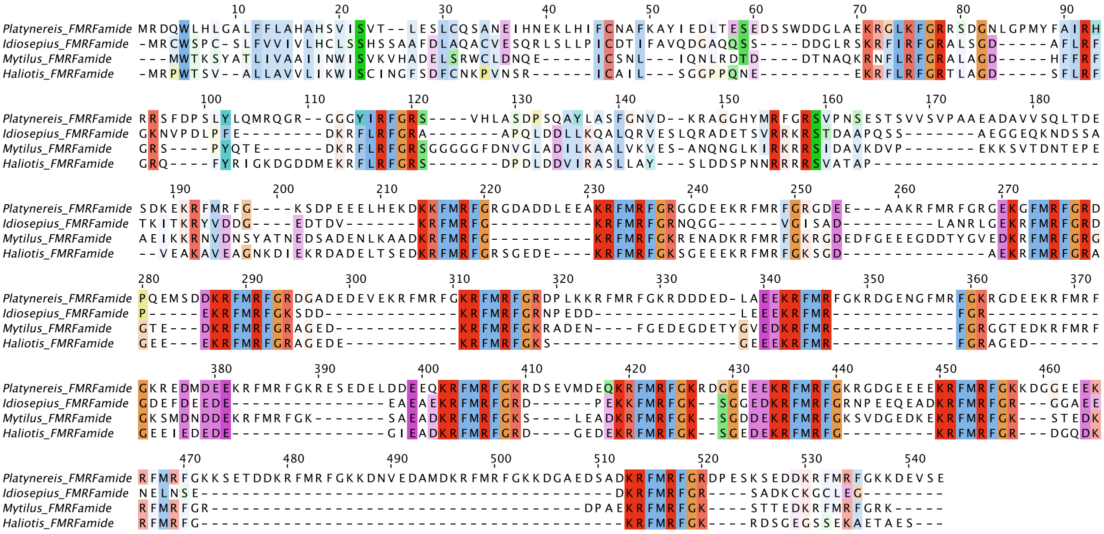
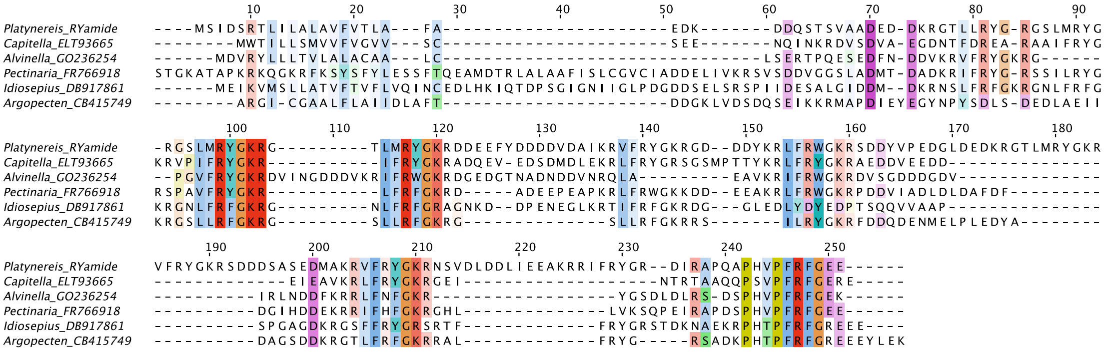
Additional file 10: list of multiple sequence alignments

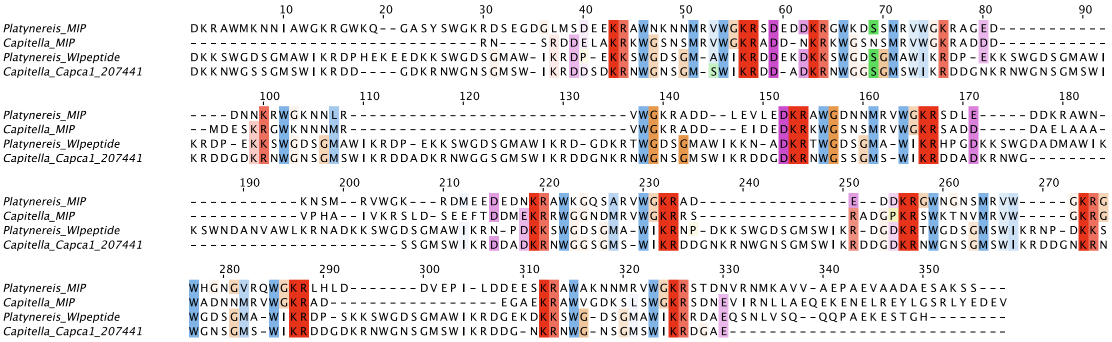
Platynereis pNPs belonging to eumetazoan pNPs families:



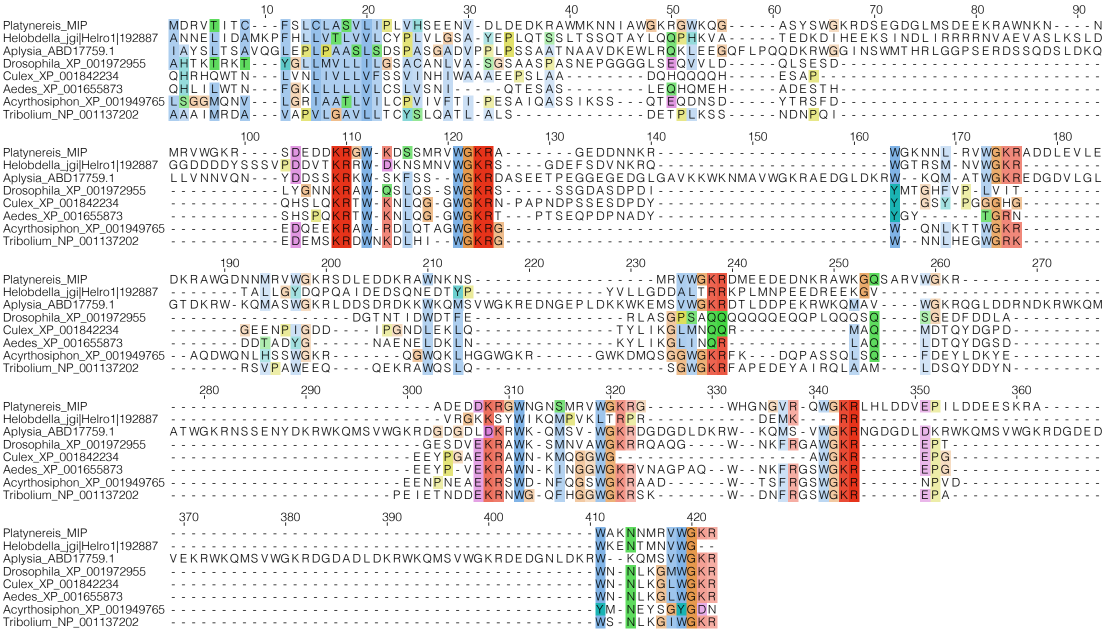
Multiple sequence alignment of annelid and mollusk FMRFa pNPs.



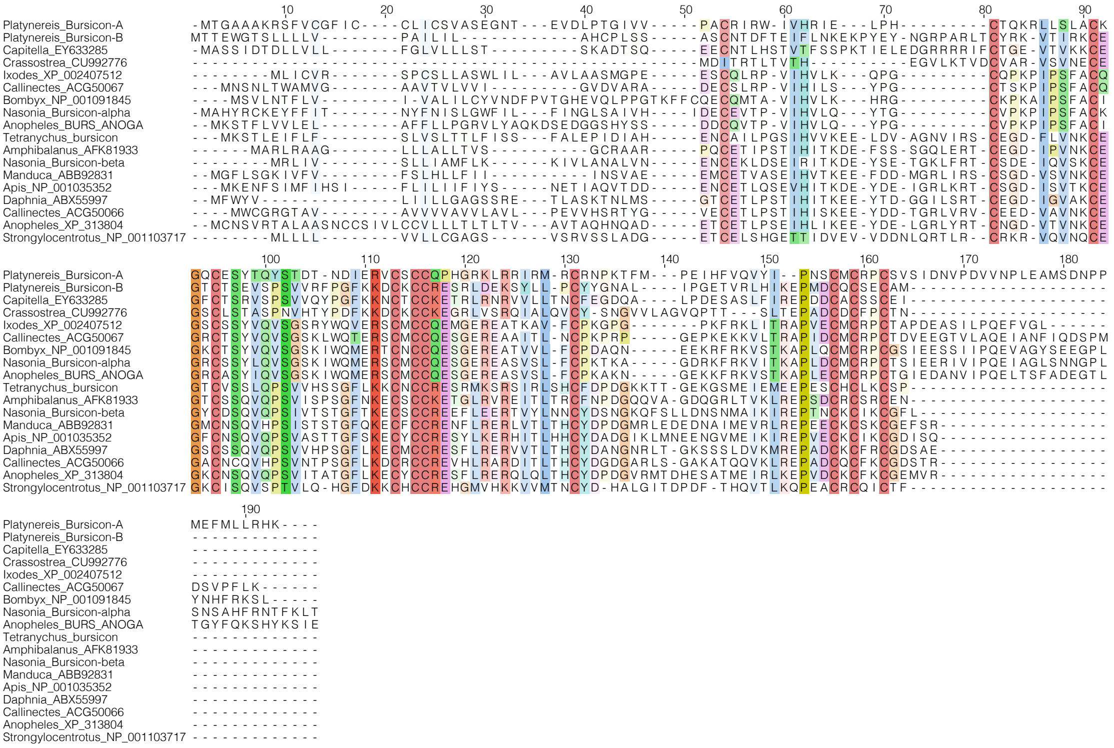
Multiple sequence alignment of annelid and mollusk RYa pNPs. These pNPs also share a conserved peptide in the C-terminus of the precursor, potentially yielding Pro rich RFamide-related peptides.



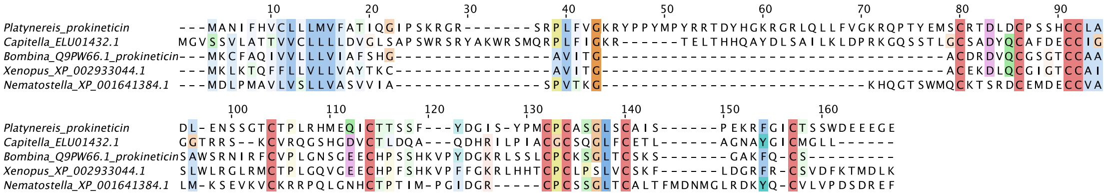
Multiple sequence alignment of trimmed *Platynereis* and *Capitella teleta* WI peptide and MIP pNPs. The mature WI peptides share two conserved Trp-residues with MIPs.



Multiple sequence alignment of *Platynereis* MIP pNP with protostome MIP/allatostatin-B pNPs.

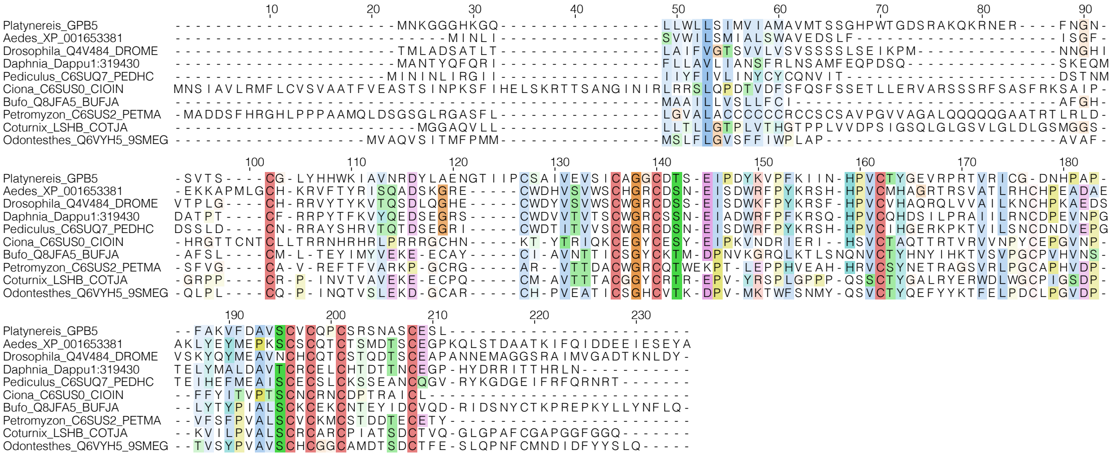


Multiple sequence alignment of *Platynereis* bursicon alpha and beta with bilaterian bursicon pNPs.

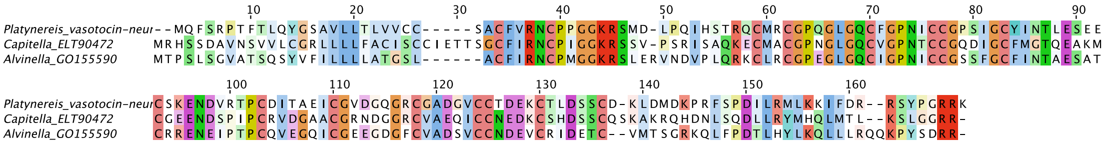


Truncated multiple sequence alignment of *Platynereis* prokineticin with bilaterian and cnidarian prokineticin pNPs. In *Platynereis* and *Capitella teleta*, this pNP also gives rise to amidated peptides located at the N-terminus of the pNP.

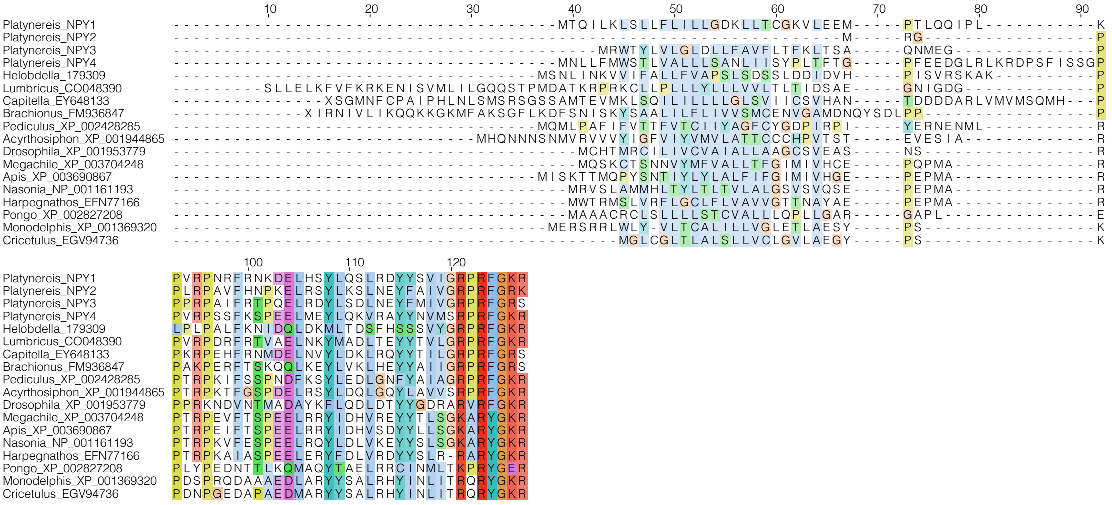
Platynereis pNPs belonging to bilaterian pNPs families:



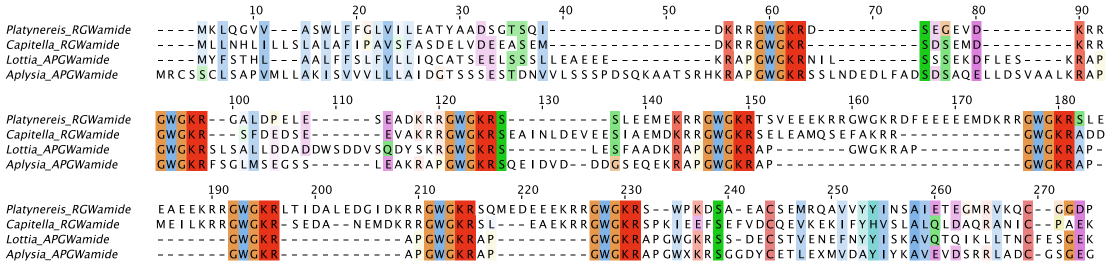
Multiple sequence alignment of *Platynereis* glycoprotein beta with bilaterian glycoprotein beta pNPs.



