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18S rRNA dataset

>KR607489.1 Brachiomonas submarina strain SAG 7-2b -mating small subunit ribosomal RNA gene, partial sequence

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>FR865585.1 Chloromonas perforata genomic DNA containing 18S rRNA gene, ITS1, 5.8S rRNA gene, ITS2, 28S rRNA gene, culture collection CCAP 11/43

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>U70791.1 Chloromonas reticulata 18S ribosomal RNA gene, partial sequence

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>AJ781310.1 Chlamydomonas subcaudata partial 18S rRNA gene, isolate SAG 12.87

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>AB007370.1 Chlamydomonas tetragama gene for 18S rRNA, partial sequence

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>KJ756821.1 Dunaliella polymorpha strain CCAP 19/7A 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence

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>KJ756819.1 Dunaliella primolecta strain CCAP 11/34 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete

sequence; and 28S ribosomal RNA gene, partial sequence

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>KU641615.1 Dunaliella pseudosalina isolate MAH 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence

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>KJ756824.1 Dunaliella quartolecta strain CCAP 19/8 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence

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>JQ315781.1 Dunaliella salina strain KMMCC 1428 18S ribosomal RNA gene, internal transcribed spacer 1, 5.8S ribosomal RNA gene, internal transcribed spacer 2, and 28S ribosomal RNA gene region

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>KJ756820.1 Dunaliella tertiolecta strain CCAP 19/6B 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence

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>GU292342.1 Ettlia carotinosa strain SAG 213-4 18S ribosomal RNA gene, partial sequence

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>AF159369.1 Haematococcus lacustris strain SAG 34-1b culture-collection SAG:34-1b 18S

ribosomal RNA gene, complete sequence

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gttctagcggtccgcctctggtgagtactgctatggcctatctttctgccggggacggtctctgggcttaactgtccggagtccggaatcggcgag
gttactttgagtaaattagagtgttcaaagcaagcctacgctctgaatacattagcatggaataacacgataggactctggcctatcttgttggtctgta
ggaccggagtaatgattaagagggacagtcgggggcattcgtatttcattgtcagaggtgaaattcttggatttatgaaagacgaacatctgcgaa
agcatttgccaaggatgttttcattaatcaagaacgaaagttgggggctcgaagacgattagataccgtcgtagtctcaaccataaacgatgccga
ctagggattggcaggtgtttcgttgatgaccctgccagcaccttatgagaaatcaaagtttttgggttccgggggggagtatggtcgcaaggctgaa
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gaggattgacagattgagagctctttcttgattctgtgggtggtggtgcatggccgttcttagttggtgggttgccttgtcaggttgattccggtaacg
aacgagacctcagcctgctaaatagtcacggctaccggtagtcgcttgacttcttagagggactattggcgtttagccaatggaagtgtgaggcaa
taacaggtctgtgatgcccttagatgttctgggccgcacgcgcgctacactgatgcattcaacgagcctatccttggccgagaggtccgggtaatc
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ccctgccctttgtacacaccgcccgtcgctcctaccgattgggtgtgctggtgaagtgtccggattggctccagcgggggaacctctgctgttgct
gagaaggtcattaaaccctcccacctagaggaaggagaagtcgtaacaaggtttccgtaggtgaacctgcggaaggatcattg

>KM020022.1 Tetracystis pulchra strain SAG 97.80 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 26S ribosomal RNA gene, partial sequence

ccatgcatgtctaagtatatatactgtgaaactgcgaatggctcattaaatcagttatagtttatttgatggtaccttactcggataaccgtagtaattcta

gagctaatacgtgcgtaaatcccgacttctggaagggacgtatttattagataaaaggccagccgggcttgcccgactcatggcgaatcatgataa
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ggtgacggaggattagggttcgattccggagagggagcctgagaaacggctaccacatccaaggaaggcagcaggcgcgcaaattacccaat
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gttactttgagtaaattagagtgttcaaagcaagcctacgctctgaatacattagcatggaataacacgataggactctggcctatcttgttggtctgta
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gaggattgacagattgagagctctttcttgattctgtgggtggtggtgcatggccgttcttagttggtgggttgccttgtcaggttgattccggtaacg
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taacaggtctgtgatgcccttagatgttctgggccgcacgcgcgctacactgatgcattcaacgagcctatccttggccgagaggtccgggtaatc
ttcgaaactgcatcgtgatggggctagatcattgcaattattggtcttcaacgaggaatgcctagtaagcgcgagtcatcagctcgcgttgattacgt
ccctgccctttgtacacaccgcccgtcgctcctaccgattgggtgtgctggtgaagtgtccggattggctccagcgggggaacctctgctgttgct
gagaaggtcattaaaccctcccacctagaggaaggagaagtcgtaacaaggtttccgtaggtgaacctgcggaaggatcattg

>KM020020.1 Tetracystis texensis strain SAG 99.80 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 26S ribosomal RNA gene, partial sequence

ccatgcatgtctaagtatatatactgtgaaactgcgaatggctcattaaatcagttatagtttatttgatggtaccttactcggataaccgtagtaattcta
gagctaatacgtgcgtaaatcccgacttctggaagggacgtatttattagataaaaggccagccgggcttgcccgactcttggcgaatcatgataa
cttcacgaatcgcacggcttcacgccggcgatgtttcattcaaatttctgccctatcaactttcgatggtaggatagaggcctaccatggtggtaacg
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gttactttgagtaaattagagtgttcaaagcaagcctacgctctgaatacattagcatggaataacacgataggactctggcctatcttgttggtctgta
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acttaaaggaattgacggaagggcaccaccaggcgtggagcctgcggcttaatttgactcaacacgggaaaacttaccaggtccagacacgggg
gaggattgacagattgagagctctttcttgattctgtgggtggtggtgcatggccgttcttagttggtgggttgccttgtcaggttgattccggtaacg
aacgagacctcagcctgctaaatagtcacggctaccggtagtcgcttgacttcttagagggactattggcgtttagccaatggaagtgtgaggcaa
taacaggtctgtgatgcccttagatgttctgggccgcacgcgcgctacactgatgcattcaacgagcctatccttggccgagaggtccgggtaatc
ttcgaaactgcatcgtgatggggctagatcattgcaattattggtcttcaacgaggaatgcctagtaagcgcgagtcatcagctcgcgttgattacgt

ccctgccctttgtacacaccgcccgtcgctcctaccgattgggtgtgctggtgaagtgtccggattgactacagcgggggaacctctgctgttgttg
aaaaggacattaaaccctcccacctagaggaaggagaagtcgtaacaaggtttccgtaggtgaacctgcggaaggatcattg

PTOX dataset

>ENA|HAGC01036235|HAGC01036235.1 TSA: Dinobryon sp. LO226KS, strain LO226KS, contig comp32964_c1_seq2, transcribed RNA sequence.

TLKDEARWKLSQLKLSNDAIWEREKSRKAPWIIKGPYLILCFLLDALFDNKPISRFYFLE
TVARMPYFSYITMLHTYETLGWWRRSAEVKRIHFAEEYNEYHHLLIWESLGGDQDWSVRF
FAQHSAIVYFFVLIVMWIFSPSLAYNFSELIEAHAVDTYAEFAESNKEILQSMDAPPVAK
AYYEAPDMYVFDEFQTSRAPRRPVINSLYDVVCNIRDDEQEHVATMAQCQDPQVLV

>ENA|HAGF01022324|HAGF01022324.1 TSA: Epipyxis sp. PR26KG, strain PR26KG, contig comp28076_c0_seq3, transcribed RNA sequence.

NRLKDELPTSLKLKLTNDAVKQTELTREAHPIARSLYDAGCTAIDYLFDNRPIERFWFLE
TVARMPYFVCVSMLHLYESFGWLRA-PSLRKVHEAEEWNELHHLLIMESLGGDKNWFDRF
MGYHSAIAAYWLLIGTYLYSPQIAYQFMELLETHAVDTYGTFVEENVEILRSLPPPDIAV
AYYTGNDLYTFDDFQVSRGSRRPPCDNLYDVFCNIRDDEKEHVSTMVACQDYSTIG

>CAMPEP_0174979518 /NCGR_PEP_ID=MMETSP0004_2-20121128|14827_1 /TAXON_ID=420556 /ORGANISM=Ochromonas sp., Strain CCMP1393 /LENGTH=562 /DNA_ID=CAMNT_0016231057 /DNA_START=1 /DNA_END=1687 /DNA_ORIENTATION=-

GQQEQSLPGSLGFKLSNKAVAEAERIRDVHPIAQILYDVGCYCIDEYFDERPIPRFWLLE
TIARIPYFSFVSMLHLYESFGWLRQ-PSMRKVHNAEEWNELHHLLIMESLGGDKEWKDRF
IGYHAAIVYYWLIIAVYVLSPRIAYQCMELIECHAADTYATFLRENAATLRSLPAPNVAR
SYYLSEDLYFFDDFQVTRGTRRPPCDNMYDVFKNILDDETEHISTMQACQEYCLSG

>XP_002946776.1 hypothetical protein VOLCADRAFT_79367 [Volvox carteri f. nagariensis]

QEFKEIRARLDQLRLDADDVIAVERERESPLWVKAPFYALCWLLDIMYDNKPIEKFWVLE
TVARIPYFAYISILHLYESLGFWRAGAELRKIHFAEEWNEMHHLQIMESLGGDRAWMDRF
IAEHSAVFYYWVLILFYLVSPRMAYNFMQRVELHAADTYTAFLQRNAAVLESIPPPMVAL
QYYYSEDLYLFDEFQTASPPRRPRCETLLDVFKNIRDDEMEHVKTMIACQNSTIAK

>KXZ56602.1 hypothetical protein GPECTOR_1g541 [Gonium pectorale]

QEFKQIRAKLDRLELDVADVVAVERRRSSPLWVRAPFYALCWVLDVMYDSKPIEKFWVLE
TVARIPYFAYISILHLYESLGFWRAGAELRKIHFAEEWNEMHHLQIMESLGGDRAWVDRF
IAEHAAVLYYWVLIGFYLVSPRMAYNFMQRVELHAADTYTAFLERNAELLSSIPPPLVAL
QYYCSEDLYLFDEFQTASPPRRPRCESLLDVFTNIRDDELEHVKTMVACQNSGIAR

>XP_001703466.1 plastid terminal oxidase [Chlamydomonas reinhardtii]

QEFKQIRAKLDKLELSVSDVVAVEHARTSPAWVKAPFYALCFVLDVMYKNKAIEKFWVLE
TVARIPYFAYISILHLYESLGFWRAGAELRKIHFAEEWNEMHHLQIMESLGGDRAWFDRF
IAEHAAVFYYWVLIAFYLVSPRMAYNFMQRVELHAADTYSAFVERNRTALADIPPPLVAL
QYYYSDDLYLFDEFQTASPPRRPPCENLLDVFTNIRDDELEHVKTMVACQESTIAK

>ABF85790.1 plastid terminal oxidase [Haematococcus lacustris]

AEFDEIKDKLSKLTICNEAVARREAARATPIAVKLPFLALCWVLDVVYDKRPIQKFWVLE
TVARIPYFAYISILHLYESLGFWRAGAELRKIHFAEEWNELHHLQIMESLGGDQAWFDRF
LAEHAAVLYYWLLIAFYLVSPKVAYNFMQRVEHHAADTYCEFLESNRELLASIPPPVVAL
NYYRNQDLYLFDSFQTSSVQRRPDCNTLLDVFINVRDDELEHVATMFAMQNEEIAK
>GAX78356.1 hypothetical protein CEUSTIGMA_g5798.t1 [Chlamydomonas eustigma]
EEWEEIREKLTKLKLDNQAIVEVEKARYTPFWVKLPFLFLCLVLDVLYEGKPIQKFWVLE
TVARIPYFAYISILHLYESIGFWRAGAELRKIHFAEEWNEMHHLQIMESLGGDQSWFDRF
VAEHSAIAYYWLLIFFYLVSPKLAYNFMQRVELHARDTYAVFVENNKELLETIPPPKVAL
SYYLNQDLYLFDEFQQGSTPRRPSCNNLYEVFNNIRDDENEHVKTMDACEKETIAL
>PRW56883.1 plastid terminal oxidase [Chlorella sorokiniana]
PEQKEVLAKVRALKLDDAKVSAREQRRKTNWGIQAAYYSLCWVLDVVYANRPIERFWFLE
TVARMPYFVYISMLHLYESLGWWRAGAELRKVHFAEEWNELHHLQIMEALGGDLRWGDR
F
LAEHAAVFYYWVLVAIYLVSPSASYQFMEMVEEHAADTYAEFAEQNREQLQGIPPPLVAL
NYYKSGDLYLFDEFQTSWELRRPPCNNLYDVFINIRDDELEHVKTMAACQDGSVAL
>AFR58668.1 plastid terminal oxidase [Dunaliella salina]
SECRKIRQKLQQLTLSNKAVAEREHTRETTWYIRLLYDAVCLMLDVVYNNRPLQRFWFLE
TVARMPYFSYISCIHLYETLGWWRAAAELRKIHFAEEWNELHHLQIMEALGGDCMWFDRF
LAYHSAIAYYWVLVALYIFSPRLSYNFSELLEAHAVDTYSEFVSSNEVLLKSLEPPLVAA
QYYRSPDLYMFDEFQTDIEKRTPKCDNLYDVFVNIRDDEAEHVKTMNACQDAEIMD
>GBF89019.1 plastid terminal oxidase [Raphidocelis subcapitata]
EDCQNIRQRLSDLKLSDAAVWAREAARPAPWWIKAPFWALCVVLDLLFANRPIQRFWVLE
TVARIPYFSAISLLHLYESLGFWRAGAELRRIHFAEEWNELHHLQIMEALGGDLLWFDRF
VAEHAALVYYWVCIAFYMAAPKNAYQFSELVEWHAVDTYAQFCETNEALLKSIPPPRVAV
AYYRNEDLYMFDEMQTCSEPRRPSCNNLYDVFSNIRDDEVEHVRTMRACQSPAIAV
>AXB99491.1 plastid alternative oxidase [Caulerpa cylindracea]
DECMQIRAKLNGLKLSNDAVWDRERARTAPWYINLAYYTLCYLLDVLFNNRPLQRFWFLE
TVARMPYFSYISMLHLYESLGWWRQGSILRKVHLAEEWNELHHLQIMESLGGDQYWSDRF
LGQHAAIFYYWILLLFYVFSPRLAYNFSELIEAHAVDTYGEFVDANKELLQSLPPPFVAV
QYYRGDDLYLFDEFQTSGETRRPECNNLYDVFVNIRDDEGEHVKTMKGCQDETIVR
>XP_002950383.1 hypothetical protein VOLCADRAFT_90709 [Volvox carteri f. nagariensis]
NECKAIRSKLKQLKLSNQAVWDREHARETPWFIKGVYLSLCVLLDVLFNNRPIQRFWFLE
TVARMPYFSYISVLHLYESFGWWRAGAELRKIHFAEEWNELHHLQIMESLGGDKLWFDRF
CALHAAVVYYWILLALYVFSPELAYNFSELIEAHAVDTYGEFVDANEELLKSLPPPLVAA
MYYRSQDLYMFDSFQTSQNPRRPPCKNLHDVFCNIRDDELEHVKTMRACQDATVQQ
>XP_005649673.1 hypothetical protein COCSUDRAFT_46597 [Coccomyxa subellipsoidea C-169]

SDCSDVREKLKMLRLENAPVWEREKRRKAPFIINVAYTTLCVVMDVLYNKRPIQRFWFLE
VVARMPYFSYISMLHLYESLGWWRAGAELRRIHFAEEWNELHHLQIMESLGGDQFWIDRF
AAQHAAVFYYWVIVGFFAFSPQLAYVFSELVEGHAVDTYEEFVEENAELLKTLPPPVVAL
EYYKNGDLYLFDELQTTGPKRRPSCNNLYDVFCNIAGDEREHVKTMRACRTYEIVS
>KXZ53636.1 hypothetical protein GPECTOR_6g553 [Gonium pectorale]
NECQEIRVKLKQLKLSNKAVWDREHARKTPWFIKGVYLSLCYLLDFLFDNRPVQRFWFLE
TVARMPYFSYITMLHLYESFGWWRAGAELRKIHFAEEWNELHHLQIMESLGGDQLWFDRF
AALHAAVVYYWILVALYVFSPELAYNFSELIEYHAVDTYGEFVDANEELLKSLPPPLVAA
VYYRSPDLYMFDSFQTSQNPRRPTCKSLYDVFRNICDDELEHVKTMRACQDSTVQQ
>XP_011402281.1 Ubiquinol oxidase 4, chloroplastic/chromoplastic [Auxenochlorella protothecoides]
PKERKVLEKLQALRLDDRRVIAREHKRKAPWLIKGSYVFLCWVLDILYANRPIQRFWVLE
TVARMPYFAYISMLHLYESLGWWRAGAELRRIHFAEEWNELHHLQIMETLGGDHLWIDRF
FAEHAAVFYYWVIILMFFASPSAAYVFSELVENHAVDTYSEFLEENKEVLQGIPPPLVAV
TYYKSGDLYLFDALHTEWSIRRPECNNLYDVFVNIRDDELEHVATMKACAENTIKP
>AAM12876.1 quinol-to-oxygen oxidoreductase [Chlamydomonas reinhardtii]
NNCAEIRSKLKQLKLSNKAMWDREHARETPWLIKGVYLSLCLLLDFLYENRPIQRFWFLE
TVARMPYFSYISMLHLYESLGWWRAGAELRKIHFAEEWNELHHLQIMESLGGDQLWFDRF
AAQHAAILYYWILLGLYVFSPRLAYNFSELIEYHAVDTYGEFWDANEELLKSLPPPLVAA
VYYRSQDLYMFDSFQTSQNPRRPSCKTLYDVFKNICDDEMEHVKTMKACQDETVSQ
>GBF99932.1 plastid terminal oxidase [Raphidocelis subcapitata]
KQCREVRARLKQLKLDNGAVWAREHARETPWLVKGVYLALCVFLDKAYDNRPIQRFWFLE
TVARMPYFVYISCLHLAESMGWWRAGADLRIVHAAEEWNELHHLQVMESLGGDVLWWD
RF
LGTHAAFIYYWVLVGLFVASPSLAYNFSELIEAHAVDTYGEFVDANEELLKSLPPPLVAA
EYYCGQDLYMFDAFQTSDTPRRPKVKNMYDVFANIRDDEKEHVKTMQACQDFTVAG
>ABF85789.1 plastid terminal oxidase [Haematococcus lacustris]
EECAEIRQRLSRLILSNHAVSERERVREAPWYVRGVYNILCLLIDVLFENRPIQRFWFLE
TVARMPYFSYISCLHLYESLGWWRAAAELRKLHFAEEWNELHHLQIMESLGGDQLWFDRF
VGYHSAIVYYWVLVLLYVASPSLAYTFSELLEAHAVDTYGEFLDANEPLLKSLAPPLVAA
EYYRSCDLYLFDEFQTSNTPRNPPLENLYDVFCAIKEDEGEHVKTMHACVDSSLVA
>PSC72506.1 plastid terminal oxidase isoform A [Micractinium conductrix]
EEQRQVLAQVRALSLDDSLVSARERARGASLPITAAYVSLCWVLDFLYAGRPIQRFWILE
TVARMPYFVYISMLHLYESLGWWRAGAELRKVHFAEEWNELHHLQIMEALGGDLRWIDRF
VAEHAAVFYYWVLVVIYLISPSASYQFMEMVEGHAADTYAEFAAQNKEPMQAIPPPLVAL
NYYKSGDLYLFDEFQTSWERRRPACNNLYDVFVNIRDDELEHVKTMVACQDGTVAL

