http://app.pan.pl/SOM/app70-Cleland_etal_SOM.pdf

SUPPLEMENTARY ONLINE MATERIAL FOR

Protein and chitin preservation in polymeric sheets in Miocene *Ecphora gardnerae* shells from Maryland, USA

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Supplementary Online Material

Supplementary Methods

Mass Spectrometry Data Analysis

After filtering by FDR and Score >= 9, peptide sequences were filtered if they were present in the extraction blank results. The following peptides were filtered: SLDSSRAEAAELINDDIFPIK, TICLIANFDVGGAK, INADVCLVTSWAK, DVEDKANTYFQQIYNMPPHLTMTIDDVLEMLK, TTLGYPVLEEDGAK, RVDDAINAVR, ANPSYSLDR, KTMTYEK, EISLSAVDTISDTK, DMARLERNEALGQMEQILK, FSTNNRFTDYGVRFEEGDVIGAMLDLESR, INAAATLWGDMLGK, NITINSR, QWIFKQAEDLAK, TTAQYVVDLRNRIEETCK, QSGRNWNNLLHSHLIQNPVCSEYLK, KAGEGVDSSQWKK, PATLGSGR, TAALSGEEAGR, SERSLPR, TILNFGEAFDKSYGLLQGAK, GQPDRVVWTPGCKESFSLLK, LTMQNAKYWTEILCQQYNFDRDNVEVEFLK, KMGIPINDDMKAK, SLVCLATER, PSTALSNR, AGGKDIISDMKER, KMPSVGK, TQKPTSPSSLSVGK, MPALVSSRESQQK, LIHTNPKSFICDICNKAFSFACNLK, QLNKSTLDMDSAK, HYDTNDLNESDSK, LIMHRISCNGEESYPGNLSVTVTFQVTEENELK, LNMTVSGGGAAR, EVFIDCLR, WTDGELYGAVFRGVNCLDDYTVEFEDGSQLILK, GEGKGEGGGFRGVAK, ELMICEQIINTYRPELK, KKMLEQQAEAER, GKEKVFHANMLK, RSVATFPAR, VRAQIWQSVSDNQFVDLLK, PTANISR, IPKLEVSGK, KAVVEGLR, QGETFFMLSIKK, DLLFVQGDWNAK, IGGSGMDKDALGIR, NTVDVLVCHGADANPQDERGDTPLLSAAK, IAGAVFSHIMR, TSTGSPGSDSNEREN, THPGGGGGGGGGGGGGGGGGGR, KDFPSMK, KEMFEAK, ECITKECITRECITK, GETLVNGSSGEEGGGK, DLQLDSR, KHWNNNIKEWMELTLAK, LSPCFRTAFKIVPADDYAK, TVDVVFPEPYKTVPKVHLSIVHLDTDK, MVVTSAKGFNGDTRMVVTSAK, SLSQVSRSAR, LGPRQIR, PGQSCPSFVSWMPLK, TSTSKKTDAGEYLETQVAAK, NAELDPGVQSELIKEAEVMK, IKGFSETVDLKTTTADEMVK, GGEGGYLENSLNTIPSYR, VLSDSLSEDLRAK, EAFYQLTGAR, FSEISEAYEVLGNTK, WEIITSQESKNK.

Table S1. Unique detected peptides and their protein accessions from each sample and extraction. NCBI match descriptions are based on BLASTp results or presence only in *Strombus* database. Mixed represents a variety of species beyond Gastropoda or Mollusca.

Accession	Sample Type	Age	Base Sequence	Protein Accession	Protein Name	Database	NCBI Result
CMM-I-6359	Hydroxylamine	8	EGTNKPEK	elysia_rna-gnl-WGS:RQTK-Echl_13966_R0	NA	Strombus	Mixed
CMM-I-6359	Hydroxylamine	8	KAEAGAEEKK	pomacea_rna-gnl-WGS:PZQS-C0Q70_mrna06558_R0	NA	Strombus	Mixed
CMM-I-6360	Hydroxylamine	8	QNLVPNLPPLTIKSDVTEKVQSHK	pomacea_rna-gnl-WGS:PZQS-C0Q70_mrna15801_R6	NA	Strombus	Gastropoda
CMM-I-6359	Hydroxylamine	8	EIYQAIEQLKNCK	pomacea_rna-gnl-WGS:PZQS-C0Q70_mrna03174_R9	NA	Strombus	Gastropoda
CMM-I-6360	Hydroxylamine	8	NASNFNSAVFKAAK	pomacea_rna-gnl-WGS:PZQS-C0Q70_mrna01606_R6	NA	Strombus	Gastropoda
CMM-I-6357	Hydroxylamine	10	NASNFNSAVFKAAK	pomacea_rna-gnl-WGS:PZQS-C0Q70_mrna01606_R6	NA	Strombus	Gastropoda
CMM-I-6360	Hydroxylamine	8	TLSFRHNPLR	pomacea_rna-gnl-WGS:PZQS-C0Q70_mrna05328_R5	NA	Strombus	Mixed
CMM-I-6360	Hydroxylamine	8	EGTNKPEK	elysia_rna-gnl-WGS:RQTK-Echl_13966_R0	NA	Strombus	Mixed
CMM-I-6357	Hydroxylamine	10	EGTNKPEK	elysia_rna-gnl-WGS:RQTK-Echl_13966_R0	NA	Strombus	Mixed
CMM-I-6359	Hydroxylamine	8	RSAPTQPGQNLR	lottia_rna-XM_009067641.1_R0	NA	Strombus	Gastropoda
CMM-I-6359	Hydroxylamine	8	ALADYGSQVDVDK	lottia_rna-XM_009047100.1_R0	NA	Strombus	Gastropoda
CMM-I-6359	Hydroxylamine	8	KLPTNTYELR	pomacea_rna-gnl-WGS:PZQS-C0Q70_mrna01933_R0	NA	Strombus	Mixed
CMM-I-6358	Hydroxylamine	10	QQALANINAPVPDK	lottia_rna-XM_009067640.1_R0	NA	Strombus	Gastropoda
CMM-I-6357	Hydroxylamine	10	VYHELVEIQHR	pomacea_rna-gnl-WGS:PZQS-C0Q70_mrna18766_R1	NA	Strombus	Gastropoda
CMM-I-6360	Hydroxylamine	8	KASEATIRVWCFFGR	lottia_rna-XM_009048959.1_R1	NA	Strombus	Gastropoda
CMM-I-6360	Hydroxylamine	8	GKVAYQNGSASLHK	pomacea_rna-gnl-WGS:PZQS-C0Q70_mrna14120_R1	NA	Strombus	Gastropoda
CMM-I-6360	Hydroxylamine	8	TKNVEQYK	lottia_rna-XM_009054684.1_R0	NA	Strombus	Mixed
CMM-I-6359	Hydroxylamine	8	TLRSSSDCRILR	lottia_rna-XM_009054189.1_R5	NA	Strombus	Mixed
CMM-I-6360	Hydroxylamine	8	MICFGHTK	pomacea_rna-gnl-WGS:PZQS-C0Q70_mrna15946_R0	NA	Strombus	Mixed
CMM-I-6359	Hydroxylamine	8	TPCGLQTPEHVSSFMEAMKDFQLTK	pomacea_rna-gnl-WGS:PZQS-C0Q70_mrna16344_R0	NA	Strombus	Gastropoda
CMM-I-6357	Hydroxylamine	10	AAASPMRAKTASDK	canidula_rna-CUNI_LOCUS6705_R1	NA	Strombus	Gastropoda
CMM-I-6359	Hydroxylamine	8	EDAVKQYK	pomacea_rna-gnl-WGS:PZQS-C0Q70_mrna16880_R0	NA	Strombus	Mixed
CMM-I-6359	Hydroxylamine	8	KGTFQSPGFPDK	pomacea_rna-gnl-WGS:PZQS-C0Q70_mrna10487_R0|pomacea_rna-gnl-WGS:PZQS-C0Q70_mrna10487_R1	NA	Strombus	Mollusca
CMM-I-6357	Hydroxylamine	10	QQALANINAPVPDK	lottia_rna-XM_009067640.1_R0	NA	Strombus	Gastropoda
CMM-I-6359	Hydroxylamine	8	SNALMSITR	elysia_rna-gnl-WGS:RQTK-Echl_15544_R3	NA	Strombus	Gastropoda

CMM-I-6357	Hydroxylamine	10	PNATASAVSAR	pomacea_rna-gnl-WGS:PZQS-C0Q70_mrna02610_R0	NA	Strombus	Mixed
CMM-I-6359	Hydroxylamine	8	AAASPMRAKTASDK	canidula_rna-CUNI_LOCUS6705_R1	NA	Strombus	Gastropoda
CMM-I-6359	Hydroxylamine	8	GAAQNIIPASTGAAK	A0A2C9KRC2	Gp_dh_N domain-containing protein	Gastropoda	Mixed
CMM-I-6357	Hydroxylamine	10	GASAQNFLDTLK	A0A2C9LTC8	Coiled-coil domain-containing protein 62	Gastropoda	Gastropoda
CMM-I-6357	Hydroxylamine	10	IVCGNRFTNNAAK	V4ABZ9	Deleted in malignant brain tumors 1 protein-like	Gastropoda	Gastropoda
CMM-I-6360	Hydroxylamine	8	GAAQNIIPASTGAAK	A0A2C9KRC2	Gp_dh_N domain-containing protein	Gastropoda	Mixed
CMM-I-6359	Hydroxylamine	8	ATMQEVNDR	A0A2T7NYB1	Nesprin-1	Gastropoda	Gastropoda
CMM-I-6360	Hydroxylamine	8	ATMQEVNDR	A0A2T7NYB1	Nesprin-1	Gastropoda	Gastropoda
CMM-I-6359	Hydroxylamine	8	KNNDIELSK	A0A0B7BSL6|A0A0B7BUC3	DDE_3 domain-containing protein (Fragment)	Gastropoda	Mixed
CMM-I-6359	Hydroxylamine	8	ELDEIRLQQAK	A0A2T7NFW9	Ephrin_rec_like domain-containing protein	Gastropoda	Gastropoda
CMM-I-6359	Hydroxylamine	8	TANEDFKK	A0A2C9K8F3	Kinesin motor domain-containing protein	Gastropoda	Mixed
CMM-I-6359	Hydroxylamine	8	QTINLYEMLQTK	A0A2C9LXF9	Apple domain-containing protein	Gastropoda	Gastropoda
CMM-I-6357	Hydroxylamine	10	VTQEKGTER	V4AP49	Peptide-methionine (R)-S-oxide reductase	Gastropoda	Mixed
CMM-I-6357	Hydroxylamine	10	NLSHLVNNVMETK	A0A433TWG4	Dynein heavy chain 5, axonemal (Fragment)	Gastropoda	Gastropoda
CMM-I-6360	Hydroxylamine	8	ASGGVSFYNILQWGSEDAMSK	A0A433U8D9	Carboxypeptidase	Gastropoda	Gastropoda
CMM-I-6360	Hydroxylamine	8	AVSNFGQADPEYGRR	A0A1R7T094	Catalase	Gastropoda	Gastropoda
CMM-I-6357	Hydroxylamine	10	VSDFVQQINANNK	V4AWL2	Microtubule-associated protein futsch	Gastropoda	Gastropoda
CMM-I-6358	Hydroxylamine	10	GASAQNFLDTLK	A0A2C9LTC8	Coiled-coil domain-containing protein 62	Gastropoda	Gastropoda
CMM-I-6360	Hydroxylamine	8	TVSVSALR	A0A2C9KFM6	Serine/threonine-protein kinase 11-interacting protein	Gastropoda	Mixed
CMM-I-6359	Hydroxylamine	8	SAYEVRVK	A0A2T7PMJ5|A0A2T7PMJ9	CD109 molecule|A2M_N_2 domain-containing protein	Gastropoda	Mixed
CMM-I-6359	Hydroxylamine	8	LTVSPSKLLN	A0A2C9KSI9	C-type lectin domain-containing protein	Gastropoda	Gastropoda
CMM-I-6357	Hydroxylamine	10	VTSPSEWIK	A0A8S3Z172	Hypothetical protein	Gastropoda	Gastropoda

CMM-I-6359	Hydroxylamine	8	GTEVGCDHEK	A0A2T7NXN1	SRCR domain-containing protein	Gastropoda	Gastropoda
CMM-I-6360	Hydroxylamine	8	KADENVPASGSK	V4ADN6	TINF2_N domain-containing protein	Gastropoda	Gastropoda
CMM-I-6360	Hydroxylamine	8	LSLSGDSGSFR	A0A2C9JF75|A0A2C9JF79|A0A2C9JF87	Ubiquitin-like domain-containing protein|RNA-binding motif protein, X chromosome	Gastropoda	Gastropoda
CMM-I-6360	Hydroxylamine	8	KLKSNDK	A0A3S1B8F9	Tropomodulin	Gastropoda	Mixed
CMM-I-6359	Hydroxylamine	8	GTPSLSSTCTLKK	A0A8S4A6G9	Hypothetical protein (Fragment)	Gastropoda	Gastropoda
CMM-I-6360	Hydroxylamine	8	KELMMKLTEMAK	A0A433TAQ0	Ion_trans domain-containing protein	Gastropoda	Gastropoda
CMM-I-6357	Hydroxylamine	10	AREMAKIEEQQK	A0A2C9M4A7	Limbin	Gastropoda	Mollusca
CMM-I-6360	Hydroxylamine	8	KLFGKETSSNTNTSQGLFQAK	A0A433SZ38	RRM domain-containing protein (Fragment)	Gastropoda	Gastropoda
CMM-I-6359	Hydroxylamine	8	GQNIFAPSREETK	A0A2T7P9J8	TIR domain-containing protein	Gastropoda	Gastropoda
CMM-I-6359	Hydroxylamine	8	QVFAVRSGGAMGVVMKGPEEK	A0A433U182	Mic1 domain-containing protein	Gastropoda	Gastropoda
CMM-I-6359	Hydroxylamine	8	AVSNFGQADPEYGRR	A0A1R7T094	Catalase	Gastropoda	Gastropoda
CMM-I-6357	Hydroxylamine	10	KSRSPSPER	A0A2C9LTG9	Sine oculis-binding protein homolog	Gastropoda	Mixed
CMM-I-6359	Hydroxylamine	8	SSFDSAGFLEEVK	A0A2T7P0R4	Copper-fist domain-containing protein	Gastropoda	Gastropoda
CMM-I-6357	Hydroxylamine	10	IVFTNVMGIEGHK	A0A3S1B970	PDZ domain-containing protein	Gastropoda	Gastropoda
CMM-I-6360	Hydroxylamine	8	SNTELDGAK	A0A3S0ZQ02	Rho guanine nucleotide exchange factor 17	Gastropoda	Mixed
CMM-I-6360	Hydroxylamine	8	ELDEIRLQQAK	A0A2T7NFW9	Ephrin_rec_like domain-containing protein	Gastropoda	Gastropoda
CMM-I-6359	Hydroxylamine	8	DLQNKTEAVER	A0A2T7PE22	Coiled-coil domain-containing protein 157	Gastropoda	Gastropoda
CMM-I-6359	Hydroxylamine	8	IVCGNRFTNNAAK	V4ABZ9	Deleted in malignant brain tumors 1 protein-like	Gastropoda	Gastropoda
CMM-I-6360	Hydroxylamine	8	IVCGNRFTNNAAK	V4ABZ9	Deleted in malignant brain tumors 1 protein-like	Gastropoda	Gastropoda
CMM-I-6359	Hydroxylamine	8	SALYRSREAVSQNK	A0A2T7PX67	UPF0764 protein C16orf89 homolog	Gastropoda	Gastropoda
CMM-I-6358	Hydroxylamine	10	TGYSWKIVCGNRFTNNAAK	V4ABZ9	Deleted in malignant brain tumors 1 protein-like	Gastropoda	Gastropoda

CMM-I-6359	Hydroxylamine	8	TFLDKVR	A0A8S3YDX0|A0A8S3ZLT8|A0A8S3ZSR5	Hypothetical protein	Gastropoda	Mixed
CMM-I-6357	Hydroxylamine	10	ENQSAESNTLKK	WGS:RQTK_2998|WGS:RQTK_4078|WGS:RQTK_4840	NA	Conus betulinus	Gastropoda
CMM-I-6359	Hydroxylamine	8	LVTIEEELR	WGS:PZQS_2213	NA	Conus betulinus	Mixed
CMM-I-6357	Hydroxylamine	10	KIMGQLSFNAPGSK	WGS:RQTK_3897	NA	Conus betulinus	Gastropoda
CMM-I-6357	Hydroxylamine	10	GTGGSDNNNSVTLTDDQTFLLK	Candidula_rna-CUNI_LOCUS15157_R1 gene=gene_22751 chr=JADBJO010000831.1 strand=-1 interval=650..5041 ref-gene=Candidula_gene-CUNI_LOCUS15157 aa=341 raa=389 score=735 prediction=1 bestScore=1067 ce=7 rce=5 pAA=0.5837 iAA=0.4593 lpm=25 maxScore=1990 maxGap=32 nps=0 start=M stop=* evidence=1 sumWeight=1.0	NA	Conus betulinus	Gastropoda
CMM-I-6359	Hydroxylamine	8	ALGAGAPKQSK	Candidula_rna-CUNI_LOCUS19021_R0 gene=gene_5119 chr=JADBJO010000239.1 strand=1 interval=3881..29794 ref-gene=Candidula_gene-CUNI_LOCUS19021 aa=696 raa=763 score=1033 prediction=0 bestScore=1033 ce=17 rce=18 pAA=0.6015 iAA=0.3729 lpm=24 maxScore=3991 maxGap=20 nps=0 start=M stop=* evidence=1 sumWeight=1.0|Candidula_rna-CUNI_LOCUS19021_R2 gene=gene_32504 chr=JADBJO010016926.1 strand=-1 interval=158..26991 ref-gene=Candidula_gene-CUNI_LOCUS19021 aa=590 raa=763 score=855 prediction=2 bestScore=1033 ce=18 rce=18 pAA=0.5355 iAA=0.3471 lpm=24 maxScore=3991 maxGap=52 nps=0 start=M stop=* evidence=1 sumWeight=1.0|WGS:AMQO_5907|Candidula_rna-CUNI_LOCUS19021_R0 gene=gene_5119 chr=JADBJO010000239.1 strand=1 interval=3881..29794 ref-gene=Candidula_gene-CUNI_LOCUS19021 aa=696 raa=763 score=1033 prediction=0 bestScore=1033 ce=17 rce=18 pAA=0.6015 iAA=0.3729 lpm=24 maxScore=3991 maxGap=20 nps=0 start=M stop=* evidence=1 sumWeight=1.0|Candidula_rna-CUNI_LOCUS19021_R2 gene=gene_32504 chr=JADBJO010016926.1 strand=-1 interval=158..26991 ref-	NA	Conus betulinus	Gastropoda

				gene=Candidula_gene-CUNI_LOCUS19021 aa=590 raa=763 score=855 prediction=2 bestScore=1033 ce=18 rce=18 pAA=0.5355 iAA=0.3471 lpm=24 maxScore=3991 maxGap=52 nps=0 start=M stop=* evidence=1 sumWeight=1.0|WGS:AMQO_5907			
CMM-I-6357	Hydroxylamine	10	VGMHASANCRVR	Candidula_rna-CUNI_LOCUS17455_R0 gene=gene_31283 chr=JADBJO010000403.1 strand=-1 interval=164873..176921 ref-gene=Candidula_gene-CUNI_LOCUS17455 aa=310 raa=334 score=779 prediction=0 bestScore=779 ce=10 rce=10 pAA=0.6628 iAA=0.5349 lpm=34 maxScore=1694 maxGap=16 nps=0 start=M stop=* evidence=1 sumWeight=1.0	NA	Conus betulinus	Gastropoda
CMM-I-6359	Hydroxylamine	8	GGAERMMATLKK	WGS:RQTK_4326	NA	Conus betulinus	Gastropoda
CMM-I-6357	Hydroxylamine	10	VTQQQTVSR	WGS:RQTK_1409|WGS:RQTK_2791|WGS:RQTK_5103|WGS:RQTK_5815	NA	Conus betulinus	Mixed
CMM-I-6359	Hydroxylamine	8	QVEQNLR	WGS:PZQS_7282	NA	Conus betulinus	Mixed
CMM-I-6360	Hydroxylamine	8	GKQEEGLGQQK	WGS:PZQS_5954	NA	Conus betulinus	Gastropoda
CMM-I-6357	Hydroxylamine	10	SPSSATGKER	WGS:RQTK_4240	NA	Conus betulinus	Gastropoda
CMM-I-6359	Hydroxylamine	8	EKALSQALLEMMFAMELTVK	WGS:PZQS_5025	NA	Conus betulinus	Gastropoda
CMM-I-6359	Hydroxylamine	8	TFVIQVR	WGS:PZQS_3512	NA	Conus betulinus	Mixed
CMM-I-6359	Hydroxylamine	8	TVLDGNLGAGTRR	WGS:AMQO_792	NA	Conus betulinus	Gastropoda
CMM-I-6359	Hydroxylamine	8	NAFRPLGSSSGKNK	Candidula_rna-CUNI_LOCUS10700_R1 gene=gene_19679 chr=JADBJO010001434.1 strand=1 interval=213940..236256 ref-gene=Candidula_gene-CUNI_LOCUS10700 aa=255 raa=268 score=426 prediction=1 bestScore=626 ce=5 rce=5 pAA=0.5113 iAA=0.3537 lpm=14 maxScore=1460 maxGap=40 nps=0 start=M stop=* evidence=1 sumWeight=1.0	NA	Conus betulinus	Gastropoda
CMM-I-6359	Hydroxylamine	8	QGLLNTPRGSGGGQYGGR	WGS:PZQS_10520	NA	Conus betulinus	Gastropoda
CMM-I-6359	Hydroxylamine	8	PEKQTPK	WGS:PZQS_7546	NA	Conus betulinus	Mixed
CMM-I-6360	Hydroxylamine	8	SLLTPTGGGGGGGGGGGK	WGS:RQTK_4740	NA	Conus betulinus	Gastropoda
CMM-I-6360	Hydroxylamine	8	VTQQQTVSR	WGS:RQTK_1409|WGS:RQTK_2791|WGS:RQTK_5103|WGS:RQTK_5815	NA	Conus betulinus	Mixed
CMM-I-6359	Hydroxylamine	8	SHDLNNKFIDK	WGS:PZQS_2022	NA	Conus betulinus	Gastropoda
CMM-I-6357	Hydroxylamine	10	SLLTPTGGGGGGGGGGGK	WGS:RQTK_4740	NA	Conus betulinus	Gastropoda

CMM-I-6359	Hydroxylamine	8	AGIALSSGQTWK	Candidula_rna-CUNI_LOCUS889_R5 gene=gene_14137 chr=JADBJO010000294.1 strand=1 interval=714006..720699 ref-gene=Candidula_gene-CUNI_LOCUS889 aa=514 raa=493 score=628 prediction=5 bestScore=761 ce=7 rce=3 pAA=0.5767 iAA=0.3457 lpm=12 maxScore=2559 maxGap=22 nps=0 start=M stop=* evidence=1 sumWeight=1.0 alternative="Candidula_gene-CUNI_LOCUS891"	NA	Conus betulinus	Gastropoda
CMM-I-6360	Hydroxylamine	8	STDPRTAGNHLWNTAGR	WGS:PZQS_5098	NA	Conus betulinus	Gastropoda
CMM-I-6357	Hydroxylamine	10	SLSFKSHSR	WGS:PZQS_12031	NA	Conus betulinus	Gastropoda
CMM-I-6359	Hydroxylamine	8	PAGSVDGSSLRQGK	WGS:PZQS_10017	NA	Conus betulinus	Gastropoda
CMM-I-6359	Hydroxylamine	8	KEPFTGILAK	WGS:PZQS_10520	NA	Conus betulinus	Gastropoda
CMM-I-6357	Hydroxylamine	10	NVDREAITMLDAK	WGS:PZQS_11854	NA	Conus betulinus	Gastropoda
CMM-I-6359	Hydroxylamine	8	SLSFKSHSR	WGS:PZQS_12031	NA	Conus betulinus	Gastropoda
CMM-I-6357	Hydroxylamine	10	QITPFTSAGANNNK	WGS:PZQS_394	NA	Conus betulinus	Gastropoda
CMM-I-6359	Hydroxylamine	8	QLRSSADSR	WGS:PZQS_11545|WGS:PZQS_13281|WGS:PZQS_13385|WGS:PZQS_35|WGS:PZQS_3873|WGS:PZQS_6017	NA	Conus betulinus	Mixed
CMM-I-6360	Hydroxylamine	8	QLRSSADSR	WGS:PZQS_11545|WGS:PZQS_13281|WGS:PZQS_13385|WGS:PZQS_35|WGS:PZQS_3873|WGS:PZQS_6017	NA	Conus betulinus	Mixed
CMM-I-6359	Hydroxylamine	8	NIQLQRQIMEEEFDEKK	WGS:PZQS_9032	NA	Conus betulinus	Gastropoda
CMM-I-6357	Hydroxylamine	10	KASPSAHSDPPPPAK	WGS:AMQO_2079	NA	Conus betulinus	Gastropoda
CMM-I-6359	Hydroxylamine	8	DNIQQGITKPAIR	Candidula_rna-CUNI_LOCUS16438_R0 gene=gene_29198 chr=JADBJO010034609.1 strand=1 interval=9334..9645 ref-gene=Candidula_gene-CUNI_LOCUS16438 aa=104 raa=104 score=524 prediction=0 bestScore=524 ce=1 rce=1 pAA=1 iAA=1 lpm=104 maxScore=524 maxGap=0 nps=0 start=M stop=* evidence=3 sumWeight=3.0 alternative="Candidula_gene-CUNI_LOCUS2762,Candidula_gene-CUNI_LOCUS2766,Lottia_gene-LOTGIDRAFT_145439,Lottia_gene-LOTGIDRAFT_146028,Lottia_gene-LOTGIDRAFT_146029,Lottia_gene-LOTGIDRAFT_146923,Lottia_gene-LOTGIDRAFT_147261,Lottia_gene-LOTGIDRAFT_147329,Lottia_gene-	NA	Conus betulinus	Mixed

