

MRVSTVAVECTEVVVAASADAERE CGEREIETIRNQQCGSGRRNDMSAASSDIMEIKERKRNESEECNEGCSWEETFEVC

>Ascop Locus 20650.0 t1 Insulin-like peptide 15
MSTLSVAPPLIVSVICLLSVSSNAEILCGSDIPKAMAMACAFGRKSGPTRPEGLTRQQRVRFPSLTGDNNTDVFDRHLKRQWKGIADYCCDRGCTLDELASAVC*

>Ascop Locus 12564.0 t1 Insulin-like peptide 16
MKLLIALLCVTVAVVCLAVSDAMRICGESLTEQSNAGCTHGVRTASDKRSNSFARRFVKRSASEECCHEGCSWEEIYEGC*

>Ascop Locus 14352.0 t2 Insulin-like peptide 17
MKFAVVCFVAVLLAAAEASHYCGVDYENYRFEVYNHHKRDLDQASDTYLSSNKQRDMRHECCSGSGCTWNEVHDDCNRG*

>Ascop Locus 16747.0 t1 Insulin-like peptide 18
MMCSVNILRVLMLLSVIMASLIVISDAGHYCNIEMDKWRQVCAGKTRLLPLFYFYRGMSKREANFLENERVSLVKRSVYHECCDEGCSDDEEVNESCEPLSNQENYQEFVDSGGMVAIYNR*

>Ascop Locus 11131.0 t1 Insulin-like peptide 19
MKVIAACLIVVAFALAYCDDEEQYTMYCGEALQCKIVDTCHLIQORRRSDTFFRRALPRIHELLWGMKEECCSDEGGCVDEEVEDKCPIIHFLMPEPIIMVDPPIKPLPTLIVDPVEPIIGKGGENPFPEPPKAKRRHH*

>Ascop Locus 16610.0 t2 Insulin-like peptide 20
MKRLCFMLIVSLHVPSFLSDTTVVAEAIIICGRDISRALAMACAFGRKSAPTSITTTTRKRRRLDLPPDQTQITTOKRWGIAHYCCQIGCDINQLAAAVC*

>Ascop Locus 13690.0 t2 Insulin-like peptide 21
MNLAFVSVLTLLCVVAIVDADEYYNYCGIDLVKWYQLCRNKRDSFAEGLSKRRNVDELVSIRDLHNECCNENCKDEBIAERC*

>Ascop Locus 11179.0 t3 Insulin-like peptide 22
MKLALFVCILVLAIVCGADIKQLCGNEGLATIKEIQSEKCIKTPHHHHEKKPAKKPAGGEGGEGGEGGAGGEGGAGRGQAPIMQKRSADTYLSEMKRGDILEKCCSKGCSVEEIREAC*

>Ascop Locus 11179.0 t4 Insulin-like peptide 23
MKLALFVCILVLAIVCGADIKQLCGNEGLATIKEIQSEKCIKTPHHHHEKKPAKKPAGGEGGEGGAGRGQAPIMQKRSADTYLSEMKRGDILEKCCSKGCSVEEIREAC*

additional Ascoparia sp. preproneuropeptide candidates:

>Asco 16273.0 t6 [3' missing] (alternative signal peptide MTSHGRTSTLLLVLSFGFAISKA)
MTSHGRTSTLLLVLSFGFAISKADAAYSTTELDGAFARRLRAKIDQIIERSQLDELIDNRAIPVKRTTPEWLDDELKDDINDAKRAIPVRRRAIPVKKAIPVKRVESELDEKRAIPVKKAIPVKREE

>Asco 17603.0 t1
MVNPVVAVFICISVQSHIISGVLVKPPSGFGFDTFVSSPNGKRMPPFPIDRLTVNGRTTPARENCKHLIPEDKLMVTKLAFFPDDRNVNCRSPANDKRISFPTMIKKRSANCKRAFFPDDRFKVNCRSPANCKRDYFPDDRFRKVNCRAPANCKRVFSPGERFEVNGRSPANCKLDFFLDRLDVGRSTNGNDMQIFNHTIDLTDFELFQLAYKQVENELMKEITNNNDCKADRNHEFVNNRNNNLGFWKIDRAD*

Childia submaculatum

>Csub_c30872_g1_i1_FNMamide
WYQRRVLPVFFFFVAVALAHYQDPSPGSRSLSDSFEEYPHLMFEFSDLEDALEKRAYAFNMGKRIAEFTEDKKPYAFNMGKKAYAFNMGKKAYAFNMGKKAYAFNMGKKLDEEDFTQDKKSYAFNMCKRPPYAFNMCKRPPYAFNMGRR*

>Csub_c355_g1_i1_SFVNamide
MKNSMFFSFVFAFLALTSTISSFRVFAPATRRGILFQKTVARELGKRVGLRTWNWHEDEQEFFFKRSFVNGKRSFVNGK*

>Csub_c12842_g1_i1_PSFamide (FxxxFamide)
MNIOYKKTLYLCFELFLCITINLSLNSAHLTPQTQIIPHKGRLRGEELRAKSELNQGASFKKPTANCQGGCPFLLGKQSEFADIFNIYLTSTGKTSSSSSWKRFSSSFCKRFTASFCKRFQPSFCKRFRPSFKKRFKRLDDLFGQTFKFSIGERLSESKNSTFTPSFKKDKMSKEDIPIPKLRGTLQPRLRSSQCTHALV*

>Csub_c14012_g1_i4_GRL peptide (alternative signal peptide MKVAAILVLFMVGLVAVVLCIS)
MKVAAILVLFMVGLVAVVLCISDESSSEGNLNLDKRGRLGSSPWEKRGRLGFSPWDKRGRLGLSSWDKRGRLTLNKRREDGLVSPAQPLDDDFESKMETKRGRLSLPSWL*

>Csub_c14972_g1_i1_AWD peptide
MKITSFFIGSILLITLQVCQYTSGHSIQVPDDIDGPVSLKRAMAWDFHHGGNGKRAIAWDFLRNDENEENTGRRLNIAWDLVKQASQNEGSPGQKRAMWDFNKRNSQEKRAMGWNFLH*

>Csub_c13095_g1_i1_MRF peptide (alternative signal peptide MKNIGLIVLAALFVCLQLACCAG)
MKNIGLIVLAALFVCLQLACCAGIDQDGLSRTEYKSDIDKRRFAPRSNHPQETFTKRDENDLEKRMRFRENDDRWKRMRFISQRRMRVFPEKRMRFIPEKRMRFAPKRMRFSPHKRMRFAPH*

>Csub_c13564_g1_i1_LWD peptide
MKCNLVALYLAILFSTLKGVESVPDDQLNEVKSGSQEDGHNEAKKLWDYGASTKRHPDVEENTEKRLWDYGQSKRLSDNEPSKRLWDYGPAKRFVENEPSKKLWD

>Csub_c12811_g1_i1_amidated_MFGYG peptide (MxGFG petide) [3' missing]
MKFPKIVNVFSTIIFAILFQCILTNHSHLNQELSTGEKYPESKRIFGYTGEMAGHEKRMFGYGGDMAAGKRMFGYGGDMATGKRMFGYGGDMAAGKRMFGYG

>Csub_c28735_g1_i1_LRFamide [5' missing]
STWGNIRFGKRFHDKAWDAYNVGEPEVKRYLRFKGRFEDPSADKRYLRFKRYLRFKGR*

additional Childia submaculatum preproneuropeptide candidates:

>Csub_c17540_g1_i2 [5' missing]
AEYMGGEDNGLCKREGEDSGLCKRDGEDKGLCKREGEDNGVKREGDDNGVGKKEEDNGVKREGEDNEPSKKEEEDNGVKREGEDNELCKKDEVEDNAGCKREGDDNVVKREGEDNGERLVEGDKEEACTRERDEKGQEGVIGNRGDNWTGSDGKITGGEDTNCIGKQEEKRGEEQENDTCGRADSAEENGKMERVDNVPGTMANGETLDDSGVIKGNVDKDTHEFVGIKLDEEQLSDTGLY*

>Csub_c17540_g1_i1 [5' missing]
AEYMGGEDNGLCKREGEDSGLCKRDGEDKGLCKREGEDNGVKREGDDNGVGKKEEDNGVKREGEDNEPSKKEEEDNGVKREGEDNELCKKDEVEDNAGCKREGDDNVVKREGEDNGERLVEGDKEEACTRERDEKGQEGVIGNRGDNWTGSDGKITGGEDTNCIGKQEEKRGEEQENDTCGRADSAEENGKMERVDNVPGTMANGETLDDSGVIKGNVDKDTHEFVGIKLDEEQLSDTGLY*

Convolutriloba macropyga

>Cmac_8297.1_amidated_SS_peptide
MKLAPLLFVSICCLSTALSSDQNGAAEDSNLIIFPGDLVDLSTPDLIELLDHSDEVKRSSFHCKFRKRILGSDPFEEHTRSSILGEYKRGVDVKVEDQKTRRSSFHGNYKRRSSFHGNWKRSSFHGNFKKSSPSLSLHGTFCKRSSLSLHGDFGKRAAWYNKLGHQSSFDEIYKGRDFLGDEIQNTPEESGQLGYLVNVY*

>Cmac_1031.1_AWD peptide (alternative signal peptide MSSDSMLSSSLFVISCYCCVSLITCEDATGPAAPALIAPEPISLHGCHIPAQLLMKRGVAWDFTKKVPVKGRNLAWDFTRRSSDDTEGKRALAWDFTRRSGDECKQSMPWDLCKRNLAWDFTKRTFVALIPEDKRALAWDFTKKYDSDKRALAWDFTKKSVIPVETIASNSPPYDKRALAWDFTR*

>Cmac_643.1_SSAMHFF_peptide (SSxxxF peptide)
MSRAANHSGVSKLMFGFVAVTIFVQETTALTIIVPTEQDALLYSEDSSDPTSVDYKRSAMHFFKRESPLTEEELIKRSSPWHYKRSSPWHYKRSSPWHYKRSSAMHFFKRSNGYPYLDESSSEGFYA*

>Cmac_3219.1_MHFamide (SSxxxFamide) (alternative signal peptide MICLSILIANCLINLSS)
MICLSILIANCLINLSSQSVVDRDLSSEQFYAASNLVAPPILIKRAHRMHFKRAPDSSSEDFEQPYSYYLEPLIPEKRSNSMHFKRASSLWRLEAPQFNSKKEAGSSMHWGR*

>Cmac_1299.1_SSFRSF_peptide (SSxxxF peptide)

MSGSGSQLASFLNIFLISVVLCLVSALYCSGDYYPTDLDFKRTEDLFESPDLRNNWSSLRGFNRRNWSSFRSFRKRSQQRWSSFRSFKRRSTDNPLD*

>Cmac_6993.1 PSFamide (FxxxFamide) (alternative signal peptide MSQVLTFAVTITIAISCFNFNGSAA)
MSQVLTFAVTITIAISCFNFNGSAIAPSLSWVSKDSSSRVSPVSLGLGVPVFMGTASDPATDIDRRAFMVKRNSVEDPNFTRGLFMSPDASWGNQFPVQWMSVKRLGAKSHFSPSFGRKMTFAPSFGR
QPSAALFQSGRGQTVGQGSASEKKRMARKREFYPSFKRNLNVNFMENQAKFPFPQVNRK*
a
>Cmac_1739.1 LWD peptide
MSTNLLPFVLLSAVLCFSSSLVTSRSLSESGGSPVLFLSDPENNHPLIHSGNNPDKRLWDYQYKRNSGLPVSLGAENPDEKRLWDYQYKRAVGLPEGVATGGDEKRLWDYQYKRNAGAAGDVIGEOK
RLWDYRMLPKKTAFA*

>Cmac_2537.1 LYDImamide
MRFGHIFLVVAGSLQLLSEVSSREIPQFTRQKSSNYMLGKRSVDLGLQKRWGLSGVVDVSVNVASDAIDSADDLKDKAIEQAANSAAAKTVTDKVADVTDTVNNEASNLDLEDAFEVADELGLPTDL
DTVIGVAGDLGIPVTQQGVVIDLAQEMQIEEMMAQMPVEDLIAMGQDLAQAVGGGSEAATVSIIEILDKLATAEAMVDNLASCKSSKDSDEGIQARKKDVKKAGGLLYDTMGKRAGGLLYDTMGKRESG
DLYNVLKKRGELDDFAKRTHLYNIMKKRAGGHLYDIMGKRAGGHLYDIMGKRAGGHLYDIMGKRDDGGLLYDIMGKRDEGEVAQILPSENSDVMDDLLSTGLGLATDLALPMATGGLIG
GGGAAPDNGNLYILDNVNELLIKLNKLQSA*

>Cmac_607.1 MxGF peptide
MQQMKNQGNLFMAGFLLLGLFALFGQGARATEETYPVDVETRAIYDFGQPLGNLMGSPDVRFGPVSDEEAKRMGGYSAFEKRMGGYGGLGLKKRMGGYSNFEKRMGTGFGMAKRMGGYSILKRMAGY
QI*

additional Convolutriloba macropyga preproneuropeptide candidate:

>Cmac_78.1 [3' missing]
MNKFLLFLAAFAVLVALSEARSKHSKRKFPTTFARSDDHHRKROGDQGTQVDDDKDKDKDTDKGDKKGEGGAGKKGGESGTVGDGKKGTTGGMGGDKKGGAGGMGGDKKGGAGGMGGDKKGGAGG
MGGDKKGGAGGMGGDG

>Cmac_321.1
MKSVSQVPCAKLTAVAFALFTCALILSCWTAVISADESPVEPERLRCARDSTDCVEKAKRLVKRAIGCDLSNPYMDCFSKRNVAAKRAIGCDLSNPYMDCFSKRVPiVYESMDMAKRAIGCDLSNPYM
DCFSKRHAAPVPVVOADKRAIGCDLSNPFMDCAKRSEPEPKRAIGCDLSNPYMDCFSK*

>Cmac_822.1 [N-terminal pyroglutamic acid]
MKSFSAVSLFGSFLVLVLLHVISTTRAQYLSPESNVGPDSVDKRSYQFLIPEKRSYQFLIPEKRSYQFLIPEKRSYQFLIPEKRTTVV*

>Cmac_844.1
MKSASVSFAPSLLVLSIAFVWTSVTSAGVGDKRSSSIHVVDGNRLQSEFYPGSETNSGQQFWKRLVSSMFAPOQQLRQSPNSRGEIEEGGLDENGLEDEFEGSKRYGEKEAPGFYQRGDENGEEEEEE
MKRAQLMEFERSLRANSAYPVMKRGRIHMNCQRFKTFQQGSGLC*

