

Did an ancient chlamydial endosymbiosis facilitate the establishment of primary plastids?

Jinling Huang Johann Peter Gogarten

1. Materials and Methods

Data sources: Protein sequences for the red alga *Cyanidioschyzon merolae* were from *Cyanidioschyzon merolae* genome database [73]. The *Chlamydomonas* predicted protein sequences were obtained from green alga *Chlamydomonas* genome sequencing project [74]. Several EST sequences were obtained from the Taxonomically Broad EST Database [33] and all other sequences were obtained from the NCBI databases

Phylogenetic analyses: Sequences were selected for major groups within each domain of life. Phylogenetic analyses were performed with a maximum likelihood method using PHYML [78] and a distance method using the program *neighbor* of PHYLIP version 3.65 [79] with maximum likelihood distances. All maximum likelihood calculations were based on the JTT substitution matrix and a mixed model of 4 gamma-distributed rate classes plus invariable sites. Maximum likelihood distances for bootstrap analysis were calculated using TREE-PUZZLE [80] and PUZZLEBOOT v1.03 (by Michael E. Holder and Andrew J. Roger, available from [81]).

2. Protein sequence alignments used for phylogenetic analyses and resulting phylogenetic trees. Each sequence name includes GI number from GenBank followed by species name. Numbers above the branches of the gene tree show bootstrap support values for maximum-likelihood analyses and distance analyses, respectively. Asterisks indicate support values below 50%.

1. Phosphoglycerate mutase

CLUSTAL X (1.83.1) multiple sequence alignment

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15605455_Chlamydia_tracho      LLILLRHGQSVWNQKNLFTGWVDIPLSQQGIQEAIAGESIKPIDCIFTS
15836396_Chlamydomonada_pneumo LLILLRHGQSVWNEKNLFTSGWVDIPLSQQGIIEEAFSAGRAIQPIDCIFTS
50912843_Oryza_sativa          ALILIRHGESLWNEKNLFTGCVDVPLTPKGVDEAIEAGKRICPVVDIYTS
42563306_Arabidopsis_thalia    ALILIRHGESLWNEKNLFTGCVDVPLTQKGVGEAIEAGKKISPVDLIFTS
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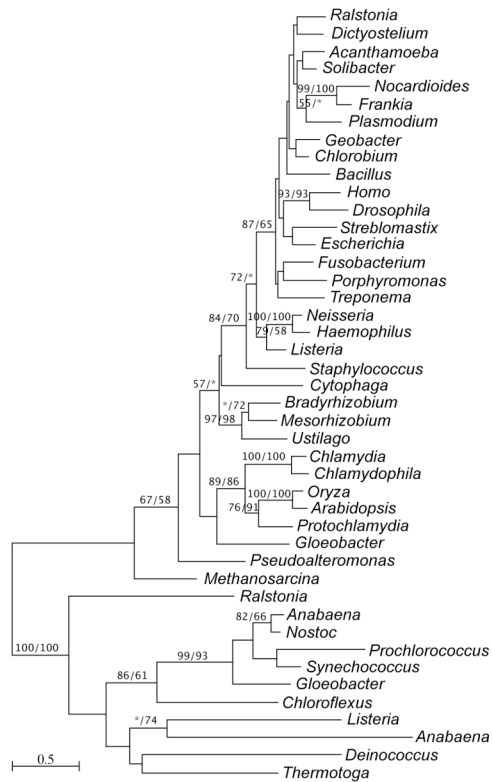


Figure 1. Phylogeny of Phosphoglycerate mutase. Note that green plant sequences form a monophyletic group with chlamydial (Particularly *Protochlamydia*) homologs. Most of the cyanobacterial sequences form a well-supported clade. The cyanobacterial *Gloeobacter* contains multiple copies of this gene (either due to duplication or gene transfer), one of which groups with plant and chlamydial sequences with insignificant support. *Acanthamoeba_pgm* and *Streblomastix_pgm* are EST sequences obtained from Taxonomically Broad EST Database.

2. 2-C-methyl-D-erythritol 4-phosphate cytidyltransferase (*ispD*)

CLUSTAL X (1.83.1) multiple sequence alignment

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67924037_Crocospaera_watson        YLLIPAAGMGKRMGNKLLNLLGKPLLSWTLWIGIIGQPYGGETRQQSV
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46399602_Proteobacteria_amoeb
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71542892_Syntrophomonas_wolfei
68269972_Moorella_thermo
67933737_Solibacter_usitat
42628890_Haemophilus_influe
75241862_Escherichia_coli
30138746_Nitrosomonas_europa
46197745_Thermus_thermop
66796900_Deinococcus_geothe
29607624_Streptomyces_avermi
68174235_Frankia_sp.
76782527_Mycobacterium_tuberc
77743258_Rhodopseudomonas_palu
17739863_Agrobacterium_tumefa
87310771_Blastopirellula_marin
82749957_Staphylococcus_aureus
82749960_Staphylococcus_aureus
60494614_Bacteroides_fragil
48855261_Cytophaga_hutchi
4981956_Thermotoga_mariti
45601697_Leptospira_interrog

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78169602_Synechococcus_sp.
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67924037_Crocospaera_watson
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48855261_Cytophaga_hutchi

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45601697_Leptospira_interrog

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35213360_Gloeobacter_violac
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66796900_Deinococcus_geothe
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76782527_Mycobacterium_tuberc
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4981956_Thermotoga_mariti
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33639743_Prochlorococcus_marin
78169602_Synechococcus_sp.
75702355_Anabaena_variab
67924037_Crocospaera_watson
35213360_Gloeobacter_violac
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CM1057_Cyanidioschyzon_merolae
71542892_Syntrophomonas_wolfei
68269972_Moorella_thermo
67933737_Solibacter_usitat

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75241862_Escherichia_coli	DLALAEFYL
30138746_Nitrosomonas_europa	DLKLAELIL
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17739863_Agrobacterium_tumefa	DIAMADEKL
87310771_Blastopirellula_marin	DLVIAEATL
82749957_Staphylococcus_aureus	DLKVANAI I
82749960_Staphylococcus_aureus	DLKVANAI I
60494614_Bacteroides_fragil	DLKVASALL
48855261_Cytophaga_hutchi	DLAMAEAIL
4981956_Thermotoga_mariti	DLELARIIA
45601697_Leptospira_interrog	DLDLAEVFS

* :

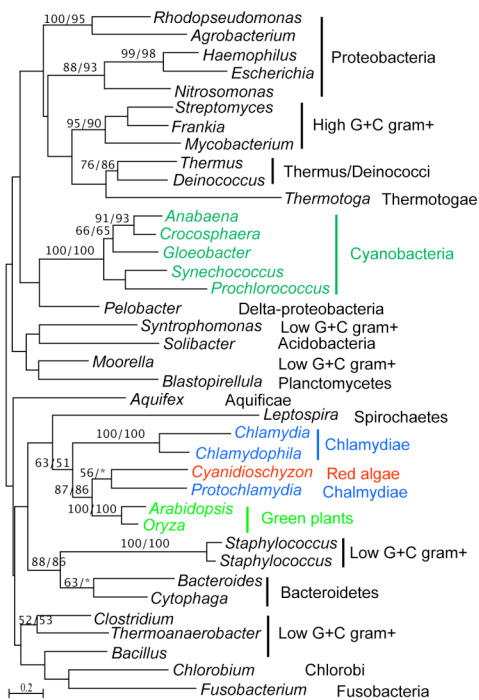


Figure 2. 2-C-methyl-D-erythritol 4-phosphate cytidyltransferase (*ispD*). Note that sequences of primary photosynthetic eukaryotes form a monophyletic group with those of chlamydiae (in particular *Protochlamydia*) whereas cyanobacterial homologs form another distinct group. This gene is part of the DXP pathway that is mainly limited to bacterial and plastids of photosynthetic eukaryotes.

3. Polynucleotide phosphorylase

CLUSTAL X (1.83.1) multiple sequence alignment

46446277_Protochlamydia_amoebo
15605577_Chlamydia_tracho
29840519_Chlamydomyces_caviae
50934417_Oryza_sativa
6006870_Arabidopsis_thalia
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51892669_Symbiobacterium_therm
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56543019_Zymomonas_mobili
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3323203_Treponema_pallid
48894082_Trichodesmium_erythr
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21674467_Chlorobium_tepidu
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24943088_Homo_sapien
24651641_Drosophila_melano
50910551_Oryza_sativa

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51892669_Symbiobacterium_therm
16078732_Bacillus_subtil
56543019_Zymomonas_mobili
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56751675_Synechococcus_elonga
6459851_Deinococcus_radiod
46106240_Rubrobacter_xylo
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48766529_Rhodospirillum_rubrum
45509695_Anabaena_variab
17133532_Nostoc_sp.
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15605776_Aquifex_aeolic
21674467_Chlorobium_tepidu
32141272_Streptomyces_coelic
15827380_Mycobacterium_leprae
24943088_Homo_sapien
24651641_Drosophila_melano
50910551_Oryza_sativa

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46446277_Proteochlamydia_amoebo
15605577_Chlamydia_tracho
29840519_Chlamydia_caviae
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CM1081_Cyanidioschyzon_merolae
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16078732_Bacillus_subtil
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48784235_Burkholderia_fungor
45658536_Leptospira_interr
15644097_Thermotoga_mariti
56751675_Synechococcus_elonga

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6459851_Deinococcus_radiod
46106240_Rubrobacter_xylano
15073173_Sinorhizobium_melilo
48766529_Rhodospirillum_rubrum
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56543019_Zymomonas_mobili
49176320_Escherichia_coli
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50934417_Oryza_sativa
6006870_Arabidopsis_thalia
CM1081_Cyanidioschyzon_merolae
16803371_Listeria_monocy
42523058_Bdellovibrio_bacter
51892669_Symbiobacterium_therm
16078732_Bacillus_subtil
56543019_Zymomonas_mobili
49176320_Escherichia_coli
55981108_Thermus_thermo
30248196_Nitrosomonas_europa
19712941_Fusobacterium_nuclea
48784235_Burkholderia_fungor
45658536_Leptospira_interr
15644097_Thermotoga_mariti
56751675_Synechococcus_elonga
6459851_Deinococcus_radiod
46106240_Rubrobacter_xylano
15073173_Sinorhizobium_melilo
48766529_Rhodospirillum_rubrum
45509695_Anabaena_variab
17133532_Nostoc_sp.
3323203_Treponema_pallid
48894082_Trichodesmium_erythr
53715606_Bacteroides_fragil
15605776_Aquifex_aeolic
21674467_Chlorobium_tepidu
32141272_Streptomyces_coelic
15827380_Mycobacterium_leprae
24943088_Homo_sapien
24651641_Drosophila_melano
50910551_Oryza_sativa

MDAGVPIKAPVAGIAMGLIILDRAILSDISGIEDHLGDMDFKVAGTAKGI
MDAGVPIKTPVAGIAMGLIILDNVTILSDISGLEDYLGDMDFKVAGNTEGI
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MDAGVPIKPPVSGAAMGLIKEGVRVLTDIQGIEDFLGDMDFKVAGTDAGI
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MDAGVPIKPPVSGAAMGLIKEDVRILTDIQGIEDFLGDMDFKVAGTDSGI
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46446277_Protoclamydia_amoebo
15605577_Chlamydia_tracho
29840519_Chlamydomonas_caviae
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45509695_Anabaena_variab
17133532_Nostoc_sp.
3323203_Treponema_pallid
48894082_Trichodesmium_erythr
53715606_Bacteroides_fragil
15605776_Aquifex_aeolic

TAFQMDIKVEGITIEIMRVALKQAKEGRVHILNKMLAVCPTYKGEMSRYA
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TSVQMDIKVKGITKEIMLDALKQAREGRLYILEKMYEAIPEPRKEPHPYT

21674467_Chlorobium_tepidu
32141272_Streptomyces_coelic
15827380_Mycobacterium_leprae
24943088_Homo_sapien
24651641_Drosophila_melano
50910551_Oryza_sativa

TACQMDIKIDGLDYHILETALEQARKGRHLILDVMAEAI PESRADIGKYA
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TALQLDTKLDGIPSOVLGALAQAKDARLTILEVMAEAI DRP-DEMSPYA
TALQADIKLPGIPIKIVMEAIQQASVAKKEILQIMNKTI SKPRSRKENG
TAIQADLKIPGIPLKVVME SLQKATDAKSNILDIMSEAI REPRKYPKESW
TAIQLDIKPAGIPLDIICESLEPARKARNQILDRMDQEISSARAFNDGSS
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32141272_Streptomyces_coelic
15827380_Mycobacterium_leprae
24943088_Homo_sapien
24651641_Drosophila_melano
50910551_Oryza_sativa

PRIETIQIKPSKIAVVIKQIRAIIEQTGVQIDIDGLVNIAAIDLVSIEKA
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PLILIMKVHPSKVYSLIKKVKSI IEEESGVEIDMQGTVKI MAIDVASLERA
PKIKIINIDPKRIGDVIRVRSI IEACGGEIDIEGVVSI LGPETELLERA
PKIITLNIKPEKIKDVIKQINAI IDETGVKIDIEGTVYIASQDQAMNRKA
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PKILTMTINPKIRDVIKQINKI I EETGVKIDIEGTIFISSTDESGNQKA
PRIETMSVPKDKIRDVIKVI REIVATTGAKVDIEGTVRLSSSDPANIEEA
PRIHTIKINPKIKDVISVIRALTEETGT TIEIEGTVKIAATDGEKAKHA
PRILSLKVPVEKIGLVKNVRALEE-LGVEVDIEGTVRIYSSDLQAALEA
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PRVEVIQIPTDKIGLLIKTINALQDEYGVNISVEGTVYVAGVEGMSVKA
PRIEMNIPVDKIREVIVKVI REIVKTKGAKINIDGTVKIASASAKEIEEA
PRITTIKVPQKQVREVIKVI REITEVTGTKIDIEGTIKIASADAEATQRA
PRLLTIKIDPDMIGLVIKT IKGITEETGAKIDIEGTVTISAVDENKAKRA
PRLTIKIDPDMIGLVIKT IKGITEETGAKIDIEGTVTISAVDENKAKRA
PHIESFKIAVEKIGALIKTVKSLSDQYRV TINTDGTVTVSGRDAQSVFDA
PRLLSFKIDPEMIGLVIKT IKGITEETGAKIDIDGTVTIAAADGEKAKQA
PRIETMTIPKEFIGAVIKI IQGMQEETGATITIEGRIEISGNTKKSIDDA
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PRLTTIQIPVDAIGMVIETRSITEETGAEINIDGTVTIACSSPEATKAA
PRIITTIKIPVDKIGEVIKMINQIQEDTGADITIEGTIYI GAAQGSQAEAA
PRVITIKVPEVVKIGEVIVKVINAI EETGAQISIEGTVFGATDGLSAQAA
PVVETVQVPLSKRAKRVYNLKKLQAE TGVTISQVETFSVFAPTSPVMHEA
PVSETLTVEPQQAQLILHMKRIYLETG TSLTAVTHFNVFAPSQAAMDEA
PRLATLSFSSDSLRLKLLFHRKKIEQETGARVSVSGT VTTI VAKTQPI MDKA
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55981108_Thermus_thermo
30248196_Nitrosomonas_europa
19712941_Fusobacterium_nuclea
48784235_Burkholderia_fungor
45658536_Leptospira_interr
15644097_Thermotoga_mariti
56751675_Synechococcus_elonga
6459851_Deinococcus_radiod

KAIHGLTIEIGRIYSGKAIS IAPFGVFVEILPGKEGLCHIVKQGDMLMV
KELIEGLTVEVGKVVYNGRVTS IATFGVFVEVLPGKEGLCHIVKEGDKLAV
KSMIEGLVVEVGKIYEGRVTS IVPFGAFVEILPGKEGLCHIVKQGDILAV
KAIIANLTPKVGEIYNCEIKT IAPYGA FVEIAPGREGLCHIFKVGDRI DV
KAIISGLTPSVGDYINCEIKSMAPYGA FVEIAPGREGLCHIVKVGDRIDV
ARMIRNITVEVPSQVQARVTKVLPFGAYVELDPGKEGLHILREDQVIAV
IAIIEDIVVEVGEVYTGKVRRI EKFGAFVELFKGTDGLVHILKLGDEVTV
IAMINDIIAEVGTKYKGRIVKIAEFGAFVEILPNTQGLLHILKEGEI DV
RQMIEALVPEPGMIYTGVRTRLMQFGAFVEILPGKEGLVHIVNIGDEVTV
KKIIEDLVVEVGLYLGKVKRI EKFGAFVEIFSGKDGLVHIVKIGDEILV
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IRRIEETIEVGRVYTGKVRTRIVDFGAFVAIGGGKEGLVHILQMGQEVVP
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RKRIEDITVEVGRIYEGTVLKLDFGAI VSVLPKGDGLLHILKEGQTVRV
LKLVD SFVVEYNEVEYGRVVS IMKFGAFMEILPGKEGLLHILSVGDVFKV
KKRIENITVEVGVYEGTVLKLDFGAI VNILPGKDGLLHILKDGQOVKV
AKMVDGFFVEVGVKIYEGKVKRIADFGAFVEILPGKEGLCHIVKEGDI IRV
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KSIIEGMTITAGDVYIGKVTRI IPIGAFVEFLPGKEGMIHILTVGDEVVV
KARIEAVTAKVGEFEFGTVVKIAPFGAFVNLFPQDGLMHLITVGDKLVK

46106240_Rubrobacter_xylano VSAIKGMTVEAGDIYVGKVVKTTFNGAFVELTPGRDGLLHILNEGDVVKV
15073173_Sinorhizobium_melilo RKWIHSIVPEVGVQVYEGTVVKTADFGAFVNFPGARDGLVHIVKEGDKVWV
48766529_Rhodospirillum_rubrum VDVIKGIPEIGVYVYTKVVKIMDFGAFVNFGLGTRDGLVHIVNVGDQVKV
45509695_Anabaena_variab RNIVQGMTLNEGDVYAGRVTRIIPIGAFVEFLPGKEGMIHIVAVGDEVIV
17133532_Nostoc_sp. RNIVQGMTLNEGDVYAGRVTRIIPIGAFVEFLPGKEGMIHIVAVGDEVIV
3323203_Treponema_pallid KVAVVGLTPRVGRVYQGVVKRIVEFGAFVEIFPGKEGLCHVLOEGQRICV
48894082_Trichodesmium_erythr CNIIQGMTLNPGDVYVGRVTRIIPIGAFVEVFAGKEGMVHILAIGDEVIV
53715606_Bacteroides_fragil IRLIKGIVPEVGEVYKGVRSIMPYGAFFVEFLPGKDGLLHIKEGDEIEV
15605776_Aquifex_aeolic KOMIQDIVVEVGAVYKGTITRVEPYGVFVELWPGKIGLLHVYKVGEEIIV
21674467_Chlorobium_tepidu VETIKTLVPEVGTIYMGKVRDIRDLGAFVEFLPKTDGLVHILKVGDRIV
32141272_Streptomyces_coelic RATINGIAPVGERYLGTVVKTTFNGAFVSLPGKDGLLHILVGVAKVQV
15827380_Mycobacterium_leprae INKINAIAPTVERFLGTVVKITEFGAFVSLPGRDGLVHIVNVGDKLRV
24943088_Homo_sapien RDFITEICLEFGAVYTATI TEIRD TGVMVKLYPMTAVLLHNLEVGQEIQV
24651641_Drosophila_melano KELIEGYMLFEGGIYTAKITELRDTGVMVILYPMPALLHNLEVGQEIQV
50910551_Oryza_sativa IEKVEFLVIEVGRYKGVSSIKEYGAFVEFNGGQQLLHIVSVGQVLSL

