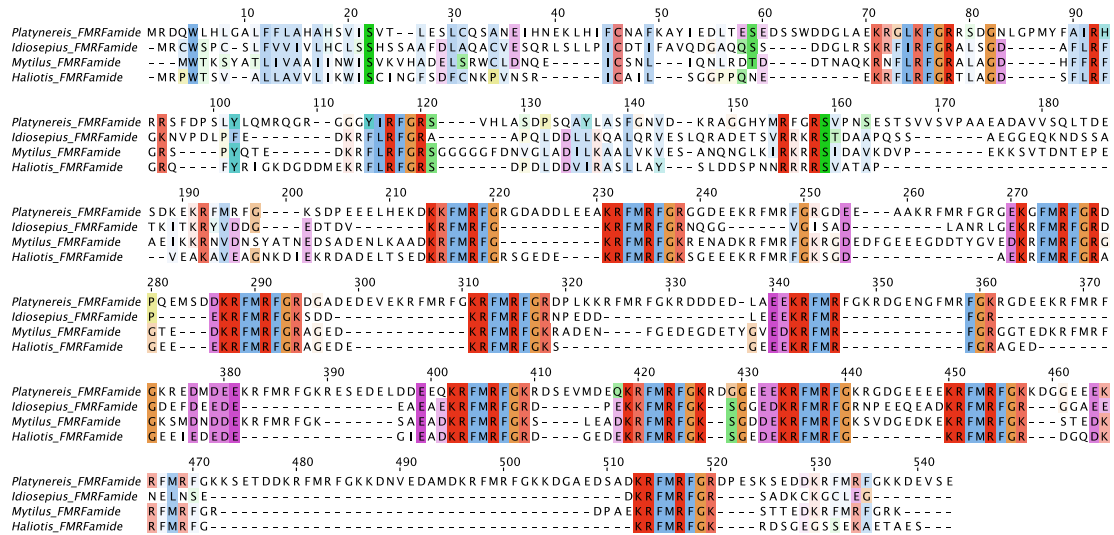
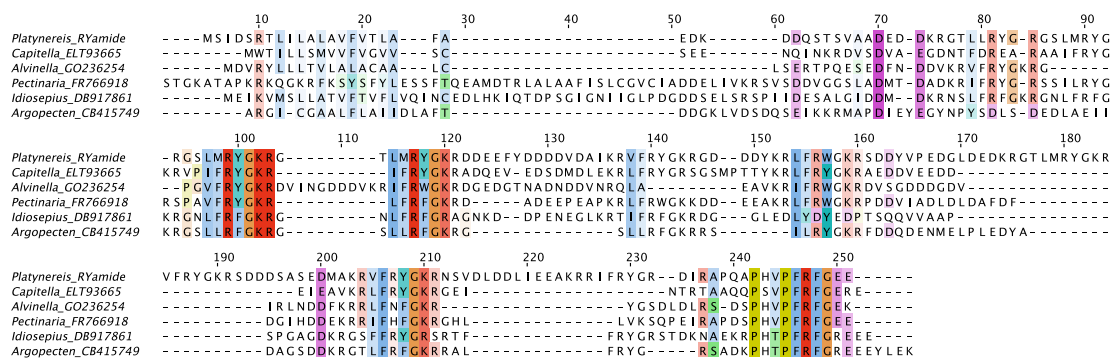


Additional file 10: list of multiple sequence alignments

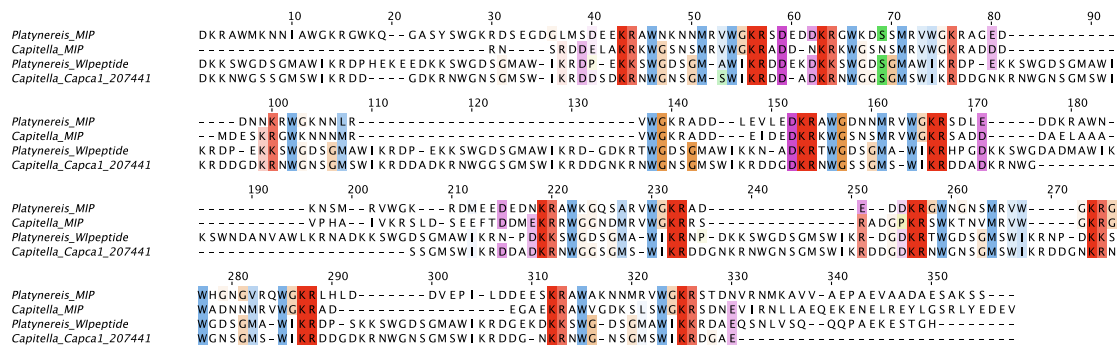
Platynereis pNPs belonging to eumetazoan pNPs families:



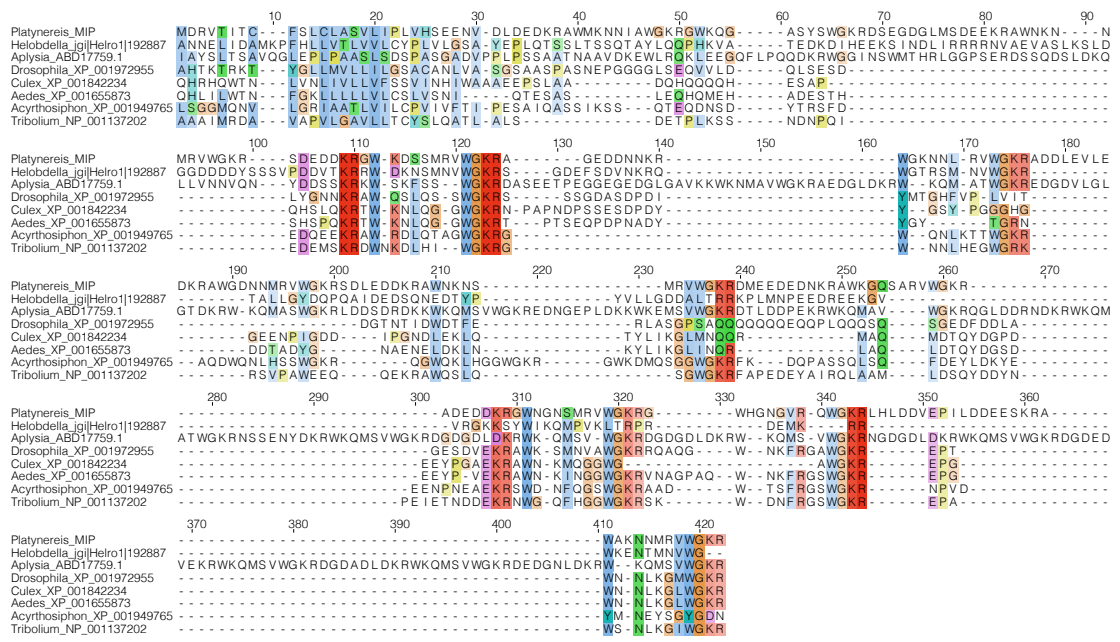
Multiple sequence alignment of annelid and mollusk FMRFa pNPs.



