

Abbreviations of species names

ABBREVIATION	SPECIES NAME	COMMON NAME	PHYLUM
Acal	<i>Aplysia californica</i>	California sea hare	<i>Mollusca</i>
Agam	<i>Anopheles gambiae</i>	African malaria mosquito	<i>Arthropoda</i>
Amel	<i>Apis mellifera</i>	Worker honeybee	<i>Arthropoda</i>
Apis	<i>Acyrtosiphon pisum</i>	Pea aphid	<i>Arthropoda</i>
Apom	<i>Alvinella pompejana</i>	Pompeii worm	<i>Annelida</i>
Asch	<i>Acanthopagrus schlegelii</i>	Japanese black porgy	<i>Chordata</i>
Bflo	<i>Branchiostoma floridae</i>	Lancelet/Amphioxus	<i>Chordata</i>
Bmor	<i>Bombyx mori</i>	Silk moth	<i>Arthropoda</i>
Bpli	<i>Brachionus plicatilis</i>	Marine rotifer	<i>Rotifera</i>
Bvar	<i>Bombina variegata</i>	Fire-belly toad	<i>Chordata</i>
Cele	<i>Caenorhabditis elegans</i>	Caenorhabditis elegans	<i>Nematoda</i>
Cgig	<i>Crassostrea gigas</i>	Giant oyster	<i>Mollusca</i>
Cint	<i>Ciona intestinalis</i>	Sea squirt/ascidian	<i>Chordata</i>
Ctel	<i>Capitella telata</i>	Capitella	<i>Annelida</i>
Dmel	<i>Drosophila melanogaster</i>	Fruit fly	<i>Arthropoda</i>
Dple	<i>Danaus plexippus</i>	Monarch butterfly	<i>Arthropoda</i>
Dpon	<i>Dendroctonus ponderosae</i>	Mountain pine beetle	<i>Arthropoda</i>
Dpul	<i>Daphnia pulex</i>	Water flea	<i>Arthropoda</i>
Drer	<i>Danio rerio</i>	Zebrafish	<i>Chordata</i>
Ecom	<i>Eurythoe complanata</i>	Common fireworm	<i>Annelida</i>
Ggal	<i>Gallus gallus</i>	Chicken	<i>Chordata</i>
Gros	<i>Globodera rostochiensis</i>	Yellow potato cyst nematode	<i>Nematoda</i>
Hasi	<i>Haliotis asinina</i>	Donkey's ear abalone	<i>Mollusca</i>
Hdiv	<i>Haliotis diversicolor</i>	Abalone	<i>Mollusca</i>
Hduj	<i>Hypsibius dujardini</i>	Waterbear	<i>Tardigrada</i>
Hmel	<i>Heliconius Melpomene</i>	Postman butterfly	<i>Arthropoda</i>
Hrob	<i>Helobdella robusta</i>	Californian leech	<i>Annelida</i>
Hsap	<i>Homo sapiens</i>	Human	<i>Chordata</i>
Hvit	<i>Homalodisca vitripennis</i>	Glassy-winged sharpshooter	<i>Arthropoda</i>
Iobs	<i>Ilyanassa obsoleta</i>	Mud snail	<i>Mollusca</i>
Ipar	<i>Idiosepius paradoxus</i>	Northern pygmy squid	<i>Mollusca</i>
Ipun	<i>Ictalurus punctatus</i>	Channel catfish	<i>Chordata</i>
Isca	<i>Ixodes scapularis</i>	Deer tick	<i>Arthropoda</i>
Lgig	<i>Lottia gigantea</i>	Giant owl limpet	<i>Mollusca</i>
Llon	<i>Lutzomyia longipalpis</i>	Sand fly	<i>Arthropoda</i>
Lmig	<i>Locusta migratoria</i>	Migratory locust	<i>Arthropoda</i>
Lsta	<i>Lymnaea stagnalis</i>	Great pond snail	<i>Mollusca</i>
Mdom	<i>Monodelphis domestica</i>	Gray short-tailed opossum	<i>Chordata</i>

