

protein	sequence name used in Fig. 4	contig number or accession number	predicted evolutionary type	N-terminal length (amino acid residues in blue in the next column)	N-terminal amino acid sequence blue, predicted N-terminal extension (dollar sign; cleaved site predicted by SignalP) red, region matched with the homologous sequence in a cyanobacterium (see the next column)	cyanobacterial sequence compared	SignalP prediction ^a	TargetP prediction ^b
DXS	Karenia	0178117440 Karenia brevis Wilson	VI	115	MYKISLLLAACACAGQGR\$RVQSSQGGSTPCSESTAGLTLRNRITATSFKGSGPAARSSADNPTLAARRPVAP NRLDRVPAISMGPEDGEKAKISGTFPPRATPLDLSLNDCC PQKMRSMDEV EQ	Synechocystis sp. PCC 7509	Y	S (4)
DXS	Karlodinium	0169082592 Karlodinium micrum CCMP2283	EA	67	XGYGRRHCTRIGQQDQEESRKSAGHPLQTLSTLMLISRGFTQRRIQSVSSRPQVAMEFDAGPRITPL LDQV TYPQDLRSFSINELKQ	Synechocystis sp. PCC 7509	N	- (4)
DXS	Lepidodinium-1	comp18684_c0_seq1 Lepidodinium chlorophorum NIES-1868	VI	170	WSINSCITLCRRRLDKMACNEASDCKRPRHRSRALVLAAGCGCSAGAIGLWSRCQQVQQAQHRAFPLSPNAR LQSRHTGEVQQRPAQSGGHRASPSDSRLATFIANGAVAATAAMFAIRSRFRSRHRHQASEARSADSSKLD TPAQGHFPPMPTLLDLSLNNEG PEGIRMSIQ	Synechocystis sp. PCC 7509	N	- (3)
DXS	Lepidodinium-2	comp57335_c0_seq1 Lepidodinium chlorophorum NIES-1868	VI	159	VDIGPAITGTLFGRSFHTILRLKVPVSGKKHRVMRSVAVLAVLLLVKDFAVGNVLDKAVHVLVDRMLDRFDQGLEA WPLHFTELYNTSLARLVGSSSVLQHLRAIGATGVTHSSKASMESLRCPMPRATLSPEQKPPFTFRGTFPARPTPL LDLSLNDEG PQALHSMTNEELQQ	Synechocystis sp. PCC 7509	N	- (4)
DXR	Karenia	0114735228 Karenia brevis Wilson	VI	137	IACHSLGLLNLAMPAMRKIALLLGCLACAGHGK\$RVQTPGSKLQSLARAEQGPELEKASLLQSFDSQAFAALT GSRHPLGSAASLNSPVASLNAGGRVGNVLFMSASEGSSWAKGRNLVGTNTAERSNVVPE KSITLIGSTGSI GTQTLDI	Synechocystis sp. PCC 7509	Y	- (5)
DXR	Karlodinium	0169122770 Karlodinium micrum CCMP2283	VI	100	MQGLPESNVLTRQGTDRDRSVPLKSLAEVLAVASNFPAHRLRTEGKSSSLVGRHHVQLLRAGCNGVAMTA SPESSWAKGRNLVGTNTAQRSNVVPVE KKITILGSTGSI GTQTLDI	Synechocystis sp. PCC 7509	N	- (3)
DXR	Lepidodinium-1	comp117701_c0_seq1 Lepidodinium chlorophorum NIES-1868	VI	150	MADDHMYQIASGVDFOPASVRRRFPGLAALLFGFSVALVCLVLAIVSRPMEHRTAAASTRLVDSPLVSKMT KLSGKPOLGMTASLTSGRSVAPGASWPSLWSKLRGVANERHHKPVYLVCHAAQSSWECGRNLVATNTARDSND PPV KKIALIGSTGSI GTQTLDI	Synechocystis sp. PCC 7509	N	- (3)
