

Supplementary Material for

## **Metallomics reveal a persisting impact of cadmium on the evolution of metal-selective snail metallothioneins**

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† deceased. We want to dedicate this work to our longtime cooperation partner, Silvia Atrian

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### **This PDF file includes:**

Tables S1 and S2

Figs. S1 to S5

FASTA-file sequence alignments S1 to S5

References

37 **Table S1:** PCR conditions for the neutral markers COI and 18SrDNA: a) Thermal cycles followed <sup>1</sup> with  
 38 the annealing temperatures adjusted according to the particular primers, samples, and polymerase used. b)  
 39 PCR mix for MyTaq Polymerase c) PCR mix for Rotorgene probe-PCR for samples which did not amplify  
 40 with MyTaq Polymerase

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<b>a) Thermal cycles:</b>	<b>step</b>	<b>temperatur e</b>	<b>time</b>	<b>cycles</b>
	Intitial step	95°C	4 min	1x
-	denaturation per cycle	95°C	30 s	38x
	annealing per cycle	50 - 65°C	45 s	
	elongation per cycle	72°C	150 s	
	final step	72°C	10 min	1x
<b>b) PCR mix for MyTaq Polymerase</b>	<b>reagent</b>	<b>volume (µl)</b>		
	dH <sub>2</sub> O	5.55		
	5x PCR Buffer	2.00		
	BSA 100µg/µl (final conc. 10µg/µl)	1.00		
	each primer (final conc. 0.2µM)	0.20		
	MyTaq polymerase Bioline	0.05		
	template DNA	1.00		
<b>c) PCR mix for Rotorgene probe-PCR</b>	<b>reagent</b>	<b>volume (µl)</b>		
	dH <sub>2</sub> O	3.6		
	2x Rotorgene Mastermix Qiagen	5.00		
	each primer (final conc. 0.2µM)	0.20		
	template DNA	1.00		

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47 **Table S2** – Lists of primers and cycling parameters applied for PCR confirmation of MT sequences

48 **2A:** Description of applied gene-specific primers used for Long Distance PCR

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<i>Species</i>	<i>MT Isoform</i>	<i>Primer</i>	<i>Sequence 5'-3'</i>	<i>T<sub>m</sub> [°C]</i>	<i>T<sub>mAn</sub> [°C]</i>
<i>Neritina pulligera</i>	MT1	Fw	TCA TCG TAC TCA CCA CTC CA	58.4	57
		Rev	TGG ACA AGG GGG TAA ACG A	57.5	
	MT2	Fw	CAG TGT CGT GTG CAG AGA GA	60.5	58
		Rev	CAG TCC AGA ATG TCT TCT TCC	59.5	
<i>Deroceras reticulatum</i>	CdMT	Fw	GGC TTA AAC GAG GAC CTG	56.3	54
		Rev	AGC TTG ATT ATT TGT CAG GTA C	56.4	
	CdMT2	Fw	CAG TCC AGA ATG TCT TCT TCC	59.5	54.5
		Rev	CTT GAA TCT TGA GAG TGG CA	56.4	
<i>Marisa cornuarietis</i>	MT1	Fw	CGT GTT GTT GTG GTT GTT	51.4	49.5
		Rev	GCA CAT ACA GAC AGG AAT	51.4	
	MT2	Fw	GTC GAC AAC CGA ACC ATC CT	60.5	58.5
		Rev	GCA GAC ATC GTG TCA CTT GC	60.5	
<i>Anentome helena</i>	MT	Fw	TCA CTT TTC CGT GAC TTG CT	56.4	54.5
		Rev	AAA GGC TTA CAA GGC GGG G	59.5	
<i>Aplysia californica</i>	MT	Fw	CGT ACG TCA CCA CCA GAG AT	60.5	54
		Rev	AAT GCT CTC CGC ACG CTA	56.3	
<i>Alinda biplicata</i>	MT1	Fw	GTC AAG TTT ACG ATC TGC G	52.9	52
		Rev	TCA ATC CCA TCC AAC CAA C	52.9	
	MT2	Fw	AGG TCA AGT TTA CGA TCT GCG T	60.1	58
		Rev	CCT AAC CAC ACA ACT CCC GT	60.5	
	9md-MT	Fw	TCC TCG TAC CGT ATC TCA GC	60.5	58
		Rev	ACG CTC AAT GTA GTC TTA TGT TGC	62.0	
	10Md-MT	Fw	TCC TCG TAC CGT ATC TCA GC	60.5	58
		Rev	ACG CTC AAT GTA GTC TTA TGT TGC	62.0	
<i>Patella vulgata</i>	MT1	Fw	GAC GCA CAC AAT CAG A	48.1	47
		Rev	AGC CAT TGC ACG AGA C	50.6	
	MT2	Fw	AGT AAG ACA CCC ACA GTC AG	58.4	53
		Rev	ACG GGG ATA GAA GAC ACA A	55.0	
<i>Lottia gigantea</i>	MT1	Fw	CTT CTC AAA GCT TCT ACA GAA T	56.4	53
		Rev	CAA GAT TGT GTG CAT GAT GAA	55.4	
	MT2	Fw	CCG CAG AGT ACA GCA ATT CAT A	60.1	55.5
		Rev	GGT ATG TGA GTC AAC AAA GAG	57.5	

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51 **2B:** Applied cycling conditions, using the Advantage 2 polymerase PCR system (see Material and  
52 Methods).

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	<i>Temp [°C]</i>	<i>Time</i>	<i>Cycles</i>
Denaturation	95	1 min	1
Denaturation	95	30 sec	30
Annealing	See table 1	30 sec	
Extension	68	40 sec – 1 min	
Final Extension	68	5 min	1

55 **Table S3:** List of gastropod Metallothionein sequences applied for the present study. Gastropod clades and major lineages (first column) with family names (second  
56 column), species names with consecutive numbers (bold blue letter fond in square brackets) (third column), MT designations (fourth column), sequence data source  
57 and databank deposition (fifth column), PCR confirmation (sixth column), kind of metal selectivity (seventh column), reference numbers (eighth column) and  
58 consecutive sequence numbers (ninth column) are shown. MT sequences with red consecutive numbers (last column) were sequenced *de novo* and are published in  
59 the present study for the first time. All other MT sequences (last column, black consecutive numbers) are reported from previous studies (see references) or were  
60 identified from publically available databases (see material and methods). Metal selectivity features (Cd – red; Cu – blue; yellow - unspecific) of single MTs (seventh  
61 column) were either directly determined by MS methods (☞), derived from other kinds of experimental evidence combined with sequence homology (●), or only  
62 deduced from sequence homology by alignment with related sequences of known metal-binding character (no symbol).  
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<i>Clade</i>	<i>Family</i>	<i>Species</i> [Species Number]	<i>MT Name</i>	<i>Data source and Acc. No.</i>	<i>PCR-confirmed</i>	<i>Kind of Metal selectivity</i>	<i>References</i>	<i>Sequence No.</i>
<i>Patellogastropoda</i>	<i>Lottiidae</i>	<i>Lottia gigantea</i> [1]	MT1	GenBank MK770430	yes	Cd ☞		1
			MT2	GenBank MK770431	yes	Cd ☞		2
	<i>Nacellidae</i>	<i>Nacella polaris</i> [2]	MT	SRA; SRR2061227	no	Cd		3
	<i>Patellidae</i>	<i>Patella vulgata</i> [3]	MT1	GenBank MK443472	yes	Cd		4
			MT2	GenBank MK443472	yes	Cd		5
<i>Vetigastropoda</i>	<i>Fissurellidae</i>	<i>Megathura crenulata</i> [4]	MT	GenBank AY102647.1	-	Unspecific ☞	2,3	6
	<i>Haliotidae</i>	<i>Haliotis diversicolor</i> [5]	MT	GenBank EU071824.1	-	Unspecific		7
			MT	GenBank KT895222.1	-	Unspecific		8
			MT	GenBank GEAU01019532.1	no	Unspecific		9
			MT	GenBank GFTT01185788.1	no	Unspecific		10
	<i>Tegulidae</i>	<i>Tegula atra</i> [9]	MT	GenBank GFBI01039752.1	no	Unspecific		11
<i>Neritimorpha</i>	<i>Neritidae</i>	<i>Nerita peloronta</i> [10]	MT1	SRA; SRX644686	no	Unknown		12
			MT2	SRA; SRX644686	no	Unknown		13
		<i>Neritina pulligera</i> [11]	MT1	GenBank MK577683	yes	Unknown		14
			MT2	GenBank MK577684	yes	Unknown		15
	<i>Titiscaniidae</i>	<i>Titiscania limacina</i> [12]	MT	SRA; SRX644702	no	Unknown		16

<b>Caenogastropoda</b>	<i>Littorinidae</i>	<i>Littorina littorea</i> [13]	MT	GenBank AY034179.1	-	Cd $\mathcal{R}$	<sup>3,4</sup>	17
	<i>Pomatiiidae</i>	<i>Pomatias elegans</i> [14]	MT1	GenBank KY636305.1	-	Cd •	<sup>3</sup>	18
			MT2	GenBank KY646306.1	-	Cd •	<sup>3</sup>	19
	<i>Nassariidae</i>	<i>Tritia obsoleta</i> [15]	MT	GenBank FK716482.1	no	Cd	<sup>3</sup>	20
	<i>Calyptraeidae</i>	<i>Bostrycapulus sp.</i> [16]	MT	SRA; SRP042651	no	Unknown		21
		<i>Crepidula fornicata</i> [17]	MT	SRA; SRP042651	no	Unknown		22
	<i>Ampullariidae</i>	<i>Pomacea bridgesii</i> [18]	MT1	GenBank KY963504.1	-	Unspecific $\mathcal{R}$		23
			MT2	GenBank KY963505.1	-	Unspecific $\mathcal{R}$		24
		<i>Pomacea canaliculata</i> [19]	MT20-III like variant X-1 like	GenBank XM_025255587.1	-	Unspecific		25
			MT20-III like variant X-2 like	GenBank XM_025255589.1	-	Unspecific		26
			MT20-III like variant X-3 like	GenBank XM_025255590.1	-	Unspecific		27
		<i>Marisa cornuarietis</i> [20]	MT1	GenBank MK577687	yes	Unspecific		28
			8md-MT	GenBank MK577688	yes	Unspecific		29
<i>Buccinidae</i>	<i>Anentome helena</i> [21]	MT	GenBank MK577685	yes	Unspecific		30	
<b>Heterobranchia</b>	<i>Aplysiidae</i>	<i>Aplysia californica</i> [22]	MT	GenBank MK577686	yes	Unknown		31
	<i>Clionidae</i>	<i>Clione limacina</i> [23]	MT	GenBank GESV01103158.1	no	Unknown		32
	<i>Limacinidae</i>	<i>Limacina retroversa</i> [24]	MT	GenBank GBXC01058817.1	no	Unknown		33

<b>Heterobranchia</b> <i>Panpulmonata</i> <i>Hygrophila</i>	<i>Plakobranchidae</i>	<i>Elysia crispata</i> <a href="#">[25]</a>	MT	GenBank KY963503	-	Unknown		<b>34</b>
		<i>Elysia cornigera</i> <a href="#">[26]</a>	MT	GenBank GBRW01068275.1	no	Unknown		35
	<i>Physidae</i>	<i>Physella acuta</i> <a href="#">[27]</a>	MT1	GenBank GU259686.1	-	Unspecific	<sup>5</sup>	36
			MT2	SRA; SRP042651	no	Unspecific		37
		<i>Physella caroliniae</i> <a href="#">[28]</a>	MT	SRA; SRP042651	no	Unspecific		38
		<i>Physella hendersoni</i> <a href="#">[29]</a>	MT	SRA; SRP042651	no	Unspecific		39
		<i>Physella gyrina</i> <a href="#">[30]</a>	MT	SRA; SRP042651	no	Unspecific		40
	<i>Lymnaeidae</i>	<i>Galba cubensis</i> <a href="#">[31]</a>	MT	SRA; SRP042651	no	Unspecific		41
		<i>Galba trunculata</i> <a href="#">[32]</a>	MT	SRA; SRP042651	no	Unspecific		42
<i>Lymnaea stagnalis</i> <a href="#">[33]</a>		MT	GenBank FX201894.1	yes	Unspecific •		43	
<i>Planorbidae</i>	<i>Biomphalaria glabrata</i> <a href="#">[34]</a>	MT + genomic variants	GenBank KY963495.1	-	Unspecific R	<sup>5,6</sup>	44	
<i>Panpulmonata</i> <i>Stylommatophora</i>	<i>Agriolimacidae</i>	<i>Deroceras reticulatum</i> <a href="#">[35]</a>	CdMT1	GenBank MK672823	yes	Cd		<b>45</b>
			CdMT2	eSnail database CL8321.Contig1	yes	Cd		46
	<i>Arionidae</i>	<i>Arion vulgaris</i> <a href="#">[36]</a>	AvMT1	GenBank MF155618.1	-	Cd R	<sup>7</sup>	47
			AvMT2	GenBank MF155619.1 MF155620.1	-	Cu R	<sup>7</sup>	48
	<i>Limacidae</i>	<i>Lehmannia nyctelia</i> <a href="#">[37]</a>	CdMT	eSnail database CL1241.Contig1	no	Cd		49
		<i>Limax maximus</i> <a href="#">[38]</a>	CdMT	GenBank MH574544	-	Cd		50
<i>Panpulmonata</i>	<i>Clausiliidae</i>	<i>Alinda biplicata</i> <a href="#">[39]</a>	CuMT1a	GenBank MK648138	yes	Cu		<b>51</b>

<i>Stylommatophora</i>		CuMT1b	SRX7671047	no	Cu		52	
		CuMT2	GenBank MK639793	yes	Cu		53	
		9md-MT	GenBank MK648139	yes	Cd		54	
		10md-MT	GenBank MK648140	yes	Cd		55	
	<i>Cochlicellidae</i>	<i>Cochlicella acuta</i> [40]	CdMT	eSnail database Unigene52262	no	Cd	<sup>7</sup>	56
			CuMT	eSnail database Unigene18701	no	Cu	<sup>7</sup>	57
			CdCuMT	eSnail database Unigene65576	no	Unspecific	<sup>7</sup>	58
	<i>Helicidae</i>	<i>Arianta arbustorum</i> [41]	CdMT (MTa)	Uniprot P55946	-	Cd •		59
		<i>Cornu aspersum</i> [42]	CdMT	GenBank EF152281.1	-	Cd •		60
			CuMT	GenBank EF178297.2	-	Cu •		61
			CdCuMT	GenBank EF206312.1	-	Unspecific •	<sup>8,9</sup>	62
			<i>Cepaea hortensis</i> [43]	CdMTV1	GenBank MH574545	-	Cd •	<sup>7</sup>
			CdMTV2	GenBank MH574546	-	Cd •	<sup>7</sup>	64
			CdCuMT	GenBank MH574547	-	Unspecific •	<sup>7</sup>	65
		<i>Cepaea nemoralis</i> [44]	CdMT	GenBank GFLU01086707.1	no	Cd		66
			CuMT	GenBank GFLU01065470.1	no	Cu		67
			CdCuMT	GenBank GFLU01003885.1	no	Unspecific		68
		<i>Helix pomatia</i> [45]	CdMT	GenBank AF399740.1	-	Cd $\mathcal{R}$	<sup>10-12</sup>	69
			CuMT	GenBank AF399741.1	-	Cu $\mathcal{R}$	<sup>10-12</sup>	70
			CdCuMT1	GenBank KY420172.1	-	Unspecific $\mathcal{R}$		71
			CdCuMT2	GenBank KY420171.1	-	Unspecific $\mathcal{R}$		72
		<i>Theba pisana</i> [46]	MT	eSnail database CL8321.Contig1	no	Cu		73
	<i>Helicoidea</i>	<i>Nesiohelix samarangae</i> [47]	CdMT (MT)	GenBank EU437399.1	-	Cd		74

65 **Table S4:** Distance analysis with Identity and Similarity values (Means and Standard Deviations) of N-terminal  
 66 versus C-terminal domains of Cd-selective MTs of Patellogastropoda, Caenogastropoda and Heterobranchia with  
 67 the same sequences as adopted in **Fig. 3**, and for unspecific gastropod MTs. For N-terminal domains, calculation  
 68 was performed without the N-terminal extension up to the first Cys position. For C-terminal domains, the linker  
 69 region was included. Note that both similarity and identity scores are significantly higher for C-terminal domains.  
 70 This supports the hypothesis of a higher degree of conservation for C-terminal domains of gastropod Cd-selective  
 71 MTs. Calculations were performed using the openly accessible program package SIAS (Sequence Identity And  
 72 Similarity) of the Immunomedicine group of the Universidad Complutense Madrid  
 73 (<http://imed.med.ucm.es/Tools/sias.html>).