>Cmac_1033.1
MNYKVAADVVISITLTVTLPTVEATAFYPPMDRRSRIYRQKRSGYPPAVINNKKRLSFLQTAVSNMOTRPHWL*

>Cmac_1118.1
MNSKVLIAIFLCVSGVLAEREKTPRGLPELREVKDAGLVESPEPPVVLDTRFRAESLTKRDVEVIPISGEGRAPESLHLQPISERAMEKRGAIKATASEQKVL*

>Cmac_1194.1
MAFFMKSTACIQMFAIVCLATLASSFYMPEDDFSGLDDESKRGVPPKVDPNCRDNYSRITCYHRANQCRTHTSLRMNCKQTCQVCRLPYKG*

>Cmac_2039.1
MESKFACFCIVVCLLLALYLSPVIGYEEEEPELKRRNFHAMSGYMKRGYEGNYAEEEEKKRNGLGOLDTWMDDKKWYRKSFPH*

>Cmac_2152.1
MKSYSQSVSFVFTSAVVLTTFFIAVCQISDDAKLPGPDIRAASMGARSAPGLMQARELANQMKRNWNSMRKRENGAWMQAAALANGLNDESYSPYRMMRQMRLK*

>Cmac_2219.1 [5' missing]
RNLKKKHGVEENIQCSSFFVFSFKSFIIEFCDKVVMGSKLVVALLSMTIVLVFQAEQSSALEKRHGFGTTGTGDSGPQCKKREMETAERAEENFKRNNHLFESLHDQ*

>Cmac_4469.1 [5' + 3' missing]
KRMDFNNEIDKRMDFNDEMKRMDFNNEKRMDFNDGTRMDFNNDKLLKNKRMQFNDELEKRFYLTPAEIHNPYRQQNMWRHNYDNEENTEKRAVRRTRHRRIRPKGGYRHKREEDLEPVEEEEREPP
YVSEGERHEDTKLNRKRLSTEFGLYDDKKRSLASDVAGWSKRDPEENQGYDTQKRSLASDVAGWSKRDPEENQGYDTQKRSLASDVAGWSKRDPEENQGYDT

>Cmac_7555.1
MIKFLSLNMYAFALLMTLWAFSAVKAATLEDEELDEKRGYFLNKAHKRELGDNEEKRYLVHSFLRPSSKRAYFRNEALKGLANEEKKRDFDPEYLDLSLKKRGFFTREMLDHLGEDKKRGYFTQEMI
DRLGEEKRGYFSREMVGSLGQGDG*

>Cmac_15344.1
MNRNLLISFSLLLLTIACCNGPNTVQEFONDSSKRGYFLNNAMLQDDKKRGFFLSKTRAKRVFSDENSDETENKRGFFTDFVNNMGENYNYRRLQRNV*

Diopisthoporus gymnopharyngeus

>Dgym_c11555_g1_i2 DRFamide (FxxxFamide)
MFTLLFGLGLVCFCTCITQISSHSSSNVFPVHEKQDLIDNDGDPYFVNQPEKRLAFVDQFKRSEFVDRFKRADFADQFVNMPRFVDKFGDNADFVDQFKRSFVDRFKRAYTVDQSEKEPDFVNR
FGKSGFVDRFKSDFDVSQRKPDFVDRFKIDFVNQLEKPDFVDRFK*

>Dgym_c12227_g1_i3 ASALHFamide isoform 1
MASSETNFARCHQSSPAQMPFSLFLASLVLSLASTCRALELMNPELTSMESQEIFPDSQESGEGLYYRDLDDKRASALHFKRASALHFKRASALHFKRASALHFKRASALHFKGRK*

>Dgym_c12227_g1_i4 ASALHFamide isoform 2
MASSETNFARCHQSSPAQMPFSLFLASLVLSLASTCRALELMNPELTSMESQEIFPDSQESGEGLYYRDLDDKRASALHFKRASALHFKRASALHFKRASALHFKGRK*

>Dgym_c12147_g1_i1 AMNAARLNFamide [3' missing]
MVTNYSKNKTWICWSFVTTLLFEMMYWSPVCSAHEVNDKNKSDILNKFEKHHLTTAKIDEGIPKDSLEDEKNIDDIGVPMKSDLENEFSKNFPVSGNLFEKAMNAARLNFKKAMNAARLNFKK
AMNAARLNFKK

>Dgym_c12581_g1_i2 LHFamide_2 [5' missing]
AEYMRMPRNHSTSSHPhYLAKTRLSTLLPSLLALIFLLNGLLAGADYLYDSLDDNNAMYDGGLEPNMVNFDDAEESSNYWYYPPIENSANSIPYNKRVSPLHIKRVSPLHFKRVSPLHFKRVSPL
HFKRVSPHHIK*

>Dgym_c12998_g1_i1_i2 FNMamide
MALRVVLVPPFFVFAVALAHYQDPSGSRSLSDSFEEYPHLMFSDSDALKKRAYAFNMKKIAEDFTEDKKPYAFNMKKAYAFNMKKAYAFNMKKAYAFNMKKLDEEDFTQDKSYAFNMKKPYA
FNMKKRPAYAFNMGR*

>Dgym_c13842_g1_i5 AWD peptide isoform 1
MKMSIMFHLALYSLGTFIMWQISVTAAFDVEDKRGMAWDFKRAGELNELNLPLQNGYDKRGMAWDFKKRYVPVDNPDDKRGMAWDFKKRDHELDKKRGMAWDFKKRDVNSEKKGIWDFKRLPLISTKR
GVAWDFK*

>Dgym_c13842_g1_i1_i2_i3_i4 AWD peptide isoform 2
MKMSIMFHLALYSLGTFIMWQISVTAAFDVEDKRGMAWDFKRAGELNELNLPLQNGYDKRGMAWDFKKRYVPVDNPDDKRGMAWDFKKRDHELDKKRGMAWDFKKRDHELDKKRGMAWDFKKRDVNSEK
RGIWDFKRLPLISTKRGVAWDFK*

>Dgym_c14376_g1_i6 WLP peptide
MTLIMKCTILPVFVIFHTCEVANGLSQSLEDISGEGDLKYFSKEEPPDLIYISNFGNYEDMDHLNSFENAKKKIGSWLPSKSDFEEDDSFSEEWNGGEAKKTIGTWLPSKSKFDSSDEIFLPE
ERSLYFNTPNVVYKKIGAWLPNKKRAIGTWLPNKKRAIGAWLPNKKRAIGAWLPNQKRAIGTWLPN*

>Hmia 98013351 SALHFamide

MTYPGLSFFIQIISILLIASLILTOTFAOEIDEDERSALHFGKRIDDPMERSSALHFGKRFSSGNODKRTTFEDRDVGLHWGKRGKRTSALHFGR*

>Ipul_5671.1 [5' + 3' missing]
LHSLNWDNGGNCVDNRIGNICAGKPAATHPVIPEPVLMVALNTLLAAAGLLLLAPLARSSSEDWLEERFDPDSIYDLDEYDIERRVDPYMAHLNGNIEERSVNHPMANLONIOGRNIDEDPREDEMLS
VRMHDFGGVMDDDLHGRSMDGGLQWGEDEDERGYHPHSCKREGDGLVSFAFGGYEERGLAQSMASCKRGLAQNM

>Ipul 701.1 (no oxidation of methionine detected)
MAAEMGSCGGGDWRGLRHLPSRSQPNRSQQQTAAAAARMKLSLSLLLMVALSALFVDNASGSSIRKEMKRRLGCPLDDPFLACSLVKRSRDQMLPQGSMQEKRRLLGCALDDPWMPCELVKRSAAETEE
*

Meara stichopi

>Msti 3522.1 WDLamide
MARQIQIAVFVILIGVILARVPSVDKRRKMSFDLCKRKLNWDLCKRGMDLSDLSEEEYDELLDSYNGCKRAMNFDLCKRAMNFDLCKRTLWDLCKREDDGEKRRLSWDLCK*