>XP_013906748.1 Alternative oxidase 4 [Monoraphidium neglectum]
AQCREVRAKLQQLTLSNAKVWEREHKRETPWVVKAVYLALCVFLDVAYDKRPIQRFWFLE
TVARMPYFSYLTMLHLLETLGWWRAGAELRKVHFAEEWNELHHLQIMEALGGDQLWIDRF
MAQ----------LAYNFSELIEAHAVDTYSEFADANEELLKSLPPPLVAA
EYYTGPDLYLFDSFQTSQQPRRPSVNTLHDVFLNIAADEGEHVKTMRACQDYSVAG
>XP_005850335.1 hypothetical protein CHLNCDRAFT_12129, partial [Chlorella variabilis]
----------IRAAYASLCWALDVMYAGRPIERFWILE
TVARMPYFVYISMLHLYESLGWWRAGAELRKVHFAEEWNELHHLQIMEALGGDLRWGDR
F
LAEHAAVFYYWALVLIYLISPAASYQFMEMVEGHAADTYAEFAEQNRERLQAIPPPLVAL
AYYKSGDLYLFDQFQTSWELRRPRCNNLYDVFINIRDDELEHVKTMAACQ------
>XP_001421713.1 predicted protein, partial [Ostreococcus lucimarinus CCE9901]
------RAKMDALRLDADAIWARERARSAPWILKVPYVALCVMLDKLFETQPVQRFWFLE
TVARMPYFSYTSMLTFYEILGWWRRSSELRKVHFAEEWNEYHHLLVMESLGGDACWRDRF
LGQHAAIVYYFVLVALWLISPALAYNFSELIEGHAVDTYGQFVDQNAELLKSMPAPRIAV
EYYEAADLYLFDEFQTARRLRRPQIRSLFDVFSNIRDDEGEHVNTMNACQREDSDI
>XP_003083541.1 Alternative oxidase [Ostreococcus tauri]
TMPKELRVKLEALRLDSDAIWEREKNRPAPWLLKAPYLALCFMLDKLFETKPVQRFWFLE
TVARMPYYSYTAALTFYEILGWYRGGAELRKIHFAEEWNEYHHLLIMESLGGDVSWRDRF
LGQHAALVYYGVLILLWFMSPALAYNFSELIEAHAVDTYAQFVDQNAELLKTMPAPRIAV
EYYEGADLYLFDEFQTARRTRRPRIRTLYDVFSNIRDDEGEHVSTMNACQKEDAAV
>GAX73707.1 hypothetical protein CEUSTIGMA_g1160.t1 [Chlamydomonas eustigma]
PEVQARRDLLGKLTLSNQAVWDREHARKSPWVIKVPYYVLCWVLDVLFDGRPIQRFWLLE
TVARMPYFSYINLLHLYETLGWWRRSLEARKVHFAEEWNEAHHLLIMESLGGDQRWADRF
IAQHAAVVYYVVLNILWFLSPTLAYNFSELIEAHAVDTYGQFVDENEAILKQLPPPRMAR
LYYESEDMYLFEKFQTERGSRHVAVMSLYDVFCNIRDDEAEHVATMHAMQRQDVLD
>QDZ20645.1 ubiquinol oxidase [Chloropicon primus]
ELCVTFEDQLKKLTLDAEGIYERELKRKKSWIIKGPYIVLCWALDRLYKDRPIQRFWLLE
TVARMPYFSYISMLHLYETLGWWRKGAAVKSVHFAEEWNEFNHLLIMESLGGDDSWIDRF
AGYHGAIVYYWVLNLLWLISPYLAYQFSELLENHAVDTYSQFVDENEELLRTLPAPAVAK
NYYQNEDLYMFDEFQTSRSRRRPQINTLYDTFSNIRDDELEHVKTMVACQNTNKSV
>XP_002509380.1 quinol-to-oxygen oxidoreductase [Micromonas commoda]
ELMSELRDQLATLTLSNDAIWAREKARPAPWIIKAPYLALCVFLDLVFENRPIQRFWFLE
TVARMPYFSYNTMLTVYELLGWWRRSSELRRVHFAEEWNEYHHLLIHESLGGDAAWRDRF
LGFHSALLYYGALNVAWLLSPALAYNFSELIEAHAVDTYAQFAEENKATLRKLPAPRIAR
KYYEEGDLYLFDEFQTARSSRRVRVTTLYDAFCAIRDDEAEHVATMAECQMEDSAM

>XP_003061387.1 predicted protein, partial [Micromonas pusilla CCMP1545]
------RDQLATLTLSNAAIWERERSRPAPWIIKAPYFALCTFLDLVFEDRPIQRFWFLE
SVARMPYFSYNTMLTLYELLGWWRRSSELRRVHFAEEWNEYHHLLIMESLGGDALWRDRF
LAQHAALAYYLVLIALWLISPALAYNFSELIEAHAVDTYAQFADENKEKLRTLPAPRIAR
AYYENDDMYLFDEFQTARSSRRPRVRTLHDTFCAIRDDENEHVATMKECQMEDSAM
>XP_007508715.1 predicted protein [Bathycoccus prasinos]
RQGELLLEYLERMKLSNAKIWEREKRLESPWIIEGPYYLLCKVLDLWFENKPVQRFWFLE
TVARMPYFSYTTMLTLYELLGWWRRSSELRKVHFAEEWNEYHHLLIMESLGGDRRWSDRF
LAQHAALVYYFGLVVVWLLSPKLAYNFSEKIETHAVATYAQFTEENKELLESLPAPEVAK
KYYEAEDLYLFDEFQTTTSVRRPKIETLYDVFSNICEDEKEHVGTMNACQIEGVTL
>XP_013899483.1 Alternative oxidase 4, chloroplastic/chromoplastic [Monoraphidium neglectum]
EECKEIRANLAQLKLDDATVWAREEERPAPWWIKAPFWGLCVVLDLLFANRPIQRFWVLE
TVARIPYFSAISLLHFYESLGFWRAGAELRKVHFAEEWNELHHLQIMESLGGDLLWFDRF
VAEHAALAYYWVCT----------
----AEGVWLAGALG---RRGAP----------SPILVC-------
>PNH11360.1 Ubiquinol oxidase 4, chloroplastic/chromoplastic [Tetrabaena socialis]
--------RNAPFRISAVAQSPEASSPRKPEFIRGVYLSLCLLLDVLYENRPIQRFWFLE
TVARMPYFSYISILHLYESLGWWRAGAELRKIHFAEEWNELHHLQIMESLGGDLLWFDRF
AALHSAIAYYWILLGLYVFSPRLAYNFSELIEYHAVDT----------
----------FQSSRAPRRPPCRSLLDVFTNIRDDEGEHVQTMRACQDSSVRS
>chlamydomonad sp. NrCl902
EQFEEIKAQLDSLRLSNEAVAARERARETPMCIKLPFLLLCWILDSIYEDRPIAKFWVLE
TVARIPYFAYLSCLHLYETLGLWTAGAELRKVHFAEEWNELHHLQIMECLGGDQSWFDRC
IAHNAALLYYWVLVLFYLVSPKWAYNFMQRVELHASDTYTEFIESNRATLAGLPPPRVAL
EYYLGEDTYLFDQFQSGNPKRRPRCESLLDVFINIRDDENEHVKTMEACQGSAQGQ
>Polytomella parva
PEFQKELEHIESLTLTSHQVEEVEHARDSPLWVKVPFFALCWLLDALYENRPIQKFWVLE
TVARIPYFAYISILHLYESLGLWRAGAELRKVHFAEEWNEMHHLQIMESLGGDQHWFDRF
FGQWAAVGYYWLIIAFYMFSPKIAYNFMQRVELHAYDTYAAFVEVNRDLLKQIPPPMVAL
SYYRTKDLYLFDEFQQNPQKRRPECSDLYDTFVNIRDDEFEHVRTMIACQDDTVAK
>CAA06190.1 Immutans protein [Arabidopsis thaliana]
--QATILQDDEEKVVVEES-FKAETSTLEQGVNVFLTDSVIKILDTLYRDRTYARFFVLE
TIARVPYFAFMSVLHMYETFGWWRR-ADYLKVHFAESWNEMHHLLIMEELGGNSWWFDRF
LAQHIATFYYFMTVFLYILSPRMAYHFSECVESHAYETYDKFLKASGEELKNMPAPDIAV
KYYTGGDLYLFDEFQTSRNTRRPVIENLYDVFVNIRDDEAEHCKTMRACQTLGSLR
>XP_015633460.1 ubiquinol oxidase 4, chloroplastic/chromoplastic [Oryza sativa Japonica Group]

EAMRTQREKEQTEVAVEESFPFRETAPLEQSVNIFLTESVITILDGLYRDRNYARFFVLE
TIARVPYFAFISVLHMYETFGWWRR-ADYIKVHFAESWNEFHHLLIMEELGGNSLWVDRF
LARFAAFFYYFMTVAMYMVSPRMAYHFSECVERHAYSTYDKFIKLHEDELKKLPAPEAAL
NYYLNEDLYLFDEFQTARCSRRPKIDNLYDVFVNIRDDEAEHCKTMKACQTHGNLR
>XP_024367795.1 uncharacterized protein LOC112278476 [Physcomitrella patens]
LEQDELRAALKKLTLSNQAVWDRENAREAPWWILGPYYLLCLMLDVIFNDRPIQRFWFLE
TVARMPYFSYISMLHLYETLGWWRIGAEVRKVHFAEEWNEMHHLRIMESLGGDLEWGDRF
FAQHAAFFYYWVLNLMFLISPKVAYNFSELIEMHAVDTYGEFADANEELLKTLPPPPAAL
EYYESEDLYMYDEFQTSQETRRPKINNLYDVFKAISGDELEHVKTMSACQTLDMPI
>PTQ49270.1 hypothetical protein MARPO_0003s0157 [Marchantia polymorpha]
IEQDELREQLKKLKLSNKKVWEREKAREAPWWILGPYYFLCWMLDVIFEDRPIQRFWFLE
TVARMPYFSYISMLHLYETLGWWRSGAEVRKVHFAEEWNEMHHLKIMESLGGDLEWGDR
F
FAQHAAFFYYWTLNAMFLISPTVAYNFSELIESHAVDTYGEFADENEELLKTLPPSPVAV
AYYESGDLYMYDEFQTSRESRRPKMGSLYDVFMAICGDEGEHVKTMVACQQLDTQV
>XP_002984492.2 uncharacterized protein LOC9644228 [Selaginella moellendorffii]
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F
FGQHAAFFYYWILNFMFFVSPKVAYNFSELIEMHAVDTYGQFFDENEELLKQLPPSPEAV
AYYENEDLYMFDEFQTSRESRRPKVDSLYDVFVAIKGDEFEHVKTMAACQRAETVA
>GAQ78184.1 Hypothetical protein KFL_000090280 [Klebsormidium nitens]
AEMDELRKKLSQLKLSNDKVWERERSREAPWYILGPYYFLCLILDVIFNGRPIQRFWFLE
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F
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EYYRGEDLYMFDEFQTSRATRRPKVDNLYDVFCNIRDDEFEHVKTMVACQDGGQPI
> XP_028109225.1 ubiquinol oxidase 4, chloroplastic/chromoplastic isoform X1 [Camellia sinensis]
--QATVLQDDEQKAAVENS-FQRKTIVFEQSVNILLTDSVIKILDVLYRDRDYASFFVLE
TIARVPYFAFMSVLHLYESFGWWRR-TDYLKVHFAESWNEMHHLLIMEELGGNSWWFDRF
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>Polytomella magna
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NYYRTKDLYLFDEFHQRAEPRRPKCDNLFDTFVNVRDDEYEHVKTMIACQDDTVAK
>Nitzschia sp.
RLEMMASPQDSSPTVLSSSNSTLLPSTFNKNLIDTLYKIMCILYPVKGNDRDFVRFYILE
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QYYEVGDPCFFDQFSTVPHRIRPPLQSLYDVFVLVRDDEKEHWRTLCNLVQFQEMN
>Spumella sp.
SFDSDVQRKIGTLTLSNRAVEAAERFRQVNFISRLLYSIGCKLLDVLFESKPIQRFWFLE
TIARIPYFSYLTTLHLYETLGLWRK-HALRRVHNAQEWNEHHHLLIMETLGGNKSLMDRL
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EYYTGKDLYYFDEFQVFTGTRRPKIKTLFDVFQNICLDEKEHVKTMQACQTYSTDG
>CEM05282.1 unnamed protein product [Vitrella brassicaformis CCMP3155]
ENTIRLRQELSRLRLDNDAVWRREEERNSPLLLKIPYLFLCWLLDVLYNERPIQRFWFLE
TVARMPYFAYISMLHLYETLGWWRVGTEVRKVHFAEEWNEMHHLFIMESLGGDQAWLDRF
LARHAAIVYYWVLILLFLISPTWAYNFSELIEWHAVDTYGQFVSQNKQILKRLPAPAVAM
EYYKSGDLYMFDEFQTSRQSRRPQINNLYDVFTTIRDDELEHVKTMSACQRLEAAM
>CEM04265.1 unnamed protein product [Vitrella brassicaformis CCMP3155]
EETIRLRQELSRLSLDDDGVIRREEERNAPLLIKVPYLFLCWLLDRLYAGRPIQRFWTLE
TVARIPYMSYISMLHLYETLGWWRVGVEVRRVHFAEEWNEMHHLFIMESLGGDQAWFDRF
LARHAAIVYYWVVIFLFLISPTWAYNFSELVEWHATDTYAEFVEQNKDRLKRLPAPAVAL
EYYNGGDLYLFDEFQSSRESRRPNIDNLYDVFVTIRDDELEHVKTMSACQRLESAM
>VEU38912.1 unnamed protein product [Pseudo-nitzschia multistriata]
GGEPEITDMTAASPQXSLSTPAEIEPVFNKLLIDTVYDVICFLYPVKGTERDFARFYVLE
TVARVPYFAYLSVMHLRETFGERYGSSERMRTHYAEADNELHHLLIMESLGGNSNIIDRT
LAQTMAFFYYWYVIAIYVWNEPAAYHLSELIEDHAFNTYTKFTAEYGDRLKNEPVPDIAR
KYYERDNPFLFDLFCTVKSERRPQLSSLYDVFVNIRDDEKEHWKTLCNLVQYDDMN
>OEU10955.1 plastid terminal oxidase-like protein [Fragilariopsis cylindrus CCMP1102]
AAESSTTTTTTIPFPSSTSNGAVTPDIFNKAVIDTVYDIICFLYPVKGTERDYARFYVLE
TVARVPYFAYLSVMHLRETFGERYPKSDRMRTHYAEADNELHHLLIMESLGGNSNIIDRT
LAQTMAFGYYWYVIVIYTFNESAAYHLSELIEDHAYNTYSKFTEEYEERLKLEPVPDVAR
KYYELDNPFLFDLFCTVKSSRRPQLTSLYDVFINIRDDEKEHWKTLCNLVQYDDMN
>XP_009033364.1 hypothetical protein AURANDRAFT_20495 [Aureococcus anophagefferens]
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TVARVPYFAYLSVMHLRETFGDRDPGSERMRTHYAEADNELHHLLIMESLGGNSSAVDRT
LAQTMAFFYYWYVTVVYSFSEPAAYHLSELIEDHAFNTYDGFLRDHGPKLKGMPVPDIAR
KYYERDDPFLFDQFCTVKSRSRPPLESLYDVFVNIRNDEKEHWKTLCNLVQLDDTQ

>XP_009034449.1 hypothetical protein AURANDRAFT_14460, partial [Aureococcus anophagefferens]
----------ATKGAIDALYE----------GRDFARFYVLE
TLARVPYFAYLSVMHLRETFGDRRPGSERMRTHYAEADNELHHLLIMESLGGNSSAVDRT
LAQSMAFFYFWYVTVVYSFSEPAAYHLSELIEDHAFNTYDDFIKDHGPKLKGMPVPDIAR
KYYERDDPYLRDQFLTVKSRSRPPLESLYDVFVNIRDDEKEHWKTL----------
>EWM22362.1 immutans protein [Nannochloropsis gaditana]
PIFKSMAANQDGELQRDNSDSSEQAKVANKAIVSSIKD----ALVAVYGDRHYARFHALE
TIARVPYFAYTSVLHLYETLGWRRR-ADLMKIHFAESWNELHHLLIMEELGGNAEWLDRL
VAVHLAFFYYWMAIALYMASPETAYNLNEMVERHAYDTYDKFLETHEEELKALPPPQIAK
EYYQTGDLYMFDEFHTNSERRRPKIESLYDVFVNIRNDEREHFMTMAVMQGHSGDA
>EJK63007.1 hypothetical protein THAOC_16363 [Thalassiosira oceanica]
----SARRTSLGSAIAPPDDPDRQLGSLNKSSIDFLKST---VFDSFFEDRAYARFYALE
TIARVPYFSYLSVLHLYETLGKWRR-AKYLKLHFAESWNELHHLLIMEELGGSERFLDRF
LAQHIAFGYYAVVILLYVLNPVQAYNLNQDVEEHAFETYDKYLKDNEEKLKNLPAPKAAI
DYYVDGDMYMFDEFQTGCEFRRPKIENLYDVFVAIRDDEAAHVQTMEQLQTELDVA
>XP_002293901.1 predicted protein [Thalassiosira pseudonana CCMP1335]
PITTAVRTTSHHSSLFASSTAPENERAANRFAIGFLKGT---IFDTFFEDRAYARFYALE
TIARVPYFSYLSVLHLYETLGKWRR-VKYLKLHFAESWNEMHHLLIMEELGGSERFFDRF
LAQHCAFGYFLIVITLYLINPVQAYNLNQDVEEHAFATYDTFLKENAEMLKTKPAPKVAI
EYYRHGDMYMFDEFQTECELRRPEINNLYDVFVAIRDDEMAHVKTMEKLQTELDVS
>XP_002182610.1 predicted protein [Phaeodactylum tricornutum CCAP 1055/1]
GVSNPLRTERTQPVVSANTVSTLPETKRNRQLVHQLKSV---LFDQVYMDRAFARFYALE
TIARMPYFSYLSVLHLWETLGMWRR-AEYLQVHFAESWNELHHLLIMEELGGNGRWGDRF
VAQHIAFFYYWIVVTLYAVNPTMAYNLNQAVEEEAYETYDGFLQTHAEYLQSQPAPQAAI
RYYTGDDLYLFHAMHDTREQRRPTCETLYDTIRNIRDDELEHVKTMACLQDESV--
>OEU09946.1 plastoquinol terminal oxidase-like protein [Fragilariopsis cylindrus CCMP1102]
VDKEDRLPDCLNFILTNESVKNAEIERDSHPVSQTLYDLGCLVLDNLFDNRPIQRFWFLE
TIARIPYFSYVSMLHLYESFGWFRA-VELRKIHSAEDWNELHHLLIMESLGGNTKWSDRF
VAYHTAFLYYWFLILVYLGSPRIAYQFMELLEAHAVDTYTTFVKVNKQRLSELPPPSVAV
SYYKYGDLYMFDDFQTTRGSRRPPCDTLLDVFTNIAIDEGEHVKTMQACQDYAKFG
>GAX22341.1 hypothetical protein FisN_3Hh453 [Fistulifera solaris]
PTLAGIRRDASSILKSSSTADNSDTK-GHRQVVKTIKSI---LFDNLYLDRSYARFYALE
TIARMPYFAYTSVLHFLETTGKWRQ-ADRLALHFAETWNELHHLLIMEELLTQSKFRDRF
VAQHVAFFYFWFAVGLYLVRPDAAYSLNQAVEEEAYATYDAFLKEREDYLKSQPAPEVAI
NYYNGSGQDMFDRMSKALSSRRVECKTLYDCFVAIRDDELEHSQTMELLKREPFEL

