cells

MDPI

Article

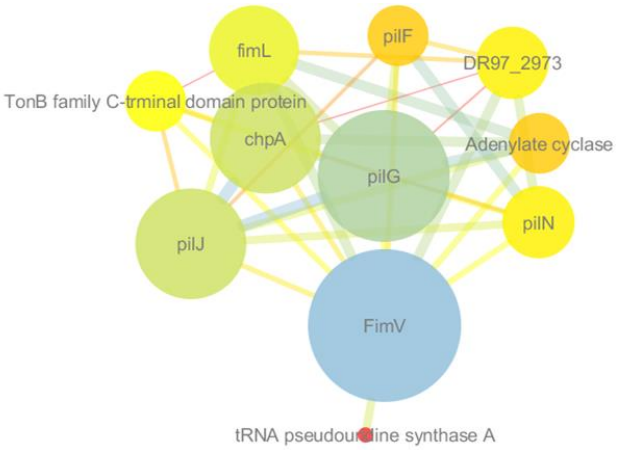
Novel Modular Rhodopsins from Green Algae Hold Great Potential for Cellular Optogenetic Modulation across the Biological Model Systems

Mayanka Awasthi [1,#], Kumari Sushmita [2,#], Manish Singh Kaushik [2] and Peeyush Ranjan [1,*]and Suneel Kateriya [2,*]

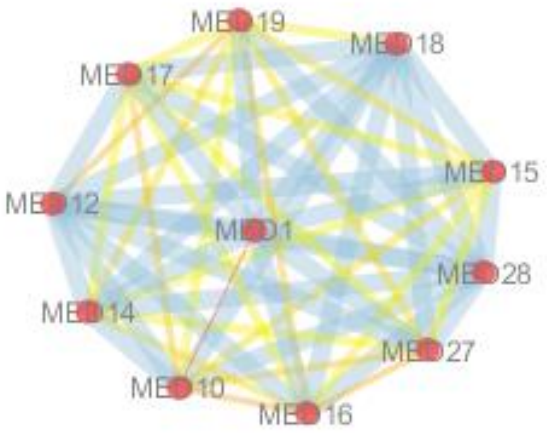
[1] Department of Cell Biology and Molecular Genetics, University of Maryland, College Park, USA.
[2] Laboratory of Optobiology, School of Biotechnology, Jawaharlal Nehru University, New Delhi, India.
\# These authors have contributed equally to this work.
* Correspondence: skateriya@jnu.ac.in (P.R.); rpeeyush@umd.edu (S.K.)

Published: xxx

Supplementary Material-1:

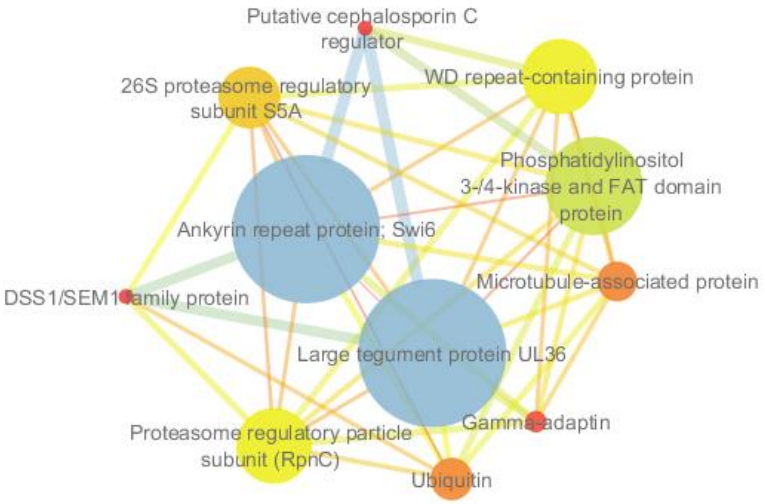


(**A**)

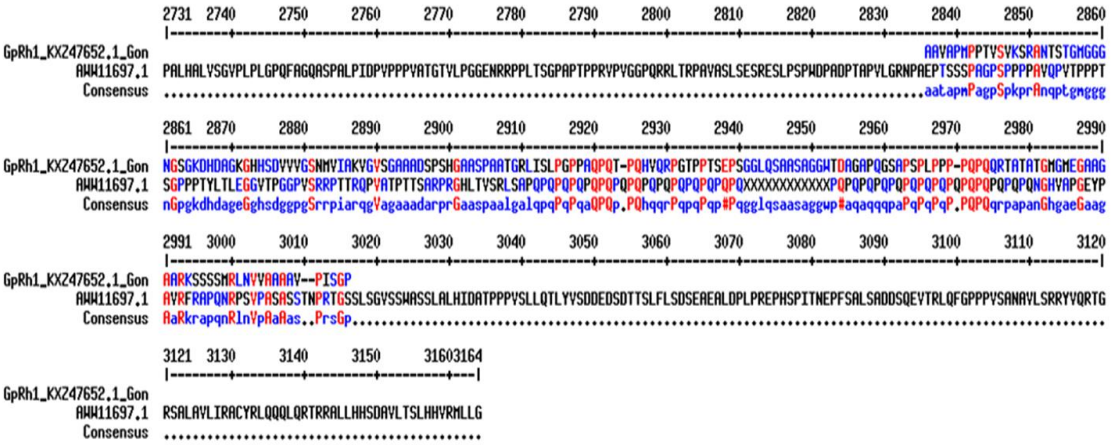


(**B**)

Figure 1. Protein-Protein interaction network showing interacting partners of (A) FimV and, (B) mediator complex subunit 15 (MED15) domains of modular ChRs. Protein-protein interaction was performed using String version 11 (https://string-db.org/) and further modified by CytoScape 3.7.2 using node degree analysis. Size of the nodes represent number of interactions of each nodes and Color scale represent combined score from low to high degree values.



(**A**)



(**B**)

Figure 2. (A) Protein-Protein interaction network showing interacting partners of UL36 domain of modular ChR, GpRh. Protein-protein interaction was performed using String version 11 (https://string-db.org/) and further modified by CytoScape 3.7.2 using node degree analysis. Size of the nodes represent number of interactions of each nodes and Color scale represent combined score from low to high degree values. (B) The sequence alignment of UL36 domain of modular channelrhodopsin (GpRh) from G. pectorale with the C-terminal segment of UL36 (accession no: AWW11697.1) of human alpha herpes Virus-1. The sequence of UL36 domain of GpRh aligned well against the C-terminal segment of HSV-1 UL36 protein having proline/alanine rich region which is crucial for viral replication.

Supplementary Material-2:

Supplementary Table1. Sequence identity of modular rhodopsin used in the analysis.

S.no	Seq. name	Sequence identifier	Organism	Genome database link
1	>Cop5	AAQ16277.3	*Chlamydomonas reinhardtii*	https://www.ncbi.nlm.nih.gov/protein
2	>Cop6	Cre11.g467678.t1.1	*Chlamydomonas reinhardtii*	https://phytozome.jgi.doe.gov/pz/portal.html#!info?alias=Org_Creinhardtii
3	>Cop7	Cre01.g038050.t1.1	*Chlamydomonas reinhardtii*	https://phytozome.jgi.doe.gov/pz/portal.html#!info?alias=Org_Creinhardtii
4	>Cop8	Cre07.g329900.t1.1	*Chlamydomonas reinhardtii*	https://phytozome.jgi.doe.gov/pz/portal.html#!info?alias=Org_Creinhardtii
5	>Cop9	Cre15.g643503.t1.1	*Chlamydomonas reinhardtii*	https://phytozome.jgi.doe.gov/pz/portal.html#!info?alias=Org_Creinhardtii
6	>Cop10	Cre15.g643503.t2.1	*Chlamydomonas reinhardtii*	https://phytozome.jgi.doe.gov/pz/portal.html#!info?alias=Org_Creinhardtii
7	>Cop11	Cre17.g733150.t1.1	*Chlamydomonas reinhardtii*	https://phytozome.jgi.doe.gov/pz/portal.html#!info?alias=Org_Creinhardtii
8	>Cop12	Cre17.g733150.t2.1	*Chlamydomonas reinhardtii*	https://phytozome.jgi.doe.gov/pz/portal.html#!info?alias=Org_Creinhardtii
9	>Vop5	Vocar.0044s0018.1	*Volvox carteri*	https://phytozome.jgi.doe.gov/pz/portal.html#!info?alias=Org_Vcarteri
10	>Vop6	Vocar.0009s0380.1	*Volvox carteri*	https://phytozome.jgi.doe.gov/pz/portal.html#!info?alias=Org_Vcarter
11	>Vop7	Vocar.0001s0831.1	*Volvox carteri*	https://phytozome.jgi.doe.gov/pz/portal.html#!info?alias=Org_Vcarter
12	>Vop8	Vocar.0069s0008.1	*Volvox carteri*	https://phytozome.jgi.doe.gov/pz/portal.html#!info?alias=Org_Vcarter
13	>MspRh1	62803	*Micromonas species*	https://phytozome.jgi.doe.gov/pz/portal.html#!info?alias=Org_MspRCC299
14	>MspRh2	61324	*Micromonas species*	https://phytozome.jgi.doe.gov/pz/portal.html#!info?alias=Org_MspRCC299
15	>MpuRh1	70932	*Micromonas pusilla*	https://phytozome.jgi.doe.gov/pz/portal.html#!info?alias=Org_MpusillaCCMP1545
16	>MpuRh2	40573	*Micromonas pusilla*	https://phytozome.jgi.doe.gov/pz/portal.html#!info?alias=Org_MpusillaCCMP1545
17	>GtRh1	146834	*Guillardia theta*	https://phycocosm.jgi.doe.gov/pages/search-for-genes.jsf?organism=Guith1
18	>GtRh2	148916	*Guillardia theta*	https://phycocosm.jgi.doe.gov/pages/search-for-genes.jsf?organism=Guith1
19	>GtRh3	148915	*Guillardia theta*	https://phycocosm.jgi.doe.gov/pages/search-for-genes.jsf?organism=Guith1
20	>GtRh4	107802	*Guillardia theta*	https://phycocosm.jgi.doe.gov/pages/search-for-genes.jsf?organism=Guith1
21	>GtRh5	122016	*Guillardia theta*	https://phycocosm.jgi.doe.gov/pages/search-for-genes.jsf?organism=Guith1
22	>GtRh6	149064	*Guillardia theta*	https://phycocosm.jgi.doe.gov/pages/search-for-genes.jsf?organism=Guith1
23	>GtRh7	138313	*Guillardia theta*	https://phycocosm.jgi.doe.gov/pages/search-for-genes.jsf?organism=Guith1
24	>GtRh8	145205	*Guillardia theta*	https://phycocosm.jgi.doe.gov/pages/search-for-genes.jsf?organism=Guith1
25	>GtRh9	144198	*Guillardia theta*	https://phycocosm.jgi.doe.gov/pages/search-for-genes.jsf?organism=Guith1
26	>GtRh10	144226	*Guillardia theta*	https://phycocosm.jgi.doe.gov/pages/search-for-genes.jsf?organism=Guith1
27	>OtRh1	46936	*Ostreococcus tauri*	https://phycocosm.jgi.doe.gov/Ostta1115_2/Ostta1115_2.home.html
28	>OtRh2	199419	*Ostreococcus tauri*	https://phycocosm.jgi.doe.gov/Ostta1115_2/Ostta1115_2.home.html
29	>OlRh1	25667	*Ostreococcus lucimarinus*	https://phycocosm.jgi.doe.gov/Ost9901_3/Ost9901_3.home.html

30	>OlRh2	89413	*Ostreococcus lucimarinus*	https://phycocosm.jgi.doe.gov/Ost9901_3/Ost9901_3.home.html
31	>OlRh3	28080	*Ostreococcus lucimarinus*	https://phycocosm.jgi.doe.gov/Ost9901_3/Ost9901_3.home.html
32	>OlRh4	47806	*Ostreococcus lucimarinus*	https://phycocosm.jgi.doe.gov/Ost9901_3/Ost9901_3.home.html
33	>DsRh1	Dusal.0121s00015.1	*Dunaliella salina*	https://phytozome.jgi.doe.gov/pz/portal.html#!info?alias=Org_Dsalina
34	>KnRh1	kfl00193_0190_v1.1	*Klebsormidium nitens*	http://www.plantmorphogenesis.bio.titech.ac.jp/cgi-bin/blast/blast_www_klebsormidium.cgi
35	>KnRh2	kfl00421_0020_v1.1	*Klebsormidium nitens*	http://www.plantmorphogenesis.bio.titech.ac.jp/cgi-bin/blast/blast_www_klebsormidium.cgi
36	>KnRh3	kfl00037_0310_v1.1	*Klebsormidium nitens*	http://www.plantmorphogenesis.bio.titech.ac.jp/cgi-bin/blast/blast_www_klebsormidium.cgi
37	>GpRh1	KXZ47652.1	*Gonium pectorale*	https://www.ncbi.nlm.nih.gov/protein
38	>GpRh2	KXZ46245.1	*Gonium pectorale*	https://www.ncbi.nlm.nih.gov/protein
39	>GpRh3	KXZ47741.1	*Gonium pectorale*	https://www.ncbi.nlm.nih.gov/protein
40	>GpRh4	KXZ54193.1	*Gonium pectorale*	https://www.ncbi.nlm.nih.gov/protein
41	>GpRh5	KXZ55246.1	*Gonium pectorale*	https://www.ncbi.nlm.nih.gov/protein
42	>CsRh1	PRW60699.1	*Chlorella sorokiniana*	https://www.ncbi.nlm.nih.gov/protein
43	>ApRh1	XP_011395544.1	*Auxenochlorella protothecoides*	https://www.ncbi.nlm.nih.gov/protein
44	>AsRh1	5151	*Asterochloris species*	https://phycocosm.jgi.doe.gov/Astpho2/Astpho2.home.html
45	>AsRh2	77589	*Asterochloris species*	https://phycocosm.jgi.doe.gov/Astpho2/Astpho2.home.html
46	>AsRh3	6282	*Asterochloris species*	https://phycocosm.jgi.doe.gov/Astpho2/Astpho2.home.html
47	>AsRh4	6192	*Asterochloris species*	https://phycocosm.jgi.doe.gov/Astpho2/Astpho2.home.html
48	>BgRh1	89464	*Bigelowiella natans*	https://phycocosm.jgi.doe.gov/Bigna1/Bigna1.
49	>BgRh2	139324	*Bigelowiella natans*	https://phycocosm.jgi.doe.gov/Bigna1/Bigna1.
50	>TsRh1	AGF84747.1	*Tetraselmis subcordiformis*	https://www.ncbi.nlm.nih.gov/protein

Sequence of modular rhodopsin and reference sequences used in this analysis:

>**KnRh3**_GAQ79757.1_Klebsormidium nitens kfl00037_0310_v1.1
MTVDAHSTVDAHSTVTDSHSAGNGTESCYVADFLGMHHESHEGALYSVYKSLEWGCFLISIGLFVFYLQQYRKKTAGWEVIYIAFIESFKYIFEIFW
PHNNPAQLNIYGVNKSVPWVRYMEWMITCPVILMALSNISGEEGEYTHRSMQLLATDQGAILCAITAAASEGAISAVFYAIGVCYGICTFYFCLQIYI
EAYFTLPETCHSAVKWMAVIFYAGWLCYPCFFLAGSEGWGNLSYEGSAIGHCIADLLSKNAWGVMHWWIRCQLEEYKHTHNGQLPHYSLETRA
KMRAEAGHIIAGSLGSVLHVAGHQHHHFHFDEDSGMQGAQIQGQPLAQANERANLKASLLNGNAVNYNQAVQAQPQAFQIQSGEDGYVISMNQ
GESSASGSRRTTQNIEGPKKDPVASAFSKALGSMKSKVTEHFTKDLPPSARPDSPSRRGSARGGADAPTAQPQQSMKIDLRDLANNPQLQQQLSMM
LKGQMAGGYALKTDLKDLANNPQLQQQLSMMLKGQMGAGNSNTNQGSNNGSPRARPVSEELAQPARLQKAQSARATSNLDDEIEEQAPAQMSR
RPSARVPRATAAADEEQAPARTLSRKISRGDGGEPVSEERLQKRPSYRAAKAAAEAADEDMTDAPAPALARRPSARAPAADADEETAPVRTASLR
RAGSKSPGNSLPSSPSRRVSRANSLRAPVSASVLLCDADGDMGDFFLDQFAAVPNSKCSVKVVATPDELIDALATGRAYDFVMVPKGVITSDPEISE
EIRAHAQTPLVAFGPALEGMAVAEVKAHMFELDVDDYIGLPKRGQEYPVEDLEALVWKYKKVADDSN

>**TsRh1**_AGF84747.1_Tetraselmis subcordiformis
MGFQLNPEYLNETILLDDCTPIYLNVGPLWEQKVARGTQWFGVILSLAFLIYYIWITYKATCGWEELYVCTIEFCKIVIELYFEFSPPAMIYQTNGEV
TPWLRYAEWLLTCPVILIHLSNITGLNDDYSGRTMSLITSDLGGICMAVTSALSKGWLKWLFFVIGCCYGASTFYHAALIYIESYYTMPHGVCKNM
VLAMAAVFFTSWFMFPGLFLAGPEGTNALSWAGSTIGHTVADLLSKNAWGMIGHFLRLEIHKHIIIHGDVRRPITVNTLGREVTVSCFVDKEEEDED
ERISTKTYANRASFMKMRNDMEQRGIQTRKSLEMLAPPPALNDGSIVLAVADPMTLTFFTQQLSQLDATIRATPAMGQGQLEQVLEKGGFDGVLV
SPEYIQQVGLVQRLKDKYHMPVYAFGWGKSSPWRSVIEGSGVDGWLEGPYFGSTFDTDALSDAIAEMQRIKTSYSMVVNGVGMNGAGMNGVG
MNGMGMDGVGMNGAGMNGVGMNGMGGYGSVGNNMHSMPMMSQQAVMMPQSAPQMMGGMSQTQQPAMMGGMQGASPHYSVGNLQNME
GQQAVGSPQVLASSWQQSALHGGMGQQQQYGQVQQMPMMVGMQTPASPGGVQTPPHTMAGQPQMSPQQLQQQLYFMQQLQQRQLQQQQYQ
GGTGQR

>**GpRh1**_KXZ47652.1_Gonium pectorale
MSELRQAWGTVANVSQWFAFGVSVAILLFYAYEAYIATCGWEEVYVCCVELTKVVLEYFHEFDSPAMLYLGVGTRVQWLRYSEWLLTCPVILIH
LSNLTGLKEDYSFKTMRLLVSDIGTIVFGATSAVCTGYLKWVFFAIGCVYGGFTFFTAGKVYREAYEAAPAGRCKWLVKVNAVIFFSSWTMYPVL
FVLGPEGTGVISLLESTTAHTFVDLMSKNIWGLVGHTLRVAVWRHILTNGEASAGTMRQSISVSRAEVGKAMQRMSIGSQYGGANRVSIGSQNGG
TASGPAGGNRLSIGSQSGILIPTGAATGAATGGRNSVCSQTGMAVPAVSTSGIVWTTTGAADQDDHKNRSSFWPSVGKGSAAVAPMPPTVSVKSR
ANTSTGMGGGNGSGKDHDAGKGHHSDVVVGSNMVIAKVGVSGAAADSPSHGAASPAATGRLISLPGPPAQPQTPQHVQRPGTPPTSEPSGGLQSA
ASAGGWTDAGAPQGSAPSPLPPPPQPQQRTATATGMGMEGAAGAARKSSSSMRLNVVAAAAVPISGPVDAIEDVEEEEVPPPTVPVEPPPPSDRRR
SSVGDPASRPYTSQQRQQAQSPRTYPHLTAADI

>Cop5_AAQ16277.3
MPATSRRFGVLLYLLASYLICTSNLGDPELTAQFHAQADPNAYTWPMVAFGTAFGLNFITLLFERESAKFQLALLACYINFLAGFSDYMSWKGYAP
IVRDSWGQGFQLLRTV**M**WLL**T**TPAMVY**L**LSIISDFSRLKVYSVMLADVLMITFGILAFLAYNKVMSILFYMVAWCLFAYVVHSMWSMFHASIAE
ARHDSSRVSLEVLRLFAVGLWFTFPVIWIVVK**M**GLVDIRT**E**EWTWCAC**D**FLG**K**VMFSSSLLHGNFLTIEQRRLIAMRIVEEGNRIQVIQELKDLVEQ
KERFMSSMSHELRTPLNGIIGLSDALLVGSCGEINDQALKTITTIKTSGARLLNLINDILDAASMRKGKLTIKHEKVNLKRVVDDVIDLCQPLAKRGV

KLVNDLRENVPFVLGDTGRIIQVFHNLIGNSCKFTHSGNISISAAVKDDEVEVAVADTGIGIPEDKFDQIFLAFEQVDMSVTRKYGGTGLGLNLVKQ
LVEAHGGRISVKSRENQGTTFYFTLKIHSEHPNEGQPQMTPTESVAAIPPPEHSQLATVRGTAPSAGGLPPSSSGATAGPRRAPSRRGSFTDKMLGAL
GAGMGGHHKKPPSETESRDGPYASNAGPGGGGNAGQGSAMVRRVSRDAHGSNPPNPKSVTAGPQVSGPMSLSDAAALMKGALKRKSSFRERGA
KVRVLSVDDDPVNQLVIQNLLAPVGYEILQAMDGQEALKVLTEEERLPDVILLDVMMPGMSGYEVCRKLREMYPLSCIPVIMISAKSKEEHIVEGL
AAGSNDYVVKPFGRQEILARIAAHLRFRDTVYQAGEIAGAIPGDVRPERVLLRGGANGGGLDLTPFLTGPARFTSLPPRIARGI**EAGTTSTTLQMFE**
SLTLLEVRLVNLGDLLASVPASDLLVALASLFHDLDTLLEQHGCYLLEGLDESHLIVSGLDNVGDQVLHALGLARSLIAAADTFALGGRRS
KLHLAVGVHTGPAQGVLVGYSHPLIFFTGQLPAEVHMLQATCPPNCVHVSARVLESVAHSEREHFVPAGVMASGATTYLMKVGGWEGGGI
VAASEATSRWSKAKRGMHDGLATDARRMRPIQLALLDMAQANPAFLVDIASAAHGAAGGGAGTSSDGQGERGGGGGGSEELSKLKREYESLER
QMEEVSGEAARLQDLVDELEEQLLARSNTAAASTAATAAASQQAAVAAADAASLKAHVAELEGQLAEAARERNGLEAALAEMEQRLVATHAAL
ATANHEAADRARAHTPAPQELPPHHPHSASRSHLHVLPQQNTPRVETASMAPSASGSEANFASGLSALGGGSLFGGGALMPRGAMPLGVPMRMP
NLAALRAHAGDMRGLLDELGLGSLASRFEAEDVSPGLLPYLDDAAMRELGASSVGARLKLRLAAQALFM