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.

```

10          20          30          40          50          60          70          80          90
Platynereis_Bursicon-A  -MTGA AAKRSFVCGFIC---CLICSVASEGNT---EVDLPTGIIVV---PACRI RW-IVHRIE---LPH-----TOKRLLSLAKK
Platynereis_Bursicon-B  MTTFEWSL LLLLV---PAI LIL---AHCP LSS---ASCNTDFTEIFLNKPKPEY-NGRPARLTCYRK-VTIRKKE
Capitella_EY633285      -MASS IDTDL LLL---FGLVLLST---SKADTSQ---EACNTLHSTVTFSSPKTIELEDGRRRRIFCTGE-VTKKKE
Crassostrea_CU992776    ------MLICVVR---SPCSLLASWIL---AVLAASMGPE---ESCQLRP-VIHLVK---OPG-----CQPKPIPSFAAQ
Ixodes_XP_002407512     -MNSNL TWAMVG---AAVTVLVVI---GVDFARA---DECSLRP-VIHILS---YPG-----QTSKPIPSFAAQ
Callinectes_ACG50067    -MSVLTN FVL---I-VALLICYNDPFPVTHEVOLPPTGKFFCOEOMTA-VIHLVK---HRG-----CKPKAIPSAFAI
Bombix_NP_001091845    -MAHYRCKEYFFIT---NYFNISLGWFI L---FINGLSAIVH---IDCEVTP-VIHLVK---YTG-----CVPKPIPSFAAQ
Nasonia_Bursicon-alpha Anopheles_BURS_ANOGA  -MKSTFLV LLE---AFFLLPGRVLYAQKDESDGSHYSS---DDCQVTP-VIHLVQ---YPG-----CVPKPIPSFAAI
Tetranychus_bursicon  -MKSTFLV LLE---SLSLTLF LISS---FALEP D IA H---ENGA I L P G S I H V V K E E - L D V - A G N V I R S - C E G D - F L V N K C E
Amphibalanus_AFK81933 -MARLRAAG---LLLALLTVS---GCRAR---POCETIPSTIHIKDE-FSS-SGQLERT-CEGD-IVNCKE
Nasonia_Bursicon-beta  -MRLIV---SLLIAMFLK---KIVLANALVN---ENCKLDEIRITKDE-YSE-TGKLFRT-CSDE-IOVSKCE
Manduca_ABB92831      -MGFLSGKIVFV---FSLHLLFII---INSVAE---MCETVASEIHVTKEE-FDD-MGRLLRS-CSGD-VSNKCE
Apis_NP_001035352     -MKENFSIMF IHSI---FLILIF IYS---NETIAGVTD D---ENCETLQSEVHIKDE-YDE-IGRLKRT-CEGD-IVNCKE
Daphnia_ABX55997      -MFWY---LII LLGAGSSRE---TLASKTNLMS---GTCTLPSTIHIKKEE-YTD-GGILSRT-CEGD-IGVAKCE
Callinectes_ACG50066  -MWCGRGTAV---AVVVAVVLA VL---PEV VHSRTY G---VECE TLPSTIHSKEE-YDD-TGRLYRV-CEED-VAVNCKE
Anopheles_XP_313804   -MCNSVRTALAASNCCSIVLCCVLLLT LTV---AVTAQHNOAD---ETCETLPSEIHLI KEE-YDE-LGRLYRT-CNGD-VTNKCE
Strongylocentrotus_NP_001103717 -MLLLL---VVLLCGAGS---VSRVSSLADG---ETCELSHGELTIDVEV-VDDNLQRTLR-CRKR-VQVNOCE

100          110          120          130          140          150          160          170          180
Platynereis_Bursicon-A  GOCESYTOYSLDT-NDIEFVSCCPHGRKLRIRM-RGRNPKTFM--PEIHFVQVYI--PNSCMCRPQSVSINDVNPVNPLEAMSDNPP
Platynereis_Bursicon-B  GCTISEVSPVVVRFPGFKKDKCKCESRLDEKSYLL-PPYGNAL--IPGETVRLHIKEPMDCCSCAM-----
Capitella_EY633285      GCTISEVSPVVVRFPGFKKDKCKCESRLDEKSYLL-PPYGNAL--IPGETVRLHIKEPMDCCSCAM-----
Crassostrea_CU992776    GSGLSTASPNVHTYDPDKDKCKCKEGRLVSRQIALQVQY-SNGVVLAVGVPQT--SLTEPADCCFPSTN-----
Ixodes_XP_002407512     GSCSYVQVSGSRYWQVRSOMCCOESGEREATKAV-FQPKPGP---PKFRKLIIRAPVCMCRPCTAPEASILPQEEVGL--
Callinectes_ACG50067    GRCISYVQVSGSKLWQTERSCMCCOESGEERAAITL-NQPKPRP---GEPKCKVLTIRAPIDCMCRPCTDVEEGVLAQEI ANF IQDSPM
Bombix_NP_001091845    GKCTSYVQVSGSKIWOMERTNCCOESGEREATVVL-FQPDQAN---EERFRKRVSTKAPLQCMCRPQSVSIEESIIPQEVAGYSEEGPL
Nasonia_Bursicon-alpha GRCSSYLOVSGSKIWOMERSMCCOESGEERASVSL-FQPKTKA---GDRKFRVITKAPLQCMCRPCTI EERIVIQEILAGLSNNGPL
Anopheles_BURS_ANOGA  GRCSSYLOVSGSKIWOMERSMCCOESGEERASVSL-FQPKAKN---GKFRKRVSTKAPLQCMCRPCTI EDANV IQEILSFADGGL
Tetranychus_bursicon  GTQVSLQPSVVHSSGFLKKNCKCESRMKRSIRLSHFQDPDKKTT-GEKGSMEIEMEPEPESCHLCKOSP-----
Amphibalanus_AFK81933 GTQVSLQPSVVHSSGFLKKNCKCESRMKRSIRLSHFQDPDKKTT-GEKGSMEIEMEPEPESCHLCKOSP-----
Manduca_ABB92831      GYCCSOVQPSVIVTSTGFTKESCCREEFLEERTVYLLNNOVDSNGKQFSLDNSNMAIRIREFNCKQIKQGF L-----
Apis_NP_001035352     GYCCSOVQPSVIVTSTGFTKESCCREEFLEERTVYLLNNOVDSNGKQFSLDNSNMAIRIREFNCKQIKQGF L-----
Daphnia_ABX55997      GYCCSOVQPSVIVTSTGFTKESCCREEFLEERTVYLLNNOVDSNGKQFSLDNSNMAIRIREFNCKQIKQGF L-----
Callinectes_ACG50066  GACNQVQPSVIVTSTGFTKESCCREEFLEERTVYLLNNOVDSNGKQFSLDNSNMAIRIREFNCKQIKQGF L-----
Anopheles_XP_313804   GACNQVQPSVIVTSTGFTKESCCREEFLEERTVYLLNNOVDSNGKQFSLDNSNMAIRIREFNCKQIKQGF L-----
Strongylocentrotus_NP_001103717 GACNQVQPSVIVTSTGFTKESCCREEFLEERTVYLLNNOVDSNGKQFSLDNSNMAIRIREFNCKQIKQGF L-----

190
Platynereis_Bursicon-A  MEFM L L R H K ---
Platynereis_Bursicon-B  -----
Capitella_EY633285      -----
Crassostrea_CU992776    -----
Ixodes_XP_002407512     -----
Callinectes_ACG50067    DSVPLFK-----
Bombix_NP_001091845    YNHF R K S L ---
Nasonia_Bursicon-alpha SNSAHFRNTFKLT---
Anopheles_BURS_ANOGA  TGYFQKSHYKSI E ---
Tetranychus_bursicon  -----
Amphibalanus_AFK81933 -----
Nasonia_Bursicon-beta  -----
Manduca_ABB92831      -----
Apis_NP_001035352     -----
Daphnia_ABX55997      -----
Callinectes_ACG50066  -----
Anopheles_XP_313804   -----
Strongylocentrotus_NP_001103717 -----

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

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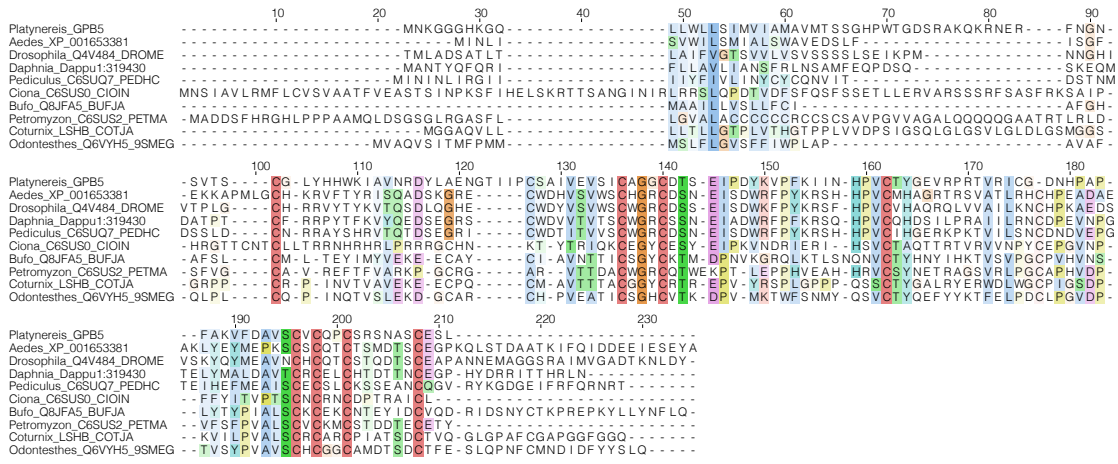
10          20          30          40          50          60          70          80          90
Platynereis_prokineticin  ---MANI FHVCL LLMVFATIQGIPSKRGR-----SRPLFVCKRYPYPYRRTDYHGKRGR LQLLFVGGKROPTYEMS CRTDLDPSSSHCLLA
Capitella_EL01432.1      MGVSSVLATTVCLLLLDVGLSAPSWRSRYAKWRSMQRPLFIKCR-----TELTHQAYDLSAILKLDPRKKGSSSTLGC SADYQCAFDECCIG
Bombina_Q9PW66.1_prokineticin --MKCFAQIVVLLLVIAFISHG-----AVITC-----ACDRDVGCGSGTCCAAI
Xenopus_XP_002933044.1  --MKLKTQFLLVLLVAYTKC-----AVITC-----ACEKLDGIGTCCAI
Nematostella_XP_001641384.1 ---MDLPMAVLVSLLVASVVI A-----SPVTKC-----KHQGT SWMQCKTSRDEEMDECCVA

100          110          120          130          140          150          160
Platynereis_prokineticin  DL-ENSSGTETPLRHMEIETTTSSFF--YDGIS-YMPCASGSLCAIS-----PEKRFCTETSSWDEEEGE
Capitella_EL01432.1      GTRRS-KVROGSHGDVCTLDQA--QDHRILP IACCGSQGLFETL-----AGNAVCIEMGLL-
Bombina_Q9PW66.1_prokineticin SAWSRNIRFVPLGNSGEECHPSSHKVVPYDGKRLSSLCPCCKSLVCSKS-----GAKFQ-SS-----
Xenopus_XP_002933044.1  SLWLRGIRMTPLGQVGECHPFSHKVVPYFGKRLHHTCPCCLPSSKSF-----LDGRER-CSVDFKTMDLK
Nematostella_XP_001641384.1 LM-KSEVKVCKRRPQLGNHCTPTIM-PGIDGR----CPCSSGLTCAITFMDNMGLRDKVQ-CVLVPSDRFE

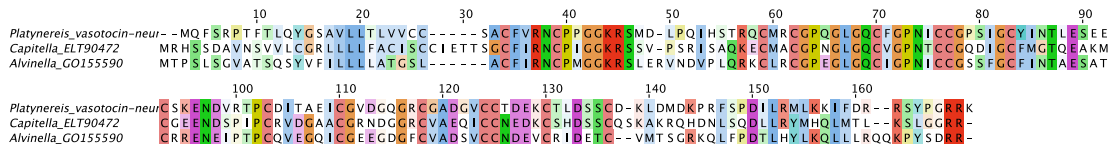
```

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.

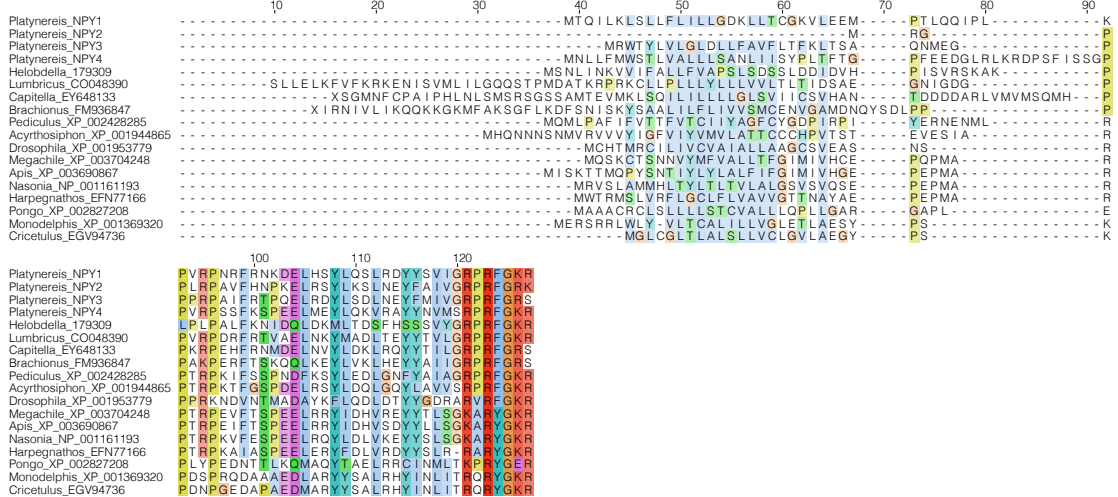
Platynereis pNPs belonging to bilaterian pNPs families:



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 (SYAmide in *Platynereis* and SLGamide in *Capitella teleta*).



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

```

10      20      30      40      50      60      70      80      90
Platynereis_RGWamide  ----MKLQGVV---ASWLFVFLVILEATYAADSGTSQLI-----D-KRRGWCKRD-----E-EVD-----KRR
Capitella_RGWamide  ----MLLNHLILLSLALAFIPAVSFASDELVDDEASEM-----D-KRRGWCKR-----DSEMD-----KRR
Lottia_APGWamide    ----MYFSTHL---AALFFSLVFLVLIQCATSEELSSSLEAEAE-----KRAPGWCKRNIL-----SEKDFLES---KRAP
Aplysia_APGWamide   MRCSCLLSAPVMLLAKISVVVLLLAIDGTSSESSTDNVVLSSSPDSQKAATSRHKRAPGWCKRSSLNDEDLFADDSAQLLDSVAALKRAP

100     110     120     130     140     150     160     170     180
Platynereis_RGWamide  GWCKR--GALDPELE---SADKRRGWCKR--SLEEMEKRRGWCKR--TSVEEEKRRGWCKRDFE-----EEMDKRRGWCKRSLLE
Capitella_RGWamide  GWCKR--SFDEDEE---EVAKRRGWCKR--EAINLDEVEESIAEMDKRRGWCKR--SELEAMQSEFAKRR-----GWCKRADD
Lottia_APGWamide    GWCKRSLSALLDDADDWSDVSDYSKRGWCKR--LESFAADKRAPGWCKRAP-----GWCKRAP-----GWCKRAP
Aplysia_APGWamide   GWCKR--FSLMSEGS---LEAKRAPGWCKR--QEI DVD--DDGSEQEKRAPGWCKRAP-----GWCKRAP-----GWCKRAP

190     200     210     220     230     240     250     260     270
Platynereis_RGWamide  EAE EKRRGWCKRLTIDALEDGIDKRRGWCKRSOMEDEEEKRRGWCKRS--WPKDA--EACSEMRAQVYVYINSALIEGMRVKO--GGDP
Capitella_RGWamide  MEILKRRGWCKR--SEDA--NEMDKRRGWCKRSL--EAEKRRGWCKRSPKIEEF--EFVDCQEVKEKIFYHVSLLQLDAQRANIC--PAEK
Lottia_APGWamide    GWCKR--APGWCKR--APGWCKR--APGWCKR--APGWCKR--APGWCKR--APGWCKR--APGWCKR--APGWCKR--APGWCKR--
Aplysia_APGWamide   GWCKR--APGWCKR--APGWCKR--APGWCKR--APGWCKR--APGWCKR--APGWCKR--APGWCKR--APGWCKR--APGWCKR--