>TFJ81505.1 hypothetical protein NSK_007176 [Nannochloropsis salina CCMP1776]
------RPPKASINRSPEAITRREEIRETPWFVLLPYYALCAFLDAVYEGRPLARFWFLE
TVARMPYFSYISMLHLYETLGWWTIGTDVRRVHFAEEWNELHHLQIMESLGGDARWLDRF
LARHSAIAYYWVLNLMFLISPRLAYNFSELIESHAVDTYSQFLDENEDLLRRLPAPRVAL
DYYVMGDLYMFDEFQTTRQTRRPLIRSLYDVFSAIRDDESEHVKTINACQVADEVI
>CBJ31032.1 conserved unknown protein [Ectocarpus siliculosus]
PKGRPLLDEQSPTSASDSSATVVSPGRFMNDFNAGVVDFLKGLMVQYYGERTYARFYALE
TIARVPYFGYLCVLHLYETLGKWRQ-AEYLKVHFAESYNELHHLLIMEELGGNVLFRDRW
FAQHAAFFYFFVVVGLYLSNPRNAYNLNQHVEEHAFSTYDSFLSDNQEALKQQPAPEASL
G------------------------------CLVRNDEWEHVKTMKAMQL-----
>XP_002296917.1 predicted protein [Thalassiosira pseudonana CCMP1335]
PRQRELQAKLNELTLSSDAIWERERARVAPYIIKIPYYALCFMLDVVFEGRPFSRFFLLE
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MAQHSALAYYIALCMLWMLSPTLSYKFSEMLETHAVDTYGQFVDENEDKLKELPPSIAAV
EYYTGVSDPMFGEYQTASRVRVPNLRSLYDVFVAIRNDEGDHVSTMKSCLDPKEAT
>CBJ25453.1 alternative oxidase, mitochondrial protein [Ectocarpus siliculosus]
PEVVDLQNRLNELKLSNKAIEDRETARQTPWYVMAPYKALCWFLDVVFEDRPIQRFWFLE
TVARMPYFSYLSMLFLYETLGWWSGAAEVRKVHFAEEYNEMQHLRIMESLGGDTRWSDRF
LARHAAIIYFSVLILGYLVSPFLAYNFSELIESHAVDTYTEFAEANEELLKSLPPTPQAL
DYYHGGDMYLFDEFQTSRFSRRPRIQNLYDVFSCIRDDELEHVKTMFACERGTGAL
>GAX11985.1 hypothetical protein FisN_8Lh079 [Fistulifera solaris]
QQQRDFRDELEQLTLNSTEIWAKEFADVAPWIIKIPYLVVCYMLDVLFEKEVFARFFLLE
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EYYAGSSDSFYAEFQTSAEIRRPQIRSLYDVFHTIRDDESDHASTMASCLNPDSNL
>EJK59088.1 hypothetical protein THAOC_20735 [Thalassiosira oceanica]
PRQKELQAKLGQLTLNSTAIWERERARVAPLVIKFPYYALCFLLDVVFEGRAFSRFFLLE
TVARMPYFSYITMLHLYESLGFWRRSSDIKRIHFAEEWNEFHHLLIMESMGGDQPYWVRF
LAQHSAVAYYVALCLLWIASPSLSYKFSEMLETHAVDTYGQFVDENESKLKELPPSLVAV
EYYTGLSDPMFGEYQTASGVRKPSMNSLYDVFCAIRNDEGDHVQTMSSCLDPKVST
>XP_002185130.1 predicted protein [Phaeodactylum tricornutum CCAP 1055/1]
DSQKELHAQLDALTLNATGIWDREMQNEAPFVIKIPYFGLCYMLDEVFDGKIPSRFFLLE
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LAQHSAIVYYVALCLLWGISPSLSYRFSELLETHAVSTYGQFLDENEEALKKLPPPLPAI
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>KOO33882.1 plastoquinol oxidase immutan [Chrysochromulina sp. CCMP291]

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TVARVPYFGYLSVMHLKETFGNRAVGKDRMRTHYAEADNELHHLLIMESLGGNSSLFDRT
LAQSMAFGYYWYVVGVYSFSEQAAYHLSELIEDHAYNTYDKFLSTNEDTLRKMPVPAIAR
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>XP_005794311.1 hypothetical protein EMIHUDRAFT_447503 [Emiliania huxleyi CCMP1516]
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TVARVPYFAYLSVMHLRETWGERDASRERMRVHYAEADNELHHLLIMESLGGNSSAVDRA
VAQGLATAYYWWVVFVFAHDERAAYHLSELVEDHAYRTYDAFLASHEVELRALPVPEVAR
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>XP_005787845.1 hypothetical protein EMIHUDRAFT_462437 [Emiliania huxleyi CCMP1516]
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IIARIPYFSYVSMLHLYESFGWWRG-PELRKVHNAEEWNELHHLLIMEALGGNAQWSDRF
LGYHVAFAYYWFLIGVYLCSPRIAYQFMELLEAHAVDTYSTFVKENRERLSQLPPPAVAR
SYYTEGDLYYFDDFQVDRGSRRPACDSLLDVFENIAIDEGEHVKTMRACQDYAVLG
>XP_005840480.1 plastid terminal oxidase [Guillardia theta CCMP2712]
EDSPVISENFDSMFRKDGTTWGSKSYPVTKSIAQALVTVLKGSLDWYYHKKDFARFFVLE
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IAQHAAFAYYWFCVTFYFLHPRGAYYVMSLIENHAYHTYSKYIEANKSWLASQPSPAIAK
EYYEGGDLYLFDAFHTTRQERRPRVQSLLDTFESIRDDESQHHRTMLSLVERGRP-
>XP_005824706.1 centrin/plastid terminal oxidase fusion protein [Guillardia theta CCMP2712]
PEARRLQEKVARLVLDNDAVAKREEIRATPALIMVPYTFLCWLIDVLFVNRPIQRFWFLE
TVARMPYFSYITMLTLYESLGWWRSSMDSRRVHFAEEWNEVQHLKIMEALGGDRSWFDRF
MGRHAAIFYFIILNHIWLLSPSLAYNFSELIEFHAVDTYGEFVDANEELLKSLPPPQEAV
EYYNSKDLYLFDEFQTGRKSRRPVIRSLYDVFCNIRDDELEHVKTMFQCQTSLQQI
>Monotropa hypopitys
LQPRKLFRVQATVLQDDEQKAAVENSFFEQSVNILLTDSVIKILDVLYRDRDYASFFVLE
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LAQHIAVFYYFMSVFMYALSPRMAYHFSECVESHAFETYDKFIKTRGEELKKLPAPEVAV
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FNR dataset

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AGKFKGLAWLFLGVANTDSLLYDADWQKIKEKYPENFRVDYALSREQSNKSGGKMYIQDK
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WHV

EVY

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AAAFKGLAWLFLGVANTDSLLYDEDWQKIKAKYPNNFRLDYALSREQNNKKGGKMYIQD
K

VEEYADEIFERLEKGAHIYFCGLKGMMPGILEMLESVSVKKGIDWKEKLTHLKEEGQWHV
EVY

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GQSLGVIPPGINAKGKPHTNRLYSIASTRYGDDMKGTSVTLCVRRATYFDELGREPAKKG
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EVY

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HV
EVY
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(+),score=78.61,sp|Q9S9P8|FNRR2_ARATH|60.63|1e-138,NAD_binding_1|PF00175.16|2.7e-
23,FAD_binding_6|PF00 [Rhodelphis limneticus]
EKVTLAPTHLENGKVPMNTWRNEKPYKGKILSIEKIVGPKAPGEIYHIVIDHRGEMPYWE
GQSFGVLPPGTDPKGKPYGVRLYSIASSRYGDHFDGRTASFCIRRAVYVDKTGKEPSKKG
VCSNYICDLKPGDEVSLAGPTGKVLLMQEECTKPQIMIATGTGIAPFRSFVRRLFLENVP
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GQSCGVIPPGTNSKEVPHGTRLYSIAASRYGDNFDGNTMTLCVRQATYFDELGSEPAKKG
ICSDFLCNATPGTEVAMTGPTGKSLLLVKDPLATFICVATGTGIAPFRSFWRRMFYEDIP
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>Polytomella parva
VSKKEVSKGLEGGKLPLNTFSTKKPYTAKVLSVEKIVGPKATGETFHVVLDTQG-VKYHE
GQSLGVIPPGTNSKEVPHGTRLYSIASSRYGDNFEGNTTTLCIRRAVYTDKTGKEPAKQG
ICSNYLTKAAPGTEVTVTGPTGKVLLLPEDASQTVICVATGTGIAPFRSFWRRCFVENVP
GYKFNGKLWLFMGVANSDSKLYDEELQALKKAYPEQFRLDYALSREQKNSKGQKMYIQDK
VEEYADEVFSLLDNGAHIYFCGLKGMMPGIQGMLERVAKSKGLVYADWVEKLKHKSQWH
V
EVY
>XP_005644145.1 ferredoxin-NADP+ reductase [Coccomyxa subellipsoidea C-169]
LKKNKVPAELEKGDLPMNTFNNKKPFKATVKSVERIVGPKATGETCHIVIETRGEIPYWE
GQSYGVIPPGTNSKEVPHGTRLYSIAATRYGDTFDGKTTSLCVRRAEYWCEMKANPAKKG
ICSNFLCDAKPGDEITMTGPTGKILLLPEDKNAAIIMVATGTGIAPYRAFWRRFFLEEIE
GYKYTGLAWLFMGVANSDAKLYDDELQAILKAHPDQFRVDYALSREQTNKNGGKMYIQD
K
VEEYSDEVFDLLDNGAHIYFCGLKGMMPGIQEMLERVASEKGMVWEEFFQKLKKNNQWH
V
EVY
>XP_002954986.1 ferredoxin-NADP+ reductase [Volvox carteri f. nagariensis]
VSKRTVPTALEEGEMPLNTYSNKAPFKAKIRSVETITGPKATGETCHIIIETEGKIPFWE
GQSYGVIPPGTNSKEVPHGTRLYSIASSRYGDDFDGKTASLCVRRAVYVDETGKEPAKKG
ICSNYLCDATPGTEIVMTGPTGKVLLLPADANAPLICVATGTGIAPFRSFWRRCFMENVP
SYKFTGLFWLFMGVANSDAKLYDEELQALAKAYPSQFRLDYALSREQKNRKGGKMYIQDK
VEEYSDEIFDLLDNGAHMYFCGLKGMMPGIQEMLERVAKSKGLNYEEWVEGLKHRNQWH
V
EVY
>KXZ46591.1 hypothetical protein GPECTOR_42g802 [Gonium pectorale]
VTKRTVPTQLEEGEMPLNTYGNKAPFKAKVRSVETITGPKATGETCHIIIETEGKIPFWE
GQSYGVIPPGTNSKEVPHGTRLYSIASSRYGDDFDGKTASLCVRRAVYVDETGKEPAKKG
ICSNFLCDAKPGTEIAMTGPTGKVLLLPADANAPLICVATGTGIAPFRSFWRRCFMENVP
SYKFGGLFWLFMGVANSDAKLYDEELKALAAAYPSQFRVDYALSREQKNRKGGKMYIQDK
VEEYADEIFGLLDGGAHMYFCGLKGMMPGIQEMLERVAKSKGLNYEEWVEGLKHKNQWH
V
EVY
>XP_003084170.1 Ferredoxin-NADP+ reductase [Ostreococcus tauri]

NGRAKVPLEMEKMELPLNTYKNKEPFVGTIRSVERIVGPNATGETCHIIIEHGGKMPFWE
GQSYGVIPPGTNSKEVPHGVRLYSIASSRYGDSYDGLTATLCVRRATYWDEMNAEPAKKG
ICSNFLCDAKPGQEVMMTGPTGQVMLLPKDPATPVIMVATGTGIAPMRSYLRRFFLEDIP
SWEFKGLAWLFMGVANSDAKLYDDEFQEMVKRFPDQFRIDYALSREDTNKNGGKMYIQDK
VEEYKDQVFQLLDGGAHMYFCGLKGMMPGILSMLEGVCKEKGISYEEWLEGLKKNGQWH
V
EVY
>XP_001697352.1 ferredoxin-nadp reductase [Chlamydomonas reinhardtii]
MSKRTVPTKLEEGEMPLNTYSNKAPFKAKVRSVEKITGPKATGETCHIIIETEGKIPFWE
GQSYGVIPPGTNSKEVPHGTRLYSIASSRYGDDFDGQTASLCVRRAVYVDETGKEPAKKG
LCSNFLCDATPGTEISMTGPTGKVLLLPADANAPLICVATGTGIAPFRSFWRRCFIENVP
SYKFTGLFWLFMGVANSDAKLYDEELQAIAKAYPGQFRLDYALSREQNNRKGGKMYIQDK
VEEYADEIFDLLDNGAHMYFCGLKGMMPGIQDMLERVAKEKGLNYEEWVEGLKHKNQWH
V
EVY
>XP_003064407.1 ferredoxin-NADP oxidoreductase [Micromonas pusilla CCMP1545]
GGRAPVPLELEKMPLPLNTFKNKAPFTGKIKSVERIVGPNATGETCHIIIEHGGKMPFWE
GQSYGVIPPGTNSKEVPHGVRLYSIASTRYGDEFDGNTATLCVRRATYWDEKNAEPAKKG
ICSNFLCDAKPGAEVMMTGPTGQVMLLPEDPATPVIMVATGTGIAPMRSYIRRFFVEDVK
NWEFKGLAWLFMGVANSDAKLYDDEFSECIKRFPGQFRVDYALSRESQNRKGGKMYIQDK
VEEYKDQVFQLLDGGAHMYFCGLKGMMPGILEMLEGVCKEKGIDYEEWLEGLKKKGQW
HV
EVY
>P53991.1 RecName: Full=Ferredoxin--NADP reductase, chloroplastic; Short=FNR; Flags: Precursor [Chlamydomonas reinhardtii]
MSKRTVPTKLEEGEMPLNTYSNKAPFKAKVRSVEKITGPKATGETCHIIIETEGKIPFWE
GQSYGVIPPGTNSKEVP-TARLYSIASSRYGDDGDGQTASLCVRRAVYVDETGKEPAKKG
LCSNFLCDATPGTEISMTGPTGKVLLLPADANAPLICVATGTGIAPFRSFWRRCFIENVP
SYKFTGLFWLFMGVGNSDAKLYDEELQAIAKAYPGQFRLDYALSREQNNRKGGKMYIQDK
VEEYADEIFDLLDNGAHMYFCGLKGMMPGIQDMLERVAKEKGLNYEEWVEGLKHKNQWH
V
EVY
>KXZ48298.1 hypothetical protein GPECTOR_29g73 [Gonium pectorale]
VSKRTVPTKLEEGQLPMNTFSPKATLKARIKSVEKLTGPKATGETYHIIIETEGKIPYWE
GQSFGVIPPGTNSKEVPHGTRLYSIASSRYGDYFDGATATLCVRRAVYVDETGAEPAKKG
VCSNFLCDAAPGTEINMTGPTGKVLLLPSDPNATLICVATGTGIAPFRSFWRRLFMEDTG

RPAFGGLFWLFMGAANADATLYDAELQALAAAHPEHFRLSYALSREQKNKRGGKLYIQDK
VEEYADEVFSLLDGGAHMYFCGLKGMMPGIQEMLSRVAGEKGLTYEHWVEGLRARGQWH
V
EVY
>PRW50852.1 ferredoxin-NADP+ reductase [Chlorella sorokiniana]
LKRADVPLELEEIGLPMNTFGPKNPFIGKIVSVETITGPKATGETCHIIIQTDKKIPFVE
GQSYGVIPPGTNSKEVPHGTRLYSIAATRYGDSFDGMTTSLCVRRAVYVDETGKEPAKKG
ICSNFLCDAKPGQEITMTGPTGKVLLLPEDPNAVIICVATGTGIAPFRTFYRRMFLENVP
NYKFTGLFWMFMGVANSDNKLYDEEMQAIAKAYPEQFRLDYALSREQKNRNGGKMYIQD
K
VEEYADEVFDLLNNGAHIYFCGLKGMMPGILEMLERVAKSKGLEYSEWFEGLKHKNQVHV
EVY
>CAA55406.1 ferredoxin NADP reductase, partial [Chlamydomonas reinhardtii]
----------KIPFWE
GQSYGVIPPGTNSKEVPHGTRLYSIASSRYGDDFDGQTASLCVRRAVYVDETGKEPAKKG
LCSNFLCDATPGTEISMTGPTGKVLLLPADANAPLICVATGTGIAPFRSFWRRCFIENVP
SYKFTGLFWLFMGVANSDAKLYDEELQAIAKAYPGQFRLDYALSREQNNRKGGKMYIQDK
VEEYADEIFDLLDNGAHMYFCGLKGMMPGIQDMLERVAKEKGLNYEEWVEGLKHKNQWH
V
EVY
>KDD75893.1 hypothetical protein H632_c449p0, partial [Helicosporidium sp. ATCC 50920]
VVRRPVPTELEGIGVPMNTYSMKKPFKARVMSVDKLVGPRATGETYHVVIETRGEIPFAE
GQSYGVVPPGSNSRTVPHATRLYSIASTRYGDRFDGRTASFCIRRATFWDELGREPEKKG
ICSNFLCDAAPGTEIDLSGPTGKLLLMPDDPHADVITVATGTGIAPFRAFWRRRFFEAVP
SEQGRGHMWLFMGVANSDAKLYASEIEAVEQAHPTRFRVDYALSREQTNASGGKMYVQDR
LEQHADEVFDRLSAGAHIYFCGLKGMLPGILETLERVAGEKGIDWPAFLEGLKKEHRWHV
EVY
>OAO96703.1 RFNR1 [Arabidopsis thaliana]
KSKVLVTPLLEDKETPLNLFRPKEPYTATIVSVERIVGPQAPGETCHIVIDHDGNVPYWE
GQSYGVIPPGENPKGAPHNVRLYSIASTRYGDSFDGKTASLCVRRAIYYDETGKEPSKAG
VCSNFLCNAKPGDKVKITGPSGKVMLLPDDPKATHIMIATGTGVAPYRGYLRRMFMENVP
NFKFDGLAWLFLGVANSDSLLYDEEFAGYRKDYPENFRYDKALSREEKNKKGGKMYVQDK
IEEYSDEIFKLLDNGAHIYFCGLKGMMPGIQDTLKRVAEERGESWEQKLTQLRKNKQWHV
EVY
>OAP18471.1 RFNR2 [Arabidopsis thaliana]
SSKVTVSPILEDKDPPLNLYKPKESYTAKIVSVERVVGPKAPGETCHIVIDHDGNLPYWE