>Cop6_Cre11.g467678.t1.1
MKLRQRTVGAQLRSQPVSSAGGPANSGPPATPSGGIAPVSIFGAAEALADPEARGWILTWSWTFTGFFVYITASWLSGLWYTTDPLAYAALRAQVP
TLVYQMSSTAFFTALVLNLTSLLFEDNAPKRQLALLSCAIKGAACHTDLLLVTGGATVLYDAYGSICIPQRYV**Q**WLV**T**TPTMVY**I**LSKISDFTPRQT
ATAIGLDVLMVLSGLVANFLRSPYLWVAFLTSTAA**FIGVLYMMGLMVYSAVKEHTSANSRRSLLFIYMCTLFIWNLFPLAWILHVVHRGSPA**
AEYLNVFANFMAKVLFSSSIMYGNYMTIAQRRLLAQQDAENANRVQMIQDLRDSVTRKDQFMSLMSHELRTPLNGIIQLSDALVRGAGGEMNP
KGQHFVRTIKNSSNHLLNIINDILDVAALKEGKLTIKHEVCSLAKAVDHVVDIVAPLAKKEVTMERWVDPATPLIIADFSRVIQILYNLTGNALKFTN
KGRVGVRVEPSADGTHVLLQVSDTGIGIPKDRLHSIWGAFEQVDMSVTRKYGGTGLGLNIVKQLVEAHEGTIEVASVEGRGTTFTVELPVLQSSTR
RSLEGQVLDSLTRCGHAAARDTMVQRRTRSRPSLGLEDTITQFARGVQRRASGLLGVAKAAQEAGSNAGTGPAGSTGAGAGGGGGAGGGGQRD
SLDREEGEQLLRKRTHELEHESRLGDLARRTVHKQSMEEADLASRQLLLSDYERRAERDTRSLERIDSGQPGLTNGGGEGAGGAAGGGAGSGGGG
GSAPGSAGKAGVAGGSCRGDVRGGGTDGRGGGGGGAGGAGGGGGGNGGGGASGGGGRRSGAPTSGRASLGELPSGGSGGGGGGGGGGGDG
TPESPRSAIARRGLLAMRQSSLSNLRGATSARAGGAAGGAAASGGGVSVGRWASTTDTGFANQGAAAAAWRGDSHRTLPGVEGGCVSVSSANG
NSIADVYEALQLARASNESGGGGGGGGGGGGGGNGSSLKASGGSLALRMSAYGRTGYGGANGGGGGANGLNGYGGGGGALGGSGASGSLLK
SALESDLYRNGPSPRDPYDCDASSVGADSEYEWVGDGGGAGGGGAFGGRSRGPTSTGSLALGGMACGPGGRRHQPPKPSLRSGKLTPMLSNAAA
AAAAITAVPPGLTLDKLAYSDMYGTIQVLSVDDEDINQIVLEEILTDSGYAFARCMDGAEALEWLCASDTMPDLILLDCMMPVMSGHEFCATLRK
VIPGNVLPVIMVSAKSDEENIVEGLRSGSNDFVRKPYQREELLARIETQLRLKSDSWWLAELVNNVDGRETESMKLLKNILPESIIARMQQGQKFVA
DSHGHVVILFSDIVGFTSLSSKLPTAEVFLMLSNMFTAFDKLTDRFSVYKVETIGDAYMVAAGHDEDEDKEAKGSPLMRVLGFARAMLDVVRNIT
APNGERLRIRIGVHCGPAFAGVIGMKCPRYCFLGDTVNTASRMESTGFPMCIHVSENVFKHHPAAEAELQEVGERDIKGKGHMRTYVVRTGAWEQ
ALRDFAARQQAAAAAAQAQAQTLALARQQAALLQQQHEQLQLQLQANGGGGGGGATANAAKAAADALAQLPASLSFDSASAGSTSSMLPLSG
GSVAGAAARTANSLAPGAGGGGAAAGAADGGGGGNGCGGGGGAVRMGHLLSTVAEEGSLPGSPSSFAAAAAAAAALSPSAAAQQQQQQAPGYH
PSHLRTASAGAGRSPLSRGELPAAASSPLQPGGGAAAGAAGSSPLLPPLLRGANHYTDPRLAGGLRPSFSTGGYVLEDDSDDGGTSTNTGVGGGTG
HGMGSSLGEGRAGSISLTGIGARSFTGASCGGGAGGGGGGGLRMLNSPTGQYDTGDAGENGSSGPGGSGGGGGEVGGSGGTPSGLRVHVPRSLS
GLSGGSYGSGGSTGIGMSRAGLGSATAAAAAAASGACFLTSDAADASFSGGVLAATTSHAALGSGGAADSQHAPSAAGAVMGSSPAAALQVSPAS
PGGAAAGGLGSGLSPQSSLYGGAQLLLSPNSAGLHSGHANTTLAYLEQRIASLGTQLATEALSRQRLQDELDAERRRAAGAMQQASLLMQQLRN
ATQAAGGGSGGAPSSVAAAAAAAGQEQHLARLQLGSGGGGADAASGGGGGAALPPSAAVPLSRLPPPPRGAGGAVASLRAAGGANELLPTSNEA
NSNADADVIIGGGGMSSTVVPAAQPPSSSAFGSAGAATSGGSGNDDQEITLASPFVSDLPAYALEAGDVVPNSLDFASQGFDPGSSGAGGRGGGGG
SRHAGRAAAAQQRPSSKVQRMNVGDAAALMLQPPKAQQLQPGSQSTAFVEAGGVGRSGASGGGIAEPLPGSAAEAYSGYSRQQLEDQLLLPVPM
PTSITALMPGGGTAAATAAVGTATAASTTTTTTTTVSHHRHVFHTSAAAGLALSAHPAPGSSPLPAPSSSSPCTALQPLQLQPPPLPCYSLDALFVDL
GLEPYLPRFRDEAIRLDMLLSMDAQQLERLGLKPLGYRIRVREAVVELARGLLRSSEDAAVLVEMSQQHQHQQQYRSQQAQQLQQQHQPLER*

>Cop7_Cre01.g038050.t1.1
MGALPEAERSSAHLIWTLGPRRNFVGQLYSVDTPVLLWCCLGSLSYACCALGLHQLDSTVREESDQGQEAVEWTIQVQTAAFGAVLLLNVLNLG
MRQHLLPFKCNLLLLFINAVAFATDLIIWRRGTPLYPLSPGLGLGLLRPGAAAAAGDRAFVPLRYV**Q**WLH**S**TPTMIY**M**VGLLAEVRGWQLALPVL
CDVAMVVTGLAACCTTGLTKAFFTAVSF**ATFAVVLRRIHAMFDKTLRSGDVAADQRGTLRAVRALLLALWGAFPLVWLAADWRLVSPQAE**
AVAWGVCDYLAKAVFSSQLWQSNLTGVHVRREVALEAWEAHNRVEAVARLSSLLAQRDELLSTLSHELRTPLAGIVALTGALYRDVASALP
ASARTLGAVRAAATCMLHIVASTLDAFAGQRAERGAAGADAGAAGGSSSNATASSGSNGGQAYNQQALALKAPAGGAAGGATGGSGGGGGGGG
SVSAAVVDLRPLVETVAAVLRPLAHDGVAVAAELPEGLPAVTADATRLNQVLYNLVGNALRFTSSGEVRVSARVLGPDGAVWRCREPNSSGDSG
AVGLSSDSPHAAAAAVRGRRSEDFTASSSSVARSPLPGGRNSGNNAPGSAGLWRRRPRTSASSEHSAAMAAPGGAGGPLGAEAAAAAALPPGCVVE
VAVEDTGVGISQAQLDALMAPAYRPLGTADTAAAANAAAAAGYAASASIRAGDAGGTLSDDSAARKRSNKSRRRAAKAGKAAAASSSSLFYTGAP
ASGAISIGGTGLGLYLVRLALRAQGSELTAESAAGIGSMFRFRLPVATAACALALASKQAAQQQGQQGQQQQQQGAAVAAEEQGAVNMAREASV
AWMAAAGEGEGSQPGPTSAAAPAPAKVSTAPVVPRSEPSAIARLTCRVNGGAAAAAADGASSSGAADGVGAGGALMRYAQSCCSPLAATGSVP
GDAGDSGGFPLPSGSTAAASHLGSGVPAMTGYLGRPPLERGLSCSACNGPGGLRAASGVSVVMAAGAAAAAAAAAAAAASSAVGSAGSADGALV
PGGSAPRERSSLLGYPKREVLDVRNLAGACGGPAAVTGEGALVPAPVAAAAPVANNFRHCNNGTLQVLSVDDDPINQLVAGQMLTSQQWKVVK
CMDGPQALKFLRLPAAPEPRASASGGATAADALAEALAAADAAAPPLDPVPDCVLLDVMMPGMTGFEVCRRLRRRYPHAALPVIIVSAKSDAAA
VEEAFAAGADDYMTKPYKRAEMVARIKAQIRIRDSMAAAAAAGVPGGSVEVPPLGNDLRVQARAQDPAAAAAAEPQQPAAGSRPQLHAPGGHV
AGSLASLLGGAAGSDSAITPPGAYARRRSVAHASPAAAMASGASTPCGSNSAAATVSPPRASLNGATGAFGSRMLGGSTCVTENGMQAPAPPRGV
ATGPAGLGSFGGGAAAAAGLFFSPGLPSGGGGGGGGGGGGGGGIFSATSTLTGTGQFRYVEDACASELALVTTTSITTGPTPPRAAALTVAFVDAE
SSGAGGAAAGALRAAATPAVAASPVSIRTAEGGVAGLSSGKLLMLPADTASAPTVSGGLTSAPVSGAAADAAAAGVSLQQQPPPTPIPLAALSPPF
PPAGGAAASPAVAASPAATAAAAAAAAAAAAVPMDLASLMAELLAEVRRSRVLEADVSKLTARVAALQTACGTLAADRDGWCRQARDLRALL
ASGLAAATAGIAGGGAAAPPPSLAFGGSPAAYGGSAAGGFTSLNLVGQPTSSAGPASVVVRANSLLNEAALAAANGSTASADSSNHALPLATYGA
AANANGGGGGGGSVAAQLEDLRRETAALRQQLRLALASIGNGSNSVSGGGGAQGSVPPVRAGSGISGGGLPSTGASAGINNGSSSSAAQMGRAY
GAGAGAGAPAIPGTGAGSAAANAANGCAATSPQPQRAVQADGNGGAPGPAMTGPVAGAAPAATSGGADAGLSAGSGLVAAPWGPHHQLLPNP
LFASSTADMLLHTAGSAASASASAGSGAAPHGLAAAATTVAAAAAAAGAGHAEPAGSVIAAKDAVAAAIDASARTADATTAAAGAADAGLPSG
DVPTPTRANGDAGSGPGARRGGGGASAHAHAQLPPAEAQAHMGVTSLSSDLPPQVRRGNAGSNGVTATANGQSCAAGAAGADHGHGGHGCGG
AAADAGIFRGGGVSGRSENSRGGSTPSVPTTGSVQGGDGTPKVADRALILPGAQPLTASTPVTPAAAALAAASAVAGSGRDGARGRSGGATAGILR
LLCSRGAVPVNGVDSK*

>Cop8_Cre07.g329900.t1.1
MVGYACNMILTLLKVIFESSRSKLDLHLVSCYINALAAASYLMLWTGFSPIVPDINSCLYIPQRWL**L**YFF**T**APAIIH**I**LSQISNYSTRMRIWVVLLNAF
MLAAGGFGTVPWISWTHKVFWYTLACVPFPSILCHMWRMVTHALDETQDPSS**KRAISFIRIFSITTWNFFPIVYFAAIDGALPLEISEPLWAALD**
WLTKMVYSSSLMEANFFTTHWRELTLRAIEEANRLSTIQQLSLDIERKDEFLSAMSHELRTPLNGIIGLSDSMIAGACGPLPEKAVKTISTVKLSG
KRLLQLINDILDAAKMKQGMLVIKHEKVDIKRLVSDVLDLSLPLVRKGVRLINNVGNVPKIVGDNGRIVQILYNLVGNATKFTRAGTVSVSAGVVE
GKVYITVSDTGVGIPPDKIDKIFEAFEQVDMSTTRRFGGTGLGLHLVKELVKAHSGRISVQSKVGVGSSFTVWLPINQEEIDFGDAFTPSRLRQASED
SNDAGSTRLGGNSVKWMDASANPAAAAGAGGDAALAAAAQAAAAARTFNREVGMGGGAARSEAEADDAAIVAAAMEAERRAGGRSPPPMEA
SRNMPDDAQTLLSVTKSGFKLVKPFYRERNGGCMVLSVDDDPINQLVVENLLLPEGFKVEQAMCGSEALDWLQHTPLLPDVILLDIMMPDMSGYE
VCQEVRRRFSTVCIPILMVSANGTPEHVMKGLEAGAVDYVKKPFNRQELLGRIRAQVRNREVVDAEMETRLVNKMLHRMLPAPVVEALQGGAG
VSGFVELHEDVTLLAADVGSWLNTSGLMMSVEGCRALLGVVNGMHAAFDKLLLKYKAFRVVSTLDHYLVVCGHDGTPDHVRRGLSLAEELVTA
ARSLTLPPGCGGGQLRVRCGLHTGPLTSVVVGVDSPHYAVFGETVGVVAGLVSRGFDNTVHCSFAVHAALRIKSQDRISASFVPAHLLLKLPGKLP
PVQTYLYKCGDWEQALKQLDDEEGERETAESAMAELSARERKWKEEQAAAEAAAELTAASLEEERAALEALAARLVTERAELEAARGEVARLR
GEVEAARAGGAAASAGAALAAAEADTALAAARAEVEALTVRLAESEAERSRMKITYEARLIEARETAAAAAASVHRSMLPMRGYGAHHEYGAV
LGHRPGDSPHQQMLLAQHQQQQVQQHVRPAGVSRISAASHNGAPGVSAPQAPLVPQASGGAAGAFLPYSYPYSYTPGRRAPSIGGASSLNMSGGS
FWTQPYRIESFMRDIGLPQYAAVLRSQDVTPAVLAGMRESDLEAMGVPTLGARLRILEAARQYGSQSTVRMALLCKDGQDGADGAEQMLSDALG
QGGVESAATWAHMGGGDSEDTAAGGAGSGNERL*

>Cop9_Cre15.g643503.t1.1
MPGDRQHSSVGPPVPASTSVSAPTEHLKEAYNTLVLLVSCAAIWMVCSYIDATYTPRDFNYIPSRSLIISYQWCMVGYASNLILTLMKVIFETNRSKL
KLHMVSCYINILAATSYCMLWTGFSPIVPDVQSCLYIPQRWL**L**YCF**T**APAIIY**I**LCQISDYTTRMRVWVIMLNVFMLAAGGLGTVPWISWTHKVYW
YVMSCVPFPSILVHMWRMVSSAVDETMDPTSKRAIKFIRLFSITTWNLFPFVYFAAI**D**GALSLEI**S**EPLWAAL**D**WLT**K**MVYSSSLMEANFFTIAQRR

EFAVRAIEEANRLATIQQLSTAIERKDDFLSVRKGVRLVNNVGNVPKIVGDNGRIVQILYNLVGNAAKFTRQGIISITAGVSEDNAKVYVSVTDTGV
GIPKEKISKIFGAFEQADMSTTRRYGGTGLGLHLVKELVKAHCGDITVESEVGVGSSFTVWLPIAQDGAMAGSVEESDREGREEKPYTLDFNGPLR
RISEDSEEGGYLQAAAAAAAAAGGGGGGGRSGGGGGGGTNRRSSQENRNNGGGRAGGGGGGGGRGGERGHAESDGEQDGPGGGGGGGGGGG
AGGEEQEGDEGTPRGGRGGGGGGRGGRGGGGGGGASNQSNHFGFYSNGDSGASGGPGGGGGGGGRGGGGGGGQGDSGPQGDSGGGGGGGGG
GGGGNGGGAGGGGSGGRGLGKGPSGRGRESSAENLLTVTKSGFKVMKPFYREKFGGCMVLSVDDDPINQMVVENLLSPEGYKVEQAMSGSEAL
DFLKRTTTLPDVILLDIMMPDMSGYEVCQEIRRRYSAVSIPIIMVSAKGHPEHVMKGLEAGSVDYVKKPFHRQELLSRIRAQVRNREIFEAEMESRK
VTEMLKRILPLSVIQRLQQGQSMIADAHDEVTVLFAGQFMIADAHDEVTVLFAGQFMIADAHDEVTVLFAGQSMIADGEVTVLFADVAGWLSSQE
LSARTTSDVVIVLNEMYGAFEKLLLKYQVFRVEHTGESYLVVSGHDGTQDHMRRMLSMAADMLSAVQQLAFPGGEPLRLRVGLHTGPAYAGVV
GIDNPRYCVFGDTVSVANALEARGFANAVHCSNAVYEAMRSKDRDRAGAMFAPARKSMAAGPSVMDTFVYKVGNWESALKELEEEEQQKEAA
DREAREKDDAARAAEAEAAAAAAAAAAAAAAAAVAEAASREREELAAACARAEELERKVNTLAAEKEAAEAAAAAARAAADALRARAADEAAE
RGRLHASIATYERLLAEAREAVTLAAARAGSAGGAGGGGAGGLAAAAAAGAAAAAQRRGSPAGIQHHHHQQLQLQLPPNLAGSPSSMLPPGHH
HGPQHAHQHAGLGAEDSGGLGLGGLGSGLGGLGSGGGGLGSGLGGLGGGGLFSPTGSDVFPLYPGGGGGAGSVAGSGGGGSVAGQAVAQSFWT
MAYPIDMFMRAAPSPSPPPDDAGPVSPRADGQDGDPALEIPGAGVQPAGAQELEELGIPPAAAAALRDALQPQEFELPGIPEIDEERRLYESRLPGKD
GAERIPRFESVRIPQVPIDPPDIRSFLLDVCVRALAQREASPTTTESSVKAMLASVFNALDRPGASERDREIASYIPRTFKEVLTLVTVLEPACRWPQLY
RYKMCKCGFIYRGAHQSASVCHGIVKAQGGGVEACGISCEQAREVTYSSIANYVERAYANPEIAADLSSWRQRQAFPRMVERIAARERERVAAHQ
AANAAAGRPGDPIPPKTPEEKAEDERDSQASTDSMFDMVDGELVKEALRKDPAFAADPRNLLVVLVSDPFIVPADEHERSSIPYLLLPVNASPENRH
HLGFATLLSLIGGNVKPPGSKKPDPLNPNHMMALIRDELAFLEKYGIRVWDASKNEFFICRVKCISFISDYRGLHKHLGMKGSPAKCACFKCWHEG
HVVGRKAVYPHNAAHLPCLHVLRTSLVGRHVPPPKKPPKKQAAAGAAKPQPTRATAPGDGTRAAAPGAKRTAAAPPVTGAAAGGGKRLRGAQG
AAGGRASDSGSSSSSDGGSSSASEYSDVEVESEDEAKRLRRQQQQRQQQPQQPRQQQAVRGRGPAVDPNLATPPARRTKAEMWYACNSPTPGAS
LVPVPWRITLEDPIGLAFPLYELDSFDPIGGINYDGMHTIYGVMRDTVVRYVQSFRKRSAAMEEYDKKNDIITVSGRGAGKVVENFRGALAVIAAN
VPRAIAGRLARLTTAGKKAKSHSFFLLAGPFGAYAVKKAGMPPRLEAAMLSIVNACSRLWDKVQRRSQLGQLRTAVVEAICLVERHMSATELDIK
LHNLMHLVDGIEQLGPLFTHSMFKPESIWGQLGRWAHSKRHMEMSMFFMALDREVSLRLRQLHPASVDAPQRHKEAQRQLYVGEEAQMSGEAAP
VLRIQARHDADGEEEVPDEGEATMWDEAKFFEADPVIYWGRFSGSRDWFDAESKEVEALYESAGLEHAMGSTVQSVRMLKEIYVGSVKLSRGSW
FMCRAANDLPDWWFGRVVEVVLHKGADDTERALVRAEWFTGATKEEAGAVSVPICDQILAPVVASRPANIIVETGPWYLPEAIVPWPCHLEPHPG
NPNVQVALARLWHILRNLFPYPTVADAVRVSRPFP*