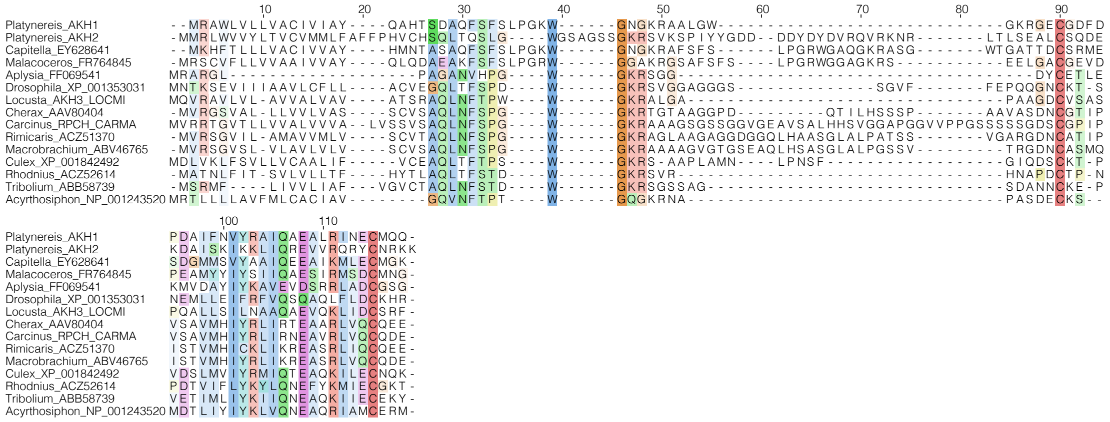
Multiple sequence alignment of annelid vasotocin-neurophysin pNPs shows a potential C-terminally located peptide (SYPamide in *Platynereis* and SLGamide in *Capitella teleta*).



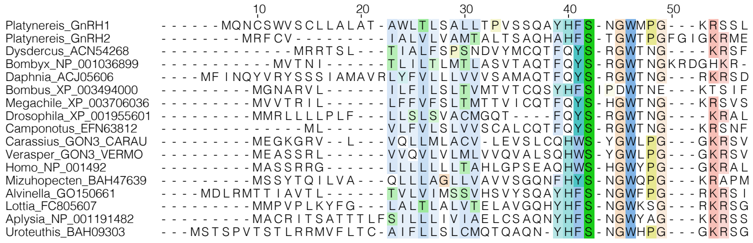
Truncated multiple sequence alignment of *Platynereis* NPY pNPs with bilaterian NPY/NPF pNPs.



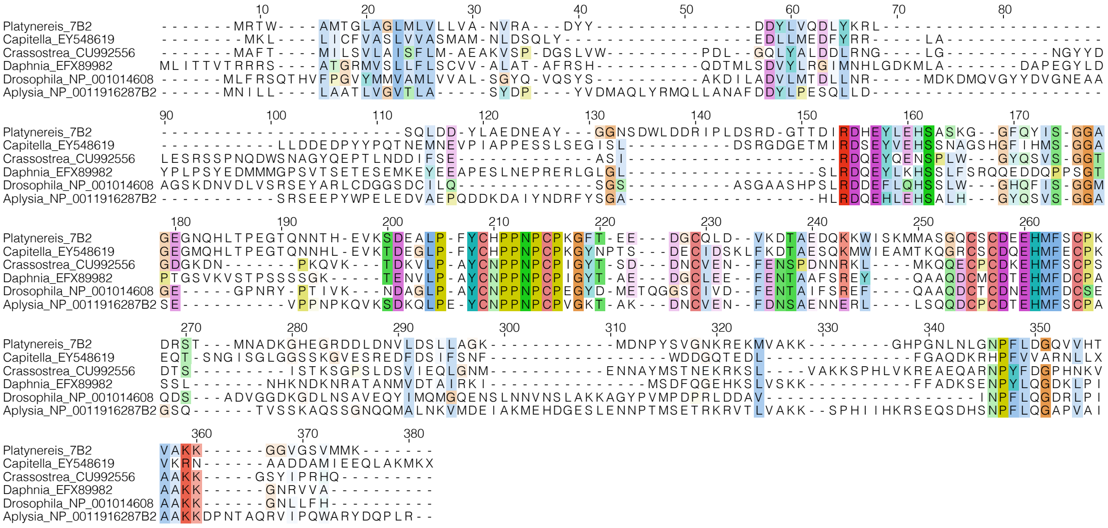
Multiple sequence alignment of annelid and mollusk RGWamide and APGWamide pNPs. These precursors share a Cys-containing stretch at the C-terminus of the precursor.



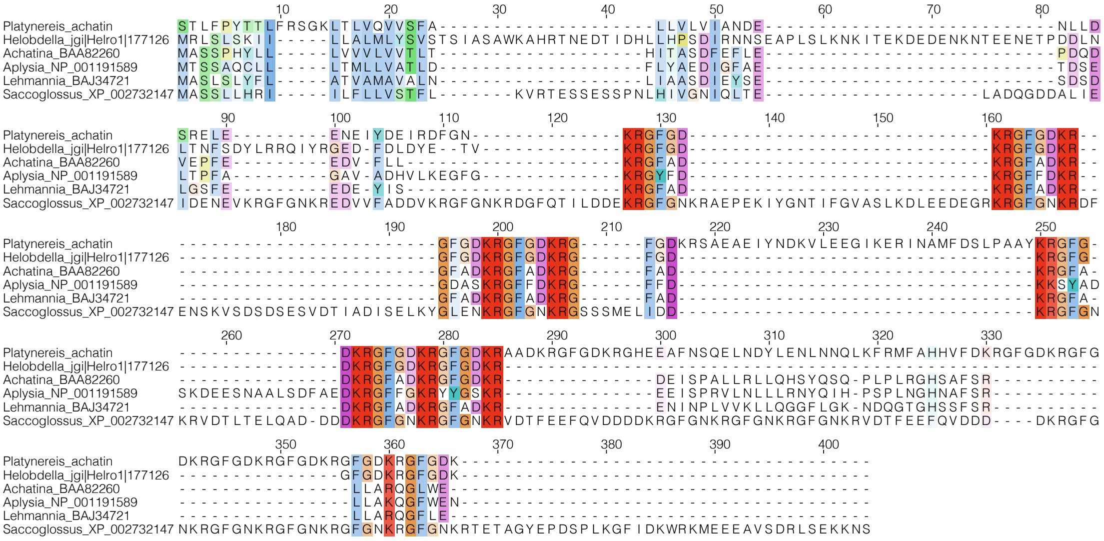
Truncated multiple sequence alignment of *Platynereis* AKH pNPs with protostome AKH/RPCH pNPs.



Truncated multiple sequence alignment of *Platynereis* GnRH pNPs with bilaterian GnRH/corazonin pNPs.

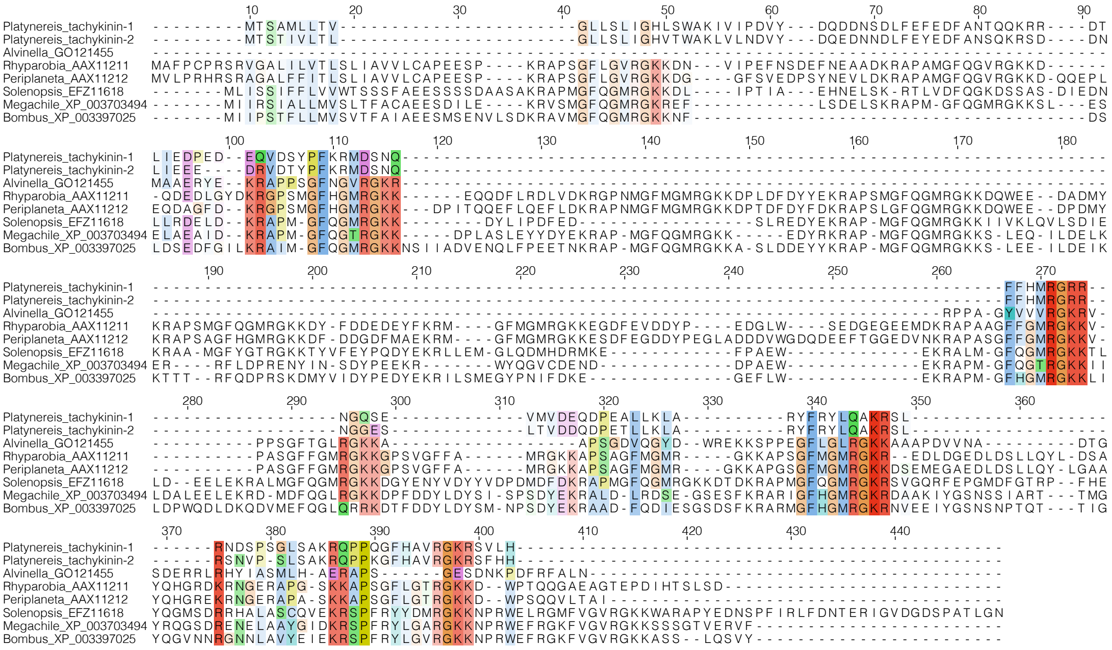


Multiple sequence alignment of *Platynereis* 7B2 pNP with protostome 7B2 pNPs.



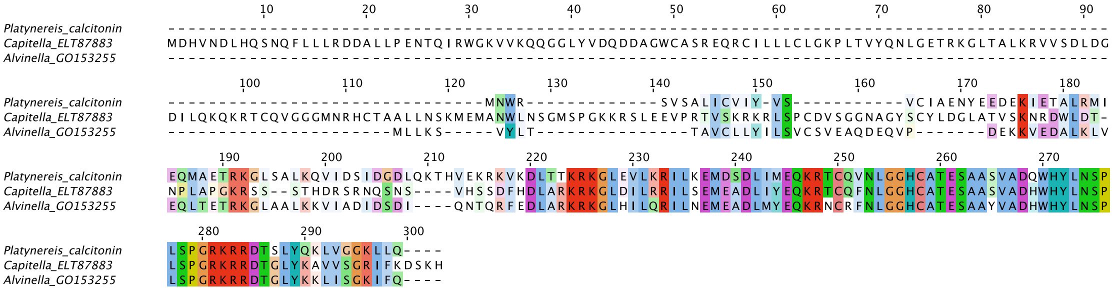
Multiple sequence alignment of *Platynereis* achatin pNP with bilaterian achatin pNPs.

Multiple sequence alignment of *Platynereis* luqin pNP with bilaterian luqin pNPs showing the conservation of a small amidated peptide and a C-terminal Cys-containing peptide.