DXR	Lepidodinium-2	comp116845_c0_seq1 Lepidodinium chlorophorum NIES-1868	VI	125	MELASLSTARLGAFLSAGARDGKAVRRTNALAGATHMGRPSLKRVAAPDPTHRLQALTCSLFSSSGGAALLA MVAGAAAGSRSKARGGKRAISLQAESSWAQGRNLVGTNTLEKSNPEPID KQISILGSTGSI GTQTLDI	Synechocystis sp. PCC 7509	N	- (5)
IspD	Karenia	0174195266 Karenia brevis CCMP2229	LA	141	MCKIALLLASLVCGVGHRAQ\$SSSGRFHFKPAESKSLRLNLSVRTSHSFTGSKSRDHESVNTVNLPLKVVSM FFLALKPPAFNPSPGVMWPTWRSTSSGLNPRALSISKLSNLEKLGARARTFMEEAASPVDTGSA FVLLAGGS GKRMGA	Synechococcus sp. WH 7805	Y	S (4)
IspD	Karlodinium	0169274054 Karlodinium micrum CCMP2283	VI	NA	Lack the N-terminal extension or the extension is too short to analyze	Leptolyngbya sp. PCC 6406	NA	NA
IspD	Lepidodinium-1	comp105386_c0_seq1 Lepidodinium chlorophorum NIES-1868	LA	134	MACFNVLWRNLVSAITA\$ELATNRGGDQPPGFHYADLDGTLTKGHQIVVSPRGLPHAPSPVYDSSSHLPL FLRPTVYQQIQLGQVPAQTDYPSHAHGKTMQSRSEVQVMAIPTRASSKVPKXVGVLL AGGKGRTRM	Synechocystis sp. PCC 7509	Y	S (3)
IspD	Lepidodinium-2	comp140699_c0_seq1 Lepidodinium chlorophorum NIES-1868	VI	130	MSRNALRFGARTRHGRRLLSAASKIKGAFVAILAFVSRRIIPPLSFAASSAPSLHKTWRDQAVKVGCFHGKPGS GCMAGASSATIAFAGAAVAATITATRGKCNKVASHAACRAALDEPSAAATV G VLL SAGV GKRM	Synechocystis sp. PCC 7509	N	M (2)
IspE	Karenia-1	comp89287_c0_seq1 Karenia brevis	EA	96	ALVVLVYALCAPAQAAGF\$EDLQSNRREIPEKSLKTLIKFLGSSKTTAGWQLSGQGCGRHIAHDLRRPGAGLKFC VTSSGLDKVYSEVYGDTPAL SL SAPCKINLFLRI	Synechocystis sp. PCC 7509	Y	S (3)
IspE	Karenia-2	comp129272_c1_seq1 Karenia brevis	VI	113	MCCWALAVRLQLCIVLIVHAEAF\$CPSWHSSELVLRPQRCTSLQPQRPIAARASGEPNITSHPLALGFFAGCALA TIGSARGRRSQAARLAKGVHAARQATPVSTEHSALK L FSPAKINLFLR	Synechocystis sp. PCC 7509	Y	S (1)
IspE	Karlodinium	comp176232_c0_seq1 Karlodinium micrum	VI	84	MATSVWRWMLVALVSMLSIAHT\$FVPPINHGRLVETSSHMRLGQLLLATSRVSPYVERNLRQVTRGANRVTK VTSGATDIAEGRSLHLFSPAKVNLFL	Synechocystis sp. PCC 7509	Y	S (1)
IspE	Lepidodinium-1	CCC15094 Lepidodinium chlorophorum	VI	38	MLGLVAAQRRRPRKCRMRHGNRLRHQSLVERAADPQ E KSLQLFSPAKVNLFL	Synechocystis sp. PCC 7509	N	M (3)
IspE	Lepidodinium-2	comp47335_c0_seq1 Lepidodinium chlorophorum NIES-1868	VI	131	MRSITRVLLALFWVGCAGE\$GIVDKMVKMLDKMRSFFDAAALGAMPIQOAVYVNHKRIALATRLVNHGGLPPR AQAPLRVDORSIHVGVASPWSSHTSPLGTRVMSGRDNRLLEAVEGTALPAPAVKADGA TL L F SPAKVNLFL	Synechocystis sp. PCC 7509	Y	S (1)
