

Sequences and adjusted gene models

The following supplemental information describes the protein sequence data used in the phylogenetic analysis presented in this paper. Table 1 describes the default source of protein sequences. Any modifications to *Ostreococcus tauri* sequences are also described below. Sequences information is presented for novel gene models, existing gene model alterations, and inference of gaps in *O. tauri* sequences based on orthologous sequences in *Ostreococcus lucimarinus*.

Table 1 Locations of protein sequence data used in this paper.

Species	Database	URL	Version
<i>Ostreococcus tauri</i>	BEG	https://bioinformatics.psb.ugent.be/gdb/ostreococcus/O.tauri	Dec-2006
<i>Ostreococcus lucimarinus</i>	UniProt	http://www.uniprot.org/uniprot/?query=organism%3a436017+keyword%3a181&force=yes&format=fasta	Nov-2012
<i>Saccharomyces cerevisiae</i>	KinBase	http://kinase.salk.edu/kinbase/FastaFiles/Bakers_Yeast_kinase_protein.fasta	Nov-2012
<i>Arabidopsis thaliana</i>	TAIR	ftp://ftp.arabidopsis.org/home/tair/Proteins/TAIR10_protein_lists/	TAIR 10
<i>Homo sapiens</i>	KinBase	http://kinase.salk.edu/kinbase/FastaFiles/Human_kinase_protein.fasta	Nov-2012

Sequences of novel gene models

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>Ostreococcus tauri|Ot03gTAP42 Chromosome 3 - 14703: 15716 sequence
ATGACGCGAGAACTCCCGCTCGCGGCGTTGTTTCGCGCGCGCCGATCGCGCGGACGCGTCGGTGGAGACGTGTGAG
GCGTTCAGGGACGCCGTGCGCGCGACCGGGGGACTGGGACGGGCGGAGACGTTGGATGATTTGGATCGCATCGGG
CTAAAGCTTTCGCTGGGGCATCGATTGGCGGGACGCGCGCACGCGCGATGCGGACGCGATGGCGTGAACGGGGC
ATCGATGCGTTGGAGGCATTCGTCTCGCTCGTTCGCGGAGCTCGATGGGGTGCCGCGGGAGGAGATGGCGGCGTGC
GAGGGAGAGGAAGAGGGGACGTCGCGGCGGGCGCGGGGGCGGAGACGGACGCGCGGATAAAAGTGCAGATTTAAG
GCGAAAAGGCGGTGTGAGAAGAGAATGGAGGAGATTGAGGAGATTTTGAAGCGACGATCGAGGGTGGAGGAGGAA
TCTGGGAGTGAATCCGCGTCGGAGGAGGATGAGACGGATCACGACGCGCTCGAGCGGGAGTATTGGATGAAACGC
ATCGAGCTCGAGACGTACGAGACTTTGGACGAACTCCCGAGCCTGAGAATGGAGAGAGAGATGTTTTTGGAGACGG
GATGAGCTCGAGGAGGCGCGACGGGCCGAGCGAGAGCGCATGGACGCGGATGAGCGCGTCGGACGCGACGCCAGG
ATCGAGACGTACACGATCGAGCGCGAGGACGTGAACGCGCTCGCGGGGCCGTCCATTCTCACCGCCGATCCGCGC
ACGAGATTCGGAACCGAGGTCTTCAGACCCACGGTGGCGTTACCCACGATGACGGTTCGAGCAGTTCGGCGAGATC
GAGCGTCGGGAGATGCTCGAACGCGAGCTCCGCTCGGGCGGAGCGGAGCTCGAGCGCGCCGCCATCCGCGCCGCC
AAAACAGAGGAACAAATCGAGGAAGAAGAGCTCGCCGAGACGCGTCGATGGGACGCGTTCAAGGACGACAATCC
TACGGCTCGGGGAACTCCCGGCTCCGGCCGTGTTTCGTAG
>Ostreococcus tauri|Ot03gTAP42 Chromosome 3 - 15342: 15716 MW: 14389.101
05/06/06 sequence
MTRELPLAALFARADRADASVETCEAFRDAVRATGGLGRAETLDDLDRIGLKLLALGHRLAGRAHARCGRDVERA
IDALEAFVSLVRELDGVPREEMAACEGEEEGTSRRRARGGDGRADKVRRFKAKRRCEKRMEEIEEILKRRSRVEEE
SGSESASEEDET DHDALEREYWMKRIELETYETLDELPSLRMEREMFLRRDELEEARAERERMDADERVGRDAR
IETYTIEREDVNALAGPSILTADPRTRFRTEVFRPTVALPTMTVEQFGEIERREMLERELRSAERELERAAIRAA
KTEEQIEEEELAEATRRWDAFKDDNPYGSNSRLRPCS
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Sequences for proteins with adjusted gene models

The most critical gene model adjustment was S6K (Ot09g03470). The existing gene model contained a gene fusion and a frame-shift near the activation loop, which would almost certainly result in a non-functional protein. We compared the genomic sequence of Ot09g03470 to *O. lucimarinus* (OSTLU_3119) and found an extremely high level of conservation at the nucleotide level. We suggest that the two deletions in Ot09g03470, near the activation loop, are the result of sequencing errors as it is likely they would result in a non-functional protein. We were unable to find any reasonable splicing solutions which would accommodate these deletions and retain a functional protein. If these deletions were genuine we would not expect such a high degree of conservation in this region, and in the region of the potential intron (if the gene was spliced to the correct frame). There is a single copy of S6K in the *O. tauri* genome. It is therefore unlikely, given the high degree of conservation, that Ot09g03470 is a pseudogene. The following alignment shows the conservation of S6K in *O. tauri* and *O. lucimarinus*. The proposed sequencing errors, which resulted in two deletions, are highlightd.

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<i>O.tauri</i> Ot07g02590	1	GAGGAC	TTT	GAG	ATTT	TTAAAG	TTGGT	CGGG	CAAGGG	CGCTTC	CGGGAAGG	TTT	TTTCAG	GTGAA	GAA	GAAG	ATTC	GG	78	
<i>O.lucimarinus</i> OSTLU_3119	1	GATGAT	TTT	CGAT	ATA	TTG	AAAT	TTGGT	CGGG	CAAGGG	CGCTTC	CGGGAAGG	T	TTTCAG	GTGAA	GAA	GAAG	ATTC	GG	78
<i>O.tauri</i> Ot07g02590	77	GGG	TGATT	TAT	CGCAT	GAAAGG	TGAT	GAA	GAAGG	ATTC	CGGAT	CAT	CGAGA	AAGG	ATCAAG	CGAG	TACACG	CGAG	CGGA	152
<i>O.lucimarinus</i> OSTLU_3119	77	GGG	CGATA	TAT	CGCAT	GAAAGG	TGAT	GAA	GAAGG	ATTC	CGGAT	CAT	CGAGA	AAGG	ATCAAG	CGAG	TACACG	CGAG	CGGA	152
<i>O.tauri</i> Ot07g02590	153	CGG	GGAT	ATTTT	GACGG	CGGT	GACG	CAC	CGTTC	CATCG	TGAG	TTT	G	AGT	ATTC	GTTC	CAGAC	CGAC	GA	228
<i>O.lucimarinus</i> OSTLU_3119	153	CGG	AGAC	ATTTT	GACGG	CGGT	GACG	CAT	CGTTC	CATCG	TGAG	T	TG	CGT	ATTC	GTTC	CAGAC	CGAC	GA	228
<i>O.tauri</i> Ot07g02590	229	TAT	TAA	TCC	TCG	ATTT	CAT	CAAT	GGT	GGGC	ATTT	ATTT	CTT	CAG	TTG	TAT	CAG	CAG	GG	304
<i>O.lucimarinus</i> OSTLU_3119	229	TACT	TGAT	TTT	TAG	AATTT	TAT	TAAC	GGC	GGGC	CACT	TTG	TTT	TTC	AG	TTG	TAT	CAG	CA	304
<i>O.tauri</i> Ot07g02590	305	TC	ACA	AAG	TTTT	TAC	CG	CGG	AG	ATTT	TG	TCT	CG	GG	T	GG	ACA	TTT	G	380
<i>O.lucimarinus</i> OSTLU_3119	305	TG	AC	AAG	TTTT	TAC	AT	T	CGG	AA	ATTT	TG	TCT	CG	CA	T	GG	ACA	TTT	380
<i>O.tauri</i> Ot07g02590	381	AA	AG	CCG	GAGA	ACAT	CTT	AG	T	CGAT	A	CCG	AG	GG	AC	AC	GT	G	A	456
<i>O.lucimarinus</i> OSTLU_3119	381	G	AA	AC	CG	GAGA	ACAT	AT	T	GG	T	CGAT	A	CCG	AG	GG	AC	GT	G	456
<i>O.tauri</i> Ot07g02590	457	G	AA	GA	TGG	T	CG	A	CGA	ATTC	CG	CT	CG	GG	A	TC	GAT	C	G	530
<i>O.lucimarinus</i> OSTLU_3119	457	G	AC	GA	TAA	CG	CG	A	CGA	ATTC	CG	CT	CG	GG	A	TC	GAT	C	G	532
<i>O.tauri</i> Ot07g02590	531	GG	AAG	ACGG	CGG	ATT	GGT	GG	T	CGG	GG	GG	T	GG	A	CA	AT	G	T	606
<i>O.lucimarinus</i> OSTLU_3119	531	GC	AAG	ACGG	CGG	ATT	GGT	GG	T	CGG	GG	GG	A	CA	AT	G	T	GG	T	608
<i>O.tauri</i> Ot07g02590	607	AA	T	AA	GC	AG	CG	GT	G	CA	AA	AG	GC	CA	AT	CT	G	A	AG	682
<i>O.lucimarinus</i> OSTLU_3119	609	G	AA	C	AA	G	C	A	G	CG	GT	G	CA	AA	AG	GC	CA	AT	CT	684
<i>O.tauri</i> Ot07g02590	683	GGG	TTG	AT	TAA	AGG	TTA	CT	T	CG	CA	AA	AG	T	CC	AT	CG	T	G	758
<i>O.lucimarinus</i> OSTLU_3119	685	GGG	CT	CAT	CA	AG	GG	TTA	TT	GG	CA	AA	AG	T	CC	AT	CG	T	G	760
<i>O.tauri</i> Ot07g02590	759	AGG	GC	CA	CA	AT	CTT	C	AA	G	CG	T	GA	A	CG	T	G	CA	AG	834
<i>O.lucimarinus</i> OSTLU_3119	761	AA	AG	T	C	A	C	A	A	T	A	A	G	C	G	T	G	G	A	836
<i>O.tauri</i> Ot07g02590	835	CGT	T	CA	GG	T	CA	CA	CT	G	CG	CA	CT	G	CG	CA	CT	G	CG	910
<i>O.lucimarinus</i> OSTLU_3119	837	CGT	T	CA	GG	T	CA	CA	CT	G	CG	CA	CT	G	CG	CA	CT	G	CG	912
<i>O.tauri</i> Ot07g02590	911	ACG	CCC	CGT	G	TC	CGG	CGA	G	CA	AG	AAA	G	TT	T	A	T	CG	TT	958
<i>O.lucimarinus</i> OSTLU_3119	913	ACG	CCC	CGT	G	TC	CGG	CGA	G	CA	AG	AAA	A	TT	C	T	CG	AT	T	960

The following nucleotide sequence is the corrected sequence for the *O. tauri* S6K (Ot07g02590), based on the assumption that the two sequencing errors we inferred previously are correct. We have supplemented the nucleotides from *O. lucimarinus* S6K (OSTLU_3119) at these deletion sites, based on their alignment.