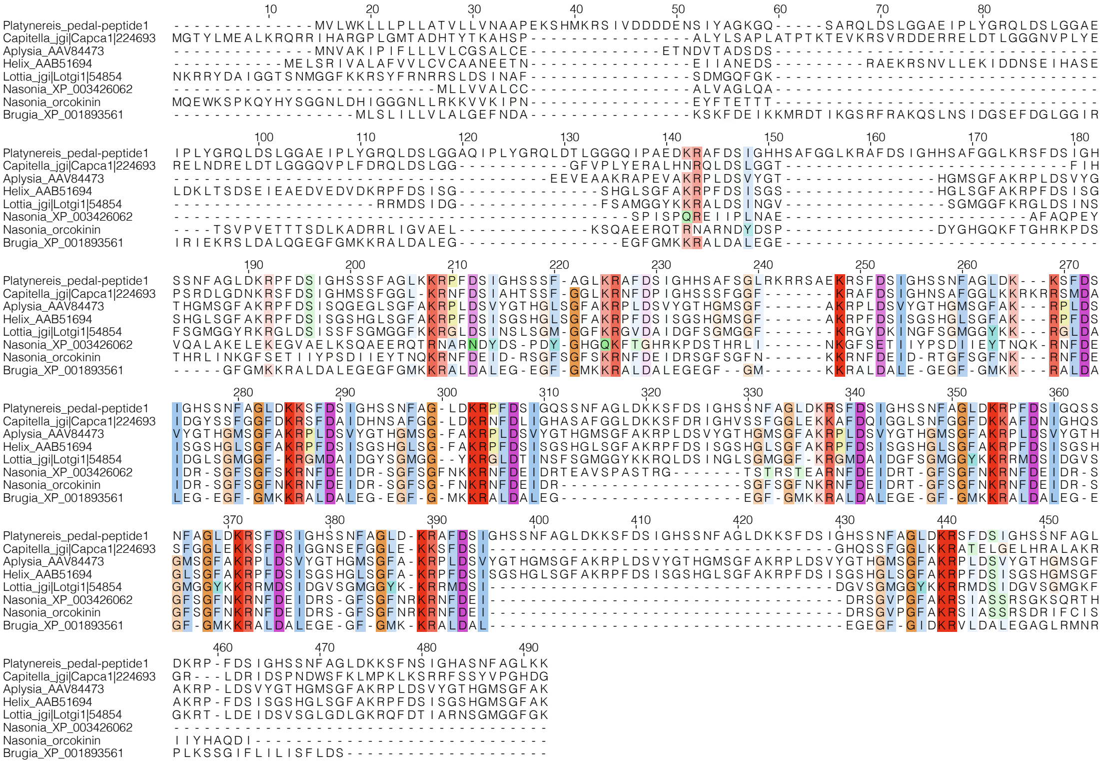
```
Platynereis_tachykinin-1   ---------MTSAMLLTV-----------------------GLLSLIGHLSWAKIVIPDVY---DQDDNSDLFEFEDFANTQQKRR----DT
Platynereis_tachykinin-2   ---------MTSTIVLTL-----------------------GLLSLIGHVTWAKLVLNDVY---DQEDNNDLFEYEDFANSQKRSD----DN
Alvinella_GO121455         --------------------------------------------------------------------------------------------
Rhyparobia_AAX11211        MAFPCPRSRVGALILVTLSLIAVVLCAPEESP----KRAPSGFLGVRGKKDN---VIPEFNSDEFNEAADKRAPAMGFQGVRGKKD------
Periplaneta_AAX11212       MVLPRHRSRAGALFFITLSLIAVVLCAPEESP----KRAPSGFLGVRGKKDG----GFSVEDPSYNEVLDKRAPAMGFQGVRGKKD-QQEPL
Solenopsis_EFZ11618        -------MLISSIFFLVVWTSSSFAEESSSSDAASAKRAPMGFQGMRGKKDL----IPTIA---EHNELSK-RTLVDFQGKDSSAS-DIEDN
Megachile_XP_003703494     -------MIIRSIALLMVSLTFACAEESDILE----KRVSMGFQGMRGKREF------------LSDELSKRAPM-GFQGMRGKKSL---ES
Bombus_XP_003397025        -------MIIPSTFLLMVSVTFAIAEESMSENVLSDKRAVMGFQGMRGKKNF--------------------------------------DS

Platynereis_tachykinin-1   LIEDPED--EQVDSYPFKRMDSNQ--------------------------------------------------------------------
Platynereis_tachykinin-2   LIEEE----DRVDTYPFKRMDSNQ--------------------------------------------------------------------
Alvinella_GO121455         MAAERYE--KRAPPSGFNGVRGKR--------------------------------------------------------------------
Rhyparobia_AAX11211        -QDEDLGYDKRGPSMGFHGMRGKK------EQQDFLRDLVDKRGPNMGFMGMRGKKDPLDFDYYEKRAPSMGFQGMRGKKDQWEE--DADMY
Periplaneta_AAX11212       EQDAGFD--KRGPSMGFHGMRGKK---DPITQQEFLQEFLDKRAPNMGFMGMRGKKDPTDFDYFDKRAPSLGFQGMRGKKDQWEE--DPDMY
Solenopsis_EFZ11618        LLRDELD--KRAPM-GFQGMRGKK--------DYLIPDFED-----------------SLREDYEKRAP-MGFQGMRGKKIIVKLQVLSDIE
Megachile_XP_003703494     ELAEAID--KRAPM-GFQGTRGKK-----DPLASLEYYDYEKRAP-MGFQGMRGKK-----EDYRKRAP-MGFQGMRGKKS-LEQ-ILDELK
Bombus_XP_003397025        LDSEDFGILKRAIM-GFQGMRGKKNSIIADVENQLFPEETNKRAP-MGFQGMRGKKA-SLDDEYYKRAP-MGFQGMRGKKS-LEE-ILDEIK

Platynereis_tachykinin-1   ----------------------------------------------------------------------------------FFHMRGRR--
Platynereis_tachykinin-2   ----------------------------------------------------------------------------------FFHMRGRR--
Alvinella_GO121455         ----------------------------------------------------------------------------RPPA-GYVVVRGKRV-
Rhyparobia_AAX11211        KRAPSMGFQGMRGKKDY-FDDEDEYFKRM----GFMGMRGKKEGDFEVDDYP----EDGLW----SEDGEGEEMDKRAPAAGFFGMRGKKV-
Periplaneta_AAX11212       KRAPSAGFHGMRGKKDF-DDGDFMAEKRM----GFMGMRGKKESDFEGDDYPEGLADDDVWGDQDEEFTGGEDVNKRAPASGFFGMRGKKV-
Solenopsis_EFZ11618        KRAA-MGFYGTRGKKTYVFEYPQDYEKRLLEM-GLQDMHDRMKE------------FPAEW------------EKRALM-GFQGMRGKKTL
Megachile_XP_003703494     ER----RFLDPRENYIN-SDYPEEKR-------WYQGVCDEND-------------DPAEW------------EKRAPM-GFQGTRGKKII
Bombus_XP_003397025        KTTT--RFQDPRSKDMYVIDYPEDYEKRILSMEGYPNIFDKE--------------GEFLW------------EKRAPM-GFHGMRGKKLI

Platynereis_tachykinin-1   ------------------NGQSE-------------VMVDEQDPEALLKLA----------RYFRYLQAKRSL-------------------
Platynereis_tachykinin-2   ------------------NGGES-------------LTVDDQDPETLLKLA----------RYFRYLQAKRSL-------------------
Alvinella_GO121455         ----------PPSGFTGLRGKKA------------------APSGDVQGYD--WREKKSPPEGFLGLRGKKAAAPDVVNA---------DTG
Rhyparobia_AAX11211        ----------PASGFFGMRGKKGPSVGFFA------MRGKKAPSAGFMGMR-----GKKAPSGFMGMRGKR--EDLDGEDLDSLLQYL-DSA
Periplaneta_AAX11212       ----------PASGFFGMRGKKGPSVGFFA------MRGKKAPSAGFMGMR----GKKAPGSGFMGMRGKKDSEMEGAEDLDSLLQY-LGAA
Solenopsis_EFZ11618        LD--EELEKRALMGFQGMRGKKDGYENYVDYYVDPDMDFDKRAPMGFQGMRGKKDTDKRAPMGFQGMRGKRSVGQRFEPGMDFGTRP--FHE
Megachile_XP_003703494     LDALEELEKRD-MDFQGLRGKKDPFDDYLDYSI-SPSDYEKRALD-LRDSE-GSESFKRARIGFHGMRGKRDAAKIYGSNSSIART---TMG
Bombus_XP_003397025        LDPWQDLDKQDVMEFQGLQRRKDTFDDYLDYSM-NPSDYEKRAAD-FQDIESGSDSFKRARMGFHGMRGKRNVEEIYGSNSNPTQT---TIG

Platynereis_tachykinin-1   ------RNDSPSGLSAKRQPPQGFHAVRGKRSVLH-----------------------------------------------
Platynereis_tachykinin-2   ------RSNVP-SLSAKRQPPKGFHAVRGKRSFHH-----------------------------------------------
Alvinella_GO121455         SDERRLRHYIASMLH-AERAPS------GESDNKPDFRFALN----------------------------------------
Rhyparobia_AAX11211        YQHGRDKRNGERAPG-SKKAPSGFLGTRGKKD--WPTQQGAEAGTEPDIHTSLSD---------------------------
Periplaneta_AAX11212       YQHGREKRNGERAPA-SKKAPSGFLGTRGKKD--WPSQQVLTAI--------------------------------------
Solenopsis_EFZ11618        YQGMSDRRHALASCQVEKRSPFRYYDMRGKKNPRWELRGMFVGVRGKKWARAPYEDNSPFIRLFDNTERIGVDGDSPATLGN
Megachile_XP_003703494     YRQGSDRENELAAYGIDKRSPFRYLGARGKKNPRWEFRGKFVGVRGKKSSSGTVERVF------------------------
Bombus_XP_003397025        YQGVNNRGNNLAVYEIEKRSPFRYLGVRGKKNPRWEFRGKFVGVRGKKASS--LQSVY------------------------
```

Multiple sequence alignment of *Platynereis* tachykinin pNPs with protostome tachykinin pNPs. Deuterostome sequences were not included because of low sequence identity.

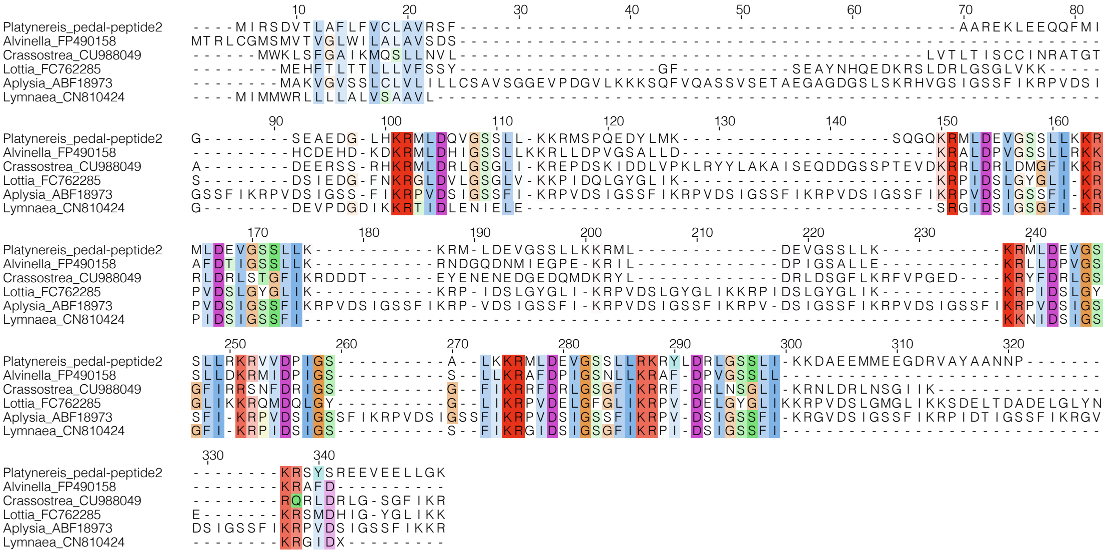


```
Platynereis_calcitonin  --------------------------------------------------------------------------------------------
Capitella_ELT87883      MDHVNDLHQSNQFLLLRDDALLPENTQIRWGKVVKQQGGLYVDQDDAGWCASREQRCILLLCLGKPLTVYQNLGETRKGLTALKRVVSDLDG
Alvinella_GO153255      --------------------------------------------------------------------------------------------

Platynereis_calcitonin  -------------------------------MNWR-------------SVSALICVIY-VS-----------VCIAENYEEDEKIETALRMI
Capitella_ELT87883      DILQKQKRTCQVGGGMNRHCTAALLNSKMEMANWLNSGMSPGKKRSLEEVPRTVSKRKRLSPCDVSGGNAGYSCYLDGLATVSKNRDWLDT-
Alvinella_GO153255      ----------------------MLLKS-----VYLT---------------TAVCLLYILSVCSVEAQDEQVP-------DEKKVEDALKLV

Platynereis_calcitonin  EQMAETRKGLSALKQVIDSIDGDLQKTHVEKRKVKDLTTKRKGLEVLKRILKEMDSDLIMEQKRTCQVNLGGHCATESAASVADQWHYLNSP
Capitella_ELT87883      NPLAPGKRSS--STHDRSRNQSNS----VHSSDFHDLARKKKGLDILRRILSEMEADLIYEQKRTCQFNLGGHCATESAASVADHWHYLNSP
Alvinella_GO153255      EQLTETRKGLAALKKVIADIDSDI----QNTQRFEDLARKKKGLHILQRILNEMEADLMYEQKRNCRFNLGGHCATESAAYVADHWHYLNSP

Platynereis_calcitonin  LSPGRKRRDTSLYQKLVGGKLLQ----
Capitella_ELT87883      LSPGRKRRDTGLYKAVVSGRIFKDSKH
Alvinella_GO153255      LSPGRKRRDTGLYKKLISGKIFQ----
```

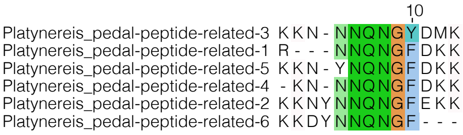
Multiple sequence alignment of annelid calcitonin pNPs shows an additional conserved C-terminal amidated peptide (e.g., DTSLYQKLVGamide in *Platynereis*).



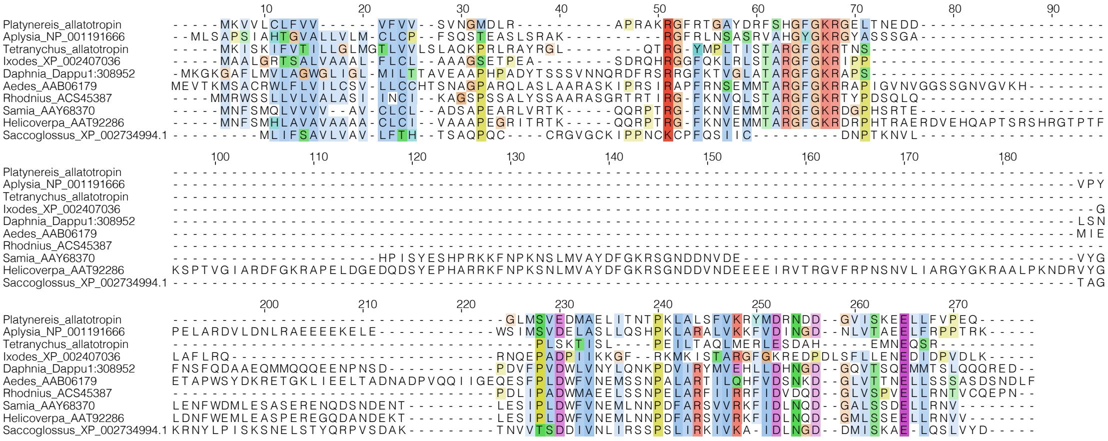
Truncated multiple sequence alignment of *Platynereis* pedal-peptide-1 pNP with protostome pedal-peptide-1 and orcokinin pNPs.



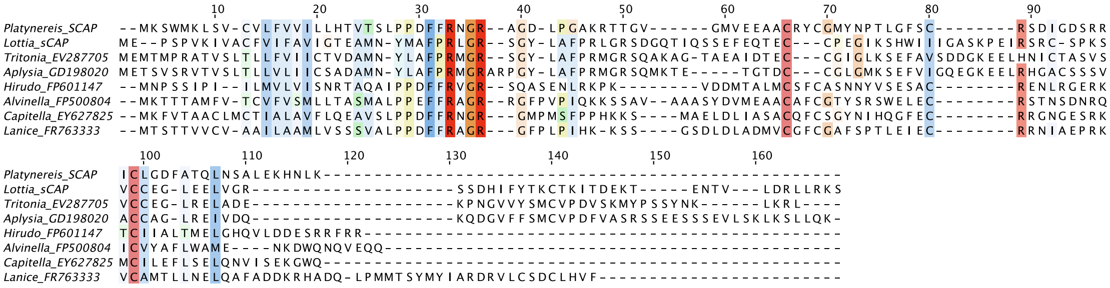
Truncated multiple sequence alignment of *Platynereis* pedal-peptide-2 pNP with annelid and mollusk pedal-peptide-2 pNPs.



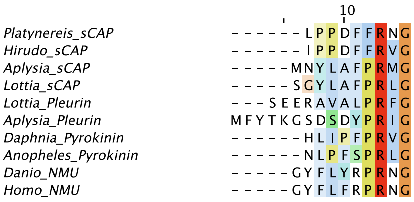
Multiple sequence alignment of *Platynereis* pedal-peptide-related peptides.