Minc	<i>Meloidogyne incognita</i>	Root-knot nematode	<i>Nematoda</i>
Name	<i>Necator americanus</i>	Hookworm	<i>Nematoda</i>
Oarc	<i>Onychiurus arcticus</i>	Springtail	<i>Arthropoda</i>
Oana	<i>Ornithorhynchus anatinus</i>	Platypus	<i>Chordata</i>
Ocun	<i>Oryctolagus cuniculus</i>	Rabbit	<i>Chordata</i>
Olat	<i>Oryzias latipes</i>	Medaka fish	<i>Chordata</i>
Onub	<i>Ostrinia nubilalis</i>	European corn borer	<i>Arthropoda</i>
Ovul	<i>Octopus vulgaris</i>	Common octopus	<i>Mollusca</i>
Pmai	<i>Peregrinus maidis</i>	Maize planthopper	<i>Arthropoda</i>
Pmar	<i>Petromyzon marinus</i>	Sea lamprey	<i>Chordata</i>
Pmon	<i>Penaeus monodon</i>	Giant tiger prawn	<i>Mollusca</i>
Ppac	<i>Pristionchus Pacificus</i>	Nematode	<i>Nematoda</i>
Psau	<i>Phyllomedusa sauvagei</i>	Sauvage's leaf frog	<i>Chordata</i>
Psed	<i>Peripatopsis sedgwicki</i>	Velvet worm	<i>Onychophora</i>
Psin	<i>Pelodiscus sinensis</i>	Chinese softshell turtle	<i>Chordata</i>
Rpro	<i>Rhodnius prolixus</i>	Triatomid bug	<i>Arthropoda</i>
Skow	<i>Saccoglossus kowalevskii</i>	Acorn worm	<i>Hemichordate</i>
Spur	<i>Strongylocentrotus purpuratus</i>	Purple sea urchin	<i>Echinodermata</i>
Tcas	<i>Tribolium castaneum</i>	Red flour beetle	<i>Arthropoda</i>
Tspi	<i>Trichinella spiralis</i>	Whipworm	<i>Nematoda</i>
Turt	<i>Tetranychus urticae</i>	Red spider mite	<i>Arthropoda</i>
Vphi	<i>Venerupis philippinarum</i>	Manila clam	<i>Mollusca</i>
Xind	<i>Xiphinema index</i>	Fan-leaf virus nematode	<i>Nematoda</i>

Abbreviations of peptide names

AVP, vasopressin; Oxt, Oxytocin; TK, Tachykinin; GnRH, Gonadotropin-Releasing hormone; Crz, Corzaonin; CCK, Cholecystokinin; SK, Sulfakinin; NMU, Neuromedin U; Neuromedin S, NMS; Ple, Pleurin; Pk, Pyrokinin; NPY, Neuropeptide Y; PYY, Peptide Tyrosine Tyrosine; PAHO, Pancreatic Hormone; NPF, Neuropeptide F; HCRT, Hypocretin/Orexin; AT, Allatotropin; CRH, Corticotropin-Releasing Hormone; UCN, Urocortin; ELH, Egg-Laying Hormone; DH44, Diuretic Hormone 44; CGRP, Calcitonin Gene-Related Peptide; Calc, Calcitonin; IAPP, Islet Amyloid Polypeptide; ADML, Adrenomedullin; ADM2, Adrenomedullin 2; DH31, Diuretic Hormone 31; NPS, Neuropeptide S; CCAP, Crustacean Cardioactive Peptide; NPFF, Neuropeptide FF; SIFa, SIFamide peptide; NMB, Neuromedin B; GRP, Gastrin-Releasing Peptide; CCHa, CCHamide peptide; Gal, Galanin; Galp, Galanin-like Peptide; Buc, Buccalin; TRH, Thyrotropin-Releasing Hormone; KiSS1, Metastin/Kisspeptin; QRFP, Ox26/RF-amide family 26 amino acid peptide; PTHY, Parathyroid Hormone; PTH, Parathyroid Hormone; PTHrP1, Parathyroid Hormone related Peptide 1; TIP39, Tuberoinfundibular Peptide 39/PTH2; GIP, Gastric Inhibitory Peptide; PACAP, Pituitary Adenylate Cyclase-Activating Peptide; VIP, Vasoactive Intestinal Peptide; PHM, Peptide Histidine-Methionine; Sct, Secretin; Gcg, glucagon; GLP, Glucagon-Like Peptide; Lk, Leucokinin; ETH, Ecdysis-Trigginger Hormone; Ple, Pleurin; Lq, Luqin; RYa, RYamide peptide; Prct, Proctolin; PDF, Pigment-Dispersing factor;

Color coding in alignments of homologous precursor sequences

Signal peptides are indicated in blue, dibasic residues (Lys/K and Arg/R) in red, Cysteines in purple, conserved C-terminal features (e.g. RFamides) in green. C-terminal amidation was not indicated; instead glycine residues just before dibasic cleavage sites were highlighted in orange in precursor sequences. Signal peptides were verified using SignalP 4.0 (Petersen, Brunak et al. 2011).