				LOTGIDRAFT_147488,Lottia_gene-LOTGIDRAFT_147781,Lottia_gene-LOTGIDRAFT_148042,Lottia_gene-LOTGIDRAFT_148108,Lottia_gene-LOTGIDRAFT_148116,Lottia_gene-LOTGIDRAFT_148724,Lottia_gene-LOTGIDRAFT_148824,Lottia_gene-LOTGIDRAFT_148840,Lottia_gene-LOTGIDRAFT_176226,Lottia_gene-LOTGIDRAFT_176527,Lottia_gene-LOTGIDRAFT_177025,Lottia_gene-LOTGIDRAFT_202861,Pomacea_gene-C0Q70_13947"|Candidula_rna-CUNI_LOCUS16438_R1 gene=gene_7861 chr=JADBJO010035468.1 strand=-1 interval=2150..2461 ref-gene=Candidula_gene-CUNI_LOCUS16438 aa=104 raa=104 score=524 prediction=1 bestScore=524 ce=1 rce=1 pAA=1 iAA=1 lpm=104 maxScore=524 maxGap=0 nps=0 start=M stop=* evidence=3 sumWeight=3.0 alternative="Candidula_gene-CUNI_LOCUS2762,Candidula_gene-CUNI_LOCUS2766,Lottia_gene-LOTGIDRAFT_145439,Lottia_gene-LOTGIDRAFT_146028,Lottia_gene-LOTGIDRAFT_146029,Lottia_gene-LOTGIDRAFT_146923,Lottia_gene-LOTGIDRAFT_147261,Lottia_gene-LOTGIDRAFT_147329,Lottia_gene-LOTGIDRAFT_147488,Lottia_gene-LOTGIDRAFT_147781,Lottia_gene-LOTGIDRAFT_148042,Lottia_gene-LOTGIDRAFT_148108,Lottia_gene-LOTGIDRAFT_148116,Lottia_gene-LOTGIDRAFT_148724,Lottia_gene-LOTGIDRAFT_148824,Lottia_gene-LOTGIDRAFT_148840,Lottia_gene-LOTGIDRAFT_176226,Lottia_gene-LOTGIDRAFT_176527,Lottia_gene-LOTGIDRAFT_177025,Lottia_gene-LOTGIDRAFT_202861,Pomacea_gene-C0Q70_13947"|Candidula_rna-CUNI_LOCUS16438_R2 gene=gene_1043 chr=JADBJO010031623.1 strand=1 interval=16154..16465 ref-gene=Candidula_gene-CUNI_LOCUS16438 aa=104 raa=104 score=524 prediction=2 bestScore=524 ce=1 rce=1 pAA=1 iAA=1 lpm=104 maxScore=524 maxGap=0 nps=0 start=M stop=* evidence=3			

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				LOTGIDRAFT_202861,Pomacea_gene-C0Q70_13947"|Candidula_rna-CUNI_LOCUS16438_R4 gene=gene_15913 chr=JADBJO010028021.1 strand=-1 interval=17565..17876 ref-gene=Candidula_gene-CUNI_LOCUS16438 aa=104 raa=104 score=524 prediction=4 bestScore=524 ce=1 rce=1 pAA=1 iAA=1 lpm=104 maxScore=524 maxGap=0 nps=0 start=M stop=* evidence=3 sumWeight=3.0 alternative="Candidula_gene-CUNI_LOCUS2762,Candidula_gene-CUNI_LOCUS2766,Lottia_gene-LOTGIDRAFT_145439,Lottia_gene-LOTGIDRAFT_146028,Lottia_gene-LOTGIDRAFT_146029,Lottia_gene-LOTGIDRAFT_146923,Lottia_gene-LOTGIDRAFT_147261,Lottia_gene-LOTGIDRAFT_147329,Lottia_gene-LOTGIDRAFT_147488,Lottia_gene-LOTGIDRAFT_147781,Lottia_gene-LOTGIDRAFT_148042,Lottia_gene-LOTGIDRAFT_148108,Lottia_gene-LOTGIDRAFT_148116,Lottia_gene-LOTGIDRAFT_148724,Lottia_gene-LOTGIDRAFT_148824,Lottia_gene-LOTGIDRAFT_148840,Lottia_gene-LOTGIDRAFT_176226,Lottia_gene-LOTGIDRAFT_176527,Lottia_gene-LOTGIDRAFT_177025,Lottia_gene-LOTGIDRAFT_202861,Pomacea_gene-C0Q70_13947"|Candidula_rna-CUNI_LOCUS16438_R5 gene=gene_23204 chr=JADBJO010034868.1 strand=1 interval=8954..9265 ref-gene=Candidula_gene-CUNI_LOCUS16438 aa=104 raa=104 score=524 prediction=5 bestScore=524 ce=1 rce=1 pAA=1 iAA=1 lpm=104 maxScore=524 maxGap=0 nps=0 start=M stop=* evidence=3 sumWeight=3.0 alternative="Candidula_gene-CUNI_LOCUS2762,Candidula_gene-CUNI_LOCUS2766,Lottia_gene-LOTGIDRAFT_145439,Lottia_gene-LOTGIDRAFT_146028,Lottia_gene-LOTGIDRAFT_146029,Lottia_gene-LOTGIDRAFT_146923,Lottia_gene-LOTGIDRAFT_147261,Lottia_gene-LOTGIDRAFT_147329,Lottia_gene-LOTGIDRAFT_147488,Lottia_gene-			

				LOTGIDRAFT_147781,Lottia_gene-LOTGIDRAFT_148042,Lottia_gene-LOTGIDRAFT_148108,Lottia_gene-LOTGIDRAFT_148116,Lottia_gene-LOTGIDRAFT_148724,Lottia_gene-LOTGIDRAFT_148824,Lottia_gene-LOTGIDRAFT_148840,Lottia_gene-LOTGIDRAFT_176226,Lottia_gene-LOTGIDRAFT_176527,Lottia_gene-LOTGIDRAFT_177025,Lottia_gene-LOTGIDRAFT_202861,Pomacea_gene-C0Q70_13947"|Candidula_rna-CUNI_LOCUS16438_R6 gene=gene_7780 chr=JADBJO010027693.1 strand=-1 interval=13635..13946 ref-gene=Candidula_gene-CUNI_LOCUS16438 aa=104 raa=104 score=524 prediction=6 bestScore=524 ce=1 rce=1 pAA=1 iAA=1 lpm=104 maxScore=524 maxGap=0 nps=0 start=M stop=* evidence=3 sumWeight=3.0 alternative="Candidula_gene-CUNI_LOCUS2762,Candidula_gene-CUNI_LOCUS2766,Lottia_gene-LOTGIDRAFT_145439,Lottia_gene-LOTGIDRAFT_146028,Lottia_gene-LOTGIDRAFT_146029,Lottia_gene-LOTGIDRAFT_146923,Lottia_gene-LOTGIDRAFT_147261,Lottia_gene-LOTGIDRAFT_147329,Lottia_gene-LOTGIDRAFT_147488,Lottia_gene-LOTGIDRAFT_147781,Lottia_gene-LOTGIDRAFT_148042,Lottia_gene-LOTGIDRAFT_148108,Lottia_gene-LOTGIDRAFT_148116,Lottia_gene-LOTGIDRAFT_148724,Lottia_gene-LOTGIDRAFT_148824,Lottia_gene-LOTGIDRAFT_148840,Lottia_gene-LOTGIDRAFT_176226,Lottia_gene-LOTGIDRAFT_176527,Lottia_gene-LOTGIDRAFT_177025,Lottia_gene-LOTGIDRAFT_202861,Pomacea_gene-C0Q70_13947"|Candidula_rna-CUNI_LOCUS16438_R7 gene=gene_6173 chr=JADBJO010006100.1 strand=1 interval=134951..135262 ref-gene=Candidula_gene-CUNI_LOCUS16438 aa=104 raa=104 score=524 prediction=7 bestScore=524 ce=1 rce=1 pAA=1 iAA=1 lpm=104 maxScore=524 maxGap=0 nps=0 start=M stop=* evidence=3 sumWeight=3.0			

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<table>
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<tr><td>CMM-I-6359</td><td>Hydroxylamine</td><td>8</td><td>GPVYFKIDGGSSPR</td><td>Candidula_rna-CUNI_LOCUS15984_R0 gene=gene_30307 chr=JADBJO010000413.1 strand=1 interval=74446..133271 ref-gene=Candidula_gene-CUNI_LOCUS15984 aa=930 raa=1736 score=1188 prediction=0 bestScore=1188 ce=18 rce=15 pAA=0.3673 iAA=0.2721 lpm=20 maxScore=9201 maxGap=347 nps=0 start=M stop=* evidence=1 sumWeight=1.0</td><td>NA</td><td>Conus betulinus</td><td>Gastropoda</td></tr>
<tr><td>CMM-I-6359</td><td>Hydroxylamine</td><td>8</td><td>VGMHASANCRVR</td><td>Candidula_rna-CUNI_LOCUS17455_R0 gene=gene_31283 chr=JADBJO010000403.1 strand=-1 interval=164873..176921 ref-gene=Candidula_gene-CUNI_LOCUS17455 aa=310 raa=334 score=779 prediction=0 bestScore=779 ce=10 rce=10 pAA=0.6628 iAA=0.5349 lpm=34 maxScore=1694 maxGap=16 nps=0 start=M stop=*</td><td>NA</td><td>Conus betulinus</td><td>Gastropoda</td></tr>
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CMM-I-6359	Hydroxylamine	8	NVDREAITMLDAK	WGS:PZQS_11854	NA	Conus betulinus	Gastropoda
CMM-I-6359	Hydroxylamine	8	TAFTSEQLLELEKEFHSK	WGS:AMQO_2050	NA	Conus betulinus	Mixed
CMM-I-6357	Hydroxylamine	10	GTKHQASQSQVAAK	WGS:PZQS_6033	NA	Conus betulinus	Gastropoda
CMM-I-6360	Hydroxylamine	8	ALGAGAPKQSK	Candidula_rna-CUNI_LOCUS19021_R0 gene=gene_5119 chr=JADBJO010000239.1 strand=1 interval=3881..29794 ref-gene=Candidula_gene-CUNI_LOCUS19021 aa=696 raa=763 score=1033 prediction=0 bestScore=1033 ce=17 rce=18 pAA=0.6015 iAA=0.3729 lpm=24 maxScore=3991 maxGap=20 nps=0 start=M stop=* evidence=1 sumWeight=1.0|Candidula_rna-CUNI_LOCUS19021_R2 gene=gene_32504 chr=JADBJO010016926.1 strand=-1 interval=158..26991 ref-gene=Candidula_gene-CUNI_LOCUS19021 aa=590 raa=763 score=855 prediction=2 bestScore=1033 ce=18 rce=18 pAA=0.5355 iAA=0.3471 lpm=24 maxScore=3991 maxGap=52 nps=0 start=M stop=* evidence=1 sumWeight=1.0|WGS:AMQO_5907|Candidula_rna-CUNI_LOCUS19021_R0 gene=gene_5119 chr=JADBJO010000239.1 strand=1 interval=3881..29794 ref-gene=Candidula_gene-CUNI_LOCUS19021 aa=696 raa=763 score=1033 prediction=0 bestScore=1033 ce=17 rce=18 pAA=0.6015 iAA=0.3729 lpm=24 maxScore=3991 maxGap=20 nps=0 start=M stop=* evidence=1 sumWeight=1.0|Candidula_rna-CUNI_LOCUS19021_R2 gene=gene_32504 chr=JADBJO010016926.1 strand=-1 interval=158..26991 ref-gene=Candidula_gene-CUNI_LOCUS19021 aa=590 raa=763 score=855 prediction=2 bestScore=1033 ce=18 rce=18 pAA=0.5355 iAA=0.3471 lpm=24 maxScore=3991 maxGap=52 nps=0 start=M stop=* evidence=1 sumWeight=1.0|WGS:AMQO_5907	NA	Conus betulinus	Gastropoda
CMM-I-6359	Hydroxylamine	8	TDITGAKISWLK	WGS:AMQO_4183|WGS:AMQO_4553	NA	Conus betulinus	Gastropoda

CMM-I-6360	Hydroxylamine	8	TAQNRSSPSSTITSFQR	WGS:PZQS_13865	NA	Conus betulinus	Gastropoda
CMM-I-6360	Hydroxylamine	8	DLLFLPLCFLVGCPANVINMAVFYK	WGS:PZQS_12885	NA	Conus betulinus	Gastropoda
CMM-I-6360	Hydroxylamine	8	SPSKSPSR	WGS:PZQS_544	NA	Conus betulinus	Mixed
CMM-I-6359	Hydroxylamine	8	SPSKSPSR	WGS:PZQS_544	NA	Conus betulinus	Mixed
CMM-I-6360	Hydroxylamine	8	VGMHASANCRVR	Candidula_rna-CUNI_LOCUS17455_R0 gene=gene_31283 chr=JADBJO010000403.1 strand=-1 interval=164873..176921 ref-gene=Candidula_gene-CUNI_LOCUS17455 aa=310 raa=334 score=779 prediction=0 bestScore=779 ce=10 rce=10 pAA=0.6628 iAA=0.5349 lpm=34 maxScore=1694 maxGap=16 nps=0 start=M stop=* evidence=1 sumWeight=1.0	NA	Conus betulinus	Gastropoda
CMM-I-6360	Hydroxylamine	8	GKQEEGLGQQKR	WGS:PZQS_5954	NA	Conus betulinus	Gastropoda
CMM-I-6359	Hydroxylamine	8	PVEAPPSVR	WGS:PZQS_5575	NA	Conus betulinus	Mixed
CMM-I-6359	Hydroxylamine	8	VGEAAGFR	WGS:PZQS_750	NA	Conus betulinus	Mixed
CMM-I-6359	Hydroxylamine	8	RMMITSSSR	WGS:AMQO_410	NA	Conus betulinus	Gastropoda
CMM-I-6360	Hydroxylamine	8	VGEAAGFR	WGS:PZQS_750	NA	Conus betulinus	Mixed
CMM-I-6359	Hydroxylamine	8	AICMRLDGLEGK	WGS:PZQS_3029	NA	Conus betulinus	Gastropoda
CMM-I-6357	Hydroxylamine	10	VGEAAGFR	WGS:PZQS_750	NA	Conus betulinus	Mixed
CMM-I-6359	Hydroxylamine	8	INDLKKSNQDAK	WGS:PZQS_10472	NA	Conus betulinus	Gastropoda
CMM-I-6359	Hydroxylamine	8	NDGSVKGIR	WGS:PZQS_8143	NA	Conus betulinus	Mixed
CMM-I-6359	Hydroxylamine	8	AKQEQTK	Candidula_rna-CUNI_LOCUS10160_R7 gene=gene_31647 chr=JADBJO010000089.1 strand=-1 interval=1036047..1037338 ref-gene=Candidula_gene-CUNI_LOCUS10160 aa=86 raa=70 score=104 prediction=7 bestScore=130 ce=2 rce=2 pAA=0.5341 iAA=0.3523 lpm=6 maxScore=369 maxGap=18 nps=0 start=M stop=* evidence=1 sumWeight=1.0	NA	Conus betulinus	Mixed
CMM-I-6360	Hydroxylamine	8	AKQEQTK	Candidula_rna-CUNI_LOCUS10160_R7 gene=gene_31647 chr=JADBJO010000089.1 strand=-1 interval=1036047..1037338 ref-gene=Candidula_gene-CUNI_LOCUS10160 aa=86 raa=70 score=104 prediction=7 bestScore=130 ce=2 rce=2 pAA=0.5341 iAA=0.3523 lpm=6 maxScore=369 maxGap=18 nps=0 start=M stop=* evidence=1 sumWeight=1.0	NA	Conus betulinus	Mixed

CMM-I-6359	Hydroxylamine	8	FITDNTVEERIVERAEMK	WGS:AMQO_4830|WGS:PZQS_9527	NA	Conus betulinus	Mixed
CMM-I-6360	Hydroxylamine	8	LVTIEEELR	WGS:PZQS_2213	NA	Conus betulinus	Mixed
CMM-I-6359	Hydroxylamine	8	KVQLKYQPR	WGS:PZQS_346	NA	Conus betulinus	Mixed
CMM-I-6359	Hydroxylamine	8	WKEAEEGK	WGS:AMQO_748	NA	Conus betulinus	Mixed
CMM-I-6360	Hydroxylamine	8	KAFSDSSTLTK	WGS:RQTK_701	NA	Conus betulinus	Mixed
CMM-I-6360	Hydroxylamine	8	DVQKNLDTK	WGS:RQTK_1182	NA	Conus betulinus	Gastropoda
CMM-I-6358	Hydroxylamine	10	SPSSATGKER	WGS:RQTK_4240	NA	Conus betulinus	Gastropoda
CMM-I-6360	Hydroxylamine	8	SPSSATGKER	WGS:RQTK_4240	NA	Conus betulinus	Gastropoda
CMM-I-6358	Hydroxylamine	10	VTQQQTVSR	WGS:RQTK_1409|WGS:RQTK_2791|WGS:RQTK_5103|WGS:RQTK_5815	NA	Conus betulinus	Mixed
CMM-I-6359	Hydroxylamine	8	KEGWEITQR	Candidula_rna-CUNI_LOCUS419_R0 gene=gene_10627 chr=JADBJO010006747.1 strand=-1 interval=83911..93393 ref-gene=Candidula_gene-CUNI_LOCUS419 aa=276 raa=320 score=691 prediction=0 bestScore=691 ce=6 rce=5 pAA=0.591 iAA=0.4806 lpm=16 maxScore=1685 maxGap=25 nps=0 start=M stop=* evidence=1 sumWeight=1.0	NA	Conus betulinus	Gastropoda
CMM-I-6359	Hydroxylamine	8	VTQQQTVSR	WGS:RQTK_1409|WGS:RQTK_2791|WGS:RQTK_5103|WGS:RQTK_5815	NA	Conus betulinus	Mixed
CMM-I-6359	Hydroxylamine	8	ENQSAESNTLKK	WGS:RQTK_2998|WGS:RQTK_4078|WGS:RQTK_4840|WGS:RQTK_2998|WGS:RQTK_4078|WGS:RQTK_4840	NA	Conus betulinus	Gastropoda
CMM-I-6358	Hydroxylamine	10	SLSGCPRAAK	WGS:PZQS_6446	NA	Conus betulinus	Mollusca
CMM-I-6357	Hydroxylamine	10	QITPFTSAGANNNK	Candidula_Candidula_rna-CUNI_LOCUS12334_R0 gene=gene_7061 chr=SDAX010000281.1 strand=1 interval=94..14398 ref-gene=Candidula_Candidula_gene-CUNI_LOCUS12334 aa=336 raa=450 score=362 prediction=0 bestScore=362 ce=13 rce=15 pAA=0.4844 iAA=0.3289 lpm=15 maxScore=2262 maxGap=44 nps=0 start=M stop=* evidence=1 sumWeight=1.0	NA	Conus consors	Gastropoda
CMM-I-6359	Hydroxylamine	8	QVEQNLR	WGS:PZQS_1289	NA	Conus consors	Mixed
CMM-I-6359	Hydroxylamine	8	QLTYVPSNLASTGYVCIR	WGS:RQTK_158	NA	Conus consors	Gastropoda
CMM-I-6359	Hydroxylamine	8	EVVYWPRMNLDIENFIK	WGS:AMQO_1837	NA	Conus consors	Gastropoda
CMM-I-6359	Hydroxylamine	8	DVQKNLDTK	WGS:RQTK_469	NA	Conus consors	Gastropoda
CMM-I-6359	Hydroxylamine	8	KIDSNLKK	Candidula_Candidula_rna-CUNI_LOCUS848_R0 gene=gene_1382 chr=SDAX010011036.1 strand=-1	NA	Conus consors	Mixed

				interval=9932..10723 ref-gene=Candidula_Candidula_gene-CUNI_LOCUS848 aa=264 raa=199 score=256 prediction=0 bestScore=256 ce=1 rce=1 pAA=0.5243 iAA=0.3221 lpm=13 maxScore=1027 maxGap=22 nps=0 start=M stop=* evidence=2 sumWeight=2.0 alternative="Elysia_Elysia_gene-EGW08_003279"			
CMM-I-6359	Hydroxylamine	8	KDETVDNVFADK	WGS:PZQS_575	NA	Conus consors	Gastropoda
CMM-I-6359	Hydroxylamine	8	SLSHTVDQSK	Candidula_Candidula_rna-CUNI_LOCUS18549_R0 gene=gene_6044 chr=SDAX010001501.1 strand=1 interval=9058..10659 ref-gene=Candidula_Candidula_gene-CUNI_LOCUS18549 aa=534 raa=627 score=1104 prediction=0 bestScore=1104 ce=1 rce=1 pAA=0.6086 iAA=0.4105 lpm=18 maxScore=3370 maxGap=23 nps=0 start=M stop=* evidence=3 sumWeight=3.0 alternative="Elysia_Elysia_gene-EGW08_004074,Lottia_Lottia_gene-LOTGIDRAFT_114344"	NA	Conus consors	Gastropoda
CMM-I-6360	Hydroxylamine	8	QITPFTSAGANNNK	Candidula_Candidula_rna-CUNI_LOCUS12334_R0 gene=gene_7061 chr=SDAX010000281.1 strand=1 interval=94..14398 ref-gene=Candidula_Candidula_gene-CUNI_LOCUS12334 aa=336 raa=450 score=362 prediction=0 bestScore=362 ce=13 rce=15 pAA=0.4844 iAA=0.3289 lpm=15 maxScore=2262 maxGap=44 nps=0 start=M stop=* evidence=1 sumWeight=1.0	NA	Conus consors	Gastropoda
CMM-I-6357	Hydroxylamine	10	FQGFARLAAESTK	WGS:PZQS_190	NA	Conus consors	Gastropoda
CMM-I-6359	Hydroxylamine	8	NIQLQRQIMEEEFDEKK	WGS:PZQS_1478	NA	Conus consors	Gastropoda
CMM-I-6359	Hydroxylamine	8	DNIQGITKPAIR	Candidula_Candidula_rna-CUNI_LOCUS16438_R0 gene=gene_6145 chr=SDAX010681882.1 strand=1 interval=108..419 ref-gene=Candidula_Candidula_gene-CUNI_LOCUS16438 aa=104 raa=104 score=524 prediction=0 bestScore=524 ce=1 rce=1 pAA=1 iAA=1 lpm=104 maxScore=524 maxGap=0 nps=0 start=M stop=* evidence=3 sumWeight=3.0 alternative="Candidula_Candidula_gene-CUNI_LOCUS2762,Candidula_Candidula_g	NA	Conus consors	Mixed

				ene-CUNI_LOCUS2766,Lottia_Lottia_gene-LOTGIDRAFT_145439,Lottia_Lottia_gene-LOTGIDRAFT_146028,Lottia_Lottia_gene-LOTGIDRAFT_146029,Lottia_Lottia_gene-LOTGIDRAFT_146923,Lottia_Lottia_gene-LOTGIDRAFT_147261,Lottia_Lottia_gene-LOTGIDRAFT_147329,Lottia_Lottia_gene-LOTGIDRAFT_147488,Lottia_Lottia_gene-LOTGIDRAFT_147781,Lottia_Lottia_gene-LOTGIDRAFT_148042,Lottia_Lottia_gene-LOTGIDRAFT_148108,Lottia_Lottia_gene-LOTGIDRAFT_148116,Lottia_Lottia_gene-LOTGIDRAFT_148724,Lottia_Lottia_gene-LOTGIDRAFT_148824,Lottia_Lottia_gene-LOTGIDRAFT_148840,Lottia_Lottia_gene-LOTGIDRAFT_176226,Lottia_Lottia_gene-LOTGIDRAFT_176527,Lottia_Lottia_gene-LOTGIDRAFT_177025,Lottia_Lottia_gene-LOTGIDRAFT_202861,Pomacea_Pomacea_gene-C0Q70_13947"|WGS:AMQO_1887			
CMM-I-6360	Hydroxylamine	8	TMQESAEHVTR	WGS:AMQO_552	NA	Conus consors	Gastropoda
CMM-I-6359	Hydroxylamine	8	QVINWFNGTAASVVSGAMSAAK	WGS:AMQO_232	NA	Conus consors	Gastropoda
CMM-I-6359	Hydroxylamine	8	TDITGAKISWLK	WGS:AMQO_1848	NA	Conus consors	Gastropoda
CMM-I-6357	Hydroxylamine	10	PGLPRDNTMAVTAK	WGS:AMQO_556	NA	Conus consors	Gastropoda
CMM-I-6359	Hydroxylamine	8	MQDKEVLAGR	WGS:RQTK_828	NA	Conus consors	Gastropoda
CMM-I-6360	Hydroxylamine	8	KIDSNLKK	Candidula_Candidula_rna-CUNI_LOCUS848_R0 gene=gene_1382 chr=SDAX010011036.1 strand=-1 interval=9932..10723 ref-gene=Candidula_Candidula_gene-CUNI_LOCUS848 aa=264 raa=199 score=256 prediction=0 bestScore=256 ce=1 rce=1 pAA=0.5243 iAA=0.3221 lpm=13 maxScore=1027 maxGap=22 nps=0 start=M stop=* evidence=2 sumWeight=2.0 alternative="Elysia_Elysia_gene-EGW08_003279"	NA	Conus consors	Mixed
CMM-I-6359	Hydroxylamine	8	FITDNTVEERIVERAEMK	Candidula_Candidula_rna-CUNI_LOCUS15734_R0 gene=gene_2294 chr=SDAX010001313.1 strand=1 interval=1775..24102 ref-gene=Candidula_Candidula_gene-CUNI_LOCUS15734 aa=957 raa=1020 score=3724 prediction=0 bestScore=3724 ce=23 rce=23 pAA=0.7931 iAA=0.7267 lpm=84 maxScore=5340 maxGap=22 nps=0 start=M stop=* evidence=1	NA	Conus consors	Mixed