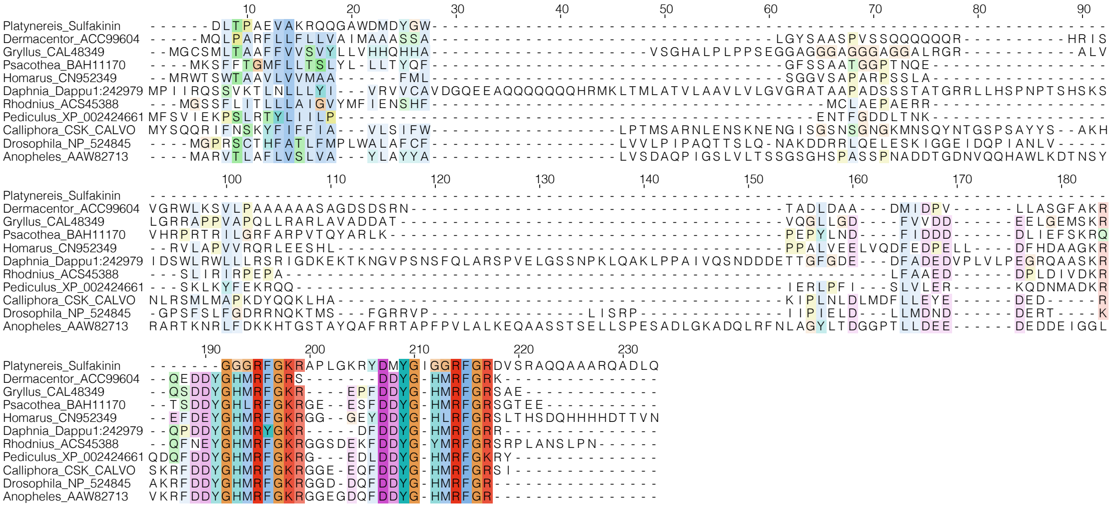
Multiple sequence alignment of *Platynereis* allatotropin pNP with bilaterian allatotropin pNPs. The *Platynereis* pNP shares an N-terminal GF/Yamide peptide with protostome pNPs, and a C-terminal conserved cryptic peptide with protostome and *Saccoglossus* pNPs.



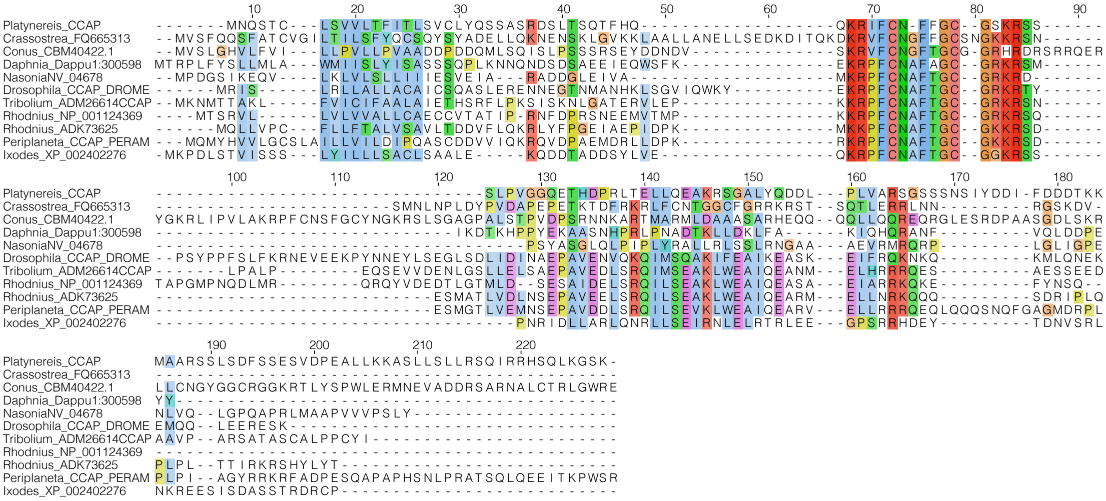
Multiple sequence alignment of annelid and mollusk pyrokinin-related sCAP pNPs.



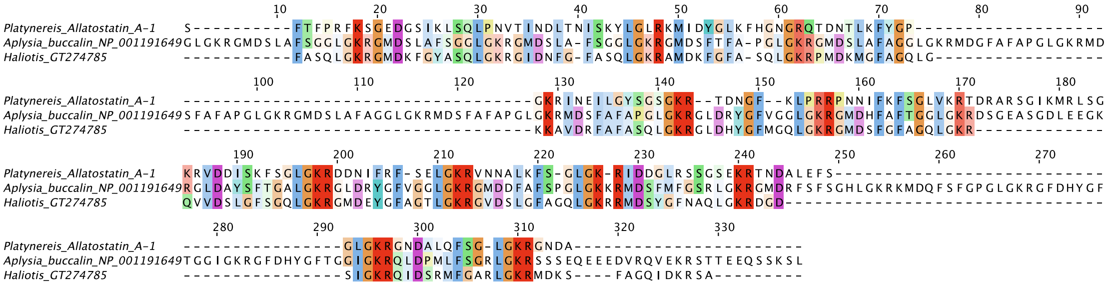
Multiple sequence alignment of bilaterian pyrokinin-related peptides, including annelid/mollusk sCAP, mollusk pleurin, insect pyrokinins and vertebrate neuromedin-U.



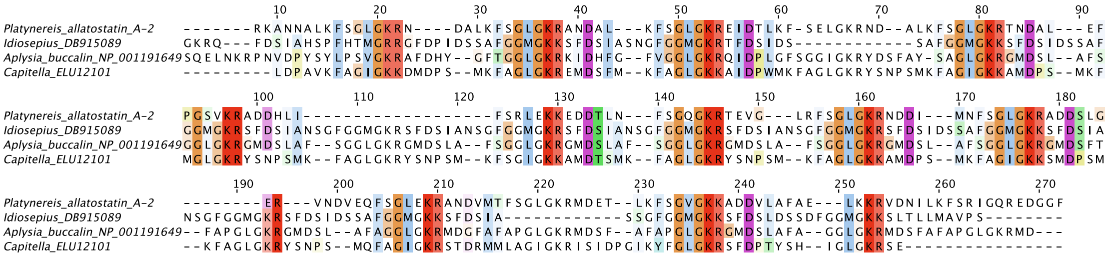
Multiple sequence alignment of *Platynereis* sulfakinin pNP with arthropod sulfakinin pNPs.



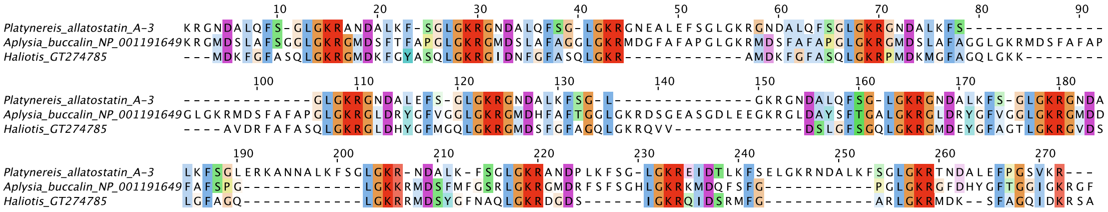
Multiple sequence alignment of *Platynereis* CCAP pNP with protostome CCAP pNPs.



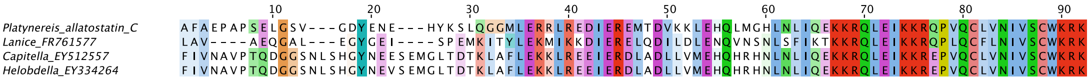
Multiple sequence alignment of trimmed *Platynereis* allatostatin-A-2 pNPs with mollusk allatostatin-A-2 pNPs.



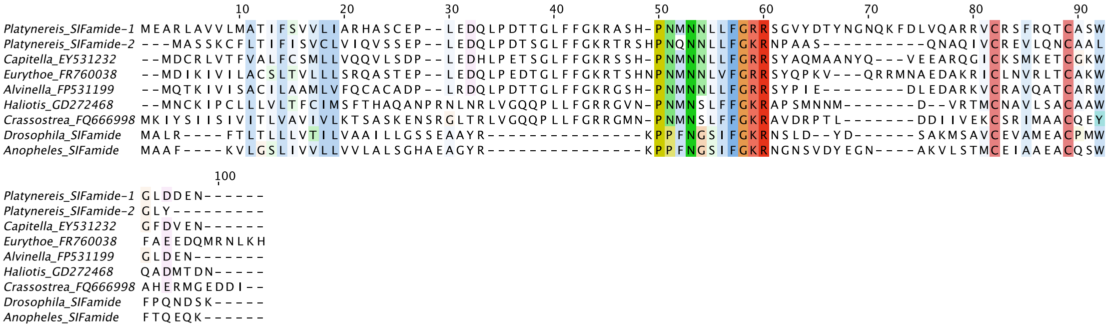
Multiple sequence alignment of trimmed annelid and mollusk allatostatin-A-2 pNPs.



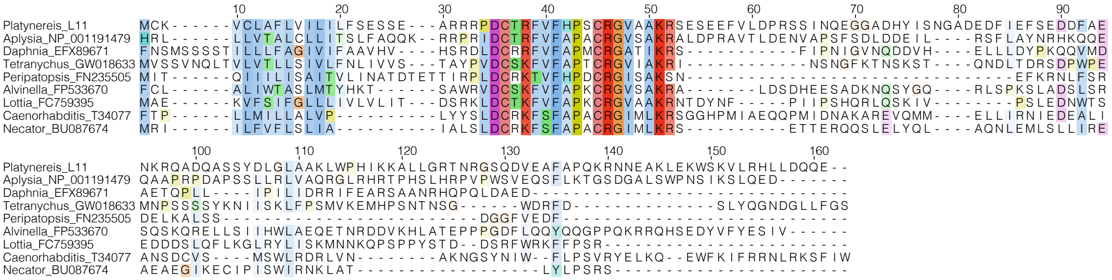
Multiple sequence alignment of trimmed annelid and mollusk allatostatin-A-3 pNPs.



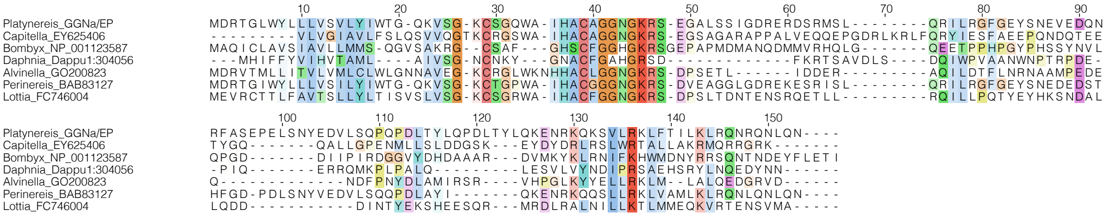
Multiple sequence alignment of trimmed annelid allatostatin-C pNPs. Besides the Cys-containing allatostatin-C peptide, these pNPs share other conserved peptide stretches (e.g., QLEI peptides).



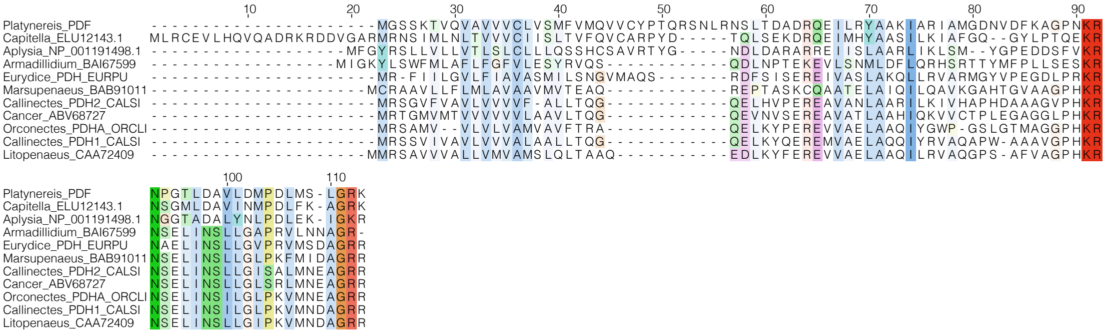
Multiple sequence alignment of lophotrochozoan FFamide and arthropod SIFamide pNPs shows besides a conserved amidated peptide conserved cystein-residues in the C-terminus of the pNPs.



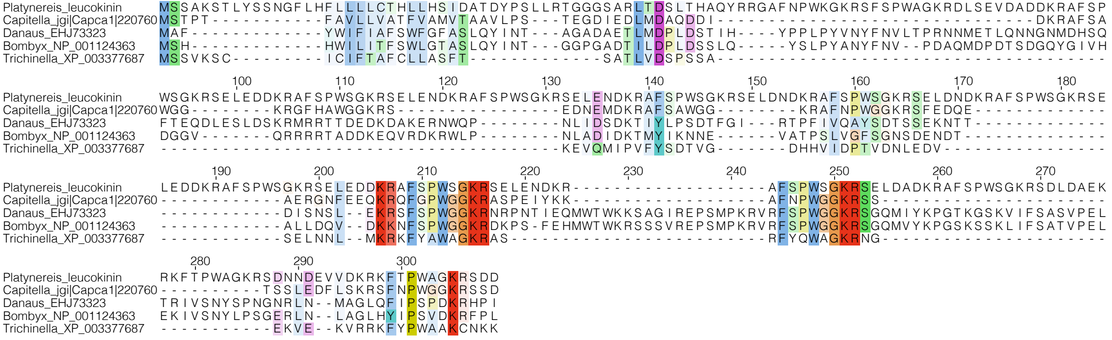
Multiple sequence alignment of *Platynereis* L11 pNP with protostome L11 pNPs.



Multiple sequence alignment of *Platynereis* GGNa/excitatory peptide pNP with protostome GGNa/ excitatory-peptide/CCHa pNPs.

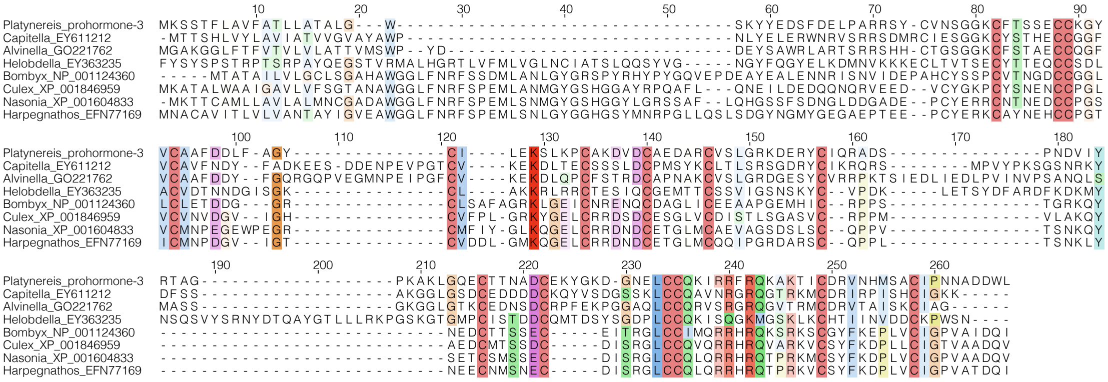


Multiple sequence alignment of *Platynereis* pdf pNP with protostome pdf/cerebrin pNPs.



Truncated multiple sequence alignment of *Platynereis* leucokinin pNP with protostome leucokinin pNPs.

