

**Fig. S1.**

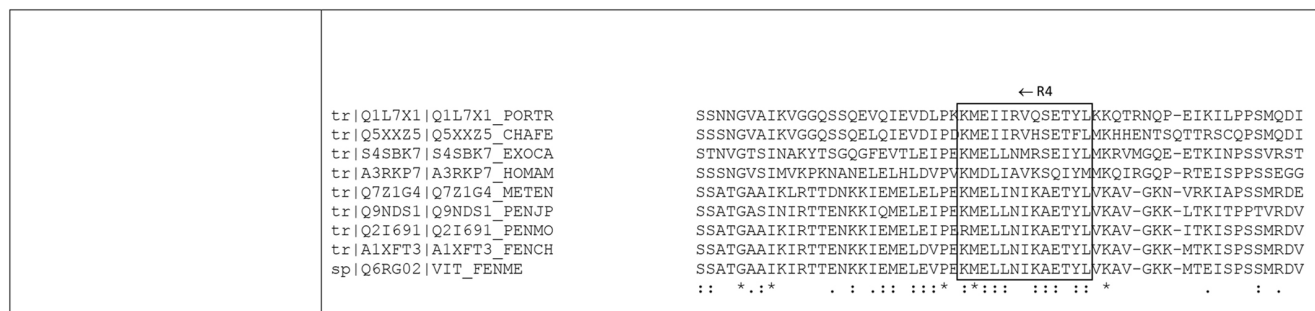
Accession numbers	CLUSTAL Omega Alignment
<p>Q1L7X1 <i>P. trituberculatus</i>                      Q5XXZ5 <i>C. feriatata</i>                      S4SBK7 <i>E. carini cauda</i>                      A3RKP7 <i>H. americanus</i>                      Q7Z1G4 <i>M. ensis</i>                      Q9NDS1 <i>P. japonicus</i>                      Q2I691 <i>P. monodon</i>                      A1XFT3 <i>F. chinensis</i>                      Q6RG02 <i>P. merguensis</i></p>	<pre>                     tr Q1L7X1 Q1L7X1_PORTR                     tr Q5XXZ5 Q5XXZ5_CHAFE                     tr S4SBK7 S4SBK7_EXOCA                     tr A3RKP7 A3RKP7_HOMAM                     tr Q7Z1G4 Q7Z1G4_METEN                     tr Q9NDS1 Q9NDS1_PENJP                     tr Q2I691 Q2I691_PENMO                     tr A1XFT3 A1XFT3_FENCH                     sp Q6RG02 VIT_FENME                      tr Q1L7X1 Q1L7X1_PORTR                     tr Q5XXZ5 Q5XXZ5_CHAFE                     tr S4SBK7 S4SBK7_EXOCA                     tr A3RKP7 A3RKP7_HOMAM                     tr Q7Z1G4 Q7Z1G4_METEN                     tr Q9NDS1 Q9NDS1_PENJP                     tr Q2I691 Q2I691_PENMO                     tr A1XFT3 A1XFT3_FENCH                     sp Q6RG02 VIT_FENME                      tr Q1L7X1 Q1L7X1_PORTR                     tr Q5XXZ5 Q5XXZ5_CHAFE                     tr S4SBK7 S4SBK7_EXOCA                     tr A3RKP7 A3RKP7_HOMAM                     tr Q7Z1G4 Q7Z1G4_METEN                     tr Q9NDS1 Q9NDS1_PENJP                     tr Q2I691 Q2I691_PENMO                     tr A1XFT3 A1XFT3_FENCH                     sp Q6RG02 VIT_FENME                 </pre> <p style="text-align: center;">F1 →</p> <pre>                     MTTHTVLLLLALTAATAA...VGGTTQLCSTECPLAA-AKLSFIPGKTYSYTSGKSIVQL                     MTHTV-LLLALAAAAA...VGSTIQLCSTECPLVAA-AKLAFTPGKTYSYTSGKSQVQL                     -MTYSALFVFAILAAA...WPSTTNLCSRECPVAGSPKLFYAPEKTYVYSYTGKSRINL                     MTTSTALLVPLVVGAG...WGGNTPRCSTECPLVAGSPKLFYQPEHTYTYTSGKSHIHL                     