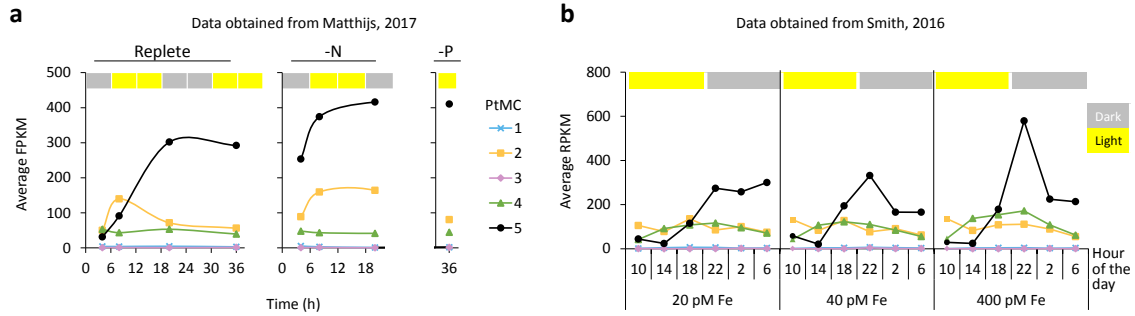
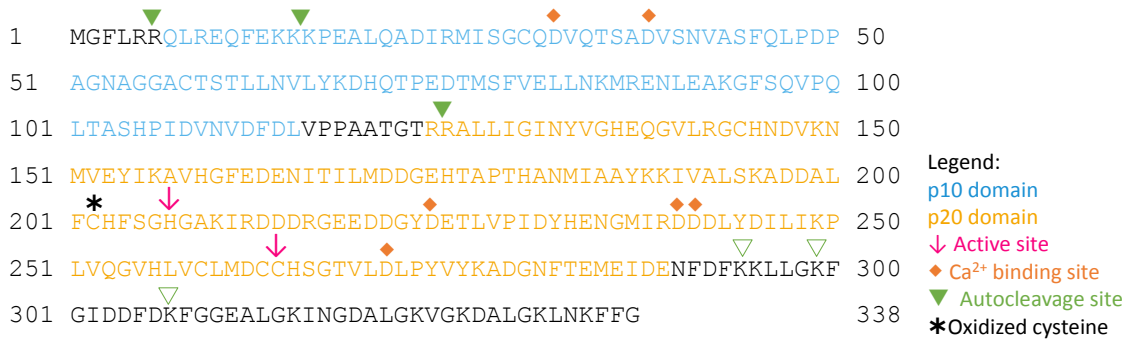


Supplementary Figures and Tables

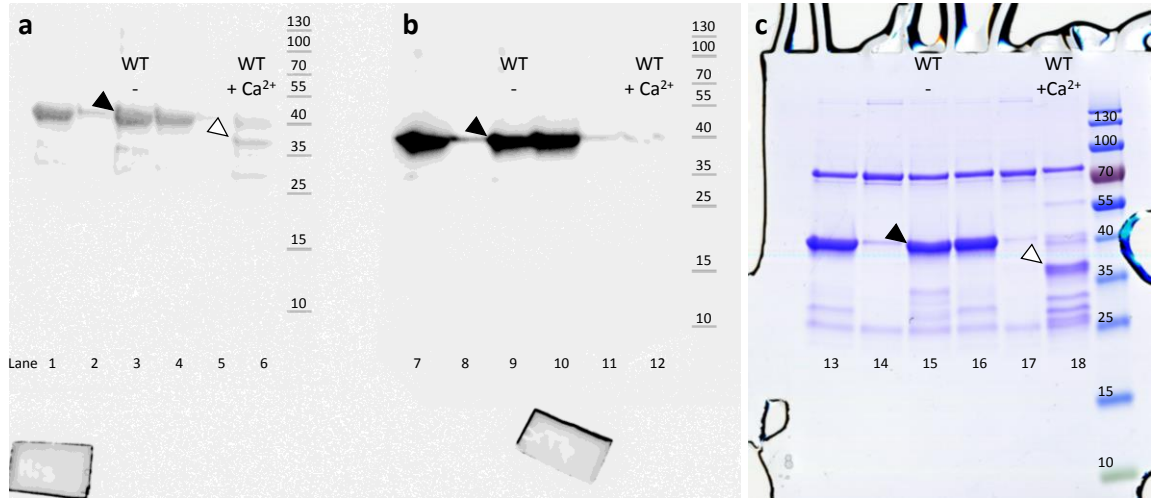


Supplementary Fig. 1 *P. tricornutum* MCs expression in published transcriptomes.

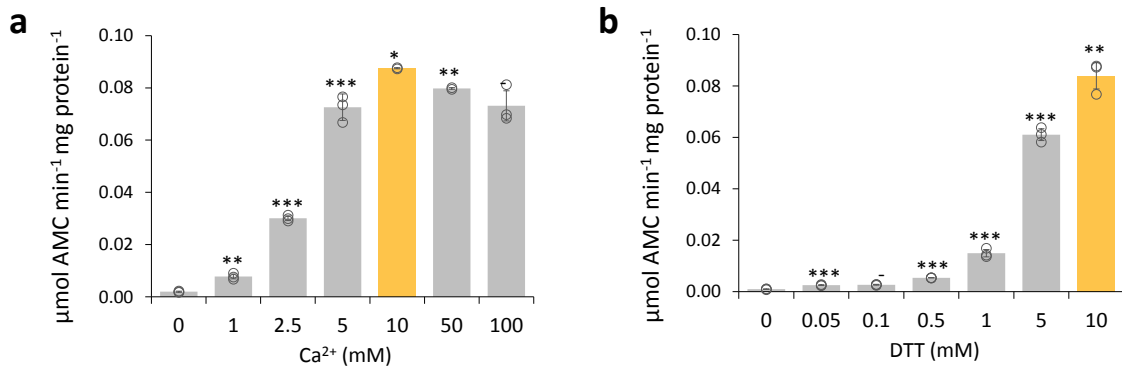
a *P. tricornutum* MCs expression, presented in fragments per kilobase of exon per million fragments mapped (FPKM) as obtained from Matthijs *et al.*¹ during 36 h growth in replete, nitrogen or phosphate deplete media. **b** *P. tricornutum* MCs expression, presented in reads per kilobase of transcript per million (RPKM) values as obtained from Smith *et al.*² after 30 generation acclimation to 20, 40 or 400 pM Fe, during 20 h growth diel cycle. Light regime is indicated in yellow (light) or gray (dark).



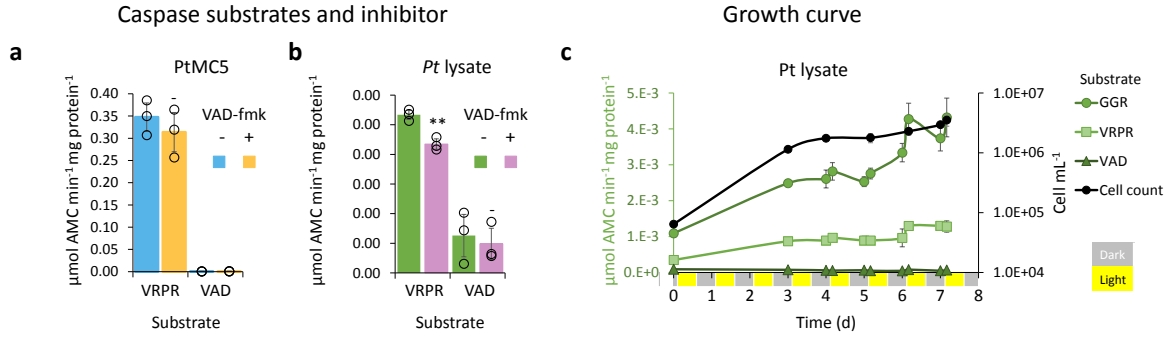
Supplementary Fig. 2 PtMC5 protein sequence and conserved features.



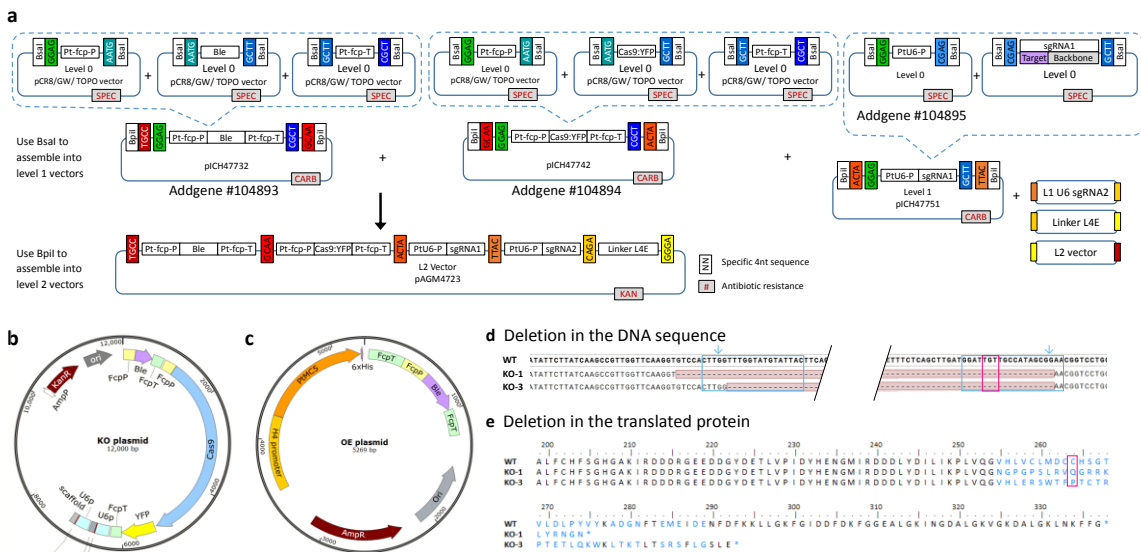
Supplementary Fig. 3 Full membranes and gels used to reconstruct Figure 2b. Immunoblot with (HRP) α His (a) or α T7 (b) tags, and Coomassie stained SDS-page (c). About 2.5 μ g protein extracts per lane were incubated with activity buffer containing 10 mM DTT, 0.1% CHAPS and without / with 10 mM CaCl_2 for 30 min prior to gel loading. Full length PtMC5 (~40 kD), auto-cleaved PtMC5 (~37 kD) were detected. Lanes 1, 2, 4, 5, 7, 8, 10, 11, 13, 14, 16 and 17 are not discussed in this manuscript. Protein ladders are present in the right, size in kD.



Supplementary Fig. 4 PtMC5 *in vitro* activity require high concentrations of Ca^{2+} and DDT. Recombinant PtMC5 protease activity, measured as release of AMC from GGR-AMC in increasing concentrations of Ca^{2+} (a) or DTT (b). In orange marked 10 mM (Ca^{2+} or DTT), as this concentration was used in the rest of the manuscript. Standard curve was used to convert the relative fluorescence units into μ mole of free AMC released per min per mg of total protein. Single measurements are indicated in circles, bars are means \pm s.d. of triplicates, each concentration was compared to 1 lower concentration, $-P > 0.05$, $*P < 0.05$, $**P < 0.005$, $***P < 0.001$.

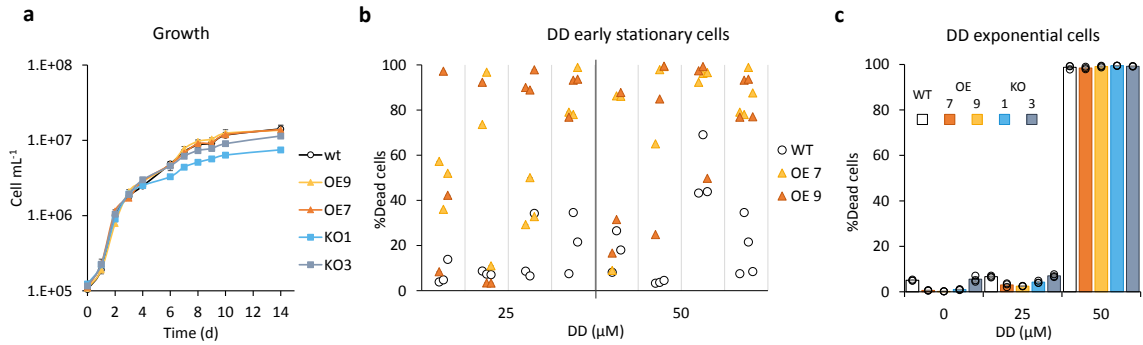


Supplementary Fig. 5 PtMC5 and *P. tricornutum* protease activity in response to caspase inhibitor and during a growth curve. Recombinant PtMC5 (a), *P. tricornutum* protein extract (b), protease activity measured as release of AMC from peptidyl substrates, with or without 100 μM of the pan-caspase inhibitor VAD-fmk. Standard curve was used to convert the relative fluorescence units into μmole of free AMC released per min per mg of total protein. Single measurements are indicated in circles, bars are means \pm s.d. of triplicates, significant relative to no inhibitor, $-P>0.05$, $**P=0.004$. c Protease activity of *P. tricornutum* protein extracts measured as in b (primary Y axis). Cell abundance (secondary Y axis) measured during 8 days of growth. Points are means \pm s.d. of triplicates.

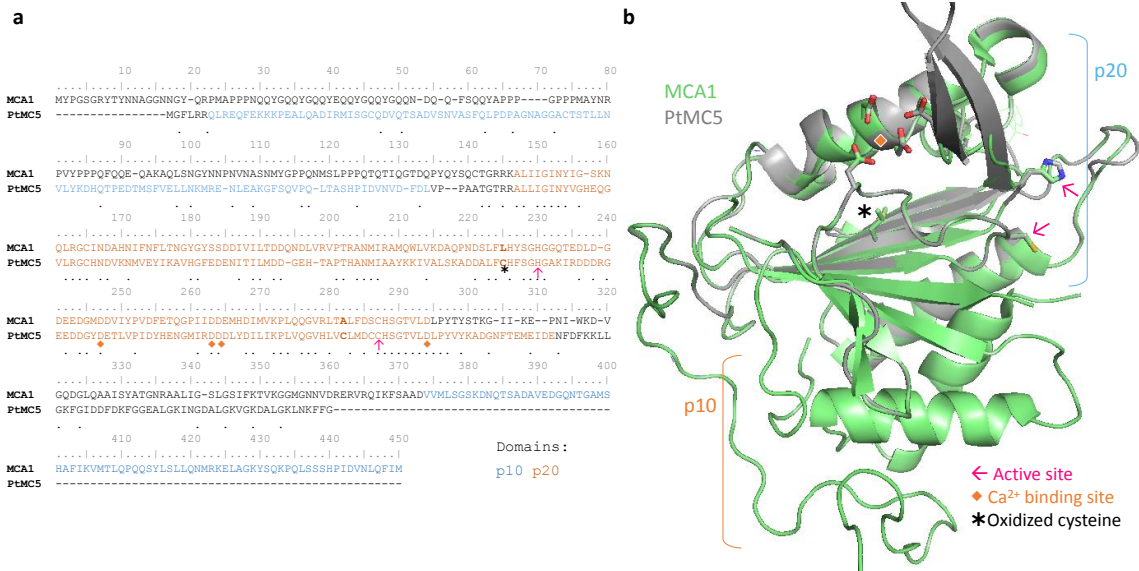


Supplementary Fig. 6 Schematic representation of assembly, final transformation vector for PtMC5 knockout and overexpression, and the exact deletion in the DNA and protein sequence.

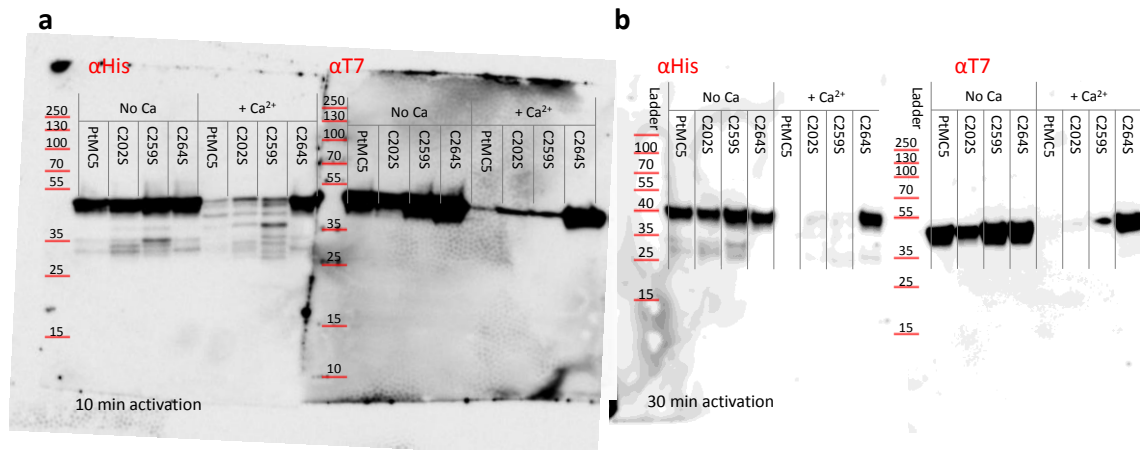
a Schematic view of Golden Gate assembly for CRISPR/Cas9-mediated PtMC5 KO vector. GG 4 nt sites are marked in colored boxes, bacterial antibiotic resistance, Spec, Carb or Kan are marked in gray boxes. Schematic representation of *P. tricornutum* transformation vectors used for PtMC5 KO (b) or PtMC5 overexpression (c). The OE vector includes bacterial antibiotic resistance (ampicillin resistance), diatom antibiotic resistance (Bleomycin resistance under *P. tricornutum* Fcp promoter and terminator) and His-tagged PtMC5 cDNA under histone 4 promoter (H4) and Fcp terminator. Plasmid maps were generated using Snapgene. **d** DNA sequence of clones KO1 and KO3 aligned to the WT PtMC5 gene. The sgRNAs are indicated in blue frame, the expected sgRNA cut positions are indicated by blue arrows. The active-site (C264) is marked in magenta frame. **e** Translated protein, based on DNA sequence, of WT and the two KO lines, starting from amino acid 199. The active-site (C264) location is marked in magenta frame, frameshifts are marked in bold blue text.



Supplementary Fig. 7 Phenotype of *P. tricornutum* cells with PtMC5 overexpression or knockout **a** Growth curve of *P. tricornutum* WT, overexpression (OE7, 9) and knockout (KO1, 3) lines over 14 days, presented as means \pm s.d. of triplicates. **b** Induction of cell death 24 h after DD treatment of early stationary cultures, measured as Sytox positive cells. Eight individual experiments are separated by vertical lines, each replica is marked in a circle (WT) or triangle (OE). **c** Induction of cell death 24 h after DD treatment of exponential cultures ($1.1 \cdot 10^6$ cells·mL⁻¹), measured as Sytox positive cells. Single measurements are indicated in circles, bars are means \pm s.d. of triplicates. Flow cytometry, analysis is based on fluorescent measurements of at least 10,000 cells per sample.



Supplementary Fig. 8 Protein sequence and structure of PtMC5 aligned to *S. cerevisiae* MC (MCA1). **a** Protein sequence alignment of *S. cerevisiae* MC (MCA1) and PtMC5. The p20 domains marked in blue, the p10 domains in orange. identical amino acids are marked with dots. **b** Cartoon representation of MCA1 structure³ (green) aligned with PtMC5 (gray), practically only the p20 domain is modeled. Key amino-acids side chains presented as sticks with conventional coloring, oxygen in red, nitrate in blue and Sulphur in yellow. The active site is marked in magenta arrows, Ca²⁺ binding site is marked with orange rhombus, and C202 in PtMC5, detected as oxidized in lethal stresses marked in black asterisk.



Supplementary Fig. 9 Full membranes used to reconstruct Fig. 4c, and similar membranes following longer activation of PtMC5. Immunoblot with (HRP) α His or α T7 tags of PtMC5, PtMC5^{C202S}, PtMC5^{C259S}, and PtMC5^{C264S}. Similar amounts of protein extracts per lane were incubated with activity buffer containing 10 mM DTT, 0.1% CHAPS and without / with 10 mM CaCl₂ prior to gel loading. **a** Full membranes used to reconstruct Fig. 4c, ~0.88 μ g protein per lane were incubated for 10 min in activity buffer. **b** About 4 μ g protein per lane were incubated for 30 min in activity buffer. Protein ladders are presented in the left of each membrane, size in kD.

*C. debilis*1 KRAVLIGINYVQ-EGELSGCHNDVIRIKDYLNIFQGFEEERHTLLMDDGININPTKGRIRAYRRIVKVSAGDITVF

*P. alata*5 KRAVLIGINYVQ-SGELSGCHNDVFNKDYLVNVLGFENRHTLLMDDGLNTSPTRENITAYRDLVNRSPAGDVAF

*C. curvisetus*4 KRAVLIGINYVQ-NGELSGCHNDVKNMKYELMNVHGFESNMTVLMDDGYHLNPTRYNITNAYQNLVRSMPGDSVF

*C. debilis*2 KRAVLIGINTGQ-QGELSGCHNDVKNMKEYLITVHGFEEQNMLILMDDNYPHNPTRMNLVAYRNLVRSKPGDITAF

*H. sinensis*3 RRAVLIGINYVQ-QQLSGCHNDVKNMKYLMQVHGFEEHNMTILMDDGYHREPTRYRNVAYKDVVRQSLPGDITVF

*C. curvisetus*1 KRAVLVGINYVGL-PGQLSACHYDVKNMKEYLITELGFEEKNMIILMDDHHTRPTRYAIIITAYRNLVRSKAGDITVF

*D. brightwellii*4-4 KRALLIGINYVQ-NGELSGCHNDVLNKEYLMDVLFGEEDNIMVLMDDGIIHEPTRDSILSGYRRLVAESVAGDITVF

*S. dohrnii*3 QRAVLIGINYKQ-KGQLSGCHNDVHNVQYKLVQGFVKDENITILMDDGMHKPPTKSAIIISAFKRLVKQTKEGDVVF

*S. marinoi*3 QRAVLIGINYKQ-KGQLSGCHNDVHNVQYKLVQGFVKDENITILMDDGMHKPPTKSAIIISAFKRLVKQTKEGDVVF

Skcos16234 QRAVLIGINYKQ-KGQLSGCHNDVHNVQYKLVQGFVKDENITILMDDGMHKPPTKSAIIISAFKRLVKQTKEGDVVF

*T. antarctica*4 QRAVLIGINYTGQ-SGELSGCHNDVHNVQYKLVQGFVKDENITILMDDGAHKPPTKAGIVNAKRLVKESKGDVVF

*T. miniscula*4 QRAVLIGINYTGQ-SGELSGCHNDVHNVQYKLVQGFVKDENITILMDDGMHKAPTKSAIIIGAYKRLVKESREGDVVF

*T. gravida*1 KRAVLIGINYTGQ-KGELSGCHNDVKNVARYLSEVQGFVKDENITILMDDGNHKKPPTKTAIIISAYKRLVKESKGDVVF

*T. rotula*4 KRAVLIGINYTGQ-KGELSGCHNDVHNVQYKLVQGFVKDENITILMDDGNHKKPPTKSAIIISAYKRLVKESKGDVVF

*T. pseudonana*3 QRAVLIGINYVQ-KGQLSGCHNDVLNVAKEYLQVGFVKDENITILMDDGNHKSPTKSAIIISAYKRLVKESKGDVVF

*T. weissflogii*1010-2 KRAVLIGINYTGQ-SGELSGCHNDVKNISYKLVQGFVKDENITILMDDGQHKPPTKSAIIISAYKRLVKESKGDVVF

*T. oceanica*2 KRAVLIGINYTGQ-PGELSGCHNDVKNKEYYIKAVHGFEENITILMDDGNHRSPTKAAIIISAYKRLVKESKGDVVF

*D. brightwellii*4-1 KRALLIGINYTGMPGELTGCNDVKNVKEYLMEHSFKEENITVLMDDNVHESPTKANIISYKRLVKESKGDVVF

*D. brightwellii*4-2 RRAVLIGINYTGMPGALTGCNDVKNKEYYIMDVHGFEEHTITVLMDDGKHPPPTKANIISAYKRLVKESKGDVVF

P. tricornerum5 RRALLIGINYVGHQGVLRGCHNDVHNVQYKLVQGFVKDENITILMDDGEHTAPTHANMIIAYKRLVKESKGDVVF

A. mhiphoral RRALLIGINYVGHQGVLRGCHNDVHNVQYKLVQGFVKDENITILMDDGEHTAPTHANMIIAYKRLVKESKGDVVF

*F. solaris*1 RRALLIGINYVGHQGVLRGCHNDVHNVQYKLVQGFVKDENITILMDDGEHTAPTHANMIIAYKRLVKESKGDVVF

*A. glacialis*1 RRALLIGINYVGHQGVLRGCHNDVHNVQYKLVQGFVKDENITILMDDGEHTAPTHANMIIAYKRLVKESKGDVVF

*A. glacialis*2 KRALLIGINYIGQ-QGELSGCHNDVNMVEYKLVQGFVKDENITILMDDGEHTNPTRSNIIISAYKRLVKESKGDVVF

*E. spinifer*4 KRALLIGINYVQ-QGQLSGCHNDVLMVVEYKLVQGFVKDENITILMDDGSHVNPTRSNIIISAYKRLVKESKGDVVF

*E. spinifer*2 KRALLIGINYIGQ-QGELSGCHNDVNMVEYKLVQGFVKDENITILMDDGEHTNPTRSNIIISAYKRLVKESKGDVVF

*P. alata*2 KRALLIANYVQ-KGELTGCINDALNMKEYYIMDVHGFEEENITIMDDGHEMPTRENIINAYNDLVIQSEAGDSIF

*P. alata*3 KHALLIGINYVQ-SGELSGCHNDVNIISYKLVQGFVKDENITILMDDGSHSPTRENIMSAFRMLVKSQVGGDSAF

*S. menzeli*1 QRALLIGINYKQ-TGQLSGCHNDVHNVQYKLVQGFVKDENITILMDDGMHKPPTKSAIIISAFKRLVKQTKEGDVVF

...*. * . * * * * * . : . : . * : : : * . : * : . : ***

*C. debilis*1 CHYSGHGGRTKDLDG-DESDGLDETLIPVDYQASAGQIIDDLLFKELVQPMSEGVAHCLMDCCHSGTVLDLPHYFTAE

*P. alata*5 CHYSGHGGFVDDTSG-DEEDGRDETLIPVDYQASAGQITDDELLKDLVHPKAGVLTCLMDCCHSGTVMDLPHYFTAD

*C. curvisetus*4 CHYSGHGGVVRTDTS-DEDDGDFDETLIPVDYQASAGQIIDDLLFKELVQPLPKGVLMCLMDCCHSGTVLDLPHYFTAD

*C. debilis*2 CHYSGHGGSVKDYSG-DEEDGDFDETLIPVDYQASAGQIIDDLLFKELVLRPMSTGVMLCLMDCCHSGTVLDLPHYFTAD

*H. sinensis*3 CHYSGHGGSVRDASG-DEEDGDFDETLIPVDYQASAGQIIDDLLLENLKVPLSRDVLMTCLMDCCHSGTVLDLPHYFTAD

*C. curvisetus*1 CHFSGHGSRVDTSG-DEDDGDFDETLIPVDYQASAGQIIDDLLKLVKPMKAGVLTCLMDCCHSGTVLDLPHYFTAD

*D. brightwellii*4-4 CHYSGHGGRLVDDDG-DEDDGDFDETLIPVDYQASAGQIIDDLLKLVPMKAGVLTCLMDCCHSGTVLDLPHYFTAD

*S. dohrnii*3 CHYSGHGGRLPDDNG-DEDDGDFDETLIPVDYQASAGQIIDDLLKILVHPMPAKVTMTCLMDCCHSGTVLDLPHYFTAD

*S. marinoi*3 QYSGHGGRLPDDNG-DEDDGDFDETLIPVDYQASAGQIIDDLLKILVHPMPAKVTMTCLMDCCHSGTVLDLPHYFTAD

Skcos16234 QYSGHGGRLPDDNG-DEDDGDFDETLIPVDYQASAGQIIDDLLKILVHPMPAKVTMTCLMDCCHSGTVLDLPHYFTAD

*T. antarctica*4 CHYSGHGGRLPDDNG-DEDDGDFDETLIPVDYQASAGQIIDDLLKILVHPMPAKVTMTCLMDCCHSGTVLDLPHYFTAD

*T. miniscula*4 CHYSGHGGRLPDDNG-DEDDGDFDETLIPVDYQASAGQIIDDLLKILVHPMPAKVTMTCLMDCCHSGTVLDLPHYFTAD

*T. gravida*1 CHYSGHGGRLPDDNG-DEDDGDFDETLIPVDYQASAGQIIDDLLKILVHPMPAKVTMTCLMDCCHSGTVLDLPHYFTAD

*T. rotula*4 CHYSGHGGRLPDDNG-DEDDGDFDETLIPVDYQASAGQIIDDLLKILVHPMPAKVTMTCLMDCCHSGTVLDLPHYFTAD

*T. pseudonana*3 CHYSGHGGRLPDDNG-DEDDGDFDETLIPVDYQASAGQIIDDLLKILVHPMPAKVTMTCLMDCCHSGTVLDLPHYFTAD

*T. weissflogii*1010-2 CHYSGHGGRLPDDNG-DEDDGDFDETLIPVDYQASAGQIIDDLLKILVHPMPAKVTMTCLMDCCHSGTVLDLPHYFTAD

*T. oceanica*2 CHYSGHGGRLPDDNG-DEDDGDFDETLIPVDYQASAGQIIDDLLKILVHPMPAKVTMTCLMDCCHSGTVLDLPHYFTAD

*D. brightwellii*4-1 CHFSGHGSQIKDDDFEEDGDETLIPVDYQASAGQIIDDLLKILVHPMPAKVTMTCLMDCCHSGTVLDLPHYFTAD

*D. brightwellii*4-2 CHFSGHGGMLPDDNG-DEDDGDFDETLIPVDYQASAGQIIDDLLKILVHPMPAKVTMTCLMDCCHSGTVLDLPHYFTAD

P. tricornerum5 CHFSGHGAKIRDDDRGEEEDGDETLIPVDYQASAGQIIDDLLKILVHPMPAKVTMTCLMDCCHSGTVLDLPHYFTAD

A. mhiphoral CHYSGHGCKIRDDDRGEEEDGDETLIPVDYQASAGQIIDDLLKILVHPMPAKVTMTCLMDCCHSGTVLDLPHYFTAD

*F. solaris*1 CHYSGHGAKIKDDEQGEEDKDYDETLIPVDYQASAGQIIDDLLKILVHPMPAKVTMTCLMDCCHSGTVLDLPHYFTAD

*A. glacialis*1 CHYSGHGGSTRDDDRGEEEDGDETLIPVDYQASAGQIIDDLLKILVHPMPAKVTMTCLMDCCHSGTVLDLPHYFTAD

*A. glacialis*2 CHYSGHGGKLRDDD-GDEEDGDFDETLIPVDYQASAGQIIDDLLKILVHPMPAKVTMTCLMDCCHSGTVLDLPHYFTAD

*E. spinifer*4 CHYSGHGGKLRDDD-GDEADGDFDETLIPVDYQASAGQIIDDLLKILVHPMPAKVTMTCLMDCCHSGTVLDLPHYFTAD

*P. alata*2 CHYSGHGGKLRDDN-GDEEDGDFDETLIPVDYQASAGQIIDDLLKILVHPMPAKVTMTCLMDCCHSGTVLDLPHYFTAD

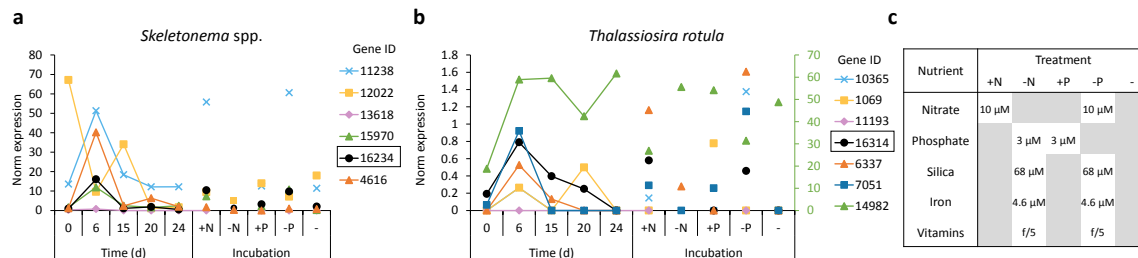
*P. alata*3 CHYSGHGGKLRDDN-GDEADGDFDETLIPVDYQASAGQIIDDLLKILVHPMPAKVTMTCLMDCCHSGTVLDLPHYFTAD

*S. menzeli*1 **CHYSGHGGRLPDDN-GDEDDGDFDETLIPVDYQASAGQIIDDLLKILVHPMPANVSMTC**LMDCCHSGTVLDLPHYFTAD

...*. * . * * * * * . : . : . * : : : * . : * : . : ***

2 Cysteines
Active site

Supplementary Fig. 10 Protein sequence alignment of the p20 domain of diatoms 2-Cys MCs, and *S. menzeli* MC1. PtMC5 is marked in bold, active site marked in red, 2-Cys in blue.



Supplementary Fig. 11 Differential expression of 2-Cys MCs in a natural diatoms bloom. MCs relative expression from a metatranscriptome of *Skeletonema* (a) & *Thalassiosira* (b) natural bloom in Narragansett Bay, data obtained from Alexander *et al.*⁴. Relative expression of MCs in the natural bloom as sampled for 24 days, or following 48 hour incubation of day 15 samples. 2 Cys MCs are marked in black circles. Added nutrients for incubation experiments described in c.

Supplementary Table 1 All PtMCs peptides detected in redox proteomics in response to lethal treatments of DD or H₂O₂ in compare to non-lethal treatments

PtMC	Cysteine	Peptide (Cys)	H ₂ O ₂ (μ M)		DD (μ M)							
			0	150	5 - 25	5 - 25	5 - 25	5-25 avg	25	25	25	25 avg
2	134	AVL IGINYTGQQQLSG C HNDVK	0.082	0.106				ND				ND
4	135	AVMIGINYTGQQQLSG C HNDVK	0.135	0.175				ND				ND
5	144	G C H NDVK	ND	ND	0.285	0.324	0.584	0.398	0.419	0.538	0.557	0.504
4	193	AGDAIF C HYSGHGGK	0.226	0.139	0.202	0.234	0.424	0.287	0.311	0.397	0.305	0.338
5	202	ADDALF C HFSGHGAK	0.272	0.340	0.214	0.197	0.142	0.189	0.387	0.424	0.383	0.398
					0.182	0.215	0.183		0.361	0.421	0.413	

In Rosenwasser *et al.*⁵, *P. tricornutum* cells were treated with 150 μ M H₂O₂ (lethal). Treated and untreated cells were sampled after 20 min. In addition, *P. tricornutum* cells were sampled 2 h after treatment with 25 μ M DD, with (non-lethal) or without (lethal) pre-treatment of 5 μ M DD 4.5 h before sampling. PtMC number, Cys number, and detected peptide (oxidized Cys marked in bold red) are shown. Average degree of oxidation in each H₂O₂ treatment⁵, and individual and average degree of oxidation in each DD treatment are shown. ND - not detected.

