

Supplemental Material to:

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PPR proteins of green algae

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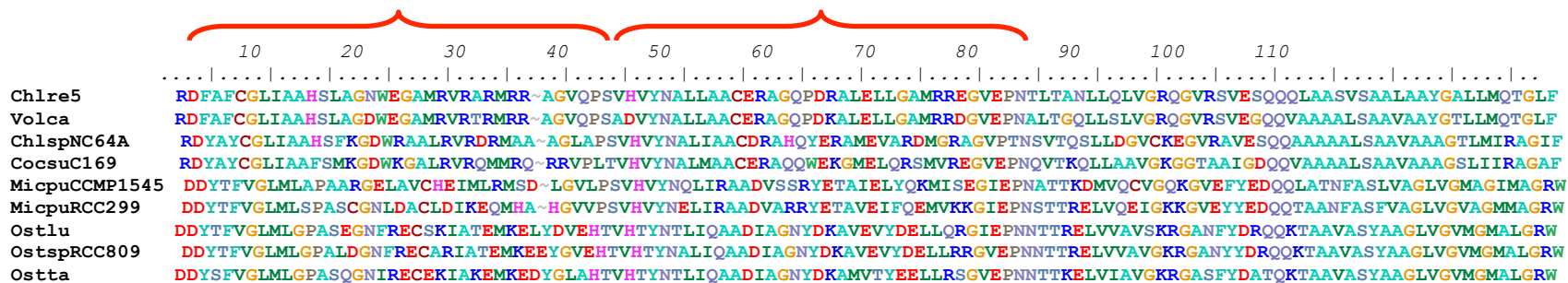
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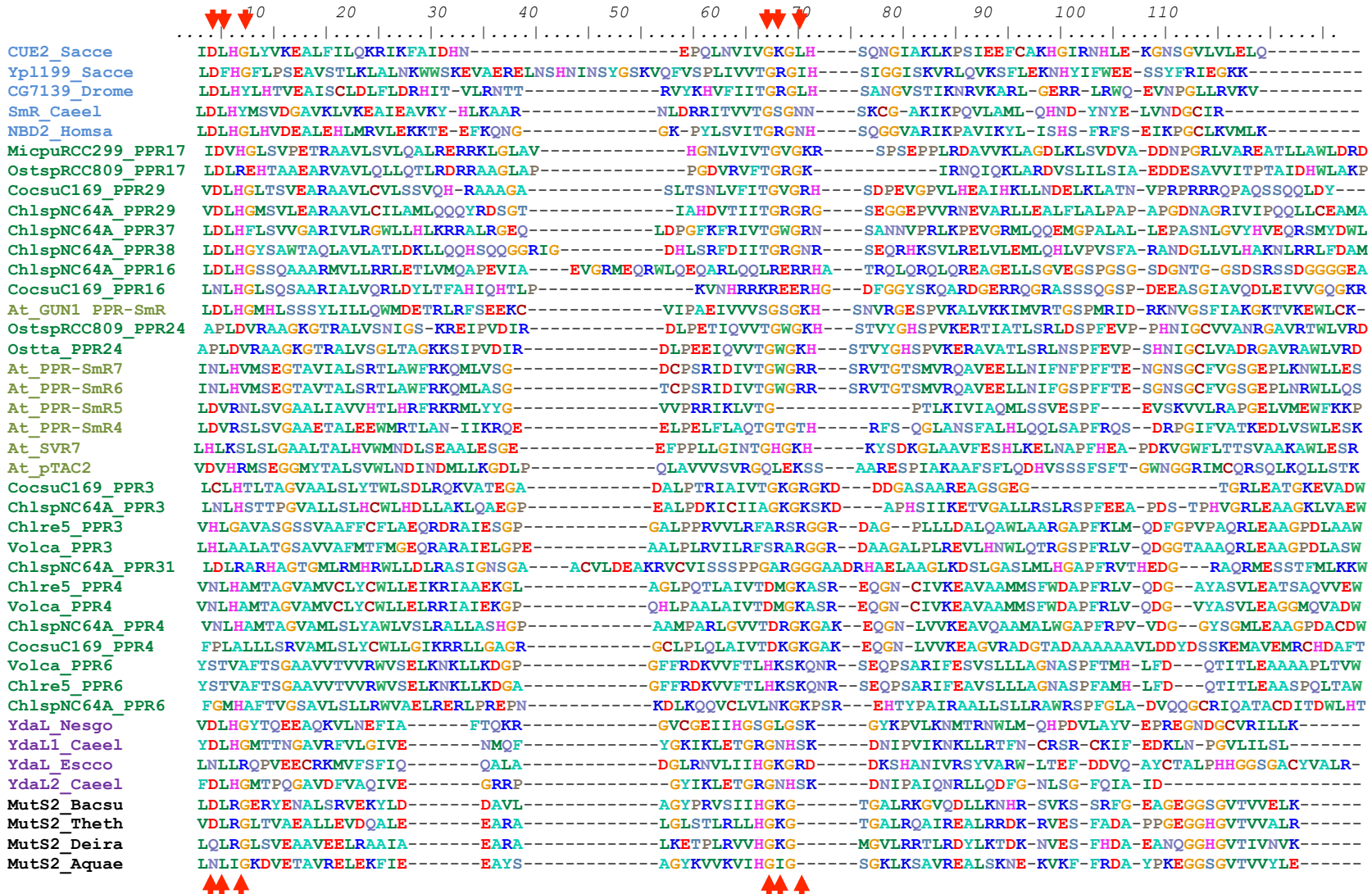
Supplemental Files:

- 1. 2012RNABIOL0232-T1: Supplemental Table 1**

Supplemental Figure 1: Multiple sequence alignment of the MCA1-C domain, after the last two PPR repeats of MCA1. The repeats are indicated by brackets. Note perfect conservation of the length of the MCA1-C domain



Supplemental Figure 2: Alignment of the SmR and SmR-like domains of PPR-SmR and PPR-cyclin proteins (titles in dark and light green for Chlorophyta and for Arabidopsis, respectively), along with representative SmR domains from subfamilies 1 (titles in black), 2 (titles in blue) and 3 (titles in purple). The residues mentioned in the text are marked by arrows. Species names are abbreviated as such: Sacce: *Saccharomyces cerevisiae*; Drome: *Drosophila melanogaster*; Caeel: *Caenorhabditis elegans*; Homsa: *Homo sapiens*; Nesgo: *Neisseria gonorrhoeae*; Escco: *Escherichia coli*; Bacsu: *Bacillus subtilis*; Theth: *Thermus thermophilus*; Deira: *Deinococcus radiodurans*; Aquae: *Aquifex aeolicus*



Supplemental Figure 3: alignment of Methyl-transferase_4 domains in Trm8, TrmB and PPR-MT4 proteins.