GQSYGVIPPGENPKGAPHNVRLYSIASTRYGDFFDGKTASLCVRRAVYYDETGKEPSKNG
VCSNFLCDSKPGDKIQITGPSGKVMLLPSDPNATHIMIATGTGVAPYRGYLRRMFMENVP
NKTFSGLAWLFLGVANTDSLLYDDEFTKYLKDHPDNFRFDKALSREEKNKKGGKMYVQDK
IEEYSDEIFKLLDNGAHIYFCGLKGMMPGIQDTLKRVAEERGESWDLKLSQLRKNKQWHV
EVY
>BAE98556.1 ferredoxin-NADP+ reductase [Arabidopsis thaliana]
PVKVVKESKKQEEGIVVNKFKPKNPYTGRCLLNTKITGDDAPGETWHIVFTTEGEVPYRE
GQSIGVIPEGIDKNGKPHKLRLYSIASSAIGDFGDSKTVSLCVKRLVYTNDGGEI--VKG
VCSNFLCDLKPGDEAKITGPVGKEMLMPKDPNATIIMLGTGTGIAPFRSFLWKMFFEEHE
DYKFNGLAWLFLGVPTSSSLLYKEEFEKMKEKNPDNFRLDFAVSREQTNEKGEKMYIQTR
MAEYAEELWELLKDNTFVYMCGLKGMEKGIDDIMVSLAAKDGIDWLEYKKQLKRSEQWN
V
EVY
>NP_001077566.1 ferredoxin-NADP[+]-oxidoreductase 2 [Arabidopsis thaliana]
AKKVEKVSKKNEEGVIVNRYRPKEPYTGKCLLNTKITADDAPGETWHMVFSHQGKIPYRE
GQSVGVIADGIDKNGKPHKVRLYSIASSALGDLGNSETVSLCVKRLVYTNDQGET--VKG
VCSNFLCDLAPGSDVKLTGPVGKEMLMPKDPNATVIMLATGTGIAPFRSFLWKMFFEKHD
DYKFNGLAWLFLGVPTTSSLLYQEEFDKMKAKAPENFRVDYAISREQANDKGEKMYIQTR
MAQYAAELWELLKDNTFVYMCGLKGMEKGIDDIMVSLAANDGIDWFDYKKQLKKAEQW
NV
EVY
>XP_015629836.1 ferredoxin--NADP reductase, root isozyme, chloroplastic [Oryza sativa Japonica Group]
ESKVAVKPLLESNEPPLNTYKPKEPYTATIVSVERIVGPKAPGETCHIVIDHGGNVPYWE
GQSYGIIPPGENPKGAPHNVRLYSIASTRYGDSFDGRTTSLCVRRAVYYDETGKEPSKNG
VCSNFLCNSKPGDKVKVTGPSGKIMLLPEDPNATHIMIATGTGVAPFRGYLRRMFMEDVP
KYRFGGLAWLFLGVANTDSLLYDEEFTSYLKQYPDNFRYDKALSREQKNKNAGKMYVQD
K
IEEYSDEIFKLLDGGAHIYFCGLKGMMPGIQDTLKKVAEQRGESWEQKLSQLKKNKQWHV
EVY
>XP_015646844.1 ferredoxin--NADP reductase, embryo isozyme, chloroplastic [Oryza sativa Japonica Group]
KSKVAVKPLLDNKEPPLNLYKPKEPYTATIVSVERLVGPKAPGETCHIVIDHGGNVPYWE
GQSYGVIPPGENPKGSPNTVRLYSIASTRYGDSFDGKTASLCVRRAVYYDETGKEPTKKG
ICSNFLCDSKPGDKVQITGPSGKIMLLPDDPNATHIMIATGTGVAPYRGYLRRMFMEDVP
SFKFGGLAWLFLGVANTDSLLYDEEFTNYLQQYPDNFRYDKALSREQKNKNGGKMYVQDK

IEEYSDEIFKLLDGGAHIYFCGLKGMMPGIQDTLKRVAEQRGESWEQKLSQLKKNKQWHV
EVY
>XP_015625198.1 ferredoxin--NADP reductase, leaf isozyme 2, chloroplastic-like [Oryza sativa Japonica Group]
TTKVEKVSKKQVDGVVTNKYRPKEPYTGRCLLNTRITGDDAPGETWHMVFSTDGEIPYRE
GQSIGVIPDGIDKNGKPHKLRLYSIASSAIGDFADSKTVSLCVKRLVYTNDQGEI--VKG
VCSNFLCDLKPGSDVKITGPVGKEMLMPKDPNATIIMLGTGTGIAPFRSFLWKMFFEEHD
DYKFNGLAWLFLGVPTSSTLLYREEFERMKEIAPERFRLDFAVSREQTNAAGEKMYIQTR
MAEYKDELWELLKDNTYVYMCGLKGMEKGIDDIMIDLAAKDGIDWLDYKKQLKKSEQW
NV
EVY
>XP_015640980.1 ferredoxin--NADP reductase, leaf isozyme 1, chloroplastic [Oryza sativa Japonica Group]
PAKKEKISKKHDEGVVTNKYRPKEPYVGKCLLNTKITADDAPGETWHMVFSTEGEIPYRE
GQSIGVIADGVDKNGKPHKLRLYSIASSALGDFGDSKTVSLCVKRLVYTNDQGEI--VKG
VCSNFLCDLKPGSDVKITGPVGKEMLMPKDPNANIIMLATGTGIAPFRSFLWKMFFEKYD
DYKFNGLAWLFLGVPTSSSLLYKEEFDKMKAKAPENFRVDYAVSREQTNAQGEKMYIQTR
MAEYKEELWELLKDHTYVYMCGLKGMEKGIDDIMVSLAAKDGIDWADYKKQLKKGEQW
NV
EVY
>XP_024384495.1 ferredoxin--NADP reductase, embryo isozyme, chloroplastic-like [Physcomitrella patens]
ASKVALTADLEGPEPPMHLFKNKEPFIGTVKSVERIVGPNATGETCHIVIDHGGQMPYWE
GQSYGIIPPGENPKGQPNTVRLYSIASTRYGDEFDGKTASLCVRRAVYWCELQAEPAKKG
ICSNFLCDCKPGDKVQITGPSGKVMLLPSDPNATHIMVATGTGIAPYRGFLRRMFMEDVP
TFKFGGLAWLFLGVANSDSLLYHDEFTKYKEAFPENFRYDTALSREEKNSKGGKMYVQDK
IEEYSEELFNLLDKGAHIYFCGLRGMMPGIQDTLKRVAEARGENWEEKLAKLKKNKQWHV
EVY
>XP_024356607.1 ferredoxin--NADP reductase, embryo isozyme, chloroplastic-like [Physcomitrella patens]
TPQVATGPKLEAKEPPMHLFKNKEPFIGTIKSVERIVGPKAPGETCHIVIDHEGNVPYWE
GQSYGIIPPGENPKGQPNSVRLYSIASTRYGDDFDGRTASFCVRRAVYWDETGKEPAKKG
ICSNFLCDSKPGDKVQIVGPSGKVLLLPEDPSATHIMVATGTGIAPYRGYLRRMFMEDT-
EFKFNGLAWLFMGVANTDSLLYHDEFNTYLKEYPDNFRYDIALSREQKNSRGGKLYVQDK
MEEYSEELFDKLDKGAHIYFCGLRGMMPGIQDMLKRVAESRGESWETKLAALKKNKQWH
V

EVY
>PTQ28452.1 hypothetical protein MARPO_0163s0011 [Marchantia polymorpha]
VSKVKV-PLLEEKEPPLNLWKNKAPYKGVIKSVERIVGPNATGETCHIVIDHDGNVPYWE
GQSYGIIAPGENPKGTPNTVRLYSIASTRYGDNFDGKTTSLCVRRAVYWDETQKEPAKKG
VCSNFLCDAKPGDEVQITGPSGKVLLLPEDPNAVHIMVATGTGIAPYRAYLRRMFMEDVP
NFQFGGLAWLFLGVANTDSLLYHDEFSSYKEQYPENFRYDLALSREQKNQRGGKMYVQDK
IEEYSSELFDLLDKGAHIYFCGLRGMMPGIQDTLKRVAEEQGIVWEEKLSQLKKNKQWHV
EVY
>OAE30389.1 hypothetical protein AXG93_3612s1120 [Marchantia polymorpha subsp. ruderalis]
AVKEAKVSKKNEHGLVTNVYKPKTPYEGICLTNGKIVGDDAPGETFHMVFSTEGKIPYRE
GQSVGVVPPGVDEKGKPHKLRLYSIASSAPGDFGDYKTVSLCVKRLVYTNDKGEE--VKG
VCSNFLCDLKAGDKVNLTGPVGKEMLMPTDEKATVIMLATGTGIAPFRGFLWRMFFEKHD
DYKFQGLAWLFLGVPTSSSLLYREEFEKMQQDYPDNFRLDFAVSREQTNAKGERMYIQTR
MADYAEELWQMLQDNTFVYMCGLKGMEKGIDDIMVSLAARDGIDWVEYKKTLKKGEQW
NV
EVY
>XP_024542927.1 ferredoxin--NADP reductase, embryo isozyme, chloroplastic [Selaginella moellendorffii]
AKVATTAAPLDTSDPPLNLFKPKTPYTATIKSVERIVGDKAPGETCHIVIDHGGNVPYWE
GQSYGVIPPGENPKGTPNAVRLYSIASTRYGDDFDGKTASLCVRRAVYWDETGKEPAKKG
VCSNFLCDRKPGDKVQITGPSGKIMLLPSNPKAAHIMIATGTGIAPFRGYLRRMFMEDV-
SFKFGGLAWLFLGVANRDSLLYHDEFEGYLKEYPDNFRYDIALSREQNNKRGGKMYVQDK
IEEYSEEVFKLLDEGAHIYFCGLKGMMPGIQDTLKRVAEERGESWEEKLSMLKKKKQWHV
EVY
>EFJ16776.1 hypothetical protein SELMODRAFT_179376 [Selaginella moellendorffii]
AKVATTAAPLDTSDPPLNLFKPKTPYTATIKSVERIVGDKAPGETCHIVIDHGGNVPYWE
GQSYGVIPPGENPKGTPNAVRLYSIASTRYGDDFDGKTASLCVRRAVYWDETGKEPAKKG
VCSNFLCDRKPGDKVQITGPSGKIMLLPSNPKAAHIMIATGTGIAPFRGYLRRMFMEDV-
SFKFGGLAWLFLGVANRDSLLYHDEFEGYLKEYPDNFRYDIALSREQNNKRGGKMYVQDK
IEEYSEEVFKLLDEGAHIYFCGLKGMMPGIQDTLKRVAEERGESWEEKLSMLKKKKQWHV
EVY
>XP_002985709.1 ferredoxin--NADP reductase, embryo isozyme, chloroplastic [Selaginella moellendorffii]
--MSRLLKLLERNKPPFHLYTSQLPYTATVSSIQRLT---RDGQVSHIVIDHGGNVPFWE
GQSYGILPPGENSKGTRHPYHLYSIASSRYGDDLSGRSASLCVKRAIYVDQTGEEPSKKG
VCSNFLCDCKPGDKVDLVGPFGKLMLLNSNPSDSHIMVATGTGVAPFRGFLQRLLEDKMR

PRKFEGSAWLFMGAPTAGRLLYNEEFERYARDLPWSFRYDTALSRESCNKRGGRFYVQDR
MEEHGEEIFKLLDGGSHIYFCGRKDMLVGVEAVFEEVARRMGEDWRGKLAKLKKNRQWH
V
EVY
>XP_002977684.1 ferredoxin--NADP reductase, root-type isozyme, chloroplastic [Selaginella moellendorffii]
MRRLVLPRSLELKKAPTNLYTRKSPYIATIESVHRLTTGENGGDTYHIVIDHGGNVPFWE
GQSYGILPPGTNPKGAPPPNRLYSLASSRYGDDLSGRTASLCVKRIVSYD----NPNSTG
ICSNFLCDARPGDQVRIVGPFGSSLLLNENPRGAQIMVGTGTGVAPFRGFLRRMFVEEVP
-FKFDGLAWLFLGVASSKSLLYHDEFERIARDFPSSFRYDLALSREMVDRSGGKFYVQHR
IKERGKEVLELLESGGHIYFCGREEMMEGIQETFRKLC---GDSWHEKLSGWKRNKQWHV
DVY
>XP_002993724.1 ferredoxin--NADP reductase, leaf isozyme 1, chloroplastic [Selaginella moellendorffii]
TETVEKVKKKDEEGVVTNLFRPKEPYVGRCLLNTKIVGDDAPGETWHMVFTTEGKIPYRE
GQSIGIVPPGLDAKGKPQKLRLYSIASSAPGDFGDYKTVSLCVKRLVYVNDKGEE--VKG
VCSNFLCDLKPGDEVSITGPVGKEMLMPVDPNATIIMLGTGTGIAPFRGFLWRMFFEKHD
DYKFNGLAWLFLGVPTSSSLLYKEEFEKMKEKFPNNFNLDFAVSREQTNAKGEKMYIQTR
MAEYAEQLWDLLKDNTYVYMCGLKGMEKGIDDIMTSLAAKEGIDWAEYKKQLKKGEQW
NV
EVY
>GAQ80250.1 ferredoxin-NADP reductase [Klebsormidium nitens]
QTATEVFPALEESDPPMNTAKNNAPFTGTIKSVERIVGPNATGETKHIVIDHEGKLPYWE
GQSYGIIPPGENPKGKPHTVRLYSIASTRYGDDFDGKTASLCVRRAVYVDETGKEPEKAG
ICSNFLCDSKPGDKVQITGPSGKVMLIPEDPNATHIMIATGTGIAPFRAYLRRFFMEDVP
SFKFGGLAWLFLGVANTDSLLYHDEFSKYKEEFPDNFRYDLALSREQKNKEGGKMYIQNK
VAEYGNEVFDMLDKGAHIYFCGLKGMMPGIQDSLKQIAESRGESWEEKLTQLKKNKQWHV
EVY
>GAQ83927.1 ferredoxin-NADP reductase [Klebsormidium nitens]
KAKAKKESKKDDEGISVNLFKPKEPYTGRTLLNTKIVGDDAPGETWHMVFSHEGKVPYRE
GQSIGIVPPGMDANGRPHKLRLYSIASSAPGDFGDYKTVSLCVKRLVYTNDKGEE--VKG
VCSNFLCDLKAGDEVQITGPVGKEMLMPKDPNANVIMLGTGTGIAPFRGFLWKMFFEKRS
DYKFNGLAWLFLGVPTSSSLLYREEFELMQKKHPKNFRLDFAVSREQNNAKGEKMYIQTR
MAEYAEELWGLLKDNTYTYMCGLRGMEKGIDDIMTSLAQRDGMDWAEYKKELKKDERW
SV
ETY

>EJK44714.1 hypothetical protein THAOC_36724 [Thalassiosira oceanica]
AAVRDAQHFLE-GELPLNFAKPNQPVTATVLGRTKLIDDDAPGDIEHVILKLPEGFHYVE
GQSLSLIPPGVDAKGRKHKPRLYSIASTRYGDVLDGNTISLCVRRAEYVDVTGEKPAKQG
VCSNFLCDVRAGDEVSVAGPVGKTMLLPKDSNTDIIMIATGTGIAPFRGFMHRLFMENTL
ARHFGGRAWLVLGVPVTGGLLYKEEFDCMQRNGADQLRIDYAISREMTAKTGGKMYVQN
V
IAENGREVFDRLDNGAVIYFCGLKGMMPGILDSLEEVAASQGIVWSEKLAELKKNHQWHV
EVY
>GAX27166.1 ferredoxin--NADP+ reductase [Fistulifera solaris]
SVLDDAQHWLEDIGLPSNTVKPKEPLPAQVLGRARLIGDDAPGDIQHIVLQLPAAFHYVE
GQSLSVIPPGLDTTGKPHKPRLYSIASTRYGDLLDGRTVSLCVRRAEYYDITGVAPEKQG
VCSNFLCNTQVGDVVQVAGPVGKTMLLPEDPSKDIIMVATGTGIAPFRGFLHRLFMENTV
SRHFNAKAWLILGVPVRSGLLYQEELQAMQQNSVADLEVTYAISREMKNAQGGKLYVQDV
LAARADELFSKLDHGAVIYFCGLKGMMPGILTALEQVATRQGIDWSTKLKEWQANHQWHV
EVY
>OEU11321.1 ferredoxin NADP reductase [Fragilariopsis cylindrus CCMP1102]
EMLYSSQCWLE-PYVAPTFAKATNPVKAIVLGRTSLITEDAPGDIQHIVLRLPEGFHYVE
GQSLSVIPPGLTEKGKKQKPRLYSIASTRYGDLLDGTTVSLCVRKAEYYDITGIIDSKAG
ICSKFLCSATPGTEIDVAGPIGKTMILPKDSTKDIIMVATGTGIAPFRSFMHRLFVEQTT
ARHYTGNAWLILGVPTSGSLLYKTEFDSMLQQQLNNLKINYAISREMTNKEGGKLYVQDV
LKENSIELFSKLEAGAVIYFCGLKGMMPGILLALEEVATSQGIDWSTTLKKYQSNHQWHV
EVY
>XP_002291633.1 predicted protein, partial [Thalassiosira pseudonana CCMP1335]
----------PLNFAKPQAPATATVLGRTKLIADDAPGDIEHVIMKLPEGFHYVE
GQSLSVIPPGTDAKGRNHKPRLYSIASTRYGDTLDGTTISLCVRRAEFIDVTGEKPEKQG
VCSNFLCNVNPGDTVSVAGPVGKTMLLPEDPTKDVIMVATGTGIAPFRGFMHRLFMENTL
ARHFGGSAWLVLGVPVSGGLLYKEEFDCMLRNSPNQLRIDYAISREMTNTIGGKLYVQHV
IAQNGKELFNRLDNGAHIYFCGLKGMLPGILESLEGVAKEQGVDWTAKLSELKKNNQWHV
EVY
>VEU44392.1 unnamed protein product [Pseudo-nitzschia multistriata]
EMLHAAQCWLEDSPVPPPFCTAKSPVTATVLGRTPLIESDAPGDIQHIVLRLPEGFRYVE
GQSISVIPPGTDPSGRPHKPRLYSIASTRYGDLLDGTTVSLCVRRAEYTDATGKVPSKAG
VCSGFLCDAVPGQKVSVAGPVGKTMLLPHSGSVDLIMVATGTGIAPFRSFLHRLFTEHTP
ANHFNGKAWLILGVPTSGSLLYKPEFDAMLRTPTPSLRIDYAISREMTNASGGKLYVQDV
LRENAGELMERLENGAVIYFCGLRGMMPGILEALEEVATASGMDWAETLKKYKANHQWHV
EVY