Supplementary Table 2 Abundance of 2-Cys MCs across diatoms species

Genus	Species	Isolate	#detected MCs	#2 Cys MCs	Classification
<i>Amphiprora</i>	<i>sp.</i>	CCMP467	5	1	Raphid Pennate
<i>Amphora</i>	<i>coffeaeformis</i>	CCMP127	7	-	Raphid Pennate
<i>Asterionellopsis</i>	<i>glacialis</i>	CCMP134	3	2	Raphid Pennate
<i>Chaetoceros</i>	<i>affinis</i>	CCMP159	3	-	Polar Centric
	<i>curvisetus</i>	Unknown	3	2	
	<i>debilis</i>	MM31A-1	4	2	
	<i>neogracile</i>	CCMP1317	3	-	
<i>Corethron</i>	<i>pennatum</i>	L29A3	6	-	Radial Centric
<i>Ditylum</i>	<i>brightwellii</i>	GSO104	7	3	Polar Centric
<i>Extubocellulus</i>	<i>spinifer</i>	CCMP396	5	2	Polar Centric
<i>Fistulifera</i>	<i>solaris</i>		4	1	Raphid Pennate
<i>Fragilariopsis</i>	<i>kerguelensis</i>	L26-C5	6	-	Raphid Pennate
	<i>cylindrus</i>		5	-	
<i>Hemiaulus</i>	<i>sinensis</i>		3	1	Polar Centric
<i>Nitzschia</i>	<i>punctata</i>	CCMP561	5	-	Raphid Pennate
<i>Phaeodactylum</i>	<i>tricornutum</i>	CCMP2561	5	1	Raphid Pennate
<i>Proboscia</i>	<i>alata</i>	PI-D3	6	3	Radial Centric
<i>Pseudo-nitzschia</i>	<i>australis</i>	10249 10 AB	3	-	Raphid Pennate
	<i>fraudulenta</i>	WWA7	4	-	
<i>Skeletonema</i>	<i>costatum.</i>	Skcos16234	5	1	Polar Centric
	<i>dohrnii</i>	SkelB	3	1	
	<i>marinoi</i>	SkelA	3	1	
	<i>menzelii</i>	CCMP793	3	-	
<i>Thalassionema</i>	<i>nitzschioides</i>	L26-B	4	-	Araphid Pennate
<i>Thalassiosira</i>	<i>rotula</i>	CCMP3096 (+Throt)	7	1	Polar Centric
	<i>antarctica</i>	CCMP982	3	1	
	<i>gravida</i>	GMp14c1	2	1	
	<i>miniscula</i>	CCMP1093	4	1	
	<i>oceanica</i>	CCMP1005	3	1	
	<i>pseudonana</i>	CCMP1335	6	1	
	<i>weissflogii</i>	CCMP1010	3	1	
<i>Thalassiothrix</i>	<i>antarctica</i>	L6-D1	6	-	Araphid Pennate

Supplementary Table 3 A list of primers used in this study

#	Name	Target	Sequence (5' – 3')
Heterologous expression of PTMC5			
1	C202S F	PtMC5 in pET-21	GATGATGCGCTCTTTAGCCACTTTTCCGGTCAC
2	C202S R	PtMC5 in pET-21	GTGACCGGAAAAGTGGCTAAAGAGCGCATCATC
3	C264S F	PtMC5 in pET-21	TGCTTGATGGATTGTAGCCATAGCGGAACGGTC
4	C264S R	PtMC5 in pET-21	GACCGTTCCGCTATGGCTACAATCCATCAAGCA
5	SDM C259S F	PtMC5 in pET-21	CACTTGGTTAGCTTGATGGATTG
6	SDM C259S R	PtMC5 in pET-21	GACACCTTGAACCAACGGC
7	T7 F	Pet21	GCGAAATTAATACGACTCACTATAGGG
8	Pet Rev	Pet21	GCTAGTTATTGCTCAGCGG
Assembly of GG and CRISPR/cas9 plasmids			
9	GG PtFcpP F	PH4 plasmid	TGGTCTCAGGAGACATACCTTCAGCGTCGTC
10	GG PtFcpP R	PH4 plasmid	AGGTCTCACATTCTTGACATCTGGCAACCGTG
11	GG Ble F	PH4 plasmid	TGGTCTCAAATGGCCAAGTTGACCAGTG
12	GG Ble R	PH4 plasmid	AGGTCTCAAAGCTCAGTCCTGCTCCTCGGC
13	GG PtFcpT F	PH4 plasmid	AGGTCTCAGCTTCCTTCCTTAAAAATTTAATTTTCA TTAGTTGC
14	GG PtFcpT R	PH4 plasmid	TGGTCTCAAGCGCTCGAGAAAACCTCATCCTG
15	SDM F fcpP	Level 0 fcpP	AGCGTCGTCTACACTGTCAC
16	SDM R fcpP	Level 0 fcpP	GAAGGTATGTCTCCTGAGACC
17	SDM F fcpT	Level 0 fcpT	CACTAGCTCGACTTCACCATGG
18	SDM R fcpT	Level 0 fcpT	TTATTCCTGACTGTGAAACCAAAG
19	GG PtU6 Prom F	<i>Pt</i> Genome	TGGTCTCAGGAGGTTGGCTCGGAAGTTGGTG
20	GG PtU6 Prom R	<i>Pt</i> Genome	AGGTCTCACTCGACTTTGAAGGTGTTTTTTGAC
21	GG sgRNA1 F	Scaffold	AGGTCTCACGAGGGATTGTTGCCATAGCGGAAGTTT TAGAGCTAGAAATAGCAAG
22	GG sgRNA2 F	Scaffold	AGGTCTCACGAGGTAATACATACCAAACCAAGTTT TAGAGCTAGAAATAGCAAG
23	GG SG R*	Scaffold	TGGTCTCAAGCGTAATGCCAACTTTGTACAAG
Scan and sequence of transformants			
24	Cas F*	L2 plasmid	CCGAGACAAGCAGAGTGGAAAG
25	Cas R*	L2 plasmid	AGAGCCGATTGATGTCCAGTTC
26	PtMC5 ex2 F	<i>Pt</i> Genome	GTGAACGATGACTTTGACTTGGTCC
27	scan KO R	<i>Pt</i> Genome	CGTCAATTTCCATTTCTGTAAAGTTTCCG
28	PtMC5 R seq	<i>Pt</i> Genome	CCTTAACTTTCATTCTGATGTGCAGCAC
29	PtMC5-KpnI 5'	PtMC5 in pET-21	ATATGGTACCGGATCTCAGTAGTGGTGGT
30	PtMC5 3'	PtMC5 in pET-21	CGGATCCGAATTCATGGGTTTCCTT
31	H4 T → gene	PH4 plasmid in <i>Pt</i>	GCAAGGATGCCCATTTGTGC
32	H4 P → gene	PH4 plasmid in <i>Pt</i>	ACAGTCAATACCGAAAACAAAC
qPCR			
33	qMC5 F	<i>Pt</i> Genome	CAAGTTCCTCAGCTAACCGCG
34	qMC5 R	<i>Pt</i> Genome	TTGACGTCGTTATGGCAACCTCTC
35	TBP F**	<i>Pt</i> Genome	ACCGGAGTCAAGAGCACACAC
36	TBP R**	<i>Pt</i> Genome	CGGAATGCGCGTATAACCAGT

*These are primers 6,21,22 from Table 1, Hopes *et al.*⁶.

**Primers from Table 1, Siaut *et al.*⁷.

Supplementary Data 1 Full protein sequences of all the MCs used in this study.

Codes for all species presented in Table 2:

Pyezoensis	<i>Pyropia yezoensis</i>
Ngaditana	<i>Nannochloropsis gaditana</i>
Cparadoxa	<i>Cyanophora paradoxa</i>
Cc	<i>Chondrus crispus</i>
Ppurpleum	<i>Porphyridium purpleum</i>
Aa	<i>Aureococcus anophagefferens</i>
At	<i>Arabidopsis thaliana</i>
Cv	<i>Chlorella variabilis</i> NC64A
Cr	<i>Chlamydomonas reinhardtii</i>
Cs	<i>Coccomyxa subellipsoidea</i> C-169
Es	<i>Ectocarpus siliculosus</i>
Fc	<i>Fragilariopsis cylindrus</i>
Mrc	<i>Micromonas pusilla</i> RCC299
Os	<i>Oryza sativa</i>
Pp	<i>Prymnesium parvum</i>
Pt	<i>Phaeodactylum tricorutum</i>
Tp	<i>Thalassiosira pseudonana</i>
Vc	<i>Volvox carteri</i>
Pn	<i>Pseudo-nitzschia multiseriata</i> CLN-47
Eh, Ehux	<i>Emiliana huxleyi</i>
symbA1	<i>Symbiodinium A1</i>
Pf	<i>Plasmodium falciparum</i>
Gt	<i>Guillardia theta</i>

Putative domains, marked on MCs full protein sequences, where available, or longest sequence where full ORF not available.

The putative p20 domain is marked in orange, the putative p10 domain is marked in blue.

```
>Pyezoensis1 contig1 GFKY01015919,GFKY01026864
MGKKAVLIGCNYPGTTKAALEGCCNDVDIMYDVLQRYKGFDAEITILKDDGSCSDELIPTGANIRKALTKL
CGEAQEDDIIIFVHFSGHGTQVPADDDDPEDDRKDEAICPTDMSLIVDDDLRAIVSTIPDGCRLTLVTDCCH
SGSMLDHSEVAIEGEKDGNSKASLLEESASLMSLLTGGTREVGGVDVKNRALPITDVASLLTQITGRSVQP
GNIRSTLGEFFGGDAGRLALQYFLKSGKSGSGMSGGLAAMAGMLAASQGGGQSSSSGGGSSGLAGLAGS
LLGGKKQSQSSGGGSAALMGLAGSLLGGKKPQQSSHSSGGGSLTAAMGMSMLSGSGGGSSGGSHSTS
HSLGGSLSEDKGILITGCQAHETSADVRPPGGKAFGALTNSIQTVLKTNPDASYDDVVSQARTVLSQAKHA
QNPCLECSEKNSRLPFIC
```

```
>Pyezoensis2 GFKY01000140,contig_9228_g2199
MSGAPPPDTWSSSSRGVGGSGGYGGYGAPSPGSGGYGPPPGGAYGQPPAHGPPPSGFDAEYEAIRIQQNEE
EARGAGGGGQTPYGSLLGPYPPQQQDPYQHPQQQQHTYAGAHGGYRAQPPSYHAQPPHPPSYAHGAPPS
NYGAAPPIQHVPPTPHVFPFGPAHPATGYVQPPNAPAPQYGPSASGPATGWTTPSGRKRALLIGINYKGTPSAL
AGCVNDVRYIQYLLASKFGFRPSDFVILTDERVDVPGARTGPPTRASILAEMRALLSGAQPGDSLFLHFSG
HGKQIKDVSQDEEDGLDEAILPSDYLRSGHIVDDEMYHILVRPMPRGRVRLTAIIDACHSATGLDLPYVHGA
PGGSQYGGGAVAAQGRGGLSSLLSGGGGNAALASMAAALGGGKPMIGGGGGSGGGGGSLGAILSAVV
MGASGKPLSGKQQAARMVEKRQPNPNAGEVIAFSACEDHATAADTHGAAGGYATGACTYSFIQAIEHGRDW
HSYTFESLLVEMRRKMRKGLKQVPQLTSSFPMSISSRFIV
```

```
>Pyezoensis3 GFKY01041200,contig_32374_g7869
```

MTIPTGHDTWTSSRTVDGGTGAANVLPFRGPPAYPLPRSNHHPFLTTPFAAAASATSSAGPDTWTPRRRPP
TGAGNLLPWGHPAAGESASSPWRTSAPPPAAPRAVHDALIGEEIERGARVDALMRPPLSGGLPVRPVHMPW
STAAAAPAAAASSSHFQPRKYALLVGINYWGNIHFMPTLRGCVADVNRVRRLLTSRGGYDPADIVTLTDEPL
DGIGGAWGKFPHTDAILAEMRALVAKPKAGDSLFFHFSGHGAQEPDASGDEIDGMDETFVPADGTPTGRTI
LDDNVHKLKLVKALPPGVRLMALIDACHSATALDLPHLLDEPWGAGHGCNAACGTEKGCDDRVI SLGACRD
DSAAADWHRAGRGTSSAGAMTSFFIDAVERNVTGTTTHRAVLNRYVRRRILEEGMTQEPQLSSSSPLDPYARL
EL

>Ngaditana GAGR01012758

PTNSRPYRRSLRRPPWPSTQAPTNLTYTPVGGFVANNVATPPPSQQGRPSSSLSSFPSPGYQPPRPAP
SFPPSSSAAYRPPHRPPSSPSPLPEGSTYQRPNDLHGALPFPSSPCNGRRKALFVGITYAGTRAEKGCVN
DVKNLHAFIQRTYGFQPEMRVLTDDPGFSEGTPTRQNIQGMRLVGGARHGDSLFFHFSGHGGSVRDQN
GDEADGMDETILPLDHARAGQIIDDEIHDLLVKPLVQGVRLTAVFDSCHSGSVMDLFPYKVDGSLEIVQV
DNTAKVVNSLANAGLAYLSGNKAVALMSGLEAVGTMLFGPKTNHDARRRTEENNQSPADVIQFGGCRDDQT
SADTRIDGQATGALSVALIRVLSQGNQDYAQLVKNMRQLLRGKYTQIPQISSSHKIDLFSPFKM

>Cparadoxa1 Contig8192

MPPPPPGYRQAPAPAPGVRPTQNLLYDPSKRRRAVHVVAISYKHDEDNFLPGCWNDKSMVDLGMKQYGFKS
KDIKMLTDEDFNKNFSPFTHLIEGARPGDILLFTFSGHGGQIKDLGDGDEIDGKDETLIPVYETAGEITDD
ELAALFAKLPRGVRLICFLDCCHSGTGLDLPYHNNILPAPKAGQQLRNYLPASRNKALPAPSYAPPPMAKT
SMDPETPKKKHHEPFLDAIFGPIVHPESYQDQYGNHSQQLQARAYGVGGPMDAGHEMRPIVVQTNLRENT
GILNFGKA

>Cparadoxa2 Contig7118

MSWNPFGGAPEPPVPGVPVGFVAVNQPPPPYGAAPT VHYPVPPGNVTKKALLIGINYLRTPECRLSGCIND
VNCMKYLLMTKYKYEERNILCMTDDQSDPLKQPTRHNIVQGMRLVMGTKANDTLFFQFSGHGSQVRDHSG
DEADGMDETILPCDFKQAGQITDDEIYQLLRCRPLPYGSPPTPHSLPPHAFGSQRWRMDCCHSGTGFDLPY
THSLNFFGQLSTTTEPMQPNWCCQGAWIAKRAPTRAIETSFAQKTTLYGQLVVSMLNEVQADAPTVINLA
LEFDCHWNSGLVL

>Cparadoxa3 Contig26116

MPTKRALIVGIKYEIWPRTLNLCVNDAKEIITGTFGYAEENVKMIIEKPGFVQPTRANIMEGLSWLPGDQ
LFFGYSGHGSQRADEGKDEVDGKDECLVPMDFQTEGYIRDDELNKLKLVVQPPPGRCLLTLGQIFDCCHSG
SGIDLDTYTIMTAAGFSLATATAAKDPMGKGVLDLDEGDGVRAAAGADAEP SIDTVVVAQVANMQAKAVGSK

>CcMCP1 XP_005717184.1 metacaspase type II, MCP1 [Chondrus crispus]

MGKYAVVIGVNYTKNPEAALQGCCNDARLMVNLLHSGKFEDEDIKLLVDDDDSNDSPNHVNVKALDWLCT
GRSEGDTIFMFHSGHGTQVPADDDDDVEEDKLEAICLEELFLMADDDDLKQYFSQLPEGVRATVVMDCCHSG
SMLDGOEVAIQGAKDEDSAVPPQESDDLNVNLGGSREAVSNRSLPISTICNVMSQKLGSPVSPTGSGVNGA
MAQVFGGTAGKLMKFKALGQMAKQDGGSSNPLVGMGLGMMGGKSTSSSGSNPLAAMMGGGSTSSSGSNPLAA
MMGGGGSTTSSNPLASMMGGGESTTSSNPLASMMGGGESTTSSNPLASMMGGGGSTTSSNPLASMMGGGGGS
TTSSNPLASMMGGGGSTEQNGNPMGSLMGLGGGNASSGGSNPLASMMGGGATETETAAPQSQNPMAMLSG
LMGGMGLGGQEDSGDAPAYNPAHQPMRDVCTLITGCQASETSADV RPAGEEAFGALTKTLTTLYEKNPET
TYHDLVSNVRSLSRGGFKQNPCLCESETMAHQPFIC

>CcMCP2 XP_005713893.1 MCP2 [Chondrus crispus]

MRDRGLPLPQSL SAYQRQAEASQVETVPDPPRLDGLNRKPSISPAAADYVPELPVGY SARMNRRKALLIG
IGYRKHKYLNVLPGCKNDVTAMFNLLTSELFGFPQDEVRLSDELNMLGSHVQAPTRFNILRDLWLTED
VGEEDSAVFFFAGHGDFIEDVSGDEIETGVDQCIMPIDCLPEPKHRTGQTFKGVPPILDDTIYERLVRGVP
AGAKVTAIVDACRSGSVCDLPMHGDGDKYRASGGDPPQRSSPHKGAGGFVLFSGSADDQQSIDMTIAT
GRNGEVESFGVMTRSFVDAVQEMAMHRCPETYDGVESWYTYGQLFQRVRELWERTSSILPHYIEKQEPQM
STSHTFDTWQAPFSI

>CcMCP3 HG001672 [Chondrus crispus]

MQRHMDPNPSSPQSGLSSRRKAPPRVSLDLCEPPTGNYGARMVENGEIRSPLAAGAFQVKPKIRPARTR
YLSLDLYAERNMQDVPMSPLVTRGGPVKSLADSGETDVRSPYSRSLSRNRRLSNVPYNASPKNSSRKAVL
IHACYINTEGAQRLRSQSNLASMYDLLVLSLGFSGRNVVWVLTDEPKTI PGAVNFTPTRGNILNSMRWLKVG

SSAKHQLLFCFSGHGCRVLKERNPVAVFEDCILPCDYPMSSPISETEIKQILVQNLNRNGATLTSLLDCQNS
AQLMNLPIYIHAAARGAKGSFFLREEPEAQRFTSASTPGVVLNSVLRFSKLRGGAEQRRMAAEERRNANAA
TCFDNGTVICISWSFETERECPSISSPNNHGCLTHAFVRYLKHSAAEKSKPSYSTALCAMSAWLSSRGGN
LPQFSSTHKVSPDKPISLL

>CcMCP4 XP_005710904.1 unnamed protein product [Chondrus crispus]
MSNPGVFPDGLDPEYSRRINANNASKPRGHLYPSSAYPPQPYPYPPGYRPPHGYSPIYAQPQNPYPPQPFH
PPPPPPPHPPQHPYAPQQPYPAHPPQPSYNPHGPPALAQASASHMTSPFRPSGRKALLVGINYRGTSSALR
GCVRDVTFVHLLVSKFGFRKKDFVVLTDSEVNI PGVRKGPPTRRVILDSLKWLVSRSRSGDSLWFSFSGH
GAQVRDVSGDESDGFDETI PVVDHKRAGHI IDDELYEIVRHVARGARLTVLLDACHSGTGLDLPYQHDVFG
TSGSQRISGGKGMSLTSGLLNVAGALLNGSASGALNAGFNMATGGKKKKKTPGDPNAGEVLLFSGCKDNQ
TSADTSKLTGGLPTGAMTFALIEHSTVGDWRNYNYRQLLQTMRQKLRAAKMTQVPQFSTSHPFDLSTS
FML

>Ppurpleum1 evm.model.contig_3552.1
MWSSSYAPGSAPQQPGTFYGAQPPPPPPQXX
XXPYQQYPPEQPI LASMVSSNALGTTKLSIN
YYQDSRLPASAXXXXXXXXXXXXXXXXXXXXXXXXXXXXXPVQHPGYGPAAPKAPATGRRKAVLIGINYTGTRN
QLKGCVNDVRFIKHLLQTRFGFKDEDFILTDEDPKISGVRRAAPTRYNI IDALRWLIGGVTAGDSLFFHF
SGHGSQVRDTNGDEEDGYDETI LPVDFQQRAGQIVDELHAILVKPLPAGARLTALIDACHSGTGLDLPYVM
DVDQYDPSAVAASGYGRGAQQRGGGNERGLIGAMIGAGLMSASYGAPPNKRKKYQKKVPLAPACAGDAV
LFSGCDDHQTADTSGLSGGTSTGAMTYCFVEAIEHGSVSDWHQYTYGSLLSMTRSKLLKKGYKQRPQLSS
GKPMASSTPFRI

>Ppurpleum2 evm.model.contig_2187.3
MVAKRAVLVACNYPGTNAELKGCISDAKIHKSIIEKKGFKESDIKVLIDDESELTSYAPPTGENIKKAL
TELCESAQPGDFLFFSFGHGTQVPGGAEEEDGKNEALCPTDMNLLVDDDIRDIVNKTCKGVTTLTVCDCC
HSGGMIDHSSILIDSDDKADPDAPPVEFRSRELPI SGVAERLSQLLGKTVDPNGTAVRGAIEHEKYGAAASK
FAVGMFENYTGKKMGTEKKKLTGMITSCFSALGVGGGGGGSDHSNAAPAVSGGSAGGPPKKVGHMVHVD
EEMGILITGCRAHETSADVRENGQAFGALSKNLHLYLETKPDATFYEVVHGARDRLADKGFTQNPCLECAK
DNAALPYICPNV

>AaMC1 AA0026G00590
ALLVGCNYPGSSAELRGCVNDVLRMRALLLGGQGFPEQQIVILRDDRGGQQRPTRRATEGLRWLAAGAGRG
DSLFFHFSGHGSQERDRTGDEADGYDETI VPCDYKSAGQITDELHAILVRPLPDGARLTSIMDCCHSGTG
LDLPYCFTPGRGWQTDVPCFSRQDVQLFSGCEDDQCSADTYANAAAGGAMTNAFLKALAENPMPPLYPDFL
TALHRELRRKGFQKQPLSSQRFDLNQRVFSLTEGFI PNSNQTI GRRPGMRRKKSRRRGRGAGVGMETML
AAGIGA AVLSSLF

>AtMC1 AT1G02170
MYPPPPSSIIYAPMLVNCSGCRTPLQLPSGARSIRCALCQAVTHIADPRTAPPPQSSAPSPPPQIHAPPG
QLPHPHGRKRAVICGISYRFSRHELKGCINDAKCMRHLLINKFKFSPDSILMLTEETDPYRIPTKQNMRRM
ALYWLQVQCTAGDSL VFHYSGHGSRQRNYNGDEVGDYDETLCLDFETQGMIVDDEINATIVRPLPHGVKL
HSIIDACHSGTVLDFLFLCRMNRAGQYVWEDHRPRSLGWKGTAGGEAISI SGCDDDDQTSADTSALSKITST
GAMTFCFIQAIERSAQGTTYGSLLSMRTTIRNTGNDGGGSGGVVTTVLSMLLTGGS AIGGLRQEPQLTAC
QTFDVYAKPFTL

>AtMC2 AT4G25110
MLLLVDCSSCRTPLHLPPGATRIRCAICHAFTLIAPEPRLQSHASASPPFPNNSPAPSTFIYPPPTPSPY
THAPHAPSPFNHAPPDSYFPTHAPPASSPFNHAPPGPPPVHVGQKRAVIVGVSYKNTKDELKGCINDANCM
KFMLMKRFQFPESCILMLTEEEADPMRWPTKNNITMAMHWLVLSCKPGDSL VFHFSGHGNNQMDNGDEV
GFDETLPLVDHRTSGVIVDDEINATIVRPLPYGVKLAIVDACHSGTVMDLPYLCRMDRLGNYEWEDHRPK
TGMWKGTS GGEVFSFTGCDDDDQTSADTPQLSGSAWTGAMTYAFIQAIERGHGMYGSLLNAMRSTVHEIFD
KNKGRELVEVGADFLSTLLGLLILGASPPDEEEVNPAPQKTQEPQLSANEAFVYKPFSL

>AtMC3 AT5G64240

MASRREVRRCRCGRMWVQPDARTVQCSTCHTVTQLYSLVDIARGANRI IHGFQQLLRQHQPQHHEQQQQQM
MAQPPPRLLEPLPSPFPGKRAVLGCVNYKGSYSLKGCISDAKSMRSLLVQQMGFPIDSILMLTEDEASPQ
RIPTKRNIKAMRWLVEGNRARDSLVFHFSGHGSQQNDYNGDEIDGQDEALCPLDHETEGKIIDDEINRIL
VRPLVHGAKLHAVIDACNSGTVLDLPICRMERNGSYEWEDHRSVRAYKGTGGAAFCFSACDDDESSGYT
PVFTGKNTGAMTYSFIKAVKTAGPARTYGHLLNLNLMCSAIREAQSRALAFNGDYTSSDASAEPLLTSSEEFDV
YATKFVL

>AtMC4 AT1G79340

MTKKAVLIGINYPGTKAELRGCVNDVRRMYKCLVERYGFSEENITVLIIDTDESSTQPTGKNIRRALADLVE
SADSGDVLVVHYSGHGTRLPAETGEDDDTGFDECIVPCDMNLITDDDFRDLVDKVPVPGCRMTIISDSCHSG
GLIDEAKEQIGESTKKEAEDEDESEESSRFGFRKFLRSKVEGAIESRGFHIGGNKDEDEAEIEIETKEIE
LEDGETIHAKDKSLPLQTLIDILKQQTGNNDIEVKGIRPSLFDAGDDSSPKVKKFMKVILGKLQAGNGEE
GGLMGMGLKGLASGFLEGLNDEDYVKPAMQTHVGSKEEVYAGGSRGSPVPLPDSGILISGCQTDQTSADATP
AGKPTAYGAMSNSIQTILEETDGEISNREMVTRARKALKKQGFTQQPGLYCHDGYANAPFIC

>AtMC5 T1G79330

MAKKAVLIGINYPGTKAELRGCVNDVRRVHKSIVDRFGFSEENITELIDTDESSTKPTGKNIRRALNLVE
SAKPGDVLVVHYSGHGTRLPAETGEDDDTGYDECIVPCDMNLITDDEFRLDVEKVPKEAHITIIISDSCHSG
GLIDEAKEQIGESTKPKKESGGSSGLGKGFVREAVEEALESKGIAPHHKDEKDNKTKELKLEDGAK
VHVVNKSLPLQTLIDILKQNTGNNDIEVKGIRPTLNFVFGEDASPKVKKFMKVILTKLQEGKTEGGILGMI
GKLAQEFLLKHLNDDEEYVKPAMKTHVGNKQEVYAGASNGSLADNGILISGCQTDQTSADASPOGHPPEMAY
GAFTNAVQIILEETKGMITYKELVVKARKLLKKQGFSSQRPGLYCSDFSFNAPFIC

>AtMC6 AT1G79320

MAKKALLIGINYPGTKAELRGCVNDVRRMRISLVERYGFSEENIKMLIDTSSSIKPTGKNIRQALLDLVE
PAKSGDVLVHYSGHGTRLPAETGEDDDTGYDECIVPSDMNLITDDDFRDLVDMVPKDCPITIIISDSCHSG
GLIDEAKEQIGESTKPKKDSGDSSTINKETEAEIEVGNRSLPLETLIDMLKQETGNDDIEVKGIRTTFLD
MFGDDSSPKVKKFMNVLNSLQETTTTIQTVSDEVLGSVENLAQEFLEQKLSDDVKPAIQDVYAGAINGAL
PDNGILISGCQTDQTSADASPPGHPELAYGALTNAIQIIIGETKGIISNKDLVVKARKLLRQGFQRPGL
YCNDAVYNARFIC

>AtMC7 AT1G79310

MAKRALLIGINYPGTTEELQGCVNDVHRMHKCLVDRFGFAEEDITVLIIDTDESYTQPTGKNIRQALSELIK
PAKSGDVLVHYSGHGTRVPPETGEEDDTGFDECIVPSDLNPIPDDEFRLDVEQVPEGCQITIVSDSCHSG
GLIDEAKEQIGESTTTKPNRESKVSSFEFEFKNCLHSIFVKLLAFCGIGSSHVETREIVEVGEDEVVRSR
YLPLERFIELLKQQTGDNIEIGKIRPTLFDVFGEDSSPKIKKFMKVILTKLRKTNDQSTLLGKIEESARG
YIEETLNDEHYMKPAMQAQVKSREIYGGRSSNGLFPDRGILLSGCQTDQTSADVKKKGEAFGAFSNAIQM
VLSETHDKDKITNKEMVLRAREILKKQMFIIQRPGLYCNDRFVFNAPFIC

>AtMC8 AT1G16420

MAKKALLIGINYPGTAVELRGCVNDVHRMQKCLIELYGFANKDIVIMIDTDKSCIQPTGKNICDELNDLIA
SGQSGDFLVHYSGHGTRIPPGIEDSEDPTGFDECITPCDMNLIKDQQFREMVS RVKEGCQLTIIISDSCHS
GGLIQEVKEQIGESHMKPVDKVKEQIEESHMKQPKLGIASYFLNIVMNLATCGVSKSQDRGGGEESEFRG
EIELEKDETLDIKTRYLPFESYLSLLKEQTGQTNIEPVRIQTLKLFKGFEDPSPNRQRGLSDLGNCEVDAG
DSGASRLNAVTDNGILLSGCQTDQRSEDEVYVTRTGKAYGAFSDAIQMILSAPRKDKKKITNKELVSEARVF
LKKRGYSQRPGLYCHDRFVDPKPFICY

>AtMC9 AT5G04200

MDQQGMVKKRLAVLVGCNYPNTRNELHGCINDVLAMKETILSRFGFKQDDIEVLTDEPESKVKPTGANIKA
ALRRMVDKAQAGSGDILFFHYSGHGTRIPSVKSAHPFKQDEAIVPCDFNLITDVFRELNVQLPKGTSFTM
ISDSCHSGGLIDKEKEQIGPSSVSSNISPAIETTNTKITSRALPFKAVLDHLSLGTGITTSDIGTHLLELF
GRDAGLKFRLPAMDLMDLLETMTAREKHVDSGILMSGCQADETSADVGVNGKAYGAFSNAIQRVLNENEG
AMKNKQLVMMARDVLERLGFHQHPCLYCSQDNADATFLSQP

>CvMC1 CNC64A_020G01030

GRKKAFICGINYFGTSAKLNCGINDAKCMEYLLKSKFGFKQENILMMTDDCPDPMRRPTRANMFQGFWRWT
MDMRPGDSLVSFHYSGHGSQTRDYSGEETDGMNETLCPMDFRQAGEIVDDELNRCLINPLPTGVKLHCIIIDA
CHSGSVMDLPFQAHVRRGGYQWEASYHFTRAHKGTAGGFVQFGASKDSQTAADT

>CrMC1 CR12G07090
MYGYPPPAYGAPPAGYGAPAAPSPYGAAPPYGAAPPAYGAYGAPQPAYGAPPAPAYGGYGAPPAPAYGAQ
PAYGTPYGGQAQPSAYTYGQPSANPQORPATAPAPAYMPPTTYAPAPTNGGRRRRALLVCGCYPGTREALN
GCLNDVNCIKFCLMNRFGFTEQQILILRDDTRQPDFISTKANIIFRGIQWLMTDQQPGDSLFFHFSGHGSQQ
YDRNGDEEDGYDETICTDFRRAGQIVDDELNRMMVQPLMPNVTLHAVI DACHSGTALDLPYRAKVDHSGR
WYWKGRARYDKCTRGGTAFQFGACKDSQVAADTNKLSGKAYTGAATFSFIEAIEKYGVQQTIVGVLGHHMQ
TLRAMNGGMVSSGATGILASLLLGSSISSGQEPVLSCDKQVDLYASRLNI

>CrMC2 CR03G07540
MPGKKAFLVIGCNYPGTNAALRGCINDVWGMKEILITYYGFTDADLTILIDTDKSYLQPTGKNIAKAKITEMV
SAAQDGDVLFVLFHFSGHGTQIPSADGDEKDKDEAICPTDMNLICDDDLRVLLKPLETKPGVKFTFIADCCCH
SGTLLEDHESVQISGPKSGAPPPPAIDMGALAGFLGALGQPDGRDLKNRALPFSELGMLSQLLGGVPVDAR
TVRSMGTIFGADSSAKIQQFIGMYQALTAGTKGAAAGGAGGILQMLCACLAPPADQNGPSGTPANAQSGP
GAHYAAPAAAGNLAEPDLKVNYPGAKPPANEQLGADVGLITGCSNETSADACPSGNPDKAHGALSNAI
QTVIKQQQQSPGQPI TYRNLVIAVREMLTKTGFAQNPCLECSNKNADTPFIVC

>CsMC1 CV04G04400
APAHQQPAPGQTYNPTGRKKALLCACNYRGSSELRGCINDAHCLRHLITSRFNFRDSDIVMLTDDSPNPQ
AWPTRANMLYQMQLLWNAQPGDSLVSFHYSGHGTQIRDQYGDSESDGLNETICPCDFKTAGYIVDDEMNRLL
VNPLPHGVRLHAIIDACHSGSALDLEFKCKVKDTGVRWKNYTRRTS IYKGTAGGEALQIGAARDKQTAAD
TATMSGSVSTGAATFAFIQAIERQGHITYLQLLQSMNQALEQLHASTGNRPPKLPKVGGLFGGLVSKVV
NGALDMAGLSGQTPVICSNVPFDL

>CsMC2 CV10G02150
PPPLQDGYGAPPQPPQGYGEPPAQQRKRALICACNYAGTDNALNGCINDAKCMQYLLKTRFRGFKEEDITM
LTDDQNDPAKWPTGNMRAHMRLVGDQATGDSLIFHFSGHGSQADWVGDEDDGYNETLCPCDFKQGGQI
VDDELNQLLVNPLRPGVRLHAIIDACHSGSVLDMEYRAEFHNGMPVWTNEFSKRPSIYKGTAGGEAFQFGA
ARDSQTAADTSQLSGNVSTGAATFAFIQVI IWDIVVCLDSRVLSMEGIRSEHHLNCF

>CsMC3 CV05G02260
MGHCASKSQFDREVEEVRERPDAATVYSSQRGTPMKDLGLVNGKYSKHSIPAEPEPQRDTIPARPGTP
SVSEIFQEPLRPSPLPTSKALPGVMSGRQLPYAAPVPPPSLPPPEYAHLAASGAWQPGRRRALLVAAN
YSRSADGSARLRGCINDVHCLKHLLTSKFGFQDNNIVLLHDEQPHGDYWP TKDNILAAVRWLLDQCPLDS
LVFAFSGHGS LDTLCDEHGRDGILPDSDFLEAGPIYEDEL YEGLVARLVKGSRLHCFVDTCRGIFALGLPSC
EDERGLDSGFASLRPQPDGEVVMLSSTLSEDEDLMDSTDYSHYASTGAVTFSLIQAVEQQAATYNVLL
RAMRYSLKNGPQHFPKVPPELSASQDFDLNRPFLL

>EsMC1 ES0009G00290
MEDDGTTINGTMDIGPEQDNSGDPGPDTRAEDMSDDDFDTEIADGIKADVRMFGSGCQDQQT SADVHDVTK
FGVPKSDGGAGGACTNALLVNVKDDEPDSWMSLLKGMRTTLSTKKFKQIPQMATS SKKLDIHS PSLAGGEG
GKHRALLIGINYVGDKSAELKGCHNDVAQMKDYIVEHGYSGEDEDLKIVMDDGEHTAPTRANIIEAIEWFV
EGAAPGDSL FMHYSGHGGSVEDNDNNEKDKRDETMIPVDYRVSGHIKDDELLAEVLVPLPEGVVLSVVMDC
CHSGS ILDLPYTFDADEGALQLVDDGGS AVVHKKAKFNMSKMKKAQKAKLGS PYMKAIRAKAAAAAAKAA
AAEAAAAETAATEAASEDQDQDQDQDQDKDQNDQEE SPQSGS GATFKVDSKVAVEA AAKAKELAAAKA
ASQNQDQDQEQEQERKQPANGSTGGATKQPPSEDVAPSATVAPKQLSIETE VVKAMESGGYVTPDPVAF
KSFTSCEAAEEDGKDDCDLSVFVVTPSSVDEESGHEHAAGISMLWVDESSTGYSIKHLTKGDARFDGKR
AVYIEATKGEGEE PFLVAVFAPEDFKPASVGGNTRVAPESAEFVWVCDKLAHSRDETLNWTACGSFVGTK
VKRTSATSATGERLVIVGALDEHNEGRVFGYGTSLGNEDLQ MSTFPKPRAMAASNQOVSTVQASALEKDGE
TFAIAVALPAAIPKETAAGDSSDTSDDETEIRPSMLYAQSLNDPGFYAGRIEIPGDTRCFMTPPAYGLKT
DVYVAGSKKAMWYDDRSWDGSTESAGVCVNAVDFTS PAKEMRTMLDKQYIRHV FILLENGKLLYTSQDPEE
GSKFDEPIDILPNVEAFSCHIDSIGNVHVNINKNGNLMHMMMQGTGLWMQKEVMVSGRDAREHLLSVVD
LKVTS LKKTAGKKTAKDLMDDAEADLPTISLSCGSGAMFRINGKGLMHKDKIVNVQPNMNGSVRIGQFVD
SFSVPHVAIRMEGLDRPLEIMCGNILTKKLEKMDASALKDAKSRDAMGDDAESLIDDPDDGDLNDFVDAVA

QLAKGFEVLSPTFEFPPKNDVDGIFRLTGGAFNDKNKFVAFVDEGPAFEEEEVDDGPPSPGYESTTRQIGGG
VESIGGELKEMASQPQRPTSVFRGDSALRGRGPVRRFTTKHRCAPDPFGMGHIGVERVRRVECRNMGNLAKK
ARENADEAIYETKKHAAESLKSLSNAERAQEATEYAAEATKWAGEAKQAAEAVRWTQAAVEAAEA AVKA
SEEVEMKASQDIGEMKAAQAFGARKASQDSQVDIILGVEGPEEEAARAMEAAARAVEAAGVAQQKSEQAKA
IERLQGSQDGLVDAGDFEAGGFLSAEYSRGRFFGPPVAKKLWLAEEAKRAGARPRGRDSSYLPVRRARHGQSPA
WPGRSPGYPRSPAIGVRYRRTAASTPAAHSDVVEAVEAAGQAVEAAAQAMERAEQAKEALGEDTGEPERK
GDDPDDNNPREYGSAPSNKGGFFDSIANELRELADEAKREAEKEAAQAGHGPPGHTSSGLFGSEAMEGETT
TRRPIINSTAECLTEPRWEEARKKAERTALEAARLVKAAQTAAFELKAVEEAEAAEALDSEDEGEDDIDG
DDGAYGSTEHTSRGIGGWVKKTTKKAKSGVQSAANKTKKAAQTAARKAEAAKQAKREAEERIAKDAARKAE
AAALQAKREAEKAAKAVAQAAEQTKKAGGLVANEVADKAKIAADVAKQAAEGAGKLAEDAGNEVGDVAGDI
KDGVDAAAGTVKDGIVNAADKVKDVAKDTVEVVDVDMTKVVEVVEEVVVEVWEHTPEGLKVKVARKVSKVVK
KGVDFVVKIGKVYVHFVETKLEQLIKALDWLWDKIKTGIMKAI EWLANFFKYKEILKTAEILEAQVLAGMD
EFIKSIPQGDIKEYFNEIRQMLQKKTGLDLDAQDMSKEDTAQDDREIDPKENFVQHHAESGTFHESAGPA
DEEEDSSDSDSDSDSGKDSMADKLQYLYGKFKKEGLNFMMSALAEGFLDVLEASTKAMMDPLKNAANAVRAW
LADGGTQYIPVISEIYKLIITGRKLLKALFFMLAIPVITYASKALLGKWSELGLIDPAMDTNSSTMAIVE
EDVQSSGTGAPAHLTRSLPGDNSSSEFVYTSRSGEKESDKGSETKKKVVWALLKVASIVMSGIVIPFQGDG
KFAQLIGFDVAVKRQRCSSSSILRPIATAYKTTWLERTSCSFSRVLYGQRPVPRRCKHRKYSPPFFWVRVE
MPLSNRMHVCANHLTAVLGCVHCLLFRIA AVVDVSKVPGQRRFPRGHRVFKIISLAKVIQKLLDRGASMVY
VGDYFDKTKNRENKKKTVLKKGDKGLFWFTFALEVGGTVADAALGFSEQGHPHAGGLEHNTPOGGTLPVIV
YDACEGIAEIAKGARLMWLAIEFGEGGFQOGTMVFQGVHGVFKGASQLAKAYSFKLVPPNKPPEYKIMVIL
FAAHMKYRTNVWPLGIASVAVQLIGADKADTEDQEQTNDAYWTACHAYL