Platynereis pNPs belonging to protostome pNPs families:



```
                                 10        20        30        40        50        60        70        80        90
Platynereis_prohormone-3 MKSSTFLAVFATLLATALG---W---------------------------------SKYYEDSFDELPARRSY-CVNSGGKCFTSSECCKGY
Capitella_EY611212       -MTTSHLVYLAVIATVVGVAYAWP--------------------------------NLYELERWNRVSRRSDMRCIESGGKCYSTHECCGGF
Alvinella_GO221762       MGAKGGLFTFVTVLVLATTVMSWP--YD----------------------------DEYSAWRLARTSRRSHH-CTGSGGKCFSTAECCQGF
Helobdella_EY363235      FYSYSPSTRPTSRPAYQEGSTVRMALHGRTLVFMLVGLNCIATSLQQSYVG-----NGYFQGYELKDMNVKKKECLTVTSECYTTEQCCSDL
Bombyx_NP_001124360      -----MTATAILVLGCLSGAHAWGGLFNRFSSDMLANLGYGRSPYRHYPYGQVEPDEAYEALENNRISNVIDEPAHCYSSPCVTNGDCCGGL
Culex_XP_001846959       MKATALWAAIGAVLVFSGTANAWGGLFNRFSPEMLANMGYGSHGGAYRPQAFL---QNEILDEDQQNQRVEED--VCYGKPCYSNENCCPGL
Nasonia_XP_001604833     -MKTTCAMLLAVLALMNCGADAWGGLFNRFSPEMLSNMGYGSHGGYLGRSSAF--LQHGSSFSDNGLDDGADE--PCYERRCNTNEDCCPGS
Harpegnathos_EFN77169    MNACAVITLVLVANTAYIGVEAWGGLFNRFSPEMLSNLGYGGHGSYMNRPGLLQSLSDGYNGMYGEGAEPTEE--PCYERKCAYNEHCCPGT

                              100       110       120       130       140       150       160       170       180
Platynereis_prohormone-3 VCAAFDDLF-AGY---------------CI----LEKSLKPCAKDVDCAEDARCVSLGRKDERYCIQRADS---------------PNDVIY
Capitella_EY611212       VCAVFNDY--FADKEES-DDENPEVPGTCV----KEKDLTECSSSLDCPMSYKCLTLSRSGDRYCIKRQRS--------MPVYPKSGSNRKY
Alvinella_GO221762       VCAAFDDY--FGQRGQPVEGMNPEIPGFCV----KEKDLQPCFSTRDCAPNAKCVSLGRDGESYCVRRPKTSIEDLIEDLPVINVPSANQLS
Helobdella_EY363235      ACVDTNNDGISGK---------------CL----AKKRLRRCTESIQCGEMTTCSSVIGSNSKYC--VPDK-----LETSYDFARDFKDKMY
Bombyx_NP_001124360      LCLETDDG---GR---------------CLSAFAGRKLGEICNRENQCDAGLICEEAAPGEMHIC--RPPS---------------TGRKQY
Culex_XP_001846959       VCVNVDGV--IGH---------------CVFPL-GRKYGELCRRDSDCESGLVCDISTLSGASVC--RPPM---------------VLAKQY
Nasonia_XP_001604833     VCMNPEGEWPEGR---------------CMFIY-GLKQGELCRRDNDCETGLMCAEVAGSDSLSC--QPPV---------------TSNKQY
Harpegnathos_EFN77169    ICMNPDGV--IGT---------------CVDDL-GMKQGELCRRDNDCETGLMCQQIPGRDARSC--QPPL---------------TSNKLY

                            190       200       210       220       230       240       250       260
Platynereis_prohormone-3 RTAG-------------------PKAKLGQECTTNADCEKYGKD-GNELCCQKIRRFRQKAKTICDRVNHMSACIPNNADDWL
Capitella_EY611212       DFSS-------------------AKGGLGSDCEDDDDCKQYVSDGSSKLCCQAVNRGRQGTRKMCDRIRPISHCIGKK-----
Alvinella_GO221762       MASS-------------------GKGGLGTKCEDNSDCRPFEKPGGAQLCCQRVSRGRQGVTRMCDRVTAISKCIAG------
Helobdella_EY363235      NSQSVYSRNYDTQAYGTLLLRKPGSKGTGMPCISTDDCQMTDSYSGDPLCCQKISQGKMGSKLKCHTIINVDDCKPWSN----
Bombyx_NP_001124360      ----------------------------NEDCTTSSEC-----EITRGLCCIMQRRHRQKSRKSCGYFKEPLVCIGPVAIDQI
Culex_XP_001846959       ----------------------------AEDCMTSSDC-----DISRGLCCQVQRRHRQVARKVCSYFKDPLLCIGTVAADQV
Nasonia_XP_001604833     ----------------------------SETCSMSSEC-----DISRGLCCQLQRRHRQTPRKMCSYFKDPLVCIGPVAADQV
Harpegnathos_EFN77169    ----------------------------NEECNMSNEC-----DISRGLCCQLQRRHRQTPRKVCSYFKDPLVCIGPVATDQI
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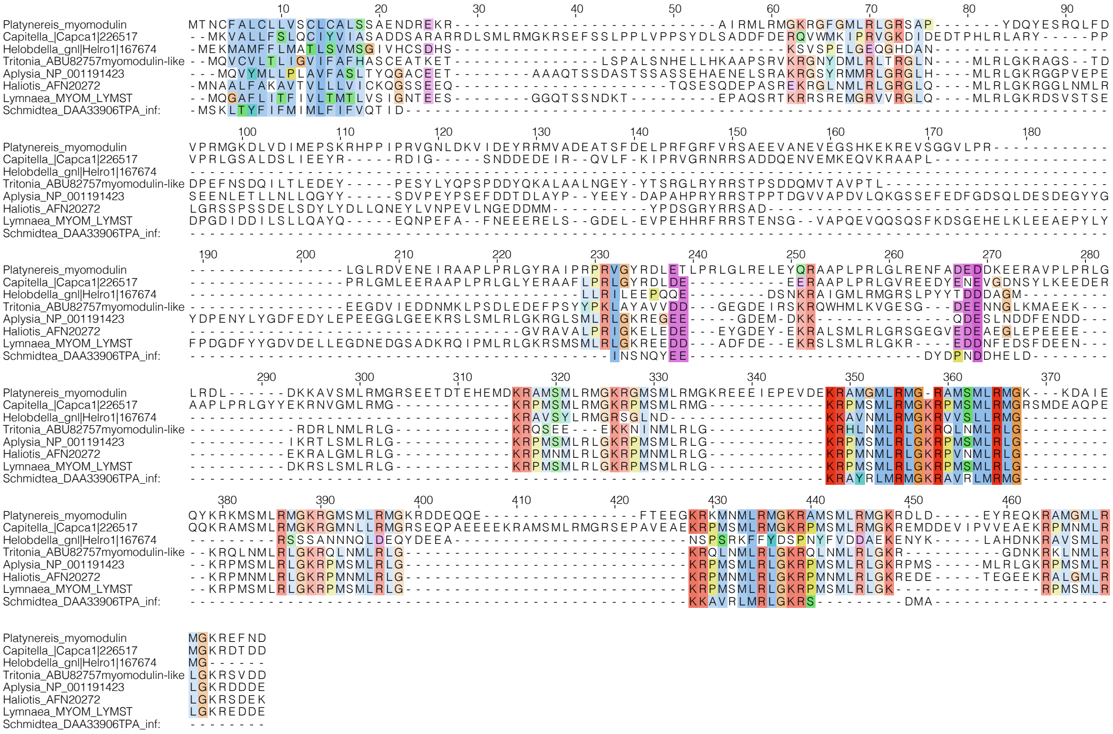
Multiple sequence alignment of *Platynereis* prohormone-3 pNP with protostome prohormone-3 pNPs.



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                                         10        20        30        40        50        60        70        80        90
Platynereis_myomodulin           MTNCFALCLLVSCLCALSSAENDREKR---------------------------AIRMLRMGKRGFGMLRLGRSAP-------YDQYESRQLFD
Capitella_|Capca1|226517         --MKVALLFSLQCIYVIASADDSARARRDLSMLRMGKRSEFSSLPPLVPPSYDLSADDFDERQVWMKIPRVGKDIDEDTPHLRLARY-----PP
Helobdella_gnl|Helro1|167674     -MEKMAMFFLMATLSVMSGIVHCSDHS----------------------------------KSVSPELGEQGHDAN------------------
Tritonia_ABU82757myomodulin-like --MQVCVLTLIGVIFAFHASCEATKET---------------LSPALSNHELLHKAAPSRVKRGNYDMLRLTRGLN----MLRLGKRAGS--TD
Aplysia_NP_001191423             ---MQVYMLLPLAVFASLTYQGACEET--------AAAQTSSDASTSSASSEHAENELSRAKRGSYRMMRLGRGLH----MLRLGKRGGPVEPE
Haliotis_AFN20272                -MNAALFAKAVTVLLLVICKQGSSEEQ----------------------TQSESQDEPASREKRGLNMLRLGRGLQ----MLRLGKRGGLNMLR
Lymnaea_MYOM_LYMST               --MQGAFLITFIVLTMTLVSIGNTEES--------GGQTSSNDKT---------EPAQSRTKRRSREMGRVVRGLQ----MLRLGKRDSVSTSE
Schmidtea_DAA33906TPA_inf:       -MSKLTYFIFMIMLFIFVQTID------------------------------------------------------------------------

                                    100       110       120       130       140       150       160       170       180
Platynereis_myomodulin           VPRMGKDLVDIMEPSKRHPPIPRVGNLDKVIDEYRRMVADEATSFDELPRFGRFVRSAEEVANEVEGSHKEKREVSGGVLPR------------
Capitella_|Capca1|226517         VPRLGSALDSLIEEYR-----RDIG-----SNDDEDEIR--QVLF-KIPRVGRNRRSADDQENVEMKEQVKRAAPL------------------
Helobdella_gnl|Helro1|167674     ----------------------------------------------------------------------------------------------
Tritonia_ABU82757myomodulin-like DPEFNSDQILTLEDEY-----PESYLYQPSPDDYQKALAALNGEY-YTSRGLRYRRSTPSDDQMVTAVPTL-----------------------
Aplysia_NP_001191423             SEENLETLLNLLQGYY-----SDVPEYPSEFDDTDLAYP--YEEY-DAPAHPRYRRSTPPTDGVVAPDVLQKGSSEFEDFGDSQLDESDEGYYG
Haliotis_AFN20272                LGRSSPSSDELSDYLYDLLQNEYLVNPEVLNGEDDMM----------YPDSGRYRRSAD-----------------------------------
Lymnaea_MYOM_LYMST               DPGDIDDILSLLQAYQ-----EQNPEFA--FNEEERELS--GDEL-EVPEHHRFRRSTENSG--VAPQEVQQSQSFKDSGEHELKLEEAEPYLY
Schmidtea_DAA33906TPA_inf:       ----------------------------------------------------------------------------------------------

                                190       200       210       220       230       240       250       260       270       280
Platynereis_myomodulin           ----------------LGLRDVENEIRAAPLPRLGYRAIPRPRVGYRDLETLPRLGLRELEYQRAAPLPRLGLRENFADEDDKEERAVPLPRLG
Capitella_|Capca1|226517         ----------------PRLGMLEERAAPLPRLGLYERAAFLPRLGYRDLDE----------EERAAPLPRLGVREEDYENEVGDNSYLKEEDER
Helobdella_gnl|Helro1|167674     ----------------------------------------LLRILEEPQQE--------DSNKRAIGMLRMGRSLPYYTDDDAGM---------
Tritonia_ABU82757myomodulin-like ----------------EEGDVIEDDNMKLPSDLEDEFPSYYPKLAYAVVDD---GEGDEIRSKRQWHMLKVGESG---DEENNGLKMAEEK---
Aplysia_NP_001191423             YDPENYLYGDFEDYLEPEEGGLGEEKRSLSMLRLGKRGLSMLRLGKREGEE-----GDEM-DKK--------------QDESLNDDFENDD---
Haliotis_AFN20272                ----------------------------------GVRAVALPRIGKELEDE---EYGDEY-EKRALSMLRLGRSGEGVEDEAEGLEPEEEE---
Lymnaea_MYOM_LYMST               FPDGDFYYGDVDELLEGDNEDGSADKRQIPMLRLGKRSMSMLRLGKREEDD---ADFDE--EKRSLSMLRLGKR----EDDNFEDSFDEEN---
Schmidtea_DAA33906TPA_inf:       -------------------------------------------INSNQYEE------------------------DYDPNDDHELD--------

                                      290       300       310       320       330       340       350       360       370
Platynereis_myomodulin           LRDL------DKKAVSMLRMGRSEETDTEHEMDKRAMSMLRMGKRGMSMLRMGKREEEIEPEVDEKRAMGMLRMG-RAMSMLRMGK---KDAIE
Capitella_|Capca1|226517         AAPLPRLGYYEKRNVGMLRMG------------KRPMSMLRMGKRPMSMLRMG------------KRPMSMLRMGKRPMSMLRMGRSMDEAQPE
Helobdella_gnl|Helro1|167674     ---------------------------------KRAVSYLRMGRSGLND----------------KKAVNMLRMGKRVVSLLRMG---------
Tritonia_ABU82757myomodulin-like -----------RDRLNMLRLG------------KRQSEE---EKKNINMLRLG------------KRHLNMLRLGKRQLNMLRLG---------
Aplysia_NP_001191423             ----------IKRTLSMLRLG------------KRPMSMLRLGKRPMSMLRLG------------KRPMSMLRLGKRPMSMLRLG---------
Haliotis_AFN20272                ----------EKRALGMLRLG------------KRPMNMLRLGKRPMNMLRLG------------KRPMNMLRLGKRPVNMLRLG---------
Lymnaea_MYOM_LYMST               ----------DKRSLSMLRLG------------KRPMSMLRLGKRPMSMLRLG------------KRPMSMLRLGKRPMSMLRLG---------
Schmidtea_DAA33906TPA_inf:       -----------------------------------------------------------------KRAYRLMRMGKRAVRLMRMG---------

                                  380       390       400       410       420       430       440       450       460
Platynereis_myomodulin           QYKRKMSMLRMGKRGMSMLRMGKRDDEQQE----------------FTEEGKRKMNMLRMGKRAMSMLRMGKRDLD-----EYREQKRAMGMLR
Capitella_|Capca1|226517         QQKRAMSMLRMGKRGMNLLRMGRSEQPAEEEEKRAMSMLRMGRSEPAVEAEKRPMSMLRMGKRPMSMLRMGKREMDDEVIPVVEAEKRPMNMLR
Helobdella_gnl|Helro1|167674     ---------RSSSANNNQLDEQYDEEA------------------------NSPSRKFFYDSPNYFVDDAEKENYK-----LAHDNKRAVSMLR
Tritonia_ABU82757myomodulin-like --KRQLNMLRLGKRQLNMLRLG-----------------------------KRQLNMLRLGKRQLNMLRLGKR----------GDNKRKLNMLR
Aplysia_NP_001191423             --KRPMSMLRLGKRPMSMLRLG-----------------------------KRPMSMLRLGKRPMSMLRLGKRPMS-----MLRLGKRPMSMLR
Haliotis_AFN20272                --KRPMNMLRLGKRPMNMLRLG-----------------------------KRPMNMLRLGKRPMNMLRLGKREDE-----TEGEEKRALGMLR
Lymnaea_MYOM_LYMST               --KRPMSMLRLGKRPMSMLRLG-----------------------------KRPMSMLRLGKRPMSMLRLGK----------------RPMSMLR
Schmidtea_DAA33906TPA_inf:       ---------------------------------------------------KKAVRLMRLGKRS---------DMA------------------

Platynereis_myomodulin           MGKREFND
Capitella_|Capca1|226517         MGKRDTDD
Helobdella_gnl|Helro1|167674     MG------
Tritonia_ABU82757myomodulin-like LGKRSVDD
Aplysia_NP_001191423             LGKRDDDE
Haliotis_AFN20272                LGKRSDEK
Lymnaea_MYOM_LYMST               LGKREDDE
Schmidtea_DAA33906TPA_inf:       --------
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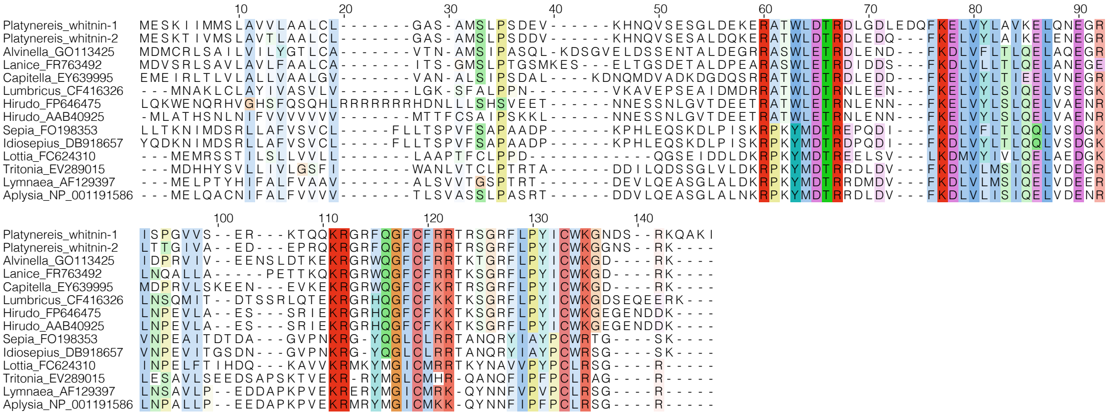
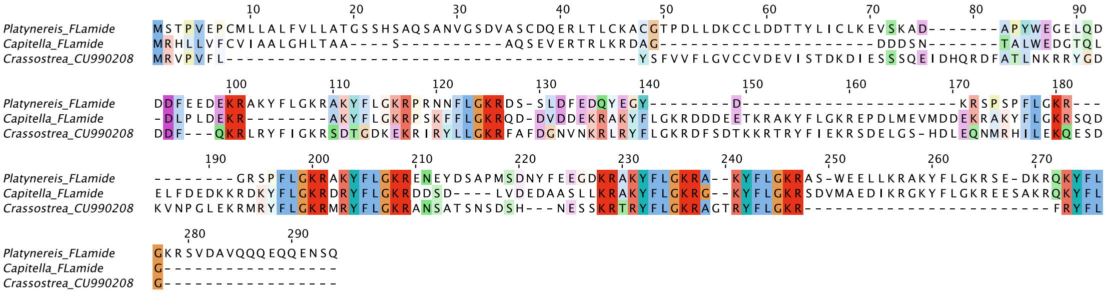
Multiple sequence alignment of truncated *Platynereis* myomodulin pNP with lophotrochozoan myomodulin pNPs.

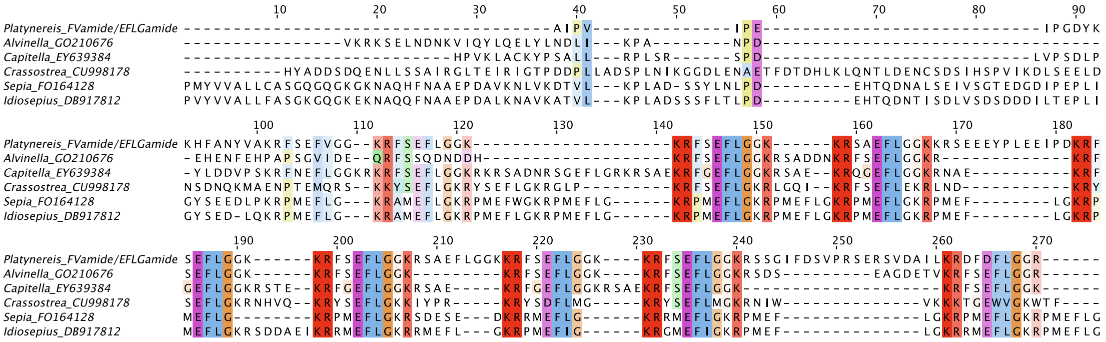


Multiple sequence alignment of *Platynereis* whitnin with annelid and mollusk whitnin/SPTR pNPs.

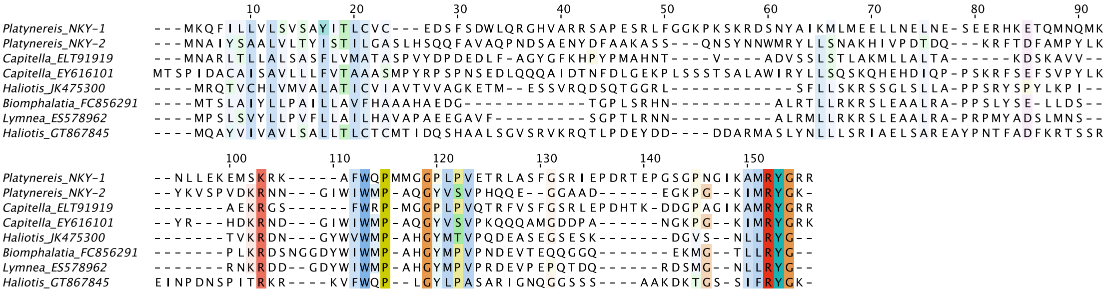
Platynereis pNPs belonging to lophotrochozoan pNPs families:



Multiple sequence alignment of annelid and mollusk FLamide/Fulicin pNPs.



Multiple sequence alignment of annelid and mollusk EFLGamide/EFLamide containing ESTs.