>XP_002183949.1 predicted protein, partial [Phaeodactylum tricornutum CCAP 1055/1]
----------KPAAPVPAKVLSRRRLIADDAPGDVQHIIMSLPKGLHYVE
GQSLSVIPPGTNPQGRPHKPRLYSIASTRYGDDLRGNTVSLCVRRAEYVDQTRKVPTKAG
VCSNFLCDMVPGTIVQVAGPVGKTMLLPKANQQDIIMVATGTGIAPFRAFLRRLFLENTV
AKQYQGQAWLILGVSVTGGLLYADEFERMQQPWPGQLRVDYAISREMKNQQGGKLYVQD
V
LSEEAEMLWTKLEDGAIIYFCGLKGMMPGILEALEDVAKARGKVWSQTLRRLKANGQWHV
EVY
>GAX27626.1 hypothetical protein FisN_13Hh283 [Fistulifera solaris]
SVLDDAQHWLEDIGLPSNTIKPKEPVLAQVLGRARLIGEDAPGDIQHIVLQLPAEFHYVE
GQSLSVIPPGVD-QGKPHKPRLYSIASTRYGDLLDGQTVSLCVRRAEFYDITGLAPEKQG
VCSNLLCNTQVGDMVQVAGPVGKTMLLPDDPSKDIIMVATGTGIAPFRGFLHRLFIENTV
SRHFNAKAWLILGVPVRSGLLYEEELQAMQQNSAADLEVTYAISREMKNTAGGKLYVQDV
LAAGPMNCFSN----------

>TFJ81270.1 hypothetical protein NSK_007231 [Nannochloropsis salina CCMP1776]
QDFLEANPYSDQSNIPLNTYKNKEPHTGKIVSVKRIVGPKATGETCHIIIDHGGAMPYWE
GQSYGVVPPGINPKGKPNNVRLYSIASTRYGDDMKGQTASLCVRRATYWCELNAEPAKKG
ICSNYLCDAKPGDSVALAGPTGKVMLIPKTPEADLIMVATGTGIAPYRTFVRRLFVEDTP
ARKFKGLAWLFLGVANKDSLLYDDEWQEVKKAYPNNFRVDYALSREQENKKGGKMYIQD
K
MEEYADEIFDRLSKGAHIYFCGLKGMMPGIQDTLERVAQEKGIEWKEMLEGLKKNHQWHV
EVY
>EWM23857.1 Ferredoxin reductase-type FAD-binding domain protein [Nannochloropsis gaditana]
QDFLEANPYFDQSNIPLNTYKNKEPHTGKIVSVKRIVGPKATGETCHIIIDHGGAMPYWE
GQSYGVVPPGINPKGKPNNVRLYSIASTRYGDDMKGQTASLCVRRATYWCELKAEPAKKG
ICSNYLCDAKPGDSVALAGPTGKVMLIPKTPEADLIMVATGTGIAPYRTFVRRLFVEDTP
ARKFKGLAWLFLGVANKDSLLYDDEWQEVKKAYPNNFRVDYALSREQENKKGGKMYIQD
K
MEEYADEIFDRLSKGAHIYFCGLKGMMPGIQDTLERVAQEKGIEWKDMLEGLKKNHQWHV
EVY
>XP_002180502.1 predicted protein [Phaeodactylum tricornutum CCAP 1055/1]
QDFLEAEPYWDQSSVPVNVYKNKAPFTGKVVSTKRIVGPLATGETCHVVIDHEGNFPYWE
GQSWGVIPPGVREKGKPHSVRLYSIASTRYGDDMTGKTGSLCVRRATYWCELKAEPTKKG
VCSNFLCDTRPGEEVQMTGPAGKVMLMPENPDTDYIMVATGTGIAPYRGFVRRLFTEKTP
AAEYKGQAWLFLGVANSDALLYDDEWQEVKTNNPNQFRLDYALSREQENKKGGKMYIQD

K
VEEYADEIFQKLDAGAHIYFCGLKGMMPGIQEMLQTVCTQKGVEYDEWLKGLKAKKQWH
V
EVY
>XP_009034033.1 hypothetical protein AURANDRAFT_52453 [Aureococcus anophagefferens]
APAAPTLDFLEYAEIPKTAFKPTAPYKSAIRSVKRAIGPDAPGEICHVVMTTEGKLPYVE
GQSVGVVPPGN--KGKPHQQRLYSIASTRYGDDGAGDSVSLCVRRAVYVDETGEEPAKKG
ICSNFLCDGSPGDVVALTGPVGKGLLLPESPDADVIMVATGTGVAPYRGFVKRLFDEQTP
ANDFTGRAWLFFGGPTSDSILYPELWDAAKASKPDQFDLTLAISREQTNEDGGRMYVQHR
IVEHADEIFDRLDNGAHFYLCGLKGMQPGIEAALEEVCDKKGLVFKDWVKALKKDKRYHV
EVY
>GAX13172.1 ferredoxin--NADP+ reductase [Fistulifera solaris]
QDFLEAEPYWDQSTVPVNVYKNKAPFTGKVVSTKRIVGPKATGETCHIIIDHNGDFPYWE
GQSWGVIPPGVREKGKPHSVRLYSIASSRYGDDMTGKTGSLCVRRATYWCELKAEPAKKG
ICSNFLCDTKPGDEIQMTGPAGKVMLIPENPNTDLIMVATGTGIAPYRGFIRRLFFEDTP
AANYKGTAWLFMGVANSDALLYDDELQEVKKKFPNNFRLDYALSREQENKKGGKMYVQD
K
VEEYADEIFTKLDNGAHIYFCGLKGMMPGIQDMLKSVAESKKIDYEEWVKELKAKKQWHV
EVY
>XP_002184856.1 predicted protein [Phaeodactylum tricornutum CCAP 1055/1]
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ICSNFLCDTKPGDEVNMTGPAGKVMLLPEEPDTDYIMVATGTGIAPYRGFVRRLFTEETP
AGEYKGQAWLFLGVANSDALLYDDEWQTVLKEYPENFRLDYALSREQENKNGGKMYIQD
K
VEEYADEIFAKLDSGAHIYFCGLKGMMPGIQDMLKSVCEEKKVDYDEWLKGLKSKKQWH
V
EVY
>XP_002295321.1 ferredoxin-nadp reductase [Thalassiosira pseudonana CCMP1335]
QDFLEAEPYYSQDTVKTNTYKNKAPFTGKVVSTKRIVGPKATGETCHIIIDHNGDFPYWE
GQSWGVIPPGTREKGKPHSVRLYSIASSRYGDDMTGKTGSLCVRRATYWCELKADPAKKG
ICSNFLCDTEPGAEVMMTGPAGKVMLMPEDPKTDYIMVATGTGIAPFRSFVRRLFFEDTP
AAAYKGEAWLFLGVANSDALLYDDEFQDAKARYPENFRLDYALSREQENKNGGKMYIQDK
VEEYADEVFNKLDNGAHIYFCGLKGMMPGIQDMLAEVCKSKGLDYEEWIKELKGKKQWH
V
EVY

>EJK72001.1 hypothetical protein THAOC_06509 [Thalassiosira oceanica]
QDFLEYTPYYDHSAVKVNTHKNKAPFTGKVVSTKRIVGPKATGETCHIIIDHEGDFPYIE
GQSWGVIPPGTREKGKPHAVRLYSIASSRYGDDMTGKTGSLCVRRATYWCELQADPAKKG
VCSNFLCDTTPGDELKMTGPSGKVMLMPEDPNTDYIMVATGTGIAPYRGFIRRLFFEDTP
AADYKGQAWLFLGVANSDALLYDDEFQDAKARYPDNFRIDYALSREQENKKGGKMYIQDK
VEEYADEIFNKLDSGAHIYFCGLKGMMPGIQDMLKAVCEEKGISYDEWLKGLKQAKQWHV
EVY
>OEU22459.1 chloroplast ferredoxin dependent NADH oxireductase [Fragilariopsis cylindrus CCMP1102]
QNFLEAEPYYDQSTVPVNVYKNKAPFTGKVVSTKRIVGPKATGETCHIVIDHKGDFPYWE
GQSWGVMPPGNREKGKPHSVRLYSIASSRYGDDMTGQTGSLCVRRATYWDTLKADPAKKG
ICSNFLCDTQPGDDVAMTGPAGKVMLMPEDPSTDYIMVATGTGIAPYRGFIRRLFNEDTP
AGRYKGEAWLFLGVANSDALLYDDEFQEAKSRYPENLRIDYALSREQNNTKGGKMYIQDK
VEEYADEVFNKLESGAHIYFCGLKGMMPGIQDMLKGVAEKKGLNYDEWLKGLKKAKQWH
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EVY
>VEU37418.1 unnamed protein product [Pseudo-nitzschia multistriata]
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GQSWGVIPPGTREKGKPHAVRLYSIASSRYGDDMTGKTGSLCVRRATYWCELKADPAKKG
ICSNFLCDTNPGDEITMTGPAGKVMLMPEDPNTDYIMVATGTGIAPYRGFIRRLFNEDTP
AARYKGEAWLFLGVANSDALLYDDEFQEAKSRFPDNLRIDYALSREQTNAKGGKMYIQDK
VEEYADEVFTKLENGAHIYFCGLKGMMPGIQDMLKGVAEKKGIDYDEWLKKLKKAKQWH
V
EVY
>OEU15208.1 chloroplast ferredoxin dependent NADH oxireductase [Fragilariopsis cylindrus CCMP1102]
EDFLEAEPFYDQSTVPVNVYKNKSPFTGKVVSTKRIVGPQATGETCHIIIDHDGDFPYWE
GQSWGVMPPGTREKGKPHSVRLYSIASSRYGDDMTGKTGSLCVRRANYWCELKADPAKA
G
ICSNFLCDSVPGTEVKMTGPAGKVMLMPEDPTIDYIMVATGTGIAPYRGFVRRLYAEDTP
AARYKGEAWLFLGVANTDALLYDDEFQLAAKK---GLRIDYALSREQENTKGGKMYIQDK
VEEYADEVFAKLEGGAHIYFCGLKGMMPGIQEMLKGVAEKKNVDYDAWLKGLKKAKQW
HV
EVY
>XP_002290014.1 ferredoxin--NADP+ reductase [Thalassiosira pseudonana CCMP1335]
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GQSWGVIPPGTREKGKPHSVRLYSIASSRYGDDFTGNTGSLCVRRATYWCELKADPAKKG
ICSNFLCDTTAGDEVMMTGPAGKVMLMPEDPKTDYIMVATGTGIAPFRGFVRRLFFESTP
AAKYQGQAWLFLGVANSDALLYDDEFQEAKSKFPDNFRLDYALSREQNNKKGGKMYIQDK
VEEYADEVFNKLNNGAHIYFCGLKGMMPGIQDMLAEVCKSKGLDYDEWIKELKGKKQWH
V
EVY
>CBJ31206.1 hypothetical protein Esi_0238_0041 [Ectocarpus siliculosus]
TRSLEREPYWDMSELPMHTFKAKAPYTGTIETVEKLVQPGASGEVFHVKLRHEGNMPYWE
GQSLGVTPPGLDAKGKPHKVRLYSIASTRYGDDGDGRTVSLCVRRATVIDETGKEPSKEG
VCSNFLCRARAGQEVTLTGPSGKIMLLPETPDADVIMVGTGTGIAPYRGFLQRLFKEDTP
AARFTGTAWLFLGVATTEGLLYHDDWMEMLRKFPFNFRCE---GREEKNASGGKMYIQDR
VEQYADEVFERLDGGAHIYFCGLKGMMPGITDMLARVAGERGISWDAKLKELKSKGQWH
V
EVY
>VEU42932.1 unnamed protein product [Pseudo-nitzschia multistriata]
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ICSNFLCDTQPGDEVTMTGPAGKVMLMPEDPKTDLIMVATGTGIAPYRGFIRRLFAEDTP
AAEYKGQAWLFLGVANSDALLYDDEFQAAKKAFPENFRLDYALSREQTNVKGGKMYIQDK
VEEYADEVFEKLENGAHIYFCGLKGMMPGIQDMLKGVAEKKDIDYDEWLKKLKKAKQWH
V
EVY
>GAX17478.1 ferredoxin--NADP+ reductase [Fistulifera solaris]
QDFLEAEPYWDQTNVPVNVYKNKAPFVGKVISTKRIVGPKATGETCHIIIDHKGDFPYWE
GQSWGVIPPGVREKGKPHSVRLYSIASSRYGDDMTGKTGSLCVRRATYWCELKADPAKKG
ICSNFLCDTKPGDEVQMTGPAGKVMLLPENPSTDYIMVGTGTGVAPYRGFIRRLFVENTP
AAAYKGQAWLFLGVANSDALLYDDEWQAVKKDHPEQFRLDYALSREQTNAKGGKMYIQD
K
IEEYADEVFNKLENGAVIYFCGLKGMMPGIQEMLETVAKKKGIDYEEWIKGLKAKKQWRV
EVY
>GAX13963.1 ferredoxin--NADP+ reductase [Fistulifera solaris]
QDFLEAEPYWDQTNVSVNVYKNKAPFVGKVISTKRIVGPKATGETCHIIIDHKGDFPYWE
GQSWGVIPPGVREKGKPHSVRLYSIASSRYGDDMTGKTGSLCVRRATYWCELKADPAKKG
ICSNFLCDTKPGDEVQMTGPAGKVMLLPENPNTDYIMVGTGTGVAPYRGFIRRLFVENTP
AAEYKGQAWLFLGVANSDALLYDDEWQAVKKEHPEQFRLDYALSREQTNAKGGKMYIQD
K

IEEYADEVFNKLENGAVIYFCGLKGMMPGIQEMLETVAKKKGIDYEEWIKGLKAKKQWRV
EVY
>OEU17081.1 ferredoxin NADP reductase [Fragilariopsis cylindrus CCMP1102]
QEFLEATPYYDQSSVPVNVYKNKAPFTGKVVSTKRIVGPKATGETCHIIVDHKGDFPYWE
GQSWGVIPPGTREKGKPHSVRLYSIASSRYGDDMTGKTGSLCVRRATYWDELKADPAKKG
ICSNFLCDTQPGDDVVMTGPAGKVMLMPEDPSTNYIMVATGTGIAPYRGFIRRLFNEDTP
AARYKGEAWLFLGVANSDALLYDDEFQEAKTRFPENLRIDYALSREQNNTKGGKMYIQDK
VEEYADEVFNKLESGAHIYFCGLKGMMPGIQDMLKGVAEKKGLNYDEWLKGLKKAKQWH
V
EVY
>VEU42375.1 unnamed protein product [Pseudo-nitzschia multistriata]
QDFLEADPYWDQSTVPVNTFKNKAPFTGKVVSTKRIVGPKATGETCHIVIDHNGDFPYWE
GQSWGVIPPGTREKGKPHAVRLYSIASSRYGDDMTGKTGSLCVRRATYWCELKADPAKKG
ICSNFLCDTKTGDEVTMTGPAGKVMLMPQDPTTBYIMVATGTGIAPYRGFIRRLFNEDTP
AARYKGEAWLFLGVANSDALLYDDEFQEAKSRFPENLRIDYALSREQTNSKGGKMYIQDK
VEEYADEVFSKLENGAHIYFCGLKGMMPGIQDMLKGVADKKGLNYDEWLKKLKKNKQW
HV
EVY
>XP_009040433.1 hypothetical protein AURANDRAFT_31888 [Aureococcus anophagefferens]
QDFLEASPYWDQSTVPVNTYKNKSPYTTKVVSCKRIVGPEATGETCHIIFDHQGKMPYWE
GQSFGVIADGTNPKGKPHTVRLYSIAASRYGDDMTGKTTSLCVRRATYWDEMGKDPAKKG
VCSNFICDSKPGDAVKMTGPSGKVMLMPEKADTDYIMVATGTGIAPYRSFIRRLFTETTP
AGEYKGTAWLFLGVANSDALLYDEEWQATLAKYPDNFKLDYALSREQSNSKGGKMYIQDK
VEEYADEIFDRLGKGAVMYFCGLKGMMPGIQDMLKSVCDKKGLDYDEYIKDLKKKGQWR
V
EVY
>XP_009035092.1 hypothetical protein AURANDRAFT_23206 [Aureococcus anophagefferens]
QDFLEASPYWDQSTVPVNTYKNKSPYTTKVVSCKRIVGPEATGETCHIIFDHQGKMPYWE
GQSFGVIADGTNPKGKPHTVRLYSIAASRYGDDMTGQTTSLCVRRATYWDEMGKDPAKKG
VCSNFICDSKPGDPIKMTGPSGKVMLMPEKADTDYIMVATGTGIAPYRSFIRRLFTETTP
AGEYKGTAWLFLGVANSDALLYDEEWQATLAKYPDNFKLDYALSREQTNTKGGKMYIQDK
VEEYADEIFDRLGKGAVMYFCGLKGMMPGIQDMLKGVCDKKGLDYDEYIKGLKKAGQWR
V
EVY
>CBN78345.1 ferredoxin-NADP oxidoreductase [Ectocarpus siliculosus]
LDFLEADPYFDQSNVPVNTYKAKDPMIGKVVSVKRIVGPEATGETCDVVISHGGKMPYWE

GQSYGVIPPGNNWKGKPNGVRLYSIASSRYGDDMTGTTTTLCVRRATYWDEMGKEPAKKG
VCSNYLCDAEPGAKLKLTGPSGKVMLMPDKPETDLIMIATGTGIAPYRSFVRRLFAEATP
AKEYKGQAWLFLGVANSDALLYDAEWQQVLKEFPDNFRLDYALSREQENKSGGKMYIQD
K
VEEYGDEVFQKLSKGAHIYFCGLKGMMPGILNMLEKVATKKKMNWETTLKDLKKKEKWM
N
KRT
>Polytomella magna
VSKRDVAPGLEGGKLPLNTYSPKKPFKAKILSVEKIVGPKATGETFHVVLDTQG-VKYQE
GQSFGIIPPGTNSREVAHGTRLYSIASSRYGDNFEGNTATLCVRRAVYVDKTGKEPEKKG
ICSNYLTSTPSGTEVTLTGPTGKVLLLPEDPSVPVICVATGTGIAPFRSFWRRCFVENIP
GYKFTGKLWLFMGVANSDSKLYDDELQALSKAHPEQFRLDYALSREQQNKKGQKMYIQDK
VEEYADELFNLLDNGAHIYFCGLKGMMPGIQGMLERVAKEKNLVYAEWVEKLKHKNQWH
V
EVY
>chlamydomonad sp. NrCl902
IVKSDVPLELEKGPMPLNTYNNKKPFKATIKSVQKIVGPKATGETYHIVINHDGKLPFWE
GQSYGIIPPGSNSKEVAHGVRLYSIASSRYGDNFDGKTTTLCVRRAVYTDETGKEPAKKG
LCSNFLADAAPGTELNVTGPTGKILLMPEDPNAVLICVATGTGIAPFRSFYRRCFYENVP
NYKFNGTFWLFMGVANSDSKLYDDELKALLATHPKQFRLDYALSREQKNLKGGKMYIQDK
IEEYADEVFGLLDKGAHMYFCGLKGMMPGITDMLERVAKEKGIDYAQWQEKLKHNNQWH
V
EVY
>Monotropa hypopitys
KPKVSISPLLEDNEPPLHLHKPKEPYTATIVSVERLVGTKAPGETCHIVIDHGGNVPYWE
GQSYGVIPPGENPKGTPQNVRLYSIASTRYGDFFDGKTASLCVRRAVYYDETGKEPSKKG
VCSNFLCDSMPGDKIKITGPSGKIMLLPEDPNATHIMIATGTGVAPFRGYLRRMFMESVS
TFKFGGLAWLFLGVANTDSLLYDEEFTKYLQDYPNNFRFDRALSREQKNKGGGKMYVQDK
IKEYSDEIFKRLDGGAHIYFCGLKGMMPGIQDTLKRVAEERGESWENKLSQLKKNKQWHV
EVY
>Nitzschia sp.
GGTVSAQAWLEDLGVPSPFAKNTKPVTATVLGRAKLISDDAPGDIQHVLLKLPEGMHYVE
GQSISVIPPGVDEKGKAHKPRLYSIASTRYGDLLDGNTVSLCVRRAQYKDATGQIDSKAG
VCSNFLCNSEPGTTVQVAGPTGKTMLLPEDPNTDVIMVATGTGIAPFRSFLHRLFVENTP
ARHFNGHAWLILGVPVTGGLLYPEELDAMKTTAGSQLDVTYAISREMQNKQGGKLYVQDV
LSEQADVLFAKLQAGANIYFCGLKGMMPGILESLEKVATEKGLDWSKTLTHYKNNHQWHV