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**S4A: Cd-selective MTs**

	<b>N-terminal Domain</b>	<b>C-terminal Domain</b>	<b>Difference (mean)</b>
<b>Identity:</b>			
All Cd-selective MTs	53.47% ( $\pm$ 20.78%)	66.17% ( $\pm$ 12.02%)	-12.70%
Patellogastropoda versus Littorinoidea	34.68% ( $\pm$ 3.07%)	66.56% ( $\pm$ 5.89%)	-31.88%
Patellogastropoda versus Stylommatophora	31.62% ( $\pm$ 2.69%)	59.10% ( $\pm$ 6.19%)	-27.47%
Littorinoidea versus Stylommatophora	47.49% ( $\pm$ 4.35%)	62.79% ( $\pm$ 5.97%)	-15.30%
<b>Similarity:</b>			
All Cd-selective MTs	58.01% ( $\pm$ 20.05)	71.47 ( $\pm$ 11.36%)	-13.46%
Patellogastropoda versus Littorinoidea	36.97% ( $\pm$ 3.82%)	69.31% ( $\pm$ 5.31%)	-32.34%
Patellogastropoda versus Stylommatophora	36.39% ( $\pm$ 2.99%)	63.17% ( $\pm$ 7.82%)	-26.78%
Littorinoidea versus Stylommatophora	54.70% ( $\pm$ 4.37%)	66.86% ( $\pm$ 7.64%)	-12.16%

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84 **S4B: Unspecific MTs**

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	<b>N-terminal Domain</b>	<b>C-terminal Domain</b>	<b>Difference (mean)</b>
<b>Identity:</b>			
All unspecific MTs	61.91% ( $\pm$ 16.11%)	59.10% ( $\pm$ 15.30%)	+2.80%
Vetigastropoda versus Ampullariidae	57.64% ( $\pm$ 5.43%)	55.86% ( $\pm$ 7.94%)	+1.78%
Vetigastropoda versus Hygrophila	49.36% ( $\pm$ 7.44%)	51.85% ( $\pm$ 8.33%)	-2.49%
Ampullariidae versus Hygrophila	52.75% ( $\pm$ 5.92%)	54.54% ( $\pm$ 5.63%)	-1.79%
<b>Similarity:</b>			
All unspecific MTs	67.087% ( $\pm$ 14.63%)	63.60% ( $\pm$ 14.60%)	+3.48%
Vetigastropoda versus Ampullariidae	62.35% ( $\pm$ 5.55%)	63.06% ( $\pm$ 7.54%)	-0.71%
Vetigastropoda versus Hygrophila	55.02% ( $\pm$ 7.87%)	56.14% ( $\pm$ 8.90%)	-1.12%
Ampullariidae versus Hygrophila	60.24% ( $\pm$ 7.30%)	60.03% ( $\pm$ 8.41%)	+0.21%

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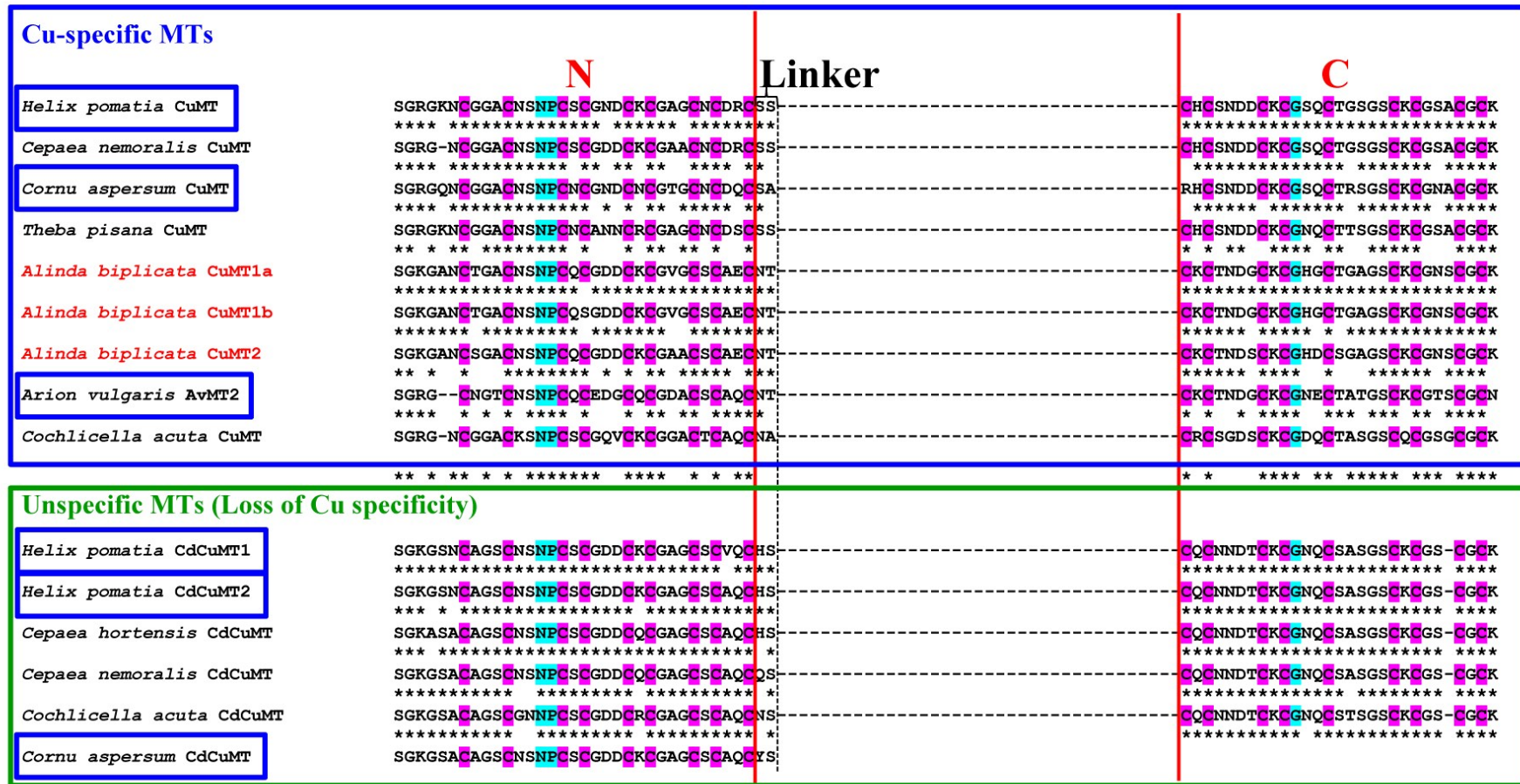
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90 **Figure S1:**

91 Metal-binding domain organization and amino acid sequence alignment of Cu-selective (CuMTs, (framed in blue) and unspecific MT isoforms (called CdCuMTs, framed  
 92 in green) from terrestrial snail and slug species of the order of Stylommatophora (clade Heterobranchia). Cys positions are underlaid in pink, conserved non-Cys positions  
 93 through sequences of all species are underlaid in blue. Identical amino acid positions between pairwise aligned sequences are indicated by black stars. Domain boundaries  
 94 of the N-terminal and the C-terminal domains (designated above the alignments as N and C in red letters) are symbolized by perpendicular bold red lines. The linker region  
 95 between the N and the C-terminal domains are designated in black letters, their boundaries are symbolized by perpendicular dotted black lines. The gaps between the two  
 96 domains indicate the lack of a second N-terminal domain (present in other gastropod MTs). MTs of species shown in red letters were sequenced for this study *de novo* and  
 97 are published here for the first time. Sequences of all other species (in black letters) were identified from publically available publications or databases. Species for which  
 98 metal selectivity features of respective MTs were documented experimentally by us through MS or NMR methods elsewhere are framed in blue. The bold red arrow on the  
 99 right hand of the alignments points to sequence similarities between Cu-selective and unspecific MTs.

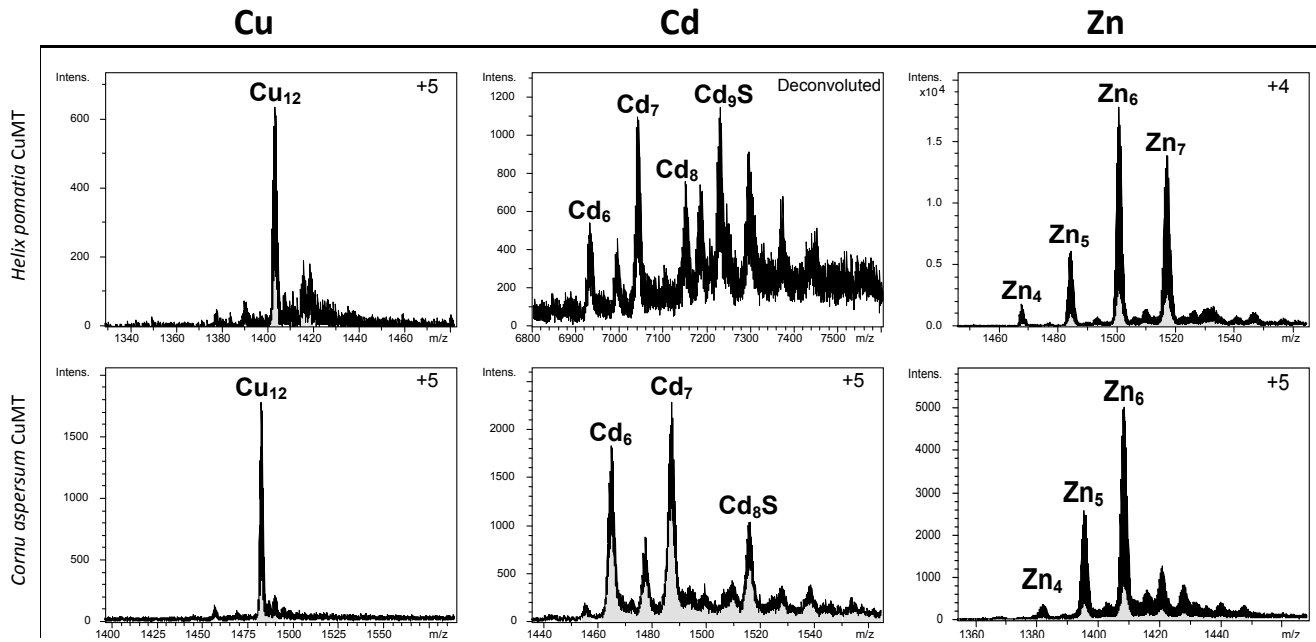
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139 **Figure S2:**

140 Cu-selective MTs from terrestrial snails *Helix pomatia* and *Cornu aspersum* of the order of Stylommatophora  
141 (Heterobranchia). ESI-MS spectra of MT species recombinantly produced in different meal-enriched media (Cd, Zn  
142 and Cu) at the corresponding charge state (as indicated in the upper right corner) or deconvoluted. Spectra are re-  
143 drawn from data reported in <sup>11</sup> and <sup>9</sup>.

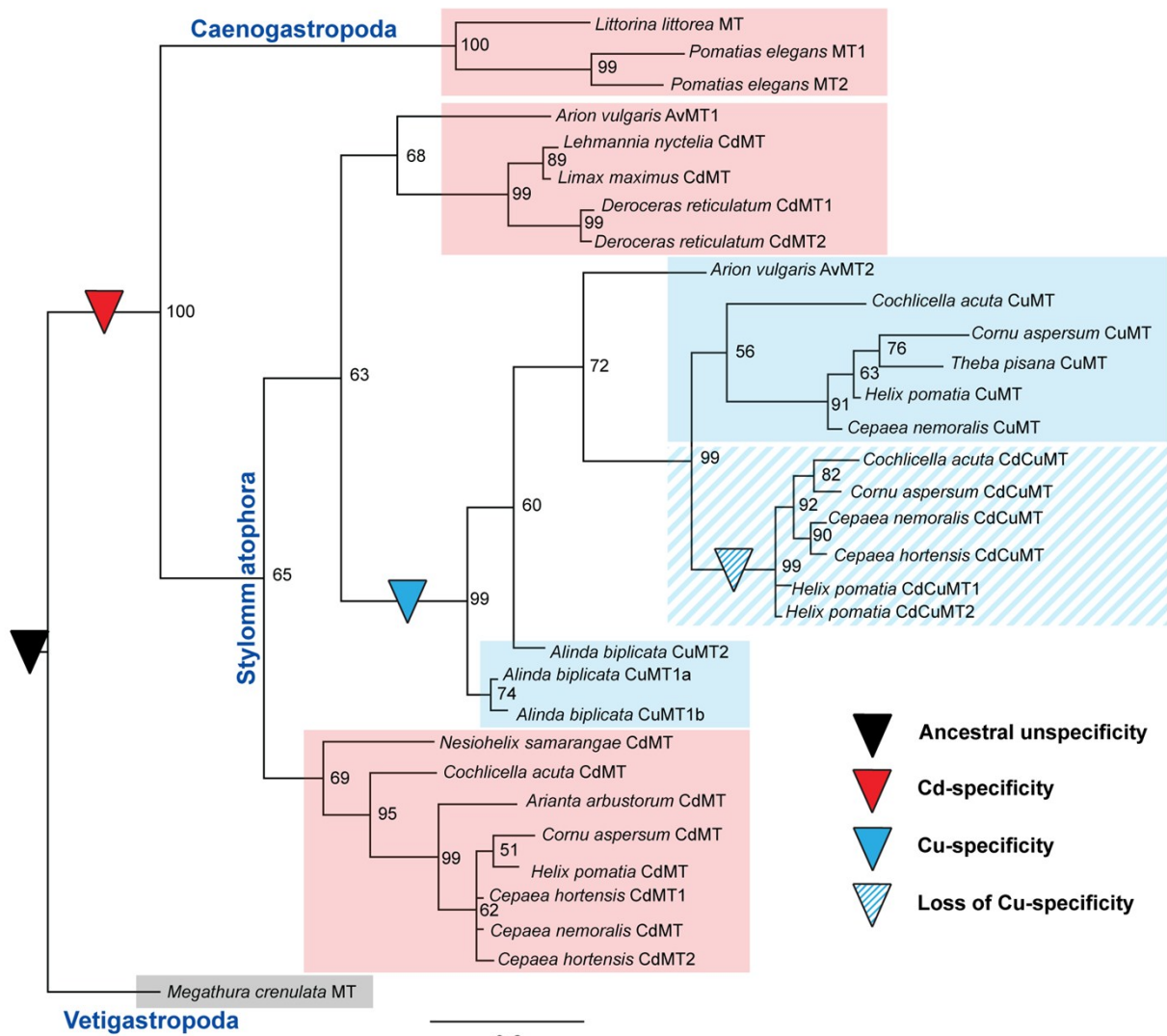
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152 **Figure S3:**

153 Bayesian Inference tree with bootstrap support values of metal selectivity features in MTs of the clade of  
 154 Caenogastropoda and in the order of Stylommatophora (a taxon of Heterobranchia with land snails and slugs), rooted  
 155 against the unspecific MTs of Vetigastropoda (represented by *Megathura crenulata*, underlaid in gray). Ancient  
 156 unspecificity of MTs at the root of Vetigastropoda is indicated by a black triangle. Gain of Cd selectivity in MTs at  
 157 the root of divergence between Caenogastropoda and Heterobranchia (represented only by Stylommatophora) is  
 158 indicated by a red triangle, species possessing Cd-selective MTs are underlaid in pink. Gain of Cu selectivity in MTs  
 159 of Stylommatophora is indicated by a blue triangle, respective species possessing Cu-selective MTs are underlaid in blue.  
 160 Secondary loss of Cu selectivity in CdCuMTs of land snails and slugs is indicated by a blue hatched triangle,  
 161 species with unspecific MT isoforms are highlighted within a blue hatched square. Bayesian inference calculations  
 162 were made based on a manually edited MUSCLE alignment (see **alignment S5**) using the free software MrBayes (see  
 163 Material and Methods)



204 **Alignment S1:**  
205 Concatenated NEXUS alignment of the mitochondrial COI sequences (position 1-580, start=3rd codon position) and the ribosomal 18SrDNA sequences (position 581-2158;  
206 aligned using the SINA Alignment tool v. 1.2.11) of the nineteen gastropod species analysed for neutral phylogeny markers, applied for the mirrored Maximum Likelihood  
207 tree represented in **Figure 6**

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209  
210 *Patella vulgata*  
211 CGGCCTTAGTATATTAATTCGAGCTGAACCTGGTCAGCCAGGCGCT---CTTTTAGCGGATGACCAACTTTATAATGTTATGTTACTGCTCAGCCTTTTGTATAATTTCTTTTTAGTAATGCCTATAATAATGGGGGTTTTGGTAATTGATTAG  
212 TGCCACTTATGCTTGGGGCCCTGATATAGCTTTTCCCGACTTAACAACATAAGATTTTGACTTCTCCCTCCCTCTCTATTTCTTCTTTTAGCCAGAAGAGCTGTTGAAGGTGGGGTAGGTACAGGTTGAACAGTTTTATCCTCCTTTATCTTCAAAT  
213 ATTGCCACTCAGGCCCTTCGGTAGATTTAGCTATTTTTCTCTCCACCTAGCTGGTGCCTCTCAATTCGGGAGCTGCTAATTTTATTAGAACGGCCGCAACATTCGTTGAGAAGCTATGCAACTTGAACGAATGCCTTTGTTGTCTGATCTGT  
214 AAAGGTAACCCATTTTATTACTTCTATCTTTACCTGTTTTAGTCCGGGGCAATTACTATACTATAACTGACCCTAATTAATACTGTTTCTTTGACCCTAGGGTTCA-GGCT----TGTTCCTTTCGGGGAGCGAGCCGAAACTGCGAACGGC  
215 TCATTAG-TCAGATAAGGTTCTTGGCGAAAA----GCGGGTCGGTTAATGGATAACTGTGGTAATCTAGAGCTAATACATGC--AA-CGCACCGT-GGTC-CCCCC-T-TTCGTTTCTCGACAAAGAGG----GG-AAACGGC-ATTTAT  
216 TCTCTATACCAGATCGCC-CTAGCCTGCGAAGCTACCGTC--A-----AAAGTA-GC-----GACGGGGCGAA-GCGACAAGT-GTTGAA-ATCCGAATAACTGTG--CCGATCGCGGGTCTTTC-CGGGC-----CCCCGACCACTT  
217 TGCCATGAAGTGTCTGTCCCATCAATTTGGCGATGGTCGGCGACCTGCCTACCACGGTGTGACGGGTAACGGGGAATCAGGGTTCGATTCCGGAGAGGGAGCCTGCGAAACGGCTACCACCTCCAAGGAGGGCAGCAGGCGCGCAACTTACCCAACTC  
218 CGACAGCGGGAGGTGAAATTTGTATCCGCTCGGGACGACTCGAA-GCGAAAGCGCTGGCCCCGGACCTTCCCTTAATCCAGAACGAAG-GTGGGTGGAGCAAAGACGATCAGATACCGTCTGATGACCGACGGTAAACCGTCCCGACCGGGCCGGAC  
219 GAGTTGCTGCGGTTAAAAAGCTCGTCTGGATCTCGGAGGCGGCACGGTCGGGCGCGATACGCT--GCGGGTCCGACC-----GGCGAT-TTCT--C--G-----GCC--GT-C-  
220 -----C-C-T--AA-CC-G-CGCGCGGG---GCGAGGTGG--ACTTCACGG--TC--CTGCCTCGTTTTCTCCTT-C-GCGG-GAGAGA----ACCGCGG-CATTTTCTGCTACCTTGAAAAAATTAGAGTGTAAAGGCAGGCTAAACCC  
221 -CGA-----GCCTGAATATTTCTGTCATGGAATAAGCGGGGATGCTTTTTCCGGAGGGTGGTCCGGCCGACTTGG----CGACGTCGCTTTCGCTGTGCGTTTCGCGGAGA-GCTAGGATTCGAGAGGAACGGTGGGGGGCGAGCGTACC  
222 GGGAGAGGTGAAATTTGTATCCGCTCGGGACGACTCGAA-GCGAAAGCGCTGGCCCCGGACCTTCCCTTAATCCAGAACGAAG-GTGGGTGGAGCAAAGACGATCAGATACCGTCTGATGACCGACGGTAAACCGTCCCGACCGGGCCGGAC  
223 GA-GGCTCGAGAACAGCGGTTATGGACCCGTCGTTGGCGGCTT-CGGGCAACCTGAGAGTTACGGGTTCCGGGGGTAGTATGGTCGCAAGGCTGAAACTTGAAGGAATTGACGGAAGGGCACCACAAGGAGTGGAGCCTGCGGCTTAATTTGACTCA  
224 ACACGGGGCAACTTACCCGGTCCGGACATCGTCAGGATTACAGACGCTCGTGCAGTCTTTCTCGATTGATGGTGGTGGTGCATGGCCGTTCTGTGGTCG