>Cop10_Cre15.g643503.t2.1
MPGDRQHSSVGPPVPASTSVSAPTEHLKEAYNTLVLLVSCAAIWMVCSYIDATYTPRDFNYIPSRSLIISYQWCMVGYASNLILTLMKVIFETNRSKL
KLHMVSCYINILAATSYCMLWTGFSPIVPDVQSCLYIPQRWLLYCFTAPAIIYILCQISDYTTRMRVWVIMLNVFMLAAGGLGTVPWISWTHKVYW
YVMSCVPFPSILVHMWRMVSSAVDETMDPTSKRAIKFIRLFSITTWNLFPFVYFAAIDGALSLEISEPLWAALDWLTKMVYSSSLMEANFFTIAQRR
EFAVRAIEEANRLATIQQLSTAIERKDDFLSVRKGVRLVNNVGNVPKIVGDNGRIVQILYNLVGNAAKFTRQGIISITAGVSEDNAKVYVSVTDTGV
GIPKEKISKIFGAFEQADMSTTRRYGGTGLGLHLVKELVKAHCGDITVESEVGVGSSFTVWLPIAQDGAMAGSVEESDREGREEKPYTLDFNGPLR
RISEDSEEGGYLQAAAAAAAAAGGGGGGGRSGGGGGGGTNRRSSQENRNNGGGRAGGGGGGGGRGGERGHAESDGEQDGPGGGGGGGGGGG
AGGEEQEGDEGTPRGGRGGGGGGRGGRGGGGGGGASNQSNHFGFYSNGDSGASGGPGGGGGGGGRGGGGGGGQGDSGPQGDSGGGGGGGGG
GGGGNGGGAGGGGSGGRGLGKGPSGRGRESSAENLLTVTKSGFKVMKPFYREKFGGCMVLSVDDDPINQMVVENLLSPEGYKVEQAMSGSEAL
DFLKRTTTLPDVILLDIMMPDMSGYEVCQEIRRRYSAVSIPIIMVSAKGHPEHVMKGLEAGSVDYVKKPFHRQELLSRIRAQVRNREIFEAEMESRK
VTEMLKRILPLSVIQRLQQGQSMIADAHDEVTVLFADVAGWLSSQELSARTTSDVVIVLNEMYGAFEKLLLKYQVFRVEHTGESYLVVSGHDGTQ
DHMRRMLSMAADMLSAVQQLAFPGGEPLRLRVGLHTGPAYAGVVGIDNPRYCVFGDTVSVANALEARGFANAVHCSNAVYEAMRSKDRDRAG
AMFAPARKSMAAGPSVMDTFVYKVGNWESALKELEEEEQQKEAADREAREKDDAARAAEAEAAAAAAAAAAAAAAAVAEAASREREELAAAC
ARAEELERKVNTLAAEKEAAEAAAAAARAAADALRARAADEAAERGRLHASIATYERLLAEAREAVTLAAARAGSAGGAGGGGAGGLAAAAA
AGAAAAAQRRGSPAGIQHHHHQQLQLQLPPNLAGSPSSMLPPGHHHGPQHAHQHAGLGAEDSGGLGLGGLGSGLGGLGSGGGGLGSGLGGLGG
GGLFSPTGSDVFPLYPGGGGGAGSVAGSGGGGSVAGQAVAQSFWTMAYPIDMFMRAAPSPSPPPDDAGPVSPRADGQDGDPALEIPGAGVQPAG
AQELEELGIPPAAAAALRDALQPQEFELPGIPEIDEERRLYESRLPGKDGAERIPRFESVRIPQVPIDPPDIRSFLLDVCVRALAQREASPTTTESSVKAM
LASVFNALDRPGASERDREIASYIPRTFKEVLTLVTVLEPACRWPQLYRYKMCKCGFIYRGAHQSASVCHGIVKAQGGGVEACGISCEQAREVTYS
SIANYVERAYANPEIAADLSSWRQRQAFPRMVERIAARERERVAAHQAANAAAGRPGDPIPPKTPEEKAEDERDSQASTDSMFDMVDGELVKEAL
RKDPAFAADPRNLLVVLVSDPFIVPADEHERSSIPYLLLPVNASPENRHHLGFATLLSLIGGNVKPPGSKKPDPLNPNHMMALIRDELAFLEKYGIRV
WDASKNEFFICRVKCISFISDYRGLHKHLGMKGSPAKCACFKCWHEGHVVGRKAVYPHNAAHLPCLHVLRTSLVGRHVPPPKKPPKKQAAAGAA
KPQPTRATAPGDGTRAAAPGAKRTAAAPPVTGAAAGGGKRLRGAQGAAGGRASDSGSSSSSDGGSSSASEYSDVEVESEDEAKRLRRQQQQRQQ
QPQQPRQQQAVRGRGPAVDPNLATPPARRTKAEMWYACNSPTPGASLVPVPWRITLEDPIGLAFPLYELDSFDPIGGINYDGMHTIYGVMRDTVVR
YVQSFRKRSAAMEEYDKKNDIITVSGRGAGKVVENFRGALAVIAANVPRAIAGRLARLTTAGKKAKSHSFFLLAGPFGAYAVKKAGMPPRLEAA
MLSIVNACSRLWDKVQRRSQLGQLRTAVVEAICLVERHMSATELDIKLHNLMHLVDGIEQLGPLFTHSMFKPESIWGQLGRWAHSKRHMEMSMF
FMALDREVSLRLRQLHPASVDAPQRHKEAQRQLYVGEEARGGRAAPVLRIQARHDADGEEEVPDEGEATMWDEAKFFEADPVIYWGRFSGSRD
WFDAESKEVEALYESAGLEHAMGSTVQSVRMLKEIYVGSVKLSRGSWFMCRAANDLPDWWFGRVVEVVLHKGADDTERALVRAEWFTGATKE
EAGAVSVPICDQILAPVVASRPANIIVETGPWYLPEAIVPWPCHLEPHPGNPNVQVALARLWHILRNLFPYPTVADAVRVSRPFP*

>Cop11_Cre17.g733150.t1.1
MLGRAFLHNPAGLAELRIQVPNAVYDRSSSIFLTALAIDVLNIVFEQQTIKLDCVLLPAFIKGMASTTNVLVRFFTPVIAMTDLGRPVVVQRYICWM
HTTPSILMLLKMISTTITPRETMIAIFFDEVMVVTGVLALVTTGWQRVLWSLVTHAAMLPVVPYMHKAFTECIATHVAAAPTMAPLWAAPSAGSA
GRRGGSGAVSIGYDAVGFDGGGSGGGGRPGLLARAMEQIRTRPLQLTMLCIYVLNLVLWCTFAITWDLALLGWISVTMEEVLYVGCDFSAK
VLFSSTLMLSSFKEIEARRENAMRVIEGSSKAKLIAELQALLEQKERFMSSVSHELRTPLNGIIGISEGMLSGCCGVLPEGVRRQIYIIRTSGARLLAL
INDVMDAAALRQNKLVLKQEHVVLRHVVDDVLDLTRSLVDGEVALVNLVPPRMMVVGDTGRIVQILNNLLGNAAKFTRRGQIRVTARQVESGR
KVAVTVSDTGIGIPRNKLATIFLPFEQVDMSISRKYGGFGLGLNIVQELVKAHGGTINVSSIEGKGSAFTFTMPLLRAMGRESLEEGRNAAHRAAAA
GGATKMIGGTGMSTTDTSSQLGGSTSGSGGAHGTGGAGTISGAVSTATPRGDSRTPGGGGAGTNTISDYPGGDTDTMYTRRSDVSESSRVRGGGG
GGMGGESQSGADATAELEQYGELKYNAAELSALASSRPYAQSAVRDSLPSLAADGSGMLPHPSGPLSPSVGLDGSAGGAGGAAGSGGMGRGSSS
QLPTVLPAGASSAVAAAARARSRAVERGGAGGRGGTTGGGGGGAAGAGVELPGGRIMPGPKPFHYTMYKRFQLLSVDDDPVNQSVVKSLVQGT
GYEVVSARSGAEALRHVAAAPALPDLVLLDCMMPEMDGYEVLQRLRAMTPHVHLPIIMVSAQTEEDHVVCGLDLGADDYVTKPFKRAELLARIR
SQLAYGEWEQDEGVFDTISTMDGGELANVAAAAANAAAGRGPLGGPAAAPRPGAAGGGSDDSEAGAVSAALGNLNLGPAGVTAASDGLGGAS
GAEQRLIVCIDDDDVNQVVLHGMLASQHYRYVRASTGAQGLAFVCGPTNGGIPPDLVLLDCSLPDTTGFDVCRVIRQMYNKQQVPIIMLSARHNE
SAVVEGLKCGANTYVTKPFRRNELLARIRLHLRARDGPIQRGTSINDMGQVDESAAAAAAAASMVGADGAGLAFGGMLPSSSHQAGLGGGGGS
YAQQASLAQPPSAHPLLLASGSGSAVFPDSAVLVVAVADYAGLCGMLLPGEMAELSGRMLAAFERAVRAAGALPIEAGSGIMSAALLPPPPAAAE
ADGGAAAGLRLAALHRVGRALLDTASTIPVPGTTTCLQLQQALALGALTVSAGGGGGGGTTSSSFFGPVLVELLDLARRAPPMTIVTPDAEAEALR
ACGATADIRGPLFLEADDVGGGAGGAVAGPLVSRRLWLVEAHPLAHQYLPPQLLYASGAARGAFFQVQPGATGAGEAAHQAAPLAAGAPGAHA
GGVGVMGFGFAEQQQPGTRSGSAALLAGAGGGVGGGGAAAAAGMVPVSVHPTPGVSAAASEAAAGSGGAGRGFGSSSIASYGAAGGGGSAA
GATAASLGLGGPGMGIGLYTNGMGVSRGVSRAFSHTFGLDSDNHGRANSAAAGSAAGGSVAGGGSVAGGGVHTGHTAGTSGNGGSQGSVLTNG
RGGGGSGGASDVAAATAMTAALPGGSAVGGLDSSSVAGITFSLQAAAAAAVAAASTGGGGPAQQHLQTPAGAGSGLHDSAGASGLYFNSSAGGG
AGRSPLQPFGVVGGGGGGAGSGMTHNSQPLQLQQQQQQQQQQFDMVSAAAAEPQIRALRHELAAMRQQLEALQGAASTSSASNVMAGGGQGNG
GQPQLSQQQLSQQLTQQQLSPQMTQLLLQQQMSMHQGFVDAALAAAAAAVAAAPGGSASGVVPMTIGSGAAGLPGVASSVGSAVPPAGTEGDA
AGALSTAGSAVPAEKASKKGGKISRLFKMGSSKSSK*

>Cop12_Cre17.g733150.t2.1
MLGRAFLHNPAGLAELRIQVPNAVYDRSSSIFLTALAIDVLNIVFEQQTIKLDCVLLPAFIKGMASTTNVLVRFFTPVIAMTDLGRPVVVQRYICWM
HTTPSILMLLKMISTTITPRETMIAIFFDEVMVVTGVLALVTTGWQRVLWSLVTHAAMLPVVPYMHKAFTEAMEQIRTRPLQLTMLCIYVLNLVL
WCTFAITWDLALLGWISVTMEEVLYVGCDFSAKVLFSSTLMLSSFKEIEARRENAMRVIEGSSKAKLIAELQALLEQKERFMSSVSHELRTPL
NGIIGISEGMLSGCCGVLPEGVRRQIYIIRTSGARLLALINDVMDAAALRQNKLVLKQEHVVLRHVVDDVLDLTRSLVDGEVALVNLVPPRMMVV
GDTGRIVQILNNLLGNAAKFTRRGQIRVTARQVESGRKVAVTVSDTGIGIPRNKLATIFLPFEQVDMSISRKYGGFGLGLNIVQELVKAHGGTINVSS
IEGKGSAFTFTMPLLRAMGRESLEEGRNAAHRAAAAGGATKMIGGTGMSTTDTSSQLGGSTSGSGGAHGTGGAGTISGAVSTATPRGDSRTPGGS
GAGTNTISDYPGGDTDTMYTRRSDVSESSRVRGGGGGMGGESQSGADATAELEQYGELKYNAAELSALASSRPYAQSAVRDSLPSLAADGSGM
LPHPSGPLSPSVGLDGSAGGAGGAAGSGGMGRGSSSQLPTVLPAGASSAVAAAARARSRAVERGGAGGRGGTTGGGGGGAAGAGVELPGGRIMP
GPKPFHYTMYKRFQLLSVDDDPVNQSVVKSLVQGTGYEVVSARSGAEALRHVAAAPALPDLVLLDCMMPEMDGYEVLQRLRAMTPHVHLPIIM

VSAQTEEDHVVCGLDLGADDYVTKPFKRAELLARIRSQLAYGEWEQDEGVFDTISTMDGGELANVAAAAANAAAGRGPLGGPAAAPRPGAAGG
GSDDSEAGAVSAALGNLNLGPAGVTAASDGLGGASGAEQRLIVCIDDDDVNQVVLHGMLASQHYRYVRASTGAQGLAFVCGPTNGGIPPDLVLL
DCSLPDTTGFDVCRVIRQMYNKQQVPIIMLSARHNESAVVEGLKCGANTYVTKPFRRNELLARIRLHLRARDGPIQRGTSINDMGQVDESAAAAAA
AAASMVGADGAGLAFGGMLPSSSHQAGLGGGGGSYAQQASLAQPPSAHPLLLASGSGSAVFPDSAVLVVAVADYAGLCGMLLPGEMAELSGRM
LAAFERAVRAAGALPIEAGSGIMSAALLPPPPAAAEADGGAAAGLRLAALHRVGRALLDTASTIPVPGTTTCLQLQQALALGALTVSAGGGGGGG
TTSSSFFGPVLVELLDLARRAPPMTIVTPDAEAEALRACGATADIRGPLFLEADDVGGGAGGAVAGPLVSRRLWLVEAHPLAHQYLPPQLLYASGA
ARGAFFQVQPGATGAGEAAHQAAPLAAGAPGAHAGGVGVMGFGFAEQQQPGTRSGSAALLAGAGGGVGGGGAAAAAGMVPVSVHPTPGVSA
AASEAAAGSGGAGRGFGSSSIASYGAAGGGGGSAAGATAASLGLGGPGMGIGLYTNGMGVSRGVSRAFSHTFGLDSDNHGRANSAAAGSAAGGS
VAGGGSVAGGGVHTGHTAGTSGNGGSQGSVLTNGRGGGGSGGASDVAAATAMTAALPGGSAVGGLDSSSVAGITFSLQAAAAAVAAASTGGG
GPAQQHLQTPAGAGSGLHDSAGASGLYFNSSAGGGAGRSPLQPFGVVGGGGGGAGSGMTHNSQPLQLQQQQQQQQQFDMVSAAAAEPQIRALR
HELAAMRQQLEALQGAASTSSASNVMAGGGQGNGGQPQLSQQQLSQQLTQQQLSPQMTQLLLQQQMSMHQGFVDAALAAAAAAVAAAPGGS
ASGVVPMTIGSGAAGLPGVASSVGSAVPPAGTEGDAAGALSTAGSAVPAEKASKKGGKISRLFKMGSSKSSK*

>Vop5_Vocar.0044s0018.1
MGGGGKASTLPAHLQDRIDAIETNQRDTDAQAFQKAVERRARVSFSVAIAGFGVLMFLLSAYLLCTSGIGDPELTAEFHSKTDPNCYTWPMVAFST
AFGLNFITLLFERESAKFQLALLACYINFLAGFNDYLSWRGYSPIVRDSWGQGFQLLRTVMWLLTTPAMVYLLSIISDFSRIKVYSVMLADVLMISF
GILAFLAFNKYLSILLYLVAWVFFSYVVYSMWTMFHASIAEARHDSSRVSLEVLRLFAVGLWFTFPGIWIIVKLGLVDVHTEEWMWCACDFLGKV
MFSSSLLHGNFLTIEQRRLIAMRIVEEGNRYALKTITTIKTSGARLLNLINDILDAASMRKGKLTIKHEKVNLKRVVDDVIDLCQPLAKRGVKLVNDL
RENVPFVLGDTGRIIQVFHNLIGNSCKFTHNGFISIAASVKDDEVEVAVSDTGIGIPEDKFDQIFLAFEQVDMSVTRKYGGTGLGLNLVKQLVEAHG
GRISVKSKEGQGTTFFFTLKIHSSAEHPNEGQPQGTPTEAVAGPAEHSQLAAIRGTAAAPGGGGGHGHGPPRRAPSRRGSFTDKMLGAKKTPSEAG
KSSLAPGGQNAGAHGQPGGAARAAAAAASAAASPQSGEGHGGPAGGAESDLSYARFVRHMMPIRVSTRPTYLPDEALFQLLAYVTCVALHDDSH
DNGKLTKPNCQRAVGRPHARTHAHTRREKTLFVFATTPPPTPTPSPTSPARFHSPPGGIPGGSDAAAAATAATGVPGSGAGVVRRVSRETGGPGGG
GAPAAGRSVTAGPQANAGFLVDIASVSPEAKDSGSFVSAGVAMPAIASANGGRPAAAGGADGGGGGGGGGDAAAAAAAAAAEIAKLKKDYESLE
KQLEEVSNEAARLQDLVDDLEEQLIAKNGATEEASAQAAAASAQATAAAAQAAAAAAELAALRTQVSELECQLEEAARERGGLEAALAEMEQR
LVATHAALASANHEAADRARSRPSALPEPRIETASMASGSEAGFGALGGGGGTAGGAVGATGSSGMSLSTLLGGGGVLAHRAAMPLGMSMRLPS
LASLRAHGGDMRSVLEELGLATLAARFEAEDISPGLLPYLDDTALRELGATSVGARLKLRIAAQALFLG*

>Vop6_Vocar.0009s0380.1
MRKRTGLPLPRQRENAPAQNSVNSTLGEDNGDPEAFRGWVKTWTWTLTGFCFYMTASWVVDACLPANPVASVELFKQVPLLVYQMSSTAFFTA
LVLNLTSLLFEDNAPKRQLALLSCAIKGAACHTDMLLVTGRARVVFDAFGAIVIPQRYVQWMVTTPTMVYILSKISDFTPQQTATAICMDVVMVL
SGLMANFAPGPYLNWLMFSVSMLSFVGVLYMMGRMVFSAVKEHSSPSSRRSLLFIYMCTLLIWSMFPVAWVLHLLNSSSPYGEYLNIFANFMA
KVLFSSSIMYGNYMTIAQRRLLAQQAAENAHRVRMIQELRDAVTRKDQFMSLMSHELRTPLNGIIQLSDALVRGAGGEMNPKGQHFVKTIKNSS
NHLLNIINDILDVAALKEGKLTIKHELCSLAKAVEHVVDIVAPLARKDVAIERSVDPHTPLIIADFSRVIQILYNLAGNALKFTHRGRVCVRVSPSAD
GSSVTLQVADTGIGIPPERISGIWGAFEQVDMSVTRKYGGTGLGLNIVKQLVEAHEGKIEVQSAEGRGTTFTVTLPVLQPCTRQSLELQVMESLSKC
GHASARAAVSRRRSNRLASTSGRKPSLEETASKLARGTTRHASGLTSPSRRDAADGNVSGSNSQEKEDVLYRRRTQELERENLMGELQRRAEHKR
SMEEAHRVSRQLQLSEPERQAERDSRSLERLDLQIAARPPPSLPAPAAAAGGSCLRNSSETGVKSSPGSITAAGSLGSFQAWRGEASEVAHRAVTGH
SSRTSGEAREALATRGSVGGGGGGGGCSGSTAVSTGGNSLADVYEHLLLARGSTDSHSGHGLVRKLSATSVGGGSKSNTVREALRMSTYGRTPGG
GGCGGGGGGGGGGGMHSHSGPVPGGTSHLLLKALDSDLYRGARESHDDGSSVGADSESDGLRAAGRRSQKGPGPVSRSGKIMPASASLNSTNALV
TASSLSPPPGLTLDKLPYSDMYGTVQILSVDDEEVNQIVLEEILTSTGYHFARCMDGLEALDWLCASETMPDLILLDCMMPNMSGHEFCATLRKVIP
GNVLPVIMVSAKSDEDNIVEGLRSGSNDFVRKPYRREELLARIETQLRLKSDSWWLAELVNNVDGRETESMKLLKNILPESIIARMQQGQKFVADS
HPHVVILFSDIVGFTSLSSKLPTAEVFLMLSNMFTAFDKLTDRFSVYKVETIGDAYMVAAGHDEDEDKARKGSPLTRVLGFAKAMLDVVRNITAPN
GERMRIRIGVHCGPAFAGVIGMKCPRYCFLGDTVNTASRMESTGFPMCIHVSEDVYQHHPNMEGEFVEVGEREVKGKGRMRTYLVRVGAWEQA
LRDYAPRQQTAAASTSASASAAGQQQQQQQHQRPAQATTMQQQQQQLQQQQQLSCQQPEREGLHGGAAEGAKSTGVSSGGLGGGELHPQPQLSQ
LSHRASFGAVSPGGSRSAGQVMLCPSSSSAAAAAAAAAAAANDGNHNNGRFVHLLSTVAEEVSVPPSPLLLPDATAAVTDGNGVGFGLVRPQLTG
SAMGVRSPLSRPELSAPRLPPRTTFGSEAYYCDETSDDGANSTLNGMIMASGGALRSCSGSLTGLLPASPFLLQTAPATGAGAGARRAVSDASGYG
NTGDGGDSGRQPGHASVLDVAAEFGLGVGGAAATAPAVAHLREDGLAFAPATAAGGAGRVGSVTGGAVIPATGYLEQQITRLGTQLAAETSKRQ
RLQADLDEERRRSASALQHVTLLQQQAAALATAAAFTSSATSSTAGRQDSTDRNGAVATSYGSCSASTKHPCNNLPSGGPSAKNGTKHGGNSVRQ
QKQLEQQLRDQEQQQQQQQPISQCDSSYAPDAEIVILGPADDDADIGDGSGGSGGGSGGAAGTAGPDSDEGPALEQQRVPSRFPLHLPVAASSGSV
EGGASPRAGLDPRVTTMQGTGNSSNLMRDSPLVLTDIEWHSNGLRRPDDATAAAETGSPEAAVAVGRRETGGGVHVHATDARGGGTGGALVSSP
VSPPLHPLHSPPAGLLAARPASDSTTNDTTTDQKLFYDSGARVNAAVEPFHTSLSHGLKAAVIVRAGTAGGTGGCHVVQSGWLMPRYSLDVLFEE
LGLLPYLGAFQEEAIRLDQLLGMDTGQLERLGLRPLGYCLRLREAVLDLARRLLRACEEAARLPQPLALTDAAPVLGAPHAAAAEAIPSSINSGGG
GGGGGGDGGGGGGGGGGAAMRSG*