```

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.

```

10      20      30      40      50      60      70      80      90
Platynereis_AKH1     --MRAWLVLLVACIVIAY---QAHTDAQFSFSLPGKW---GNGKRAALGW-----GKRGECGDFD
Platynereis_AKH2    --MMRLWVVYLLTVCVMMFLAFFPHVCHQSLTQSLG---WGSAGSSGKRSVKSPYYGDD--DDVDYDVRQVRKNR-----LTLSEALCSQDE
Capitella_EY628641  --MKHFTLLLVAGIVVAY---HMNTRSAQFSFSLPGKW---GNGKRAF SFS---LPGRWGAQGRASG-----WTGATDCSRME
Malacoceeros_FR764845 --MRSVCFLLVVAIVVAY---QLQDAEAKFSFSLPGRW---GAKRGSFAFSF---LPGRWGAGKRS---EELGACQEV
Aplysia_FF069541    MRARGL---PAGANVHPG---W---GKRSVGAGGGS-----SGVF-----FEPQOQCKT-S
Drosophila_XP_001353031 MNTKSEV I I I AAVLQFL--ACVEGQLTFSPD---W---GKRAAGAGGGGGG-----PAAGDVSAS
Locusta_AKH3_LOCOMI  MGVRAVLV L AVVALVAV---ATSRQLNFPW---W---GKRTGT AAGGPD-----QTILHSSSP-----AAVASDNCGTIP
Cherax_AAV80404     --MVRGSVAL-LLVVLVAS---SCVSAQLNFSPPG---W---GKRAAAGSGSSGGVGEAVSALHHSVGGAPGGVPPGSSSSGSDGCGP IP
Carcinus_RPCH_CARMA MVRRTGVTLLVVALVVA---LVSSVSAQLNFSPPG---W---GKRAAAGSGSSGGVGEAVSALHHSVGGAPGGVPPGSSSSGSDGCGP IP
Rimicaris_ACZ51370  --MVRSGVIL-AMAVVMLV---SCVT AQLNFSPPG---W---GKRAAAGSGSSGGVGEAVSALHHSVGGAPGGVPPGSSSSGSDGCGP IP
Macrobrychium_ABV46765 --MVRSGVSL-VLAVLVLV---SCVSAQLNFSPPG---W---GKRAAAGSGVGTGSEAQLHSAAGLALPGSSV-----TRGDNCSMO
Culex_XP_001842492  MDLVKLFVLLVCAALIF---VCEQLTFSPD---W---GKRS-AAPLAMN---LPNSF-----GIQDSQKTP
Rhodnius_ACZ52614   --MATNLFIT-SVLLVLTTF---HYTLAQLTFSTD---W---GKRSVR-----HNAPDCTP-N
Tribolium_ABB58739  --MSRMF--LIVLVIAF---VGCTAQLNFSSTD---W---GKRSGSSAG-----SDANNCKE-P
Acyrtosiphon_NP_001243520 MRTL LLLAVFMLCACIAV---GQVNF TPT---W---GQGRNA-----PASDECKS--

100     110
Platynereis_AKH1     PDAIFNVYRAIQAEALRINEOMQO-
Platynereis_AKH2    KDAISKIKKLLQREVVVRQRYCNRKK
Capitella_EY628641  SDGMMSVYAAIQEAIKMLEOMGK-
Malacoceeros_FR764845 PEAMYIYSIIQAESIRMSDDMNG-
Aplysia_FF069541    KMDVAYIYKAVVDSRRLLADCGSG-
Drosophila_XP_001353031 NEMMLEIFRFVQSAQLFLDOKHR-
Locusta_AKH3_LOCOMI  PQAALLSILNAQAQVQKLLDQSRF-
Cherax_AAV80404     VSAVMHIYRLIRNEAVRLVQOQEE-
Carcinus_RPCH_CARMA VSAVMHIYRLIRNEAVRLVQOQEE-
Rimicaris_ACZ51370  ISTVMHIYRLIKREASRLVQOQEE-
Macrobrychium_ABV46765 ISTVMHIYRLIKREASRLVQOQEE-
Culex_XP_001842492  VDSLMIYRMIQTEAOKILEGNQK-
Rhodnius_ACZ52614   PDTVIFLYKIQNEFYKMIIEGCK-
Tribolium_ABB58739  VETIMLYKIQNEAOKIIECEKY-
Acyrtosiphon_NP_001243520 MDTL IYIKLVQNEAORIAMQERM-

```

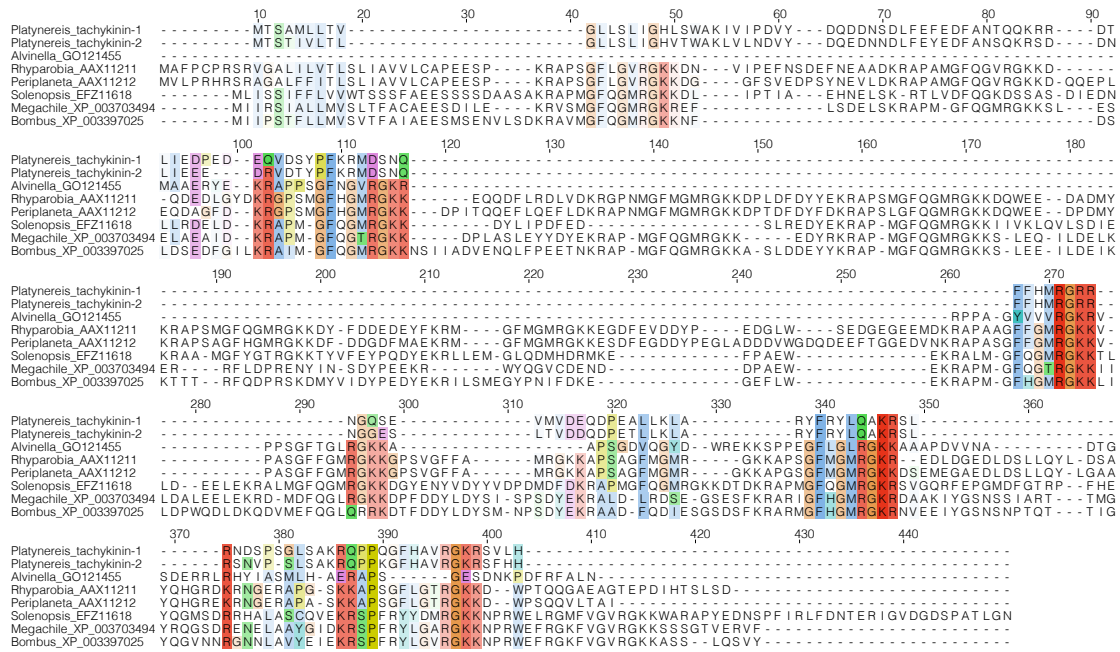
Truncated multiple sequence alignment of *Platynereis* AKH pNPs with protostome AKH/RPCH pNPs.

```

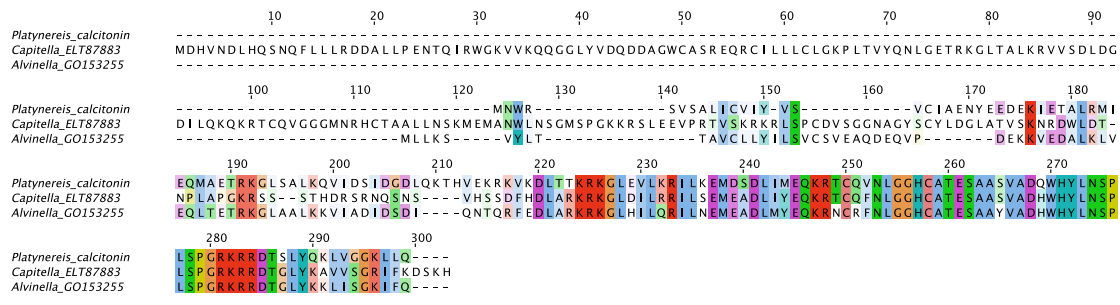
10      20      30      40      50
Platynereis_GnRH1    -----MONGSWSVSCLLALAT-AWLTLSALLTPVSSQAYHF--NGWMPG--KRSLS
Platynereis_GnRH2    -----MRFVCV-----IALVLVAMTALTSAOHAHF--TGWTPGFGIGKRME
Dysdercus_ACN54268  -----MRRTSL---TIALFSPSNDVYMCOTFOYS--RGWTNG--KRSF
Bombyx_NP_001036899 -----MVTNI---LTLTLMTLASVTAOTFOYS--RGWTNGKRDGHKR-
Daphnia_ACJ05606    ----MFINQVYRYSIIAMAVRLYFVLLLVVVSAMAQTFQYS--RGWTNG--RKRSD
Bombus_XP_003494000 -----MGNARVL---ILFJLSLVTMTVTQSYHFF--PDWTNE--KTSIF
Megachile_XP_003706036 -----MVVTRIL---LFFVFLTMTTIVICOTFOYS--HGWTNG--KRSVS
Drosophila_XP_001955601 -----MMLLLLPLF---LLLSVACMGQT---FOYS--RGWTNG--KRAL
Camponotus_EFN63812 -----ML-----VLFVLSLVVSCALCOTFOYS--RGWTNG--KRSNF
Carassius_GON3_CARAU -----MEGKRV--L---VOLMLLACV-LEVSLCOHWB--YGLWPG--GKRSV
Verasper_GON3_VERMO -----MEASSRL---VQVVLVLMVYQVALSOHWB--YGLWPG--GKRSV
Homo_NP_001492      -----MASSRRG---LLLLLLTALHLPSEAOHWB--HGWPYGP--GKRAL
Mizunohopecten_BAH47639 -----MSSYQILVA---QLLLAGLLVAVVSGQNFHY--NGWOPG--KRAPM
Alvinella_GO150661  -----MDLRMTTIAVTL---TLVLIIMSSVHVSQAYHFS--NGWPG--RKRSI
Lottia_FC805607     -----MMPVPLKYFG---LALTLALVTELVAVGQHYHFS--NGWKSQ--RKRSG
Aplysia_NP_001191482 -----MACRITSATTLFSLILLIIVIAELCSAQNYHFS--NGWYAG--RKRSS
Uroteuthis_BAH08303 -----MSTSPVTSTLRRMVF L T C-AIFLLSLCMTQAQN-YHFS--NGWHPG--GKRSG

```

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



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



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

10

```

Platynereis_pedal-peptide-related-3 KKN - NNO10NGYDMK
Platynereis_pedal-peptide-related-1 R - - NNO10NGFDDK
Platynereis_pedal-peptide-related-5 KKN - YNO10NGFDDK
Platynereis_pedal-peptide-related-4 - KN - NNO10NGFDDK
Platynereis_pedal-peptide-related-2 KKNY NNO10NGFEKK
Platynereis_pedal-peptide-related-6 KKDY NNO10NGF - -
  
```

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

```

10      20      30      40      50      60      70      80      90
Platynereis_allatotropin  --- -- MKVYLCLFVYV --- -- VVVV - SVNGMDLR --- -- APrAK  RGFRTGAYDRFSHSFGKRGELTNEDD --- --
Aplysia_NP_001191666     --- -- MLSPFSIAHIGVALLVLM  CLCP - FSOSMEASLSRAK --- --  RGFRLNSABRVAHGYSKRYVASSSGA --- --
Tetranynchus_allatotropin --- -- MKISKIFVTILLGLMGL  LVVLSLAQKPLRAYRGL --- --  OTRGYMP10LTISTAR10GFKRTNS --- --
Ixodes_XP_002407036      --- -- MAALGR10T10SALVAAL  FLCL - AAAGSETPEA --- --  SDROHGGF10OKL10LST10AR10GFKR10IPP --- --
Daphnia_Dappu1:308952    --- -- MKKGAF10LMVLAGWGL  IGL - M10L10T10AVEA10AP10HPADY10TSS10VNN10Q10H10DFRS --- --  RGF10KT10VG10LAT10AR10GFKR10APS --- --
Aedes_AAB06179          MEVTKMSACRWFLVILCSV  LLOCHTSNAGPARQLASLAARASKIPRS  IAPFRN10SE10MMT10AR10GFKR10AP10  IGVN10VG10SS10GN10V10GKH --- --
Rhodnius_AC345387       --- -- MMRWSSLV10LVALAS10  I - INC10I - KAGSPSSALYSSAARASGRRTIR  R - FKNV10OL10ST10AR10GFKR10Y10PS10D10SLQ --- --
Samia_AAY68370         --- -- MNFSM10LV10VV - AV - CLCL - ADSAP10EARL10VRT10K - -- QORPT  R - FKNV10EM10MT10AR10GFKR10DR10PH10SR10TE --- --
Helicoverpa_AAT92286    --- -- MNFSM10LV10VVAAA  A - CLCL - VAAAP10EGR10IT10RT10K - -- QORPT  R - FKNV10EM10MT10AR10GFKR10DR10PH10SR10TE --- --
Saccoglossus_XP_002734994.1 --- -- MLIFSA10LVAV - LFT10H - TSAQ10ROC - -- CRGVGCK10IP10NC10CP10Q10S10I10IG - -- DNF10KNVL --- --
100     110     120     130     140     150     160     170     180
Platynereis_allatotropin  --- --
Aplysia_NP_001191666     --- --
Tetranynchus_allatotropin --- --
Ixodes_XP_002407036      --- --
Daphnia_Dappu1:308952    --- --
Aedes_AAB06179          --- --
Rhodnius_AC345387       --- --
Samia_AAY68370         --- --
Helicoverpa_AAT92286    --- --
Saccoglossus_XP_002734994.1 --- --
200     210     220     230     240     250     260     270
Platynereis_allatotropin  --- -- GLMSVE10DMAELI10TNT10PK10LALS10FV10KRY10M10DR10ND10 - GVISKE10EL10LV10PEQ --- --
Aplysia_NP_001191666     --- -- WIMS10VDE10LAS10LQSH10PK10LAL10LV10K10F10V10DI10NGD - NLV10TAEL10FR10P10TRK --- --
Tetranynchus_allatotropin --- -- PLSK10ISL - -- RE10IL10TL10AO10LMER10LES10DAH - -- EMN10QSR --- --
Ixodes_XP_002407036      --- -- RNOEPAD10I10IKGF - -- R10MK10IS10AR10GFK10RED10PL10S10LE10ED10VD10LDK - --
Daphnia_Dappu1:308952    --- -- PDV10F10VD10LV10NY10LONK10PD10IR10YM10VE10H10L10DH10NGD - GOV10T10SO10EM10T10S10LOO10RED - --
Aedes_AAB06179          --- -- ETAPW10Y10DK10RET10GK10LEEL10T10AD10NAD10P10VQ10I10GE10QES10F10PL10DF10W10V10NEM10SS10N10AL10ART10I10L10HF10V10D10SK10D - GLV10T10T10N10EL10SS10S10AS10DS10N10DF --- --
Rhodnius_AC345387       --- -- POL10IP10AD10WMAEEL10SS10N10PL10ART10I10RR10FD10VOD - GLV10SP10VEL10LR10IV10COE10PN --- --
Samia_AAY68370         --- -- LEN10FD10M10LES10ASERENQ10DS10N10ENT - -- LES10IP10L10DF10W10NEM10L10N10PD10ARS10V10VK10FD10L10NO - GALS10DE10LL10R10NY --- --
Helicoverpa_AAT92286    --- -- LDN10F10WEM10LEAS10PEREGQ10DANDEKT - -- LES10IP10L10DF10W10NEM10L10N10PD10ARS10V10VK10FD10L10NO - GML10SE10EL10LR10N10V --- --
Saccoglossus_XP_002734994.1 --- -- KRNYLP10ISK10NE10LST10Y10QRP10VS10DAK - -- TNV10V10SD10I10V10N10L10IR10SS10SL10IR10K10LV10KA - I10DL10NGD - DMI10SKA10 - LOS10LV10YD --- --
  