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46446277_Proteochlamydia_amoebo KVLDINERGQIKLSR
15605577_Chlamydia_tracho KLLSINEKGQLKLSH
29840519_Chlamydophila_caviae KLLSINEKGQYKLSH
50934417_Oryza_sativa KLIEINDKGQLRLSS
6006870_Arabidopsis_thalia KLIEVNEKGQLRLSV
CM1081_Cyanidioschyzon_merolae KVLEVNARGQVRVSR
16803371_Listeria_monocy KVIEVDQQRVNLRSR
42523058_Bdellovibrio_bacter KVLEVDRSGRVKLSR
51892669_Symbiobacterium_therm KVTEIDRLGRINLSI
16078732_Bacillus_subtil KVTEIDKQGRVNLRSR
56543019_Zymomonas_mobili KVLEIDNRGKVRLSM
49176320_Escherichia_coli KVLEVDRQGRIRLSI
55981108_Thermus_thermo KVHRIDERGKIDLIR
30248196_Nitrosomonas_europa KVLEADEKGRRLLSM
19712941_Fusobacterium_nuclea RVISM-EGGKISLSK
48784235_Burkholderia_fungor KVIQTDEKGRVRLSA
45658536_Leptospira_interr KVLNVDKTGKIDLSR
15644097_Thermotoga_mariti QVINIDDLGRLQFKR
56751675_Synechococcus_elonga KVREIDQKGRVNLTR
6459851_Deinococcus_radiod KIANIDDRGKIDLIR
46106240_Rubrobacter_xylano RVLEIDKQNRISLEM
15073173_Sinorhizobium_melilo KLMGFDERGKVRLSM
48766529_Rhodospirillum_rubrum KCVGFDDRKGKIKLSM
45509695_Anabaena_variab KVREIDNKGRINLTR
17133532_Nostoc_sp. KVREIDNKGRINLTR
3323203_Treponema_pallid KLIDIDRMGRNLNSY
48894082_Trichodesmium_erythr KVREIDSKGRVNLTR
53715606_Bacteroides_fragil KLIDIPKTGKFKLSR
15605776_Aquifex_aeolic KVLDDLDELGRPRFTT
21674467_Chlorobium_tepidu KLIDVPRTGKFALSI
32141272_Streptomyces_coelic EIAEIDSRGKLSLIP
15827380_Mycobacterium_leprae EIADIEKRGKISLVL
24943088_Homo_sapien KYFGRPADGRMRLSR
24651641_Drosophila_melano KYFGRPVSGFMRLSR
50910551_Oryza_sativa TCIGQDLRGNIKLSL

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46446277	<i>Parachlamydia</i>	FYLQYSPFPYVSVGEVGRVAPGRREIGHGKLAERALMAVPTKEQFPYTRLESNITESNG	442
15605577	<i>Chlamydia</i>	FYLQYFPFPFVSVGEVGRIGSPGRREIGHGKLAEKALSHVLPETSRFPYIIRLESNITESNG	436
29840519	<i>Chlamydophila</i>	FYLQYFPFPFVSVGEVGRIGSPGRREIGHGKLAEKALSHLTPDPAKFPYTRLESNITESNG	435
50934417	<i>Oryza</i>	FYLQYTFPPSSVGEVGRIGAPNRREIGHGMLAERALEPILPPEEDFPYTRVLESNITESNG	570
6006870	<i>Arabidopsis</i>	FYLQYTFPPSSVGEVGRIGAPNRREIGHGMLAERALEPILPPEEDFPYTRVLESNITESNG	595
cm1081	<i>Cyanidioschyzon</i>	FYLQYMFPPFAVGEVGRIGAPGRREIGHGMLAQRALPVPVPPREVFPYTRVLESNITESNG	555
16803371	<i>Listeria</i>	FMHHYNFPQFVSVGETGPRRAPGRREIGHGALGERALQYVIPSEEEFPYTRVLESNITESNG	438
48833185	<i>Magnetococcus</i>	FYLNYTFPPYCVGETGRMGAPGRREIGHGKLATRALTAIVPSAEVFPYTLRITSEITESNG	439
42523058	<i>Bdellovibrio</i>	FMLHYNFPFYVSVGEVGRMGSSTRREIGHGNLAERAIKAVLPDFEKFYTRVLESNITESNG	439
1892669	<i>Symbiobacterium</i>	FMHHYNFPFYVSVGETRPLRGPGRREIGHGALAEALPVPVPEEEFPYTRVLESNITESNG	450
16078732	<i>Bacillus</i>	FMHHYNFPQFVSVGETGPMRGPGRREIGHGALGERALEPVPSEKDFPYTRVLESNITESNG	437
56543019	<i>Zymomonas</i>	FMLHYNFPFYVSVGEVGRFGAPGRREIGHGKLAERALEPVPVPSKADFPYTRVLESNITESNG	434
49176320	<i>Escherichia</i>	FLFHYNFPFYVSVGETGMVGSPPKREIGHGRLAKRGLAVMPDMDFPYTRVLESNITESNG	459
55981108	<i>Thermus</i>	FLVHYNFPFSTGEVRRLRGVSRRVEVGHGNLAKRALKAVMPKEEDFPYTRVLESNITESNG	448
30248196	<i>Nitrosomonas</i>	FMLHYNMPPFATGETGRVGTPKRREIGHGRLAKRALLAVIPVVEEFGYSMRVSEITESNG	436
19712941	<i>Fusobacterium</i>	FYLHYNFPFYVSVGEVGRMGSPPRREIGHGSLAERALSYPVPEEEFPYTRVLESNITESNG	449
56415214	<i>Salmonella</i>	FLFHYNFPFYVSVGETGMVGSPPKREIGHGRLAKRGLAVMPDMDFPYTRVLESNITESNG	436
48784235	<i>Burkholderia</i>	FMLHYNMPPFATGETGRVGSPPKREIGHGRLAKRALAACLPSADEFGYSIRVSEITESNG	441
45658536	<i>Leptosira</i>	FMLHYNFPFAFVSVGEVRRSSGPRREIGHGNLAERALKLVLPKDFEFPYTRVLESNITESNG	435
15644097	<i>Thermotoga</i>	FMLHYNFPFCTGEVVKPLRGPGRREIGHGHLAERALKMNLPEEEFPYTRVLESNITESNG	438
56751675	<i>Synechococcus</i>	YLHYNMPPYVSVGETRPMRGPGRREIGHGALAEALPVLPSKEEFPYTRVLESNITESNG	445
6459851	<i>Deinococcus</i>	FLHYNMPPYVSVGETKRMGQSRREIGHGNLAKRAIRAVLPSFEEFPYTRVLESNITESNG	471
46106240	<i>Rubrobacter</i>	YMHYYPFPYSTGETRGLGPPRRREIGHGALAEALPVPVPEEEFPYTRVLESNITESNG	416
8766529	<i>Rhodospirillum</i>	FMLHYNFPFYVSVGEAGRMGSPGRREIGHGKLAERAIHPMMPAKDAFPYTRVLESNITESNG	436
23349057	<i>Bruceella</i>	FMLHYNFPFYVSVGETGRMGSPPRREIGHGKLAERAIHPMLPAEAFQFPYTRVLESNITESNG	438
45509695	<i>Anabaena</i>	YLHYNMPPFVSVGETKPLRAPGRREIGHGALAEALPVLPPKEQFPYTRVLESNITESNG	446
17133532	<i>Nostoc</i>	YLHYNMPPFVSVGETKPLRAPGRREIGHGALAEALPVLPPKEQFPYTRVLESNITESNG	446
3223203	<i>Treponema</i>	FILHYNFPFVSVGEIGRMGV--GRREIGHGCLAHRSLSAVLPDEQFPYTRVLESNITESNG	434
48894082	<i>Trichodesmium</i>	YLHYNMPPFVSVGETKPLRQPGRREIGHGALAEALPVPKSDIFPYTRVLESNITESNG	446
53715606	<i>Bacteroides</i>	FLHYNMPPFVSVGETGEAKAQRGGRREIGHGNLAHRALKRMIP--EDYPVVRVSDILESNG	438
15605776	<i>Aquifex</i>	FMLHYSMPFVSVGEAKPWGPPRRREIGHGALAEALPVLPEEEFPYTRVLESNITESNG	435
21674467	<i>Chlorobium</i>	FMLHYNMPPFVSVGEIGRVGAGRREIGHGNLAERAIKVMPSQEFYTRVLESNITESNG	453
32141272	<i>Streptomyces</i>	YMHYNMPPYVSVGETGRVGSPPKREIGHGALAEALPVLPTREFPYTRVLESNITESNG	460
6968686	<i>Campylobacter</i>	FMVYNMPPFVSVGEASPIKAPGRRELGHGNLAKRALYPSV--DENYPYTRVLESNITESNG	457
15827380	<i>Mycobacterium</i>	YMHYNMPPFVSVGETGRVGSPPKREIGHGALAEALPVLPSVEEFPYTRVLESNITESNG	474
24943088	<i>Homo</i>	FMLHYEFPYATNEIGKVTGLNRRRELGHGALAEKALYVPIV--RDFPPTTRVLESNITESNG	481
24651641	<i>Drosophila</i>	FMLHYEFPYATNEIGKVTGLNRRRELGHGALAEKALYVPIV--RDFPPTTRVLESNITESNG	479
50910551	<i>Oryza</i>	FMLHYSFPFVSVGEVGRIGVGRREIGHGALAEKALYVPIV--RDFPPTTRVLESNITESNG	500

Figure 3a. A segment of multiple protein sequence alignment of polynucleotide phosphorylase showing conserved residues shared by chlamydiae, red algae and green plants.

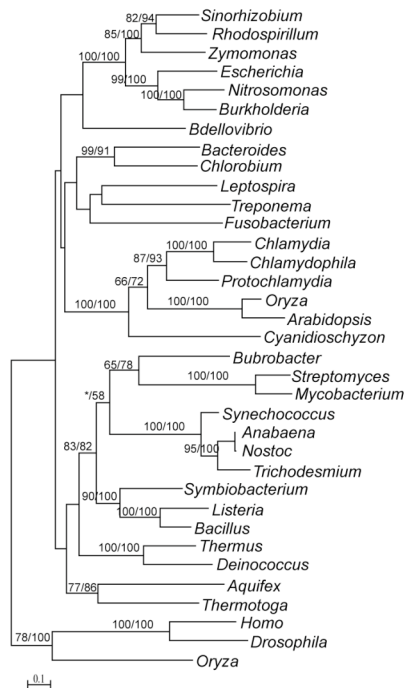


Figure 3b. Phylogeny of polynucleotide phosphorylase showing that sequences of chlamydiae, red algae and green plants form a monophyletic group that is distinct from those of cyanobacteria.

4. Aspartate transaminase

CLUSTAL X (1.83.1) multiple sequence alignment

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15605813_Aquifex_aeolic            FSDRLKVLPPYLFAELDRKKQEKIVIDLGVGDPDMPTPKPIVEAAKKALE
45505954_Anabaena_variab          FAKRLEKIPPYLFAEINRKRREALIINIGVGDPPKTPAHILQAMREAI
48894959_Trichodesmium_erythr     FAKKLEKISPYPLTEINRKKNELIINFGAGDPDQPTPNHIVQAMHEAIK
67920389_Crocospaera_watsonii     RADRLNALPPYVFARLDELKAKARLIDLGMGNPDGMAPQPVIDGAIALQ
68270744_Moorella_thermo          EARRIRELPPYLFARIEKKAIEARIISLIGIDPDMPTPSHVIDKLVAEAH
57234493_Dehalococcoides_ethen    LSKRIENLPPYLFVQISKKIAEKRVISFAIGDPLPTPKHILAEELCKAAE
67917639_Chlorobium_limico        QFDKIKRLPKYVFAAVNELKMAERVIDFSMGNPDGPTQHIVDKLVESIN
57168677_Campylobacter_coli       RFNTIERLPPYVFAEVNAIKMAARIIDFSMGNPDGKTPQHIIDKLCESAN
70731920_Pseudomonas_fluore       RFARIDRLPPYVFNITAEKMAARIIDLSMGNPDGPTPHIVEKLVTVAQ
26248758_Escherichia_coli         RFTRIDRLPPYVFNITAEKMAARIIDFSMGNPDGATPPHIVEKLVTVAQ
68558669_Ralstonia_metall         RFARIDRLPPYVFNITAEKMAARIIDMSMGNPDGATPHIVAKLVDAQAQ
48765475_Rhodospirillum_rubrum    DFYRIKRLPPYVFAEVNAMKARARIIDLGMGNPDQPTQHIVDKLCEAAT
68193651_Mesorhizobium_sp.        EFHKVRRLLPPYVFEQVNRKASARIIDLGMGNPDLPTPKAIVDKLCEVVR
45509383_Anabaena_variab          PADRIQQLPPYVFARLDELKAKARLIDLGMGNPDGATPPVVDAAIQALQ
52079908_Bacillus_lichen          HSDVLKQLPEQFFASLVKKVNEKIVINLGGQGNPDQPTPEHIVDTMAQAVR
89894681_Desulfitobacterium_ha     KARRLSSLGASVFTMDDLKLELEINLSIGSPDRSPSAEIRKVLAEGLV
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68004982_Geobacter_metall         NDNYLKLKAGYLFPEIGRRVREFSVIRLIGDVTTRPLPAPVIAKAFHDAVD
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45505954_Anabaena_variab          EASNYPPEYEGTQEFREAAVKWMERLNPNTVEVSSIGSKEAINTFLAFEA
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67917639_Chlorobium_limico        KPRTYSVSKGIYKLRGAVGSWYRRLDLDRVVVVTMGSKYVHLVQAINP
57168677_Campylobacter_coli       KDKTYSTSMGIYKLRLAICNWKRLDPESEVVATMGSKYVHLVQAINP
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68558669_Ralstonia_metall

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48765475_Rhodospirillum_rubrum
68193651_Mesorhizobium_sp.
45509383_Anabaena_variab
52079908_Bacillus_lichen
89894681_Desulfitobacterium_ha
18893347_Pyrococcus_furios
53796147_Chloroflexus_aurant
56784224_Oryza_sativa
14601942_Aeropyrum_ernix
CM2642_Cyanidioschyzon_merolae
37703720_Oryza_sativa
21436149_Arabidopsis_thalia
37703722_Oryza_sativa
25315768_Arabidopsis_thalia
62184887_Chlamydomypha_abortu
8163283_Chlamydia_muridarum
46399960_Protoclamydia_amoebo
48895399_Trichodesmium_erythr
72382904_Prochlorococcus_marin
23124300_Nostoc_puncti
67924273_Crocospaera_watson
56750696_Synechococcus_elonga
53713935_Bacteroides_fragil
67916709_Clostridium_thermo
68004982_Geobacter_metal
45658671_Leptospira_interr
84489723_Methanosphaera_stadtm
2621088_Methanothermobacter_th
89896148_Desulfitobacterium_ha

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11498021_Archaeoglobus_fulgid
15605813_Aquifex_aeolic
45505954_Anabaena_variab
48894959_Trichodesmium_erythr
67920389_Crocospaera_watsonii
68270744_Moorella_thermo
57234493_Dehalococcoides_ethen
67917639_Chlorobium_limico
57168677_Campylobacter_coli
70731920_Pseudomonas_fluore
26248758_Escherichia_coli
68558669_Ralstonia_metal
48765475_Rhodospirillum_rubrum
68193651_Mesorhizobium_sp.
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53796147_Chloroflexus_aurant
56784224_Oryza_sativa
14601942_Aeropyrum_ernix
CM2642_Cyanidioschyzon_merolae
37703720_Oryza_sativa
21436149_Arabidopsis_thalia
37703722_Oryza_sativa
25315768_Arabidopsis_thalia
62184887_Chlamydomypha_abortu
8163283_Chlamydia_muridarum
46399960_Protoclamydia_amoebo
48895399_Trichodesmium_erythr
72382904_Prochlorococcus_marin
23124300_Nostoc_puncti
67924273_Crocospaera_watson

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56750696_Synechococcus_elonga
53713935_Bacteroides_fragil
67916709_Clostridium_thermo
68004982_Geobacter_metall
45658671_Leptospira_interr
84489723_Methanosphaera_stadtm
2621088_Methanothermobacter_th
89896148_Desulfitobacterium_ha

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19915595_Methanosarcina_acetiv
11498021_Archaeoglobus_fulgid
15605813_Aquifex_aeolic
45505954_Anabaena_variab
48894959_Trichodesmium_erythr
67920389_Crocospira_watsonii
68270744_Moorella_thermo
57234493_Dehalococcoides_ethen
67917639_Chlorobium_limico
57168677_Campylobacter_coli
70731920_Pseudomonas_fluore
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62184887_Chlamydomonas_reinhardtii
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68004982_Geobacter_metall
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84489723_Methanosphaera_stadtm
2621088_Methanothermobacter_th
89896148_Desulfitobacterium_ha

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SAEFVGRLLIDEAGIVCTPGNGFGEYGEYFRISLTVPTERLLEAAER
STEFITLLLDKCGIVVPPGVYGVSGEGYFRIALTICEERLHEAIQR
SQEFATLLEKCGIIVVPGNAYGTSGEYFRIALTVEDKRISOALQR
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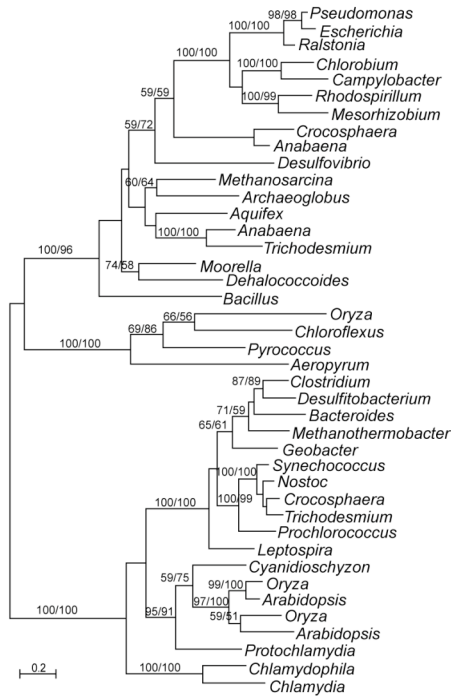


Figure 4. Phylogeny of Aspartate transaminase. It appears that gene duplication, differential losses and gene transfer were involved in the evolution of this gene. In the lower part of the tree, red algae and green plant sequences form a monophyletic group with *Protochlamydia* homolog with strong support whereas cyanobacterial sequences form another distinct clade. Two other chlamydial sequences appear to be more distant from those of *Protochlamydia*, red algae and green plants.