>Vop7_Vocar.0001s0831.1
MESDVLGHQSRVVLKTVSRMPRTFISQLYAVDMAVTGWVSFGSLSYAACAIYLASQNVDRSCAAGIGEQVASVEWTFQVQTAAFGAVLLLNLLN
LGMRQHLLPFKCNLLLLFINGVAFVTDLLLWRGATMVMFSSSGRPFAPLRYVQWCHSTPTMIYMLALLADCGGCQLAVPLLSDVLMVASGLAAC
YTRGFLKDAMTIVSFGTFIVVLYYVYGMFHKTLSSDVSPEQRSTLRTVLALLLALWSAFPVVWLAADWHLMGPQMEAICWGVCDYLAKVV
FSSQLWQSNLTEVQLRRDRALEAWEASNRVEAVTRLTALLKQRDDLLSTLSHELRTPLAGIVALSESLCQEVSAALPSSAQNLATVRATATCMLNI
VTSTLDSFAARRVGEPGGAPYVGDDGSGPVTPSVPLVALDLRPLVETVTTVLRPLAHDGVAIVSDLPSVLPLVAADSTRLSQVLYNLVGNAMRFTT
HGEVRVAARMVLPEGAETTSGRPGDGGAAAATAATADLAPTTSNTSANGGGGGIWRYGRPRLSQSSVSSWSSVASFPAGTQVEVSVEDTGIGIAQ
DLLDELFLPYRTGHETQVGGASGESSSPNGLAPTSTGRVSRSIGGTGLGLYLVRLALRAQGSDITAESAPGIGSVFRFRLPLAQQSQQQHPGHHHHH
HHYHTHHHVNGTAQPSSPPQPLTGPHHQQQQVVLVEEVSNQTHQQQQSHADYESGSHAQLSGSGFDCGEARFSYPVSAVTTASDGSGAERVSAA
PSSPKPTVPSSPKPWVACATARLVKLSAGAAAAGSRTGDGDGESGAAIASAGPQHPPTSAFLLGESPGPLHSRPLRMSLDEQRRNLLFPQHKQPSSA
SASAGSRCKASCTAECCGREPPAQGAAVLGVASKAAASTDILSAVADAGLGVAVPQVTTVPPLRLVTPTLTPAPTPTAAMTRNSTGNVMSSLTPFD
VAHAMEEGRQLARSGLRPNFRHRNNGTLQVLSVDDDPINQLVAGQMLTSQSWKVVKCMNGPEALAHLQLAPKPGTVAAAAAAASASVSEQPV
MGASASAAAASLAAAAAAAQPLLLPAVLPDCVLLDVMMPGMSGFEVCRKMREHFSSAQLPIIIVSAKGDSAAVDEAFESGADDYMTKPYKRTEMV
SRIKAQIRTRDSILDAAARAAAAAAMLPAQPAQELSPPAPITSGSTTTAWTGLGTGGTPRACCSSAAARMLPACSGAASEVPSPSPSPLHQVAHQGP
HLDARPTSVDVFLLQQPTPNVIKMRMGASRGGLDGSWGRVGLYKRDGMLSRTGLVEGTVTPWDAGLREGPLKDPVTAPAIVLGSPMIDLQPVEG
SLTGAAGVSASAGAPGSSSDTIHKQVVEPLAPAAGLAEAAAAEVGVAIGMSKPPEALPEATMVEPAKELASTANTPGLCLAGGQSPAATSGTGRCS
SDAGSVTAAGIVAALVDVATASGASEGAVAEGAASSRGDGGSSSGCRGCGDGGEPSGAAALMREVLTEVRRSRVVEADIERLTSRVAALRTACCT
LAAERDGWRRQARDLRALLAAGLGGAIAVPAVSMPVQAKARNSAQPHLALAEALAAAHGSRSSADSLGITGGGAPNGGAVAAQLEDLKKEAAL
LRQQLSMALASVGGNGSIALGGATDTGGSRNFGLPSSCFPAVRPQRGLLGAPRTSDSPHSAAITRVGATGDQDRSGGGGGNDGAPPWGVSVFPNT
AYVPPPDIFLTTEASGLSAGSGPGGGACEGCASGEAGAGGCHAAGAAARHGKRALTRAASSGVAGAPGLVSRAGLAAAAEIAIAKHANGGGGGG
AAAAGGSVGKEDNAAAPVRASGDGTSDAAVALALPQLPKGDTAQVLGELRGSSVASEGGRRATASTSAGDEMCRVSSTARAPVVQASSSRGSRS
KGGGGGVAGTSGILRLLCSKGAAPTGSSPNVSPHRRNPHHQQQQQ*

>Vop8_Vocar.0069s0008.1
MSCVPFPSILVHMWRMVSSAVDETMDPTSKRAIKFIRLFSITTWNLFPFVYFAAIDGALSLEISEPLWAALDWLTKKMVYSSSLMEANFFTIAQRREF
AVRAIEEANRLATIQQLSTAIERKDDFLSAMSHELRTPLNGIIGLSESLMAGACGQLPEKAVKTISTVKLSGKRLLQLINDILDAAKMKQGTLVIKHE
KVDIKRLVTDVLDLSLPLVRKGVRLVNNVGNVPKIVGDNGRIVQILYNLVGNAAKFTRQGVISITAGVSEDNIKVYVTVSDTGVGIPKEKVPKIFGA
FEQADMSTTRRYGGTGLGLHLVKELVKAHGGEITVESEVGVGSSFTIWLPISQDGVLTSVDDSEMKEPYALDLNEPLRRISEESEEGGYHRNHVMG
SRNTSEGDSDGDDDGGGGGGGGGGKRRSSSATAAGGGGGGGDRSDSGGQEGVSGLGGGGSGSRRRLRTSAGGGAGGGSGTAGMENLITVTKTGF
KVMKPFYREKYGGCMVLSVDDDPINQMVVENLLSPEGYKVEQAMSGSEALDFLKKTATLPDVILLDIMMPDMSGYEVCQEIRRRYSAVSIPIIMVS
AKGHPEHVMKGLEAGSVDYVKKPFHRQELLSRIRAQVRNREIFEAEMESRKVTEMLKRILPMSVIQRLQQGQSMIADAHDEVTVLFADVAGWLSS
QSLSSRSTSDVVLVLNEMYGTFEKLLLKYQVFRVEHTSESYLVVSGHDGTSDHIKRILSMAVDMLSAVQQLTFPGGQQINIRIGVHTGPAYAGVVGI
DNPRYCVFGDTVSVANALEAKGFDNTIHCSNAVYGAVRSKERDRGNVMFVPGRKSMTTGPTVMDTFIYKAGSWETALKQLEDEEREKEAAEREA
KLVEEGAAATRREGQEALAAQERARAEALAAQIEALEAERRSTEARVEMEAAEKRRVQERLAAEAAAKAAAQQRLEAERVAAKAARAEAEALR
NRAEAVEAERLRLKPFPIFLGRKSMAGVVTQKVYLLAIYTPLRMQSQPCQVLLFPASCQTDTDTSTLNSNPTICVRNLNRTRVPSTQGYATALRPER

RSGVEGSGRGGGGGAGRSGGAGKGAGRSGGAGKGAGRSGGAGKGAGRSGGASGRIVGGSSRGGSGGGDGGRPWLRAGRGRHS
GASCSRLHQLLIACS*

>MspRh1_62803 *Micromonas species*
MTTDAPGSESLPRVKAKHVFLLFALFAFVNTSLRRVFSPKDGLADSISLPDGSSSDGIERDHAFAAMMLFGAAFMFNMNAAMWSLHVTKTSLNLQ
VAYISAVAAWTHYEMWLGKDWYVSYMGSRFMGGNAVAFSGLRQLEWCFTTPILLTIVQNIHAYAFAAAGTSDKGKRNPATYQPVNRAVLIAAD
ECMLLCGLVLPLASGVERAVFLTAAVACFVFIIYHSVHALLDVMTFSELSHMDSARLTAIVALKVIAWSGYPITYFATEFGYIDCKTQHDWYLYND
VITKFSYTLIISAGSLRFIEVLEERRKAFAIQMSRVQRAFFFNITHELRTPLNSIIGFNTLAMESGELTEFTESFIKASLTSAEALLGLINQILDFAKFEGA
KDKSGGSNATIELSDDVFTLRQLVEQVMDISQKASSRGVDLIFSITSPEHFNTKLVGDFFRLRQCCVNLVDNAIKYSSNVNGRTALVEFSMGIAPGA
KPDSLAITFAVEDNGVGIKLEKQHTLFVPFCQPADHKTAKEKGTGLGLVITKAIIECMGGDIDFESVEGTGTKFFFTLDFERAREASIDGGDDADFVE
DAAQLEALPPKARVVFHPAMNESTRKHVTCIMKCFGAKPGVNYVTVPGEDTLKDKIRQASLLGVPVVLTDVINLNSSLDFIKATPRAGIIIFGLPYQ
LMELHKNISDMRNVQTVLKPVKPSDLLKAIAKLTHQGATREIDFLNDTTDSEDGAVQKRLEHAEIKAAENALIKVEPPDVAEGTGELKGMTVLLVE
DNIMNQQMAKFSILKCGADLEIAMHGQEAVDMVTARFDQGKPGYDCILMDMMMPIMDGATATTEIRALEQRRRLTPQTIVGLSANVGPEYTARV
KAAGMDGSMSKPFYPATLRNTLLNVKKGTYVGFGSSRLSIDRIHTTIEEKPGN*

>MspRh2_61324_Micromonas species
MATTMSRPRVSSGDEIQGSTLLALFAALVALNALVAPHLAGCPIGDGGSGAKGTGGTCAATDASIGGSRDVAVFAAAMFVAATAFALVNAAMTA
SPDRSRHFQSAAYVNACAAFAHLQMVRGENWHVSSADGFSISGLRLLEWLFGTPVMIVLAKQLYALSREPPVDYVSAAVKLFERDRGADGVYIPP
PSIRLVQADVLMLVCGCFIANLAPAPPAVRNGALFVGVATFGYVISHLSRCLAGSAVYSAIAGVRKDAKFGYALAVFNVVSWCVFPTAYFLHVSG
RIDAARLDLGYAIGDAFAKFSCTMLYVTGCGRIMDLAEDEAAQRTDAQVAEQREYIRAVCAELKAPLDAIVGYGQMSADYDENGEKTPSQVRRF
QRAILTSAESMRELVSQAAQYSKVHGEIHARGRMMTGKEGEDVGLPRVAWRKEGGDSRAFPLPPMLPTPGRRFSRVSRESFDGDDETDPPSSVFTL
GKLQDLVVKAANIPVGFELTCEISPPAATHTEHFRANTRLLRQALATLCETAAAQPSVVRRAGGVEAARARGAPPCVRLSASLGATRKMEIAPVID
PNDESRDESLETSDLPEWTDATFTASLILDRRVGSHPSDASNSGNPHSLGVGVTPEELAKRRRLDLSTTVAKTVVTAMGGSLIRRQSDSMSGDASG
DQFSFTVPLLRTSRDESECDFVPVMPLPPGRTVGAVLLRARGAVGAGAMSANHVEHVASSLISYGAKVDKCEHESDAASQLSEFASTDDVYPVLV
MAADDEGDDENSWRHERLLAAAGARGSVVLFSSDASDDVGSDPKPSRHRRYANDSNVVVVARNATGEEVHEALCGVLAHVAANDANPTAAEP
SNQATPSEDVSNPTNDEERRREKFDHSASGAWFKELGESEHLTRANSEHRKSRASHDADEDPYAFHGSPSPQKRLVDESSQKNDAIPERTVAKPEP
ASTASKVKHGFKDDELDGLDVLVVEDNHFQLRIVKATLQRSGVTLDVALHGAEAVAHVRRRVDAGGKLYDLILMDSMMPVMDGATATREIRAM
ESAYRSSKTGDELRDAGNAQPMIIVGLSAEGGPGYEQESRDAGMDGTLGKPCRPETMRKTLKEVHRGEWKRGTFQSASKRASLHF

>MpuRh1_jgi|MicpuC3v2|8757|wlab.149627.1 in phycocosm or 70932 in phytozome
MGNAAVASTEPVSVARTQVMPTVSPWNLAGMATAFVLLNRAIQRVIPGISVGVPNADGSVESVDESHARMAFVVFTAALFFNVNAAAFSIHDSKR
KLNLQVAYISTIAAYTHYEMAEGRDWYVNTFGPSGEVVSGLRQLEWACTTPILLLLVQNLHAFVFAALPRAMGPKKTSLTTTRDGTTKAANAIAP
YVPVNRIALILADELMILCGLVAPLTRGLERFAFLSVAMACFGFIIYHSLFALVDITRRADGLSVADAGRVKCIAALKMIAWTVYPAVYFAVLFGV
MTPARQHEIYLYNDVLTKFSYSLVISAGSMRFVEMVDQKRTQLTAHMAGMQRTFFFNITHELRTPLNSIIGFNTLAMESGELTEFTESFIKASLTSAE
ALLSLINQILDVAKFEGAKDAGSSDGPAIELSEDVFTLRQLIEQVTDISQKASSSGVDLVIHIEHPEHFNTKFVGDFFRLRQCCVNLVDNAIKYSSNVQ
GRSSLVEFTMSICRARGQRAGSARGERGGGDSRGQRDQQSEKGDESIFDDVRDVSGITFSVKDNGVGIPAAKQHNLFVPFSQPADHKAAKEKGTGL
GLVITKNIIECMGGEIEFESKEDEGTKFFFTVDFKHARLSAVDYEEEFEGATDLGFGSAVSGGGLDTEHEQSLPANARVVLHPGMSASSRKHVVNIL
KCFGGRAGVNYVSVPSADKLAGKIEQASGLGIPIVLADIEDTEKTLNLVKQTPKKAGVVIFGLPYQLIDFHRRTSDLRNVQTVLRPVKPSDFLRAAW
KLANVNALGEPDWMHDTGGECDDGVAERLRAAEANADHNAGRAAADSGASASPGDEGDGATAAAASSASAEDLKHELLAGMRVLLVEDNVM
NQQMAKFSIIRSGAELEIAQHGKEAVDMVSSRLEQKLPNYDCVLMDMMMPVMDGATATVLIRELEKKHGAEKPHAIVGLSANVGPEYTDKVKK
AGMNGSLSKPFYPATLRNVLEQVYKGTYAGFSGKGGKDAAAADIQSKPGN*

>MpuRh2 micromonas pusilla (40573)
MRAGSPRGVAAAATAPAHPARADELSGRALLLLFLAFLAADACLTPVFLSSSDAAPRRDDAPSSSATASATSFRRDVAVFGTALFTAATTLSVVSA
LWATHPARRRHFWSATYVNAVAGVAHLQMMRGGEWWLVGDARTRGDLPSGLRLLSWFFSTPVMIVLMRQFHGLARKPPLSSLTTVSKSAFKGG
KKGGNRAAADGGGAAKAKTRASSSSYAPPPASHLAWGTVFMLACGCGGVIAPGMPPPIARVLVVLGGGAFAWVLTQMVRILLGAAEGSAFDS
VRRDRGRIRVLVFINVCAWCVFPLVFLARRAGLIDDDEAHLGFSAGDGCAKFSLSALYLVGCGRILDLAEEDVRRRVQEGMADQLAFYHSLS
FELRQPLSAVIGFGQLALEYPGPEKVPSAVRDFQRAILASAESMRSLVVQASEYSRLEAEIRNLGILKRPAIDRDENAEGDGEVMGFSPATLLDDVM
TSATTALTLGVEVVVETRPKTLLRAAPSTAKTTFVGNVDALRDCLVTLTQGACACRESKEGDCGGAVRCVKLLMELGDATSDEDHFHGATYSEA
TFTAFVPVNGVPSSSSKGPGASAPSSSSPSSPSSSRRVVSCRHLDEMGMDAAKNKMLGLSMTVARAVVEAMGGDLSYALHPEDASEPDCFSISVPL
RRVLYTGPHTTASAHSPPPGDDDSFDFDLLPALPRPRGSKTIAMTHPSLSRHFAAYVSDVARGSGVVVATAIEEAGGGVVAPDDESDPDPGATLAA
AWRRLGADPDAFPVLIAPADAFGGGEGAGGGDAGVGVAAAAREFRDLVCEGGSRASGVLVCATAAATADARAALRERDAVSVVRRPCTTRDLH
AALLACVNGALARARVARQSSLGQSGGGGGGGGGGRRDSVDGGGRRASIDIEEFASLSTSRYMGAGSGKEGRLEKGEVPATASAASASSPLHSDD
EWATPVAAAEKSKEKSPPPSKESSGSFSEIRPKPASKATSTLKDDELDGLDVLVVEDNHFQLRIIRATLQNSGVSLDVALHGEEAVDRVRGRIDRGE
KLYDLVLMDSQMPIMDGATASREIRALEKAHREGKNAAAAAVLNPETMIIVGLSAEAGHEYEREARAAGMDGALGKPCRPETMRKTLKEVHAG
RWKRGSFNTAAKRAVSHF

>**GtRh1**_XP_005821993.1_Guillardia theta (146834)
MSTTQNSTTTVLDVVINQNISSNTPSGFQNLTFSDLIGEYNSTTSTNYLGIQYADFNPYTLWYICMALFLAAASIILALTFSIESFQRNCLLYWIFSLQF
LITASMYLFMSLNIGLLYEVYDVKVEPGIILQPGVMLHRPTNPPVYWMRNVFWTFSTSIDLFILTVVVDSSKNISKQKKYKTLINWEYKTYLFMINA
ALHTCGVIGTIVPASQISKVCKWTYWVFGLGLFVMLMNQLASSQCPLMKTAERNMVLQSYKKLVRVVIITWSLYPALWAIGDGSGTIAWNLKEV
MYAVIDFISKFSFIAMFLHCTNSPSCHWNVSLASFASWFRLCLGDDGGLKVLCMQMDAMQPLACFAKAIKLKRHYGWRRVAPMLYRMKKFPQTL
VFPDLTRFDPDDINAVNGIHGIFLEKNEDTGEFLINSHGKYGKARSVRTFEPWVIQYRTPPRPPAELKEYMECMALDAYYAEPPRCMNVRQALKKQ
VSVNHAKVWKEWHIAAFDDARFLHPVLSDARNPPVPSPSWLLDQWEYEITKFKARGSRKTETTNLPGKDFGSIGILSGKGRFWFCESKSYEIGCGL
RLDTKWPILFYTKNGVVGHPAEVDVSHDVSKSHKRLVTGVSLWQPIFSGVNNVKADAFYHKKAGVMHGASLFVDYRDVRYRPDAKVAACLDRF
YQAFLADGFLARNMLMGFMLKRLSRETIDTYMGEARNMAVVVCMDVVPASEPCLNEYPDHEQLRRDRRERRYFSQRKRELGDLLSRIGEMSRRN
PDKRKEHDKICEALRKRREAMDHVLKERKYRLEREQRERVDLQCEARELDNFRLEIEKKMMSSVLADKDWSAEMEPILFEKERAFERKLEQRTAR
LRKEFEERCTAESEALLKEYEGRSPVLFAEDDGDLRYDTMDTEEHTFFENENKWLFSTGLARMSAFLDENGERIPEITCEGEVEDDYDESTFIF

>**GtRh2**_jgi|Guith1|148915|fgenesh2_pg.256_#_8 (148916)
MSTSSVAYLRTPVVQALDWIGFISLGGTAAVLAYRLMNFKPPNKDILYFFGYREKGMISLYVNLFAAVAYYARITSHLSGDVGAATNIVLYKYFDY
LITCPLLVGTKSKRGETFDLLTTLNLPYKITYAVYVQITIFTGFMSANTPPPATFLWFAFGMLLFSYTWFNIISLVQVRFIQYFAKKGNTTQSRRVSVA
SKAGFRNKNVRNPLQTALSTYFCIWMVYPVLWLLLKTKVIDQVTEHCINVVMDVLAKSMYGFALLRFQLLMDKASLEMSELKVTKSDLMEDFN
AEKKKMRELRRRQQAEMEGEELSDDEEEAHGNSRQNQIKGGNHVSGTSSPISQEQLGMLLSQMTTMQQMSSPRQMAPIGQPASPLQASMMPGGM
PNSFMSAPPPRMIDENAGNAPANWMSAQQVQQSAAGGVGGAQPNNWRQAFDDLDQGRGMSRDV

>**GtRh3**_jgi|Guith1|148916|fgenesh2_pg.256_#_9 (148915)
MSTSSVAYLRTPVVQALDWVGFISLGGTAAVLAYRLMNFKPPNKDILYFFGYREKGMISLYVNLFAAVAYYARITSHLSGDVGAATNIILYKYFDY
LITCPLLVGTKSKRGETFDLLTTLNLPYKITYAVYVQITIFTGFMSANTPPPATFLWFAFGMLLFSYTWFNIISLVQVRFIQYFAKKGNTTQSRRVSVA
SKAGFRNKNVRNPLQTALSTYFCIWMVYPVLWLLLKTKVIDQVTEHCINVVMDVLAKSMYGFALLRFQLLMDKANLELSELKVTKSDLMEDFN
AEKKKMRELRRRQQAEMEAQEMSDDDEDVDDQAGESNQSQKSKAGKQSSGKNSPISQEQLGMLLSQMATMQQMSSPRQMSQPSQMMMSPMQ
TSMMPGGMPNSFMSAPPPRMIDENAGNAPANWMSAQPVQQSAAGGVGGAQPNNWRQAFDDLDQGRGMSRDV

>**GtRh4**_XP_005833164.1_Guillardia theta (107802)
MTGSVPGDSDDAVIMEKTKFVKMQISFLFVICMLMDIGGICFQISKKKRALNSLVFFINTVSFVVYLSACFGWIPAIYSLDGKRVSVERFFQWMNTT
PCMIFVLSALGNTLQKYLIHDVKELVKCVLWDEAMIFAGLLHAYLGFSLLGWMFLLTACFCFYQVMQKLHGAILISISKVATVYEVVSLRVLEIFTI
VLWSLFPLVHVLYFSGTITFTQYDIAQSFVDLATKAIYSVTLITGNFFLLDTVAELRLEQLQAEKDARNSKVVRSEMMDHAMQMAVIEAETSARLS

SRFLANISHELRTPLNSIIAFNSLLLESDDLSTTQTEYVTSSLTSAESLLSVINQVLDFAKLDSESKLFKTSGEEETPKALQPFFLEQVCDNVCDMMSSR
VAAREVDFAVKVSGHHGHEEGKKLMLVGDSFQLCQCLVNLCDNAVKFARKTGGEAHMRVSLQRSSSDWAVVQVEVQDNGVGIARESLDLLFKP
FSQISSHYSREHGGTGLGLAITHKIVTSMGGTITCCSDGLEKGSTFRSHLASPAPPPFVPAPPAPAPSSLTPAPISSALGVALTCNRMVVPFAIYKQEEV
ADELPAEEEKSHSSEDKLHRHDDKPLPHDLQLVLCMARGPSFRSVELFCRNHKMKPESFAYDGPEPSNMSMIRLVSKIKRTLGSDSPPVFLVQIEVY
KELLKKQMQLPSRLLIFGYIDSQFELIESQDDMATRLVPRPIKHSLLHSKIHSMLLITAAKTERSSSVASGDSEKISELDDVSHPDEERQQEKKLRVLV
VDDHFANQKVAVALLNKVLGKDAVIADIASDGVEALKLVEDNKDDPYNLILMDIQMPNMDGLEATRRVRLLEKKDFDDASSSDNLRVGG

>**GtRh5**_XP_005818773.1_Guillardia theta (122016)
MEKERREQQVFENLQVEGYADAEFLDKRPSCDSRMDEGLPEPLRPLSPPHESRSEAPLNQQEDHQRVPAFFRQSRHFSQSFKLPSLKQATQVDQKF
MIRATMNDVPGLFLFALWLMVYVVFVYALRSYSSACANVQTDESEYYTMKKTMFVKILAVFLFSICILMDLSGMLFQISAKKRTLNSLVLFINLVA
CTVYLSYVTGVLPVLHDLEGRQMFIERYF**Q**WMN**T**TPCMLF**V**LHALGSSMEKELVISFSSLFRVLISDELMILTGLVHAVVGNSMIGCVACFLSCCFF
LDVLRGVHAFTNSSVARAATTYEIASLRSLEISTFLLWSVFPVVHLLHY**G**GFISTFQ**Y**DIAQTFV**D**ILT**K**SVYTVTLLTGNFCILDTVAEVRIAQLQAE
KETKHKNVIRTELMNQALQTAMLEAETSSRLSRHFLANISHELRTPLNSVVAFNSLLESEDLSAAHKDYVRSSLTSADALLTVINQVLDYPKLEAK
EDNEKEGKGGEEKEGSELMEEFSLLKLGEDLSDLIASCIKSDLDFAVDIQVSEADAELFLYGDAFHIRQCAMNLCDNAMKFSPEQGGEVTLRMRLS
DLDEASSVCLLHVEVEDNGIGIPEDKLNLLFKPFSQVSSQYTRLHQGTGLGLAITKKLVDSMHGSISCQSRGAEAAKSRGGAAAGGTGTVFCITVPL
HFTRQPVGVNSTLEIPGLQEGTVILATRKGPSSALIMRLCKERKVRVVDLRQDKGPVSKQLLVKLQAAVKAQGDRPFCVVVDMLVYEQLSAMATE
LSCLKSFLILGGMTSQLCLLKKKRHDEASNVIPLPIKPSVLFSKIFSSFTEEKKSPALPSFPYAAKVAKETVSSGNVPALEEAVKKEAEEDNRMRILVV
EDQIANQKVAVALLQRVFGKDKVAVDIANNGEEGVAAASSGSYDLILMDIQMPIMDGLEASRKIREWEKEKDRKKICIIAVTAHTSPAHVEECMQ
AGMDRHFSKPLSLSLMRSIVEDFDDWKGSRV