Residues deemed important for binding the AdoMet substrate are indicated by **red arrowheads**, and for catalysis by **blue arrowheads**; aromatic residues which in the Bacillus enzyme stack with the guanine ring are indicated by **green arrowheads**; the basic region believed to bind the D-arm of the tRNA is **bracketted**.

Color code in sequence names is as follows: **cyan** for Amoebozoa (Enthi: *Entamoeba histolytica*; Dicdi: *Dictyostelium discoideum*; Plopa: *Polysphondylium pallidum*); **black** for secondary endosymbionts (Guith: *Guillardia theta*; Cryne: *Cryptococcus neoformans*; Perma: *Perkinsus marinus*; Phatr: *Phaeodactylum tricornutum*; Thaoc: *Thalassiosira oceanica*); **green** for Opisthokonts (Cael: *Caenorhabditis elegans*; Sacce: *Saccharomyces cerevisiae*); **pink** for Viridiplantae (Arath: *Arabidopsis thaliana*; Phypa: *Physcomitrella patens*; Chlvu: *Chlorella variabilis*; MicpuRCC299: *Micromonas sp. RCC299*; Ostta: *Ostreococcus tauri*; Batpr: *Bathycoccus prasinos*; Volca: *Volvox carteri*; Cocsu: *Coccomyxa subellipsoidea C-169*); **dark green** for bacteria other than Chlamydiae; **blue** for Chlamydiae; the Archaeal sequence used as an outgroup is **highlighted** (Thesp: *Thermococcus sp. 4557*)

Enthi_Trm8 -----GIKPFHRVHAHRNPLADSPSTNPITPQSLDVKLYFPN-----GKPA--EMLDIGCGWGGVLREVG-MIQEKN-----VLGMEIRDPAVQYGLEKIQAAREKN
Dicdi_Trm8 -----AIKPYHRIKAHANPADSYNFFYPTGPEYDWTKNYPQQAMN-----EKVV--E1ADVGCYGGLLISLSSLPFERL-----SVGMELRDKVQYVEERIDKLRREKH
Flopa_Trm8 -----PIKPYHRIKAHANPQSDSNFDYVPSVPCYDWSKHYNKTLSEQP-----EKRV--TIADVGCYGGLLVGLASTFPDRL-----ALGLEIRDKVVQYVEDRIEKLKRDN
Guith_Trm8 -----VKRRKFRSRAHANPLADPQFEYVPSVPCVDSVLYPELCEGAETM-----PRPV--EYADVGCYGGLLVGLERFPDRI-----SIGVEIREKVASVYDQRIKALRQAN
Cryne_Trm8 -----VPQKRFYRQRAHANVFDHIELEYPKRPELMDWSTHYPAYFSQPNEDG---TITPGEKVV--EWADVGCYGGLLMALAPLFPPEKL-----MLGMEIRTSVTKVYDRIAATQAEQ
Caeel_Trm8 G-----LPQKKHYRQRAHNSPHSDHDIEYPLTFNMDWTKYYGDYTKG-----RQV--DFADIGCGYGGLLMRLSPKYPDNL-----MIGMEIRVKVSDYVNEKIQALRKH
Sacce_Trm8 GQ-----KIDLPKKRYRQRAHNSPFDHLEXYVPSVPCVDSVLYPELCEGAETM-----MTKKV--TIADVGCYGGLLMRLSPKYPDNL-----ILGMEIRVQVTNYVEDRIEALRNN
Arath_Trm8_1 -----LPRKRFYRARAHSNPLSDSHFPIIPISPAHVDSLHFKFVEADNKF-----IKKV--EYADVGCYGGLLISLATLFPDNL-----MIGMEIRVQVTNYVEDRIEALRNN
Phypa_Trm8_1 AOVKAGKQKGLPKKRFYRARAHSNPLSDCQFSVPTTPEFDWSESPFEFFAQEBTT-----DLKV--RFADIGCGYGGLLVQMSPLFPKTL-----MVGMEIRLDKVEYVKEKRIALRQ
Chlvu_Trm8_1 -----PKQMYRRAHNSNPLNDAHFVPLSDHLEXYVPSVPCVDSVLYPELCEGAETM-----V-----PPQVQ--EYADVGCYGGLLVQMSPLFPKTL-----IMAMEIRLDKVEYVKEKRIALRQ
MicpuRCC299_Trm8_1 RVREKGAHLDRPWSLTYLRNKGVTQRAKEAWRTLWQYQIDVQTHAGGGGPPRLDFREVFADREAP-----FALVEVGCYGGLLVQMSPLFPKTL-----FVGVVEVHPGKGAALQIQRREDEL
Ostta_Trm8_1 QKENYRELFDAHGIRFDARPTMRGSGDDGSDTSDEASRMKRYETLDWDRAPFGGGGGG-----GEPRR--RVLELGCGLGDLNLIAAAEFETVY-----FLGVEVHRPGVATALGEIEARGLT
Ostta_Trm8_2 ATSTTLVNVTSGKKKNINRRMKMTNPLAAPPYQTPKTLDEAHWAVFVGG-----DALKR--LIVDIGTAKGGFIKALAREADACTRAKSIEYNLVGVVEIYEPVIAANAWQVQNRGS
Arath_Trm8_2 -----EEVGHVIRIQHVNPLS--SSFSKPAVPP--VWDEVYKD-----PSLP--LMVDIGSGSGRFLMVAQANKVRESR-----NYLGLEIRQLVKRANFVWNLGLSN
MicpuRCC299_Trm8_2 -----QKVGGRVVRQHVNLK--ASLQSQAPVP--AWTDVYAS-----TARP--LIVDIGCGGRFLMMAKVPET-----NFLGVDIRAPLVERGNKWEYAGVVD
Chlvu_Trm8_2 -----AFAGGVRVVRQHVNLK--KELQVPTPEP--VWEEVYEQ-----PGR--MVLDIGCGYGGLLVQMSPLFPKTL-----NMAGLEIRAPLVERGNKWEYAGVVD