EVY
>Spumella sp.
SPSLEADPYWDQMRIPMNTYTIAQPFQAKVAAVRPLVNANATAEFYEMVIEHGGRMPFWE
GQNVGIIPPGTDPEGLPLPTRLYTVASTRYGDDTRGTSMTLCFKRCLREKTEPIEPAKYG
VCSDYMSNLRPGDSVLMTGPAGREILLRDKPESDIIMVATGTGVAPFRAFVRRLLVEDNP
ASRFSGLAWLFLGATTQDSVLYHDLWTSLTAAHPDRFRYTLALSRDQTNAQGGKMYIQDQ
VQLHSEEIFERMAKGAVLYCCGRRAMMPSIMANLDLHATSRGLKWQKVFESWVRNEQLKI
EVY
>CEM11286.1 unnamed protein product [Vitrella brassicaformis CCMP3155]
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GQSYGVIPPGINPKGKPQGVRLYSIASTRYGDDMTGNTASLCVRRAVYNDETGEEPEKKG
VCSNYLCDAQPGDELKLTGPAGKVMLMPDKPAADLIMVATGTGIAPYRGFLRRLFVEQTP
ARDFKGLAWLFLGVANSDSLLYDEEWQSILKEHPDKFRLDYALSREQNNKKGGKMYIQDK
MEEYAEEIFDRMDKGAHMYFCGLKGMMPGILEMLKGVAESKGKTWEDVLKSWKENKQW
HV
EVY
>ABF73016.1 plastid ferredoxin NADPH reductase protein precursor [Karenia brevis]
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FAKFKGLAWLFLGVANSDALLYDEDWKAIEKENPDNFRYDVALSREMTNKDGGKMYIQDK
VEEYGDEVFDRLDKGAHIYFCGLKGMMPGIQGMLEKVAGAKGLNYEEFIKKLKKNGQWH
V
EVY
>XP_002788137.1 ferredoxin--NADP reductase, putative [Perkinsus marinus ATCC 50983]
ARRKPKIISSRGRSVEVNKHKLKHPLQAVCLSNTPATREAKPADVRHIVLDTGGDLEYLE
GQSVGIIPPGA-------KTKVYSIASAGQGDLSDGTTVSLCVKRLVEVDDYGEVEDYRG
VGSNYLCDLKPGDTVAITGPTGKELLLPDDPDSKVLMLATGTGIAPFRGFLTSEFCRGID
---GEGKLWLILGVADRSSILYPQELSDCVSANSDRLRVDYALSREEKDEQGRKMYIQSK
MRQCGEDIWRWLQPNFHLYMCGMKAMESGVHEALSEICASHGSDWKEILARMRKEGRYH
A
EVY
>AKR52926.1 chloroplast ferredoxin-NADP+ reductase [Polykrikos lebourae]
TKAPAGTRVVEGRSIPWNMWSVKAPLPADVVENTTTQTGDANWETCHITFNHRGEYSYVE
GQSLGIIAPGPDKKESPAKIRLYSIASSATGDDETSKTVSLCVKRVVEVDEVGEDPDYRG
VASNHICDARPGDTVQITGPTGAEMLLPEIDDPNIVMLATGTGIAPMRSYLRYLFHDKAG

GERFKGLAWLFLGVPYKASLLYDAEHQDYVKRFPDQFRFDYAVSREDKNAAGQKMYIQTK
MAEYGEELWELLKPKTHFYLCGLKGMEAGMAEVFGPIAEKNGIVWADYFKQLKKEHRMH
V
EVY
>AAW79314.1 chloroplast ferredoxin-NADP{+) reductase, partial [Heterocapsa triquetra]
ATKKKGVKVVHGKEIPWNIFMPKAPYTGKVVANDTEDTGDANWETTHLTFDHDGKVPYLE
GQSIGIIAPGPDKKETPAKIRLYSIASSAVGDDQTSKTVSLCVKRVVELDEVGEDPDYRG
VCSNHICDMSVGDDVLITGPTGAEMLLPEDPKANIIMLATGTGIAPMRSYMRLLFHDKAG
GSRFQGLAWLFMGVPYSKSLLYDDEHLAYVKNYPDQFRFDYAVSREQTNAAGQKMYIQTK
MAEYTDELWELMQENTHIYMCGLKGMEAGMEECFSAKAEAAGLVWKEFAKSMKKADRY
HV
EVY
>PHJ21926.1 ferredoxin nadp+ oxidoreductase fnr [Cystoisospora suis]
ESSTFQSLEHLDSDVPINTFRPSAPLLCRVVSVLPATGEGRAPEIYTVVLHHACRLRFVE
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VCSTFICNAKPGDEFEVTGPMGKTLLLPKQEDAPLVMLATGTGVAPFRGHIQRLRRMAAG
HTSRQPRILLFVGARTAEAVPYLNEWKACSSDESSGVELHLALSRQMHREDGKRLYIQDL
VWRERAKVWKALQDGGHLYVCGLKSMLSGVEDVLARVARECAGSGMDFVRQLKQERRW
HV
EVY
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GQGIGIMPPSRAAQKRRLLPRIYSIASSRDGDDGCGSTLTLCVKKHIYADVTGKRRQKDG
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AQPNRPKVLLFIGARTAAAVPYMNEWRDIEAQRDGNFDIHFALSRQMKNPQGKKLYIQDV
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WHV
EVY
>XP_966214.1 ferredoxin--NADP reductase [Plasmodium falciparum 3D7]
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YCSGFIKNLKINDDIYLTGAHGYFNLPNIQKNTNFIFIATGTGISPYISFLKKLFAYDKN
RNSYTGYITIYYGVYNEDSILYLNELEYFQKMYPNNINIHYVFSYKQ-NSDATSFYVQDE
IYKRKTEFLNLFNYKCELYICGHKSIRYKVMDILKSHDQ----------FDEKKKKRVHV
EVY
>XP_005835894.1 hypothetical protein GUITHDRAFT_162347 [Guillardia theta CCMP2712]

LEFLEAKPYWDQSGVQVNIAKQKNPLIGKIISVQRIVGPNSPGETCNIIIDHQGQAPLLG
GPVLRCRPPGIDPKNKPYGVRLYSIASTRYGDDKTGKTTTLCVRRATYWCELKAEPAKKG
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VEEYADEVFDALDKGAHIYFCGLKGMMPGIQDMLRGVCESKGLNFEEYLEGLKKKGQWH
V
EVY
>KOO53489.1 ferredoxin-NADP reductase [Chrysochromulina sp. CCMP291]
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VCSNFLCDAKPGDELMLTGPSGKVMLIPKDPNVDLIMVATGTGIAPYRSFIRRLFVEKTP
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VKEYADEVFTRMDNGAHMYFCGLKGMMPGITEMLEEVSSKKGLVWEDKLKEWKEKGQW
HV
EVY
>XP_005790923.1 hypothetical protein EMIHUDRAFT_361737 [Emiliania huxleyi CCMP1516]
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GQSYGVIPPGTNPKGKPNSVRLYSIASSRYGDDMTGTTTTLCVRRATYWCELKADPAKKG
VCSNYLCDSKPGDDVKLTGPSGKVMLIPKDPNVDLIMVATGTGIAPYRSFIRRLFVEETP
FGEYSGLAWLFLGVANSDALLYDDEWQSVLKAHPKNFRLDYALSREQKNKDGGKMYIQDK
VAEYSDEIFTRMDNGAHMYFCGLKGMMPGITEMLEGVCKEKGLKWEDKLTQWKKAGQW
HV
EVY
>XP_005770769.1 hypothetical protein EMIHUDRAFT_432385 [Emiliania huxleyi CCMP1516]
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GQSYGVIPPGTNPKGKPNSVRLYSIASSRYGDDMTGTTTTLCVRRATYWCELKADPAKKG
VCSNYLCDSKPGDDVKLTGPSGKVMLIPKDPNVDLIMVATGTGIAPYRSFIRRLFVEKTP
FGEYTGQAWLFLGVANSDALLYDDEWQEVLKKYPDNFRLDYALSREQKNKDGGKMYIQD
K
VAEYSDEIFSKMDNGAHMYFCGLKGMMPGITEMLEGVCKDKGLVWEDKLSEWKKAGQW
HV
EVY
>AAW79315.1 chloroplast ferredoxin NADP(+) reductase, partial [Isochrysis galbana]
QDFLEASPFWDQSNIPINTYKNKAPFTGKIISVKRIVGAAATGETCDIVMSHGGKMPYWE
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VCSNFLCDSKPGDEVKLTGPSGKVMLIPQDATADLIMVATGTGIAPYRSFIRRLFVEKTP
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K
VAEYSDEIFTRMDNGAHMYFCGLKGMMPGITEMLEGVSKAKGIVWEDKLKEWKSKGQWH
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EVY
>KOO34261.1 hypothetical protein Ctob_009005 [Chrysochromulina sp. CCMP291]
QGFLEFDPYFDKTNLPKNTFKAKAPFVAKVISTKKISGPKANGETWDVVLSHGGDMPYIE
GQSYGVIPPGVNPKGKPNSVRLYSIASSRYGDDMTGKTTTLCVKRALYWDELKAFPAKKG
ICSNYLCDLKPGDEVLLTGPAGDVMLLPENPNADIIMLATGTGIAPMRTFLRRLFFEDTP
YARFKGLAWLFFGVYNSDALLYEDEWQTILKKHPGRFRYDKAISEEMKNKDGGNMFVQHK
MEEYADEIFDRLEKGAHMYLCGLRGMLPGVQESLKKVAEAKGIDYDEFLKNLKEKGQWH
V
EVY
>KOO34449.1 ferredoxin--NADP+ reductase [Chrysochromulina sp. CCMP291]
PSHLEFEPYFDISTMPLNTFKNKAPHTGTIVSAKRIVGDKAPGEVCHVHIKSGAVFKYIE
GQSLGVIPPGNCPKGKPNTVRLYSIASTRYGDDLDGESVSLCVRRAVYWDDLGREPAKKG
VCSNYLCDAKPGQLVTLTGPTGKVMLMPATPEADLIMVATGTGIAPYRGFLRRLFIEQTP
AAAFRGLAWLVLGVPTSDGLLYDEDWQAIAKRHPKHFRVTYAISREQETADGRKMYVQDR
LAESAQELFERLDKGAHIYFCGLKGMMPGIVETLEKVAASKGVDWDEKLEHLKKNGQWH
V
EVY
>XP_005789289.1 hypothetical protein EMIHUDRAFT_42969, partial [Emiliania huxleyi CCMP1516]
---LECDPYHAAANLPLNTYKNKAPLAGAIISAKRIVGPAAPGEVCHIRIGTGDNFRYWE
GQSLGVIPPG------PNAVRLYSIASTRYGDDAKGSSVSLCVRRALYWDDTGAHPAKKG
VCSNFLCDSSPGDEVHLTGPTGKVMLMPHEPATDLIMLATGTGIAPYRGFLRRLFLEPTP
AADFRGLAWLFLGVANRDALLYDDEWQAILQRSAAQGREDGARRRSATRPVGGKMYIQDK
VAQHADEVFERMDNGAHMYFCGLKGMMPGITEMLEGVCKEKGLVWEDKLSEWKKAGQ
WHV
EVY
>OSX71405.1 hypothetical protein BU14_0537s0012 [Porphyra umbilicalis]
GSATLRMAATKRANVPLNLFRPKTPYEATVLYNARIVGKDAPGETVHLIFQHDGNVPYLE
GQSIGVMAPGLDAKGKPHKVRLYSIASTRYGDFGDGKTVSLSVKRLLYNDDEGKE--VKG
VCSNFLCDLAPGDKVSITGPVGTAMLMPEDPNATVIMLATGTGIAPFRTYMRRAFTEKHS
DYKFTGKMWLFLGVPTSSTLLYQTEFEEMMHNYPDQLRCDWAISREQTDADGNKMYLQT

R
MKEYAEELYQLVTSKAYIFLCGLKGMTAGIDEMFGELFKKDGLDWNEYRKAMKKEGRYEA
EVY
>ADM64306.2 ferredoxin-NADP+ reductase [Pyropia yezoensis]
------MAATKRTDVPLNLFRPKAPYEATVLYNARIVGKDAPGETMHMIFNHDGNVPYME
GQSIGVIAPGVDAKGKPHKVRLYSIASTRYGDFGDGKTVSLSVKRLVYEDADGKE--VKG
VCSNHLCDLTPGDKVHITGPVGTAMLMPEDPNATIIMLATGTGIAPFRTYMRRAFTEKHA
DYKFTGKMWLFLGVPTSSTLLYQTEFEEMMHNHPDQLRCDWAISREQTDAEGNKMYLQTR
MKEYAQELYELVTAKAHIFLCGLKGMTAGIDEMFGELFEKDGLNWNDYRKAMKKEGRYEA
EVY
>XP_005706517.1 ferredoxin--NADP+ reductase [Galdieria sulphuraria]
YGVRMAAPASSKREVPLNIFRPNKPFEATCLSNELIVDKDAPGETWHMVFNTDGALRYIE
GQSIGVIPPGSDDKGKPHKVRLYSIASTSHGDHKDDKTLSLCVKRLVYTDSTGEE--RRG
VCSNYLCDLKANDKVNISGPVGTVMLMPEDQKANIIMLATGTGIAPFRAFLLRAFMENNP
DYRFEGKMWLFFGVPTTSSLLYYDELEKMAKENPNHLKIDYAISREQKDANGKKMYIQNR
MAEYKEELYELFHPNTYIYMCGLKGMESGLDEVMGPVFEERGQDWQEFRKQLKKEKHLLI
ETY
>XP_005719376.1 Ferredoxin-NADP+ oxidoreductase [Chondrus crispus]
PAARINMATIDKSKIPLNVYRPKNPYTAKVLYNERIVGEDAPGETMHMIFNHDGNVPYLE
GQSIGIVAPGTDKKGRPHKPRLYSIASTQHGDFGDGKTVSLSVKRLVYQDADGNE--VKG
VCSNHLCDLKAGDDVKISGPVGVTMLMPTDPNATLIMLATGTGVAPFRAFMRRAFSEDNP
DYKFTGTMWLFLGVPTASTLLYQQEFEEMKANFPENVRLDYAISREQTDPDGNKMYLQNR
MKEYEDELYELFQDNTYVYMCGLKGMESGIDGFMTSRFERDGKDWIAYRKSMKKAKRWE
V
ETY
>PXF41619.1 Ferredoxin--NADP reductase, cyanelle [Gracilariopsis chorda]
RAATIRMASRDRSKIPINLFRPKNPYVATVVYNERIVGEDAPGETKHMIFNHDGNVPYLE
GQSIGVIAPGLDGKGKPHKVRLYSIASTRHGDFGDGKTVSLSVKRLVYTDDDGNE--VKG
VCSNHLCDLKAGDKVQISGPVGTAMLMPEDPNATIIMLATGTGVAPFRTFMRRAFAENNS
DFKFTGTMWLFLGVPTSSTLLYQEEFEEMKANYPGQVRLDYAISREQQDADGKKMYLQNR
MKEYEEELYELFQENTYVYMCGLAGMEGGIDEFMSARFEKDGRDWNEYRRSMKKAGRW
EV
ETY
>XP_005538366.1 ferredoxin-NADP+ reductase [Cyanidioschyzon merolae strain 10D]
RPATLRMVAAE-KKVPVNLYKPNDPLIGTCIYNKKIVGDDAPGDTCHVIIHHDGKLPYLE
GQSVGIIPEGTDEKGRPHKLRLYSIASTAAGDFGDYKTLSLVVKRLVYTNEKGEE--VRG

VCSNYLNDIKPGTPVKMTGPVGKEMLMPDDPNATIIMLATGTGIAPFRAFMRKAFVEKHA
DYQFKGKMILYLGVPTSSSLLYRDELEEMKANAPDQVELHYAISREMKNKQGGKYYLQDA
MAERGEEIWQLLQDNTYVYMCGLKGMDSGIDAFMKDLAAKDGVDWATFKKQLKQQHRY
NV
EVY
>BAF42337.1 ferredoxin-NADP+ oxidoreductase [Cyanidium caldarium]
GSATLHMVAAE-KKVPVNLFKPSSPLVGTCIYNKKIVGDDAPGDTCHVIIHHDGKLPYLE
GQSVGIIPEGTDDKGRPHKLRLYSIASTAAGDFGDYKTLSLVVKRLVYTNEKGEE--VRG
VCSNFLNDIKPGEPIKMTGPVGKEMLMPDDPNATIIMLATGTGIAPFRAFMRKAFVEKHA
DYQFKGKMILYLGVPTSSSLLYRDELEEMKANFPDQVELHYAISREMKNKQGGRYYLQDS
MAERGEEIWQLLRDNTYVYMCGLKGMDSGIDSFMTDLAAKDGVNWADFKKQLKQQHRY
NV
EVY

Dataset of plant type MMT

>BAB62076.1 APG1 [Arabidopsis thaliana]

RFIQHKKEAYWFYRFLSIVYDHVINPGHWTEDMRDDALEPADLSHPDMRVVDVGGGTGFT
TLGIVKTVKAKNVTILDQSPHQLAKAKQKEPLKECKIVEGDAEDLPFPTDYADRYVSAGS
IEYWPDPQRGIREAYRVLKIGGKACLIGPVYPTFWLSRFFSDVWMLFPKEEEYIEWFKNA
GFKDVQLKRIGPKWYRGVRRHGLIMGCSVTGVKPASGDSPLQLGPKEFLLGTLAAAWFVL
IPIYMWIKDQ