>EsMC2 ES0024G00620

MNSMGVKQGGEEERAPAAAAAAPAAGGGHGQHAAGGGGGGGKGGKRGHRAKDI PDEEFDAE IAGGIRAD
VRMFGCEDVQTSADVHDVAKFGLPDATGAGGACTNAVLANVKDSKPDSSWMSLLKGMIRSTLKEKKFKQIPQ
LATSKKMDIHSFPDLSSGDESGNHKALLIGINYTGKGGELKGCNDVQKREYITTHGYPADGANLKI VSD
DGEHEEPSKENILKAIKWL VHGAKAGDSL FMHYS GHGGSVKDNTGDEEDNKDETMIPVDYMKSGQIKDDEI
LKELVMPLEPGVVL SVVMDCCHSGS ILDL PYSF DAKDGALELVEAGGSGVMQKKKNFNVKKMKHKAQGGK

>EsMC3 ES0394G00050

MEDDGNTTNGVMIDAPEQNSNDHGSQDPPSPDTRAEDMSDDDFDTEIADEIKADVRMFGCQDKQTSADVH
DVTKFGVPNSDGGAGGACTNALLVNVDDEPDSWMSLLKGMRTTSLTKKFKQIPQMATSKKLDIHSFSLA
GGEGGKHRALLIGINYVGDPSVELKGCNDVAQMKDYIVEHGYPAEEGEDLKIVMDDGEHTAPTRANIIEA
IEWLVEGAAPGDSL FMHYS GHGGSVEDTDNNEKDKRDETMIP TDYSMSGHIKDELLSELVPLPEGVVLS
VVVDCCHSGS ILDL PYP TFD ADEGALQLVDDGGSGVVLKAKFNMTKIRKARKLNLRGYPYMKAIRAKAAAA
AAKAAAAKAASEKQQEQEQEQTPQPVGGSSTAFKVGSKVAAAAAKARASAAAKAASQQEQEQEKPAANGGTA
DTAKDQPPSEDVAPSSTVMQAPTFKLSIETEVIKSMETGGYITPDPTAFKSFTSCEADMEEDGQDDCDLSV
FVVTPSVDEESGHEHAAGISMLWVDESSTGYSMKHLTKGDARFDGKRAVYIEATKGEGEEPFLVAVFAPE
DFKPASAGGGSGVAPESTE FVVVWCDKLAHSRNETLNWTACGSIVGTVKVRTSATTSTSGERLVI VEALDV
KNEARVFGTSLGNDLQMSMFPPTPRAMRASNQVSTVQASTLEKDGETFAIAMALPATIPKKT PVAGDSS
DTSDDETEIRPSMLYAQSLNDPGFYAGSIEIPGDTRCFMTPPAYGLKTDVYVAGTKKVIWYDDRAWDSTE
KAGVSLNSVDFTSPAEMRTMIDKQFIRHVFILLENGKLLYTSQDPEEGSIFDEPVDILPNVEAFSCHADS
IGNVHVNNINKDGNLMHMMMDQGTSLWMQKEVMVAGGAAREHLISIVDLKVTALEKTSGKKTANDLMQAAE
AEADLPTISLSCGSGAMFRINGKGHLMHKDKKVEVRPNMSGLVRIGQFVDSFSVPHVTIRMPGLDRPLEIM
CGNILT KLEKMDASALKGAKSRDAMGDDAESLIDDPDDGLNDFVDAVAQLAKGFKVLSPTFEFPPKNDVD
GIFRLTGRAFNEENQFVAFVDEGPAFEEEEVDDGPPSPGGAPS PRQGGAGAEP IGGELKEMATPQRRTSVF
RGDSALHGRRPVRRFTTKHRCAPDPFGMGHLGVERVRRVECRNMGNLAKKARENADEAIYETKKHAAESLK
AKLSNAERAQEATEYAAEATKWAGEAKQAAEAVRWTQAAVEAAEA AVKASEEVEMKASQDIGEMKAAQAF
GARKASQESQVDIILGVEGPDEEAARAMEAAARAVEAAGVAQQTSEQAKAMERGQGSQDGLVDVDFEAGG
FLSAEYSSGRFFGPPVAKKLWLAEEAKRAGARPRGRDSSYLPVRRARHGQSPA WPGRSPGYPRSPAIAARYR
PAASTPAHSDVVEAVEAAGQAVEAAAQAMERAEQAKEALGEDTGEPERRDDAGDLNPREYGSAESNKGFF
DSIAKELRELADEAKREAEKEAAQAAHGPPGYTSSGLFDTMDAGIPTRRPI TDTTAECLKEPKWEAVRQEA
EKTAMEATRLV KAAQTA AFELKAVEEVEVAEALDSEDEEEDHIDGDY GAYGSTEYTSRKF GDRIK KATK
VKSGVQNAAKKTKQAAQTAARKAEAAKQAKREAEERIAKDAARKAEAAALKAKREAEKSAKAVAQAAKEVK
KAGELVAKEVADKAQIAAAAAKQAAEGA KLAENAVNEVGDVAGDIKDGVEDAADKVKDGVVHAADKVKDV
AKDAAEVVDVTKMVDVVEEVVEEVWEHTPEGLKVKVARKVAKVVKGVDFVVKIGKVYVHFVETKLEQLV
KALDWLWDKIKTGIMKAI EWLASFFKYKEILKTAEILEAGAIY GIDQFIATIPSEDAVKEFFNDLRLMLER

KTGLDLDAQDMSTEDTTPDDREVDPKENFVQHHSTCGTFEGAGTPADAKDDSKDQEKASEDSDDDDPGMDT
VAEKLNLYLYEKLKEGLNFAFMSALAEIVDLEGGTQLMVKILKFVAKKFRDWLADGGPIYIPIIIESEIYKLI
TGRKLLKALAKLFFIFAIPTVYMAKAVLGKWPVSQMVSVQDLTGAKGNTLSIAGQAPDSTDAAMIDITKIIPAG
DRNFLTNRFFKSHPIFKIISYGRALQKILNLASTMVYVGDYFTGPKTPLKRKDKAFFSFLTMFDAAGVLVS
LKVDGGQASEPGAGGLVNMNATEGGQTPNNATVPAIIFDMADGIAEIAKGSRLIALANELDEGGRQERTMK
FQGSHGIFKQASQMATAFGKQIVKSPADPATKVAVIIVAAGLKWITKVPLGMASVVLQLEGS AEGKDEDKD
LKNNAYWIACFAYL

>EsMC4 ES0414G00090

MGGFMDSIKASCTKMAKQINEAMAGDKKESASGGGSAATGTRAPEDAAYAKKVAEAIKADVRMFGSCMD
SQTSADVVDVSKFGLPADGAGGACTNAMLLTLSDEHSDSWLGLLKGMSVLTTRKFSQVPQLSTSRIDV
NDKFSLRNTAGGGSTKCLLIGINYIGQQGELAGCHNDVDMKKYITTHGYSMDDPADCKVLMDDNVHGMPDH
KGVIEGFRWLTADAKAGDSLFMHYSGHGGSVKDTSGDEADNMDLTPVDYKSSGQITDDEILKELVMVLP
EGVTLTVVMDCCHSGSILDLPYALKADEGTISAVEAGEVSSSISANPGFDFAKRAHGGGGV DIEELPRVV
YPIFVTS

>FcMC1 FC007G01280

MDAKIQDAIPAKFVMLSGCEDKQTSADVGNVGFSLPDPGGKAGGACTSSLLKVLNENQGREMSWIDCLHR
MRSVLKSKGFDQIPQLSSSRMLDVNHQFEIVPQESI QARGARRAVLIGINYVGGQGELSGCHNDVKNIKKY
LIGKEGFLEKDMILMDDGRGHPTRQNIQAFDRITQYSKAGDVVFIHYSGHGGRVVDTSGEDEDDGYDET
LIPLDFKKSQIVDDEIYERLVKKMPANVTVVCLMDSCHSGTALDLPYEINATESKM HANKGFNMGLQNP
AMIAGCCLCLFPLMLMDD

>FcMC2 FC007G03890

MNDQSNPSIITWADLLRKMKNEINDIEYVQAPIISSTRKFDLNTPFSLVPESFDKSTGKKRSL LIGCNYHG
TEGAELKASHDDIRSMKDYIVNVHGFPEPDDMMTILLDDKEHKSPTFTNIVEAFKSLSEQS QPGDSVFIQF
AGHGGRI L DSPINNNVESYDEIIAPSDYNKSGIIRD TLIYKTL LAMP RYGVHVTVIIDCCDTGMMLDLPYS
WS

>FcMC3 FC008G00950

EAQRAFENDKPDMSMRKDVRMISGCDTQTSADVSNVNSFQLPDPAGRAGGACTSTLLNLIYKDGQTPEDTM
SFTEVLDKMRINLKENGYSQIPQLTSLNPIDITDFTLVPDATGGVRRAVMIGINYVGHEQGELSGCHND
VLNMKKYIMNEHGFDEDNIVVLMDDGQHTSPTKSNMINAYKQIVADSEDGDTIFLHYSGHGTKVRDESGDE
EDGYDEALCPLDYNESGLLVDDDLFAILIEPLQQGVHVMVSLMDCCHSGTILDLPIYIFKPIPNEDGSMPTSM
KLDDTINLDGLIEQFG

>FcMC4 FC059G00280

MLGQLGKKYAGDVANKVEELTLKLNLRYPQQD TDNSNSSTSSSNKVLNSNGNKTTEKLHKISGRRAV F
IGINYIGQKNELKGCINDVINIKNFFRSHYHIDDIMILTDDKRAEPETNYVPTRNILSAFRWL IKGAKSG
DSL L LHYSGHGSKVKNLDGTEASGYDQTLVPVDHQKSGQI IDDDVHDVLCRKLKKGVR LTAIFDCCHSESI
MDLPFTYNINGNLEI IENDKNQSIATLVAAGTRFLLDGNK KETKQIFKTEITNLVQSALGNETKQDSAKAK
VME TNQTQADVIMFSGCKDDQTSADTKINGMSSGAMSYALIH TLK KHRKGGKQ QILTYTELLREMRRTLEG
KYTQVPQLSAGRKLVLDPFRV

>FcMC5 FC073G00110

FDEQAEEAI PADVRMISGCHDEQTSADVNNVGSFNL PDPAGRSGGACTSAILQVYKEHQNSSKHLTFMDV
FLQTRDVIKSGGFEQIPQLSSRRIDINQPFDMSTNKSQGTTRYAVLIGINYTSHKQGQLSGCHNDVQNI
RKYIMDVGNVQSKNITILMDDGGKHTDPTRGNIMNALTDLTRKCCQAGDIAFVHYSGHGGRVKDETGEESG
YNSTLVPVDFHIAGQIIDELYRHLV CAMPRGTTLTCLMDCCHSGSVL DLPFN FVADGEQTEM

>MrCMC1 MRCC299_04G00220

MPSASKPPTGASNPTPKPRDAQKEKDYERKKQRVKEAHRKKRVRALMKSAPGEPVKLHYDTDCRSPATEAH
VVMFSGVSSSESKGEIAGSSGMGWY GMPRRAGKGGAGGACANALLHYLKE SDRTKPPDRSWLTTMVG MQWL
SKEGYTTVPRLSAGNNNFDFKRPFSILNPQCVNSQRLSGRTRAVLIGCNYPGTESALDGAWADVSKMKRYI
ASVGFNSDGDLSMVLRRDDPNGKSGELQPTKENILEALH LALGAAEGD SLLLFHSGHGVRVNRPKASETDD
ETVVAEDGLVPCDYKTEGPILDREVQEILVSRLPKGCSLVMFLDCCRGGSAVELPYNFKLTPKQYAFEKER

MAVGWPVRRNPLAALVDRTVMNVPNNCKRALRIGAKTADATCETIGGVLQAAADSFLPKLIKREYQRGKRK
IHKLTGVKVQFEPHDERTHRFLF

>OsMC1 OS01G58580

MGRKRALLVGINYPGKAEKLGCHNDVDRMHRCLVDRFGFDEDDIRVLLDRDSSGTQPTGANIRRALAQLV
GDARPGDFFLFFHYSGHGTRLPAETGQNDTGYDECIVPSDMNLITDQDFRELVQKVPNGCLFTIVSDSCHS
GGLLDSAKEQIGNSTRQNQTQSREREPPSDSGSGFRSFLKETVRDVFESSEGIHLPRSRHSQSHYGGEDQYE
TYAQPTDGHTKNRSLPLSTLIEMLKEKTGKDDIDVGSIRMTLFNIFGDDASPKVKFKMKVMLGKFQQQSG
EQGGLMGMVGS LAQEFKVKLEGNEEEAFKPAIEQEVHVSDEVYAGTKTWAPNNGILISGCQSNQTSADAT
TPQGSSYGALSNAIQITILADKRGVNSNKDLVMKARSLAKQGYTQQPGLYCSDDHVHVSFIC

>OsMC2 OS03G27120

MDHFGGRALGFGGGGGCGAVRCRHCASLPPAMPGARVIQCAQCYGVTRVGGRRRRHPNPVEPWRPAVPMP
VAGGGFFPGSRGKRAVLIGITYAGMRRRGSQLMRGPVNDVKCMRYLLCERFGFPNDCVLILTDEEKDPCR
LATKENIRMAMNWLVGQCSGDSLVFHFSGIGVQVPDDDDGDEVDGYDEAICPMDSFSQGPILDDEINEAIV
RPLVHGAKLHAVVDAEHSSTVLDLPLFLCCLSSRSGGWQWEDHRPPTGAYKGSQAMLFSGCSDGNNKHS
LLPEASTVGAMTHSFIAVECEPRATYGSLLTTMRSIMRDGGVTCNLQGPIGAPIRKVANFSGIQEPNLSC
SEMFDIYRKPFVL

>OsMC3 OS03G27170

MGCNCLVGGKGNTRPAATTSARPSSSRCAHCGAGLAVPRPGPGGAAAVTTVRCALCHRMTCVDRRGGRD LG
GGGGGGALEASSSSWAPAEASFLRRDAPSGYPFVPGKRALLVGVSYKGSSEYELEGTVNDVDCMRLLGES
FGFPADSILVLTTEELGEGDPSRSPTRANLLAAMRWLVEGCDAGDSLVFHFSGHGVQKLDVNGDEVDGYNEA
LCPVDFERSGKILDDEINETIVRPLVAGAKLHAIVDTC HSGTILDLPLFLCRLSRTGYWQWENHCRRPELAK
GTSGGLAISISGCSDQKSADSSGFSSEQAAAAAIGAMTYSFIRAVESEPGTTYGRLLAAMRATIREGQQ
GSSVRLLPGRLGFSVVRKMIPSGGVQEPQLCASEVFDIYRKPFLL

>OsMC4 OS03G27190

MAVVS GKRALLVGVSYKGDTSRELTGAAEDVKNMNSLLKKFLFPEESI HMLTEELGAKDPLKAPTRENIM
KEMRWLVEGCRAGDSLVFHFSGHGRQKDDNGDEVDGRDEELCPVDYKVSIGNILDDDINDAIVKPLTQGVK
LHAIIDTCHSGTMLDLPYLCRFNRMG LCSRYSKWKVQTRWRRLSPKKEWAMVPVGGHAISISGCKDYQNSLEP
DNTAGGGVMTWSFLEAVGSRRTMTYGELLDSMRAKVHRLQSSSGKCLVTGCLGSLAAKCLPCCFLSVQE
PQLCSSKEFNVEEQFIL

>OsMC5 OS03G27210

MASARPPRGTAWCGGCGAYLAVPPGARSVRCALCRAVTRVERRGHGGHGGALGFIKGLISAFAPPPPLTP
SAGAAAAASYPRVSGKKRALLVGI SYAATGYELKGTVNDVNCMSFLLRERFAFPADCILVLTQENGDPYR
VPTRANLLAAMRWLVEGCSAGDSLVLFHFSGHGVQKLDVDGDEADGYDEALCPVDFERAGVILDDEINETIV
RPLVAGVKLHAIVDTC HSGTILDLPLFLCRLSRTGYWQWENHCRRPELAKGTSGGLAISISGCGDSQTS SDT
TAFSGGAATGAMTYSFIKAVETE PGTTYGRLLSAMRATIRGGGGEVGI PGPLGAFFRRVITFSCAQEPQLC
ASEPFDIYRKPFLL

>OsMC6 OS05G41660

MGRKRAVLVGINYAGTEGELKGC LNDVARMRRCLVDRFGFDEADIRVLADADPSTPQPTGANIRLELERLV
GDARPGDTLFFHYSGHGLQLPIETGGDDDDTGYDECIVPCDMNLIKDQDFTELQKVPDGLFTMVSDSCH
SGGLIDKTKEQIGSSTKQSKIQQRERELRQQAPS PGTCSCASLLQIALRHLPRRGGQRIIGSRSRDGVGE
DQPPRSQAELLAADATRAGIKNRSLPLSTFVEMLRERTGKDDVGVGSIRTTLFHFFGDDASPKIRRLVNAM
LGRRHGSATASEEHPDKAKPERVDGEGEAAAQKQAGAPETRPLPRNGVLI SGCQTDSETSADATTPEGVSYGA
LSDAIQSVLAEERRGKVTNMELVRRARELLAKQGYTQQPGLYCRDKHANVAFIC

>OsMC7 OS05G41670

MGGRKRALLVGINYPGKAEKLGCHNDVARMRRALVDRFGFDEADIRVLADADRSAPQPTGANIRRELARL
VGDARPGDFFLFFHYSGHGTRLPAETGQDDDTGYDECIVPSDMNLITDQDFTELQKVPDDCLFTIVSDSCH
SGGLLIDKTKEQIGHSTKQNAQQIKREERSDSGTGGFRSFLKETLKETVRDAFESRGVHIPHQSSRRNDDE
DEEPHMGSSSHGGDRIKNRSLPLSTLIEMLKEKTGKDDIDVGSIRMTLFSLFGDDASPKIKFKMKVMLTKL
QEGQHGGVMGLVGALAEFMAKLEGNQEADALEPAMKQEVHVSVEAYAGTTARVSNGLVLI SGCQTDQTS A
DATTPKGVSYGALSNAIQITILSEKSGRVTNKELVLRARELLSKQGYTQQPGLYCSDKHTSVAFIC

>OsMC8 OS11G04010
MERGQKKKLATLVGCNYAGTPNELQGCINDVAAMRDALVARFGFAPADVTVLTDDRGSVLPPTGANIKRAL
ADMVARAAPGDVLFHYSGHGTLVPPVKGRRRHGHGECDEAIVPCDFNLITDVFRRLLVDRVPRGASFTMVS
DSCHSGGLIDLEKEQIGPSVLAAGAAPAAAAASTTATRATAARFLPYAAVVEHLSGVSGVDAAHHVADHLL
ALFGADASAKFHRDAEQPVRTDDDGILLSGCQTDETSADVPGDDEVAAGGKACGAFSNAIQTVLASHPAPV
SNRQLVSMARAVLSDQGFEQHPCLYCSDGNAETPFLWQEEDKKTVTAAEQAMTAL

>PpMC1 PP00016G01500
MGGQRRIKCSSCQVETLVTLSPGTRSIICEHCLAVIQVTPVEAPSIPSKPDTYSPRHVLPYWEWSKRAVIC
GISYGGTSELKGLNDAKCMSYLLMSKFHFPESAILVLTEQVDPRRQPTKYNIMQALEWLQGCQAGDS
LVFHFSGHGSQQPNYIGEELDGFDETLIPVDFMTAGQIVDDINTTIVRPLPTGVDLHAIVDACHSGTVLD
LPFLYRYSGHEAFVWEDHRPATGTWKGTAGGNVYSFSGCDDHQTVFDTMNLGRSTSTGEMTYCFIQAIERG
YGTTYGSLNAMRSAIHMAENQLVTSIDMLLKGSYEGGDTPEPQLTSSRCFDVSTPFRL

>PpMC2 PP00043G01330
MVRRALLVGCNYPGEPCELKGSANDVDRMHVLLTKKFGFKPTEILVLVDIDPRSRQPTGANIRKSLRKLVD
GAEPGDVLFHYSGHGTQVPPDRGRRDETGYEECIVPSDMNLLTDDDFRELVDRIPPGCNFTFIADACHSG
GLIDNEKEQIGDRYSMGEGLGGRPRPPLRPEAGGGGLTDLVAEGIEAFSGAGGGKQNSFMDAGVRYGGY
LDSGDYGYSGKPHHTPLKNKSLPLNLTLSILSQTGRSVKPGNIYQNLVDFGEDASPTVKVFRILLNKL
EGEDGGRSHGLLGKIGGLASSLLKTKIDNDPSGGYPEDRQGEELRRHRRRQRRNYDAGILISACEPHESSA
DANPTNDPRDAYGALSNAIQTVIGESRGLTNRQVMAARRLLNEQGYKQHPCLYCSDRNADAYFLQPPPM

>PpMC3 PP00043G01350
MSKRALLVGCNYPGTVQLHGCANDVRRMKALLIDRFQFDERDILVMLDTPALPQPTGANIRKCLDKLIE
NTQPGDCLVFHYSGHGTQVPAESGQEDDTGAEAAIVPTDMNLLTDDDFRELVNKIPVGVTFNFLSDSCHSG
GLIDSTKEQIGHTVKDVEEGEKEKRGFRGFLSKAKAKYDSHKGRKEEERPDTONFDFESQYMEETGHQVKN
KNLDINSLTEILSQTGHEVQVGNIRTTFLDFMGDDASPKVKTFFVSVILNQLQSGAGEGGFMGMVSGMAGQ
FLKSKLESDSPDHISLMAAAGSAHPSNPRSAYAGVRPSASHRVREDAGILVSGCQHNETSADATPGGDHS
QSYGAFSNALIGVLAHKDGPITNRDLVLQIRESLAKSGFKQHPCLFCTDQNAHAHFICVD

>PpMC4 PP00065G00020
MLVNCGRCRTPLVLPPGAMSIQCALCRHVTPAIYDRAAPSHSTPQISDPYRNSSHAPQYTPTPPNVHGRKK
AVLVGINYFNSRHMLKGCINDSNMRHMLTTKFGFPAASILTLEEQPSAVMKPTRYNMHMAMVWLIQGCQ
AGDSL VFHYSGHGSQQRDYSGEEADGFNETLCPVDFETAGMIVDDEINDTIVKPLPHGVRLHAIIDACHSG
TVLDLPFLCRFNRYGQFTWEDHRPANRRWKGTSGGQAYSFSGCDDSQTSADTSALSKITSTGAMTFCFIQA
IERGHAQTYGSLLCAMREAIRTTKVNSGMGTGTITSLMEMLVSGGSLTGGLTQEPQLTANEAFDINS PFHL

>PpMC5 PP00165G00360
MSKRALLVGCNYPGTVKCELHGCANDVRRMKELLMNRFQFDEIDILVMLDTPSLPQPTGANIRKSLAQLIQ
STEAGDCLVFHYSGHGTQVPAESGQEDDTGADEAIVPTDMNLLTDDDFRELVNQIPVGVTFNFLSDSCHSG
GLIDSAKEQIGNTGISAFSGKRDVEEGEEEGGFRGLLSNMRSRFGSGNRDNDEERPDLQNFDFESQYLEE
TSQQVKNRNLIDINTLSEMLSEQAGHPVEVGNIRTTFLDFMGDDASPKVVFVNILLSRIQSGGEEGGFMGM
LSSAAGHYLKSCLDSESPDEAANYMAAAGSVHPSTARAAYGGVRPSASHRAREDAGILLSGCQHNETSADA
TPAGDHSQSYGAFSNALIGVLAETEGPISNRELVLKIRESLASSGFKQHPCLYCTDENADAHFICVD

>PpMC6 PP00373G00150
MPTKKALLVGINYEGQPHHALRGCWKDVERMGECLVSRYGFPKESICTLVDRPGTSPDLMPGTGEIIRRKLE
ELTRDLKWDGDCIVFHFSGHGLQMPPEGEPEDETGMKEAVVPVDANMITDDDFRILVDKIPDGVFFTFIADCC
HSGGLIAHCEQQVGSHPEDRYAAPNFGNSHEGFRGSYNGNLETVQPGAWPYGGANLQSSGRYDANLATS
KYTSKRSMVHAVTQMLSARAGHTVEPGNICANLYDLFGDKSSVTCKEIVHTVFNGLRSKGGSKREILKRI
SSKSIDFLSAKLHSSSLRDSNYQQQTATRDLTDATPENLSHIPKRPDRCILITACQSDETA SEHRNEIHGA
FTKTLLEDIVDEHKGPLDNHRLVYECRQLARKPYGQHPCLYSTPAQAHHVFICY

>PtMC1 PTI_02G05190 pink: my p10 red: CDD p10
MGNADSKATTSLAEAETVPTGIGRKESCLRSFNDSFEETKNTAADPIHPISGRSDRKETAQARDDEISSHI
TDDQVHVNLAMADLMAYLQVVANSSHLPLTRRDDPDLRIEGLASEEYGGKSAAFIPSDVRVIAGVFTR

YGRVWDLPTSEEYNAVDGNHEPGRSYGGACCNALLKVLYDAANDHVDAFHAVAATSASIFDDDDDEEEDLYA
GMGQSYKSGCSLEYTNPYSVTITWCDLLRRMKAEMKDIEHVQVPKISTSRKIDLSKPFSLIPSNFDPINGQ
KRSLLIGCNYSDIPEAQLKASHDDVRSIKDYIVNVHGFPEACGLMTVLMDDKNHKKPTFLNIVEAFKALSE
EAQPGDAIFIQFSGHGGRVLDSDHIDTEAESYDEVLPVPCDYLSGLIRDTLIFKTLAPMRYGVTVTILIDC
CDNGMVLELPYSWSTKGDRRSSQPKLALNEDFSFKRFLKVVRTLYESSSFTQLGRTVDIALNPMNATFKST
TITNDESSVLFQPEKAVNAASRSSILDNFSLACSTKTLSTPRGDGDDGIVNSTGLSVMKHYSLTKQSLLO
QVMNCTLLSPEVDEDFSFDETYQTRTEDHNTFDEEDRSVGYNSSFRSCVTEYEEESRRRGRRRRR

>PtMC2 PTI_16G01290 (plus manual correction)

MASFDEKIKQAI PAEFHMI S GSHDSQTSADVNTGKFLPNPAGRAGGACTSALLQVLYNNGVAAGELSWV
QCLRQMRTALNGMFGDQVPQLTSSRLIDVNTPMAIVPPTATGRKRAVLIGINYTQQGQQLSGCHNDVKNII
KFLTKVHGFNETEMLILMDDGQHHSPTKKNIEDAFTRITQYSQAGDVVHVHYSGHGGRVRLDGDDEDDGFD
ETLIPVDFKQAGQI IDDDILKILVKPMRQGVTVTVLMDCCHSGTVLDDL PYRFSADDSKMRIDQGNANSLFG
KLGDMVAQVACCACLAYVVADMLLN

>PtMC3 PTI_08G02260

MGYEQLPQLSSSRWIDVNRPLTIVPKSGRRRAIVVGINIVGQKQKELKACHNDANNVLKYLIEAQGFDP
S QILILMDDGKHTEPTRRNIEDAFVRMTQYSQPGDVVWVFSFGHGGRAVDISGDEDDGYDETLIPLDFMKHGQ
I IDDDILDMFVKPMKKGVNVTGDFRSRDFPWKVLMDCCHSGTVLDDL PYTYSSGDQKMRTEKNFDFGDKN
ATNAKKQKEMEKAERKAAGENS DSDDEGDKKKKKVKEKEEDPNEGLYDQSPI PPPQPRPPTDLPPPPTP
PNQCCRIL

>PtMC4 PTI_16G02000

MSNYLERAEELI PAEVRMISGCRDEQTSADVSNVASFSLPDPAGSAGGACTSAMLKVLVYANHKAPQKDL
S FQEVLMKMRGILSQGRYTQIPQLSSSRPLDIHQSFNIVPANFTGTRRAVMIGINYTQQGQQLSGCHNDV
KNM IEFIKDIHG FEDENITILMDDGAHTEPTYKNILAAAYHELVS SAKAGDAIFCHYSGHGGKVRDD
DGDEADGY DETLVPVDFNAAGQIRDDDI FSALIGMPAGVTLT SVMDCCHSGTVLDDL PYVFKADGE
QNMAPPDFDFS KLAAMFQAYMVQQGANGQGGIDPNDIAIAIVAKECCNIL

>PtMC5 PTI_16G02030 (plus manual correction)

MGFLRRQLREQFEKKEKPEALQADIRMI SGCQDVQTSADVSNVASFQLPDPAGNAGGACTSTLLNVLYK
DHQ TPEDTMSFV ELLNKMRENLEAKGFSQVPQLTASHPIDVNVDFDLVPPAATGTRRALLIGINIVG
HEQGVLR GCHNDVKNMVEYIKAVHGFEDENITILMDDGEHTAPHTANMIAAYKKIVALSKADDALFCH
FSGHGAKIRD DDRGEEDDGYDETLVPIDYHENG MIRDDDL YDILIKPLVQGVHLVCLMDCCHSGT
VLDDL PYVYKADGNFTE MEIDENFDFKLLGKFGIDDFDKFGGEALGKINGDALGKVGKDALGKLNKFFG

>TpMC1 TP20G01470

MGGDDNNNEGHTMTKEEFKATKPELTKDIRMISGCADHQTSADVSNVSSFQLPDPAGRAGGALTSTLLK
VLYADEQKTDFTVEVMERLRGHLKGRYSQIPQLSSMNPIDVETKFDLVPDSATGTRRAVMIGIN
YIGDNPGE LSGCHNDVNLMMKYYIMDVHGFEDNIVVLMDDGEHTEPTHDNIMNAYKKVIADAEDGDA
IFLHYSGHGTKL RDDDFGEEKDGYDEALCPRDFASAGMIRDDDL YDILVKGCPDGVHVMVSLMDC
CHSGS IMDLPYIFKGDG SQ TEMILDPDMNIDAFIEQITGKLVEFIKAKMAAGF

>TpMC2 TP10G02670

MRRIPNTPRGSIGIPPNGRHKAL IIGINYTGTRAAKGCVNDAKSMQQLLMRNGFGDDGSHMLLLT
DERSR GREYQPNATNIMKAFAWFMKDVQKGDVLFHFHSGHGGQVPDKTGHEADGFNETIVPLDYERAG
QISDDVLW GSLVYPMPEGCRILALMDMCHSGTGLDLFPDYNVDTRRWKEDVNPAPHS PGDVVLFSG
CEDAQT SAD

>TpMC3 TP02G04700

MTDKKRSSKSGKASSIRTPPPPKRSPSSGGRS KSGRS IKSSADATPTLSSSATRGTKKNGDAEPR
EQS RSKRSRSKSRGAHRRDGRRSRSKSRPKQQNKQEQQLVHSSSEARPKQRKSKSKSLSNKSKS
SKSNNGS SARSAPSPSSKSGKNKAVASEFNVKRQKQK FANQAKMI PAEVFMI S GSHDAQTSADV
SNINSSFALPNPA GKAGGACTAALMQVLYDAYDDRREDSLSWVDVLRMRDVLDSKNYDQIPQLT
SSRMIDVHDPFVITPKSFS KKNNTQRAVLIGINIVGQKQQLSGCHNDVNLVAKYLKEVQGF
RKENMTILMDDGNHKSPTKSAILSAYKKI VKESKEGDVVFCHYSGHGGRKIDNDGDEDDG
HDETLIPVDFEKAGQIRDDDL LKILVHPMAAGVRMTCCMD CCHSGTVLDDL PYRFTADGD
VEEMEMNERVNFTDALWTGMSIAVGVAAAGNAVASAVTS AVAPEMMILGGGPN AIQ

>TpMC4 TP05G02130
MPSNMSWADLLRKMKTEMQGVGFSQAPALTSSYKFDLNTPFSLIPPNFKAGINKKRALLIGCNYRKT PDAG
LKASHDDVRSMKDFLVNVYGFPE TSDLMTVLMDDKHHQHPTHENITEAFKRLAEKSQPGDAVVVLFSGHGC
RVLDSPIDSEAE SYDEALVPSDYNVSGNIRD TLFVFKTLLAPMKKGVTMT C I IDCCHTGMMMDL PYIWSKN
DKGEQLPKMSLNNEFSFVRFLKVVKTLYESSVFTKIGKT V GSEL DKQLPAKDDETVTETV GSLVTI PENEP
PKREASLFQLLSCQNPQCLATKVINCTLHEPEYSDDDTIPKDN TMDEFYDDVSHDSYSTGSGR

>TpMC6 TP18G00030
MTIVENPTGVKRAVLIGINIVGQQGQLSGCHNDVRNIQDFLQRVHGFQQHNMTVLMDDGRHKEPTYAKIMA
AFDWIVKESMAGD TVWIHYSGHGGRVADQDGEDDDGYDETLIPVDFQRKGQIRDDDLLKHLVKPMRKGVVV
TALMDCCHSGTVL DLPY

>VcMC2 VC0004G01350
MPSKRAVLIGCNYPGTNAALRGCINDVWGMKAILEEFFGFGPSDITILIDTDPQYLKPTGKNMKAKISEMV
AAAQDGDVVCVLHFSGHGTQIPSYGGDEKDGKDEAICPTDMNVICDDDLRALLKPLEAKPGVKFTFIADCC
SGTLLDHETVQISGPKDGAPRPPQIDMGVLSLFGTLGQPDGRDFKNRALPFNDLCGMLSELLGGAPVDAR
NVRSNLGT L FAGDASAKVQQFMQVFMFTAGQKEGGGAGGVPAMGLLQLL CACLAPSADQSGSGPTGQPAN
ANSFGPATYAVGNLNEPDLKINLPTPGTKPPGDQQLSSDVGILITGCQSHETSADACPSGNPDKAHGALS
AIQT VVRTHHQQNPQPLTYRNLVIVRELLAKTGF AQNPCLECSDTNADTPFIMH

>Pn1 jgi|Psemu1|257123|estExt_Genewise1Plus.C_2100062
MTDARIKNAIPASFVMSGCEDEKQTSADVSNVGAFLPDPKKGAGGACTS SLLKVLNESGGREMSWIDLLH
RMRSVLTSKGFQDIPQLSSSRMMDVNNRFEIVPSWAQGRRAVLIGINIEGQQGELSGCHNDAKNIQS YLI
NEQGFRESDMI VLMDDGVNNPPTKRNIIDALDRVVEYSQAGDVVFIHYSGHGGRQRDADGDEEDGYDETLI
PVDFKSAGQIVDDDL YAHLV LKMREGVAVVALMDCCHSGTALDLPYNINATESEM HATEGFNFGLLDNAQM
AMGCCFLLMSLLSMFD

>Pn2 jgi|Psemu1|188031|e_gw1.73.141.1
MFRRNDRDLRHGEDVATSISNNNNNNDFDKQAQYLVAEVRMISGCHSLETSADVSNIH SIVGRGKLPSP
GRAGGACTTALLSIFITFQKLLLELRRRLAQTGVSQIPQLTSSRPLELEETPFSLRGTPREGRGGTATATA
TQRALLVGINIYGGQNGQLSGCINDVANVKKYL CNHCGFEEKHVLLI DDGRNHHPTRDNIIRALRRLVEHS
KPGDSVYFHYSGHGGLLDPNYWNRFKAGVSKKEYDETLYPVDHARAGQIRDFNLFHFFVKPMAAGVTVTCV
MDCCHSGSVL DLPYSYR

>Pn3 jgi|Psemu1|188378|e_gw1.76.57.1
MFGTLGKKYAAQVAEKVEQLALQALNERNPQTVQNEKTTEQLHKISGRRKAVFIGINIKGQK GELRGCIND
VKNIKNFFQTHYQLDDVLVLTDDKQAEPE TKYPPTRANILNAFKWLTGAKPGDSL LLLHYSGHGGKVKNH
TEASGYDQTLIPLDHQKSGHILDDDVHDALCRKLPKGVRLTAIFDCCHSETIMDLPYVYNI DGNLDIVLN
DKNESVATLVSAGTRFLLDGNKKA KAVFQAELTNLVKGA VLGGNPEADSARRKQNIENNETSADVIMFSG
CKDDQTSADATIKGEATGAMSFALVKT LKAHHKDSKRITYTELLREMRQVLE GKYTQVPQMSAGRKLMLDQ
PIQI