Volca_Trm8_2 -----MQIGKTRVRQHVNLK--REFQOQTAAP--DWSAVFSD-----PSLP--LALDIGSGYGGLLVQMSPLFPKTL-----NYLGLEIRQLVKRANFVWNLGLSQ
Cocsu_Trm8_2 -----VRCRQHVNLK--KELQVPLAPP--DWGAIYD-----TARP--LIVDIGCGSGRFLVLSRRFRQ-----NLLGLDTRAKLIMERANEWARLLELQ
uncma_TrmB -----INPNKG--LLNFNK-----LFLSPNN--VTLEVGFNGDLSLEMAIQPNLN-----FLGIEVYVYAGV--GRLINEASKN
uncba_TrmB -----SDFGIEVNEKVVINEFDE-----VFANQD--VTLEVGFNGDLSLEMAIQPNLN-----FLGIEVYVYAGV--GRLINEASKN
uncga_TrmB -----WPNYGVSLTDN--QLNFVE-----LEFNSHD--VTLEVGFNGDLSLEMAIQPNLN-----FLGIEVYVYAGV--GRLINEASKN
Rahsp_TrmB -----WVPMGVVEFQAE--PLAIDA-----LFGRPAD--VVLEIGFGMGTSLVMAKQNPQN-----FIGIEVHSPGV--GACLATAHEE
Sheha_TrmB -----QWPIMLDLYTPE--SIDLVE-----VFGREAP--VTLEIGFGMGASLVAMAKASPELN-----FIGIEVHSPGV--GACLATAHEE
Shibl_TrmB -----WVPMGVVEYAAQ--PLDLSA-----LFGREAP--VVLEIGFGMGASLVAMAKANPHQN-----FIGIEVHSPGV--GACLATAHEE
Escoc_TrmB -----WVPMGVVEFSED--MLDFPA-----LFGREAP--VVLEIGFGMGASLVAMAKDRPEQD-----FIGIEVHSPGV--GACLATAHEE
Nitha_TrmB -----WPRYGISLGAE--PMDLEA-----IFNRKAE--RILEIGFGMGASLVAMAKASPELN-----FLGIEVHSPGV--GHLLEAE
Truura_TrmB -----WRRFQFPLEWAA-----QPFPHDPAALHVEVGFNGDGRYTVRRALAPQER-----FVGLIESSASL--QRGLKRVRE
Meisi_TrmB -----SLEFPFLSQTK-----LFGREGR--LVLEVGHGDRFTAETARRNPDWN-----ILGVEVSAGSV--ARALKRMRRE
Sanke_TrmB -----RTSVDPGYLDAAE-----VFGRSAR--LVVEVGSQGEAVAHAAAESEPTD-----FLAVEVYTPGV--AQTLQRRLTS
Mycav_TrmB -----AEDPDRPGPLDIDA-----WFGRRAP--VVLEIGCGNGTSLTAMAKKEEGVD-----VIAVEVYRRLG--AQLLCAIDRD
Clodi_TrmB -----LRDDIDKLGKW-----NLKFRNDP--IHVEFGTGKGFITTLAKQNPDN-----YIAMELKEEVL--LKAVERKADAS
Bacsu_TrmB KPWADDFLAENADIAISNPADYKGNWT-----VFGNDP--IHEVGTGKGFISGMKQNPDN-----YIGIEVHSPVI--VTAVKRQKDS
Dicth_TrmB -----ISNNKANYFLDLRD-----IFQNEP--IFLEIGMNGEFIVHMAKENPNAN-----FIGIDVSKEIF--RKALSRVKS
Dictu_TrmB -----LNQKSNYFLDWKE-----VFNENP--IFLEIGMNGEFIVHMAKENLMAN-----FIGIDVSKEIF--RKAVSRVKS
Proam_TrmB -----PGWTH-----DQTFADQK--TYLECSNGAWIASKAIEQSQYN-----WVGEIKKFDRT--RKIWSKIKKF
Chlmu_TrmB -----VPSYYPKYEYFVMPVWQ-----LFANRHP--VCELCGNGDWWVQALKDTIN-----WIAVEKRFDRV--RKIWSKMSNH
Chlps_TrmB -----IPEHYFKHQFEMPSWEE-----FFGNHP--IFCELCGNGDWWVAQANKPNMN-----WIAVEKRFDRV--RKIWSKMHNS
Chltr_TrmB -----VPNYYSRYEEFVMPVWQ-----LFPANGP--IFCELCGNGDWWVQALKDTIN-----WIAVEKRFDRV--RKIWSKMHNS
Chlab_TrmB -----IPEHYFKHQFEMPSWEE-----FFGNHP--IFCELCGNGDWWVAQANKPNMN-----WIAVEKRFDRV--RKIWSKMHNS
Chlca_TrmB -----IPNHYFKHQFEMPSWEE-----FFGNHP--ISCELCGNGDWWVQAQNPQMN-----WIAVEKRFDRV--RKIWSKMHNS
Chlfe_TrmB -----VPEHYFKHQFEMPSWEE-----FFGNHP--ISCELCGNGDWWVQAQNPQMN-----WIAVEKRFDRV--RKIWSKMHNS
Chlps_TrmB -----IPEHYFKHQFEMPSWEE-----FFGNHP--IFCELCGNGDWWVAQANKPNMN-----WIAVEKRFDRV--RKIWSKMHNS
Wadch_TrmB -----VPEYDNDQFPPGWEA-----PSLGNKPS--VVIEYCSNGAWIVEKAKSNPQNN-----WIAVEKRFDRV--RKIWSKMHNS
Simne_TrmB -----VPTYDYKYEYFVMPVWQ-----LFGNDHP--VHIEYCSNGEWILERAKAHPVN-----WIAVEKRFDRV--RKIWSKMHNS
Entdi_PPR-MT4 -----SKEVFMYPREINVLHFEVEVFK-----NKNP--INIELCSGYGELITKAEEKKEN-----WIGIELYRDRV--YNSWATKIFA
Enthi_PPR-MT4 -----EVFQMPYPREINVLHFEVEVFK-----NKNP--INIELCSGYGELITKAEEKKEN-----WIGIELYRDRV--YNSWATKIFA
Entin_PPR-MT4 -----QLYPKATEIISFEKVFV-----NTNP--VNIEMCSGYGELITKAEEKKEN-----WIGIELYRDRV--YNSWATKIFA
Entnu_PPR-MT4 -----EVFQMPYPREINVLHFEVEVFK-----NKNP--INIELCSGYGELITKAEEKKEN-----WIGIELYRDRV--YNSWATKIFA