```
>Ot07g02590 a proposed corrected sequence based on identification of
potential sequencing errors. The two inserted bases (bold and underlined)
are proposed from the alignment with O. lucimarinus
ATGACGACATCCGCGAGCGACGCCGAGGCGCGCCGCGCTGAGGCTCAGTGGACTCGGATACGCGATCGCGGAG
GGCGATGGGACGCGCGCCGCGGGCGGGGACGCGAAAGATGGATGGGTTTCGACGTGCGAGCGACGAGCGATGGG
ACGGAGACGCCGACGTTGAAGCGACAAACACAGCTCCGGGGTGAGCATGCTCAGCGCGAACCTGCGACGGATCGAT
AGTGGGTTGTTGCTGGACGAGACGCCGAGCGCGAGCGGGGGCGGAGAGACGAAAAAGTTGTCCGGGAGGACTTTT
GAGATTTTAAAGTTGGTTCGGGCAAGGGGGCGTTTCGGGAAGGTTTTCAGGTGAAGAAGAAGGATTCGGGGGTGATT
TATGCGATGAAGGTGATGAAGAAGGATCGGATCATCGAGAAGGATCAAGCGGAGTACACGCGAGCGGAGCGGGAT
ATTTTGACGGCGGTGACGCACCCGTTTCATCGTGAGTTTGGAGTATTCGTTCCAGACGACGAGCAAGCTGTATTTA
ATCCTCGATTTCATCAATGGTGGGCATTTATTTTCAGTTGATATCAGCAGGGAACGTTTCGGGGACGAGCTCACA
AAGTTTACGCCCGGAGATTTGTCTGGCGGTTGGACATTTGCACTCGCTCTCCATCGTGCACCAAGATTTAAAG
CCGGTAACATCTTAGTCGATAACGAGGACACGTGAAGATCACCGATTTTCGGTTTAGCGAAGAAGATTCGGAA
GATGGTTCGCACGAATTCGCTCCCGGGATCGATAGATTACATGGCGCCGGAGATTTTGGAGCCAAAGGCCACGGG
AAGACGGCGGATTGGTGGTCCGTGGGGGTGTTGATTTTCGAAATGTTATCCGGTACGCTCCCGTTCAAGGGGAAA
AATAAGCAGGCGGTGCAAAAGGCCATCTGTAGCGAGAAGGTTAAGGTGCCAAATTACTTCCAACCCGACGCGGTG
GGGTTGATTAAGGGTTACTCGCCAAAGATCCATCGTTGCGTCTCGGTCGCGGGGAGACTGGCACC GCGGACGTC
AAGGGGCACAAGTACTTCAAGAGCGTGAATGGTGAAGATCGCGCTGAAGCGATCAATCCACCGTTCAAGCCG
AACGTTCAAGGTCAGCACTGCGTCGCAACTTCGACGCGCGCTGGACGGACGTCGATCCCGTGGACTCGGTCGCC
GCCACGCCCCTGTCCGGCGAGCAAGAAAAGTTTATGGGTTTACCTTTGTCTCAAATTCATGGAGGAAGCGGCC
GTCAGGCTCGCATCGACGACGATTTATCCTCCGCGAGCGCGTCCGAGGA
```

The following amino acid sequence is the translation of our proposed *O. tauri* S6K (Ot07g02590) sequence.

```
>Ostreococcus tauri|S6K|AGC|Ot07g02590 We have removed an incorrect gene
fusion and resolved a frame shift error which affected the activation loop
(targeted by PDK1). We speculate there is a sequencing error (as there is
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no deletion in *O. lucimarinus*, which is highly conserved at the genomic level).

```
MTTSASDAEARRAWALSGLGYAIAEGDGTRAAAAGTRKMDGFVDRATSDGTETPTLKRQHSSGVSMLSANLRRID
SGLLLDETPSASGARETKKLSPEDFEILKLVGGQAFGKVFQVKKKDSGVIYAMKVMKKDRIIEKDQAEYTRAERD
ILTAVTHPFIVSLRYSFQTTSKLYLILDFINGGHLFFQLYQQGTFGDELTKFYAAEICLAVGHLSLSIVHRDLK
PENILVDNEGHVKITDFGLAKKISEDGRNLSLPGSIDYMAPEILSAKGHGKTADWWSVGVLI FEMLSGTLFPFKGK
NKQAVQKAICSEKVKVPNYFQPDVAVGLIKGLLAKDPSLRLGRGETGTADVKGHKYFKSVEWSKIALKAINPPFKP
NVQGGQHCVANFDARWTDVDPVDSVAATPVSQGEQEKFMGFTFVSNFMEEAAVRLGTAGSRATAEEDIDDDLSSASA
SED
```

The following amino acid sequences are the result of corrections to the underlying gene-models based on bioinformatics analysis. The corrected sequences are used for all phylogenies presented in this paper. Amino acid sequences that are derived from *O. lucimarinus* have been underlined.

>*Ostreococcus tauri*|Ot09g03470

```
MGGDAGTRSATTTRATVIRILGDAASAVDVREAYAFGVELGRGQFGEVREVVDSTGRALACKSISKRGLKSESSR
EMVRNEVRIMHHLGIRRLVSVHEDATHVHLIMEKLDGPEWFDITEQFDEAPYSEAEAAAQFRNVARTVEYLHA
MDVMHRDLKPENFVLKSKEKDSPICAIIDFGLSTFFLPDQEFTELVGSPYYVAPEVMGYKYSNEADVWSCGVILYI
LLSGVPPFWGSSEKQIFDEIKRYKTGATSLDFASEPWPSVSDAAKELVQGM LTVNRKDRMTIEDVLSHPWLADPG
VAPKTALDNIVLQRFKNFAGMDKFKRFG LHAMARSMPEEEVIGLGVMFKELDKDKSGKITIVELRQGLKLSAEAA
AAQLEEVVASVDLDGSGDLDYEEFIVATIARSKRESRAAVQRAFDFDIDGDGSITADEFQRALESLSVERTNL
GDVNELLAAADTNGDGVDFDEFMAAMSSD TDAR
```

>*Ostreococcus_tauri*|AGC|PDK1|Ot03g02170 Later start site and changes to splicing

```
MIQEQQELVTLPTKLDYFTDVHRSKDTRTIVELPPKEPSEEEEDPPQGFARIFACCFAPKILCFTKFPSPVAVS
VNPPSRLGRSPGSAHAFAVTTARRLACRLAIERARTPPRTPPFEISDFVTVDVIGEGSYSDVREVFLSSRPSERYAL
KVMDKAHIVRESKSRVATERTLLAGRLRECEHVARLMFTFQD TYSLYMGFELCPGGDLFWQLKRSEEGVMEETK
VVFYVSEVLVAVQDCHARGVVHRDVKPENVLIDASGHVKICDFGSALDLRHEVTSALTALASEKRCASFVGTAEY
VAPEILDGCEETTTAVDLWSIGIMTFQLLTGRVPFKGKTEYLTMQERTSTRLSANISESAKDFIDSLLTRDPKKR
LGYENETSIRNHPFFAAVDDWSELRSREAPRVL TATGVGSDATVTDSECDHDDGTD TDEWRARVNAAAAALDAL
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>*Ostreococcus tauri*|CK1|Ot02g06160

```
MSASNGGLELRVGNKYRLGRKIGSGSFGDIYLGTHIKTNEEVGIKLESCKTKHPQLLYETR LYKILQGGTGVPNV
RWYGIIEGDYINIMVMDLLGPSLEDLFNFCNRKLSLKTIVMLADQLVSR IEYVHKSFIHRDIKPDNFMGLGKRAN