5. Bacterial tyrosyl-tRNA synthetase
 CLUSTAL X (1.83.1) multiple sequence alignment

17935718_Agrobacterium_tumefa	RGFIHQIVTAYIGYDPTASSLHVGHLLTQIMMLHWMQKGTGHQPISLMGGGT
13470335_Mesorhizobium_loti	RGFIHQIVTAYVGYDATATSLHIGNLISATMLYWLQETGHRPIALMGGGT
67916376_Clostridium_thermo	RGYIAQLITFYIGFDPTADSLHVGHFLOMMVMAHMOKAGHRPIALIGGGT
34764162_Fusobacterium_nuclea	RGYLKQLVTFYIGFDPTADSLHVGHFIAMMFMAHMQQHGRPIALAGGGT
15639820_Treponema_pallid	RGFIRQCLTFYVGVDPDPTGSSLHVGHMLPMFALKHLCDAGHRGCVLIGGGT
16768608_Drosophila_melano	RGFFHGIQSIYAGFDPTADSLHVGNLLVIMGLIHCQRAGHRPIALVGGAT
7705710_Homo_sapien	RGLFKDFQTIYCGFDPTADSLHVGHLLALLGLFHLQRAGHNPIALVGGAT
89306341_Tetrahymena_thermo	RELLFQCF SAYAGFDPTADSLHMGNLSISILTMIRLSLLGIKPIILLVGGAT
66815010_Dictyostelium_discoi	RGFIHQMVSLYAGFDPTADSLHIGNLLTLMVMLHFKRHGHNPPIALMGGAT
34914470_Oryza_sativa	RGLVEATLKAYCGFDPTAESLHLGNLLGLVVLVSWFRRCCGHNAVALVGGAT
6957729_Arabidopsis_thalia	RGLLESILRVYCGFDPTAESLHLGNLLGIIVLSWFQRCGHQAVGLIGGAT
153655_Chlamydomonas_reihd	RGLIQEVLVSVYCGFDPTADSLHLGNLLGIIVLAWFQRCGHEPVALVGGAT
46400444_Protochlamydia_amoebo	RGFIDAVIKVYCGFDPTADSLHLGNLVAIMGLAWFQRFQGHTPVAIVGGAT
CM3397_Cyanidioschyzon_merolae	RGLIDAVVAVYVGFDPDPTADSLHIGNLLGLLVLRFQKLGHRPVAIIGGAT
76788775_Chlamydia_tracho	RGILDNSVSAYLGFDPDPTAPSLHIGHWIGICFLRRLAAYGITPVALVGGAT
15618276_Chlamydomonas_pneumo	RNILENFIAAYLGFDPDPTAPALHIGHWIGICFLKRLAALGITPVALVGGAT
66854407_Anaeromyxobacter_deha	RSLVHDQITGYVGFDPDPTADSLHVGHLLAVMSLAWLQRCGGTPIIVVGGGT
53711359_Bacteroides_fragil	RGMVHDMVTAYVGDPTADSLHIGHLCGMILRHFQRCGHKPLALIGGAT
16080019_Bacillus_subtil	RGLIQMIRLYSGFDPTADSLHIGHLLPILTLRRFQLAGHHPPIALVGGAT
29376289_Enterococcus_faecal	RGLVYQVVKLYIGFDPTADSLHIGHLLPILMLRRFQONGHVPPIALVGGGT

75212974_Escherichia_coli
22125858_Yersinia_pestis
59800530_Neisseria_gonorr
34498527_Chromobacterium_viola
32446275_Rhodopirellula_baltic
6325160_Saccharomyces_cerevi
75907148_Anabaena_variab
71675409_Trichodesmium_erythr
33861885_Prochlorococcus_marin
46579366_Desulfovibrio_vulgar
15595865_Pseudomonas_aerugi
16080897_Bacillus_subtil
4980991_Thermotoga_mariti
15606818_Aquifex_aeolic
67919131_Chlorobium_limico
45657564_Leptospira_interr
6460463_Deinococcus_radiod
76260159_Chloroflexus_aurant

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17935718_Agrobacterium_tumefa
13470335_Mesorhizobium_loti
67916376_Clostridium_thermo
34764162_Fusobacterium_nuclea
15639820_Treponema_pallid
16768608_Drosophila_melano
7705710_Homo_sapient
89306341_Tetrahymena_thermo
66815010_Dictyostelium_discoi
34914470_Oryza_sativa
6957729_Arabidopsis_thalia
153655_Chlamydomonas_reiherd
46400444_Protochlamydia_amoeba
CM3397_Cyanidioschyzon_merolae
76788775_Chlamydia_trachoma
15618276_Chlamydomonas_pneumoniae
66854407_Anaeromyxobacter_dehalogenans
53711359_Bacteroides_fragilis
16080019_Bacillus_subtilis
29376289_Enterococcus_faecalis
75212974_Escherichia_coli
22125858_Yersinia_pestis
59800530_Neisseria_gonorrhoea
34498527_Chromobacterium_violaceum
32446275_Rhodopirellula_baltica
6325160_Saccharomyces_cerevisiae
75907148_Anabaena_variabilis
71675409_Trichodesmium_erythrorhizon
33861885_Prochlorococcus_marinus
46579366_Desulfovibrio_vulgaris
15595865_Pseudomonas_aeruginosa
16080897_Bacillus_subtilis
4980991_Thermotoga_maritima
15606818_Aquifex_aeolicus
67919131_Chlorobium_limicola
45657564_Leptospira_interrans
6460463_Deinococcus_radiodurans
76260159_Chloroflexus_aurantiacus

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67916376_Clostridium_thermo
34764162_Fusobacterium_nuclea
15639820_Treponema_pallid

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 34764162_Fusobacterium_nucleatum
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 16768608_Drosophila_melano
 7705710_Homo_sapient
 89306341_Tetrahymena_thermo
 66815010_Dictyostelium_discoi
 34914470_Oryza_sativa
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 46400444_Proteochlamydia_amoebos
 CM3397_Cyanidioschyzon_merolae
 76788775_Chlamydia_trachomatis
 15618276_Chlamydomonas_pneumoniae
 66854407_Anaeromyxobacter_dehalogenans
 53711359_Bacteroides_fragilis
 16080019_Bacillus_subtilis
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 75212974_Escherichia_coli
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76260159_Chloroflexus_aurant

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17935718_Agrobacterium_tumefa
13470335_Mesorhizobium_loti
67916376_Clostridium_thermo
34764162_Fusobacterium_nuclea
15639820_Treponema_pallid
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66815010_Dictyostelium_discoi
34914470_Oryza_sativa
6957729_Arabidopsis_thalia
153655_Chlamydomonas_reihd
46400444_Protoclamydia_amoebo
CM3397_Cyanidioschyzon_merolae
76788775_Chlamydia_tracho
15618276_Chlamydomonada_pneumo
66854407_Anaeromyxobacter_deha
53711359_Bacteroides_fragil
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22125858_Yersinia_pestis
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32446275_Rhodospirillum_baltic
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6460463_Deinococcus_radiod
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67916376_Clostridium_thermo
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15639820_Treponema_pallid
16768608_Drosophila_melano
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34914470_Oryza_sativa
6957729_Arabidopsis_thalia
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46400444_Protoclamydia_amoebo
CM3397_Cyanidioschyzon_merolae
76788775_Chlamydia_tracho

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 33861885_Prochlorococcus_marin
 46579366_Desulfovibrio_vulgar
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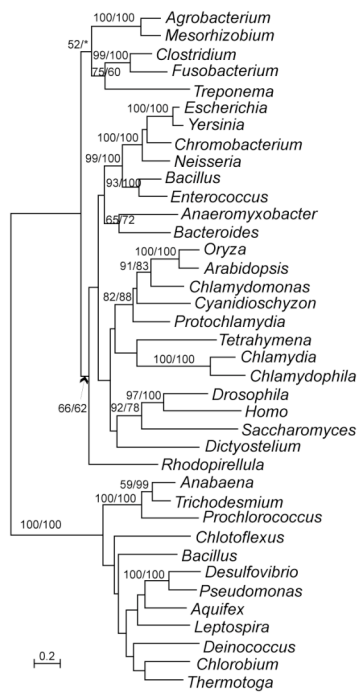


Figure 5. Phylogeny of bacterial tyrosyl-tRNA synthetase. Again, sequences of red algae, green plants and *Protochlamydia* form a monophyletic group. Sequences of *Chlamydia* and *Chlamydomonada* group with *Tetrahymena* homolog, but with insignificant support. The sequences of *Dictyostelium*, *Saccharomyces*, and *Homo* are annotated to be mitochondrial precursors and therefore of likely α -proteobacterial origin.

6. Oligoendopeptidase F

CLUSTAL X (1.83.1) multiple sequence alignment

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15835007_Chlamydia_murida
46400453_Protoclamydia_amoeb
CM3763_Cyanidioschyzon_merolae
87310907_Blastopirellula_marin
32446842_Rhodopirellula_baltic
2688150_Borrelia_burgdo
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WDL SRLYLEEYLR IARVIERVYTYAHL LHDEDLHTRYAEQTSFLEPELVE
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WNI ELLFLKASTGVDRIA EKVGNYAFLQKSSNEVTELSAATSWLMPAIME
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WDL SALFIGEYENLSDAIGRIMS YAFLVFAEDTCNEISEHLLFFEIEFGD
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76259709_Chloroflexus_aurant
55379750_Haloarcula_marism
15790868_Halobacterium_sp.
68194738_Enterococcus_faeciu
16414804_Listeria_innocu
65318570_Bacillus_anthra
56379199_Geobacillus_kausto
68056395_Exiguobacterium_sibir
27467608_Staphylococcus_epider
66856279_Anaeromyxobacter_deha
56380195_Geobacillus_kausto
83319855_Mycoplasma_capric
19714448_Fusobacterium_nuclea
65317438_Bacillus_anthra
27467983_Staphylococcus_epider
34483139_Wolinella_succin
57240464_Campylobacter_lari

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LHNL SKKEERVILRKKASKCF SKTLKQNKLLVYIFNMIKSELASICELR

77740978_Rhodopseudomonas_palu
15075820_Sinorhizobium_melilo
78193764_Geobacter_metal

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77740978_Rhodopseudomonas_palu
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56380195_Geobacillus_kausto
83319855_Mycoplasma_capric
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VYAPISYEEAVSLICDSLTPGLDNYVEALRKGGLGWVDKYENQNKRS GAYS
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MYAPLPYEDAVKSVLASLAPLGDEYLRVASAGLRWVDRYENKGRSGAYS
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TYVPI TWDAQVNVVLESQPLGDEYVSTLEEGLRWADRYENRKGQSGAFS
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VYVPLPYNEAVDIITEALKPLGEEYVKTIRNGLGWVDKYENEGKRSGAFS
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27467983_Staphylococcus_epider
34483139_Wolinella_succin
57240464_Campylobacter_lari
77740978_Rhodopseudomonas_palu
15075820_Sinorhizobium_melilo
78193764_Geobacter_metall

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RNAPLWNEARDTVLSAYHAFAPEMAAIARRFFGWIDAPVRPGKAPGAF
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33235980_Chlamydomydia_pneumo
15835007_Chlamydia_murida
46400453_Protoclamydia_amoeba
CM3763_Cyanidioschyzon_merolae
87310907_Blastopirellula_marin
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SGCYDPYILLNYTNTLYDVSVAIEAHEAGHSMHSYFSREAYHDAQYPLFLAE
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83319855_Mycoplasma_capric
19714448_Fusobacterium_nuclea
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77740978_Rhodopseudomonas_palu
15075820_Sinorhizobium_melilo
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56380195_Geobacillus_kausto
83319855_Mycoplasma_capric
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 15075820_Sinorhizobium_melilo
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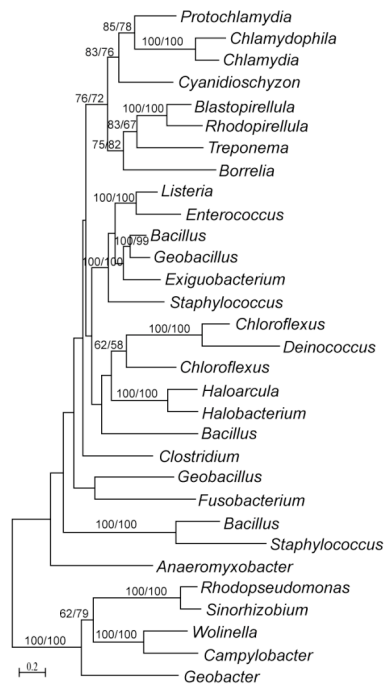


Figure 6. Phylogeny of Oligoendopeptidase F, showing that red algal and chlamydial sequences form a monophyletic group. No significant hits were found in GenBank non-redundant protein sequence database using red algal and chlamydial (*Chlamydomphila* GI 15618060, *Protochlamydia* GI 46400453) sequences as queries.

7. 4-diphosphocytidyl-2-C-methyl-D-erythritol kinase (*ispE*)

CLUSTAL X (1.83.1) multiple sequence alignment

77741291_Rhodopseudomonas_palu
 14026931_Mesorhizobium_loti
 30180818_Nitrosomonas_europa
 47573077_Rubrivivax_gelati
 28868320_Pseudomonas_syring
 46133381_Haemophilus_influe
 50877624_Desulfotalea_psychr
 52216746_Bacteroides_fragil
 67939927_Chlorobium_phaeob
 4981944_Thermotoga_mariti

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 WHAHAKINLALHVTGRRADGYHLIDSLAVFTRFGDRVEINLVLKARDALP
 FPAPAKLNLFHVIGRRREDGYHLLQTVFRFDIDHSRDLHFVLCVRAAKLLL
 VPAPAKLNLFHVIGRRDDGYHLLQSVFALIDWADTLHFVLCVRAAKLLL
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3322649_Treponema_pallidum
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10172673_Bacillus_halodu
17132325_Nostoc_sp.
71676002_Trichodesmium_erythr
67924114_Crocospaera_watson
35210662_Gloeobacter_violac
73659963_Dehalococcoides_sp.
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84518232_Prochlorococcus_marin
54018383_Nocardia_farcin
29607239_Streptomyces_avermi
6460432_Deinococcus_radiod
87310106_Blastopirellula_marin
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166959_Chlamydomonas_reinhard
34908970_Oryza_sativa
46400864_Protochlamydia_amoeb
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19713437_Fusobacterium_nuclea
45599560_Leptospira_interrog

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46133381_Haemophilus_influe
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52216746_Bacteroides_fragil
67939927_Chlorobium_phaeob
4981944_Thermotoga_mariti
67934269_Solibacter_usitat
3322649_Treponema_pallidum
47096183_Listeria_monocyt
10172673_Bacillus_halodu
17132325_Nostoc_sp.
71676002_Trichodesmium_erythr
67924114_Crocospaera_watson
35210662_Gloeobacter_violac
73659963_Dehalococcoides_sp.
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54018383_Nocardia_farcin
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2983445_Aquifex_aeolic
29834922_Chlamydomyxa_caviae
15834807_Chlamydia_murida
166959_Chlamydomonas_reinhard
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67934269_Solibacter_usitat	GLF
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47096183_Listeria_monocyt	ALI
10172673_Bacillus_halodu	GLV
17132325_Nostoc_sp.	ALC
71676002_Trichodesmium_erythr	ALT
67924114_Crocospaera_watson	TLC
35210662_Gloeobacter_violac	GLA
73659963_Dehalococcoides_sp.	TLL
33632756_Synechococcus_sp.	ALF
84518232_Prochlorococcus_marin	AIF
54018383_Nocardia_farcin	FLC
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87310106_Blastopirellula_marin	ALC
2983445_Aquifex_aeolic	FFG
29834922_Chlamydomyxa_caviae	VSY
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166959_Chlamydomonas_reinhard	CFG
34908970_Oryza_sativa	GIG
46400864_Protochlamydia_amoebo	CIG
CM4233_Cyanidioschyzon_merolae	ALG

19713437_Fusobacterium_nuclea TFV
 45599560_Leptospira_interrog GLV

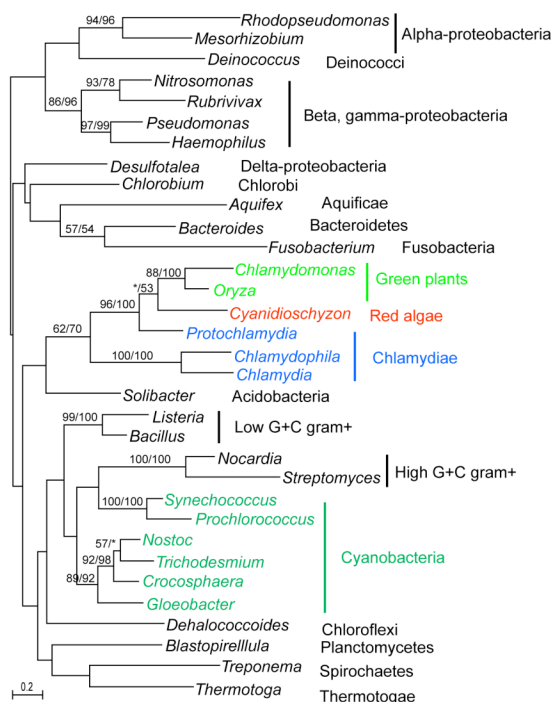


Figure 7. Phylogeny of 4-diphosphocytidyl-2-C-methyl-D-erythritol kinase (*ispE*). Note that sequences of primary photosynthetic eukaryotes form a monophyletic group with those of chlamydiae (in particular *Protochlamydia*) whereas cyanobacterial homologs form another distinct group. This gene is part of the DXP pathway that is mainly limited to bacterial and plastids of photosynthetic eukaryotes.

8. Enoyl-ACP reductase (*fabI*)

CLUSTAL X (1.83.1) multiple sequence alignment

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35214762_Gloeobacter_viol      TLAGKKALITGIANNRSIAWIAQAFHAAGAALAVQIAALFETIAQKWGQ
32447170_Rhodopirellula_baltic  QFEGKKGLIIGVANDHSIAWIAQAEILKQGGKCGFDIRTIFFHTEKTFGK
67932874_Solibacter_usitat     LLEGKFALILGIANKWSLAYIAQAFSREGATLVLDLALTESLQGFQRP
16413428_Listeria_innocu       SLEGKTYVVMGVANKRSIAWAIARSLNEAGAKLVFAITATFETIKDKAGK

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67916335_Clostridium_thermo
16765044_Salmonella_typhim
68058530_Haemophilus_influen
68558071_Ralstonia_metall
2983915_Aquifex_aeolicus
13476200_Mesorhizobium_loti
13474637_Mesorhizobium_loti
67458967_Rickettsia_felis
86155412_Campylobacter_fetus
76259288_Chloroflexus_aurant
39982876_Geobacter_sulfur
68555265_Ralstonia_metall
51857752_Symbiobacterium_therm
50944223_Oryza_sativa
18396215_Arabidopsis_thalia
89898427_Chlamydia_felis
76167348_Chlamydia_tracho
32307472_Bigelowiella_natans
32423792_Phaeodactylum_tricor
46400427_Protoclamydia_amoebo
34555736_Toxoplasma_gondii

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48853605_Cytophaga_hutchin
60491878_Bacteroides_fragilis
67919153_Chlorobium_limico
86740599_Frankia_sp.
66737267_Mycobacterium_tuberc
6459755_Deinococcus_radiod
46199980_Thermus_thermop
23128764_Nostoc_punct
78712168_Prochlorococcus_marin
CM4316_Cyanidioschyzon_merolae
86606338_Synechococcus_sp
35214762_Gloeobacter_viol
32447170_Rhodopirellula_baltic
67932874_Solibacter_usitat
16413428_Listeria_innocu
67916335_Clostridium_thermo
16765044_Salmonella_typhim
68058530_Haemophilus_influen
68558071_Ralstonia_metall
2983915_Aquifex_aeolicus
13476200_Mesorhizobium_loti
13474637_Mesorhizobium_loti
67458967_Rickettsia_felis
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76259288_Chloroflexus_aurant
39982876_Geobacter_sulfur
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51857752_Symbiobacterium_therm
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89898427_Chlamydia_felis
76167348_Chlamydia_tracho
32307472_Bigelowiella_natans
32423792_Phaeodactylum_tricor
46400427_Protoclamydia_amoebo
34555736_Toxoplasma_gondii

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48853605_Cytophaga_hutchin
60491878_Bacteroides_fragilis
67919153_Chlorobium_limico
86740599_Frankia_sp.