Dicfa_PPR-MT4 -----EQQQQLKKTAAEESGNTGSS-----NLYKNIAG-----NQ-----YINQNL--VKMEICSGHGHVITERAKRDLESD-----WVSVETRYDRV--FQIWTKKVLE
Dicdi_PPR-MT4 -----PDSTLS--SFNGLFNSYK-----KGGG--NFNSNRS--LKMEICSGHGHVITERAQDLDAD-----WISLEIRYDRI--FQIWSKMILE
Dicpu_PPR-MT4 -----RISDESSGKELD--AFNELFNQYK-----KGGVYVYKGTDDV-----DLNTNRY--LKMEICSGHGHVITERAQDLDAD-----WISLEIRYDRI--FQIWSKILE
Polpa_PPR-MT4 QQLSKQQRKLCPLMEQSKRVNFSVPTFKNLNIEENKELENKWFDLKLFKDR-----DQESPRQ--VKMEICSGHGHVITERAQDLDAD-----WLSVEIRYDRV--FQIWSKLILD
MicpuCCMP1545_PPR26 -----GAELR--LGVDAFD-----DASLP--VRVEVCSGHGDWVTSRAAADATRRN-----WLAIEMRKRV--AMTWHKAIRR
MicpuRCC299_PPR26 -----EGAAANVKKPLCFKVEF-----GNDLP--VRLEVCVSGHGDWVTSRAAADATRRN-----WLAIEMRKRV--AMTWHKAIRR
Batpr_PPR26 -----VHKQRELAETPAIEKFWASRYER-----KGAFMK--AKLEVCVSGHGDWVTSRAAADATRRN-----WLAIEMRKRV--AMTWHKAIRR
Ostta_PPR26 -----EQATNVRILGGGSDKTVDA-----ADAGAD--VRIECSGHGDWVTSRAAADATRRN-----WLAIEMRKRV--AMTWHKAIRR
Ostta_PPR19 -----SERKVKRAIRKVISDGTIRDFRMSHRLKDD-----ERE--LNLEVAAGNDWAVQAATDSSD-----WISLELRHDRV--YSIFSRVCS
MicpuCCMP1545_PPR19 -----FDLRFSAKQFERHVSQKYEIRNRE-----ARQ--VKMEICAGNDWVTSRAAADATRRN-----WLAIEMRKRV--AMTWHKAIRR
Ostlu_PPR19 -----RKVIKADGTIRDFRMSHRLKDD-----KRE--LNLEVAAGNDWAVQAATDSSD-----WISLELRHDRV--YSIFSRVCS
Batpr_PPR19 -----KRLKKTIDSKTGQINFKLFLHGVQKEA-----KVNE--ISLEVAAGNDWAVQAATDSSD-----WISLELRHDRV--YSIFSRVCS
Perma_PPR-MT4 -----EQVVDNVEEFAANMKNLNGKLIKITDD-----DRG--VCLVEVSGSGDWWVLSRAKRDWSQQ-----WIAAEKRFDRV--HIFSRVCS
Phatr_PPR-MT4 -----RALRDDGTINFDVFGCTAK-----GRP--LDIELGAGFGDWIARQAFHRPKRN-----HIAVELRADRV--HQIFAKGTQA
Thaac_PPR-MT4 -----CVDFDRIFFSTGDRDKK-----C-----HGGAG--LYLELGSVSGDWWVLSRAKRDWSQQ-----WIAAEKRFDRV--HIFSRVCS
Guith1_PPR-MT4 -----KMLSPKGLVFERELFG-----NTLP--VKLEICSGAGWAVIAQAKADQDAN-----WMALEIRIDRV--HQIFRMIHF
Guith2_PPR-MT4 -----SGYFNQDARLSWERIFSSSDSSRG-----AS-----GDRSRP--VRMEICSGSEWIVEQAKTEQASD-----WVSLERHDSQ--QQTVVKMALS
Guith3_PPR-MT4 -----SSSNVDKGNLKTGLSKLLRAV-----GPKP--LVVELCAGSSEWVLDRAVGEDAN-----WIAVEVYRDRV--HEILFRSLL
Thesp_C5M_Archae VRTALTVPVVDVILKILEYKTPVIRLWDYREKGEVIGQDLASAYVAHVLP-----EPGE--RVLDLAAAPGSKTFHAAALMENKGE-----IIAVDYSYDRL--MRMKEKMLL

Enthi_Trm8 E-----LKNVWIIQCNCMKYVDN---YFVK--GQLLKIFITFPDPHFKN-----SVKRRRIINPHFAAMYVYLLKPGE-----GMLYTASDVK-ELFDWNTQSLDQQP--
Dicdi_Trm8 VG-----QFQNISVIRTNAMKYLPN---YFEK--GQLQKIFLFPDPHFKN-----ATHKRRRIISPTLLSEYAYILAPG-----AYAYFISDVE-ELYLWMFEHFKNHP--
Plopa_Trm8 EEK-----NQYQNISVLKTNAMKYLPN---LFYK--GQLEKIFLFPDPHFKN-----ANKHRRRIISPALLEAYAYIVKVG-----GLAYFISDVE-ELYLWMFEHFKNHP--
Guith_Trm8 K-----GRFQNISVVRTNAMKCIAN---FVVK--GSLEKLFVCFADPHFKT-----KNHRRRIINRNSISEFAYVLKGE-----GFLYVVTDVK-ELHDWQVEHLNAHP--
Cryne_Trm8 SLLPAGSVDTKPGGYQNVSVIKANSMKHMPN---FFAK--GQLEKIFLFPDPHFKN-----RKHKARIITPALLAEYAYVLRPG-----GILYTVTDVK-DLHEWMAHHLAHP--
Caeel_Trm8 -----AEAGHYRNVAVLRSNAMKYLPN---YFHK--GQLSKMFFLFPDPHFKN-----KKHKWRIITPALLSEYAYVLRPG-----GIYITITDVK-DLHEWMAHHLSEHP--
Sacce_Trm8 -----ASKHGFMQINVLIRGNAMKFLPN---FFEK--GQLSKMFFCFADPHFKQ-----RKHKARIITPALLSEYAYVLRPG-----GIVYITITDVK-DLHEWMAHHLSEHP--
Arath_Trm8_1 SE-----GQYENISVVRTNSMKYIPN---YFEK--GQLSKMFFLFPDPHFKE-----KNHRRRIVISTHLLDEYAYVLRAG-----GIYITITDVE-ELGEWMKSCLEKHP--
Phypa_Trm8_1 -----GQYENISVLRNTAMKYLPN---YFEK--GQLTKMFFLFPDPHFKE-----KNHRRRIISTALLAEYAYIMAVG-----GILYITITDVQ-ELGEWMKAHLDAHP--