>Msti 6636.1 GFGN peptide (achatin) (alternative signal peptide MRNYFVILELAILALITSA)
MRNYFVILELAILALITSAAFEEISSNDNFDLCKRGFGNCKRGFGNCKRGFGNCKRSIDDEIDTKQELVDKLVSIVMKDETIENRDERGFGNCKRDYTGPLAGIGTYSRGFGNCKRGFSEPLSGIG
YRFSRGFGNCKRSPPGGVKHVFVIEGVCDSSGENSDNFFLSEFVNLLNLKPCKHETENGIIHQVVQGVKCAAGALI*

>Msti 11548.1 FRamide
MVTCKSAIKCLIFTFVFTLILISETQGRSSNDAYRSAPGGYSFRCKRLPKSVMDFRCKRLPYPGFLEFRCKRNFNSSDDIDENGNDSPYSVSVPSYSSGGCKILNLN*

>Msti 5141.1 calcitonin-like 1
MVAMPTVQPVLYVMGLLLIFSCLVHSTCNNHKLGDQSSDENYYWPIRDIARQIARVKTSDNSDYWVVRDASQRLSPVKRCQTMSTCLLNRLSQHMTSNMKKPRYTGVKSPCK*

>Msti 7629.1 calcitonin-like 2
MYVPLTCLASLLLLATVGTSMSTRQRAILEDQAQGSWDEFSNSPIYGPFKRLMPLSKRCDFSTCLGDRVSSGLLGGINVGAFSPCK*

>Msti 6316.1 GnRH-/AKH-like
MKVVLRVLLIHLAICMCMTATNGWTSVSNWLPCKRKSQLPVEAHDIDPEALQAEPDDETVPCTICSLPTNDRRRYFKSAVNYILWDSEGNPVSVVPQSCKRDD*

>Msti.22299.1 Insulin-like peptide 1
MNTVNFLILVVVSATAICTVSAIFCKDMKWSGRLCKGSKLADKWTCLDDYTSNYTMSILYLSHIRQANLANPKNVLQNFGRSMPTILKRRMRSENINSDELVDLCLKTCGFTTLVRFCSISEHWEKL
FEDLLEGKISAEFLDKIDQINMKSTNRI*

>Msti.rna.tri.12781.1 prokineticin like
MHGNOHRLLENKFLTICIFILFSQRVASFHMEAKYQPTDDFGLKSQWGIEISSNSLLKHVDKRMMIHVECSVDDDCGAGRCSSNSRNRQIRTKSLHGVDDFCLPHIPEWGIQYERQHVWCPVQEAICEN
VAGRKAGRCVLVKK*

additional Meara stichopi preproneuropeptide candidates:

>Msti 5165.1 [5' missing]
NGRLQTGFYVNGRLQTGFYVNGRLQTGFYVNGRLQTGFYVNGRLQTGFYVDGRLHELADV*

>Msti 43027.1 [5' missing]
RRLHHGLGRHLHLYLHHGLRRLHHGLGRHLHLYLHHGRHLHHGLGRLYHGLGRLHHDQQHCLRRLDQVLKYQMFPNT*

>Msti 44607.1 [5' missing]
RTGWRPECLRWGRCTCWRIQCLRWGRGTGWRPECLRWGRCTCWRIQCLRWGRGTGWRIQFLRWGRCTGWRI*

Nemertoderma westbladi

>Nwes 37655.0 t1 GFGN peptide (achatin)
MSFQIGFGLFALMGIFVYSECLRIIPSPCRNQDGTIVNRVPMVTPPQGVQLQHTRTTNKGLLHAMORRGFGNCKYYPGNSLPSEDVQTVTKQSGHAVETRFGNCKRYPGDTVMTVKRYGKEVVTRFGNK
RFPGDYMQIARRLVGTAMPNKDDEFTPRAKENAVRMEMFGDSPGSNGNSGTRSC*

>Nwes 49866.0 t1 LRIGamide isoform 1
MKSCIWIGVLAALVLIAYLTVTDATDEFKRLRIGCKRHISAENSAEHSNSNVEKRLRIGCKRDMMKRLRIGCKRSDDDSREKRLRIGCKRDNGLDKRLRIGG*

>Nwes 36484.0 t1 LRIGamide isoform 2
MKSCIWICLMAALVLIAYLTVTDANAEEFKRLRIGCKRSHHSDENSDNHDSSSVEKRLRIGCKRDVMKRLRIGCKRNDDSREKRLRIGCKRDNGMEKRLRIGG*

>Nwes 7201.0 t1 LRVGamide (LRIGamide) [3' missing]
MGTSMWVVAALVVMMAHIVHWPDSSDVKRLRVGCKRSDDFEKRLRVGCKRDDDEEMDKRLRVGG

>Nwes 60610.0 t1 AWD peptide
MKITSFFIGSILLIITLQVCQYTSCHSIQVPGDIDGPMSLKRAMAWDFHHGGNGKRAIAWDFLKRNDENEENTGRRLNIAWDLVKQASQNEGSPGOKRAMAWDFNKRNSQKRAMGWNFLN*

>Nwes 35014.0 t1 TFFNamide (SFxNamide)
MVKLIVVAFVIIVSLTMBITSKPYESSQISAFHTNPWIELLSPEYQSLKKCRDELDEKRTFFNGKRTFFNGKRRDCDFSCLFSPEYNSLMEKYGEEVDKKRTFFNGKRRNGEFNNMDK*

>Nwes 54093.0 t2 t3 t7 t8 t14 t15 t21 t24 WSFTNamide 1
MGNKIRFYAGVILFVLVLEAIVSDAQKDVRNKL EEVELPND AENQLVHRMKKWSFTNGKRNINSNDKRWSTNGKRSYENADKRWSTNGKRWSTNGKRSVS*

>Nwes 44523.0 t2 t6 t7 WSFSNamide 2
MNRRTLHLIIALGLIIMNSLVKGDHNVDVLYGEKGDCKRWSFGGCKRWSFGGCKRSFNDAKRWWSFSNGKRNNDQETI*

>Nwes 52296.0 t8 t19 t2 LKIamide
MSALVRYICFLLCLLVTLDSIFARHWGHFVEDGGDVANDLEKRLKICKRMYDEPYRSIDLKRLKICKRSEENLSESEDEINEDKRLKICKRLKICKRLKICKRFFW*

>Nwes 37502.0 t1 t2 ELamide 1
MPAALSFTTLTILFVICHVSMAFTVYELCKRGRNDNDSDSMERRAPFVYELCKRRLQPGFTNEYTNRRKNFVYELCKRSIRSVENQMKTILGNNAK*

>Nwes 33619.0 t1 ELamide 2
MLMRLLTITLLFWCSLQSRARYVYELCKRGDSSEFLKSAVALDPTNKRFVYELCKRSSILKSSPEWNEQQRRDSDEPQORSYVYELCKRSYE*

>Nwes 32435.0 t1 LWD peptide [3' missing]
MKCNLVALYLAILFSTLKGVESVADDQLKEVEGSEQEDGHNEAKKLWDYGASTKRHQPDVEENTECKRLWDYGQSKRLSDNEPSKRLWDYGPAKRFVENEPSKKLWDYGPSKKLWDYGPSKKLW

>Nwes 32435.0 t2 LWD peptide [5' missing]
YGPSKKLWDYGPSKKLWDYGPSKKLWDYGPSKKLWDYGPSKKLWDYGPSKKLWDYGPSKKLWDYGPSKKLWDYGPSKKLWDYESSKXHSSNDEVN*

>Nwes 6928.0 t1 WDLGamide partial 1 [3' missing]
MTSCSEILNWRLLFIFVFGYILLSSVDAEVDPNDRKPIGWDLGCKRPIISCKRGLNWDLGCKRGLNWDLG