MNSSSLVFLVALVAG...REDEAPRCSTECPLVAGSPKLFYQPEHTYTYTSGKSKVQL                     MTTSSLLFVLALVAG...WGADLPRCSTECPLVAGSPKLFYQPEHTYTYTSGKSRVQL                     MTTSTLLFVILAVFT...WGADLPRCSTECPLVAGSPKLFYQPEHTYTYTSGKSRVHL                     MTTSNLLFVLAVAG...WGADLPRCSTECPLVAGSPKLFYQPEHTYTYTSGKSTVQL                     MTTSTLLFVLAVAG...WGADVPRCSTECPLVAGSPKLFYQPEHTYTYTSGKSTVQL                     : : : : * ** * : : * : * : * : * : * : * : * : * : * : * : * : * : *                 </pre> <p style="text-align: center;">F2 →</p> <pre>                     RVQRVCSHPDDDTWAINM...KGVVSAIQISLPSLSISNSGLNFTETDVLGTCPTYEYVQGE                     RVQRVCSHPDDDTWAINM...KGVVSAIQISLPSLSISNSGLNFTETDVLGTCPTYEYVQAE                     RVMESCAHPDDDVSNM...KGIASAFQNSLPSNSINTGLNFTETDVLGNCSTMYEVKNE                     RVQHVCTHPEDDVVSN...IKKIASAFQNSLPSNSTINSQNTETDVLGKCPHYEVERE                     RVQHVCAHPEDQFWAIN...LKKGVASALQNSIPSLSPVAGSITVTETDVLGKCPHYKVKTE                     RVQHVCAHPEDQFWAIN...LKKGVASAFQNSIPSLSPVSSGIVTETDVLGKCPHYIETE                     RVQHVCAHPEDQFWAIN...LKKGVASAFQNSIPSLSPVSSGIVTETDVLGKCPHYIETE                     RVQHVCAHPEDQFWAIN...LKKGVASAFQNSIPSLSPVSSGIVTETDVLGKCPHYIETE                     RVQHVCAHPEDQFWAIN...LKKGVASAFQNSIPSLSPVSSGIVTETDVLGKCPHYIETE                 </pre> <p style="text-align: center;">** * ** : * : * : * : * : * : * : * : * : * : * : * : * : * : * : * : * : * : * : *</p>

<pre> tr Q1L7X1 Q1L7X1_PORTR tr Q5XXZ5 Q5XXZ5_CHAFE tr S4SBK7 S4SBK7_EXOCA tr A3RKP7 A3RKP7_HOMAM tr Q7Z1G4 Q7Z1G4_METEN tr Q9NDS1 Q9NDS1_PENJP tr Q2I691 Q2I691_PENMO tr A1XFT3 A1XFT3_FENCH sp Q6RG02 VIT_FENME  tr Q1L7X1 Q1L7X1_PORTR tr Q5XXZ5 Q5XXZ5_CHAFE tr S4SBK7 S4SBK7_EXOCA tr A3RKP7 A3RKP7_HOMAM tr Q7Z1G4 Q7Z1G4_METEN tr Q9NDS1 Q9NDS1_PENJP tr Q2I691 Q2I691_PENMO tr A1XFT3 A1XFT3_FENCH sp Q6RG02 VIT_FENME  tr Q1L7X1 Q1L7X1_PORTR tr Q5XXZ5 Q5XXZ5_CHAFE tr S4SBK7 S4SBK7_EXOCA tr A3RKP7 A3RKP7_HOMAM tr Q7Z1G4 Q7Z1G4_METEN tr Q9NDS1 Q9NDS1_PENJP tr Q2I691 Q2I691_PENMO tr A1XFT3 A1XFT3_FENCH sp Q6RG02 VIT_FENME </pre>	<pre>           