				sumWeight=1.0			
CMM-I-6360	Hydroxylamine	8	KAFSDSSTLTK	WGS:AMQO_1977	NA	Conus consors	Mixed
CMM-I-6360	Hydroxylamine	8	DVQKNLDTK	WGS:RQTK_469	NA	Conus consors	Gastropoda
CMM-I-6359	Hydroxylamine	8	EILMKTTQLQDK	WGS:RQTK_1667	NA	Conus consors	Gastropoda
CMM-I-6360	Hydroxylamine	8	ITTEVLQTAPMDDEKGLCLK	WGS:PZQS_2460	NA	Conus consors	Gastropoda
CMM-I-6359	Hydroxylamine	8	KELVSLLETK	Candidula_Candidula_rna-CUNI_LOCUS15080_R1 gene=gene_2446 chr=SDAX010066343.1 strand=1 interval=292..5405 ref-gene=Candidula_Candidula_gene-CUNI_LOCUS15080 aa=249 raa=251 score=237 prediction=1 bestScore=259 ce=4 rce=5 pAA=0.55 iAA=0.275 lpm=13 maxScore=1359 maxGap=23 nps=0 start=M stop=* evidence=1 sumWeight=1.0	NA	Conus consors	Mixed
CMM-I-6357	Hydroxylamine	10	DQTAQMEAQLKK	WGS:PZQS_1417	NA	Conus consors	Gastropoda
CMM-I-6360	Hydroxylamine	8	KKLGGSDK	WGS:AMQO_1785	NA	Conus consors	Mixed
CMM-I-6359	Hydroxylamine	8	TVYIQTR	Candidula_Candidula_rna-CUNI_LOCUS22262_R0 gene=gene_11411 chr=SDAX010012142.1 strand=-1 interval=2476..11611 ref-gene=Candidula_Candidula_gene-CUNI_LOCUS22262 aa=1830 raa=1885 score=2300 prediction=0 bestScore=2300 ce=7 rce=8 pAA=0.5758 iAA=0.3567 lpm=36 maxScore=9614 maxGap=59 nps=0 start=M stop=* evidence=1 sumWeight=1.0	NA	Conus consors	Mixed
CMM-I-6360	Hydroxylamine	8	VTSQTAATVLDPSSAIHFTSSK	WGS:AMQO_729	NA	Conus consors	Gastropoda
CMM-I-6357	Hydroxylamine	10	EWGAKVDFVRNK	WGS:PZQS_669	NA	Conus consors	Gastropoda
CMM-I-6358	Hydroxylamine	10	LQEAVSSASR	WGS:AMQO_1153	NA	Conus consors	Gastropoda
CMM-I-6357	Hydroxylamine	10	AKDYPEDNLFQEAR	WGS:PZQS_1585	NA	Conus consors	Gastropoda
CMM-I-6359	Hydroxylamine	8	VQEPQVK	WGS:RQTK_36	NA	Conus consors	Mixed
CMM-I-6360	Hydroxylamine	8	TSSLSFGTDLGLSQK	WGS:AMQO_241	NA	Conus consors	Gastropoda
CMM-I-6360	Hydroxylamine	8	AKDYPEDNLFQEAR	WGS:PZQS_1585	NA	Conus consors	Gastropoda
CMM-I-6359	Hydroxylamine	8	KDGALRLCIDFR	WGS:PZQS_3880	NA	Conus consors	Gastropoda
CMM-I-6360	Hydroxylamine	8	WYESLGK	Candidula_Candidula_rna-CUNI_LOCUS14076_R1 gene=gene_11046 chr=SDAX010077650.1 strand=-1 interval=512..3249 ref-gene=Candidula_Candidula_gene-	NA	Conus consors	Mixed

				CUNI_LOCUS14076 aa=124 raa=205 score=189 prediction=1 bestScore=625 ce=3 rce=3 pAA=0.43 iAA=0.3333 lpm=19 maxScore=1096 maxGap=27 nps=0 start=M stop=* evidence=1 sumWeight=1.0			
CMM-I-6360	Hydroxylamine	8	SSGDRPFPTDRR	WGS:PZQS_1667	NA	Conus consors	Gastropoda
CMM-I-6359	Hydroxylamine	8	TQISFLSR	WGS:AMQO_1813	NA	Conus consors	Mixed
CMM-I-6359	Hydroxylamine	8	LVFSQVR	WGS:PZQS_3130	NA	Conus consors	Mixed
CMM-I-6360	Hydroxylamine	8	GEIVTNCFK	WGS:PZQS_870	NA	Conus consors	Mixed
CMM-I-6357	Hydroxylamine	10	VTQQQTVSR	WGS:RQTK_1384	NA	Conus tribblei	Mixed
CMM-I-6359	Hydroxylamine	8	EVTFGLSIGGEAVGK	WGS:PZQS_304	NA	Conus tribblei	Gastropoda
CMM-I-6357	Hydroxylamine	10	HRAIYDAFSLAAK	WGS:PZQS_1822	NA	Conus tribblei	Gastropoda
CMM-I-6359	Hydroxylamine	8	DVQKNLDTK	WGS:RQTK_1123	NA	Conus tribblei	Gastropoda
CMM-I-6359	Hydroxylamine	8	VHGEEGLGVRGGDPCE PEASREGQTPTK	WGS:RQTK_1543	NA	Conus tribblei	Gastropoda
CMM-I-6360	Hydroxylamine	8	VTQQQTVSR	WGS:RQTK_1384	NA	Conus tribblei	Mixed
CMM-I-6359	Hydroxylamine	8	SLSHTVDQSK	Candidula_rna-CUNI_LOCUS18549_R0 gene=gene_526 chr=LFLW010274540.1 strand=-1 interval=2443..4053 ref-gene=Candidula_gene-CUNI_LOCUS18549 aa=537 raa=627 score=1102 prediction=0 bestScore=1102 ce=1 rce=1 pAA=0.6044 iAA=0.4082 lpm=18 maxScore=3370 maxGap=23 nps=0 start=M stop=* evidence=3 sumWeight=3.0 alternative="Elysia_gene-EGW08_004074,Lottia_gene-LOTGIDRAFT_114344"	NA	Conus tribblei	Gastropoda
CMM-I-6360	Hydroxylamine	8	HSIITALARDYFNGSR	WGS:AMQO_686	NA	Conus tribblei	Gastropoda
CMM-I-6359	Hydroxylamine	8	HSIITALARDYFNGSR	WGS:AMQO_686	NA	Conus tribblei	Gastropoda
CMM-I-6360	Hydroxylamine	8	LNSMSPAAQR	Candidula_rna-CUNI_LOCUS20925_R0 gene=gene_1328 chr=LFLW010252434.1 strand=-1 interval=1973..8678 ref-gene=Candidula_gene-CUNI_LOCUS20925 aa=473 raa=508 score=1149 prediction=0 bestScore=1149 ce=9 rce=9 pAA=0.6692 iAA=0.5164 lpm=15 maxScore=2604 maxGap=13 nps=0 start=M stop=* evidence=1 sumWeight=1.0	NA	Conus tribblei	Mixed
CMM-I-6359	Hydroxylamine	8	LEAMAEVKPETMAEVK	WGS:AMQO_1386	NA	Conus tribblei	Gastropoda
CMM-I-6360	Hydroxylamine	8	KGDACVNILQGSR	WGS:PZQS_4028	NA	Conus tribblei	Gastropoda
CMM-I-6357	Hydroxylamine	10	KHLRDSNIASNSK	WGS:AMQO_1799	NA	Conus tribblei	Gastropoda

CMM-I-6360	Hydroxylamine	8	TISSTFMAASGLNEASRQANK	WGS:AMQO_509	NA	Conus tribblei	Gastropoda
CMM-I-6357	Hydroxylamine	10	PGLPRDNTMAVTAK	WGS:PZQS_2432	NA	Conus tribblei	Gastropoda
CMM-I-6360	Hydroxylamine	8	SPSKSPSR	WGS:PZQS_3571	NA	Conus tribblei	Mixed
CMM-I-6359	Hydroxylamine	8	SPSKSPSR	WGS:PZQS_3571	NA	Conus tribblei	Mixed
CMM-I-6360	Hydroxylamine	8	KAFSDSSTLTK	WGS:AMQO_2426	NA	Conus tribblei	Mixed
CMM-I-6360	Hydroxylamine	8	KYEGRNTITK	WGS:PZQS_3524	NA	Conus tribblei	Gastropoda
CMM-I-6360	Hydroxylamine	8	DVQKNLDTK	WGS:RQTK_1123	NA	Conus tribblei	Gastropoda
CMM-I-6357	Hydroxylamine	10	WTSPHAVAFLDK	Candidula_rna-CUNI_LOCUS21112_R0 gene=gene_2267 chr=LFLW010892047.1 strand=1 interval=353..3429 ref-gene=Candidula_gene-CUNI_LOCUS21112 aa=191 raa=193 score=330 prediction=0 bestScore=330 ce=5 rce=5 pAA=0.6587 iAA=0.4279 lpm=29 maxScore=1010 maxGap=11 nps=0 start=M stop=* evidence=1 sumWeight=1.0	NA	Conus tribblei	Gastropoda
CMM-I-6359	Hydroxylamine	8	KYEGRNTITK	WGS:PZQS_3524	NA	Conus tribblei	Gastropoda
CMM-I-6358	Hydroxylamine	10	VTQQQTVSR	WGS:RQTK_1384	NA	Conus tribblei	Mixed
CMM-I-6359	Hydroxylamine	8	VTQQQTVSR	WGS:RQTK_1384	NA	Conus tribblei	Mixed
CMM-I-6360	Hydroxylamine	8	SSFQNLKK	WGS:RQTK_2223	NA	Conus tribblei	Mixed
CMM-I-6358	Hydroxylamine	10	APSSSSGAVSR	WGS:RQTK_2442	NA	Conus tribblei	Gastropoda
CMM-I-6360	Hydroxylamine	8	ETVLINGSNSR	WGS:PZQS_571	NA	Conus tribblei	Gastropoda
CMM-I-6360	Hydroxylamine	8	LTWAEYVTSVQGSFSENKELAK	WGS:PZQS_550	NA	Conus tribblei	Gastropoda
CMM-I-6359	Hydroxylamine	8	LLYSVRSNDQHHEGVAVILK	WGS:PZQS_99	NA	Conus tribblei	Gastropoda
CMM-I-6360	Hydroxylamine	8	LLYSVRSNDQHHEGVAVILK	WGS:PZQS_99	NA	Conus tribblei	Gastropoda
CMM-I-6360	Hydroxylamine	8	LSRDITIAR	WGS:PZQS_2473|WGS:PZQS_2911	NA	Conus tribblei	Gastropoda
CMM-I-6360	Hydroxylamine	8	ERCKQIYTIFMPSASSAVGK	Candidula_rna-CUNI_LOCUS802_R6 gene=gene_1757 chr=LFLW010588647.1 strand=1 interval=792..6038 ref-gene=Candidula_gene-CUNI_LOCUS802 aa=284 raa=396 score=450 prediction=6 bestScore=725 ce=9 rce=8 pAA=0.5352 iAA=0.3769 lpm=25 maxScore=2055 maxGap=34 nps=0 start=M stop=* evidence=1 sumWeight=1.0	NA	Conus tribblei	Gastropoda
CMM-I-6359	Hydroxylamine	8	TVYIQTR	WGS:PZQS_3515	NA	Conus tribblei	Mixed
CMM-I-6360	Hydroxylamine	8	DINLVVNDISECILK	WGS:PZQS_1083	NA	Conus tribblei	Gastropoda
CMM-I-6359	Hydroxylamine	8	QIQTEKGR	WGS:RQTK_1073	NA	Conus tribblei	Mixed

CMM-I-6359	Hydroxylamine	8	SSFQNLKK	WGS:RQTK_2223	NA	Conus tribblei	Mixed
CMM-I-6360	Hydroxylamine	8	SWLSEDTISMIEER	WGS:RQTK_482	NA	Conus tribblei	Gastropoda
CMM-I-6357	Hydroxylamine	10	TNSVKSMELLNNK	WGS:AMQO_1606	NA	Conus tribblei	Gastropoda
CMM-I-6359	Hydroxylamine	8	TNPPSIPPSVAN	WGS:RQTK_2024	NA	Conus tribblei	Gastropoda
CMM-I-6357	Hydroxylamine	10	LSQVVSEMR	WGS:PZQS_3634	NA	Conus tribblei	Mixed
CMM-I-6359	Hydroxylamine	8	EWIELASMIQTR	Candidula_rna-CUNI_LOCUS7435_R0 gene=gene_763 chr=LFLW010099223.1 strand=1 interval=4584..12160 ref-gene=Candidula_gene-CUNI_LOCUS7435 aa=580 raa=594 score=1408 prediction=0 bestScore=1408 ce=5 rce=6 pAA=0.6517 iAA=0.4859 lpm=14 maxScore=3148 maxGap=19 nps=0 start=M stop=* evidence=2 sumWeight=2.0 alternative="Elysia_gene-EGW08_002624"	NA	Conus tribblei	Gastropoda
CMM-I-6360	Hydroxylamine	8	PGLPRDNTMAVTAK	WGS:PZQS_2432	NA	Conus tribblei	Gastropoda
CMM-I-6360	Hydroxylamine	8	KLSDSLIMSEKAR	WGS:PZQS_4511	NA	Conus tribblei	Gastropoda
CMM-I-6359	Hydroxylamine	8	RGMFYKAGEK	WGS:PZQS_1676	NA	Conus tribblei	Gastropoda
CMM-I-6359	Hydroxylamine	8	EDAVKQYK	WGS:PZQS_1196|WGS:PZQS_4096	NA	Conus tribblei	Mixed
CMM-I-6359	Hydroxylamine	8	EGKGFQLAMLNLR	WGS:RQTK_362	NA	Conus tribblei	Gastropoda
CMM-I-6359	Hydroxylamine	8	DKLALALAEK	Candidula_rna-CUNI_LOCUS20925_R0 gene=gene_1328 chr=LFLW010252434.1 strand=-1 interval=1973..8678 ref-gene=Candidula_gene-CUNI_LOCUS20925 aa=473 raa=508 score=1149 prediction=0 bestScore=1149 ce=9 rce=9 pAA=0.6692 iAA=0.5164 lpm=15 maxScore=2604 maxGap=13 nps=0 start=M stop=* evidence=1 sumWeight=1.0	NA	Conus tribblei	Gastropoda
CMM-I-6357	Hydroxylamine	10	MDLAIYCQHFQER	WGS:PZQS_2426	NA	Conus tribblei	Gastropoda
CMM-I-6359	Hydroxylamine	8	TNLHTNER	WGS:PZQS_2776	NA	Conus tribblei	Mixed
CMM-I-6359	Hydroxylamine	8	GLRTQDNGLR	Candidula_rna-CUNI_LOCUS16115_R4 gene=gene_1316 chr=LFLW010161969.1 strand=-1 interval=5240..5722 ref-gene=Candidula_gene-CUNI_LOCUS16115 aa=161 raa=155 score=158 prediction=4 bestScore=313 ce=1 rce=1 pAA=0.6894 iAA=0.3354 lpm=10 maxScore=866 maxGap=3 nps=0 start=M stop=* evidence=1 sumWeight=1.0	NA	Conus tribblei	Gastropoda
CMM-I-6357	Hydroxylamine	10	APSSSSGAVSR	WGS:RQTK_2442	NA	Conus tribblei	Gastropoda
CMM-I-6360	Hydroxylamine	8	DTFPLPR	WGS:PZQS_2600	NA	Conus tribblei	Mixed

CMM-I-6359	Hydroxylamine	8	QNIPEDVLKVSR	Candidula_rna-CUNI_LOCUS15019_R0 gene=gene_5770 chr=LFLW010034030.1 strand=-1 interval=7063..9525 ref-gene=Candidula_gene-CUNI_LOCUS15019 aa=167 raa=103 score=129 prediction=0 bestScore=129 ce=2 rce=2 pAA=0.4251 iAA=0.2754 lpm=9 maxScore=548 maxGap=24 nps=0 start=M stop=* evidence=2 sumWeight=2.0 alternative="Candidula_gene-CUNI_LOCUS15021,Elysia_gene-EGW08_009932"	NA	Conus tribblei	Gastropoda
CMM-I-6359	Hydroxylamine	8	GAVKDTELLMGTNK	WGS:PZQS_2840	NA	Conus tribblei	Gastropoda
CMM-I-6359	Hydroxylamine	8	QGVGTISETDR	WGS:RQTK_1119	NA	Conus tribblei	Gastropoda
CMM-I-6359	Hydroxylamine	8	SGATIQVLQRGGVLEGIFYQR	WGS:RQTK_588	NA	Conus tribblei	Gastropoda
CMM-I-6359	Hydroxylamine	8	KPTSQQQQQAGGASK	WGS:PZQS_3374	NA	Conus tribblei	Gastropoda
CMM-I-6359	Hydroxylamine	8	ITPITYSSNGSSAAK	WGS:PZQS_1005	NA	Conus tribblei	Gastropoda
CMM-I-6359	Hydroxylamine	8	ENLVQSNTTVFK	WGS:PZQS_532	NA	Conus tribblei	Gastropoda
CMM-I-6359	Hydroxylamine	8	GDLRWETEHGGNQGR	Candidula_rna-CUNI_LOCUS19432_R6 gene=gene_3249 chr=LFLW010485785.1 strand=-1 interval=855..1232 ref-gene=Candidula_gene-CUNI_LOCUS19432 aa=126 raa=125 score=101 prediction=6 bestScore=148 ce=1 rce=1 pAA=0.6742 iAA=0.2273 lpm=12 maxScore=752 maxGap=7 nps=0 start=M stop=* evidence=1 sumWeight=1.0	NA	Conus tribblei	Gastropoda
CMM-I-6359	Hydroxylamine	8	GVSPDPEKIEAIVNMK	WGS:RQTK_1892	NA	Conus tribblei	Gastropoda
CMM-I-6357	Hydroxylamine	10	QITPFTSAGANNNK	WGS:PZQS_858	NA	Conus ventricosus	Gastropoda
CMM-I-6359	Hydroxylamine	8	KPPNCDDVLLKQMEDTFIDNLR	WGS:AMQO_1386	NA	Conus ventricosus	Gastropoda
CMM-I-6359	Hydroxylamine	8	LYGTDVKR	Candidula_rna-CUNI_LOCUS20322_R1 gene=gene_17905 chr=CM031618.1 strand=-1 interval=54165824..54167869 ref-gene=Candidula_gene-CUNI_LOCUS20322 aa=336 raa=349 score=681 prediction=1 bestScore=685 ce=2 rce=2 pAA=0.68 iAA=0.42 lpm=18 maxScore=1835 maxGap=11 nps=0 start=M stop=* evidence=1 sumWeight=1.0	NA	Conus ventricosus	Mixed
CMM-I-6360	Hydroxylamine	8	PSPGWTAGGPLCDPSR	WGS:PZQS_5787	NA	Conus ventricosus	Gastropoda
CMM-I-6359	Hydroxylamine	8	TKTKMNTK	WGS:AMQO_5188	NA	Conus ventricosus	Mixed
CMM-I-6357	Hydroxylamine	10	VTQQQTVSR	WGS:RQTK_4436	NA	Conus ventricosus	Mixed

CMM-I-6357	Hydroxylamine	10	DALHTPRSLVGDR	WGS:PZQS_3007	NA	Conus ventricosus	Gastropoda
CMM-I-6359	Hydroxylamine	8	QVEQNLR	WGS:PZQS_9398	NA	Conus ventricosus	Mixed
CMM-I-6359	Hydroxylamine	8	TLGNTLVNDKLDAGK	WGS:AMQO_3280	NA	Conus ventricosus	Gastropoda
CMM-I-6359	Hydroxylamine	8	LGKSADDFK	WGS:AMQO_244	NA	Conus ventricosus	Mixed
CMM-I-6360	Hydroxylamine	8	TRKLGEESR	WGS:PZQS_8785	NA	Conus ventricosus	Mixed
CMM-I-6359	Hydroxylamine	8	PSPGWTAGGPLCDPSR	WGS:PZQS_5787	NA	Conus ventricosus	Gastropoda
CMM-I-6360	Hydroxylamine	8	TKTKMNTK	WGS:AMQO_5188	NA	Conus ventricosus	Mixed
CMM-I-6359	Hydroxylamine	8	PSANISTR	WGS:RQTK_76	NA	Conus ventricosus	Mixed
CMM-I-6359	Hydroxylamine	8	DVQKNLDTK	WGS:RQTK_5546	NA	Conus ventricosus	Gastropoda
CMM-I-6358	Hydroxylamine	10	TIFCSIRSRTTTTIFDHK	WGS:RQTK_5223	NA	Conus ventricosus	Gastropoda
CMM-I-6359	Hydroxylamine	8	TAAMTPGKVHGIR	WGS:PZQS_7111	NA	Conus ventricosus	Gastropoda
CMM-I-6358	Hydroxylamine	10	ISSGVVSNQR	WGS:PZQS_9524	NA	Conus ventricosus	Mixed
CMM-I-6360	Hydroxylamine	8	VTQQQTVSR	WGS:RQTK_4436	NA	Conus ventricosus	Mixed
CMM-I-6359	Hydroxylamine	8	TVSPSDKRR	Candidula_rna-CUNI_LOCUS7421_R0 gene=gene_4128 chr=CM031603.1 strand=1 interval=62239529..62252107 ref-gene=Candidula_gene-CUNI_LOCUS7421 aa=463 raa=610 score=1007 prediction=0 bestScore=1007 ce=8 rce=4 pAA=0.5703 iAA=0.4412 lpm=30 maxScore=3165 maxGap=67 nps=0 start=M stop=* evidence=1 sumWeight=1.0	NA	Conus ventricosus	Mixed
CMM-I-6360	Hydroxylamine	8	STDPRTAGNHLWNTAGR	WGS:PZQS_1067	NA	Conus ventricosus	Gastropoda
CMM-I-6360	Hydroxylamine	8	NNLNPSPGPAMPEANR	WGS:PZQS_502	NA	Conus ventricosus	Gastropoda
CMM-I-6359	Hydroxylamine	8	IEWKTFQTGDVR	WGS:PZQS_6244	NA	Conus ventricosus	Gastropoda
CMM-I-6359	Hydroxylamine	8	GSGIIMVGEK	WGS:AMQO_3443	NA	Conus ventricosus	Mixed
CMM-I-6359	Hydroxylamine	8	PAGTLLPR	WGS:PZQS_10604	NA	Conus ventricosus	Mixed
CMM-I-6360	Hydroxylamine	8	GSGIIMVGEK	WGS:AMQO_3443	NA	Conus ventricosus	Mixed
CMM-I-6360	Hydroxylamine	8	PLMIEDVSEELDPALDNVLEKNFIK	WGS:AMQO_3262	NA	Conus ventricosus	Gastropoda
CMM-I-6360	Hydroxylamine	8	QLMLSAQSR	WGS:AMQO_510	NA	Conus ventricosus	Mixed
CMM-I-6359	Hydroxylamine	8	SVETGVPSKMSAAK	WGS:AMQO_678	NA	Conus ventricosus	Gastropoda
CMM-I-6359	Hydroxylamine	8	QLRSSADSR	WGS:PZQS_1443	NA	Conus ventricosus	Mixed
CMM-I-6360	Hydroxylamine	8	QLRSSADSR	WGS:PZQS_1443	NA	Conus ventricosus	Mixed
CMM-I-6359	Hydroxylamine	8	DNIQGITKPAIR	Candidula_rna-CUNI_LOCUS16438_R0 gene=gene_6933 chr=CM031629.1 strand=-1 interval=36705754..36706065	NA	Conus ventricosus	Mixed

				ref-gene=Candidula_gene-CUNI_LOCUS16438 aa=104 raa=104 score=524 prediction=0 bestScore=524 ce=1 rce=1 pAA=1 iAA=1 lpm=104 maxScore=524 maxGap=0 nps=0 start=M stop=* evidence=3 sumWeight=3.0 alternative="Candidula_gene-CUNI_LOCUS2762,Candidula_gene-CUNI_LOCUS2766,Lottia_gene-LOTGIDRAFT_145439,Lottia_gene-LOTGIDRAFT_146028,Lottia_gene-LOTGIDRAFT_146029,Lottia_gene-LOTGIDRAFT_146923,Lottia_gene-LOTGIDRAFT_147261,Lottia_gene-LOTGIDRAFT_147329,Lottia_gene-LOTGIDRAFT_147488,Lottia_gene-LOTGIDRAFT_147781,Lottia_gene-LOTGIDRAFT_148042,Lottia_gene-LOTGIDRAFT_148108,Lottia_gene-LOTGIDRAFT_148116,Lottia_gene-LOTGIDRAFT_148724,Lottia_gene-LOTGIDRAFT_148824,Lottia_gene-LOTGIDRAFT_148840,Lottia_gene-LOTGIDRAFT_176226,Lottia_gene-LOTGIDRAFT_176527,Lottia_gene-LOTGIDRAFT_177025,Lottia_gene-LOTGIDRAFT_202861,Pomacea_gene-C0Q70_13947"|Candidula_rna-CUNI_LOCUS16438_R1 gene=gene_28936 chr=JAFLJL010002299.1 strand=1 interval=30433..30744 ref-gene=Candidula_gene-CUNI_LOCUS16438 aa=104 raa=104 score=524 prediction=1 bestScore=524 ce=1 rce=1 pAA=1 iAA=1 lpm=104 maxScore=524 maxGap=0 nps=0 start=M stop=* evidence=3 sumWeight=3.0 alternative="Candidula_gene-CUNI_LOCUS2762,Candidula_gene-CUNI_LOCUS2766,Lottia_gene-LOTGIDRAFT_145439,Lottia_gene-LOTGIDRAFT_146028,Lottia_gene-LOTGIDRAFT_146029,Lottia_gene-LOTGIDRAFT_146923,Lottia_gene-LOTGIDRAFT_147261,Lottia_gene-LOTGIDRAFT_147329,Lottia_gene-LOTGIDRAFT_147488,Lottia_gene-LOTGIDRAFT_147781,Lottia_gene-LOTGIDRAFT_148042,Lottia_gene-LOTGIDRAFT_148108,Lottia_gene-LOTGIDRAFT_148116,Lottia_gene-LOTGIDRAFT_148724,Lottia_gene-			