>Nwes 32008.0 t1 t2 WDLGamide partial 2 [3' missing]
MMLIRDRLSLLWRVLFTFATIGFAVNADSDSDTLDNKKPIGWDLGCKRGLNWDLGCKRALNWDLGCKRGLN

>Nwes 27067.0 t1 WDLGamide parital 3 [5' missing]

GKKRGLNWDLGGKKRGLNWDLGGKKRALNWDLGGKKRGLNWDLGGKKRGLNWDLGGKKRGLNWDLGGK*KRGLNWDLGGK*

>Nwes_12264.0 t1 t2 WDLGamide partial 4 [5' missing]
WDLGGKKRGLNWDLGGKKRGLNWDLGGKKRALDRENNKPKGLNWDLGGK*

>Nwes_25514.0 t1 PxFVamide_1 [3' missing] (alternative signal peptide MDQTLMTSLLLIVILAISTVTS)
MDQTLMTSLLLIVILAISTVTSQSQSGVADDKNAQAVSVSHSQDTPRLVRRYVPQFVGKKRHPVSDAADTGDGPEADADAPPELSENQLNEQELLELLSDYDFNRFDDGENHEDLDVNVQDVVNGDDKSD
GVDDTLPLSDSDSIDNSQEEKKRYVPFSFVGKKRYIPNFVGKKRYVP

>Nwes_14711.0 t1 PxFVamide_2 [5' missing]
SFVGKKRYIPSFVGKKRYVPFSFVGKKRYQPTFVGKKRYVPNFVGKKRYQPLFVGKKRYQPTFIKKRENEDKKRYRPMFVGKKRYVPFSFVGKKRYVPFSFVGKKSTVDSTDEMTGVNSDESTPVLVEKKRSAPQAETL
SSDEDNHLRHKKRSLIEMEDKKRTWGPWAVRDILTQKSLEGTKKRFAPEFVGRRDSISTLSALKALQVARSEPRLATKKRFQAPLFIKKRSSHEDSSLYWNKLNIDPLTESYLQELQEMQL*

>Nwes_51167.1 t1 t7 t8 t15 t20 t22 t24 t26 t27 t47 LHFamide [5' missing]
LGRNTRTQLHIKKRTRIQLHIKKRIIRTQLHMKRRLTTLQLHFKKRTRTQLHTSSTTRIQPHTRWTTQYLIPTHVYQLNSRITTPVGFLRVHFEPEHPRPTPNQRP*

>Nwes_46971.0 t4 Calcitonin-like
MSKLLSLSVVVLVVALFLASTDAEHASIIINREKLIKRCCTTMSTCLVNRVTEGLMGNANKGRYVGPSPSGRRRRFAKQKR*

>Nwes_61081.0 t1 Glycoprotein hormone alpha
MMEIIFIINLLKLVLVLSILIDRCFTKEAYGCHVAHYVLSLEYPSCESQHIPLLACKGYCESFSYSSPMGNVRKFQVSOQQCCRIIESNQVEFYQRCEDGLYRGYTVNATQCHCSHCKLETMTMKNINKRS
THGRTLHKHSNNSSKTLIDDDVDWDDRIWQHKLFTEP

>Nwes_30166.0 t2 Glycoprotein hormone alpha (alternative signal peptide MNFFENSKLLIFFPLVLVIA)
MNFFENSKLLIFFPLVLVIAENKSKQEDDVDSGDGCFLTEYTMKLDFTDCETKHIHLYACRGYCVSYAYSQQWRHSVNTPRFIAHSSCCRIYGFTRVNFNYICEDGIYTGSVPNATSCYCDNCELPEGS
QSRVTRGTQRAVRLKKNLPAPLRNATHITDQKQFQQLTPKHNSKIFKP

>Nwes_43918.0 t3 GnRH-/AKH-like_01
MEPRVIVIVCIIAIIIVDSCTAANGFSGSSNWHPSGKRNKGSSEGSNENPSSNEISGELGPGVCSCGADGVKKYFKTIDEIKELSSGSGSGSSEES*

>Nwes_45035.0 t1 GnRH-/AKH-like_02
MEFRSVIILVVIVFEIGSSSANGFTGSSNWLPSSKKRGIQYNGVKGKADIGPGVCSTPDGTTKHFTSVKEIMKEGDQT*

>Nwes_49732.0 t1 GnRH-/AKH-like_03
MEFRVLVALVILVVTADIAKANGFTGASNWFPCKKKNNMANLRQTGLATSMKAMANARAPKTKPETGPGVCFLPGGNLYKFESIEHEVPRIEGPDID*

>Nwes_29216.0 t1 GnRH-/AKH-like_04
MSSHYTMKSYSALLLLSSVLLFIVYTTVDAAETANGFTGSHNWSPGCKKRTANGFTGSHNWSPGCKRNAPSGISAQEQLQIYGPCICIAPDGSTKYVASLSDPEISEKNP*

>Nwes_64678.0 t1 Neuropeptide Y/F-like_01
MPLSSGSRLLWCVSAILTLGLLCLILPAGLGSATPLWSRGDQSGGDQPVFKTPEELRRYLQDMNEYAIVNRPRYCG*

>Nwes_43226.0 t10 Neuropeptide Y/F-like_02
NTNTITMNRVTCTLLFVALALVLSVTCQPDSMLAPPGRPFVERPSDQLRRYLKALNDYYAIVGRPRFGKSADKQTLGQAFEQQAVGNE*

>Nwes_64887.0 t1 Neuropeptide Y/F-like_03 [5' missing]
RRVHGNSDSSSALTSSRSTSNSSSKDAAMIDVFENPFELRNYLKQLRELYAIRNRPRFGK*

>Nwes_Locus_30704.0 t1 Insulin-like peptide 1
MYLKRFPETPRWKYYLYIWTLLFSTLFQVGWQDYICGSDVPRAIVRACAAQKRSVGNYYENPLSKNNLMKSLKLKRAASGIASHCCAAGCSSGDLAFC*

>Nwes_Locus_5627.0 t1 Insulin-like peptide 2 (alternative signal peptide MAVYIRTRCICFCLLLCTTMA)
MAVYIRTRCICFCLLLCTTMAESKYICDGQQLSRAILRACAFFKRDGRSNINNQGIQDGAADFNSMEFFVKPKISQLHHKNLRSKRVGDGVASHCCQKGCMSMRQLSSVC*

>Nwes_Locus_45386.0 t1 Insulin-like peptide 3 (alternative signal peptide MFLLVAVLVSMILLQG)
MFLLVAVLVSMILLQGIPLSSQEILCGSAVPRAIVRACASQKRS SHMPYQSQWQNVERRNDLIRVYRSGMRGIASHCCSYGCSSSDLVAFCC*

>Nwes_Locus_57309.0 Prokineticin like [5' missing]
TVAYSMASTCSSNLDCPDQCCGQPVYDVVLNLAKTCKPYAKQGQCGHGNILFASCDCEQGLTCVEHTGLLSFLHTDKGTCRTDASTDHKTGTSAGILDLCFKK

additional *Nemertoderma westbladi* preproneuropeptide candidates:

>Nwes_37876.0 t1
MTKAWLNFGALVILAQLFPISDAFRGENWMMFYKDLCQDGSIDCVLRDLPEVIMWGS DGN DQEFTAKKSLIGQRLGYEQNSPEKKIFINQGLGNDPKKRMFVNQRLGNYPKKRMFINQRLGNAPDKRMFV
SQRLIKKR*