F3 →          ← R1 GARVLVKKERNHRLCKEHYPTPDEINLFLYLGKGLPIQESRBIICRQEIDSGIISVVVEDK GAKVLVKKERNHRLCQEHYPTPDEIDLPHLKGPLPIQESQBIICRQEIDSGIISVVVEDK GEKVVVMKKNHRFCQDHFISRAESTKAWLKAPLFMEESFBECKQEITKGVYTSITCKDK GKLVIVKKEKNNRLCKKRYPTPAETQMPWLKAPLPLEESGCRCKQEITNGIYSSIIICDK GRELIVTKKEHRHCTEHFPTPNEVPAFPMWKAPLPLEESGPECKQVIENGIYTAITCEDK GEKVIIVKKNHRHCQQRYPPTPAETPAFPLWKAPLPIEESKBECKQEITNGIYTSIMCHDK GEKVIIVKKNHRHCQERYPTPAETPAFPLWKAPLPIEESKQCRQEIANGIYTAITCQDK GEKVIIVKKNHRHCQERYPTPAETPAFPLWKAPLPIEESKQCRQEIANGIYTAITCQDK GEKVIIVKKNHRHCQERYPTPAALPAFPLWKAPLPIEESKQCRQEIANGIYTAITCQDK *.:.*.*:*** *.:. . :*.*.*:*** *:* * .*: .:.*.*            F4 → KVLRPSYGIYKYVEAKQESTLRLTSSDVSAPDTISRIGQDELVPRSLRYDYEPKAKDPTL KVLRPSYGMKYVEAKQESTLRLTSSDVSAPDTISRIGQDELVPRSLRYDYETAJKDPSL NIIRPAYGSYKYIEAVQESTLRFESSETDN-VPPAVSQLPFRFIRKTLRYDQHTMKKDPSP KVVPRSYGAYKYVEAKQESTLRYVSLSSQ-Q--PPAIPQGSVLRKSLRYSYHTLNKDPSP HIVRPAFLYKYVEANQESTLRFISESSD-TSAISGITRGELEIESLLFN-ETTKDPEL NIVRPAIGIYKYVEANQESTLRFISESSD-TSAITAI PRGEMHIESLLYNH-ETMKDPEL NIVRPAIGIYKYVEASQDSTLRFISESSD-TSAISGIHSGEVHIESLLYNH-ETMKDPQL NIVRPAIGIYKYVEASQDSTLRFISESAD-TSAISGIPSGELHIESLLYNH-ETMKDPQL NIVRPAIGIYKYVEASQYSTLRFISESSD-TSAISGIPSGELNIESLLYNH-ETMKDPQL .:.:.*.*:*** *.*: * . . :.*.*:*** *:* * .*: .:.*.*  VPELEQTLRYLCEITRDGVEADTAAQLEKAVNLMRRIPEQSFNDIYTKVRNKQICPQHTK VPELEQTLTYLCEITKDGVEADVAHLSKAVHLMRRIPEQGFNEIYTKVHNKQICPQHSR VVKLDAMLKEVCQKMKHGVQEDTASYFANALQYMRVPEEAIPQTLKIRGGQICEQRQK VAELDQMTQICEKTKDVERDAALVAKAVQLLRVPEEAIVKQTLDKIRAGRYCQDHSK APEIDELMKEICDKTENTVEAADAALVAKALHMLRSVPAEVVEVAEKVRGGRYCGHSER APELDQLMKEICDKTKDVEAADAALVAKALHMLRRVPEVVEVAEKVRGGHYCSDSAR APELDQLMKEICAKTKDVEAADAALVAKALHMLRRVPEVVEVAEKVRGGHYCSDSAR APELDQLMKEICDKTKDVEAAGALVAKALHMLRRVPEVVEVAEKVRGGHYCSDSAR APELDQLMKEICDKTKDVEAAGALVAKALHMLRRVPEVVEVAEKVRGGHYCSDSAR .:.:.*.*:*** *.*: * . . :.*.*:*** *:* * .*: .:.*.* </pre>
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	← R2
tr Q1L7X1 Q1L7X1_PORTR	LESFLMDAIAFVHEPESVEMVKELVEGRRTGLAALYSTAFYLVPRPDVKAIQALEPLF
tr Q5XXZ5 Q5XXZ5_CHAFE	LESFYKDAIAFVHEPESVEMVKELVEGRATGLAALYSTGFYLVPRPDVKAIQALEPLF