QVNIIDFGLAKKYRDPKTHLHI PYRENKNLTGTARYASINTHVGIEQSRRDLES LGYVLIYFLRGLPWQGLKA
ATKKQKYEKISEKKMTTPIEVLCKGFPEFVTFYQVVRSLRFS DKPDYSYLRKLF RDLDFIREGYQYDYVFDWTIL
KYQQTQALTRPTAGLGGQAQAGTSGDQGDQDRTLRRQTTLERQSSATRAAGGKEVLATERSSSFARAYERQRSSS
RPLTSRDDDGGRAYQ
```

>*Ostreococcus tauri*|TOR|Ot01g05130

```
MCAIESEGEDDKDVCAEGSGNGGEERGRGDFLGFRNSVHARVGAMIGSADTAKKMGG LRAIDQLIDVEFGEEVE
KVRKFAEYVLEVMPPGGEERAQTKGEGARHPVDARNPLWGLPSAPQLIELMTAVIGRLVAHGGALTTDIVDSHVQ
RAVDLLETKEKNKEALSMKHAAVRTLSELARNAPTIFNVHVQIVVVAIWSALRDP SLQVREAAVSALRDCLMVI
EQRETRYRVQWYYSLYESCRVGLRSESSVEAMHGSL LALGELLRYTGEFMLSRYREVAQTIFRLQDCKASII RRT
IVLLIPKLAVFSPRRFAESYLVE SCALILTTIRASSDSGAGFEALS QLADAMSHVINLSTISPEKADVGGVLLRY
LPEVSAVMYDLFTTRARDQQTPEAL KCAGSLMNSLNEAWKPHFMNMT PPMFGDLSEALVSGLD FVAKSSPELM
PEIQMKLADSIESAISQGPETVTPNRKTVQ LALRTMRTFFFEAVALLRAIKKNVVPYLS DSSAETRLEAALTCCS
TLRLRVGSSKSATRAVEY IMAALIPVAVGDTDASIRSSLLSDFCRPCASIDSYLGQA KSLRALFLTVNDESVTIR
MLGIELLGH LATRNPAYVLPALRAHMLQLLAELEFSS ESLHREESAKVLAVLIRSCPRFVAPYLSAILNVL TATL
RADEGGSSATSTSTRESMTALKGR LQRTGSSSGS GALTSSIPATLRKRRDVTGREKAAVLGTIGELANVSGSEIKP
FVQPLLALLLIALKSPSTRDEAVVTLGKLI ESSGYVADPFTTHPQLLPQLLRILANERGIARNEVLR TLGCLGAL
DPYAHKANELLIRLHGEVLSADGVRGVRQASL KLAAGTGEDDILDEF LNADGDDEIDVLP TLHLTSLSDEYYPTI
ALNSLLRILRDPTRTSHRLMVIRSI VYIFQVLDTGCVQYLPVNLVPMV LNVIRTSDPSRREDMFVELATLVS VVKA
HIRRYLTDIFELMHLTWDVTGMSKNTILLCEELS FALNDEFKRNLP TIIPSVVAALGAEERLKYDLVPHILHAL
ECFGVSLNDHLYLLMPPIMRLLKHSVIVSVPVEIKKCTLES LRLLPIMNLS DQAALIVHSLTRVLD DDERMELRME
ALCVLTSLEVSLGRDYALFLPVVKRAVSKCGVNDPAFDEMVKRVESGNVLLYPDEELETSSV VATAARKKPD IQRR
LSVNQLAIRRAWESSQRSTKEDWLEW MRQLALDLLKSSPLPSLRACSELAQVQPNLARDLFCASFVSCWAE LNES
HREVLVRSLEAALGSPTIPPEIVSILLNLCEFM EHDEKPIVDVRTLGMIAERSRAYAKALHYKELEFVTNPGAC
VAIIA IANNQLQLPEAARGVLVYAQENLSVVIKESWY EKLEQWDDALEAYKRKMDEVMHV TTPNAMEERREAMAG
QLRCLNALAEWEEIHRISEIATKSNVDWDDYSIDVTTIATKAAWY LGDWEQMEVLTDKLERDQRSQGR LPTADRA
ELVSKHKTSVVNVTD CDFYKSI IAFRKG NQEEARTHLSAARDKLGTEL PALVRESYDRSYRALIRAQQ LTELDEVE
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IEYAQLTAVASPAALQRQEVIRKMRDRYIYLVKRDVEVWQELLQVRSVLVLPMSSEETDIWLKFAALNRKQGRDRQS
RRTLLRLLGYPMLCAEETAGFGAGSGRPKVMFAFIKHLWHTGQKRQAFMRLQSLAHELRTWENQRSSGQPPEV
EHNKTVSRAFLKLGKWRWALTDNMDETLDVLMFRATAADQQWSKAWHHWALFNATAMEHFHRQGGASTQDA
MQHVAPAI SGFFRSIALGGGKTNAKQGGSLQDILRLLTLWFNHGGTAEVETALIEGFGHVSIDTWLAVI PQIVAR
IHTHVI PVRNLIYQLLIRVGRQHPQAVLYPLLVACKSQSTSRRAANA ILDNVRQHSALLVEQAQIVSLELIRVA
IVWHEAWHEALEEASRLYFGEQNVDMMAVLTPLHHILERQGAETLQEMGFVQNYGRELQEAHDLQCQYQMSKRE
EELNQAWDLHYHVKRITKQLPTMTTLELQYVSPRLLNSRGLLELCVPGNYISRATEQAKSEHGKDYGYLLKGHED
LRQDERVMQLFGLVNTLLNSNMTTQQKDLGIARYAVVPLSPNSGLIGWVPCDTLHALIREYREAHKIPLNLEHR
MMLAMAPDYDHLPLVNKVEIFMHAVENTSGGDLAHVLWLKSRSSSEQWLERRTTYTRSLAVMSMVGYLGLGDRHP
SNLMI DRYSGKVLHIDFGDCFEASMYREKFPKVPFRLTRMLVRAMEVSGIEGNFRSTCESVVTVLRDNKDSVMA
MLEAFVHDPLINWRLLTHKIVPDNDENEVQEVALLRSSASDSGNSTPQPKSRGAGSKRPPSVGVVDTSPGVPVSS
SSVIGVEAAHAMAAMSSVRDHPSQAGSVLFRRTELIHALETYGMDDGANEALNERAVSVMQRMSAKLTGRDGEH
HHVDTMLPDTVEKQVRRRLVAEATSAENLSVSYVWGCPWW

>*Ostreococcus tauri*|ABC1|Ot04g02190

MVHGGTVIVRVS DRARKSGSGKARRRRRGRDPYDDLRFGEFDKPKLLRFFRRRPLQVAGRLATIIRVGRVIRQWK
AQESWDPEERTRGAILREAMTRLGPVFKIGQTLRQRPDLIGEEAADELKLLQSQSNEFPNALAWKTIVEDLEWD
GPIAPNHPYRARNPDAEPLFAKFSEQPIAAASLGQVYKAKTWDGQDVAVKVQRPKVVRQVALDWTWCWSLSLSTLK
RLWGTTELDVIADEVGQGVWQELDYTQEAHMDEFNERHKWLGFRAPHWLPEYTGPPGRARIITTEWINGQHI
AALPPEKKLIMAQMAVEACVAQLIYTGFBVHADPHEGNMMLDDNDMLVFLDFGLMSEVEPFIMEGFAGKIQHMISG
NWEGLVLFVQEVGFTPKGEFLKRDDRSPTYKPALEEMTKAVADTLSTEELGGQSRFGALATGLAKLSANFKFLTP
PYIILLIRTFLEGLIAEKADPDFNIYTAALPYAIRRAMAPSTPEGQIAMRNFLNESDELWRDRIEELVLTDTV
DEDDSKESADAENAEGAFGDSQALMARRSKEVVGRLLGSTEGVALRRVANSANTEKIVEYLSGPKGTALRAKSIR
MLSRNLKDLWTARRFVRRATPQIDSLPVWPESEARRIRERQDRAQKRALAFIFGTHMARLIRKPWLLVRLTVT
AYIVVTAFFVYALAVTVWDYLKWLNRFTPWGLVWRLASRGAPSGPS
SDALGSTSVP

>*Ostreococcus tauri*|DSP|Ot16g02430+A4S8J9

MPHVVDSDDDAPPRAAWCRACGHDPGTTTCVCGHRRVDDDDLLDPRPRLGHDEPIIEVIDKFLCLGAFEHT
SKEDVLLACGIRTVMNAPPECTPCCSSKNICVFTAPVKRGCSTTLDLGETVKKLEALHARAMRADEAGAANRVLV
YCMMSGQSRAPSVAVAYLMYSERRRMDALKALQRRYPRGYNGVTIKQKDVDELKMFEAELFPPGAS

>*Ostreococcus tauri*|Actin|Ot16g00370