```

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.

```

10      20      30      40      50      60      70      80      90
Platynereis_sCAP         --- -- MKSWMKLSV - CVL10FV10VL10LL10H10VT10SL10LP10DF10F10R10NGR - -- AGD - LP10GAK10RT10CV - -- GMVEEAA10CR10Y10GM10YN10PT10LG10FC - -- -- RSDIGDSRR
Lottia_sCAP             ME -- P10SP10YK10IV10AC10FV10IF10AV10IG10TE10AMN10-YMA10FP10LR10GR - -- SGY - LA10FP10RLGR10SDQ10T10QSS10E10F10EQ10TC - -- CP10E10G10IK10SHW10I10IG10ASK10PE10IR10SRC - SPKS
Tritonia_EV287705       MEMT10MP10RA10TV10SL10TL10LV10IV10IT10VD10AMN10-YLA10FP10MCR - -- SGY - LA10FP10MRGR10SOAK10AG10-TAEA10ID10TE - -- CG10IL10KL10SE10FA10VSD10DK10EEL10H10NI10CT10AS10VS
Aplysia_GD198020        MET10SV10SR10TV10SL10LL10VL10I10CS10ADAMN10-YLA10FP10MCR10AR10FP10GY10-LA10FP10MRGR10SQMK10TE - -- TGT10DC - -- CGL10GM10K10SE10FV10I10G10EG10K10EEL10HG10AC10SS10SV
Hirudo_FP601147        --MNP10SS10IP10I - I10LM10VL10I10SN10RT10AQ10IP10PD10F10VGR - -- SQAS10EN10LR10K10PK - -- -- VDD10MT10AL10MC10S10FC10ASN10Y10VS10E10AC - -- -- REN10LR10GER10K
Alvinella_FP500804      --MKT10TT10AM10FV - TV10FV10S10ML10TA10SM10AL10PP10E10F10R10AGR - -- RGF10FP10V10I10Q10KS10SAV - -- AAAS10Y10DV10ME10AA10CAF10CG10YS10R10SWE10LE10C - -- -- RST10NS10DN10R10K
Capitella_EV627825     --MK10F10Y10T10AAC10LM10CT10I10AL10AV10LQ10E10AV10S10LP10PD10F10R10AGR - -- GMP10MS10F10PP10H10KS - -- MAE10LD10L10IAS10A10C10FC10SG10Y10I10HQ10GF10EC - -- -- RR10NG10SE10R10K
Lanice_FR763333        --MT10ST10TV10CV - AA10LAAM10LV10SS10S10VAL10PD10E10F10R10AGR - -- GFP10LP10I10HK10-KSS - -- GSD10LD10LAD10MV10CG10FG10A10FS10PT10LE10IE10C - -- -- RR10NI10A10E10PR10K
100     110     120     130     140     150     160
Platynereis_sCAP         I10CLGDFATQ10LNSALEKHNK - --
Lottia_sCAP             VCCEG - LE10ELVGR - --
Tritonia_EV287705       VCCEG - LR10ELADE - --
Aplysia_GD198020        ACCAG - LR10E10IVDQ - --
Hirudo_FP601147        TCII10AL10TM10EL10G10H10VL10DD10E10RR10FR - --
Alvinella_FP500804      IC10VY10AF10LWAME - -- NK10DW10QN10VEEQ - --
Capitella_EV627825     MCII10LE10FL10SE10LQ10NV10I10SEK10GWQ - --
Lanice_FR763333        VCA10MT10LL10NEL10QA10FAD10DK10RHAD10 - LPM10MT10SY10MI10ARD10RV10LC10SD10CL10HVF - --
  
```

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

```

10
Platynereis_sCAP         --- -- LP10PD10DF10FR10NG
Hirudo_sCAP             --- -- IP10PD10DF10FR10VG
Aplysia_sCAP           --- -- MN10YL10AF10PR10LG
Lottia_sCAP            --- -- SG10YL10AF10PR10LG
Lottia_Pleurin         --- -- SEER10AV10AL10PR10FG
Aplysia_Pleurin        MFY10TK10GS10D10YP10RI10IG
Daphnia_Pyrokinin      --- -- HL10IP10FP10RV10G
Anopheles_Pyrokinin    --- -- NL10FL10SP10RL10GG
Danio_NMU              --- -- GY10FL10YR10PR10NG
Homo_NMU               --- -- GY10FL10FR10PR10NG
  