tr S4SBK7 S4SBK7_EXOCA	LESFMDLDAFVHEPESVEMVKELVSGKATSGRAALYAAAMTFMFRPCIHSEALKPLF
tr A3RKP7 A3RKP7_HOMAM	LESFLDAVAFVHEPESVEMVKELVMAARATSGRAALYAAAFYLPQPCIHAMALKPMF
tr Q7Z1G4 Q7Z1G4_METEN	LESIFPDVAFVHEPESVEMVVEIENGRATSGRLALYTAALYTPRPNIKAVKALPLF
tr Q9NDS1 Q9NDS1_PENJP	LESIFLDAVAFVHEPESVEMVQELINGRATSGRLALYTAALYTPRPNIEAVKALPLF
tr Q2I691 Q2I691_PENMO	LESIFLDAVAFVHEPESVEMVQELINGRATSGRLALYMAAVLYTPRPNIEAVKALPLF
tr A1XFT3 A1XFT3_FENCH	LESIFLDAVAFVHEPESVEMVQELINGRATSGRLALYTAALYTPRPNIEAVKALPLF
sp Q6RG02 VIT_FENME	LESIFLDAVAFVHEPESVEMVQELINGRATSGRLALYTAALYTPRPNIEAVKALPLF :***:*.:::**:* :* ***.*: ::** ***.:::**:*** :*** :*** :*** :*** :*** :***
tr Q1L7X1 Q1L7X1_PORTR	KSSADLSSAKLAAAMVNTYCRHHPHCYNETPFVRNLAQALKQKIEEDLSSSS-EDTQKQA
tr Q5XXZ5 Q5XXZ5_CHAFE	KSNADLSSAKLAAAMVNTYCRHHPHCYEEFPVRNLAQALKQKIEEDLSSSSRETTQKQA
tr S4SBK7 S4SBK7_EXOCA	EYQRFPTTLGASMVHTYCRQKPKQEKAPVRLAETLSSKVOQVCTPSPNEETKQA
tr A3RKP7 A3RKP7_HOMAM	ESSQLPRATLAAAMVNTYCRHNNHCYEEAPVKSIVEALGNLQKQCSFSDERTOKAA
tr Q7Z1G4 Q7Z1G4_METEN	ESARPKPTMLAAAMVNVKYLVPNCQEAVERIAELANKVERHCPTPSAGEEAEIEI
tr Q9NDS1 Q9NDS1_PENJP	ESPRPMPSSLAAAMVNVYCRHTPHCHQEAVERIAELAAKVEGHCSPSIGVEEKEEA
tr Q2I691 Q2I691_PENMO	EALKPSPSSLAAAMVNVYCRHTPACYEAPVAGIAELANRVQSHCSFSGAEDKEVA
tr A1XFT3 A1XFT3_FENCH	ESPRPMPSSLAAAMVNVYCRHTPACYEAPVAGIAELANRVQSHCSFSGAEDKEVA
sp Q6RG02 VIT_FENME	ESPRPMPSSLAAAMVNVYCRHTPACYEAPVAGIAELANRVQSHCSFSGAEDNEVA : **.*:**. ** : **.* ** : **.* ** : **.* ** : **.* ** : **.* ** : **.* **
	FS →
tr Q1L7X1 Q1L7X1_PORTR	LSALKSLGNMGVTPFAVTRAAVHCIEEGLTSSRVRAAAQAFRQANCF---RFAVEKLVH
tr Q5XXZ5 Q5XXZ5_CHAFE	LSALKSLGNMGVTPFAVTRAAVHCIEEGLTSSRVRAAAQAFRQANCF---RFAVQKLVQ
tr S4SBK7 S4SBK7_EXOCA	LVLLKSLGNMGVTPFAVTRAAVHCIEEGLTSSRVRAAAQAFRQANCF---RFAVQKLVQ
tr A3RKP7 A3RKP7_HOMAM	LATLKTGNMGVTPFAVTRAAVHCIEEGLTSSRVRAAAQAFRQANCF---RFAVQKLVH
tr Q7Z1G4 Q7Z1G4_METEN	VAALKALGNMGVTPFAVTRAAVHCIEEGLTSSRVRAAAQAFRQANCF---RFAVQKLVH
tr Q9NDS1 Q9NDS1_PENJP	LAIFFKALGNMGVTPFAVTRAAVHCIEEGLTSSRVRAAAQAFRQANCF---RFAVQKLVH
tr Q2I691 Q2I691_PENMO	LAIFFKALGNMGVTPFAVTRAAVHCIEEGLTSSRVRAAAQAFRQANCF---RFAVQKLVH
tr A1XFT3 A1XFT3_FENCH	LAIFFKALGNMGVTPFAVTRAAVHCIEEGLTSSRVRAAAQAFRQANCF---RFAVQKLVH