>XP_015647024.1 2-methyl-6-phytyl-1,4-hydroquinone methyltransferase 1, chloroplastic [Oryza sativa Japonica Group]

RFIQHKKEAFWFYRFLSIVYDHVINPGHWTEDMRDDALEPAELYHHGLKVVDVGGGTGFT
TLGIVKHVDNENVTLLDQSPHQLEKARQKVALNGVNIIEGDAEDLPYPTDTFDRYVSAGS
IEYWPDPQRGIREAYRVLKLGGVACLIGPVHPTFWLSRFFADMWMLFPKEEEYIEWFQKA
GFQDVKIKRIGPKWYRGVRRHGLIMGCSVTGVKRSSGDSPLQLGPKAFVMGTICASYYVL
VPIYMWMKDQ

>GAQ88660.1 MPBQ/MSBQ methyltransferase [Klebsormidium nitens]

RFIQHKQEAFWFYRFLSIVYDHVINPGHWTEDMREDALEVADLNDPNLKVVDVGAGTGFC
TQGVVRTIPGKNVTMIDQSPHQLAKARKKPELQDVTILEGDAEDLPFATDTFDRYVSAGS
IEYWPDPQRGIVEAYRVIKPGAKACLIGPVHPTHPISRFFADQWMLFPTEAEYMEWFTKA
GFEDVQIKRIGPSWYRGVRRHGLIMGCSVTGVKSNPGESPLNLGPKALILGSLAGAYYVI
IPIYMWLKNL

>XP_001692712.1 MPBQ/MSBQ methyltransferase [Chlamydomonas reinhardtii]

RLVQHKSEAYWFYAGLSQVYDHIVNPGHWTEDMRDDALAPAKLDDPNLKVVDVGGGTGF
C
TLGVVKTVKPENVTLMDQSPHQLAKAKAKPALKGVTILEGDAEDLPFPTDTFDRYVSAGS
IEYWPEPQRGIREAYRVVKEGGLACMIGPVHPTHPVSRFFADAWMLFPTEEEYIEWFTKA
GFTDVKMTRIGPKWYRGVRRHGLIMGCSVTGVKPKAGDSPLVMGPKALILGTAAGFYYFC
LPIYMYIKNL

>XP_005650939.1 S-adenosyl-L-methionine-dependent methyltransferase [Coccomyxa subellipsoidea C-169]

RFIQHKKEALFFYAFLSQVYDYIVNPGHWTVDMRTEALEPAKLDNPKLKVVDVGGGTGFC
TQGIVKTISPINVVLMDQSPQQLAKAKKKKDLQGVTIVEGDAEDLPFPTDSFDRYVSAGS
IEYWPEPQRGIKEAYRVIKEGGLACMIGPVHPTFWLSRFFADMWMLFPTEDEYREWFTKA
GFTDVKIKRIGPKWYRGVRRHGLIMGCSVTGIKPKAGDSPLEMGPKVLIIGSLAGFYYFV
LPVYMWLKNL

>KXZ49108.1 hypothetical protein GPECTOR_23g39 [Gonium pectorale]

RFIQHKNEAKAFYAGLSQVYDHIVNPGHWTEDMREDALVPAKLDDPNLKVVDVGGGTGFC

TLGIVKSINPSNVTLIDQSPHQLAKAKAKPALKEVTILEGDAEDLPFATDSFDRYVSAGS
IEYWPEPQRGIREAYRVIKEGGVACVIGPVYPTFWLSRFFADVWMLFPKEEEYIEWFTKA
GFTDIKITRIGPKWYRGVRRHGLIMGCSVTGVKPKAGDSPLVMGPKALILGTAAGFYYFC
VPVYMYLKNL
>PRW18401.1 MPBQ MSBQ methyltransferase [Chlorella sorokiniana]
RLIQHKNEAKAFYAFLSQVYDYIVNPGHWTTDMREDALQPAQLDSPDLKVVDVGGGTGFC
TQGIVKAVLPTNITLIDQSPQQLDKARGKADLQGVTILEGDAEDLPFPADSFDRYVSAGS
IEYWPEPQRGICEAYRVIKPGGLACMIGPVHPTHPVSRAMADLWMLFPTEEEYLQWFKAA
GFEDVQLKRIGPSWYRGVRRHGLIMGCSVTARKPAGGDSPLQLGPKAVVLGSVGGFWYFL
LPVYMWLKNL
>XP_002952409.1 hypothetical protein VOLCADRAFT_81811 [Volvox carteri f. nagariensis]
RLIQHKNEAYWFYAGLSQVYDHIVNPGHWTEDMREAALVPAMLDNPDLKVVDVGGGTGF
T
TLGIVKAIKPGNVTLIDQSPHQLAKAKAKPALKGVTILEGDAEDLPFRTDSFDRYVSAGS
IEYWPEPQRGIKEAYRVIKEGGVACVIGPVHPSFWLSRFFADVWMLFPKEEEYIEWFTKA
GFVDVKITRIGPKWYRGVRRHGLIMGCSVTGVKPKAGESPLVMGPKVLIMGTAAGFYYFC
VPIYMYLKNL
>KAA6422115.1 MPBQ MSBQ methyltransferase [Trebouxia sp. A1-2]
RLIQHKEEAFWFYRFLSIFYDTIVNPGHWTEDMRTDALAVAELNDANLKVCDVGGGTGFC
TLGVVETVKPENVTLVDQSPHQLSKAKAKPALQRVTIKEGDAEDLPLPTDGFDRYVSAGS
IEYWPDPQRGIKEAYRVVKSGGLACLIGP----------WFTRA
GFEDVQIKRIGPKWYRGVRRHGLIMGCSVTGRKTKDGDSPLQLPPKPLLLGSTAGFYYFV
LPVYMWIKDK
>Monotropa hypopitys
RFIQHKKEAFWFYRFLSIVYDHIINPGHWTDDMRDDALEPADLTDRNLVVVDVGGGTGFT
TLGIVKHVDAKSVTILDQSPHQLAKAKEKEPLKECTIIEGDAEDLPFPTDYADRYVSAGS
IEYWPDPQRGIREAYRVLKLGGKACLIGPVYPTFWLSRFFADVWMLFPKEEEYIEWFEKA
GFKDVKLKRIGPKWYRGVRRHGLIMGCSVTGVKSASGDSPLQLGPKVFVLGATAAMYYVL
VPVYMWLKDQ
>OSX72407.1 hypothetical protein BU14_0438s0002 [Porphyra umbilicalis]
GLIQHKREAFWFYRFLSIVYDTIVNPFHWTVGMRDKSLAQAGLASRNLVTVDVGGGTGFN
TEGVLAYVDPQYVTLLDQSPHQMAKAKAKPALQGVTFVEGDAENLPFATGYADRYTSAGS
IEYWPEPQRGIAEAYRVLKPGGKATIIGPVRATNWFSRFWCDLWMLFPMESEYRKWYEAA
GFYDIQVGYIGPEAYKGVRSHGLIMGLTITGTKPMNGEPLCQLGPMEWIIGLIAGGYYFV
LPFCVMLYAA
>XP_005711647.1 Putative uncharacterized protein [Chondrus crispus]

GLIQHKREAFWFYRFLSIVYDTIVNPFHWTKEMRDRSLTQAMLECRDLKTVDVGGGTGFC
TEGVAQYIDTKNITLLDQSPHQMAKAKAKESLKGVTFVEGDAENLPFQSGEFDRYTSAGS
IEYWPEPQRGIKEAYRVLKPGGVATMIGPVRATNWFSRFWCDLWMLFPMESEYIKWFTAA
GFTNLEVSYIGPSAYKGVRQHGLIMGLTVTGTKPAQGESPLQMGEMLWFIGVLAGGYYFV
LPFLIILYAA

>PXF43311.1 2-methyl-6-phytyl-1,4-hydroquinone methyltransferase 2, chloroplastic [Gracilariopsis chorda]

GLIQHKREAFWFYRFLSIVYDTIVNPFHWTKEMRDRSLAQAQLECRDLKTIDVGGGTGFC
TEGVANYIDTKHITLLDQSPHQMAKAKAKKTLQGVTFVEGDAENLPFNSAQFDRYTSAGS
IEYWPEPQRGIAEAYRVLKPGGVATLIGPVRATNWFSRFWCDLWMLFPMETEYRKWFTAA
GFKDLKISYIGPNAYKGVRQHGLIMGLTITGTKPADGESPVQLGEMLWMLGVIAGGYYFI
LPFLIILYAA

>XP_005704060.1 MPBQ/MSBQ methyltransferase [Galdieria sulphuraria]

GLIQHKKEAFWFYRFLSIVYDTIVNPFHWTVEMRDTSLKQAELVSRDLKVLDAGGGTGFT
TEGIVQYVDAHNITLLDQSPHQMAKAKKKPKLSSVNFVEGDAENLPFPSNSFDRYISAGS
IEYWPEPQRGISEAYRVLRCGGVATVIGPVRATHWFSRFWCDLWMLFPTEEEYRYWFQKA
GFEDIRVSYIGPAAYKGIREHGLIMGLTISGKKPVNGEPVCRLGPMQWLLGCIAGFYYFL
LPFFIMFYAA

>XP_005535393.1 probable MPBQ/MSBQ methyltransferase [Cyanidioschyzon merolae strain 10D]

GLIQHKREAFWFYRFLSLVYDTVVNPFHWTTEMRDASLRQAGLEEPDFKVLDVGGGTGFC
TEGIVQYVSPSQVTLLDQSPHQMQVAKRKPSLQGVTFVQGDAEALAFPTDSFDRVVSAGS
IEYWPEPQRGIAEAYRVLKPGGLATIIGPVRATNPVSRFFCDLWMLFPMEEEYRVWFTRA
GFTDLKVSYIGPPAYKGIRQHGLIMGLTITGRKPAPGEAKIQLGPMRWILGCIAGFYYFV
LPFAIMLYAA

>KAA8494213.1 2-methyl-6-phytyl-1,4-hydroquinone methyltransferase, chloroplastic [Porphyridium purpureum]

GMMQHKREAFWFYRWLSFFYDVVVNPFHWTREMRDEALLRAQLDSPCLRVVDVGGGTGF
S
TLGIVRYVAARYVVLMDQSAAQMSYAAQKRELSGVTFIEGDAENIPIRTNYADRYVSCGS
IEYWPNPQQGIGEAYRILKPGGLACMVGPVRATNPLSRFFCDTWMLFPTEQEYIYWFAAA
GFRNIKVSEITPAAYKGVRRHGLIMGLVVTGEKPLNGDLPLTMEDRVQMLGTVAGFYYFV
LPIAIMLYAA

>XP_005838443.1 hypothetical protein GUITHDRAFT_65997 [Guillardia theta CCMP2712]

RLIQHKAEAFWFYRYLSIVYDKIVNPGHWTEDMREDALKPAQLTSPDLDVVDVGGGTGFC
TLGIVKAVRPEKIVLMDQSPHQLEKARAKKGLEGVTIMEGDAEDLPFETDSKDRYVSAGS
IEYWPDPQRGICEAYRVVKPGGIACCIGPVHPTFPLSRIFADLWMLFPTEEEYIEWFTKA

GFEDVKITRIGPWWYHGVRRHGLIMGCSVTGRKPEAGLPKLQLGPKELILGTLGGFYYFL
VPVYMFLKHL

Dataset of divergent type MMT

>XP_002952366.1 hypothetical protein VOLCADRAFT_105494 [Volvox carteri f. nagariensis]
GLGLTLFALKRVLDTPSRKYDNNVGKEYDAWTEEGVLEYYWGEHIHLGYYSDEEGYFKQA
KFDFVDEMLKFSGAQDPKKILDVGCGFGGTSRHLAKKFKEASVTGITLSPKQVARGTELA
QQQGVNNVQFQVMDALAMEFPDDTFDLVWACESGEHMPDKKKYVEEMTRVLKPGGTLVI
A
CWCQREETAQDKEDLQFLYDEWAHPYFISIQEFERLMKGTGKLQNVHTDNWNKNTLASWR
HSIWVGVFDPWIVVSKPRIWYKTVREIVTIERMHQAFAKGLMEYGMMAGSKA

>KXZ49093.1 hypothetical protein GPECTOR_23g25 [Gonium pectorale]
GLGLTAYTLKRILDTPSRKYDNNVGKEYDAWTEEGVLEYYWGEHIHLGYYSDEEGYFKQA
KFDFVDEMLKFSGAQNPKKILDVGCGFGGTSRHLAKKFKDASVTGITLSPKQVQRGTELA
KEQGVGNVQFQVMDALAMEFPDDTFDLVWACESGEHMPDKKKYVEEMTRVLKPGGTLVI
A
CWCQREETAQDKEDLQFLYDEWAHPYFISIEEFGRLMNGTGKLEKVHTANWNKNTLASWR
HSIWVGVFDPWIVVFKPRIWYKTVREIVTIERMHQAFAKELMQYGMMAGTKA

>XP_001692723.1 predicted protein [Chlamydomonas reinhardtii]
GLGLSLFALKRILDTPSRKYDNNVGQEYDAWTEEGVLEYYWGEHIHLGYYSDEEGYFKQA
KFDFVDEMLRFSGAKNPATILDVGCGFGGTSRHLAKKFRDANVTGITLSPKQVQRGTELA
KEQGVGNVKFQVMDALAMEFPDNSFDLVWACESGEHMPDKRKYIEEMTRVLKPGGTLVIA
CWCQREEGPQDKEDLQFLYDEWAHPYFISIAEFGRLMNGTGKLDGVKLEDWNKNTISSWR
HSIWVGVFDPWVVVFKPRIWYKTVREIVTLERMHQAFEKGLMEYGMMTATKK

>PNH02628.1 putative tocopherol O-methyltransferase, chloroplastic [Tetrabaena socialis]
GLGLTAFTIKRILDTPSRTYDNNVGQEYDAWTEEGVLEYYWGEHIHLGYYSDEEGYFKQA
KFDFVDEMLGFSGAKAPQKILDVGCGFGGTSRHLAKKFRDASVTGITLSPKQVARGTELA
QQQGVTNVKFQVMDALAMDIPDDTYDLVWACESGEHMPDKKKYVEEMTRVLKPGGTLVI
A
CWCQREETPADKADLQFLYDEWAHPYFISIEEFGRLMNGTGKLQAVTTANWNQNTLASWR
HSIWVGVFDPWIVISKPRIWYKTVREIVTIERMHQAFATGLMEYGMMTGTKS

>KAA6422171.1 MPBQ MSBQ transferase cyanobacterial type (ISS) [Trebouxia sp. A1-2]
GVALTFFALKRVFDTPSRAYKENVGDEYDSWTEDGVLEYYWGEHIHLGYYTEQEGYFKQA
KLDFVDQMLKWSGAKSPSRVLDVGCGIGGTTRILAKNFPDANTQGITLSKSQVKRGTELA
AEQGLSNCSFQVMDALHMDFPDDTFDLVWACESGEHMPDKKLYIEEMTRVLKPGGTLVIA
CWCQREESSEEKDQLQFLYDEWAHPYFISNLEFGRLMEGTGKLQAVEVEDWTQPTIDSWR
HSIWVGVYDPWIVVFKPVVWYRTMREIVTLERMHRAFDKGLMQYGMMKAVKS

>PRW61310.1 S-adenosyl-L-methionine-dependent methyltransferase [Chlorella sorokiniana]
GAVLAGYGIKKVFDTPSRSYDQNVGQEYDAWTEEGVLEYYWGEHIHLGYYTEEEGYFIQA

KYDFIDEMFKWSGSDTPQKVLDVGCGIGGTSRFLAAKFPQASVTGITLSPNQVKRGTELA
AERGLGNVKFQVMDALKMEFPDNSFDLVWACESGEHMPDKKAYVDEMVRVLKPGGTLVI
A
TWCQREETESDRERLQFLYEEWAHPYFVSKEEYGRIMEGTGQLDNVATADWTAPTINSWR
HSIWVGVWDPWIVVFKPRIWYKTVREIVTLERMHRAFDDGLMEYGMMKAKKK
>XP_005650891.1 S-adenosyl-L-methionine-dependent methyltransferase [Coccomyxa subellipsoidea C-169]
GVAVVVLAVKKLFDTPSRTYDPNVGDEYDSWTEEGILEHYWGEHIHLGYYTEEEGYFKQA
KFDFVDEMLRWSGAEQPKRILDVGCGIGGTSRHLAAKFPGAQVQGITLSSKQVARGTELA
KERGLTNVNFQVMNALAMEFEDDTFDLVWACESGEHMPDKKAYVEEMARVLKPGGHMVI
A
TWCQREETDKERADLQFLYDEWAHPYFVSVQEYGRLLEGTGKMESVDIDDWTPQTLPTWR
HSNWVGVWDPWPVIFKPFVWYKVLREIVTLERMHRAFDSGLMEYGMAKAVKK
>Polytomella parva
GLAASAVAIKNVFDNPSRKYHGNVGQEYDAWTSEGILEHYWGDNIHLGYYSEKEGYFKKA
KVDFIDEMFRFSGSQSPRAVLDVGCGFGGSSRHLARKFPDSTIIGITLSAEQVKRARELA
AEQGLTNVHFFVMDALYMSLPAETFDLVWACESGEHMPDKRRFVSQMSRVLRPAGNLVIA
CWCQRDSSAQEQKELDFLYHEWAHPFFVSKEAFGRMLSEMGKFKNIQIQNWTRFTLPTWH
HSILVGVWDPWIVLSKPRIWYKTLREVVMIQRMHKAFAKGLMEYGMISAVKA
>Polytomella magna
GLAVGATAVIKVFNNPSRKYNNNVGQEYDAWTSEGVLEHYWGDNIHLGYYSEEDGFFKYA
KVEFIDRMLEFSKSESPKEILDVGCGFGGSSRHLAKKFPAASVQGITLSPKQVERGIELA
AEQGLTNVTLQVMDALKMDFPDNSFDLVWACESGEHMPDKRQFVEEMLRVLRPGGRLVIA
CWCQRDAGKQEQRELNFLYDEWAHPFFVSKEAFGRIMQDTGSLGD----------

>Nitzschia sp.
AAIAGIGFTKAVLDKPSRPYKGSVGEEYDAWTSQGIVEYYWGEHIHLGYYPMDVGQISDA
QVLLMEQLCQFGGVQGNPKILDVGCGFGGTTRFLARQFSGADVTGISLSKEQVQRASEIS
SEQGVTNTKFVVEDAMELSFDDNSIDLVWACESGEHMPDKKRYVEQMVRVLKPGGRLIIA
TWCQRDDSTRDRRDLDYLYGEWSHPYFVSKELYAGLLKGTTVMQNIKVDNWAQETLPTW
R
KTIQLAFLNPWGWLFKPTTYMRCLRDAYCMERMHRAFHRGLMEYGVLCATKQ
>Spumella sp.
VYLLYLMKLSEISTKRSRKFEQTVAREYDQWTREGLVEYYWGEHIHLGYYERPPTDFVEA
KVRFVDRLLDVSGLRQPLRVLDVGCGIGGTTRHLARCLSGVSVTGIAISGAQIERAEALS
REQQVAGTAFARMDAQEMTFPDESFNVVWVCESSEHMPDKAKLVSEMMRVLKPGGRLVL