>Pn4 jgi|Psemu1|320764|estExt_fgenesh1_pm.C_7970004
MKDENRDDLQRRNSIIKDDQVLVNLAMADLMAYLQVVANN SNNLPLTRRDDPELTRMVTNLSSEVYARKS
AAFIPADVRVIAGSFLKYGNVWDLPTSEEYVASDGAQEPGRSYGGACSN SMLKVLYDAASEAADVGNIDKD
ACDALFDDDDDES LSTLPLTRNNTFASLDMNGQSNPSTITWAE LLRKMKTEIDEIEYVQAPTIGATRKFDL
NQPFSLVPESFDKSTGKKRSL LIGCNYNGTEGAELKASHDDICSMKDYIVNVHGFPE SDDMMTVLLDDDQH
RPPTFMNIVEAFKSLSEESQPGDAVFIQFSGHGGRILDS PINNSVESYDEILVPSDYSKSGVIRDTLIFKT
LLAPMRYGVCVTIVL DSCDTGMVV DLPYSWSTRSDKAGSVAKMKQSENFSFVRFLKVVKTLYESS TFTQLG
RTVGSALGEQPTVDESSDEEAEDEEEEGEKT LSTIERTKTEEMQEGSVLGLCTPRGRAADSTYSRSENDR
DAFSLIEKMLGCNFLVHDLDDDFSDGETFENTTYNTFDDTHTMTNASTFDLSLSDGEYRRSSRRRRSRN

>Pn5 jgi|Psemu1|320057|estExt_fgenesh1_pm.C_3800004
MATTYDEQIEEEIPGTFVFSILDAEEDERNNAVSSLEDYELPGNVVQGETSSGGVCA YALLNVLKQKNK
GAGKKKKPKKTWADALEAMQAEIRNERGLD TYPTLSTSRPTDLWSEPMQIASSSSEGVKRALLIGLHY
ENDGEDDGD DDDDDDAEDA KLSCHDDIRKMRQYLIHEEGFEPQNILVAMDDNGRHHEPTKEFILECVV
RLCEI SESGDSIFFHFSGHGGRLLDEEEDDDCEI PHELLAPSDYRKGEILTND ELYSSFVREV PAGVHVVA

I IDTCHPSPSGCAMEL PYVCEAGDDEVRDSSGGFRSARA IMATV TAAAGTATVASKKKKKGKDVEKKGKQKK
KTVDS DNSDDESENGETEDENDEESSQSEK GKTEKKPNKKKQKKDEEEEEAEEMEVPNDMEESS
QSEK GKPEKSKKKKKKKGDEPPPKEEEASEEQEEDKPKKKKKEDKKKKSKKQKDVSNSSDDV GSEGD
DDPPEQAPK KKKKEKEDAPK KKKKTKKK

>EhMC1 jgi|Emihu1|43172|gw1.322.10.1
TRASLNGNRRSVLIGINYSGLSSPSELRGCVNDVKRMRPFVERLGFPSNEGSQMVLLDDGSTPLAPTMANI
RGAI AWLVEGAAAGDALFFQYSGHGGRIQGSDFHETLCPLDMASEGQLLDTL FETLVAPLPSPGCR LTVI
LDSCHSAGALNLPFLFTGT EGNLKSALAGEAVQMAMSRNWL RDVIAITGCRSDQTSADVGNVDLQFDLQPT
ARSGAGGALTSAFIEALD GREAA PSYLELLEAIRLKLAE EGF TQVPQLASSLLVDLTSAFSML

>EhMC2 jgi|Emihu1|202860|gm1.1700383
MGAQPSLFDVHAPALDPRDVTQVFELLDKDGSGRLAGSEVTKMFAAMCGRPVKVHGAKSSYSLNEFIEAVE
DMGRRQPFLNITGNLVKYVRENKEKMPVDAFSDERIEAVSTFLDKDKSGAIEPDELLRFLQYLHIPLFTI
FGVNSSGVIKSNAQLQRLLRKLAKQCPQLEIEQKI IKISGDIHAGDASKPPQYQEATASAEPPEPAAGR
KKALLIGINYTGSRMPLRGCINDVKSQYNVLTTFKGYSSSEIRLMTDDTNDSSKVPNKNMMAALKWLV EG
VKPGDELFFHYSGHGSQCPDRSGREPDKNECLCPTDCTKGFPEYVITDDQM QNFFSQIPEGAKITCLFDC
CHSATMGDL CVNRELGLEEDIVPSTKQVWTL SGCQDNQTSADAVIGGVPRGAFSWALMGALEDN NYKLYD
DLLAQTRHKLRRRMGEGSGDSSHFRSAYLETSWCGSSWTALQLGGRYFCIDMRP

>Ehux1-EhMC5 metacaspase-scaffold16
MELAAGAGVAAAAAAGGAAYLRSRRGPASGKEGTTKWQWRAAAVKERRALCICCSYPGTQWALPGCVPDQE
AMVKTLIRNSYAVTF LADHTPAWQPKPSALSNNRNI LAELEALCRWLHAAPGRQGWVSYSGHGTQTADRG
GDEADGLDEAMVPCDFK MAGLLTDDKLR TIRFGAGSSLMFFFDCCHSGTILDLPYTLRHTLSGPEYPIET
EAGAI FCI SASKDDQ SAYETAEGGVCTRAFLGAYTPSVSPAATLRLMRRYAERKGMPTIMMASNRPFTEA
DASFVEAEPEGGGGFCAAFHRCQNLGCSKGRSKAGDFGGENPAARSLELN RGEASGRGPKLHPSCPDPLS
TTKGRAYVAARRAKLAAPP

>Ehux2-EhMC8 metacaspase-scaffold276
MSAAVMSLQPHVFTRYEWLPKSTSGTSTKHRALCIAAYPGT SYELHGTVKDQEALKKGLEDN GYSVTFLS
DADDKHAVPTKANILKEIANLCDWLNEEKGRMGWISYAGHGTQTKATVAGEEPDGKDEAMVPTDYPTAGLL
TDNELNQTMLKSHKVQNGCAMIIFMDCCHSASILDIPYALETEPVGPKYVEDKSIGDIFGVSAAADDKVAY
ETAAGGVCTRAFLIEAVRKLK GALPAEILLEMRYAKDQNM DQLITMHSNRQFTFGDFQIMKGV DVVKEAA
PPVSAPPAPAPATAPSPAAPPGHAGYNPAAHTSHVYTAPATSKPDLTKVKGGEELNRPPAQAPPTAPATS
GKKAGGK GAGTKPATQPQSSCCVVC

>Ehux3-EhMC6 scaffold120 440238|estExtDG_fgenesh_newKGs_kg.C_1200066
MTDQSAAGPTTNFNLYKTGAGKTERKALCICCSYPGTQLALPGCVRDQAAMVDMLPKQGYDVTFLTDGDNY
HEKPTKANIVREMKKLCAWLSEKEGRQGWISYSGHGAQVPDDEIQKVGYSSEKDGMD EAMVNI DYQSVGLL
TDDELKEVLVFSKGS SLMVFMDCCHSGTILDLPYRLTHEATGPAYDVI PDCGTIFCVSAALDEQCAYETSE
GGVCTRAFLGAYRKGQPPGQMLQKMRAYAQA KMPQ QITMNSNRPF TDADGSFIDADPASGICESLLNCLT
GETSATRSIEIGNKQDKGQIPPSKPCTAAGKILPQPTKDYVKSIREKNGYVAQL

>Ehux6-EhMC3 scaffold111_jgi|Emihu1|223690|gm1.11100063
MPNSFTGMMWESKAATAGDRKVVTKALCVCCSYPSNTEVKGLPKWASTGKHALPGCVGDQMRMKDMLKKEG
VKVRFLTDHKKLSKEKDYSTKKNIVAE LKLVKWL DGAKEDGPVRQAWFVYSGHGVINPKRPYSLLPEDAP
DPGGHGFMLESIVPCDYFTTSELLSEVELEETLQGFNENGALLAFMDCCHSGTILGLPWDLELDES GEMV
GCRAPHPEAIIERYSKGRILCISAALDAEVAYETKAGGVCTNAFLESHNKGDPPAKVLIAMNQYARDHYM
KQTINMSSNVEFTDADA AVIAGGI PHWSRSLGKIMSAPAALARS LAPKQP VVERAVAF EKHPSAGAVSDF
LYATALARHAGECGERALEIASQGASKAARLASTGKAPEEADEANTYARGLIDDGVARRRGL

>EhMC7-9 correct65 452661 471262|estExtDG_fgeneshEH_pg.C_9100002
MGGCSSSQKTTAEPEQRTPRRRALLVGM DYRGAPAGWPIINGTRNDVKVFD TLLREHWGFSEEDIVT VTD
PAEQSTESLLAALTAFKASLRPGDTAVIFYSGHGKQVFDANGDEVTRKGESAPDIMDEALCTTNGTLLDDD
LTVLMQGI AASAAQLFWFC DACYSGGFVDQSGSSLPEN VVLIASSLETQKSEDALRIETDKETGKMAMFY
QGTGTRWLKAAVDGGGLPPRATHQQLFDALAAERAKDKRTSVQNP FIVASATARQLTLWM

>Amphiprora1 CAMPEP_0186511138
MGFLKKAFRDVFEDKKPKELKADIRMISGCEDAQTSADVSNVASFCLPDPAGRAGGACTSTLLNLLYKDHK
DTRDDMSFVEVLTKVCIVGSQASAPLWMMDDSLRVGVAVFRRHNNRCEKIWAAVAFPKFPNXSASSPIDIS
TTFDLVPDGATGKRRALLIGINYIGHSQGVLSGCHNDVLMVVEYIKEVHGFEEDESITVLLDDGEHDAPKE
NILAAYKKMVAEAE PGDSL FCHYSGHGCKIRDDDRGEEEDGFDEALVPVDYQTAGLIRDDDLFDII IKPMP
DGANLFCFLDCCHSGTILDLPLYKADGTMEVMEIDESFDFKLLGKFGTLVDGFFD

>Amphiprora2 CAMPEP_0186511756
XAIPAEIHMISGSHDAQTSADVFN TGQFQLPDPAGRAGGACTSALLKTYRLEEQQGGANGKVSQVLLRTM
RGE LRQMGYDQVPQLTSSRLIDVNKPMYVPPDFKPAAGRKRAILIGINYVGQQQLSGCHNDVKNIKKYL
TEVQGFNESEMLILMDDGNHHPTRKNIIDAFKRIGEYSNAGDVV FVHYSGHGGRV RDTSGDEDDGYDETL
IPVDFQRAGQIVDDDILKILVKPIKAGVYVTVLMDCC HSGTVL DL P YRF SADD SQMRI DQGFNMNSMLGKL
GGAADVAACACLG LCV AQLLADILAG

>Amphiprora4 CAMPEP_0186484142
XMRFRSSRRHGQNGAGETNTS QKGS AQQFSQQVQHLIPAEVRMISGCHSEQTSADVVESTSRDFSLLPNP
KKGAGGACTSALLDILYEHHRSSLSFQQLLLQLRSALAQRGFDQIPQLTSSRPLEMQQTPFSCISPYEG
NPQTPHQQCRRALLVGINYRGQSGELSGCQNDVYRMRDYL CQVQGYLPSNVVLLVDDGKAHYPNRKNII S
VLQQLVLQSTSGDSVFFHYSGHGGLLEP SLCNNAWKRSVEDYDEILYPLDHKQAGHIRDYSLFRHFVKPMP
AGVTVTCVMDCC HSGGVLDLPYSYKATPGGTIAMERSMGLNLLALLYLLAGGRLPGGGLFHNVS DSIQGV
TGESVESLQGAGMTEEDAQDGITDFTGDNGGDVVAESIENDITADDLGDDDIAPGDLGENDIGADDLGEND
VGTEDIARTGDFPEPMPDPDLPLEPPVFD TNGNPI SDTGLDGP I GAPP I FDSNGDQYGGGDAVYDTNNVPG
YDDNRMAGFAGNSDLGFMQASPYGYDQGGRAEY EYGGT DYGGMGDNGEDADCDCGGCISELLQNLADDE

>Amphiprora7 CAMPEP_0186516142
XTLRDTKDQHRIQTSIMPTREEVLAKAE EYIPATVRMISGCRDEQTSADVSNVASFCLPDPAGRAGGACTS
SLLQILYADHKKPEVDLSFQETLLAMRKVLSAKGFSQIPQLSSSRPLDINQTFDLVPPEHVSGTRRAVVVA
INYVGQQGELRGCHNDALNMIEYIKDVHGFPEENITVLMDDGQHT EPT RDNILAAYRKVV R DSEPGDVVFT
HYSGHGKLRDQDGD EKDGYDETLVPVDYASSGQIRDDDLFKYLVAPMAAGVMTCLMDCC HSGTVL DL P F
EFVADGEQTEMHVKPDFDPQTLINL FQAFQTF SNGECS PETLMEQAQMLKGCN I L

>Amphiprora8 CAMNT_0029300213_6
YTNISYCFACVVT TTTTTRSIHNMGSGNFDDKVHKCIPAEFFMISSSQDSEISNEAYNTGSFELPDPAGKA
GGACTSAILEVFYSRGHEVGGMSWVDVLKDMHEQLKKQKFDQVPQLSSSRWIDVNQPMFIVPPKSGVRRRA
MLIGINYVGQKQKACHNDVENVKDYLIKAQGFRESEMLILKDDGRHEMPTKQNI MDG FVRLTQYSQPGD
VVFVFSGHGGRVVDTS GDEDDGFDES LIPVDFQEVGQIVDDDILDI FVKKMKGGVTCTVVMDCCHSGSVM
DL PYYFSADGKEMETEKNFQFGSGGTDGEVPPKHKRTFDKHGKAVKVHEKEEQDKAEKKAPKRTVHEAPIK
KIKPRAPPRDRKPPPPPPPPQR

>Acoffeaeformis1 CAMPEP_0186537396
MSVEEQAE EAI PAVVRMFSGCEDRQTSADVSNVGSFQLPDPAGRAGGALTSALLNTTYADHANTGADLTFK
ETLITAREKLRREMGEFQVPQLSCSRATDL DQPF SII PPDFEGTRRAVMIGINYVGHDPGELSGCHNDVFN M
AEYIKDCHGFTDDDIVYLLDDGEHTPPTAANIIEAFQTLASQAQPGDACFLHYSGHGCSIPDQDGEDDDGK
DEALCPVDYAENGI LRDDHVLQMLVAPMPRGVTLT C I MDCCHSGTILDL PFLFLADG SQEEMEADPDFEFG
PFLTVMVSSFAAAGLEGLKQLHAEGKARRKKRRQWLKSR LGF

>Acoffeaeformis2 CAMPEP_0186537718
MAEDLIRAEVRMISGCRDSQTSADVSNVAEFQLPDPAGRAGGACTSAMLQVLYADHQT PEDDL SMQEVLLQ
MRDILRSSGYTQIPQLSSSRCLDIHTPFRLVPEDFSGTRRAVVI AIN YVGQQGELRGCQNDAHNMIEYIKN
VHGFEDENILILMDDGIHPDPTYENIITAYRQLVASCEPGDAV FCHYSGHGKLVDE DGEEDGYDETLVP
VDYQSAGQIRDDTLYKELV GALPEGVMMTSVMDCCHSGTVL DL P YV FVADG EEEEMHENPGFDMNAMAGFA
SAAGIAMALASGADPIEVAMQACCAIL

>Acoffeaeformis3 CAMPEP_0186529544
MGRFLKKLAKLKDKVEDRIADFREEEPAARAAFEDAKPEAMKNDIRMISGCEDAQTSADVSNVNSFSLPDP
AGRAGGACTSTLLNIIYADEKVPEDDLSYTVLEKMRANLKKKGF S QIPQLTASNPI DVNTDFDLVPPAAT
GTRRAVMIGINYVGHDPGELRGCHNDVLMNKYIMAVHGF AEENIQVLMDDGEHTPPTKENILAAYKKVIA

ETQSGDAVFLHYSGHGTKLRDDDDWKEEEDGYDEALVPVDYQEGAGMIRDDDDLYEILVKPLAHGAHMVSLMD
CCHSGTILDLPIYIFKADGTDQEMHLDP TLNLDGLIQSFGGHVTNLMSKFKFFK

>Acoffeaeformis4 CAMPEP_0186534122
MSSFNEKVINTIPSQVFMISSSSDKQTSDEAYNAGAFNLPNPNKGQGGACISSLLQVLYERGHEKGSMTWI
SCLEDMWQQLKNLGFQVLPQLSSSRWIDVYRPMYIVPPNSGKRRAMIIGINYVGGQQLKACHNDADNIKD
YLINAQGFREEMLVKDDGKHMMPKQNIIMDGFTRLTQYSQPGDVVVFVFSFGHGGRVVDTSGDEEDGYDE
SIIIPVDFRENGQIIDDLLDLFVKRLKGGVFCVVVMDCCHSGTVMDLPYAFSANRKKMAIERNFPFDDDDK
TRKRAFKNQKHAERRGDASMAGDDKTVSTTRTKPKKKQRPKPSIREMPIEPVPPRPPRRSVPPPPPPKQC
CTIM

>Acoffeaeformis5 CAMPEP_018654023
MSLEQAQQAIPAVVRMFSGCEDKQTSADVSNVASFKLDPDPAGRAGGALTSALLNVTYADHKDTGKDLTFKE
TLYAVRTSLQGGFEQTPQLSSSRPTDLEEHFAILPKNFAGKRRAVMIGINYTGDNPGELRGCHNDVHNMK
EYIKNCHGFTDADITLLDDGKNTAPTAANILAAFKKLASEAKAGDACFVHYSGHGCSIRDDDGDEADGMD
EALCPVDYKKSGLRDDDVLEKLIAPLPRGVTLTCLMDCCHSGTILDLPYLFLADGMQEQMQPDPDFDFGP
LITMVSSFAKLGFEGLKHLKQKVRKKERQWLKNRLGL

>Acoffeaeformis6 CAMPEP_0186520996
MSSIDERIKQAI PAEFHMI SSGSADSQTSADVQNTGKFQLPDPAXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
XXXXXXXXXXXXXXXXXXXXXXXXX RAGGACTSALLQVWYRDGHATGEKTWVQCLREMRSNLLQMGFDQVPQLTSS
RMIDVNMKIMHIVPPGSTGRRAVLIIGINYVGGQQLSGCHNDVNNIKKYLIAAQGFKESEMLILMDDGRHH
APTRKNIEDAFRRITEYSNAGDVVVFHYSGHGGRVVDTSGDEEDGYDETLIPVDFRSAGQIVDDNILDMLV
KPMRAGVTVTVMDCCHSGTVLDPYRFSADDSQMRDLQGMNMDNFLGKLDPGSVALCACLGFMMMNMLDF

>Acoffeaeformis7 CAMPEP_0186541908
MGGDFEGKAHELIPADVMI SGCQDAQTSADVGNVATFSLPDPAGRAGGACTSALLKVLYQQDGTESFSFV
DVLMMRMTVLRSGSYPQIPQLSCSRKMDVQEKFTLVPESSTPYGSKRALLIGINYVGGQELRGCHNDVG
NIKRYIMDVHGFQEEIDIVLMDDDGNHELPTYDNI IAAFRRLVNDTESGDCAFFHYSGHGGRLPDDNGDEED
GYDETLIPVDYQSAGQIRDDLLYSDLVGRMPEGSTLTCLMDCCHSGSVLDPYTFQADGEQQEMGENPKAN
MGRQLQAMAVGFLVRKIFGTGPAAQMVMSLATSGLAMAQSGGSSGGQKTGGANNVLLPLLX

>Aglacialis1 CAMPEP_0199875840
MGFLSRMKKRIEERFDEKQGAVIPADVMI SGCQDSQTSADVWNVQSFGLPDPAGRSGGACTSALLKVLYA
DHRKLDLDDTLFVEVLDKMREILSEGEYTQIPQLSSSRAMDLELPFHLVSQQEDATDKRRALLIGINYVGHE
SGVLSGCHNDALNMKEYIMDVHGFEEENITLLDDGEHDPPTKENILNAYKKLVEESEKGDVSFCHYSGHG
GSTRDDDRGEEEDGKDETLIPVDYKTAGIIRDDDLFDTLVHPMKEGVTLTCLMDCCHSGTILDLPYTFKAD
GSGNVDMSIDDDFNFDKLFKKIGEVFD

>Aglacialis2 CAMPEP_0199894872
MPSIEEAIPANVRMISGCRDEQTSADVSNVATFSLPDPAGRAGGACTSGLLKILYADKHKPDDDL SFQEV
LNLRDVMSSGRFTQIPQLTSSRPLDVHTPFTLVPDECTGTKRALLIGINYIGQQGELSGCHNDVLMVEYL
KDVWGFEEHNITILLDDGEHTNPTRSNILSAYQQIVAEAESGDVAVYCHYSGHGGRLRDDDGDEEDGYDETL
VPLDYQRAGQIRDDDLFNILVGPMAKAGVLTVMDCCHSGTVLDPYCFVADGEQEEMTLKPDFDMEKLMG
LAQALMAASNGDPMALAQACCTIL

>Aglacialis3 CAMPEP_0199871010
MVDGAFDSQAIEAIPADVMI SSGSHDKQTSADVSNVGFQQLPDPAGKPGGACTSALLKVLYKDKHAAAPM
SWVDTLQRMRSILRGMGYDQIPQLTSSRMIDVKSTMYIVPPGSTGRRAVLVGINYIGQQGQLSGCHNDVH
NIKDYLINVQGFKEQDMLILMDDGRSHEPTRENILKSLKRVTEYSEPGDVVFFHYSGHGGQVRDTSGDEED
GYDETLIPVDYKRSQIIDDLLSDVLVKSLLKGVTLTALMDCCHSGTVLDPYRFDADGSDAMIRDEKMDF
GKFLDSASEVVGCLLCLYICILGLVSDF

>Caffinis1 CAMPEP_0187013496
MPPQLEKVKREIRFQDQDTTIPPGGEYDLATADSPSENLLFDEIVEKVYPAEILMIGGCRDSQISVEVDAP
GASLASMLSSGGETHHSKEVSINLSQLRNTHFRLPNNIDGRSSGVCTKAFLSCLQGNHATVSWFQLLKS
MQIHLKGYNQDPQLSSSRLIEVDQPFIEVRNKNGTKRAVMIGVNYTGQKGEKLSGCHDDVESITSYLIESHG

FEKENMTVLMDDGIHEPPTYRNIMVACRAIVRESKPGD TVFFHYSGHGGRIQDINKDEADGFDETIIPSDY
FRAGQITDDDLNKTTLVKPMKGGVYVVALMDCCHSGTVL DLPYVCTEGSHMTRQTQLNLDLKKTKFCGFFYS
CIRAN

>Caffinis2 CAMPEP_0187019438
MTSEQAQN AIRSEFRMISGCEDEKQTSADVSNVGSFQLPDPAGRAGGACTSTLLNVLYRDKVRPDDKSFKEL
LLEMREILQSKDFTQIPQLSSSRNL DVDTKFDITPDGFHGTKRAVMIGIN YVGGEGELAGCHNDV LNMKEY
LMDIHEFEEENMTILMDDGVHPDPTRDNIMYAYRKIVAESQAGDVVYLHYSGHGGKLRDDGNDEEDGYDET
LIPLDYQSAGQIRDDDLRLTLVPMQEGV FVTSVMDCCHSGTVL DLPYNYQGE GDSMQEQDFKYDAAFSIL
GALATGNTSAAASVAMDECCTVS

>Caffinis3 CAMNT_0029934239_2
HKSTLLIFHNSHKRLTSASNLYFIYNKKRKNIKTKMSYPGNRRPQNRPAQPQKQNSVGFNGQPTQFDEMAI
KAFPAEFQMISGCHDSQTSADVSNLNSQFSLPNPQ GKAGGACTAALLSVLYDSHRNGTFSSMSWVTL LRS
RQNLLNKGFDQVPQLTSSRLIDV NKPLKLVNDDANASYGTRRAVMIGIN YTGQQGQLSGCHNDVKNMIEYL
KSYQGFEEDRNMTVLMDDGYHHDPTYYNIMDAYRTVVRESRPGD TVFLHYSGHGGRRV RDTSGDEDDGFDETL
IPVDYQRSQIVDDDLCTQLVKAMPQGV LVTSLMDCCHSGTVL DLPYRFTADGDAMVRQNEFD FGDIAVVA
LAACCLFDLLCCLCSALGGMVDGFD M

>Ccurvisetus1 CAMPEP_0187040390
MDAEQQIEFDTKAKEQIPASIRMISGCRDSQTAADVTDLGSFSLPSPDGRSGGASTAVFLK TLYDAKNDGT
LSSLNWVDLLQAMKEKLDGKGY SVPVQLSSSSMMNIKEPVK FVNDDPNGTKRAVLVGIN YVGLPGQLSACH
YDVKKVKEYLITELGFEEKNMIILMDDDHHTRPTKYA IILTAYRRLVEESKAGD TVYCHFSGHGSRV VDTNG
DEDDGYDETLIPVDYF RAGQIVDDDLKLFVKPMAKGV LMTCMFDCCHSGTVL DLPYFNA DDDEKMQRL
SDFKFKKKYLWCRLSVAFRFVYSPVSGSSYV VNSLEKHMVKIFVSDTALPGILYL

>Ccurvisetus2 CAMPEP_0187047062
SADVSNVGSFNL PDPAGRAGGACTSALLNVLYADKKK PDDDL SFKQVLLSMRDLGSKNFTQIPQLSSSRE
LDVDTKFDITPDGFSGTKRAVLIGIN YVGGEGELAGCHNDV LNMKEYLMDVHEFEEDNMHVLLDDGVHEDP
TYDNIMNAYRQLVSSSVEGDCVYI HYSGHGGKVRDRDGD EADGYDETLIPLDYMNAGQIKDDDLRLTLVIP
MQRGV FVTSVMDCCHSGTVL DLPYVFKADGEHDQMEHDEDYDFDPMMSILGDAGMI GTGLAVAAVA DSEC
CTIS

>Ccurvisetus4 CAMPEP_0187051206
LITTKGKMNDFDQKAEQAI PADVHMI SGCCHDSQTSADVSNVGNFQLPNPQGRAGGACTAALLQ TLYDAHRN
GSLPTLSWVTL LRSRMTNLLNKGFDQVPQLTSSRMIDVEKPVQFVNDSNNYGTKRAVLIGIN YVGGQNGELS
GCHNDVKNMKEYLMNVHGFPE SNMTVLMDDGYHLNPNTRYNITNAYQNLVRQ SMPGDSV FCHYSGHGGRV R
TSGDEDDGFDETLIPVDFQSSGQIIDDDL FKNLVQPLPKGV LMTCLMDCCHSGTVL DLPYRFTADGDVSAG
MQRIDGDFDFDELLMIGLICCLPDL LYCFGDLFGCLYGLLDF

>Cdebilis1 CAMPEP_0200872066
MIYQQRYSILRHRIRRP SLKEAFVATAIFSCLLLLVPFLHKASDDNILETQEKGAPTQTVNYVSSLVVG
YPSTSPPYNSTVEFII SPKDPSCIEDPGHLFYYPFAEEADDPDPTIYNCTWLANTRRPNLICDYEIFNTGF
ENLQPAREVCPVTC DSCYLLHPSAVPTPTPSFSSHPSSEPSVSARPTLLPSTEPSGSPTS IPTQRPTACPE
DPDAIFFRTELE DATKPIFHTCKELSEFKYPENTCKFLTQSWTEEIEEDQKPI SINYYYPAKDICRNTCS
TCVIESPNPSNGPSISPSRTPSKFPTQNPSEVPTIPGIPSPRRTPNPSITPSKNPSLRPSNSPTGT PKIVE
FDLTMTFVKDPND SAPNEDFNEEPLTEVVTETLMSSFENQKDGNF EVVSRVKSQESFGERRYLR LQSSGSQ
SQTILSRRSGSNRSRQLQVSGQRVIFLIVVENNSGRSLKSIKNASENTFESEESQRKFLKELRNRDSSFVI
YNGVVSTDEVKPSLTPR VAVTKRKAWIIVLSVVLGVSILLV LILLGLLYLFKRKKDEVKKEIEGNDKI
DTVMPPPPSITDLSIPPDPKFPPTNSNDNENAF LISNDSPKQEHNTETS DNGEIEQANSSTTEATGDGE
SALDSDSGMQPNADSIQ PSEPIGPSVSDTSNAQKDRDKNVGMRERGYNSYSEYSSQDDYSSDSDSYEDSLSG
SDFRYGDNSEESVTR SDESLVSLKCTVHMI SGCRTQTSADVDEVGKFC LPNPLGKSGGACTAALLQ TLYD
FHGSEKTRSLTCSWAGILL SMRENLSQGY SVPVQLTSSKPINVNDTFHISNPWKYGTKRAVLIGIN YV
QEGELSGCHNDVIRIKDY LINFQGFEE RHITLLMDDGININPTKGRIIRAYRRIVK VSKAGD TVFCHYSGH
GGRTKDL DGD ESDGLDETLIPMDYQSAGQIIDDDL FKELVQPMSEGVHATCLMDCCHSGTVL DLPYHFTA
SDASKGIQRGRAPHSSYREIRQNTQKKPEI IPLPAKNMKNPRVGKVKPSPGTGHEFD DVFRIDHACISPEL
HLPPMISEGKIAITVPSGPLGFATVDNPTNGIRASEVFAMKQSSILAGKIRNGDR LIALDGI DTSSSLTAAE

VTKLIISRSSKSRDMVFRSDRGKPTDMRTIDEGSVSSHGINDYTCCKTGTSELTKLIDGVAEHEAVSVISV
ASEDNESVCSMISC

>Cdebilis2 CAMPEP_0200886990

MSDFDQKAEQAI PADIRMISGCQDSQTSADVSNVGNFQLPNPQGKSGGACTAALLQTLTKVHREGAEISWV
DLLRAMRDNLLEKGFQDQIPQLTSSRMKIVESPLKIVNDTDVYGTGTKRAVLIGINYTGQQGELSGCHNDVK
NMKEYLITVHGFEEQNMLILMDDNYHPNPTRMNVLNAYRNLVRESKPGDTAFCHYSGHGGSVKDYSGDEED
GFDETLIPVDFQRSQGIIDDDLFKELVRPMSTGVLMTCLMDCCHSGTVLDDLTPYRFTADGDVVSQGMQRISGF
NFDDLLVVGVFVCCCLPDLGLGCLFEILG

>Cdebilis3 CAMPEP_0200879288

MFSEKAEGAIPAEFRMISGCQDRQTSADVSNVASFRLPDPAGHAGGACTSAILNVLVYADKHKPDDDLTFKD
VLMKMRDMLDTKGFQAIQPLSASRDIDVDTKFDITPDDFSGTKRAVLIGINYVGQDDELAGCHNDVLMKE
YLMDVHEFEEDNIHVLLDDGVHEDPTSENI IAAAYRRIVAESVDGDCVYCHYSGHGGKVRDDNGDEADGYDE
TLVPLDFQEAGQIRDDDLKTLVIMPRKGVFVTSVMDCCHSGTVLDDLPTFKADGEQESMQHDESFNFDPM
MGILANAALGGAAVVVAANECCTIS

>Cdebilis4 CAMNT_0047068781_6

KQFFHIIYSISSSSIMSEFDKKAENIPAEIRMISGCKDEQTSADVGNVTSFGLPDPAGRAGGACTSAIL
KVLVYADKKRPDKDLSFKDVLLKMRDVLDDKRFEQIPQLTSSRNLDVDTKFDITPDDFNKRAVLIGINYV
GQNGELAGCQNDALNMKEYLKDVFHDFKDENIQLLDDGTNTNPTKRNILKAYAKIAEESDAGDVVYLHYAG
HGGHKS DRGGDEKDRDETLPVDFQKQWGVGEILDDDIYQKLVKLKKGVFATSVMDCCCHSGTVLDDLPHYK
VGDGKQEGGMNANEGFNFGTAKGGCIIIL

>Cneogracile1 CAMPEP_0200990868

MISGCEDKQTSADVSNVASFKLDPDPAGRAGGACTSAILNVLVYADKKKPDGDLDFKDVLLQMRGMLDGKGF
QIPQLSASRNLDVDSKFDITPDNFSGTKRAVMIGINYVGQDDELAGCHNDVLMKEYLMDVHEFEEDNMMI
LMDDGEHVEPNQANILSAYRRVVALSQPGDVVYLHYSGHGGKLRDDNNDEEDGYDETLPDYNSAGQIRD
DLLLLRILVLPQAGVYVTSVMDCCHSGTVLDPYFNFKGDGEQESMNESENFDSTPMGILSTLTSNASLMN
SVASAAEECCTIS

>Cneogracile2 CAMPEP_0200992636

MSNYPGNRRPQAEKQQSIQYSSNATGYDRQAEETFPAEFHMISGCHDSQTSADVSNLNTQFSLPNPQGRAG
GACTASLLSVLYEEHRKGSIDSLSWVNLRLNRMQDLLNKGFDQVPQLTSSRLIDVKNKPLELINKSSDAAYG
TKRAVMIGINYRGQGGELSGCHNDVKNMVEYLKKNKQGFQESNMTIMDDGYHTNPTYSNIMNAYRTLVRTS
QKGDVTFIHYSGHGGRRVRLNGDEDDGFDETLPVDFKQAGQIVDDDLCKELVKAMPQVLTSLMDCCHS
GTVLDDLTPYRFTADGEAMVRQDQDFDGDVIGGVVAMCCCFEIMLND

>Cneogracile3 CAMNT_0047211831_3

IMDQSTDNNDEHANDTSHNHESNNAMFHILISACDSDTAADVSDINSQFSLPNSQGGKSGGACTAALLNLY
AAHENGITDSMSWVGLLKEMRKDLIKKEYDQIPQLTSSHRIEVDKPKIVNDSPDSMSGTKRAIMIGINYV
GQQGELSGCHTDVKNMRKYLVEVYGFKKSDIIVLMDDGIHNNPTKHNIMKAYRKIVRDSLPGDVFVLFHFSG
HGGQRVDLNGDEDDGYDETLPVDFQEAGQIVDDDLWVELVKAMPQVLTSLMDCCHSGTVLDDLPHYQYAA
DEDNVVSSGDCSDNSTGSLQDDQSPETPETAAASSTVSEARLYELITSKNWKRAEEFLDDKSTFNEEEKL
ENLQYQDSNGYTPLVKAVLKKSAVSLIKTMINLGKRETLEVTNDSDNVNLHWAAYSNNVSLVFKLILEK
SNRDVIYAKNNYDKTPEILLNRNKAAFIDKTLALLVKEQLLSDQKTTVDRLCTSWSTIKTLAWAHLPE
EKDIVLERPLFKAILNSTFICPRYIFISMMDLYMQIALVLFVFFLRNIIQSSTPFLSLIILVVCVWF
LIREMTELMLTYLKNYFLEPTNVDIIQFVLLAGSIVIIFASGIDDLNPLSTIDHAFVISATCVAWLKLL
FVVGNLVYNGAVFANGVITIIIGKIVPFLFTSAVLLLMFMSHYLMWAGHYFCSQFFKSDDEWTCNLPSY
HETFSMFLGLNSEVQVSTFAISYVYGFISILMMNILIAICYSYAKVLESGDRTFWRNRLKFAECQCF
NMFCCAERHNRIRNESTRYGRIDSEIITNFDLNVQDGDPPQDNGPQVHILKNDRISFGTHDWSIYNKKIG
ANDKREFFGWVWETSVTSTPSLRIRLKYFFSRALWEDIICPGQEFENILLGIQYNKSGRGLRFFVRLVCY
VLIPFSLIIILMFCFGSVSFGLLWHRKMRHLFAEDTNKFKSEQVEARDTLKEEIFIELQEYETNINDSL
EQLVRKHEEKIGKQFAILSKKQKMNFKQNEHEYRFVDIDEHLSDIKKMLSEMGNK

>Cpennatum1 CAMPEP_0200351432

MSFQEQAEKLIAAEVRMISGCADSQTSADVSNVKEFELPDPAGKAGGACTSALLNILYNDGVAAGEMSWVD
MLRRMRVELQGDTYQVPQLSSSRQFDLSNTFEFAKTGYGGTKRAVLIGINYVQSGQLSGCHNDVLNIQKY
IMDVHGFQEEENIEVLMDGGYHTSPTRHNITVAYQRIAEVVSQSGDAVFCHYSGHGGKLPDDNGDEDDGYDET
LIPVDYEHAGQMRDDELLQRLVPLRAGVTMFSLMDCCHSGTILDLPYRFRADGDTEEFQEEESGYNFGGYM
GLLGESAETVFCCFMLLKFFVWDMVM

>Cpennatum2 CAMPEP_0200351262
MPFSFNGAFQNLKDRFDDDDDEPSYEERATNMI PATVTMLSGCKDCQTSADVVDVKSFGLPDPAGKAGGAC
TSALLKLLYHEEQVPDDDLTYVEVLNMGMRDNLNDNYTQVPQLSSSRPFDLTPFVFAEGIGTRRALLIGIN
YGGQNGELSGCHNDVINIKGYIEKVHGFSEDNMTILMDDAEHEEPTKRNILKGFALVKSCAEAGDSVVFVHY
SGHGGSIKDDDSGEEEDGMDECLCPVDYALNGVIRDDDVYSTLVAGMPPGARVTCMLDCCHSGSILDLPLY
YTAGSEECCLKENEKFKFGKLFQLLGNLAEDFLDLF