sp Q6RG02 VIT_FENME	LAIFFKALGNMGVTPFAVTRAAVHCIEEGLTSSRVRAAAQAFRQANCF---RFAVQKLVH : **.*:**. ** : **.* ** : **.* ** : **.* ** : **.* ** : **.* ** : **.* **

<pre>tr Q1L7X1 Q1L7X1_PORTR tr Q5XXZ5 Q5XXZ5_CHAFE tr S4SBK7 S4SBK7_EXOCA tr A3RKF7 A3RKF7_HOMAM tr Q7Z1G4 Q7Z1G4_METEN tr Q9NDS1 Q9NDS1_PENJP tr Q2I691 Q2I691_PENMO tr A1XFT3 A1XFT3_FENCH sp Q6RG02 VIT_FENME</pre>	<pre>YALRPEENTEVRIAAYLAAVRCANYEDLQEIIVTKISY--EENTQVRGFILSHLINLQKS YALRPGQNTQEVRIAAYLAAVRCANYEDLQHIIVTKISY--EENTQVRGFILSHLINLQOS VVLDPKKTQEVRIAGSYLAAVRCAYEDLKKITDKIAI--AENTQVRSFILSHLQNVRES IAVHPAKNTEFRIASYLAMAMRCVRQKDLQMIVNNYHEK--SKNTQVRGFILSHLLNQDQT IATHPDFTEVRIASYLAAIKCAEMEDLEKIIINKITE--EKNTQVRSFVLGHLINIQUES IATRPTEFTEVRIASYLAAIRCAEMEHLEQIIIEKISE--EENTQVRGFVLGHLINIQUES IAVRPAFTEVRIASYLAAIRCAEMEDLEIEIEKISV--EENTQVRGFILGHLINIQUES IAVRPAFTEVRIASYLAAVRCAEQEHLETIIEKISK--EENTQVRGFVLGHLINIQUES IAVRPAFTEVRIASYLAAVRCAEQEHLETIIEKISK--EENTQVRGFVLGHLINIQUES . **.* : ** * : : . : . * : * : : :*****:*.** * : : :</pre>
<pre>tr Q1L7X1 Q1L7X1_PORTR tr Q5XXZ5 Q5XXZ5_CHAFE tr S4SBK7 S4SBK7_EXOCA tr A3RKF7 A3RKF7_HOMAM tr Q7Z1G4 Q7Z1G4_METEN tr Q9NDS1 Q9NDS1_PENJP tr Q2I691 Q2I691_PENMO tr A1XFT3 A1XFT3_FENCH sp Q6RG02 VIT_FENME</pre>	<pre>DAPEKQSLRYMMTNIVLPQDFEADIRKYSQNLDSLVSFSESLGVGAEVESNLIYAPGSMIP DAPGKRLRYLLTNILLPQDFETDIRKYSQNLDSLVSFSPSA--AGLESNMIYAPGSMIP TASFKNLKNMLETIVLPSNFTKDWKYSRNVDLSYAPTFVGVGAGMESNLIYAPGSFVP NTPHKDYLRYLLTNILLPQDFETDIRKYSRNIDMSYFAPSLGVGAGVESNLIYVPGSFVP TCPKSKHLRYLLTNVVIPTDFEKDFRFRSRNVMSYHAPAFMGADLESNLIYAPGSFVP TCPTKENLRYLLTNVVIPTDFEKDFRFRSRNIDVAYHAPAFMGAGLESNLIYAPGSFIP TCPAKENLRYLLANVVIPTDFEKDFRFRSRNIDMAYHAPAFMGAGLESNLIYAPGSFVP TCPAKENLRYLLANV-IPTDFEKDFRFRSRNIDVAYHAPAFMGAGLESNLIYAPGSFVP * * : : * : : * : * : * : : * : * : * : : * : * : * : : * : * : * : : *</pre>