```

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

```

10      20      30      40      50      60      70      80      90
Platynereis_Sulfakinin  -----DLTPAEVAKKROGAWDMWDYGW-----
Dermacentor_AC039604  -----MQLPARELFLFLVVAIAAASSA-----
Gryllus_CAL48349      -----MGCSMLTAAFFVVSYYLLVHHQHA-----
Pscocotha_BAH11170   -----MKSFFTGMLFLLSLYL-LLTYQF-----
Homarus_CN952349     -----MRWTSWTA AVLVMMAA-----FML
Daphnia_Dappu1:242979 MP I I R Q S V K T L N L L Y I I -----V R V V C A V D G Q E E A Q Q Q Q Q Q H R M K L T M L A T V L A A V L V L G V G R A T A A P A D S S T A T G R R L L H S P N P T S H S K S
Rhodnius_ACS45388    -----MGS S F I T L L L L A I Q V Y M F I E N S H F-----
Pediculus_XP_002424661 MF S V I E K P S L R T Y L I L P -----
Calliphora_CSK_CALVO MY S Q Q R I F N S K Y F I F F I A -----V L S I F W-----
Drosophila_NP_524845 -----M G P R S C T H F A T L F M P L W A L A F C F-----
Anopheles_AAW82713  -----M A R V T L A F L V S L V A -----Y L A Y Y A-----
-----LV S D A Q P I G S L V L T S S G S G H S P A S S P N A D D T G D N V Q Q H A W L K D T N S Y

100     110     120     130     140     150     160     170     180
Platynereis_Sulfakinin  V G R W L K S V L P A A A A A A S A G D S D S R N -----T A D L D A A -----D M I D P V-----L L A S G F A K R
Dermacentor_AC039604  L G R R A P P V A P Q L L R A R L A V A D D A T-----V O G L L G D-----F V V D D-----E E L G E M S K R
Pscocotha_BAH11170   V H R P R T R I L G R F A R P V T Q Y A R L K-----P E P Y L N D-----F I D D D-----D L I F S K R Q
Homarus_CN952349     -----R V L A P V V R O R L E E S H L-----
Daphnia_Dappu1:242979 I D S W L R W L L R S R I G D K E K T K N G V P S N S F Q L A R S P V E L G S S N P K L O A K L P P A I V O S N O D D E T T G F G D E-----D F A E D E V P L V L P E G R O A A S K R
Rhodnius_ACS45388    -----S L I R I R P E P A-----
Pediculus_XP_002424661 -----S K L K Y F E K R Q O-----
Calliphora_CSK_CALVO N L R S M L M A P K D Y Q Q K L H A-----
Drosophila_NP_524845 -----G P S F L F G D R R N Q K T M S-----F G R R Y P-----L I S S R P-----I P I E L D-----L L M D N D-----D E R T-----K
Anopheles_AAW82713  R A R T K N R L F D K K H T G S T A Y Q A F R R T A P P V L A L K E Q A A S S T S L S P E S A D L G K A D Q L R F N L A G Y L T D G G P T L D E E-----D E D D E I G G L

190     200     210     220     230
Platynereis_Sulfakinin  -----G G G F F G K R A P L G K R Y D M Y G I G G R F G R D V S R A Q Q A A A R Q A D L Q
Dermacentor_AC039604  -----G D D Y G H M R F G R S-----D D Y G-----H M R F G R K-----
Gryllus_CAL48349      -----Q S D D Y G H M R F G R K-----E P-----D D Y G-----H M R F G R S A E-----
Pscocotha_BAH11170   -----T S D D Y G H L R F G K R G E-----E S F D D Y G-----H M R F G R S G T E E-----
Homarus_CN952349     -----E F D E Y G H M R F G K R G G-----G E Y D D Y G-----H L R F G R S L T H S D Q H H H H D T T V N
Daphnia_Dappu1:242979 -----Q P D D Y G H M R Y G K R-----D F D D Y G-----H M R F G R R-----
Rhodnius_ACS45388    -----Q F N E Y G H M R F G K R G S D E K F D D Y G-----Y M R F G R S R P L A N S L P N-----
Pediculus_XP_002424661 Q R F D D Y G H M R F G K R G E-----E O F D D Y G-----H M R F G R S I-----
Calliphora_CSK_CALVO S K R F D D Y G H M R F G K R G G E-----E O F D D Y G-----H M R F G R S I-----
Drosophila_NP_524845 A K R F D D Y G H M R F G K R G G D-----D O F D D Y G-----H M R F G R-----
Anopheles_AAW82713  V K R F D D Y G H M R F G K R G G E D O F-----D D Y G-----H M R F G R-----

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

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10      20      30      40      50      60      70      80      90
Platynereis_CCAP       -----M N O S T C-----L S V V L T F I L S V C L Q Y S S A S R D S L I S Q T F H Q-----O K R I F O R F F G G-----G S K R S S-----
Crassostrea_F0665313  -----M V S F Q Q S F A T O V G I L T I L S F Y Q C C Y Y A D E L L Q K N E N K L B V K K L A A L L A N E L L S E D K D I T Q D-----K R V F O G F G S G N B K R S N-----
Conus_CBM40422.1      -----M V S L G H V L F V I-----L L V L L P V A A D D-----D D M L S Q I S L P S S R S E Y D D N D V-----S K R V F O G F T G G-----B R H D R S R R Q E R
Daphnia_Dappu1:300596 MT R P L F Y S L L M L A-----W M I I S L Y I S A S S O P L K N N O N D S D A E E I E Q W S F K-----E K R P F C A F A G O-----G K R K S M-----
NasoniaNV_04678      -----M P D G S I K E Q V-----L K L V L S L L I I I E S V E I A-----A D D G L E I V A-----M K R P F C A F T G O-----G K R K S M-----
Drosophila_CCAP_DROME -----M R I S I-----L R L L A L A C A I C S Q A S L E R N E N G I M A N H K L S G V I Q W K Y-----E K R P F C A F T G O-----G K R K T Y-----
Tribolium_ADM26614CCAP Q D F M K N M T F A K L-----F V I G I F A A L A I E I H S R F P K S I S K N L S A T E R V L E P-----K R P F C A F T G O-----G R K R S N-----
Rhodnius_NP_001124369 -----M T S R V L-----L V L V A L L C A E C C V T A T I P-----N F D P R S N E M V T M P-----K R P F C A F T G O-----G K R K S Q-----
Rhodnius_ADR73625    -----M Q L L V P C-----F L L T A L V S A V L D D V F L O K R L Y F P G E I A E P I D P K-----M K R P F C A F T G O-----G K R K S D-----
Periplaneta_CCAP_PERAM -----M Q M Y H V V L G C S L A I L L V I L D I P O A S C D D V V I O K R Q V D A E M D R L L D P K-----R K R P F C A F T G O-----G K R K S D-----
Ixodes_XP_002402276   -----M K P D L S T I S S S-----L Y I L L L S A C L S A A L E-----Q O D D A A D D S Y L V E-----O K R P F C A F T G O-----G K R K S S-----

100     110     120     130     140     150     160     170     180
Platynereis_CCAP       -----S L P V G G O E H D P R L T E L L O E A K R S G A L Y Q D D L-----P L V A S G S S S N S I Y D D I-----F D D T K K
Crassostrea_F0665313  -----S M N L N P L D Y P D A P E P E I K T D F R K R L F C N T G G C F G R R K R S T-----S O T L E R R L N N-----R G S K D V-----
Conus_CBM40422.1      Y G K R L I P V L A K R P F C N S F G C Y N G K R S L S G A G A L S T P V D P S R N N K A H T M A R M L D A A A A R H E Q O-----O O L L O R E Q R G L E S R D P A A S G D L S K R
Daphnia_Dappu1:300596 -----I K D T K H P P E K A A S N H P L R N A D T L L S L R N G A A-----K I O H O R A N F-----V O L D I P E
NasoniaNV_04678      -----R S Y A G G I O L P I P L Y R A L L R L S L R N G A A-----A E V R I R K K O-----L G L I G P E
Drosophila_CCAP_DROME -----P S Y P P F S L F K R N E V E E K P Y N N E Y L S E G L S D L I D I N A E P A V E N V O K I M S Q A K I F E A I K E A S K-----E L F R R K N K O-----K M L O N E K
Tribolium_ADM26614CCAP -----L P A L P-----E Q S V E D N E L G S L L E L S A P A V E D L S R O I M S E A K L W E A I O E A N M-----E L H R R K O E S-----A E S S E E D
Rhodnius_NP_001124369 T A P G M P N Q D L M R-----O R Q Y V D E D T L G T M L D-----S E S A I D E L S R O I L S E A K L W E A I O E A S A-----E L A R R K O K E-----F Y N S Q-----
Rhodnius_ADR73625    -----E S M A T L V D U N S E P A V E D L S R O I L S E A K L W E A I O E A R M-----L L N R K O O-----S D R F I Q
Periplaneta_CCAP_PERAM -----E S M G T L V E M S E P A V D D L S R O I L S E V K L W E A I O E A R Y-----L L R R R Q E O L Q Q S N O F G A G M D R P L
Ixodes_XP_002402276   -----P N R I D L L A R L Q N R L L S E I R N L E L R T R L E E-----G P S R R H D E Y-----T D N V S R L

190     200     210     220
Platynereis_CCAP       M A A R S S L S D F S S E S V D P E A L L K K A S L L S L L R S Q I R R H S Q L K G S K-----
Crassostrea_F0665313  L L C N G Y G G C R G G K R T L Y S P W L E R M N E V A D D R S A R N A L C T R L G W R E
Conus_CBM40422.1      Y Y-----
Daphnia_Dappu1:300596 N L V Q-----L G P Q A P R L M A A P V V V P S L Y-----
NasoniaNV_04678      E M Q O-----L E E R E S K-----
Drosophila_CCAP_DROME E M Q O-----L E E R E S K-----
Tribolium_ADM26614CCAP A A V P-----A R S A T A S C A L P P C Y I-----
Rhodnius_NP_001124369 -----
Rhodnius_ADR73625    P L P L-----T T I R K R S H Y L Y T-----
Periplaneta_CCAP_PERAM P L P I-----A G Y R R K R F A D P E S Q A P A P H S N L P R A T S Q L O E E I T K P W S R
Ixodes_XP_002402276   N K R E E S I S D A S S T R D R C P-----

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

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10      20      30      40      50      60      70      80      90
Platynereis_Allatostatin_A-1 S-----F T F P R F X S G E D G S I K L S Q L P N V T I N D L T N I S K Y L G L K M I D Y G L K F H N G R Q T D N T L K F Y G P-----
Aplysia_buccalin_NP_001191649 G L G K R G M D S L A F S G L G K R G M D S L A F S G L G K R G M D S L A F S G L G K R G M D S F T F A P G L G K R G M D S L A F A G L G K R M D G F A F A P G L G K R M D
Haliotis_GT274785     -----F A S Q L G K R G M D K F G Y A S Q L G K R G I D N F G-----F A S Q L G K R G M D K F G A-----S Q L G K R P M D K M G F A G Q L G-----

100     110     120     130     140     150     160     170     180
Platynereis_Allatostatin_A-1 -----C K R I N E I L G Y S G S G K R-----T D N G F-----K I P R R P N N I F K F S L V K R T D R A R S G I K M R L S G
Aplysia_buccalin_NP_001191649 S F A F A P G L G K R G M D S L A F A G L G K R M D S F A F A P G L G K R G L D R Y G F V G L G K R G M B H A F T G L G L K R D S G E A S G D L E E G K
Haliotis_GT274785     -----K A V D R F A F A S Q L G K R G L D H Y G F M G Q L G K R G M B S F A G Q L G K R-----

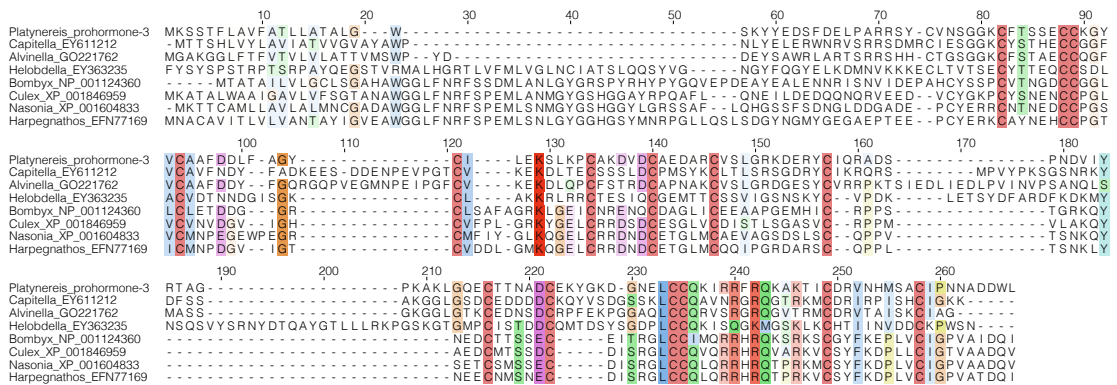
190     200     210     220     230     240     250     260     270
Platynereis_Allatostatin_A-1 K R V D D I S K F S G L G K R D D N I F R F-----S E L G K R V N N A L K F S-----G L G K-----R I D D G L R S S G S E K R T N D A L E F S-----
Aplysia_buccalin_NP_001191649 R G L D A Y S F T G A L G K R G L D R Y G E V G L G K R G M D D F A P S P L G K R G M D S F M G S R L C K R G M D R F F S G H L G K R K M D Q F S F G P G L G R G F D H Y G F
Haliotis_GT274785     Q V V D S L G F S G L G K R G M D E Y G A G T L G K R G V D S L G F A G L G K R G M D S Y G F N A Q L C K R D G-----

280     290     300     310     320     330
Platynereis_Allatostatin_A-1 -----G L G K R G N D A L Q F S G-----L C K R G N D A-----
Aplysia_buccalin_NP_001191649 T G G I G K R G F D H Y G F T G I C K R Q L D P M L F S G R L C K R S S S E Q E E D V R Q V E K R S T T E E Q S S K S L
Haliotis_GT274785     -----S I C K R Q I D S R M F E G A R L G K R M D K S-----F A G Q I D K R S A-----

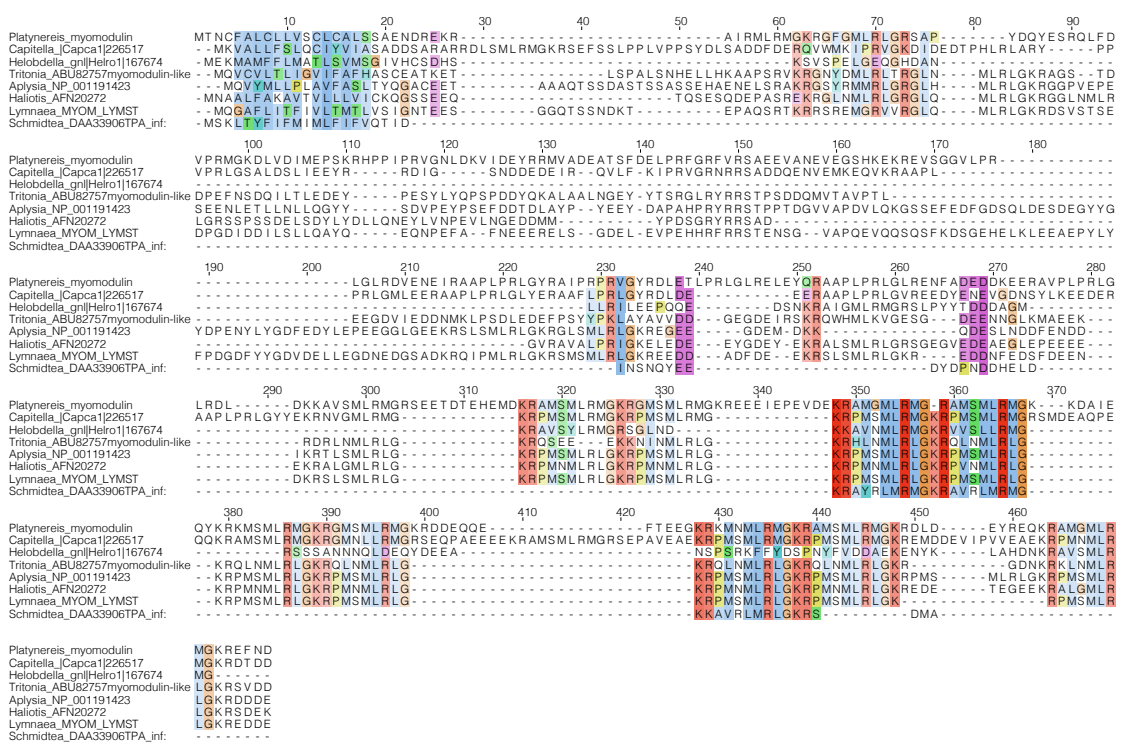
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Multiple sequence alignment of trimmed *Platynereis* allatostatin-A-2 pNPs with mollusk allatostatin-A-2 pNPs.