225  
226 *Alinda biplicata*  
227 AGGGCTTTCTTTATTAATTCGATTAGAGTTAGGAACAAGAGG-----GTATTACTTGATGATCATTTTTTTAATGTAATTGTACAGCGCACGCCCTTCTGTTATAATTTTTTTTATAGTTATACCGGTAATAATTTGGGGGTTTTGGCAATTGAATAG  
228 TACCCCTTCTCATTGCTGCACCTGATATAAGATTTCCCTCGAATAAATAATAAATAAGCTTTTGGTTATACCTCCGGCTTTCCTTTTATTAATTAGTAGTAGAATAGTGAAGGGGGGCTGGTACAGGTTGAACCGTATATCCGCCCTTAAGAGGTATT  
229 GCCGCCCATGGTGGCGCCTCTGTTGATTTGGCAATTTTTCTTTGACCTTGCAGGAATATCCTCTATTTTAGGGGCTATTAATTTTATCACTACGGTATTTAATATACGTAGAAGAGGGATAAATATAGAACAGGTAAGTCTTTTGTATGATCTAT  
230 TTTAGTGACGGTTTTTTTTTACTACTTAGCTTACCAGTATTAGCTGGTGGCATCTACTATGTTATTAACCTGATCGAAATTTAATACTTGTTTTTTGTATCCCGCAGTTCACA-CT-----GTCTC-AC----GGTGA----AACCGCAATGGC  
231 TCATTAATCAGTTCGAGTTCTTAGATGACA-----CGA-T-CC-TACTTGGATAACTGTGGCAATCTAGAGCTAATACATGCTTAC----CA-AG--CTC-CGACC--C-TC-GC-----GG-AA--AGA-CGCTTT  
232 TATTAGTTC-AA--AAC-CAAT-----CGG-CGTCGCCCT-----TCG-C-----GGGGT-GCG-TCGTCC-----AAC-T-GGTG-A-CTCTGGATAACTTTGTGCTGATCGCATGGC----CTCACGT-----GCC-GGCGACGCA  
233 TCTTTCAAATGTCTGCCCTATCAAATGTCGATGGTACGTGACATGCCTACCATGTTTGTAAACGGGTAACGGGGAATCAGGGTTCGATTCCGGAGAGGGAGCATGAGAAACGGCTACCACATCCAGGAAGGCAGCAGGCGCGCAACTTACCCACTCCC  
234 GGCACGGGGAGGTAGTGACAAAAATAACAATACGGGACTCTTCGAGGCC-CGTAATTTGGAATGAGTACACTTAAACCCCTTAAACGAGGATCTATTGGAGGGCAAGTCTGGTGGCA-GCAGCCCGGTAATTCAGCTCCAATAGCGTATATTA  
235 AGTTGTGTCAGTTAAAAAGCTCGTAGTTGGATCTC-----AGGCGCAGGCGGGCC-GTCC-GGC-----TCGC-----GCCGT-CACT--G--C-----CCT-G--T--  
236 -----T-TCC--TG--CCC-T-ACCCGTC---TGCCGGCT----CTCTCCCGCG--GTGC---TCTTCACTGAG-C-GTCCCGGGT-----GCCG--G-----CGGTTTACTTTGAAAAAATTAGAGTGTCAAAGCAGGC----CGC  
237 -AGCT-----GCCTGAATAAT-GGTGCATGGAATAATGGAATAGGA-----CC---TCGGTTCT---A-TTTT-----GTTGGTT---TTCGGAACGAGGTT--A-----ATGATTA-ACAGGGACAAACGGGGGCATTTCGTATTCG  
238 GCGTTAGAGGTGAAATTTCTGGATCGCCGCAAGACGAGCTACT-GCGAAAGCATTTGTCAAGAATGTTTTCATTAATCAAGAACGAAA-GTCAGAGGCGGAAGACGATCAGATACCGTCTGATGTTCTGACCATAAACGATGCCAACTAGCGATCCGC  
239 AGGAGT-T-----GCTT-CGATGACTCTGCG--GGCAGCTTCCGGGAAAC--AAAGTGTTTGGGTTCCGGGGGAAGTATGTTGCAAAAGCTGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTTAATTTGACTC  
240 AACACGGGAAACTCACCCGGTCCGGACACTGTAAGGATTGACAGA---TTGATA-GCTCTTCTTGATTGCGGTGGTGGTGGTGCATGGCCGTTCTTAGTTG

241  
242 *Aplysia californica*  
243 AGGTTTAAAGTCTTTTAAATTCGATTGAGCTTGGTACCCTGGAGCT--TTCCTAGGGGATGATCACTTCTATAATGTTATGTTAACTGCTCAGCCTTTTGAATGATTTTTTTTTTATAGTTATGCTATATAAATGGTGGATTGCGGAATTGAATGG  
244 TACCTTTATTAATTTGGTCTCCTGATATAAGATTTCCCTCGTATAAATAACATAAGTTTCTGACTTCTTCCCCCTTCTTTTTACTTCTTTTAGTCTCTAGACTAATAGAAGGTGGAGCTGGAACAGGATGAACAGTTTTATCCTCCTCTATCAGGTCCT  
245 ATTGCACACGGAGGAACCTTCGTTGATTTAGCTATTTTTCTTTACATTTAGCAGGGATGCTTCAATTTTAGGTTGCTATTAATTTTATTACTACTATTTTAAATATACGATCGCCAGGAATTAATTTTGGAGCGATTAAGCTTATTTGTTGATCTGT  
246 TCTAGTAACAGCTTTCTTACTTCTTCTTTTACCAGTATTAGCTGGTGCATATACGATGCTTTTAAACGGATGCTAATTTTAAACGACCTTCTTCGACCCCTCGGGTTTACA-CT-----GTTTC-AC----GGTGA----AACCGCAATGGC  
247 TCATTAATCAGTTCGAGTTCTTAGATGACA-----CGA-T-CC-TACTTGGATAACTGTGGCAATCTAGAGCTAATACATGCTTGC--CA-AG--CTC-CGACC--C-TC-GT-----GG-AA--AGA-CGCTTT  
248 TTATTAGTTC-AA--AAC-CAAT-----CGT-CGTTTCGCGC--TTT-G-----GCGCGG--GCG-GCGTCC-----AAT-T-GGTG-A-CTCTGGATAACTTTGTGCTGATCGCATGGC----CTTTTGT-----GCC-GGCGACGC  
249 ATCTTCAAATGTCTGCCCTATCAAATGTCGATGGTACGTGATATGCCTACCATGTTTGTAAACGGGTAACGGGGAATCAGGGTTCGATTCCGGAGAGGGAGCATGAGAAACGGCTACCACATCCAAGGAAGGCAGCAGGCGCGCAACTTACCCACTCC  
250 CGGCACGGGGAGGTAGTGACAAAAATAACAATACGGGACTCTTTTCGAGGCC-CGTAATTTGGAATGAGTACACTTAAACCCCTTAAACGAGGATCTATTGGAGGGCAAGTCTGGTGGCA-GCAGCCCGGTAATTCAGCTCCAATAGCGTATATTA  
251 AAGTTGTGTCAGTTAAAAAGCTCGTAGTTGGATCTC-----AGGTGACGGCGGGC-GTCC-GGC-----TCGC-----GCCGTTCAC-T-G--C-----CC--G--T--  
252 -----ATCTCC--TG--CCC-T-ACC-GTC---TGCCGGT---CTCTCCCGCG--GTGC---TCTTCCGTTGAG-C-GTCCCGGGT-----GCCG--G-----TGGTTTACTTTGAAAAAATTAGAGTGTCAAAGCAGGC-----CT  
253 C-GGTA-----GCCTGAATAAT-GGTGCATGGAATAATGGAATAGGA-----CC---TCGGTTCT---A-TTTT-----GTTGGTT---TTCGGAAC-GGAGGT--A-----ATGATTA-ACAGGGACAAACGGGGGCATTTCGTATTCG  
254 GGCGTTAGAGGTGAAATTTCTGGATCGCCGCAAGACGAGCTACT-GCGAAAGCATTTGTCAAGAATGTTTTCATTTAGTCAAGAACGAAA-GTCAGAGGCGGAAGACGATCAGATACCGTCTGATGTTCTGACCATAAACGATGCCAACTAGCGATCCG

255 CAGGAGT-T-----GCTT-TGATGACTCTGCG--GGCAGCTTCCGGGAAACC--AAAGTTTTGGGTTCCGGGGGAAGTATGGTTGCAAAGCTGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTTAATTTGACTC  
256 AACACGGGAAAACCTACCCGGTCCGGACACTGTAAGGATTGACAGA---TTGATA-GCTCTTCTTGATTCCGGTGGTGGTGCATGGCCGTTCTTAGTTG  
257  
258 *Arion vulgaris*  
259 AGGTCTATCTCTTTAATTCGCTTTAGAGTTAGGAACAACCTGGT-----ATTTTACGTGATGATCAATTTTTTAATGTTATTATCACTGCACACGCTTTTGTAAATAATTTTTTTATAGTTATACCCTAATAATTTGGAGGTTTCGGTAATTGAATAG  
260 TTCCTCTACTTATTTGGAGCTCCCGATATGAGATTTCCACGTATAAATAATATAAGATTTTGATTATTGCCCCACTCTTTACTTTTACTTATTGCTCCAGTATAGTAGAAGGAGTGCGGGGACAGGTTGACCGTTTACCCCCCTTAAGAGGTTCC  
261 TTAGCACATAGTGGAGCTCAGTAGACTTAGCAATTTTTTTCATTACACTTGGCTGGTATATCTTATTTTAGTGGCAATTAATTTTATTCTACTATTTTAAATATACGCCCTAAAGCCTTATCATTGGAGCGTATAAGTTTGTGTTGATCCAT  
262 CTTGATTACGGTTTTTTTTTACTACTATCTCTGCCCGTATTGGCGGGGGCTATTACCATACTATTAACAGACCGTAATTTTAACTACTAGATTTTTTGATCTCGCGGTTTACA-CT-----GTCTC-AC----GGTGA-----AACCGCAATGGC  
263 TCATTAATCAGTCGAGGTTCAATAGATGACA-----CGA-T-CC-TACTTGGATAACTGTGGCAATTTAGAGCTAATACATGCTTAC----CA-AG--CTC-CGACC--C-TC-GT-----GG-AA--AGA-GCGCTT  
264 TTATTAGTTC-AA--AAC-CAAT-----CGC-CGTTACCCT----TTG-C-----GGGGT--GCG-GCGTCC-----CAC-T-GGTG-A-CTCTGGATAACTTTGTGCTGATCGCATGGC----CTCATGT----GCC-GGCGACGC  
265 ATCTTCAAATGTCTGCCCTATCAAATGTCGATGGTACGTGACATGCATGCCCTACCATGTTTGTAAACGGGTAACGGGGAATCAGGGTTCGATTCCGGAGAGGGAGCATGAGAAACGGCTACCACATCCAAGGAAGGCAGCAGGCGCGCAACTTACCCTCC  
266 CGGCACGGGGAGGTAGTGACGAAAAATAACAATACGGGACTCTTTTCGAGGCC--CCGTAATTTGGAATGAGTACACTTTAAACCCCTTTAACGAGGATCTATTGGAGGGCAAGTCTGGTGCCA-GCAGCCCGGTAATTCAGCTCCAATAGCGTATATTA  
267 AAGTTGTTGACGTTAAAAGCTCGTAGTTGGATCTC----AGGCGCAGGCGGGCG-GTCC-GGC-----TCGC-----GCCGGTCACT--G--C-----CC--GT-T-  
268 -----GTCTCC--TG--CCC-T-ACC-GTC----TGCCGGCT----CTCTCCGTTG--GTGC---TCTTCACTGAG-C-GTCCCGGTG-----GCCG--G-----CGCGTTTACTTTGAAAAAATTAGAGTGTTCAAAGCAGGC-----CT  
269 C-AGCT-----GCCTGAATAAT-GGTGCATGGAATAATGGAATAGGA-----CC---TCGGTCT---A-TTTT-----GTTGGTT---TTCGGAATGGAGGTT--A-----ATGATTA-ACAGGGACAACGGGGCATTCGATTTGC  
270 GCGGTTAGAGGTGAAATTTCTGGATCGCCGCAAGACGAGCTACT-GCGAAAGCATTGTCAAGAAATGTTTTCATTAATCAAGAACGAAA-GTCAGAGGCGCAAGACGATCAGATACCGTCTGAGTCTGACCATAAACGATGCCAATAGCGATCCG  
271 CAGGAGT-T-----GCTT-CGATGACTCTGCG--GGCAGCTTCCGGGAAACC--AAAGTTTTGGGTTCCGGGGGAAGTATGGTTGCAAAGCTGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTTAATTTGACTC  
272 AACACGGGAAAACCTACCCGGTCCGGACACTGTAAGGATTGACAGA---TTGATA-GCTCTTCTTGATTCCGGTGGTGGTGCATGGCCGTTCTTAGTTG  
273  
274 *Biomphalaria glabrata*  
275 TGGATTATCATTATTGATTGCTTTGGAGCTTGGAACTACTCTT-----GTTTTGATAGATGAACATTTTTATAATGTTGTTGTACAGCTCATGCTTTTTATTATAATTTTTTTTATAGTTATACCTATAATAATTTGGTGGTTTTGGTAATTGAATGG  
276 TTCCTTTATTAATTTGGTGTCTCCAGATATAAGTTTTCTCCGGATAAATAATATGCTTTTTTGATTACTTCCGCCTTCATTTATTTTATTGTTAGTATCTAGTATAGTTGAGGGTGGAGTAGGTACAGGTTGAACGTATATCTCCCTTAAAGTGGTCTT  
277 ATTGCTCATGGNGTGTCTCTGTTGATTTAGCTATTTTTCTTTACATTTAGCAGGAATAAGTTCAATTTTAGTGCTATTAATTTTATTACTACAATTTTAAATATGCGTGTCTCCCGGTTTACAATGGAACGTTTATCATTATTGATGATCTGT  
278 ATTAGTTACAGCATTTTTTACTTTTTTACTTTTACTGTTTTAGCAGGGGCTATTACAATTTTAAACAGATCGAAATTTAACTACTGTTTTTTGATCTCGAGTTTACA-CT-----GTCTC-AC----GGTGA-----AACCGCAATGGC  
279 TCATTAATCAGTCGATGTTTATTAGATGAAA-----CTA-T-CC-TACTTGGATAACTGTGGCAATTTAGAGCTAATACATGCTTAC----CA-AG--CTC-CGACC--C-TC-GT-----GG-AA--AGA-GCGCTT  
280 TTATTAGTTC-AA--AAC-CAAT-----CGC-CGTTGCCCT----TCG-C-----GGGGC--GCG-GCGTCC-----GAT-T-GGTG-A-CTCTGGATAACTTTGTGCTGATCGCATGGC----CCTA-GT----GCT-GGCGACGC  
281 ATCTTCAAATGTCTGCCCTATCAAATGTCGATGGTACGTGATGCCCTACCATGTTTGTAAACGGGTAACGGGGAATCAGGGTTCGATTCCGGAGAGGGAGCATGAGAAACGGCTACCACATCCAGGAAGGCAGCAGGCGCGCAACTTACCCTCC  
282 CGGCACGGGGAGGTAGTGACGAAAAATAACAATACGGGACTCTTTTCGAGGCC--CGTAATTTGGAATGAGTACACTTTAAACCCCTTAAACGAGGATCAATTTGAGGGCAAGTCTGTGTGCCA-GCAGCCCGGTAATTCAGCTCCAATAGCGTATATTA  
283 AAGTTGTTGACGTTAAAAGCTCGTAGTTGGATCTC----AGGCGCAGGCGGGCG-GTCC-GGC-----TCGC-----GCCGGTCACT--G--C-----CC--GT-T-  
284 -----GTCTCC--TG--CCC-T-ACCCTC----TGCCGGCT----CTCTCCGTTG--GTGC---TCTTCGCTGAG-C-GTCCCGGTG-----GCCG--G-----CGCGTTTACTTTGAAAAAATTAGAGTGTTCAAAGCAGGC-----C  
285 G-AGCT-----GCCTGAATAAT-GGTGCATGGAATAATGGAATAGGA-----CC---TCGGTCT---A-TTTT-----GTTGGTT---TTCGGAATGGAGGTT--A-----ATGATTA-ACAGGGACAACGGGGCATTCGATTTGC  
286 GCGGTTAGAGGTGAAATTTCTGGATCGCCGCAAGACGAACTACT-GCGAAAGCATTGTCAAGAAATGTTTTCATTAGTCAAGAAACGAAA-GTCAGAGGCGCAAGACGATCAGATACCGTCTGAGTCTGACCATAAACCTATGCCAATAGCGATCCG  
287 CAGGAGT-T-----GCTT-CGATGACTCTGCG--GGCAGCTTCCGGGAAACC--AAAGTTTTGGGTTCCGGGGGAAGTATGGTTGCAAAGCTGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTTAATTTGACTC  
288 AACACGGGAAAACCTACCCGGTCCGGACACTGTAAGGATTGACAGA---TTGATA-GCTCTTCTTGATTCCGGTGGTGGTGCATGGCCGTTCTTAGTTG  
289  
290 *Cepaea hortensis*  
291 CGGGCTGTCTCTATTAATCCGTTTAGAACTTGGTACCCTGGT-----GTATTAAGTACGATCATTTTTTATAATGTTGTTGTTACTGCTCATGCGTTTTGTTATGATTTTTTTTATAGTTATACCAATTATAATTTGGGGGTTTGGAAATTGAATAG  
292 TTCCTTTGCTAATTTGGTGTCTCTGACATAAGCTTTCTCCGGATAAATAATATAAGTTTTTGGTTATTACCTCCAGCATTTTTATTGCTTATTAGTAGTAGTCTCGTAGAAGGAGGAGCTGGAACCGGTTGAACCGTTTTATCCGCCCTAAGAAGCTTA  
293 ATTGGGCATAGGGGTGCATCAGTTGACTTAGCTATCTTTCTTGCACCTCGCAGGTGTGTCATCTATTTTAGGGGCTATTAATTTTATTACTACTATTTTAACTCGGACCTGGAATAACACTTGAACGTATGAGCCTTTTTGTTTGAATCAAT  
294 TCTAGTAACTGTTTTTTTACTTCTTCTTCTTCCGTTTTCGCTTCCGTTTTCAGAGGTGCTATTACAATATTGTTAACTAGTCAAAATTTAGCACTTCCGTTTTTTGATCCTGTGTTTACA-CT-----GTCTC-AC----GGTGA-----AACCGCAATGGC  
295 TCATTAATCAGTCGAGGTTCCCTTAGATGACA-----CGA-T-CC-TACTTGGATAACTGTGGCAATTTAGAGCTAATACATGCTTAC----CA-AG--CTC-CGACC--C-TC-GC-----GG-AA--AGA-GCGCTT  
296 TTATTAGTTC-AA--AAC-CAAT-----CGT-CGTTGCCCT----TCG-C-----GGGGC--GCG-GCGTCC-----CAC-T-GGTG-A-CTCTGGATAACTTTGTGCTGATCGCATGGC----CTTACGT----GCC-GGCGACGC  
297 ATCTTCAAATGTCTGCCCTATCAAATGTCGATGGTACGTGACATGCCTACCATGTTTGTAAACGGGTAACGGGGAATCAGGGTTCGATTCCGGAGAGGGAGCATGAGAAACGGCTACCACATCCAAGGAAGGCAGCAGGCGCGCAACTTACCCTCC  
298 CGGCACGGGGAGGTAGTGACGAAAAATAACAATACGGGACTCTATCGAGGCC--CGTAATTTGGAATGAGTACACTTTAAACCCCTTAAACGAGGATCTATTGGAGGGCAAGTCTGGTGCCA-GCAGCCCGGTAATTCAGCTCCAATAGCGTATATTA  
299 AAGTTGTTGACGTTAAAAGCTCGTAGTTGGATCTC----AGGTGACAGGCGGGCG-GTCC-GGC-----TCGC-----GCCGGTCACT--G--C-----CC--GT-T-  
300 -----GT-TCC--TG--CCC-T-ACC-GTC----TGCCGGCT----CTCTCCGTTG--GTGC---TCTTCGCTGAG-C-GTCCCGGTG-----GCCG--G-----CGCGTTTACTTTGAAAAAATTAGAGTGTTCAAAGCAGGC-----CT  
301 C-GGCT-----GCCTGAATAAT-GGTGCATGGAATAATGGAATAGGT-----CC---TCGGTCT---A-TTTT-----GTTGGTT---TTCGGAATTGGAGGTA--A-----ATGATTA-ACAGGGACAACGGGGCATTCGATTTGC  
302 GCGGTTAGAGGTGAAATTTCTGGATCGCCGCAAGACGAGCTACT-GCGAAAGCATTGTCAAGAAATGTTTTCATTAATCAAGAACGAAA-GTCAGAGGCGCAAGACGATCAGATACCGTCTGAGTCTGACCATAAACGATGCCAATAGCGATCCG  
303 CAGGAGT-T-----GCTT-CGATGACTCTGCG--GGCAGCTTCCGGGAAACC--AAAGTTTTGGGTTCCGGGGGAAGTATGGTTGCAAAGCTGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTTAATTTGACTC  
304 AACACGGGAAAACCTACCCGGTCCGGACACTGTAAGGATTGACAGA---TTGATA-GCTCTTCTTGATTCCGGTGGTGGTGCATGGCCGTTCTTAGTTG  
305  
306 *Anentome helena*  
307 AGGATTAAGTTTATTAATTCGTTGAGCTAGGACAACCTGGAGCT--TTACTTGGTATGATCAACTTTATAACGTGATGTTTACAGCTCATGCTTTTTGTTATAATTTTTTTTTTAGTTATAGCTATAATAATTTGGCGTTTTTGGAAATTGATTTGA