<pre>tr Q1L7X1 Q1L7X1_PORTR tr Q5XXZ5 Q5XXZ5_CHAFE tr S4SBK7 S4SBK7_EXOCA tr A3RKF7 A3RKF7_HOMAM tr Q7Z1G4 Q7Z1G4_METEN tr Q9NDS1 Q9NDS1_PENJP tr Q2I691 Q2I691_PENMO tr A1XFT3 A1XFT3_FENCH sp Q6RG02 VIT_FENME</pre>	<pre>RSLGVNLTAAALDGTGIPMNLGEI GARLEGLEPILA QLLGPASYLKTSSYSKMFNDLVSFI RSLGVNLTAAALDGTGIPINIAADV GARVEGLEPIIA QLLGPASYLKTSSYSKIFNDLVSFI RSVNLNLTGALGA--TPFNIGEIGARFEGIESIIEEMFGPESYLKRTSSRQILRDLSSNI RSVDFNFTAALFEG--ISMNIGEIGARLEGLEPVIIEVFGPEGLQRTSFSQILDTMTTFV RALTMNLKADIDE--THLDIGEIGARFEGVDSIIEEHFGPEGLRKRATFGKIMQDITGFA RAVNLKMKADVDE--MHMDIAEIGARFEGIDSIEELFGPEGLRKRATFGKIMQDITGFA RAVNLKMKADVDE--MHMDIAEIGARFEGIDSIEELFGPEGLRKRATFGKIMQDITGFA RAVNLKMKADVDE--MHMDIAEIGARFEGIDSIEELFGPEGLRKRATFGKIMQDITGFA RAVNLKMKADVDE--THMDIAEIGARFEGVDSIIEELFGPEGLRKRATFGKIMQDITGFA RAVNLKMKADVDE--THMDIAEIGARFEGVDSIIEELFGPEGLRKRATFGKIMQDITGFA * : : : : * : : * : * : * : : * : * : * : : * : * : * : : * : * : * : : *</pre>

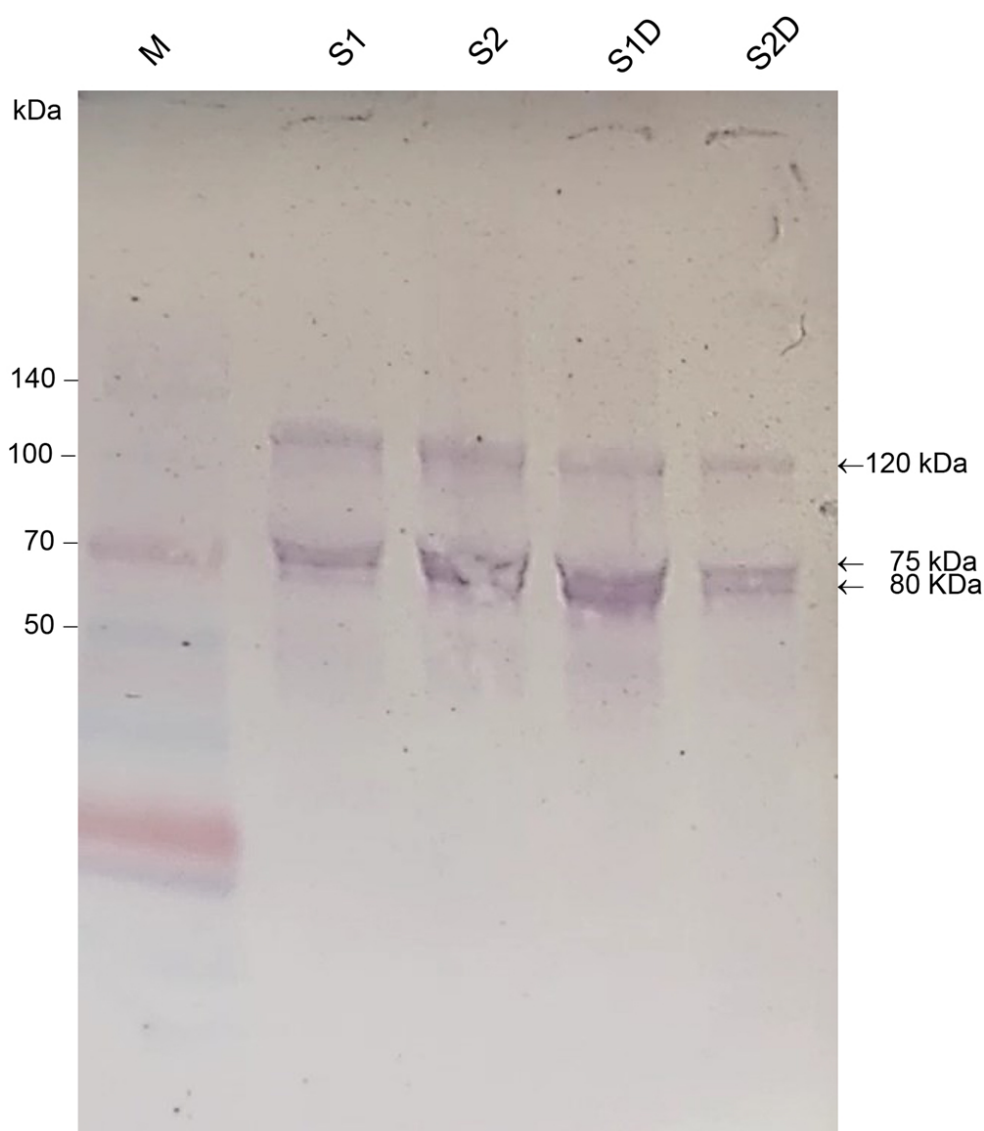
	<pre> tr Q1L7X1 Q1L7X1_PORTR                QKNWSTIKQELEVAIRERRSVDAALESIIISKLYGPHYGKQADDFARFLGQEIINYASLS tr Q5XXZ5 Q5XXZ5_CHAFE                QQNWSTIKQELEVAIRERRVTDDATIESIISKLYGPHYGKQADDFARFLGQEIINYASLS tr S4SBK7 S4SBK7_EXOCA                EETFNKINERLQGSFRQRSIDLQISHLFDKLYGNRH-MQKADDFARINNQEMAFGSLM tr A3RKP7 A3RKP7_HOMAM                EOKGNKILEKLQDLRQRSSIDLSTLINFGLNLYDQSRVTRADVFARFMQEIITFASLA tr Q7Z1G4 Q7Z1G4_METEN                EEKGYKVMHEHLNLRTRRSIDASTIADFFNKLYGERASDVRAEVEFARIMGQEVYANIA tr Q9NDS1 Q9NDS1_PENJP                EEKGLKVMHEIKQTLRTRRSIDSSVIDFFGKLYGEGRSHTHAEVFAIRIMGHEITYADVA tr Q2I691 Q2I691_PENMO                GEKGLKVMHEIKHTLRTRRSIDSSVIDFFGKLYGEGRSHVHADLFARFMGHEITYADVA tr A1XFT3 A1XFT3_FENCH                GEKGLKVMHEIKGTLRTRRSIDSSVIADFFGKLYGEGRSRSHTHAEVFAIRFMGHEITYADVA sp Q6RG02 VIT_FENME                    GEKGYKVMQKHLRTRRSIDSSVIADFFGKLYGKSRSHTHAEVFAIRFMGHEITYADVA   .. .: .: .: .: * : * : * : : : : * * .   * : . : * : * : * : * : . .  tr Q1L7X1 Q1L7X1_PORTR                DNLQDINIQHLEASVRYLKRMLSSLKNDLDMVKA-AQLGVDYSL-PTIQGTPLKMKLE tr Q5XXZ5 Q5XXZ5_CHAFE                EHLQDINMHHLVEASVRCPMQLSSLKNVNLDKVKA-VQLGVDYSL-PTIQGTPLKITSE tr S4SBK7 S4SBK7_EXOCA                GNMKNIMEELINMFDSDMINRAENLTVRA-AQLYLDYHL-PTMQGLPLKMKLE tr A3RKP7 A3RKP7_HOMAM                GDLKHISADEMIESFFSYDIPPMQKNLAHQFOHERLKLTLDYHLSPPSRAYHSLKQLN tr Q7Z1G4 Q7Z1G4_METEN                