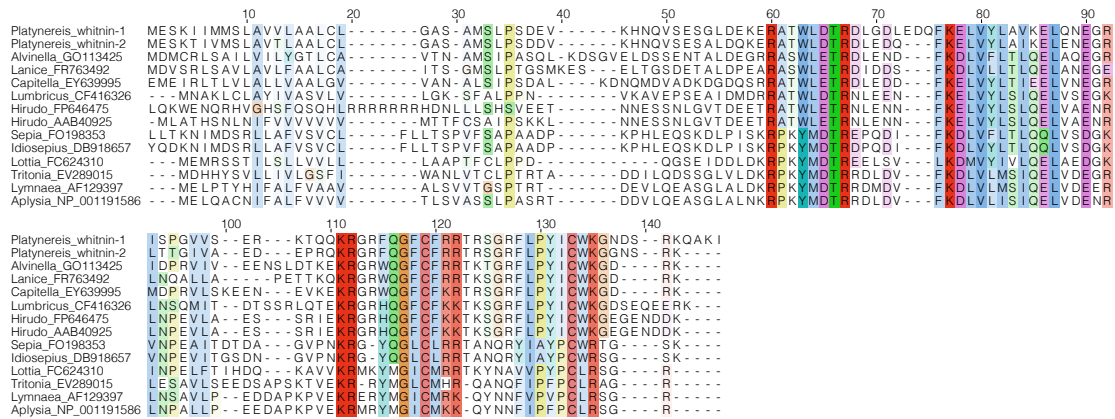
Platynereis pNPs belonging to protostome pNPs families:



Multiple sequence alignment of *Platynereis* prohormone-3 pNP with protostome prohormone-3 pNPs.

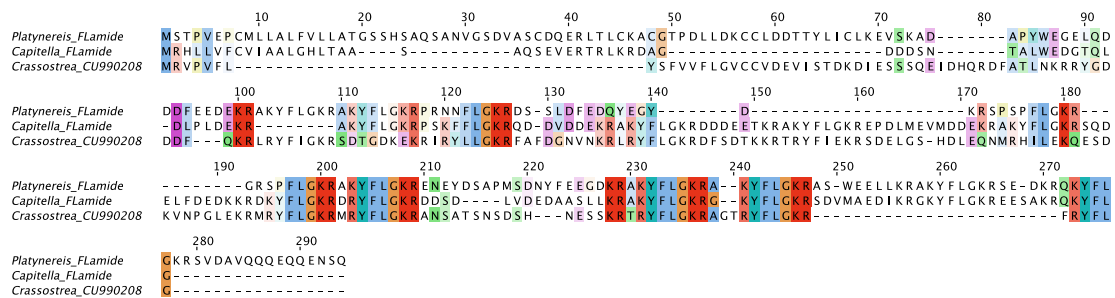


Multiple sequence alignment of truncated *Platynereis* myomodulin pNP with lophotrochozoan myomodulin pNPs.

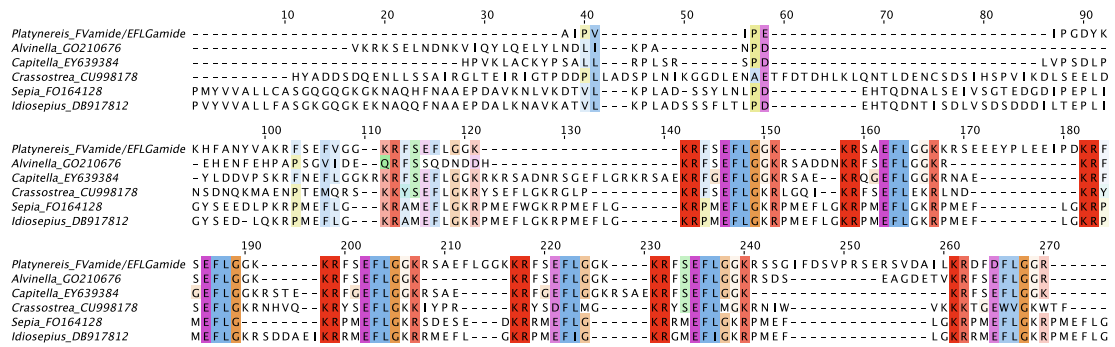


Multiple sequence alignment of *Platynereis whitnin* with annelid and mollusk whitnin/SPTR pNPs.

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.


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10      20      30      40      50      60      70      80      90
Platynereis_NKY-1  ---MKQFILLVLSVSAYITLCVCF--EDSFSDWLQRGHVARRSAPESRLFGGPKSKRDSNYAIKMLMEELLNLENE-S EERHKETQMNGMK
Platynereis_NKY-2  ---MNAIYSAALVLTYSTITLIGASLH5QQFAVAQPNDSAEYDFAAKASS---QNSYNNWMRYLLSNAKHIVPDTQ---KRFTDFAMPYLYK
Capitella_EL191919 ---MNAARLTLALLSASFVLMATASPVYDDEDLF-AGYGFKHYPYMAHNT---V---ADVSLSLTLAKMLLALTA-----KDSKAVYV-
Capitella_EY616101 MTSPI DACAI SAVLLLVYTAASMPYRPPSPNS EDLQQQA IDTFDLGKPLSSSTSA LAWIRYLLSQSKQHEHDIQP-P SKRFSEF5VPLYK
Haliotis_JK475300 ---MRQTVCHLVMLVALATICVIAAVTVACKETM---ESSVRQDSQGTGGRLL-----SFLLSKRS5GLSLLA-PPSRYSPLYKPI-
Biomphalaria_FC556291 ---MTSLAIYLLPAILLAVFHAHAHEDC-----TGPLSRHN-----ALBTLBKRSL5EAALRA-PPSLYSE-LLDS-
Lymnea_ES578962 ---MPSLSVYLLPVFLLA ILHAVAPAECAVFF-----SGLT LRNN-----ALRMLLRKRSLEAALRA-PRPMYADSLMNS-
Haliotis_GT867845 ---MQAYVIVAVLSALLTLCTMCTIDQSHAALS5GVS5RVKQRTLPEYDDE---DDARMA5LYNLLLSRI5AELSAREAYPNTFADFKRT5RSR

100     110     120     130     140     150
Platynereis_NKY-1  --NLLLEKEMSKRK-----AFWQPMMGGLPLVETRLASFGSRIEPDRTEPGSGPNGIKAMRYGRR
Platynereis_NKY-2  --YKVSPPVDKRN---GIWIWMP-AQGYVSVPHQEE---GGAAD-----EGKPG---KIMRYGK-
Capitella_EL191919 ---AEKRG5-----FWRP-MGGGLPVQTRFV5FGSRL5PDRHTK-DDDGPAGIKAMRYGRR
Capitella_EY616101 ---YR---HDKRND---GIWIWMP-AQGYVSVPKQQQAMGDPA-----NGKPG---KIMRYGRK
Haliotis_JK475300 ---TVKRDN---GYVWVWMP-AHGYMTVPQDEASEG5ESK-----DGV5---NLLRYG--
Biomphalaria_FC556291 ---P LKRD5NGGDYWIWMP-AHGYMPVPND5EVT5EQ5GQ-----EKM5---TLLRYG--
Lymnea_ES578962 ---RNRD5---GDYWIWMP-AHGYMPVPR5EVP5EP5TDQ-----RDSM5---NLLRYG--
Haliotis_GT867845 EIPND5P5IT5KR---K5FWQ5---L5GLP5ASAR5IGN5GQ555---AAKDKT5G5-SI5FR5Y5GK-

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Multiple sequence alignment of annelid and mollusk NKY pNPs.

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10      20      30      40      50      60      70      80      90
Platynereis_FVRla  QAEEIAELENPPYKRRVSGFVRI GRDP5K5KASSFVRI GRGSS5FVRI GRNPWGDKRV5S5FVRI GK5SND5VPAYLPYDDALV5EDQEK5RARS
Pomatoceros_GR308449 -----MENA5EK5R5S5FVRI GK5S-----SDPR5FIY5R5P-----S5FVRI GK5SDE5FAM5DA-----
Capitella_EY646590 VANELDN5YDEDD5M5DK5R5K5S5FVRI GRNF-----LP5FVRI5T5Q5RHK-----S5FVRI GR5ST5D-----
Aplysia_EY421845 -----AI5K5RA5S5FVRI GK5AP-----S5FVRI GR5NP-----S5FVRI GR5N-----
Lottia_FC795696 LK5SAIQD5GDT5P5QAV5K5RP5S5FVRI GRNP-----S5FVRI GR5AF-----GR5I5R5I5G5N-----

100     110     120     130     140     150     160     170     180
Platynereis_FVRla  GFVRI GK5V5GDE5EK5RAS5FVRI GK5SVD5EP5NYIED5GHE5Y5EE5E5P5EK5RAS5AFVRI GRP5S5FVRI GRDP5I5K5RAS5FVRI GK5RSAD5S5EM5ED5SK5R
Pomatoceros_GR308449 -----MENA5EK5R5S5FVRI GK5S-----MP5AAA5E5I-----DNE5K5RAS5FVRI GRP5-----
Capitella_EY646590 -----S5LE5K5RP5S5FVRI GK5S-----PYM5K5RP5S5FVRI GK5K5SDN-----E5E5K5RAS5FVRI GK5AG-----
Aplysia_EY421845 -----P5S5FVRI GK5S-----E5LP5D5ED5F-----A5E5K5RAS5FVRI GK5N-----
Lottia_FC795696 -----DP5N5K5RL5S5FVRI GK5S-----DP5N5K5R5I5S5FVRI GK5SQ5EF-----NQ5EP5K5R5Q5S5FVRI GK5SP5EL5NE5IP5N5K5R

190     200     210     220     230     240     250     260     270
Platynereis_FVRla  ASS5FVRI GK5S---VD5E5K5RN5H5FVRI GK5S5E5ED5L5K5RV5S5FVRI GK5S5L5D5E5K5R5A5S5FVRI GK5AL5E5D5E5E5K5R5GI5R5EG5FVRI GK5AK5S5GFVRI
Pomatoceros_GR308449 ---S5FVRI GK5K---DNG5-----G5K5RV5S5FVRI GK5K---DE5Y5D5E5AD5AL5NS5Q5LQ5DEL5Y5NE5QA5K5RA---S5FVRI GK5S-----
Capitella_EY646590 ---SK5FVRI GK5S5D5S5LD5NG5E5EQ5DR5Y5RV5G5E5AL5N5K5RP5S5FVRI GK5S5D5E5E5E5K5R5A5FVRI GK5AL---A5E5K5RP---S5FVRI GK5K---
Aplysia_EY421845 -----I5GYD---L5G5S5L5G5Y5D5DL5A5ADF5S5Q5D5ML5K5RA5S5FVRI GK5S-----G5NG5ED5K5RA---S5FVRI GK5S-----
Lottia_FC795696 Y5S5FVRI GK5S---M5D5G5S5LEN5P---D5K5RV5S5FVRI GK5N-----I5EN5EL5T5N5AG5L5K5AP---S5FVRI GK5S-----

280     290     300     310     320     330     340     350     360
Platynereis_FVRla  GKAK5SGFVRI GK5SMD---DE---K5RA5S5FVRI GK5K---D5VG5DE---EK5RAS5FVRI GK5---NP5L5GE5K5RP5GG5FVRI GK5---
Pomatoceros_GR308449 -----Y5D5E5TP-----K5RA5S5FVRI GK5S5Y5G5D5DEL5T5D5QL5SQ5AD5K5RAS5FVRI GK5A---S5P5FG5K5R5M5N---FVRI GK5-----
Capitella_EY646590 -----S5D5E5I5ET5ME---E5TP5M5K5RP5S5FVRI GK5S5L5G5E5D5G5AL5IP5V5D5E---EK5RAS5FVRI GK5---K5RP5S5---FVRI GK5---
Aplysia_EY421845 -----G5D5S5G5P5H5L5VD5GT5D5D5G5K5RT5S5FVRI GK5S---G5MD5NA5AD5G5AL5S5D5K5RAS5FVRI GK5AL5S5P5V5AP5AQ5S---V5G5S5P5M5S5L
Lottia_FC795696 -----Y5FA5EP5G5DM5D---A5E---K5RL5N5FVRI GK5S---G5L5E5E5P5EM5EQ5K5RA5FVRI GK5---K5IP5S5AFVRI GK5---

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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  MRVLLLAGLL---LCV---YSAPLQQH-SKRL5RAKAAEQVIFGNHGNAR-VK5K5G5P5GLA-----TP5L5P5L5G5P5Y5K5G5D5E5QA5ID5K5K5AL5VT
Capitella_EY541915 MQVF-QIVPVLVF5L5L5AP5L5EQ5Q5AD5ND5IN5N5K5RAE-I5M5Y5G5H5GN5SAR-MK5K5G5P5VLV-----DP5VE5Q5E5P5AD5D5V5D-----
Lottia_FC765189 MQLYTVL5S5I5L5CS5VV---W5TAP5LA---ENE5I5EL5AK5RAK5ET5IM5GN5Q5N5SP5RR5K5K5S5L5L-----TK5D5V5ND5AD5L5K5H5-----
Crassostrea_HS232296 MKL5FVALL5P5L5F5L---GLV---Y5CA5APT5DI5E5K5R5AM5Y5K5RA5EQ5VM5F5G5N5Q5N5K5P5R-I5K5K5D5P5E-----P5AL5P5DL5K5G5S-
Mytilus_ES401399 MLL-LI5V5P5L5L---G5VV---M5AAP5LA---E5ERN5I5K5Y5K5RA5ET5IM5GN5Q5N5SN5K5Q5V5K5K5D5P5E5V5P5L5H5D5I5P5D5V5K5A5E5I5LP5D5D5G5S-

100     110     120     130     140     150     160     170     180
Platynereis_GNxQN  SKVTS55ED5Q5V5PA5EV5EQ5D5L5DD5L---E5TD5TK5GH5LA5E5E5E5E5K5LAP5LA5E5D5S5D5AS5Q5D5ATA5AD5MK5D5E5T5E5AG5S5SQ5E5D5ATE5QS5L5EQ5L5N5E5F
Capitella_EY541915 LV5DE5VT5NE5I5PA5E5T5EK5E5L5VE5E5V5TP5E5GD5L5AL5Q5K5E5D5D5L5N5K5AG---DAL5E5V5D5R5E5E5T5V5E5I5L5S5G5D5A5E5G5EN5Q-
Lottia_FC765189 V5IAMP5ARD5VP5AD5AV5K5ED5N5LP5TD5V---E5SDA---S5TE5V5Q5AS5D5N5IP5L5K5P5D-----T5E5BN5K5S5D5VT5E5P5E5D5ID5P5D5Q5D5ML5Q5S5D5
Crassostrea_HS232296 --V5TANK5A5E5D5FA5E5T---K5TA5E5LP5K5-AI---EK5-----E5L5E5D5S5D5V5M5E5P5K5E5S5-----D5I5T5S5E5G5E5P5T5D5E5L5E5D5F5P5E5T5E5AK5E5--
Mytilus_ES401399 --V5E5ASK5A5E5D5I5E5S---K5S5D5E5P5E5D5L---NT5---V5VK5A5E5L5E5N5E5E5K5A5S-----D5LL5AD---D5T5S5Q5T5G5E5ANI5P5Q5AD5D5S5Q5T5E

190     200     210     220     230     240     250     260     270
Platynereis_GNxQN  KIP5SQA5Q5Q5G5FP5LDL5FG5KN5Q5Q5G5E5Y5M5D5P5TY5DY5Q5N5PY5L5R5R5K5R5L5TP5HK5AR5AV5NA5E5D5M5M5G5S5AG5I5AN5S5G5R5SK5R5DL5Q5E5RY5M5W5ND5L5D5Y5P5E5V

280     290     300     310     320     330     340     350     360
Platynereis_GNxQN  ER5RG5E5E5EG5P5E5L5E5EQ5Q5E5AL5K5ML5R5D5E5I5L5K5YN5EMA5E5V5D5N5E5T5G5E5E5R5P5Y5E5P5EQ5EA5Q5D5L5I5N5Y5L5R5NG5YA5E5AP5EQ5D5P5E5EQ5G5P5E5P5W5E5D5M5G
Capitella_EY541915 -----M5E5S5I5P5NG5D5I5ATT5L5M5K5EQ-----S5E5I5D5N5S5V5D5Q5K5E5---T5E5P5AM5N---W5DY5L5N5I5D5G-----Y5K5P5Y5P5D5Q5D-
Lottia_FC765189 -----M5W5S5E5E5D5D5---E5P5V5E5D5S5Y5N5P5AL5P5G5Q5N5E5D5Q5LAN---W5Y5H5L5L5Q5Y5G-----D5L5D5N5S5Y5SR5Q5NR--
Crassostrea_HS232296 -----L5EN5K5ND5K5E5K5S5---E5E5I5N5N5AS5E5K5S5---S5E5N5K5E5G5E5N---S5V5R5T5D5N5D5E-----D5ML5E5L5E5E5W5Y5N5N5P
Mytilus_ES401399 -----D5E5N5I5P5Q5AD5E5A5I---E5E5L5K5N5I5G5E5D5S---Q5G5D5S5E5N5Q5P---I5T5N5V5AS5D5E-----Q5NY5D5NY5D5L-

370     380     390     400     410     420     430     440     450
Platynereis_GNxQN  P5AA5E5AL5P5E5E5E5P5FN5PY5G5Q5Y5A5E5DN5V5M5S5AP5Y5L5AK5R5Q5L5S5F5V5P5G5M5R5K5R5G5N5D5F5Y5P5Y5G5P5D5AR5W5N5AM5V5T5E5D5T5E5K5R5A5E5R5M5E5R5L5L5R5L5A5A5L
Capitella_EY541915 -----R5TK5R5S5AQ5S5EQ5P5L5TA-----E5E5I5N5N5AS5E5K5S5---S5E5N5K5E5G5E5N---S5V5R5T5D5N5D5E-----Y5FK5D5H5K5D5S5N5K
Lottia_FC765189 -----N5KY5Y5A5Y5R5R5R5S5L5L5R-----Y-----Y5FK5D5H5K5D5S5N5K
Crassostrea_HS232296 A-----L5AL5R5Y5R5AY5Q5S5FP5N-----Y-----Y
Mytilus_ES401399 -----Y5K5L5Y5R5E5Y5Q5N5I5R-----Y-----Y5N5Y5R5L5Y5D5V5N5Y

470
Platynereis_GNxQN  R5DR5R5D5E5L5E5A5QR5FYA5E5DF5P5E5K5
Capitella_EY541915 M5P5D5S5P5Q5R5K5R5D5L5T5D5D5E5L5K5E5W5L
Lottia_FC765189 AV5K5R5G5R5I5K5R5D5L5D5D5L-----D5L-----D5L
Crassostrea_HS232296 -----D5L-----D5L
Mytilus_ES401399 R5K5R5R5M5A5I5R5K5R5R5F5M5G5R5S-----

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Multiple sequence alignment of annelid and mollusk GNXQN peptide pNPs.

Multiple sequence alignment of annelid and mollusk LXR peptide pNPs.

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Platynereis_LXRX      MKELTCLLVVATIQALSAAAPSQNKVVRMKRNYEQPDLQFHQPDEALVRIKRRRS-AMEPTLVVKRD--EQLKRYKREKRDVE-
Mytilus_ES394341     -MVVPVFLVLFVCFPS--TFTETVRSHTIT-KREAEKPSLEQL---ENELRRVVKRLKDTAEVLPVVKRMKRDEHSERELSRIKRLK--SLK-
Haliotis_GT276618    MYAFKMLLLPVGVLVLT-SIAGLSQGSIG-KRSTERAIDLDL---ESQLSRVVKRLDPG--VPELSRTK-----RDVEN
    10          20          30          40          50          60          70          80          90
Platynereis_LXRX      EELQORVRRQRDTEELHRFKRQRDTEAELEEYKRRKSGVEVDPLEARTKRFKREAE-----EPPQRVYKREKRDAAEELHRFKRQKR
Mytilus_ES394341     PGLSRVVKRTRASSELVLPFLSRAKRFKDL-----EVDVSMLSRVVKRLKRSPTYKTLTVDHYEPLSLRMKRQRSSVEFSLH-----
Haliotis_GT276618    DGLSRMKRYNTD--EMP SLSREKR-----GIEENALSRMKRGDVEDD-----NPVLSREKRDLEENIGLSRMKRGDE
    100         110         120         130         140         150         160         170         180
Platynereis_LXRX      DTEQLERYRRDRDLEPELSTRKREKRDVESPPTLAKKGLKESRAAGDRRRNQKALKREKKTMMNHRWEKHQKRRNGNKHHSIPRMKK
Mytilus_ES394341     --EKDLSRVKRFHDPNTIELSLVRLKRSERVK-----RIPSS
Haliotis_GT276618    S-HALELSREKR-HADSLALSTRKREK-----
    190         200         210         220         230         240         250         260         270
Platynereis_LXRX      NVLKRERSDLLANHALRNHLVSRQNKLGSKLAKHVRKRTQKIQHGHYKLEADVAKLGRRLRDIALNLHIANLNKNAAKRRVKTTHAKKN
Mytilus_ES394341     NVHKIKRNRNKNLNY-----LKGTKRHFKAHEHLDRNIDLKTAKQELSRQSGALXRRK-----EKTRAQ--
Haliotis_GT276618    LLKRVK-----VDPDSVELDRAKRGEVILIRK-----RRITDD--
    280         290         300         310         320         330         340         350         360
Platynereis_LXRX      KKIAAKKH
Mytilus_ES394341     -----
Haliotis_GT276618    -----
    370

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Multiple sequence alignment of annelid and mollusk LXR peptide pNPs.

Multiple sequence alignment of annelid and mollusk CLCCY pNPs.