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6459755_Deinococcus_radiod
46199980_Thermus_thermop
23128764_Nostoc_punct
78712168_Prochlorococcus_marin
CM4316_Cyanidioschyzon_merolae
86606338_Synechococcus_sp
35214762_Gloeobacter_viol
32447170_Rhodopirellula_baltic
67932874_Solibacter_usitat
16413428_Listeria_innocu
67916335_Clostridium_thermo
16765044_Salmonella_typhim
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89898427_Chlamydomydia_felis
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32307472_Bigelowiella_natans
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46400427_Protoclamydia_amoebo
34555736_Toxoplasma_gondii

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: : . * * : . . * :

48853605_Cytophaga_hutchin
60491878_Bacteroides_fragilis
67919153_Chlorobium_limico
86740599_Frankia_sp.
66737267_Mycobacterium_tuberc
6459755_Deinococcus_radiod
46199980_Thermus_thermop
23128764_Nostoc_punct
78712168_Prochlorococcus_marin
CM4316_Cyanidioschyzon_merolae
86606338_Synechococcus_sp
35214762_Gloeobacter_viol
32447170_Rhodopirellula_baltic
67932874_Solibacter_usitat
16413428_Listeria_innocu
67916335_Clostridium_thermo
16765044_Salmonella_typhim
68058530_Haemophilus_influen
68558071_Ralstonia_metall
2983915_Aquifex_aeolicus
13476200_Mesorhizobium_loti
13474637_Mesorhizobium_loti
67458967_Rickettsia_felis
86155412_Campylobacter_fetus
76259288_Chloroflexus_aurant
39982876_Geobacter_sulfur
68555265_Ralstonia_metall
51857752_Symbiobacterium_therm
50944223_Oryza_sativa
18396215_Arabidopsis_thalia
89898427_Chlamydomydia_felis

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86606338_Synechococcus_sp
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32447170_Rhodopirellula_baltic
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16413428_Listeria_innocu
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67916335_Clostridium_thermo
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16765044_Salmonella_typhim
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68558071_Ralstonia_metall
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39982876_Geobacter_sulfur
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68555265_Ralstonia_metall
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18396215_Arabidopsis_thalia
PLGSRAAKAIGFIDTMI EYSYVNAFLQTADEVGNTAAFLSPLASAITGS
89898427_Chlamydomydia_felis
PLASRAGKAIGFIEKMDYLDWSPITTEQVGAFLVSSLASAITGE

76167348_Chlamydia_tracho PLASRAGKAIGFIERMVDYYQDWAPLPEAEQVGAAAFLVSPLASAITGE
32307472_Bigelowiella_natans PFGSRPARAIGFIERVINYSYKNAPIESAMEVGTAGFLLSPLAFAITGQ
32423792_Phaeodactylum_tricor -----TSQQV-----
46400427_Proteochlamydia_amoebo PLRSRAARAIGFIDRMINYSQVNPAPLQKACEVANVA AFLGSDLACAITGS
34555736_Toxoplasma_gondii PLKSRAASAIGKIDYAIIDYSYNNAPLRHSDDVGGAAFLLSPLARAVSGV

48853605_Cytophaga_hutchin NLMHDGGFSSSTGM
60491878_Bacteroides_fragilis NLFHDGGFSSVGM
67919153_Chlorobium_limico NLFHDGGYSSMGA
86740599_Frankia_sp. IVHVDGGVHAVGI
66737267_Mycobacterium_tuberc ILYADGGAHTQLL
6459755_Deinococcus_radiod TIYVDAGLSIMTV
46199980_Thermus_thermop VVYVDAGYHIMGM
23128764_Nostoc_punct VLYVDAGYEIMGM
78712168_Prochlorococcus_marin TIYVDAGYCINGM
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86606338_Synechococcus_sp VIYVDSGYSILGF
35214762_Gloeobacter_viol TIYVDCGFSIMGG
32447170_Rhodopirellula_baltic ILHVDGGYHAMGS
67932874_Solibacter_usitat CLFVDAGMQVLGF
16413428_Listeria_innocu VIHVDSGYHIIIGF
67916335_Clostridium_thermo VIHVDSGYNIMGI
16765044_Salmonella_typhim VVHVDGGFSAAM
68058530_Haemophilus_influen IVHVDAGFSITAM
68558071_Ralstonia_metall ITYVDGGYNIVGT
2983915_Aquifex_aeolicus VVHVDNGYHIMGV
13476200_Mesorhizobium_loti VHHVDSGYHVVGM
13474637_Mesorhizobium_loti IHYVDSGYHIVSM
67458967_Rickettsia_felis IHYVDCGYNIMGS
86155412_Campylobacter_fetus IHYVDAGYNIMGM
76259288_Chloroflexus_aurant IHYVDAGFNVVVP
39982876_Geobacter_sulfur VHFVDSGYNIIGL
68555265_Ralstonia_metall TVYVDGGVHVMA-
51857752_Symbiobacterium_therm TIYADNGFHIMGV
50944223_Oryza_sativa TVYVDNGLNTMGL
18396215_Arabidopsis_thalia TIYVDNGLNAMGV
89898427_Chlamydophila_felis TLYVDHGANIMGI
76167348_Chlamydia_tracho TLYVDHGANVMGI
32307472_Bigelowiella_natans VVYVDNGLSPMGL
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34555736_Toxoplasma_gondii TLYVDNGLHAMGQ

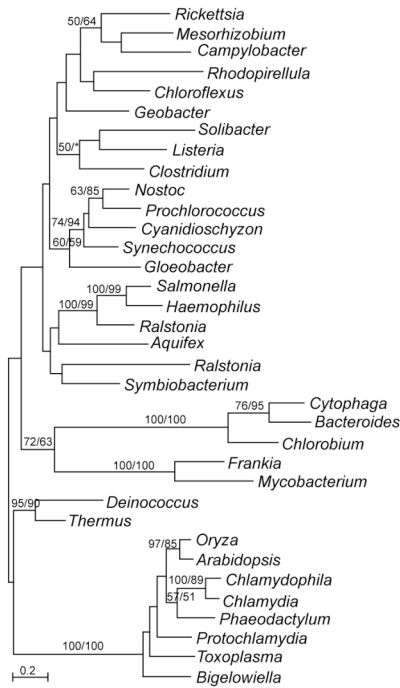


Figure 8. Phylogeny of Enoyl-ACP reductase (*fabI*). Note that sequences from green plants, diatoms, chlorarachniophytes, apicomplexans and chlamydiae form a strongly supported group whereas cyanobacterial and red algal sequences form another group. See discussions in the text.

9. 23S rRNA (Uracil-5-)-methyltransferase

CLUSTAL X (1.83.1) multiple sequence alignment

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82740724_Shewanella_sp.      RRRARLATLFCQVLAKPLSDLIVPFAKLLLGHLELIAADNGLSFTPGNFV
75827716_Vibrio_choler      RRRARLSLWCPVLEPSLNALLPDLNALLGHVELVKGDNTLSFLPSHF I
39983735_Geobacter_sulfur   GYRCRAQFKICVICDPAINLTLRDLRLVLIPQIDAATGEDGLSFRGGF S
2982968_Aquifex_aeolic     NYRVRVQFKICLLAHERINELIPHIREVLVHVNYSPTRDE-YRVSNDSF F
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75825214_Vibrio_choler     AFRNKAKMVVCPLYPQPMQELLAYLENWILKFILLTRSENSMVRPKS F F
71366121_Nocardioides_sp.  GVRNKAKMVVCP LHTPGIQAALPVLADFVLKYL LVTESPD-LHLRPQS F F
39983433_Geobacter_sulfur  HYRNSAKLVVCP LHHPLINRVVTVAVKEGILRYLVVRIERTFTTISPR S F F
18893255_Pyrococcus_furios  GHRNRIDLAVCPVFGKTSKKAIERLREYILRYMVLREGKFTYLIHPNS F F
18892856_Pyrococcus_furios  EFRNISNFIVCPVFSNRTPLYIRAMKEFLVHYLQVREGKFTYLLRPGIF F
40068573_Nanoarchaeum_eqita YRNRMDYPICKMLSKEAEI I INEFNKFILRYLVIREGKFTYYISPNS F F
14195332_Chlamydia_muridarum RGRNKMEFSFCLMIDERAIDILNYTRSWWLCTLTVRIGNVSFHVRPRS F F
33236756_Chlamydomphila_pneumo RGRNKMEFSFCLLIHEQ TMDILKLTREWWLCTLTVRTGSPQFSLRPRS F F
46400819_Protochlamydia_amoebo HYRNMELTFCLLANGWFAQAARAIQKWWLRTLTLREGLRTFRISPSAF F
42565079_Arabidopsis_thalia HYRNMELTFCLLQSEPGNLVLA AVQDCWLKHLMLRTGRNVFQISANS F F
34906470_Oryza_sativa     RYRNKMEFSFCLLQSEPADKVLAI VQETWLKHLMIRTGRNIFQISANS F F
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47094248_Listeria_monocy
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53763114_Synechococcus_elonga
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33634926_Prochlorococcus_marin
46401273_Proteochlamydia_amoebo
42565237_Arabidopsis_thalia
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19712946_Fusobacterium_nuclea
4981638_Thermotoga_mariti
45600206_Leptospira_interrog
69299484_Silicibacter_sp.
41819164_Treponema_denticola
66797570_Deinococcus_geothe

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82740724_Shewanella_sp.
75827716_Vibrio_choler
39983735_Geobacter_sulfur
2982968_Aquifex_aeolic
82743019_Shewanella_sp.
75825214_Vibrio_choler
71366121_Nocardioides_sp.
39983433_Geobacter_sulfur
18893255_Pyrococcus_furios
18892856_Pyrococcus_furios
40068573_Nanoarchaeum_equita
14195332_Chlamydia_muridarum
33236756_Chlamydia_pneumo
46400819_Proteochlamydia_amoebo
42565079_Arabidopsis_thalia
34906470_Oryza_sativa
21645898_Chlorobium_tepidu
29337947_Bacteroides_thetai
50756251_Gallus_gallus
54641671_Drosophila_pseudo
45599387_Leptospira_interog
47094248_Listeria_monocy
65317856_Bacillus_anthra
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65317755_Bacillus_anthra
23125360_Nostoc_puncti
53763114_Synechococcus_elonga
35213705_Gloeobacter_violac
33634926_Prochlorococcus_marin
46401273_Proteochlamydia_amoebo
42565237_Arabidopsis_thalia
CM4438_Cyanidioschyzon_merolae
19712946_Fusobacterium_nuclea
4981638_Thermotoga_mariti
45600206_Leptospira_interrog
69299484_Silicibacter_sp.
41819164_Treponema_denticola
66797570_Deinococcus_geothe

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QTNSYQAVNLVVDLYSGVGLFSLQIANEVKKGIVGIEVVEAEVMAIIVD
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QPQITQAAKIIILLDLYCGAGTIGIMLSPYVKNVIGVEIIPDASAVIIVD
QPNTQAEKLYVVDLYCGTGTGLGICSAKYVKEVIGIELSRESVLDVAVVD
QTNTHQAEVLYVLDLFCGTGTIGLTLARRAKHVYGYEVPQAITDAVVD
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QTNTQAEKLYVVDLYCGTGTITLYLARHCKQAIGIEVPEAVKDAIVVD
QTNSEQAYNLVVDLYTGTGTIANFVSRQARQVIGIEVPEAIEDAIITD
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82740724_Shewanella_sp.
75827716_Vibrio_choler

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PARAGAEGIVDQAKRVVYVSCNPATLARDSQSLLFRLEKLGMLDMFPHTS

39983735_Geobacter_sulfur
2982968_Aquifex_aeolic
82743019_Shewanella_sp.
75825214_Vibrio_choler
71366121_Nocardioides_sp.
39983433_Geobacter_sulfur
18893255_Pyrococcus_furios
18892856_Pyrococcus_furios
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42565079_Arabidopsis_thalia
34906470_Oryza_sativa
21645898_Chlorobium_tepidu
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54641671_Drosophila_pseudo
45599387_Leptospira_interog
47094248_Listeria_monocy
65317856_Bacillus_anthra
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65317755_Bacillus_anthra
23125360_Nostoc_puncti
53763114_Synechococcus_elonga
35213705_Gloeobacter_violac
33634926_Prochlorococcus_marin
46401273_Proteochlamydia_amoebo
42565237_Arabidopsis_thalia
CM4438_Cyanidioschyzon_merolae
19712946_Fusobacterium_nuclea
4981638_Thermotoga_mariti
45600206_Leptospira_interog
69299484_Silicibacter_sp.
41819164_Treponema_denticola
66797570_Deinococcus_geothe

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PPRAGAEQIAQLPLISYVSCNPVTFARDAEVLVYKLNWVQVDFRWS
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82740724_Shewanella_sp.
75827716_Vibrio_choler
39983735_Geobacter_sulfur
2982968_Aquifex_aeolic
82743019_Shewanella_sp.
75825214_Vibrio_choler
71366121_Nocardioides_sp.
39983433_Geobacter_sulfur
18893255_Pyrococcus_furios
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14195332_Chlamydia_muridarum
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46400819_Proteochlamydia_amoebo
42565079_Arabidopsis_thalia
34906470_Oryza_sativa
21645898_Chlorobium_tepidu
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54641671_Drosophila_pseudo
45599387_Leptospira_interog
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23125360_Nostoc_puncti
53763114_Synechococcus_elonga

HIEAMALFEL
HLESMAFLVK
HIESVTLIR
HIESIALLEV
HFEVLAMLVK
HAEVLTLLVR
HYEVLALLER
HVENIALLVK
HIELVGLRR
HVEAVIKLRK
HIENVILMCK
HLENVLLER
HLENIILLER
HVENITLLTL
HIECVLLEL
HIECICVLEL
HIETVACFER
HVENVLLLEL
HCELLILFER
HTELVILFER
HLESVSVFTK
HVETVLLQL
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HVEAAFLVL
HVETVALLEL

35213705_Gloeobacter_violac	HVECVATLER
33634926_Prochlorococcus_marin	HIECLALLTR
46401273_Protochlamydia_amoebo	HIELLTLFER
42565237_Arabidopsis_thalia	SIEVLAVFKR
CM4438_Cyanidioschyzon_merolae	HLEMVAVFDR
19712946_Fusobacterium_nuclea	HIECVGLIER
4981638_Thermotoga_mariti	HVETAVTLVK
45600206_Leptospira_interrog	HLESVAFLKR
69299484_Silicibacter_sp.	HTELAASFSL
41819164_Treponema_denticola	HIETLGIFRK
66797570_Deinococcus_geothe	HVEVSVLER

* :

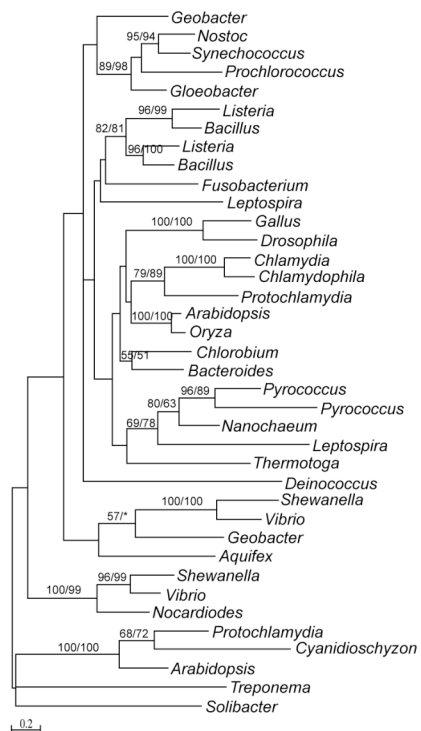


Figure 9. Phylogeny of 23S rRNA (Uracil-5-)-methyltransferase. Note that this gene contains two copies in green plants. One groups with red algal and *Protochlamydia* sequences with strong support (lower branch). BLAST search of GenBank protein nr sequence database using the red algal sequence had significant hits (Evalue < e-8) only to *Protochlamydia* and *Arabidopsis* sequences.

10. CMP-KDO synthetase

CLUSTAL X (1.83.1) multiple sequence alignment

34397752_Porphyrromonas_gingiv	IPARFASSRFPKPLADMLGKSMIQRVHERIVPRAVVATDDDERIRQAVED
48853699_Cytophaga_hutchi	IPARYASTRFPGKPLIQINGKTMIQCVYDQVITEVLVATDDDRIEAEVLR
33635764_Prochlorococcus_marin	VPARLESSRLPNKVLADIGMPMLQRVLERCPNAVVLCTDSDRLKEMAED
2983277_Aquifex_aeolic	IPARLGSTRLKEKPLKNLLGKPLIRVVVEGLGERVILATDSERVKEVVED
77545625_Pelobacter_carbin	IPARYASSRFPKPLARILGKTMIQRVYERTIDRVVVATDSDRIADVSG
39983882_Geobacter_sulfur	IPARFASTRFPKALADIAGKPMVQHVYERTVSEVVVATDDDRIAQAVRG

67930978_Solibacter_usitat
56686778_Synechococcus_elonga
82738953_Pseudomonas_putida
48766205_Rhodospirillum_rubrum
77690215_Rhodopseudomonas_palu
84712599_Polaromonas_naphth
72117710_Ralstonia_eutrop
82736692_Pseudomonas_putida
68056808_Haemophilus_influe
32448211_Rhodopirellula_baltic
32261715_Helicobacter
60493187_Bacteroides_fragil
83859819_Oceanicaulis_alexan
15835072_Chlamydia_murida
29834703_Chlamydomydia_caviae
46400100_Protochlamydia_amoebo
7688437_Zea_mays
51854266_Oryza_sativa
30695393_Arabidopsis_thalia
24197538_Leptospira_interr
19714354_Fusobacterium_nuclea
24195250_Leptospira_interr
84517633_Prochlorococcus_marin
67935837_Chlorobium_phaeob

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IPARYASERLPGKVLVLLPIAGRPMLQWVYEATFDQVAIATEDPRVVEAAAA
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IPARMASTRLPKPLLDIGVPMIVHVLRRRAIGRVAVATDTPEDIAEAVIA
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IPARYASSRFPKPLVQILGKPMIQRWERTVLDHVVVATDDERIAECCRG
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34397752_Porphyrromonas_gingiv
48853699_Cytophaga_hutchi
33635764_Prochlorococcus_marin
2983277_Aquifex_aeolic
77545625_Pelobacter_carbin
39983882_Geobacter_sulfur
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82738953_Pseudomonas_putida
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72117710_Ralstonia_eutrop
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15835072_Chlamydia_murida
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30695393_Arabidopsis_thalia
24197538_Leptospira_interr
19714354_Fusobacterium_nuclea
24195250_Leptospira_interr
84517633_Prochlorococcus_marin
67935837_Chlorobium_phaeob

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34397752_Porphyrromonas_gingiv
48853699_Cytophaga_hutchi
33635764_Prochlorococcus_marin
2983277_Aquifex_aeolic
77545625_Pelobacter_carbin
39983882_Geobacter_sulfur
67930978_Solibacter_usitat

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56686778_Synechococcus_elonga
82738953_Pseudomonas_putida
48766205_Rhodospirillum_rubrum
77690215_Rhodopseudomonas_palu
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15835072_Chlamydia_murida
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19714354_Fusobacterium_nuclea
24195250_Leptospira_interr
84517633_Prochlorococcus_marin
67935837_Chlorobium_phaeob

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77545625_Pelobacter_carbin
39983882_Geobacter_sulfur
67930978_Solibacter_usitat
56686778_Synechococcus_elonga
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48766205_Rhodospirillum_rubrum
77690215_Rhodopseudomonas_palu
84712599_Polaromonas_naphth
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7688437_Zea_mays
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24197538_Leptospira_interr
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84517633_Prochlorococcus_marin
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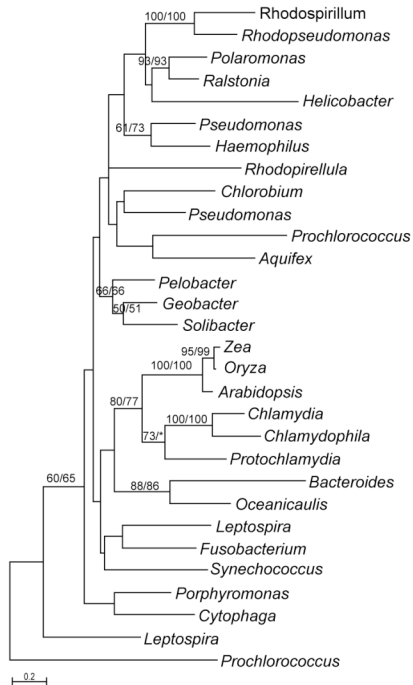


Figure 10. Phylogeny of CMP-KDO synthetase, showing sequences of green plants and chlamydiae form a monophyletic group.

11. ATP/ADP translocase

See the following for phylogeny:

1. Wolf, Y. I., Aravind, L. & Koonin, E. V. Rickettsiae and Chlamydiae: evidence of horizontal gene transfer and gene exchange. *Trends Genet* 15, 173-5 (1999).
2. Linka, N. et al. Phylogenetic relationships of non-mitochondrial nucleotide transport proteins in bacteria and eukaryotes. *Gene* 306, 27-35 (2003).
3. Greub, G. & Raoult, D. History of the ADP/ATP-translocase-encoding gene, a parasitism gene transferred from a Chlamydiales ancestor to plants 1 billion years ago. *Appl Environ Microbiol* 69, 5530-5 (2003).
4. Amiri, H., Karlberg, O. & Andersson, S. G. Deep origin of plastid/parasite ATP/ADP translocases. *J Mol Evol* 56, 137-50 (2003).
5. Schmitz-Esser, S. et al. ATP/ADP translocases: a common feature of obligate intracellular amoebal symbionts related to Chlamydiae and Rickettsiae. *J Bacteriol* 186, 683-91 (2004).