>**GtRh6**_jgi|Guith1|149064|fgenesh2_pg.274_#_4 (149064)
MPSTCSFSHDSQMEKERREQQVFENLQVEGYADAEFLDKRPSCDSRMDEGLPEPLRPLSPPHESRSEAPLNQQEDHQRVPAFFRQSRHFSQSFKLPS
LKQATQVDQKFMIRATMNDVPGLFLFALWLMVYVVFVYALRSYSSACANVQTDESEYYTMKKTMFVKILAVFLFSICILMDLSGMLFQISAKKRT
LNSLVLFINLVACTVYLSYVTGVLPVLHDLEGRQMFIERYF**Q**WMN**T**TPCMLF**V**LHALGSSMEKELVISFSSLFRVLISDELMILTGLVHAVVGNSMI
GCVACFLSCCFFLDVLRGVHAFTNSSVARAATTYEIASLRSLEISTFLLWSVFPVVHLLHY**G**GFISTFQ**Y**DIAQTFV**D**IL**T**KSVYTVTLLTGNFCILDT
VAEVRIAQLQAEKETKHKNVIRTELMNQALQTAMLEAETSSRLSRHFLANISHELRTPLNSVVAFNSLLLESEDLSAAHKDYVRSSLTSADALLTVI
NQVLDYPKLEAKEDNEKEGKGGEEKEGSELMEEFSLLKLGEDLSDLIASCIKSDLDFAVDIQVSEADAELFLYGDAFHIRQCAMNLCDNAMKFSPE
QGGEVTLRMRLSDLDEASSVCLLHVEVEDNGIGIPEDKLNLLFKPFSQVSSQYTRLHQGTGLGLAITKKLVDSMHGSISCQSRGAEAAKSRGGAAA
GGTGTVFCITVPLHFTRQPVGVNSTLEIPGLQEGTVILATRKGPSSALIMRLCKERKVRVVDLRQDKGPVSKQLLVKLQAAVKAQGDRPFCVVVDM
LVYEQLSAMATELSCLKSFLILGGMTSQLCLLKKKRHDEASNVIPLPIKPSVLFSKIFSSFTEEKKSPALPSFPYAAKVAKETVSSGNVPALEEAVKKE
AEEDNRMRILVVEDQIANQKVAVALLQRVFGKDKVAVDIANNGEEGVAAASSGSYDLILMDIQMPIMDGLEASRKIREWEKEKDRKKICIIAVTAH
TSPAHVEECMQAGMDRHFSKPLSLSLMRSIVEDFDDWKGSRV*

>**GtRh7**_jgi|Guith1|138313|fgenesh2_pg.31_#_17 (138313)
MVLFSVWIVFYSLLIFLVHWISSRMTGSVPGDSDDAVIMEKTKFVKMQISFLFVICMLMDIGGICFQISKKKRALNSLVFFINTVSFVVYLSACFGWIP
AIYSLDGKRVSVERFF**Q**WMN**T**TPCMIF**V**LSALGNTLQKYLIHDVKELVKCVLWDEAMIFAGLLHAYLGFSLLGWMFLLTACFCFYQVMQKLHGA
ILISISKVATVYEVVSLRVLEIFTIVLWSLFPLVHVLYF**S**GTITFTQ**Y**DIAQSFV**D**LAT**K**AIYSVTLITGNFFLLDTVAELRLEQLQAEKDARNSKVVRS
EMMDHAMQMAVIEAETSARLSSRFLANISHELRTPLNSIIAFNSLLLESDDLSTTQTEYVTSSLTSAESLLSVINQVLDFAKLDSESKLFKTSGEEETP
KALQPFFLEQVCDNVCDMMSSRVAAREVDFAVKVSGHHGHEEGKKLMLVGDSFQLCQCLVNLCDNAVKFARKTGGEAHMRVSLQRSSSDWAV
VQVEVQDNGVGIARESLDLLFKPFSQISSHYSREHGGTGLGLAITHKIVTSMGGTITCCSDGLEKGSTFRMVVPFAIYKQEEVADELPAEEEKSHSSE
DKLHRHDDKPLPHDLQLVLCMARGPSFRSVELFCRNHKMKPESFAYDGPEPSNMSMIRLVSKIKRTLGSDSPPVFLVQIEVYKELLKKQMQLPSRL
LIFGYIDSQFELIESQDDMATRLVPRPIKHSLLHSKIHSMLLITAAKTERSSSVASGDSEKISELDDQEKKLRVLVVDDHFANQKVAVALLNKVLGKD
AVIADIASDGVEALKLVEDNKDDPYNLILMDIQMPNMDGLEATRRVRLLEKKDFDDASSSDNLRVGG*

>**GtRh8**_jgi|Guith1|145205|fgenesh2_pg.99_#_1 (145205)
MPGQTSRAEEPCCEIRGLKEERKMPTSGMPGREDSEKDLTSSSNRDLASVLQKGGIASPSTISRLIKMGSSLKREHLFQSDDLDEQTPQQLTLKEKLL
FWAIDAPGIVLFTIWCLVYISFTFACWWYAPFSTPSIKGMEPMPNVHVIMHQAKFVKVVLATCIFGICIIIDIAGVLFQVSSKKRQLNSLVLFINLVSFT
VYLSTIYDLYPSMYDFQGNPIYVQFFA**Q**WMN**T**TPVMIL**V**LASLGSSMQDSLVQDWGIVIRAILWDEVMLTLGLTHTFLGPGLYGWICFGCAGCCF
MTVMWYIHSISSISLSNAATTYEIMSLRGLEAITYMLWVLFPSLHILHH**L**GLLDTLQ**Y**EIARTVV**D**VVV**K**AIYSVALMSGNFCLLDTVATLRVAQLR
SERDSKQTAVVRAEVMNRALQMACVEAETSARLSRRFVANISHELRTPLNSVIAFNSLLLDAEELDPLHREYVKSSLTSAEALLGIINQVLEYAKLE
AREDSDTGKGKGDGAPAIELNKQPFLLTDICEDLCDILSARVNMRKVDFAVDVAKQKKFEMLPALVGDSFRLRQCLINLCDNAIKFARDDHGKVIL
RIHVDSQEKDLAQLRIEVWDNGEGIPEEKQKLLFKPFSQVSSHLRNHNGTGLGLVITKRIVNAMGGNVECRSSVGGGGTTFTVTVPLPIAKSEDVKR
EEATQDGLSGRVLVVLREGPGLEFVRGLCEEWGLQSSVISFEENPHGHARAIATSQRLLEALKAQDEAVLVMDCQVYLHLIADSPSSLASRRLLLV
GHLDDQSKLPPKSMAQFVLRPIKPSLFRSKLEAAFSLTPAPVETSVVKPQKPQTEAEEAAPTGEDRMQILIVEDHPVNQKVAIAMLHKALGKDKVNI
VLANNGQEGLDLATARGHAFDLILMDRTDPPYFIVAMTAHASQADVEECLSSGRRREKERRMGGGGGTRVKGEGEGEEKDCEVVGVDGMAGM
DRYASKPLNLNVMRDLMAEFLTWRSANPRVSPTA*

>**GtRh9**_jgi|Guith1|144198|fgenesh2_pg.84_#_1 (144198)
MPGNPSVVMSSHSASLHDENTSTSNSHEPSREKKDVAIASSFRPSTASEQNLRARLTKESAIAKAESSSFVNKSSKSSFIHSPDKGSRQGSFRIDTADK
KWSLGMIRSEAPGVVLFIAWCFMYALVLSGARQLSAYCRQQSASGTRNEQVIMDKAKFVKVLAAFIFGICVVMDLAGMIFQVSAKKRPLNSFALFI
NLVSFIVYVSTILDYFPLMFDFDGNPVQIQFYV**Q**WMN**T**TPIMIL**I**LACLGTSMQDVLVQDWGVVVNAILWDETMLVLGLVQTMLGSSIIGWVCCV
CSGCCMVVVFRRIHQISNASVNNAATTYEIASLRGIEWFTYMLWSLFPCVHVLYF**L**RRIDLVQ**Y**EIMRTFV**D**VVA**K**AVYTVALLTGNFCILDTVAT
LRIKQLQAERDSKDKTVLRAEVMNRALQMACVEAETSARLSRRFVANISHELRTPLNSVVAFNSLLLDADDLNPVHREYVKSSLTSAEALLGIINQ
VLEYARLESKADGSESGSSRQDLLPSSIELTEKPFFLADLCDELCDILTARVNLRKVDFAIELCTEYKGGSVPCLYGDSFRIRQCLINICDNAVKFAKD
EGGQVVLRIELLEEAPDGSAFLSMEVWDNGEGIPQDQQDLLFKPFSQ

>**GtRh10**_jgi|Guith1|144226|fgenesh2_pg.84_#_29 (144226)
MEKDFPSVNGVAKSRVVHIASPSEAPLISSYRNKMSQNSFHTKTKSSSFISDSGSNDEKGSFSTRIKKAQKEMPGVALFIVWCFIYVGFVYGSWVLS
GYCKPKMGFSAQSDEVTLDKSKFVNVLAAFIFGVCIIMDISGMVFQVSAKKRQLNSLALFINMVAFVVYVSTVLDVFTPMYDTTGEPIAVQFFM**Q**
WMC**T**TPIMIL**V**LASLGTSMEENLVPDWPLVINAICWDELMLVLGLTHNIIGSCFIGWAVFCCAASCFVVVYYRIWQIIDRNVKQAATTYEITSLRGL
QIYTYLLWLSFPTLHILHH**L**HVLDDTQ**F**SICRTFV**D**VLA**K**AIYTVALMTGNFCILDTVATLRLQQMETEKDSKERTVLRTEVMNRALQMACVEAET
SARLSRKFIANISHELRTPLNSVVAFNSLLLEADDLNSIHREYVSSSLTSAEALLGIINQVLEYAKLEAKADGSDDGSQSSKHEMIPSSIDFTEKPFHLG
ELSDELSDIMAARVSGKQVDFAVQLCLSCKLGTCPFLLGDSFRLRQCLINLCDNAVKFCRDEGGQEEAPADSAFVCLEVWDNGEGIPLEQQDLLFK
PFSQLPSKHMSNNGGTGLGLAITKRIVSAMCGTIECVSNTDGRGTTFRIVVPLPVCSGRDFELTFPKFMARDSLRGKVRLVLPEGPTKTMMKEMLRF
WGMDIDDIFTAASAMDLTLKQMERLKAELRDKKEKEAKEGRPSVLIIDSQLQNGLLDGWSKDELNSLLVVGYLDEQGGGKYKVSCDLHKLVLRP
VKMSALYSKLLVTVLPSSLLAC*

>**OtRh1**_jgi|Ostta4221_3|72114|OT_ostta17g01230T0.. >jgi|Ostta1115_2|46936|gw1.24.242.1
MAVDARSWRGFARGKVNGMGVRLSALLVLFLSFVVVTEWVRDREGERFSAFTPRLIRQQRAVDARTGERLMVSGDVNANASATGPDPFEDLRT
YVDHGVVRLEAEVCGSTSLMALTVFAVCASIGLNDIMWTPSRSRRSVSSTVL**Y**ITIVACY**T**HYLMVQGSDLLKQGVEGTYYSLLRYL**E**WMM**T**TPV
LLI**L**VFQLHALCVGDERAPYRTDMWCACIADEIMLITGWLTNELSGKVHGVCLTISMLCFTYVISRCVGLFRELLTSNLVAGDRMRFIILACAKTIC
WTSFPIVYMAKE**M**EFIDTSA**E**HEWFLSC**D**VLT**K**AVYCLLLSAGSIRVLDVTRDEELADIERLTKMQREFFFNITHELRMPLNSVIGFNTLAVESGEL
TDVTNGFIKNSLTSAEALLGLINQVLDYAKFNRKGVEVSGGHGLELSNDNFTLEELIDQTLSICQRADYTGNLFVRIDPSLFPMTYICDFFRLRQCLV
NLVNNALKFSNHLDRPGCVMIDVRGYLDESEAHLTFSVEDNGVGIPEERQSAVFVPFSQQSDYSALRVQGTGLGLTITKTIIELMGGTIHFTSKEDV
GTKFNISLPMGYKSADKMRIAPKNLMALIGLRPGLQMRTLRNILACYQLNVRDMIEVGLVGQDREQVEHYIMHGHTSNKHVVLCIEEEQYFQNED

WLKSIKPEPKIMIISKSSRMKDLPHVANVRSIMKPVAMMPTIEALEYFSREGEGECFVDETESQGVGSIMKSESDTAASKSATDLDGDVDISSMRVLL
VEDNRMNQQVAIQSMKKCRVTVDVADNGLIATQMIEDTIHGVIAPYDVIFMDVMMPVMDGNEATRKIRQMEKEAPETYKRNLIIALSANVGPEHT
IAVTEAGCDGSLGKPFYPSTLRQLLYSIFMDEYEGFAAQETFFARPG
>**OtRh2_**OUS45390.1_Ostreococcus tauri (199419)
MGRMGARDGTLTKGARTQVPALVMRSVENARVAIDDGKLDTAIKAMKSTDALCSRVVAPPTVHGLCLRVLADAYVSKKAAEGAGGLAGGAMT
EGDGSGGGEAQSSGEGDDGVNEDYAELAKEALKRGIDMCKVHEGKAGMNAYMRHDLLGRLGDLYAALGEIYREEGNHKEAIRALRHGLARFEK
NNQNDFTAATYNRVAYCYMEQNVWDAALDTLQSAERAATGNDAESILLSTTHAYRAQCYRALDQIQPAREAFEKALTFAMACGNEPVVREAEE
FLAETQAHSAAQTRATAMAVDARSWRGFARGKVNGMGVRLSALLVLFLSFVVVTEWVRDREGERFSAFTPRLIRQQRAVDARTGERLMVSGDV
NANASATGPDPFEDLRTYVDHGVVRLEAEVCGSTSLMALTVFAVCASIGLNDIMWTPSRSRRSVSSTVLYITIVACYTHYLMVQGSDLLKQGVEGT
YYSLLRYL**E**WMM**T**TPVLLI**L**VFQLHALCVGDERAPYRTDMWCACIADEIMLITGWLTNELSGKVHGVCLTISMLCFTYVISRCVGLFRELLTSNLV
AGDRMRFIILACAKTICWTSFPIVYMAKE**M**EFIDTSA**E**HEWFLSC**D**VLT**K**AVYCLLLSAGSIRVLDVTRDEELADIERLTKMQREFFFNITHELRMPL
NSVIGFNTLAVESGELTDVTNGFIKNSLTSAEALLGLINQVLDYAKFNRKGVEVSGGHGLELSNDNFTLEELIDQTLSICQRADYTGNLFVRIDPSLFP
MTYICDFFRLRQCLVNLVNNALKFSNHLDRPGCVMIDVRGYLDESEAHLTFSVEDNGVGIPEERQSAVFVPFSQQSDYSALRVQGTGLGLTITKTIIE
LMGGTIHFTSKEDVGTKFNISLPMGYKSADKMRIAPKNLMALIGLRPGLQMRTLRNILACYQLNVRDMIEVGLVGQDREQVEHYIMHGHTSNKHV
VLCIEEEQYFQNEDWLKSIKPEPKIMIISKSSRMKDLPHVANVRSIMKPVAMMPTIEALEYFSREGEGECFVDETESQGVGSIMKSESDTAASKSATD
LDGDVDISSMRVLLVEDNRMNQQVAIQSMKKCRVTVDVADNGLIATQMIEDTIHGVIAPYDVIFMDVMMPVMDGNEATRKIRQMEKEAPETYKR
NLIIALSANVGPEHTIAVTEAGCDGSLGKPFYPSTLRQLLYSIFMDEYEGFAAQETFFARPG

>OlRh1_jgi|Ost9901_3|25667|estExt_fgenesh1_pg.C_Chr_160087 (25667)
MARSKSTPIDARRERRMSAGARDARTWRAFARGRVDGTGVRLSALTVLFLSFVVLTEWIRDREGEKFSAFTPRLIRSRHVLDVTTGERVMMTEER
ARGSGLNAGNASGAAAANLRTYMDHGVVRLEAEVCGSTSLMALTVFAVCASIGLNDIMWTASRQRRRVSSTVMYITIIACYTHYLMVQGSDLLM
KSIEGTYYSLLRYL**E**WIF**T**TPVLLI**L**VFQLHALVVGGAKSRFRTEMYAICVADEIMLITGMLVNEMNGTVRGMLLTVSIGCFMYVITTCIQLFREVL
ANELTKGDRTRFVILAIAKTVCWTSFPLVFMAKE**L**NYIDTSA**E**HEWFLSC**D**VLT**K**AAYCLLLSAGNIRVLDAARDEEMADIERLTKMQRDFFFNIT
HELRMPLNSVIGFNTLAVESGELTDVADGFIKNSLTSAEALLGLINQVLDYAKFNRKGAEVDQAHGLELTNDDFTIEELIDQTLSISQRQDYTGNVF
VRIDPSLFRMTYKSDFFRLRQCLVNVVNNALKFSSNLDRSGNVIIDVRGYLEEQEARLTFSVEDNGVGIPEEKQSAVFVPFSQQSDYSALRVQGTGL
GLTITKTIIELMGGVIDFTSREDVGTKFNITLPLGYKATEKQHTAPRDLKVLIGLRPGLQMRTVRNILACYQVNVQDMLEVGLEDAQDREQVEHYV
RHSHKANRPAVLCIEEEQYFAHESWLNSIDPEPHILIISKSSRMKDLPHSACKRAIMKPIAMSAFIETLEYLAADAKNGEVDENAMRTRGLGGRDEST
SSLAENSMMRSERTSSDSKRAPKSSAEQPDIDISSMRVLLVEDNRLNQQVAIHSMKRCNVFVDVAENGLIATHKVEDTIRGNSKPYDVIFMDMMMP
VMDGNDATRRIREMEQSAPPGYKRNLIVALSANVGPEHTLAVTEAGCDGSLGKPFYPSTLRSLLYSIFLDEYEGFEGETMNTASRPGH

>OlRh2_jgi|Ost9901_3|89413|ost_16_006_019 (89413)
MRGAAKLRSDRADVARPSSTSDLAARGARRSTNRDDPNGLGASTTARRASDDDARAMARSKSTPIDARRERRMSAGARDARTWRAFARGRVDG
TGVRLSALTVLFLSFVVLTEWIRDREGEKFSAFTPRLIRSRHVLDVTTGERVMMTEERARGSGLNAGNASGAAAANLRTYMDHGVVRLEAEVCGS
TSLMALTVFAVCASIGLNDIMWTASRQRRRVSSTVMYITIIACYTHYLMVQGSDLLMKSIEGTYYSLLRYL**E**WIF**T**TPVLLI**L**VFQLHALVVGGAKS
RFRTEMYAICVADEIMLITGMLVNEMNGTVRGMLLTVSIGCFMYVITTCIQLFREVLANELTKGDRTRFVILAIAKTVCWTSFPLVFMAKE**L**NYIDT
SA**E**HEWFLSC**D**VLT**K**AAYCLLLSAGNIRVLDAARDEEMADIERLTKMQRDFFFNITHELRMPLNSVIGFNTLAVESGELTDVADGFIKNSLTSAEAL
LGLINQVLDYAKFNRKGAEVDQAHGLELTNDDFTIEELIDQTLSISQRQDYTGNVFVRIDPSLFRMTYKSDFFRLRQCLVNVVNNALKFSSNLDRSG
NVIIDVRGYLEEQEARLTFSVEDNGVGIPEEKQSAVFVPFSQQSDYSALRVQGTGLGLTITKTIIELMGGVIDFTSREDVGTKFNITLPLGYKATEKQH
TAPRDLKVLIGLRPGLQMRTVRNILACYQVNVQDMLEVGLEDAQDREQVEHYVRHSHKANRPAVLCIEEEQYFAHESWLNSIDPEPHILIISKSSRM
KDLPHSACKRAIMKPIAMSAFIETLEYLAADAKNGEVDENAMRTRGLGGRDESTSSLAENSMMRSERTSSDSKRAPKSSAEQPDIDISSMRVLLVE
DNRLNQQVAIHSMKRCNVFVDVAENGLIATHKVEDTIRGNSKPYDVIFMDMMMPVMDGNDATRRIREMEQSAPPGYKRNLIVALSANVGPEHTL
AVTEAGCDGSLGKPFYPSTLRSLLYSIFLDEYEGFEGETMNTASRPGH

>OlRh3_jgi|Ost9901_3|28080|eugene.1600010136 (28080)
MSAGARDARTWRAFARGRVDGTGVRLSALTVLFLSFVVLTEWIRDREGEKFSAFTPRLIRSRHVLDVTTGERVMMTEERARGSGLNAGNASGAA
AANLRTYMDHGVVRLEAEVCGSTSLMALTVFAVCASIGLNDIMWTASRQRRRVSSTVMYITIIACYTHYLMVQGSDLLMKSIEGTYYSLLRYL**E**W
IF**T**TPVLLI**L**VFQLHALVVGGAKSRFRTEMYAICVADEIMLITGMLVNEMNGTVRGMLLTVSIGCFMYVITTCIQLFREVLANELTKGDRTRFVILAI
AKTVCWTSFPLVFMAKE**L**NYIDTSA**E**HEWFLSC**D**VLT**K**AAYCLLLSAGNIRVLDAARDEEMADIERLTKMQRDFFFNITHELRMPLNSVIGFNTLA
VESGELTDVADGFIKNSLTSAEALLGLINQVLDYAKFNRKGAEVDQAHGLELTNDDFTIEELIDQTLSISQRQDYTGNVFVRIDPSLFRMTYKSDFFR
LRQCLVNVVNNALKFSSNLDRSGNVIIDVRGYLEEQEARLTFSVEDNGVGIPEEKQSAVFVPFSQQSDYSALRVQGTGLGLTITKTIIELMGGVIDFT
SREDVGTKFNITLPLGYKATEKQHTAPRDLKVLIGLRPGLQMRTVRNILACYQVNVQDMLEVGLEDAQDREQVEHYVRHSHKANRPAVLCIEEEQ
YFAHESWLNSIDPEPHILIISKSSRMKDLPHSACKRAIMKPIAMSAFIETLEYLAADAKNGEVDENAMRTRGLGGRDESTSSLAENSMMRSERTSSDS
KRAPKSSAEQPDIDISSMRVLLVEDNRLNQQVAIHSMKRCNVFVDVAENGLIATHKVEDTIRGNSKPYDVIFMDMMMPVMDGNDATRRIREMEQS
APPGYKRNLIVALSANVGPEHTLAVTEAGCDGSLGKPFYPSTLRSLLYSIFLDEYEGFEGETMNTASRPGH*