>Cpennatum4 CAMPEP_0200356122
XTQKPDAMASTGNFHQQAVELIPATVRMISGCHSEQTSADVSNVASVAQLPSPAGRAGGACTSALLDILHR
TPPGSLSFQDLLGQLRQNLNSNGFDQIPQLTSSRSLDVGRTPFHLVGGSGQRRRAVLVGINYRGQSGELSGC
HNDVFNMKKYIMDVHGFQERNILVLVDDTRHPITRQKIIAALEALVANSVAGDNVYFHYSGHGGLLEPEA
NLFKLGGGDTYDETLPLDHTRAGQIRDYSLFNRFVKPMAAGVTVTCVMDCCCHSGSVLDLPYSFQPTPGGG
IRSVQNFDAISNLAFLYVLAGLLPSAGFGDIAANIGDQVGGDISDYQGAGIEAEAQDDEAYEGDGPDPFGD
FADGDGAPDDFGPGGVPDDPGGYEMGGDRGFGGGDAGEGYDTGDGDRGFGGFGMRTRDVGDDGDEGPGFGG
FDMAGGDDGFGMAGGDMGGDDGPGVDCDCLIDSINSLLETTGEEE

>Cpennatum5 CAMPEP_0200357564
MTFQEQAEKLIAAEVRMISGCADCQTSADVSNVKEFELPDPAGKAGGACTSALLNILYNDGVAAGAAEMSWVD
MLRRMRVELQGDTYQVPQLSSSRQFDLSNTFEFAKTGYGGTKRAVLIGINYVQSGQLSGCHNDVKNIKRY
IMDVHGFQEEENIEVLMDGGHHTSPDRRNIMEAYARIAEESQPGDAVFCHYSGHGGKLPDDNGDEDDGYDET
LIPVDYEHAGQIRDDELLKKLVLPLQAGVTMFSLMDCCHSGTILDLPYRFRADGDTEEFQEEGGYNFGSYM
DLLGDSGATVFCCFMILQWVMSMLW

>Cpennatum7 CAMNT_0046377579_4
KSEGSQASKKREVINSRYPCVSTLLLLIPSNRSFSLTIQPINIPL*PRQIFNMPISFNDQFRKLKNRFD
DEDPSLEERATVMI PANVIMISGCKDAQTSMDVFDVGFDPNPAGKAGGACTSALLKLLYNDEVVPDDDL
TYVEVLNGIRDNLDDDYTQVPQLSSSRPFNLEKPFVLAEGEGTRRALLIGINYVGMGDELGDCHNDVLMNK
SYIEKVHGFKNSNISILMDGKNRHANPTKKRILRNFKKLVRECEEGDSVVFVHYSGHGVSRLDKDRNEKDG
MDECLCPLDYTAKGYIRDDDIYSTLVAAMPAGVRMTCIMDCCHSGSILDLPYAYKAKTRKNGSEQSKKLT
GYAKSSVFEENKFKFDKLFKCLGNLTEDFLDASDDSDVSD

>Cpennatum8 CAMNT_0046377197_3
LPTQKSDTMASDTDNFHQQAVDLIPATVRMISGCHSEQTSADVSNVASVAHLPSAGRAGGACTSALLDILH
RAPPGGLSFQDLLGRLRQHLGAGFEQVPQLTSSRSLDVGRTPFHLVGGGGQRRRAVLVGINYRGQSGELSG
CHNDVFNMKKYIMDVHGFHERNIIVLVDDTSHVPVTRHRIIAALEALVSNVAGDNVYFHYSGHGGLLAPE
ANLFLKGGGGDDGYDETLPLDHTRAGQIRDYSLFNRFVVRPMAAGVTVTCVMDCCCHSGSVLDLPYSFQPTP
GGGIRSVRNFDSLNLAFLYVLAGLLPPSGFGDVAAHIGDRVGGDMSDYTGAGIAAEAQDDEAYEGGDPD
VGDFADGDGAPDDFGPGGVPEDPGGYEMGGDRGFGGAETGGGEAGEGYGMGEGDPGFGGFGMTRDVEGD
DGGPGFGGFGMAGGEMGGDDGGFGMADLMGGDDNDPGVDCDCLIDSINTLLETTGDEE

>Dbrightwellii4-1 CAMPEP_0193954124
MGWLVKKIREFKEEQKAHLIKAEVRMISGCDDSQTSADVSNVSMFELPDPAGKAGGACTSAYLSVLYKDKK
ASGAELTFVEVLQKNEGSSPEKKYTQIPQLSSSKPIDLNEFPQLVPDTATGTRKALLIGINYTGMPGELT
GCHNDVKNVKEYLMNEHSFKEENITVMLDDNVHESPTKANIISGYKKLTKESQPGDAVFCHFSGHGSQIKD
DDWFEEDGLDETLPVDFKENGQIRDDDI FDIILVPMKEGVTLTCTFFDCCHSGTVMDLPFTYRADS
SSQ MVLDKKLDGKVFREVGDFFNKKEETNAK

>Dbrightwellii4-2 CAMPEP_0193979726
XQAI PAEVRMISGCADAQTSADVSNVNFELPDPAGRSGGACTSALLKVLYTNKKKPD TDL SFRDVLQRVR
DILAEGKYAQIPQLSSSRPFVKTTHFALVPKGEHGTTRRAVLIGINYTGMPGALTGCHNDVHNKHYIMD
VWGFKEEHITVLLDDGKHKPPTANILGAYAALAAKCPGDVAVFCHYSGHGGMLPDDNGDEDDGDFETLIP

LDFKRTGQIRDDDLFKILVVPKAGVTLTCLFDCCHSGTVLDDL PYNFQADDHEFTEEKNYKFTPLLSIAAE
LKANCINCTNPADPAANCTVS

>Dbrightwellii4-3 CAMPEP_0193978290
XFPLKDKNIHFLSIGTCKMGNDNSREAESTPEVAEFRMISGCQDSQTSADVSNVNEFELPDPAGRAGGACT
SALLKVLVYHDEKTPEDTYSFVEVLKMMRDELSEGEYTVQPQLTSSSTIIDLNEPFDLVPEKSTGTRRAVLVG
INYVGMNGELSGCHNDVYNIKKYIMDVHGFEEENIVMLVDDGCEMPTRENMMNAYKWLVESSEAGDAVFT
HFSGHGGQLRDQDGDGDEADGFDETLIPVDYLENGQIRDDDLVDTLVKPMKVGVVVTSLMDCCCHSGTVLDDL P
YTFRADSDKFEMEMEEGFDLGLKLLGKIGA

>Dbrightwellii4-4 CAMPEP_0193955922
MADFDTKAKAAIRAEVRMISGCHDAQTSADVSNVGSFQLPDPAGRAGGACTSALLNVLYRDHQASEDLVSW
DTLRQMRREILSSKDFEQIPQLTSSRYIDVNETMQIVKGHGAKRALLIGINIVGQNGELSGCHNDVNIKEY
LMDVLGFEEEDNIMVLMDDGIHHEPTRDSILSGYRRLVAESVAGDTVFCHYSGHGGRLVDDDDGDEDDGYDET
LIPVDFEHAGQIRDDVLFNEFVRPMAEGVTVTCLMDCCCHSGTVLDDL P YRFVADGDDVQMRADESVDFEGFL
GPAFWTAGIIAASSLGGGGGGVGEIFGAIMIAAGVYVGLSWIPVSVYVGVYVTV

>Dbrightwellii4-5 CAMPEP_0193981564
LTFQDLLLQLRSSLNSGFDQIPQLTSSRPLDVQPCPFHLVGGTGARRALLVGINYLQNGELSGCFNDVY
NIKKYLQNHGFGAPKDIVLMDGKHSFPTRQRIIQELKKLVSCSIGGDSVFFHYSGHGGLLDADGFNLFK
AANPNAKQYDETLYPVDHGTSGQIRDFSLYSHFVQPMKEGVFVTCLMDCCCHSGSVLDDL P YSFQPTSGGGIR
TGRNLDLTLNLAFLYVLGGMLPSHGFENVNTHIENNVDGTLDDYQGTQVEQLEMDDVACEEAQFDDPEGV
GYGEGIDDDVEYGHYDDFGDDDDTEERFVGNVDGDDVGEYMNDPDPNPMGSPGFDGGPPPFEDDAMDG
PLSRPMEYDQAPPDIVQGTFFVDDGDRGGEFVGGDDFAEDEAVNYFPPQEEVQGGFGEYDDAGGDDAEIDC
GCLGDLMSALMEDEE

>Dbrightwellii4-6 CAMNT_0038558635_2
ITPSITSSMFSYPGQKRRPKRPTGPPPLSLSLRFWDYDTRGGSLDREEVSAALLHTPPFNHRGADS
VRETVYSVWAAFDDHDSGSIDKREFCAPGGLGESLLAYTTQHHQPPPKPAHTYPPQTTHTRPPQTYQPYQ
PATNTTQSNDDPIYVPAYGSNNQTHQETHQHNSPAPSAPPVYSSGSNTWNCQNTFANSNTDPRCQMCNA
AAPAGIAAHNHQPPAPAPYHQPPAPAPYHQPPAPAPYQPPNHHHQPPSYQQPTHHQPTRHQHTQQSPQYQ
TMRINIPAGTVPGQRLKIKTPGGHEHMTI PERHQWHSQHPPVFDVQVPVAPAVVVQAAPIHNPTPSGGHY
APAPPPKPAQTPWQSWESFRGHTFQQVPMATTNVPHEISHSSNIPASGRRKALLIGINIKGTRAAALRG
VNDAKNIKNLLMENGFRDDPTHMVMLVDEGARNSNYLPTRANIMRGFQWLQVGVSEGDALFFHFSGHGSQV
PDKSGFEEDGLNETILPVDYQKQISDDVIWSSIVYPLPSGVKLTVMDCCHSGTGLDL PFDYMLDSKRWV
EDTNPAAHSGKHVVSFSGCEDSQTSADTIEKYQAGGAMTQSFISAYRQNPMTYPEFMAAIHRRLLKQRFKQ
RPQLTSSQAFDVKNVTFVSTEGFQPNKNQVIGRIQRKKIRPGSTGDRRQSGVNDLLFGGLMVGALAFADA
LFG

>Dbrightwellii4-7 CAMNT_0038593613_3
ALGLRNNSKRISHIKANILLDSLTKHPPTKPTHTTSLPQAHQSAYSHQGVNVSTGSAPQLQTS HQSEHNH
HHTMMMSVPHTTMRPPHTYHSTHSHQGVNVSTGSAQQLQTYQSHQSEHNHHTMMMSVPHTTMRPPQTYH
STYSHQGVNVSSGSAPRIQNYQSHQHQIRPYHTVAMSTKDYPGSQVHTVTTPKIDEAHSQNAAGDVVEVH
AAPSVAQNHQOQPTFNQHPAQKHQSHQNHQYHAMTMSAPQASAPPELPPKDPTVSQDHKVTTPKIDEAQS
QNNTSVDVEVPAAPSVAQNHQPQSTSNQPPSHQKHQSQQNHHHAMAMSAPOASAPGQTPKIDI PERPDHI
AAAFERIKLQNAATYDENPNTEGQGLVDRSDEHSTVAPPVLLRPNQTPWQSWESFRGYPFKEVPLATT
DIPSNVYNDASNVIASGRRKALLIGINYAESAPLQGCVNDAKNIKNLLIENGFTDDPTHMVMLTDEEQN
SKYLPKANIRRGFQWLQVGVSEGDVLFHFSGHGSQVSDAEGMEEDGLNETILPMDYQKQITDDMIWSS
VVYPLPSGVKLTVMDCCHSGTGLDL PFDYEPYTGWRVEETNPAHSGKHVVLFASCEDAETSADAIGKYQA
GGAMTQSFILAYKENPMPKYPEFMAAIHGHILDRHFKQRPQLTSSQELDTKNSRFSLEIGIQRNKNRTIGR
IQRKKIRPGSTGDRRNFLFR

>Espinifer1 CAMPEP_0200425734
PTATTLAPPLTDPYSWFDYDQDNSGTLQDEVVSGLLNAFYQKQSSSTADEQHGGTNQSGNDAAPPSVDTI
RESIKAIWPAFDIDGDGQIDREEFCSPGGMAESLLAATTGGIPPGQAETTDGFFSSHHASGGGGYPGAR
PHHSSGGGGYPAARPQQHQAYVPTAKPVASSGMMAGVYNPHAHQQQQQPAPTAPPPPRPAAATVQVVQP
VYKTIQVQIPPGMGPGQKLKVLTDAGKEAAIVTIPDRAKWRANARTGQPFDIRVAEKPKPAPTVPVVQ

GHSVSGSPGRHSAGASVSSVTSSMAAMSTGAAAGPAAVTFKAWERFGGHSYHAPSLGMRRVPHLPITSMSNV
HASGRRRALLIGINYKGTAAALRGCINDANNMERLLVQHGFPRDSCHMVKLVDSSRNRNYLPTRANITKAC
QWLLQGVSKGDVLFHYSGHGAQVPDRSGMESDGYNETILPMDYRSGQITDDALWNSLIAPLPDGTRLTSV
MDCCHSGTGLDLPYDVDIRTGRWKEDVNPAAHQGDAILFSGCEDAQTADTMDKFQAGGAMTQSFIKAYQD
NPMATYPEFMAS IHRHLKRRGFHQRPQLTASQKFDVRSRIIFSFTDGIENHNPQIGRMKRRHVRPAKAGYK
KNNMNDLLFSAGGAIALAGLANLFLDG

>Espinifer2 CAMPEP_0200438730

XLFAAMKQERKSI SLVTA[~]AAVSLALNIALARATTLTDTSWRS[~]DLGVDSQTW[~]SLAMRASGRLALLDLHDLYV
KEPSK[~]LQSVRLPPFRGGGAGEDGDG[~]SERNKDD[~]VDLYN[~]PRLSL[~]STAWSASSAQLPAPSQSATKAAIRECAES
SQSVSPANDLQ[~]TTPGGASAGSCGQDMQ[~]QVCAGSRRTNTVST[~]TRASGQARALVVVWASWNILNGALLTLTP
KDSYDFAAYLVEAIGAVRVSHGLQLFLAAGANI[~]SAQKVMGVGILVRLVFLAASFALGT[~]YETLQ[~]TQSKAPFL
LSAGVMSMAAFSLLSNKGRPMLMANL[~]FSTTTCIKGMNMI[~]FRPFASNRLFGMGFTD[~]GELYWILHSSEKSSH
SSLGQSDC[~]DFFXIPLLN[~]VI[~]GTKIPGKYRSLGFHLV[~]ISSVFMNALS[~]HGMPIRAAGLSAATWLALLAELTF
VSGGYRRLSDVPRVYLFFLASALVCSIVFL[~]TDT[~]PRKHVDSSVGDALS[~]SVSGWRSDEEGASQEILWKQEDVY
PLMYERDDNNTSDV[~]RSIRIIXL[~]AYSTSLTGTILLELSLRDGRK[~]PWCCECGKSGAALGRSAPMIDSTDSID
STDSIDSHHDDGRQEDKTRHQ[~]QRSGALLLCAAAAAARSAAAAAARGESYMYMSCRELRRSRGKILF
ASYFPQRRSGRGPKIRAFHLIYGFAKLPSLIVLRSRLIRVLP[~]CRVAEGGCCGHQTLTEVANKNNR[~]NAEAE
TLEAAEKAI[~]PAEVRMISGCQDSQTSADVSNVASFSLPDPAGRAGGACTSALLK[~]VLYADHHRTEEDLSFQET
LLKMREILSSGRYTQIPQLTSSRPMNIQESFDLVPDCSGERRALLIGINYIGQQGELSGCHNDVMNIKEY
IIDVHGFPEENITILLDDGEHRDPTRENILDAYKALVSASKAGDACFCHYSGHGGKLRDDDDGDEADGYDET
LVPLDYQ[~]RAGQIRDDDI[~]FNTLIGPMPKGVTLTCIMDCCHSGTVL[~]DL[~]PYVFKADGESEEMTADPDFDFGPLL
QLAVSLFSDGIQKEDFLKIGSSLLSGVFS

>Espinifer3 CAMPEP_0200433120

MTKKSNSSTDVDP[~]SAIIPATV[~]HMISGCE[~]DRQTSADVTN[~]VDAFSLPDPAGRAGGACTSALLK[~]VLYYI[~]SRSK
T[~]PLSFVDVLMNMRGILSEESFSQIPQLTSSRLLNVSDAFYIVPPTCTGT[~]KRALLIGINYVGQSGELSGCHN
DVLNIKEYLIDVLGFKEKNITVLMDDNESERPTGSNIIDAFKDLASLSKSGDAVYFHYSGHGGKLRDLNGD
EKDGYDET[~]VIPVDYDTYGQIRDDTLYK[~]KLIGAMRSGVNLTCVMDCCHSGTVL[~]DL[~]PYK[~]FVANGSTTEMALDD
DANLNLQEF[~]AADLELEGRWLLPCIGVLLLMALIAIVLWFLGRA

>Espinifer4 CAMPEP_0200482898

MGDFLAEAEKAI[~]PAEVRMISGCMDSQTSADVSNVASFSLPDPAGKAGGALTSSLLK[~]VLYADHRKPDGDL[~]SF
QEVLMKVRGVLGGSY[~]TQIPQLSSSRPMDINTPFEIVPDGCTGT[~]KRALLIGINYVGQQGQLSGCHNDVLMNV
EYLKDVWGFPPQ[~]NITVLLDDGSHVN[~]PTRSNILNAYRTLVAESQPGDAVYCHYSGHGGKLRDDDDGDEKDYD
ETLVPLDYQ[~]SAGQIRDDDLFNTLVGPMKKG[~]VQATCIMDCCHSGSILDL[~]PYVFKADGEQTEMAPSPDFDMGP
LLALAGALASGASITEALSQQDPQQLMAMAQQCCTIL

>Espinifer5 CAMPEP_0200484576

MAELDRFMNGLASPSPNHLANRSVAASAGNADSGAGDDDTKAATIVLGGANLVGTIPTSGPIDVDEVSQSS
LVEEINAPSGAASSGILLARDGDKTTQEAEKDASVAAAVAPIVATLSMLSASKSRGGTEASMKKSKSQKK
VTIVEQIDEKSLNDT[~]NENAVDSETIP[~]PRNSNMSVCSSHHTDDASTV[~]VSLQFKVEK[~]KKK[~]KRKTSQNPASISR
EASSTASSTVMVDNTAGGKGRSNGGKTVFRSLK[~]KL[~]SNK[~]KVPSASSVSVSVVGGGPDA[~]IRILSGCSH
SNASDIVPNTSSLPYPSGTTGGACASSLLQVLYDAEGGKAKAAGASKKKHGDGATSKLSYVDILVKMRSDLT
TRGYDQIPQLAASH[~]PVDIAAPFRLKSGKGTARALLVGINYAE[~]EEENQSSSHNDVKNMHRYLTEVAGFDADN
VTMLMDDGDCLPSKANI[~]IETW[~]KELAEDSKAGDSVFFHFSGK[~]GSETIAPVDYENAGQICDGD[~]MYNAFVKKI
PKGVTVTCLMDSCHSGTVLEL[~]PYVFKADGTDIRSKTMMMNQGFN[~]SSK[~]FFF[~]GD[~]T[~]FNQLIGESRNGFSTPPRR
SSNGR[~]KVASSPSTPTTNSACDDDLGDDAVTMVSI

>Fkerguelensis5 CAMPEP_0188144146

MSSTLAQAE[~]EYIPANVRMISGCQDSQTSADVSNVATFQLPDPAGRAGGACTAAMLK[~]TLYNDEDNPAMDLSF
QDTLLQMRDVLSEGKY[~]TQIPQLSSSRPLDIHTKFDLVPDSGFSGT[~]KRSVLIGINYVGQDGELAGCHNDVGN
MTRYIQVHGFTE[~]THMTVLMDDGSHQ[~]APTYDNIMSAFRQLVQDTQEGDAV[~]FVHYSGHGGK[~]VADQDGDEADG
YDETLVPVDFQAGQIRDDDI[~]FKVLIGMPRNV[~]TMT[~]CVMD[~]CCHSGTVL[~]DL[~]PYTFVADGTQEEMMETPGFDF
GTLMKLYQSFQTFKQG

>Fkerguelensis8 CAMPEP_0188102320

MGRFMKRLRQRLEDKIDTVTTSITDGTLSMPEGYPGIAPSQQHEAQRSFESNKPESMRKDVRMISGCEDSQ
TSADVSNVRQFQLPDPAGGGGACTSTLLNILYKDEQIVEDTYSFTEILEQMRINLGKSGYTQIPQLTSLN
PIDVTTDFQLIPEDASGTRRAVMIGINYVGHAGQQLSGCHNDVLMKKYIMDVHGFEEENIVVLMDDGIHS
SPTASNMIQAYQQIVADSEGDGDAIFLHYSGHGTKLRDDNGDEDDGYDEALVPVDFNEGGGMIRDDDLFDIL
IKPLAQNVHMVSLMDCCHSGTILDLPIYIFAPKLNTDGSYSMPQEMTLDETIIDLGLVEQFGGQAMGLLV
NFLQKSLGQN

>Fkerguelensis9 CAMPEP_0188100640

MGRFSINNLQTSVERIEKLLLEKFQKLLHSHKEDHENAQRDFEERKPDPTMKKSVVLIISGCEDRKTSTMS
NIDMFTLPDSAGRCGGIVTAALLNVLYWNDDKQKLEVKQQIQTRTNEIEKSNQDTSERAASYRKVAEDTL
PLLQLLVNDGGNLVDRMEEI IKPTEDEDDTEEDVQEMRKQMDYILSYDLFVNLDKAKKIYKAFNTSSPLF
VSGNIAGCAQIYREAAEKNILPLLPSNDDLQNKLEVIASKYDDPAEETRAFREQFDHILSYNEWTDSDKK
FEEALDNAKQCIVEAIDNGATYLDDEDYDSIASIHRKSAEEKILPLLNSDLQSRLESVIATEYSDTCVE
AAAFLEPFNYILDWTENKEKLLKCMKNNCSKEEAQHLYVDVIDKLRSSIKNSGHDQKQPQLTSLTLIDIN
TEFKLVDPDNFKGRRRAVMVIGISYDGGLIGCHNDVINMKKYLIERCDFKEYYVDVLMDDGVHTLPTKSNIMN
ALLRVVNDNCNDGDAVFFFGHGTEIVDENGDEKDGDECLVPCDYLEYENFKDGVISDDDLFDNIISELP
SDVHMVALMDCCHSGTILDLPIYILKANEDGSMPEMVLDDTIDLKSLIKQYGGRRKLDLLLNSVSKLFIEK
EMPPMHVNPVKLGRVLLLADEDAYRHSFARFEGDELNGLIDEKLPARGKECKVVTVWGDQTITAFDDGTR
FDFPFESVEAQLHVMEMPEAESNEGEHTPTVIFKLHSSLNSVIDIYEVDRDGTVMVGSISKEDEDSGTLHMDT
HYGHSFRFCTHEESTTSSQQMDMAKSLISTAISIGAPAYNTGDIPECARIYKETALQIAPMLPQNLTGLE
ATIQQTFKNANEEAWAFRKNFDSIMSFVPSSSFKIYYIDQCNGPHQTCVVTSDDDDEESNNDEEDSDDDGEE
GGEDEEKSDDDDEESDDDEEDGDDNGEEGGEDEKESVDDDEVSDDDGEEEDGEEDGEDDEESENDDKE
SL

>Fkerguelensis10 CAMPEP_0188069114

MNTTNNRFLSYDECQQFERNKPGELRDADIWMIISGCDDHQTSADVSNVASFQLPESNGKAGAGGACTATLL
QVLYEEEEETPHDDYTFTQVLEKMRQRLRSKGFQTIQPLSSTKPIDMSTEFKIVPDDLPGTSRAVLIGINIR
GQKQKELGCHNDVFNLYNIQDWYGFQDENVTVLADDGDHQLPTKQNILAAYHRIVRQSRSGDSIFLHYSG
HGTVKVPDLNGDEDDGYDEALVPLDFDRSGVILDEDELYEIVFKGLPSNVHVVALMDCCHSGTVLDPYIFKA
DGNFASKMEIDRGSLSASKLFGQLGGMALKIVMGGSNNGGSGQLVEGFIKHFLR

>Fkerguelensis15 CAMPEP_0188088198

XTLQSIICIMFQQGRERRQNRGDRRTDRQERRGNNRSRPARPATTTTTTTRATTTTTSTKGRSTAARETT
TTATVNDEGLSFDEQAEQAI PADVRMISGCHDVQTSADVSNVSDFALPDPAGRAGGACTSALLQVIYNEHH
LDPTYHQLSFMDVFLQTRDVIDGMGYQPVPQLSSSRRIDIHQPFNMMKNDSDTGPGSGTRYAVLIGINITS
HKQGGQLSGCHNDVGNIKKYIMDVGKIKAHNITTLMDDAGISIPPTKRNIMKAFDELTRKCPGDCAFVHYS
GHGSRQKDYTGQEEESGYNSTLVPIDFNEAGQIVDDELYEHLVLMKMPRGSTLTCLMDCCHSGTVLDPFNFV
ADGEQTEMVEMENFPFLQLLQCVGKALQEAGVSQLRDLRDKDKREQVKAALVENGVGEQLAAARAGAAANA
GGAGAGSGQRGGVAGGTVRDNIKSRQERRENRRKFLR

>Fkerguelensis17 CAMNT_0031427971

TMDEEKIRNAIPANFVMLSGSEDKQTSADVNGVGFSLPDPAGKAGGACTSALLKVVNENQGRQMSWIDLL
HRMRNVLKDKGFDQIPQLSSSRMIDVNNQFEIVPRQSINEQGARRALLIGINIVGQGGELSGCHNDVKNIK
KYLIRKEGFQEKDMLILMDDGRQHAPTRQNIEMAFDRITQYSKAGDVVFIHYSGHGGKIRDTSGDEADGYD
ETLIPLDFKQAGQIVDDEIYSRFVTKMPGNVTVVVVMDCCHSGTVLDPYEINATQSKMSLNLKGFNMGLLN
NATVAIGCCLCILSMLDI

>Npunctata1 CAMPEP_0199328580

MGFLNEQQRRAFEEEEKQALRADIWMVSGCEDRQTSADVSNVATFQLPEPSGNAGGACSATLLNVLYEDEK
NPLDRFTFTQVMEKMRGILKRKGFQTIQPLSSTRPIDMNDKFLVPDDLPGNRRRAVLIGINIRGQKQKELRG
CHNDVFNMYNYIQDYGFQDEEDITVLVDDADHPPTKANI IAAYQSVVAKSQPGDAIFLHYSGHGTKLPDD
NGDEDDGYDEALVPLDFKSAGMIRDDYLYDIIVKALPSGVHVAVMDCCHSGTVLDPYVFKANGEYRME
IEDKDFDNKIFRIFGGGKMGAMMTKVMGKMAKGMKQFLR

>Npunctata2 CAMPEP_0199330992

MESRINDAIPAKFVMIISGSEDKQTSADVNVVGSFQLPDPAGKAGGACTSTLLKVLHDNGNRPMWIDLLHK
MRDVLRLQKGYDQIPQLSSSRMIDVSHKFEIVPTETIERNGARRAILIGINIVGQKQKQLSGCHNDANNIKNY

LINNQGFLKEDMLIILMDDGRHHQPTRANIMNAFDRIVQYSKAGDVVFIHYSGHGGRVVDTSGDEADGYDET
LIPVDFQRAGQIVDDDLKHLVKRMPAGVHVTVLMDCCSHGTALDLPYEIDATQSKMSFNKGFNMGLLDDP
GAMCCLAICAACLFDDIIGGIMSGLAD

>Npunctata3 CAMPEP_0199330036
MEDAIEQAKKTIPAEIHMISGCRDEQTSADVSNVNSFQLPDPAGRAGGALTSALLNVTYKDEEDTGKDLFS
QETLLRVRDQLKKGFSQIPQLSSSRPMDISKKFDIVPDNMHGTRRAVMIGINYVGDNPGEIRGCHHDVFN
MKKYIMDVHGFQEENITVLMDDGEHIPPTRENILGAYRKIVAESESGDVVFCCHYSGHGGKLRDDNGDEEDG
FDETLVPRDYQTAGQIRDDALYDTLVAPMKAGVFATFVMDCCSHGTVDLDPFNFDVADGEQEEMKLEQGFDF
SPLLAFAAAYMASQQAGDDPVSGLLSACGACLIQ

>Npunctata4 CAMPEP_0199338742
LPSPAGRSGGACTCALLSILYDAEQNKKPIITFQKVLLELRRRLSESGMTQIPQLTGSRPLDLHETPFVFN
PRENSINTRRALLVGINYFGQNGQLSGCINDVNNVKKYLCQYEGYLEKNILVLTDDGRNPHNPTREKIIRA
LRQLVAQSVSGDSVYFHYSGHGGLLDPDYWNRFKAGKHLKEYDETLYPVDHERAGQIRDFSLFNHFVKPMS
AGVTVTVMDCCHSGSVLDLPYSYRPT SAGTIRMQRSMDTLTNLAFILYILAGGMLPHHGGLFDSVTQNLQD
VTGVSVDLGLTGVVEEMTFDVEGLGDYGDHMIQDNGGSPDITVDALDNQYQGDRAFDFEQGDVPDVGIG
HTFSRNFVIGESGFVSDTGGDGSDLNGTDDVDCGENDIDCADCGDIGDILGNILEDL

>Npunctata6 CAMPEP_0199343924
MGRFLRKLRRERRRRRIGNQEEAQRAFEEEEKPDAMRKDVIRMI SGCEDKQTSADVSNVHSFQLPDPAGRAGG
ACTSTLLRILYKDETIIPEDTLSFTQVLEKMRDLAEQGYTQIPQLTANNPIDVEADFDLVPSTATGTRRAV
MIGINYIGDDPGEIRGCHNDVFNMKKYIMEVHGFEEEDNIVVLMDDGEHDPPTRDNIIAAYEKVVADSEAGD
AIFLHYSGHGKLRDDDDGDEDDGYDEALVPRDYNEAGMIRDDDLIDILIKPLADGVMVSLMDCCHSGTVL
DLPYIFKADGGATPNVMQLDDTIDLGLIQQFGGHAIGFLKNFLEQQG

>Palata1 CAMPEP_0200176934
LERDELISGVIRAAPKNDAAANIADAVYALWSSWDVDGDGRISVDEFRCRKGGLGEEIVRNLNLEVNDKGDTR
VNFYGPFAVNPFAHNLQPYTNTASTAASQQAVPSQPATWNCLACTFIXFIESNILQPCVFFLLKDVNKHNO
CFPLILSLLCLGHSHVNSILGVCTTDVPTAVPSQPATWNCLACTFINLSSQTSCKACGTPQVTTPTIHA
FSPSAISQPYPHGSSQVPSSPHAGHKTFRVKVPPGMKPGQKVKVSTGPTTSDAVVVIIPRHAWSNNDHNSN
GRWEPSTFEVTVTMGDNQENIYQSPNATNHTYTHHSPNHTANHTNHTYTNHSTNHTSHIPNRINNSYHHIP
ERFHDGRYSGDVPWMPFHQFQSQKYKPPPTKMI STPLTSNHSPINASGRRKALLIGINYTNTRASLRGCV
NDAMKIKGLLVENGFTDDAAHMTLLIDETPEPHAGGGGAVSSYLPTKANIVKGLQWLVSGRKGDVLFHFH
SGHGAQVPDATGQEADGLNETILPLDYQKAGMISDDTIWGSVMYPLAEGVRLTALMDCCHSGTGLDLPFEC
QLKRNLSVNNNTDYQWVEDINPAHSRGDVVLLSGCEDAQT SADAFDRHRKEAGGAMTTAFIDAYRAHPAGS
TYPEILNSISEQLRRKNFAQRPLTTSQRFDVRRRIFSLVEGIEPNGNAQIGRLKRRHFKPAKNVTAIDPR
LNELLFGGALAIGLASILFD

>Palata2 CAMPEP_0200175712
MTEITPYDYDVVTPGTADERDYIGETYQQSDVISYWHGLGRGGNTDDVSSLNSEGIQEYINGALIIISILL
LIFIVIWGGIIIFLRIYDDCIPGKIKFLSGWRFENTSSTSLMPFIIRITFIFCAICVYIFTMIYVQKGIHG
FEDATKIAQAQNTFRFRDVEEADRVTITMLANGEEASGLKDRIKRDI PYLCPKRNISNLGTDLFLTLNKYT
NSLDQLGDFYIDQRWKPAEMWVERLLNITVKFDDTIDEINLPLFAIHWIPLIVLTTILLIATLLSIYDNGR
EDLKIRLAPWFQWCLKKIVFPLFTLWSIGTFFLAAAVAFGLVVNSDL CAGGPGAGSPDFPFMRLVDSSGLE
GTRTGGAVYKFIKYSRGC DKRFRDKGSTFYEGNLTRALSQTEYITDFILDKGTIEMSDDCGNDVTGLMVA
LDELTRHMQLKVGTKRIRDVLRCKRLNNIYTELFYNGLCYHSVNALAWSYCSLLAIGFFSMLMVTLRSSI
LPSYEYSWSEEFDIDGDNVSDDQTMEEEDSYELESNTMAFPAIVRMI SGCQDSQTSADVSNVASFSLPDPAG
RAGGACTSALLKVLVSLIDSSCEISWEDLLIKMRENLNDDGYKQIPQLTSSRPTDLKSNFELVPSDGSATG
AKRALLIAINYVGQKGEELTGCINDALNMKKYIMDVWGFEEENITMIMDDGEHMEPTRENILNAYNDLVIQS
EAGDSIFCHYSGHGGKLRDDNGDEEDGYDETLPVDYARSGQIRDDDLYEILVGCMPRGVYMTCLMDCCHS
GTVLDLPYKVFVAPERRR

>Palata3 CAMPEP_0200178272
MSPSTLCCRKNFAVADTENAIRSTVRMISGCMDSQTSADVSNVSQFQLPDPAGRAGGACTSAFLRVMYNE
QQRPSYDLTFAEVLGMGRDVLNNGSYSQIPQLTSSHALDINEPFQLHSLTSFRGKHKALLIGINYVQSGE
LSGCHNDVWNIRSYLIDVHGFEEERYITILMDDGSHTSPTRENIMSAFRMLVKSSVGGDSAFCHYSGHGGKI

RDNNNDES DGYDETLVPLDHYASGQIRDDDVYDALVGPMPNSVTLTCLMDCCHSGTVL DLPYKFKPDNTAT
DKMVLDPNFDNAKLVRFARKLFLGLATETG IKRNDTFVDKEGQLWRKAEDGEPLPFKLYKHQLIQRDIEEHN
NENI IKKIEDMG IKVYIVSHNSSDLLQCIDDDVAEEVSNFSIKTNGRKRCCFLILTEEGRLYNLALGGNVGK
TINGLAGQWEALLNSFSGLEATIAIAVLARSFGCAEVGKGYELRPGYLSLILGYILSEEMGLSWQNVAMFV
RGIPRISQLNPWIYPE

>Palata4 CAMPEP_0200144054

MGLFSRLREKLESLDDEKVVIKADV RMI SGCMDAQT SADVSNVDDFQLPDPAGKPGGACTSALLKVLYDEE
KTPTDDLTFSEVLEQMRTVLDEEYEQIPQLSSSHALDVSTPFTVVGEGTKRALLIGINYGQNGELSGCH
NDALRIKKYLM DVYGYEEENFTYLM DNGVYDDPTYDNILAAFDDIVAKSEAGDSV FVHYSGHGGFLADDSC
DEEDGKDETLIPVNYTEAGQIRDDTVFNRLVLPMAADDVTLTCLMDCCHSGTIL DLPYKFKAGMGESVMSLQ
PGFRFDNFFRKIGLSDEE

>Palata5 CAMPEP_0200147548

MSAFGEQAQKVIPSEFRMISGCHDAQT SADVSNVGAFLPNPCGKAGGACTAALLKVLYEMNERRETWSWV
DVL RKMRTNLDGMGYEQVPQLTSSRMISVTD SMEIVPATQQGVRRAVLIGINYGQSGELSGCHNDVFNVK
DYLNVNLGFENRHITLLDDGLNTSPTRENITYAYRDLVNR SAPGDVAFCHYSGHGGFVDDTSGDEEDGRD
ETLIPVDFQSAGQITDDELLKDLVHPMKAGVLTCLMDCCHSGTVMDL PYRFTADGDNIQMREN PSSNMLE
YGDLIATFAGAYALTGLLGAGGGMGGMGGSPNNTGEEEEAD CCTCIMDLVNSFL

>Palata6 CAMPEP_0200160162

MSSTLEQAKEYIPANVRMISGCKDSQTSADVSNVASFSLPDPAGRAGGACTAAMLKTYLNDEEDRGVDLSF
QDTLLQMRKVL DQGSYTQIPQLSSSRKLDIHTKFDLVPDDGFEGTKRAVMIGINYGQSGELAGCHNDVGN
MKRYIQKVHGFTDEHMTVLMDDGQHEEPTYGNIMAAFRQLVENTKEGDAV FVHYSGHGGKLRDDDGDEADG
YDETLVPLDYQEAGQIRDDDFSTLIGPMPRNVMTVMDCCHSGTVL DLPYSFVADGSQDEMTETPGDFD
GTLIKLQSFQNGGGGGISPEVMQGIQKIASKCFMSF

>Paustralis1 CAMPEP_0199647600

MPLRLNRKDRSGRENAAAVSQONNPSHSKNAATSKNNFDEQVEYLIP AQVRMISGCHSLET SADVSNIIHSI
AGKGLPSPEGRAGGACTTALLSILYDAQKRKNDNHYSGDGSTTFQQLLELRRRLAQTGMSQVSQLTSSR
PLELEETPFSLRSIPATNQQQQQQQHG GGGTQRALLVGINYYGQRGQLSGCINDVNLVKKYLCNYQGFLE
KHVLLIIDDGRNHHPTRDNIIRALQRLVKQSKPGDSVYFHYSGHGGLDPNYWNR YKAGVSNKKYDETLYP
VDHLKAGQIRDFNLFNFVKPMAAGVTVTCVMDCCHSGSVLDL PYSYRPTSDGTIRMRQSMDSL TNLAFLY
ILAGGMLPDLGFESIAQNL ENATGETMDNLQIGIVEELSSDIGGYTNDYTNDGDVVTGATCDNTDLTGIAG
DDRDICSSNGDFAYEGDEITGEDITYDIDSGGFVDVGGTNLGG AQDGF LADDYNPDGCEGNECDGCDVIG
EILNTLFEDS