MADEGEVSALVCDNGSGMVKAGFAGDDAPKAVFPSPVGRPRHHGVMVGMGQKDCYVGDEAQSKRGILTLYPLEH
GIVTNWDDMEKIWHHTFYNELRVDPAEHPVLLTEAPMNPKANREKMCQIMFETFNVPAMYVSIQAVLSLYASGRT
TGIVLDCGDGVSHTVPIYEGYALPHAILRLDLAGRDLTDYMKVILTERGHSFTTSAEREIVRDIKEKLAYVALDF
EEEMATSQSSSSIEKSYELPDGQMITIGSERFRCPVLFQPSLIGMENPGIHETTYNSIMRCDVDIRRDLYANIV
LSGGTTMFPGIADRISKELTALAPSSMKIKVVAPHERKYSVWIGGSILASLSTFQQMWIAKSEYNEAGPSIVHRK
CF

>O.tauri|Ot12g01390 New Gene model Tubulin alpha subunit gene model 201785:
203233 MW: 49240.094

MREVISIHIGQAGIQGTGNSCWELYCLEHGIQPDGQMPMDGSAGQEDDSFNTEFFSETGAGKHVPRCVFLDLEPTVI
DEVRTGAYRQLFHPEQLISGKEDAANNFARGHYTIGKEIVDVALDRIRKLADNCTGLQGFLVFNVAVGGSGLG
SLLLERLSVDYGGKSKLGFTIYSPAVSTAVVEPYNSVLSSTHALLEHTDVAVMLDNEAVYDICRRSLDIERPTYT
NLNRLLAQVISSLTASLRFDGALNVDVTEFQTNLVPYPRIHFMSSYAPVISAEKAYHEQLSVAEVTASAFEPAS
MMAKCDPRHGKYMACLMLYRGDVPKDVNAAVANIKTKRTIQFVDWSPGTFKCGINYPPTVVPGGDLAKVQRAV
CMISNSTAIAEVFSRLDHKFDLMYGKRAFVHWYVGEEMEEGEFSEAREDLAALEKDYEEVGASSAAEGFEDEY

>O.tauri|Ot08g03630 New Gene model Tubulin alpha subunit 601890: 603406
MW: 49658.703

MREVISIHIGQAGVQGTGNSCWELYCLEHGIQPDGQMPSPDKTIGASDDAFNTEFFSETGAGKHVPRCIFLDLEPTVI
DEVRTGAYRQLFHPEQLISGKEDAANNFARGHYTIGKEIVDLALDRIRKLADNCTGLQGFLVFNVAVGGSGLG
SLLLERLSVDYGGKSKLGFTIYSPQVSTAVVEPYNSVLSSTHALLEHTDVAVMLDNEAVYDICRRSLDIERPTYT
NLNRLIAQVISSLTASLRFDGALNVDVTEFQTNLVPYPRIHFMSSYAPVISAEKAYHEQLSVAEVTNSAFEPAS
MMAKCDPRHGKYMACLMLYRGDVPKDVNAAVASIKTRRTIQFVDWCPTGFKCGINYPPTVVPGGDLAKVQRAV
CMISNSTAIAEVFSRLDHKFDLMYAKRAFVHWYVGEEMEEGEFSEAREDLAALEKDYAEVGAASSLSTGYEEMDE
Y

>O.tauri|Ot05g05090 New Gene model Ubiquitin-conjugating enzyme 800704:
801366 MW: 17131.406

MSDKDKAKSLSNSARRIQKELAEISLEPPTNCSAGPKGDNLYEWVSTIVGPSESPYSGGVFFLDIQFPDPYPFKA
PKVTFRTRIYHCNVNSSGQICLDILKEQWSPALTIKSVLLSICSLTLDANPHDPLVGSIAQQFLNDKENHDKTAQ
EYAQG

>*Ostreococcus tauri*|SNRK|Ot06g03970+A4RZA4 (NB incorrect n terminal
sequence removed before genomic gap)

MEGGEDSGTHASGGASRGQAEIYLPNYRIGKTLGIGSFGKVKVAEHVLTGHKVAIKILNRKKIKAIIDMEEKVRRE

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SAGNWSDMSTTSDDGMLRMCHTSLAPTKPRRWTKGDNLGEFSFGSVWLALNGDTGELFALKEVRFSSDKHREE
SIEQLEQEVDVLSRLVHPNIVRYIGVTREEAALYIFLEYVPGGSIASLVHRFGKFEENVIRVYTRQLLIGLSYLH
SQRVLHRDIKGANILVEKSGRIKLADFGMAKVLENVSHGKSFKGSACWMAPEVIRQKNVGFEDIWSVGCTVYEM
ATGAPPWSDCSTQVQIIFKIASSEEIPVPEHLSPDGQDFLRRLCLQRDATRRPEAVALLDEPFVVDHRSSNATN
IPGLQYDTWASSSVLSFRDDEASVRSRSGDGTVGGMRSNQSSMRHVAWGDL

>*Ostreococcus tauri*|TKL|Ot11g00940 New Gene model TKL CTRL-like 169582:

172309 MW: 100334.7 [*Ostreococcus tauri*]

MFSRSNSDDVVEARAHATANAPDRDRIVGVKHEAASTRDSFVREVRDGENSRATDDDASTSGDARDGGGEGSEE
AGNVNGRSGRERQSEGANAGRMALNARRPSRDHERTPNKFLPWLSNTPTLDGTLEKRQETEGWWASLFGGGTEQ
WGLRYFLLYDTHLFWGKGFSTMHGYSVTLSVREVPPELGPSTFAVEMMAVPKRNLRSFNDNVNFDLISGLCCKP
AGFRVMYLRATSPKEMQRWMEGFRCRGTSDTPVSTRMPLDFSEEIPSPRISTDSELSIDTFSGTGTRTRYEEPPP
PLSPGGASREFLNTSPETEDVPLFRLDANGESGEFNHSTQQKSPVTRSVLKSNSMLRNHEQRQSVGNCSSKSVT
FDDHVESVVIARSPVKQQGIVPAQETDREFRTRRLLKAAGSFKISESELQIGAKLIGSFGVVYRAKWNDDVA
YKVMLQDKMNYETVNAFAEEIRMMRGLRHPNIVLFIGAVIQPNRLGIVSELMKRGNLEFLLHGNSTMGRQLRENG
MLRRQMAADCARGMLYLHLSLRPVVHDLKPANLVVDSNWTLVKVSDFGMAQLKSYTYDSVSGAPGGTPEWMSPEA
LRGDKANERSDVYSFGVILWELMTVSFPWAEELSSPVQIVAQVAFHRRLKVPWEIEKPMADLLHSCWAREPEERP
TFEKIVEQLAGEYPAWVSLGQVDSADEQAANILAMMSTGKGASSTEADSADSSNEEEFVDNVVEVSVISAFAPR
GLKPIRTPPTVTDVVKQTDTLDEEDSSEESNSLDAPNGRASASANGTVMTTVNEFRPRLRSRRRAPSSRPRSP
PSQTAPAVDAVRCIITSHPSRALKIALGAVTTNWSTPAVDARPPARTARRSAQKPPAPLSTRTASRARASPARSW
IPRCSRPR

>*Ostreococcus tauri*|Ot12g02970 New Gene model Histone H3 (Lys4)

methyltransferase complex, subunit CPS25/DPY-30 (ISS) - 470097: 470484 MW:
12800.328 [*Ostreococcus tauri*]

MDDARCARSRARSIPRRDGTSDGRDVRGAAIGFLKRARRAEDAPTPSVPREDEPKAAEPSAEDSNERGESVKAYL
EETVSKTLHDGMMRLANERPSAPLKFLGEYLLLEKSRERGE

Sequences for proteins with patched gene models

The following sequences are gene models that have been patched from *O. lucimarinus*. Amino acid sequence was transferred from the most similar *O. lucimarinus* gene to gaps in *O. tauri* where there was a high degree of conservation in the surrounding region. These sequences were used in phylogenetic analysis throughout this paper. Amino acid sequences that are derived from *O. lucimarinus* have been underlined.