				LOTGIDRAFT_148824,Lottia_gene-LOTGIDRAFT_148840,Lottia_gene-LOTGIDRAFT_176226,Lottia_gene-LOTGIDRAFT_176527,Lottia_gene-LOTGIDRAFT_177025,Lottia_gene-LOTGIDRAFT_202861,Pomacea_gene-C0Q70_13947"|Candidula_rna-CUNI_LOCUS16438_R2 gene=gene_13019 chr=JAFLJL010015254.1 strand=1 interval=943..1254 ref-gene=Candidula_gene-CUNI_LOCUS16438 aa=104 raa=104 score=524 prediction=2 bestScore=524 ce=1 rce=1 pAA=1 iAA=1 lpm=104 maxScore=524 maxGap=0 nps=0 start=M stop=* evidence=3 sumWeight=3.0 alternative="Candidula_gene-CUNI_LOCUS2762,Candidula_gene-CUNI_LOCUS2766,Lottia_gene-LOTGIDRAFT_145439,Lottia_gene-LOTGIDRAFT_146028,Lottia_gene-LOTGIDRAFT_146029,Lottia_gene-LOTGIDRAFT_146923,Lottia_gene-LOTGIDRAFT_147261,Lottia_gene-LOTGIDRAFT_147329,Lottia_gene-LOTGIDRAFT_147488,Lottia_gene-LOTGIDRAFT_147781,Lottia_gene-LOTGIDRAFT_148042,Lottia_gene-LOTGIDRAFT_148108,Lottia_gene-LOTGIDRAFT_148116,Lottia_gene-LOTGIDRAFT_148724,Lottia_gene-LOTGIDRAFT_148824,Lottia_gene-LOTGIDRAFT_148840,Lottia_gene-LOTGIDRAFT_176226,Lottia_gene-LOTGIDRAFT_176527,Lottia_gene-LOTGIDRAFT_177025,Lottia_gene-LOTGIDRAFT_202861,Pomacea_gene-C0Q70_13947"|Candidula_rna-CUNI_LOCUS16438_R3 gene=gene_28934 chr=JAFLJL010002299.1 strand=1 interval=1558..1868 ref-gene=Candidula_gene-CUNI_LOCUS16438 aa=94 raa=104 score=430 prediction=3 bestScore=524 ce=2 rce=1 pAA=0.9038 iAA=0.9038 lpm=51 maxScore=524 maxGap=10 nps=0 start=M stop=* evidence=3 sumWeight=3.0 alternative="Candidula_gene-CUNI_LOCUS2762,Candidula_gene-CUNI_LOCUS2766,Lottia_gene-LOTGIDRAFT_145439,Lottia_gene-LOTGIDRAFT_146028,Lottia_gene-			

				LOTGIDRAFT_146029,Lottia_gene-LOTGIDRAFT_146923,Lottia_gene-LOTGIDRAFT_147261,Lottia_gene-LOTGIDRAFT_147329,Lottia_gene-LOTGIDRAFT_147488,Lottia_gene-LOTGIDRAFT_147781,Lottia_gene-LOTGIDRAFT_148042,Lottia_gene-LOTGIDRAFT_148108,Lottia_gene-LOTGIDRAFT_148116,Lottia_gene-LOTGIDRAFT_148724,Lottia_gene-LOTGIDRAFT_148824,Lottia_gene-LOTGIDRAFT_148840,Lottia_gene-LOTGIDRAFT_176226,Lottia_gene-LOTGIDRAFT_176527,Lottia_gene-LOTGIDRAFT_177025,Lottia_gene-LOTGIDRAFT_202861,Pomacea_gene-C0Q70_13947"			
CMM-I-6357	Hydroxylamine	10	ENQSAESNTLKK	WGS:RQTK_2998|WGS:RQTK_4078|WGS:RQTK_4840	NA	All conus	Gastropoda
CMM-I-6357	Hydroxylamine	10	KIMGQLSFNAPGSK	WGS:RQTK_3897	NA	All conus	Gastropoda
CMM-I-6357	Hydroxylamine	10	VGMHASANCRVR	Candidula_rna-CUNI_LOCUS17455_R0 gene=gene_31283 chr=JADBJO010000403.1 strand=-1 interval=164873..176921 ref-gene=Candidula_gene-CUNI_LOCUS17455 aa=310 raa=334 score=779 prediction=0 bestScore=779 ce=10 rce=10 pAA=0.6628 iAA=0.5349 lpm=34 maxScore=1694 maxGap=16 nps=0 start=M stop=* evidence=1 sumWeight=1.0	NA	All conus	Gastropoda
CMM-I-6359	Hydroxylamine	8	KPPNCDDVLLKQMEDTFIDNLR	WGS:AMQO_1386	NA	All conus	Gastropoda
CMM-I-6359	Hydroxylamine	8	LYGTDVKR	Candidula_rna-CUNI_LOCUS20322_R1 gene=gene_17905 chr=CM031618.1 strand=-1 interval=54165824..54167869 ref-gene=Candidula_gene-CUNI_LOCUS20322 aa=336 raa=349 score=681 prediction=1 bestScore=685 ce=2 rce=2 pAA=0.68 iAA=0.42 lpm=18 maxScore=1835 maxGap=11 nps=0 start=M stop=* evidence=1 sumWeight=1.0	NA	All conus	Mixed
CMM-I-6360	Hydroxylamine	8	PSPGWTAGGPLCDPSR	WGS:PZQS_5787	NA	All conus	Gastropoda
CMM-I-6357	Hydroxylamine	10	VTQQQTVSR	WGS:RQTK_1384|WGS:RQTK_1409|WGS:RQTK_2791|WGS:RQTK_4436|WGS:RQTK_5103|WGS:RQTK_5815	NA	All conus	Mixed
CMM-I-6359	Hydroxylamine	8	QVEQNLR	WGS:PZQS_9398	NA	All conus	Mixed
CMM-I-6359	Hydroxylamine	8	LGKSADDFK	WGS:AMQO_244	NA	All conus	Mixed
CMM-I-6360	Hydroxylamine	8	GKQEEGLGQQK	WGS:PZQS_5954	NA	All conus	Gastropoda

CMM-I-6360	Hydroxylamine	8	TRKLGEESR	WGS:PZQS_8785	NA	All conus	Mixed
CMM-I-6359	Hydroxylamine	8	PSPGWTAGGPLCDPSR	WGS:PZQS_5787	NA	All conus	Gastropoda
CMM-I-6359	Hydroxylamine	8	EKALSQALLEMMFAMELTVK	WGS:PZQS_5025	NA	All conus	Gastropoda
CMM-I-6359	Hydroxylamine	8	TFVIQVR	WGS:PZQS_3512	NA	All conus	Mixed
CMM-I-6359	Hydroxylamine	8	NAFRPLGSSSGKNK	Candidula_rna-CUNI_LOCUS10700_R1 gene=gene_19679 chr=JADBJO010001434.1 strand=1 interval=213940..236256 ref-gene=Candidula_gene-CUNI_LOCUS10700 aa=255 raa=268 score=426 prediction=1 bestScore=626 ce=5 rce=5 pAA=0.5113 iAA=0.3537 lpm=14 maxScore=1460 maxGap=40 nps=0 start=M stop=* evidence=1 sumWeight=1.0	NA	All conus	Gastropoda
CMM-I-6359	Hydroxylamine	8	PSANISTR	WGS:RQTK_76	NA	All conus	Mixed
CMM-I-6359	Hydroxylamine	8	GKQEEGLGQQKR	WGS:PZQS_5954	NA	All conus	Gastropoda
CMM-I-6359	Hydroxylamine	8	DVQKNLDTK	WGS:RQTK_5546	NA	All conus	Gastropoda
CMM-I-6359	Hydroxylamine	8	VHGEEGLGVRGGDPCEPEASREGQTPTK	WGS:RQTK_1543	NA	All conus	Gastropoda
CMM-I-6359	Hydroxylamine	8	TAAMTPGKVHGIR	WGS:PZQS_7111	NA	All conus	Gastropoda
CMM-I-6358	Hydroxylamine	10	ISSGVVSNQR	WGS:PZQS_9524	NA	All conus	Mixed
CMM-I-6360	Hydroxylamine	8	VTQQQTVSR	WGS:RQTK_1384|WGS:RQTK_1409|WGS:RQTK_2791|WGS:RQTK_4436|WGS:RQTK_5103|WGS:RQTK_5815	NA	All conus	Mixed
CMM-I-6359	Hydroxylamine	8	SHDLNNKFIDK	WGS:PZQS_2022	NA	All conus	Gastropoda
CMM-I-6359	Hydroxylamine	8	TVSPSDKRR	Candidula_rna-CUNI_LOCUS7421_R0 gene=gene_4128 chr=CM031603.1 strand=1 interval=62239529..62252107 ref-gene=Candidula_gene-CUNI_LOCUS7421 aa=463 raa=610 score=1007 prediction=0 bestScore=1007 ce=8 rce=4 pAA=0.5703 iAA=0.4412 lpm=30 maxScore=3165 maxGap=67 nps=0 start=M stop=* evidence=1 sumWeight=1.0	NA	All conus	Mixed
CMM-I-6357	Hydroxylamine	10	SHDLNNKFIDK	WGS:PZQS_2022	NA	All conus	Gastropoda
CMM-I-6359	Hydroxylamine	8	AGIALSSGQTWK	Candidula_rna-CUNI_LOCUS889_R5 gene=gene_14137 chr=JADBJO010000294.1 strand=1 interval=714006..720699 ref-gene=Candidula_gene-CUNI_LOCUS889 aa=514 raa=493 score=628 prediction=5 bestScore=761 ce=7 rce=3 pAA=0.5767 iAA=0.3457 lpm=12 maxScore=2559 maxGap=22 nps=0 start=M stop=*	NA	All conus	Gastropoda

				evidence=1 sumWeight=1.0 alternative="Candidula_gene-CUNI_LOCUS891"			
CMM-I-6360	Hydroxylamine	8	SHDLNNKFIDK	WGS:PZQS_2022	NA	All conus	Gastropoda
CMM-I-6360	Hydroxylamine	8	NNLNPSPGPAMPEANR	WGS:PZQS_502	NA	All conus	Gastropoda
CMM-I-6357	Hydroxylamine	10	SLSFKSHSR	WGS:PZQS_12031	NA	All conus	Gastropoda
CMM-I-6357	Hydroxylamine	10	NVDREAITMLDAK	WGS:PZQS_11854	NA	All conus	Gastropoda
CMM-I-6359	Hydroxylamine	8	SLSFKSHSR	WGS:PZQS_12031	NA	All conus	Gastropoda
CMM-I-6359	Hydroxylamine	8	IEWKTFQTGDVR	WGS:PZQS_6244	NA	All conus	Gastropoda
CMM-I-6359	Hydroxylamine	8	GSGIIMVGEK	WGS:AMQO_3443	NA	All conus	Mixed
CMM-I-6360	Hydroxylamine	8	GSGIIMVGEK	WGS:AMQO_3443	NA	All conus	Mixed
CMM-I-6360	Hydroxylamine	8	QLMLSAQSR	WGS:AMQO_510	NA	All conus	Mixed
CMM-I-6359	Hydroxylamine	8	SVETGVPSKMSAAK	WGS:AMQO_678	NA	All conus	Gastropoda
CMM-I-6357	Hydroxylamine	10	KASPSAHSDPPPPAK	WGS:AMQO_2079	NA	All conus	Gastropoda
CMM-I-6359	Hydroxylamine	8	DNIQGITKPAIR	Candidula_Candidula_rna-CUNI_LOCUS16438_R0 gene=gene_6145 chr=SDAX010681882.1 strand=1 interval=108..419 ref-gene=Candidula_Candidula_gene-CUNI_LOCUS16438 aa=104 raa=104 score=524 prediction=0 bestScore=524 ce=1 rce=1 pAA=1 iAA=1 lpm=104 maxScore=524 maxGap=0 nps=0 start=M stop=* evidence=3 sumWeight=3.0 alternative="Candidula_Candidula_gene-CUNI_LOCUS2762,Candidula_Candidula_gene-CUNI_LOCUS2766,Lottia_Lottia_gene-LOTGIDRAFT_145439,Lottia_Lottia_gene-LOTGIDRAFT_146028,Lottia_Lottia_gene-LOTGIDRAFT_146029,Lottia_Lottia_gene-LOTGIDRAFT_146923,Lottia_Lottia_gene-LOTGIDRAFT_147261,Lottia_Lottia_gene-LOTGIDRAFT_147329,Lottia_Lottia_gene-LOTGIDRAFT_147488,Lottia_Lottia_gene-LOTGIDRAFT_147781,Lottia_Lottia_gene-LOTGIDRAFT_148042,Lottia_Lottia_gene-LOTGIDRAFT_148108,Lottia_Lottia_gene-LOTGIDRAFT_148116,Lottia_Lottia_gene-LOTGIDRAFT_148724,Lottia_Lottia_gene-LOTGIDRAFT_148824,Lottia_Lottia_gene-LOTGIDRAFT_148840,Lottia_Lottia_gene-LOTGIDRAFT_176226,Lottia_Lottia_gene-LOTGIDRAFT_176527,Lottia_Lottia_gene-LOTGIDRAFT_177025,Lottia_Lottia_gene-LOTGIDRAFT_202861,Pomacea_Pomacea	NA	All conus	Mixed

				_gene-C0Q70_13947"|Candidula_rna-CUNI_LOCUS16438_R0 gene=gene_29198 chr=JADBJO010034609.1 strand=1 interval=9334..9645 ref-gene=Candidula_gene-CUNI_LOCUS16438 aa=104 raa=104 score=524 prediction=0 bestScore=524 ce=1 rce=1 pAA=1 iAA=1 lpm=104 maxScore=524 maxGap=0 nps=0 start=M stop=* evidence=3 sumWeight=3.0 alternative="Candidula_gene-CUNI_LOCUS2762,Candidula_gene-CUNI_LOCUS2766,Lottia_gene-LOTGIDRAFT_145439,Lottia_gene-LOTGIDRAFT_146028,Lottia_gene-LOTGIDRAFT_146029,Lottia_gene-LOTGIDRAFT_146923,Lottia_gene-LOTGIDRAFT_147261,Lottia_gene-LOTGIDRAFT_147329,Lottia_gene-LOTGIDRAFT_147488,Lottia_gene-LOTGIDRAFT_147781,Lottia_gene-LOTGIDRAFT_148042,Lottia_gene-LOTGIDRAFT_148108,Lottia_gene-LOTGIDRAFT_148116,Lottia_gene-LOTGIDRAFT_148724,Lottia_gene-LOTGIDRAFT_148824,Lottia_gene-LOTGIDRAFT_148840,Lottia_gene-LOTGIDRAFT_176226,Lottia_gene-LOTGIDRAFT_176527,Lottia_gene-LOTGIDRAFT_177025,Lottia_gene-LOTGIDRAFT_202861,Pomacea_gene-C0Q70_13947"|Candidula_rna-CUNI_LOCUS16438_R0 gene=gene_6933 chr=CM031629.1 strand=-1 interval=36705754..36706065 ref-gene=Candidula_gene-CUNI_LOCUS16438 aa=104 raa=104 score=524 prediction=0 bestScore=524 ce=1 rce=1 pAA=1 iAA=1 lpm=104 maxScore=524 maxGap=0 nps=0 start=M stop=* evidence=3 sumWeight=3.0 alternative="Candidula_gene-CUNI_LOCUS2762,Candidula_gene-CUNI_LOCUS2766,Lottia_gene-LOTGIDRAFT_145439,Lottia_gene-LOTGIDRAFT_146028,Lottia_gene-LOTGIDRAFT_146029,Lottia_gene-LOTGIDRAFT_146923,Lottia_gene-LOTGIDRAFT_147261,Lottia_gene-LOTGIDRAFT_147329,Lottia_gene-LOTGIDRAFT_147488,Lottia_gene-LOTGIDRAFT_147781,Lottia_gene-			

				LOTGIDRAFT_148042,Lottia_gene-LOTGIDRAFT_148108,Lottia_gene-LOTGIDRAFT_148116,Lottia_gene-LOTGIDRAFT_148724,Lottia_gene-LOTGIDRAFT_148824,Lottia_gene-LOTGIDRAFT_148840,Lottia_gene-LOTGIDRAFT_176226,Lottia_gene-LOTGIDRAFT_176527,Lottia_gene-LOTGIDRAFT_177025,Lottia_gene-LOTGIDRAFT_202861,Pomacea_gene-C0Q70_13947"|Candidula_rna-CUNI_LOCUS16438_R1 gene=gene_28936 chr=JAFLJL010002299.1 strand=1 interval=30433..30744 ref-gene=Candidula_gene-CUNI_LOCUS16438 aa=104 raa=104 score=524 prediction=1 bestScore=524 ce=1 rce=1 pAA=1 iAA=1 lpm=104 maxScore=524 maxGap=0 nps=0 start=M stop=* evidence=3 sumWeight=3.0 alternative="Candidula_gene-CUNI_LOCUS2762,Candidula_gene-CUNI_LOCUS2766,Lottia_gene-LOTGIDRAFT_145439,Lottia_gene-LOTGIDRAFT_146028,Lottia_gene-LOTGIDRAFT_146029,Lottia_gene-LOTGIDRAFT_146923,Lottia_gene-LOTGIDRAFT_147261,Lottia_gene-LOTGIDRAFT_147329,Lottia_gene-LOTGIDRAFT_147488,Lottia_gene-LOTGIDRAFT_147781,Lottia_gene-LOTGIDRAFT_148042,Lottia_gene-LOTGIDRAFT_148108,Lottia_gene-LOTGIDRAFT_148116,Lottia_gene-LOTGIDRAFT_148724,Lottia_gene-LOTGIDRAFT_148824,Lottia_gene-LOTGIDRAFT_148840,Lottia_gene-LOTGIDRAFT_176226,Lottia_gene-LOTGIDRAFT_176527,Lottia_gene-LOTGIDRAFT_177025,Lottia_gene-LOTGIDRAFT_202861,Pomacea_gene-C0Q70_13947"|Candidula_rna-CUNI_LOCUS16438_R1 gene=gene_7861 chr=JADBJO010035468.1 strand=-1 interval=2150..2461 ref-gene=Candidula_gene-CUNI_LOCUS16438 aa=104 raa=104 score=524 prediction=1 bestScore=524 ce=1 rce=1 pAA=1 iAA=1 lpm=104 maxScore=524 maxGap=0 nps=0 start=M stop=* evidence=3 sumWeight=3.0 alternative="Candidula_gene-			

				CUNI_LOCUS2762,Candidula_gene-CUNI_LOCUS2766,Lottia_gene-LOTGIDRAFT_145439,Lottia_gene-LOTGIDRAFT_146028,Lottia_gene-LOTGIDRAFT_146029,Lottia_gene-LOTGIDRAFT_146923,Lottia_gene-LOTGIDRAFT_147261,Lottia_gene-LOTGIDRAFT_147329,Lottia_gene-LOTGIDRAFT_147488,Lottia_gene-LOTGIDRAFT_147781,Lottia_gene-LOTGIDRAFT_148042,Lottia_gene-LOTGIDRAFT_148108,Lottia_gene-LOTGIDRAFT_148116,Lottia_gene-LOTGIDRAFT_148724,Lottia_gene-LOTGIDRAFT_148824,Lottia_gene-LOTGIDRAFT_148840,Lottia_gene-LOTGIDRAFT_176226,Lottia_gene-LOTGIDRAFT_176527,Lottia_gene-LOTGIDRAFT_177025,Lottia_gene-LOTGIDRAFT_202861,Pomacea_gene-C0Q70_13947"|Candidula_rna-CUNI_LOCUS16438_R2 gene=gene_1043 chr=JADBJO010031623.1 strand=1 interval=16154..16465 ref-gene=Candidula_gene-CUNI_LOCUS16438 aa=104 raa=104 score=524 prediction=2 bestScore=524 ce=1 rce=1 pAA=1 iAA=1 lpm=104 maxScore=524 maxGap=0 nps=0 start=M stop=* evidence=3 sumWeight=3.0 alternative="Candidula_gene-CUNI_LOCUS2762,Candidula_gene-CUNI_LOCUS2766,Lottia_gene-LOTGIDRAFT_145439,Lottia_gene-LOTGIDRAFT_146028,Lottia_gene-LOTGIDRAFT_146029,Lottia_gene-LOTGIDRAFT_146923,Lottia_gene-LOTGIDRAFT_147261,Lottia_gene-LOTGIDRAFT_147329,Lottia_gene-LOTGIDRAFT_147488,Lottia_gene-LOTGIDRAFT_147781,Lottia_gene-LOTGIDRAFT_148042,Lottia_gene-LOTGIDRAFT_148108,Lottia_gene-LOTGIDRAFT_148116,Lottia_gene-LOTGIDRAFT_148724,Lottia_gene-LOTGIDRAFT_148824,Lottia_gene-LOTGIDRAFT_148840,Lottia_gene-LOTGIDRAFT_176226,Lottia_gene-LOTGIDRAFT_176527,Lottia_gene-LOTGIDRAFT_177025,Lottia_gene-LOTGIDRAFT_202861,Pomacea_gene-C0Q70_13947"|Candidula_rna-			

<table>
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				LOTGIDRAFT_148116,Lottia_gene-LOTGIDRAFT_148724,Lottia_gene-LOTGIDRAFT_148824,Lottia_gene-LOTGIDRAFT_148840,Lottia_gene-LOTGIDRAFT_176226,Lottia_gene-LOTGIDRAFT_176527,Lottia_gene-LOTGIDRAFT_177025,Lottia_gene-LOTGIDRAFT_202861,Pomacea_gene-C0Q70_13947"|Candidula_rna-CUNI_LOCUS16438_R8 gene=gene_17410 chr=JADBJO010031431.1 strand=1 interval=720..1031 ref-gene=Candidula_gene-CUNI_LOCUS16438 aa=104 raa=104 score=524 prediction=8 bestScore=524 ce=1 rce=1 pAA=1 iAA=1 lpm=104 maxScore=524 maxGap=0 nps=0 start=M stop=* evidence=3 sumWeight=3.0 alternative="Candidula_gene-CUNI_LOCUS2762,Candidula_gene-CUNI_LOCUS2766,Lottia_gene-LOTGIDRAFT_145439,Lottia_gene-LOTGIDRAFT_146028,Lottia_gene-LOTGIDRAFT_146029,Lottia_gene-LOTGIDRAFT_146923,Lottia_gene-LOTGIDRAFT_147261,Lottia_gene-LOTGIDRAFT_147329,Lottia_gene-LOTGIDRAFT_147488,Lottia_gene-LOTGIDRAFT_147781,Lottia_gene-LOTGIDRAFT_148042,Lottia_gene-LOTGIDRAFT_148108,Lottia_gene-LOTGIDRAFT_148116,Lottia_gene-LOTGIDRAFT_148724,Lottia_gene-LOTGIDRAFT_148824,Lottia_gene-LOTGIDRAFT_148840,Lottia_gene-LOTGIDRAFT_176226,Lottia_gene-LOTGIDRAFT_176527,Lottia_gene-LOTGIDRAFT_177025,Lottia_gene-LOTGIDRAFT_202861,Pomacea_gene-C0Q70_13947"|Candidula_rna-CUNI_LOCUS16438_R9 gene=gene_24450 chr=JADBJO010029231.1 strand=-1 interval=8377..8688 ref-gene=Candidula_gene-CUNI_LOCUS16438 aa=104 raa=104 score=524 prediction=9 bestScore=524 ce=1 rce=1 pAA=1 iAA=1 lpm=104 maxScore=524 maxGap=0 nps=0 start=M stop=* evidence=2 sumWeight=2.0 alternative="Candidula_gene-CUNI_LOCUS2762,Candidula_gene-CUNI_LOCUS2766,Lottia_gene-			