>Paustralis2 CAMPEP_0199652308

MDAKIESAIPANFVMISGCEKQTSADVGNVSTFALPDPQKAGGACTSLLKVLNENQGGSMSWIDLLHR
MRSVLKSKGFDQVPQLCSSRMIDVNNQFEIVPEEAQGCRRAVLIGINYE GQQGELSGCHNDVKNINKFLRK
EQGFHQSDMMILMDDGSSTPPTRRNIMDAFDQVVQNSTAGDVVFIHYSGHGGNVPDESGDEEDGYDETLIP
VDFQSAGQIIDDELYERLVTKMPAGVTVVVLMDCCHSGTALDLPYQINATQSQMSLSEGFNFSLLDNAAGV
IGCCLCLMSILDMVM

>Paustralis3 CAMNT_0045498567

FQKLIPTYMGRFFKFTQHVQNQVKAAMGDQSDAQAAFEDQKPD SMRNKDVRMISGCEDAQT SADVSNVAN
FCLPDPAGRAGGACTSTLLNILYKDDQVPEDTLSFTQVLEQMRSDLGSGGYSQIPQLTSLNKIDVETDFEL
VPSTATGVRRAVMIGINYGVHSPGELRGCHNDVNLMMKKYIMDVHGFEEENIVILMDDGIHESPTKENMVA
YKQIVADSEEGDAIFLHYSGHGTKLVDKSGDEDDGYDEALVPLDFQEVGMIMDDDLFDIL IAPLQDGVH MV
SLMDCCHSGTILDLPYIFKPNQDGSMP LGMMLDESIDL DGLLQFQGGQAVGILLNFMQKACC

>Pfradulenta1 CAMPEP_0199827318

MGRFFKFRQNI REKIEEAIGDAIGADGGGFIGNQEEA QNEFEDKKPDSMRGKDIRMISGCEDSQT SADVF
NVVDFQLPDPAGRAGGACTSALLRILYKDEHIPEDTLSFTQVLELMREDLSEEGYRQIPQLTSLNKIDVET
DFELVPHTATGVRRAVMIGINYGQD GELRGCHNDVNLMMKYLMDVHGFEEENIVILMDDGVHDEPTREN
IEAYQQIVDESEDGDAVFLHYSGHGTKLVDGSGDEEDGYDEALVPLDYDEAGMLLDDDLFEILIEPLAEGV
HMVSLMDCCHSGTILDLPYIFKPNDDGSM PHAMKLD DDTINLDGLVEQFQGGQALGLLVNFVAESF

>Pfradulenta2 CAMPEP_0199811974
MDAKMRNAIPARFVMI SGSEDKQTSADVGNVGTFSLPDPAGKAGGACTSTLLKVLNENGGQPMSWIDLLQK
MRSVLKYKGFQDQIPQLSSSRVIDVNNQFEIVPESSGGRRAVLI GINYEQQGELSGCHNDVNLKKNYLVR
EEGFQEQDMI ILMDDGQHNL PTRKNILDAFDRIVQYSKAGDVVFIHYSGHGGRVYDSSGDEADGYDETLIP
LDYQSAGQIVDDDLRQLVTRMPEGVTVVVLMDCCHSGTALDLPYEINATESEMRTNPGFNMALLDAGAVV
SCCLCLNVLFELLASLDGGDGGDRGRDRYDSGE

>Pfradulenta3 CAMPEP_0199786516
MPSLFNRKNRHGGGLGSDNFDATTTGTDNDFDQVRQLIPAEVIMISGCHSLETSADVSNVKTIDGHLPSF
EGRAGGACTTALLSILYESLKTTRNNSPREISFQQLLLRLRGRLAQSGMSQIPQLTSSRPLELEERPFSL
KSNPNNGGTRRALLVGINYYGQSGQLSGCINDVLNVKYLKCNHHGFLEKHVLLLI DDGRNHKPTRENIIRA
LRLVVEHSKAGDSVYFHYSGHGGLDPDYWNRYKAGKKDKQYDETLYPVDHARTGQIRDFSLFNHFVKPMT
AGVTVTCVMDCCSHSGSVLDLPYSYRPTEDGTIRMQRMSDSLTLNLSFLYILAGGMLPDFGFESIAENLQSAT
GEAMDALQGTGVEEFSSDLGGINGYGLGNGDDVDDAMNYTSGLETGNVDTGFDDSNVDYGGNGVDDFDLQ
NTDIAENAYGDGRGDAFFGAFRDITYFADETVDGADCGDVNCGDADCNDGCDVVGAILGALMDSDS

>Pfradulenta4 CAMNT_0045629199
RQQQQQKQQQQQVLRRTDQONT SRLSGKRLSCGTLANKKATKATTRTTQHSHTRHEIQATIGANKQ
TNMFGKLGKQYAAQVAEKVEAFALEKLNERNPQSTVTEETTEKLKLSISGNRKALFIGINYGQRGELKGCV
NDVNIKKFFRTHYTLNDTLVLTDDKRAEPETDHAPTRKNILNAFKWLKVGAKPGDLLLLHYSGHGGKSKN
HDGTEASGFQDTLIPVDYKAGQILDDDVHDLCKSLPKGVRLTAIFDCCHSESIMDLPFVYVNGNLEIV
ENDRNQS IATIMATGTRFLLDGNRKKAGQALKNEITSMLSVMAGGQDPAQEARKKVIASNQTKADIIMF
SGCKDMQTSADTSQQGEAGGAMS FALIKTLEKHHRDKDLTYTELLREMRQVLEGGYTPVQLSA
GRRLLVDHPPFRV

>Sdohrnii1 CAMPEP_0192149910
XISGCHDAQTSADANITSFQLPNPAGRAGGACTAALLQVLYDRPSIAAGNDNTSWVQVLRMRRENLEQGF
EQVPQLSSSRIIDVNERMTIVNDNPSGVKRAVLI GINIVGQQGELSGCHNDVKNISSYLQVQGFQNM
TLMDDGVHDNPTYDRILQAFQVWVNESQAGDTVWIHYSGHGGRVEDDNGDEDDGYDETLIPVDFQRKQIR
DDDLLRRLVVKPMREGVLMTCMLDCCHSGTVLDPYRFIADGDHYQMERNDDFDMDHLEIVAKIAATVAASL
GGMAQSVIQSSGLVEEIDECCVIL

>Sdohrnii2 CAMPEP_0192135274
MGFFNKLKEAALKEAKKIMEELGLGGDDDETKPTMTTEEFKTKPDEL RKDIRMISGCQDRQTSADVSNV
SSFQLPDPAGKAGGACTSTLLNILYADEHVPEDDLSFVEVLEEMRIKLSGGYSQIPQLSSMNPIDVNTKF
DLVPDTATGTRRAVMIGINYGDDPGELSGCWNVDVLMKKYIIDVHGFEENIVILMDDGIHTEPTKANI
DAYKTI IAQAEENDAI FLHYSGHGTCLRDDGDGSDGYDEALVPRDFQTSGMIRDDDL YELLFKNLPDGVH
MTSLFDCCHSGTILDLPYLFKGDGSQTEMTLDPNMNLDAFIEKLTGKLMEFLQAKMAASLSL

>Sdohrnii3 CAMPEP_0192159136
RGKPPPPRRQSSSTAGQSKKADATIKRSSSTREARPVKSNANSKSSRRDSQSRKSRPRDDSRNSKPRD
KRSRSKSRPRSSPRNNENDTQQRSSKSSSSRSKPPQSKGNRSKSSPRSGTLHGKRSSSSSNKGNKAQA
ESFNAKKRQKQFASQAKKAIPTNVRMISGSHDAQTSADVGNINAQFELPNPAGRAGGACTAALLQVLYDAH
DRGDINMSWVDALREMREILHEKGFQDIPQLSSSRMIDVCDPFFVITPESFDPGFNKRRAVLI GINYGQKQ
QLSGCHNDVHNVTQYLKEVQGFKDENITILMDDGMHKPPTKSAIISAFKRLVKQTKEGDVVFCCHYSGHGGR
LPDDNGDEDDGYDETLIPLDFQKSGHIRDDDLKILIHMPAKVTMTCLMDSCHSGTVLDPYRFVGDGDH
VEMEMNDRVNFTEALWTGLSVAAGVVAGNAIADAVNVAPEMMILGGPNAIHEHX

>Smarinoi1 CAMPEP_0192232734
MGFFNKLKEAALKEAKKIMEELGLGGDDDETKPTMTTEEFERTKPDEL RKDIRMISGCQDRQTSADVSNV
ASFQLPDPAGEAGGACTSTLLNILYADEQVPEDDLSFVEVLEEMRIKLSGGYSQIPQLSSMNPIDVNSKF
DLVPDTATGTRRAVMIGINYGDDPGELSGCWNVDVLMKKYIQDVHGFEENIVILMDDGIHTEPTKANI
DAYKTI IAQAEENDAI FLHYSGHGTCLSDDDGDGSDGYDEALVPRDFQTNMIRDDDL YELLLKNLPDGVH
MTSLMDCCHSGTILDLPYLFKGDGSQTEMTLDPNMNLDAFIEKLTGKLMEFLQAKMAASLSL

>Smarinoi2 CAMPEP_0192224422

XQIPSEVRMISGCHDAQTSADANITSFQLPNPAGRAGGACTAALLQVLYDRPSIAAGNDNTSWVEVLRRMR
ENLDEQGFQVLPQLSSSRIIDVNERMTIVNDNPSGVKRAVLVGINYVGGQGELSGCHNDVKNISSYLQVQV
GFRPQNMITLMDGVDNPTYDRILQAFQWVVNESQAGDTVWIHYSGHGGRVEDDNGDEDDGYDETLIPVD
FQRKGQIRDDDLLRYLVKPMREAVLMTCLMDCCHSGTVLDDLPRFIADGDHYQMERNDFFDMDHLIEVAKI
AATVAASLGGMAQSVIQSSGLVEEIDECCVIL

>Smarinoi3 CAMNT_0036352755
PRSSPRNNENDTQQGRSKSKSSSSRIKPPQSKGTRSKSSPRSGTPHGKSSSSSSSNKGNKAQAESFNAKKR
QQKFASQAKKAIPTNIRMISGSHDMQTSADVGNINAQFELPNPAGRAGGACTAALLQVLYDAHDRGDVNMS
WVDALREMREILHEKGFQDQIPQLSSSRMIDVCDPFVITPESFDPGFNKQRAVLIGINYKGGKQGLSGCHND
VHNVTQYLKEVQGFKDENITILMDGDMHKPPTKSAIIISAFKRLVKQTKEGDVVFCQYSGHGGRLPDDNGDE
DDGYDETLIPLDFQKSGHIRDDDLLKILIHMPMPAKVTMTCLMDSCHSGTVLDDLPRFVGDGDHVEMEMNDR
VNFTEALWTGLSVAAGVVAGNAIADAVNVAPEMMILGGGPNAIHEHSDTACCAVS

>Smenzeli1 CAMPEP_0192261006
XRCRLNIYQGEKDDSPATASSYTCIPLQCRRRGDHQAEESIRRLHHPGSLKTQVKAGLIQHSRDPHQREE
RQDQPSLMLTTKPEDEIEVGANPDQEMIIIVTQNRGTSLDPGANRDPDPLEKIMNTIHKRDGGANQNLLR
PGANTXAKSNRSKSNPRSSAPQAKSSSSSKGNKAQAESFNAKKRQQKFASQAKKAIIPANVRMISGSNDVQT
SADVGNINSQFELPNPAGRAGGACTAAILQVLYDANDRGDVMDSWVDALREMREILHEKGFQDQIPQLTSSS
MINVSDPFDITPQSFDPNLKQRALLIGINYKGGTQGLSGCHNDVHNVSQYLOEVQGFKEDNITMLMDGDM
HKPPTKSAIIISAFKRLVKQTKEGDVVFFHYSGHGGRLPDDNGDEDDGFDETLIPLDFKKSQIRDDDLLKI
LVHPMPANVSMTCLMDCCHSGTVLDDLPRFVGDGDHVEMEINDRVNFTEALWTGLSVAAGVVAGNATADVA
PEMMILGGGPNAIHEYS

>Smenzeli2 CAMPEP_0192280530
MGFFNKLKEAAVKEAKKIMEELGLGDEKDDDTKPTMTTEEFENTKPELTKDIRMISGCQDCQTSADVSN
VSSFQLPDPAGRAGGACTSTLLNIIYADEHVPDDLLSFTFVLEQMRVKLRRGGYSQIPQLSSMNPIDVSTK
FDLVPDTATGTKRAVMIGINYVGDSPGELSGCWNVDVLMKKYIQDVHGFEEENIVILMDGDNHTEPTKANI
IDAYKTIIGQAEENDAIIFLHYSGHGTCLRNDNGDEGDGYDEALVPRDFQTSGMILDDDLIYDLIKDLDPGV
HMTCLMDCCHSGTMDLPLFKGDSQTEMILDPNMNLDAFIEKLTGKLMLEYLQAKMAASLSL

>Smenzeli3 CAMNT_0036412763
ADCSDIVAEPIKQYSVLSRNKMPSFAEKVASQIPSEVRMISGCHDAQTSADANITTFQLPNPAGRAGGAC
TAALLQVLYDRPSIASANDNTSWVEVLRRMRGNLEQQGFQVLPQLSSSRIIDVNEPMTIVNDNPSGVKRAV
LIGINYVGGQGELAGCHNDVKNISKYLQVQVGFQVQNIITLMDGIDHNPTYDKIMQAFQWVVNESQAGDT
VWILYSGHGGRVDDNGDEDDGYDETLIPIDFQRKGQIRDDDLLRYLVKPMRQGVLMTCMLDCCHSGTVLD
LPRFIADGDHYKMERNDFFDMDHLIAVAQMAAAVASSFDVGSVGRMAQSVIQSTGLVEEIDECCVIL

>Skcos11238
QTQYQTANNGSSYATQQQQHHTSYVTQPMPTSAVXPTTSTQPLQPPVATAYASGGGGTSAPPVVATAYV
PSSTNATTASSATAAPILATAYIPANELDDGHTRPSAPPMPNSYNPNYSATTGNNNFHTHQDEFWECSVCT
FPNRQSETHCKGCGNAQPGGNSSSYNSKPQAPSAVQSSAAPSYSYTMNDINSHMASISLGTGTYPNGINMMS
SSAPPPSSTSGTMKVHIPAGMRSGQKLVKVRSPAGDEVVKTIPNQSEWSYEIDGRPYFRLQFGPSQTAAAST
ASPAMSAASTMKVHIPNGMGXPQXIKVRSPTGSEVVKTIPNQSEWSYEIDGRXFFRMAFGDEXNATNYSYS
TTLSTPPPHSTTWREFHTRASSRYNPPPIGMKPVQHVPRGVSSITPNGRHKSLLIGINYTGTRAAALRGC
NDAKNMQTLLKNGFPNDGSHMLMLTDERHRGSEYQPNASNIMKAMSWMKDAQKGDVLFHFGHGGQV
DKTGHEADGFNETLIPLDHTRAGQISDDVWLGSLVYNLPEGARLTALMDMCHSGTGLDLPYDYNVNTTRWT
EDVNPASRSGDVVLFSGCEDSQTSADVQYSGXGGAMTLAFTKAYQCCSSSTYHEFLSVVXKXELRKKRHSQ
RPQLTSSQQFDASSRIIFSLGHDNGGITSMIEPNHNPQVGRQKRRHVRPARQGFGRAGGGNDLFLGLGIAAVG
AALFADALF

>Skcos12022
GVEVLRRMRENLDEQGFQXPQLSSSRIIDVNERMTIVNDNPSGVKRAVLXGINYVGGQGELSGCHIDVKN
ISSYLQVQVGFQV*NMITLMDGVDNPTYDRILQAFQWVVNESXAGDTVWIHYSGHGGRVEDDNGDEDDG
YDETLIPVDFQRKGQIRDDDLLRYLVKPMREGLLMTCLMDCCHSGTVLDDLPRFIADGDHYQMERNDFFDM
DHLIEVAKIAATVTASLGGMAQSVIQSSGLVEEIDECCVIL

>Skcos13618
GELWRRNFAINATVHKSSKFTVMSAKNNDLEEEYEVEKVVVDHRYRKTAFPDGSHDEYLKWKGYPSSENTWE
PESNLNPSALAEARTLKWTTTEQFENTKSDELKDXLCISACNDXATAADVHNKXFKLPDAAGKFGGGGG
GACSSLLSILYADEKVLLEEDLSFKEI IWKMRKTLIKDPYRQIPQMSMNPXDVNTKFDLFPDTATGTKRA
VMIGVNYVGDENELSGSHNDVLMKRYI IQEVRGFEEENIVILMDDGKHTNPTKKNIIHACKKVIRQAEE
NDAILFLYSGHGTRVEDDNGDERDGFDEAIVPRDFEENGFI LDDDLYEILIKDL PKGVSMFSLFDCCHSAT
IMDLPYLFKGDDEMOTEMTLDPKFNLDAFIEKITGNLKEFVQAKMAAKQKKAAGSKRKKVPEPSKEKKKKL
EQEHE

>Skcos16234
SRGKPPPPPPRRQSSSAAGQSRKAELTIKSSSSTRGEARSVKSHANSKSRRDNQSRKSRPRDDSRNSKP
RDKSRSRKSRPRSSPRNNENDTQRRSKSKSSSRKPPQSKGTRSKSSPRSGTPHGKSSSSSSSNKGNK
AQAESFNAAKRQKQFASQAKKAIPTNIRMISGSHDMQTSADVGNINAQFELPNPAGRAGGACTAALLQVLY
DAHDRGDVNMSWVDALREMREILHEKGFQDQIPQLSSSRMIDVCDPFVITPESFDPGFNKQRAVLIGINYKG
QKXLSGCHNDVHNVTXYLKEVQGFKDENITILMDDGMHKPPTKXAIISAFKRLVKQTKEGDVVFCQYSGH
GGRXPDDNGDEDXGYDETLIPLDFQKSGHIRDDLLKILIHMPAKVTMTCLMDSCHSGTVLDPYRFVGD
GDHVEMEMNDRVNFTEALWTGLSVAAGVVAGNAIADAVNVAPEMMILGGG

>Skcos4616
LAKMGNQESVPSVPGDEEIPMDASPQVGKHSKSLHSPQYMEGVPEPNKSSNRSKSKDKRSSRERPERGE
AREDENRDSVEQHNNKRI SPASTDPSMSYANNFATLPPRGNKRITDDQVHLDLPMAELMAYLQMVANHS
SNLPLTRRDDPDLGRTVSSLTAD EYAFKCAAFIPSKIRILGGQFGKYGKVWDLPTSEEFNAKSSSTREPGIS
YGGACSNALLKAIYDTESEINNVASPHMVDAANLFEDDDQTVNTAGFSIDQNSKSFDKLSFDDSNATSLT
WAQLLHKMKGEMHGMGFNVPAITSSYKFDLNKPFSLVPEFKVGVNKKRTLLIGCNRYKTRDAQLKACHD
DVTSIKDFLVN VYGFPEPDLMTILMDDKHKSPHKNITEAFKRLAEQSQPGDAVFVLTGHGCRIMDSP
IDATAESYDEALLPSDYEESGIIRD TLMFKTLFAPMKKGVTVTCIMDCAHTGVMIDL PYLWTSKDSKKEEQ
QAKMSLNDFSFVRFLKVVKTLYESSVFTRIGKTVGAELAKQLSAADDETAVD SVASLETMPENDINDKDN
AGILCSI AKLITCQPDEYSDEEHFDDTGSYDSR

>Tnitschioides1 CAMPEP_0200188848
MGRFFKKIFGSSGAGSKISDQQQARDAFEEQKPAGLRKDIRMISGCEDAQTSADVSNVASFALPDPAGRAG
GACTSTLLRILYKDDTVPEDDLSYTVLTVQMRDDLAAQGFQIPQLTASNPIDVNTDFDLVPATATGTRRA
VMVGINYVGHNPGE LRGCHNDVLMKRYI IAVHGFEEENIHVLMDDGEHEEPTRANLIAAYEKIVAETESG
DAIFLHYSGHGTKLRDDDGDEDDGYDEALVPLDFKETGMIRDDDLFDIVCKPLADGAHMVSLMDCCHSGTI
LDLPYIFKADGSSTQMQLDDSIDLDGLLQQFGGAAISFLQNFLG

>Tnitschioides2 CAMPEP_0200208386
MSDFDAQVQKLIPAEVNMI S GSHDSQTSADVYNVSQFQLPDPKGRAGGACTSAVLKVLYNDSQEPSEQLTW
VTLLRRMRSVLSMGMFQDQIPQLTSSRMIDVNKPMYIVPPNANGMKRAILIGINYTGQRGQLSGCHNDVDNI
SEYLQKVHGF EATNMLRLVDNGVDHAPTHANIMSAFSRIGDYSKAGDVVFLHYSGHGSRVPDRDGEDDDGY
DETLPVDFERSGQIVDDDI LRKLVKPLAAGVTMTCLMDCCHSGTVLDPYRFADGDVW

>Tnitschioides3 CAMPEP_0200209970
MGDLLEKAKRAIPADVRMYSGCRDEQTSADVSNVTSFSLPDPQGRAGGACTATMLQILYADEKKLEEDLTF
QEVLLKMRDVLKEKGFQIPQLSASRPIDIKEKFDLVPDNIAGTKRAVMIGIN YVGDNPGE LRGCHNDVFN
MKKYIQDVHGFEDENITILMDDGNHTVPTRENILAAYSKIVEESQPGDAVFCHYSGHGKLDKDDNGDEADG
YDETLVPVDYKTAGQIRDDLLYKNLVGGFKEGVFCTFVMDCCCHSGSVLDFPFQFQADGESDSMEAPADDFD
GPLLSLAASLAGGQNI GTDPGKLLAMCGSCIVS

>Tnitschioides4 CAMNT_0046182537
ALPYNPHYQPSPTAVQPVT AQPVMAQPVAAQSFNAQSVTTPQPVMAQPVTAQSFNAQSVTTPLPVMAHPIT
AQPSNAHSVTTPLPVM AHPVTAQPVGGQPAIAQPVMAQPVMAQPVMAQPVMAQPMSTQQQPVVAQAFVPPQYQQPQ
LVAPVPAQVYNPYAVPSLPPPSLNTSAWFDYD KDRSGSLKSEIMQGLLYTFGAKTPNEQYSLQGTVDS
IWSIFDTRNGTLDKREFCAPGGFGESLQAAMASNGKATATTPHQPVVSSTGNSWTCTKCTFANSMADSYC
KMCQAIRVGGGGATNNAIAPAPGVYVANSSSAAATTIYGGAATNNTITSVPGVYVPGSSAAAATTTTNSWN
CTKCTFANATSQSHCRMCQFPRNGTTMNASAPVNTKIRVGI PQDSSPGQRIKIQT PAGKSEIAIIPRSEW
VFLNTGQPAFDYSIATTSTTTTASAVSVPAPTNTTIRVGI PQGTNAGQRIKIKTPAGGSEIVTVPQSQW

YLNTGQAAFDYELPTATSASAVHVQSSSQHPWQEQITKSSYQSPAPLGVMTVPISIGSMIQPSGRRA
LLIGINYTGTRAAALRGCINDAKNMRNVLIRKHAFPGDTCHEMMLTDEPSRGRNYQPTYSNIRRLQWLLQG
VSQGDVLFHFHSGHGAQVPDKTGHEADGLNETILPLDYENKQITDDELWGSIVYPLPAGARLTALMDCCHS
GTGLDLPFEMYKQNKHNKYNQSSWMEDLNPAHSQGDVVLISGCKDDQTSADAFQQGTAGGAMTQAFLTAY
EQHPYCTYPELLQAIHQALKQRRFTQRPQLTASQPFNTQERIFSLVEGIEPNHQSSIGRLKKKHIRPGRGT
GGGGGNAGNMLLGAAGIFGALALGDALFDF

>Tantarctica1 CAMPEP_0200089382

MSYQDNIDAEIPAEVRMLSGCHDTQTSADANITTFELPDPAGRRGGACTAALLQVLYNDNDGDPQDCSDQS
WVEVLRAMRNNLAAEGFTQVPQLSSSRMIEINDPMQIVNNPQGTKRAVLIGINYVGHDPGELSGCHNDVAN
ISKYLGKGLGFEQDNMMVLMDDHRHEEPTYRNIMRAFWDWIVSESQPGDTVWIHYSGHGGRLDQDGEDDG
YDETLCPIDFQTAGQIRDDLLKHLVKPMKGVLMTCMLDCCCHSGTVLDPYNFIADGEHAGMERNENFDL
GNVMGMLGAVAGAAMASGAVGEIADECCVIL

>Tantarctica2 CAMPEP_0200100074

MGGFNNIKAAAIEKVKEEIFASLGLDGGDDGDGGQMTTEQFEKSKPDELKRDIRMISGCQDKQTSADVSN
VSSFQLPDPAGNAGGACTSTLLKILYADEQVPEEDLSFTEVLEQMREHLSTEGYTQIPQLSSMNPIDVNHK
FDLVPDTATGTRRAVMIGINYVGDSPGELSGCWNVDVLMKNYIMDVHGFEEENIVILMDDGENIEPNYENI
IDAYKAVVSQSEDGDAIFLHYSHGHTKLRDDNNEEADGYDEALCPRDFQSSGMIRDDDLYEILVKELRDGV
HMTSLMDCCHSGSIMDLPYIFKGDGSQTEMILDPENMMDAFIEQITGKLMFLMCKLGL

>Tantarctica4 CAMPEP_0200125594

MTEEKRPSKSSSHRSNPPPPRRQNSSGGGKERSKRENNGGDAGRSVGTKSMATKASVRSRSTHETN
HTNRSSRSKSRPRESPGKSRSRKSRPREAPRESRSTLDIKSKPSDEKSRSRKSRPRQSSSKSQPDDTR
SSSNKQSKSPKQSKKSPKPKHNSNTTKSKSHNNGNGTRSSLKQPSVKKREKFGNFAHKAIIPAAVRMISG
SHDAQTSADVSNISSQFQLPNPAGRSGGACTAALLQVLYQSHEYGKDDISWVDVLRQMRDVLDEKGFQIP
QLTSSRMIDVHDPFAITPTSFSHKNTQRAVLIGINYTGQSGELSGCHNDVHNVAKYLMQVQGFKKENVTI
LMDDGAHKPPTKAGIVNAYKRLVKEKSGEDVAFCHYSHGGRPLPDDNGDEEDGYDETLIPVDYDKKGQIRD
DDLLKILVHPLQEGVTMTCLMDCCHSGTVLDPYRFTSDGDLEEMEINDRTNFKDALWTGMGLGVGMAAGN
AIGNAVVSAVTPDPEMMILGGGPNAIHEYSDTDCCVIS

>Tgravidal1 CAMPEP_0200700714

MSGEKRSSKKKTSVQSIRTHPPPPPPRPNRQSSSSSGIGKEKSKRENGGSGRSVGTKVSSTVRSRSTRE
SSRTNRSTRSKSRTRDAQSSRSRSKSRPRETPREGRSQSGRSTGSRKSKTTGDRSRSRSRARPQDGRSS
PTKQQSKNNSNPKSISSSKSKSQKNGRSRSPKQTSSTKKREKFNASNAQQAIPASVRMISGSHDSQTSADVS
NINSQFQLPNNAGRSGGACTAALLQVLYQSHEYGHDDISWVDVLRQMRDVLNEKGFQIPQLTSSRMIDVQ
DRFAITPVDGFSFSQKNNTKRAVLIGINYTGQKQKELSGCHNDVKNVARYLSEVQGFKKENVTILMDDGNHKP
PTKTAIIISAYKLVKESKKGDDVVFCHYSHGGRPLPDDNGDEEDGYDETLIPVDFEKRQIRDDLLKILVS
PMSEGVTMTCLMDCCHSGTVLDPYRFTSDGDLEEMEMNERCNFKDGLWSGMGLALGMAAGSAVVDVLTTP
PEMMILGGGPNAIHEYSDSDCCVIS

>Tgravida2 CAMPEP_0200710618

MGGFNTLKNQAIAAAKEGMLSSLGVDADGSDGEQMTKSQYEEKSPDELKRDIRMISGCQDKQTSADVSNVE
QFELPDPAGQAGGACTSTLLNILYADEKVPEEDLSFAEVVSTMREQLSEGSYTVQVPQLSSMNPIDLNAKFD
LVPDTATGTRRAVMIGINYVGDVDRPGELSGCHNDVHNMKKYITDVHGFDEENIRILMDDGENEAPTRSNIIA
AYKAVVDEAEEDGDAIFLHYSHGHTKLRDQNGDEADGYDEALCPRDFQAGMIRDDDLYDILVKALPDGVHM
VSLMDCCHSGSIMDLPYIFKGDGSQTEMELDPENMLDAFIEGISEGLVDLFLKSLGL

>Tminiscula1 CAMPEP_0201031444

MSYQDRIDAEIPADVHMISGCHDTQTSADANITQFELPDPAGRRGGACTAALLRVFYNDGDDDPQDFQGGQS
WVDVLRMRRENLAAGFSGVQVPQLSSSRMIDVESPMRILNSPSGTKRAVLIGINYVGHNPGLSGCHNDVRN
ITKYLGKGLGFEFSNMRVLMDDGRHEQPTYRNIMRAFWDWIVNSQPGDTVWIHYSGHGGRLPDQDGEDDG
YDETLCPIDFNTAGQIRDDLLKHLVKPMREGVLMTCMLDCCCHSGTVLDPYNFIADGEHYGMERNENFDL
SNLMDAAMGVAAAAAAGVAGDIVDECCVIL

>Tminiscula2 CAMPEP_0201033658

XAGGACTSAILQVIYKEEQPSCEINTFMDVFLQTRVIVKSNQFEQIPQLSSSRCIDVNPQFDLMTNKGNE
GTRYAVLIGINYTSHRRGRLRGCHNDVHNICKYIMDVGNVEESNITILLDDGTSTPPTRENIMQALDELTO
KCQPGDTAFVHYSGHGGRVKDETGEDPTGFNSTLVPLDFNKRGVGHILDKELYEHLVCAMPSGTSLTCLMD
CCHSGTVLDDL PYNFVADGEQTEMPVKDFPFVKLIMLRQALREAGVERLMDLRDSDKREQVKAAMAEL
LARLGHNFVDRADFACGAKEEWRQERHEAGGNVFGGVYVLCDCNX

>Tminiscula3 CAMPEP_0201021774

XELEGEATNTQYHQSIAPRIVTMGFFNKIKEAAIEKAKQEMLAQLGMSGDDEEGGQOMTTEEFERSKPEL
RKDIRMISGCEDRQTSADVSNVSSFQLPDPAGRAGGACTSTLLKILYADERVPEEDLSFTEVLEQMRHLS
SGGYTQIPQLSSMNPIDVSHKFDLVPDTATGTRAVMIGINIVGDNPGELSGCWNDVLMNKYIMDVHGFE
EDDIVILMDDGHEIEPTAENIINAYKTVVAEAEEGDAIFLHYSGHGTCLKDDDHNEEADGYDEALVPRDYQ
STGMIRDDDLYEILVKGCPDGVHMIISLMDCCHSGTILDLPIYIFKGDGSQTEMILDPENLDSFIEMLTGKL
MDFMMKKLGLGGD

>Tminiscula4 CAMPEP_0201050048

XSWARKGDSRSRNRNHPAKIAVILLRRRDGATAVAAGGREIKEMVRVQWGLATLHPCRDRLERARRRKF
TIAPITIVGAEANPNRENROETALEANLDPEKRINPKTKTEAVAERIAAGTEEGIGRQIRIMTKLTNGETRV
AAVANLDPDNPNLNRKTKVTAMLAXSPQKQSKKPSKHNNNSNTRSNSQRQHRNSGTRSSPAKPKQPSSK
KRQKFADAAQKAI PATVRMISGSHDAQTSADVSNINSQFQLPSPAGKSGGACTAALLQVLYQHYENDEDED
DLSWVDVLRMRNILLDDKGFQIPQLTSSRFIDVRDPFVITPTDGSFNYKHNTQRAVLIGINYTGQSGELS
GCHNDVHNVARYLLEVEQGRKENVITILMDDGMHKAPTSAIILGAYKRLVKSREGDVVFCYSGHGGRLLPD
DNGDEEDGYDETLIPVDYDKKQIRDDDLKILIHMPKGVMTMCLMDCCHSGTVLDDL PIRFTADGDVEEM
EMNERCDFKDALWSGFLAVGMAAGNAVANAASALTPDPPAPEMMILGGGPNAIHEYSDTDCCAIS

>Toceanica1 CAMPEP_0192891684

MGFFSSLKKAACDAKQKIYEELGISQSDAQPSGQMSREDYEANKPELDRKDVRLSGCADHQTSADVSS
VSKFKLPDPAGSAGGACTSTLLKILYADEENPETQLSFTEVLETMREDLKGNRYSQIPQLSSMNPIDVSDT
FDLVPPEATGTRAVMIGINIVGDSPGELSGCWNDVLMNKRYIMQVHGFDEENIVILMDDGHEATPTFRNI
IDAYKIVISQAEEGDSIFLHYSGHGTMMKDDDGDEEDGYDEALCPRDYASAGLIRDDDLIDLKELPDGV
HMFSLMDCCHSGS IMDLPYVFKGGIDSEMHLDPENLDAFIQQISGKLKEYIERRLRERWG

>Toceanica2 CAMPEP_0192912886

XDDGALRTPHGGDDGKVLARAFYDRATDEEXPMSLAICEPYPAENKVKVLYSQKAGCYDVKRSLASQLLSS
YRLTQALSIESFLLTGCRKMPDRQNSRRQKSTSGRRRKEDDAAKQKSTHRRRSSSRKRQPSTSERRSKSR
GRKKTQSRDTRKSARTDVRSRKSKQPRTGVGSKSARTEKTKPDASSRSQKSRSGRNSQGGKRKSSGA
KGRRAVGPNKTPSAKRSSHFAEEANKAIPALVTMISGCHDAQTSADVANLSSQFKLPNPAGKSGGACTAAL
LEVLHCSSSDDEREMSWVDVLRMRIVLNKKGFDQCPQLTCSRMINVKDRFFITPPDFNEVNNTKRAVLIG
INVTGTPGELRGCHNDCLNVARFLREQGRDENVTMLLDDNKHRSPTKAAIILSAYKKLVRESKPGDVVFC
YSGHGGRLLPDDNGDEDDGWDETLIPVDFKTAGQIRDDDLFKFLVHPMPANVTMCLMDCCHSGTVLDDL PIR
FTADGDLDEMQINDRCDFKSALYHGLVLGAGLAVGDVVASTVISGAVNAFTKPSDLDTAGMVLGGGHSMS
DMIVATSFEX

>Toceanica3 CAMPEP_0192912014

MSSFQSRIEEIPADFHMSGCDHQTADVHNISFQLPDPQGRAGGACTAALLQVLYRGDPSQDQSSSW
VDVLRQMRNLAAMGYEQHPQLSSRLIDVNSPMRITNGHGGTRRAVLIGINIVGQQGQLSGCHNDVRNIA
KYLSSMGFQQHNMTILMDDGMHEEPTYRNIMEAFKWIIVQESQPGDTVWIHYSGHGGSVEDDDGDEEDGRDE
TLIPLDFQRAGQIRDDDLKYLKPKMRGVLVTCLMDCCHSGTVLDDL PYNFYADGRQTSMRNEDFDMGHL
MEIAAFGVMTMAMASDLAGMAAGAAGFASAASGGGAEIILDECCVIL

>Trotula1 = throt11193 = GS1 CAMPEP_0192965622

MLRERARAAARQRMDDFVDETFGPPSPQADDRDVEITDDDAPTSDPEFDQRAEEAIPANVRMISGCHDTQT
SADVSNVDTFQLPDAAGMAGGACTSAILQVVYKEEPPSEDLTFMDVFLQTRDVIESKGFQIPQLSSSRC
IDVQPPFDLMSNEYGNEGTRYAVLIGINYTSHRRGRLRGCHNDVHNICKYIMDVGVVEESNITILLDDGEA
TEPTRANIMEALDELCKCEPDDTAFVHYSGHGGRVKDETGDPTGFNSTLCPVDFDQPGVGQILDKELYE
HLVCAMPAGTSLTCLMDCCHSGTVLDDL PYNFIADGEQTEMPNQDFPFLKLLAMRQALREAGVETFRDLFD
EEKREQLKASYDAAYNESMEGLGRDIGGGENFGRAARRERRQRNRRANRRKR

>Trotula2 = throt1069 = GS4 CAMPEP_0192960494
MGGFNTLKNQAI A A A A K E G M L S S L G V D A D G T D G E Q M T K S Q Y E E S K P D E L R K D I R M I S G C Q D K Q T S A D V S N V E
Q F E L P D P A G Q A G G A C T S T L L R I L Y A D E K V P E E D L S F A E V V S T M R E Q L A E G N Y T Q V P Q L S S M N P I D L N A K F D
L V P E S A T G T R R A V M I G I N Y V G D R P G E L S G C H N D V H N M K K Y I M D V H G F E E E N I R T L M D D G E N E A P T R S N I I A
A Y K A V I A E A E E G D A I F L H Y S G H G T K L R D Q N G D E A D G Y D E A L C P R D F Q Q A G M I R D D D L Y D I L V K G L P N G V H M
V S L M D C C H S G S I M D L P Y I F K G D G S Q T E M E L D P E M N L D A F I E C I S G K L V E F L K K S L G L