1. Alignment of bilaterian Vasopressin (AVP)-like precursors (family 1)

```

                *           20           *           40           *           60           *
AVP_Hsap  -----*-----MPDTMLPACFLGLLAFSSACCYFQNCPRCGKRA-----MSDLELRQ
Oxt_Hsap  -----*-----MAGPSLACCLLGLLALTSACYIQNCPLCGKRA-----APDLLDVR-----K
Vtc_Trub  -----*-----MPQCALLLSLLGLLALSSACYIQNCPRCGKRA-----LPETGIR-----Q
Iso_Trub  -----*-----MTGTAISVCLLFLLSVCSACYISNCPICGKRS-----IMDAPQRK
AVP_Cint  -----*-----MYRQFSIVLILLANSILIDACCFFRDCSNMDWYRKRGQEITDPRKQLFQELPEFLDNRPFQ
AVP_Bflo  -----*-----MWRFGMVLVSVLLLVVVAATVGHSACYIINCPRCGKRA-----LENRSGP---AARE
AVP_Skow  -----*-----MFGTPERLSWKVLTIAVIFVCATTTCEACFISDCARGCGKRS-----PGSALTGAGHPLRQ
AVP_Spur  -----*-----MMSVKSIVTCLFSLVLALWIGGSFACFISNCPKCGKRS-----NSRPLR-----Q
AVP_Ctel  MRHSSDAVNSVVLCGRLLLLFACISCCIETTSGCFIRNCPICGKRS-----SVPSRIS---AQKE
AVP_Lgig  -----*-----MCFSSFQYILSLFVFMCVIFGANSCFIRNCPTCGKRA-----IEASEIG-----HK
AVP_Dpul  -----*-----MAGLWTFCLIALSMTEMIIPLTAKPCFIINCPPGCGKRS-----SQLVEPS---SYLE
AVP_Tcas  -----*-----MSTIITSIILLVLSESLVSGCLITNCPRCGKRS-----KFAISEN---AVKP
AVP_Cele  -----*-----MGSSPILLVLAISIGLASACFINSCPYRRYGRTI-----R
<----- signal peptide -----> vasopressin-like

```

```

                80           *           100           *           120           *           140
AVP_Hsap  CLPCGPGGKRC--FCPSICCAD---ELGCFVGTAEALRCQEENYLP--SP-----CQSGQKAC----GS
Oxt_Hsap  CLPCGPGGKRC--FCPNICCAE---ELGCFVGTAEALRCQEENYLP--SP-----CQSGQKAC----GS
Vtc_Trub  CMSCGPRDRRC--FCPNICCGE---GLGCLMGSPETARCAGENYLL--TP-----CQAGGRPC----GSE
Iso_Trub  CMSCGPGDRRC--FCPGICCGE---SFGCLMGSPESARCAEENYLL--TP-----CQAGGRPC----GSE
AVP_Cint  CNKDESNTGNECKFSQKICCQETDDGQVICAVSATELQHRFLSSGVLQQVQRILHEFVEISSRGA---PQK
AVP_Bflo  CPRCGPSLSQCIGPTT--CCSP---QAGCTRSLRVALECSMENLVP--VP-----CRLSGPSC--TLPGQQ
AVP_Skow  CISCGSNNSGHC--IGPSICCGD---FGCYFGTQETAVCQEEKSIP--VP-----CESKGTPC--GEYG
AVP_Spur  CLECGPGGVRC--MEPGICCGP---TIGCHINTQHTLSCMRENEIS--TP-----CELPGNPC---QTVP
AVP_Ctel  CMACCGENGLQC--VGPNTCCGQ---DIGCFMGTQEAKMGEENDSP--IP-----CRVDGAAC---GRND
AVP_Lgig  CMSCGPGNVEQ--VGPNICCGR---FGCYIGTKETEICEHENDST--VA-----CRVEGKLC---GSRQ
AVP_Dpul  CAPCGPAGKGTC--LGANLCCGS---HFGCFFKTEETNVCLLTNLKSTQICNQHFWKTDLKSASCSLNGDKI
AVP_Tcas  CVSCGPGQSEQ--FCPSICCGP---FGCLVGTPETLRCQREGFFHEREP-----CIAGSAPC---RKN
AVP_Cele  CSSCGIENEEVC--ISEGRCCTN---EECFMSTE---CSYSAVCPELF-----CKIGHHP-----
<----- signal peptide -----> neurophysin -----