```

Platynereis_CLCCY    -MSSIYKMAILLVLCALLLALASSRPSATNQEVEEQANVARLKR-----RTKCGFLEACDPYENS CCGPMKCANLFGGYLCSGIEKMCML
Capitella_ELU03629.1 MPMAVGIPRVVIFLVILTAAYVHSAPSRGSAAKHL-LERLTNVNR-----CRYQTEEGHPYKDTCCGEMQCLLIRGHCIYGLTICICL
Alvinella_GO205196.1 ----MQALKLTFVAVSLVICVVLVLRADGATDFDSRGAALRLLGFGSAKKTCLWQMDENPYEDVCCGKMKCANAGISYGRVREKGYCV
Tritonia_EV285052.1 ----MHRYALTFIFGVIMTII LPEVLSLPRLSRQMPVPOQFRLRPS S S ADKWGNVMESEI PWKTKCGSLTGMNLAEGYELVPLEDKKQ
Aplysia_EB255556.1  MESGRRTPTLLTVLLALCACSLHTVLSALRPLRSTRQLVPLQAKP-----DKVQNYMSTGVWESPCCGSMALNLARGYGLVPLEEGFCH
    10          20          30          40          50          60          70          80          90
Platynereis_CLCCY    PTSY--GV-----
Capitella_ELU03629.1 PARLHDNRRTGNRYR
Alvinella_GO205196.1 PNSY--GKALPYNWN
Tritonia_EV285052.1 KVGR-ADIF-----
Aplysia_EB255556.1 KPDV--DIY-----
    100

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Multiple sequence alignment of annelid and mollusk CLCCY pNPs.

Multiple sequence alignment of annelid and mollusk CCWamide pNPs.

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Platynereis_Plectoxin/VI-like -MRW-----IIFCFLLIVFSHTVLCWRIQDFANTDNEADDDTSARYRQERRLLDYLRDVKRHHVHKDRQVQKPP--YELTSAMQOE
Crassostrea_FP002705        -MTY-----FIAGIWIILLISNFGSSC-----MYAYDYDDDYIQNKALDLEFSSMDRRNYL-----RQPIQNSWNR
Aplysia_GD218738           -MSW-----TCERLWLLVLLVLP LCL-----SLRYTDYMTSPEYRHDA LKTLRN IKKLPQPSMSVSRSGYSEOKRLWNO
Haliotis_GT275645          MKKSWWKVSLLQLSGLVYVLLLVLPASS-----QYDRDLINRORRNDALQQLRSIKRRVSYRYVSKRR--KTLEGREWNO
Lottia_FC753680            -----XLMIPYSS-----LQLYDRGYSMRNYNDFDALDKLTKIKRVSFRFRNQVPE-----RTGRWRRA
    10          20          30          40          50          60          70          80          90
Platynereis_Plectoxin/VI-like PCDPTNNVHTCCDEEDGLVCKCFWANGKGVSRLLWGR
Crassostrea_FP002705        HCLPWSNEIQHSCC--GGLAKKCNLWGNCRGTTQLWGR
Aplysia_GD218738           PCEPWTSDPSRAACNPRRHVCCCLWLNCRGRTLLWGR
Haliotis_GT275645          FCVPWSSEYEETCCNPRRLVGRCLWMCNCRGVSRTWGR
Lottia_FC753680            PGIWTSPEGEACGTSANLVGRCLWMLNCRGVRGRTWGR
    100         110         120

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Multiple sequence alignment of annelid and mollusk CCWamide pNPs.

Multiple sequence alignment of annelid and mollusk QSGamide pNPs.

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Platynereis_QSGamide    -MPNSQVLIATVIFCVAVSCV-CSKSIQVFNHNERLKRRLIGDLQIAHQHQAICL-L-KHW-PKGCVEIGCGLFDIAAGCRKRKSYSNNVEDF
Pomatoceros_GR310530.1  -MQTSQVLFVSVLL-VVFACV-FARVSPDY---RNRVRRGFADVLMKSHQANIGL-RNLGPKACKEFACGLVDIAAGCRKRKSYSNNVEDF
Crassostrea_HS121817.1  -MHLNLTVFKVIFLFCVIFVCATNCRNLE-----SRVRRGNADVVKAT EYFARLAL-ERM-PTDQLIGCGLVLDLQESGKKRKT-----DTQ
Lottia_FC598192.1       MPRFGVALCSIVLVFVLSLTLTESKLS-----RQKRQLADLKTSELSALISLGGRYAPRGCKDVACGLVDIFKSGKRNGN-----NRY
Argopecten_CB413348.1   -MTYTKVVAKVLVLCVAVFGCIAYGRSVEGK---LKRRLRRAGDVKTA EYWARLAL-ERSRARGCALIGCGLIDIVQSGKKRDG-----RTS
    10          20          30          40          50          60          70          80          90
Platynereis_QSGamide    LNNENELRRRESNRLVLRQRIADELMRES--
Pomatoceros_GR310530.1  AMSRDEFDYDYSRLALLERVLDTIMEDEDS-
Crassostrea_HS121817.1  SS-----PYH-KRRLKILVQLLIPKKEQ--
Lottia_FC598192.1       LR--DLSLEE-RQLIRNLIQRAAERKA-
Argopecten_CB413348.1   QSLQGLDLETES-RAKLLTM-----
    100         110         120

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Multiple sequence alignment of annelid and mollusk QSGamide pNPs.

Multiple sequence alignment of annelid and mollusk CCRFamide pNPs.

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Platynereis_CCRFamide    MQVKITITLTYSLITLVQWEVTKALPTFPDMSCQAFCKANFQGE-QHIACLTDICRSMYRGRISRFGKRVSHVMEDDLQEPLEPTALKDR
Lottia_FC748821         -----MAIRCFIIVC-AVTLTLLAVIDAKGRNYSQSAFCNKNVSKTSKSL EYCLSYICNRIYHFYKVTIRFGKRSSYDFDEGSEM-DRPSLLDFFL
    10          20          30          40          50          60          70          80          90
Platynereis_CCRFamide    LYAAYMKVLQHDOIRGSKRLPGEQEKRSWPFALS LD
Lottia_FC748821         IY PDS-----DY-----
    100         110         120

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Multiple sequence alignment of annelid and mollusk CCRFamide pNPs.