A
AWCQRDDRAEDSAQLQTLYDDWAHPHFVSIERFTELLASNGA-ADIVAQDWTAPTLPSWL
HSITVGILDPRPFLRQPGLIFGALREARTLALMHRAFRSGLMRYGVLTATKP
>CAMPEP_0174960874 /NCGR_PEP_ID=MMETSP0004_2-20121128|3933_1 /TAXON_ID=420556 /ORGANISM=Ochromonas sp., Strain CCMP1393 /LENGTH=400 /DNA_ID=CAMNT_0016209269 /DNA_START=89 /DNA_END=1291 /DNA_ORIENTATION=+
LFTALKSWADKALWTPSRTYSNSVGKEYDAWEEEGILEYYWGEHIHLGYYGEKESQFIQA
KYDFIDEMLKFGQFDVPLQILDVGCGIGGTSRYLAKKFQDTTVVGITLSQNQVNRATALA
KEQDVPNARFEVMDALDMTFPDNSFDYVWACESGEHMPDKKKYVEQMTRVLKPGGRIVI
A
TWCQRDEGDEEKRMLNFLYSEWTHPFFISISDYKKLMDGTGQLEDLATDDWTPQTIASWL
HSIWVGVFDPWPVFSKPKLWWKTFRDGLTLVRMHKSFNSKLMEYGMMTGTKK
>ENA|HAFO01015914|HAFO01015914.1 TSA: Uroglena sp. WA34KE, contig comp194936_c1_seq2, transcribed RNA sequence.
AILAIGKWVDEKLWTPSRTYNNTVGKEYDAWEEEGILEYYWGEHIHLGYYAEKDSLFIEA
KYDFIDEMLNFGRINAPAQILDVGCGIGGTSRYLAKKFTDTKVIGITLSNNQMKRATELA
KEQGVTNAEFLVMDALDMQFPDNSFDYVWACESGEHMPDKKRYIEEMTRVLKPGGKIVVA
TWCQRDEGNDEKRMLNFLYSEWTHPFFISISDYKKLMESTEVLNDIITDDWTPQTIASWL
HSIWAGVFDPWPVFSRPHLWWKTFRDGLTLVRMHKSFDSKLMEYGMMAAVKS
>ENA|HAGC01013791|HAGC01013791.1 TSA: Dinobryon sp. LO226KS, strain LO226KS, contig comp25212_c0_seq1, transcribed RNA sequence.
AFSAFARWFNRMLWTPSRVYNNTVGKEYDAWQEEGILEAYWGEHIHLGYYEPEYKAFIQA
KYDFIDAMLQFSGFDVPVKILDVGCGIGGTSRYLAKKFRQVEVTGITLSGNQKRRATELA
TEQQCDNAVFQVMDALQMEFEDESFDLVWACESGEHMPDKKRYVEEMTRVLKPGGQLVIA
TWCQRDEGESENRMLNFLYSEWTHPFFISISDYAQLMLGTGSLTSIRTDDWTPQTIASWL
HSIWVGVFNPWPVFRQPRLWWKTFRDGLTLYRMHNSFASGLMQYGMMTATKT
>ENA|HAGF01018081|HAGF01018081.1 TSA: Epipyxis sp. PR26KG, strain PR26KG, contig comp25997_c0_seq1, transcribed RNA sequence.

------------------------CGIGGTSRYLAKKFENAQVTGITLSPFQVKRATQLA
KEQFVSNAEFKVMDALNMNFPDNSFDYVWACESGEHMPDKKKYVEEMTRVLKPGGRIVIA
TWCQRDEGAQDRRMLDFLYSEWSHPYFISINDYKSLMLGTQQLGEVGTDDWTVPTIPSWR
HTLWAGVFDPRP--
>GGOE01001753.1 TSA: Euglena longa strain CCAP 1204-17a Contig1765, transcribed RNA sequence MPBQ/MSBQ methyltransferase
MLGVLFLALKKLFDTPSRKYNVNVGREYDAWTEEGVLEYYWGEHIHLGYYSPELGNFIEA

KVEFVNKMFDWSGAKGPRTILDVGCGIGGTSRQLAERLPAAQVTGITLSPKQVERGMELV
KERGIKNCELKVMDALKMDFPDNSFDLVWGCESGEHMPDKKKYVEEMVRVLKPGGTLVIA
TWCQREETQKEKGKLQFLYDEWAHPYFISKEAYVRIMHGTGQLECVGCEDWNEYTIDSWR
HSIWVGVRDPMGLFCKPAVLYKCLRDAITLEKMHRAFACGLMEYGMLKAKKK
>GEFR01007101.1 TSA: Euglena gracilis EG_transcript_7105 transcribed RNA sequence
VLSVVALGVKKVLDTPSRKYNVNVGKEYDAWTEEGVLEYYWGEHIHLGYYSPELGNFIEA
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KERGIKNCDLRVMDALKMDFPDNSFDLVWGCESGEHMPDKKKYVEEMVRVLKPGGTLVIA
TWCQREETQKEKDKLQFLYDEWAHPYFISKEEYVRIMNGTGQLQSVVTEDWNEYTIDSWR
HSIWVGVRDPMGLFCKPAVLYKCLRDAITLERMHRAFASGLMEYGMLKAQKK
>VEU41615.1 unnamed protein product [Pseudo-nitzschia multistriata]
TALAGTGFVKLFLDKPSRTYGGTVANEYDEWTEEGILEYYWGEHIHLGYYGPDVKYLNEA
QYTFIDEMMKFGGIDPAAKVLDVGCGFGGTSRYLARALPEAEVTAITLSPKQVERAQELA
IEQDTHNVNFMVEDALEMSFPDNSFDIVWACESGEHMPDKKKYIEQMMRVLKPGGKFVMA
TWCQRDDRKRDKRDLQYLYEEWTHPYFISKEEYTQLIDNTGVMNKVTAANWVRETIASWR
HTIFKGAKDPRGFIFKPKKYIKTLRDAYCIERMHRAFKRGLMEYGMLTATKK
>OEU07966.1 MPBQ/MSBQ methyltransferase [Fragilariopsis cylindrus CCMP1102]
AAMASTGFVKLFLDKPSRTYGGTVAQEYDEWTEEGILEYYWGEHIHLGYYGPDVKYLKDA
QYAFIDEMMKFGGIDPKAKVLDVGCGFGGTSRYLARALPESSVTAITLSPKQVERAKELA
IEQDTPNVKFMVEDALEMSFPDNSFDIVWACESGEHMPDKKKYIDQMMRVLKPGGKFVMA
TWCQRDDRKRDKRDLQYLYEEWTHPYFISKEAYAELIAETGVMNKATTADWVKETIATWR
HTILKGIKDPWGFIFKPKKYIKTLRDAYCIERMHRAFKRGLMEYGMLTATKK
>XP_002293723.1 sterol-c-methyltransferase [Thalassiosira pseudonana CCMP1335]
GAILTTATIK-YLDKPSRTYSGSVAREYDAWTQDGILEYYWGEHIHLGYYNEEEGYFIQA
KYDFIDEMMKFGGIDAGAKVLDVGCGFGGTSRYLADKLPKAEVTGITLSPNQVKRGTELA
MERNLPNAKFTVMNALEMDFPDNTFDIVWACESGEHMPDKEAYINEMMRVLKPGGKFVM
A
TWCQRDDRKRDKRDLRFLYEEWTHPYFISIEAYKELIDATTLMSNVKTADWVTPTIASWR
HSIWVGVYDPMGWIFKPTKYVKCARDAYCLERMHRAFKRGLMEYGMFAAVKK
>GAX14460.1 hypothetical protein FisN_11Hh079 [Fistulifera solaris]
AALAGTAGVKLILDKPSRTYAGSVGDEYDAWTSEGILEYYWGEHIHLGYYTPEEGYFIQA
KYDFIDKMMEFGDIDPKAKVLDVGCGFGGTSRYLAKALPSSHVTGITLSPNQVKRGTELA
VEQGVANTKFMVMDALKMDFPDNSFDIVWACESGEHMPDKKTYIEQMMRVLKPGGKFVM
A
CWSQREEGKRDKRDLQYLYEEWSHPYFVSINYFKKLIDDTGVMGEVKTANWVDETIASWR
HSVWVGIFDPRGWIFKPKQYYKCVRDAYCLERMHRAFKRGLMEYGMWAATKK

>XP_002186194.1 predicted protein [Phaeodactylum tricornutum CCAP 1055/1]
AAVAGTATVKLVLDKPSRTYGDTVAKEYDAWADDGILEYYWGEHIHLGYYSPEEGYFVQA
KYDFIDEMMTFGGIDAKAKVLDVGCGFGGTSRYLAKKLSDAHVTGITLSPKQVQRGTELA
VEQGVANTRFTVMDALQMDFPDNSFDIVWACESGEHMPDKKAYISEMMRVLKPGGTFVM
A
CWSQRDDSQRDKRDLQYLYEEWTHPYFISIKDFRKLIDDTDVMNPVTTANWVDETIASWR
HSIWVGVFDPRGWIFKPKTYVKCFRDAYCLERMHRAFKRGLMEYGMWTATKK
>EJK64762.1 hypothetical protein THAOC_14472 [Thalassiosira oceanica]
AAVAGTAGVKFILDRPSRAYNDSVAKEYDEWTQDGILEYYWGEHIHLGYYSEEEGYFIQA
KYDFIDEMMKFGGIDAGAKVLDVGCGFGGTSRYLADKLPKAEVTGITLSPNQVKRGTELA
EERGLPNAKFQVMNALEMDFPDNSFDIVWACESGEHMPDKEAYINEMMRVLKPGGKFVM
A
TWCQRDDRKKDKRDLRFLYEEWTHPYFISIEAYEELIDATKLMGGVKTADWCEPTIASWR
HSIWVGVYDPRGFIFKPTKYLKCARDAYCLERMHRAFKRGLMEYGMFAATKK
>CBJ31646.1 MPBQ/MSBQ transferase [Ectocarpus siliculosus]
AVGLLGAVAIKVLDTPSRPYDNTVGNEYDAWTEDGILESYWGEHIHLGYYNEEEGAFIQA
KYDFIDEMAKWGGVVAPKKVLDVGCGVGGTSRYLAKKLPETSVTGITLSPKQVERATQLA
EEQGVPNAKFQVTNALDMTFEDESFDLVWACESGEHMPDKGKYIEEMTRVLKPGGQLVVA
TWCQRDNSPEEERKLDFLYSEWTHPHFISINDYAKLMEGTGQLEQVETDDWAEQTTPTWR
LSIWVGVVNPWPWLRVPRSYYKTVRDAWCIERMHQAFKKGLMQYGMIKSVKK
>CEM04269.1 unnamed protein product [Vitrella brassicaformis CCMP3155]
AALAAGVAVKKVLDTPSRPYDGSVAREYDAWTEEGILEHYWGEHVHLGYYDDEDGSFKQA
KDDFVLKMLEFAKVDVPKDTLDLGCGIGGTARILAKAFPQSRILGIAISPNQIARANELA
TEQGVSSCKFMVMDGMKMTVPDNTFDFVWVCESTEHMPDKQKAIQEMTRVLKPGGRLVV
A
VWSQRDDTKRERRRLDYLYSEWSHPFFTSVPQFVEMLQDTGVMENIETADWAQQTLPSWR
HQIWLGIKDPLPWLTKPKFYWKCVRDAWCLNRMHQAFKEGLMQYGMITATKK
>KOO24628.1 hypothetical protein Ctob_000658 [Chrysochromulina tobinii]
VVALAFAWLARVLNTPSRVYDNSVGREYDAWTSEGILEYYWGEHIHLGYYGEKEPFFIEA
KYDFIDKMLEFSQAQAPLKVLDVGCGIGGTSRYIAKKFPKATVTGITISPEQQRRATALA
AERGVSNAKFEVCDALDMTYEDNTFDLVWACESGEHMPDKVKYVEEMARVLKPGGRIVIA
TWCQREEGPKERDTLDYLYGEWTHPYFISIEEYGRIMQRTGKLQKIVTADWATETIPAWR
HSVWVGVWDPWPVIRRPKLWWKVIRDAWCLEIMHRAFTNGLMQYGMMTATKP
>XP_022840839.1 Methyltransferase type 11 [Ostreococcus tauri]
GIVALAYGTKTIFDTPSRTYVNTVGTEYDAWTEEGILEYYWGEHIHLGWYSDEDGAFIQA
KFDFVDQMADWSEARAPARVLDVGCGIGGTSRHLARRFVGTEVTGITLSPNQVKRATELA

SEQGVTNANFQVMNALEMTFEDDTFDLVWACESGEHMPDKKKYVEEMVRVLKPGGKIVIA
TWCQRETPQKEKDNLQFLYEEWAHPYFISYEEYERLLRGTGSMESAASEDWVKNTLVSWR
HSIWVGVWDPWPVVFAPRQWYKVVREIVTLERMARAFESGLMTYGMIKGTKK
>EWM22420.1 Methyltransferase type 11 [Nannochloropsis gaditana]
VAGLLAARLPGVIARGWRSYNNSVGREYDAWTREKILEHYWGEHIHLGYYTEEDGYFIGA
KYDFIDRMMAFAKLDGPAKVLDVGCGIGGTTRYIAKKLTTSQVSGITLSQEQVRRAKELA
EEQDVTNAEFQVMDALHMSYPDNSFDLVWACESGEHMPDKKAYVEEMVRVLKPGGTLVIA
CWCQRDAKRSEQKRVDFMCTEWSHPYFISIQDFERLALGTGVMENVRTEDWAKFTLPSWR
HSVWVGVFDPFFWMLRPHLWVKILRDAFTLNVFHNAFKDGLMGYGMIYAQKK
>XP_009039696.1 hypothetical protein AURANDRAFT_12910, partial [Aureococcus anophagefferens]
----------RPYDNSVGREYDAWTKEGILEHYWGEHIHLGYYTDAEGYFIEA
KYNFTQRMMDWGGVTTDVKILDVGCGIGGTSRYMATTLPESSVTGITLSGEQRDRATKLA
AERDIPNAKFQVMDALNMDFEDNSFDVVWGCESGEHMPDKKKYVTEMARVLKPGGKMVI
A
TWCQRDNAAEEEQALDFLYSEWTHPYFISIPDYAKSLKKDAAMVDVETDDWNKNTIASWR
HSIWVGVFDPWPVIRAPRMWYKCLRDGICLERMHRAFKRGLMEYGMIKGTK-
>XP_003055537.1 predicted protein [Micromonas pusilla CCMP1545]
SLAFAFCKLKKNLDTPGRPW-TTVGKEYDAWTDEKILEYYWGEHIHLGYYKDEDGAFVEA
KLDFVDEMLAWSRFNGPRKVLDVGCGIGGATRHLANKFSNTRVTGVTLSPKQARRAGELA
LKQGVPNAEFLVMDALEMDFPDDHFDVVWACESGEHMPDKGKYVEEMVRVLKPGGTLVI
A
TWCQRSTPPREVVNLNYLYEEWAHPYFISINDYAMLLKGTMKMDTVETDDWTRQTIASWR
HSIWVGVWDPMPVFSRPRIWYKTLRDIVCLERMRRAFGCGLMQYGMIKGTKS
>XP_005841094.1 hypothetical protein GUITHDRAFT_91786 [Guillardia theta CCMP2712]
-------VAAFLLNKPSRAYQNTVGKEYDAWTEEGILEYYWGEHIHLGFYNKSDNPFKET
KYKFIDEMYKWSGAEAPLKVLDVGCGIGGTSRYLAKKLGDTKVTGITLSPNQVQRATELA
KEKGLDNVEFKVMDALKMEFPDNTFDLVWGCESGEHMPDKYKYVEEMTRVLKPGGTLVI
A
TWCQRETPESEKDKLKFLYEEWAHPYFISIEEYERHCKKTGKLEAISGANWVKETIHAWR
HSIWVGIWDPWIVIWKPWIWWKVIREIVTLERMHRAFDSGLMTYGMIRAKKQ
>XP_005787794.1 hypothetical protein EMIHUDRAFT_98396 [Emiliania huxleyi CCMP1516]
LVATIFAWVLRVFNTPSRSYRNSVGEEYDAWTSEGILEYYWGEHIHLGYYEEGQPLF---
----------PSKVLDVGCGIGGTSRYIAKKFPSADVTGITISPEQRRRAEQLA
TERGIGNAKFELVDALNMTFADNSFDLVWACESGEHMPDKERYVQEMSRVLKPGGRIVIA
T-------AKERATLDYLYGEWSHPYFISIEEYGRIMERTGELDQVVTDDWAKQTIPAWR

HSIWAGVWDPWPVFRRPRLWYKVLRDSWCLEVMHRAFTNGLMRYGMMTATKK
>KAA8496924.1 2-methyl-6-phytyl-1,4-hydroquinone methyltransferase [Porphyridium purpureum]
VIVVLALIIKKDLDTPKRPYTDGVGAEYDKWTMDGILEYYWGEHIHLGYYSKEEGAFKQA
KIDFTKQMLYWTGVKAPRRILDVGCGIGGTSRILAKEFPHAEVIGISLSSEQVQRATALA
EKEGLDNVTFRLMDALHMDFDDDTFDLVWGCESGEHMPDKAAYVNEMTRVLAPQGTLAI
A
TWCQRDTPQTEKDRLQYLYDEWSHPHFISYQEYMRIMQRTNVMGDVIGEDWNDVTLPSW
R
HSNWVGVVDPWPVIFKPALWYWVIREIVCLERMHRAFRDGLMQYGMIKGVKK
>XP_002777996.1 3-demethylubiquinone-9 3-methyltransferase, putative [Perkinsus marinus ATCC 50983]
---------TGTQTQPERYRPGGVGNEYDKWTNDGLVETYWGEHIHLGAYTTDEWFFKEQ
KFTFVDDLLSWGGFDATLRILDVGCGIGGSSRIMAKRY--EAVTGITLSDAQVERASELS
REAGLNNVTFKKMDALRMEFPDASYDLIWSCECGEHVPDKAKYIEEMCRVLKPGGRLIVA
TWCEKDDRDHQKWLLRFLYEEWSHPMFISIEKYEDILRKNSLMEGVESADWTPQTLPSWR
HSIFVGVWWPWPVIIRPRVWWSTIREIVTIERMHEAFRDGVMRYGVFRATK-
>chlamydomonad sp. NrCl902
GLCLAAAGYMLFQKGSRAYKGSTVGAEYDAWTEEGILEHYWGEHIHLGYYSEAEGYFKAA
KYDFVDAMLEFSGVKS-ASILDVGCGFGGTSRHLAKKFPDAKVTGITLSPKQVERGTQLA
HEQGVGNAEFKVMDALAMTLPSDSFDLVWACESGEHMPDKRRYVEEMVRVLKPGGTLVIA
CWCQREETPQETRELRFLYDEWAHPHFISIQEFTRIMEGTGQLAGVTGEDWTAHTLPSWR
HSLWVGVDDPWPVIAKPRIWYKTLREAVTLERMHRAFASGLMEYGLMRATKL