```

```

                *           160           *           180           *           200           *
AVP_Hsap  GGRCAAFGVCC-NDESCVTEPEC-REGFHRRARASDRSNATQLDGPAGALLLRLVQLAGAPEPFEPAQPDAY
Oxt_Hsap  GGRCAVLGLCC-SPDGCHADPAC-----DAEATSQR~~~~~
Vtc_Trub  GGRCAVSGLCC-NSESCAVDSDC-----LGETEALEPGDSSAGSSPTELLLRLLHMSSRVEPHKCTLI~~~
Iso_Trub  GGRCASSGLCC-DAESCTMDQSC-----LSEEEGDERGSLFDGSDSGDVILKLLRLAGLTSPHQTH----
AVP_Cint  RRYCIKVGVC-SWDRCRPQVSC-----SYKDQDIPSHKEVFQDQTALVNRISHLLQDMY~~~~~
AVP_Bflo  TGTCVGEGMCCMDGEKCSLSPEC-----SMRTAEDEEARRQERRSVLPNWVLPGNTPPDIQKWW~~~
AVP_Skow  HCNCVADKICC-EEYNCSYDANC-----TTKNDGFQKADSSSSTAFKRAFKDLLEDK~~~~~
AVP_Spur  SGTCGAMGVCC-NSNSCSEDASCLMIEEDDSLKRFEQMSREENGSTRKDLRVKLLDLLNMQDQ~~~~~
AVP_Ctel  GGRCVAEQICC-NEDKCSHDSSC-----QSKAKRQHDNLSQDLLRYMHQLMTLKSLGRR~~~~~
AVP_Lgig  QQCVANGICC-DS~~~~~
AVP_Dpul  DGICVADLLCC-SLGNLPQDDL~~~~~
AVP_Tcas  TERCAFDGICC-SQDSCHADKSC-----ASDDKSPIDLYTLINYQAELAGDK~~~~~
AVP_Cele  GYCMKKGYCC-TQGGCQTSAMC~~~~~
<----- signal peptide ----->