				LOTGIDRAFT_145439,Lottia_gene-LOTGIDRAFT_146028,Lottia_gene-LOTGIDRAFT_146029,Lottia_gene-LOTGIDRAFT_147261,Lottia_gene-LOTGIDRAFT_147329,Lottia_gene-LOTGIDRAFT_147781,Lottia_gene-LOTGIDRAFT_148042,Lottia_gene-LOTGIDRAFT_148108,Lottia_gene-LOTGIDRAFT_148116,Lottia_gene-LOTGIDRAFT_148724,Lottia_gene-LOTGIDRAFT_148840,Lottia_gene-LOTGIDRAFT_176527,Lottia_gene-LOTGIDRAFT_202861"|WGS:AMQO_5860|WGS:AMQO_5900|WGS:AMQO_6106|WGS:AMQO_6113|WGS:AMQO_6157			
CMM-I-6357	Hydroxylamine	10	TEYLPSLDPR	WGS:PZQS_4453	NA	All conus	Mixed
CMM-I-6359	Hydroxylamine	8	TEYLPSLDPR	WGS:PZQS_4453	NA	All conus	Mixed
CMM-I-6359	Hydroxylamine	8	VGMHASANCRVR	Candidula_rna-CUNI_LOCUS17455_R0 gene=gene_31283 chr=JADBJO010000403.1 strand=-1 interval=164873..176921 ref-gene=Candidula_gene-CUNI_LOCUS17455 aa=310 raa=334 score=779 prediction=0 bestScore=779 ce=10 rce=10 pAA=0.6628 iAA=0.5349 lpm=34 maxScore=1694 maxGap=16 nps=0 start=M stop=* evidence=1 sumWeight=1.0	NA	All conus	Gastropoda
CMM-I-6360	Hydroxylamine	8	TAFTSEQLLELEKEFHSK	WGS:AMQO_2050	NA	All conus	Mixed
CMM-I-6360	Hydroxylamine	8	TVSPSDKRR	Candidula_rna-CUNI_LOCUS7421_R0 gene=gene_4128 chr=CM031603.1 strand=1 interval=62239529..62252107 ref-gene=Candidula_gene-CUNI_LOCUS7421 aa=463 raa=610 score=1007 prediction=0 bestScore=1007 ce=8 rce=4 pAA=0.5703 iAA=0.4412 lpm=30 maxScore=3165 maxGap=67 nps=0 start=M stop=* evidence=1 sumWeight=1.0	NA	All conus	Mixed
CMM-I-6360	Hydroxylamine	8	LNSMSPAAQR	Candidula_rna-CUNI_LOCUS20925_R0 gene=gene_1328 chr=LFLW010252434.1 strand=-1 interval=1973..8678 ref-gene=Candidula_gene-CUNI_LOCUS20925 aa=473 raa=508 score=1149 prediction=0 bestScore=1149 ce=9 rce=9 pAA=0.6692 iAA=0.5164 lpm=15 maxScore=2604 maxGap=13 nps=0 start=M stop=* evidence=1 sumWeight=1.0|WGS:PZQS_8992	NA	All conus	Mixed
CMM-I-6359	Hydroxylamine	8	NNLNPSPGPAMPEANR	WGS:PZQS_502	NA	All conus	Gastropoda

CMM-I-6359	Hydroxylamine	8	NVDREAITMLDAK	WGS:PZQS_11854	NA	All conus	Gastropoda
CMM-I-6359	Hydroxylamine	8	TAFTSEQLLELEKEFHSK	WGS:AMQO_2050	NA	All conus	Mixed
CMM-I-6359	Hydroxylamine	8	TDITGAKISWLK	WGS:AMQO_2901|WGS:AMQO_448	NA	All conus	Gastropoda
CMM-I-6360	Hydroxylamine	8	TAQNRSSPSSTITSFQR	WGS:PZQS_13865	NA	All conus	Gastropoda
CMM-I-6360	Hydroxylamine	8	DLLFLPLCFLVGCPANVINMAVFYK	WGS:PZQS_12885	NA	All conus	Gastropoda
CMM-I-6357	Hydroxylamine	10	PSANISTR	WGS:RQTK_76	NA	All conus	Mixed
CMM-I-6360	Hydroxylamine	8	PSANISTR	WGS:RQTK_76	NA	All conus	Mixed
CMM-I-6360	Hydroxylamine	8	VGMHASANCRVR	Candidula_rna-CUNI_LOCUS17455_R0 gene=gene_31283 chr=JADBJO010000403.1 strand=-1 interval=164873..176921 ref-gene=Candidula_gene-CUNI_LOCUS17455 aa=310 raa=334 score=779 prediction=0 bestScore=779 ce=10 rce=10 pAA=0.6628 iAA=0.5349 lpm=34 maxScore=1694 maxGap=16 nps=0 start=M stop=* evidence=1 sumWeight=1.0	NA	All conus	Gastropoda
CMM-I-6360	Hydroxylamine	8	GKQEEGLGQQKR	WGS:PZQS_5954	NA	All conus	Gastropoda
CMM-I-6359	Hydroxylamine	8	VGEAAGFR	WGS:AMQO_280	NA	All conus	Mixed
CMM-I-6360	Hydroxylamine	8	VGEAAGFR	WGS:AMQO_280	NA	All conus	Mixed
CMM-I-6359	Hydroxylamine	8	SLFGDSLSSR	WGS:PZQS_2218	NA	All conus	Gastropoda
CMM-I-6359	Hydroxylamine	8	AICMRLDGLEGK	Candidula_rna-CUNI_LOCUS21787_R0 gene=gene_26062 chr=CM031609.1 strand=1 interval=31980052..32012872 ref-gene=Candidula_gene-CUNI_LOCUS21787 aa=338 raa=423 score=872 prediction=0 bestScore=872 ce=10 rce=10 pAA=0.5789 iAA=0.4943 lpm=43 maxScore=2184 maxGap=48 nps=0 start=M stop=* evidence=1 sumWeight=1.0	NA	All conus	Gastropoda
CMM-I-6357	Hydroxylamine	10	VGEAAGFR	WGS:AMQO_280	NA	All conus	Mixed
CMM-I-6359	Hydroxylamine	8	INDLKKSNQDAK	WGS:PZQS_10472	NA	All conus	Gastropoda
CMM-I-6359	Hydroxylamine	8	FITDNTVEERIVERAEMK	Candidula_Candidula_rna-CUNI_LOCUS15734_R0 gene=gene_2294 chr=SDAX010001313.1 strand=1 interval=1775..24102 ref-gene=Candidula_Candidula_gene-CUNI_LOCUS15734 aa=957 raa=1020 score=3724 prediction=0 bestScore=3724 ce=23 rce=23 pAA=0.7931 iAA=0.7267 lpm=84 maxScore=5340 maxGap=22 nps=0 start=M stop=* evidence=1 sumWeight=1.0	NA	All conus	Mixed

CMM-I-6360	Hydroxylamine	8	KAFSDSSTLTK	WGS:AMQO_1195	NA	All conus	Mixed
CMM-I-6360	Hydroxylamine	8	DVQKNLDTK	WGS:RQTK_5546	NA	All conus	Gastropoda
CMM-I-6359	Hydroxylamine	8	ENQSAESNTLKK	WGS:RQTK_2998|WGS:RQTK_4078|WGS:RQTK_4840	NA	All conus	Gastropoda
CMM-I-6357	SPEED	10	MTKGTLSANEGDIR	pomacea_rna-gnl-WGS:PZQS-C0Q70_mrna00036_R0	NA	Strombus	Gastropoda
CMM-I-6358	SPEED	10	MTKGTLSANEGDIR	pomacea_rna-gnl-WGS:PZQS-C0Q70_mrna00036_R0	NA	Strombus	Gastropoda
CMM-I-6359	SPEED	8	SVIHTDQPTTERK	elysia_rna-gnl-WGS:RQTK-Echl_20674_R4	NA	Strombus	Gastropoda
CMM-I-6358	SPEED	10	TVTDRTSAHWMTLEVKQAK	pomacea_rna-gnl-WGS:PZQS-C0Q70_mrna19955_R6	NA	Strombus	Gastropoda
CMM-I-6357	SPEED	10	NFRHLSTSVYMR	pomacea_rna-gnl-WGS:PZQS-C0Q70_mrna03906_R0	NA	Strombus	Gastropoda
CMM-I-6357	SPEED	10	HLPPGTFVDASRFETAKDLGK	pomacea_rna-gnl-WGS:PZQS-C0Q70_mrna03861_R4	NA	Strombus	Gastropoda
CMM-I-6359	SPEED	8	KEMGSYLLSYEVR	lottia_rna-XM_009046999.1_R1	NA	Strombus	Gastropoda
CMM-I-6358	SPEED	10	KSANQLLMKTLGGCLSNLIK	A0A3S1BDZ5	Exocyst complex subunit Sec15 C-terminal domain-containing protein (Fragment)	Gastropoda	Gastropoda
CMM-I-6357	SPEED	10	KQVGSTEGMQTTVMTSELMQHR	A0A2T7NGX0	Lysine--tRNA ligase	Gastropoda	Gastropoda
CMM-I-6357	SPEED	10	VFTFSKGQTMDHK	A0A8S3ZRH4	C2H2-type domain-containing protein	Gastropoda	Gastropoda
CMM-I-6357	SPEED	10	VSDFVQQINANNK	V4AWL2	DUF4592 domain-containing protein	Gastropoda	Gastropoda
CMM-I-6359	SPEED	8	VASLSPIR	A0A3S0ZMH9	PLAT domain-containing protein	Gastropoda	Mixed
CMM-I-6359	SPEED	8	SLSERLK	A0A0B6YM18	MCM AAA-lid domain-containing protein (Fragment)	Gastropoda	Mixed
CMM-I-6357	SPEED	10	HQQGPDTELFPLK	A0A433TAC1	Uncharacterized protein (Fragment)	Gastropoda	Gastropoda
CMM-I-6357	SPEED	10	KCRSLQSMMELK	A0A2C9KHY9	Uncharacterized protein	Gastropoda	Gastropoda
CMM-I-6358	SPEED	10	AREMAKIEEQQK	A0A2C9M4A7	CARD domain-containing protein	Gastropoda	Mollusca
CMM-I-6359	SPEED	8	KCRSLQSMMELK	A0A2C9KHY9	Uncharacterized protein	Gastropoda	Gastropoda
CMM-I-6358	SPEED	10	YGFIADLCLGDSGFK	A0A2C9JZT4	VWFA domain-containing protein	Gastropoda	Gastropoda
CMM-I-6357	SPEED	10	HEEERSKVDELR	A0A0B7BB55|A0A2C9K354|A0A2T7NWK6|A0A3S1BJS8|A0A8S3Z7J2|W5VJC5	AAA+ ATPase domain-containing protein|AAA+ ATPase domain-containing protein (Fragment)|26S protease regulatory	Gastropoda	Mollusca

					subunit 4-like protein (Fragment)		
CMM-I-6359	SPEED	8	YGFIADLCLGDSGFK	A0A2C9JZT4	VWFA domain-containing protein	Gastropoda	Gastropoda
CMM-I-6359	SPEED	8	QFGRGVYATEDIK	V4AK22	MYND-type domain-containing protein	Gastropoda	Gastropoda
CMM-I-6359	SPEED	8	QKKTSSSVSSPAVTSQR	A0A2T7PKU6	BTB domain-containing protein	Gastropoda	Gastropoda
CMM-I-6360	SPEED	8	PMSVEQVFTPMRSVLVLICILLMNSVVVLPICVSVYFDWSFNLDKNR	A0A2C9KN53|A0A2C9M4J1|A0A2C9KN53|A0A2C9M4J1	G-protein coupled receptors family 1 profile domain-containing protein	Gastropoda	Gastropoda
CMM-I-6359	SPEED	8	MADPTPRSLPR	A0A2T7PXR9	Uncharacterized protein	Gastropoda	Gastropoda
CMM-I-6360	SPEED	8	LEGMFKDMTVSNTINEEFK	V4AYZ2	Cullin family profile domain-containing protein	Gastropoda	Gastropoda
CMM-I-6359	SPEED	8	HTVMDLKWHHNGNWMLTASRDHLLK	A0A3S1BDQ9	Uncharacterized protein	Gastropoda	Gastropoda
CMM-I-6360	SPEED	8	AYANLMQAMWKGKNESYVSPDPFK	A0A0B6Z572	USP domain-containing protein (Fragment)	Gastropoda	Gastropoda
CMM-I-6357	SPEED	10	HVAVTMNTSMSGDKGR	A0A2T7PUJ9	Cation efflux protein cytoplasmic domain-containing protein	Gastropoda	Gastropoda
CMM-I-6359	SPEED	8	QMVNGSRTNSFNGSVDMPDFARDIK	WGS:PZQS_1451	NA	Conus betulinus	Gastropoda
CMM-I-6359	SPEED	8	ILFCPMKGTHYK	WGS:RQTK_1770	NA	Conus betulinus	Gastropoda
CMM-I-6358	SPEED	10	GLGASEQGIVDMRK	Candidula_rna-CUNI_LOCUS5061_R0 gene=gene_20016 chr=JADBJO010005870.1 strand=1 interval=77176..139055 ref-gene=Candidula_gene-CUNI_LOCUS5061 aa=714 raa=752 score=1476 prediction=0 bestScore=1476 ce=19 rce=18 pAA=0.6392 iAA=0.4906 lpm=17 maxScore=3959 maxGap=34 nps=0 start=M stop=* evidence=1 sumWeight=1.0	NA	Conus betulinus	Gastropoda
CMM-I-6357	SPEED	10	GLGASEQGIVDMRK	Candidula_rna-CUNI_LOCUS5061_R0 gene=gene_20016 chr=JADBJO010005870.1 strand=1 interval=77176..139055 ref-gene=Candidula_gene-CUNI_LOCUS5061 aa=714 raa=752 score=1476 prediction=0 bestScore=1476 ce=19 rce=18 pAA=0.6392 iAA=0.4906 lpm=17 maxScore=3959 maxGap=34 nps=0 start=M stop=* evidence=1 sumWeight=1.0	NA	Conus betulinus	Gastropoda

CMM-I-6359	SPEED	8	DPYVLLPPPPNVVDAPYSAR	WGS:AMQO_3246	NA	Conus betulinus	Gastropoda
CMM-I-6360	SPEED	8	KTAGKSEHGGTGGDFK	WGS:PZQS_5086	NA	Conus betulinus	Gastropoda
CMM-I-6357	SPEED	10	SSFQVTQYKGDNFVRLSGDAEEFAK	WGS:PZQS_5658	NA	Conus betulinus	Gastropoda
CMM-I-6357	SPEED	10	PFAAHWYVGFGFK	WGS:AMQO_2801	NA	Conus betulinus	Gastropoda
CMM-I-6357	SPEED	10	IAAPTKQK	WGS:RQTK_937	NA	Conus betulinus	Gastropoda
CMM-I-6357	SPEED	10	MTGFLSNLIQACR	WGS:PZQS_4399	NA	Conus betulinus	Gastropoda
CMM-I-6357	SPEED	10	GREGPSPQVMAMSRR	WGS:PZQS_6514	NA	Conus betulinus	Gastropoda
CMM-I-6360	SPEED	8	SSFQVTQYKGDNFVRLSGDAEEFAK	WGS:PZQS_5658	NA	Conus betulinus	Gastropoda
CMM-I-6360	SPEED	8	NSYEVMLYANKLQFENNK	WGS:PZQS_8791	NA	Conus betulinus	Gastropoda
CMM-I-6360	SPEED	8	ELGQGSFGMVYSGK	WGS:RQTK_1359	NA	Conus betulinus	Gastropoda
CMM-I-6359	SPEED	8	NRPSLPR	WGS:PZQS_1126	NA	Conus betulinus	Mixed
CMM-I-6359	SPEED	8	IAAPTKQK	WGS:RQTK_937	NA	Conus betulinus	Gastropoda
CMM-I-6357	SPEED	10	DPYVLLPPPPNVVDAPYSAR	WGS:AMQO_3246	NA	Conus betulinus	Gastropoda
CMM-I-6359	SPEED	8	TNKQTKFETSGNK	WGS:RQTK_1959	NA	Conus betulinus	Gastropoda
CMM-I-6357	SPEED	10	SANVFQGGAGGAQSWGGAR	WGS:PZQS_3647	NA	Conus betulinus	Gastropoda
CMM-I-6359	SPEED	8	GGPFNGPPDRFGGPR	WGS:PZQS_5625	NA	Conus betulinus	Gastropoda
CMM-I-6359	SPEED	8	DGGLQNMEVHGILK	WGS:AMQO_894	NA	Conus consors	Gastropoda
CMM-I-6357	SPEED	10	LLIACAAGQKGSSWECLLIK	WGS:PZQS_2302	NA	Conus consors	Gastropoda
CMM-I-6357	SPEED	10	MTGFLSNLIQACR	WGS:AMQO_254	NA	Conus consors	Gastropoda
CMM-I-6358	SPEED	10	APSYNVLISMTVTINDK APSYNVLISMTVTINDK APSYNVLISMTVTINDK	WGS:RQTK_2313	NA	Conus consors	Gastropoda
CMM-I-6359	SPEED	8	FAHIDGDHLTLLNVYHAFK	WGS:RQTK_182	NA	Conus consors	Mixed
CMM-I-6357	SPEED	10	GREGPSPQVMAMSRR	WGS:PZQS_143	NA	Conus consors	Gastropoda
CMM-I-6360	SPEED	8	TIVMNFSQVMFAELDSETK	WGS:AMQO_1035	NA	Conus consors	Gastropoda
CMM-I-6358	SPEED	10	LLIACAAGQKGSSWECLLIK	WGS:PZQS_2302	NA	Conus consors	Gastropoda
CMM-I-6360	SPEED	8	APSYNVLISMTVTINDK APSYNVLISMTVTINDK APSYNVLISMTVTINDK	WGS:RQTK_2313	NA	Conus consors	Gastropoda
CMM-I-6357	SPEED	10	SAPSMKNYTSIALK	WGS:PZQS_2969	NA	Conus consors	Gastropoda
CMM-I-6357	SPEED	10	GEVGDWKNYLTVAQSERLDAAMTLLK	WGS:PZQS_1723	NA	Conus tribblei	Gastropoda
CMM-I-6360	SPEED	8	DLADQAKDDEAAK	Candidula_rna-CUNI_LOCUS16253_R0	NA	Conus tribblei	Gastropoda

				gene=gene_10232 chr=LFLW010006165.1 strand=-1 interval=1121..11865 ref-gene=Candidula_gene-CUNI_LOCUS16253 aa=296 raa=299 score=939 prediction=0 bestScore=939 ce=6 rce=6 pAA=0.7826 iAA=0.6355 lpm=17 maxScore=1516 maxGap=2 nps=0 start=M stop=* evidence=2 sumWeight=2.0 alternative="Elysia_gene-EGW08_017459"			
CMM-I-6357	SPEED	10	CTPLLAALMYRVSSMIIK	WGS:PZQS_1296	NA	Conus tribblei	Gastropoda
CMM-I-6360	SPEED	8	PSHPQSPLNSNHQHAHRPQGTQPDR	Candidula_rna-CUNI_LOCUS18204_R0 gene=gene_642 chr=LFLW010228811.1 strand=-1 interval=87..3322 ref-gene=Candidula_gene-CUNI_LOCUS18204 aa=822 raa=823 score=1213 prediction=0 bestScore=1213 ce=2 rce=2 pAA=0.6086 iAA=0.3914 lpm=29 maxScore=4290 maxGap=29 nps=0 start=M stop=* evidence=1 sumWeight=1.0	NA	Conus tribblei	Gastropoda
CMM-I-6357	SPEED	10	ELEAHNAITFAKRLEDFR	WGS:PZQS_2674	NA	Conus tribblei	Gastropoda
CMM-I-6358	SPEED	10	KNDPHNPLELTDSR	Candidula_rna-CUNI_LOCUS14918_R0 gene=gene_10655 chr=LFLW010411421.1 strand=1 interval=691..4590 ref-gene=Candidula_gene-CUNI_LOCUS14918 aa=172 raa=153 score=519 prediction=0 bestScore=519 ce=3 rce=3 pAA=0.7093 iAA=0.5698 lpm=17 maxScore=853 maxGap=19 nps=0 start=M stop=* evidence=2 sumWeight=2.0 alternative="Lottia_gene-LOTGIDRAFT_228377"	NA	Conus tribblei	Gastropoda
CMM-I-6358	SPEED	10	WTSPHAVAFLDKTESK	Candidula_rna-CUNI_LOCUS21112_R0 gene=gene_2267 chr=LFLW010892047.1 strand=1 interval=353..3429 ref-gene=Candidula_gene-CUNI_LOCUS21112 aa=191 raa=193 score=330 prediction=0 bestScore=330 ce=5 rce=5 pAA=0.6587 iAA=0.4279 lpm=29 maxScore=1010 maxGap=11 nps=0 start=M stop=* evidence=1 sumWeight=1.0	NA	Conus tribblei	Gastropoda
CMM-I-6359	SPEED	8	KNDPHNPLELTDSR	Candidula_rna-CUNI_LOCUS14918_R0 gene=gene_10655 chr=LFLW010411421.1 strand=1 interval=691..4590 ref-gene=Candidula_gene-CUNI_LOCUS14918 aa=172 raa=153 score=519 prediction=0 bestScore=519 ce=3 rce=3 pAA=0.7093 iAA=0.5698 lpm=17 maxScore=853 maxGap=19 nps=0 start=M stop=* evidence=2 sumWeight=2.0 alternative="Lottia_gene-	NA	Conus tribblei	Gastropoda

				LOTGIDRAFT_228377"			
CMM-I-6358	SPEED	10	ADMTGKGLKGDLDR	WGS:PZQS_4367|WGS:PZQS_4368|WGS:PZQS_4369	NA	Conus tribblei	Gastropoda
CMM-I-6357	SPEED	10	KYFSGFSMRSSTK	WGS:RQTK_573	NA	Conus tribblei	Gastropoda
CMM-I-6359	SPEED	8	SLTDPGDGHVLGTTR	WGS:PZQS_4456	NA	Conus tribblei	Mollusca
CMM-I-6357	SPEED	10	SLTDPGDGHVLGTTR	WGS:PZQS_4456	NA	Conus tribblei	Mollusca
CMM-I-6359	SPEED	8	FPLASHSLSAPIEFVITGWTAEMTDLAK	WGS:PZQS_2220	NA	Conus tribblei	Gastropoda
CMM-I-6357	SPEED	10	FPRIYACATMWHETETEMAQLLK	WGS:AMQO_76	NA	Conus ventricosus	Gastropoda
CMM-I-6358	SPEED	10	NPTKWSSKLHNFVESCLIK	WGS:PZQS_10151	NA	Conus ventricosus	Gastropoda
CMM-I-6358	SPEED	10	QEKQASGSRATSAR	WGS:PZQS_7090	NA	Conus ventricosus	Gastropoda
CMM-I-6358	SPEED	10	KGSLTAESLVDGGAK	WGS:PZQS_2037	NA	Conus ventricosus	Gastropoda
CMM-I-6357	SPEED	10	TSLTGHKTSMTGQK	WGS:AMQO_3507	NA	Conus ventricosus	Gastropoda
CMM-I-6357	SPEED	10	QYGKSAGSGHVSEQQK	WGS:PZQS_4403	NA	Conus ventricosus	Gastropoda
CMM-I-6357	SPEED	10	KMTPRGNGPGHSEK	WGS:AMQO_5620	NA	Conus ventricosus	Gastropoda
CMM-I-6357	SPEED	10	KGSLTAESLVDGGAK	WGS:PZQS_2037	NA	Conus ventricosus	Gastropoda
CMM-I-6360	SPEED	8	PSANISTR	WGS:RQTK_76	NA	Conus ventricosus	Mixed
CMM-I-6359	SPEED	8	STQVMTSMQQLIK	WGS:AMQO_829	NA	Conus ventricosus	Gastropoda
CMM-I-6359	SPEED	8	FAHIDGDHLTLLNVYHAFK	WGS:PZQS_1759|WGS:RQTK_1014	NA	Conus ventricosus	Mixed
CMM-I-6357	SPEED	10	GREGPSPQVMAMSRR	WGS:PZQS_4130	NA	Conus ventricosus	Gastropoda
CMM-I-6360	SPEED	8	QYGKSAGSGHVSEQQK	WGS:PZQS_4403	NA	Conus ventricosus	Gastropoda
CMM-I-6357	SPEED	10	LTKCEQGYATVEK	WGS:RQTK_5555	NA	Conus ventricosus	Gastropoda
CMM-I-6360	SPEED	8	ELGQGSFGMVYSGK	WGS:RQTK_2448	NA	Conus ventricosus	Gastropoda
CMM-I-6359	SPEED	8	NRPSLPR	WGS:PZQS_1667	NA	Conus ventricosus	Mixed
CMM-I-6358	SPEED	10	SQTSFIDVFITTCIFSINTSKGVIK	WGS:PZQS_3969	NA	Conus ventricosus	Gastropoda
CMM-I-6357	SPEED	10	SPTKWMSSANILK	WGS:RQTK_4310	NA	Conus ventricosus	Gastropoda
CMM-I-6358	SPEED	10	DSLMTLSLVKYADLFITMSLVLCHDSLMTLSLVKYADLFITMSLVLCR	WGS:RQTK_4926	NA	Conus ventricosus	Gastropoda
CMM-I-6359	SPEED	8	EEILSTSPYASVFYDVIHDSEIERLK	WGS:PZQS_5300	NA	Conus ventricosus	Gastropoda
CMM-I-6360	SPEED	8	TGRSNNTGTAYTFFTPSNANK	WGS:RQTK_53	NA	Conus ventricosus	Gastropoda
CMM-I-6357	SPEED	10	CRASTICVHNDHLYGTEFTQR	Candidula_rna-CUNI_LOCUS8306_R2 gene=gene_12745 chr=CM031616.1 strand=-1 interval=45119490..45123913 ref-gene=Candidula_gene-	NA	Conus ventricosus	Gastropoda