IspF	Karenia-1	0173950708 Karenia brevis CCMP2229	EA	101	SSPLAMHVITVMLAALACESHARRMHTTRDARLQSHREAAALAHAPHRALGALLALDPAAGWHIFGLGHGRGKAP FPSYCSORQGVSRCRQIHALATAPEP AMRIGHYDIH	Synechocystis sp. PCC 7509	Y	S (2)
IspF	Karenia-2	011485984 Karenia brevis Wilson	VI	76	XGNDYMAGRKVLVDLRAGFKRKPASLDWATEATHWNQDRSGHCCFLEGPSQPQRKIKISTNSKNYDESEWI AEP SVRIGHGFDIH	Synechocystis sp. PCC 7509	N	- (3)
IspF	Karlodinium	0169223484 Karlodinium micrum CCMP2283	VI	115	MAATHQPPLVGGIGILLNRFRQDXNNIDVGLSKTVMLSDSFAFMRGLDLSLLALRPMATFTGNSDGHVDSR RPFSAPELAGIRRLRYDAVSSAEATGEDQDLSLNDWAEP IRIGHGFDIH	Synechocystis sp. PCC 7509	N	- (4)
IspF	Lepidodinium-1	comp109737_c0_seq1 Lepidodinium chlorophorum NIES-1868	VI	147	MASTDMLGYVQVREDLGTNTSRTRRQALSIGLAVLISLMVWNGIAPWALLSLVSCQPRVQIARAYRSGIDTL AVWPSMQQRASGESIQRPGFHTKQSQVQEAQRKFLNKRSTQQRKASTSELVGLQCECNASGWDVEPL MRIGHGFDIH	Synechocystis sp. PCC 7509	N	- (3)
IspF	Lepidodinium-2	comp84031_c0_seq1 Lepidodinium chlorophorum NIES-1868	VI	116	MFDSTAFLAASRDGLASPRRLAPEVGLRPIEGASLAHTYDAIGFLQVSMLLGVCGLARAVKRRRDRPFGAART LARAQELRVGDGEDAGE\$SFFPTTSEQTVEANGVPSDPL LRIGHYDIH	Synechocystis sp. PCC 7509	N	- (5)
IspG	Karenia	0173636972 Karenia brevis CCMP2229	VI	108	XMSTRTISAFMLSGGDAKANKPVLDRPGYHLRSSVPVAAAARPSAAGSSTLGSGAARALVAGALATLWAQLVR GQRRRSGPSRSSNCRVAVARSAIPAGGYCETVE TCTRRKTRSVNVG	Synechocystis sp. PCC 7509	N	- (5)
IspG	Karlodinium	0169104574 Karlodinium micrum CCMP2283	VI	139	MSSRKLIMFLVLAHTHFA\$R\$RLWRDQESNAASESAGASKVLSLLGLRIPTVNSQSSMARLPAAMTRTQMMRP SLSAPCSRYPYRQGRSSAAMQERASSASMEVSSPVKEKEKAAVATLSIDELALPLPPGGYCDSS STSTRKRT RTV	Synechocystis sp. PCC 7509	Y	S (3)
IspG	Lepidodinium-1	comp95833_c0_seq1 Lepidodinium chlorophorum NIES-1868	VI	127	MFGAPLSQVFLMPDGGRSVGTARNPTNAIFPRAAVNGARMLEDQSKPSPQTTVFASSAVVAIASLAMRAQKRR QRQLMRHARKLHILREAPVLAPEVKSEKSGVDSLSEPSLPAGGYCEAVERLV RRKTRTVKIGSVNIG	Synechocystis sp. PCC 7509	N	M (4)
IspG	Lepidodinium-2	comp110402_c0_seq1 Lepidodinium chlorophorum NIES-1868	VI	124	MKIQAHLMVRRVAVTILLIAVAQAH\$DKPEMDELDTLVDLFPDRHGMQFHALMGNTLGAHGRLASQAALG HSMLSAASKQPLPCRGLLSGRHSLATRRDSFPTCAVPOGVYCEQLNEC IRRPTRTVTIG	Synechocystis sp. PCC 7509	Y	S (3)