>Nwes_21237.0 t1
MLLFAISSLMYLIIVNVQIINTDIESTITSKWNNYVHDDGGHGSQNFSNVKGDLGENVTGDFKKNVTDGDKNVTDDVGENDTDDIKKNVYTGDIKKIVTGEVKKIVTGDVKNVTSKVKKNVSTEFSEI
TITPTDVVYLVPNICHFTWLNPIPFPHSYLSLISAYKNLNPSPRDIRCLTL*

>Nwes_15548.0 t1 [5' missing]
SRVYKKRGGEILIPHVYKKRGGEILFPVRYKKRGGEILIPRVYKKRGGEILLPRVYKKRGGEILIPRVYKKRGGEILLSRVYKKRTGEILIPRAYKKRAFGGKGDHFIPVNVNEDKHDAIVIPSRHKKR
GGGVFIPSAYSRPDEGE*

>Nwes_15548.0 t2 [5' missing, 3' missing]
LCATSSVTINRLRYHNSVALSLIFAAAVLLHSSQLGISATDLOKKRGAEVYIRHVYKKRSALSIDGRDEPQQRPAAANIYD TDDSLALAGYNKEAKKPAFTLPYNSKNEKKRGAEILIPRVYKKRTGEIL
LSRVYKKRGGEILFPVRYKKRGGEIL

***Sterreria* sp.**

>Sterr_c21028_g1_i1 WDLamide isoform_1 (alternative signal peptide MKAHFHQCLPAVLLFAAIGTQVA)
MKAHFHQCLPAVLLFAAIGTQVAHCEFELSQTNEKKRPMTWDLKKRPISWDLKKRSDKKRPMSWDLKKRSDKKRPMSWDLKKRPMSWDLKKRSDSAESDKDFEELIAKKRPMSWDLKKRSSDKRRR*

>Sterr_c21028_g1_i2 WDLamide isoform_2 [3' missing] (alternative signal peptide MKAHFHQCLPAVLLFAAIGTQVA)
MKAHFHQCLPAVLLFAAIGTQVAHCEFELSQTNEKKRPMTWDLKKRPISWDLKKRSDKKRPMSWDLKKRPMSWDLKKRSDKKRPMSWDLKKRSDDKRPMSWDLKKRSD

>Sterr_c21856_g1_i1 LRIGamide [5' missing]
YQRRVRAEESGDIDKKRLRIGKKRAYDEKKRLRIGKKRSDDELEATKKRLRIGKKRAYDEKKRLRIGQKKRRRRV*

>Sterr_c16337_g1_i1 ELamide [5' missing]
TNAEYGDQGNENSDQFADKKMRHEWWEKKRLRPEWWEKKRSMQPEWWEKKRLRPEWWEKKRAPRHEWWEKKRLRPEWWEKKRSGDGEFESS*

>Sterr_c22814_g1_i1 Calcitonin-like_1
MGRSSSPQWLVSIVVILLISSSSSFIMRRFDLTLEGNEEQNLNLQEMARRSDVIPLHIAYKRFMSEAKRC TNSPTCLLNRVTEGLGSRYRNYPRYTGAFFSPKKK*

>Sterr_c17081_g1_i2 Calcitonin-like_2
MNLLVPLLVISIALSITDGRNLRSEMTKMKVKNPLAKNLFAKRC EGLGTCLLNRVTSGMLGKGPSVGAWSFGKK*

>Sterr_c4877_g1_i1 GnRH-/AKH-like_01
QRRVRGFALSLLVVMAIDMTLAANGFTGSTSWLPGKKKRS PSFSVDDSA PFSEENAQPAQLGPGVCVCLHPDGSRRYFKTVVNVYLLNKDGEEISAKFDEEPNKKERFF*

>Sterr_c566_g1_i1 GnRH-/AKH-like_02 [5' missing]
QRRVRGSTSWLPGGKKRSQEPVVTDTKEQAVLGPCCVLNQMARDTVLRKLLTTYSGTKMTNLWLPKKYHNLKTNLFSRQTPVVTQSL*

Xenoturbella bocki

>Xboc_12867.1 SFWNamide
MNYIYIPLFLAILLWYQLPLTASEETLADYMKEDGTTDSGIGIRSFWNKKRAWADQGLDEMINEEARAFWNKKRSFWNKKRSFWNKKRAPVETDFDEDKRSFWNGKREPDVGENYDDALLKKSFWNGKRSFWNGKRSFWNGKRSFWNKKRADDQOREDIPPVEYMEFLDRLFGHQSDGKLAP*

>Xboc_21216.1 PxLFAmide
MTNMAIISVCVLLVLAVNIVNGSADFCEQFPDLCDDAEMSKRQLNVFPWYEVWNSKKRQDVEIRREPPLFVKKRREPPLFVGKREEASYFVGEKK*

>Xboc_836.1 LRFDIamide (alternative signal peptide MKLFDLFCVTLVAGIASVYCA)
MKLFDLFCVTLVAGIASVYCAEAEFGMPASSDVKRLKFDIGKKRHFDDKRLRFDIGKKRAWEEGQENDYAQELVLGMADGVHDYLANNADDSVSKRLYDMSKRLRFDIGKRLKFDIGKRLGADSNDLVVIGGVEIPVCAQDEPEGLSLCGFAPMGSRWWPICS DNCEELKADSYD*

>Xboc_2558.1 GFGN peptide (achatin)
MSCTSVTVCYWLLMCVLMCATVLSFPVGELGVYDDADLKDNLGDISDTSAQETARLVSSCLSYSELMRSDVDNALMLDIDDRGFNGKRIAGFGNKRIPGFGNKPFGFGNKGFGN*

>Xboc_1521.1 SLQFamide [5' missing]
GRRSLQFGRRSLQFGRRSLQFGRRSLQFGRRSLQFGRRSLQFRHLSMSHARRFPNTQQGRR*

>Xboc_4670.1 Calcitonin-like (alternative signal peptide MNNKTLIVLSMVLSTMLVLASS)
MNNKTLIVLSMVLSTMLVLASSAPTDAANSKKRDLESDLAAVKFIEALLNLEDNVERISYEKELYEQPMPINMESNPVRRCTCSMSVCLQSQIAHALLSRPKGPDGTANSPGK*

>Xboc_4807.1 Glycoprotein hormone beta
MKSTFAFILLILVCSFAAEGLATTTTLEDDLVMCKREYRQHIASMSGCRDERILTVA CWGRCE TQMVPKLEPPYKESFHSVCIPYNYTIGQIQMQDCDEGVDPITYSFPQPGICMCQSCADQGYVVAACH

>Xboc_39242.1 Bursicon beta
MLTLLLLTLAVGWGAATEGTAETCHVVFSDTTIRQQVDYGAEGQAVCTGTVTLHRC EGNCSQARPSVLHGFASSCNCRETVLVETEVLVLLCDFGAGDGDHLPDVRVYTLRIQEPVECACSRCYN

>Xboc_26735.1 Glycoprotein hormone alpha (alternative signal peptide MHHRTLIVIVVTLVVVHCIPILT)
MHHRRTLIVIVVTLVVVHCIPILTFPTLTNGLSPMDHTRLGGPLYFRGFHNGSRAVGEEDSRILNVKIRENKARSKRSIGVGC HLVGYIQRVEIDCCTPVNVAMNACRGYCVSYAYPTNPGGPYILFTASTQC CRITERHRVPFIVCDNNGKYQGFFLSARACACGICDYES

>Xboc_6444.1 GnRH-/AKH-like
MFTIYSQAMP RMDRRAMMAIGLVLMVLVQSCLAANGFTGSSNWLPAKKRSFMDQETPAPDDVEENGGEKTIGFCVCAVLDNKRRYFKTVINYMLWDEKQAHNDRMQANRRDLLDDKLWL*

