVRREIFRLIARLKEIGVTTV

                       190       200       210       220       230       240
T. elongatus      MTTERVDEYGPVARFGVEEFVSDNVVILRNVLEGERRRRTVEILKLRGTTHMKGEYPFTI
Synechococcus     MTTERIEEYGPIARYGVEEFVSDNVVILRNVLEGERRRRTLEILKLRGTSHMKGEYPFTI
Synechocystis     MTTERVEEYGPIARFGVEEFVSDNVVVLRNVLEGERRRRTVEILKLRGTTHMKGEYPFTI
WH 8102           MTTERIDEYGPIARYGVEEFVSDNVVILRNVLEGERRRRTVEILKLRGTTHMKGEFPFTM
A.variabilis      ITTERSEEYGPVASFGVEEFVSDNVVIARNVLEGERRRRTIEILKLRGTTHMKGEYPFTI
Anabaena          ITTERSEEYGPVASFGVEEFVSDNVVIARNVLEGERRRRTIEILKLRGTTHMKGEYPFTI
Prochlorococcus   MTTERVDDYGPIARYGVEEFVSDNVVLLRNVLEAEKRRRTLEVLKLRGTVHMKGEFPFTM

                                N-terminal Domain ←──┼──→ C-terminal Domain
                       250       260       270       280       290       300
T. elongatus      N-NGINIFPLGAMRLTQRSSNVRVSSGVKTLDEMCGGGFFKDSIILATGATGTGKTLLVS
Synechococcus     TDHGINIFPLGAMRLTQRSSNVRVSSGVVRLDEMCGGGFFKDSIILATGATGTGKTLLVS
Synechocystis     THDGINIFPLGAMRLTQRSSNARISSGVQTLDEMCGGGFFKDSIILATGATGTGKTLLVS
WH 8102           GTHGISIFPLGAMRLTQRSSNVRVSSGVPRLDEMCGGGFFKDSIILATGATGTGKTLLVS
A.variabilis      TNDGVNIFPLGAMRLTQRSSNVRVSSGVKTLDGMCGGGFFKDSIILATGATGTGKTLLVS
Anabaena          TNDGVNIFPLGAMRLTQRSSNVRVSSGVKTLDGMCGGGFFKDSIILATGATGTGKTLLVS
Prochlorococcus   GDDGIIVFALGAMRLTQRSSNIRISSGVKDLDEMCGGGYFQDSIILATGATGTGKTMLVS

                       310       320       330       340       350       360
T. elongatus      KFLETGCQQGERALLFAYEESRAQLSRNASSWGIDFEELERRGLLRIICAYPESAGLEDH
Synechococcus     RFVENACANKERAILFAYEESRAQLLRNAYSWGMDFEEMERQNLLKIVCAYPESAGLEDH
Synechocystis     KFLQEGCRQRERAILFAYEESRAQLSRNASSWGIDFEEMEHKGLLKLLCTYPESAGLEDH
WH 8102           KFIEDACRNKERAILFAYEESRAQLLRNGTSWGIDFEQMEQDGLLKIICAYPESTGLEDH
A.variabilis      KFLQNGCVNNERAILFAYEESRAQLSRNAYSWGIDFEELESQGLLKIICTYPESTGLEDH
Anabaena          KFLQNGCVNNERAILFAYEESRAQLSRNAYSWGIDFEELESQGLLKIICTYPESTGLEDH
Prochlorococcus   KFIEDAYNNKERAILFAYEESRAQLNRNATSWGIDFEKMENEGLLKIICAYPESTGLEDH

                       370       380       390       400       410       420
T. elongatus      LQIIKSEIADFKPSRVAIDSLSALARGVSNNAFRQFVIGVTGFAKQEEITGFFTNTTDQF
Synechococcus     LQIIKSEINDFKPARIAIDSLSALARGVSNNAFRQFVIGVTGYAKQEEITGLFTNTSDQF
Synechocystis     LQMIKSEISEFKPSRIAIDSLSALARGVTNNAFRQFVIGVTGYAKQEEITGFFTNTTDQF
WH 8102           LQIIKTDIGQFKPSRMAIDSLSALARGVSHNAFRQFVIGVTGYAKQEEIAGFFTNTSEEF
A.variabilis      LQIIKSEIAYFKPARIAIDSLSALARGVSNNAFRQFVIGVTGYAKQEEITGFFTNTTDQF
Anabaena          LQIIKSEIAYFKPARIAIDSLSALARGVSNNAFRQFVIGVTGYAKQEEITGFFTNTTDQF
Prochlorococcus   LQIIKSQINEFKPKRLAIDSLSALARGVSLNAFRQFVIGVTGYSKQEEIAGFFTNTAEEF

                       430       440       450       460       470       480
T. elongatus      MGSNSITESHISTITDTILLLQYVEIRGEMSRAINVFKMRGSWHDKGIREYVITEKGAEI
Synechococcus     MGAHSITDSHISTITDTIILLQYVEIRGEMSRAINVFKMRGSWHDKAIREFMISDKGPDI
Synechocystis     MGAHSITESHISTITDTILMLQYVEIRGEMSRALNVFKMRGSWHDKGIREYSISHDGPDI
WH 8102           MGSHSITDSHISTITDTILMLQYVEIRGEMARALNVFKMRGSWHDKGIREFVITGNGPQI
A.variabilis      MGSHSITDSHISTITDTILMLQYVEIRGEMSRAINVFKMRGSWHDKGIREYNITADGPEI
Anabaena          MGSHSITDSHISTITDTILMLQYVEIRGEMSRAINVFKMRGSWHDKGIREYNITADGPEI
Prochlorococcus   MGSHSITDSHISTITDTILLLQYVEIKGEMARAINVFKMRGSWHDKRIREYIITGQGPEI

                       490       500       510       520
T. elongatus      RDSFRNFEGIISGTPTRISVDEKTELARIAKGMQDLESE--
Synechococcus     KDSFRNFERIISGSPTRITVDEKSELSRIVRGVQEKGPES-
Synechocystis     RDSFRNYERIISGSPTRISVDEKSELSRIVRGVKDKTAE--
WH 8102           KDSFSNFERIISGVPHRVTTDERSELSRIARGVSSED----
A.variabilis      QDSFRNYERIVSGSPTRVSIDEKAELSRIVRRFEDKQGSDS
Anabaena          QDSFRNYERIVSGSPTRVSIDEKAELSRIVRRFEDKQGSDS
Prochlorococcus   KDSFSNFEQIFSGAPHRVISDQ--SIPNVFKGIEKN-----
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