```
                              10        20        30        40        50        60        70        80        90
Platynereis_NKY-1     ---MKQFILLVLSVSAYITLCVC---EDSFSDWLQRGHVARRSAPESRLFGGKPKSKRDSNYAIKMLMEELLNELNE-SEERHKETQMNQMK
Platynereis_NKY-2     ---MNAIYSAALVLTYISTILGASLHSQQFAVAQPNDSAENYDFAAKASS---QNSYNNWMRYLLSNAKHIVPDTDQ---KRFTDFAMPYLK
Capitella_ELT91919    ---MNARLTLLALSASFLVMATASPVYDPDEDLF-AGYGFKHPYPMAHNT----V----ADVSSLSTLAKMLLALTA------KDSKAVV--
Capitella_EY616101    MTSPIDACAISAVLLLFVTAAASMPYRPSPNSEDLQQQAIDTNFDLGEKPLSSSTSALAWIRYLLSQSKQHEHDIQP-PSKRFSEFSVPYLK
Haliotis_JK475300     ----MRQTVCHLVMVALATICVIAVTVVAGKETM--ESSVRQDSQTGGRL------------SFLLSKRSSGLSLLA-PPSRYSPYLKPI--
Biomphalatia_FC856291 ----MTSLAIYLLPAILLAVFHAAAHAEDG------------TGPLSRHN----------ALRTLLRKRSLEAALRA-PPSLYSE-LLDS--
Lymnea_ES578962       ----MPSLSVYLLPVFLLAILHAVAPAEEGAVF---------SGPTLRNN----------ALRMLLRKRSLEAALRA-PRPMYADSLMNS--
Haliotis_GT867845     ----MQAYVIVAVLSALLTLCTCMTIDQSHAALSGVSRVKRQTLPDEYDD----DDARMASLYNLLLSRIAELSAREAYPNTFADFKRTSSR

                           100       110       120       130       140       150
Platynereis_NKY-1     --NLLEKEMSKRK-----AFWQPMMGGPLPVETRLASFGSRIEPDRTEPGSGPNGIKAMRYGRR
Platynereis_NKY-2     --YKVSPVDKRNN---GIWIWMP-AQGYVSVPHQQE--GGAAD------EGKPG--KIMRYGK-
Capitella_ELT91919    -------AEKRGS------FWRP-MGGPLPVQTRFVSFGSRLEPDHTK-DDGPAGIKAMRYGRR
Capitella_EY616101    --YR---HDKRND---GIWIWMP-AQGYVSVPKQQQAMGDDPA------NGKPG--KIMRYGRK
Haliotis_JK475300     -------TVKRDN---GYWVWMP-AHGYMTVPQDEASEGSESK-------DGVS--NLLRYG--
Biomphalatia_FC856291 -------PLKRDSNGGDYWIWMP-AHGYMPVPNDEVTEQQGGQ-------EKMG--TLLRYG--
Lymnea_ES578962       -------RNKRDD--GDYWIWMP-AHGYMPVPRDEVPEPQTDQ------RDSMG--NLLRYG--
Haliotis_GT867845     EINPDNSPITRKR----KVFWQP--LGYLPASARIGNQGGSSS----AAKDKTGS-SIFRYGK-
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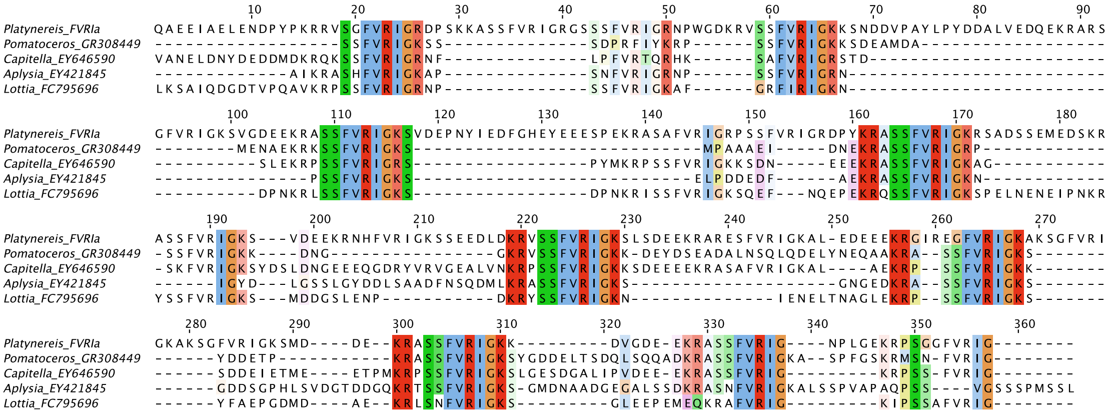
Multiple sequence alignment of annelid and mollusk NKY pNPs.



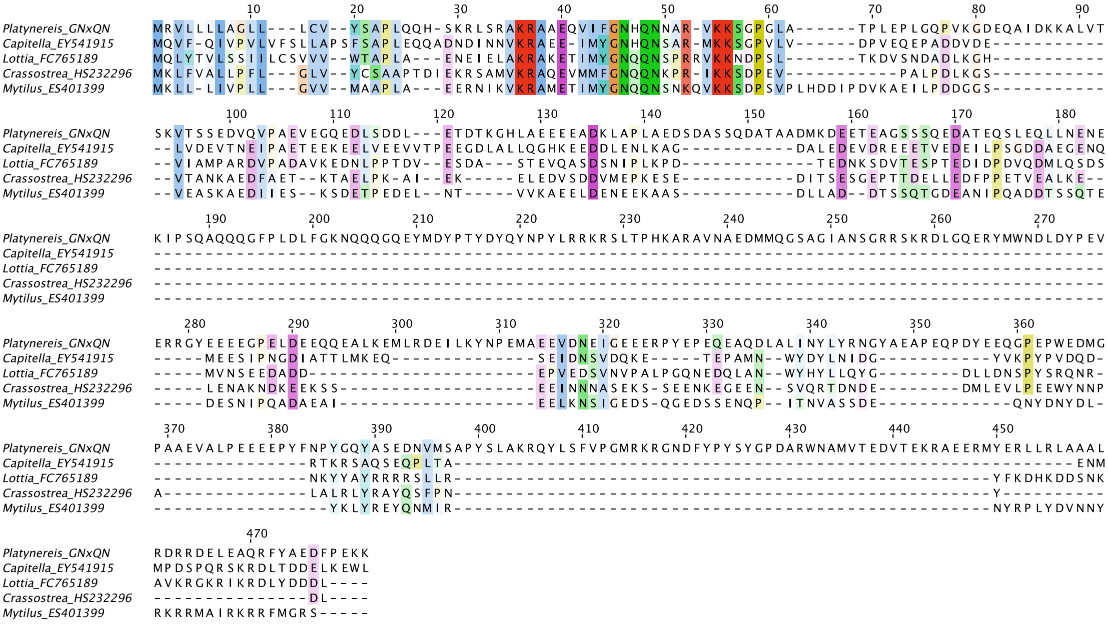
```
                              10        20        30        40        50        60        70        80        90
Platynereis_FVRIa     QAEEIAELENDPYPKRRVSGFVRIGRDPSKKASSFVRIGRGSSSFVRIGRNPWGDKRVSSFVRIGKKSNDDVPAYLPYDDALVEDQEKRARS
Pomatoceros_GR308449  ------------------SSFVRIGKSS--------------SDPRFIYKRP------SSFVRIGKKSDEAMDA------------------
Capitella_EY646590    VANELDNYDEDDMDKRQKSSFVRIGRNF--------------LPFVRTQRHK------SAFVRIGRSTD-----------------------
Aplysia_EY421845      -------------AIKRASHFVRIGKAP--------------SNFVRIGRNP------SSFVRIGRN-------------------------
Lottia_FC795696       LKSAIQDGDTVPQAVKRPSSFVRIGRNP--------------SSFVRIGKAF------GRFIRIGKN-------------------------

                           100       110       120       130       140       150       160       170       180
Platynereis_FVRIa     GFVRIGKSVGDEEKRASSFVRIGKSVDEPNYIEDFGHEYEEESPEKRASAFVRIGRPSSFVRIGRDPYKRASSFVRIGKRSADSSEMEDSKR
Pomatoceros_GR308449  --------MENAEKRKSSFVRIGKS----------------------------MPAAAEI-----DNEKRASSFVRIGRP------------
Capitella_EY646590    ----------SLEKRPSSFVRIGRS-----------------PYMKRPSSFVRIGKKSDN-----EEEKRASSFVRIGKAG-----------
Aplysia_EY421845      ---------------PSSFVRIGKS---------------------------ELPDDEDF------AEKRASSFVRIGKN------------
Lottia_FC795696       ----------DPNKRLSSFVRIGKS-----------------DPNKRISSFVRIGKSQEF---NQEPEKRQSSFVRIGKSPELNENEIPNKR

                         190       200       210       220       230       240       250       260       270
Platynereis_FVRIa     ASSFVRIGKS---VDEEKRNHFVRIGKSSEEDLDKRVSSFVRIGKSLSDEEKRARESFVRIGKAL-EDEEEKRGIREGFVRIGKAKSGFVRI
Pomatoceros_GR308449  -SSFVRIGKK----DNG----------------GKRVSSFVRIGKK-DEYDSEADALNSQLQDELYNEQAAKRA--SSFVRIGKS-------
Capitella_EY646590    -SKFVRIGKSYDSLDNGEEEQGDRYVRVGEALVNKRPSSFVRIGKKSDEEEEKRASAFVRIGKAL----AEKRP--SSFVRIGKK-------
Aplysia_EY421845      ------IGYD---LGSSLGYDDLSAADFNSQDMLKRASSFVRIGKS--------------------GNGEDKRA--SSFVRIGKS-------
Lottia_FC795696       YSSFVRIGKS---MDDGSLENP-----------DKRYSSFVRIGKN--------------IENELTNAGLEKRP--SSFVRIGKS-------

                       280       290       300       310       320       330       340       350       360
Platynereis_FVRIa     GKAKSGFVRIGKSMD----DE--KRASSFVRIGKK---------DVGDE-EKRASSFVRIG----NPLGEKRPSGGFVRIG--------
Pomatoceros_GR308449  ------YDDETP-----------KRASSFVRIGKSYGDDELTSDQLSQQADKRASSFVRIGKA--SPFGSKRMSN-FVRIG--------
Capitella_EY646590    ------SDDEIETME----ETPMKRPSSFVRIGKSLGESDGALIPVDEE-EKRASSFVRIG---------KRPSS-FVRIG--------
Aplysia_EY421845      ------GDDSGPHLSVDGTDDGQKRTSSFVRIGKS-GMDNAADGEGALSSDKRASNFVRIGKALSSPVAPAQPSS----VGSSSPMSSL
Lottia_FC795696       ------YFAEPGDMD----AE--KRLSNFVRIGKS---------GLEEPEMEQKRAFVRIG---------KIPSSAFVRIG--------
```

Multiple sequence alignment of trimmed annelid and mollusk FVRIamide pNPs.