ETLKGVTDADKIIEFFSFLVDDLEELKGLNLTAKELKLLHLYYSL-PTIQGLHRSRSPWK tr Q9NDS1 Q9NDS1_PENJP                ESLKGVTDADTLIETFFSFFESLEQMKGLNLTART-AQLYMDYSL-PTIQGTPLRKLKA tr Q2I691 Q2I691_PENMO                ESLKGVTDADTLIETFFSFFENSLEHMKDLNLTART-AQLSMDYSL-PDIQGTPLRKLKA tr A1XFT3 A1XFT3_FENCH                ESLKGVTDADTLIETFFSFFENSLEHMKDLNLTART-AQLSMDYSL-PTIQGTPLRKLKA sp Q6RG02 VIT_FENME                    GSLKGVTDADTLIETFFSFFENSLEHMKDLNLTART-AQLSMDYSL-PTIQGTPLRKLKA   : : . . : : . : : : : : : * : . . :  tr Q1L7X1 Q1L7X1_PORTR                TVAVAGIKMQTNLNL--FSGQSSGSLFKILPSPFVETHGFIGYDAYISKSGLKMNTTV tr Q5XXZ5 Q5XXZ5_CHAFE                TMAVAGIKMETNNLNL--FSGQSSGSESKLILPSPFVETHGFIGYDAYISKSGLKMNTTV tr S4SBK7 S4SBK7_EXOCA                GTAMVGLKMEASRVGL----MSGTPGVMMFYPSLSTQIDAFIGYDCHIVRTGIKMRNRI tr A3RKP7 A3RKP7_HOMAM                GKAVGGLKMQGNLNLIDILFNWRNGENLPKIIPSLSVQVDGFGVYDYSNKLGLEMRNTI tr Q7Z1G4 Q7Z1G4_METEN                GTAVAGLKMEGFNHIAHILANPGLNLTAKILYPLGSIHTTGFVGFDAFIKAKGEMKNTI tr Q9NDS1 Q9NDS1_PENJP                GTAVAGLKMEGFNIAQILSDPGLNLTGKILFPLSVQATGFVGFECRLTRVGIEMENTI tr Q2I691 Q2I691_PENMO                GTAVAGLKMEGNVNIGQILSDLNSQGTGKIFPPLSVQATGFVGFACGTRVGIEMQNTI tr A1XFT3 A1XFT3_FENCH                GTAVAGLKMEGNVINVAQILSDLNSQGTGKIFPPLSVQATGFVGFECRLTKVGIEMQNTI sp Q6RG02 VIT_FENME                    GTAVAGLKMEGNVNIAQILSDLNSQGTGKIFPPLSVHATGFVGFDWLLARVGIEMQNTI   * : * : * : . .   . : * : * : .   . : * :   : * : * : . . </pre>
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**Fig. S1. Multiple alignment of VTG amino acid sequences from nine different crustacean sources.** The sequences were chosen from the GenBank SwissProt database and aligned using Clustal Omega (<https://www.ebi.ac.uk/Tools/msa/clustalo/>). The figure shows the alignments based upon which the CODEHOP primers have been designed. An asterisk (\*) denotes identical residues; a colon (:) denotes a conserved residue substitution; a full stop (.) denotes partial conservation of the residue. The arrows above the amino acid sequences indicate the position of the sense (F →) and antisense (← R) primers chosen from a group of candidate primers obtained from the j-CODEHOP programme. The sequences of the sense and antisense primers, shown inside the boxes, were obtained from the Clustal Omega alignments