Chlvu_Trm8_1 P-----GKYQNCVSVRTNAMKFITN---FFRK--GQLTKLFFLFPADPHFKA-----ANKHRRRIITRLLAEYAYVLRPG-----GLLYITITDVE-DLGDWQRDRLEAHP--
MicpuRCC299_Trm8_1 G-----DGWVDNVRVVRMDALWLVR---DFIPR--ESLSDVCVYFPDPWSDA-----QAHRRIIVNPFLLALIEPCMAKTG-----GRHLSTDDD-SYAEHMFVRVMSAE--
Ostta_Trm8_1 -----NAKVCEMDALWLMTG---EYVED--ASIDECLVHFPDPWRDE-SG-----LDRKAHRRIVNETLTLTSLERTLRPG-----TGRLSVATDDD-QYARHLERFVEQFARP--
Ostta_Trm8_2 -----LKRRAHFVHCNAMVSLKS---LNLPN--IRAICVQFPDPWRSRA-----RHKRRRIVMTDFARTIADVLPSG-----GELYCCSDVR-ALAEEMDVVAANDDF--
Arath_Trm8_2 -----VHPIFANAMVSFEHLIS---SYPG--PLEIVSILCPDPHFKK-----RHQKRRVVQKPLVNSILQNLKPG-----CKIFVQSDVL-DVAQDMRDQDDEESN--
MicpuRCC299_Trm8_2 N-----LHFAECNATVSMGKWLK---SYAEDCGSKVETVAIQFPDPHFKK-----RHHKRRVVQPALVRAALAEGLTPG-----ARVFLQSDVK-DVSEDMRDKFERFG--
Chlvu_Trm8_2 S-----VFLRGNATITLQHTTG---GXPG--PLDVLVQVFPDPHFKA-----RHKRRRIVVQRTVEALGRIMAPG-----ARVFLQSDVL-GVAEHMRDTEPQHGSA--
Volca_Trm8_2 R-----VHLYFSNATVSLTTLG---SYPG--PITDVFIQFPDPHFKR-----RHHKRRVVQPQLVTRALDMPRG-----GRLLQLSDVE-EACVAMVMPFEKYAGE--
Cocsu_Trm8_2 S-----VHFMMANATVLSLEMLA---TYPG--PLSLVSIQFPDPHFKT-----RHHKRRVVQPQLVRAIARMPGTG-----GRVFLQSDVE-EAVALMHMFRQHG--
uncma_TrmB -----KLT-NLKIIDDAVEVLN---NNIPD--DSISHFQLEFPDPWHKK-----RHHKRRRIVQTSFLLDLLTKKLKNN-----GIVHIATDWE-NYAEHMETLESHS--
uncba_TrmB -----NIS-NLMIIDDAVEVMT---NNIAD--DSISHFQLEFPDPWHKK-----RHHKRRRIVQTSFLLDLLSKLKD-----GTVHIATDWE-NYAEHMETLEMHH--
uncga_TrmB -----QLS-NLKIIDDAVEVLQ---NHIPD--DGLSKFQLEFPDPWHKK-----RHHKRRRIVQTSFLLDLLTKKLTD-----GIVHIATDWE-NYAEHMETLKSQH--
Rahsp_TrmB -----GVS-NLRVMCHDAVEVLE---KMIIPD--GSLDMVQLEFPDPWHKA-----RHHKRRRIVQTSFLLDLLTKKLKVG-----GVFHMATDWE-PYAEHMLVMSVTSLE--
Sheha_TrmB -----GVT-NLRVYHDAVEVLE---NSIAE--GSLACVQLEFPDPWHKT-----RHHKRRRIVQAPFAELIRSKLVG-----GVFHMATDWE-NYSEHMLVMSNAAP--
Shibl_TrmB -----GVT-NLRVMCHDAVEVLE---NMIPC--NSLSMVQLEFPDPWHKA-----RHHKRRRIVQPFPAELVKSCLKLG-----GVFHMATDWE-PYAEHMLVMSVTTID--
Escoc_TrmB -----GLS-NLRVMCHDAVEVLH---KMIIPD--NSLRMVQLEFPDPWHKA-----RHHKRRRIVQPFPAELVKSCLQLG-----GVFHMATDWE-PYAEHMLVMSVTTID--
Nitha_TrmB -----GVD-NIRVICDDAWKVLQ---HHLPE--QSLQGVQLEFPDPWPKK-----RHHKRRRIVQPFVVDLWHLKLPD-----GWHLATDWE-NYAAQMMAVLSQHP--
Trura_TrmB -----GVA-NVKKLVGAFAVR---HLFPP--GSLASITVNFPPDPWPK-----RHEGRLLLRASFRRALAAARLAPR-----GVILLATDHP-EYLAFAQREAEASG--
Meisi_TrmB -----GTR-TVRLYHGEARFALR---NFIAF--RSLRYVYVNFPPDPWPKA-----KHEENRLQTESGFRRRLSTRLLDG-----GQLLLTDDH-EYVRFAQEQAAQSG--
Sanke_TrmB -----GST-NVRLMQADAMVVG---TIIAP--ASVDELWLFPDPWHKS-----RHTKRRRIVTAPASLVARVLRPG-----GTWRLATDWA-DYARQMRVLAASE--
Mycav_TrmB -----NVT-NIRLRGNALDVLQ---RLIAP--ASLTGVRVFPDPWPKA-----RHHKRRRIVQPGTVGLIADRLLPG-----GVLHVATDHA-GYAEHIADVAGEP--
Clodi_TrmB -----NLN-NILFLWGDVSNILD---YFEAK--ELSRIVNFCDPWPKN-----RHHKRRRIVQTESGFRRRLSTRLLDG-----GIFHFKTDNR-KLFEHMRTDETAANN--
Bacsu_TrmB -----EAQ-NVKLLNIDADTLTD---VEFEP--GEVKRVYLNFSDPWPKK-----RHEKRRRIVYSHFLKKYEVVMKGG-----GSIHFKTDNR-GLFSEYLSKSEYVG--
Dicht_TrmB -----GLK-NIRIMRIEGSEFLC---KRVRS--KTLGVIYNFPDPWPKK-----SRKEERLVNEPFIYILSDRLKEG-----GVFIFVSDNE-DYAMTVWELLKFT--
Dicut_TrmB -----GLK-NIRLMRIEGSEFLC---KRVKS--ETLSGVYNFPDPWPKK-----SHKERRLVNEPFIYILVSDRLKNE-----GIFHFVSDNE-EYTKVSWGLLKKFD--
Proam_TrmB -----ELD-NLLTICGEGFHVTR---DFFAN--ESVDVAVNFPPDPWPKK-----RHAHRRIVQPAFVKEIHRILKSD-----KLFTLVTDHA-AYSKIMIDVLIQYG--
Chlmu_TrmB -----KVN-NLLIVCGEAQTFPT---HYVTD--ASFQKIVVNFPPDPWPKF-----RHKHRLFDVDFVQDMVRVLVEG-----GQLTLVTDH-TYLTNSIQVMLN--