>OlRh4_jgi|Ost9901_3|47806|estExt_GenewiseEukaryote.C_Chr_160302 (47806)
MMTEERARGSGLNAGNASGAAAANLRTYMDHGVVRLEAEVCGSTSLMALTVFAVCASIGLNDIMWTASRQRRRVSSTVMYITIIACYTHYLMVQ
GSDLLMKSIEGTYYSLLRYL**E**WIF**T**TPVLLI**L**VFQLHALVVGGAKSRFRTEMYAICVADEIMLITGMLVNEMNGTVRGMLLTVSIGCFMYVITTCIQ
LFREVLANELTKGDRTRFVILAIAKTVCWTSFPLVFMAKE**L**NYIDTSA**E**HEWFLSC**D**VLT**K**AAYCLLLSAGNIRVLDAARDEEMADIERLTKMQRD
FFFNITHELRMPLNSVIGFNTLAVESGELTDVADGFIKNSLTSAEALLGLINQVLDYAKFNRKGAEVDQAHGLELTNDDFTIEELIDQTLSISQRQDY
TGNVFVRIDPSLFRMTYKSDFFRLRQCLVNVVNNALKFSSNLDRSGNVIIDVRGYLEEQEARLTFSVEDNGVGIPEEKQSAVFVPFSQQSDYSALRV
QGTGLGLTITKTIIELMGGVIDFTSREDVGTKFNITLPLGYKATEKQHTAPRDLKVLIGLRPGLQMRTVRNILACYQVNVQDMLEVGLEDAQDREQ
VEHYVRHSHKANRPAVLCIEEEQYFAHESWLNSIDPEPHILIISKSSRMKDLPHSACKRAIMKPIAMSAFIETLEYLAADAKNGEVDENAMRTRGLG
GRDESTSSLAENSMMRSERTSSDSKRAPKSSAEQPDIDISSMRVLLVEDNRLNQQVAIHSMKRCNVFVDVAENGLIATHKVEDTIRGNSKPYDVIFM
DMMMPVMDGNDATRRIREMEQSAPPGYKRNLIVALSANVGPEHTLAVTEAGCDGSLGKPFYPSTLRSLLYSIFLDEYEGFEGETMNTASRPGH*

>DsRh1_0121s00015.1_**Dunaliella** **salina**
MLREKANVVAPRPGDAKEAIRISTRVWLGVGTTSYLTCAFGLWSTFINGNSVAHEQNLARLHAEVPGQYLEWPMSAFAAVLVLNVLNLALRQNT
TKFRTNLLLLFINGVAFTTDLLINLDLTPVFQAANGRMFHPLRYL**Q**WSH**S**TPTLIY**M**IWLSSDPEEVEAPQLMYAVANDVVMILTGPASTCSSGSM
QLL**WGAVSFATFFAVLITVSKMFRSNIDNLEDSEARGIVRAVLFLMLGLWNLFPVVWLLAELRMISPAMEHLCWGLCDYAAKAVFVSQLW
QSNIASVYERREIALRMWEESNRVLVIDKLQRLVDAKEQLLNVISHELRTPVLGIMALSGSLVKDVQQKVPINVNHLCMMKSSAAFLNNLISASIET
AKNKDQKPQAAHEAVYMYELVEEVCTLICPLVREGVTLTNAIPSELPPVVGDRTRLMQVLFNLVGNASRFTMHGHIHVRARILDNYIEISVEDTGIG
VAQEDIEAIFQPYLTLTSGVASSCGGTGLGLYLVKLALDGHNADVNVESEVGKGSAFH

>**KnRh1_**GAQ84541.1_Klebsormidium nitens (kfl00193_0190_v1.1)
MADEVPSTPPGGPPAAQEGEKEGPPSPVVPVPRGAVPQLLELLDSERSLRKPPRTWLIASSVSALVATFAVLVLLLRQWHPPAGRQAPFDPTRHSTE
VGMVAFGCAFILFTCSLICRTDKEKRTAAFLVCYINAIAFSTNMLLYYSATPVVLDFFGRPCFPVRYV**Q**WLH**T**TPTMIF**M**AAKISSFTSPQVVVAVL
YDMLMLATGLTASLAPSWPVMAAAISCSCAAFLAVLVLVWNMFRSALREARDLASYRNLQFLQAHMVFTWNIFPLVWALSA**L**HVITPET**E**AYLY
LAG**D**LSA**K**VVFSALLLEGSFLSIEEKRRAAAAVQEENSKNALIAELRQAVSQKDRFLASVSHELRTPLNGIIGLSDTVLQGSCGPVTEVLLHTLGTIK
KSGHRLQNLVNDILDVSSARSGPLVLRYDRVKLRPCVDHVLDLTTPSLKWSVKLHNDVPAGLPELQCDPARLIQVLHNIVGNAAKFTDEGEIRVSA
RLRKNQTGQDVVAVTVKDTGIGIPAERIADIFSAFEQGSDAIVQQHGGTGLGLSLAETLVRAHHGSISVTSRLGEGSAFTFVLPLVQPKREKEESAPE
EPEPSRSRPPSAPSPQREADRRERASSSADSAASDGEAAPKFARSSLTKFQRESASGYTLKQQITGHCASEGFEDGAGRLHRSFFDVNGQYEILSVDD
DPVNQMVVEGMLRPAAYKITKKMDGMEALAYLERSDTTPDLILLDVMMPGLSGYEVCRKVRQMFPASALPVIMVSAKSQEGDIVEGLKAGAND
YLTKPFKRLEILARIETQLKIKKLWKVEM**EAAKSYQLLKKMLPES**IIHRLNSGQSLIADSHPEVTILFSDIVGFTEIAGCSRTADLIFMLNDMFTGFDE
LVDKHGVYKVETIGDAYMVVAGHDGAADHAGRVLRMAMDMLALVHAIKQPNQRESVRIRIGVHSGPAYAGVIGVKCPRYCFFGDTVNTASRME
SNGYAQAVHCSPATHDLTKHLFDFATVPRRHIKGKGPMETYLLKHGEWELAHRALLADAAAAPPLERAGTGWWLXMAVGGRVPEDKGKEDGE
KSAEEKAPAQSETENRLSDSRIRASSEPVPPLRQEVDKRPPVQDPGTQPSSKLAADEPPGVSPVADASARARFTSLRITPPGGPLHPASPRIRSPLSRSY

SSPDLKVLINREAFQAAYPESSPSLEGMSPAPANGTPSPKPSVRSTSAGGSLGSTPVSESERRVSDGSPKLELHSTKFVQVGKTAWVLKRPPSISGAK
GDPAAPIVGFGVAGKAAAPPAAKDTRMEHLKMMLGSDPGSYVRRLSDTSIISDLDGPHEDG**GPPERGTA**PAGVPAADGSRTKAESERAGRPAETS
LAKETPSAKDSEVKAHTTKPTAEKSPPSTDDVSRGAPKREEKRKEEQATEKAPPRSLPVMVQRNLAAALEGPAAGGGGVLGASGSLRQYSRVSRT
ELVCLAASSCGFSDPHSRDVSNSGTPEGSKRPSFETPEGSKRSSLEERDPPVGGPVADPAHDKGFSHLRPGQDDRAPPGVEQQVCGRVGEPGRKPR
WSGRDPSPLKPRPDIAGIPLNLTRLEEEVKPLALPLADRSMANVEEEFPVVTKPSLENGTGTEANGTLSNDQGVSSDDEQVAPLTAKKDGSRSPERS
PRRYTDFAPAPLRVATSSAHAAHRRSVSQWLPERNSPPGAPPPQPTGSPAQRTKAEALAQQPGQRRKTSVVSPGGSSQDRSPEHRAPERPVPDPLSS
QTRAAAAAVAAARGIKVPAKPRLAEGVELDAATLERLTEAITEQVLSHLGTPRGSTSSISSSRGSPSGQDRAQRSLSASPLRGAGWGPWRVPARGIP
LDEASRDSSGKTSPGGSRSPRGRMAFTEFAAHDDGWAREESRFASDPAYPGAAASSLPIQGRHVAGFPWQLELTRSYSEDGVAARYERDRSEARA
PPGGWADVASDVSSGSWSSFESTYTGGAPGFDRYRPEVTSAEGDDLQARGANGARLADASGNGHLAGGRDAPGEIARFLTGLGLGHYLDTLEQIV
LPTLLTGIVRGAARTRSARETVLLFADVILPSRWQEEVTLAVLSRLTLQQLKEVGVHPLGARMRILEAFKARTPH

>KnRh2_GAQ88354.1_Klebsormidium nitens (kfl00421_0020_v1.1
MESPLRAEARCTQLTVFLMIFAAALVTALALFVRSLYLDASQYTTGPPPGDHTRAALVAYINGTALLTYVLLDRDYTPVLVDHFGRPHYPARFL**Q**
WML**T**TPIMIY**L**TASISGQSHRQIILNTFCDLFILMVGLNGLLSSSNLMSGVCLTAAGFAFVTLLRNVHRMTNDAVLETRDSGCHWSFHLLQIYILTT
WTAFPCVAFLSE**T**NLVSPIM**E**AHMFLAL**E**LAC**K**FVFSALLLEGKFLSLEENRRVAEVARDESNKSALIEQLQQAITEKNRFLASVSHELRTPLNGIIG
LSDAMLLNLDGRLQGSLGEVNEDMKKTLETIKQSGGRLKNLVNDILDVESLRQRKLTLHYEVVYLRHLVDHVMDLTSPMVKWNVKLYNDVSKD
IPEIDCNQARLIQILHNLVGNAAKFTDGGEIRVCARVRETDDGHEFMIVDVRDTGIGIPSHKLQTIFLAFEQVNETSMDQRGGTGLGLFLVDSLVRAH
GGTISVTSEIGHGSCF**TLKLPLKHVDVNKSKPGPAPRSRLVSLAVKTPDDGLNSTPKTASSKATSPKATSPKGTSPKAVTPPGARSPKNTSPKA**
ASPAAASPMAASLKQKLTGSPGRMFVCSDGKGHVTLTPKTALAAIPDSDVTQDEKRAVTFEAGGAGIPKGDGGSTPESGKKGSLSRCASTRLV
GNLYVGEFELPKRAVSAPATAGQESSKIARKAGSLWPDLRSLKPVEVELSFKDQTEDHSSTAVHYPTKLRSHYEVHGQYEILSVDDDRVNQMVVD
GLLRPAGYKITKKMDGMEALAYLEGSEVIPDLIMLDVMMPGLDGYEVCKKVREMFPSSALPVIMVSAKSQEGDIVKGLRAGSNDYLTKPFKRLEI
LARIEVQLKIKRLWRVEIEAKKSYQLLKKML**P**DSIIERLSAGQSLIA**D**SHKEVTILFSDIVGFTEISGSSATEDLILMLNEMFTAFDALVDKHGVYKVE
TIGDAYMVVAGHDGSPDHALRIVRMAMDMLAKVRDVKQPNHVDPVRIRVGIHTGPAYAGVIGTKCPRYCFFGDTVNTASRMESNGFQMSIHTSM
TTYERCQDSFEFAPVGRRIIKGKGPMETFLLKYGEYEAGLQALRAENRPTLARSDSSPDLLKRHAKIDPASLPPSVSPLLKQSLEGPSRKTSRFKSEGP
RREQDVEFAQDLPSGYVSDDVSCGGGPAPGRERKLDRTRTGPRKEQDLEYARDLPSGYVSDDVSCGGGPAPGREKKLERTRTPPRRSLGSALLGIT
PLRRSGSFSGMTAQKEESAPAVNPDPVRTLRVDESSVNNIPVVAAQALNRSGDRPLPEHVTSHVAVPRPSTDLGRVAAQQMPSGRETPAQEDGIKW
RTGLGVQDGLSDPTGL**F**EILDGMGLGRYASVLEEAEVTVDILATMTPEQLKEAGVQAIGARLRILEAFRAPKATGST

>GpRh2_KXZ46245.1_Gonium pectorale
MDSQALVFRGAALDIVPAAVYDRSTSIFLTALAIDLLNILFERQTIKLDCVLLPTFIKGMASTTNVLVRFYTPVVGLTNLGRPVVIQRYI**C**WMH**T**TPS
ILM**L**LKMISTSITPREAAVAILFDEIMVVTGVIALVTTGWQRVFWSCITHLAMLPVVPYMHKAFTEAMEQVRTRPLQLTMLCIYVLNLILWCTFAVT
WDLAL**L**GWISVMT**E**EVLYVAC**D**FSA**K**VLFSSTLMLSSFKEFEARRESAMRVIESSSKAKLIAELQALLEQKERFMSSVSHELRTPLNGIIGISEGMLS
GCCGVLPEGVRRQIYIIRTSGARLLALINDVMDAAALRQNKLVLKQEQVVLRHVVDDVLDLTRSLVDSEVQLVNLVPPRMLVVGDTGRIVQILNN
LLGNAAKFTRRGQIRVTARQVEGGRKVAVTVSDTGIGIPRNKLATIFLPFEQVDMSISRKYGGFGLGLNIVQELVKAHGGTINVSSIEGKGSTFTFTL
PLARAMGRESLEEAKAAAKRSQQGLGIAITDASSSQVGGGSVSGSGAGPAGKDGTSGSVTASGISPRGAGGGDDSSTIVSSSDASRRPGQKGSTAG
GVPNPAEVEQYGELNYNAAELSALASSRPYAQSARESLPASYEGNRSSSAHSPSIQPAVSMRSGRSGGPPSAAPVPARSRGDSSISGAGGAAVGGTS
DVPQLASDAKIVHGPRPFHYTMYKRFLLLSVDDDHVNQSVIKSLLSSTGYEVVAVPSGPEALRYVSTAPALPDLVLLDCMMPEMDGYEVLQRLRA
MTPHVHLPIIMVSAQTEEDHVVCGLDLGADDYVTKPFKRNELLARIRAQLVYGDWEQDEGALETLSSLAIGEVGGASAGHASPGNGGSSMHILDS
GNNMGDAAHAAAAAAAAAAATAALSPGGLADSGRRNSLPGVGGSDQRLIVCIDDDDVNQVVLQGMLTSQHYRYVRASTGSQGLSYVCGTNSGGI
PPDLVLLDCSLPDMTGFDVCRCIRQMYNKQQVPIIMLSARHNESAVVEGLKCGANTYVTKPFRRNELLARIRLHLRSREAHHGSTPDSSNEDSDPR
AGSNAASALTDAGASTPGKSSNGGRALQRAHDPVVASAAAAVGPGSMDAVRVWPEAAVLVVAVADYGGLCRMLLPAEMAELSGRMLAAFDRA
VTAHGAVRVEASSGVMSAAMLPAAVAPGPGAAADPADAALGLRLATLHRVGRALIEAAATIGVPGTNTCLQLQQALALGPLMGHSTPPVFGGLP
GQGGGAGSGMLYFGPVLAELLDLARRAPPMTIVTPDMEAQALRSSGATADIRGPLFLEADDVGGPAAAALAARRLWLVEAHPLAHQYLPPQLLH
AASNVLRAGGFFNRSGTDDMDKSSLAASTVAGPSPLGPRGGGQGGSTLASGLSGGAGGGAGSASHGHGAAGGSSLLGAGEHGGQAAASAASTSV
GFNTSLGFGLYGGHNISRAASRAFSQTFGLDSDALGRMGQQLAASGGNTGTGSGNGASQGSGATTGVSPGGATGSARGGGGSTGSPLGGGQNMI
DSSSGGAAGITFSLQAAAAAVGASTGGGSGPSGVAANADLYSIGGGSSVLLSVPPSNPFAVPHAPSGPSFLYGTAATPGLRASG
GVPSAVGGGGSGSQVSPSEQDAMAEPHIRALRNELAVMRQQLEALQSGSASVRSEAHAGTSGGSHAQPPPTPQALLVQHLQQQQQQAAQQQQQP
QHFLAPAVQAGPQHADSGALQSLASVGEQGLVGARGSEAGGGGLVAAASGSIGGESLGAGLAEKAQKKGSKLTRLFGKSSKSGAK

>GpRh3_KXZ47741.1 Gonium pectorale
MDPHVCLDPVPPLVYQMSSTAFFTALVLNLTSLMFEDNATKRQLALLSVAIKGAACHTDMLLVTGRATVVFDAFGAICIPQRYV**Q**WCV**T**TPTMV
Y**I**LSKISDFTPSQTATAIAMDVTMVITGLLANFTPWPLNLLMFGASMLAFGGVLYMMGRMVYGAVKEHTSAASRRSLLFIYMCTLLIWCLFPLAW
LLHV**A**SPESAAGEYLNVFA**N**FMA**K**VLFSSSIMYGNYMTISQRRLLAQAEAENANRVRLVADLRDAVTRKDQFMSLMSHELRTPLNGIIQLSDAMV
RGAGGEMNPKGQHFVRTIKNSSNHLLNIINDILDVAALKEGKLTIKHELCCLDKAVDHVVDIVAPLAKKDVAIERSVDPRTPLIIADFSRVIQILYNL
TGNALKFTHRGRVAVRVTPAADGGAVTLVVSDTGIGIPKERIPSIWGAFEQVDMSVTRKYGGTGLGLNIVKQLVTAHDGNITVSTTVTVTSEEGVG
TTFTVTLPVLQPSARRSLEVQVHDSLAKCGYQVPRAREKPRSRAVSGLEDTFTQLTRGITRKASGLLSPKQEPPGQSDSVADRADRADKERDERDV
LYRRRTQELERENLMGDLQRRTEHKRSMDEAHLASRSLEMTGLERRAERDTTSLDRRGGGGGGGGGAAEPPAQLPAAGPSDSSRLSASPTGLSGL
LSARSSMVGGGGGSARQLAGGGGNSFWRSDAWEQQQQLNNNNNNNLRRSSIESQRGGGGGGQPSGLVRKSSNVSLSSRTGGPMGQPYGMPMRG
FGRPSNAGAAANGGGTSLLKSALESDLYRLPYRDSWDGASSFGADSESEGARLSRRHHHVAAATKLAAAGGSVAGGGGGGGSFSMGTAAAATA
SPPGLTLDKLAYSDMYGTIQILSVDDEEVNQIVLEEILTSTGYGFVRCMDGLEALEWLCASETLPDLILLDCMMPNMSGHEFCATLRRVIPGNVLPVI
MVSAKSDEENIVEGLRSGSNDFVRKPYQREELLARIETQLRLKKDSWWLAELVNNVDGRETESMKLLKAMLPESIIARMQQGQKFVADSHSHVVI
LFSDIVGFTSLSSKLPTAEVFLMLSNMFTAFDKLTDRFSVYKVETIGDAYMVAAGHDEDDDKAAKGPPLSRVLGFARAMLDVVRNITAPNGERLR
VRIVSSGGSEGGEGKGERG

>GpRh4_KXZ54193.1_Gonium pectorale
MIAFSTAFGLNFITLLFERESAKFQLALLACYINFLAGFSDYLSWKGISPIVRDSWGQGFQLLRTV**M**WLL**T**TPAMVY**L**LSIISDFSRIKVYVVMLADV
LMIAFGILAFLAHNWILTILLYTIAWSLFTYVVYSMWSMFHASIAEARHDSSRISLEVLRLFAVGLWFTFPAIWIVVK**L**GLVDVRT**E**EWLWCAS**D**FL
G**K**VMFSSSLLHGNFLTIEQRRLIAMRIVEEGNRIQVIQELKDLVEQKERFMSSMSHELRTPLNGIIGLSDALLVGSCGDVNDQALKTITTIKTSGARLL
NLINDILDAASMRKGKLTIKHEKVNLKRVVDDVIDLCQPLAKRGVKLVNDLRENVPFVLGDTGRIIQVFHNLIGNSCKFTHSGHIAISATVKDDEVE
VAVTDTGIGIPEDKFDQIFMAFEQVDMSVTRKYGGTGLGLNLVKQLVEAHGGRIGVRSKENAGTTFFFTLKIHSEHSTEGQGGSPSDAAPSSVGEHS
QLTAVRGGPGASTGHQHPAPRRAPSRRGSFTDKMLGGHKKTPSETGKSMLGAVVSGSQLGAVTAARAAMQGGGGGGGGGGATSGSGMAQGAE
ERERHGASLDQQQQQQTSRKSREGAHPHGPASFTKGPQVSGPMSLNDAAALMKGALKRKSSFRTKGTKVRVLSVDDDPVNQLVIQNLLAPVGYEI
LQAMDGQEALQVLTEEERLPDVILLDVMMPGMSGYEVCRKLREMYPLSCIPVIMISAKSKEEHIVEGLAAGSNDYVVKPFGRQEILARIAAHLRFR
DTVYQAGEIAGAIPGEVLPSRVLLRGGAGGALDLAPFLTGPARFTSLPPRVAKGI**EAG**TTSTTLQMFDQLTLLEVSIPQLGDLLSSVPASELLVALAQ
LFHDLDTLLEQHGCFLLEGVDDSFIIVSGLDNLGDQVLHALGLARSLIAAADTFTLGGRRLKMALSIGIHTGPAQGVLVGHNHPTLYFTGQLPAEVH
MLAATCPANCVHVSARVVEAVGTEREHFVAAGHMNSGSTSTYLMKVGSWEAGGIVATSDNTARWGKGKLGVHEGINTEARRMRPIQLALLAM
AQTNPGFLVDIASGGPEASQKHAGGAPSDPAAAGAGSSAAGGAAAGGDPAAAAAEIARLTREYEALEKQLEEVSNEAARLQDLVDDLEEQLIAKN
GCSAAATQQAEAAAAGAQALKTQVATLESQLAEAARERSGLEAALAEMEQRLVATHAALATANHEAADRARSRTPAPEPRVETASMASGSEAGF
ASAAAAAHGSGSMFGGMGGGGALAPRVAMPLGVGMRLPNIASLRAAGGDMRAVLEELGLSSLAPRFEAEDISPGLLPYLDDGAMRELGATSVGA
RLKLRLAAQALFMGA