>*Ostreococcus tauri*|Ot10g02860+A4S411

MDGERRARDDDDARDARSGGTRASASADEDGTNKSFDFAGCSQSQRDERRGATRGTARSQNGESQEFGGPDFIT
PADAQFDAYGGYEDKENFRGARSPCALSSPARNKRPRFGLDLGASQGTQEFASQPLDATQPSQSQGEFGGGFRVPR
 NREPTRGVGSRSGLPRAATSPPCARNALFLPDDEQPPETSSAHARRANCTSAAQLATMSRFRADFDLGCIARGGFS
 KVHKVIGRLDGCRYALKRTSEQLKNERDRSEALREVHVMASLVTCPQIVRYHSAWENDHLYIHMELCEEGCASR
 MVDSRDGERMNDALQARCLRDISTALAFAHDRGLAHMDVKPDNIFICKEGFKLGDWGRATQLSGARRSSAVDEGD
 ARYLPELLNDNFNDLDRSDVFSLGASLYELAIGTSLPSHGSYQALRQGVVPTGAVAASLHALCVAMMSPIPLD
 RPSAADVLSKHCTL

>*Ostreococcus tauri*|Ot07g04140+A4S0Q4

MGAPRSPGGARASDDDDARGRPSAPDELKNYEKLGRIGEGTYGVVYKARCRATNEIVALKRVMDRERDGMPLTSL
 REIKILQRCAHENVISLKRVIQGETPSNVFLVFEYCEHEMARLIDFVKTKFTTSEVKSLMMQTLRAVEYLHERKV
 FHRDLKLSNLLLNRGELKLCDFGLARTYDPIEAGIYTPKVVTLWYRAPELLFGEEQYTAIDMWSCGCVFAEFL
 KHAPLFPASTEIELMQMICALLGNPNSNIWPGWDSLPHARKFKLPEQPYNFLEINFPKLSAAGVNLDDVLLTFDP
EKRGTATEALAHPPFFQESPPPKPPAEMPTYPSTHSAPERGAERRNAKRSRGALDERIGAVF

>*Ostreococcus tauri*|CMGC|Ot01g05560+A4RRZ9

MRKKERAAPAGDMFGEDSDEEAFYLRDASGEGEGGDGAKVTGGAVDMSKGLTDNWDDAEGYCARIGEVLDGRYT
 ITAHLGKGVFSNVLRAVDKREGEMEVAIKVIRCNQTMHKAQLEIDILQKLSGSDPENKRRHCVRFLRHFEYREHV
 FMVFESLSMNLRVVIKKFGRNVGINIRAVQAYATQLFIALRHLKNCGVVHADIKPDNILVNETKSVLKVCFGSA
 MFDGDNELTPYLVSRYRAPEVILGLPYSHPMDLWSVGCCLYELFTGSIAFPGRSNNHMLKLMLELKGVPVQKVL
 RRALFTENHYDHTGAFAVIEEDPVTKKSIRRLIRDAKPTKDLTKIFTRDSDMSDGERK

>*Ostreococcus tauri*|CMGC|Ot07g04140+A4S411

MGAPRSPGGARASDDDDARGRPSAPDELKNYEKLGRIGEGTYGVVYKARCRATNEIVALKRVMDRERDGMPLTSL
 REIKILQRCAHENVISLKRVIQGETPSNVFLVFEYCEHEMARLIDFVKTKFTTSEVKSLMMQTLRAVEYLHERKV
 FHRDLKLSNLLLNRGELKLCDFGLARTYDPIEAGIYTPKVVTLWYRAPELLFGEEQYTAIDMWSCGCVFAEFL
 KHAPLFPASTEIELMQMICALLGNPNSNIWPGWDSLPHARKFKLPEQPYNFLEINFPKLSAAGVNLDDVLLTFDP
EKRGTATEALAHPPFFQESPPPKPPAEMPTYPSTHSAPERGAERRNAKRSRGALDERIGAVF

>*Ostreococcus tauri*|CMGC|Ot09g02480+A4S2P7

MTRSSSDTSSSDARDVDDVDSRSASSSDEDEGTDGYKRGYHPVSIGERYNDDRYVVVKLGWGHFSTCWLVEDV
 GSGREMNGKVTYRALKIQKSSGSYTEAAKDEIEILTQCKDQAASAEEREELGSDNVVRLHDHFTHQPNGTHVCMV
 FDVLDGNLLTLIKRYEYLGVPPLGKALTRAMLRGLRYLHDVKNIIHTDLKPENVLLTLALPEKRGRKSKNKVV
 DPRKDVKAGTPTLVDQIERLDVASSKRESGQVENDTSKETNSEDDIDCVDLLPYSLLKRLDAKICDLGNACWVDR
 QFTQDIQTRQYRAPEVILGAKYDTSADIWSLACIVFELATGDVLFDPPRSGKDYDRDEDHLALMMELVGRMPKHLA
 LSGKYSKEFFNRSSELRHIRSLKFWPCERVLIEKYNMPEKDAKDLSDFLVPMPLDFNPSKRATAEKMLEHRWLQF

>*Ostreococcus tauri*|CMGC|Ot09g00650+A4S284

MRALGVGLIHHPKTVQSFCEQLLVAVRYVHSLGLVHTDLKPENVLLMSNSYRENATHRVPVDHTIRLIDFGSTTFI
 DRHHSVVSTRHYRAPEIILGLGWSYPCDMWSIGCMMIELLTGEALFQTHDNLEHLAMMQHALSRTIPNAVVKRV
 PKDKLRDLFNRNGALNWPNEKTDAESYAALGNTGVVRQLLEKHLSGEVLVSLFADLVGKLLDFDPKRRITSKSAVN
 HAFSLDLKIDWRIMRNGDGRVLGVKK

>*Ostreococcus tauri*|Ot15g02970+A4S7Z1

DYDNRTPLHVAASEGSFAVADWLVKSGVTINPVDRWGSTPLESAVYGNHSDLVKMLAKNGAKIKDRVSGTFVPLE
ESHLSGVFHTQLPADTMAWEIPDGEFRTSKRLVPALGVVNTGMWPGTKVCLKQLHKHLNADEVAQAEFRLELKIM
 QQLHHPHIVQFLGTTTSTEGTLTSIVSEFMGGGSLEQVFRNEELLSLKLATQMALDCARGMAYLHGRSPLPVIHRD
 LKPGNLMLTTNRTLKIGDFGLSKTLSVRNKLPQEMSQAFNMTGETGSYRYMAPEVFRHEFYGPV
 DVYAASMIYYQLFSFQQPFSGRNPVDACRAARLHAPRSRRLVTRMWDPIVKKRDPDFTE
 IIQILTPVAARYAAQPDASAAGPACCVVQ

>*Ostreococcus tauri*|Ot04g05350+A4RWS0

MRSSSTSRRAANDLARGTALGTHGRYEIVEMINRGGLDRVSRHQLHANLHPAALTTDALVLMTTEMVGLYFLSTV
 LLVREQLPEEYRAIITEALGADLEFRFYAKFYELIFMASAALTVISLYAKHVTAASTVKVPLAARRAQIKYATRL
 MGGNGSNAGVPGVVRLNPNVNHGEDVLVLFELAKGVDALDYINQHGGRLDEDEARRLFAQLVEAVRAIHDLGFC
 HRDVKPENAIVCEDGNLRLIDFGLAKGLESAKTRAVGTPDYMSPPELLDKLDRDGKARTEKYDA
 AACDVWSSGVFLFIMLTGRYPFQDPNRPNNVKATLQNIVKGNVAPLRVDVSDDDVRDLLRCMLTPDPRKRITLQKV
 AKHPWLSGSLGRRKKPSLVDRLKQSFTFRATTSD

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>*Ostreococcus tauri*|AGC|Ot09g00870+A4S2A2

MCVEDFEPLKLIGRGAFGEVRLVQRKDTGEIFAMKKLKKSEMVRGQVDHVKAERNLLAEVNSRAVVKLYYSFQD
DQFLYLVMFEFLPGGDVMTLLIRRDTLTHEETRFYLAQTVAALETIHRHNF IHRDIKPDNLLLDKDGHMKLSDFGL
CKPIDPTYQQAVLPEILENESMGPSDPPRTEDEDSKRAEEVANWQKSRRLAFSTVGTDPDYIAPEVLLKKGYGLE
CDWWSVGAI AFEMLMGYAPFYSDEPLTTCRKIVHWRHHLRI PDDSPISPEARDLIERLLCDADQRLGTHGGVEEI
KSHKFFKGLDWNALYTMTPPYRPVVSRLDTRNFEDFEEDDSMRKKS^{GT}VEGEGAPKDENFIGYTYKNVEIVGEE
VKKLN^{IAR}PSLTSVFP^{TSK}

>*Ostreococcus tauri*|MAP3K|STE|Ot11g01380+A4S4M0 (NB incorrect n terminal
sequence removed before genomic gap)

MGR^TKQ^RGK^TL^TLGE^FFA^ET^STQ^RT^SG^LLGA^RLA^RAV^DGA^TDG^GDD^GDD^SYAE^FT^VE^IGN^AS^VR^CAE^QE^GS^YD^V
RAFAREGRNAGGKVIKSVTFVFGKMGERRVTEAPFEVQYRCETSDVDEVAVQFHRALNARPVRELHAIELSSEE
REFSRSFAVEVKRRALMKVLGKDKGDAEVDVRRRAESRS^SLL^EES^SQ^SR^GV^DAW^TV^QD^VSE^WL^RS^IE^LE^EL^VER^FAK
AKINGYELLRLTEKDLRESLHLERNLERVRAIRAINVLRASAGAADAENDKSATPPLSAPLGAPRGGLS^PLE^LE
LDVSWIEFVSEKARASVLI^GW^FM^HV^LDE^VK^AKE^FDE^PG^PQ^LS^VY^CE^AT^LQ^AS^KS^CE^DA^LE^ER^VL^DI^LE^ST^PG^WD^P
RTKMFPSTCDLTKLNDQ^LM^EL^YL^EV^KA^FE^EF^AA^LN^MD^DR^GE^HE^RS^RS^TP^PK^MP^GE^SS^PA^IP^RL^NR^AE^SL^TT^PS^V