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                              10        20        30        40        50        60        70        80        90
Platynereis_GNxQN     MRVLLLLAGLL---LCV--YSAPLQQH-SKRLSRAKRAAEQVIFGNHQNNAR-VKKSGPGLA------TPLEPLGQPVKGDEQAIDKKALVT
Capitella_EY541915    MQVF-QIVPVLVFSLLAPSFSAPLEQQADNDINNVKRAEE-IMYGNHQNSAR-MKKSGPVLV------DPVEQEPADDVDE-----------
Lottia_FC765189       MQLYTVLSSIILCSVVV--WTAPLA---ENEIELAKRAKETIMYGNQQNSPRRVKKNDPSL-------TKDVSNDADLKGH-----------
Crassostrea_HS232296  MKLFVALLPFL---GLV--YCSAAPTDIEKRSAMVKRAQEVMMFGNQQNKPR-IKKSDPEV----------PALPDLKGS-----------
Mytilus_ES401399      MKLL-LIVPLL---GVV--MAAPLA---EERNIKVKRAMETIMYGNQQNSNKQVKKSDPSVPLHDDIPDVKAEILPDDGGS-----------

                           100       110       120       130       140       150       160       170       180
Platynereis_GNxQN     SKVTSSEDVQVPAEVEGQEDLSDDL---ETDTKGHLAEEEEADKLAPLAEDSDASSQDATAADMKDEETEAGSSSQEDATEQSLEQLLNENE
Capitella_EY541915    --LVDEVTNEIPAETEEKEELVEEVVTPEEGDLALLQGHKEEDDLENLKAG-----------DALEDEVDREEETVEDEILPSGDDAEGENQ
Lottia_FC765189       --VIAMPARDVPADAVKEDNLPPTDV--ESDA---STEVQASDSNIPLKPD-------------TEDNKSDVTESPTEDIDPDVQDMLQSDS
Crassostrea_HS232296  --VTANKAEDFAET--KTAELPK-AI--EK-----ELEDVSDDVMEPKESE-----------DITSESGEPTTDELLEDFPPETVEALKE--
Mytilus_ES401399      --VEASKAEDIIES--KSDETPEDEL--NT-----VVKAEELDENEEKAAS-----------DLLAD--DTSSQTGDEANIPQADDTSSQTE

                         190       200       210       220       230       240       250       260       270
Platynereis_GNxQN     KIPSQAQQQGFPLDLFGKNQQQGQEYMDYPTYDYQYNPYLRRKRSLTPHKARAVNAEDMMQGSAGIANSGRRSKRDLGQERYMWNDLDYPEV
Capitella_EY541915    --------------------------------------------------------------------------------------------
Lottia_FC765189       --------------------------------------------------------------------------------------------
Crassostrea_HS232296  --------------------------------------------------------------------------------------------
Mytilus_ES401399      --------------------------------------------------------------------------------------------

                       280       290       300       310       320       330       340       350       360
Platynereis_GNxQN     ERRGYEEEEGPELDEEQQEALKEMLRDEILKYNPEMAEEVDNEIGEEERPYEPEQEAQDLALINYLYRNGYAEAPEQPDYEEQGPEPWEDMG
Capitella_EY541915    -----MEESIPNGDIATTLMKEQ--------------SEIDNSVDQKE-----TEPAMN--WYDYLNIDG-----------YVKPYPVDQD-
Lottia_FC765189       -----MVNSEEDADD----------------------EPVEDSVNVPALPGQNEDQLAN--WYHYLLQYG--------DLLDNSPYSRQNR-
Crassostrea_HS232296  -----LENAKNDKEEKSS-------------------EEINNNASEKS-SEENKEGEEN--SVQRTDNDE--------DMLEVLPEEWYNNP
Mytilus_ES401399      -----DESNIPQADAEAI-------------------EELKNSIGEDS-QGEDSSENQP--ITNVASSDE-------------QNYDNYDL-

                      370        380       390       400       410       420       430       440       450
Platynereis_GNxQN     PAAEVALPEEEEPYFNPYGQYASEDNVMSAPYSLAKRQYLSFVPGMRKRGNDFYPYSYGPDARWNAMVTEDVTEKRAEERMYERLLRLAAAL
Capitella_EY541915    ---------------RTKRSAQSEQPLTA------------------------------------------------------------ENM
Lottia_FC765189       ---------------NKYYAYRRRRSLLR----------------------------------------------------YFKDHKDDSNK
Crassostrea_HS232296  A--------------LALRLYRAYQSFPN----------------------------------------------------Y----------
Mytilus_ES401399      -----------------YKLYREYQNMIR----------------------------------------------------NYRPLYDVNNY

                             470
Platynereis_GNxQN     RDRRDELEAQRFYAEDFPEKK
Capitella_EY541915    MPDSPQRSKRDLTDDELKEWL
Lottia_FC765189       AVKRGKRIKRDLYDDDL----
Crassostrea_HS232296  ---------------DL----
Mytilus_ES401399      RKRRMAIRKRRFMGRS-----
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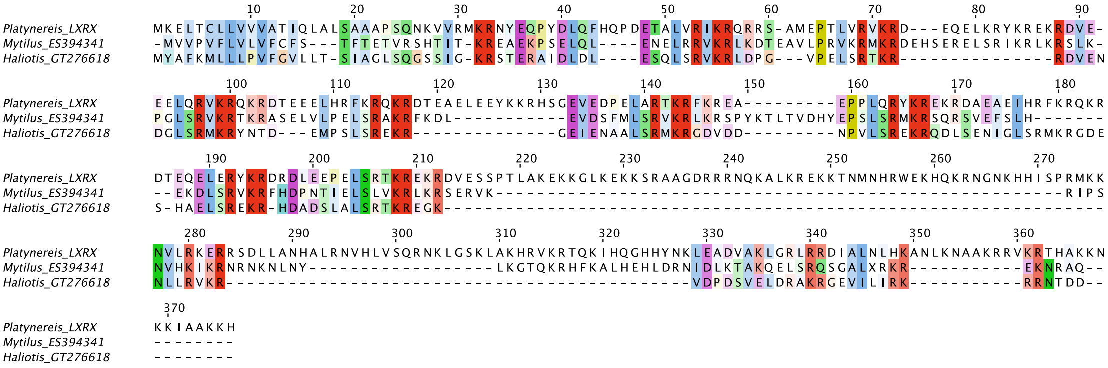
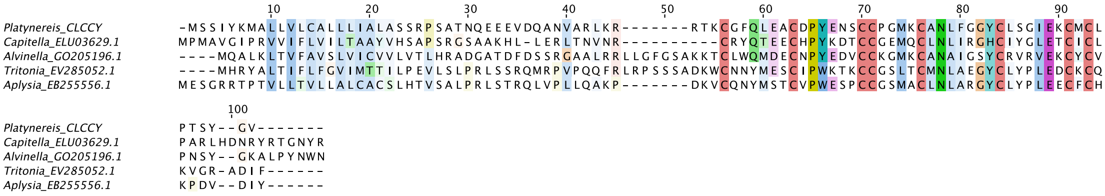
Multiple sequence alignment of annelid and mollusk GNXQN peptide pNPs.



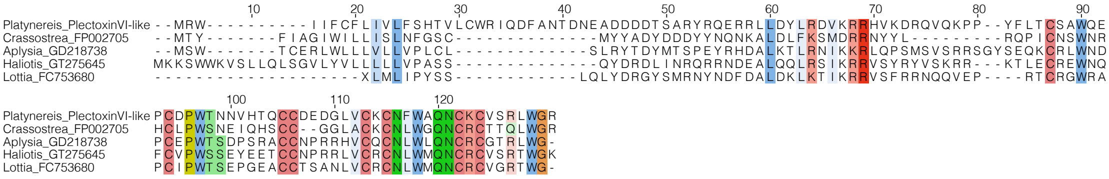
```
                            10        20        30        40        50        60        70        80        90
Platynereis_LXRX   MKELTCLLVVVATIQLALSAAAPSQNKVVRMKRNYEQPYDLQFHQPDETALVRIKRQRRS-AMEPTLVRVKRD---EQELKRYKREKRDVE-
Mytilus_ES394341   -MVVPVFLVLVFCFS---TFTETVRSHTIT-KREAEKPSELQL----ENELRRVKRLKDTEAVLPRVKRMKRDEHSERELSRIKRLKRSLK-
Haliotis_GT276618  MYAFKMLLLPVFGVLLT-SIAGLSQGSSIG-KRSTERAIDLDL----ESQLSRVKRLDPG---VPELSRTKR---------------RDVEN

                          100       110       120       130       140       150       160       170       180
Platynereis_LXRX   EELQRVKRQKRDTEEELHRFKRQKRDTEAELEEYKKRHSGEVEDPELARTKRFKREA---------EPPLQRYKREKRDAEAEIHRFKRQKR
Mytilus_ES394341   PGLSRVKRTKRASELVLPELSRAKRFKDL-----------EVDSFMLSRVKRLKRSPYKTLTVDHYEPSLSRMKRSQRSVEFSLH-------
Haliotis_GT276618  DGLSRMKRYNTD---EMPSLSREKR--------------GEIENAALSRMKRGDVDD---------NPVLSREKRQDLSENIGLSRMKRGDE

                        190       200       210       220       230       240       250       260       270
Platynereis_LXRX   DTEQELERYKRDRDLEEPELSRTKREKRDVESSPTLAKEKKGLKEKKSRAAGDRRRNQKALKREKKTNMNHRWEKHQKRNGNKHHISPRMKK
Mytilus_ES394341   --EKDLSRVKRFHDPNTIELSLVKRLKRSERVK-------------------------------------------------------RIPS
Haliotis_GT276618  S-HAELSREKR-HDADSLALSRTKREGK----------------------------------------------------------------

                      280       290       300       310       320       330       340       350       360
Platynereis_LXRX   NVLRKERRSDLLANHALRNVHLVSQRNKLGSKLAKHRVKRTQKIHQGHHYNKLEADVAKLGRLRRDIALNLHKANLKNAAKRRVKRTHAKKN
Mytilus_ES394341   NVHKIKRNRNKNLNY------------------LKGTQKRHFKALHEHLDRNIDLKTAKQELSRQSGALXRKR-----------EKNRAQ--
Haliotis_GT276618  NLLRVKR---------------------------------------------VDPDSVELDRAKRGEVILIRK-----------RRNTDD--

                    370
Platynereis_LXRX   KKIAAKKH
Mytilus_ES394341   --------
Haliotis_GT276618  --------
```

Multiple sequence alignment of annelid and mollusk LXRX peptide pNPs.



```
                               10        20        30        40        50        60        70        80        90
Platynereis_CLCCY     -MSSIYKMALLVLCALLLIALASSRPSATNQEEEVDQANVARLKR-------RTKCGFQLEACDPYENSCCPGMKCANLFGGYCLSGIEKCMCL
Capitella_ELU03629.1  MPMAVGIPRVVIFLVILTAAYVHSAPSRGSAAKHL-LERLTNVNR----------CRYQTEECHPYKDTCCGEMQCLNLIRGHCIYGLETCICL
Alvinella_GO205196.1  ----MQALKLTVFAVSLVICVVLVTLHRADGATDFDSSRGAALRRLLGFGSAKKTCLWQMDECNPYEDVCCKGMKCANAIGSYCRVRVEKCYCV
Tritonia_EV285052.1   ----MHRYALTIFLFGVIMTTILPEVLSLPRLSSRQMRPVPQQFRLRPSSSADKWCNNYMESCIPWKTKCCGSLTCMNLAEGYCLYPLEDCKCQ
Aplysia_EB255556.1    MESGRRTPTVLLTVLLALCACSLHTVSALPRLSTRQLVPLLQAKP-------DKVCQNYMSTCVPWESPCCGSMACLNLARGYCLYPLEECFCH

                           100
Platynereis_CLCCY     PTSY--GV-------
Capitella_ELU03629.1  PARLHDNRYRTGNYR
Alvinella_GO205196.1  PNSY--GKALPYNWN
Tritonia_EV285052.1   KVGR-ADIF------
Aplysia_EB255556.1    KPDV--DIY------
```

Multiple sequence alignment of annelid and mollusk CLCCY pNPs.