				CUNI_LOCUS8306 aa=693 raa=742 score=629 prediction=2 bestScore=645 ce=4 rce=4 pAA=0.5442 iAA=0.283 lpm=9 maxScore=3938 maxGap=14 nps=0 start=M stop=* evidence=1 sumWeight=1.0			
CMM-I-6359	SPEED	8	GHLLHLSSSADGAAALMK	WGS:PZQS_2965	NA	Conus ventricosus	Gastropoda
CMM-I-6359	SPEED	8	QMVNGSRTNSFNGSVDMPDFARDIK	WGS:PZQS_1451	NA	All conus	Gastropoda
CMM-I-6357	SPEED	10	GEVGDWKNYLTVAQSERLDAAMTLLK	WGS:PZQS_1723	NA	All conus	Gastropoda
CMM-I-6357	SPEED	10	GLGASEQGIVDMRK	Candidula_rna-CUNI_LOCUS5061_R0 gene=gene_20016 chr=JADBJO010005870.1 strand=1 interval=77176..139055 ref-gene=Candidula_gene-CUNI_LOCUS5061 aa=714 raa=752 score=1476 prediction=0 bestScore=1476 ce=19 rce=18 pAA=0.6392 iAA=0.4906 lpm=17 maxScore=3959 maxGap=34 nps=0 start=M stop=* evidence=1 sumWeight=1.0	NA	All conus	Gastropoda
CMM-I-6357	SPEED	10	QYGKSAGSGHVSEQQK	WGS:PZQS_4403	NA	All conus	Gastropoda
CMM-I-6357	SPEED	10	LLIACAAGQKGSSWECLLIK	WGS:PZQS_2302	NA	All conus	Gastropoda
CMM-I-6358	SPEED	10	GLGASEQGIVDMRK	Candidula_rna-CUNI_LOCUS5061_R0 gene=gene_20016 chr=JADBJO010005870.1 strand=1 interval=77176..139055 ref-gene=Candidula_gene-CUNI_LOCUS5061 aa=714 raa=752 score=1476 prediction=0 bestScore=1476 ce=19 rce=18 pAA=0.6392 iAA=0.4906 lpm=17 maxScore=3959 maxGap=34 nps=0 start=M stop=* evidence=1 sumWeight=1.0	NA	All conus	Gastropoda
CMM-I-6360	SPEED	8	KTAGKSEHGGTGGDFK	WGS:PZQS_5086	NA	All conus	Gastropoda
CMM-I-6357	SPEED	10	KMTPRGNGPGHSEK	WGS:AMQO_5620	NA	All conus	Gastropoda
CMM-I-6360	SPEED	8	PSANISTR	WGS:RQTK_76	NA	All conus	Mixed
CMM-I-6358	SPEED	10	WTSPHAVAFLDKTESK	Candidula_rna-CUNI_LOCUS21112_R0 gene=gene_2267 chr=LFLW010892047.1 strand=1 interval=353..3429 ref-gene=Candidula_gene-CUNI_LOCUS21112 aa=191 raa=193 score=330 prediction=0 bestScore=330 ce=5 rce=5 pAA=0.6587 iAA=0.4279 lpm=29 maxScore=1010 maxGap=11 nps=0 start=M stop=* evidence=1 sumWeight=1.0	NA	All conus	Gastropoda

CMM-I-6359	SPEED	8	STQVMTSMQQLIK	WGS:AMQO_829	NA	All conus	Gastropoda
CMM-I-6359	SPEED	8	FAHIDGDHLTLLNVYHAFK	WGS:PZQS_1759|WGS:RQTK_1014|WGS:RQTK_182|WGS:RQTK_310	NA	All conus	Mixed
CMM-I-6357	SPEED	10	GREGPSPQVMAMSRR	WGS:PZQS_4130	NA	All conus	Gastropoda
CMM-I-6360	SPEED	8	QYGKSAGSGHVSEQQK	WGS:PZQS_4403	NA	All conus	Gastropoda
CMM-I-6357	SPEED	10	LTKCEQGYATVEK	WGS:RQTK_5555	NA	All conus	Gastropoda
CMM-I-6360	SPEED	8	ELGQGSFGMVYSGK	WGS:RQTK_2448	NA	All conus	Gastropoda
CMM-I-6359	SPEED	8	NRPSLPR	WGS:PZQS_1667	NA	All conus	Mixed
CMM-I-6358	SPEED	10	SQTSFIDVFITTCIFSINTSKGVIK	WGS:PZQS_3969	NA	All conus	Gastropoda
CMM-I-6357	SPEED	10	STQVMTSMQQLIK	WGS:AMQO_829	NA	All conus	Gastropoda
CMM-I-6358	SPEED	10	DSLMTLSLVKYADLFITMSLVLCHDSLMTLSLVKYADLFITMSLVLCR	WGS:RQTK_4926	NA	All conus	Gastropoda
CMM-I-6360	SPEED	8	TGRSNNTGTAYTFFTPSNANK	WGS:RQTK_53	NA	All conus	Gastropoda
CMM-I-6357	SPEED	10	CRASTICVHNDHLYGTEFTQR	Candidula_rna-CUNI_LOCUS8306_R2 gene=gene_12745 chr=CM031616.1 strand=-1 interval=45119490..45123913 ref-gene=Candidula_gene-CUNI_LOCUS8306 aa=693 raa=742 score=629 prediction=2 bestScore=645 ce=4 rce=4 pAA=0.5442 iAA=0.283 lpm=9 maxScore=3938 maxGap=14 nps=0 start=M stop=* evidence=1 sumWeight=1.0	NA	All conus	Gastropoda
CMM-I-6359	SPEED	8	GHLLHLSSSADGAAALMK	WGS:PZQS_2965	NA	All conus	Gastropoda

Table S2. Sequence coverage in percentage of each shell and extraction based on the length of the comparison protein.

Accession and Database	CMM-I-6357-hydroxylamine	CMM-I-6358-hydroxylamine	CMM-I-6359-hydroxylamine	CMM-I-6360-hydroxylamine	CMM-I-6357-SPEED	CMM-I-6358-SPEED	CMM-I-6359-SPEED	CMM-I-6360-SPEED
A0A2C9LTC8 Gastropoda	0.50398992	0.50398992						
A0A2C9LTG9 Gastropoda	0.804289544							
A0A2C9M4A7 Gastropoda	1.03626943					1.03626943		
A0A3S1B970 Gastropoda	5.098039216							
A0A433TWG4 Gastropoda	0.665983607							
A0A8S3Z172 Gastropoda	2.903225806							
Candidula_Candidula_rna-CUNI_LOCUS12334_R0 gene=gene_7061 chr=SDAX010000281.1 strand=1 interval=94..14398 ref-gene=Candidula_Candidula_gene-CUNI_LOCUS12334 aa=336 raa=450 score=362 prediction=0 bestScore=362 ce=13 rce=15 pAA=0.4844 iAA=0.3289 lpm=15 maxScore=2262 maxGap=44 nps=0 start=M stop=* evidence=1 sumWeight=1.0 Conus consors	4.166666667			4.166666667				
Candidula_rna-CUNI_LOCUS15157_R1 gene=gene_22751 chr=JADBJO010000831.1 strand=-1 interval=650..5041 ref-gene=Candidula_gene-CUNI_LOCUS15157 aa=341 raa=389 score=735 prediction=1 bestScore=1067 ce=7 rce=5 pAA=0.5837 iAA=0.4593 lpm=25 maxScore=1990 maxGap=32 nps=0 start=M stop=* evidence=1 sumWeight=1.0 Conus betulinus	6.451612903							
Candidula_rna-CUNI_LOCUS17455_R0 gene=gene_31283 chr=JADBJO010000403.1 strand=-1 interval=164873..176921 ref-gene=Candidula_gene-CUNI_LOCUS17455 aa=310 raa=334 score=779 prediction=0 bestScore=779 ce=10 rce=10 pAA=0.6628 iAA=0.5349 lpm=34 maxScore=1694 maxGap=16 nps=0 start=M stop=* evidence=1	3.870967742		3.870967742	3.870967742				

sumWeight=1.0 Conus betulinus								
Candidula_rna-CUNI_LOCUS21112_R0 gene=gene_2267 chr=LFLW010892047.1 strand=1 interval=353..3429 ref-gene=Candidula_gene-CUNI_LOCUS21112 aa=191 raa=193 score=330 prediction=0 bestScore=330 ce=5 rce=5 pAA=0.6587 iAA=0.4279 lpm=29 maxScore=1010 maxGap=11 nps=0 start=M stop=* evidence=1 sumWeight=1.0 Conus tribblei	6.282722513					8.376963351		
V4ABZ9 Gastropoda	0.436241611	0.637583893	0.436241611	0.436241611				
V4AP49 Gastropoda	5.113636364							
V4AWL2 Gastropoda	1.593137255				1.593137255			
WGS:AMQO_1606 Conus tribblei	12.26415094							
WGS:AMQO_1799 Conus tribblei	8.552631579							
WGS:AMQO_2079 Conus betulinus	4.777070064							
WGS:AMQO_556 Conus consors	4.281345566							
WGS:PZQS_11854 Conus betulinus	0.894085282		0.894085282					
WGS:PZQS_12031 Conus betulinus	2.083333333		2.083333333					
WGS:PZQS_1417 Conus consors	1.312910284							
WGS:PZQS_1585 Conus consors	4.416403785			4.416403785				
WGS:PZQS_1822 Conus tribblei	5.019305019							
WGS:PZQS_190 Conus consors	1.608910891							
WGS:PZQS_2426 Conus tribblei	3.274559194							
WGS:PZQS_2432 Conus tribblei	5.761316872			5.761316872				
WGS:PZQS_3007 Conus ventricosus	1.388888889							
WGS:PZQS_3634 Conus tribblei	2.195121951							
WGS:PZQS_394 Conus betulinus	3.365384615							
WGS:PZQS_6033 Conus betulinus	11.47540984							
WGS:PZQS_669 Conus consors	2.285714286							
WGS:PZQS_750 Conus betulinus	0.722021661		0.722021661	0.722021661				
WGS:PZQS_858 Conus ventricosus	3.218390805							
WGS:RQTK_1384 Conus tribblei	2.922077922	2.922077922	2.922077922	2.922077922				

WGS:RQTK_1409 Conus betulinus	2.686567164	2.686567164	2.686567164	2.686567164				
WGS:RQTK_2442 Conus tribblei	5.882352941	5.882352941						
WGS:RQTK_2998 Conus betulinus	4.87804878		4.87804878					
WGS:RQTK_3897 Conus betulinus	0.627240143							
WGS:RQTK_4240 Conus betulinus	4.237288136	4.237288136		4.237288136				
WGS:RQTK_4436 Conus ventricosus	2.950819672			2.950819672				
WGS:RQTK_4740 Conus betulinus	12			12				
canidula_rna-CUNI_LOCUS6705_R1 Strombus								
elysia_rna-gnl-WGS:RQTK-Echl_13966_R0 Strombus								
lottia_rna-XM_009067640.1_R0 Strombus								
pomacea_rna-gnl-WGS:PZQS-C0Q70_mrna01606_R6 Strombus								
pomacea_rna-gnl-WGS:PZQS-C0Q70_mrna02610_R0 Strombus								
pomacea_rna-gnl-WGS:PZQS-C0Q70_mrna18766_R1 Strombus								
WGS:AMQO_1153 Conus consors		17.54385965						
WGS:PZQS_6446 Conus betulinus		1.733102253						
WGS:PZQS_9524 Conus ventricosus		2.824858757						
WGS:RQTK_5223 Conus ventricosus		8.256880734						
A0A0B7BSL6 Gastropoda			2.786377709					
A0A1R7T094 Gastropoda			2.946954813	2.946954813				
A0A2C9K8F3 Gastropoda			0.35971223					
A0A2C9KRC2 Gastropoda			6.302521008	6.302521008				
A0A2C9KSI9 Gastropoda			3.086419753					
A0A2C9LXF9 Gastropoda			1.785714286					
A0A2T7NFW9 Gastropoda			0.112693372	0.112693372				
A0A2T7NXN1 Gastropoda			0.303122158					
A0A2T7NYB1 Gastropoda			0.084301236	0.084301236				
A0A2T7P0R4 Gastropoda			1.867816092					
A0A2T7P9J8 Gastropoda			0.712328767					
A0A2T7PE22 Gastropoda			1.401273885					
A0A2T7PMJ5 Gastropoda			0.647773279					
A0A2T7PX67 Gastropoda			1.778907243					

A0A433U182 Gastropoda			5.660377358					
A0A8S3YDX0 Gastropoda			1.386138614					
A0A8S4A6G9 Gastropoda			0.892244338					
Candidula_Candidula_rna-CUNI_LOCUS15080_R1 gene=gene_2446 chr=SDAX010066343.1 strand=1 interval=292..5405 ref-gene=Candidula_Candidula_gene-CUNI_LOCUS15080 aa=249 raa=251 score=237 prediction=1 bestScore=259 ce=4 rce=5 pAA=0.55 iAA=0.275 lpm=13 maxScore=1359 maxGap=23 nps=0 start=M stop=* evidence=1 sumWeight=1.0 Conus consors			4.016064257					
Candidula_Candidula_rna-CUNI_LOCUS15734_R0 gene=gene_2294 chr=SDAX010001313.1 strand=1 interval=1775..24102 ref-gene=Candidula_Candidula_gene-CUNI_LOCUS15734 aa=957 raa=1020 score=3724 prediction=0 bestScore=3724 ce=23 rce=23 pAA=0.7931 iAA=0.7267 lpm=84 maxScore=5340 maxGap=22 nps=0 start=M stop=* evidence=1 sumWeight=1.0 Conus consors			1.880877743					
Candidula_Candidula_rna-CUNI_LOCUS16438_R0 gene=gene_6145 chr=SDAX010681882.1 strand=1 interval=108..419 ref-gene=Candidula_Candidula_gene-CUNI_LOCUS16438 aa=104 raa=104 score=524 prediction=0 bestScore=524 ce=1 rce=1 pAA=1 iAA=1 lpm=104 maxScore=524 maxGap=0 nps=0 start=M stop=* evidence=3 sumWeight=3.0 alternative="Candidula_Candidula_gene-CUNI_LOCUS2762,Candidula_Candidula_gene-CUNI_LOCUS2766,Lottia_Lottia_gene-LOTGIDRAFT_145439,Lottia_Lottia_gene-LOTGIDRAFT_146028,Lottia_Lottia_g			11.53846154					

ene-LOTGIDRAFT_146029,Lottia_Lottia_gene-LOTGIDRAFT_146923,Lottia_Lottia_gene-LOTGIDRAFT_147261,Lottia_Lottia_gene-LOTGIDRAFT_147329,Lottia_Lottia_gene-LOTGIDRAFT_147488,Lottia_Lottia_gene-LOTGIDRAFT_147781,Lottia_Lottia_gene-LOTGIDRAFT_148042,Lottia_Lottia_gene-LOTGIDRAFT_148108,Lottia_Lottia_gene-LOTGIDRAFT_148116,Lottia_Lottia_gene-LOTGIDRAFT_148724,Lottia_Lottia_gene-LOTGIDRAFT_148824,Lottia_Lottia_gene-LOTGIDRAFT_148840,Lottia_Lottia_gene-LOTGIDRAFT_176226,Lottia_Lottia_gene-LOTGIDRAFT_176527,Lottia_Lottia_gene-LOTGIDRAFT_177025,Lottia_Lottia_gene-LOTGIDRAFT_202861,Pomacea_Pomacea_gene-C0Q70_13947" Conus consors								
Candidula_Candidula_rna-CUNI_LOCUS18549_R0 gene=gene_6044 chr=SDAX010001501.1 strand=1 interval=9058..10659 ref-gene=Candidula_Candidula_gene-CUNI_LOCUS18549 aa=534 raa=627 score=1104 prediction=0 bestScore=1104 ce=1 rce=1 pAA=0.6086 iAA=0.4105 lpm=18 maxScore=3370 maxGap=23 nps=0 start=M stop=* evidence=3 sumWeight=3.0 alternative="Elysia_Elysia_gene-EGW08_004074,Lottia_Lottia_gene-LOTGIDRAFT_114344" Conus consors			1.872659176					
Candidula_Candidula_rna-CUNI_LOCUS22262_R0			0.382513661					

gene=gene_11411 chr=SDAX010012142.1 strand=-1 interval=2476..11611 ref-gene=Candidula_Candidula_gene-CUNI_LOCUS22262 aa=1830 raa=1885 score=2300 prediction=0 bestScore=2300 ce=7 rce=8 pAA=0.5758 iAA=0.3567 lpm=36 maxScore=9614 maxGap=59 nps=0 start=M stop=* evidence=1 sumWeight=1.0 Conus consors								
Candidula_Candidula_rna-CUNI_LOCUS848_R0 gene=gene_1382 chr=SDAX010011036.1 strand=-1 interval=9932..10723 ref-gene=Candidula_Candidula_gene-CUNI_LOCUS848 aa=264 raa=199 score=256 prediction=0 bestScore=256 ce=1 rce=1 pAA=0.5243 iAA=0.3221 lpm=13 maxScore=1027 maxGap=22 nps=0 start=M stop=* evidence=2 sumWeight=2.0 alternative="Elysia_Elysia_gene-EGW08_003279" Conus consors			3.03030303	3.03030303				
Candidula_rna-CUNI_LOCUS10160_R7 gene=gene_31647 chr=JADBJO010000089.1 strand=-1 interval=1036047..1037338 ref-gene=Candidula_gene-CUNI_LOCUS10160 aa=86 raa=70 score=104 prediction=7 bestScore=130 ce=2 rce=2 pAA=0.5341 iAA=0.3523 lpm=6 maxScore=369 maxGap=18 nps=0 start=M stop=* evidence=1 sumWeight=1.0 Conus betulinus			8.139534884	8.139534884				
Candidula_rna-CUNI_LOCUS10700_R1 gene=gene_19679 chr=JADBJO010001434.1 strand=1 interval=213940..236256 ref-gene=Candidula_gene-CUNI_LOCUS10700 aa=255 raa=268 score=426 prediction=1 bestScore=626 ce=5 rce=5 pAA=0.5113 iAA=0.3537 lpm=14 maxScore=1460 maxGap=40 nps=0 start=M stop=* evidence=1 sumWeight=1.0 Conus betulinus			5.490196078					

Candidula_rna-CUNI_LOCUS15019_R0 gene=gene_5770 chr=LFLW010034030.1 strand=-1 interval=7063..9525 ref-gene=Candidula_gene-CUNI_LOCUS15019 aa=167 raa=103 score=129 prediction=0 bestScore=129 ce=2 rce=2 pAA=0.4251 iAA=0.2754 lpm=9 maxScore=548 maxGap=24 nps=0 start=M stop=* evidence=2 sumWeight=2.0 alternative="Candidula_gene-CUNI_LOCUS15021,Elysia_gene-EGW08_009932" Conus tribblei			7.185628743					
Candidula_rna-CUNI_LOCUS15984_R0 gene=gene_30307 chr=JADBJO010000413.1 strand=1 interval=74446..133271 ref-gene=Candidula_gene-CUNI_LOCUS15984 aa=930 raa=1736 score=1188 prediction=0 bestScore=1188 ce=18 rce=15 pAA=0.3673 iAA=0.2721 lpm=20 maxScore=9201 maxGap=347 nps=0 start=M stop=* evidence=1 sumWeight=1.0 Conus betulinus			1.505376344					
Candidula_rna-CUNI_LOCUS16115_R4 gene=gene_1316 chr=LFLW010161969.1 strand=-1 interval=5240..5722 ref-gene=Candidula_gene-CUNI_LOCUS16115 aa=161 raa=155 score=158 prediction=4 bestScore=313 ce=1 rce=1 pAA=0.6894 iAA=0.3354 lpm=10 maxScore=866 maxGap=3 nps=0 start=M stop=* evidence=1 sumWeight=1.0 Conus tribblei			6.211180124					
Candidula_rna-CUNI_LOCUS16438_R0 gene=gene_29198 chr=JADBJO010034609.1 strand=1 interval=9334..9645 ref-gene=Candidula_gene-CUNI_LOCUS16438 aa=104 raa=104 score=524 prediction=0 bestScore=524 ce=1 rce=1 pAA=1 iAA=1 lpm=104 maxScore=524			11.53846154					

maxGap=0 nps=0 start=M stop=* evidence=3 sumWeight=3.0 alternative="Candidula_gene-CUNI_LOCUS2762,Candidula_gene-CUNI_LOCUS2766,Lottia_gene-LOTGIDRAFT_145439,Lottia_gene-LOTGIDRAFT_146028,Lottia_gene-LOTGIDRAFT_146029,Lottia_gene-LOTGIDRAFT_146923,Lottia_gene-LOTGIDRAFT_147261,Lottia_gene-LOTGIDRAFT_147329,Lottia_gene-LOTGIDRAFT_147488,Lottia_gene-LOTGIDRAFT_147781,Lottia_gene-LOTGIDRAFT_148042,Lottia_gene-LOTGIDRAFT_148108,Lottia_gene-LOTGIDRAFT_148116,Lottia_gene-LOTGIDRAFT_148724,Lottia_gene-LOTGIDRAFT_148824,Lottia_gene-LOTGIDRAFT_148840,Lottia_gene-LOTGIDRAFT_176226,Lottia_gene-LOTGIDRAFT_176527,Lottia_gene-LOTGIDRAFT_177025,Lottia_gene-LOTGIDRAFT_202861,Pomacea_gene-C0Q70_13947" Conus betulinus								
Candidula_rna-CUNI_LOCUS16438_R0 gene=gene_6933 chr=CM031629.1 strand=-1 interval=36705754..36706065 ref-gene=Candidula_gene-CUNI_LOCUS16438 aa=104 raa=104 score=524 prediction=0 bestScore=524 ce=1 rce=1 pAA=1 iAA=1 lpm=104 maxScore=524 maxGap=0 nps=0 start=M stop=* evidence=3 sumWeight=3.0 alternative="Candidula_gene-CUNI_LOCUS2762,Candidula_gene-CUNI_LOCUS2766,Lottia_gene-LOTGIDRAFT_145439,Lottia_gene-LOTGIDRAFT_146028,Lottia_gene-LOTGIDRAFT_146029,Lottia_gene-LOTGIDRAFT_146923,Lottia_gene-LOTGIDRAFT_147261,Lottia_gene-LOTGIDRAFT_147329,Lottia_gene-LOTGIDRAFT_147488,Lottia_gene-LOTGIDRAFT_147781,Lottia_gene-LOTGIDRAFT_148042,Lottia_gene-LOTGIDRAFT_148108,Lottia_gene-LOTGIDRAFT_148116,Lottia_gene-LOTGIDRAFT_148724,Lottia_gene-LOTGIDRAFT_148824,Lottia_gene-			11.65048544					