308 TTCCATTGATATTAGGAGCACCAGATATGGCATTTCCTCGTTTTAAATAATATAAGATTTTGATTATTACCACCTGCTTTACTTCTTTTATTATCTTCACCAGCTGTTGAGAGTGGTGTGGAACTGGGTGAACTGTTTATCCACCTCTTGCAGGAAAT  
309 ATAGCTCATGCTGGCGGTTCTGTAGATTTAGCTATTTTTTTCATTACATCTTCAGGAGTATCATCAATTTAGTGCGGTAATTTTATTACAACATTTAATATACGATGACGTGGTATGCAATTTGAGCGACTTCTCTTATTTGTTGATCTGT  
310 AAAGATTACTGCTATTTTACTACTTTTATCATTACTGTATTAGCTGGAGCTATTACTATACTTTAACTGATCGAAATTTAATACTTCTTTTTTTGACCCCTGCAGTTTACA-CC-----CTCGT-AC----GGTGA-----AACCGCAATGGC  
311 TCATTAATCAGTCGAGGTTCCCTTAGATGATC-----CGA-A-AT-TACTTGGATAACTGTGGTAATTTAGAGCTAATACATGC--CC----AACAG--CTC-CGACCC-T-TA-C-----G-----GG-AA--AGA-GCGCTT  
312 TTATTAGTTC-AA--AGC-CAGT-----CGGGT-----TCT-----GC-CCGTTT-----T-T-T-GGTG-A-CTCTGGATAACTTTGTGCCGATCGCATGGC----C-TC-GA-----GCC-GGCGACGC  
313 ATCTTTCAAATGTCTGCCCTATCATATGACGATGGTACGTGACTGCCTACCATGTTAGCAACGGGTAGCGGGGATCAGGGTTCGATTCGGAGAGGGAGCATGAGAAACCGGTACCACATCCAGGAAGGCAGCAGGCGCAACTTACCCTCC  
314 TGGCAGCGGGAGTGTGACGAAAAATAACAATACGGAATCTTTTTGAGGCT--CGTAATTTGGAATGAGTACACTTTAAACCCCTTAAACGAGGATCTATTGGAGGGCAAGTCTGGTGCCA-GCAGCCCGGTAATTCAGCTCCAATAGCGTATACTA  
315 AAGTTGTTGCGATTAAAAGCTCGTAGTTGGATCTC-----AGGCATGGGCGCAG-GTCC--GC-----CTCGC-----GGCGGT-CACT--G--T-----GC--GT-T-  
316 -----T-TGT--TT--CCCATCTACGCT----TCCCGGTTG--TTCAGCTCA-TG--GTGC---TCTTCGCTGAG-C-GCTATGGGTG-----GCCG--G-----AACGTTTACTTTGAAGAAATTAGAGTGTTCAAAGCAGGC-----G  
317 C-GTC-----GCCTGAATAAT-GGTGCATGGAATAATGGAATAGGA-----CC---TCGGTCT---A-TTTT-----GCTGGTT---TTCGGAACACGAGGT--A-----ATGATTA-AGAGGGACAGACGGGGCATCCGTATTGC  
318 GGTGTAGAGGTGAAATTTCTGGATCATCGCAAGACGAACT--GCGAAAGCATTTGCCAAGCATGTTTTATTAGTCAAGAACGAAA-GTCAGAGGTTCCGAGACGATCAGATACCGTCTGAGTTCTGACCATAAACGATGCCAAGTACGATTCG  
319 CTGGTGT-T-----GCTT-CATCGACTCTGCG--GGCAGCTTCCGGGAAACC-AAAGTTTTCGGGTTCCGGGGGAAGTATGGTTGCAAAGCTGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGAGTGAGGCTTAAATTTGACTC  
320 AACACGGGAAACTCACCCTCGGACACTGTAAGGATTGACAGA---TTGATA-GCTCTTCTTGATTTCGGTGGGTGGTGCATGGCCGTTCTTAGTTG

321  
322 *Cornu aspersum*

323 AGGCTTGTCTTTACTCATTTCGTTTTGAACTAGGTACGTCGGGT-----GTATTAAGTATGACCATTTTTATAATGTTATTGTTACAGCGCACGCATTTGTTATAATTTTTTTCATAGTTATACCTATTATGATTGGTGGCTTTGGTAACTGAATAG  
324 TACCTTTATTAATTGGCGCTCCGGATATAAGTTTTTCGCGCATAAACAACATAAGTTTTTGATTATTACCTCCGCTTTTTTGTACTTATCAGTAGCAGCTTAGTTGAAGGAGGGGCTGGAACGATGAACTGCTATCCACCTTTGAGAGGTCTA  
325 AGCGGCCATAGTGGTGCCTCCGTAGACTTAGCAATTTTCTCGCTCCATCTTGCTGGTATGTCGTCTATTTTAGGTGCGATTAATTTTATTACAACATTTTCAACATACGTTCCGCTGGTGTGAGATTAGAACGCATAAGTTTGTGTTGGTCTAT  
326 TTGATGACTGTGTTTTTACTATTACTGCTGCTGCTTGCCTTTCGAGGCCAATTTCTAGCTATTAACCTTTCATTTTGTATCCGCGGTTTACA-CT-----GTCTC-AC-----GGTGA-----AACCGCAATGGC  
327 TCATTAATCAGTCGAGGTTCCCTTAGATGACA-----CGA-T-CC-TACTTGGATAACTGTGGCAATTTAGAGCTAATACATGCTTAC----CA-AG--CTC-CGACC--C-TC-GC-----GG-AA--AGA-GCGCTT  
328 TTATTAGTTC-AA--AAC-CAAT-----CGT-CGTTGCCCT----TCA-C-----GGGGC--GCG-GCGTTC-----CAC-T-GGTG-A-CTCTGGATAACTTTGTGCTGATCGCATGGC----CTTATGT----GCC-GGCGACGC  
329 ACCTTCAAATGTCTGCCCTATCAATGTGATGCTGACATGCCTACCATGTTTGAACGGGTAACGGGGAATCAGGGTTCGATTCGGGAGAGGGAGCATGAAAAACCGGTACCACATCCAAGGAAGGCAGCAGGCGCGCAACTTACCCTCC  
330 CGGCACGGGAGGTAGTGACGAAAAATAACAATACGGGACTCTATCGAGGCC--CGTAATTTGGAATGAGTACACTTTAAACCCCTTAAACGAGGATCTATTGGAGGGCAAGTCTGGTGCCA-GCAGCCCGGTAATTCAGCTCCAATAGCGTATATTA  
331 AAGTTGTTGCAAGTTAAAAGCTCGTAGTTGGATCTC-----AGGTGACGGCGGGC-GTCC-GGC-----TGC-----GCCGTTTACT--G--C-----CC-G--T-  
332 -----GTCTCC--TG--CCC-T-ACC-GTC----TGCCGGCT----CTCTCCCGTGG--GTGC---TCTTCGCTGAG-C-GTCCCGGTG-----GCCG--G-----CGGTTTACTTTGAAAAAATTAGAGTGTTCAAAGCAGGC-----CT  
333 C-GGCTA----GCCTGAATAAT-GGTGCATGGAATAATGGAATAGGA-----CC---TCGGTCT---A-TTTT-----GTTGGTT---TTCGGAACA-GAGGT--A-----ATGATTA-ACAGGGACAACGGGGCATTCGTTACTGC  
334 GCGCTTAGAGGTGAAATTTCTGGATCGCGCAAGACGAGCTACT--GCGAAAGCATTTGTCAAGAATGTTTTTATTAAACAAGAACGAAA-GTCAGAGGCGCAAGACGATCAGATACCGTCTGAGTTCTGACCATAAACGATGCCGACTAGCGATCCG  
335 CAGGAGT-T-----GCTT-CGATGACTCTGCG--GGCAGCTTCCGGGAAACC-AAAGTGTGTTGGGTTCCGGGGAAAGTATGGTTGCAAAGCTGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGAGTGAGGCTTAAATTTGACTC  
336 AACACGGGAAACTCACCCTCGGACACTGTAAGGATTGACAGA---TTGATA-GCTCTTCTTGATTTCGGTGGGTGGTGGTGCATGGCCGTTCTTAGTTG

337  
338 *Deroceras reticulatum*

339 GGGGCTTCTTTTTAATTCGATTAGAATTAGGAACAGCGGGA-----GTTTTACTAGATAATCATTTTTTAAATGTTAGTAGTAACTGCACATGCATTTGTTATAATTTTTTATGGTGATACCTATATAAATTGGAGGCTTTGGTAAATTGGATGG  
340 TACCCTTGTAAATTGGAGCTCCGGATATAAGTTTTCTCGAATAAATAATATAAGGTTTTGATTACTTCCCCTTCACTTTCTTTTACTAATTTGTTCTAGTATAGTAGAGGGTGGGGCGGGAACGGGTGAACAGTTTACCCCTTTAAGAGGGCCA  
341 TTAGGTCATGCTGGGCATCTGTGGATTTAGCTATTTCTCATTACATTTAGCAGGGATGCTTCTATTTTAGGTGCTATTAATTTTACTTACTACAATTTTAAATATACGGTCACCTGGGATGAGAATAGAACGTTTAAAGATTATTTGTTGATCAAT  
342 TTTAGTTACTGTGTTTTTACTTTTTATTTATCTTTTACCTGTTTTAGCGGGGCAATTTACTATACTTTAACTGATCGAAATTTAATAACAAGGTTTTTGGACCCCTGCAGTTTACA-CT-----GTCCC-AC----GGTGA-----AACCGCAATGGC  
343 TCATTAATCAGTCGAGGTTCCCTTAGATGACA-----CGA-T-CC-TACTTGGATAACTGTGGCAATTTAGAGCTAATACATGCTTAC----CA-AG--CTC-CGACC--C-TC-GT-----GG-AA--AGA-GCGCTT  
344 TTATTAGTTC-AA--AAC-CAAT-----CGT-CGTCGCCCT----TCG-C-----GGGGT-GCG-GCGTCC-----CAC-T-GGTG-A-CTCTGGATAACTTTGTGCTGATCGCACTGA----CTT--GC----TCA-GGCGACAC  
345 ATCTTTCAAATGTCTGCCCTATCAATGTGATGCTGACGTGACATGCCTACCATGTTTGAACGGGTAACGGGGAATCAGGGTTCGATTCGGGAGAGGGAGCATGAGAAACCGGTACCACATCCAAGGAAGGCAGCAGGCGCGCAACTTACCCTCC  
346 CGGCACGGGAGGTAGTGACGAAAAATAACAATACGGGACTCTTTTCGAGGCC--CGTAATTTGGAATGAGTACACTTTAAACCCCTTAAACGAGGATCTATTGGAGGGCAAGTCTGGTGCCA-GCAGCCCGGTAATTCAGCTCCAATAGCGTATATTA  
347 AAGTTGTTGCAAGTTAAAAGCTCGTAGTTGGATCTC-----AGGTGACGGCGGGC-GTCC-GGC-----TGC-----GCCGTTTACT--G--C-----CC--GT-T-  
348 -----GT-TCC--TG--CCC-T-ACC-GTC----TGCCGGCT----CTCTCCCGCG--GTGC---TCTTGTGCTGAG-C-GTCCCGGTG-----GCCG--G-----CGGTTTACTTTGAAAAAATTAGAGTGTTCAAAGCAGGC-----CT  
349 C-GGCT----GCCTGAATAAT-GGTGCATGGAATAATGGAATAGGA-----CC---TCGGTCT---A-TTTT-----GTTGGTT---TTCGGAAGTGGAGGT--A-----ATGATTA-ACAGGGACAACGGGGCATTCGTTATTGC  
350 GCGCTTAGAGGTGAAATTTCTGGATCGCGCAAGACGAGCTACT--GCGAAAGCATTTGTCAAGAATGTTTTTATTAAACAAGAACGAAA-GTCAGAGGCGCAAGACGATCAGATACCGTCTGAGTTCTGACCATAAACGATGCCGACTAGCGATCCG  
351 CAGGAGT-T-----GCTT-CGATGACTCTGCG--GGCAGCTTCCGGGAAACC-AAAGTGTGTTGGGTTCCGGGGAAAGTATGGTTGCAAAGCTGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGAGTGAGGCTTAAATTTGACTC  
352 AACACGGGAAACTCACCCTCGGACACTGTAAGGATTGACAGA---TTGATA-GCTCTTCTTGATTTCGGTGGGTGGTGGTGCATGGCCGTTCTTAGTTG