Chlps_TrmB -----QVR-NLRIVCGEAQTFFR---HYIQN--EVIQRIVVNFPPDPWPKS-----RHKHRLFDQDEFMNDIVRVLVDS-----GIILATDDK-NYLLQAIKIMQ--
Chltr_TrmB -----RVN-NLLIVCGEAQTFFS---HYVSD--ASFQKIVVNFPPDPWPKF-----RHKHRLFDQDLFVQDMMRTLVVG-----GQLTLATDDY-NYLVNATIMMLK--
Chlab_TrmB -----QVR-NLRIVCGEAQTFFR---HYIQN--EVIQRIVVNFPPDPWPKS-----RHKHRLFDQDEFMNDIVRVLVDS-----GIILATDDK-NYLLQAIKIMQ--
Chlca_TrmB -----QVS-NLRIVCGEAQTFFR---HYLKN--ETLQRIVNFPPDPWPKS-----RHKHRLFDQDEFMNDIVRVLVES-----GILVATDDK-NYLVNATIMMLK--
Chlfe_TrmB -----RVT-NLRIVCGEAQTFFL---HYLGE--AVVQRIVNFPPDPWPKS-----RHKHRLFDQDEFMNDIVRVLTP-----GILVATDDK-NYLLQAIKIMQ--
Chlps_TrmB -----QVR-NLRIVCGEAQTFFR---HYIQN--EVIQRIVVNFPPDPWPKS-----RHKHRLFDQDEFMNDIVRVLVDS-----GIILATDDK-NYLLQAIKIMQ--
Wadch_TrmB -----HLD-NLVVFCGEGFRMTQ---EYFPS--GAVDRIYNFPDPWPKK-----RHAHRRIVQRPVVEQISRIKLPQ-----GVLTLVTDHA-VYSEQMIIEVLNMQE--
Simne_TrmB -----NIS-NLLIVCGEAQVFTR---EYVPE--NSVETIYNFPDPWPKD-----RHAHRRIVQPAFMRDVLTAVRPG-----GNAQLVSDAK-EYVLQMQAEISQ--
Entdi_PPR-MT4 -----GLD-NVACVWGDAMNVLM---LNIMP--ESIDNIYLNFPPEPKY-----ENSPNTLFTIQFFQVARIKLD-----GIFCLLTDSP-IVVNIIVNQFAHSE--
Enthi_PPR-MT4 -----GLD-NVACVWGDAMNVLM---LNIMA--DSIDNIYLNFPPEPKY-----ENSPNTLFTIQFFQVARIKLD-----GIFCLLTDSP-IVVNIIVNQFAHSE--
Entin_PPR-MT4 -----EVK-NVSCIWGDAAEVIT---MALLP--NSIDNIYLNFPPEPKF-----ENAPNTLFTKQFFQVAKALKTG-----GTFNLLTDSI-IVVKIIEKVFENTP--
Entnu_PPR-MT4 -----GLD-NVACVWGDAMNVLM---LNIMA--DSIDNIYLNFPPEPKY-----ENSPNTLFTIQFFQVARIKLD-----GIFCLLTDSP-IVVNIIVNQFAHSE--
Dicfa_PPR-MT4 -----DID-NLYLLAGEAHSTIK---TNVPD--GSVDELYINYPNPPMW-----YG-AKRLIDEPFLKELNRIKRD-----GTLTIVTDNR-EYSESVVRQQTSK--
Dicdi_PPR-MT4 -----AID-NLYIVGGDAHGSKL---EIIIPD--NILNEVYINYPNPPVW-----SG-AERLNELEFLIEINRCLKDD-----GTLTIVTDNR-DYSQDIIDILTKSK--
Dicpu_PPR-MT4 -----SID-NLYIVGGDAHGSKL---EIIIPD--GVLEVYINYPNPPVW-----KG-ADRLENELEFLIEINRCLKKS-----GTLTIVTDNR-FYSQIEIDILTKSK--
Polpa_PPR-MT4 -----SID-NLYILAGEANSVLK---NSVPS--DSLVEVYINYPNPPVW-----PG-AWRLINHDFLVDIHRTLKDD-----GTLTIVTDNR-GYADSVVQLLKKSR--
MicpuCCMP1545_PPR26 -----RLT-NLALLRGTAHETLS---TRVPA--DRVEEIHVNYDPPEW-----VGSQCLVDRAFLAACHRAKLDG-----TGHTVFTVDDP-TYAMRMCRELSVAA--
MicpuRCC299_PPR26 -----RLD-NVALLCGMAHEMMG---AHVPS--GSLTEVYVNYDPPEW-----VGSQCLVDRAFLRDAHRSKLPK-----VGHLLTVTDNR-NYAMRMCRELSKLV--
Batpr_PPR26 -----GVR-NLTMCLGLAHECMR---KQIPN--EVLDEIYVNFPPDPPEW-----NGSANCLVDGAFLVESHRTLTKG-----AYLILVTDNR-GYAMRMCRELSVVP--
Ostta_PPR26 -----GVEKNLRLVCGMAHDALDV---CRAPP--GSATEVYVNYDPPEW-----VGSQCLVDRAFLRDAHRSKLPK-----GHLICVTDNR-AYAMRMCRELRKAR--
Ostta_PPR19 -----GAS-NFAAMGGDAAYVMR---RYIAP--GSVSNVFNFPPEPHHS-GDA-----AADNSLALLNEEFRRDIHAGLKKG-----XALVIFSDNH-RYMQSLECSWSYGL--
MicpuCCMP1545_PPR19 -----GIT-NLALGGDATQVLQ---NNIRP--GSISYIFINFPPEPHHS-GSR-----TADNRFHLLTSSFFECIHTVLIDD-----GVLTLFSDNH-KYMRSLANTISSLL--
Ostlu_PPR19 -----GAS-NFAAMGGDAAYIMR---RYVAS--ESVSHVFNFPPEPHHS-GDA-----AADNSLALLNEEFRRDIHACLRRAYTSTDPAGGLTIFSDNH-RYMQALARTLAELD--
Batpr_PPR19 -----KLR-NLAVVSGDAFRLLN---ESIPP--NSLHRLFINFPPEPHHS-GDE-----KSRNDLALLNKDFFVAHAALKKDKKNGDGGGLTIYSNE-RYMHTLAKMISGLT--
Perma_PPR-MT4 -----GPR-NVHIIGDARECLP---MLLPL--SCVSEVHINFPPEPVWH-----GPR-NVHIIGDARECLP-----MLLPL--SCVSEVHINFPPEPVWH-----DA
Thatr_PPR-MT4 -----PLD-NLCVVGAESEDFLK---DLRIS--GSLATVFNHPEPPTQTFGGDRSELEAIKGGGEPAMHLLTSGTLEAAANSLSHG-----GRLVIVTDNR-WYARLLASLTLKVV--