Multiple sequence alignment of annelid and mollusk HFAamide pNPs.

```

10      20      30      40      50      60      70      80      90
Platynereis_HFAamide MTRDVTAVTALASVILVALLLVQETNSFEYNGYQKMKRWRGGNLCCKNAVHFAKRTSATPPDVL-----DLPDDVTNEVES
Capitella_ELU01627.1 ---MEYPRRLRWYGLV-LVVLACCLATDAFEYSYGRKMKMVRGGNLCCKSAVHFAKRSNALSDPFI-----LDLEIPAENDV--
Alvinella_GO155586.1 ----MSAVARLFTAV-FVPALLCQVALSFEFSYGRKMKCYRGGNLCCKTAVHFAKRRQQLASDQGL--GQTYPRFDLSANGAGHYTG
Aplysia_EB352987.1 ----MGVSRYVYCCFLLSLLLQHSYSVWVSQGRHRGLYRGGILEGNAMHFAKRNKNTATSMYAPPLRPTVYARLAATPDIAAQVGA
Crassostrea_AM857389.1 ----FLFTVLGAFSVQKFCENACNRLLGGNLCRCNGFHFAKRTVLENI LPVP--NTYSSV-NGDEP INQR IQA
Doryteuthis_JK335440.1 ---MSKSS-VWVFY---LMLLCLLVAVHTFDLQKFLKRCRAVGGNLCRCCTAHFAKRS DTHAAAEAA-----AAAAANLDV--GQSRSSH

100     110     120     130     140     150     160     170     180
Platynereis_HFAamide SRAAEQLRKWFTRAA-LAVQSSKDGQAENSASELRSRAKQLLLMALKK-----LSDNSQGN-----NPWSDITE-----DRLF
Capitella_ELU01627.1 ----TNWRSLSLGG-KKLDILRQGDPAFLFA-----MR--YYLTLRR-----GGDESEDYR-----R-----
Alvinella_GO155586.1 AENV-APSGWTDDEELRLAAQLLDDDRQSLDPLAQISKAR--FGISRRR-----R--ESSNRP-----N-----
Aplysia_EB352987.1 EEE-----KIATSRRLRFE--GLED-----ELDEIJSXFASRRGNEDGASGVVPGKCRGRGKTEEAAWVNRDSDAVSPGSLRRHY
Crassostrea_AM857389.1 PSF-----TNDIQQPAPVLRRENLSRIDKTRDTQMIIQWLNNIRL-----IKSEMPKHMAYGI-----EDDLTP-----
Doryteuthis_JK335440.1 GRNNN--NEEEEEKMRIAGAAEAGPEDLQVLSMNDLLSNSQYLYPLMGV-----MP-ASSRRASLMGRLEAEDENM--ELLQGESGRIV

190     200
Platynereis_HFAamide -----DNI--
Capitella_ELU01627.1 -----
Alvinella_GO155586.1 -----
Aplysia_EB352987.1 WG-----
Crassostrea_AM857389.1 -----
Doryteuthis_JK335440.1 RDSRSDKGSRRSNLILA

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Multiple sequence alignment of annelid and mollusk HFAamide pNPs.

Platynereis pNPs belonging to annelid pNPs families:

Multiple sequence alignment of annelid FVMamide pNPs.

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10      20      30      40      50      60      70      80      90
Platynereis_FVMamide MSLVWVHVAAFSLVATAVVLAAYSDDKRFKPEYQDFVLGKRDRPSYIDFLMGKRSRRITYPEFVDFLLSSKRPSSYDFVLGKRSRPSFND FYMGR
Capitella_EY632921* MSLVWVHVAAFSLVATAVVLAAYSDDKRFKPEYQDFVLGKRDRPSYIDFLMGKRSRRITYPEFVDFLLSSKRPSSYDFVLGKRSRPSFND FYMGR

100     110     120     130     140     150     160     170     180     190
Platynereis_FVMamide AEFPSFEFFMCKKRNDAFHD FVMGKRDPN NYLDFMTLDDQHVRRRANIEQTS ESHNEANDA AVDKK-DNYGK FVMGKKN SQQDFRAFSLGKR
Capitella_EY632921* --RDRFDLFGCKKRMDESFMLGPGHAK-----RRRRAEADDKRSDDFNSEFFSGKRNDADENS EFTCKRN--DADFQSFFTGKR

200     210     220     230     240     250     260     270     280
Platynereis_FVMamide QEEKQNVDSFVMGKKN-DKDYSKFVMGKSKDKDYSNFMVGGKNGDDYSK FVMGKKNKNDYSNFMVGGKKNADKDYSN FVMGKKNQDYSK FVMGKKNNDG
Capitella_EY632921* NGD--DWANETQCKRAMNPGVDFEIQGKRSPMNADEIQGKRNPYAADFTHGKRDSQGLDFLQCKRNMQMGYADFVQKRN-PSFEEDFLGKRRM-S

300     310     320     330     340     350     360
Platynereis_FVMamide DYSK FVMGKKN DGDYSK FVMGKKN DDYSK FVMGKKN--DDYSK FVMGKKN DKNDYSN FVMGKKN-------DG
Capitella_EY632921* DPTASMLGKKN DQND FVSGKRNNAESFVLGKRDSSSDPPASSASKDDADDLNSFILGKKN SLDTDEAAQNE

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Multiple sequence alignment of annelid FVMamide pNPs.

Multiple sequence alignment of annelid DLamide pNPs.

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10      20      30      40      50      60      70      80      90
Platynereis_DLa_JF811324 MAACRQCLLTALVIFCACSQ LTHALNENSVPLEKEDLLLTGDDEKRYAFNADLGKRSQLEELYEDEDAD-----DKRSYGFSDLGKRR
Capitella_DLa_EY612748 MRMNR-AWLAGLV LNS---VLI AFLQAAAPVPPDDIAAHSIKRRFSFRADLGKRS DGEETLVDSSEDFEP LNDDLEKRYSF FRADLGKRS
Hirudo_FP646581 MKMKK---ALHVIMFC---VSVI GAACQHFPELLIHRN--KFF-----DRLPQMEFLED-----DPTYHSLHRGK

100     110     120     130     140     150     160     170     180
Platynereis_DLa_JF811324 ---MGFNADLGKRF AAFNTDLGKRY YGFNNDLGKR--YGFNNDLGKRYSGFR-----ADLGKRYMGNFADLGKRFSSFRADLGKRLRD
Capitella_DLa_EY612748 EDDMDMAAEMAKRFSAFRADLGKRFSAFRADLGKRSYGFADLGKRSYERRFLDDDDMDQVDDKRAAFRADLGKRASSFRADLGKRFQM
Hirudo_FP646581 IVDSPVVDIYLYKRRLLRS DLGKRLYDTSQ-----EDAADASPQDVTLSAALSEMEDRGRKSN-

190     200     210     220     230     240     250
Platynereis_DLa_JF811324 LDESHRAYSFRADLGKRSVPSEDLKRFMRDODLGKRY--SFRADLGKRAAFCDLGKRFSDSSDDA
Capitella_DLa_EY612748 LRPYWQPN-YLRDYGRLQ-----FRADLGKRASPSFSDLGKRAAFADLGKRS TDQLVA
Hirudo_FP646581 -ENIWQLWQ-----LKEGWKKA--PMLRGDLGKRQMRSDLG-----

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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_SLRFamide ---MLSVRWLQV LVVCLVGVCTCALP SLAGYDDGLLHYRDEEDSFAISDPDKPVRDDGNLGSLLLNLRFRDL-----SNEYHRLRPA
Capitella_ELU08166.1 MPSILNQAWCVLWVTVIVT VTVHSLPRVP-----LLGDHLEYQVDR AQPKEIRNN--GLGSLLLNLRFRDLG-----ARDLAHLNAV
Amynthas_F5508545.1 -----GRGHVSSDSFRS---DAPIRDN-QDFVRKVLDELFRVDVAYPLDYGENEDSALPSS

100     110     120     130     140     150     160
Platynereis_SLRFamide LLLKSLALKPHYQEAQETK-----EFNKRGDMSVNELAQTLNHLKARNVD-GCV-KLOS LRFGRRR
Capitella_ELU08166.1 RHEQLSADVEDEETDNNALLQ---GEMNKRSTVSVSOLAALHNLSRDLDEEGV-KLOS LRFGRK---
Amynthas_F5508545.1 SFSYS SSSGFRRGTDGNVVRRTGSGKSRGDSVVIHLAELLNTLKSRTGDDGLPPLLOS LRFG-----

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Multiple sequence alignment of annelid SLRFamide pNPs.

Multiple sequence alignment of annelid QERAS pNPs.

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10      20      30      40      50      60      70      80      90
Platynereis_QUERAS_peptide -MEKIAVFLLVATIALAFSA--SINQA----DALYLPNTRVMKRSAAA--AANNHVKISSPQQKR-YTDYQERASAFCTGLCMYEERK
Alvinella_FP537998        MATRLGLFVITIVLLVACSL--LLAQS----EALYVPKNRATLSSATGD---VAKRST-NIGQRQKR-YTDYQERASAFCTGLCMYEERK
Tubifex_CBAZ3684         MIETLMTSTERQQL-LLFVV--SYILLTVGIVTANYLPQQQD-----ADVLSLNKR-YTDYQERASAFCTGLCMYEERK
Sthenelais_FR770837     -MNKLGQYFLA--ACLV--LYAATSTLEVGAFTPHKSNALQAALKTLKSQLQRNSDISGSRQRKYFTDYQERASAFCTGLCMYEERK
Asiaticobdella_JZ184685  MSKGGKSMFGKIFILSVLCHVCLSF AVASARFVGHVYVNDDEEM-----MAKRS-LDYMDER-YTDYQERASAFCTGLCMYEERK

100     110     120     130     140     150     160     170
Platynereis_QUERAS_peptide SYSECFDLCNMYW-----
Alvinella_FP537998        SYSECFDLCNMYW-----
Tubifex_CBAZ3684         PYTDFDLCNWTGVGPSPIKLDKEKGRVAASSPAESAP----AAEQGMA----SMLRGTGAGRSRLGDKSKTRLRMGAKKATWDSY
Sthenelais_FR770837     SYSDCFDVCNMY-----
Asiaticobdella_JZ184685  PYSYCFDLCNWNKGPSWDHHDHTKDS EASKAMAFPLNR SVGGALPEGLMETQKNIIRTGY-RMRPADRNKGRNRFQEN-----

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Multiple sequence alignment of annelid QERAS pNPs.

Multiple sequence alignment of annelid MNC pNPs.

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10      20      30      40      50      60      70      80      90
Platynereis_MNC_peptide MRSFLLVILALVLSALLVS--SQSDDFSQYSSQ-----WQLESF-QPKQTEPDSISDFARDVKRLLLHLRRRKQPNAS
Capitella_EY614600     MKGSTTFCIWTVLAATLIALSSQSVVVEARSRPAIANNEEMAEPRDGAQQW--LQLE-EVMKDAPEMFDLVDKARAIFGDLKK----FTG
Eisenia_EH671930      -----LVLASQPLE--EGNSVVKEDRR-----SLESIRWLKKEKRAELATIAKRVKAEL-----

100     110     120
Platynereis_MNC_peptide PSRSASAKRFQLGQRINRHCWDVADVCCMWNVC-
Capitella_EY614600     KGTPAQPKGFLIG--LSRHCWDVADVCCMWNVC-
Eisenia_EH671930      SGRNSASDQAKRG-RINRHCWDATDLCMSNACV

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Multiple sequence alignment of annelid MNC pNPs.

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

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10      20      30      40      50      60      70      80      90
Platynereis_LEQ      ---MWHLAAAVLFATVVSNTIGAPLNP LPQ-KIHRESTK EITLLEQELKKAAGENKKRPPPAE EGVPAEAL-AD EEL-----VKELAAHDE
Alvinella_GO201158  MEKAIVRTAMLVVFLLASYG LGAPVSKVQDLDKRRESTEPEILNLEQQLKKAAGEDKQYFSATEARMPQIDGLATPEQDNSNPIDDEYGLLDD

100     110     120     130     140     150     160     170     180
Platynereis_LEQ      AVKDDKPKQSKETDEDS EEEELQEKAVAEKAAELKAKQEEQEEELK DVEKEPESEPDVAQEEEEEAQDQEEEPGNEEVHDEEELQNLGAPSNII
Alvinella_GO201158  VIEPNPEGDRQLDRIRKYA-----QLWBIIV-----KHEEYM

190     200     210     220     230     240     250     260     270
Platynereis_LEQ      NDLYEDYLNEQRAYYDAKRS GAALDNLAEQENEK DFEVSSLLETIEH ELLDEMRTGEVEEEEQQPSYNYNAPSNDQEEALRAEYLAA
Alvinella_GO201158  RSMHLHDYLGNTDGLDRIGPED EIPKRD-----ASDLSYF--SDDLEP-AMDDIYQGSDDD-----ERADSLMADYMV S

280     290     300     310     320     330     340     350     360     370
Platynereis_LEQ      TRGLQEPQQQFESYFSNPPYQGSPEYEGNEIRPPMENFNQNP SDKMAKVVAKWGYSAP E EYQKEENQAPLMEESAQEKDHEESLDQPQHL
Alvinella_GO201158  ----PEQQQFGRADGRM-----

Platynereis_LEQ      E P I M
Alvinella_GO201158  ---

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