12. 12. Glycerol-3-phosphate acyltransferase. **Note this gene is only present in chlamydiae and plastid-containing eukaryotes.**

CLUSTAL X (1.83.1) multiple sequence alignment

15834812_Chlamydia_murida PEPLYQKFQICHQTYIEAATRKIIFPPYHKKIRTPYQFGIDFFSVLIDDO
33236837_Chlamydophila_pneumo PEPLYQKFSVFHQNYIDAATKKFIFPPYHKKIRAPFRLSIDFFSLVIDDK
46400593_Proteochlamydia_amoebo KPPFAAIEEHFHSYLLATKHSYQFEIFHQSIIRSPYQFGLDFIRPLINFE
CM1432_Cyanidioschyzon_merolae STRACSVLRGWYSYEKAALAAFHFKPYHQAVSGPTAFGNRFSRPLCDLQ
7576943_Elaeis_guinee SSDIANGLEEELYNYRNAVLSQFTFSPHHQAIAREPYMFGQNYIRPLIDFR
37537152_Oryza_sativa PADVAANLEELYNYKDAVMQSFTFPPYHKAAREPYMFGQNYIRPLVDYR
30692655_Arabidopsis_thalia PANVAAGMEELYWNYKNAVLSYTFNPNYHKAAREPYMVFHTYIRPLIDFK
154139_Chlamydomonas_reih PPQLEPAWDYFYDNYKKAATSSYTFPSFHTRLIPEYDFGQRYVATLIDFQ
23619128_Plasmodium_falcip ITDHINTFKGFLRKYLYEIKKHYEFPNIHRYDOTLYEWSLKFWSSELIDKK
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46400593_Proteochlamydia_amoebo KSTVLGREQLAKIYQOMAQGDNVILLANHQTEPDQIILSMLNIDKLLAT
CM1432_Cyanidioschyzon_merolae RSYLDPSSSFACIRAQLAAGDNVCLVGNHQSSEADPFAIYHMFESGAALAE
7576943_Elaeis_guinee RSYIGNISIFSDMEEKLQGHNVVLSNHNQTEADPAI IALLRNTNSHIAE
37537152_Oryza_sativa NSYVGNISIFQDMEQKLGQGHNVVLSNHNQTEADPAI IALLRNSNPWISE
30692655_Arabidopsis_thalia NSYVGNASIFSELEDKIROGHNVVLSNHNQSEADPAVISLQLAOSPFIGE
154139_Chlamydomonas_reih NSVLGFRERFDRVQELLDQKHNVVILANHQTEADPGVFAHMLKTHPKLAT
23619128_Plasmodium_falcip NSKFLGISNIKKIEEWRDKGHNI IIFSNHHIEADANI IKYFFQDSEQISR
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15834812_Chlamydia_murida NMIFVAGDRVTS DPLARPF SMGCDLLCIYSKRHINHPPELKEEKLHNHOK
33236837_Chlamydophila_pneumo NMIFVAGDRVTS DPLARPF SMGCDLLCIYSKRH IATPELREEKLLHNOK
46400593_Proteochlamydia_amoebo EMIF IAGHRV I SDPLAI PMSGRNLLCIYSKKHISHPPEKKTQKVSHNQR
CM1432_Cyanidioschyzon_merolae SILVMAGDRVRDDPLAAPFSVGRSMLTVYSKKHILDEDDRSEKQAHNRK
7576943_Elaeis_guinee TMFVAGDRVLT DPLCKPFSMGRNLLCVYSKKHMDDPEL IEMKRRANTR
37537152_Oryza_sativa NIVYVAGDRVVT DPLCKPFSMGRNLCVYSKKHMNDPELVDMKRRANTR
30692655_Arabidopsis_thalia NIKCVAGDRVIT DPLCKPFSMGRNLCVYSKKHMNDPELVDMKRRANTR
154139_Chlamydomonas_reih DVIYVAGDRVVT DPMCKPFSMGRNLCVHSKKHMDDAPEL KAAKMETNRK
23619128_Plasmodium_falcip NIIFIGGHKIRVDPLSRPFSVTANLLCIYSKKYIENPHLKEEKTFLFNHK
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15834812_Chlamydia_murida SMRTLKMLLSEGSKF IYVAPAGGRDRKNSQELYPAEFHPDSIEMFRLLAK
33236837_Chlamydophila_pneumo SMQILKTLNLEGGKFIYVAPAGGRDRKNAERLYPSEFSPESIEVFRLLAK
46400593_Proteochlamydia_amoebo TMRKMSELLSEGGRCIYVAPSGGRDRRNSEQIT IAPFDQSELMFWLMAQ
CM1432_Cyanidioschyzon_merolae TLREMERL FADGGRCVWFAPSGGRDRRSPERVTCASFDPDAIELFRLSAE
7576943_Elaeis_guinee SLKEMALLLRGGSQI IWIAPSGGRDRPDPSEWHPPAPFDVSSVDNMRRLVE
37537152_Oryza_sativa SLKEMALLLRGGSQI IWIAPSGGRDRPDPLEWHPPAPFDASAVDNMRRLLE
30692655_Arabidopsis_thalia SLKEMATLRSGGQLIWIAPSGGRDRPNPSEWPPAPFDASSVDNMRRLVE
154139_Chlamydomonas_reih TLVAMQRKLNLEGGTLMWIAPSGGRDRPNANEVWPDNFDPAAVELMRNLVQ
23619128_Plasmodium_falcip SLNVLRLNLLNKGKQI IWLAPSGGRDRKGADKIHISPFDPKI IQTFNVFAK
: : : : * : : * * : : * * : : * : : :

15834812_Chlamydia_murida SSGKPTHFFPFAMKTYDILPPPPTI EETIGEHRVISFAP IAFNFGEELRA
33236837_Chlamydophila_pneumo ASNQTTHTFYPFALKTYDILPPPPKIENAI GEQRAIFFAPVFFNFGAELRA
46400593_Proteochlamydia_amoebo QADHPHTFYPLSLHTYDLMPPPKHVEKELGEKRTAQFTPVHLAFSSEIRA
CM1432_Cyanidioschyzon_merolae KAGRPCHYYPMAIGTFNMLPPPQVEKEKEQORVVS YARLWMSLMPQVRA
7576943_Elaeis_guinee HSSVPGHIYPLSLLCYEVMPPPQVEKQIGERRTISFHGVGLSVAPELFS
37537152_Oryza_sativa HSGVPGHIYPLSLLCYEVMPPPQVEKEIGEQRVISFHGVGLSVTEEIFS
30692655_Arabidopsis_thalia HSGAPGHIYPM SLLCYDIMP PPPQVEKEIGEKRVLVGFHGTGLSIAPEIYS
154139_Chlamydomonas_reih RAKQPGHLMPSMFSYPMPPPKTVDKSIGERRLTAFTGVG I SLCEELLA
23619128_Plasmodium_falcip RSKVKTHF IGLALNTYNICPPNTIDVEIEKERTCNYS P VYLN LGDIIIT
: * : : : * * : : : * : : . : : :

15834812_Chlamydia_murida SRVFSIVTDLYKEI
33236837_Chlamydophila_pneumo EKVFSIVKNLYEEL
46400593_Proteochlamydia_amoebo EFIWKIVRRNYELF
CM1432_Cyanidioschyzon_merolae ENLYHLVQKYTQM
7576943_Elaeis_guinee QALYNSVGEQYNVL
37537152_Oryza_sativa ESLYNSVVDQYNAL
30692655_Arabidopsis_thalia QALYKSVNEQYEIL
154139_Chlamydomonas_reih KAAHDAVKESYAVL
23619128_Plasmodium_falcip TYLYNYVNQLYKQI
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13. Isoamylase

CLUSTAL X (1.83.1) multiple sequence alignment

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29144251_Salmonella_enteri         LAIGEATPHGATGVNFTLFSAHAERVELCVFYDLPRRGD VWHGFLAGARP
48765636_Rhodospirillum_rubrum     LDAGEPWPLGAMGVNIAVFS EAATQIDLCFLPLPRTGDIWHGFLPGGGP
1707700_Sulfolobus_solfat          LRPGDPYPLGSGNVNFSLFSANA EKVELLLYIEVKKTDGDIWHVFPGLRP
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71737201_Pseudomonas_syringae     IREGLPFPLGASGVNFAVFSANA TKVELCLFIE LPTYDETYHGYLPDAH
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53756174_Methylococcus_capsul     YSTGSPPLGVHDANFALFSRH GSRVRLLLFIDLDR TGDIVHVAHVGAHR
87311865_Blastopirellula_marin    LQFTHILPYGAVGVQFVVF SRNATAMRLLMYIDF DRWGD IWSIFVPGVSA
32446352_Rhodopirellula_baltic    LQFAYSPPFGATGVQFSVFSRS ATEMRLLLYIDF DRWGDVWSLHVPGLEA
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22136708_Arabidopsis_thalia       VSSGEVSP LGVSGINFALFSQ NATSVTLCLSLVLDK TGDTHWICVEDLPL
46446740_Protochlamydia_amoebo    ITPGSPFPFGANKVNFAVY AKNIEKISLCLFIELEKTGNVWHIAIESLPP
82748503_Clostridium_beijer      IRPGFYLENGAVGVNFTIHS QSATSCKLLLFIPFP RIGNVYSMIVLGLDI
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42525620_Treponema_dentic          WYLYTADGEFSPSALFDENNYLLDPYARLI SSF PKCVVPLQKCVIYEAHV
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29840170_Chlamydophila_caviae     QYAFRVGDPTNTTAKFDFPKYLADPYAKNLH SYLKNE-PKEESIIYEMHV
15604761_Chlamydia_tracho         EYAYKLRGTDLSSQKFATDSYIADPYSKNIYS YLKHE-PKENFYIYEMHV
53756174_Methylococcus_capsul     GYAFQVDGPHPHLRFDQPAVLLDPYATALV TVAKALVHSELVIYEAHV
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48763460_Rhodospirillum_rubrum

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29141918_Salmonella_enteri
39936374_Rhodopseudomonas_palau
71737201_Pseudomonas_syringae
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82748503_Clostridium_beijer
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6457937_Deinococcus_radiod
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VTCHDGFLLNDLVSYNHKHNEANGENNRDGI ENNLSWNCGVEGETEDPEV
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ICAHDGFLLADLVTYNNKNNLANGENNDGENHNSWNCGEEGDFASISV
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: *** .: * : :.* * . ** : : : .:* :

ISLRKQIQIKMILILYISQGI PMLLMGDEMGRTOQLGNNNAYCQDNPTTWV
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ERMRKMSAKNILLTLLSAGT PPMINMGDEFVFRTOGNNNAYCQDNEMSWF
MERRRDSIHALLATLLLSQGT PMLLAGDEHGHSQHGNNNAYCQDNALTWL
RSLRDRQRNRLACL LLSLGVPMIRGGDELGQTOQGNNNVYQDNPLNWL
VICREKQKRNFMITLLVSQGT PMLLGGDELSRTQGNNNAFQDNEITWF
LGMRRQLRKNQLACLFLA QGVPLLAGDEVGNSQAGNNNAYCQDNEIGWV
NRLRQKQMRNFLTLLLGQGT PMLLGGDEFGRTOGNNNAYCQDNDISWY
LSLRNRQRNFLTLLMLLSQGV PMLLGGDEFGRTOGNNNAYCQDNEISWV
LALRARQMRNFWATLMV SQTGPMIAHGDEIGRTQYGNNNVYQDSELSW
RELGRQRNFLTLLLSQGI PMLCHGDELGRTOGNNNAYCQDNEISWI
LALRARVAQMLSTLLLA QGTPMLTAGDEWGRSQQGNNNAYCQDNAMSWL
LATRKRVARSLIATLLMAL GTPMVLAGEDESLRTOHGNNNAYCQDNELSWL
NTLRRRQMRNMLATLLLSQGT PMLLAGDEFANSONGNNNAYCQDNALSWL
NAIRERQRNFLTLLLSHGTP MLLLAGDEFGRSQMGNNNGYCQDSEISWV
LSLRERQRNMLATLLLA QGTPMLLAGDEFGRTOGNNNAYCQDNEISWV
NTLRLRQMRNFFATLLLA QGTPMIVAGDEFARTOHGNNNAYCQDSEIGWI
RQQRERQRNLLATLLLSQGT PMLLAGDEFGRTOGNNNAYCQDNEISWV
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CALRERQMRNFFLALFLS QGIPMIQSGDEYGHSAKGNNNHWCLDTKINYF
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NQLRLRQIKNFLTILFFS QGT PMLMGDPVGRTOGNNNSYCNKNSWF
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VALRDRQMRNFFVALFVA QGVPMYMGDEYGHTRKGNNTYCHDNALNWI

22136708_Arabidopsis_thalia
46446740_Protoclhamydia_amoebo
82748503_Clostridium_beijer
48894542_Trichodesmium_erythr
16330244_Synechocystis_sp.

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1707700_Sulfolobus_solfat
39936707_Rhodopseudomonas_palu
6457937_Deinococcus_radiod
48894700_Trichodesmium_erythr
57116886_Mycobacterium_tuberc
8246833_Streptomyces_coelic
73538060_Ralstonia_eutropha
48784580_Burkholderia_fungor
48763460_Rhodospirillum_rubrum
29141918_Salmonella_enteri
39936374_Rhodopseudomonas_palu
71737201_Pseudomonas_syringae
48785916_Burkholderia_fungor
29840170_Chlamydomyxa_caviae
15604761_Chlamydia_tracho
53756174_Methylococcus_capsul
87311865_Blastopirellula_marin
32446352_Rhodopirellula_baltic
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48893487_Trichodesmium_erythr
16329290_Synechocystis_sp.
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34098817_Arabidopsis_thalia
46360122_Ostreococcus_tauri
22136708_Arabidopsis_thalia
46446740_Protoclhamydia_amoebo
82748503_Clostridium_beijer
48894542_Trichodesmium_erythr
16330244_Synechocystis_sp.

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NWNLLDLDFTRELIYFRFQHPVYFRKWFDIGWYNFMIFFNAYHELIEF
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DWRLRALDFARRLIALRADHPVLRRRRFFDLVWLLFLLLLNSHWEPADF
DWKQQVLLQMVRRLLALRLRPLSLGANHFSDIAWFDLLLLNAGDTDVVVF
DWARRQMTAFVARVIALRKHQLLRETRFLDVGWFDLLMMLNANEKTLRF
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DWSGDGLARFTKQVIALRKKHSARFLDSPNIQWHGFYIAFNNSHHEPAML
QWKEQNHFRRFFSEVIKFRSHHVLLKHENFLEITWHEIYVAFNAHDYFVKA
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NWSLALDFTFKKNMINFRKRHPAIKDRIEFPVSKHGVLICINAHWETQV
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* : :

19714344_Fusobacterium_nuclea
32398065_Rhodopirellula_baltic
42525620_Treponema_dentic
29144251_Salmonella_enteri
48765636_Rhodospirillum_rubrum
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39936707_Rhodopseudomonas_palu
6457937_Deinococcus_radiod
48894700_Trichodesmium_erythr
57116886_Mycobacterium_tuberc
8246833_Streptomyces_coelic
73538060_Ralstonia_eutropha
48784580_Burkholderia_fungor
48763460_Rhodospirillum_rubrum
29141918_Salmonella_enteri
39936374_Rhodopseudomonas_palu
71737201_Pseudomonas_syringae
48785916_Burkholderia_fungor
29840170_Chlamydomyxa_caviae
15604761_Chlamydia_tracho
53756174_Methylococcus_capsul
87311865_Blastopirellula_marin

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RLPWTTIALR-EMSLVAL
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TLPWTTCLLDTARSLLLL
HLPYQKVADSAHMLLVA
SLPYEKIVDSPYSSLVA
RLPWIKAVDTRSLVVL
ILPWRMFDVDTERSMRVY

32446352_Rhodopirellula_baltic	HFPWNLFVDTRHSMRIY
48837599_Methanosarcina_barker	EIPWYRAVDTPRSVVVL
48893487_Trichodesmium_erythr	ELPWYLIVNTPRAAVIL
16329290_Synechocystis_sp.	ELPWHRLVDTPRSSVVL
CM4050_Cyanidioschyzon_merolae	TVPWLRIVDTPWSSIIL
34098817_Arabidopsis_thalia	SLPWEFPVDTSYSSIIL
46360122_Ostreococcus_tauri	KLPWKLILDTRSAVIF
22136708_Arabidopsis_thalia	LIPWFRVADTPFSSILL
46446740_Protochlamydia_amoebo	TIPWVWLVNTSYTSIAL
82748503_Clostridium_beijer	RLPWRIAVNTPRSVMIL
48894542_Trichodesmium_erythr	NIPWHIFVNTDRSIVIL
16330244_Synechocystis_sp.	ELPWHVFANTDRSVVIL

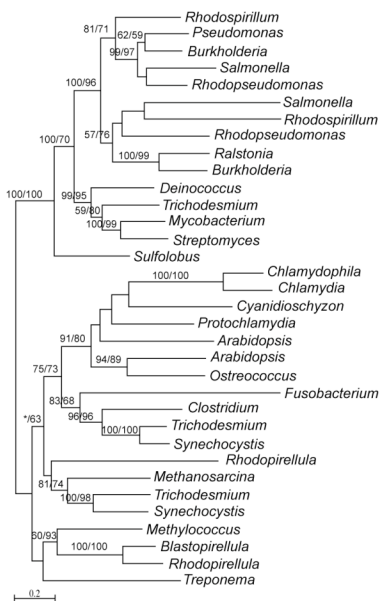


Figure 13. Phylogeny of isoamylase, showing red algal, green plant and chlamydial sequences form a monophyletic group that is distinct from cyanobacterial homologs. There are multiple homologous copies of this gene in cyanobacteria, but neither of them appears to be closely related to chlamydial, red algal and plant homologs.