>GpRh5_KXZ55246.1_Gonium pectorale

MAVAKSPLGEVDRNRRYPSRLAAASFPKDYRDDYDDSDDAVDDSEDTGNDGDARRGRSVQRRAGIKARPDKAQKVRTRGARPLTRTTATVSNG
GSGPPKRRHSARLLKQHHDQDKDGGASDRGEEEEEEEVGEGAEVGGTSDKDRGSGDGGGASSDSGSSGQEDEDEEMGDEGAAAGPRQAGSKSE
GEHADDEEDGGVWKGRYHLRGGAVNALRAIPAKRPRYNEDGGGGAKRRRREDEDDEEEDEGEEEEDEEDEDDDEEQGGKGGRVRDRARERDR
RSERDRRRERDRSRKGKGSAAPYTLRDRSRMVPMSVQEQERQKEELRRELQARKRFRDRARAHGGGKHGGAGSGGGAGHGGGGGGSGHRRS
GGGGFGGWRGGVSDDDIPDIDGTSMGNPWRNLQAAAGQLPPWQQHGAPNTPLPVLGQQANGGAQVVPSSALHGLGAGVAGTPFGGAAAAAAA
GGGLPLAPWEQALLADAAALAGGGVKEKAGNAEINPVAVDPSVGFDQVGGLDSYVEALKEMVFLPLVYPELFTRFNVQPPRGVLFYGPPGTGKT
LVARALASHASRYGGRKVSFYMRKGADVLSKWVGEAERQLRLLFEEAQKNAPAIIFFDEIDGLAPVRSSRQDQIHNSIVSTLLALMDGLDSRGQVV
VIGATNRPDALDGALRRPGRFDRELLFPLPGLQARRSILEIHTRKWSLRPSPALLDELAGLCVGYCGADLKALCAEAALHAVRRRYPQIYASEDKLL
VEPSSVNVEREDFLSAIAAVTPASNRSAAALARPLAGAAAVVLAPQLAAVLGRLQRSFPPAAQCLAAGARREGGGSATTSPEPTASSILPPGRAGPS
GSTAAGALVPRLASGTDGGAMGSLLARLPAWLMSRPRLLLCGPPGHGQGALASAVLYALEGLPSHAIGLPALLANPGARSPEEALVLAFVEARRS
APAILYLPHLHLWWRTAPPTLRATLVMLLRDLPPELPLLLLATAEVPSCELDRELRDRVFEGPGDVVALQTPGEQARRELFKASGAREPILAAAEPL
DPALLAATRSAAAAGSAAAAAAAGGAEPAGPLPKDPSMEAARAAEAAAAEELAARRAYEDDQSALRALRLMALRGVTLTLLNDRRWKMFAAPA
DAGEDPEYWQRVRREKEWASNVGSDWKVTNPMDLATLLARVDGRQYSTTSHYLADVQLIAQGARQYFGDDPQGVRQVSRAVALGDEAEHLVK
SRVPMELAQRCEHMARRGGPAPPPPGLELPEELAAAKVKAAAAGAKGKDGVGAATHGAAAAVNGAGGIVRRQRGGHGTGSDANCILMFDDPE
MLLRRMSKQQLQQQREREQQDDLVEWTYQIQTAAFGAVLLLNLLNLGMRQHLLPFKCNLLLLFINGVAFATDLLLWRGASPVLTSSAGRPFAPLR
YVQWCHSTPTMIYMLALLADCAGWQLVPPVLADVAMVLTGLGACYTEGLLKAVLTLLSFITFAYVLVYVYGLFNKTISGDVSSDQRITLRTVLVL
LLALWSAFPLVWLAAELHLISPAAEAVAWGVCDYLAKVVFSSQLWQSNLSGVQLRRDRALEAWEASNRVEAVARLTALLRQRDDLLSTLSHELR
TPLAGIVALSSSLCKDPSAVSPASSRTLASVRAAAACMLNIVTATLDSFAGRREGGEGRASKDFGAGSPAVAAGAAVEAIAVAAVDLQSLVETVVS
VLRPLAHDGVQVVTDLPSRLPHVLADATRLSQVLYNLVGNAMRFTSQGEVRISARILIPEGAELPAAAAGSALTTSGMGSSGGGITGCCSGGCEPPC
GATRSSNSGSCSGRVSGSGGSGLWRGRARRLSSSASSTSSSASAASPLPPGSEVEVLVEDTGVGMPQETLDELFQPYRSAEEGGVAAGVVAAKRRK
ATPLGGTGLGLYLVRLALRSQGSDIVAESVPGLGSTFRFRLPVVDESTAARRDGASGAAGHRGALAERANSRLIGVSLVDAGGAPGTPPARPLTGP
AVHAEAPSTALRKQRMSLDEQREQRNPSLLRVMGRDRAASSSARSVLGGPVSAGGQSAGDTAAMAAAASAMNPPAAAEPQAADPPAVAAARAG
RPQAARAPGPNFRHRNNGTLQVMSVDDDPINQLVAGQMLTSQSWKVVKCMNGPEALKRLHLDPTTGASAAGSGAGGVREDCGEAALAAAVTA
AAGAASLVLPDCILLDVMMPGMSGFEVCRRLRERYPTAQLPVIIVSAKGDAAAVEEAFAAGADDYISKPYKRDEMVARIKAQPSAAGCSTTPEPA
ALAALAPADFPCVGGSAGGGAGSSGAGSSSNNGVAVCASGQPIALLQEVLAEVRRRNHVETELAKLGARVASLQAACGSLASDRDGWRRQAREL
RALLAAGCNGAGRAATGCAMSADGFGGCNGGTSGLDTLLSAEPVRFASTNKLNLTSPGQGNGNGRNSDGSGASSVVNDLQDGGGGAGAGGVN
AAAGSGSRAVTGGGSATGGISGAVELQLQDLRREAALMRQQLMVALASVGTTRTDNSTSIGAVGGPVANSGAAEPGAGRMVQALAPDGSAAAA
RVAEIGPGGAQPAGALPRRPPAPVAGGHNRAMHDLMLATNASDLSTRSGTGASMGSGMPGHAGSGAASAVADRPAAPVIPIPPPSNPGKDTGPPV
AATRHHLNPQQYP

>CsRh1_PRW60699.1 Chlorella sorokiniana
MPASKGSMAGHSAQRTGLHEPIEELPDRRLHFSRSVTLVSLCTMSYAFWIFYLCGHSESEATLEFYRVVPPTVYMWPMVAFATAVLLNLLSMAME
RRPVKRQLCFLNVYISGVAFVFEFLAWKQSAPIYINAAGRPTSLMRFVMWAHATPIMLYTLSLISDFSTKQLYQTLGVNVFMIVAVIPGELIPAWHR
WIWNGLSCAVYPYIFHQIFYMYSAGIREARETGAQTSLRTLRNFTLSFWTFFPCVWVLVQLGWVDLYHEEVLWCVADTMGKIIFSSTLLHSNFMSI
EHRRMMAMRVVEEANRIRVIHELRQLVEQKEQFIALMSHELRTPLNGIIGLSNVLLMDVDSLPPDTCKTVTTIRNSGARLLNLINDILDAAALRKGK
LAVQQGKVNLKNVADDVVDLTEALAKPGVNIRNKITADAPLVVGDTSRIVQVLYNLIGNAAKFTERGDIWVDATSSPDGATVAVSVHDTGIGIPE
DKLDDIFAPFAQVDMSTTRRYGGTGLGLNLVKQLVEAHGGSISVASRRGKGSVFTFTLRVYAQDDGGSPGPVTAQQRHSLALAAQEAADAAAEE
LDEVSMPNPEEEPLLASGRMSRKDSEPDMMLRLSHDAQPANMLQRLSADSRLRSSYDADYANYHKAPQQLSPQAALNAFLSAGPHQVVKEIQKG
NITKPEDVAAATNGGDGNGGNGGSGGNGSQGDVEEEGPLAHDWLLADQVVQRQSSAGQVKVLSVDDDPVNQMVIQAMLGKAGFKVLKAADG
QKALDLLEESLRQGDPPHVMLLDVMMPGLSGYDVVRLVRERHPTLMLPVILVSANSREEHVVEGLQAGANDYVTKPFGRNELVARIQAQLRTRE
FSQGVRASLAAACQGLQQQQQQQAPQQGADGSLGWEGNRRLSLPVVERAASAPPDGLPPWPCMI

>ApRh1_XP_011395544.1_Auxenochlorella protothecoides
MVAFATATVLNLASACLELRPIKRQLCFLAAYITATALVFEALAARGRAPIFWSVSGRPVSLLRYVMWAHATPVIIYTLSMISDFDSLRVWRLVLV
DLVMIVTIIPGELVDAWHRWIWNIISFAVFPYICSELWAMYSSAIHASRDHATVRALSALRASTAVFWTLFPFVWTVAQARGVSTAWEELLWTCCD
LGGKIIFSTSLLHSNFLTIDDRKMRAMREVIESNRVRVIQELRTLLEQREHFISVMSHELRTPLNGIIGLSSTLLLDLAGEPLRGRGPAVTHDVAAIRSS
GVRLLNLVNDILDASALREGKLAVKLERVEVRRVAEDVLALVRQLAAPGVVILNDIPSDLPAAKADTGRLIQVMYNLIGNACKFTDKASWWWW
WWGGGSKGDGAWCLGCIMLTAGPERENMVSISVSDTGIGIPPSKLDLIFGPFAQAGGLADMSYTRRYSGTGLGLHLARQLLAAQGGTIHATSHQN
KGSTFTFTLPVYTDADSKAAAVAGVISQGRTLRNPPRIDDMLEEEAGALGLGAQPDGGAAGEDLLQLLLGQAGLDPGARGPGSAPRVGRSGLVAG
TPVCVDNFASDFQTDMLDRLSLESRSTYFLATERETQRKAPQQLSPEAAASAFTSAAGPSPGWPGAQGDWAAADAGACGAGGASGDQAMSPFLL
PSASTAESGGPPSGSDRGPLVLPPRGGGGAESRPDWQRAWQSVEDMRQRGAIRVLSVDDDPLTQTVVQGMLSRSGFQVSKAADGERALDVLEGGI
LAGRPPHIVLINLMMPKTSGFDVIRTIRSRWPGLMLPVIILSASCWEKAVVEGLQASGEVRSIKLAPLPFQAGANDYLPKPFGCFELMARIEAQLRTH
EFMAEACRQARPSEARSSEGGSGGSGSASANGVCSPDSSSDASYN

>AsRh1_jgi|Astpho1|75682|estExt_fgenesh1_pg.C_000730034 (5151)
MPGLRGWTGVLGWVGSAVVLYITLDNAAQAYWGDGSPEAAALLFAEVPQQWFRYSADFFLAALFVSLLSVLYEDSPAKKQAAVLSCLIKSVACY
ADWKLSVDGKGVIWDSAGYPFVVKRYVNFMITTPTMLYLLSGVSSFSVGEVAATAGMQWGCVVTGLIASLTYGFWKWFWVTLSFAFYGLVLRE
MQRMVNSAAKANEGTKMRLRGLNFIHNYSVVAWSLFPAAWVTGHLHLTSIGDTELLMMAGNLVAKLLYSSGIMYDNFVTVSERRDAAAAEIEQ
RQRLVMITELKSAMQRKDSFLSVMSHEMRTPLNGVIGLTDALLKGSSGKMTEKAVKLLHTIHDSANYLLNLVNDVLDAAAFRHGKLKLMVQQV
NISELVNTVFSNVLTMQQEGVKLHAEVDPRMPIIIADKDRLTQVLYNIVGNALKFTSMGTVGVLVKPFADMKSVVFTVADTGIGIPEKNFSSIFLPFE
QLDMSPTRKYRGTGLGLSICKVLVEAHGGSIAVSSEVGAGSTFTFTLPVEPPQPHSIRGDGRLSNDGSLLPKPEEGSPSRASLQLANPEKAISAGTGGS
VAAGKGPLSPLGGIGTPSAGGATESKLKVSLHHVASCQALDRRNSSTTPHSRHAYTLDHVKPLHGQENGTFLVLSVDDDPVAHLVLREMLTPEGY
EVHSELDPQKALQWVAASPFLPDIVLVDCMMPGLTGYEFTAKLRETVPRTLVPVIMVSAKAEGTLIKNGFDVGCNDFVSKPVMAEELLTRMATHL
DLRQDAPGWMQIITGGPSKLDNEALRLLRSILPDRIIRRMKEGQTLIADSHPSVCILFADICNFTPLSSSMATAEVFLLLSNLFSLFDKLTDRHGVYKV
ETIGDCYMACAGHDEDDDKKAKGSPTQRMLAMAVDMLQAVQDLTVPNGGSVRVRIGMHVGPAYAGVIGQKCPRYCFLGDTVNTASRMESNGF
PMTIHLSDAAHRELLMCMDGSSFAPLGKRAIKGKGTMETFLAKEGEWRAAVEATQHPKPGKLSKMRSLLPLIPALEARGGDASVQPGMAGDVHA
AAKQAANAGLPALAASSRHAANAEGAAASRMASESPAAVLSPSRDGSQASTLQAQLEAQQHALAAARATADAQLQQMLRVQGQLQAEILRHQM
QRDQASGSTSRVSSFSALPGADAMAHLNGGGALSLAQLQALAAAGAMGMDMYGNAYPTTPRGYPGMYPPPGGYYWPPPGPYWTPGPSSVAGAP
AAGAGPVPVPSSVDLELRLNSAPVASTRTSVDRGSGDASGNPGSPDKTPAGWTRKLFKKVGKSGHHAPPRNTSLL

>AsRh2_jgi|Astpho1|77589|estExt_fgenesh1_pg.C_001370002
MKEGTRGWPITLVVAGASVGAYYGLNQLCLKWGANDKAASAALFKEVPQIAFQRSGDAFFACFALHILNIAYENTNTKRQLALLAAVIKGIAGW
VDWQIAADGGGIIFDSSGYRPLVIRRFLNYAITTPIIVYLVSCVSDFSGWRVAGVAAMQAGVIAFGVAASLLPSPWKWFVVSMSVFLYVTVLRNIR
HMVGSALAVRSGANRENGGLQFIFIYTVVLWSVFPATWFATQLNLIGTRNSEIISMVANWVAKVVYSSNIMFSSFVTISERKADAQAVAEQEERVH
MIKDLKEAMDHKDSFLSVMSHELRTPINGIMGLSDALVRGTGGKLNEKGQQFLVTINNSAHHLLNLVNDILDAAAFKHGKLKLKVEEVDIHKVVA
QVFSTLSTLKKGDVQMWNDIDDSTPNIMADSGRVVQVLYNLLGNSLKFTSKGSVGLHVVPSDDKKDVLFKVQDTGIGIAEDKLQSIFVPFEQADM
TTTRKYGGTGLGLSICKVLAEAHGGQIEVTSTPGLGSTFTVRLPIFPRQVKDAAPPPTGAVVAPPQTSPVLKVYTLDNIESASPAAAEKQPLLAVPET
PRGEKSHKLSFAEAPGVTPPRSFDRQRPEMFTVEDQTLPQPVEQSPPPPVEQTLQTAGPQLPAVKTKGTRDRTVSRSASFKGTSTPTTRTPTYTLQDV
KPTHQDELGTILVLSVDDDPVAHMVLAEILEPMGYKLHCETDPEKALKWVNESVVLPDIVLLDCMMPKMNGHQFCAKFRETVPRSMVPVIMVSA
KTGEANVVEGLRNGCNDFLSKPVHRDELLARMETHLHVKQDASWMTHLINSGCSKVDNEAMQLLKSILPDKIIARIQGGQKFIADSHQRVTVMFS
DIVGFTPLSSSLPTAEVFMLLSNMFNTFDRLTDQYGVYKVETIGDAYMVVAGKPWHDEDDMKRSLGTPAQRVLNMATAMIDMVKALTLPNGDF
VRIRLGMHSGPAYAGVIGQKCPRYCFLGDTVNTASRMESNGFPMTIHLSEAAHKELVPVLGDDYFVSVGKRNIKGKGTLQTYLAKEGMWEEAMQ
AIKEHGQEAASVVEVATPRRLSSRTMTMSRHQLQVAALEDALSTMRAALETEQAQHLESQASIRQAQETIAAMQAQAAGQEENAKEQAAKLALL
QANLEAKQQELKTCEARLETAAEKVRRMEAELEMAQRKVEEAQKQVQDAHKDAVERQGELLRLKNAAAEVEIEEVEPAEEPAVPERRAAKADG
QRQRAAQFPSRDPPGQPQERPRSLSRPPARDEEGYLDDEGGEDGHPPRRFQEESSPPRNARAMSVTPPMSVTEWDDQPQEWDGPATIPARRPGHGE
SPMQDYLGEHSALLQEVQRKRMQRQGEGYGAYASSQPGNGGSVSPWGGKSNYTSASADEHLRGMFRAARDMAPTRHSPEGYGWEDADHERGP
SPGRRGGPRPLDTMYDSIDPRGYRSPGYRSAVDGNAGSYSPDGFPAKAARGRPTSARSHPRTPSSPQRDRSGWGPAY*

>AsRh3_jgi|Astpho1|29226|e_gw1.00088.7.1 (6282)
SQVPKQHYQISVASFLSALVINFTSLLYEAGATKKQLALLSCFIKGAAAYADLVTGTGQGIILMDPNGTPCVVNRYIQWALTTPTLVYVISRISSFST
KRVALAVGAQVVVIVTGLLSQLSPGIFFWLYICMSFFFYVFVMIEMGKMVGSVLTEESNSEARSGLLFIFWSTVVVWLAFPIYWCCQQLGILSVYN
CELGTLVANFVAKVLFSSSVMYGNFLTIAQRRALAKEAAEHANRLKLIEDLKASMKVKEEFLSVVSHELRTPLNGVIGLSEALLRPGPWQLGEKGL
HYIKTIKNSSHHLSNIINDILDAASMAKGKLVLKTERVSLNKVVDHVFDIMGHLVKKKVTLEKNLAPDLPHIIADGSRVVLYNLLGNSVKFTTEGRI
TVSVKPMPGSLPGMEMLQLSGDMTAARKFGGTGLGLNIVKRLVEAHGGTINVESTPGVGSTFTVRLPVKPPESQAQKQAEGSVGDWSNRKNMQQ
STPRNSGGEDQRSTDVGSPCLTERKPTHMEEYGNTLILSVDDEPTNHLVIEEALESAGYKMHSELDGKDALAWINGSKVLPDLILLDCMMPNMTGE
PAAWHEFCIELRKTVPQAVVPVIMISAKNNEDNVVEGLSHGCNDFLSIVNGVLQEDTEAMQILKSILPECIIARMQDGHAYIGDSYDNVAILFSDIVG
FSTMASTMSAVEVFLLLTNLYTQFDRLVDKYAVYKVETIGDGYMLAAGHDEDKDKARIGTPMERLMMMAKAMLDCAAKFRTNNGAALQIRVG
VHCGPVYAGVIGSKCPRFCFIGDTVNVASRMESNSFPMCIHLSEVAYKNLGSHMSQAVSMGKRAIKGKGEMVTYLAKVGSMLFFCCVLICLSGWH
SVVLRIRARQRPA*

>AsRh4_jgi|Astpho1|76150|estExt_fgenesh1_pg.C_000880024 (6192)
MLAQLQLDAQALGSPTSPIEFCKSVDLPDQHFLAYGAGAGLVGIATCQASSDSPSQPGVPFARQPDIVLAVPAARNAGRDIISVVFSSKSAENLLAA
AAGNHIHLFSLTASMLALQGRIAPHEGPPQGDSQMLCAVQHSADIAALSWTQAGDGLLAADTQGCVVMYRVPEPGDLSGRGSRLVHVWTGSSSM
LVQPQTLLAAGTNVMSPAASASPGSRQVTIWWPEHLPDVQDAAHQRQAHHRPSPEQVAVLAEQLRHPAGVVGLEWSPGALQHGVSPDLEEEDGD
EAGSPVAAATSQPALMTVGEDSVIRIWVEVTVGPMLGPAQGSSLGRPALPQQPAGPAAPGGGSGGARLQAPPGKGEPRRCRAKGAQVSRDAVHFL
GGIQQWSKEEPRWAQALCTTLYTSGSGARGFKLQAQLAPGTLRACWGQPDAGLAGVNHRLQSSQIMWVLAVAQQRALEGSTEPQSEQLLLWAL
DGLSGVVINGIPNNLPGTRAASVPKAVLWGQHCSALVWPKAAGQRRLACGCSTEHAAPVLQVLESCRGEGSDTLLRTFELHTVDEVTQLHVARRS
RAGISAGNQPLAMVHELPLHSLTLQRQTGHAAPVTALAQHPRQPLAASLDANGLVLLWSVPAGAPLRLLGSLSELSGAVQAPEGATAVVWLDPA
AGGAQLAVGGAHGVDIYGVSRLGEQQQTPLQVAHLAVARLPDQWRGLEHLTSLAGRPGGRQLLLGLQQQPGTATPQSTPPPVAAWQMASQATC
MAAAPQESGFDLLLGGSDGLLRLVTLGDRNSLLEQDRLVCSASGQGQPTGIPVAAAASGGSAWLAAAVQSFGSADHLVCIWQATVASDTPSFSLR
AALPLPEAPTAVVWLEGCLPGVALAVADSWPEFRVFVRGKDGGFAPIAKLPSLPDSVRQLCGANTGRLPGQQPLAGASAGEDAGLGTPALAAAGT
KPKAPATPGSSAPPGSAPQALCQQVLLGAGSLLACLSPVARATEQPDGHGRVLALVGQEVSGGSPVALAAVAAEAGGPLPQFDPRRLRMLIERGR
MQAASAAIRVMLQRLQGRSATGKPDEVPGADQKLPPPMVDAILDANFLKAFTRLSARLPESAKAAAAQAAKAAPAAPAAAARAGSGSAQTDDD
DGPMKPLHTSKGTAPNGELKGTAGSTGSRAASALPVDPFAFNMGAFDMGSSSAPATETRADQQPASADPYAFDMGSFGGDPAPAAAPPPQQAPTA
ADPFAFDMGAFGMGTDSQQEAGHQTKSQPGPPPASSGDPFAFNPDAFGMGDAAGSGHAEQPDSAAPVPAAAADPFAFNPEAFGMGQPPQQVPGS
AQAAPAPGAAADHFAFDPEAFGMDQLGQPPQQPPGSAQAGHGRDSAASNEDISVKGPQRQGAASVPGSRTTGTSLPGAAQSPARDRSQRRQQAA
AVFQPRRPGSKPADALSLEELEALERLLLPQVDPSDDEDDLAGQADKSQQMPFRSPWATGEATAALGLTHQQALEVFELAQLLCPSAAQRALPPTP
GALEPAAGALPSADWAALDAAGQQLLRRLQLALVWQHHIAAEQAAVAGAPGGAGAGRSREVSDGLMASAHTNNALLGSVTEAASWAERVGLT
PGLSSEGAMWGVLSESQEALLTDSLKLVPGSLDQEAAEKPMEFGFSTGPARKQPRHQLSWEGMRQAGAGFWLTDPQVVKSTAEALAKAQYAAT
KDPHSCALMYTALQRKALLTGLFRTANNKKVADFLGRDFSDVKNRTAASKNAFVLLGKHRHELAAAFFILAGSNKDAVGVCGHEMRDPQLALFL
ARLLEPGNPQLQQEIIDDRLLPDAQEAEDAWAVCLLQWLHGQPAAGLLTLVTSNHLMSSSDSGTPSQTPSRTLRQPQKEQALVRSASRRHGNVPRQ
APSLPSLDNVFALDLILFCLQDNLNVWPGPLPSLPELHSLATAAAQQADVQGLPSAGLEALHVASSCMHRLQGAAGQGQRHAAVLGAWQQRLVL
AVLVQGIDWQPLTALAQGQDSRPGSAMRKALTAHTAAWQDQAAALLARLDAAGIAVDQQVALQQLAIWEAALQAAVLPGLGQPGKAEGDRLS
RSHSAFSGKSLISTRHSVLGPAVFEASHELLHVEGDRLHAVCASNAGMYGYAGGEGRPFVAASGHHGLIQGEVLLLDEHYSVGADREEGLEDQRK
GSAFSALLGDMLEAVRWPGDPWTNMATPHMGGGVLAGGPHTRAATAPKPESPSAARVRAPLGQILTSTLCAHPTRQLYLSALMSGSSSGEVFLCK
FGDRFATAGYTPMPAAVTIAPSSAQSMFSAPPRSWNPAPGTSFTHWGQPQSVVWSDCGERFAGIGDGGVVATWRIDAPRLGLSKRGMDVAFLGT
GSSVLAVGGLDASGANIAIWDTQAPSYHRPVARLNHHSAAVTSLQVLPGGYHLASADASGTIAVKDLRMLGGSLANSASPRGSSARSSGHLMAGS
PRKRLSVDGSASSAAADAAARGLLWLVRPPSESAGVVCMTAGLWPAPDGSAGGTMLVTGHHDGTIHVWSAGRGRHLQAIEGAHVMPSSQQQTL
TSKDITTLIVAIAASAYFAMAAGGGDDYFPVYYNNAQSRDIFWARYIDWFLTTPLLLLDLLILTDITVATTIWIMAADIFMIIFGLFGAVSDHKTKWG
WFGVACFFEALIVVGLMLPGMKGAFARGKSTGMLFAIMAVYLSVLWWGYPIVWGLAEGSNTISADAEIGAYAGLDIVAKVVFGWIIMLLGYPMI
GKQMNMEHEQGRFLPQLLSSPINAPLSIVPTGAKAYHPVGKSNPGGPMESATGATTGSAVPAGATTASAGTKAPGANGQTIV*