>Trotula3 = throt10365 = GS3 CAMPEP_0192967966
MSYQDQIASQIPAEVRMLSGCHDTQTSADANITSFELPDPAGRRGGACTAALLQVLYDDRNGDPQDFQGGQS
WVDVLRAMRNNLAAGFSQVPQLSSSRMIEVNDPMTI INEGGGGTKWAVLIGIN YV G Q N G E L S G C H N D V H N
I T K F L T N S Q G F E Q E N M M T L L D D G H H K E P T Y R N I M D A F S W I T R A A Q P G D T V W I H Y S G H G G R V E D Q D G D E D D G
Y D E T L I P V D F Q S A G Q I R D D D L L K Y L V K P M R E G V L M T C L M D C C H S G T V L D L P Y N F I A D G E H L G M E Q N E K F D L
G G L M E V A A G V A A A A A A A G V A D D I I D E C C T I L

>Trotula4 = throt16314 = GS2 CAMPEP_0192949914
FVVPLVVVPPSHHPTATTFSNTNSNTSTANVPPINI IMSGEKRSSKKT SVQSKSIRDNPPPPPPPPRKRQS
SSSSGIGREKSKRENGGSGRSVGT KSIADTKVSKSTVDRHELVSRTAPIAAPAANPEREMP KAVAQGANLD
PEKHREAVPKVAVPLAVGANPKLEEIGAAVAE P G H K T A A X S S P K K Q Q S K K S S N S K N D S S T K S K S H K N G T
R S S P T K Q P S S R K R E K F A S N A Q Q A I P A S V R M I S G S H D S Q T S A D V S N I N S Q F Q L P N N A G R S G G A C T A A L L Q V L
Y Q S H E Y G H D D I S W V D V L R Q M R D V L N E K G F E Q I P Q L T S S R M I D V H D R F A I T P A D G S F S Q R N N T K R A V L I G I N
Y T G Q K G E L S G C H N D V N N V A R Y L S E V Q G F K K E N V T I L M D D G N H K P P T K S A I I S A Y K K L V K E S K K G D V V F C H Y
S G H G G R L P D D N G D E E D G Y D E T L I P V D F E K R G Q I R D D D L L K I L V G P M P E G V T M T C L M D C C H S G T V L D L P Y R F
T S D G D L E E M E M N E R C N F K D G L W S G M G L A L G M A A G S A V V D V L T P Q P E M M I L G G G P N A I H E Y S D S D C C V I S

>Throt14982
EERNRERRSRNGGEGSSHQHGHNNNNNNNNNNNSRSTNNRSDRDNGVGRSISPLHSSVSGSNTSGNASGSA
FGSHSDL SRVMPGGGATSPGLSSIASTKIADDTVQLDLPADLMAYLQVVANNSSNLPLTRRDDPELGRTV
SSLTAE EYAFKCAAFVPSNVRILGGQFGKYGRVWDLPTSEEFVDVT DGTREPGISHGGSCCNALLKAMYDTE
SEVNNIASPTVDAKDLFD D D D D D E T V D T A G Y T V D R T I A S F D T L V L N D G S N A S A M S W A Q L L R K M K P E M Q V G
F N Q V P A V T S S Y F K D L N E P F S L V P P D F K K G V N Q R A L L I G C N Y R R M P D A E L K A C H D D V R S V K D F L V N V Y G F P
E S P E L M T V L M D D K K H K H P T H S N M T Q A F K K L A E R S Q P G D A V F V L F T G H G C R V L D S P I D E S A E S Y D E A L V P A D
Y E E T G I I R D T L F F K T L L A P M K K G V T L T C I V D C C H T G V M I D L P Y L W T T K G D K G E V L P K M S L N N D F S F V R F L K
V V K T L Y E S S V F T R I G K T V G T E L D K Q L P G R D D E T V I E T V G S L E T M P E N E Q P E K K K T F F E K L C S P A T L A Q S I I
N C T L Q A E D H Q Y S D D E A T L G R N N T L D E E H S Q Y S Y D S

>Throt6337
KIKEDHDSRQIIASNFSLTSDPSETTNDRTAPTPTS AANDPLQSSSNFHLNPVSDI STMFGANGKKYADV
IASKLEKAVGDHLSKAPQSTESATERMGKVTGKRRA LF I G I N Y F G Q K G E L R G C I N D V H N I Q G F L T S N F R I
D E V M V L T D D Q K D P R Y I P T R Q N I L N A F K W L R N G A K A G D S L I L H Y S G H G G S V K D T D G D E E D G M D E T L I P V D Y Q
K A G Q I V D D E V H T V L C R G L P K G V R L T A I M D C C H S E S M L D L P Y I Y T I N G D L Q I I E T S K Q E G I V T L I G A G T R F L
L D G N K K N A V S N F K T G L G L L M S G G G G G N S E A R E K T I K T R S T E A D V I Q I S G C R D S Q T S A D A Q I A G Q A T G A M S H
A L I S C L K K N K N Q T Y T Q L L Q S M R G T L E G K Y T Q I P M M S A G R K L V M D H P F T I

>Throt7051
FTTLDYKSAGGSKVKISQHKMGFFKKTGALSSYPARRNRLQNEQNHNPTAANPPSNYGAHNPTPMPASVY
QTNGMSVAPAAATTTTAAVAAPYNAVAYGAFPGNNAPVQATVYIPGQASTAPT PVSTAAPVQATAYVPG
TVSSIPPAATATAQVHTAAPVQATVYNPNNDSTPAANPSFLGAQQRASFNNNGNGNYNANESSFWECVCT
FPNLRTEPNCKGCGAVIPPGMLYSAASSATAQPPPTQQRPPQDAYNNITSQMNSMGLEGAKIGGAGTTSAG
APSSAANTGAGVMRVH I P L N M T T G Q K I K V R S P D G K E V V Q T I P P Q S Q W H Y D G T Q P F F R M Q F G G S P A P P T T A Y
G R D D G N N H N T N A P T M A H D V P P M H T T A W R D F C H A P G A G H Y S S P P L A L Q S V P S T P I G S G M P M R P N G R H K C L I I
G I N Y T G S R A Q L R G C I N D A K N M Q G L L R R N G Y P D D G S H M L L L T D E R N R G R E Y Q P N K E M I T K A F A W L M K D V R K G
D V L F F H F S G H G G Q Q R D T T G M E V D G Y N E T L I P V D Y D R K G Q I S D D V L W G S L V Y R L P E G A R I T A L M D M C H S G T G
L D L P Y D Y N V D T R S W T E D I N P A H S A G D V V L F S G C E D A Q T S A D V A G A G R Q A G G A M T Q A F M G A Y N T C N N D A A T Y
H E F L T A V K K E L R K K K F S Q R P Q L T S S Q R F D A K S R V F A L G Y A S G G C G G G G S I P S V I E P N H N P K I G R M K R Q N I
R R Q R H G L G G G G G N N F F G M M A G A A G A A L F A D A L F

>Tweissflogii1010-1 CAMPEP_0193034156

MGFFNKLKNAASKAIKEDLLKSMGIDDADDGGMTRDEFEANKPDELRKDIRMISGCADRQTSADVSNVSSF
QLPDPAGRAGGACTSTLLKVLVYADERVPEEDLSFTQVLEQMRRHLKEGGYSQIPQLTSMNPIDVEAKFDLV
PETATGVRRAVMIGINYVGDPEGELSGCWNDVLMKKYIMDVHGFEEEDNIVVLMDDGENTEPTRENIIEAY
RTVVAHSEEGDAIFLHYSGHGTCLRDDDSDEADGYDEALVPRDFQENGMIRDDDLYEILVKDLADGVHLVS
LMDCCSGTMDLPIYIFKGDGEMGEMILDPDMNLDAFIEQITGKLIIEFLQSRFS

>Tweissflogiil010-2 = 36-1 CAMNT_0037344015
IAHNILINRYFLIGVVFQSLQTSFQRIMAGEPAKRKSSSRDDAPPKRSASSASHPKHSSSSSRQRSKSDADR
HDKSSSSKNGGDLKRSQSSRHGQPKSKHPKSKSPKPKPQDGGSKSKPSSNKKSTNKDSQKKSASASKKSK
PVENYGTQVATNGSANKAAAAAMNEKKAQKFNKDAQKAI PAQVRMISGSHDAQTSADVSNINSQFQLPD
PAGKSGGACTASLLEVLVDIHNGLDGVSWVDLLRDMRDVLEDKGYEQIPQLTSSRMIDVSHPPFAITPSS
FDSSKNKRAVLIGINYTGQSGELSGCHNDVKNISKYLREVQGFKKENVTIIMDDGQHKEPTKANI IASYK
KLVKDCSGDVVFCCHYSGHGRLPDDNGDEDDGHDETLPVDFEKNQIRDDDLNMLVNPMPKGVMTMTCL
MDCCHSGTVLDPYRFTADGDLEEMEMNERVDFSDEFWSGFFATAVAVAASKVDPPAEMMILGGPNAIH
EYSDTACCVIA

>Tweissflogiil010-3 = 36-2 CAMNT_0037378133
YVLINYCSITFSNHIFQTLSTMSFADKVAESIPAEVRMISGCHDVQTSADANITAFELPDPAGRRGGACTA
ALLQVLYDETNQAQDNSADMSWVEVLRAMRENLAAGYSQVPQLSSSRIIDVNEKMDIVKDPEGTRAVLI
GINYVGGQSGELSGCHNDVKNINSYLVQEVLFERENMKVLMDDGMHEEPTFENIVRAFKWVVKESAPGDTVW
IHYSGHGGRLEDQDGEDDDGYDETLIPIDFQSEGQIRDDDLKYLVPMPCEGVTMTCLMDCCHSGTVLDP
YRFIADGDHMEMERNENFEFKDFLTAAVGVAVAADIAGAAGALDECCTIL

>Txantarctica1 CAMPEP_0200975774
MEEAIENAKKAIPAEVRMISGCRDEQTSADVSNVASFQLPDPDGSAGGACTSALLNVLYADHKKLEEDLSF
QQVLLKVRDVLKEKGFQAQIPQLSSSRPIDIKNTFDLVPNHVTGTRRAVMIGINYVGDNPGLAGCHNDVGN
MKDYIQDVHDFDEENITLLMDDGEHISPTRDNILAAARRIVEESQPGDAVFCHYSGHGKLRDDNGDEADG
YDETLVPVDYATEGQIRDDLLFKNLVGGFREGVFCFVMDCCCHSGSVLDLFPQFKADGENDSMGVSSGFDF
NSLLSMAASMNDTNMFADIASNPQKLLALCGSCTIS

>Txantarctica2 CAMPEP_0200957050
MSDDKCDKLCGIDMDGICLPSKDKDNKLVQAEEGSCRQSPKSASDMEDEAETRDINETENEDTATEDKVR
KDAATAYSDNSGTDNKNRSIQADVFMLSGCEDSQTSADVSNVSSFQLPDPNAGRAGGACTSALLKVLVSNQA
AVTDLTFVKVLTVMRTVLSGGFSQNPQLTSSQEMDVNQFYIVPPRCQGTKRAVLIGINYTGQSGELSGC
QNDICINIKDYIMNVWGFEEENIVILMDDGNHTNPTRSNILEAYKNLVTNSEGDAAAFCHYSGHGGRVDDDD
RGEEADGYDETLIPVDYDTSGFIRDDDLVSNLVCAMSGVTLVSLMDCCHSATVLDLFPKYGADTTDTNQI
GSFVTFGRGKIIIIICIIIAVVITIVVLVALYLA

>Txantarctica3 CAMPEP_0200971514
MGRFFKKIFSGVREALSDKDGARNEFEDKPKDALRNEIRMISGCEDSQTSADVSNVSGSGFSLPDPAGRAG
GACTSTLLSVLYADEQVPEDDLSFTQVLNAMRVNLAEQGFQIPQLTSSNPIDVNADFDLVPANATGTRRA
VMIGINYVGDPELGRGCHNDVLMKKYIMHVGFEEDNITILMDDGEHDSPTKENILEAYKKVIEETEEES
DAIFLHYSGHGTQKVKDRDGDDEADGYDEALVVDYQEEGLINDDLIDILCKPLAKGATMVSMLMDCCHSGTI
LDLPIYIFKADGSMPEGMQLDESDFDGLIQSFGGHVIGFLTNFLK

>Txantarctica4 CAMPEP_0200971326
MSDFDAQVAKLIPAEVHMI SADSQTSADVYNVSQFQLPDPQKAGGACTSAILQVLYRDDQDYSNELTW
VALLRKMREVLNMGYDQVPQLTSSRLIDVNEPMYIVKPGTDGGVKRAILVGINYTGQSGELSGCHNDVEN
ISGYLQKVHGFPPDQMLRFLDNGVDHSPTRANLMSAFERIAAAYSEPGDVFVFMHYSGHGSRVKDYNGDEDDG
FDETLVPVDFESNGQIVDDDLKDFVKPLKSGVNMTCLMDCCHSGTVLDPYRFTADGDVVRDEGFGGLM
DSPENVLALCCCLALLADFL

>Txantarctica5 CAMNT_0047144487
QPHNNNIITPTAPFNSTQTAAPTRPPPSLSNKSASFVDFYDRDYSGKLSRDEIIRGAVETLSVPYGSKKY
NDISNTIHSVWVFDTRSGSIERHEFCGPDGFESLQAMMTMNSQSTTTTQSKKKVRVGI PSYGPG
KQVMVPSGGKTEIVTIPDRSEWIYLNLTGQATFDIEIPTSSHYSAVQQAKPQKPTTMTKTVRVGIPKGSNP
GSKVNVPTS DGKTNIVTIPDRSKWIYLNLTGQPAFDIQVPTAQPPQAAHY SAGGGTDITTSASSYHTTSSS

ASLPPWKNYNDMIPASYQPPLGMKSVSVSPQSNLSFVKTSRRRALIIGINYTGDKRAALRGCINDAKNM
KNLLLRNQFPNDGSHMVVLVDDSTSSNNHRPHTSNIFKAMQWLMQGVRRGGDVLFFHFSGHGAQVPDRTGHE
ADGLNETILPLDYKKGQITDDEMWSLVYPLPAGARLTALMDCCHSGTGLDLPFYQKGGKTTNRYGMTS
TSSSIRNANWIEDINPAHSQGDVVLFSGCQDDQTSADTFSTNTEAGGAMTQSFISAFESNPYSTYPEFLSA
IQRSLRQRRFSQIPQLTSSQAFSAEERIFSFVDGIAPNRNPHIGRIKKNKHVRPGRTSDRGRGIGP

>Txantarctica6 CAMNT_0047161225

FTLGGNNNKRALLVGINYIGQNGELRGCHNDVYNVQYLVSYHGYRERDIQILVDDYNNRSIFPTRQKIIS
ALQYLVQSSVAGDAVYFHYSGHGGLLEPNFRSSSKKDYDETLFPLDFDQSGQIRDYSLYQNFVQMPAGV
VVTCVMDCCCHSGSVLDDLPSFQPTHEVGDRLIPMGNTMTDLSNLAFLYILMGGTLPVGGFLFDSVTDTLQS
SLGDGFLEDYQGTGMGNEEMMDQFTEGGEDTAAPYGEDEDIARQGENFNYYDDNDGGGEILAPPADAQENF
GYNNNNNYEENQNNYEENQNYVDVGGDEGEEATNLPDCGSCIADVLNDLLSEGGEY

>Hsinensis1 GAUA01013815.1

MSSFYENAEKTIAAQVRMISGCEDEVQTSADVSNVSSFQLPDPAGRAGGACTSTLLKILYADKQAPDEDMSF
QDLLLLKMREVLDEKGFQIPQLSSSRPMDVATKFDLTPEDFSGVKRAVLIGINYVGGQELAGCHNDVJNI
KEYIMDVHGFEEENITVLMDDGVSDPTRENILNAYKELVASSEAGDVAFIHYSGHGGKLRDDDGDEADGY
DETLVPLDYMSAGQIRDDDLLTTLVIPAAGVFMTSIMDCCHSGTVLDPYNFKADGEQTEMQESEGFDIFS
PMLALLLA

>Hsinensis3 GAUA01014143.1

MSNFDQKVEQMI PAEVRMISGCADSQTSADVSNVSNFKLDPDPQGRAGGACTAALLQVLYRDESAPAQDL SF
VSVLRQMRQILDAKGFSQVPQLTSSRIIDVQNKFTIVNPKEATMGGTRRAVLIGINYVGGQQLSGCHNDV
KNMKKYLQVHGFEEHNMTILMDDGYHREPTYRNIVNAYKDVVRQSLPGDTVFCHYSGHGGSVRDASGDEE
DGYDETLIPVDFQTAGQILDDYLLENLVKPLSRDVLMTCLMDCCHSGTVLDPYRFTADGD

>Hsinensis4 GAUA01006240.1

VGTQVADDQIHINLAMADLMAYLQVVASNSSNLPLTRRDDPELGRTVSTLTAEYATKSAAFIPSDVRVIG
GSFLKYGRVWDLPTSEEFVSDGAQEPGLSYGGACCNSFLKVLVDIENEESVIMGQSEYMDSNNLFDDDDDE
NISVSNDSCTSLDLGNDEGSGVTWTQLLRKMKEEMREVGFSQVPTITSSRKFDLNQPFSSFFPENFDPTQNK
KLSLLIGCNYNNAVTDQIKASHDDVRSVKDYIVNVHGFPEKKGAMTILLDDKEHSPHTSNIIQAFKHLAE
ESKPGDAVFIQFSGHGRVLDTRLDSEGECEYDEVLIPSDFTTKGLIRDITLMFKTLLAPMRDGVTVTILLDC
CDTGVMMLDLPYAWTTKNDRLDIAPPKLSLNDNFSFVRFLKVVKTMYEMSTFTQLGRTVGSALN

>Fsolaris1 Scaf102 GAX16243.1

MGFLSRALKETFEQEKPPQLRGDIRMISGCLDSQTSADVSNVQSFQLPDPAGEAGGACTSALLNIVYKDDH
NTAADLSFTEVLTQMRSMKAKRYSQVPQMSASREIDVNTKFDLVPDNATGTRAVLVGINYIGHSQGVLS
GCHNDVKNMVDYIKDVHGFEEQNIIVIMDDGEHPEPTKANIVAAYKKLIEESQPGDCLFCHYSGHGAKIKD
DEQGEKDGDEVLVPVDYEQAGMIRDDDLFDILIRPMQGGVSLFCLMDCCHSGTVMDLPYIFKADGIFEN
MEIDENFDFEKLFKKVGEVAVRELGNVKNKYLDKDL

>Fsolaris2 Scaf183 GAX22319.1

MTDYAERIEHAIPAEFHMISGSHDMQTSADVFNQSFELPNPAGKAGGACTSALLQVLYKDNHAASSQMSW
VECLRKMRSELNRMGYDQIPQLTSSRLIDVNKPMPTIVPPGSTGHRRAILIGINYIGQKQQLSGCHNDAMNI
KKYLINVHGFKESEMLILMDDNKHHPPTRRNIEDAFQRITQYSQAGDVVHVHYSGHGSRIPLDGDGDESDGY
DETLVPVDFKSAGQIVDDEILKLLVKPMKAGVTCTVLMDCCHSGTVLDPYRFSADDSQMRDPRMNLEKY
LGKFDVQTVLCLALLACCLADLLN

>Fsolaris3 Scaf132 GAX18784.1

MARGNPTISDREFDQVRKQVIRSHFHMISSADHQQSEEAYHAGKFQLPNPAGKAGGACTSAFLQAMYQRGE
GANWVETLQEMHDILQGMGYAQTPLTSSRLIDVRKPLQIVPAGSGRRRALLIGINYVGGQELTACHNDV
HNIREFLTEVYGFKESEMLILMDDARHNPPTRRNIEDAMIRLTRYSQPNDAFVSVFSGHGGNTRDTSDEA
DGMDETLIPVDFRTEGHIVDDDLRLLVKKPMMDVHVTVLMDCCHSGTVLDPYKFGANDTRVQRESGFNL
DQVHESQLTVGSYHAPGTVLSSWSLHGDKEKPPKEEKKSPKSKKKKKAATFQPKKKKNKDMTKVEENEQQ
EVGPKMVGQAALPVRASKKSAAPAPGDKKCSVM

>Fsolaris4 Scaf78 GAX14314.1

MGNSDSKPEVIEIPLPGAVETLQOQDQGEVDHIDPIEASTSRNESRDERDTQDNELPVTKIRDDQVHVNLA
MADLMAYLQVVANNNSQLPVTRRDDPELDRIVSSLSSEYARKSAAFLPADIRVIGGTFTRYGRVWDLPTS
EEYTATDGALEPGRSYGGACCNTLLKVLVYDSANDAAGAAQSEAAAESLFDDDDDETDTDPLPKSPKSGISL
DFGGQSSVSINWIDLRRMKVEFKEIGYAQAPKVTTSRKIDLNKPFSLTPENFNPEKNKRSLLVGCNYHE
LKDAELKASHDDIRSMKDYIVNVHNFPEGKEYMTVLLDDGEHPPTFMNIVEAFKALSEESQPGDVVVFVQF
SGHGGRVLGDPDQVGTIYDEVVVPSDYKSSGLIRDITLMTKLLAPMRYGVTVTIIIDCCDNGMVLELPYCW
GTMHDKKESI AKVSMNKDFS FVRFLKVVKTLYESVFTQLGKT VGSALNPLSPLEDVVSRRREKEKNSEKR
NTKASKERGDTIFDALAHACTTVRFDDRVICRTGKTDNSVEEESK KASSDAGSLIEKVLNCTMMERDEDFS
DDDSFKSNSYDVGNSFDSLTEEDEPHRSRRRRR

> symbA1-2 GAKY01119793, GAKY01119787, GAKY01119790
MGNAGCCSSSDGNPQFEILAAPRDIVGRK KALLVGLNRYNRTRAELHGCINDVNNMQQVLVKQYGFKLEDIL
MLNEDQDKSQWPYK KVIIEGLQWLYKDAKAGDLLFFHYS GHGSQYQLD KKGMPADCICPLDCLDKKWP
EAVILDTEIHQELYDPLPKGCKAVCIFDCCHSATVANLCETMVVQEGPMTAARKEKMKALTDQKNKAAATVRF
YQDINSKGLDL

> symbA1-5
GAKY01160523, GAKY01160524, GAKY01160525, GAKY01160526, GAKY01133546, GAKY1133547, GAKY01133551, GAKY1133554
MLAPPERDEFGKLPLEDTTTEAPPEDDDGLLAPEETDGDHLDEIPEAPREVGSYQHQQHHYS GHHQYGHHP
YVSQLASYSGHGHGYPALASYSGPGMYGQAGDSYSGYMY SADGFQQLYQPYSGYAYHLSGLGMAPMAP
QPSQHVQISSGQAGQMVTS PSHQAAPSKPAK PETA AKLHV TGQRRAVTVGVNYIGTENELRGCINDSDTFI
TLLTEDFGFSVSDIRQLRDDHPQRMPTRKNI SAALQWLKVGAAAGDHL LFHYS GHGSQRRDSSGDEADGKD
ETIVPCDFNRSGMIADDELRRMLVDGLPKGCRLTVIMDCCHSGTGMDLSYKAKVLHDGSLTIRAVSSRQRH
PTGAEV VLLSGCRDVQTSADI SGGVAGNKAAGAMTTAFR KVISKKRDISYHLLLEMRSLFKQHSFDQVPQ
LCMEFHLNFEEPFLEADPPVAQPPAPLRSTQRRALTIGINYFSLTPGQGR LSGCINDSETMIAVLKETFK
FEDGQICRLRDRRTNLMPTKANILSAMRWLTQGVGSGDELFLHYS GHGGRAADRSGDEITGQDDTLIPCDF
QTAGQISDDELHSL LVEHLPEACRLWVLFDCCHSGTALDLAFKVTAS AALXLD SRRLRCTKMRSRHRPSG
RPATPANGEV VMI SGCKDDQTSADI QSGSSAHKAAGAMTTAFRHVVSPTI SCEDLLLQMRQFLRRNSFAQV
PQMSSDKYLQLDSAFTNYQTKRXXXXXXXXXXXXGRCAYGISATACRQRDGRGHTHSSTRGTDSRTAAQVAF
NACQSAVSCRMQHGDAAATVAPSKSRRAASGLDESKLVRPLTSSSSEHLAVQRDRKS

> symbA1-6
GAKY01019324, GAKY01019325, GAKY01019326, GAKY01019327, GAKY01019328, GAKY01019329, GAKY01019330, GAKY01019331, GAKY01019332
SSDLAPLAASAMGKVC SVLSGRPAPADICAVIKEAEHRAEEWDCWAFGDSRDVSPKAAKQEPLTGARRSL
IGCNYAGTSNELHGCANDVRRMIPVLAKLGFPSDGGSQVLLDEEGVDGPKPTHANMLEGLDWLVAEAQPG
DALLHYS GHGGREPAEEGGYHETLVPLDFETAGMLRDTL FERLVKRLPEGCR LTCILDSCHSAGALNLPY
IFVGT EELRKAVAGEAVRMALAMRWKSDLEKWRQSSKELFGDVSSLGKNLWKMYQDQSGYVTDKETTK
GVAVGEVVAITGCRSDQTSADVGDVSTFGLKQVSGSAGGALTSALVEALEGQEELTYAELLERIRQELARK
GFSQVPQF

> symbA1-8 GAKY01116216
MANFMDELATGSRRTWRDLCKKETPTVGS DGM LKGIWREAVIAAVACEKAGKAGRFADGPAGQVLDYLLER
GFNKFFTNAEQTEEAHAGRIRPSMAPSGAGAAIDSWSGGK PHEYRPGKDDGKPKGSGDLQIRCGNCGNV
YGVAVPPGTAPGATVQARCPHC GTTNQAAMP HGGGSPSSPMKFTGGGAPPRPSGRQ KALLIGVNYFGTRAE
LRGCINDVHNLFRLLTETYGWQAHNIRTLTDDGRGGGMPTRH NITQH LRWLAEDAMP GDVLF FFSFGHGAQ
KEDPQGFEE DGMNETILPVDFEHAGMMTDDEVS DYIVKPLPEGVRLTSVMDCCHSGSGFDLPFTWDP
RRGMWREAVNPF LCRGDVLMFSGCEDDDTSSDAASMYAAPGGAMTTAFCDVLRNRPRIYPELLQLLHRHLSMGG
FSQRV LSSSQQFSLDRPFSFDDIHPNMNSQLGRIFRQRFP PRPRPMSG PLADMLG PLGMLAGGLVVGALA
GEALEGGVGLLGALFG

> symbA1-9 GAKY01183850, GAKY01183751, GAKY01183753
KRLKPSVWARETMGAGDSKCNCG LCHCCGDGPLEPWRDSGGCIRMLIIALDYDYAPSAELTCTKDARTMYR
MAGRAGVDDITVITDKAGVGDPSFPTRSFVLRHMRQVAKRCEE GDFVWFVWAGHG VNVPDFNGDEKDGFDQ
AFVTPDVTGRLTESAVLIDDEFAMALDTFVPDGVRI LCINDCCHSGTICDIDSFMYKHDIYSISASQDNEE
AEDMGE GVLSTALRRAVRTLSVEYGSQEF S IMDV FQRCKRFAVRLTGEQNINLQYSGPKPSVVAWPLCFP
WWTYLQKAGLMKVDIQEFAEDGLDSDDEDWTVPVAGSPATTS PFALTPGAGVRTNG

> symbA1-10 GAKY01049302, GAKY01049303, GAKY01049304, GAKY01049305

MGKRALCVGVNYPGQEYQLYGCVNDCLDWERMLKEAYEFEETRVLIDQYPDGTPTESGAQLPTRANILAQL
GGWLVAGAQP GDVLFVVFAGHGCQVRTNERELEALVPGDYRDSALILRDEVHALMARLPSGCYITMILD
CCHGAHMLDVPCSVDTSTGPFVTVHQTARTARPQEVSRTHEAWMQAYVDHARSRPRFIPTVTASGRTRKRSPEGA
GAHVGRMTLNPVTAFLCAAARPFENARDANIKTYQCGVLTFCIHQALQDLQYRCTFEQLLERAANKMEDI
RNKYMRRMDQTIQMSFCPNSAPSAVVVFDARYAPVAQHRSQLAQQQNMSPPENLRS PGAPSPEPVRQAST
EFVPSPGYREQPDTNAVGGEVVGVGIVYVQLFSCSDLRPQGMYGQCDPYVKMTCGGVTHQSTVKRNSTHPT
WGDEENKFTFKASDCQVEMLFIEVRNAGRDELIGRVDVPLRSLPSMTWEERRQFLQNGGEVEFRVALYPER
AAANLRPQPGLGMGLGGPMGPMEQQPPAGTGYPEKPRPPSPARDLGP SLMGEYDLRAPMERRPMDEEPL
LENIFGKPNLFAAMPDLMSQLSTNAPTGFHEVLP AIPQVGG LSTPALGGLGTPVSGLPAPATAMPAPAAPA
TSRLGVASYTPPPAACFTPPSLLPTAEVGR TASRGLSLEGGYSTGGMAAAKMNTASTAVPTPQVPGSYTYS
TPSPFTYSQAQPGQSALGSNLNAASYPYSSSGT PFTGYSQQIIISGQTSQSALGTDLASYTYTAPS YTTSA
PASLTSYTPQGQIIGTTAQKALNADLSAGAYTYTSAPTALFTGYSQPGQSTGAYGARLATPSYQPPYQVLS

>symbA1-11 GAKY01048077,GAKY01048080

MSGWSPAAPRPFSPAAGAAAASGASGASAMGSRVFGPEVRHVEAPASEKVNQLRRSFTSLQAEMQLSFQR
QDGEVASEPFGAFLPNSGREGVLAPVAGGSMALGSSSSLASTVPGGAADVSPSNAKSETGELDVWLKEKAQ
KIKDHVTEMANAQRRAEDVGRSLQDHLQDLAE LRRMLRQAQADLAEELAKAQELERRRDALRQEQADLQSQ
IVLREQEFQELRSNRDDVDRQLSRALAEQGLQKNNLEASSKSFQQAELAKDIDQSKRQVLELRSSLAGR
KAVLEEKEKSLKMEETVRVEKEMVQREQLSAELDQTRTSLAEAKAVMEVSKRRFDEMEEKGRETTRKLEMA
REELHGLRAEDGESPVSRSTVEDAKA I LAQKTAKLNQQTLOVEKLEKELQDNREOLEKQSLRMAEVHAEATE
FEMKSKCLDERKLQLQDDLEDKRLLVQQSLAEKDEQRR LAEARESCARDLAVLKDDEEQRVAEARTRYAQT
ADELERDVAAKQHELQTAKSHAEI IQKVCSELEKTRSRRSLLQDRTAALQAAQARAQDLEELAGTEAEL
ATAATELQRLEKEEVERATEIEDARQKLSEVQMEIETMQARAQTSRVDDLEATSRALAESLQKAGQERTAA
REKQDALKVELHESES DLKKAEEVASLTGELEKAQSEAESL TEQVNNLLQSSSGDKSKAETLQKSVEANN
KELDATRGLLVTRQLEVEALHQVLDNENQSHRQELEALEAAAEASTQSSQELAQQRLRELERRRDEAADALA
AAESHKLAVEQEI QKVIAETERVTKETYTSL SLLKAQTPQTYAQGAEQKPDPEAVKLRQLKRQVEAEAQR
VANLRSDLAAREVEVERQASIAAALAPAGGVSELEGS LQQMMELVRAQESARKSRRQEEDLRNDLAKLKE
RTAATRDKLLYQEDHLKLOGETLAKLESQKAKSEG DVETLTLGLHKLQDQENQYLQEA IKHLMQOQVEAKHGG
SLDGWAGESCEAQVAREVARYVAEIEQWK RQTEQVRLRQKTEGVTROYQEHEVTVQTLNQRIDKLOKEI IQC
DRCAKSWEEEEKSRRTNSAPTSPTVLPGLVIFQRPLPSHHERKALLIGVNYSN SHAPLKGCINDVWNMQCL
LRYTLRYTPEQLQLLDVGDGDRSRPDRAPTKANILAGLQWLI EDVRPGDHL LLLVFSGYGAQHPRTPGSNKC
ESYLVPSDFAAADLPSDFFEVVASACKSPAQPNVIDQTAKMAAGAAPGGPEEIERQAAAAQKALGNSKASYR
LISMLEVHDFLSQLPQRCRVSLLLDACYTILPGAGPESNSPATFRKVDRGRVEYDKLRNFMSRPRFLELPP
LPVQHTPPHLPRSNSFLPCTLHCFSGCRLKEWCAEFPIEGSVQGA FSWAFLKALAQGHFHIGVYQFQQLVS
NILLNLKGYFRHIDQQPVLQLSAAASPQDVVLWT

>symbA1-12 GAKY01032711

MGSVGSQICCF LRACDPEQRVEMRSLAAQVPVPTPQPLTGYAPYAGPGQLATGVAVATPIPYASAAPVVA
CATPVEMSPVCHNGFSCTPHAESI PVTGMAVSSRSVPQTL SQAQVQLPGRRKSLLVGINYFGTEAELSGCI
ADVCRMQPFLEQLGFPSDQCCQMVL LDAPGWPHYRRPTLANMRQAIRWLVDVRTGDALFFHYSGHGGREP
STSGADGYVETLCPEDYDEEGMLLDTELFETLVRPLPSGCRLTCLMDCCHSGGVLNLPYLFTGTETHWDFW
KMPLAWAWGCGAFGRNTRPPRARTKRGSLPTKLAMSVSLWARLWQSPA AVLIRRVQM VVTSKRSSSTSSRPG
AGRC

>symbA1-13 GAKY01017080

LGVVHEVLSRSVRAMNGTGCCASSDGKPIYEALSAGPPGGRK KALLVGINYRNMGSELRGCINDTINMQEM
LVKQYGFKLEDIRMINEDQEKSSWPFKKVIFEGMEWLYQDARSGDTLVFHYSGHGSQYSADEKAMPADCIC
PLDLIIDRKWPDSVILDTEIHEKLYDPLPGCKAICVFDCCHSATVANLCETMVVKEGPITASKKEKLIKE
LTRQKDNVAAEVRFYREVNSGQLDIKKKSREEMIQLLEKHAFPKRGPYGPYSDVSTLNYNLLSTSISAFF
EDSVKAAEARLAAKEKAIKAVQSMQPGEGAEIYIGNLEQDQQTAYGKREAAKDIRLRFIPQPGMDSGDSET
AKPKLLGAGRGYRDVLGQAKYKDHLWVFGCQDEETSEDAHVDGTFQGAFTWALIKALKSDGFREAYSKL
LIQIKTYLEGGGFKQVPALSTTHKMYLDCGFLGEEL

>symbA1-14 GAKY01067445

MELLRCVAEICCGESPQKPRPLVQPGPGVTGAPAPPSQVALTGRRRSLLVGINYFGTQNELHGCVSDVQRM
LPLLDKLGFP SDAESRRVLVDAPDWPQH LHPTLANMRQGI AWLTQDAQPGDSLLFHYSGHGGMRPSDGRS
EWHETLCPVDMDAEGMLLDSELFETLVRPLPSGCRLTCILDSCHSGGVLDPFIFVGTQENLASALAGEAA

KPNATNEKCLDINNKEKKKKIKSVHYDMDEILSLKCKVYDELDTCLKCINNLTKNKKLYEQLKYYKHKLD
KDTKTKKLYDECTSEKTSYTMKDSYISSLLCNEYKLNHILNKSNNKVSDDKHILSYNHHNNKNNNINDI
NNIKHISKFVNKDNEKTLNINILNHNKDPNSGVFLPSDNTESVIYMNRRNRKLCDNNFNVSKHVLYKDS
KGTDSTRTNFYDDYSMSYVKSNDVNEKKEKIKNNINISDKYFLSETDSPIGKKALMITLNYNGLLEGC
VNDTVDMCDHLMQRFGFNDIFILLNDCNLCYRNFVTQKANKKNILSNLHNFIVNSNNGDILFFYFCGYSIKL
IDSKFTENYNFALLPQDHSKNNYIYSNEIFNIKKLQGGKQLCIIFDTTYTSYFVPVPTSITYNKNMNTTE
IYKYNFSSNQYKLSLKTFGKIRDRNVDSIFVENIKKPLLYEYKKEKENDTNTNDKIILVPSIFFFSPDCN
DRNDFEFSIKNKVRGLLTYCLGKAIELLKNDFSYHDLFVAASQILIDIKKEYNLKYVKFKLSFLNEYSRDD
IKFLSHESLFLKLLQLDEPLWPKSLKLNLNQYIQDICNMDERKMLKSSKKKCLLIFIKDIKFYTYKNID
TKNEYFVSCFIKKNVNLVRRNNTKEQRIVQDKIFFLEYITLNVTHMENANIYVELFKKKKKNYFVAR
IFNIRNVNGKFSLSDEKKNIIIGIIDLNKICVS