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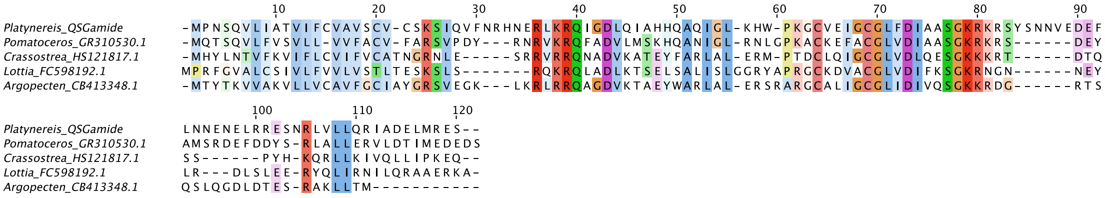
                                      10        20        30        40        50        60        70        80        90
Platynereis_PlectoxinVI-like --MRW----------IIFCFLIVLFSHTVLCWRIQDFANTDNEADDDDTSARYRQERRLLDYLRDVKRRHVKDRQVQKPP--YFLTCSAWQE
Crassostrea_FP002705         --MTY-------FIAGIWILLISLNFGSC--------------MYYADYDDDYYNQNKALDLFKSMDRRNYYL---------RQPICNSWNR
Aplysia_GD218738             --MSW-------TCERLWLLLVLLVPLCL-------------SLRYTDYMTSPEYRHDALKTLRNIKKRLQPSMSVSRRSGYSEQKCRLWND
Haliotis_GT275645            MKKSWWKVSLLQLSGVLYVLLLLLVPASS--------------QYDRDLINRQRRNDEALQQLRSIKRRVSYRYVSKRR---KTLECREWNQ
Lottia_FC753680              --------------------XLMLIPYSS------------LQLYDRGYSMRNYNDFDALDKLKTIKRRVSFRRNQQVEP----RTCRGWRA

                                    100       110       120
Platynereis_PlectoxinVI-like PCDPWTNNVHTQCCDEDGLVCKCNFWAQNCKCVSRLWGR
Crassostrea_FP002705         HCLPWSNEIQHSCC--GGLACKCNLWGQNCRCTTQLWGR
Aplysia_GD218738             PCEPWTSDPSRACCNPRRHVCQCNLWLQNCRCGTRLWG-
Haliotis_GT275645            FCVPWSSEYEETCCNPRRLVCRCNLWMQNCRCVSRTWGK
Lottia_FC753680              PCIPWTSEPGEACCTSANLVCRCNLWMQNCRCVGRTWG-
```

Multiple sequence alignment of annelid and mollusk CCWamide pNPs.



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                                 10        20        30        40        50        60        70        80        90
Platynereis_QSGamide    -MPNSQVLIATVIFCVAVSCV-CSKSIQVFNRHNERLKRQIGDLQIAHHQAQIGL-KHW-PKGCVEIGCGLFDIAASGKRKRSYSNNVEDEF
Pomatoceros_GR310530.1  -MQTSQVLFVSVLL-VVFACV-FARSVPDY---RNRVKRQFADVLMSKHQANIGL-RNLGPKACKEFACGLVDIAASGKRKRS------DEY
Crassostrea_HS121817.1  -MHYLNTVFKVIFLCVIFVCATNGRNLE-----SRRVRRQNADVKATEYFARLAL-ERM-PTDCLQIGCGLVDLQESGKKKRT------DTQ
Lottia_FC598192.1       MPRFGVALCSIVLFVVLVSTLTESKSLS-------RQKRQLADLKTSELSALISLGGRYAPRGCKDVACGLVDIFKSGKRNGN------NEY
Argopecten_CB413348.1   -MTYTKVVAKVLLVCAVFGCIAYGRSVEGK---LKRLRRQAGDVKTAEYWARLAL-ERSRARGCALIGCGLIDIVQSGKKRDG------RTS

                               100       110       120
Platynereis_QSGamide    LNNENELRRESNRLVLLQRIADELMRES--
Pomatoceros_GR310530.1  AMSRDEFDDYS-RLALLERVLDTIMEDEDS
Crassostrea_HS121817.1  SS------PYH-KQRLLKIVQLLIPKEQ--
Lottia_FC598192.1       LR---DLSLEE-RYQLIRNILQRAAERKA-
Argopecten_CB413348.1   QSLQGDLDTES-RAKLLTM-----------
```
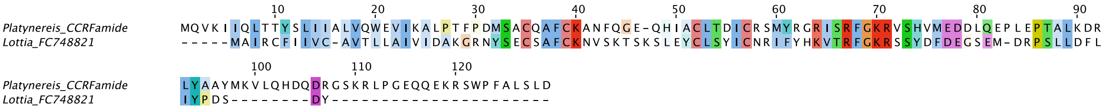

Multiple sequence alignment of annelid and mollusk QSGamide pNPs.



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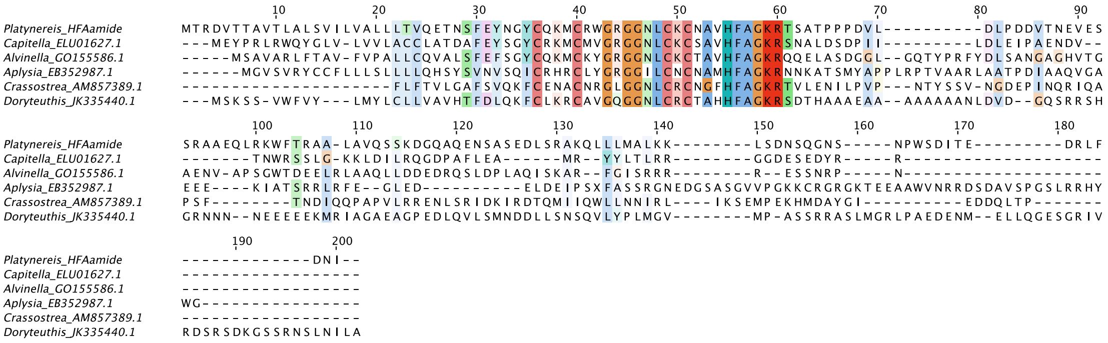
                                10        20        30        40        50        60        70        80        90
Platynereis_CCRFamide  MQVKIIQLTTYSLIIALVQWEVIKALPTFPDMSACQAFCKANFQGE-QHIACLTDICRSMYRGRISRFGKRVSHVMEDDLQEPLEPTALKDR
Lottia_FC748821        -----MAIRCFIIVC-AVTLLAIVIDAKGRNYSECSAFCKNVSKTSKSLEYCLSYICNRIFYHKVTRFGKRSSYDFDEGSEM-DRPSLLDFL

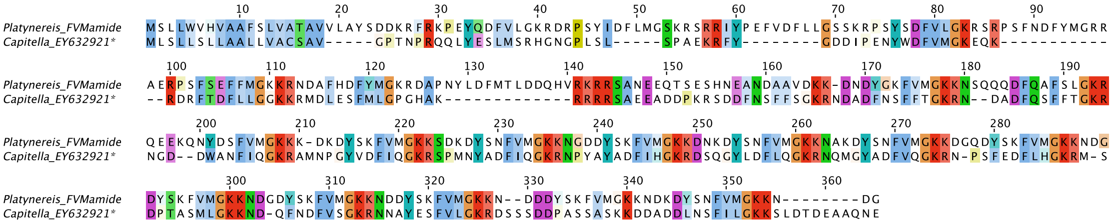
                              100       110       120
Platynereis_CCRFamide  LYAAYMKVLQHDQDRGSKRLPGEQQEKRSWPFALSLD
Lottia_FC748821        IYPDS--------DY----------------------
```

Multiple sequence alignment of *Platynereis* and *Lottia gigantea* CCRFamide pNPs.

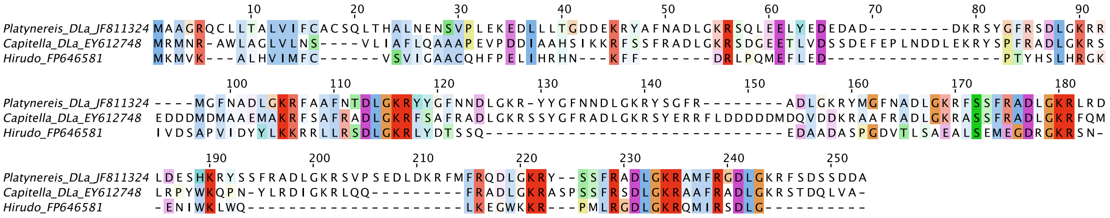


Multiple sequence alignment of annelid and mollusk HFAamide pNPs.

Platynereis pNPs belonging to annelid pNPs families:

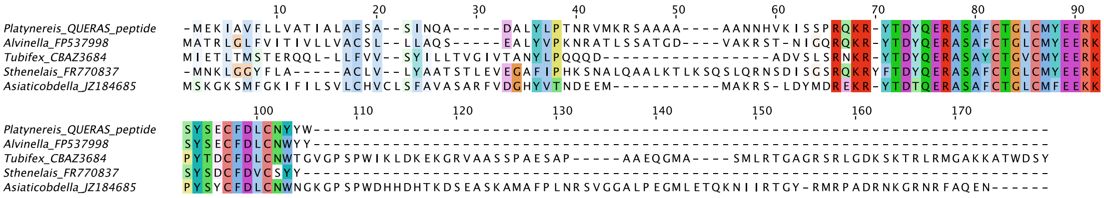


Multiple sequence alignment of annelid FVMamide pNPs.



Multiple sequence alignment of annelid DLamide pNPs.

Multiple sequence alignment of annelid SLRFamide pNPs.



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                                   10        20        30        40        50        60        70        80        90
Platynereis_QUERAS_peptide -MEKIAVFLLVATIALAFSA--SINQA-----DALYLPTNRVMKRSAAAA----AANNHVKISSPRQKR-YTDYQERASAFCTGLCMYEERK
Alvinella_FP537998         MATRLGLFVITIVLLVACSL--LLAQS-----EALYVPKNRATLSSATGD----VAKRST-NIGQRQKR-YTDYQERASAFCTGLCMYEERK
Tubifex_CBAZ3684           MIETLTMSTERQQL-LLFVV--SYILLTVGIVTANYLPQQQD-----------------ADVSLSRNKR-YTDYQERASAYCTGVCMYEERK
Sthenelais_FR770837        -MNKLGGYFLA-----ACLV--LYAATSTLEVEGAFIPHKSNALQAALKTLKSQSLQRNSDISGSRQKRYFTDYQERASAFCTGLCMYEERK
Asiaticobdella_JZ184685    MSKGKSMFGKIFILSVLCHVCLSFAVASARFVDGHYVTNDEEM-----------MAKRS-LDYMDREKR-YTDTQERASAFCTGLCMFEEKK

                                100       110       120       130       140       150       160       170
Platynereis_QUERAS_peptide SYSECFDLCNYYW--------------------------------------------------------------------------
Alvinella_FP537998         SYSECFDLCNWYY--------------------------------------------------------------------------
Tubifex_CBAZ3684           PYTDCFDLCNWTGVGPSPWIKLDKEKGRVAASSPAESAP-----AAEQGMA----SMLRTGAGRSRLGDKSKTRLRMGAKKATWDSY
Sthenelais_FR770837        SYSDCFDVCSYY---------------------------------------------------------------------------
Asiaticobdella_JZ184685    PYSYCFDLCNWNGKGPSPWDHHDHTKDSEASKAMAFPLNRSVGGALPEGMLETQKNIIRTGY-RMRPADRNKGRNRFAQEN------
```
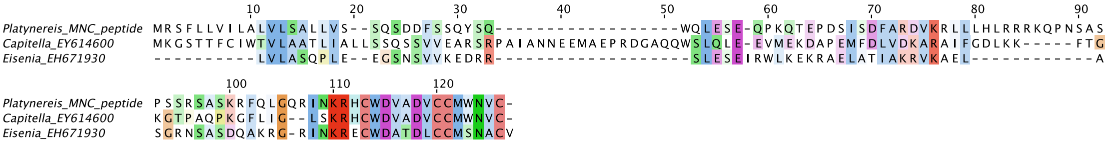

Multiple sequence alignment of annelid QERAS pNPs.



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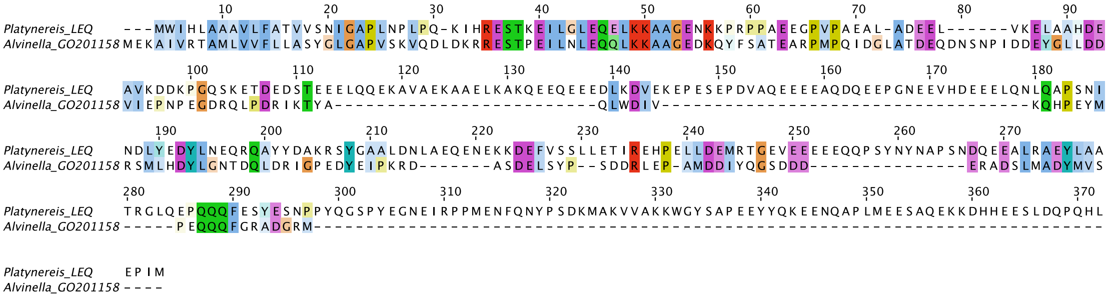
                                10        20        30        40        50        60        70        80        90
Platynereis_MNC_peptide MRSFLLVILALVLSALLVS--SQSDDFSSQYSQ-------------------WQLESE-QPKQTEPDSISDFARDVKRLLLHLRRRKQPNSAS
Capitella_EY614600      MKGSTTFCIWTVLAATLIALLSSQSSVVEARSRPAIANNEEMAEPRDGAQQWSLQLE-EVMEKDAPEMFDLVDKARAIFGDLKK-----FTG
Eisenia_EH671930        ----------LVLASQPLE--EGSNSVVKEDRR-------------------SLESEIRWLKEKRAELATIAKRVKAEL------------A

                             100       110       120
Platynereis_MNC_peptide PSSRSASKRFQLGQRINKRHCWDVADVCCMWNVC-
Capitella_EY614600      KGTPAQPKGFLIG--LSKRHCWDVADVCCMWNVC-
Eisenia_EH671930        SGRNSASDQAKRG-RINKRECWDATDLCCMSNACV
```

Multiple sequence alignment of annelid MNC pNPs.



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                           10        20        30        40        50        60        70        80        90
Platynereis_LEQ    ---MWIHLAAAVLFATVVSNIGAPLNPLPQ-KIHRESTKEILGLEQELKKAAGENKKPRPPAEEGPVPAEAL-ADEEL------VKELAAHDE
Alvinella_GO201158 MEKAIVRTAMLVVFLLASYGLGAPVSKVQDLDKRRESTPEILNLEQQLKKAAGEDKQYFSATEARPMPQIDGLATDEQDNSNPIDDEYGLLDD

                       100       110       120       130       140       150       160       170       180
Platynereis_LEQ    AVKDDKPGQSKETDEDSTEEELQQEKAVAEKAAELKAKQEEQEEEDLKDVEKEPESEPDVAQEEEEAQDQEEPGNEEVHDEEELQNLQAPSNI
Alvinella_GO201158 VIEPNPEGDRQLPDRIKTYA-------------------------QLWDIV-----------------------------------KQHPEYM

                    190       200       210       220       230       240       250       260       270
Platynereis_LEQ    NDLYEDYLNEQRQAYYDAKRSYGAALDNLAEQENEKKDEFVSSLLETIREHPELLDEMRTGEVEEEEEQQPSYNYNAPSNDQEEALRAEYLAA
Alvinella_GO201158 RSMLHDYLGNTDQLDRIGPEDYEIPKRD-------ASDELSYP--SDDRLEP-AMDDIYQGSDDD---------------ERADSLMADYMVS

                 280       290       300       310       320       330       340       350       360       370
Platynereis_LEQ    TRGLQEPQQQFESYESNPPYQGSPYEGNEIRPPMENFQNYPSDKMAKVVAKKWGYSAPEEYYQKEENQAPLMEESAQEKKDHHEESLDQPQHL
Alvinella_GO201158 -----PEQQQFGRADGRM---------------------------------------------------------------------------

Platynereis_LEQ    EPIM
Alvinella_GO201158 ----
```

Multiple sequence alignment of *Platynereis* and *Alvinella pompejana* LEQ pNPs.