<b>Clustal Omega alignment</b>		
<i>P. elephas</i>	-----TL-PTQLRSRPLAQGGLPVEESGSVCLQEIKDGIYWSITCEDE	42
QDE13857.1	GEKVVVTKLKNHRFCQDHYANRAETPKAWMKAPLPMEESYSECKQEITNGIYTSITCKDK	112
ABO09863.1	GHKVIVKKEKNHRLCKKRYPTPAETQMPWLKGPLLEESECRCCKQEITNGIYSSIICHDK	240
	:.***:*** . * ***.:*** ** *.*:	
<i>P. elephas</i>	NVIRPSYGAYKYVEANQESTT-----	63
QDE13857.1	NVIKPAYGSYKYVEAHQESVLRFSQSETDQIPPSVSQLPSRFIRKTLRYDQHTLKKDPSMA	172
ABO09863.1	KVVRPSYGAYKYVEAKQESTLRYVSLSSQPPAIPQ-GSLVRKSLRYSYHTLNKDPMSV	298
	:*.:.*:**:*:*****:***.	
QDE13857.1	<i>Macrobrachium potiuna</i>	(69.39% identity)
ABO09863.1	<i>Homarus americanus</i>	(67.92 % identity)

**Fig. S2. Alignment of VTG *P. elephas* amino acid sequences with homologous VTG sequences from GenBank.** Identity and similarity percentages are shown at the top of each Clustal Omega alignment panel. Numbers on the left indicate the positions of the amino acids in each protein. An asterisk (\*) denotes identical residues; a colon (:) denotes a conserved residue substitution; a full stop (.) denotes partial conservation of the residue.



**Fig. S3. Results of Western blot analysis using anti-VTG2 antibody.** An aliquot of all homogenate samples with concentration of VTG120-180 ng / mL were pooled into one sample (S1). Similarly, an aliquot of all samples with a concentration of VTG 200-260 ng / mL (S2) was pooled. The same S1 and S2 samples were also digested with the subtilisin protease (S1D and S2D samples). Western Blot profiles did not highlight particular differences between the samples treated and untreated with the protease. The different concentrations of VTG detected by ELISA were also not reflected in the number of immunoreactive bands to the anti-VTG2 antibody. The arrows (←) indicate the presence of an immunoreactive band of about 120 kDa and also two very close bands between 80-75 kDa.