>Xboc_7489.1 Vasotocin
MYRTVFYITLVTVLSLYADVASSCLVQGCPIGKKRSMNDAERQCSACGPGYRGVCVGLQTC CGDFGCHMGTTDAKMLCTEQINPEPCHVEKKRCGLNAYAKCVADGICCDFETCTLDEKCCQIGEGHDSWPANNNDAGVGRITAFRLSLRADQ*

>Xboc.20871.1 Insulin-like peptide 1 [3' missing]
MGIVTMVCM SLLVLLAVIGGSDAVNRHLCGAELANTLRMLCGDRGYNAPQYEGAHGVMSHSHYTIPVFITKRAAHNYLGAVVPNMMKRGTRIVQEC CRQTC SL SNLALYCAPERLPIDISSENSEESFEFLETSTVDTTSAESATDGVEEGEYSSGDSSELNEVEVIDNDGTNMIAYR

>Xboc.rna.tri.22210.1 Prokineticin like
MLGERCVGFRGIVLTTCCVVYTVVVLVTVTSAYHGLSLNDAEPPFSEDSLYTNQGIVLDQVRRSKTSSRTRHEVYNVFRAPPVEVCYKDADCRPHGCCVRSHYIPTINQCRPLAGAGQKCAPPDLFIRGLRDTDYCPC TASVTCVKVNRKDSFGYCLA*

>Xboc.rna.tri.35664.1 Prokineticin like [5'missing, 3'missing]
FGGVFTREDRFPKTIQRCS EDVDCPVSHCCAYS LFAQLKECKPLGSEGDTCNVFSFPYAYDGRQRCPCPRRHLLCN

additional Xenoturbella bocki preproneuropeptide candidates:

>Xboc_4088.1 [5' missing]
SVGSKKRSVGSKKRSVGSKKRSVGSKKRSVGLSKRRPVGSMG SIGSRLLPAGSKRLPVASPVSGP*

>Xboc_5920.1 [5' missing]
KRGERGGSVYKRGERGGPVEKRGERGGSVYKRGERGGPVEKRGERGGSVYKRGERGGPVERRGERSGSVEEIGERGGSVEKRGGSCGSVDVSITGSVTALSR SALS VASTLWASLARA*

>Xboc_1407.1 [5' missing]
LLVARVKRGGLVARVKRGGLVARVKRGGLVARVKRGGLVARVKRGGLVARVSRGGLELYKV VQLSSDSQNRSHLRSKFIADDDVAVS*

Xenoturbella profunda

>Xpro_16203_g1_i1 SFWNamide
MNYQCCPLL LLLWHHFFSTASEATLADFLKHDGTTDSGGIGVRSFWNKKRAWTDDGLGEP IETMARSFWNKKRSFWNKKRAALEVQPDFDERSFWNKKRDPALQQQQTVDLFDHHSKKSFWNGKRSFWNGKRAATDVGNVGVPVPAEYLELFELFGHQSNKRLAA*

>Xpro_12884.1 i1 i2 LRFDIamide (alternative signal peptide MKLFDIFCFALFAGVASVYCA)
MKLFDIFCFALFAGVASVYCAEDSFIPASSDVKRLRFDIGKKRHFDDKRLRFDIGKKRAWEGTDGGDYAQLVLGLADEGHEFDDETINKRLMYDINKRLRFDIGKRLRFDIGKRLGADHLKETDIDLIIIGGVEIPVCAQEGNAGMSLCGFVPLGSRWWPICSDDCEELNEENS YD*

>Xpro_21851.1 i1 GFGN peptide (achatin)
MAATSVYMTCCVLMAVLLAFTTVMCDPITNDLGVGLYDDENIQDFQEDSQLGSEARASIVSTCLGVSDLMRQDLHSEMFDIQTRGFNGKRTPGFGNKPFGFGNKRDPGFGNKGFGN*

>Xpro_9341.1 i4 Glycoprotein hormone beta
MRPWLRMMIVCLSVAVSLATTTDLLENLFCKVKKREYRQHIA SKIGCRDERVPTIACWGRCE TQMFPKLEPPYKESFHSVCIPYNYTVGHVEMQDCDEGVDP IYTYPQPGICMCQRCGEQDYTVACH

>Xpro_1530.1 i1 [5' missing] Glycoprotein hormone alpha
EVD SRILNIKIRETESRLKRTSSVGC HLVGMHVSQIDGCTPVNVAMNACRGYCVSYAYPTNPGGPYLF TAATQCCRITERHRVPFIVQCVNGEKYMGYFLSARACACGICDS

>Xpro_1888.1 i2 GnRH-/AKH-like
MFTIYNRGMTGMDQRAMMLVIGITMVLVQTCFAANGFTGSSNWLPGKKRSYTDRGTPKPDEIDENAGEKTIGFCVCAVQDNKRRYFKTVINYMLWDEKQAQNERVQADRRDLLNDKLWL*

>Xpro_9608.1 i1 Vasotocin
MDRMLFVCVLTVTVSLCTNSVSACLVQGCPIGKKRSLNAD RQCSACGPGYRGVCVGVQTC CGDFGCHMGTEDAEMCLTEQNNPEPCQLKKKRCGLNAFSKCVADGICCDIETCTLDDDCLHVTNTNYNSWATGEGGVDTIKKFLRSLRGDQ*

>Xpro_3311.1_i1 Insulin-like peptide_1
MLMKPVSVFVTLCLINQLLFTNSVNAIKCGSHLVSTLHMVCHGKYNKRWGPVELDRYSALDFLSYPLHPAAKRQVVSECCYKSC TMS E L T T Y C Q H *

>Xpro_13741.1_i Insulin-like_peptide_2

MDTVNMVCSLLLLVFAMTVSVEG GNRHL C GAELANTLRML C GDRGYNTPQYGGAHGIMSHRHYSLPVF S K R A A H N Y L G A L V P H M K R G T G R I V Q E C C R Q T C S L S N L A L Y C A P Q R R P I D I S S E E S G E E
N F Q F L D D T N Q D D T S S S Y N G G D S T A E G I A T S S S V G S D E T G A E Y E F S G D D T D A M M T E D V E L D N D G S N L I A Y R R R R R R R R R D M A E L S A E Y G F G D G L E G A E T T S E R R V L W G K W H G L P V R Q Q A T L E S E E D E V
E S P D W I R F G L P R *

additional *Xenoturbella profunda* preproneuropeptide candidates:

>Xpro_20770.1_i1 [5' missing]
NLGLF G R K T K C R H I F G R I A K F R P L F G R K P K F R P L F G R K T K F R P L R *

>Xpro_14971.1_i1_i2_i3 [5' missing]
GG G R S L P G E S G G G R S L A I E S G G R R S H T V E S G G W R S L A V E A G G R R S H T V E S G G W R S L A V E A G G G R S L D G R A A V C I I G A S Y S S C P S P A D G *

>Xpro_14077.1_i1 [5' missing]
G Y R T E M S G Y R R G X P G Y R T E M S G Y R R G X P G Y R T E M S G Y R R G X P G Y R T E M S G Y R R G X L G Y R D I G E G G Q D I G I S D R N V K T L K M T L K S Y H V S K R E K A A L L P V I L I N K Y K A E *

Signal peptide basic cleavage site C-terminal amidation + cleavage site Predicted active ligand Cysteine

>NP_000906.1 oxytocin-neurophysin 1 preproprotein [Homo sapiens]
MAGPSLACLLGLLLALTSACYIONCPLGKRAAPDLDVRLCLPCGPGGKGRCFGNICCAEELGCFVGTAEALRCQENYLPSPCQSGQACGSGGRCVAVLGLCCSPDGCHADPACDAEATFSQR