353  
354 *Elysis crispata*

355 TGGTTAAGGCTCTTAATTCGATTGAAATAGGACTTCCGGTGCC--TTTTAGGTGACGACCACTTTTTATAATGTTATTGTTACAGCACATGCTTTTGTATAATTTTTTTCATAGTTATACCTCTAATAAATTGGAGGATTTGAAATGAAATAG  
356 TTCTTATCTTATTTGGGCTCCAGATATAAGTTTTCTCGTATGAACAATATGAGGTTTTGACTTTTACTCCATCTTTTATTTTCTTCTGCTTCAAGCCCTTGGAAAGGAGTGTGGAACTGGATGGACAGTGTATCCACCCTTAGGGGACCT  
357 ATTGGCCACGGTGGTGCCTCAGTAGATTTAGCAATTTTCTCACTACATCTTGTGGTATATCTTCTATCTTAGGTGACGTTAATTTTATTACTACAATTTTAAATATACGATCTCCGGGATAAGAATAGAACGACTAAGACTCTTGTGTTGATCAGT  
358 TTTAGTTACGGCATTTTACTATTGCTATCACTACTGTACTTGCAGGAGCGATTACGATCTGCTCACCATCGTAACCTTAACTACTAGCTTTTTGATCTGCGGTTTACA-CT-----GTTCC-AC----GGTGA-----AACCGCAATGGC  
359 TCATTAATCAGTCGAGGTTCCCTTAGATGACA-----CGA-T-CC-TACTTGGATAACTGTGGCAATTTAGAGCTAATACATGCATCG----CA-AG--CTC-CGACC--T-TC-G-----GG-AA--AGA-GCGCTT  
360 TTATTAGTTC-AA--AAC-CAAT-----CGT-CGG-TCC-----CTC-G-----CGG--CCG-GCGTCT---CAC-T-GGTG-A-CTCTGGATAACTTTTGTGCTGATCGCATGGC----CTT--GC----GCC-GGCGACGC

361 ATCTTTCAAATGTCGCCCATCAAAATTCGATGGTACGTGACATGCCTACCATGTTTGTAAACGGGTAACGGGGAATCAGGGTTCGATTCGGGAGAGGGAGCATGAGAAACGGCTACCACATCCAAGGAAGGCAGCAGGCGCGCAACTTACCCACTCC  
362 CGGCACGGGGAGGTAGTGACGAAAAATAACAATACGGGACTCTTTCGAGGCC-CCGTAATTTGGAATGAGTACACTTTAAACCCCTTTAACGAGGACCCATTGGAGGGCAAGTCTGGTGCCA-GCAGCCCGGTAATTCAGCTCCAATAGCGTATATTA  
363 AAGTTGTTGAGTTAAAAAGCTCGTAGTTGGATCTC-----AGGCGCAGGCGGGCG-GTCC-GGC-----TCGC-----GCCGGTCACT--G--C-----CC--GT-T-  
364 -----GTTTCC--TG--CCC-T-ACCCGTC----TGCCGGCT----CTCTCCCG-CGCGGTGC----TCTTCGCTGAG-C-GTCCCGGTG-----GCCG--G-----CGCGTTTACTTTGAAAAAATTAGAGTGTCAAAGCAGGC-----CT  
365 T-GGTC-----GCCTGAATAAT-GGTGCATGGAATAATGGAATAGGA-----CC----TCGGTTCT----A-TTTT-----GTTGGTT----TTCGGAAGTGGAGGT--A-----ATGATTA-ACAGGGACAACAGGGGGCATTCGTATGGC  
366 GCGGTTAGAGGTGAAATTCGGATCGCCGTCAGACGACTACT-GCGAAAGCATTGTCAAGAATGTTTTCATTAATCAAGAACGAAA-GTCAGAGGCGGAAGACGATCAGATACCCTCGTAGTTCTGACCATAAACGATGCCAGCTCGCGATCCG  
367 GGGGAGT-T-----GATT-CGATGACTCCGCG--GGCAGCTCCGGGAAACC--AAAGTGTGGGTTCCGGGGGAAAGTATGGTTGCAAAGCTGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTCGCGCTTAATTTGACTC  
368 AACACGGGAAAACCTACCCGGTCCGGACACTGTAAGGATTGACAGA---TTGATA-GCTCTTCTTGATTCCGGTGGGTGGTGGTGCATGGCCGTTCTTAGTTG  
369  
370 *Helix pomatia*  
371 GGGTCTCTCTTGTAAATTCGTTGAGAGTTAGGAACATCCGGC-----GTATTAAGCGACGATCATTTCTATAATGTGATTGTAAGTGCATGCAATTTGTTCATAATTTTTTTTATGGTAATACCTATATAATGGTGGATTGGAAATGGATAG  
372 TCCCCTTACTTATTGGTGCACCTGATATAAGGTTTCTCGTATAAATAACATAAGCTTTTGACTGCTGCCCGCTCTTTTATATTAATTAGGAGTAGTTAGTTGAAGTGGGGCAGGGACGGGTTGGACTGTTTATCCACCTCTTAGCAGTTTA  
373 ATTGGCCATAGTGGAGCATCGTTGATCTCGCTATTTTTCTTTACACCTTGCTGGAATGCTTCTATTCTGGGTGCTATTAATTTTACTACTATTPTTAATATACGGTCTCCAGGTATAAGTTTATGGTGGTCTAT  
374 TCTAGTAAGTGTGTTTTACTCTTATATCCTTACCTGTTTGTAGCTGGTCTATTACTATATTTGACTGATCGAAATTTAGTACTCTTTTTTGTATCTGCTGTTTCACT-CT-----GTCTC-AC----GGTGA-----AACCGGAATGGC  
375 TCATTAATCAGTTCGAGGTTCTTAGTAGACA-----CGA-T-CC-TACTTGGATAACTGTGGCAATTCAGAGCTAAATACATGTTAC-----CA-AG--CTC-CGACC--C-TC-GC-----GG-AA--AGA-GCGCTT  
376 TTATTAGTTC-AA--AAC-CAAT-----CGT-CGTTGCCCT----TCA-C-----GRGC--GCG-GCGTTC-----CAC-T-GGTG-A-CTCTGGATAACTTTGTGCTGATCGCATGGC----CTTAYGT-----GCC-GGCAGCG  
377 ATCTTTCAAATGTCGCTGCCCTATCAAAATGTCGATGGTACGTGACATGCCTACCATGTTTGTAAACGGGTAACGGGGAATCAGGGTTCGATTCGGGAGAGGGAGCATGAGAAACGGCTACCACATCCAAGGAAGGCAGCAGGCGCGCAACTTACCCACTCC  
378 CGGCACGGGGAGGTAGTGACGAAAAATAACAATACGGGACTCTATCGAGGCC-CCGTAATTTGGAATGAGTACACTTTAAACCCCTTTAACGAGGATCTATTGGAGGGCAAGTCTGGTGCCAGC-AGCCCGGTAATTCAGCTCCAATAGCGTATATTA  
379 AAGTTGTTGAGTTAAAAAGCTCGTAGTTGGATCTC-----AGGTGCAGGCGGGCG-GTCC-GGC-----TCGC-----GCCGGTCACT--G--C-----GCGGTTTACTTTGAAAAAATTAGAGTGTCAAAGCAGGC-----CT-  
380 -----GT-TCC--TG--CCC-T-ACC-GTC----TGCCGGCT----CTCTCCCGTG--GTGC----TCTTCGCTGA--CGGTCCCGGTG-----GCCG--G-----CGCGTTTACTTTGAAAAAATTAGAGTGTCAAAGCAGGC-----CT  
381 C-GGCT-----GCCTGAATAAT-GGTGCATGGAATAATGGAATAGGA-----CC----TCGGTTCT----A-TTTT-----GTTGGTT----TTCGGAACA-GAGGT--A-----ATGATTA-ACAGGGACAACAGGGGGCATTCGTACTGC  
382 GCGGTTAGAGGTGAAATTCGATCGCCGCAAGACGAGCTGCT-GCGAAAGCATTGTCAAGAATGTTTTCATTAATCAAGAACGAAAAGTCAAGAGGCGGAAGACGATCAGATACCCTCGTAGTTCTGACCATAAACGATGCCAGCTAGCGATCCG  
383 CAGGAGT-T-----GCTT-CGATGACTCTGCG--GGCAGCTTCCGGGAAACC--AAAGTGTGGGTTCCGGGGGAAAGTATGGTTGCAAAGCTGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGC-GCTTAATTTGACT  
384 CAACACGGGAAAACCTACCCGGTCCGGACACTGTAAGGATTGACAGA---TTGATA-GCTCTTCTTGATTCCGGTGGGTGGTGGTGCATGGCCGTTCTTAGTWG  
385  
386 *Limax maximus*  
387 AGGTTTACTTTTAAATTCGTTTGAAGTACAGTGGT-----GTTTTAATAGATGATCATTTTTTCAACGTTATGTAACGGCTCATGCTTTTGAATAATTTTTTTTATAGTTATACCTATATGATGGGGTTTTGGTAATTGAATAG  
388 TTCCCTTTTTAAATTTGGGCTCCTGATATAAGGTTTCTCGTATAAATAAATAAGGTTTTGGTTACTTCTCCATCTTTTATTTTGTCTTATGTTCTAGTATAGTGAAGGGGTCAGGTACAGGGTGAAGTGTATATCCTCCTTTGAGAGTCTCT  
389 TTAGGGCATGGAGGAGCTCTGTTGATTTAGCTATTTTTTCACTTCAATTTAGCTGGTATATCTTCTATTTTAGGTGCAATTAATTTTATTACTACAATTTTAAATATACGAACTCTGGGATAACCATAGAAGCTGTGAGATTATTTGTATGGTCAAT  
390 TTTAGTACAGGATTTTACTTCTTCTTTCGCTTCTGATTTGGCGGGGCAATTAATTAATTAAGTACTAGCTTTTGTATCCAGCTGTTTCACT-CT-----GTCC-AC----GGTGA-----AACCGGAATGGC  
391 TCATTAATCAGTTCGAGGTTCTTAGTAGACA-----CGA-T-CC-TACTTGGATAACTGTGGCAATTCAGAGCTAAATACATGCTTAC----CA-AG--CTC-CGACC--C-TC-GT-----GG-AA--AGA-GCGCTT  
392 TTATTAGTTC-AA--AAC-CAAT-----CGT-CGTTACCT--TGC-C-----GGGT--GCG-GCGTCC-----CAC-T-GGTG-A-CTCTGGATAACTTTGTGCTGATCGCATGGC----CTCACGT-----GCC-GGCAGCG  
393 ATCTTTCAAATGTCGCTGCCCTATCAAAATGTCGATGGTACGTGACATGCCTACCATGTTTGTAAACGGGTAACGGGGAATCAGGGTTCGATTCGGGAGAGGGAGCATGAGAAACGGCTACCACATCCAAGGAAGGCAGCAGGCGCGCAACTTACCCACTCC  
394 CGGCACGGGGAGGTAGTGACGAAAAATAACAATACGGGACTCTTTCGAGGCC-CCGTAATTTGGAATGAGTACACTTTAAACCCCTTTAACGAGGATCTATTGGAGGGCAAGTCTGGTGCCA-GCAGCCCGGTAATTCAGCTCCAATAGCGTATATTA  
395 AAGTTGTTGAGTTAAAAAGCTCGTAGTTGGATCTC-----AGGCGCAGGCGGGCG-GTCC-GGC-----TCGC-----GCCGGTCACT--G--C-----GCGGTTTACTTTGAAAAAATTAGAGTGTCAAAGCAGGC-----CT  
396 -----GT-TCC--TG--CCC-T-ACC-GTC----TGCCGGCT----CTCTCCCGCG--GTGC----TCTTCGCTGAG-C-GTCCCGGTG-----GCCG--G-----CGCGTTTACTTTGAAAAAATTAGAGTGTCAAAGCAGGC-----CT  
397 C-GGCT-----GCCTGAATAAT-GGTGCATGGAATAATGGAATAGGA-----CC----TCGGTTCT----A-TTTT-----GTTGGTT----TTCGGAAGTGGAGGT--A-----ATGATTA-ACAGGGACAACAGGGGGCATTCGTATTCG  
398 GCGGTTAGAGGTGAAATTCGATCGCCGCAAGACGAGCTACT-GCGAAAGCATTGTCAAGAATGTTTTCATTAATCAAGAACGAAA-GTCAGAGGCGGAAGACGATCAGATACCCTCGTAGTTCTGACCATAAACGATGCCAGCTAGCGATCCG  
399 CAGGAGT-T-----GCTT-CGATGACTCTGCG--GGCAGCTTCCGGGAAACC--AAAGTGTGGGTTCCGGGGGAAAGTATGGTTGCAAAGCTGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGC-GCTTAATTTGACTC  
400 AACACGGGAAAACCTACCCGGTCCGGACACTGTAAGGATTGACAGA---TTGATA-GCTCTTCTTGATTCCGGTGGGTGGTGGTGCATGGCCGTTCTTAGTTG  
401  
402 *Littorina littorea*  
403 TGCCTTAAGTCTACTTTTCGGGCTGAATTAGGTCAACCTGGCGCT---CTCCTGGGAGATGACCAGCTGTACAACGTTATCGTTACAGCCACGCTTTGTAATAATTTCTTCTTGTATGCTTATAAATAATGGTGGGTTGGAAATGACTTG  
404 TCCCTTAATATATTAGAGCACCCGATATAGCGTTCCCTCGTTAAATAACATAAGCTTTTGATTACTCCCGCCGCTTGTGTTGTTACTATCTCTGCTGCGGTAGAAAGTGGTGCAGGGACGGGTTGAAGTGTATATCCTCCTTTATCCGGAAT  
405 TTAGCCCATGCGGAGGCTCTGTGGACTTAGCCATTTTCTCTCTTCAATTTGGCCGGTGTCTCATCTATTTTGGGGCCGTAATTTTATTAACAATATTAATAATACGATGACGAGGGATGCAATTCGAGCGATTACCTCTTTTGTGTTGATCTGT  
406 AAAAATTACAGCCATTTCTTTACTTTTATCCCTCCAGTTTGTAGCGGAGCCATTACAATATTGTTAACGTGATCGAAATTTAACACTGCCTTCTTCGATCCTGCTGTTTCACT-CC-----CTCGT-AC----GGTGA-----AACCGGAATGGC  
407 TCATTAATCAGTTCGAGGTTCTTAGTAGATC-----CCA-A-TC-TACTTGGATAACTGTGGTAATTCAGAGCTAAATACATGC--CA----ACCAG--CTC-CGACCCT--TA-C-----TG-----GG-AA--AGA-GCGCTT  
408 TTATCAGTTC-AA--AAC-CAGT-----CGGGCC-G-----TTA-A-----AC--GGTCCGTC--C-T-T-GGTG-A-CTCTGGATAACTTTGTGCTGATCGCATGGC----C-TC-GA-----GCC-GGCAGCG  
409 ATCTTTCAAATGTCGCTGCCCTATCAAAATGACGATGGTACGTGATCTGCTTACCATTGTTGGCAACGGGTAACGGGGAATCAGGGTTCGATTCGGGAGAGGGAGCATGAGAAACGGCTACCACATCCAAGGAAGGCAGCAGGCGCGCAACTTACCCACTCC  
410 TGGCAGGGGAGGTAGTGACGAAAAATAACAATACGGAACCTTTTGAGGCT-CCGTAATTTGGAATGAGTACACTTTAAACCCCTTTAACGAGGATCTATTGGAGGGCAAGTCTGGTGCCA-GCAGCCCGGTAATTCAGCTCCAATAGCGTATACTA  
411 AAGTTGTTGAGTTAAAAAGCTCGTAGTTGGATCTC-----AGGCATGGGCGCAG-GTCC--GC-----CTCGC-----GGCGGT-CACT--G--T-----GT--G--T-  
412 -----A-TGT--TT--CCCATCTACGCT---TCCCGGTTG---TTAGCCCA-TG--GTGC---TCTTCAATGAG-C-GTTTTGGGTG-----GCCG--G-----AACGTTTACTTTGAAAAAATTAGAGTGTCAAAGCAGGC-----A  
413 C-GTC-----GCCTGAATAAT-GGTGCATGGAATAATGGAATAGGA-----CC----TCGGTTCT----A-TTTT-----GCTGGTT----TTCGGAACACAGGT--A-----ATGATTA-AGAGGGACAGCAGGGGGCATTCGTATTCG