Thaac_PPR-MT4 -----PLT-NLCCVSGECSFLR---QRIRT--GTVDALFVNHPEPPTQTFHG-----NEADQSGDEPAHMLNSGSAKCLKPDGR-----GRLIIVTDNL-LYAQHLICRSYSKLV--
Guith1_PPR-MT4 -----DVQ-NLAVLGGDATQILP---CLISE--SSVNQIFVNHPEPPTQTFG-----DSEGQHLLTVDFRDMYRILAH-----GTTIVTDNL-WYAKLLGRILGKVS--
Guith2_PPR-MT4 -----KLN-NLAVLAGDAKVLVS---RRVPT--ESLSQVLFNFPPEPLWS-GGD-----GESTLHLLTADFFRSARVLEAG-----GSLTILSDNS-RYASVLLATLADLK--
Guith3_PPR-MT4 -----GLN-NLVVNLDAALVCS---DLRPP--ASVRSMLFRPEPEM-----GA-GSVFSPSFLRAVHKNLEPN-----GTFNIVTDNRGQFADMLLTLHLL--
Thesp_C5M_Archae -----GIK-NVKLVHADQSFKDKAKFKDKIILDAPCSSSGTYRQFPEVKWRF-DEN-----KIKRIVNVQRNMLRNAYENLRKG-----GEMTYSTCSI-RIDEEENVLFAIEKV

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Enthi_Trm8      -----LLERMPPDDYT-----DDYLNIVMFKTEEAKKVDREQRQK---WGACYRRRIIEEPF
Dicdi_Trm8      -----LFEQVERDIAE-----NDSCIPLIVNSTEEGRKVNRIIDGKK---WFAVFR-ITDPS
Plopa_Trm8      -----LFEVVKLEPT-----DDPCIPLILNATEEGRKVNRIIDGKK---WYGVFR-TEAP-
Guith_Trm8      -----LFEKLDDDAEK-----ADPCWDLMFNSSEEBANKVERNEGSK---FGAIYRR-ISLAE
Cryne_Trm8      -----LFEYIPTETLS-----DDPILEAARTATEEGQKVERNKGDK---WVACFR-REDPK
Caee1_Trm8      -----LFERLTEEMK-----KDPVIVMLFESTEEGQKVTNRDGGK---WPAIFRR-LPNPA
Sacce_Trm8      -----LFEKLSKEWEE-----NDECVKIMRNATEEGKKVERKGDK---FVACFTR-LPTPA
Arath_Trm8_1    -----MFEISLTQEEELV-----SDPVVELLCSATEEGQKVARNGGQT---FRAVFR-IAVVS
Phypa_Trm8_1    -----LFHPLTDEELE-----KDVCVPLLNATEEGQKVERNGGST---YKAIYRR-IAIGL
Chlvu_Trm8_1    -----LFEKRVSDDEELE-----SDPAQQLLEGTTEEGQKVARNGGKT---WRHYVRR-IPGPA
MicpuRCC299_Trm8_1 -----SSGKWEK-----VDEALLGRSGSTKYEERGRALGSEI---RNFVRYVGGSP--
Ostta_Trm8_1    -----KLDEVTYKRIGEMAEPSESMPLLENVPELDEAHKYEWKSLSDIKSEENVQPPS-----RGWVRCDFPFARFDSKYASRALEEGRSC---VDVGFRRFPSPVD
Ostta_Trm8_2    -----VLQHMDFVDTED-----KRRWLNRANPYDAHTERDIVCEGKIRPV---YRFAVIRA----
Arath_Trm8_2    -----AHLFDLIDAS-----LHDNPLGVPTEREVQTTSTNGRC---YRVLNRNNTTV-
MicpuRCC299_Trm8_2 -----WFAPCREAHGGATFCAASEPPPPQQQQH---GEQAQQGASAAGGQAQAQQQQHHHQHQQQQEQQEQEASEPQWESE---W-AASGWLRDNLPLGVPTEREVLTTEQGLPV---YRLLLRIT-
Chlvu_Trm8_2    -----DFT-----LAPQHSQCAG-----GWLVDNVPVGTPTEREHYVAQQGLPV---YRVMLTRV-
Volca_Trm8_2    -----
Cocsu_Trm8_2    -----
uncma_TrmB      -----HFKNACAGD-----H-IYSERPE---QRPLTKFENRGQKLGHV---WDIIFTNL-
uncba_TrmB      -----HFKNLAGD-----H-IYSERPK---DRPLTKFENRGHRLGHV---WDLFKNT-
uncga_TrmB      -----HFKNLTGDD-----H-IYSPRPK---HRPLTKFENRGQKLGHV---WDIIFTNS-
Rahsp_TrmB      -----NWNVLSQE-----G-NYVPRPE---SRPVTKFEMRGQRLGHV---WDLMFERK-
Sheha_TrmB      -----GYKNQSAT-----G-DVVERPD---HRPLTKFEARGHRLGHV---WDLMFERV-
Shibl_TrmB      -----GYHNCSAE-----G-NYVPRPQ---SRPVTKFQRGQRLGHV---WDLMFERM-
Escco_TrmB      -----GYKNLSES-----N-DYVPRPA---SRPVTKFQRGHRLGHV---WDLMFERV-
Nitha_TrmB      -----GFGNLAGE-----G-REAGGPG---ERPSTKFERRGQQRGYQV---WDLKLLKL-
Trura_TrmB      -----AFALIEA-----EAPP---AVFETKYALKWKGQKRL---FYQVFRAT-
Meisi_TrmB      -----LFDVKTTP-----PPPP---HHLETKYALKWKEQNRSF---YHAVFTKT-
Sanke_TrmB      -----EFD-VLDD-----APR---FAGRPVTSFERKGTTEKGRDI---ADLTAVRR-
Mycav_TrmB      -----RLRPNPND-----SPLPI-SVARPTTKYETKAQDAGSAV---TEFIWLR-
Clodi_TrmB      -----WLLKNISLD-----LGNSEYENNVTEYEDKFMSSQGMRI---FRCEAKRR-
Bacsu_TrmB      -----LLLTYVSLD-----LHNSNLEGNIMTEYEEKFSALGQPI---YRAEVEWRT-
Dicht_TrmB      -----NFSPMWDD-----GLRT-DFPEYYKTKYARKWLSLGLTI---YYIGFRKE-