SGSPTFTSPRNDMGPS^PSP^SGL^NV^GA^RS^FS^PT^PL^SD^LT^RS^SL^PE^LQ^EDE^VA^DG^DR^VM^EL^NT^EW^EI^DY^ND^IE^FE^G
VPSSKNRIGHGGFGEVFLGRYHGLVAVK^LF^NQ^DM^MG^KL^QD^FR^RE^VR^IL^SR^LR^HP^SI^VL^WL^GA^CT^QA^PN^LT^IV
LEYMDK^GSL^HQ^FL^HR^TT^TP^YT^TL^TL^TR^WA^MT^IA^QG^MV^YL^HS^AK^FP^FI^VH^CD^LN^TN^NV^LV^NR^DG^MV^KI^TD^FG^LS^KV
K^HS^SR^LS^RQ^TG^MT^GT^VN^YA^SP^EV^IR^GG^KF^SE^AS^DV^FA^YG^VI^LW^EL^LT^RR^IP^WE^DL^NE^YQ^IV^FQ^MT^SD^LD^AS^LA^AT
A^KN^LE^LP^AS^AP^EG^YR^KI^IH^GA^WA^TQ^PE^RR^SA^FK^DV^LG^DL^RE^VY^RE^QV^DI^EK^AL^RA^AR^KG^ST^SS^LS^AT^SA^PD^K

>*Ostreococcus tauri*|MAP2K|STE|Ot04g04050+A4RWE8

E^CG^ER^DG^FI^SE^CG^ER^DG^FI^LG^AA^DL^EL^VG^VI^GT^GS^GG^VR^LA^TH^KR^TG^EA^LA^VK^TI^AI^SL^AR^DE^NE^RK^RI^VT^EL^R
T^LH^KS^EC^DY^IV^RS^SG^AY^FD^RG^SV^SL^VM^EY^MD^GG^TM^SD^AT^KY^LG^KW^VE^QD^LA^AA^TS^ML^AD^GL^HL^HT^KL^NV^VH^RD^I
K^PC^NV^LL^NL^RG^EA^KL^SD^FG^VS^GH^LT^DA^SK^CH^SW^VG^TV^TY^MS^PE^RI^QG^ES^YE^YT^AD^VW^SF^AL^TM^VE^CA^LG^RF^PY^NP
P^DV^SR^RL^VF^WD^LL^DI^VV^QD^PV^PN^LR^PE^LD^VS^DE^FD^NF^VA^LG^LN^KD^PT^GR^ML^TK^NM^IA^HP^WI^FG^RD^RA^SD^KR^RI^AA
L^AA^RH^LD^AR^SK^AR^ER^EG^EK

>*Ostreococcus tauri*|ABC1|Ot08g00750+A4S118 (second gap patched)

M^PL^TS^RP^LQ^TR^EN^QS^NR^IR^SS^RA^PF^QR^LN^HT^IH^RP^RS^LV^RP^IH^LA^QP^HV^HR^VL^LR^LS^IR^IA^PL^SS^TN^RR^RR^RR^R
A^RV^SS^VQ^RP^RR^SA^LS^HE^HS^LD^RS^HR^SP^AR^RP^RP^RL^FL^PL^RA^LT^PV^HA^LR^ER^RH^HT^NQ^GR^HV^PE^QR^IX^XX^XX^XX^V
G^RR^TT^GD^AD^DD^DG^DG^RD^AR^RR^TG^RG^VH^RR^AR^AH^RS^AD^PS^RR^SW^NR^FG^LA^RL^RP^RR^AN^RL^RK^LA^TT^RE^RG^TA
L^AI^SG^PP^VI^GK^SL^EE^PI^EA^FN^KV^GF^VG^KL^RF^LR^AV^GG^AA^FG^VA^AA^SA^TL^RC^WA^PK^VH^GA^LT^VM^LV^AC^AS^TK^R
G^GD^GA^LV^RF^VE^GK^VP^GK^LG^RA^CV^RA^MA^AP^KS^AR^GT^LR^RW^AT^WQ^AI^RL^GM^RL^TA^RR^QQ^RK^VD^YS^MR^VA^PV^IA^SY^M
I^AK^RR^IG^RI^KE^VE^RD^VE^WE^KQ^HH^WG^AA^RM^RD^VI^ED^FG^GF^YR^KV^GQ^IA^GT^AK^QM^PA^PY^IE^CF^SK^TM^DN^NP^PV^SF
R^LV^RR^TL^EE^GL^GP^LG^HF^AE^LS^RK^PV^AT^AS^IA^QV^HF^GR^LL^DG^RE^VA^VK^VQ^AT^DA^AM^IG^DI^ES^ML^ST^TR^AM^RW^L
G^LD^EG^LD^FP^TI^FR^AY^LD^VI^EE^EF^DF^TI^EA^SK^MD^EF^RK^VL^DA^AG^LD^RL^AV^PQ^VI^TA^TR^RV^LI^MR^RV^RG^VK^LL^TL^F
N^RA^RA^TN^KI^PR^CP^SP^VA^QC^HA^VG^GF^GW^QG^VF^HS^MF^MA^WG^TM^ML^KH^GH^FH^TD^PH^PG^NF^MV^AH^DG^KL^IL^LD^WG^QT^KR
V^SE^VE^RM^HM^CR^LS^LY^MA^NE^DH^TN^IA^KE^IR^SH^GS^VR^LE^RP^TE^AL^SA^LS
Y^AY^FD^TR^PS^PL^AE^MN^VM^DF^KN^SP^FV^QN^KI^LQ^NT^QE^GF^FA^IR^SV^FL^LR^GM^LS^TC^AL^RM^SM^VQ^AW^EP^IA^RS^AM^IL^NG
E^AP^PS^RF^RL^KT^QF^II^NR^SL^LG^FQ^RR^FN^VG^AR^VN^AV^DE^YM^ST^KR^DK^DE^AN^GT^LW^PN^SS^SL^F

>*Ostreococcus tauri*|ABC1|Ot03g01200+A4RU11

X^PD^AL^AP^WR^GE^LR^YD^VE^AF^EA^YF^KR^RP^MK^VL^RR^AL^VV^AY^EL^GA^IG^LG^VA^AR^AG^ER^RR^RA^QR^LS^ET^LA^RL^GP^AY^IK
L^GQ^VM^ST^RA^DV^FP^VE^YV^HA^AT^SL^ET^LE^RE^LG^LG^VD^FF^EK^FH^ET^PV^AA^AS^LA^QV^YR^AT^LP^GG^QD^VA^IK^LQ^RP^GL^AE
L^VA^LD^AV^IL^RR^FA^GF^VG^YW^RN^FK^SD^VV^GI^VD^EL^VG^RI^FE^EM^DY^NK^EA^ES^CE^RF^RA^MY^AP^DG^AG^VL^AG^LV^YA^PR
V^VD^FL^ST^AT^VL^TM^EG^IV^PN^EV^LD^RG^LR^AS^SA^AD^VG^IM^HT^DP^HP^GN^LI^VA^EN^GG^LT^YL^DF^GM^TV^EV^PI^ET^RR^AM^V
R^GL^IG^FV^NR^DA^RG^LV^DD^LK^VM^DF^LP^PN^VD^RA^AE^EA^LR^SV^FA^GE^ST^TK^VR^NS^ND^FM^GV^VS^QL^ST^AL^MK^HG^FR^LP^P
Y^FS^RI^LR^AL^AA^LE^GT^AT^ID^PS^FR^VV^DR^SY^PF^VL^SR^VL^SD^RS^PE^MR^ES^LR^RL^LL^AE^DG^SI^RY^KR^LI^RL^IR^AY^GV^E
A^TP^MA^SE^TE^TR^SD^CR^QA^LD^KT^IA^GL^SE^LA^SG^EK^ES^LS^GE^DE^AR^RA^TK^TA^ME^DA^LR^FL^LS^DR^GE^TR^ER^LI^DD^FI
A^AF^EA^LL^DE^DS^GS^KT^DI^PE^GR^FT^VD^DA^IG^AA^KS^AA^TA^VG^DN^PD^LW^IP^VL^GR^AA^SE^RE^TL^AA^LR^AS^SR^VA^YD^RL^IK
L^RA^SR^RS^LG^RA^PC^ED^AK^EL^VR^KV^VH^AL^SA^PK^SP^ET^QP^TR^DS^SV

>*Ostreococcus tauri*|AGP-like|Ot06g01800+A4RYP1

M^TR^TT^DG^TR^GV^AD^AS^RE^GW^TT^RA^RG^AS^GR^RR^TV^GE^RW^AL^DD^AT^LG^RG^SF^AT^VW^RA^TC^VK^TG^AV^VA^VK^EI^AC^ER^LS
K^KL^RE^SL^KL^EV^EV^MR^RM^RD^EN^IL^RF^ID^MQ^SS^NE^TV^YI^VL^EY^CA^GG^DL^SQ^FI^RR^NG^RM^NE^TS^AR^RF^ML^QL^AR^GL^KA
M^RK^AQ^LV^HR^DL^KP^QN^LL^LT^SN^DL^NA^EL^KI^AD^FG^FA^RY^IR^DS^EG^MA^DT^VC^GS^PL^YM^AP^EV^LN^YQ^KY^DA^KA^DL^WS^VG
A^IL^FE^ML^VG^TV^PF^TG^QN^QV^QL^LR^NI^QK^TE^FK^IP^IH^IA^ED^LS^PA^CI^DL^LR^GL^LH^RN^AN^DR^IS^FE^DF^NH^PF^LK^SG
T^VG^VG^IP^SK^SG^AT^KS^QA^QE^SD^GA^SS^AD^SE^TM^PF^NM^DV^ES^NS^PS^TS^TR^VN^GQ^PQ^ER^TI^S
Q^PV^PM^LS^RQ^SS^AS^GK^MS^IA^SD^YV^LV^SS^PG^TS^IP^RS^MR^PP^SL^GS^SP^LS^RM^SL^SP^ND^GS^PG^TF^GR^AR^MS^RG^TS^PS^S
Q^PM^TL^AT^RY^QT^QS^QM^LV^TQ^LG^VR^VG^VL^EK^AA^VV^LR^DT^ST^EH^WN^VG^NK^LA^AL^SL^GL^VS^LA^AL^RS^AH^RL^AS^EI^VT^TE
Q^KS^SV^NL^SG^TS^AS^AS^GN^SS^PT^GG^NS^MA^SA^KK^AT^VR^IK^EA^YQ^AA^HT^RA^EK^AA^DA^CR^AA^GF^DM^EA^QL^PD^GM^EL^V
E^NV^CK^LA^KD^GV^RE^EL^AE^NK^QV^AL^DI^YG^RA^QT^LL^QF^LI^GE^GP^SL^HI^TP^PL^VI^DG^TH^AR^LS^SL^SA^TV^AS^RQ^QS^LV^R
L^MR^GV^R

>*Ostreococcus tauri*|Ot08g01230+XP_001419308.1

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MGLSTYEQQAERLMSKSATTSMRLEVATSVRDGIEIVHTSEYVNFLLKSCFPAPKEILTKHTSPTMEDNEMNALRH