```

2. Alignment of bilaterian Tachykinin-like peptides (family 2)

	*	20
Tk1_Hsap	~~~~~H----	KTDSEVGI MG
Tk3_Hsap	~~~~~D----	MHDFE VGIMG
Tk4_Hsap	~~~~~ASQ	EF GI MG
Tk_1_Trub	~~~~~P----	RPHQ FI GI MG
Tk_2_Trub	~~~~~H----	KINSE VGIMG
Tk_1_Drer	~~~~~P----	RPHQ FI GI MG
Tk_2_Drer	~IYLH----	KINSE VGIMG
Tk_1_Cint	~~~~~HVR	HE YGI MG
Tk_2_Cint	SIGDQPSIFNERASE	ETGI MG
Tk_1_Ctel	~~~~~LSR	GF YA ARG
Tk_2_Ctel	~~~~FS----	PKSE HFS RG
Tk_3_Ctel	~~~~AY----	PSGF TM PRG
Tk_4_Ctel	~~~~RV----	PLGF Q MVRG
Tk_5_Ctel	~~~~GL----	NKSSE FL ARG
Tk_1_Apom	~~~~LN----	PASE SF NRG
Tk_2_Apom	~~~~AP----	PSGF NG VVRG
Tk_3_Apom	~~~~RP----	PAGY VV VVRG
Tk_4_Apom	~~~~VP----	PSGF TG LVRG
Tk_5_Apom	~~~~SP----	PEGF L GLRG
Tk_Ovul	~~~~SEVKPPSSSE	FI GI MG
Tk1_1_Lgig	~~~~HP----	NFG EM GSRG
Tk1_2_Lgig	~~~~QP----	AFGF HA VVRG
Tk2_1_Lgig	~~~~QR----	TFGF VG TRG
Tk2_2_Lgig	~~~~QP----	HLGF HG MVRG
Tk2_Lgig	~~~~GL----	DQYGF TG QLG
Tk_1_Acal	~~~~FK----	PSGF EM GSRG
Tk_2_Acal	~~~~QP----	HLGF HG SRG
Tk_1_Dple	~~~~V-----	PQGF L GMVRG
Tk_2_Dple	~~~~K-----	PQGF VG VK G
Tk_3_Dple	~~~~V-----	PMGF VG MVRG
Tk_4_Dple	~~~~~A----	NIHK EF GVRG
Tk_1_Pmai	~~~~AS----	NMG FV GMVRG
Tk_2_Pmai	~~~~~AM	FV GMVRG
Tk_3_Pmai	~~~~~AV	FV GMVRG
Tk_4_Pmai	~~~~~TM	FV GMVRG
Tk_5_Pmai	~~~~~AK	FV GMVRG
Tk_6_Pmai	~~~~~AV	EM GMVRG
Tk_7_Pmai	~~~~~AM	FQ GMVRG
Tk_1_Onub	~~~~V-----	PQGF VG MRG
Tk_2_Onub	~~~~K-----	PQGF VG VK G
Tk_3_Onub	~~~~A-----	PMGF VG MRG
Tk_4_Onub	~~~~AA----	NIHQ EF GVRG
Tk_1_Dpul	~~~~TP----	NSRA FL GMVRG
Tk_2_Dpul	~~~~KM----	HGE KFL GMVRG
Tk_3_Dpul	~~~~AP----	SSNS EM GMVRG
Tk_1_Tcas	~~~~A-----	PSGF EM GMVRG
Tk_2_Tcas	~~~~A-----	PMGF EM GMVRG
Tk_3_Tcas	~~~~A-----	PSGF F GMVRG
Tk_4_Tcas	~~~~MP----	RQAG FF GMVRG
Tk_5_Tcas	~~YPYQ----	FRG KE VGVVRG
Tk_1_Dmel	~~~~AP----	TSSE FI GMVRG
Tk_2_Dmel	~~~~A-----	PLA FV GLVRG
Tk_3_Dmel	~~~~A-----	PTGF T GMVRG
Tk_4_Dmel	~~~~AP----	VNSE FV GMVRG
Tk_5_Dmel	~~~~A-----	PNG F LGMVRG
Tk_Cele	~~~~VP----	MMS LK GLVRG
Tk_Ppac	~~~~~AP	E K L VRG

3. Alignment of bilaterian GnRH-like peptides (family 3)

*

GnRH_Hsap	Q	--	HWSYGLR	PGG	~~~~~
GnRH2_Hsap	Q	--	HWSHWYP	PGG	~~~~~
GnRH_Pmar	Q	--	HWSHWFP	PGG	~~~~~
GnRH1_Cint	Q	--	HWSKGYSP	PGG	~~~~~
GnRH2_Cint	Q	--	HWSLALSP	PGG	~~~~~
GnRH3_Cint	Q	--	HWSNWWIP	CAPGYNGG	
GnRH2_Csav	Q	--	HWSNKLAP	PGG	~~~~~
GnRH_Spur	Q	VH	HREFSGWR	PGG	~~~~~
GnRH1_Ctel	Q	AY	HFSHWFP	PGG	~~~~~
GnRH_Apom	Q	AY	HFSNGWFP	PGG	~~~~~
GnRH_Ovul	Q	NY	HFSNGWHP	PGG	~~~~~
GnRH_Acal	Q	NY	HFSNGWYAG	~~~~~	
GnRH2_Lgig	Q	HY	HFSNGWKS	PGG	~~~~~
CORZ_Dmel	Q	TFQ	YSRGWTN	C	~~~~~

4. Alignment of bilaterian Cholecystinin/Sulfakinin-like peptides (family 4)

*

```

CCK_Hsap      ~~~~~~DYM-GWMDFG
CCK_Drer      ~~~~~~DYV-GWMDFG
CCK_Ipun      ~~~~~~DYL-GWMDFG
CCK_Cint      ~~~~~~NYY-GWMDFG
CCK2_Skow     ~~~~~~DHY-GWMNE~
CCK1_Spur     ~~~~~~DYG-HGMFFG
CCK2_Spur     ~~~~~~PDDYNW-GMWEF
CCK3_Spur     ~~~~DKADLYGW-GGFFG
CCK_Ctel      QGAAWDM-DYGWGGGRFG
CCK_2_Lgig    ~~~~~~F-DYNFGGGRWG
CCK_2_Hdiv    ~~~~~~NYGEYGFGGGRFG
CCK_1_Lgig    QG-AWDY-DYGLGGGRFG
CCK_1_Acal    QG-AWSY-DYGLGGGRFG
CCK_1_Hdiv    QG-AWSY-DYGLGGGRFG
CCK_2_Acal    ~~~~~~SYGDYGI GGGRFG
CCK_Apom      QG-AWDM-DYGWGGGRF~
Sk_Dmel       ~~~~~~FDDYG--HMREFG
Sk_Dpul       ~~~~~~FDDYG--HMREFG
  