14. Phosphate transporter

CLUSTAL X (1.83.1) multiple sequence alignment

94413958_Pseudomonas_aerugi	VSLVLALIFVLSFEFINGFHD
15607685_Mycobacterium_tuberc	FLLLIVVVTALAFDFTNGFHD
90588650_Flavobacterium_johnso	TLLILIIVLALIFDYINGFHDA
116254783_Rhizobium_legumi	PLLVGLVVIALLFFDFLNGLHDA
113868249_Ralstonia_eutrop	WVIALLVALLLDFDMNGFHD
73747989_Dehalococcoides_sp.	YLLIILLAI GF--AFVNGTND
94985848_Deinococcus_geothe	IGLIVI IALALAFDFINGFHD
82749132_Clostridium_beijer	TITVLIIVITVLI FDFINGFHD
30019602_Bacillus_cereus	ILTVLVVICALAFDFINGFHD

50256150_Cryptococcus_neofor
82780741_Dunaliella_viridi
68073475_Plasmodium_berghe
115503941_Trypanosoma_brucei
5803173_Homo_sapien
21356511_Drosophila_melano
32267370_Helicobacter_hepatis
15888000_Agrobacterium_tumefaciens
56695869_Silicibacter_pomero
116250630_Rhizobium_legumi
15609418_Mycobacterium_tuberculosis
59801910_Neisseria_gonorrhoeae
73852587_Emiliania_huxleyi
28569257_Tetraselmis_chuij
CM4066_Cyanidioschyzon_merolae
75906380_Anabaena_variabilis
15618590_Chlamydomonas_pneumoniae
15605425_Chlamydia_trachomatis
15643031_Thermotoga_maritima
71278581_Colwellia_psychrophila
68545472_Shewanella_amazonensis
69258455_Magnetococcus_sp.
51246480_Desulfotalea_psychrophila
46445733_Candidatus_Protococcus
115447039_Oryza_sativa
24079961_Medicago_truncatula
14521600_Pyrococcus_abyssi
11499387_Archaeoglobus_fulgidus

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LLLVCVVVGGFYTAWNIGANDVANAVGSPVSGAGALTLKQAVLIAAVFEFL
TILIIAGILGFIMAFSIGANDVANSMATAVGARAITVRQAALIAMFLEFL
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IFMFLAIIFGLYMCWIGANDVANAMGTSVGSNAITIKQAI I IAMI FEFA
AMLIMAVIFGLYMTWIGANDLANAMGTSVGAITVQKAI I IAI FEFL
ALLLILITGFYMAWSIGANDVANAMGTSVGSGLTLRQAVLIAAVLEFC
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MLSYGTLFGFYMAWNIGANDVANAMGTSVGSGLSLRQAVLTAAVLEFS
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LFIVVAGIVGFYVAVNIGANDAANSMTAVGAGAITPKQAVLIAGILEFT

* : * . . . : :

94413958_Pseudomonas_aeruginosa
15607685_Mycobacterium_tuberculosis
90588650_Flavobacterium_johnsonii
116254783_Rhizobium_legumi
113868249_Ralstonia_eutropha
73747989_Dehalococcoides_sp.
94985848_Deinococcus_geothermophilus
82749132_Clostridium_beijerinii
30019602_Bacillus_cereus
50256150_Cryptococcus_neofor
82780741_Dunaliella_viridi
68073475_Plasmodium_berghe
115503941_Trypanosoma_brucei
5803173_Homo_sapien
21356511_Drosophila_melano
32267370_Helicobacter_hepatis
15888000_Agrobacterium_tumefaciens
56695869_Silicibacter_pomero
116250630_Rhizobium_legumi
15609418_Mycobacterium_tuberculosis
59801910_Neisseria_gonorrhoeae
73852587_Emiliania_huxleyi
28569257_Tetraselmis_chuij
CM4066_Cyanidioschyzon_merolae
75906380_Anabaena_variabilis
15618590_Chlamydomonas_pneumoniae
15605425_Chlamydia_trachomatis
15643031_Thermotoga_maritima
71278581_Colwellia_psychrophila
68545472_Shewanella_amazonensis
69258455_Magnetococcus_sp.
51246480_Desulfotalea_psychrophila
46445733_Candidatus_Protococcus
115447039_Oryza_sativa
24079961_Medicago_truncatula

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AIFVPHLKVAAVGTGTIDVIFGALVGAIAWNVITWYGYIPSSSSHALIG
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GAF-SGTAVAKTVGENIVSVILGVLISAI IWNII TWYFGIPSSSSHALIG
GAM-TFTGVAKTITKDIVDILAALLAAIAWNL TWYGYIPSSSSHALIG
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GAVSLGSEVTSTISSGI ANGMICALSATFIWLLFATMMSLPVSTTHSIVG
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14521600_Pyrococcus_abyssi
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94413958_Pseudomonas_aerugi
15607685_Mycobacterium_tuberc
90588650_Flavobacterium_johnso
116254783_Rhizobium_legumi
113868249_Ralstonia_eutrop
73747989_Dehalococcoides_sp.
94985848_Deinococcus_geothe
82749132_Clostridium_beijer
30019602_Bacillus_cereus
50256150_Cryptococcus_neofor
82780741_Dunaliella_viridi
68073475_Plasmodium_berghe
115503941_Trypanosoma_brucei
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21356511_Drosophila_melano
32267370_Helicobacter_hepatis
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59801910_Neisseria_gonorrhoea
73852587_Emiliania_huxleyi
28569257_Tetraselmis_chuii
CM4066_Cyanidioschyzon_merolae
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15618590_Chlamydomonas_pneumoniae
15605425_Chlamydia_trachomatis
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46445733_Candidatus_Proteus_sibiriacus
115447039_Oryza_sativa
24079961_Medicago_truncatula
14521600_Pyrococcus_abyssi
11499387_Archaeoglobus_fulgid

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94413958_Pseudomonas_aerugi
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116254783_Rhizobium_legumi
113868249_Ralstonia_eutrop
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71278581_Colwellia_psychr
68545472_Shewanella_amazon
69258455_Magnetococcus_sp.
51246480_Desulfotalea_psychr
46445733_Candidatus_Protoc
115447039_Oryza_sativa
24079961_Medicago_trunca
14521600_Pyrococcus_abyssi
11499387_Archaeoglobus_fulgid

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90588650_Flavobacterium_johnso
116254783_Rhizobium_legumi
113868249_Ralstonia_eutrop
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15609418_Mycobacterium_tuberc
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73852587_Emiliana_huxleyi
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15643031_Thermotoga_mariti
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46445733_Candidatus_Protoc
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94413958_Pseudomonas_aerugi
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116254783_Rhizobium_legumi
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30019602_Bacillus_cereus

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71278581_Colwellia_psychr	VRNIVVSWVITLPVAGLSIVFF
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51246480_Desulfotalea_psychr	ILNIVISWVITLPAGAFMAMLFF
46445733_Candidatus_Protoc	TRDILVSWIVTVPVIGALLAII
115447039_Oryza_sativa	VREIVASWLVITVPVAVLSIFYT
24079961_Medicago_trunca	VKEICASWAVTIPVATLSVIYF
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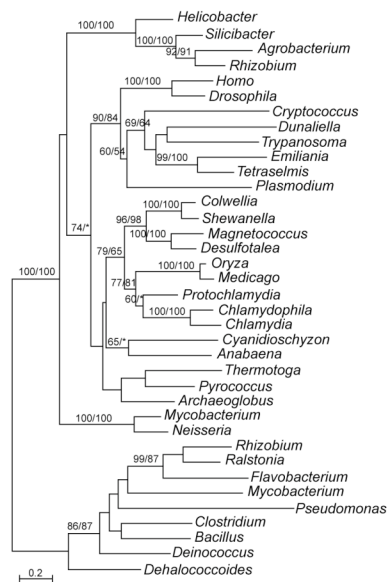


Figure 14. Phylogeny of phosphate transporter. There appears to be an ancient gene duplication and multiple subsequent genes losses, and gene transfers in the evolution of this gene. One of the paralogous copy (upper part of the tree) shows that chlamydial and vascular plant sequences form a monophyletic group, with which the red and green algal homologs are not particularly related. *Medicago* and other vascular plant sequences (*Solanum*, accession number AAT35816; *Spinacia*, accession number CAD36013) are experimentally annotated to be phosphate transporter localized in the

chloroplast inner membrane. Red algal *Cyanidioschyzon* sequence groups with cyanobacterial *Anabaena* homolog with insufficient support, but contains weak mitochondrion-targeting signal as predicted by SignalP. All other eukaryotic sequences are likely of either mitochondrial or nucleocytoplasmic origin.

15. Hypothetical protein

CLUSTAL X (1.83.1) multiple sequence alignment

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17936651_Agrobacterium_tumefa  MRISIFAVGRLKSGPEKDLAARYIERLAKTGPVIEVGETRKRREEAAMK
50365295_Mesoplasma_florum     MNIKIVCFGKLDKFFIDSFNEYANRISKYANLQVIELKVVNKNINSDDL
33634821_Prochlorococcus_marin MQLAIVAVGHKMPAWIETGFNEYTKRMPPELRIELREVKTVMQREARIG
68555467_Ralstonia_metall      MKITILAVGTKMPRWVDEAYTDYAKRFRDITLELKEIKKGIAAEHERLA
34101826_Chromobacterium_viola MRLRLIAGVSRMPKWVEEGWHEYAKRRLPSELAMELVEIPRFIRQEGEAMA
48728976_Pseudomonas_fluore    MKCLLIATGERVPTWVAQGFAYHKRLSYWLPLELVEIEQAIIEDEGRRVA
15836940_Xylella_fastid       MKLQWLTVGKTNDAYLKEGCAQYTKRRLPHYLPFEYLEIPDVLKKEEEKLD
48854617_Cytophaga_hutchi     MRLKLVAVGRLREEAYERACAERYARRLAAYARLELVEVRAGLLKEGQALD
37520906_Gloeobacter_viola    MRLHLITVGEFKLAYARAGWDEYEKRLRRYHKVQVTRVGRGTGAQASEAIA
66798153_Deinococcus_geothe   MRLRVVAVGRPRLAYARLVGEYARRMRRYAPLDLVFV-----RKGEELP
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68177625_Desulfuromonas_acetox MKLRVWVIGKTKESAIQTLTGEYLRKLSRYVATEGLEIGEALLKLDKDRPG
94967055_Acidobacteria_bacteri MKLRVLVWVGKTOEEWVRRGIDEYAGRVRRYAPLEIGEARAMRARECERLD
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68270163_Moorella_thermo      MRIRLTVVGVKVEKYLQDGVQYELKRLRPYARVEIVTPVQVMQREGERLR
51894437_Symbiobacterium_therm MRITIIAVGKIKKYLKEGKINEYSKRLSRYCKLEIIEVEQVKKREAERVK
67876341_Clostridium_thermo  MNVTIISVGKIKKYLSDAII EYSKRISRYSKLDIIEVAKILEKEAERIK
45358600_Methanococcus_maripa  MNIKIISVGKLEKYLKQGIN EYVVKRLNAYAKIELIEVPQVKEKEGERIA
68195425_Enterococcus_faeciu  MQITIIITVGLKKEKYLKQ GIAEYTKRLGAYCSIQIEIEVPQVKKKEGERIA
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50365295_Mesoplasma_florum     KLKAEIICMDVSSKNYSTEE FMSIIIVFVIGPSDGFSDKFLQONYYKVVSF
33634821_Prochlorococcus_marin ALNSVLVPLSEEGEALTSV SFAKRLLAFVIGGADGLS AELKNSTQWQLSL
68555467_Ralstonia_metall      SLSKRIVALDERGKDWTTV QLAELVAFVIGGADGLD PALKARAHTLLRI
34101826_Chromobacterium_viola AIPPRLVVMDERGNWTSVK LAEGLVVFVIGGADGLS AELKQRADVLLQL
48728976_Pseudomonas_fluore    KVGQRIVTLDEVHGKPSW TEQLAVELVNFVGGPEGLAPEVCARADQRWSL
15836940_Xylella_fastid       ALPKYAVTLDVKGKSLNSE QLAKRMLVFLIGGPEGHSQEVLNISNERWSL
48854617_Cytophaga_hutchi     RLQDQLILLDEKGNFTST EFQYILIFLIGGPYGFSDAVYKRANGKIAL
37520906_Gloeobacter_viola    QLHPHAVLLDSGGKQFTS VELADWLPVFI VGS SHGVAPMVRER AQMVVSL
66798153_Deinococcus_geothe   RAAGPLILLDRPEQFTSES LSAYLLAFVAVGGPEGHTDD LRARAHRLWSL
55980197_Thermus_thermo       KAEGRKVVLDERGRLLTTE ELYRRLVAFVGGAE GHPEAVREEADLLLSL
68177625_Desulfuromonas_acetox RIPAYVIGLDEKGRRLSSE KLAANLVCL IIGGAYGLTEALRQRCD SLLSL
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39998298_Geobacter_sulfur     KLVPRLILLDERGKQLTS PEFAAYILAF AIGGAYGFAD EFRRRADRVIAL
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34763429_Fusobacterium_nuclea QISKYNILLDLDGKEINS ENMSKYI INF IIGGSNGVNKELK NLVDMKLLF
68270163_Moorella_thermo      LIPPFVVALDREGVMLS SEELAGRLVALI IGGTLGLATF ILQOADLRLSF
51894437_Symbiobacterium_therm ALDQHVVVLDGRGKNFS SEELAAFLLA FVIGGSLGLDPAVLARAGTTLSL

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67876341_Clostridium_thermo
45358600_Methanococcus_maripa
68195425_Enterococcus_faeciu
68055317_Exiguobacterium_sp.
16799398_Listeria_innocu
16081075_Bacillus_subtil

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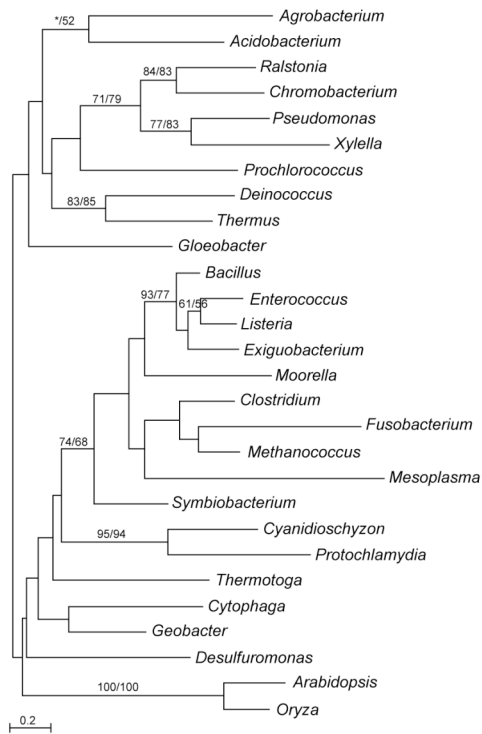


Figure 15. Phylogeny of hypothetical protein, showing red algal and *Protochlamydia* sequences form a monophyletic group. The protein sequence length of this gene is short (179 amino acids for *Cyanidioschyzon*) and the support values for many branches are low.

16. Beta-ketoacyl-ACP synthase (*fabF*)

CLUSTAL X (1.83.1) multiple sequence alignment

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89298548_Tetrahymena_thermo      LKRVVVTGIGAVSPIGLNASSSWESLIAGKSGIISTSTNKLANPDNLKKW
92908594_Mycobacterium_sp.      FPSVVVTAVEATTSLAADIESTWKLLAGESGIRVLEPVRI GGHLTRIDM
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66820316_Dictyostelium_discoi   LKRVVVTGMGIVSPLGVGIKYNWDKLLINGESGIKRFEPKVVAVRVPVQVK
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32470845_Rhodopirellula_baltic SRRVVITGLGTVTPLGCDVETLWSALLAGKSGIHELSPVHF GGDIEPKEA
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76258447_Chloroflexus_aurant
46198353_Thermus_thermophi
94984545_Deinococcus_geothe
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106895571_Clostridium_sp.
53688239_Nostoc_puncti
23124097_Nostoc_puncti
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67920030_Crocospaera_watson
116622648_Solibacter_usitat
116620290_Solibacter_usitat
47574643_Rubrivivax_gelati
82736706_Pseudomonas_putida
29653839_Coxiella_burnet

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116620290_Solibacter_usitat
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KRSGFVFMGEGSGILILEEYEHAKKRGAKIYAEFAGYGASSDAYHLTSPDP
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89298548_Tetrahymena_thermo

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15643565_Thermotoga_mariti
71367081_Nocardioides_sp.
66820316_Dictyostelium_discoi
CM2363_Cyanidioschyzon_merolae
18410739_Arabidopsis_thalia
116055175_Ostreococcus_tauri]
15834771_Chlamydia_murida
29840610_Chlamydomydia_caviae
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116061551_Ostreococcus_tauri]
15237422_Arabidopsis_thalia
108882523_Aedes_aegypti
8923559_Homo_sapien
34802538_Brachyspira_hydys
42525557_Treponema_dentic
95007196_Toxoplasma_gondii
32470845_Rhodopirellula_baltic
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67917496_Chlorobium_limico
110637801_Cytophaga_hutchin
89889944_Flavobacteria_bacter
57237499_Campylobacter_jejuni
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76258447_Chloroflexus_aurant
46198353_Thermus_thermophi
94984545_Deinococcus_geothe
22325473_Arabidopsis_thalia
102192140_Rickettsia_canade
83591758_Rhodospirillum_rubrum
106895571_Clostridium_sp.
53688239_Nostoc_puncti
23124097_Nostoc_puncti
16329903_Synechocystis_sp.
67920030_Crocospaera_watson
116622648_Solibacter_usitat
116620290_Solibacter_usitat
47574643_Rubrivivax_gelati
82736706_Pseudomonas_putida
29653839_Coxiella_burnet

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89298548_Tetrahymena_thermo
92908594_Mycobacterium_sp.
15643565_Thermotoga_mariti
71367081_Nocardioides_sp.
66820316_Dictyostelium_discoi
CM2363_Cyanidioschyzon_merolae
18410739_Arabidopsis_thalia
116055175_Ostreococcus_tauri]
15834771_Chlamydia_murida
29840610_Chlamydomydia_caviae
46446872_Proteochlamydia_amoeba
116061551_Ostreococcus_tauri]
15237422_Arabidopsis_thalia
108882523_Aedes_aegypti
8923559_Homo_sapien
34802538_Brachyspira_hydys
42525557_Treponema_dentic
95007196_Toxoplasma_gondii
32470845_Rhodopirellula_baltic
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110637801_Cytophaga_hutchin
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76259633_Chloroflexus_aurant
76258447_Chloroflexus_aurant
46198353_Thermus_thermophi
94984545_Deinococcus_geothe
22325473_Arabidopsis_thalia
102192140_Rickettsia_canade
83591758_Rhodospirillum_rubrum
106895571_Clostridium_sp.
53688239_Nostoc_puncti
23124097_Nostoc_puncti
16329903_Synechocystis_sp.
67920030_Crocospaera_watson
116622648_Solibacter_usitat
116620290_Solibacter_usitat
47574643_Rubrivivax_gelati
82736706_Pseudomonas_putida
29653839_Coxiella_burnet

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VSSTKSMTHMLGAAGALETVISVLAIRDNTAPPTINLENPDEMKIDTVM
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89298548_Tetrahymena_thermo
92908594_Mycobacterium_sp.
15643565_Thermotoga_mariti
71367081_Nocardioides_sp.
66820316_Dictyostelium_discoi
CM2363_Cyanidioschyzon_merolae
18410739_Arabidopsis_thalia
116055175_Ostreococcus_tauri]
15834771_Chlamydia_murida
29840610_Chlamydomyxa_caviae
46446872_Proteochlamydia_amoebo
116061551_Ostreococcus_tauri]
15237422_Arabidopsis_thalia
108882523_Aedes_aegypti
8923559_Homo_sapien
34802538_Brachyspira_hyodys
42525557_Treponema_dentic
95007196_Toxoplasma_gondii
32470845_Rhodopirellula_baltic
85075673_Neurospora
67917496_Chlorobium_limico
110637801_Cytophaga_hutchin
89889944_Flavobacteria_bacter
57237499_Campylobacter_jejuni
76259633_Chloroflexus_aurant
76258447_Chloroflexus_aurant
46198353_Thermus_thermophi
94984545_Deinococcus_geothe
22325473_Arabidopsis_thalia
102192140_Rickettsia_canade
83591758_Rhodospirillum_rubrum
106895571_Clostridium_sp.
53688239_Nostoc_puncti
23124097_Nostoc_puncti
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67920030_Crocospaera_watson
116622648_Solibacter_usitat
116620290_Solibacter_usitat
47574643_Rubrivivax_gelati
82736706_Pseudomonas_putida
29653839_Coxiella_burnet

KNSFGFGGVNVSLLFKKF
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SNSFGFGGHNSVVAFAFAF
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SDTLGFGGHNAALLLRRY
SNSFGFGGHNACVLFGRF
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SNSFGFGGHNVTLAFKKY
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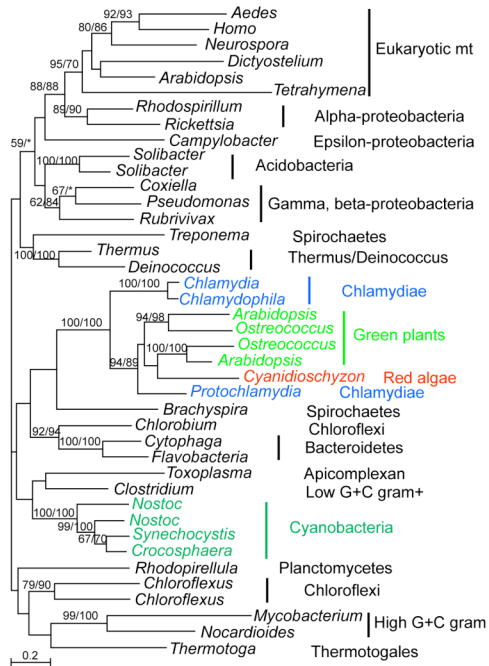


Figure 16. Phylogeny of Beta-ketoacyl-ACP Synthase (*fabF*). Note that sequences of primary photosynthetic eukaryotes form a monophyletic group with those of chlamydiae (in particular *Protochlamydia*) whereas cyanobacterial homologs form another distinct group. Mt=mitochondrial precursor