VVYEILNRLPFNEVLRPYESELLDLALESLREENEKNALLCLRVI FDLHRNFRPTMDKRVEPFIRFVHDVYEGSG
VTIDELLGSSGSTRKRKSEEKLPAPCELP SHKSFKVMMECLIVMLVYQLYNRDKFIQQEVEKMI PLMVKFTGL
QTIDIDSMSAGQREFSSDLKSAQVKTI GFITFLLRGNVSVFVEPHHEEISNAIVSLLRTPD VVATRKELLIATR
VLSSPPLCKGFFQHLDLMMDEDVIVGTGRMCIENLRPLAYSFLAELVHHMKAELTLEQIRRAIHI FSRNMQDETL
PLSTHMTCVRLMHHLVESVFRMRTDASRATEAREFLVRIMYATVAKFRTRLRNIPELLKTASGLEAAVKAKASKR
SKDAKADGVAETGATETPNKSASEKKESSDDPEPDLPSHEKLRSLSDNKAI IKTLTIGMKTLLWSITNFNNGSESV
DIGLNRSEIKRASGFIRNGVKCMQLFNGTECTEMCTHFSEALLVLEPRNFVDMMSLHFDDFFAGMLELPTMVQVP
HLLLQNTKLCRYFADAAMTYLLEKKLECLRQSSQEAQLVLKLFSLLLHAI SKHSHCESVLSTHVI FMMDACLKA
IRENDNPSAYVRLRLRYLFRAMAQAKFDVLYQEVVPI LPATLDCLLAMLNGPDPLELHDTVVELCLILPARLSSIL
PHLPKLAMPLCRALRAHANELNLLGLRTELEFVWVDSLNFELDFPCIAEVESELMLALWAMLKPQQSGSPFAGAKAMQ
LLGKLGGRNRAFALKNPLKLDKSNPEHGLRMI LMFKPDTSFLVPLDRICIPSEALVRHRRQALTFIRTCVLSI LNL
SAARALYGTVEEIESALEAAI SNGWGKKCEAMTGEVATPQLGNKTKGQLVAEQNI FKRLVVTVIAAECDSLKET
DEKFMNDVCEHVALLFVNSATCTPGEDTDNMDHDSVERPRATNLKVLETTFLDALMTSFESTKQIYLTATVKAL
ATFLDAVLI LSRDELQSLQTADDSLEKQRTPKSKSKKKTDIHDDSPYPI LASLVEAVLPRFVHCCYKREPHSII
GGVEGFNLLIERLPTS IWRRLPDILSANIRAIQ LLLPAHAPAQKKRVEQVFLQVEKFI PAEVS PRGDDAPTGV
AGVSVLVDDEL CNLSSTCASRAA IERALLGI SERTSTPMDTVLSITDEKLMTVFERPLLTRHVL S QIQTVKLINFC
LNASPHLITFRDKWENNLRAFINEAL TIAEVEDPTIMSVETRENEAMSTLRQSCVQLISSALKAPEFSADTAAE
LTVIRERISTVLFTSLTSRNKVIVEIAKKGLVEVKPYMKNKTLKQSVS P ILMNLQHLSKLSVPLLEALEY LLELL
AEWFSPTLGEKLLHEHIKYWIELDFSAPAVPGQLRKS PKDAKLIAAIVNLFHLLPKLRDKNELKPKNEKRLLPDFDI
KPLVRDIMVIESTMP PASVYSSAHS LFIVPLTKFLNRYPKESVAYFLARLDQPEHFARFVSI LKLP EAADL LKTI
TSSSSKLLHI IFGAGKGEMDEIDKIAVEGVEPIEDTKLAYNGLQLLATIAKLPDWLPKEKAI LKQLNECWDSN
DRAATLSDESKVSLPAMMETKYLAKCFLSIVKNDHSQVEILFKI ISVLC TRSSVDFTFVREFVKNEVVERYTPAE
RNAVLKQFLKEFAEQLEAIEDANPDHVTC SLKVMVNPMLKSLTDGRDDDDGEP SDKLLEIVTDDFVSELVTDVFE
PSDGGNDALYTESVLIQ LQLSTLLIRYVPKTLVDHRKELIKFGWNHLKREDSSSKQWAFVNI SYFLQHVVALLR
AYQPEQKALVTEPSKAKKEECEAKSAGRSTRASRSSKAPKDDDDDDTADEMMSDLPETETLNSMPSIGVIDEGF
KPSPAMEEIVNFLVRMTFITCEGKEQDSKELNTRTVELLSTALEMWP SARIKFTFVDKLLTLANQSNRDPSTL
LMSLSVLRAMKISDYKFFSENVEQTL SLIEPCLSSSTSERAHSLAEVVGMAFDRFKSKDNTEPESECIQRHQPI
DRVYTRAIADATVSKSLPNAEHASTTLACTLKV MATEGALRTAMIDENLPKLMKVLARLTHEFNQASAAIGLQPI
HPKRQGTPEVQPEYGSVANCMMVCIDI I SKRVINAGSEQKQIFLRLLQLLINDKSTHGNVLMAILDAMI AWAD
DSTLGEAVSDDERNRSGSLNAKETVFLFLSKLAQLTRMGLAI TQTQEWEEKLLNVTYKLC SAEGKHEPALRSEVF
LKVERLHLLGLRTRRPELRK KFFSLYHEVIGKSLFQRLQYILCIQDWDAMADTFWLMQGLDLILSTLAEDERIML
APNSALISPLLPIDLETKNPLPVPSPKPKNAKSN SPELDELIKRHAKFLHEKSNISVNDLMTPLRQVATRNAHIAY
YLWVLIFFIVWATLQREEQLQ LAKPMIGLLSKESH LRQA AVRPNVIQALLEGISLSQPQLKIPSELTKFLGKTFN
AWHTAIALLENHVVRYPQEARCFDALSELYRLLNEQDVLAGLWMQRCHSDVTRAGLSLSQHGHWQNAQEVFFEGI
QLATAGQAPGVSKTEMCLWETQWLN SAMQLNQWDLISDFSRTVEHSEL MVQSMWR LSWAGVKELLP SGALNETE
ETPEITTVRAFASLVSGRVREAEQHWANAVKSSLD RWWRLPETGSTCHI PSLHVFNAIAEVQESTRILLELSNTQ
RRGAQGLANNRTLVDIMETWR LRPNEWQMPWWEI LMWRGNMHNIMTHAAKQIGE QNPAMLQVTQQLDQLGQ
RERAWSLNKFANAARKQNLPEVALN I LNRHQGQIEVSEAFSKLREQCESYLSLGDEAVTGLNLLSESQSLEFFAPP
QKAELFRLRAKFQEQMEDYS GAYTSYATAVTLCKQLAEGWISWG HFLRKRHRNEG TGLMQATTCLLQGVRRNNVQEN
RHELLHVVRMLAFDANTS AVGGAIMRHLEYLPKWVWIPWIPQLLLSLGHNETQYARSILLQIVAAYPQALYYQLR
TSLLERRDAAARATQTARKLAAKDDKEGKSEAKASYADIQAAAQRAQEATIAFEAAKEVMEQLRVRNTNLVGELE
VLLSELGTQFACTPEERLLVVVCTLLHRCYKYP AATTGEVPENFKKELIGVYQACFSADTSVKHAD FVKEYKASY
ERDLNPEQKTFPKTVAELMSKLGWKQRLMNDVEDSL PASLRLEDESMALRHVT FNEIEVPGQYANISYGVTD RF
MKNLRIGADVHIVRRNGNCFRRLEFLGTDGSIKQFIVQTS LTPAARGEERMLQFLTNLNDVFAKHAETRRRNMCY
YTPAII PVWPQVRLLED DDDNHGTYQEVYDANFARYGREADLPITL FKAALDPAILGEVTGAEDVLELRKALMEI
TQKHVTENI FSQYMYKTL PNSSHLWTFKRQLSQQ LAMSSFLSALLRIGGRTPNKIMFAKNTGKIFMLDFHPAFDQ
KGIVEYIEPVPFRLTRNLHTFFTFPGVKGDFVASMASAAQACTAPEADLEAHLELFFRDQLMVWPWRRMGGDTPP
VSPSPSEIKNMARANVQEVLRRLPI IAPTVP LPDTS DTVPSVQKAVLHLVDAALNIRNVSRSAI WAPWY

>*Ostreococcus tauri*|Phosphatase_2C|Ot03g04580+A4RUZ8

MRASVRACAGSGALDAVSDGENAAERNFGDGETGTATGDLRGRTYVVTGTETSAIAAACARRLRDAGARVVCACV
DANEARARVDGDKGDRDEDATTANTAHERELRASGALVTMYCDVERLETIERFAREFCAKAWALDGV LNAASTT
MEEFSLTADGIERQF AVNHLAHFKLTALLMDELVRTAAASGREGRVVYLT SNLHHFSFRIRQGT PKPSRGIDFAN
INSDFGYSPLNAYGQSKLANVLHAWLSERLAKSGARVRCVAATPGLTELELDRSLSFPGGSLISAPLKYVMINT
LEEAVVTPLYCLTAPTIPPGTYFNNCV PVKASLPGRDPR LAARLWEFSEELCDAGASSVRATARS LPAYLYYRLT
RGGRTHDPGYIEQLSGTRAERLTNF IARTQVEKAAPWWIWI VIACATIGISFAGVLLQNELYETPPI TRACWRLT
LTTFFLAPMGAWERYRWESSAERDKMRAGKTWGI LLGSGFALGVHFAAWVASLDMTSLAHSLLFVTTSP LLILVE
NAIFRRHRPTNMETAGVFI GLVGAGITLLDIRDDKEVTAKGDALAF LGAVAI VFHIECGRTLRTWMPTTVYAFPV
TLIAAVFLALFALVFDERE PVFGWASSAKISWFVLLAFVSGI IGHAGFN FALGYVSSLVVSISTTMEPVIGTIIG
FLTYGTSTPKLFTLLGGPLLLAGIRADAGGAASVVRALGDACDGEASGTTVVLALVRS DGFVAVHVGDSAAYACE
TSGGGVRRARLTEDHGLGNARERARVRAEGGTIVESRGAMRVGG EYLVTRALGGTARRARGVSQTPDVVARRWRT