Dictu_TrmB      -----NFSPLWDH-----GLRR-DFPEYYKTKYARKWLAGLPI---YYIGFKKT-
Proam_TrmB      -----GFISL-----FE-----APYTTTSPYGYGSSYFEEELWREKGSKI---HYHVFRI-
Chlmu_TrmB      -----YLSPG-----MQ-----DPYYVNVKDNYGGSWFENLWRSKGEKI---FCTEFVKK-
Chlps_TrmB      -----RLLPQ-----LE-----EPYYCKMLENYGDSWFERLWRSKQGEI---FYTEFVKK-
Chltr_TrmB      -----YLSPG-----LK-----SPHYINVKDNYGGSWFENLWRSKQGEI---FCTEFIKR-
Chlab_TrmB      -----RLLPK-----LE-----EPYYCKMLENYGDSWFERLWRSKQGEI---FYTEFVKK-
Chlca_TrmB      -----CLLPT-----IE-----DPYYCKVLDNYGDSWFERLWRSKQGEI---FYTEFVKK-
Chlfe_TrmB      -----YLSPT-----ME-----DPYYCEV-ENYGNLWRSKQGEI---FYTEFVKK-
Chlps_TrmB      -----RLLPQ-----LE-----EPYYCKMLENYGDSWFERLWRSKQGEI---FYTEFVKK-
Wadch_TrmB      -----GMCSA-----HP-----EPYYVNELEGYGTSTFDALWRDKGRVI---RYHQYRQ-
Simne_TrmB      -----VSG-----W-----KPSNHQNNYGSYFDRLWRSLGREI---YYLEYL-
Entdi_PPR-MT4  -----ILRNKFQIQGK-----TMFEKKIPDGYSYFDQLWKN-GKIN---QDRFFMKI-
Enthi_PPR-MT4  -----ILRNKFQIQGK-----TMFEKKLPEGYGTSYFDQLWKN-GKIN---QDRFFMKI-
Entin_PPR-MT4  -----FLGVRFRYEGK-----EMFVNKMPADYGTSTYFDQLWKN-ANTN---EDRYFMRLV-
Entnu_PPR-MT4  -----ILRNKFQIQGK-----TMFEKKLPEGYGTSYFDQLWKN-GKIN---QDRFFMKI-
Dicfa_PPR-MT4  -----PLKRIFAPAQ-N-----NDYLADLPEEYGYSYFNKLWSN-GQRI---KRYCVYA-
Dicdi_PPR-MT4  -----KLLKIYKPVK-----ETYLIQLSEYGYSYFNKLWNN-GQRV---KRYCIVIS-
Dicpu_PPR-MT4  -----KLLKVKPASPND-----NTYLTPLAEDYGYSYFNKLWNN-GQRV---KRYCIVIT-
Polpa_PPR-MT4  -----KLAKIYKPVK-----EDYICQLDEDYGYSYFNKLWSN-GQRM---KRYCIYI-
MicpuCCMP1545_PPR26 -----GMFAPTEEGGA-RPFRAGVPEDYGGSYFDAMWTN-GNLR---DRYIYR-
MicpuRCC299_PPR26 -----RLFKPTFHGG-KPFKSGVPEGYGGSYFDEMWN-GRON---DRYI-
Batpr_PPR26     -----HLFEPATADG-KPFENRNPADYGFYSFNALWTN-GNL---DRY-
Ostta_PPR26     -----SLFETTEPEG-KPFASGVPEYGGSYFDSMWTN-GNRV---DRY-
Ostta_PPR19     -----FSSRDADVTS-----REPALYETIDGVRLYQG-IPGFLAGHRVHEQSYFDRFWE-GRHV---DRYFISVGVKA-
MicpuCCMP1545_PPR19 -----HEKDEKADEPMF-----LAEIAQGTAVDGKSGSTTFENAVGMRLYQG-LPGIGSGHIVHEQSYFDRFWKQ-GSHA---DRYFMIVSKN-
Ostlu_PPR19     -----I-----FTARD-----DVLASGAPANQYETIRGVRLYQG-VPGPSAGHRVHEQSYFDRFWEN-GQHV---DRYFISLVK-
Batpr_PPR19     -----VDDNNIAFESK-----SYGADESSDTIEASFENVEGVRLYTGSAPGKSGGFEEKYEESSFFDRFWQA-GSRI---ERYFMVFSKR-
Perma_PPR-MT4  -----CAREDKSYRNLIDSRRSRRGQLYMLACGF-----CCIL-----IIALTVLLL-
Phatr_PPR-MT4  -----RQKPDFLFRPPRPK-----EFHASNLHOMIEYFGGSTGQAGVPLYEQPNEG-----IGHVKYDVSTGASYFDRLWKS-GAGL---HAEQTRFILI-
Thaac_PPR-MT4  -----SQVDLVGVAPRE-----VHDLKRIEFSFGHSLNLYEGNPSIS-VDHVYVVKGGPSNGTSYFDRLRWT-GAGKHADMKRYIIALRTKG-
Guith1_PPR-MT4 -----EGSKAFTSIKM-----QNKNIQNQSCIDGFEVIEHG-SPGPECCHSIIKASSYFDRLWQK-GINRHATAHNDRYFLYIKNV-
Guith2_PPR-MT4 -----DEEGNEPLFVDR-----RELTDNKRISQVVRDLPLFVG-LPGEVCGHFANSYFDRLWNN-GMHN---KRYFIFVHKNA-
Guith3_PPR-MT4 -----LPSDLRDSYLKVVKSCPLFKARS-----TARREGAKKGEAVSYFDQLWRSRGFQ---ERYFIELGKVP-
Thesp_C5M_Archae -----G-----LELLDYP-----FDWDRGFLEIGDRVFRWHTKHCNCG---FFIAKMRKG-

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Supplemental Table 1.

PPR proteins of green algae, showing number of repeats, full protein length, evidence for gene model truncation at the N- or C-terminus, presence of additional domains and predictions of intracellular localization by TargetP (in red) and Predalgo (in blue): M= mitochondrion; C= chloroplast; org= mitochondrion or chloroplast; SP= secretory pathway; - or O = other compartment; *= conflicting."