17. Malate dehydrogenase

CLUSTAL X (1.83.1) multiple sequence alignment

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71069968_Giardia_lambli          VLRVCISGAAGQICYSVLFRIAAGDMLGYDQPVHIVMLEVPAALKAAEGV
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15605100_Chlamydia_tracho        TVSVAVTGGTGTQIAYSFLFSLAHGDVFGSDCGIDLRIYDIPGTERALSGV
67464753_Entamoeba_histol        PLHLVLTGAAGQIGYNLLFLIAHGLMFGPNQTVYLHLVDIM--VEAMEGV
52139822_Lycopersicon_escule     LINVSVSAGAAGMIANHFLLFKLASGEVFGPDQPVTLKLLGSESIQALEGV
11182080_Scherffelia_dubia]     TINVVVSGAAGQISNHLFLMLASGSVFGNDQPIALRLLGSESIQALEGV
116059121_Ostreococcus_tauri]   TITVAVSAGAAGQISNHLFLKIASGSVFGADQPVILRLLGSESIQALEGV
46447406_Protochlamydia_amoeba   PIKIAISGGAGQIAYSLLFRLASGELFGPNQLIELQVLEVPNALSALEGV
89306547_Tetrahymena_thermo      PIKVTVTGAAGNIGYAFVFFAGQGRVFGDQPIDLTLELPSNKRPMGMT
1054961_Trichomonas_vagina       PIHILITGAAGQIGYALTFRIAKGDLCG-DRKVVHLHLEIPFGMKALEGC
89296341_Tetrahymena_thermo      EINVCVTGAAGQIGYAFLLPLLTGQCFG-DKKINLRLLDVPQAESILQGV
24528077_Galdieria_sulphu        PINVCVTGAAGQIAYSLLPLIAGGKVFQPVQVSLRLLIEAALPSLQGV
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CM3065_Cyanidioschyzon_merolae   PLRVAVTGAAGQIGYQLVTRIASGEMLGKNQPIHLSCIETPQGMKALRGV
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24214839_Leptospira_interr       TVKVAVTGAAGQIGYSLLFRIASGQMFADTAVEIQMLELEAAIPAAGV
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71276528_Xylella_fastid          LVRVAVTGAAGQIGYSLLFRIAAGEMFGKDRSVILQMLELPKAQAALKGV
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15827536_Mycobacterium_leprae    PLKVAVTGAAGQIGYSLLFRLASGSLLGLDRPIELRLEIEPALKALEGV
29829979_Streptomyces_avermi     PVNVTVTGAAGQIGYALLFRIASGQLLGADVVKLRLLLEITPALKAAEGT

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5174539_Homo_sapient
66814308_Dictyostelium_discoi
Malawimonas_jakobiformis

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71069968_Giardia_lambli
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15605100_Chlamydia_tracho
67464753_Entamoeba_histol
52139822_Lycopersicon_escule
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116059121_Ostreococcus_tauri]
46447406_Proteochlamydia_amoeba
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24528077_Galdieria_sulphu
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CM3065_Cyanidioschyzon_merolae
95926834_Coxiella_burnet
24214839_Leptospira_interr
Acanthamoeba_castella
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Seculamonas_ecadoriensis
71276528_Xylella_fastid
84360329_Burkholderia_dolosa
15805354_Deinococcus_radiod
71365666_Nocardioides_sp.
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5174539_Homo_sapient
66814308_Dictyostelium_discoi
Malawimonas_jakobiformis

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71069968_Giardia_lambli
62185314_Chlamydomydia_abortu
15605100_Chlamydia_tracho
67464753_Entamoeba_histol
52139822_Lycopersicon_escule
11182080_Scherffelia_dubia]
116059121_Ostreococcus_tauri]
46447406_Proteochlamydia_amoeba
89306547_Tetrahymena_thermo
1054961_Trichomonas_vagina
89296341_Tetrahymena_thermo
24528077_Galdieria_sulphu
15077032_Trypanosoma_brucei
CM3065_Cyanidioschyzon_merolae
95926834_Coxiella_burnet
24214839_Leptospira_interr
Acanthamoeba_castella
30248777_Nitrosomonas_europa
Seculamonas_ecadoriensis
71276528_Xylella_fastid
84360329_Burkholderia_dolosa
15805354_Deinococcus_radiod

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84360329_Burkholderia_dolosa
15805354_Deinococcus_radiod
71365666_Nocardioides_sp.
15827536_Mycobacterium_leprae
29829979_Streptomyces_avermi
111224976_Frankia_alni
116058088_Ostreococcus_tauri]
52139818_Lycopersicon_escule
24583394_Drosophila_melano
5174539_Homo_sapient
66814308_Dictyostelium_discoi
Malawimonas_jakobiformis

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71069968_Giardia_lambli
62185314_Chlamydia_abortu
15605100_Chlamydia_tracho
67464753_Entamoeba_histol
52139822_Lycopersicon_escule
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46447406_Protoclamydia_amoeba
89306547_Tetrahymena_thermo
1054961_Trichomonas_vagina
89296341_Tetrahymena_thermo
24528077_Galdieria_sulphu
15077032_Trypanosoma_brucei
CM3065_Cyanidioschyzon_merolae
95926834_Coxiella_burnet
24214839_Leptospira_interr
Acanthamoeba_castella
30248777_Nitrosomonas_europa
Seculamonas_ecadoriensis
71276528_Xylella_fastid
84360329_Burkholderia_dolosa
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71365666_Nocardioides_sp.
15827536_Mycobacterium_leprae
29829979_Streptomyces_avermi
111224976_Frankia_alni
116058088_Ostreococcus_tauri]
52139818_Lycopersicon_escule
24583394_Drosophila_melano
5174539_Homo_sapient
66814308_Dictyostelium_discoi
Malawimonas_jakobiformis

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71069968_Giardia_lambli
62185314_Chlamydia_abortu
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67464753_Entamoeba_histol
52139822_Lycopersicon_escule
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15077032_Trypanosoma_brucei
CM3065_Cyanidioschyzon_merolae
95926834_Coxiella_burnet
24214839_Leptospira_interr

LSEAELMKEAADALK
ISLDEISQEKANVSL
ISLDEILQEKASVSL
NSEEELLEKKLEIA
KSEDELLAEKRCVAH
KTEDELVKEKECVGH
KSAEELVNEKGCVGS
LTEQELKEEREMVSS
VTTKELIEERDLALQ
ATEKELIGEKETAWK
ITTEELLSEKADAFS
ITADELYAEKAEALA
ATTELEEEERREVST
RTRKELIEERDAVRH
ETLDELREERDAVEA
ITHEELVSRNEVKE

Acanthamoeba_castella	KTNDELVSEKNGVGE
30248777_Nitrosomonas_europa	IAYDELTOELDSIKH
Seculamonas_ecadoriensis	ASLKELKEERDAVAS
71276528_Xylella_fastid	KTLAEELEERASIAH
84360329_Burkholderia_dolosa	ATLAELLEERDGVAH
15805354_Deinococcus_radiod	ATAQELEEEERDEVK
71365666_Nocardioides_sp.	ASTAELADEREAVKE
15827536_Mycobacterium_leprae	KSTAELADERMAVKQ
29829979_Streptomyces_avermi	ASVKELEEEEREAVRA
111224976_Frankia_alni	ASVRELAEEREAVRA
116058088_Ostreococcus_tauri]	ESATELTEEFELAEA
52139818_Lycopersicon_escule	ATAKELAEKSLAYS
24583394_Drosophila_melano	VTGKELQEEKDEALS
5174539_Homo_sapien	LTAKELTEEKESAFE
66814308_Dictyostelium_discoi	LTTEELVAEKTALQ
Malawimonas_jakobiformis	-----

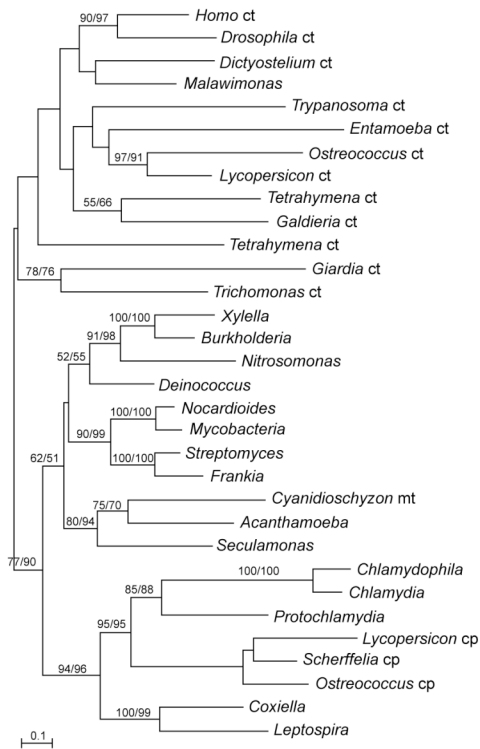


Figure 17. Phylogeny of Malate dehydrogenase, showing that green plant chloroplast precursors form a strongly supported group with chlamydial homologs. Cp = chloroplast, ct=cytoplasmic, mt=mitochondrial, based on the original sequence annotations from GenBank and *Cyanidioschyzon* genome database. The sequences of *Acanthamoeba*, *Malawimonas*, and *Seculamonas* were obtained from the Taxonomically Broad EST Database (TBestDB). No hits to cyanobacterial homologs were statistically significant (Evalue<e-8) in our search of the GenBank non-redundant protein sequence database.

18. Sodium:hydrogen antiporter

CLUSTAL X (1.83.1) multiple sequence alignment

118166492_Mycobacterium_avium
14521887_Pyrococcus_abyssi
57640815_Thermococcus_kodaka
108803861_Rubrobacter_xylano
108803863_Rubrobacter_xylano
71279344_Colwellia_psychr
109672731_Campylobacter_concis
77464578_Rhodobacter_sphaer
71280641_Colwellia_psychr
95931201_Desulphuromonas_acetox
95929830_Desulphuromonas_acetox
86144878_Vibrio_sp.
113947356_Shewanella_baltic
16752011_Chlamydomphila_pneumo
15834867_Chlamydia_murida
CM1485_Cyanidioschyzon_merolae
18402254_Arabidopsis_thalia
15222822_Arabidopsis_thalia
86134192_Tenacibaculum_sp.
86131526_Cellulophaga_sp.
118056239_Pseudomonas_mendoc
90423709_Rhodopseudomonas_palu
90422565_Rhodopseudomonas_palu
89900927_Rhodoferax_ferrir
88936799_Geobacter_uraniu
71906322_Dechloromonas_aromat

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118166492_Mycobacterium_avium
14521887_Pyrococcus_abyssi
57640815_Thermococcus_kodaka
108803861_Rubrobacter_xylano
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71279344_Colwellia_psychr
109672731_Campylobacter_concis
77464578_Rhodobacter_sphaer
71280641_Colwellia_psychr
95931201_Desulphuromonas_acetox
95929830_Desulphuromonas_acetox
86144878_Vibrio_sp.
113947356_Shewanella_baltic
16752011_Chlamydomphila_pneumo
15834867_Chlamydia_murida
CM1485_Cyanidioschyzon_merolae
18402254_Arabidopsis_thalia
15222822_Arabidopsis_thalia
86134192_Tenacibaculum_sp.
86131526_Cellulophaga_sp.
118056239_Pseudomonas_mendoc
90423709_Rhodopseudomonas_palu
90422565_Rhodopseudomonas_palu
89900927_Rhodoferax_ferrir
88936799_Geobacter_uraniu
71906322_Dechloromonas_aromat

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118166492_Mycobacterium_avium
14521887_Pyrococcus_abyssi
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108803861_Rubrobacter_xylano
108803863_Rubrobacter_xylano
71279344_Colwellia_psychr
109672731_Campylobacter_concis

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71906322_Dechloromonas_aromat

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15222822_Arabidopsis_thalia
86134192_Tenacibaculum_sp.
86131526_Cellulophaga_sp.
118056239_Pseudomonas_mendoc
90423709_Rhodopseudomonas_palau
90422565_Rhodopseudomonas_palau
89900927_Rhodoferrax_ferrir
88936799_Geobacter_uraniu
71906322_Dechloromonas_aromat

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71279344_Colwellia_psychr
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77464578_Rhodobacter_sphaer
71280641_Colwellia_psychr
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95929830_Desulphuromonas_acetox
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113947356_Shewanella_baltic
16752011_Chlamydomphila_pneumo
15834867_Chlamydia_murida
CM1485_Cyanidioschyzon_merolae

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71906322_Dechloromonas_aromat

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 : ** *:*:* .

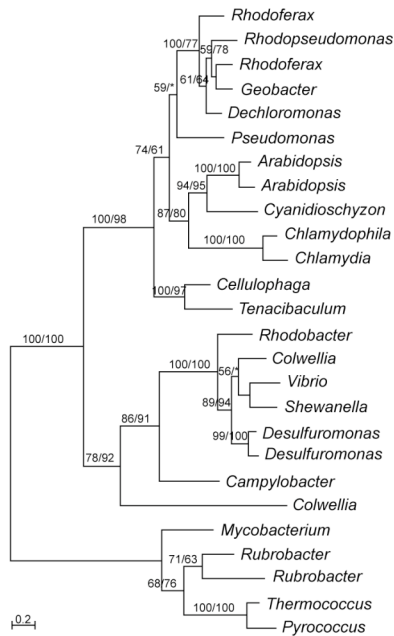


Figure 18. Phylogeny of Sodium:hydrogen antiporter, showing that red algal, green plant and chlamydial sequences form a monophyletic group. The *Arabidopsis* sequences (GI 18402254) are annotated as chloroplast precursors, but no identifiable cyanobacterial homologs were found in GenBank non-redundant protein sequence database using *Cyanidioschyzon*, *Arabidopsis* (GI 18402254) and *Chlamydomonas* (GI 16752011) as queries.

19. 4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase (*gcpE*)

CLUSTAL X (1.83.1) multiple sequence alignment

32471760_Rhodospirillum_baltic	TRPVTIGSITIGDGHPIAVQSMTATKTQNI DATVEQAEALHARGAGVVR I
17986553_Brucella_melite	SVGVSVGGVIVGGSAPVVVQSMTNTDTADVDSTVAQVAALHRAGSEIVR I
15805413_Deinococcus_radiod	TVSVNVGVMVGSAPVIVVQSMTNTDTANA EATAIQVAQLARAGSEIVR V
116620316_Solibacter_usitat	AVVVDVGGVKGVTGTHPIVVQSMTNTDTAD VASTVNQVMALARAGSELVR V
42526774_Treponema_dentic	PRTIHIGKLTGGTSPILLQTMWKESSLDLLS IVKSLNELEQLGCDIVRF
15606681_Aquifex_aeolic	TRQIRVGNVKGIGDAPVIVVQSMTSTKTHD VEATLNQIKRLEYAGCEIVR V
15645249_Helicobacter_pylori	TKQIFIGGVAIGGDAPISTQSM TFSKTADIESTKNQIDRLKLAGADLVR V
68234882_Frankia_sp.	SRQIHVGNVPVGGDAPVSIQSMCTTLLTSD V NATLQOIAQLTAAGCQIVR V
15643653_Thermotoga_mariti	RKSVKVGKVVIGGEAPVSVQSMTTTKTAD VEKTVS QIKSLERAGCEIVR V
73748214_Dehalococcoides_sp.	STEIRLGNLTI GGSAPISVQSMTKTDTRNIPATIAQIKELEECGCEI IRL
51892639_Symbiobacterium_therm	TRAVKGRVQIGGGAPITVQSMTKCDTRDVP EVLQRIRALEEAGCDIVR V
34763966_Fusobacterium_nuclea	TRVVKVGNLKGNNPIIQSMTNTNSADVEAT ARQINELEKAGCQLVRM
16079562_Bacillus_subtil	TRPVKVGPLTIGGNNEVVIQSMTTTKTHD VEATVAEINRLAEAGCQIVR V
110803791_Clostridium_perfri	TRKVKIGNIYVGGDFRVSISQSM TNDTKDVESTVKQIKELQEAGCDIVR C
26987589_Pseudomonas_putida	SRKIWVGNVPVGGDAPVAVQSMTNTDTNDV AATVAQIQRLVDAGVDIVR V

50122142_Erwinia_caroto
90579365_Vibrio_angust
46156442_Haemophilus_somnus
99080703_Silicibacter_sp.
83592086_Rhodospirillum_rubrum
56551076_Zymomonas_mobili
78188327_Chlorobium_chloro
78187812_Pelodictyon_luteol
53715645_Bacteroides_fragil
33861233_Prochlorococcus_marin
78184752_Synechococcus_sp.
CM2113_Cyanidioschyzon_merolae
75906658_Anabaena_variab
113477916_Trichodesmium_erythr
67925456_Crocospaera_watson
Cyanophora_paradoxa
Glaucocystis_nostochinera
15618288_Chlamydomonada_pneumo
34540704_Porphyrionomonas_gingiv
110638588_Cytophaga_hutchi
76788770_Chlamydia_tracho
46446374_Candidatus_Protoc
24215859_Leptospira_interr
23508024_Plasmodium_falcip
30697397_Arabidopsis_thalia
61742128_Chlamydomonada_reinha
Bigelowiella_nutans_cp
116059551_Ostreococcus_tauri
Isochrysis_galbana

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116620316_Solibacter_usitat
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90579365_Vibrio_angust
46156442_Haemophilus_somnus
99080703_Silicibacter_sp.
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78188327_Chlorobium_chloro
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33861233_Prochlorococcus_marin
78184752_Synechococcus_sp.
CM2113_Cyanidioschyzon_merolae
75906658_Anabaena_variab
113477916_Trichodesmium_erythr
67925456_Crocospaera_watson
Cyanophora_paradoxa
Glaucocystis_nostochinera
15618288_Chlamydomonada_pneumo
34540704_Porphyrionomonas_gingiv

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Bigelowiella_nutans_cp
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Isochrysis_galbana

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17986553_Brucella_melite
15805413_Deinococcus_radiod
116620316_Solibacter_usitat
42526774_Treponema_dentic
15606681_Aquifex_aeolic
15645249_Helicobacter_pylori
68234882_Frankia_sp.
15643653_Thermotoga_mariti
73748214_Dehalococcoides_sp.
51892639_Symbiobacterium_therm
34763966_Fusobacterium_nuclea
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Cyanophora_paradoxa
Glaucocystis_nostochinera
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76788770_Chlamydia_tracho
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Isochrysis_galbana

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68234882_Frankia_sp.
15643653_Thermotoga_mariti
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75906658_Anabaena_variab
113477916_Trichodesmium_erythr
67925456_Crocospaera_watson
Cyanophora_paradoxa
Glaucocystis_nostochinera
15618288_Chlamydomonada_pneumo
34540704_Porphyrionomonas_gingiv
110638588_Cytophaga_hutchi
76788770_Chlamydia_tracho
46446374_Candidatus_Protoc
24215859_Leptospira_interr
23508024_Plasmodium_falcip
30697397_Arabidopsis_thalia
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Bigelowiella_nutans_cp
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Isochrysis_galbana

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. : .