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NELGLIILTS DGTTERLKPDDACAFVVFAGKRKCD E SAKVDTSIALDGD AASSTQSS EDAWDTVEVQGNSEVMNERV
ERALKCALELGS SDNVALAAVSAGRHTQITVTVQK PSSLVAEMLSIGSNIEEYKITQLVAVSSGPYLPKTPFR
YDDMYDEEPQPTYNFGRKFEQSAIEGALTALALAPGKGEKNRVQNAITSVYVGIIDSRLARGQDEGVRAGERPFAR
GHFGEVWRAKLSRQLTAQKLE CASSAVSGDSSTVIMKRILVEQDLDLQLSADREYVYFGRLLCGASPHIARYMHTF
DKIPPSGRERWLVRDEGESLERL MYAPESEVGGDSATLQLVVSQSDWWR ETRRSATGRRVLKTI LRQIFA AVNVS
HSNFGVVHRDIK PANVFRVFRDDDIVQAKLGDFGSAMDTRRRRIQLY GSTGPSAAQETA EYSPPEVLFGN DLIERTL
KYDIWSLGM MTELLSLGSPKAFSHISRKTRLALERELRE VHPTARAVAYRLRAMLELCIVPPDTQVGTLLSWE C
TEVALMNI FKARDPLGVGLESIWALRLIRKLLSWDPNERPSAAQALEHAFFRDGD ERGWKCGADASEHEWKSRC D
ALCASPT

>*Ostreococcus tauri*|Phosphatase_2C|Ot09g03800+A4S313

MGAYLSQPVTRKDSTDGADARFAYGTTAMQGWRTNARDAHATIPELDGRTAFFAVFDGHGGKEVALYAARHLHES
LKETEGFEGDGDALKGALEESFLALDRRMLSKEAASELRALRSGSGEEEDGALGLVRTGANAE EQNRRAEINA
KLRAALIEQMKEQDPNIDERDIKFDFELEDSDDFEQPSSSEDGGVDALDRWSGPQAGATSVVVCIRGNNA YCAN
AGDSRAVFSRKGVAEDMSNDHKPMNEEERKRIMNAGGFVSEGRVNGSLALSRLALGDFEYKRNKDLSEKEQAVTA
FPEIREFELREGDEFMILACDGIWDMSSQECVTFVRERLIAGAKSETFKISRVC EELCDACLAPDTRGSGLGCD
NMSVVIVLLQKFWQPTSA

>*Ostreococcus tauri*|Phosphatase_2C|Ot01g02430+Q01GJ0

MRVNAWRSRGRGGGGVGTTRGGARRARGGTAARAAAATRLLEVSSAGAILVPHPKADKGGEDACFVLKQSGAFGVF
DGVGGWAE EWVDPAEYSEKFAEKSAQSVLRGTRDPVAVMKDAHDETVIGSCTACIAMLKDGNILDVANLGDAGA
LVAREGEVVYQTSPPQHEFNLPYQLGWAKVYPEGDRPEASERSEISLSPGDVVLVLSGDGLW DNVPHAEVAALCAE
HNGDAEECAEAIATLAFGYSCDPEYDSPFTQQARAVAE TRPEWGDRRS IIGGKMDDIAVVVAFIDSER TLS

>*Ostreococcus tauri*|PP|Ot10g01220+A4S3K6

MLGATFARDGRARGFDDATNARFTTNQRHGDRAKTTRDDASPGARCGHTLTALRWNQRTKIVCFGGATELEGAS
ASALGDGRGGSPLHGGGRDGTNWWKLSGATSDLRVDFPQGGEWDELKSGGDVPSARAAHGAPTVGGMLVHGGIG
PDGLARRRLVRVSGSDEGSERYAHVLSFVAQRFLVVI GGTDGSKCLGDTWVLDTTTKPYAWSKCNPTGPTSPRT
YASASTRTDGLLLLCGGRGADGMALNDAFGLARHRDGRWEWAEAPGKAPTRRFQHATAFVDTRLHITGGASAGGQ
LVPEETTMSMLDTSAGGSTGWRECKRDGPKTGLVQDANALVGP RCRHASVSYGPFIFVHGG LRNGTLEEGELTPC
AALRHRLSSSLGGAWTSGGAPPSFRVARVNE DSKAHANLVLVSCVSSRGDDYITGGWGDTLRTWRWDP TKGLSGG
APMTQHNDNVEFASVDVREDHEHLAISGGRDCTVRIHNDVAKRSQRGR IYAFENIASGCVWPSQTVAVGSRGGA
VMLWDAEKGTKKCTLRGHEGEITSMCTYDWNTRDTFAINTQRDATYSNGSFS SPSPEVTLRPLGSSPSSPDS P
EGMNANAEQELRHASAQEA AAAALDLVARRKFSLGGSDSGSPGGSSVHTPSPGFAGLGS PGDARRTPASEVRLHHR
AVVVAAAPYDSESKSTPRGVASMRQLSIDQFENEARRIGTPGADMYTPGDTPAKLARARRAAELGAQPVHRVVI
THLLHPHTWEPSQDRRFFLNAAA INELCDAAEHCFKNEETVLRVNGPAKIFGDLHGQFGDLMRLFAEYGS PSTAG
DIAYIDYVFLGDYVDRGAYSLETISLLLALKIEY PNSVHLLRGNHEESDINGLFGFRIECVERLGEAVGDQVWRR
FNSLFEWLPLAAVIEDRICCMHGGIGRSVTHLSQINDLKRPLTMENGGVELMDIILWSDPTENDGIEGLRPNARGP
GLVTFGPDRVRAFCE TNGIQMIVRAHECVMDGFERFAQQQLLTVFSATNYCGTANNAGAILVLGRDLTLYPKLIH
PLPPIAMESLSPSDRIDDNLWLQDVNRER PPTPRGRFGQSQPTIGLINPI

>*Ostreococcus tauri*|LST8|Ot06g02150+XP_001418442.1

MPTPSVVLATAGYDHTVRFWEATRGCYR TLQYADSQVNRLEITPDKRYLAAAGNPHVRLYE VNASNPQPVTSYD
GHTGNVTAVGFEP RGSWMYTGS EGDGTVKIWDLRAGGYQREYESRGAVTSVVLHPNGTE LMSADQNGNIRVWDLTA
NACSC ELVPEVGTAVQSLTVAGD GSMVVAGNSKGT CYVWKLQPGSKTTAHFEPLHKLNSHNGYVLKCLISPDCRL
LATTSSDKTVKLNLDGFKLERVLEGHQRWVWDCVFSVDAAYLVTASSD T TARLWDCSTGEAIRVYSGHKAVVC
CALNDSAVSDAVEAETDINS P

>*Ostreococcus tauri*|RAPTOR|Ot06g01080+A4RYH6

MKISPCARMQCWIQPMTTQPQNELDAIGKALQAQYERWQPRAKYKQLDPTTEDM KKLKISCRRNAKNERVLLHY
NGHGVPRTANGEI WVFNKS YTYIPLSVYDLHSWTGTPAIYVFD CSNAGLIVKSF LKLSDPAQPPKAGVDLEQ
RQSGGSM AFAQLEHGMRSGVQDSGFGPSATANSANECILIAACGANELL PQSSELPADIFSA CLTTPVKMALHWF
CSNSVLHEHGITVDIIDKIPGMQNNRKTPLGELNWI FTAITDTIAWNVLPRKLFQRLFRQDLLVASLFRNLLAE
RVMRANNCTPISSPRLPPTHQH PMWAAWDMAVEQCLLQMPSLISGDPDVEFVPS PFFTDQLTAFEVWLEYGSEHD
SPPEQLPIVLQVLLSQSHRLRALILLGRFLDLGLWAVELALS VGIFFPYVLKLLQTTAPELRQILVFIWTKILALD
RSCQADLVKDDSYNYFVRFLQSSSVPEERAMAAFI LAVICDGHEKGQSVCLASGLLNICLSNIHDAAPETGSP
FFLRWLCLCLGKLWEENFEAQKVACSAKAHEQLIPLFSHSSPDTRAAAVYACGTFISFGCVRESHQDDDI DRQES
HEPLMHAMSSQNLGTKTSGSGSADTPNTVGLFISP GAIASMEIT IAYQLLR TAEDASPMVRIETAVALARIATA
HSMMIRESLVAWKR DYDSVTAKRVVDAKRSEAMGVRRRRFS SGTFSFGMDHSLGNSMSTVDEDDNMPMSVESVARS
ADEQYATSDNTMPTTAGTLPPPPFRSHDSADPVE SRTPEGTKGTVYTLILQALLNLATDPVPAVAKAGCHALHAA
DIDQSHPIQMVTKAGNFAEVEPVVRRLSASQRRRPSFASLDFGTHHERSFSKDVGVSPNGGGLTRTDSWHQRLA
NLGS SLGSRLLGSPTKSKPVSKLSGNRSEQQLSPSTG SVGLRTSTIRGKGRKSQALDSPVSSAGHLPALVIPSTR
TEQLRNSPTSLSLTLRRTSNLITDHSVEQDSL GQQRIFGSHASLDSLDSTLSPRLNRSEAMHG YASDDVHDAQLP
KSIIYKRSCGHFSTPLLETAQDEDDDDDDDEIESSISPWMRPPDMKRRAERLKMIRERSKETLGGGERLKMTEYV
SSIDVGGGVTP TSI LMFPEPFAFTGDSTGRVHIWNHNS SRMVNKIETGMKSVNLLSLVNETDDALLTGCEDGT
VKIWRSYDSIQKETLVTAWNTLPAQPIVSENGEIRSG LPLSFYKPS THYKAHESTQAAI VWQQLTGCLYATGNAP

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NPFLRVWDVSSEICRDTLNLAQGTCLTAEGALLMAGTHDGAVLSYDLRAPARLLSAMQTHHTTPVISILLQGGV
NNLLVTGCSEGQLKFCDLRNASKPFLITEVTHCARWSLACSSHRIWFIARVIASGSSERAIKLWDLRGHNFAAIQ
YTNSFLGQRIGSVTALAFHPNSAYLAAGSNAGHATIYGPHF