414 GGTGTTAGAGGTGAAATTCCTGGATCATCGCAAGACGAACTACT-GCGAAAGCATTGCGCAAGAATGTTTTTCATTAGTCAAGAACGAAA-GTCAGAGGTTGCAAGACGATCAGATACCGTCGTAGTTCTGACCATAAACGATGCCAACTAGCGATCCG  
415 CTGGTGT-T-----GCTT-CATCGACTCTGCG--GGCAGCTTCCGGGAAACC-AAAGTCTATGGGTTCCGGGGGAAGTATGGTTGCAAAAGCTGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTTAATTTGACTC  
416 AACACGGGAAACTCACCCGGTCCGGACACTGTAAGGATTGACAGA---TTGATA-GCTCTTTCTTGATTCCGGTGGGTGGTGCATGGCCGTTCTTAGTTG  
417  
418 *Lottia gigantea*  
419 CACTTTGAGACTTTTAAATTCGAGTTCATTTAATACACTCTGGGAGTGGGCTACTGGTTAGAGGTACGCTGTATAACGCAAGTGTGTACGGCCCATGCTTTTTTAATAATTTCTTTATGGTAATGCCGGTCTTAATTTGGAGGGTTCGGGAATTGGTTAG  
420 TGCCATTAATGCTCCCGGCTCCTGATTTAGGTTTGCCTCCGATAAACAACTTAAAGTTTTGGTTAGTTCCTCATTGCTGGTATTTTTATAGTTTCCAGGTTAACCGATACTGCAGTGGGGACAGGCTGAACCTTGTATCCTCCGTTGCTTCTCTT  
421 GAGGGTACCATTCTCCTTGTGTGGACGAGGCAATTTTTCTTTGCATATATCAGGGATTGCTTCAATTTTTGCTAGAAATTAACTTTACTACGATTAACACGCTCGGGGGCTCATAAGAAGATGTCTTCTATACCACTTTTTGTAGTGTCTAT  
422 TGGTGTAAACGAGGGTCTACTTTTTGTTGCTGTTCTGTTTGGCTGGGGGGCTTACTATACTTATACTGATCGTAATTAACACCGCCTTTTTTGACCCAGAGGTTGAGG-CTTGTCTCTTCGG-GG----AGCGAGCCGAAACTGCGAACGGC  
423 TCATTAG-TCAGATAAGGTTCTTGGCTAAAAGCGGGTCCG-T-TT-TA-ATGGATAACTGTGGTAATCTAGAGCTAATACATGC--AACGCACCGTGGTCCCGTAGTC-T-TCTC-----GTCTCGGGGAAA-CGGCATTATTT  
424 CTCTGGACC-AG--ATCGCCCT-----AGCCTGCGA-AGC-----TACCGTCAAAAGTAGCGACGGG-GCGAAGC--GACAA-GTGTG-AAATCCGAATAACTGTG--CCGATCGCGGGGT----C-TT-TCCGGGCCCGGACGACTTT  
425 GCCATGAAGTGTCTGCCATCAATTTGGCGATGGTCCGGACCTGCCTACCACGGTGTGACGGGTAACGGGGAATCAGGGTTCGATTCCGGAGAGGGAGCCTGCGAAACGGCTACCACCTCCAAGGAGGGCAGCAGGCGCGCAACTTACCCAATCCC  
426 GACACGGGGAGGTAGTGACGAAAAATAACCTGGCGGGGCCCTTTCGTGGTCCGCCGGGGCGGAATGAGCGCAATTTAAAAGAGTGTGCGAGGAGCTATTGGAGGGCAAGCCTGGTGCCA-GCAGCCGCGTAATTCAGCTCCATAGCCTATATCCG  
427 AGTTGCTGCGGTTAAAAGCTCGCTGGTGGATCTCGGAGGGCGGACGGTCCGGCGCATACGCTGC---GGTCCG-----ACC-GGCGAT-TTCT--C--G-----GCC-GT-CC--  
428 ----C-T-A---A--C-C-A-GCG-----CGCGGGCGAGGTGGACTGC-CG--GTCC--TGCCCTGTTTCT-CCTTACGGGAGAGAAACCG--CCGCAATTTCTGTCTACCTTGAAAAAATTAGAGTGCTAAAAGCAGGC-----TAA  
429 AACCCCGAGCCTGAATATTTCTGTCATGGAATAAGCGGGGATGCTCTTTTCCGGAGGGCGGTCCGACCGA-CTGGCGACGTGCTTTCGCT----GTCCGTTT-CGCCG-AGAGCTAGGATTCGAGAGGAACGGTGGGGGGCAGCGTACCGGGC  
430 GGGAGAGGTGAAATTTTGTGATCCGCTCGGGACG-ACTCGAAGCGAAAGCGCTGGCCCGGACGCTTTCCTTAATCCAGAACGAAG-GTGGGTGGAGCAAAGACGATCAGATACCGTCTGTAGTACCAGCGGTAAACGCTGCCAGCGGGCCGCGGACG  
431 AGGC-TCGAGAACAGCGGTTATGGACCCGTCGCTGGCGGC-TTCCGGCAACCTGAGAGTTTACGGGTTCCGGGGGTAGTATGGTTCGCAAGGCTGAAACTTGAAGGAATTGACGGAAGGGCACCACAAGGAGTGGAGCCTGCGGCTTAATTTGACTCAA  
432 CACGGGGCAACTTACCCGGTCCGGACATCGTCAGGATTGACAGACGCTCGTGCAGTTCTTTCTCGATTGATGGTGGTGGTGCATGGCCGTTCTTGCTGGCT  
433  
434 *Marisa cornuarietis*  
435 TGCTTTAAGAATGCTTATTCGAGCTGAACTTGGGCAACCGGGAGCC---TTGTTAGGTGATGATCAGCTTTACAATGTCTATGTTTACAGCTCATGCTTTTGAATGATTTCTTTTGTAGTTATGCTTATAATAATTTGGTGGATTGGAAATTGACTTG  
436 TGCCATTAATATTAGGTCTCCTGACATGGCTTTTCTCGTTTAAATAATAAAGTTTTGGTTGCTTCCGCTTCTTTTACTTCTTTTGTCTCAGCTGCTGTAGAAGTGGAGTTGGACAGGTTGAACAGTTTATCCTCCTTTAGCTGGAAT  
437 CTAGCACATGCTGGTGGTCTGTAGATTTAGCAATTTTTCTTTTACATTTAGCTGGTGTCTTCTTATTTTAGGGCTGTAAATTTTATCACAACAGTAATTAATATACGTTGACGAGGCATGCAATTTGAGCGATTACCTTTGTTGTGTGATCTGT  
438 TAAAATTACGGCTATTTTACTTTTATCTTTTACCTGTTTTAGCCGGTGTCTTACTATATTACTTACGGACCGAAATTTAATACTGCTTTTTTGTATCCTGCTGTTTACA-CC-----CTCGT-AC----GGTGA-----AACCGCAATGGC  
439 TCATTAATCAGTCGAGGTTCCCTTAGATGATC-----CAT-T-TC-TACTTGGATAACTGTGGCAATTTCTAGAGCTAATACATGC--AA----CAAAG--CTC-CGACCC-GGTG-TC-----AA-AGCGG-----GG-AA--AGA-GCGCTT  
440 TTATTAGTTC-AA--AAC-CAGT-----CGG-GT-----CTC-----GGCCCCGTCCT--T-T-T-GGTG-A-CTCTGGATAACTTTGTGCGGATCGCATGGC--C-TC-GA-----GCC-GGCAGCG  
441 ATCTTCAATGCTGCTGCCCTCAATGTCGATGTCAGTGATAGGCCTACCATTGTGACTACGGGTAACGGGGGATCAGGGTTCGATTCGGGAGGGAGCATGAGAACGGCTACCACATCCAAGGAAGGCAGGCGCGCAACTTACCCACTCC  
442 CAGCTCGGGGAGGTAGTGACGAAAAATAACAATACGGAACCTTTTGGAGGCT-CCGTAATTTGGAATGAGTACACTTTAAACCCCTTAAACGAGGATCTATTGGAGGGCAAGTCTGGTGCCA-GCAGCCCGGTAATTCAGCTCCAATAGCGTATATTA  
443 AAGTTGTTGCGATTAAAAGCTCGTAGTTGGATCTC-----AGGCATGGCGGTGCG-GTCC-GTC-----TCGC-----GACGGT-CACT--GTGCGAAGCCGGGGCGGGCGGGCCCTTCGCGGG-GTTT-  
444 CGTTCGCTTTTGGCGTCCCATCCTCCGTTTATCTCC-GGTCT--CTCCGTCCA-TG--GTGC---TCTTCGCTGAG-C-GTTATGGGCG-----GCCG--G-----AACGTTTACTTTGAAGAAATTAGAGTGTCAAAGCAGGC-----T  
445 C-GTTA-----GCCTGAATAAT-GGTGCATGGAATAATGGAATAGGA-----CC-----TCGGTCT--A-TTTT-----GCTGGTT----TTCGGAACAGAGGT--A-----ATGATTA-AGAGGGACAGCAGGGGGCATCCGTATTCG  
446 GGTGTTAGAGGTGAAATTTCTGGATCATCGCAAGACGAACTACT-GCGAAAGCATTGCGCAAGCATGTTTTCATTAGTCAAGAACGAAA-GTCAGAGGTTGCAAGACGATCAGATACCGTCTGTAGTTCTGACCATAAACGATGCCAACTAGCGATCCG  
447 CAGGTGT-T-----GCTT-CATCGACTCTGCG--GGCAGCTTCCGGGAAACC-AAAGTTTTCGGGTTCCGGGGGAAGTATGGTTGCAAAAGCTGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTTAATTTGACTC  
448 AACACGGGAAACTCACCCGGTCCGGACACTGTAAGGATTGACAGA---TTGATA-GCTCTTTCTTGATTCCGGTGGGTGGTGGTGCATGGCCGTTCTTAGTTG  
449  
450 *Neritina pulligera*  
451 TGCTCTTAGTTTGTGATTCGAGCAGAGCTTGGGCAACCTGGTGTCT--TTATTGGGGATGATCAGCTTTATAATGTAATTTGTGACTGCTCATGATTTGTAATAATTTCTTTTGGTTATGCCAATGATAATTTGGTGGGTTTGGTAACTGATTTG  
452 TTCCTTAAATGTTAGGGGCTCCTGATATGGCTTTTCTCGACTAAATAACATGAGTTTTTGGACTTCTTCTCCTTCAATGACTTTGTTGTTAGCCTTCTCTCCGTTGAGAGTGGAGTAGGTACTGGTTGAACGTTTATCCTCCACTTTCTGGGAAT  
453 TTAGCTCATGCTGGTGGATCTGTTGATTTAGCTATTTTTCTTTACACTTGGCTGGTGTTCATCAATTTAGTGGTAAACTTTATTACTACTATTTAATATGCGATGACGAGGAAATGCAATTTGAGCGACTTCCCTTTGTTGTTGATGATCTGT  
454 TAAAATTACCAGCAATTTGTTGTTGCTTTCTTCTTCTGCTTGCAGGCGCAATTAATGTTGCTAACTGATCGAAATTTAATACTTCGTTTTTGTATCCAGCTGTACAAA-CC-----TTCAC-AT----GGTGA-----AACCGCAATGGC  
455 TCATTAGATCAGTTATGGTTCCCTTAGATCGTA-----CAA-C-TC-CACTCGGATAACTGTGGCAATTTCTAGAGCTAATACGTCG--AA----GAAAG--CTC-TGACC--T-CG-C-----GG-GA--AGA-GCGCTT  
456 TTATTAGTTC-AA--AAC-CAAT-----CGGGCC-----GCA-A-----GGTCTGTC--GTT-T-GGTG-A-CTCTGGATAACTTTGTGCTGATCGCACGGC--C-TC-GA-----GCC-GGCAGCT  
457 ATCTTCAAAATGCTGCCCTCAACTTTAGATGGTACGTGATATGCCTACCATTGATTAACGGGTAGCGGGGATCAGGGTTCGATTCGGGAGGGAGCATGAGAACGGCTACCACATCCAAGGAAGGCAGGCGCAACTTACCCACTCC  
458 TGGTACGGGGAGGTAGTGACGAAAAATAACAATACGGGACTCTTTCGAGGCC-TCGTAATTTGGAATGAGTACACTTCAAACCCCTTAAACGAGGATCTATTGGAGGGCAAGTCTGGTGCCA-GCAGCCCGGTAATTCAGCTCCAATAGCGTATATTA  
459 AAGTTGTTGACGTTAAAAGCTCGTAGTTGGATCTC-----GGGTTTGGCGGGCG-GTCC-GCC-----TCGC-----GGCGGT-TACT--G--C-----AC--GA-C-  
460 -----C-C-G--A--C-C-T-ACC-----TCCCGGTTT-----TCCCT-TG--GTGC---TCTTACTGAG-T-GCTTCGGGTG-----GCCG--G-----AACGTTTACTTTGAAAAAATTAGAGTGTCAAAGCAGGC-----G  
461 C-T-TC-----GCCTGAATAAT-GGTGCATGGAATAATGGAATAGGA-----CC-----TCGGTCT--A-TTTT-----GTTGGTT----TTCGGAACGAGGT--A-----ATGATTA-AGAGGGACAGCAGGGGGCACTTCGATTTAC  
462 GGTGTTAGAGGTGAAATTTCTGGATCGCCGTAAGACGAACTACT-GCGAAAGCATTGCGCAAGCATGTTTTTCAATTAACAAGAACGAAA-GTCAGAGGTTTCAAGACGATCAGATACCGTCTGTAGTTCTGACCATAAACGATGCCAACTAGCGATCCG  
463 CTGGAGT-T-----GCTT-CTATGACTCAGCG--GGCAGCTTCCGGGAAACC-AAAGTTTTGGGTTCTGGGGGAAGTATGGTTGCAAAAGCTGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTTAATTTGACTC  
464 AACACGGGAAACTCACCCGGTCCGGACACTGTAAGGATTGACAGA---TTGATA-GCTCTTTCTTGATTCCGGTGGGTGGTGGTGCATGGCCGTTCTTAGTTG  
465  
466