LOTGIDRAFT_148840,Lottia_gene-LOTGIDRAFT_176226,Lottia_gene-LOTGIDRAFT_176527,Lottia_gene-LOTGIDRAFT_177025,Lottia_gene-LOTGIDRAFT_202861,Pomacea_gene-C0Q70_13947" Conus ventricosus								
Candidula_rna-CUNI_LOCUS18549_R0 gene=gene_526 chr=LFLW010274540.1 strand=-1 interval=2443..4053 ref-gene=Candidula_gene-CUNI_LOCUS18549 aa=537 raa=627 score=1102 prediction=0 bestScore=1102 ce=1 rce=1 pAA=0.6044 iAA=0.4082 lpm=18 maxScore=3370 maxGap=23 nps=0 start=M stop=* evidence=3 sumWeight=3.0 alternative="Elysia_gene-EGW08_004074,Lottia_gene-LOTGIDRAFT_114344" Conus tribblei			1.862197393					
Candidula_rna-CUNI_LOCUS19021_R0 gene=gene_5119 chr=JADBJO010000239.1 strand=1 interval=3881..29794 ref-gene=Candidula_gene-CUNI_LOCUS19021 aa=696 raa=763 score=1033 prediction=0 bestScore=1033 ce=17 rce=18 pAA=0.6015 iAA=0.3729 lpm=24 maxScore=3991 maxGap=20 nps=0 start=M stop=* evidence=1 sumWeight=1.0 Conus betulinus			1.58045977	1.58045977				
Candidula_rna-CUNI_LOCUS19432_R6 gene=gene_3249 chr=LFLW010485785.1 strand=-1 interval=855..1232 ref-gene=Candidula_gene-CUNI_LOCUS19432 aa=126 raa=125 score=101 prediction=6 bestScore=148 ce=1 rce=1 pAA=0.6742 iAA=0.2273 lpm=12 maxScore=752 maxGap=7 nps=0 start=M stop=* evidence=1 sumWeight=1.0 Conus tribblei			11.9047619					
Candidula_rna-CUNI_LOCUS20322_R1 gene=gene_17905 chr=CM031618.1 strand=-1			2.380952381					

interval=54165824..54167869 ref-gene=Candidula_gene-CUNI_LOCUS20322 aa=336 raa=349 score=681 prediction=1 bestScore=685 ce=2 rce=2 pAA=0.68 iAA=0.42 lpm=18 maxScore=1835 maxGap=11 nps=0 start=M stop=* evidence=1 sumWeight=1.0 Conus ventricosus								
Candidula_rna-CUNI_LOCUS20925_R0 gene=gene_1328 chr=LFLW010252434.1 strand=-1 interval=1973..8678 ref-gene=Candidula_gene-CUNI_LOCUS20925 aa=473 raa=508 score=1149 prediction=0 bestScore=1149 ce=9 rce=9 pAA=0.6692 iAA=0.5164 lpm=15 maxScore=2604 maxGap=13 nps=0 start=M stop=* evidence=1 sumWeight=1.0 Conus tribblei			2.114164905	2.114164905				
Candidula_rna-CUNI_LOCUS419_R0 gene=gene_10627 chr=JADBJO010006747.1 strand=-1 interval=83911..93393 ref-gene=Candidula_gene-CUNI_LOCUS419 aa=276 raa=320 score=691 prediction=0 bestScore=691 ce=6 rce=5 pAA=0.591 iAA=0.4806 lpm=16 maxScore=1685 maxGap=25 nps=0 start=M stop=* evidence=1 sumWeight=1.0 Conus betulinus			3.272727273					
Candidula_rna-CUNI_LOCUS7421_R0 gene=gene_4128 chr=CM031603.1 strand=1 interval=62239529..62252107 ref-gene=Candidula_gene-CUNI_LOCUS7421 aa=463 raa=610 score=1007 prediction=0 bestScore=1007 ce=8 rce=4 pAA=0.5703 iAA=0.4412 lpm=30 maxScore=3165 maxGap=67 nps=0 start=M stop=* evidence=1 sumWeight=1.0 Conus ventricosus			1.943844492					
Candidula_rna-CUNI_LOCUS7435_R0 gene=gene_763 chr=LFLW010099223.1 strand=1 interval=4584..12160 ref-gene=Candidula_gene-CUNI_LOCUS7435 aa=580 raa=594			2.068965517					

score=1408 prediction=0 bestScore=1408 ce=5 rce=6 pAA=0.6517 iAA=0.4859 lpm=14 maxScore=3148 maxGap=19 nps=0 start=M stop=* evidence=2 sumWeight=2.0 alternative="Elysia_gene-EGW08_002624" Conus tribblei								
Candidula_rna-CUNI_LOCUS889_R5 gene=gene_14137 chr=JADBJO010000294.1 strand=1 interval=714006..720699 ref-gene=Candidula_gene-CUNI_LOCUS889 aa=514 raa=493 score=628 prediction=5 bestScore=761 ce=7 rce=3 pAA=0.5767 iAA=0.3457 lpm=12 maxScore=2559 maxGap=22 nps=0 start=M stop=* evidence=1 sumWeight=1.0 alternative="Candidula_gene-CUNI_LOCUS891" Conus betulinus			2.33463035					
WGS:AMQO_1386 Conus tribblei			6.425702811					
WGS:AMQO_1386 Conus ventricosus			8.301886792					
WGS:AMQO_1813 Conus consors			1.720430108					
WGS:AMQO_1837 Conus consors			10.49382716					
WGS:AMQO_1848 Conus consors			3.973509934					
WGS:AMQO_2050 Conus betulinus			11.76470588	11.76470588				
WGS:AMQO_232 Conus consors			7.028753994					
WGS:AMQO_244 Conus ventricosus			0.323275862					
WGS:AMQO_3280 Conus ventricosus			5.281690141					
WGS:AMQO_3443 Conus ventricosus			0.388953715	0.388953715				
WGS:AMQO_410 Conus betulinus			4.411764706					
WGS:AMQO_4183 Conus betulinus			2.264150943					
WGS:AMQO_4830 Conus betulinus			3.010033445					
WGS:AMQO_5188 Conus ventricosus			7.01754386	7.01754386				
WGS:AMQO_678 Conus ventricosus			3.365384615					
WGS:AMQO_686 Conus tribblei			9.696969697	9.696969697				
WGS:AMQO_748 Conus betulinus			1.990049751					
WGS:AMQO_792 Conus betulinus			1.587301587					
WGS:PZQS_10017 Conus betulinus			1.146601147					

WGS:PZQS_1005 Conus tribblei			2.803738318					
WGS:PZQS_10472 Conus betulinus			1.492537313					
WGS:PZQS_10520 Conus betulinus			3.100775194					
WGS:PZQS_10604 Conus ventricosus			1.465201465					
WGS:PZQS_11545 Conus betulinus			3.703703704	3.703703704				
WGS:PZQS_1196 Conus tribblei			7.339449541					
WGS:PZQS_1289 Conus consors			0.800915332					
WGS:PZQS_1443 Conus ventricosus			2.368421053	2.368421053				
WGS:PZQS_1478 Conus consors			5.985915493					
WGS:PZQS_1676 Conus tribblei			5.128205128					
WGS:PZQS_2022 Conus betulinus			5.069124424					
WGS:PZQS_2213 Conus betulinus			0.693909021	0.693909021				
WGS:PZQS_2776 Conus tribblei			1.275917065					
WGS:PZQS_2840 Conus tribblei			5.128205128					
WGS:PZQS_3029 Conus betulinus			3.314917127					
WGS:PZQS_304 Conus tribblei			12.5					
WGS:PZQS_3130 Conus consors			1.670644391					
WGS:PZQS_3374 Conus tribblei			1.016260163					
WGS:PZQS_346 Conus betulinus			0.788091068					
WGS:PZQS_3512 Conus betulinus			0.925925926					
WGS:PZQS_3515 Conus tribblei			2.508960573					
WGS:PZQS_3524 Conus tribblei			2.481389578	2.481389578				
WGS:PZQS_3571 Conus tribblei			0.636435959	0.636435959				
WGS:PZQS_3880 Conus consors			4.6875					
WGS:PZQS_5025 Conus betulinus			0.666222518					
WGS:PZQS_532 Conus tribblei			1.408450704					
WGS:PZQS_544 Conus betulinus			0.687285223	0.687285223				
WGS:PZQS_5575 Conus betulinus			1.239669421					
WGS:PZQS_575 Conus consors			1.081081081					
WGS:PZQS_5787 Conus ventricosus			8.938547486	8.938547486				
WGS:PZQS_6244 Conus ventricosus			0.526546731					
WGS:PZQS_7111 Conus ventricosus			1.744966443					
WGS:PZQS_7282 Conus betulinus			0.676982592					

WGS:PZQS_7546 Conus betulinus			1.486199575					
WGS:PZQS_8143 Conus betulinus			0.823421775					
WGS:PZQS_9032 Conus betulinus			5.743243243					
WGS:PZQS_9398 Conus ventricosus			0.616197183					
WGS:PZQS_99 Conus tribblei			3.100775194	3.100775194				
WGS:RQTK_1073 Conus tribblei			0.538358008					
WGS:RQTK_1119 Conus tribblei			7.913669065					
WGS:RQTK_1123 Conus tribblei			1.952277657	1.952277657				
WGS:RQTK_1543 Conus tribblei			12.22707424					
WGS:RQTK_158 Conus consors			13.13868613					
WGS:RQTK_1667 Conus consors			1.941747573					
WGS:RQTK_1892 Conus tribblei			3.791469194					
WGS:RQTK_2024 Conus tribblei			2.745995423					
WGS:RQTK_2223 Conus tribblei			6.349206349	6.349206349				
WGS:RQTK_36 Conus consors			2.011494253					
WGS:RQTK_362 Conus tribblei			1.666666667					
WGS:RQTK_4326 Conus betulinus			1.260504202					
WGS:RQTK_469 Conus consors			2.102803738	2.102803738				
WGS:RQTK_5546 Conus ventricosus			1.587301587					
WGS:RQTK_588 Conus tribblei			8.936170213					
WGS:RQTK_76 Conus ventricosus			1.324503311					1.324503311
WGS:RQTK_828 Conus consors			2.849002849					
elysia_rna-gnl-WGS:RQTK-Echl_15544_R3 Strombus								
lottia_rna-XM_009047100.1_R0 Strombus								
lottia_rna-XM_009054189.1_R5 Strombus								
lottia_rna-XM_009067641.1_R0 Strombus								
pomacea_rna-gnl-WGS:PZQS-C0Q70_mrna01933_R0 Strombus								
pomacea_rna-gnl-WGS:PZQS-C0Q70_mrna03174_R9 Strombus								
pomacea_rna-gnl-WGS:PZQS-C0Q70_mrna06558_R0 Strombus								
pomacea_rna-gnl-WGS:PZQS-C0Q70_mrna10487_R0 Strombus								

pomacea_rna-gnl-WGS:PZQS-C0Q70_mrna16344_R0 Strombus								
pomacea_rna-gnl-WGS:PZQS-C0Q70_mrna16880_R0 Strombus								
A0A2C9JF75 Gastropoda				2.570093458				
A0A2C9KFM6 Gastropoda				0.481637568				
A0A3S0ZQ02 Gastropoda				0.741962077				
A0A3S1B8F9 Gastropoda				1.971830986				
A0A433SZ38 Gastropoda				1.842105263				
A0A433TAQ0 Gastropoda				1.392111369				
A0A433U8D9 Gastropoda				4.646017699				
Candidula_Candidula_rna-CUNI_LOCUS14076_R1 gene=gene_11046 chr=SDAX010077650.1 strand=-1 interval=512..3249 ref-gene=Candidula_Candidula_gene-CUNI_LOCUS14076 aa=124 raa=205 score=189 prediction=1 bestScore=625 ce=3 rce=3 pAA=0.43 iAA=0.3333 lpm=19 maxScore=1096 maxGap=27 nps=0 start=M stop=* evidence=1 sumWeight=1.0 Conus consors				5.64516129				
Candidula_rna-CUNI_LOCUS802_R6 gene=gene_1757 chr=LFLW010588647.1 strand=1 interval=792..6038 ref-gene=Candidula_gene-CUNI_LOCUS802 aa=284 raa=396 score=450 prediction=6 bestScore=725 ce=9 rce=8 pAA=0.5352 iAA=0.3769 lpm=25 maxScore=2055 maxGap=34 nps=0 start=M stop=* evidence=1 sumWeight=1.0 Conus tribblei				7.042253521				
V4ADN6 Gastropoda				2.116402116				
WGS:AMQO_1785 Conus consors				5.095541401				
WGS:AMQO_1977 Conus consors				7.638888889				
WGS:AMQO_241 Conus consors				1.879699248				
WGS:AMQO_2426 Conus tribblei				7.638888889				
WGS:AMQO_3262 Conus ventricosus				0.56831098				
WGS:AMQO_509 Conus tribblei				3.925233645				

WGS:AMQO_510 Conus ventricosus				2.950819672				
WGS:AMQO_552 Conus consors				5.288461538				
WGS:AMQO_729 Conus consors				3.52				
WGS:PZQS_1067 Conus ventricosus				1.642512077				
WGS:PZQS_1083 Conus tribblei				5.154639175				
WGS:PZQS_12885 Conus betulinus				7.911392405				
WGS:PZQS_13865 Conus betulinus				9.139784946				
WGS:PZQS_1667 Conus consors				1.192842942				
WGS:PZQS_2460 Conus consors				3.636363636				
WGS:PZQS_2473 Conus tribblei				1.25				
WGS:PZQS_2600 Conus tribblei				2.857142857				
WGS:PZQS_4028 Conus tribblei				5.241935484				
WGS:PZQS_4511 Conus tribblei				4.924242424				
WGS:PZQS_502 Conus ventricosus				3.245436105				
WGS:PZQS_5098 Conus betulinus				1.512455516				
WGS:PZQS_550 Conus tribblei				10.18518519				
WGS:PZQS_571 Conus tribblei				6.432748538				
WGS:PZQS_5954 Conus betulinus				4.189435337				
WGS:PZQS_870 Conus consors				1.323529412				
WGS:PZQS_8785 Conus ventricosus				1.014656144				
WGS:RQTK_1182 Conus betulinus				1.807228916				
WGS:RQTK_482 Conus tribblei				5.303030303				
WGS:RQTK_701 Conus betulinus				1.806239737				
lottia_rna-XM_009048959.1_R1 Strombus								
lottia_rna-XM_009054684.1_R0 Strombus								
pomacea_rna-gnl-WGS:PZQS-C0Q70_mrna05328_R5 Strombus								
pomacea_rna-gnl-WGS:PZQS-C0Q70_mrna14120_R1 Strombus								
pomacea_rna-gnl-WGS:PZQS-C0Q70_mrna15801_R6 Strombus								
pomacea_rna-gnl-WGS:PZQS-C0Q70_mrna15946_R0 Strombus								
A0A0B7BB55 Gastropoda					2.721088435			
A0A2C9KHY9 Gastropoda					3.217158177		3.217158177	

A0A2T7NGX0 Gastropoda					2.256410256			
A0A2T7PUJ9 Gastropoda					3.319502075			
A0A433TAC1 Gastropoda					0.512820513			
A0A8S3ZRH4 Gastropoda					0.726256983			
Candidula_rna-CUNI_LOCUS5061_R0 gene=gene_20016 chr=JADBJO010005870.1 strand=1 interval=77176..139055 ref-gene=Candidula_gene-CUNI_LOCUS5061 aa=714 raa=752 score=1476 prediction=0 bestScore=1476 ce=19 rce=18 pAA=0.6392 iAA=0.4906 lpm=17 maxScore=3959 maxGap=34 nps=0 start=M stop=* evidence=1 sumWeight=1.0 Conus betulinus					1.960784314	1.960784314		
Candidula_rna-CUNI_LOCUS8306_R2 gene=gene_12745 chr=CM031616.1 strand=-1 interval=45119490..45123913 ref-gene=Candidula_gene-CUNI_LOCUS8306 aa=693 raa=742 score=629 prediction=2 bestScore=645 ce=4 rce=4 pAA=0.5442 iAA=0.283 lpm=9 maxScore=3938 maxGap=14 nps=0 start=M stop=* evidence=1 sumWeight=1.0 Conus ventricosus					3.03030303			
WGS:AMQO_254 Conus consors					1.759133965			
WGS:AMQO_2801 Conus betulinus					1.949025487			
WGS:AMQO_3246 Conus betulinus					3.875968992		3.875968992	
WGS:AMQO_3507 Conus ventricosus					8.092485549			
WGS:AMQO_5620 Conus ventricosus					5.204460967			
WGS:AMQO_76 Conus ventricosus					2.705882353			
WGS:PZQS_1296 Conus tribblei					5.732484076			
WGS:PZQS_143 Conus consors					1.762632197			
WGS:PZQS_1723 Conus tribblei					23.21428571			
WGS:PZQS_2037 Conus ventricosus					1.479289941	1.479289941		
WGS:PZQS_2302 Conus consors					2.877697842	2.877697842		
WGS:PZQS_2674 Conus tribblei					4.245283019			
WGS:PZQS_2969 Conus consors					3.317535545			

WGS:PZQS_3647 Conus betulinus					1.539708266			
WGS:PZQS_4130 Conus ventricosus					1.794258373			
WGS:PZQS_4399 Conus betulinus					1.522248244			
WGS:PZQS_4403 Conus ventricosus					1.142857143			1.142857143
WGS:PZQS_4456 Conus tribblei					15.95744681		15.95744681	
WGS:PZQS_5658 Conus betulinus					4.208754209			4.208754209
WGS:PZQS_6514 Conus betulinus					1.785714286			
WGS:RQTK_4310 Conus ventricosus					1.96969697			
WGS:RQTK_5555 Conus ventricosus					2.086677368			
WGS:RQTK_573 Conus tribblei					1.833568406			
WGS:RQTK_937 Conus betulinus					4.14507772		4.14507772	
pomacea_rna-gnl-WGS:PZQS-C0Q70_mrna00036_R0 Strombus					19.71830986	19.71830986		
pomacea_rna-gnl-WGS:PZQS-C0Q70_mrna03861_R4 Strombus					12.96296296			
pomacea_rna-gnl-WGS:PZQS-C0Q70_mrna03906_R0 Strombus					5.217391304			
A0A2C9JZT4 Gastropoda						4.178272981	4.178272981	
A0A3S1BDZ5 Gastropoda						2.322880372		
Candidula_rna-CUNI_LOCUS14918_R0 gene=gene_10655 chr=LFLW010411421.1 strand=1 interval=691..4590 ref-gene=Candidula_gene-CUNI_LOCUS14918 aa=172 raa=153 score=519 prediction=0 bestScore=519 ce=3 rce=3 pAA=0.7093 iAA=0.5698 lpm=17 maxScore=853 maxGap=19 nps=0 start=M stop=* evidence=2 sumWeight=2.0 alternative="Lottia_gene-LOTGIDRAFT_228377" Conus tribblei						8.139534884	8.139534884	
WGS:PZQS_10151 Conus ventricosus						2.564102564		
WGS:PZQS_3969 Conus ventricosus						4.970178926		
WGS:PZQS_4367 Conus tribblei						3.636363636		
WGS:PZQS_7090 Conus ventricosus						2.456140351		
WGS:RQTK_2313 Conus consors						68.91891892		68.91891892
WGS:RQTK_4926 Conus ventricosus						41.02564103		

pomacea_rna-gnl-WGS:PZQS-C0Q70_mrna19955_R6 Strombus						16.23931624		
A0A0B6YM18 Gastropoda							4.964539007	
A0A2T7PKU6 Gastropoda							0.752212389	
A0A2T7PXR9 Gastropoda							2.716049383	
A0A3S0ZMH9 Gastropoda							0.361500226	
A0A3S1BDQ9 Gastropoda							2.083333333	
V4AK22 Gastropoda							1.780821918	
WGS:AMQO_829 Conus ventricosus							5.882352941	
WGS:AMQO_894 Conus consors							3.526448363	
WGS:PZQS_1126 Conus betulinus							1.949860724	
WGS:PZQS_1451 Conus betulinus							1.588310038	
WGS:PZQS_1667 Conus ventricosus							1.703163017	
WGS:PZQS_1759 Conus ventricosus							3.58490566	
WGS:PZQS_2220 Conus tribblei							9.655172414	
WGS:PZQS_2965 Conus ventricosus							1.41955836	
WGS:PZQS_5300 Conus ventricosus							3.951367781	
WGS:PZQS_5625 Conus betulinus							3.092783505	
WGS:RQTK_1770 Conus betulinus							2.625820569	
WGS:RQTK_182 Conus consors							2.631578947	
WGS:RQTK_1959 Conus betulinus							3.52303523	
elysia_rna-gnl-WGS:RQTK-Echl_20674_R4 Strombus							6.735751295	
lottia_rna-XM_009046999.1_R1 Strombus							17.80821918	
A0A0B6Z572 Gastropoda								14.37125749
A0A2C9KN53 Gastropoda								16.43356643
Candidula_rna-CUNI_LOCUS16253_R0 gene=gene_10232 chr=LFLW010006165.1 strand=-1 interval=1121..11865 ref-gene=Candidula_gene-CUNI_LOCUS16253 aa=296 raa=299 score=939 prediction=0 bestScore=939 ce=6 rce=6 pAA=0.7826 iAA=0.6355 lpm=17 maxScore=1516 maxGap=2 nps=0 start=M stop=* evidence=2								4.391891892

sumWeight=2.0 alternative="Elysia_gene-EGW08_017459" Conus tribblei								
Candidula_rna-CUNI_LOCUS18204_R0 gene=gene_642 chr=LFLW010228811.1 strand=-1 interval=87..3322 ref-gene=Candidula_gene-CUNI_LOCUS18204 aa=822 raa=823 score=1213 prediction=0 bestScore=1213 ce=2 rce=2 pAA=0.6086 iAA=0.3914 lpm=29 maxScore=4290 maxGap=29 nps=0 start=M stop=* evidence=1 sumWeight=1.0 Conus tribblei								3.04136253
V4AYZ2 Gastropoda								2.480417755
WGS:AMQO_1035 Conus consors								3.718199609
WGS:PZQS_5086 Conus betulinus								2.182810368
WGS:PZQS_8791 Conus betulinus								2.275600506
WGS:RQTK_1359 Conus betulinus								1.157981803
WGS:RQTK_2448 Conus ventricosus								2.287581699
WGS:RQTK_53 Conus ventricosus								4.259634888

Table S3. Deamidation levels by sample and extraction type. Mean percent value for glutamine (Q) and asparagine (N) with one standard deviation included.

Accession	SampleType	NCBI match	Qdeam mean ± stdev	Ndeam mean ± stdev	Qcount	Ncount
CMM-I-6357	Hydroxylamine	Gastropoda	13 ± 29	0 ± 0	54	117
CMM-I-6357	Hydroxylamine	Mixed	33 ± 0	NA	36	6
CMM-I-6357	Hydroxylamine	Mollusca	NA	NA	2	0
CMM-I-6357	SPEED	Gastropoda	5 ± 15	6 ± 24	50	21
CMM-I-6357	SPEED	Mollusca	NA	NA	0	0
CMM-I-6358	Hydroxylamine	Gastropoda	NA	0 ± 0	4	6
CMM-I-6358	Hydroxylamine	Mixed	NA	NA	11	2
CMM-I-6358	Hydroxylamine	Mollusca	NA	NA	0	0
CMM-I-6358	SPEED	Gastropoda	0 ± 0	0 ± 0	11	19
CMM-I-6358	SPEED	Mollusca	0 ± 0	NA	6	0
CMM-I-6359	Hydroxylamine	Gastropoda	40 ± 49	18 ± 35	132	132
CMM-I-6359	Hydroxylamine	Mixed	0 ± 0	0 ± 0	82	62
CMM-I-6359	Hydroxylamine	Mollusca	NA	NA	1	0
CMM-I-6359	SPEED	Gastropoda	10 ± 31	9 ± 30	31	30
CMM-I-6359	SPEED	Mixed	NA	100 ± 0	0	6
CMM-I-6359	SPEED	Mollusca	NA	NA	0	0
CMM-I-6360	Hydroxylamine	Gastropoda	6 ± 21	1 ± 8	51	82
CMM-I-6360	Hydroxylamine	Mixed	10 ± 16	0 ± 0	41	21
CMM-I-6360	SPEED	Gastropoda	4 ± 14	0 ± 0	31	29
CMM-I-6360	SPEED	Mixed	NA	NA	0	2

Table S4. Gastropoda-only Proteins and genes used for Panther analysis.

NCBI BLAST protein result	Gene
melanopsin	OPN4
cartilage matrix protein-like	MATN1
coiled-coil domain-containing protein 62	CCDC62
RNA binding motif protein, X-linked	Rbmxl1
Bg selectin 1	
nucleoprotein TPR	TPR
muscle m-line assembly protein unc-89/obscurin	OBSCN
G-protein coupled receptor 98	GPR98
cullin-3	CUL3
catalase	CAT
similar to ubiquitin carboxyl-terminal hydrolase 2	USP2
exocyst complex component	Exoc
coiled-coil domain-containing protein 157	CCDC157
titin homolog	ttn-1
diphosphomevalonate decarboxylase	MVD
matches nothing similar to MORN repeat containing protein 1	MORN1
cytochrome P450	CYP1A2
Protein BANP-like	Banp
Low-density lipoprotein receptor-related protein 2	LRP2
Serine/threonine-protein phosphatase 6 regulatory ankyrin repeat subunit C-like	ANKRD52
Coatomer subunit delta-like	ARCN1
splicing factor ESS-2 homolog	ESS2
Formyl peptide receptor-related sequence 6-like	Fpr-s6
phosphatidylinositol 4-kinase alpha-like	PI4KA
Prolyl 4-hydroxylase	P4H1
Vitamin D3 receptor	VDR
Molluscan insulin-related peptide receptor	PTHR24416
TPA_inf: venom-related protein PPI	
FAST kinase domain-containing protein 1, mitochondrial-like	FASTKD1
kelch-like protein 36	KLHL36
Chitin synthase chs-2-like	CHS2
YTH domain-containing protein 1-like	YTHDF1
dnaJ homolog subfamily C member 30, mitochondrial-like	DNAJC30
Sulfotransferase 1A1-like	SULT1A1
heterogeneous nuclear ribonucleoprotein L-like	Hnrnpl
Calcium homeostasis endoplasmic reticulum protein-like	CHERP
constitutive coactivator of PPAR-gamma-like protein 1 homolog	fam120a
magnesium transporter NIPA2-like	NIPA2

nuclear speckle splicing regulatory protein 1	NSRP1
PiggyBac transposable element-derived protein 4-like	PGBD1
neural-cadherin	CadN
Apoptosis inhibitor 5-like	API5
beta-1,4-galactosyltransferase 2	B4galt2
tensin-1-like	TNS1
zinc finger protein Xfin	XFIN
Reverse transcriptase domain-containing protein	
bifunctional apoptosis regulator	Bfar
PE-PGRS family protein PE_PGRS30-like	PE_PGRS30
zinc finger protein 236-like	ZNF236
F-box and leucine-rich repeat protein 3	Fbxl3
Steroid dehydrogenase	Ke6
Reverse transcriptase	
ankyrin-1	ANK1
zinc finger protein 251-like	ZNF251
translin-associated protein X	TSNAX
tyrosine-protein phosphatase 99A-like	Ptp99A
coiled-coil domain-containing protein 166	Ccdc166
Mitogen-activated protein kinase kinase kinase kinase 4-like	MAPKKK4
leucine-rich repeat protein lrrA-like	lrrA
Tetratricopeptide repeat protein 21B	TTC21B
Nucleolin-like	NUCL1
dynein axonemal heavy chain 5-like	DNAH5
E3 ubiquitin-protein ligase Rnf220-like	Rnf220
gamma-tubulin complex component 5	TUBGCP5
proteoglycan 4-like	PRG4
immunoglobulin-like domain protein	
TOG array regulator of axonemal microtubules protein 1-like	Togaram1
putative ammonium transporter 1	
cysteine-rich motor neuron 1 protein	CRIM1
mitochondrial inner membrane m-AAA protease component AFG3L2-like	AFG3L2
Zinc finger swim domain-containing protein 1	Zswim1
myosin-10	MYH10
zinc finger protein aebp2-like	AEBP2
angiopoietin-2	ANGPT2
Whirlin	WHRN
high affinity cAMP-specific and IBMX-insensitive 3',5'-cyclic phosphodiesterase 8B-like	Pde8b
pre-mRNA-splicing factor SLU7-like	SLU7
protein unc-79 homolog	UNC79
Charged multivesicular body protein 3	CHMP3

serine/threonine-protein kinase unc-51-like	unc-51
polypeptide N-acetylgalactosaminyltransferase 1-like	Galnt1
peptidyl-prolyl cis-trans isomerase G-like	Ppig
probable ATP-dependent RNA helicase DDX5	DDX5
Adenylate cyclase type 9-like	ADCY9
cytosolic phospholipase A2	PLA2G4A
autophagy protein 12-like	ATG12
Eukaryotic translation initiation factor 3 subunit A-like	Eif3a
Cell surface hyaluronidase-like	Cemip2
replicase polyprotein 1a	1a
mitogen-activated protein kinase kinase kinase 4	MAPKKK4

Table S5. Specific Raman peak frequencies by sample from spectra in Figures 6, S1-S3.