ADC84429.1 neuropeptide Y prohormone 1 [Schmidtea mediterranea]
 MTFYIGFLCLTLNVNIVCSQKSLFIIEPPAKPEFFDDPELLRNYYIKKLN¹NEYFAIVGRPRFGKRFDRGFS
 >sp|P01303.1|NPY Human pro-neuropeptide Y
 MLGNKRILGSLGTLTALLSVCLGALAFYPSKPDNPNGEDAPADMARYYSALRHYINLITRQYGRKSSPETLISDLLMRESTENVPRTLEDPMAM

>sp|P01258.2|CALC_HUMAN Calcitonin Precursor
 MGFOKFSFFLLALSILVLQAGSLHAPFRSALESSPADPATLSEDEARLLLAALVQNYVQMKASELEQEEREQSSLDSPRSKRCGNLSTCMLGTYTQDFNKFHTFPQTAIGVGAPGKKRDMSSDLERD
 HRPVHSMPQAN

>NP_001076580.1 progonadoliberin-1 isoform 2 [Homo sapiens]
MKPTQKLLAGLILITWCVEGCSSQHSYGLRPGKGRDAENLIDSFQEIVKVEVGLAETQRFECTTHQPRSPRLDLKGAESLIEETGQKKI
>sp|Q5DW47|CORZ_APIME_Pro-corazoinin [Apis mellifera]
MVNSQDILLFLSLTITITIVMCTPTYSHGWTNKRSTSELEALANRAIQSDNVFANCELOQLRLLQLQGNINQLFQTPCELLNFPKRSFSENMINDHRQPAPTNNNY

[illegible]

>XP_002732147.1 [Saccoglossus kowalevskii]
MASSLLHRIILFLVLVSTPLKVRTESSESSPNLHVGNQLTELADQGDDALIEIDENEVKRGFGNKRQDVVFADVVKRGFGNKRQDGFQTILLDFEKKRGAEPKIYGNITFGVASLKDLDEDEGRK
RGFGNKRDFENSKVSDSDSESVDTIADISELYGLENKRFGFNKRGSMSMELIDDKRFGNKRVDLTLELQADDHDKRGFGNKRQDVTFFEFQVDDDDDKRGFGNKRQDVTFFEE
FOVDDDDDKRGFGNKRQDVTFFEFQVDDDDDKRGFGNKRRTETAGYEPPDSPLGFKIDKRGFMEEEEAVSDRLSEKKN*

>AQS80481.1 [Charonia tritonis]
 MTSYRYRLTLTAIVIAAVKLLLAADDLDFNDASFALGEDFEFPFGDIDF**EGRGFGN**KRGFGDKRGFGDKRGFAD**KRGFGD**KRGFAD**KRGFGDK**GRSYSPSNLMAALFRSYYHRQPLAGSIAL**KRLLEKQ**
 GIWQ

[illegible][illegible]

>Locus_56724.0 assembled from SRX1343820 [*Halicryptus spinulosus*]
MFRLYTFMLLFLFTLLLVHSLCAFEAEVESMPLLLKSVANAAKTEMYNPPSIDLANEYEREDLVELENGFDNNQEYDNEIRLEERGFGNKRGGFGNKRGGFGNKRGRSRNVLENHFQEFTRKGGFGNKRRA
DIENKRGGFGNKRGGFGNKRIGVSSAAFRLLAKLTNVRDIFDELAKSDNEKRGGFGNKRGGFGNKRGGFGNK*

>XP_002598112.1 [Branchiostoma floridae]
 MTSLEGVSPGTPRRSGHVGPQPCCQAAALVRMLLLQVLLLCVALLHSES SPVQTLTYEPPFLSSDHHGNDISGADDTFAADFQGSTTEPDDLIGIGFTRTGFG KKEAWAPYAHALSARGFGN KRGMGN K
 RGFGNKRAAEDERYAAVQOLVERLRHQAEREGLADLMRYGSOAEGGEDADVTDAKRGRFGNKRASRLAR

>ALJ99974.1 L-type SALMFamide [Asterias rubens]
MKGGQHLAVAVVVVAGSFGIIEA5PFGGYNRAPDNVWVRDAMARGSGTEDEANEQRMGTGAKRPPAGASAFHSALSYGKRGDDDSAEVERRAYHSALPFGKRTPIEKRAYHTGLPFGKRDDEAAEQD
AMMERGFNSALMPGKRLHSALPFGKRGYHSALPFGKRLDTTDEGDIERRGYHSGLPFGKRTATDEAVNDILDQLRSEEN

>L-type SALMFamide [Patiria minata] - from Elphick et al. 2015: Reconstructing SALMFamide Neuropeptide Precursor Evolution in the Phylum Echinodermata: Ophiuroida and Crinoid Sequence Data Inform New Insights. Frontiers in Endocrinology, 6. MKLYPLLAVLVFVAGPFRITIEAYSPFGGYHRRALLGNVWRASDNRARPASTPEEEANEQRMTGAKRPGAGSPVFHSALTYGKRADEADTDAAVERRAFHSALPFGKRTAMDPRRLGHSALPFGKRDDEEAADALMRRRGFNSALMFGKRIHTALPFGKRGYHSLVFGKRSDEEGGTAMERRGYHTGLFPFGKRDGTDAAVSEILSRLSD

[illegible]

>pfu_aug1.0_10475.1_31931.t1 [Pinctata fucata] – from Steward et al. 2014: Neuropeptides encoded by the genomes of the Akoya pearl oyster *Pinctata fucata* and Pacific oyster *Crassostrea gigas*: a bioinformatic and peptidomic survey. BMC Genomics, 15.
...DIDPALDFEFGSEGEIYKRSHKPIYVGKSYDEPKDDVSNIDGAYASDLDTLDNLDRLYLQHSDAQFQRDTRYKPIVGRSDENPMDGEWMEKRRSPFLFYGKRRAPIFYGKRRMHLIVGRGLDRAPKIFY
GRRSPFLFYGRRSNGRNIYRDPVFSYVMMRRSSVSGNAEYFSQASSALLLALDQSLADKSRQGRYIHPTAAQGHVAQFALPQHKRVSPSTFIKGRDTEPNNLDSYDPDNSGFDIDHQPVMVHKR
EVNPMFIKGRYSDDTIENRENNAEHSAGNIWACKSYEDFIVRVKRLASKLLVGYDLAQRLLKSMRKFFGRYIGDIIKAYOISLRMSVDSILNDF

>XP_003425678.1 [Nasonia vitripennis]
 MSSNNLSGTSAMSLTIFVCLVLSLIGGTSVAMDEQPSASSSSGVSSSSSSSHGHFPLSDVDPREQIVGKKRAYTYRSEYKRLPIYQFGLGKRWVDDKQSPQSFVGLGKTRTPYSFVGLGKSSYSEDDDSRY
 GLDLSYLIOPSDLYEOLAAORDALENVLQOOOAIAKRTGGFNFGGLGKRAEFMNRGMMREDGLHEKVPVKHSRDKYLFGLGKRFYEPATMODDEDEEMLEDA

>NP_001037036 [Bombyx mori]
 MLSGKPLLLVLGAALAAEQVAEHGAEQVAEHAAPLEKRRSPQYDFLGRKRAYSYVSEYKRLPVYNFGLGKRSRPYPFLGLGKR SAGAEQLDDDISNEADQNTLDELFDQYDDSAAVPTGYVEKRRPYSFSG
 LGLGKRF AEAPAEDEKRRKMYSGFLGRKRRSYSGFLGKR LSSKFNFLGKRDRDMHRFSFGLGKRSEDSTSENIDA