IspH	Karenia-1	0173789044 Karenia brevis CCMP2229	EA	91	MNVCEGECIGRMLRFAQYRNACAKEEALASPLQAAHPAAWSSPGAGRINLLNPRGTRLDLTLRASAPVAE GSEPMGPVPLEKITP GS L DKRAERRIMAS	Synechocystis sp. PCC 7509	N	- (3)
IspH	Karenia-2	0173843192 Karenia brevis CCMP2229	LA	147	XLKLLASIGFGNMYRIQQLFLACAGHGRRMQNSLQSSQDNQELNTFDINLDGHSDEVEQSSTLDRATGEPF AGTAFMTLLALTPAAAFVNNPLASGKRVPRDSTLHSSTVLVDKRGDVSQAPVMTSTAVERTKTKRFSR RE LRQKLLSSKNHNRQGF	Synechocystis sp. PCC 7509	N	M (4)
IspH	Karenia-3	0174063494 Karenia brevis CCMP2229	VI	100	XSSKALELNRPSPISMANVPGVLRQETSMRAAGHQGVSQVQNAQQLWATSGAAAAALAGAAFAAAQLASRRR SGRQLTSTQRHVTEKTVPLTVDRNA TKDLRKDFQRSDQY	Synechocystis sp. PCC 7509	N	M (5)
IspH	Karlodinium	0169356754 Karlodinium micrum CCMP2283	EA	77	XDLFIAVWLACGPSQVSTRSQPLEHSSQSQELATLFLSALTPOQSRSRARSVLSALKTPTDLEGVTLTKKIEP G L TDKTKERKRM	Synechocystis sp. PCC 7509	N	S (5)

Table S3. (continued)

protein	sequence name used in Fig. 4	contig number or accession number	predicted evolutionary type	N-terminal length (amino acid residues in blue in the next column)	N-terminal amino acid sequence blue, predicted N-terminal extension (dollar sign; cleaved site predicted by SignalP) red, region matched with the homologous sequence in a cyanobacterium (see the next column)	cyanobacterial sequence compared	SignalP prediction ^a	TargetP prediction ^b
IspH	Lepidodinium-1	comp91619_c0_seq1 Lepidodinium chlorophorum NIES-1868	VI	116 ^b	MSADMLSQAFLAAGGGPLRKAYGGVHPSQAVAPAAVAIGAIEVSKTSGIDDDGYFQGTSNVAAMLLLTGSLAARA AGRRRAQKRQSRQHRSSLVVVAGVDTEAAVQTPPIIDRSTTKAFRRNLMSSDKY	Synechocystis sp. PCC 7509	N	M (5)
IspH	Lepidodinium-2	comp108906_c0_seq1 Lepidodinium chlorophorum NIES-1868	VI	169 ^b	MQTMP\$VIVITLLALPVAGHAES\$ELVASGGNSAQDFIDQLVDSFSEELVDRARQDHISPTNLDNVTLAKTYQGS\$S LRPQYTRLPVSTVFVPLAR\$V\$PQTLASSRAHGSOPQRALNVLRAIQ\$RPGSSCSG\$SALHAMS\$VIAGAVKEAGRR KTIQRATAQGTKLPELDPATTKT FRRDF\$R\$S	Synechocystis sp. PCC 7509	Y	S (2)

^aPutative signal peptide (SP) was predicted by SignalP 4.1 Server with the default settings ("Y", SP predicted; "N", no SP predicted).

^bPutative intracellular localization was predicted by TargetP 1.1 Server with the default settings ("S", secretory pathway; "M", mitochondrion; "-", any other location; reliability class from 1 to 5 is provided in parentheses).