467 *Physella acuta*  
468 AGGTTTAAAGCTTGTAAATTCGTTTGGAAATAGGAACATCTCTT-----GTAAGTGTGGATGAACATTTTTATAATGTAATGTTACAGCACATGCTTTTGTAAATGATTTTTTTTATAGTTATACCTATAATAATGGAGGGTTTGGAAATGAATAG  
469 TACCTATATTAATTTGGTGTCTCCCGATATAAGATTTCTCGAATAAATAATAAGATTTTGTACTTTTACCGCTTCATTTATCTTATTATATGTAAGTCTATAGTTGAGGGTGGAGTTGGAACCTGGGTGAACGTTTACCCCTCTATCAGGACCT  
470 GTAGCTCACTCTGGTTCATCAGTAGATCTTGTCTATTTCTCATTACACTTAGCTGGGTATCATCTATTTCTAGGTGCTATTAATTTTATTACTACCATTTTAAATATACGTTACCTGGTATTACTGGAACGAATAAGCTTATTTGTTTGTATCGGT  
471 GTTAAATTAAGTCAATTTTATATTTATTTGTCTATTGCTGTTTGTAGCAGGGGCTATTACTATACTAATACTGATAGAAATTTAACTACTAGGTTCTTTGATCCAAGAGTTTACA-CT-----GTCCC-AT----GGTGA-----AACCGCAATGGC  
472 TCATTAATCAAGTCGAGGTTCTTAGATGACA-----CGA-G-TCC-TACTTGGATAACTGTGGCAATCTAGAGCAATAACATGCAAT-----GA-AG--CTC-CGACC--T-TTACT-----GG-GA--AGA-GCGCTT  
473 TTATTAGTTC-AA--AAC-CAAT-----CGG-TC-GGCC-----TCG-C-----AAGGGGTT-GCG-TCGTCCC-----ATT-T-GGTG-A-CTCTGGATAACTTTTGTGCTGATCGCATGGC---C-TC-GC-----GCC-GGCAGCG  
474 ATCTTTCAAATGTCTGCCCTATCAAATGTCGATGGTACGTGATATGCCTACCATGTTTGTAAACGGGTAACGGGGAATCAGGGTTCGATTCGGAGAGGGAGCATGAGAAACGGCTACCACATCCGAGGAAGGCAGCAGGGCGGCAACTTACCCACTCC  
475 CGGCACGGGGAGGTAGTGACGAAAATAACAATACGGGACTCTTTTCGAGGCC-CCGTAATTTGGAATGAGTACACTTTAAACCCCTTAAACGAGTATCTATTGGAGGGCAAGTCTGGTGCCA-GCAGCCCGGGTAATCCAGCTCCAATAGCGTATATTA  
476 AAGTTGTTGCAGTTAAAAAGCTCGTAGTTGGATCTC-----AGGCGCAGGCGGGCG-GTCC-GGC-----TCGC-----GCGGCTCACT--G--C-----CC--G--T-  
477 -----ATCTCC--TG--CCC-T-ACC-GTC-----TGTCGGCT-----CTCTCCCGCGG--GTGC-----TCTTCACTGAG-C-GTCCCGGTG-----GCCG--A-----CGGTTTACTTTGAAAAAATTAGAGTGTCAAAGCAGGC-----CT  
478 C-G-CT-----GCCTGAATAAT-GGTGCATGGAATAATGGAATAGGA-----CC----TCGGTTC-----A-TTTT-----GTTGGTT----TTCGGAATTGGAGGT--A-----ATGATTA-ACAGGGACAACCGGGGCATTTCGTATTGC  
479 TGCGTTAGAGGTGAAATTTCTGGATCGCAGCAAGCAACTACT-GCGAAAGCATTTGTCAAGAATGTTTTCATTAGTCAAGAACGAAA-GTCAGAGGCGCAAGACGATCAGATACCGTCGTAGTTCTGACCATAAACTATGCCACTGGCCATCCG  
480 CAGGAGT-T-----GCTT-CGATGACTCTGCG--GGCGGCTCCGGGAAACC-AAAGGTTTTGGGTTCCGGGGGAAGTATGGTTGCAAAAGCTGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGAGTGGAGCTGCGGCTTAATTTGACTC  
481 AACACGGGAAAACCTACCCGGTCCGGACACTGTAAGGATTGACAGA---TTGATA-GCTCTTCTTGATTTCGGTGGGTTGGTGCATGGCCGTTCTTAGTTG  
482  
483 *Pomacea bridgesii*  
484 AGCTTTAAGATTGCTTATTCGTTGCTGAAGTACAGGCAACCTGGTGCT---TTATTAGGAGATGACCAGCTTTATAATGTAATTTGTGACGGCTCATGCTTTTGTAAATAATTTCTTTCTAGTTATGCCAATAATGATTGGAGGATTTGGTAACTGATTTGG  
485 TTCCATTGATACTAGGGCCCCAGATATGGCTTTTCCACGGCTTAATAACATAAGATTTTGGTTATGCTCCTCTTTTACTATTATGCTCTCGGCTGCTGCGAAAGTGGTGGTACTGGTTGAACAGTTTACCCCTTTAGCTGGAAT  
486 TTAGCTCATGCTGGTGGTCTGTAGACTTAGCAATTTTTCTTTACATTTAGCTGGGGCCTCCTCTATCCTAGGTGCGGTAATTTTATTACAACGGTAATTAATATACGGTACGAGGATGCAATTTGAGCGTCTTCTCTATTCGTGTGGTCACT  
487 TAAAATTAAGTCTATTTTATTATTATCATTGCCAGTTCTTGTGGGGCTATTACTATACTAATACTGACCGAAATTTTAACTACGGCTTTTTTGTACCCGGTGTTCACA-CC-----CTCGT-AC----GGTGA-----AACCGCAATGGC  
488 TCATTAATCAAGTCGAGGTTCTTAGATGATC-----CAA-A-TC-TACTTGGATAACTGTGGCAATTTCTAGAGCTAATACATGC--AA-----ACCAG--CTC-CGACCC-GGTG-TC-----AC-AGCCG-----GG-AA--AGA-GCGCTT  
489 TTATTAGTTC-AA--AAC-CAGT-----CGG-GGT-----CTC-----GGCCCCGCTCCT---T-T-T-GGTG-A-CTCTGGATAACTTTGTGCGGATCGCATGGC---C-TC-GA-----GCC-GGCAGCG  
490 ATCTTTCAAATGTCTGCCCTATCAAATGTCGATGGTACGTGATAGGCTACCATTGTTGACTACGGGTAACGGGGAATCAGGGTTCGATTTCCGGAGAGGGAGCATGAGAAACGGCTACCACATCCAAGGAAGGCAGCAGGGCGGCAACTTACCCACTCC  
491 CAGCTCGGGGAGGTAGTGACGAAAATAACAATACGGAACCTTTTGGAGGCT-CCGTAATTTGGAATGAGTACACTTTAAACCCCTTAAACGAGGATCTATTGGAGGGCAAGTCTGGTGCCA-GCAGCCCGGGTAATCCAGCTCCAATAGCGTATATTA  
492 AAGTTGTTGGCATTAAAAAGCTCGTAGTTGGATCTC-----AGGCATGGGCGTGCG-GTCC-GTC-----TCGCGACGGTCACTGTGCGAAGCCGGGGCGGGCGGTGCCCTTCG--C-----GGGGTGT-CGT-T-  
493 CGTCTCTTTGGCGT--CCCATCTCCGTTTATCTCC-GGTCT---CTCCGTTCA-TG--GTGC-----TCTTCTGCTGAG-C-GTTATGGCGC-----GCCG--G-----AACGTTTACTTTGAAGAAATTAGAGTGTCAAAGCAGGC-----T  
494 C-GTCA-----CCCTGAATAAT-GGTGCATGGAATAATGGAATAGGA-----CC-----TCGGTCT---A-TTTT-----GCTGGTT---TTCGGAACACGAGGT--A-----ATGATTA-AGAGGGACAGACGGGGCATCCGTATTGC  
495 GGTGTTAGAGGTGAAATTTCTGGATCATCGCAAGACGAACAACCT-GCGAAAGCATTTGCCAAGCATGTTTTCATTAGTCAAGAACGAAA-GTCAGAGGTTGCAAGACGATCAGATACCGTCTGATTTCTGACCATAAACGATGCCAATAGCGATCCG  
496 CAGGTGT-T-----GCTT-CATCGACTCTGCG--GGCAGCTTCCGGGAAACC-AAAGTTTTCGGGTTCCGGGGGAAGTATGGTTGCAAAAGCTGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGAGTGGAGCTGCGGCTTAATTTGACTC  
497 AACACGGGAAAACCTACCCGGTCCGGACACTGTAAGGATTGACAGA---TTGATA-GCTCTTCTTGATTTCGGTGGGTTGGTGCATGGCCGTTCTTAGTTG  
498  
499 *Pomatias elegans*  
500 TGCTTTAAGGCTTTTAAATTCGGGCTGAATTTGGGCGAGCCTGGGAGT---TTGCTAGGTGATGATCAACTTTATAATGTTATTGTTACTGCTCATGCAATTTGTTATAATTTTTTTTTTGGTTATGCCAATAATGATTGGTGGTTTTGGCAATTGGTTAG  
501 TTCCTTTAATGTTGGGGGCTCCTGATATGGCTTTTCTCGGTTAAATAATATAAGATTTTGTACTTCTCCTCGCTTATTTTTATTGTTAATATCTGCGGCTGTAAGAGGGGAGCTGGTACTGGGTGAACAGTATATCCCTTTGGCTGGTAAAT  
502 TTAGCACATTCGGGTGGTTCGTGTGATCTTGTCTATTTTTCTGTTACATTTGGCTGGGGCACTTCTTATTTTAGGTGCTGTGAATTTCTACTACTATTGTTAATATAACAATGGTGTGGTGTTCAGTTGGAGCGGTATCTTTGTTGTTGGTTCGGT  
503 TAAAATTAAGTCTATTTTGTCTTTTACTTTCTTTTACCAGTTTTGGCTGGGGCAGTTACTATGCTTTTAAACAGATCGGAATTTTAACTACTTTTTTTGATCCTGCTGTTCACA-CC-----CTCGT-AC----GGTGA-----AACCGCAATGGC  
504 TCATTAATCAAGTCGAGGTTCTTAGATGATC-----CAA-A-TC-TACTTGGATAACTGTGGTAAATTTCTAGAGCTAATACATGC--CA-----ACCAG--CTC-CGACCTT-TC-G-----GG-----GG-AA--AGA-GCGCTT  
505 TTATTAGTTC-AA--AAC-CAGT-----CGGGT-----GCA-A-----GAC-TCGTC-----T-T-T-GGTG-A-CTCTGGATAACTTTGTGCGGATCGCATGGC---C-TC-GA-----GCC-GGCAGCG  
506 ATCTTTCAAATGTCTGCCCTATCAAATGACGATGGTACGTGATCTGCCTACCATTGTAGCAACGGGTAGCGGGGAATCAGGGTTCGATTTCCGGAGAGGGAGCATGAGAAACGGCTACCACATCCAAGGAAGGCAGCAGGGCGCAACTTACCCACTCC  
507 TGGCACGGGGAGGTAGTGACGAAAATAACAATACGGAACCTTTTGGAGGCT-CCGTAATTTGGAATGAGTACACTTTAAAGCCTTAAACGAGGATCTATTGGAGGGCAAGTCTGGTGCCA-GCAGCCCGGGTAATCCAGCTCCAATAGCGTATACTA  
508 AAGTTGTTGGCATTAAAAAGCTCGTAGTTGGATCTC-----AGGCATGGGCGCAG-GTCC--GC-----CTCGC-----GGCGGT-CACT--G--T-----GT--GG-T-  
509 -----TTTGT--TT--CCCATCTACGCT---TCCCGGTTG---TTCAGCCCA-TG--GTGC-----TCTTGAAGTACG-C-GTTTTGGGTG-----GCCG--G-----AACGTTTACTTTGAAGAAATTAGAGTGTCAAAGCAGGC-----A  
510 C-GTC-----GCCTGAATAAT-GGTGCATGGAATAATGGAATAGGA-----CC-----TCGGTCT---A-TTTT-----GCTGGTT---TTCGGAACACGAGGT--A-----ATGATTA-AGAGGGACAGACGGGGCATCCGTATTGC  
511 GGTGTTAGAGGTGAAATTTCTGGATCATCGCAAGACGAACAACCT-GCGAAAGCATTTGCCAAGCATGTTTTCATTAGTCAAGAACGAAA-GTCAGAGGTTGCAAGACGATCAGATACCGTCTGATTTCTGACCATAAACGATGCCAATAGCGATTCG  
512 CTGGTGT-T-----GCTT-CATCGACTCTGCG--GGCAGCTTCCGGGAAACC-AAAGTTTTCGGGTTCCGGGGGAAGTATGGTTGCAAAAGCTGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGAGTGGAGCTGCGGCTTAATTTGACTC  
513 AACACGGGAAAACCTACCCGGTCCGGACACTGTAAGGATTGACAGA---TTGATA-GCTCTTCTTGATTTCGGTGGGTTGGTGCATGGCCGTTCTTAGTTG  
514  
515  
516  
517

518 **Alignment S2:**

519 MUSCLE alignment (manually edited) of gastropod CdMT protein sequences applied for the mirrored Maximum  
 520 Likelihood tree represented in **Figure 6**.

521  
 522  
 523 >*Lottia gigantea* MT1  
 524 -SSEK-----PSCCIAEYECCKTKLCCDTGPADCCCKPGNKPDCCAPGKQLQCKCP-G-  
 525 TCACGVGCTGVDNCKCGAGCS-CFN  
 526  
 527 >*Lottia gigantea* MT2  
 528 -SSEK-----ASCCIAEYECCKTKSCCDTGPADCCCKPGNKPDCCAPGKQLQCKCS-G-  
 529 TCACGVGCTGVDNCKCGAGCS-CFN  
 530  
 531 >*Nacella polaris* MT  
 532 -SSEK-----AACCCIAEYECCKTKSCCKDGPADCCCKPGNTTDCCKGKV-ACKCA-G-  
 533 SCACGAGCTGQTPCKCGAGCS-CNS  
 534  
 535 >*Patella vulgata* MT1  
 536 -SSQK-----ASCCLAELECCCKTKACCAKGPANCCSPGNDPNCKS-N-ICKCN-G-  
 537 NCACGVGCTGIENCECGTGCS-CK-  
 538  
 539 >*Patella vulgata* MT2  
 540 -SSEK-----AACCLAEHECCCKTKSCCANGPADCCCKPGKTVDCCKSQN-TCKCG-E-  
 541 SCACGAGCSGVDNCKCGSGCS-CK-  
 542  
 543 >*Littorina littea* MT  
 544 -SS---VF-GAGCTDVCKQTPCGCATS--GCNCTDDCKQSC-KYAGCT---DTCKQTPCGC---GSGCNCKEDCRCQSCST-ACKCAAG-  
 545 SCKCGKCTGPDSCCKDRS-CS-CK-  
 546  
 547 >*Pomatias elegans* MT1  
 548 STSGANVIYAGAGCTGTCKQSPCGCKNSAAGCRCKDDCQCPACAKYAGCT---GTCKQSPCGCKNSAAGCGCKDDCPCACAK-SCKC--G-  
 549 TCNCGKCTGTPSNCKCDDGCS-CK-  
 550  
 551 >*Pomatias elegans* MT2  
 552 SSSGANAT-----GAGCT---ETCKESPCGCKNSAAGCKCKDDCQCTTCAK-SCKCA-G-  
 553 TCNCGKCTGTPNSCKDGGCP-CK-  
 554  
 555 >*Helix pomatia* CdMT  
 556 SGK GK-----GEKCT---SACRSEPCQC---GSKCQCGEGCTCAAC-K-TCNCTSD-  
 557 GCKCGKECTGPDSCCKGSSCS-CK-  
 558  
 559 >*Cornu aspersum* CdMT  
 560 SGK GK-----GEKCT---AACRNEPCQC---GSKCQCGEGCTCAAC-K-TCNCTSD-  
 561 GCKCGKACTGPDSCCTCGSSCG-CK-  
 562  
 563 >*Arianta arbustorum* CdMT  
 564 SGK GK-----GDLCT---AACKNEPCQC---GSKCQCGEGCACAAC-K-TCNCTSD-  
 565 GCKCGKECTGAASCKGSSCS-CK-  
 566  
 567 >*Cepaea hortensis* CdMT1  
 568 SGK GK-----GEKCT---AACRNEPCQC---GSKCQCGEGCACAAC-K-TCNCTSD-  
 569 GCKCGKECTGPDSCCKGSSCS-CK-  
 570  
 571 >*Cepaea hortensis* CdMT2  
 572 SGK GK-----GEKCT---AACRNEPCQC---GSKCQCGEGCACAAC-K-TCNCTSD-  
 573 GCKCGKECTGPDSCCKGSLCS-CK-  
 574  
 575 >*Cepaea nemoralis* CdMT  
 576 SGK GK-----GEKCT---AACRNEPCQC---GSKCQCGEGCACAAC-K-TCNCTSD-  
 577 GCKCGKECTGPDSCCKGSSCS-CK-  
 578  
 579 >*Cochlicella acuta* CdMT  
 580 SGK GK-----AESCT---AQCQSNPCQC---GDKCQCGEGCACTSC-K-TCKCTSD-  
 581 GCKCGKECTGPASCKGSSCS-CK-  
 582  
 583 >*Nesiohelix samarangae* CdMT  
 584 SGK-----GELCT---SACKSNPCQC---GDKCQCGEGCTCSAC-K-SCHCTND-  
 585 GCNCGKECTGPTSCKCDTSCS-CK-  
 586  
 587 >*Lehmannia nyctelia* CdMT  
 588 SGK-----GAKCT---GACKSEPCQC---GQNCQCGDDCSCSQC-K-TCKCSAGS  
 589 TCQCGHGCTGVESCKGNSCS-CK-  
 590  
 591 >*Limax maximus* CdMT  
 592 SGK-----GAKCT---GACKSEPCQC---GQNCQCGDDCSCSQC-K-TCKCSAGS  
 593 TCQCGHGCTGVESCKGSSCS-CK-  
 594

595 >*Deroceras reticulatum* CdMT1  
596 SGK-----GKCT---GDCKSEPCKC---GQNCQCGNDCTCSQC-K-TCKCSSS-  
597 GCQCGHGCTGVESCKCGSSCT-CK-  
598  
599 >*Deroceras reticulatum* CdMT2  
600 SGK-----GKCT---GDCKSEPCKC---GQNCQCGNDCTCSQC-K-TCKCSSS-  
601 GCQCGHGCTGVESCKCGSSCT-CK-  
602  
603 >*Arion vulgaris* AvMT1  
604 SGK-----A-CT---GACKSEPCQC---GNNCQCGGDCDCSQC-K-TCKCTNE-  
605 GCKCGQNCTGQATCSCEKSCS-CK-  
606  
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611  
612  
613

614 **Alignment S3:**

615 MUSCLE alignment (manually edited) of MTs of Panpulmonata (Hygrophila + Stylommatophora + Sacoglossa)  
616 applied for the Bayesian Inference Tree represented in **Figure 7**.