```

5. Alignment of bilaterian NMU/Pyrokinin-like peptides (family 5)

	*	20	*
NMU_Hsap	~~~~~	FRVDEEFQSPFASQSRGYFLFRPRNG	
NMS_Hsap		ILQRGSGTAAVDFTKKDHTATWGRPFFLFRPRNG	
NMU_Drer	~~~~~	ENLQGPGRIQSRGYFLYRPRNG	
Pk1_1_Lgig	~~~~~	~~~~~MNYMAFPRLG	
Pk1_2_Lgig	~~~~~	~~~~~SGYLAFPRLG	
Pk2_Lgig	~~~~~	SAGRFRYYPEVRSEERAVALPRFG	
Pk1_1_Dpul	~~~~~	~~~~~QSLIPFPRVG	
Pk1_2_Dpul	~~~~~	~~~~~HLIPFPRVG	
Pk1_3_Dpul	~~~~~	~~~~~QNLIPFPRVG	
Pk_Tcas	~~~~~	SENFTPWAYIILNGEAPIIREVHYS	PRLG
Capa_Dmel	~~~~~	~~~~~TGPSASSGLWFG	PRLG
Hugin_Dmel	~~~~~	~~~~~SVPFK	PRLG
Pk1_2_Cele	~~~~~	~~~~~LYMAR	VG
Pk1_3_Cele	~~~~~	~~~~~AFFYT	PRIG
Pk1_1_Cele	~~~~~	~~~~~LLVPY	PRVG

6. Alignment of bilaterian NPY/NPF-like peptides (family 6)

```

                *           20           *           40           *           60
NPY_Hsap  -----MLGNKRLGLSGLTLALSLLVCLGALAEAYPSKFDNPGEDAPAEDMAR
PYY_Hsap  -----MVFVRRPWPALTTVLLALLVCLGALVDAYPEAPEAPREDASPEELNR
PAHO_Hsap  -----MAAARLCLSLLLLSTCVALLLQPLLGAQGAPLEFVYFGDNATPEQMAQ
NPY_Bflo  -----MTSVRIFSYVCLLVLIYACVEVTRAQEEEDVEAPEEGK
NPY_Skow  -----MDLKTILLASLVCMVVCWDERLSARVQRDASDYQAEPTAPSRGASLAEWDR
NPF1_Ctel  -----MKLSQILILLLLGLSVIICSVHANTDDDDARLVMVMSQMHPPEKRPEHFRNMDELNV
NPF2_Ctel  -----MDAKLLKAMFVLASCLLLLLPTSCSQDMHGMEVVRPKVFRNADELRM
NPF_Lgig  -----MQKLVLSLLILAAVVMLEVTSQDSMLAPEDRPSEFRSPDELRR
NPF_Dpul  MSSSNNSIQQFLPRSCSLAALVFLVMAVLAVCVTTTKADGGDVMSGGEGGEMTAMADAIK
NPF_Dmel  -----MCQTMRCILVACVALALLAAGCRVEASNSREPRKNDVNTMADAYK
                <----- signal peptide ----->                <--- ..

                *           80           *           100          *           120
NPY_Hsap  YYSALRHYINLITRQRYGKRSSPETLISDLLMRESTENVPRTRLEDPAMW-----
PYY_Hsap  YYASLRHYLNLVTRQRYGKRDGPDTLISKTFPPDGEDRPVRSRSEGPDLW-----
PAHO_Hsap  YAADLRRYINMLTRPRYGKRHKEDTLAFSEWGSPhAAVPRELSPLDL-----
NPY_Bflo  YYKNLANYLRLLITRQRYGRRSAPDYGSRTLYRHPPYPQDIVHTLDMDGISLSLCISLNL
NPY_Skow  YLRELSLYROYADIOFGGRSDGGANNIHQQTQKNHRSNIWDYLSKKLAL-----
NPF1_Ctel  YLDKLRQYTYIIGRPFGGRNVFSEVRVHTIVLYCFCQSR LAPIRCA-----
NPF2_Ctel  YLKALNEYFAIVGRPFYGKRS SPSENPAFGEVDVDGNGRVNDDEFDQFAYGYRK-----
NPF_Lgig  YLKALNEYYAIVGRPFYGGRSVNKRSAADYLEFKPSHKNDYEYLYDERDERFSPYY-----
NPF_Dpul  YLQGLRRYDNSLVRPFGYGRGRLPYFDMEDLPLHPQVCSSSSYF-----
NPF_Dmel  ELQDLDTYYGDRARVFGYGRGSLMDILRNHEMDNINLGKNANNGGEFARGFNEEEEIF-----
..neuropeptide F/Y->