Sample	Peak Frequencies
CMM-I-6357 Internal	1085 cm^{-1} 705 cm^{-1} 206 cm^{-1} 152 cm^{-1}
CMM-I-6357 External	1087 cm^{-1} 713 cm^{-1} 281 cm^{-1} 155 cm^{-1}
CMM-I-6358 Internal	1085 cm^{-1} 704 cm^{-1} 206 cm^{-1} 152 cm^{-1}
CMM-I-6358 External	1086 cm^{-1} 713 cm^{-1} 282 cm^{-1} 157 cm^{-1}
CMM-I-6359 Internal	1085 cm^{-1} 705 cm^{-1} 206 cm^{-1} 153 cm^{-1}
CMM-I-6359 External	1086 cm^{-1} 713 cm^{-1} 281 cm^{-1} 155 cm^{-1}
CMM-I-6360 Internal	1088 cm^{-1} 1080 cm^{-1} 705 cm^{-1} 206 cm^{-1} 153 cm^{-1}
CMM-I-6360 External	1088 cm^{-1} 1084 cm^{-1} 713 cm^{-1} 281 cm^{-1} 155 cm^{-1}

Table S6. Gastropod-specific Overlapping peptides between the Little Cove Point Member and Windmill Point Member *Ecphora* shells.

Base Sequence	NCBI Match
AAASPMRAKTASDK	matches nothing
AKDYPEDNLFQEAR	Uncharacterized protein
APSYNVLISMTVTINDKAPSYNVLISMTVTINDKAPSYNVLISMTVTINDK	Uncharacterized protein
DPYVLLPPPPNVVDAPYSAR	Uncharacterized protein
ENQSAESNTLKK	Hypothetical protein
IAAPTKQK	PiggyBac transposable element-derived protein 4-like
IVCGNRFTNNAAK	hypothetical protein
KCRSLQSMMELK	uncharacterized protein
KNDPHNPLELTDSR	Steroid dehydrogenase
NASNFNSAVFKAAK	matches nothing
NVDREAITMLDAK	Tetratricopeptide repeat protein 21B
PGLPRDNTMAVTAK	Nucleolin-like
QITPFTSAGANNNK	immunoglobulin-like domain protein
QYGKSAGSGHVSEQQK	Hypothetical protein
SHDLNNKFIDK	myosin-10
SLLTPTGGGGGGGGGGGK	Uncharacterized protein
SLSFKSHSR	Uncharacterized protein
SPSSATGKER	Whirlin
SSFQVTQYKGDNFVRLSGDAEEFAK	pre-mRNA-splicing factor SLU7-like
STQVMTSMQQLIK	Charged multivesicular body protein 3
VGMHASANCRVR	replicase polyprotein 1a
YGFIADLCLGDSGFK	cartilage matrix protein-like

Figure S1. Muricoid gastropod Ecphora gardnerae (CMM-I-6357; Bed 23 Little Cove Point Member of the St. Marys Formation, Miocene, Maryland, USA) Raman spectrum of internal (blue) and external (black) surfaces. a is peaks for aragonite, c is calcite. Black arrow indicates possible calcite peak on the internal surface.

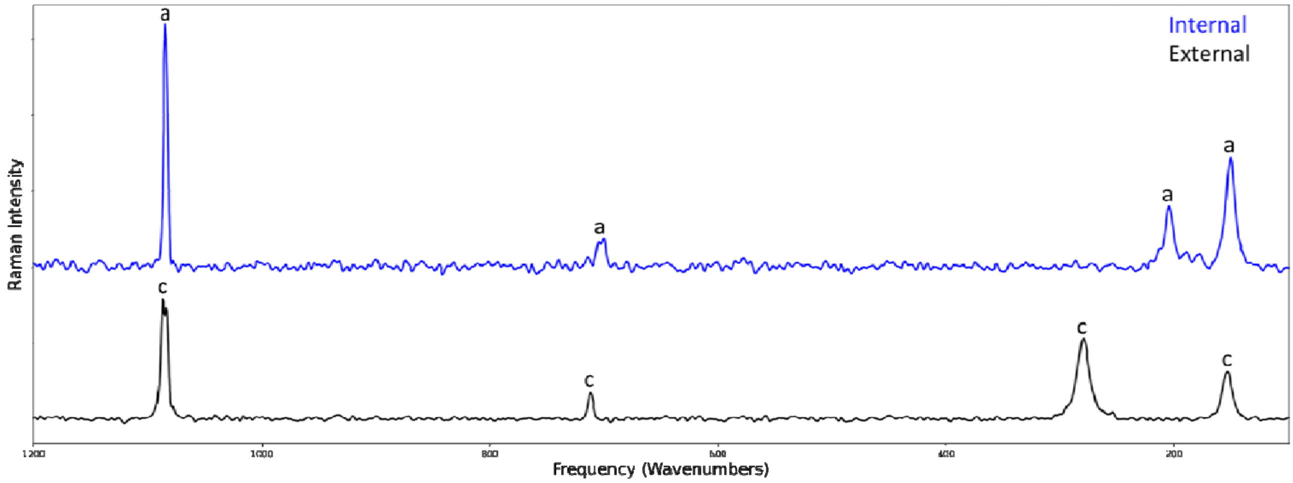

Figure S2. Muricoid gastropod Ecphora gardnerae (CMM-I-6359 Bed 24 Windmill Point Member of the St. Marys Formation, Miocene, Maryland, USA) Raman spectrum of internal (blue) and external (black) surfaces. a is peaks for aragonite, c is calcite. Black arrow indicates possible calcite peak on the internal surface.

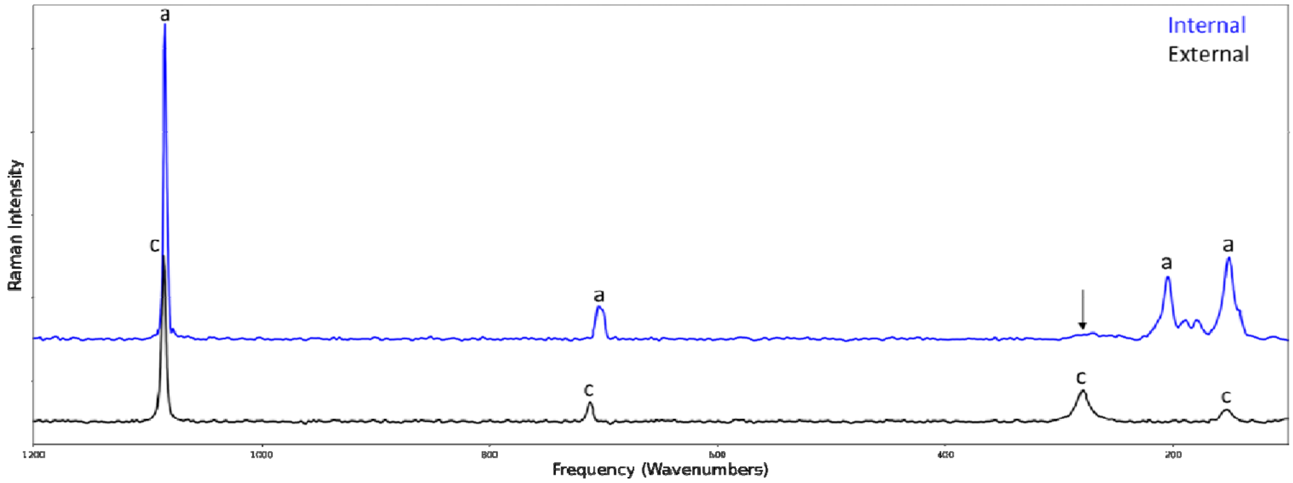

Figure S3. Muricoid gastropod Ecphora gardnerae (CMM-I-6360 Bed 24 Windmill Point Member of the St. Marys Formation, Miocene, Maryland, USA) Raman spectrum of internal (blue) and external (black) surfaces. a is peaks for aragonite, c is calcite. Black arrow indicates possible calcite peak on the internal surface.

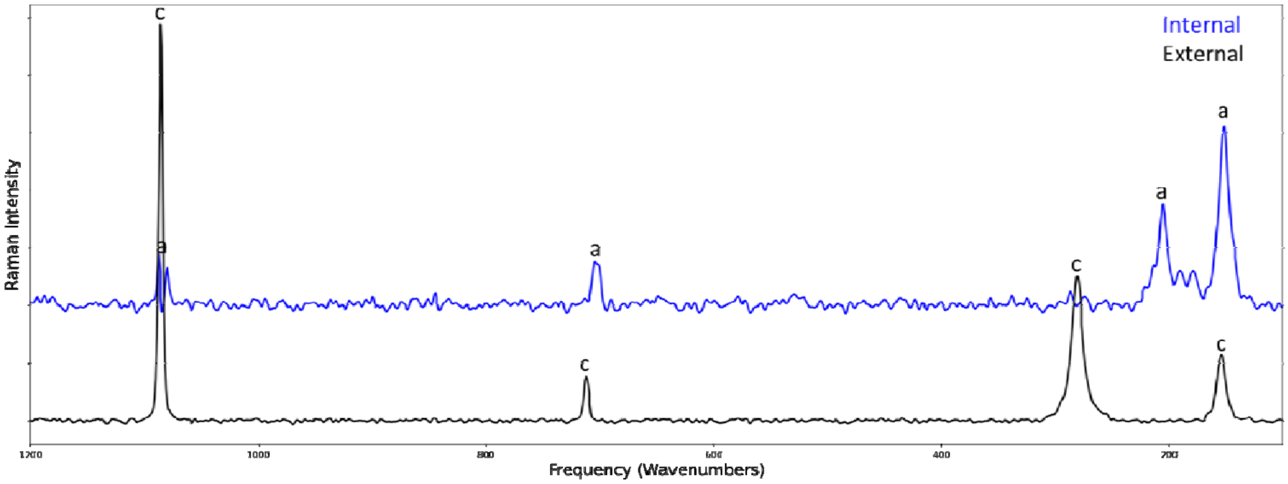

Figure S4. Example of internal (A) and external surface (B) from the Muricoid gastropod Ecphora gardnerae (CMM-I-6357; Bed 23 Little Cove Point Member of the St. Marys Formation, Miocene, Maryland, USA). Similar appearance was visibile for the other shells as well.

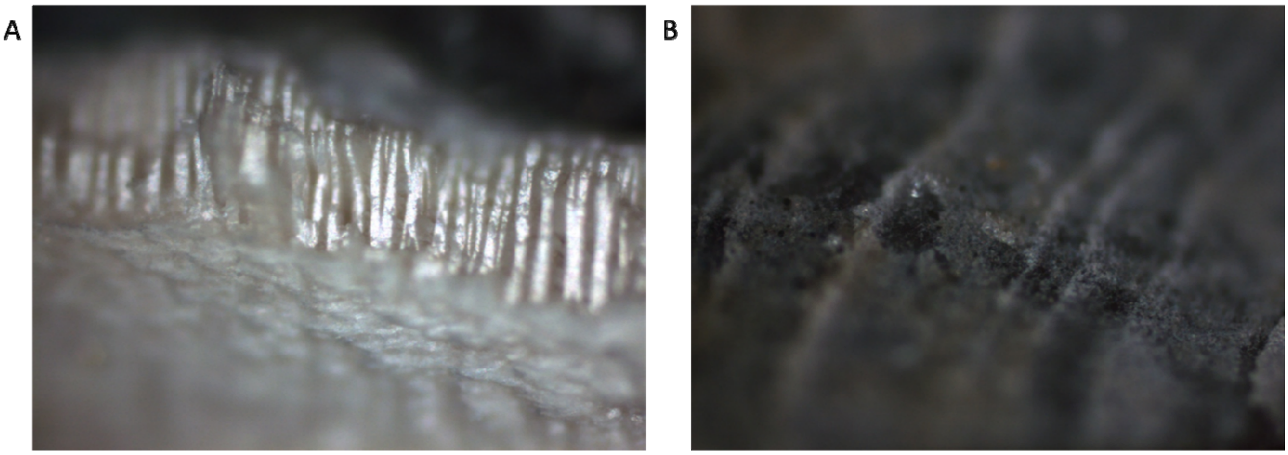

Figure S5. Raman spectra of non-*Ecphora* turritellid shells from the Little Cove Member (10 Ma; top) and Windmill Point Member (8 Ma; bottom) showing only aragonite.

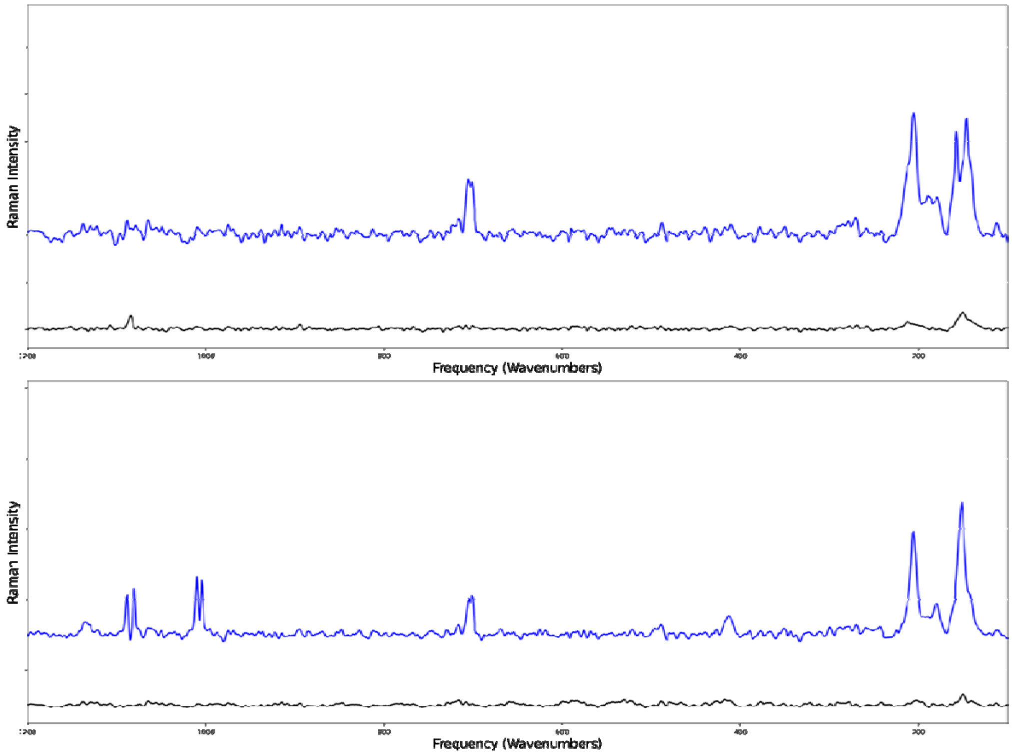

Figure S6. Scanning electron microscopy images of membranes from Muricoid gastropod Ecphora gardnerae (CMM-I-6360 Bed 24 Windmill Point Member of the St. Marys Formation, Miocene, Maryland, USA). Yellow arrows represent ~10-12 µm areas that could represent cells within the membrane network. Membranes under the HCl demineralization are ~1 µm in thickness.

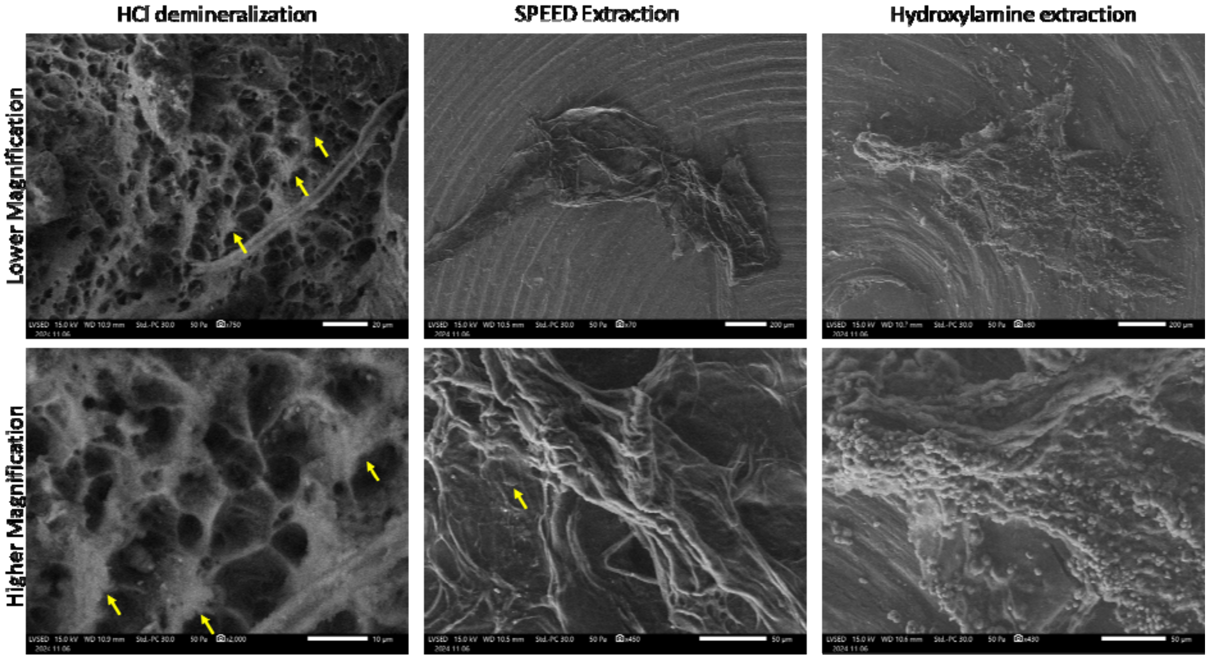

Figure S7. Scanning electron microscopy images of membranes from Muricoid gastropod Ecphora gardnerae (CMM-I-6357 Bed 23 Little Cove Point Member of the St. Marys Formation, Miocene, Maryland, USA). Yellow arrows represent ~10-12 µm areas that could represent cells within the membrane network. Membranes under the HCl demineralization are ~1 µm in thickness.

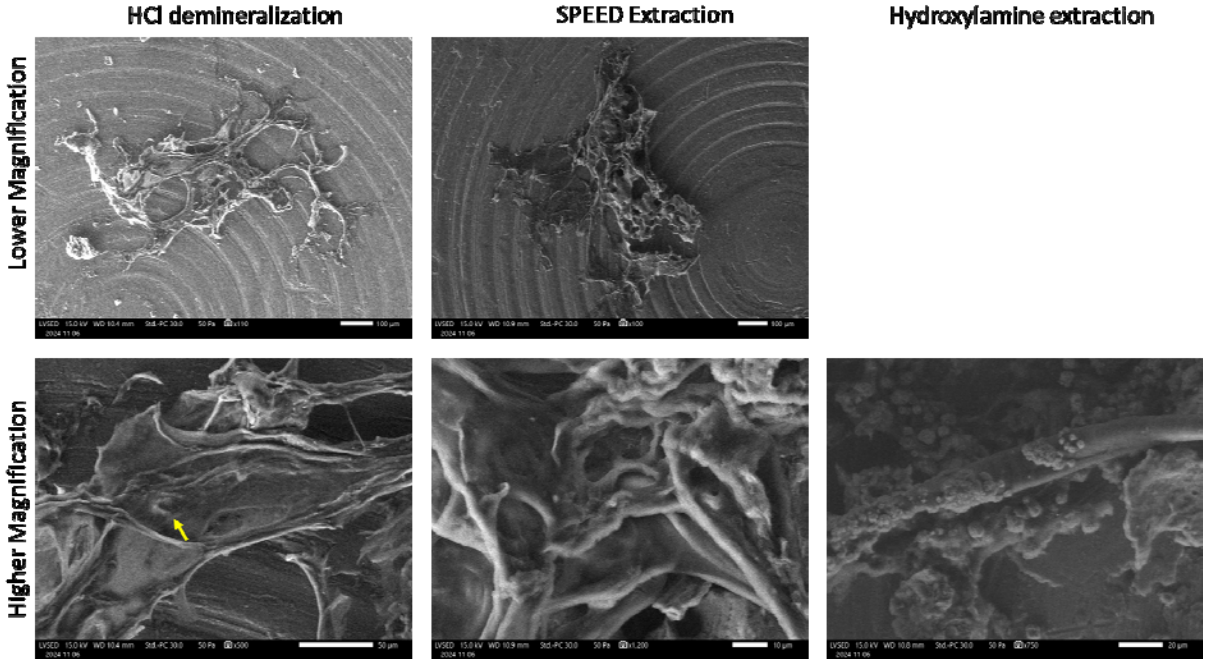

Figure S8. SEM images of the crossed-lamellar and prismatic layer of the undemineralized *Ecphora* shells.

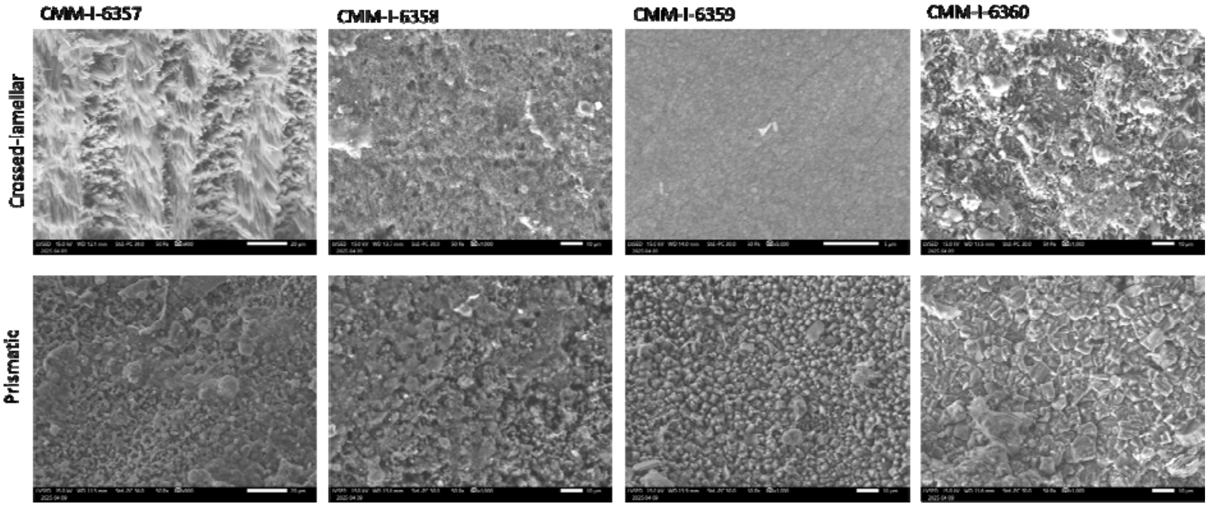

Figure S9. SEM images of HCl etched *Ecphora* shells localizing the membranes to the prismatic layer. The back scatter images show the membranes as darker areas compared to the mineralized lighter areas. CMM-I-6358 shows the boundary between the crossed-lamellar layer (top left) and the prismatic layer with the membranes

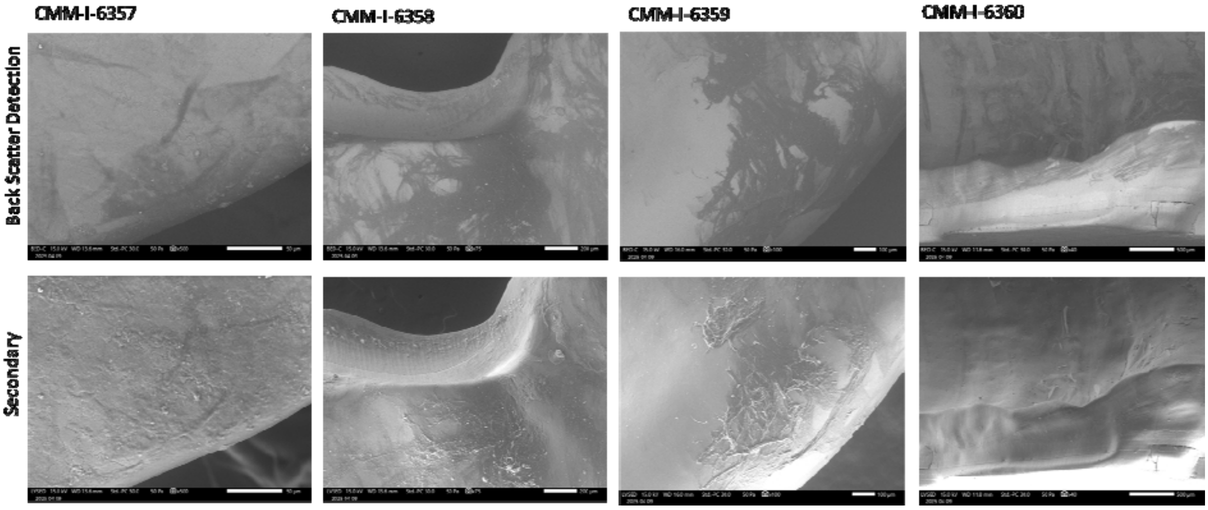

Figure S10. Video of CMM-I-6560 showing membranes releasing during demineralization.
available at http://app.pan.pl/SOM/app70-Cleland_etal_SOM/Figure_S10.mov