>BgRh1_jgi|Bigna1|89464|estExt_fgenesh1_pg.C_490145
MSTMRTSVRPKIGGHIQVGDEGHQGYGHIEKLLYPFDVLASFIETVFPNMQKYATTTGIVIVCYLAHARMVSTYPTDGVVSVVADVHTTIVVSAAI
TTFFFSVSPFYALFWERATKEGEHVGIYSRSHVGFLCICGVTFACMATHIYIAAIGQIHTLNTLGGSRVFYTTYYCEWITTTPMMIQSLFHFAEMTKR
RRIVVIRAQILNFIMFTSGSWLWGKPTLLKGVIVAYFFIGNLYSQDRLLKFSKVVSRDEPLQREWDTYNSNLRIFYTMTWMLFPMIYVLGSLEIIQPW
MEIKLFAYADLSAKVGLVNMAYRYINNATEEIAWCKKILEQERLKSDVVRYIFHETRVPLNTISLGVSNLDVSDDAKEIESVKKTLAASCDSMRHIL
DDYLVWEKMRAGKISKFKFEVATFALQEIVDMLLTRFKATAEKNDLTYTVEARVKNTSFIGDKYKIVQIASNYISNAMKFTPRGGIVSFVVEEIQPP
PNSSYRPSNLHSSIRDALEEGDICWLQFSCRDTGAGISEENQKLLFTPFVQIEPGVKKNSSGAGLGLSICKEMAAGMGGSVHLESMIGKGATFYVTLP
LPKAISRKVIPDGPLQATIGDGNKLSEEAPLRVLVTDDVKSNREFLAKRLRRMKKENGKPKYVCDVAEDGVAAIRMSQNKGPFPYDVYLMDNQM
PNLLGRDCIRKLRDEHGIKSMMIGVTGDIISEDRKLMLECGADCIHGKPVNVKALTQDISAFFEKKRNASQSKSSG*

>BgRh2_jgi|Bigna1|139324|aug1.49_g14032
MSTMRTSVRPKIGGHIQVGDEGHQGYGHIEKLLYPFDVLASFIETVFPNMQKYATTTGIVIVCYLAHARMVSTYPTDGVVSVVADVHTTIVVSAAI
TTFFFSVSPFYALFWERATKEGEHVGIYSRSHVGFLCICGVTFACMATHIYIAAIGQIHTLNTLGGSRVFYTTYYCEWITTTPMMIQSLFHFAEMTKR
RRIVVIRAQILNFIMFTSGSWLWGKPTLLKGVIVAYFFIGNLYSQDRLLKFSKVVSRDEPLQREWDTYNSNLRIFYTMTWMLFPMIYVLGSLEIIQPW
MEIKLFAYADLSAKVGLVNMAYRYINNATEEIAWCKKILEQERLKSDVVRYIFHETRVPLNTISLGVSNLDVSDDAKEIESVKKTLAASCDSMRHIL
DDYLVWEKMRAGKISKFKFEVATFALQEIVDMLLTRFKATAEKNDLTYTVEARVKNTSFIGDKYKIVQIASNYISNAMKFTPRGGIVSFVVEEIQPP
PNSSYRPSNLHSSIRDALEEGDICWLQFSCRDTGAGISEENQKLLFTPFVQIEPGVKKNSSGAGLGLSICKEMAAGMGGSVHLESMIGKGATFYVTLP
LPKAISRKVIPDGPLQATIGDGNKLSEEAPLRVLVTDDVKSNREFLAKRLRRMKKENGKPKYVCDVAEDGVAAIRMSQNKGPFPYDVYLMDNQM
PNLLGRDCIRKLRDEHGIKSMMIGVRKPEEEEEEEEENIEKTKQKLRIRYVYYSILVQVTPRSPYLVLSPDNPKSFLSRSRETLSLRTGS*

>1KGB_BR
QAQITGRPEWIWLALGTALMGLGTLYFLVKGMGVSDPDAKKFYAITTLVPAIAFTMYLSMLLGYGLTMVPFGGEQNPIYWARYADWLFTTPLLLL
DLALLVDADQGTILALVGADGIMIGTGLVGALTKVYSYRFVWWAISTAAMLYILYVLFFGFTSKAESMRPEVASTFKVLRNVTVVLWSAYPVVW
LIGSEGAGIVPLNIETLLFMVLDVSAKVGFGLILLRSRAIFG

>1UAZ_AR1
TAAVGADLLGDGRPETLWLGIGTLLMLIGTFYFIVKGWGVTDKEAREYYSITILVPGIASAAYLSMFFGIGLTEVQVGSEMLDIYYARYADWLFTTP
LLLLDLALLAKVDRVSIGTLVGVDALMIVTGLVGALSHTPLARYTWWLFSTICMIVVLYFLATSLRAAAKERGPEVASTFNTLTALVLVLWTAYPI
LWIIGTEGAGVVGLGIETLLFMVLDVTAKVGFGFILLRSRAILGDTEAPEPSAGAEASAAD

>1VGO_AR2
QAGFDLLNDGRPETLWLGIGTLLMLIGTFYFIARGWGVTDKEAREYYAITILVPGIASAAYLAMFFGIGVTEVELASGTVLDIYYARYADWLFTTPL
LLLDLALLAKVDRVTIGTLIGVDALMIVTGLIGALSKTPLARYTWWLFSTIAFLFVLYYLLTSLRSAAAKRSEEVRSTFNTLTALVAVLWTAYPILWI
VGTEGAGVVGLGIETLAFMVLDVTAKVGFGFVLLRSRAILGETEAPEPSAGADASAA

>1H2S_SRII
MVGLTTLFWLGAIGMLVGTLAFAWAGRDAGSGERRYYVTLVGISGIAAVAYVVMALGVGWVPVAERTVFAPRYIDWILTTPLIVYFLGLLAGLD
SREFGIVITLNTVVMLAGFAGAMVPGIERYALFGMGAVAFLGLVYYLVGPMTESASQRSSGIKSLYVRLRNLTVILWAIYPFIWLLGPPGVALLTPT
VDVALIVYLDLVTKVGFGFIALDAAATLRAEHGE

>1XIO_SRI
MNLESLLHWIYVAGMTIGALHFWSLSRNPRGVPQYEYLVAMFIPIWSGLAYMAMAIDQGKVEAAGQIAHYARYIDWMVTTPLLLLSLSWTAMQF
IKKDWTLIGFLMSTQIVVITSGLIADLSERDWVRYLWYICGVCAFLIILWGIWNPLRAKTRTQSSELANLYDKLVTYFTVLWIGYPIVWIIGPSGFGWI
NQTIDTFLFCLLPFFSKVGFSFLDLHGLRNLNDSRQTTGDRFAENTLQFVENITLFANSRRQQSRRRV

>1E12_HR
AVRENALLSSSLWVNVALAGIAILVFVYMGRTIRPGRPRLIWGATLMIPLVSISSYLGLLSGLTVGMIEMPAGHALAGEMVRSQWGRYLTWALSTP
MILLALGLLADVDLGSLFTVIAADIGMCVTGLAAAMTTSALLFRWAFYAISCAFFVVVLSALVTDWAASASSAGTAEIFDTLRVLTVVLWLGYPIV
WAVGVEGLALVQSVGATSWAYSVLDVFAKYVFAFILLRWVANNERTVAVAGQTLGTMSSDD

>Sodium (Na^+) ion pump (6RF6_A)

MTQELGNANFENFIGATEGFSEIAYQFTSHILTLGYAVMLAGLLYFILTIKNVDKKFQMSNILSAVVMVSAFLLLYAQAQNWTSSFTFNEEVGRYFL
DPSGDLFNNGYRYLNWLIDVPMLLFQILFVVSLTTSKFSSVRNQFWFSGAMMIITGYIGQFYEVSNLTAFLVWGAISSAFFFHILWVMKKVINEGKE
GISPAGQKILSNIWILFLISWTLYPGAYLMPYLTGVDGFLYSEDGVMARQLVYTIADVSSKVIYGVLLGNLAITLSKNKELVEANS

>RhGC (blastocladiella emersonii)
MKDKDNNLRGACSSCNCPEYCFSPTSTLCDDCKCSVTKHPIVEQPLSRNGSFRSSGASLLPSPSSPNVKITSTVGLRSRKSESQANVRGSMISNSNSG
SRSNNSGGAGGGSGGSSSSKGGSALANYQSAMSELWSWNMMLSTPSLKFLTVQFTTWIVLTTVGA**IYTL**FFHERQAYNRGWADIWYGYGAFGFG
LGLSFAYMGFTGARNPEKKALSLCLLGVNFISFMSYIIIMLRLTPTIEGTMANPVEPARYL**E**WIA**T**CPVLIL**L**ISEITQYPHDPYKVIVNDYALCLAGF
VGAISAQQPWGDLAHFVSCLCFSYVVYSLWSCFTGAIDGETQCNVEKSGLRWIRFSTITTWSLFPITWFSYT**S**GLISFTV**A**EAGFSMI**D**IGA**K**VFLTL
VLVNSTVEQAQNQKVDAITAIAEELENQINNCDAILQKMMPEGVLEQLKNGQATEAKEYESVTVFFSDITNFTVISSRTSTKDMMATLNKLWLEYD
AIAKRWGVYKVETIGDAYLGVTGAPDVVPDHAERACNFAVDIIEMIKSFKTITGESINIRIGLNSGPVTAGVLGDLNPHWCLVGDTVNTASRMESTS
KAGHIHISESTYHFIKSKFVTQPLDVMEVKGKGKMQTYWVLGRK

Rh-PDE
MGRKNAANSSMLQEASMNNYSMTSAASGASSSGRGKRRAKTRNIAIASTKEVQWQGIFMIIVWLCVMGSLIFFANPEASRRVFAKFSHLQSFYGA
TSVAFAFATGLDILAYVNAVSDEKRVLSGILAYVDGVACISYLSMATLNLYFLVDSTQGNPVWLMRYA**E**WII**T**CPTLLY**W**CGLASRADRSSVSDIA
TADALLLAGGALSSILPSWPAFFVFAGSFATYIYVMLHMWGMFGKAMQPDFQPPPPLPRHALHLLRCEIVMSWSIFPLVEFLRR**Q**GYIDFQV**G**EAM
NCVA**D**YAA**K**VGLAMIMVNCNLEQINALRVQQMHSALTGMLKVMRKTNLSSSRMAQLDGVDDDVKSWIMNEFSGSTDGKGGDDAKAQQRARG
RKGHSAAMDAEKLAASSLFTWDFDALDKSDEDLTAVCVRVFQELHVIEQFNIDEKKLRKWLQKVRTQYNKNPFHNWRHAVMVLHTTYLLLTSV
ATEFITEVELLAMLIAALSHDLDHNGLTNAFHINSRSELALVYNDQSVLENHHSHLAFEILLEKGCNVVENLDEDEFKRLRAVIINCILNTDMATHHT
KLSKMEEVNRLGGFINLAENNDQRLFVLAVLLHTADLHNPIKPFESNKRWSARLQKEFNNQVELEAKMNLPSLPFMRGNDEESLAKGEIGFINFVV
KPWHQQLSQAFPKLDFLLDTIDANLAEWKAIAESYRQMH

>ChR1
MSRRPWLLALALAVALAAGSAGASTGSDATVPVATQDGPDYVFHRAHERMLFQTSYTLENNGSVICIPNNGQCFCLAWLKSNGTNAEKLAANIL
QWITFALSALCLMFYGYQTWKSTCGWEEIYVATIEMIKFIIEYFHEFDEPAVIYSSNGNKTVWLRYAEWLLTCPWRDSRLNVILIHLSNLTGLANDY
NKRTMGLLVSDIGTIVWGTTAALSKGYVRVIFFLMGLCYGIYTFFNAAKVYIEAYHTVPKGI**CRD**LVRYLAWLYFCSWAMFPVLFLLGPEGFGHIN
QFNSAIAHAILDLASKNAWSMMGHFLRVKIHEHILLYGDIRKKQKVNVAGQEMEVETMVHEEDDETQKVPTAKYANRDSFIIMRDRLKEKGFETR
ASLDGDPNGDAEANAAAGGKPGMEMGKMTGMGMGMGAGMGMATIDSGRVILAVPDISMVDFFREQFARLPVPYELVPALGAENTLQLVQQAQ
SLGGCDFVLMHPEFLRDRSPTGLLPR**LKMG**GQRAAAFGWAAIGPMRDLIEGSGVDGWLEGPSFGAGINQQALVALINRMQQAKKMGMMGGMG
MGMGGGMGMGMGMGMGMAPSMNAGMTGGMGGASMGGAVMGMGMGMQPMQQAMPAMSPMMTQQPSMMSQPSAMSAGGAMQAMGGV
MPSPAPGGRVGTNPLFGSAPSPLSSQPGISPGMATPPAATAAPAAGGSEAEMLQQLMSEINR**LKNE**LGE

>ChR2
MDYGGALSAVGRELLFVTNPVVVNGSVLVPEDQCYCAGWIESRGTNGAQTASNVLQWLAAGFSILLLMFYAYQTWKSTCGWEEIYVCAIEMVK
VILEFFFEFKNPSMLYLATGHRVQWLRYAEWLLTCPVILIHLSNLTGLSNDYSRRTMGLLVSDIGTIVWGATSAMATGYVKVIFFCLGLCYGANTFF
HAAKAYIEGYHTVPKGRCRQVVTGMAWLFFVSWGMFPILFILGPEGFGVLSVYGSTVGHTIIDLMSKNCWGLLGHYLRVLIHEHILIHGDIRKTTKL
NIGGTEIEVETLVEDEAEAGAVNKGTGKYASRESFLVMRD**K**MKEKGIDV**RASLDNS**KEVEQEQAARAAMMMMNGNGMGMGMGMNGMNGMG
GMNGMAGGAKPGLELTPQLQPGRVILAVPDISMVDFFREQFAQLSVTYELVPALGADNTLALVTQAQNLGGVDFVLIHPEFL**RDRSSTS**ILSRLRG
AGQRVAAFGWAQLGPMRDLIESANLDGWLEGPSFGQGILPAHIVALVAKMQQMRKMQQMQQIGMMTGGMNGMGGGMGGGMNGMGGGNGM
NNMGNGMGGGMGNGMGGNGMNGMGGGNGMNNMGGNGMAGNGMGGGMGGNGMGGSMNGMSSGVVANVTPSAAGGMGGMMNGGMAA
PQSPGMNGGRLGTNPLFNAAPSPLSSQLGAEAGMGSMGGMGGMSGMGGMGGMGGMGGAGAATTQAAGGNAEAEMLQNLMNEINR**LKRE**LG
E

>VChR1
MDYPVARSLIVRYPTDLGNGTVCMPRGQCYCEGWLRSRGTSIEKTIAITLQWVVFALSVACLGWYAYQAWRATCGWEEVYVALIEMMKSIIEAF
HEFDSPATLWLSSGNGVVWMRYGEWLLTCPVLLIHLSNLTGLKDDYSKRTMGLLVSDVGCIVWGATSAMCTGWTKILFFLISLSYGMYTYFHAA
KVYIEAFHTVPKGICRELVRVMAWTFFVAWGMFPVLFLLGTEGFGHISPYGSAIGHSILDLIAKNMWGVLGNYLRVKIHEHILLYGDIRKKQKITIA
GQEMEVETLVAEEEDDTVKQSTAKYASRDSFITMRNRMREKGLEVRASLDAGGGDSGMEAGGGGAAHAQPHMAKPGTELGKTMSASFTNGAA
TSLEPGRVILAVPDISMVDFFREQFAQLPVPYEVVPALGAENTVQLVQQAAMLGGCDFVLMHPEFLRDRGPTGLLPQVKMMGQRTAAFGWSQMG
PMRDLIESSGVGAWLEGPSFGSGISQAALQQLVVKMQQAKRMAAMGSMMGGGMGNGMGMGMGMGMGMGNGMGNGMGMGNGMGNGM
GMGNGMGMGNGMGMGNGMGNGMGNGMGMGNGMGNGMGNGMGMGNGMGNGMGNGMGNGMGNGMGNGMGNGMGNG
MGNGMGMMTPGAMGMGMGGMGNLAAAAGNAMYGGGGGGGGSTMGSGNAAMMTGLVMGGGNGVGAGPGGVVANLGSSALQPQSQMMG
GGNVVGMSSPQLQLQQSSSMPLGGLAPNRIGNNPLFGAAPSPLHSQPGASPTGLSSPQLGMGAMLPAGTSVGAGGGSVGPTETDMLQQLMTEINR
LKDELGE

>VChR2
MDHPVARSLIGSSYTNLNNGSIVIPSDACFCMKWLKSKGSPVALKMANALQWAAFALSVIILIYYAYATWRTTCGWEEVYVCCVELTKVVIEFFHE
FDEPGMLYLANGNRVLWLRYGEWLLTCPVILIHLSNLTGLKDDYNKRTMRLLVSDVGTIVWGATAAMSTGYIKVIFFLLGCMYGANTFFHAAKV
YIESYHTVPKGLCRQLVRAMAWLFFVSWGMFPVLFLLGPEGFGHLSVYGSTIGHTIIDLLSKNCWGLLGHFLRLKIHEHILLYGDIRKVQKIRVAGE
ELEVETLMTEEAPDTVKKSTAQYANRESFLTMRDKLKEKGFEVRASLDNSGIDAVINHNNNYNNALANAAAAVGKPGMELSKLDHVAANAAGM
GGIADHVATTSGAISPGRVILAVPDISMVDYFREQFAQLPVQYEVVPALGADNAVQLVVQAAGLGGCDFVLLHPEFLRDKSSTSLPARLRSIGQRV
AAFGWSPVGPVRDLIESAGLDGWLEGPSFGLGISLPNLASLVLRMQHARKMAAMLGGMGGMLGSNLMSGSGGVGLMGAGSPGGGGGAMGVG
MTGMGMVGTNAMGRGAVGNSVANASMGGGSAGMGMGMMGMVGAGVGGGQQMGANGMGPTSFQLGSNPLYNTAPSPLSSQPGGDASAAAA
AAAAAAATGAASNSMNAMQAGGSVRNSGILAGGLGSMMGPPGAPAAPTAAATAAPAVTMGAPGGGGAAASEAEMLQQLMAEINRLKSELGE

>MvChR1
MSPPTSPTPDTGHDTPDTGHDTGGHGAVEICFAPCEEDCVTIRYFVENDFEGCIPGHFDQYSSHGSLHDIVKAALYICMVISILQILFYGFQWWRKTC
GWEVWFVACIETSIYIIAITSEADSPFTLYLTNGQISPQLRYMEWLMTCPVILIALSNITGMAEEYNKRTMTLLTSDVCCIVLGMMSAASKPRLKGIL
YAVGWAFGAWTYWTALQVYRDAHKAVPKPLAWYVRAMGYVFFTSWLTFPGWFLLGPEGLEVVTGTVSTLMHACSDLISKNLWGFMDWHLRV
LVARHHRKLFKAEEEHALKKGQTLEPGMPRSTSFVRGLGDDVEIDPSYELYRLKRQNHPEYFLSPAQTPRRGPSFDKRTSFEMDGGKNGMLQMMP
VTGMGMGMGMGMGGGKTVLFLDYTGGGYVSFFEQQLSNMGVNVTKCWSDDDMYNTAGVANVKQLFHFAMIPNNALGGQMVMDLRGTGLL
VVAYGPEPPMPGMGQDEFVPLQMPGVPYDESILHNLVMRHAITQGLGMNGMQGNMGQQQQMMGMQGNMNGMQGNMNGMQGNMNGMQGN
MSGMQGNMNGMQGNSGMNQGWNNQGFTNTGAFGY