32471760_Rhodopirellula_baltic
17986553_Brucella_melite
15805413_Deinococcus_radiod
116620316_Solibacter_usitat
42526774_Treponema_dentic
15606681_Aquifex_aeolic
15645249_Helicobacter_pylori
68234882_Frankia_sp.
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73748214_Dehalococcoides_sp.
51892639_Symbiobacterium_therm
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99080703_Silicibacter_sp.
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AGIATLLAEGLGDTIRVSLTEAPEKEIPVYSILQSLGLRKTMEYIACPS

CM2113_Cyanidioschyzon_merolae
75906658_Anabaena_variab
113477916_Trichodesmium_erythr
67925456_Crocospaera_watson
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76788770_Chlamydia_tracho
46446374_Candidatus_Protoc
24215859_Leptospira_interr
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Bigelowiella_nutans_cp
116059551_Ostreococcus_tauri
Isochrysis_galbana

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AGIGTLLAEGIGDTRVSLTEAPEKEIPVYSILQALGLRRTMVEYVACPS
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--VGLLCDGLGDGVFIDPDTDHSAPLAAFGLLQGSRMRTKTEYVSCPS

32471760_Rhodospirillum_baltic
17986553_Brucella_melite
15805413_Deinococcus_radiod
116620316_Solibacter_usitat
42526774_Treponema_dentic
15606681_Aquifex_aeolic
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68234882_Frankia_sp.
15643653_Thermotoga_mariti
73748214_Dehalococcoides_sp.
51892639_Symbiobacterium_therm
34763966_Fusobacterium_nuclea
16079562_Bacillus_subtil
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78188327_Chlorobium_chloro
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53715645_Bacteroides_fragil
33861233_Prochlorococcus_marin
78184752_Synechococcus_sp.
CM2113_Cyanidioschyzon_merolae
75906658_Anabaena_variab
113477916_Trichodesmium_erythr
67925456_Crocospaera_watson
Cyanophora_paradoxa
Glaucocystis_nostochinera
15618288_Chlamydomonada_pneumo
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110638588_Cytophaga_hutchi
76788770_Chlamydia_tracho
46446374_Candidatus_Protoc
24215859_Leptospira_interr
23508024_Plasmodium_falcip
30697397_Arabidopsis_thalia
61742128_Chlamydomonada_reinha
Bigelowiella_nutans_cp
116059551_Ostreococcus_tauri
Isochrysis_galbana

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CGRTYFDLERAAASIKRLSHLKLKIGIMGCVVNGPGEADADFGYVGA
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15805413_Deinococcus_radiod	APVYQDGKLLKGPRIAEEFQELLEKY
116620316_Solibacter_usitat	APVYVDGRLMLKGDRIVAEFLEILNEY
42526774_Treponema_dentic	VIIFKHGAI TDLKKLTEEEKIKAVDKA
15606681_Aquifex_aeolic	AWLFKHKGP IVDSEMVDELLKEIQNM
15645249_Helicobacter_pylori	GLIIKEGKVI LAEKDLFETTFVIEVENL
68234882_Frankia_sp.	GQIFVRGKVI VPEAQIVETLIEEAMRL
15643653_Thermotoga_mariti	VIFVKG--EIVSKEFVLERLKYLNEL
73748214_Dehalococcoides_sp.	GLLFRKGEKIVPEDELVDALLREIASL
51892639_Symbiobacterium_therm	GMLYVGGERV TTEEMVEALVELVEQK
34763966_Fusobacterium_nuclea	GILFKKGEI VVSENNLLEELKKMISED
16079562_Bacillus_subtil	GLLFRKGGKIVVPEETMVEELKKEIDIL
110803791_Clostridium_perfri	GLIFRKGEI IVKEEDLVEELIKI IETI
26987589_Pseudomonas_putida	NLIYIDGKPAL TNDNLVDELEKLRQK
50122142_Erwinia_caroto	SGFYEDGVRQF DNEQ MIDQLEAKIRAK
90579365_Vibrio_angust	SAFYEDGIRQF DNDNVIDQLESKIRAK
46156442_Haemophilus_somnus	SGYYLDGKRQF DNE DLINQLEAKIRAK
99080703_Silicibacter_sp.	GMVYLAGKASMSNDQ MIDHIVEVEEKK
83592086_Rhodospirillum_rubrum	NKVYVSGIPDINNEAMVDHLVALVEKK
56551076_Zymomonas_mobili	HMVFLSGVTDVEDAKMLDHIVSLVEAK
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78187812_Pelodictyon_luteol	ISLYVGKECVLPEVEAVDRLIDLIREH
53715645_Bacteroides_fragil	ISLYKQKEC IIP EEEAVEKLI ELIKAN
33861233_Prochlorococcus_marin	IALYRRKEEIVPEDEGVDALIRLIKDD
78184752_Synechococcus_sp.	IALYRGREEIVPEKEGVQALIQLIQED
CM2113_Cyanidioschyzon_merolae	ISLYRGREEIVPENQGV AELIKLMKED
75906658_Anabaena_variab	ISLYRGREEIVPEDKGVEELINLIKAD
113477916_Trichodesmium_erythr	ISLYRGREEIVHESQGV EELINLIKAD
67925456_Crocospaera_watson	IALYRGREEIVHEEQV EELINLIKAD
Cyanophora_paradoxa	-----
Glaucocystis_nostochinera	-----
15618288_Chlamydomphila_pneumo	IDLYVKHTCVIPMEDAE EELIRLLQEH
34540704_Porphyrromonas_gingiv	IDLYKQKICV I PQEQAVQQLIELIKEN
110638588_Cytophaga_hutchi	IALYRGQTVV VVHSDKAVDELINIKED
76788770_Chlamydia_tracho	IDLYVKHKCVIPI ENAE EELVQLLKEH
46446374_Candidatus_Protoc	IDLYVGKECVI DFADADDRLVNLIRAH
24215859_Leptospira_interr	VHLYRGKEI VVPSEI ADEKLVQLIKDN
23508024_Plasmodium_falcip	IDLYYGKELVIPEEEACDKLIELIKKH
30697397_Arabidopsis_thalia	IDLYVGKTVVIAMTEATDALIGLIKEH
61742128_Chlamydomonas_reinha	IDLYVGKEVVIPMESACDQ LIELIKEH
Bigelowiella_nutans_cp	VDLYVGKEMVIPNAEACDALIELIKEH
116059551_Ostreococcus_tauri]	IDLYVGKEVVIASEVACDELIELIKEH
Isochrysis_galbana	-----

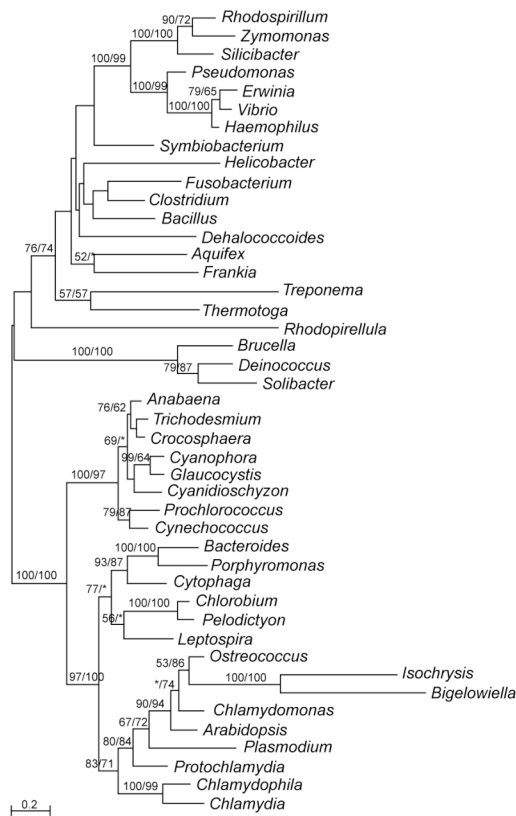


Figure 19. Phylogeny of 4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase (*gcpE*). Note that sequences from green plants, apicomplexans, chlorarachniophytes, and haptophytes form a strongly supported monophyletic group with homologs from chlamydial (in particularly *Protochlamydia*) whereas those from cyanobacteria, red algae and glaucophytes form another distinct group (see text for more discussions). *Cyanophora*, *Glaucocystis*, *Bigelowiella*, and *Isochrysis* were obtained from the Taxonomically Broad EST Database (TBestDB). This gene is part of the DXP pathway that is mainly limited to bacterial and plastids of photosynthetic eukaryotes.

20. Sugar phosphate isomerase

CLUSTAL X (1.83.1) multiple sequence alignment

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85089259_Neurospora_crassa      LLNTASTALSCITDLYFHRAVDAIVNGKLVIIIGVGKSGHIAKKLVATFNS
53711463_Bacteroides_fragil    LLQKEAQAVLNIPVTDYEKAVELIVKGLVTSGMGKAGQIAMNIATTFCS
15618437_Chlamydomonas_reinhardtii ILGKQKEAVDFFQAFAMQLAEKILSGWVFFSGVGKSGCVARKLVATLQS
15605124_Chlamydia_tracho      IFHKQKQVISQYFASFVHQLTEKLLQGS�FFSGIGKSGCIARKLVATMQS
113476650_Trichodesmium_erythr QIRLVRETMREAEAAIAEAAAWISEGSIVLTGVGKAGLIAQKLVATLAS
32476096_Rhodospirillum_baltic VISSEASALEKLSENIFNTIIEFLLTGRVIFTGIGKSGYIARKIAASFSS
102191805_Rickettsia_canade    VMTTEMNAIRCLIDEAYESIVSEIAEGKVIIFMGVGKSAHIGKLAATFAS
90573271_Clostridium_diffic    CLQEEAAAIAAAAERLVEGALALLEKAKLVIITGVGKSGIVARKIAATFSS
87123156_Synechococcus_sp.     CLQEEAAAIAVAAERLVEKALVLLERAKLVIITGVGKSGIVARKIAATFSS
33864177_Prochlorococcus_marin ILDKQHLYTNHYFETLIEKLVLELLEKSIFFTGVGKSGLVAKKIALTMVS
46447416_Candidatus_Protoc    LFOEQQEYLNHFFNTNLVEIFVKTCITGTIVCTGVGKSGFIAQKICQTLVS
Prototheca_wickerhamik
115444351_Oryza_sativa         LFGAQRRLDHFDFDLAAAFQAQALVPGAVFFFTGVGKSGIVARKLAQTLAS

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102191805_Rickettsia_canade
90573271_Clostridium_diffic
87123156_Synechococcus_sp.
33864177_Prochlorococcus_marin
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Prototheca_wickerhamik
115444351_Oryza_sativa
15232565_Arabidopsis_thalia
116185416_Vibrio_sp.
116621618_Solibacter_usitat
110636722_Cytophaga_hutchi
34762344_Fusobacterium_nuclea
67918831_Chlorobium_limico
116329828_Leptospira_borgpe
15606685_Aquifex_aeolic
109673529_Campylobacter_curvus
Rhizopus_oryzae
15964325_Sinorhizobium_melilo
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110635071_Mesorhizobium_sp.
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39996991_Geobacter_sulfur
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116185625_Vibrio_sp.
68544435_Shewanella_baltic

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15605124_Chlamydia_tracho
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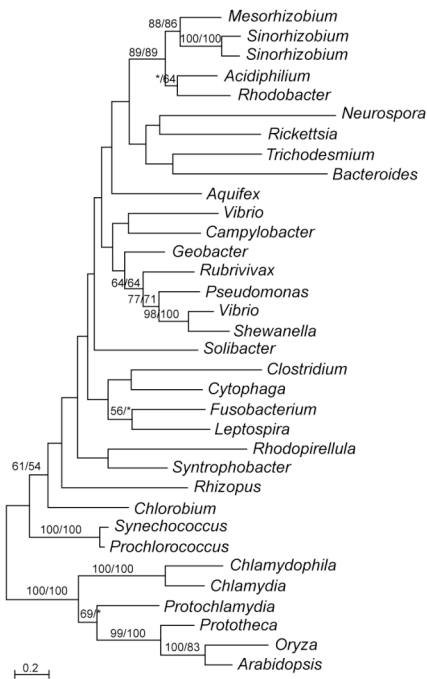


Figure 20. Phylogeny of Sugar-phosphate Isomerase, showing green plant and chlamydial sequences form a strongly supported monophyletic group. Sequences of *Prototheca* and *Rhizopus* were obtained from the Taxonomically Broad EST Database (TBestDB). No red algal homologs were identified in our search of the *Cyanidioschyzon* genome and the Taxonomically Broad EST Database.

21. Metal P-type ATPase

CLUSTAL X (1.83.1) multiple sequence alignment

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78189332_Chlorobium_chloro       NMDVLIALGSLASYLYSIASAMIITSILLGRFLEAGSRLKANNIAELAE
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67921918_Crocospaera_watson
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76258102_Chloroflexus_aurant
71366115_Nocardioides_sp.
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42526892_Treponema_dentic
28211582_Clostridium_tetani
19703603_Fusobacterium_nuclea
46445921_Candidatus_Protoc
83815585_Salinibacter_ruber
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84488951_Methanosphaera_stadtm
89340253_Mycobacterium_flaves
71368538_Nocardioides_sp.
76258037_Chloroflexus_aurant
75910063_Anabaena_variab
16331905_Synechocystis_sp.
56962051_Bacillus_clausi
52841244_Legionella_pneumo
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118058132_Pseudomonas_mendoc
114564618_Shewanella_frigid

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70606661_Sulfolobus_acidoc
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46445712_Candidatus_Protoc
45549362_Drosophila_melano
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87306843_Blastopirellula_marin
52841258_Legionella_pneumo
53713321_Bacteroides_fragil
78188927_Chlorobium_chloro
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53712588_Bacteroides_fragil
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118058132_Pseudomonas_mendoc
114564618_Shewanella_frigid

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114563186_Shewanella_frigid
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116330313_Leptospira_borgpe
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110635001_Mesorhizobium_sp.
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114564618_Shewanella_frigid

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42525989_Treponema_dentic
114563186_Shewanella_frigid
19704525_Fusobacterium_nuclea
16082160_Thermoplasma_acidop
70606661_Sulfolobus_acidoc
84489487_Methanosphaera_stadtm
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45549362_Drosophila_melano
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115444827_Oryza_sativa
56962006_Bacillus_clausi

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116330313_Leptospira_borgpe
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110635001_Mesorhizobium_sp.
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*

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114563186_Shewanella_frigid
19704525_Fusobacterium_nuclea
16082160_Thermoplasma_acidop
70606661_Sulfolobus_acidoc
84489487_Methanosphaera_stadtm
78189332_Chlorobium_chloro
71417434_Trypanosoma_cruzi
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6320475_Saccharomyces_cerevi
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16331210_Synechocystis_sp.
15643086_Thermotoga_mariti
46445712_Candidatus_Protoc
45549362_Drosophila_melano
55743071_Homo_sapien
115444827_Oryza_sativa
56962006_Bacillus_clausi
116330313_Leptospira_borgpe

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87306843_Blastopirellula_marin
52841258_Legionella_pneumo
53713321_Bacteroides_fragil
78188927_Chlorobium_chloro
67921918_Crocospaera_watson
21228430_Methanosarcina_mazei
28210589_Clostridium_tetani
89340248_Mycobacterium_flaves
83374897_Rhodobacter_sphaer
94972021_Deinococcus_geothe
76258102_Chloroflexus_aurant
71366115_Nocardioides_sp.
CM4147_Cyanidioschyzon_merolae
92875650_Medicago_trunca
15224717_Arabidopsis_thalia
115469636_Oryza_sativa
63253545_Arabidopsis_cp
89897922_Chlamydomyxa_felis
15605460_Chlamydia_tracho
53712588_Bacteroides_fragil
42526892_Treponema_dentic
28211582_Clostridium_tetani
19703603_Fusobacterium_nuclea
46445921_Candidatus_Protoc
83815585_Salinibacter_ruber
94972049_Deinococcus_geothe
77462336_Rhodobacter_sphaer
84488951_Methanospaera_stadtm
89340253_Mycobacterium_flaves
71368538_Nocardioides_sp.
76258037_Chloroflexus_aurant
75910063_Anabaena_variab
16331905_Synechocystis_sp.
56962051_Bacillus_clausi
52841244_Legionella_pneumo
118065328_Roseiflexus_casten
87311031_Blastopirellula_marin
110347018_Mesorhizobium_sp.
118058132_Pseudomonas_mendoc
114564618_Shewanella_frigid

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: : : : : ** . * .

42525989_Treponema_dentic
114563186_Shewanella_frigid
19704525_Fusobacterium_nuclea
16082160_Thermoplasma_acidop
70606661_Sulfolobus_acidoc
84489487_Methanospaera_stadtm
78189332_Chlorobium_chloro
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15606387_Aquifex_aeolic
6320475_Saccharomyces_cerevi
42573159_Arabidopsis_thalia
75907770_Anabaena_variab
16331210_Synechocystis_sp.
15643086_Thermotoga_mariti
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115444827_Oryza_sativa
56962006_Bacillus_clausi
116330313_Leptospira_borgpe
118060384_Pseudomonas_mendoc

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KKIVAVVGDGIN DAPALALSDLGIAISTGTEIAIEAADVILCGNLRGLA
NELVAMVGDGIN DAAALASSNVGVAMGGGAGAASEVSPVVL MGNRLTQLL
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53713321_Bacteroides_fragil	SVVLNSLSLA
78188927_Chlorobium_chloro	SVVSNSLRLLK
67921918_Crocospaera_watson	SVVSNALRLR
21228430_Methanosarcina_mazei	SVTTNSLLMK
28210589_Clostridium_tetani	SVLLNALRLK
89340248_Mycobacterium_flaves	FVVGNSLRLLR
83374897_Rhodobacter_sphaer	FVLTNALRLR
94972021_Deinococcus_geothe	FVLSNALRLR
76258102_Chloroflexus_aurant	FVVTNSLRLLR
71366115_Nocardioides_sp.	SVVTNALRLR
CM4147_Cyanidioschyzon_merolae	LVGLSGLRLL
92875650_Medicago_trunca	LVILNSMLLI
15224717_Arabidopsis_thalia	LVIFNSMLLL
115469636_Oryza_sativa	LVCLNSIRAL
63253545_Arabidopsis_cp	LVCLNSVRGL
89897922_Chlamydomyxa_felis	IVGLNALRLL
15605460_Chlamydia_tracho	IVGLNALRLL
53712588_Bacteroides_fragil	IAIMNAVRIQ
42526892_Treponema_dentic	LAVFNSLRRAK
28211582_Clostridium_tetani	I AVLNSMRAL
19703603_Fusobacterium_nuclea	LAVLNSFRAL
46445921_Candidatus_Protoc	LVILNSLKLM
83815585_Salinibacter_ruber	LVVGNALRLL
94972049_Deinococcus_geothe	LVTANALRLL
77462336_Rhodobacter_sphaer	LVTNLALRLL
84488951_Methanosphaera_stadtm	LVILNSFRIG
89340253_Mycobacterium_flaves	FVILNAIRAA
71368538_Nocardioides_sp.	FVIGNGVRAG
76258037_Chloroflexus_aurant	IVVLNGLRLL
75910063_Anabaena_variab	LVTLNSGLRLL
16331905_Synechocystis_sp.	IVTLNSGLRLL
56962051_Bacillus_clausi	LVALNSIRLI
52841244_Legionella_pneumo	IVIASGLRML
118065328_Roseiflexus_casten	LVTNLNGLRLL
87311031_Blastopirellula_marin	LVIANSLRLL
110347018_Mesorhizobium_sp.	LVVLNGLRLL
118058132_Pseudomonas_mendoc	LVVFNGLRLL
114564618_Shewanella_frigid	LVVGNGLRLL

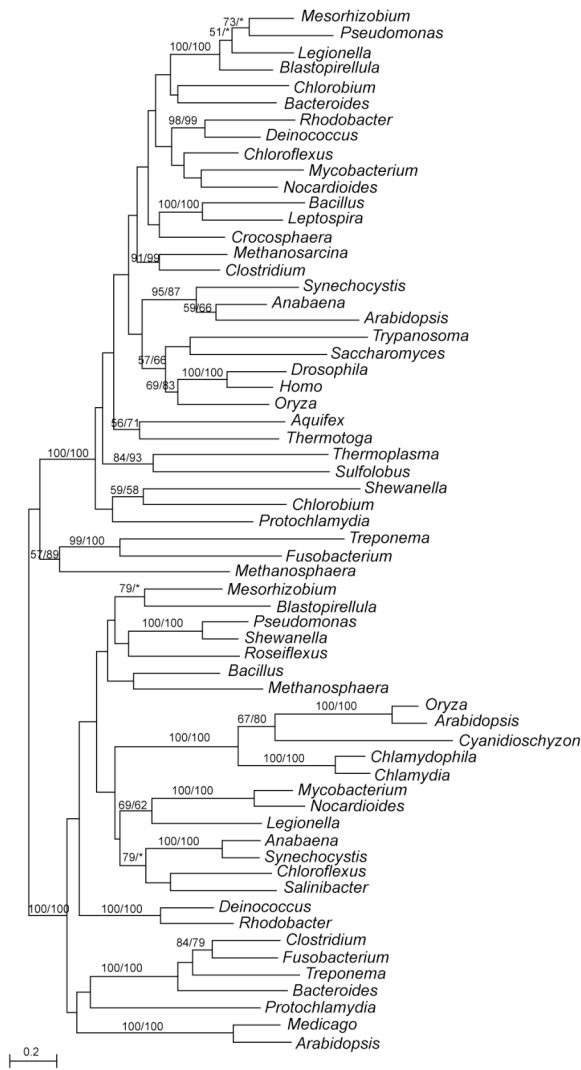


Figure 21. Phylogeny of Metal P-type ATPase. There are multiple copies of this gene. Topology of one paralogous copy (lower part of the tree) shows that red algal, green plants and chlamydial sequences form a strongly supported monophyletic group that is distinct from cyanobacterial homologs. The *Arabidopsis* sequence (GI 63253545) is experimentally annotated as a heavy metal P-type ATPase, localized in the chloroplast envelope and essential for growth under adverse light conditions.