617  
618  
619 >*Tritia obsoleta* MT1  
620 -----EGTGCAGPCKQTPCGCE--SSGGCKCGGDCSCTECGR-GAGCTDACKETPCGC-ASSGGCKCTGNCSPPSCS-----CKCGK-----  
621 -----GACKCDKG-CEGPGSCKCGPG-C-----TCKKS-----  
622  
623 >*Littorina littorea* CdMT  
624 -----SSVFGAGCTDVCKQTPCGC--ATSGCNCTDDCKCQSC-KYGAGCTDTCKQTPCGC---GSGCNCKEDCRCQSCSTA-----CKCAA-----  
625 -----GSKCKGKG-CTGPDSCCKDRS-C-----SCK-----  
626  
627 >*Pomatias elegans* MT1  
628 STSGANVIYAGACTGTCKQSPCGCKNSAAGCRCKDDCQCPACAKYAGACTGTCKQSPCGCKNSAAGCGCKDDCRCPCAKAS-----CKCGT-----  
629 -----CNCGKG-CTGPNCKCDDG-C-----SCK-----  
630  
631 >*Pomatias elegans* MT2  
632 -----SSSGANATGAGCTETCKESPCGCKNSAAGCKCKDDCQCTTCAKS-----CKCA-----  
633 -----GTCNCGKG-CTGPNCKCDDG-C-----PCK-----  
634  
635 >*Elysia crispata* MT  
636 -----SGK-GLICTAPCTNDPCGC---GENCQCGHACSHSCS-----CSCGA-----  
637 -----DCKCNQATCHEKSNCKCEAS-C-----SCRK-----  
638  
639 >*Elysia cornigera* MT  
640 -----SGK-GASCPPTCRNDPCGC---GQDCQCGQDCTCSSCS-----CLCGN-----  
641 -----ECKCTSASCSQGVRCRCDTL-C-----DCRPK-----  
642  
643 >*Helix pomatia* CdMT  
644 -----SGKKG-GEKCTSACRSEPCQC---GSKCQCGEGCTCAACKT-----CNCTS-----  
645 -----DGCKCGKE-CTGPDSCCKGSS-C-----SCK-----  
646  
647 >*Cornu aspersum* CdMT  
648 -----SGKKG-GEKCTAACRNEPCQC---GSKCQCGEGCTCAACKT-----CNCTS-----  
649 -----DGCKCGKA-CTGPDSCCKGSS-C-----GCK-----  
650  
651 >*Arianta arbustorum* CdMT  
652 -----SGKKG-GDLCTAACRNEPCQC---GSKCQCGEGCACASCKT-----CNCTS-----  
653 -----DGCKCGEK-CTGAASCKGSS-C-----SCK-----  
654  
655 >*Cepaea hortensis* CdMT1  
656 -----SGKKG-GEKCTAACRNEPCQC---GSKCQCGEGCACAAACKT-----CNCTS-----  
657 -----DGCKCGKE-CTGPDSCCKGSS-C-----SCK-----  
658  
659 >*Cepaea hortensis* CdMT2  
660 -----SGKKG-GEKCTAACRNEPCQC---GSKCQCGEGCACAAACKT-----CNCTS-----  
661 -----DGCKCGKE-CTGPDSCCKGSL-C-----SCK-----  
662  
663 >*Cepaea nemoralis* CdMT  
664 -----SGKKG-GEKCTAACRNEPCQC---GSKCQCGEGCACAAACKT-----CNCTS-----  
665 -----DGCKCGKE-CTGPDSCCKGSS-C-----SCK-----  
666  
667 >*Cochlicella acuta* CdMT  
668 -----SGKKG-AESCTAQCSNPCQC---GDKCQCGEGCACTSCKT-----CKCTS-----  
669 -----DGCKCGKE-CTGPASCKGSS-C-----SCK-----  
670  
671 >*Nesiohelix samarangae* CdMT  
672 -----SGK-GELECTSACKSNPCQC---GDKCQCGEGCTCSACKS-----CHCTN-----  
673 -----DGCNCGKE-CTGPTSCCKDTS-C-----SCK-----  
674  
675 >*Limax maximus* CdMT  
676 -----SGK-GAKCTGACKSEPCQC---GQNCQCGDDCSCSQCKT-----CKCSA-----  
677 -----GSTCQCGHG-CTGVESCKGSS-C-----SCK-----  
678  
679 >*Deroceras reticulatum* CdMT1  
680 -----SGK-GEKCTGDCKSEPCCK---GQNCQCGNDCTCSQCKT-----CKCST-----  
681 -----GSGCQCGHG-CTGVESCKGSS-C-----T-----  
682  
683 >*Deroceras reticulatum* CdMT2  
684 -----SGK-GEKCTGDCKSEPCCK---GQNCQCGNDCTCSQCKT-----CKCSS-----  
685 -----SGCQCGHG-CTGVESCKGSS-C-----TCK-----  
686  
687  
688  
689

690 >Lehmannia nyctelia CdMT  
691 -----SGK-GAKCTGACKSEPCQC---GQNCQCGDDCSCSQCKT-----CKCSA-----  
692 -----GSTCQCGHG-CTGVESCKCGNS-C-----SCK-----  
693  
694 >Arion vulgaris AvMT1  
695 -----SGK-A--CTGACKSEPCQC---GNNCQCGGDCDCSQCKT-----CKCTN-----  
696 -----EGCKCGQN-CTGQATCSCEKS-C-----SCK-----  
697  
698 >Physella acuta MT1  
699 -----SGK-GPNCTEACTGEQCTC---GRQLQV-----CCKT-----CKCED-----  
700 -----NACKCGEG-CTGPSTCKCESSDC-----ACK-----  
701  
702 >Physella acuta MT2  
703 -----SGK-GPNCTEACTGEQCTC---GDSCKCGEGCNCPSCKT-----CKCED-----  
704 -----NACKCGEG-CTGPSTCKCESSDC-----ACK-----  
705  
706 >Physella carolinae MT  
707 -----SGK-GPNCTEACTGEQCTC---GDSCKCGEGCNCPSCKT-----CKCED-----  
708 -----NACKCGEG-CTGPSTCKCESSDC-----ACK-----  
709  
710 >Physella hendersoni MT  
711 -----SGK-GPNCTEACTGEQCTC---GDSCKCGEGCNCPSCKT-----CKCED-----  
712 -----NACKCGEG-CTGPSTCKCESSDC-----ACK-----  
713  
714 >Physella gyrina MT  
715 -----SGK-GPNCTEACTGEQCN---GDSCKCGEGCNCPSCKT-----CKCED-----  
716 -----NACKCGEG-CTGPSTCKCEST-C-----ACK-----  
717  
718 >Galba cubensis MT  
719 -----SGR-GPNCTEACRGEQCNC---GDSCKCGEGCNCPSCKT-----CKCSA-----  
720 -----EDCKCDAG-SKGTGNCKC-----  
721  
722 >Galba truncatula MT  
723 -----SGK-GPNCTEACRGEQCNC---GDSCKCGEGCNCPSCKT-----CKCAA-----  
724 -----EDCKCDAG-SKGTGNCKC-----  
725  
726 >Lymnaea stagnalis MT  
727 -----SGK-GPNCTEACTGEQCNC---GDSCKCGEGCNCPSCKT-----CKCSA-----  
728 -----EDCKCDAG-SKGTGNCKC-----  
729  
730 >Biomphalaria glabrata MT  
731 -----SGK-GPNCTEACTGEQCNC---GDSCKCGEGCNCPSCKTTKGNPCTEACTGKQ  
732 CSCGDSQCQCGEGCTCSCCKKACTKECTDTECSGDSCKCGEG-CK-CSSCKAGK--CTKSDEGCKTEGHCAKGCCKS  
733  
734 >Helix pomatia CuMT  
735 -----SGR-GKNCGGACNSNPCSC---GNDCKCGAGCNCDCRSS-----CHCSN-----  
736 -----DDCKCGSQ-CTGSGSCKCGSA-C-----GCK-----  
737  
738 >Cornu aspersum CuMT  
739 -----SGR-GQNCGGACNSNPCNC---GNDNCNGTGCNCDQCSA-----RHCSN-----  
740 -----DDCKCGSQ-CTRSGSCKCGNA-C-----GCK-----  
741  
742 >Cepaea nemoralis CuMT  
743 -----SGR-G-NCGGACNSNPCSC---GDDCKCGAACNDCRSS-----CHCSN-----  
744 -----DDCKCGSQ-CTGSGSCKCGSA-C-----GCK-----  
745  
746 >Theba pisana CuMT  
747 -----SGR-GKNCGGACNSNPCNC---ANNCRGAGCNCDCRSS-----CHCSN-----  
748 -----DDCKCGNQ-CTTSGSCKCGSA-C-----GCK-----  
749  
750 >Alinda biplicata CuMT1a  
751 -----SGK-GANCTGACNSNPCQC---GDDCKCGVGCSCAECNT-----CKCTN-----  
752 -----DGCKCGHG-CTGAGSCKCGNS-C-----GCK-----  
753  
754 >Alinda biplicata CuMT1b  
755 -----SGK-GANCTGACNSNPCQS---GDDCKCGVGCSCAECNT-----CKCTN-----  
756 -----DGCKCGHG-CTGAGSCKCGNS-C-----GCK-----  
757  
758 >Alinda biplicata CuMT2  
759 -----SGK-GANCSGACNSNPCQC---GDDCKCGAACSCAECNT-----CKCTN-----  
760 -----DSCKCGHD-CSGAGSCKCGNS-C-----GCK-----  
761  
762 >Cochlicella acuta CuMT  
763 -----SGR-G-NCGACKSNPCSC---GQVCKCGGACTCAQCNA-----CRCSG-----  
764 -----DSCKCGDQ-CTASGSCQCGSG-C-----GCK-----  
765

766 >*Arion vulgaris* AvMT2  
767 -----SGR-G--CNGTCNSNPCQC---EDGCQCGDACSCAQCNT-----CKCTN-----  
768 -----DGCKCGNE-CTATGSKCGTS-C-----GCN-----  
769  
770 >*Helix pomatia* CdCuMT1  
771 -----SGK-GSNCAGSCNSNPCSC---GDDCKCGAGCSVCQCHS-----CQCNN-----  
772 -----DTCKCGNQ-CSASGSKCGS--C-----GCK-----  
773  
774 >*Helix pomatia* CdCuMT2  
775 -----SGK-GSNCAGSCNSNPCSC---GDDCKCGAGCSAQCHS-----CQCNN-----  
776 -----DTCKCGNQ-CSASGSKCGS--C-----GCK-----  
777  
778 >*Cepaea hortensis* CdCuMT  
779 -----SGK-ASACAGSCNSNPCSC---GDDCQCGAGCSAQCHS-----CQCNN-----  
780 -----DTCKCGNQ-CSASGSKCGS--C-----GCK-----  
781  
782 >*Cepaea nemoralis* CdCuMT  
783 -----SGK-GSACAGSCNSNPCSC---GDDCQCGAGCSAQCHS-----CQCNN-----  
784 -----DTCKCGNQ-CSASGSKCGS--C-----GCK-----  
785  
786 >*Cochlicella acuta* CdCuMT  
787 -----SGK-GSACAGSCGNNPCSC---GDDCRCGAGCSAQCHS-----CQCNN-----  
788 -----DTCKCGNQ-CSTSGSKCGS--C-----GCK-----  
789  
790 >*Cornu aspersum* CdCuMT  
791 -----SGK-GSACAGSCNSNPCSC---GDDCKCGAGCSAQCHS-----CQCNN-----  
792 -----DTCKCGSQ-CSTSGSKCGS--C-----GCK-----  
793

794

795 **Alignment S4:**

796 MUSCLE alignment (manually edited) of MT protein sequences of Stylommatophora versus Caenogastropoda and  
797 Vetigastropoda applied for the Bayesian Inference Tree represented in **Figure S3**.

798  
799  
800 >Megathura crenulata MT  
801 --SGK-----GENCTAECKSDPCACGD---SCKCGEGCACTTCVKTEAKTTCKCG--ESCKC-EG  
802 CKEGEACKCESGCASCK  
803  
804 >Arion vulgaris AvMT1  
805 --SGK-----ACTGACKSEPCQCGN---NCQCGDCCDCSQC-----KTCKCTN-EGCKCGQN  
806 CTGQATCSCSEKSC-SCK  
807  
808 >Lehmannia nyctelia CdMT  
809 --SGK-----GAKCTGACKSEPCQCGQ---NCQCGDDCSCSQC-----KTCKCSAGSTCQCGHG  
810 CTGVESCKCGNSC-SCK  
811  
812 >Limax maximus CdMT  
813 --SGK-----GAKCTGACKSEPCQCGQ---NCQCGDDCSCSQC-----KTCKCSAGSTCQCGHG  
814 CTGVESCKCGSSC-SCK  
815  
816 >Deroceras reticulatum CdMT1  
817 --SGK-----GEKCTGDCKSEPCCKGQ---NCQCGNDCTCSQC-----KTCKCSTGSGCQCGHG  
818 CTGVESCKCGSSC-T--  
819  
820 >Deroceras reticulatum CdMT2  
821 --SGK-----GEKCTGDCKSEPCCKGQ---NCQCGNDCTCSQC-----KTCKCSS-SGCQCGHG  
822 CTGVESCKCGSSC-T--  
823  
824 >Nesiohelix samarangae CdMT  
825 --SGK-----GELCTSACKSNPCQCGD---KCQCGEGCTCSAC-----KSCHCTN-DGCNCGKE  
826 CTGPTSCKCDTSC-SCK  
827  
828 >Cochlicella acuta CdMT  
829 SGK GK-----AESCTAQCSNPCQCGD---KCQCGEGCACTSC-----KTCKCTS-DGCKCGKE  
830 CTGPASCKCGSSC-SCK  
831  
832 >Arianta arbustorum CdMT  
833 SGK GK-----GDLCTAACKNEPCQCGS---KCQCGEGCACASC-----KTCNCTS-DGCKCGEK  
834 CTGAASCKCGSSC-SCK  
835  
836 >Cornu aspersum CdMT  
837 SGK GK-----GEKCTAACRNEPCQCGS---KCQCGEGCTCAAC-----KTCNCTS-DGCKCGKA  
838 CTGPDSTCGSSC-GCK  
839  
840 >Helix pomatia CdMT  
841 SGK GK-----GEKCTSACRSEPCQCGS---KCQCGEGCTCAAC-----KTCNCTS-DGCKCGKE  
842 CTGPDSTCGSSC-SCK  
843  
844 >Cepaea hortensis CdMT1  
845 SGK GK-----GEKCTAACRNEPCQCGS---KCQCGEGCACAAC-----KTCNCTS-DGCKCGKE  
846 CTGPDSTCGSSC-SCK  
847  
848 >Cepaea nemoralis CdMT  
849 SGK GK-----GEKCTAACRNEPCQCGS---KCQCGEGCACAAC-----KTCNCTS-DGCKCGKE  
850 CTGPDSTCGSSC-SCK  
851  
852 >Cepaea hortensis CdMT2  
853 SGK GK-----GEKCTAACRNEPCQCGS---KCQCGEGCACAAC-----KTCNCTS-DGCKCGKE  
854 CTGPDSTCGSLC-SCK  
855  
856 >Arion vulgaris AvMT2  
857 --SGR-----G---CNGTCNSNPCQCED---GCQCGDACSCAQC-----NTCKCTN-DGCKCGNE  
858 CTATGSCKCGTSC-GCN  
859  
860 >Alinda biplicata CuMT2  
861 --SGK-----GANCSGACNSNPCQCGD---DCKCGAACSCAEC-----NTCKCTN-DSCCKGHD  
862 CSGAGSCKCGNSC-GCK  
863  
864 >Alinda biplicata CuMT1a  
865 --SGK-----GANCTGACNSNPCQCGD---DCKCGVGCSCAEC-----NTCKCTN-DGCKCGHG  
866 CTGAGSCKCGNSC-GCK  
867  
868 >Alinda biplicata CuMT1b  
869 --SGK-----GANCTGACNSNPCQSGD---DCKCGVGCSCAEC-----NTCKCTN-DGCKCGHG  
870 CTGAGSCKCGNSC-GCK  
871



872 >*Cochlicella acuta* CuMT  
873 --SGR-----G-NCGGACKSNPCSCGQ---VCKCGACTCAQC-----NACRCSG-DSCCKGDQ  
874 CTASGSCQCGSGC-GCK  
875  
876 >*Cochlicella acuta* CdCuMT  
877 --SGK-----GSACAGSCGNNPCSCGD---DCRCGAGCSCAQC-----NSCQCNN-DTCKCGNQ  
878 CSTSGSCKCGS-C-GCK  
879  
880 >*Cornu aspersum* CdCuMT  
881 --SGK-----GSACAGSCNSNPCSCGD---DCKCGAGCSCAQC-----YSCQCNN-DTCKCGSQ  
882 CSTSGSCKCGS-C-GCK  
883  
884 >*Cepaea nemoralis* CdCuMT  
885 --SGK-----GSACAGSCNSNPCSCGD---DCQCGAGCSCAQC-----QSCQCNN-DTCKCGNQ  
886 CSASGSCCKCGS-C-GCK  
887  
888 >*Cepaea hortensis* CdCuMT  
889 --SGK-----ASACAGSCNSNPCSCGD---DCQCGAGCSCAQC-----HSCQCNN-DTCKCGNQ  
890 CSASGSCCKCGS-C-GCK  
891  
892 >*Helix pomatia* CdCuMT1  
893 --SGK-----GSNACAGSCNSNPCSCGD---DCKCGAGCSCVQC-----HSCQCNN-DTCKCGNQ  
894 CSASGSCCKCGS-C-GCK  
895  
896 >*Helix pomatia* CdCuMT2  
897 --SGK-----GSNACAGSCNSNPCSCGD---DCKCGAGCSCAQC-----HSCQCNN-DTCKCGNQ  
898 CSASGSCCKCGS-C-GCK  
899  
900 >*Cornu aspersum* CuMT  
901 --SGR-----GQNCGGACNSNPCNCGN---DCNCGTGCNCDQC-----SARHCSN-DDCKCGSQ  
902 CTRSGSCKCGNAC-GCK  
903  
904 >*Theba pisana* CuMT  
905 --SGR-----GKNCGGACNSNPCNCAN---NCRGAGCNCDCS-----SSCHCSN-DDCKCGNQ  
906 CTTSAGSCKCGSAC-GCK  
907  
908 >*Helix pomatia* CuMT  
909 --SGR-----GKNCGGACNSNPCSCGN---DCKCGAGCNCDCR-----SSCHCSN-DDCKCGSQ  
910 CTGSGSCKCGSAC-GCK  
911  
912 >*Cepaea nemoralis* CuMT  
913 --SGR-----G-NCGGACNSNPCSCGD---DCKCGAACNCDCR-----SSCHCSN-DDCKCGSQ  
914 CTGSGSCKCGSAC-GCK  
915  
916 >*Littorina littorea* MT  
917 -----SSVFGAGCTDVCKQTPCGC--ATSGCNCTDDCKQSC-KYGAGCTDTCKQTPCGCGS---GCNCKEDCRCQSCS-----TACKCAA-GSCKCGKG  
918 CTGPDSCCKDRSC-SCK  
919  
920 >*Pomatias elegans* CdMT1  
921 STSGANVIYGAGCTGTCKQSPCGCKNSAAGCRCKDDCQCPACAKYAGCTGTCKQSPCGCKNSAAGCGCKDDCRCPACA-----KSKC---GTCNCGKG  
922 CTGPNCKCDDGC-SCK  
923  
924 >*Pomatias elegans* CdMT2  
925 SSSGANAT-----GAGCTETCKESPCGCKNSAAGCKCKDDCQCTTCA-----KSKCA--GTCNCGKG  
926 CTGPNCKCDGGC-PCK  
927  
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