>PfMC3 XP_001348333.1 PF14_0160
MVYNNGLRGRKKEEKYIPMNRKSTSLKDPSTKNNNYIKTLDTYINEEDSPTKILSKGKKNKNENIKKR
INEKDNDTDREDAASLNDVYNKVMKYNTRGTFIEKVSSSERNIEHNNNIIRKLGSKDYSKARVQTMTTN
IGNHNALKKINPKVPSITSRTKSYTKVMNENKYNNNNNSNNNNINSMYYSKLLNNKYSTEHTQSIDNN
NITSKRLNNKKTATDKAQSTSRYSISNSVKKSYSTKGYNTDRSQTMSRYTLQNKKDSNTNTNRKGYSTHRG
QIIQDNSINNOAEEKKRNMMLKKKYIKESSNSTITGSNEKKNSSNILKKNSTCDLNYLNKEYNNNNMMHE
HAENVYNINDNEGCSMQIINDEDVQKNVPEFYTINLGSSETKNMGENYIFKNRDKKIKPNIYERNMMDLM
EHKLNDDMSYNFADHIKIDIECYINQLNESNKCNIYKECDPSKLI SPVYDNVNDNILENNQQLNEYEKHNDI
LTTSYLKYYSHTNNNNHYNDEEDVHLDLGKTNEGFSNVVKNMMDNIPWNETNKKESFSNIKKKIDHTDDRHI
AYVDNSSMKHTMNDKQYVKNVPYNNMEEVLLLNEKRGNILGSLISKNHDAKRATSNNNNINNNKYYYYD
NKYSEHGSDSVSSNIGYPHGYKNNNIYNYVNNIKDLSSPLYCNTKTKRAHKFHTDNIMSDQLNKYEDNNKN
DGKFFSGNISSKQKGNLNTNYTTHSSEYRIKIESNLTKDYRKSLEYNDIPNFDYINNTNVQNSDFGD
SHYINRNVSYKNSMNSDDIQNSNNNNNNNNNNNNMNVNPNNEYLVYTNKHYVRINNKLYEKTRDNTYIEVD
SNSNFDIINDINSSHNSPLDNKDNLTLYHNTNKKEYSDYVSSYSNINKYEDINLPNNIHVSKDGKYLKKNY
SVSQNSDDNSVQDSFFSRTSRSNSQNRDKNVNHIEQNYNNSNRDDIYYYHNLKLLERLTQQNIKS
GKYQRNIPQNDNDHNDDESEIKEVKKDKTKIDMNKHLHLNDKKIFNQVKRENTGVHMNASKTIKNNMKEVT
YRNINNDTNYNNNNVKNYLYSDELGKNKNRDTPKTKQHGDSDLNKTELKKKIYNDIINNDIINNININ
DIKSGAINNNIVNNNLINNYNADNRNVSNSIFTQHINNINNNFYNSDDERINIIDNNKRMDMTKDESDF
RNNYFVELEKRRKKNLGTNTTPIISLKNETINMMINKRNFNNYISDKVRDKILKREISCSVNTVCSSK
TNNKTNNSYSSNNNDNNNNNNNSNPFILDNSIRKSNIITTSNNAKLINNTIISKGINNINLINSNKN
SLNSAKINALGLSSRNDLNYIMNNRNTSNNHINQHLLYNNRNYSVIKIPNVHKEKRSKIPHNINIKSNL
NLEPNIKTYTNIKTPINIKAYTNIKAPTNIKAPINIKASTNIKAPTNVKAPTNVKAPTNVKAPTNVNAPT
VNAPTANAPTYVNTPTNIKRQEFNSVTLNYKGISKFDINEDKNTTIIPPLHRQSNSNFPFKNTKLNLS
MYTEKELIKCKSINNSDIYNYLRNTYNTKPSKFYRTVSYRNMMLKKNKSMLENRKRKTEKKEENLMSTFNY
TSEVDSKYIVKAVVVGCVNYVSEERSRLYGSVNDAYVFCRALVKYFDFLLENILLTDSLPSNAYIYEDFD
INRKKYINVDEEENIKNNEPLKKNIFNLFNTALYTTLKKTNEEELNCNSCKDVEIKNVDISSEKMNFL
WPTRVNILKAVNWLVRDSIPFGSYVYFAGKSVQVDNMSGWEGEGYDEAFLCSDPFNKISEHNVITAVQLK
DLLLSINESAQMTIILDCSGGQTILDPAGTENSLSYIKGCKQKGIWPIITNPTNKVHKAIDITILNNTSMK
KYFCRSRYSKLIIEVESTSAMIDPLLQSISSLPVAPKAYCLCAATWEQISIEGLFPPIEFARVSQKPKPEY
KTGEGHYQNMNKNIRAEKSNRNGPNGLINKNNNLKSKTNYEKNFNFTLNMMKMLFSNTNNNNENKLEDEK
INRLGFNENDSDYIDDNYNSDDNNNNNNYNYDGEKGFKNFQENLNNVGQKDVIKNKKFKDNYILVSHGVF
TYCLIEAIEFKEKELKYNILEKKNEQFIPMTLKNLINVIQKMQNIKYNKLLKINQKPEFTIHPGANATN
NNYFVHYSKNIHFQNYKCNFINADLSPFLNVNKAWEIEINRTTLRNRKSLSLSSSTLINTASSKYFTQKNEQF
KNSYSLKY

>GtMC1 jgi|Guith1|57223|gw1.16.206.1
GRKKALLIGINYAGTRNALRGCINDVENMQQLLRKEGFRREEMVILTDDGRGDAMPTRNEILRACQWL
VAGAGLGDVLFHFGHGSQQRDDSGMESDGYNETIVPCDMQQIVDDELWNNLVFPLPSGVRLTAVMDCCHSGT
GLDLPTWKHNRWLEDENPSHSCGDVQLFSGCQDDQTSDDGDEKFKIGGAMTNAFIRAYNAQPFQTYPEF
LSRLKSNLRSAGFGQVPLSSQAFDVNEKVFSLVEGIVPNTNVTIGRLQRRKIRPK

>GtMC2
jgi|Guith1|156638|fgenes2_kg.347_#_2_#_2724_1_CCFI_CCFN_EXT_A_EXTB
MDCFGCCPKELQAEAEKVATNEAQNAVSNATRAAPNMQNTMGAGGNSALSQALNAVGGMQGLMGMVQSLA
SGQTPSLPSTSNATDFKQAAQALPAEVHMFSGCRDEQTSADVDTSSFGLPADSGPGGAGGACTNSIMLA

LSENPNPTWIDLLNRMRTILKEKGFTQVPQLSSSKEISLDGNFQLAAASSSTKALLIGINYVGQKGELRGC
HNDVLMQKDYILKNGYDPASMRVLMDDGSNMNPNTRANILDSIKWLVKDAKSGDCLFMHYSGHGGSMKDDNG
DEADGMDTVPVVDYTTSTGQIRDDIIFQELVAPLPQGVKLTVMIMDCCHSGTILDLFSSFTANDQNTQNYTS
GMTLPMNGNFNWKKIFDIGMSMLKKYGMGGAMGGAQSGMSANV

>GtMC3 jgi|Guith1|101222|au.6_g2324
MKAEARKSDQAVLFDVDTACDDDKHAQKEAIHMIELVLKEETFTDTFSKRNSALSDQSKFRSCKFVDSLTLQ
SFESDLIFLEHPRVFGGLCMGLNEYKGELKPLETAVQDARELHDKLCSLPQSHSVLSLNPRSPSEMRKYLRK
NLKQLMPASPELVIFFYAGHGFYEPRKKDQMLVPVDVEEVKGLSTHEINDQMLS IKDLFKIFRDFENDISL
FHPMVLVIIDACREKIEGVTEELPQDQEDKKLPQNWSLLTTCGKGVASDNSIFFKALLDPREGMFACNRP
LEGLVQSCCRTCKGRQPCISMNTYTIPEDFCLVRDGEALRDIKMSIAGLNKAAKEIASSQLSDTDTSETET
FVLAYSPEDAKFRDRTKDALKYFLSQSKQRADNPRWRICSIIVLMYFLQYEDTRFCTRRLLGIFYTYMEDL
IAGPELVNDVLEYISRNKILSPSFGAWKKSQTNRISDDKLLIAIIDYTVAKELRRVISDTEELNDALELW
KKAIDPCFDSSKSWEDGMDRIERHLQKQAALECGQNLLFFYFVLEKAVAVNSYVMILKMTRLSSVFLRHCL
LEYNNKKEGEGINKLEGWRTWVSSTGWIVRRDGYRADWNHCKERWCEDMRKGFQOLEKFERPRGFQRFQDF
QKDGSVVSFAFMENGCDSNKRRLGIEYPSSTSVRGELCESPVSGPSRQEGSDGRGDQEDISILQFHMQY
ARRYDVKDFLMDRDFWSGLKWYSQDIDCYYYFRIVHTLAHFVYDNQVDIAVDTENPNEEIDSTFAHPPPSY
RAYRPAISDSPFLFGAKDLEDDDFWANINQLIEDEIFEEHHRQMVLIQAKYVDFHKVDLYVSMNDNSVDS
DDSDEFVDIPKSNSQSQF

>GtMC4 jgi|Guith1|102616|au.10_g3718
MPRQHPRIHALCIGAGEYQYIDKLDAPKDARAMHRKFEETPLCKCFLNVDPTSKEEDMQKQLQELAESSYGR
PPQVTFIFYAGHGCLTSGPLAMLPCNFKAEEETMMEEGTFTLDELIDILYESHWSWNKIPVVFVMDACR
ESIQQHSLALEAAEPRRPARTSIFCSCSRGQLASDESSFFQDLLDPEHGIFAINQPLFDGLMFALDQSRAR
VTEQWARSISPEDVPPKFCIKEDKTAKADVDQIEAAGRRIETSQQRTSPDAATVAAYS PRASEKIEHLQS
SLVQVCKGALNSFAAGTSPGKAMFVFLSLFLRYEETEFGESWLI PCLHGLLSQGVKEVSEMINSHLMKNTI
TSSSLKQWIAEKCPGIDQSKLVFAALDFSVRTELQRCSDNDNPDMARRESEGWVTNVANVCYTDAITVNVAM
DMANEYLSRLAALLSIQVFERIVETGSYVVFMRMSPLTSACLSQLAEQVRKRLHGETGADQVFRTWISS
SGWLSSTSEHRELRLQYLDDEDEEKHLMEILRGVQQLHFVLDLTRVEGQGALSLLKKQDATSSSPPLVNLIEL
VLKGDETS KHSRFRWGVAAI WTHAQERGT SVEAVI MRLNERGICLDMFDNTCLVRENELKEQLESSERAAS
ILRMWWARPEEIKQGGDWLRERQQRSEGAQVGRDLEEIFKAGMDVSRLVMRRRKREIRDERDSQEMKMNK
MCQVNLWVAGEKQQAALRDQPQSADVTAICSFSGSFDSPRVIEGMQESVLTYS SPSKTSLLLRLVMLREVL
ALGFPPDLSELWAELERLQLAAGKELDFVGMCGNILYDVIVKSSQDARAWIQRNIFGMTAEELTSALRHHA
SNNSKHELLSGCFLSVNLTHFWLRKNLILDSITQLEDALEVFLFKFEDQTNRKRAVEEYLKILVVLDA
LSSLRSIETELLHQESC VVVLKMPAVFGKMLLYLMENDCEINGSLNQQRLDRIVSDWLTPTHKLVSVREW
FAALSSSLPNVGDVSSRCERGRQGLKEQLGNMNTAVADQVMVGMIREGLGLLQEQDEVFTILRMFILDEQK
LDERQHEKCVMIKSSTSRRPRIATRGMRSAPAAPASSDKEWALLTLGELHDFCGSSSYVLQVIVEESDDDE
TETRRLQAVEVGETYRRYRVTRDFVVS VSLVNFSSDVLQTFYKSDGEAEDEGPITLKPWAHTSLENLQ
TKLDEGQERDTIILEDRRQATTLLRFFEA

>GtMC5 jgi|Guith1|111492|au.52_g12594
MQDYHLKRFSA LVEPFFNAHGWTSSV GAGPEPLVVR LTRGVQDKYIRLVSIIDLEEVGGGRQGGGGGGDP
LLQRLLCFQDDLWPDDQLYLELKTSETWRDRSREDVIHGRARNVVAAI PRAIEKRESSLSATS DAAILFDG
AQASQQLMIRAVLDDNRERLLKRNALSSQTGYPYQSSGSFYESEMVLEHARVFGGLCMGLSEYDGEFQ
PLAAA EK DAMKLHQ T L C S F K N C H S A L C S N P R T L E D M K G F L R S N L T S L E E A C P E Q V L F F F A G H A I F E P T C K D
Q L L V P T A L E A V R S L S T Q L L E S M L S I T E L F R Q F R D F E R N V A L G T P R V L V I V D A C R E K V E C K K E N L R A E S D F
QGMPTFWTLVQTC SNGQVAFDDSAFFQAF LDPCEGMFACNQSLQRALLQCCSSTNTNPKCVLTNVQNIPE
DFCVISDGKDLRVVMSSV IETQKAARYVTSN ASWRTDASGADTCVLA YSAQDSV LIRQRASQALKH FVSKK
EQDIPRWSFC SMVIMLFLQYDDTRFSSKTMLGHLLAKVKNGNVGPELCEDIQEYLRHGRI TSPSFEAWKEQ
SGLNFQDNKLLIAILDFTVTKEIRKVPDPQEQRDALLIWEIRVVKCYKSSSTSWEKGMDLIEEHLRHVTVI
DDGEDNLFYCQVLEKAADAGSFAMILKMTKLSVFLSCCLLEYNMQHNVSEL DGLSAVVSSTGWIVREDGY
NTDWTVSNALWSNELTRTFQTLERCEVGMGRSDQTS LQDQDPHNQEQRARTNSSAFYQSPSRQNNVDRLDE
ITIDEMAARTQTKADGSTTPKVI

>GtMC6 jgi|Guith1|116566|au.97_g17668
MEGYVQKRFHSL LKTFSDLQAWSSSPVSQTERLLDKLYAGMQRKTTRLISIIDLEGQDSL LERLLCFREEE
RPDDELCLHVMTSESWGARSKDEAVS GRATGGS LTRARMKAIERRRGRGSDSSTRQETRKADQAVLLGEGG

GGDDEGARELVRRVMELALEGGRADSFSSRRNRSVEVSLPELARGQSDGAELRGRDLPLGASSVYGLCMGLN
DYQGELKPLARAVAAATELHEKLCSLPQCHSVLSSNP TLSAMKRYLRRLRELEGACPELVIFFYAGHGIY
ESRSKDQMLIPTDVEEVVRLSFRMGGEMMLSMEEVFKFFRDFEQDVSQYHPRVLLVVIDACRDEIEGVSEGL
PQDPEVKALPKHWTLLLTTCGKGKTASDESKLFESLLDAETGMFACNRPLDSVLLDCARRCKESQPCVLMNI
YDIPEGFCLVSDGEALRDIRSSTAALHAAKDVVSSYPPLTDTSKADTYVLAYSPEDAKSFDRAMEAVKYF
LGEQRAG

>GtMC8 jgi|Guith1|117476|au.111_g18578
MRGTRHVKALCIGADAYTHIAPLVEAVKDARRIHRELEDSPGCSSSFLANPTTRQSMLDMLSSLAMDCQTK
RPELMLVIFYAGHAIQLSSGEIAMLTCDVVRPEVSEETRGSRVTVGDALSAMAAGAENVEGLPPLLVIIDAC
RDEAQGRERIESEIERNRTRSMKVSLFSLCSRGQRADDESAFLRDLLDKEHGMFARNMRLKQAIIEHAMLES
RREQVAVSFCTVFIPEGLCIRPDPTVPRDIQQIQGARRVAESSRRLDPTAGPTSPGPAAEVVAGYSPAA
AGTGADAFRSSLGLLQESLGSLLLEESPRWRVCSMFVFLVFLRYEGTRYGTQATRYYQTRSKKRLGPD LIR
AVNGHMSRNEIRSEELEQWVQETYETSTRGKTAVAAIDFAVREEIRRSLSHMPEEARSELRLWEEDVRLRD
FYEGDMTEEEALDEAEYLRDKMTADQDGRSLPLLAVHVLVSRVETGFSVFTFLKMTRLSCACLSVALAKRV
RATLDEESVGGDEVGFFVVLKTLGEGGALTVLGREQEVDSHVSEELKLLSSRPPAASEFTMMSLGGKRLGDP
DDIRSDDAQSVAGSDALSQASTALHSDSRSSDARSVAGSEALSQASTASVSSASSREGQQRFLSVLLDKP
ELSEALKPFDNILPGDTWEDVRGKVKYEDVVKVKGKALMKEAELIAGDFKTLMRSKEVEKLLSESRPTDVK
DFERKINAKWGPDKQDGPYKIWAKIRTRRELYLNEFSSTEKRQKHLIVAMAYLSTFNWCLTSKPGKPFY
ALPSDQKAL

>GtMC9 jgi|Guith1|117482|au.111_g18584
MRGTGRVKALCIGADAYTHIAPLVEAVKDARRMHRELEDSGSCSSSFLANPTTRQSMLDMLSSLAMDCQTK
RPELMLVIFYAGHAIQLSSGEIAMLTCDVVRPEVSEETRGSRVTVGDVLSAMAAGAENVEALPPLIIVIIDAC
RDEVQGRERIESEITNRTRSMKVSLFSLCSRGQRADDESAFLRDLLDKEDEGMFARNMRLKQAIQHAMLES
RREQVAVSFCTELIPELDCIRPEPTVLRDIQQIQGARRVAESSRRLDPTAGPTSPGPAAEVVAGYSPAA
AGTGADAFRSSLGLLQESLGSLLLEESPRWRVCSMFVFLVFLRYEGTRYGTQVTRYYQTRSKKRLGPD LIR
AVNGHMSRNEIRSEELEQWVQETYGTSTRSKTAVAAIDFAVREEIRRSLSHMPEEARSELRLWEEDVRLRD
FYEGDMTEEEAALNEAEGYLKKNKMTADQDGRSLPLLAVHVLVSRVETGFSVFTFLKMTRLSCACLSVALAKRV
RVAGQGYHEHGELEERLEKEEAEQLRALLAGVGGDEEGFVAMSKLEGGGALTVMGREQEVDSQVGEELKLL
SVVPVREIKTASRLRVHQVMRSESALSQASTASVS SAFARERHQIRILSALLDKPELSDALEPFDNISPGD
TWENVRGKVKYEDVVRVKGKALMKEAELIAGDFKTLMRSKQVEKLLGTSVERPTDVKDFERKINARWGPDI
ERGPYKIWAKISNRPECFLSRLERYLNEFLSTEERQADLIVAMAYLSTFNWCLTSKPGKPIEYALPSDQKA
S

>GtMC10 jgi|Guith1|146838|fgenesh2_pg.136_#_4
MGENACRIKTLICIGIDAYKHIP TLDNAIRDATDVHNQLESSPGCQANLLVNPSTRTAITSQISSLVDRKRT
RGLELILVFFAGHGMQLSKGDIALLTSDIVRAEESRETQSMITVADMLEALRDGAAQNSDRI PPLLVIID
ACRDSKRSAMWGMERLEHEGSNLTQRMVSLCLSCSRGQQASDES AFLKDLLDSELGMFAQNRRLKLAIEY
AVRMSYDREQKYGQYARTLCTELIPDKLCIRNDKTVAADLQQITMGVESLIQSEGMQPDSTDSGVQVVA
YSPAATRTGADVRESLLQLVRKSLFSLQDKGPRWKICSMFLLVFLSNKGTTYKKQGDGRGFFHAFKLLG
PELIKKVEKAMVADEIWSEKLERWIREEYGEIDRKKMVTAAIDFTVREEIRSSLGHMEEEADTEISWWEGE
VCLADHYSKGEKEQEEALDLAEYLLKDKITADQEGGLSPLLAVHVLTRVVETGSCVAFLKMTRLSSACMSV
MLAKSVREVLGGNGKEGLFRTWISSGWLSPREYGEEMEERMEAKEVEMLR TLLLTVGGGVSKFIDWKLE
QPDRKSLEDSKPNITMEKVDPVKKVTYREEKVPKTSKLLSADSAGVQETQLAGYFQSLPADLATGR LERN
LDSSREALFANIHFDTFVYLARSMLSVKMEIEESFDGAGIGISVGV DGETSIWMEKICQDLKVDLKRLEAH
ECAFYSDQSLEHQSMMDIWFPPQLVTALQKRLTEKEIDVLDCLDEAKESENKALRRELLEGA IMAHAL
GMNQKEKNDLIGLALRMGKEQVYRCMTKSTQRTERTWTQSLNADGSRFVEVFGSEGEPSVPADSKS
SRIQMIRINEGQELEDRITIGFLIIMRQTADIELLGKELNLLSEAEQRQEVSDRPCRIELQGAGDCKGHKSK
IEIIQQDLEQLTPAEFEKRVKEAFESEEFKPCRVRGIERIVKIEILDDGFGGKTFDRQDTGYFQAI SER
YNKQRSNQDPELGLQLVIKMRVEASVLPSSDILETLRPLDASEIETDARALGRVFPEQKAVAGRILNRLK
FVLQEEKMSLRDFEKLDFAILVFNFLTLKQQT EARMLETFLSDMTSDREC NKVVAHQAPAAEQLRKKILSI
SDKTLFVLI SDESHWALNKGSPQDLI INDPNLVKKKNFIVLQVSATPYPNLTLHSRIPEKYVKFEEDDPYK
PVQEAKEKRRVKGKDFEELHVIKWLRSRRYRTIYFRFEDFLRTLPSYVLD ECI LPGEEASADDQARE DVRNQ
LIRRENNLISLME SVKVSRRKKKEEEEAVREHVWLADFILSMLYFHKVRWDRSTGRLKSVADDLHNITLKD
LEKLLKEEYMTIANQCKSSGARQACAKLRERVKETLKEERSGSAARDCAIEVFYIKLKSEAKEESVEVND
DDSFMEADDFYQFNETDRIVKDLLSNRTHNGGLYGHMKVVRMFSIKLADQVCEELKRIRKSLFGDSVFAVI

EDYGGSELYDCIETQFRDQPLTYDKDKAPRSINSLIQGRARGKCLTSLNYKDLEGLPCILFLIEKGRMGDT
FPHSFDCLDLRVRSSDNNTTTLIQEMGRLCRYPTLREEHRFETSEEAVQVAKEKRWFEGKGRPIVVYANAAD
DEVDLSQLDGLKRLIGIAWSLSSWTQKSILOVVERGKTLSPGRRGEEDWYTLDRNVDRSAQASMAEDLKG
MLIRFPASTMNRRAVPGWDVQCLKITESRRKDETKIRVQDISQVKKYNNFGPDSTYIIVRDSASLAWLAS
RHSCPHGGVLEKELEHDLPSALVSSSLYDTLMKAVETAIEYCSKEIWEICIRLSPQLHMHMKRDRGQGLV
QKNLDLHDIRNRHVAVTRAKAEGEGSKRVKVNHCDCDHTKRRQHQLRFLHAECQIGKTGAYLHLLNLLR
REVGLRADSEYACIPQIRPEDYPIKVEFQTRLAWEMPFWRDLAGQKGLFKMKEGKYHKMVIQRLRLLAK
CLRDSRGRSSWQQLYCNGLLAPASSQNAEGECIQVKEKVIIRLLKVKSKSNSSPIEIISEGAEVKLKILDFE
RLRDIVEWDREDSMPSIVADMRTGLKTRSGETLLQSNQDKSELSSALGSKTDLQNIWEGRETTAGTSS
GLATGQVKNDFPARCLCLHTLPEKTKVLLRSLPIMRGVRIARLFGDDERRWPRI SFPFGEEQVSRYSFLR
DGRVNGAFELQGEKAIIRNWMTASYKRDAAGSIQTGRAAFLLDRSSAFKEGDRDVPVRQMLLVRPDDGEGDG
QFSSYVSEVGSEYIVVALSHEMILSEAVSELGFRSEQFEHQMPDDGKLRLTPQDGGIGYARLFAQLFAHLL
GLERVWMIIDNVLDCYQLDL SKMFASDPPLLHPPACSFATIMLQMQDMI SDAPKSSEEICRHHRKQGKGQ
ACPKTEGFFDHESMTTKSCQAVRGA AAAKAAAMERGVKSTPDI STIQDVRGNTDGYAVIGMRRDVNVFMKS
SVPFKITHSVY SFFLLNVKSTIGKGVLFPPKQWEDVDFNNLCEEAGLAVLKVNRFFHKKQHRSLHDLRLEV
DGQPEACEVVRVHVNGRQIFNVACGSEMSTLSDVYETIVKRLKRLYPQSDIKKVTCTRIQGGDISFAYKES
YRDIKELEGQEMCEAVYLDVLFVPEARERMVDEAIVTTSTSKASIPFLVSLVESQRNIFYYPPEYEMDES
EGDQPFPAEVPAGRWNEFSDTNLRNVKLKEINVMWDDVEEYKRRFFNIVRNLLRDKCEIRKINLILPAKAY
ETMKEKIDDKIKNLRIGKMTKTWTTVLPCKEASQEDDVMIEASQSDNAESTMDFVVICCSSEEEKKAAQ
DKGEGQRAEADEAKQOEAKQOEAKRQOEAKQOEAKRQOEAKRQOEAKRQOEAKRQOEAKRQOEAKRQOEAKRQ
KAAEKQDGLWRTEKWKRRKFQEGTVRVGDNISYRPAKQEAERGKVIIEGGKIEEKGRTFADVLEFFRSGGDEA
PVAKLRSVYINRDGKNIISVHDLKQEKD

>GtMC11_jgi|Guith1|146844|fgenes2_pg.136_#_10

MGENTCRICKTLCIGIDAYEHI STLDNAIRDATDVHNQLESSPGCQATLLVNPSTRTAITSQISSLVDRKRT
RGLELILVFFAGHGMQLSKGDIALLTSDIVRAEESEETKQSMITVADMLEALRDGAAQNSDRI PPLLVIID
ACRNSKRSAWMGMERLEHEGSSLIQRMVSLCLSCSRGQQASDESFALEDLLDSEQGMFAQNRRLKLAIEY
AVRMSYDREQKYGQYARTLCTELIPDKLCLRNKTVAADLQQIRMGVESLIQSEGMQPDSTDSGVQVVAA
YSPAARTRGADVRESLQLVKSLFSLQDKGPRWKICSMFLLVFLSNKGTTYKKQGDGRRGFHAFKQMVG
PELIAKTVGKAMVADEIWEKLERWIRERYGEIDRKKMVTAAIDFTVREEIRSSLRHMEEEANAIEIKWVTRN
DYLADHYSKGEQEEALDLAEYLLKDKITADQEGRLSPLLAVHVL SRVVETGSCVAFMKMTRLSSACMSV
MLAKSVREVLGGNGKEGLFRTWISSSGWLSGPREYGEEMEERMEAKEVEMLRLLLLTVGGVSKFIDWKKLE
QPDRKSLEDKPNIKMEKVDVPVKVYTYREEKVPKTSKLLSADSAGVQETPLAGSMLSVMKIEEESFDGAG
IGITVGVDEETSIMWKICQDLKIDLKRLAHECAFYSLSLEHQSMMTDISFFPQLVTALQKRLTKNKEI
NVLGCINKAKESENNDSSQKRELLEGAAMMARALGMNQREKNDLISQKLP SRGKEQIYDCMTKSTQKQTERW
TWQSLNADGSRFRFVEVFGSEGEGPSVPADSKPSRIQIMIRINEGORLEDRTIGFLIIMRQTADIELLEKEL
NLLSEAEQRQEVSDRPCRIELQGAGGCKGHKSAIEIIQDLEQLTPEEFKRVKEAFESEEFKPCRVRGI
ERIVKIEILDDGFGGRKTFDRQDTGYFQAI SERYNKQRSNQDPELGLQLVIKMRVEASVLPSSDVLETLR
PLDASEIETDARALGRVFPEQKAVAGRILNRLKFVLQEEKMSLRDFEKLDFAILVFNFLTLKQQTTEAMLE
TLFSDMTSDRECNKVVHQA PAAEQLRKKILSISDKTLFVLI SDESHWALNKGSPQDLIINDPNLMEKKNF
IVLQVSATPYPNLTLSHRIPEKYVKFEEDDPYKPVQEAKEQKTGEFDEELHVIKWKLRSSRYRTIYFRFED
FLRTLPSYVLDECILPGEEASADDQTREDVRNQLIRRENNLISTLMESVKVSRKKKEEEEAVREHVWLADF
ILSMLYFHKVWRDRSTGRLKSVADDLHNITLKDLEKLEEEYMTIANKCKSSGARQACAKLRERVKETLK
EERSGSAARDCIAEVFYIKLKSEAKEESVEVNDSDSFMEADDFQFNETDRIVKDLLSQRKHNGGLYGHMK
VVMGFSIKLADEVCEELKRIRKSLFGDSVFAVIEDYGGSELYDCIETQFRDEPLTYDKDKAPRSINSLIQG
RARGKCLTSLNYKDLEGLPCILVFLIEKGRMGDTFPHSFDCLDLRVRSSDNNTTTLIQEMGRLCRYPTLREEH
CFETSEEAVQVAKEKRWFEGKGRPIVVYANAADDEVDLSQLDGLKRLIGIAWSLSSWTQKSILOVVERGK
LSPGRRGEEDWYTLDRNVDRSAQASMAEDLKGCMILRFPSTFKIGGSPSWGDVQCLKITESRRQVDETKI
RVQDSSQVKKCPDSTYIIVRDSASLAWLASRHNCPHGGVLEKELEHDLPSALVSSSLYDTLMKAVETAIEYCS
KEIWEICIRLSPQLHMHMKRDRGQGLVSIYQKNELHDIRNQHVAVTRAKAEGEGSKRVKVNHCDCDHTK
RRQHQLRFLHAECQIGKTGAYLHLLNFLRREVGLRADSEYACIPQIRPEDYPIKVEFQTRLAWEMPFWRD
LAGQKGLFKMKEGKYHKMVIQRLRLLAKCLRDSRGRSSWQQLYCKALLAPASSQNAEGECIQVKEKVI
RLLKVKVSDSSPIEIISEGAEVKLRILDVERLRDIVEWDREDSMPSIVADMMKAGLKTRSGETLLQSNQDK
SELSSALGSKTDLQNIWEGRETTAGTSQGLATGQVKNDFPARCLCLHTLPEKTKVLLRSLPMMRGVRI
ARLFGDDERRWPRI SFPFGEEQVSRYSFLKDGRVNGAFELQGEKAIIRNWMTASYKRDAAGSIQTGRAAF
DRSSAFKEGDRDVPVRQMLLVRPDDSEGQGFSSYVSEVGSEYIVVALSHEMILSEAVSELGFRFEQFERQ
MPDDGKLRLTPQDGGIGYARLFAQLFAHLLGLERVWMIIDNVLDCYQLDL SKMFASDPPLLHPPVACSFAT

IMLQMQDMISDAPKSSEEICRQHKKQGGKQACPKTDGFFDHESMI PKSCQAVRGAAAKAAAMERGVKSTS
DISTIQDVRGNTDGYAVIGMRRD VNVFMNSSVPFKITHSVYSFFLLNVKSTIGKGVLFPPKKVWEDVDFNN
LCEEAGLAVLVKVNRFHHKQHRSLHDRLEVDDQPEACEVVCRVHVNGRQIFNVACGSDMSTLSDVYETIVK
RLKRLYPQSDIKKVT CRIQGGDISFAYKESYRDIKELEGQEMCEAVYLDVLF PYEARERMQVDEAIVTTST
SKASIPFLVSLVESQRNIFYFPSRRALDESEGDQFFAEVPAGRKWNELSDKSLDRVKLEELNIMWDDVEA
FKPFFNIVRNLLRDKECIRKINLILPAKAYESMKEKIDDKIKNLRIGNMKTWTTVLPCKEDASQEDD VDM
IEASQSDNAESTMDFVVICCSSEEEKKAAQDKGEGLRAEAEDEAKQQEAEDEAKQQEAKQQEAKPQAEESD
SSKKPKTEEPEKRKSSEPPVGESPAKKGKAAEKQGLWRIEKWKRFQEGAVRVGDNISYRPAKQEAAREGK
VIEGGKIEEKGKT FADVLEFFRSVDDGDASGSAPGQKLR SVYINRDGKNFISVHDLKQEKD

>GtMC12 jgi|Guith1|163584|estExt_fgenesh2_pg.C_400124
MSHAGVTLTSLVIDFRYRDEGNQVQDRGLGPFLEMYAFRVGNLRLERYSLHVHTLKKWSEREQHVWDRARR
ITAVNIRRCARRDETGYFKDVELYGLPVLPCSPHLRRHWRNYLDRSQDLEWDCTKLRVYHTETESKQETIR
NVRGGLKQKEEEEFDLVLQERLEVFALCIGVGGYEMLPPLPQALRDSHDFLHALRRMPCRGRVEISDPTEN
DLLYLLEKHLEVI AKFPSSWILVTFSGHVLKEGKSGELCFLKDFDASWLDRLDEEPEGAVTLGDIVKLWT
KWFEPHPPVLLLLVDGCRMTMPDQPQLHAVDLPTGWSMCMSSRRTERGETIQEASYMHSMMMMDQENGMFAGG
ERLRGVLTRIRDQAPAGIAVEESWKEDPRLPEMFSFSDIIEFPAAVLQDNDGDIREEEEQETGAGAGAGAG
AG
NLLDAAGELCVEVGRSDDAVKLFRRSIELRPEENSCKYMNGLQLMAGAESLELFLKGLALMRQELGNVAEE
KGEEAKKLRGLCSAHC SVAELYMTDLCEENAEAGILKLLIELEQLDEAEFGNLLLQVDDQYVETWYLL
ALIHFRGAHSAHHCTLSAIKILEQEGVEDEDQASRLQELHEEIEKNLRDGNNDVAMEDEEGDEDGDWMT
DDEEEAHP

>GtMC13 jgi|Guith1|144452|fgenesh2_pg.87_#_38
MEAAEEEEAEVRAIAKLLLEVYCKGSNGKYDAYTDKKLVDTCQRELGEEMVETRTGGPKGRLLRAFADKLNK
FDKFSGKTRTEALCNLAEILNKKVGPQRQPTPERQKLALIIGISNYDKEALPNCTSDARCI SEAFKSRGFE
TYLEFDTQDQESFWKVEYEDFASKIRPPCTVLFYVAAHGAQFHTDVLVFP IIPFRTKDAEKAI SMQAMINKI
STRLD PDS DVVMLLDTCRVNFSQRGHQDLEQLATLPQTWILYATKESYPVCDGPDGGNSPFTRAVLRTLKE
LGPDVEFYKFATSVNKYVRDCGMQRSELKADMTKELFI

>GtMC14 jgi|Guith1|149022|fgenesh2_pg.268_#_3
MDETREGGSRWDGSHLQVQLVAIEPGVTDKRCNVRNPPAAVLLTGTFLDPCQPCVLGRLEVSYLILTS
PSLSDLPGLALTTRCIDVCVDRRSLKSEQRGQEQLTDQDQTQEQQQLTDQEQEGRGRLEGEQDCQVDG
EIIYEENGFTSFQVGGGDSQGEPAASRGVVRNEEGRGADEEQGEHGQGAPGEGPVSTRAAASPDRIEGTPPT
RSRRSSGVSSSAEKSTGRAKSPATPGLSPDGGLDEIRQGLAKAELKEKEVEEVI EKMKSLGVRGKKDIKF
VRELIDIKTLDLTEMSKLRVEKYLKRFARKKKPASPGEEESLFRSLKQFDVHLNVQSCMFSSRMAEDFP
WNLQEEKSIEDRQRTSVNELYERLKSDDNLEVDFLYLLTVSWCLSRCDPVLGFNEFPYTCGGS LKREWR
IEREVWFLLRATSEGVPPTYIVFHLLFAGMWRESREERDCSVVGKVRMRSSTKVRSKKHVYKCTDTTKWDS
AGGGLDLRSSSMARWRWREGAEGEESMAKVRGWLVAEQEAPFAQAVTVGPCWNLAGTRRRRAALIVCNQAY
RRARCFPELYNPVPDGRQLGEVLEELGWKVEFRVDLNL EELVGAVRCFRDAIGDNE SAAMLA FVGHGVEVH
GKLFLLPTDIQLEVDNYFQREKDLAADLARC SLSF DAVQSELRGRNGTCPTL FVL DCCRSSNNSRSPIFQP
STTVQNLELKNSCIIYSTQSGQVALEGAPDGGPFMSAFAGELRKEEAELNQLVIETRKIVMNSTGGAQMA
PNQSLLELQFFFPCPEIAACL

References

1. Matthijs, M. *et al.* The transcription factor bZIP14 regulates the TCA cycle in the diatom *Phaeodactylum tricornutum*. *EMBO J.* **36**, e201696392 (2017).
2. Smith, S. R. *et al.* Transcriptional orchestration of the global cellular response of a model pennate diatom to diel light cycling under iron limitation. *PLOS Genet.* **12**, e1006490 (2016).
3. Wong, A. H.-H., Yan, C. & Shi, Y. Crystal structure of the yeast metacaspase Yca1. *J. Biol. Chem.* **287**, 29251–29259 (2012).
4. Alexander, H., Jenkins, B. D., Rynearson, T. A. & Dyhrman, S. T. Metatranscriptome analyses indicate resource partitioning between diatoms in the field. *Proc. Natl. Acad. Sci.* **112**, 201421993 (2015).
5. Rosenwasser, S. *et al.* Mapping the diatom redox-sensitive proteome provides insight into response to nitrogen stress in the marine environment. *Proc. Natl. Acad. Sci. U. S. A.* **111**, 2740–5 (2014).
6. Hopes, A., Nekrasov, V., Kamoun, S. & Mock, T. Editing of the urease gene by CRISPR-Cas in the diatom *Thalassiosira pseudonana*. *Plant Methods* **12**, 49 (2016).
7. Siaut, M. *et al.* Molecular toolbox for studying diatom biology in *Phaeodactylum tricornutum*. *Gene* **406**, 23–35 (2007).