```


7. Alignment of bilaterian Corticotropin-Releasing Hormone (CRH)/DH44 peptides (family 7 - bilaterian)

	*	20	*	40	*	60
CRH_Hsap	~~~~~	SEEPPI	SIDLTFHL	IRE---	VLEMARAEQLAQQ	AHS---NRKLMEIIG~~
Sauvagin_Psau	~~~~~	QGPPIS	IDLLELRK	---	MIEIEKQEKEKQQAAN	---NRLLDITIG~~
UCN1_Hsap	~~~~~	DNPSL	SIDLTFHL	LRT---	LLELARTQSQRERAEQ	---NRIIFDSVIG~~
UCN2_Hsap	~~~~~	IVLSL	DVPIGLIQI	---	LLEQARARAAREQATT	---NARILARVGHG
UCN3_Hsap	~~~~~	FTLSL	DVPTNIMNL	---	LFNIAKAKNLRAQAAA	---NAHLMAQIG~~
CRH1_Trub	~~~~~	SEDPPI	SIDLTFHL	IRE---	MMEMSKAEQLAQQ	AQN---NRIMMELVIG~~
CRH2_Trub	~~~~~	SEEPPI	SIDLTFHL	LRK---	MIKEAKMENQKEQELI	---NRKLIDEFC~~
UCN_Trub	~~~~~	SRLTL	SLDVPTNIMNV	---	LFDVAKAKNLRAKAAE	---NARLLAHITIG~~
CRH_Cint	~~~~~	PALGRNPFL	SLDVPLSFLSK	---	LMEVKRREEQRKIAKIKSVHNS	SSLMKRIG~~
CRH_Csav	~~~~~	AAKPKPQTNVL	SLDVPLSFLSK	---	LIEMSRREDKRQREKEISL	RNKKLMEKYIG~~
CRH1_Skow	~~~~~	NPTSGHS	IGLSLDIIRDRLEKAE	SERMQQEKQSDINRYRQ	NTELMTGLIG~~	
ELH_Acal	~~~~~	ISINQDLKAITD	---	MLLTEQIRERQRYLAD	---LRPRILEKIG~~	
ELH1_Lgig	~~~~~	SRLSINQELKSLAN	---	LLVLRENKRREAQKTK	---LRSKLLSITIG~~	
ELH2_Lgig	~~~~~	AGRLSINGALSSSLAD	---	LLVSENQRRDRLESME	---LRQRIQYLIG~~	
ELH1_Cgig	~~~~~	GRLSITADLRSLAR	---	MLEAHRKRFIASRFPYDS	--IRKKLFRYIG~~	
ELH2_Cgig	~~~~~	QRLSVNGALSSSLAD	---	MLAANGRQRMSEMAM	---NRQRLFGLIG~~	
ELH_Lstag	~~~~~	LSITNDLRAIADSY	---	LYDQHKLRRERQEEEN	-----LRRRFLELIG~~	
DH44_Hmel	~~~~~	KMPPLSINNPMEVLRQRL	---	LLEVARKQMREANQRQAVA	-NRVFLQNVIG~~	
DH44_Dmel	~~~~~	NKPSLSIVNPLDVLRQRL	---	LLEIARRQMKENSQVEL	--NRAILKNVIG~~	
DH44_Dpul	QSQSHSGSSGNHHSQ	LSIISPIEALRSRL	---	RLEMLRRQYGNQIKQ	-----NQDKLERVIG~~	
DH44_Isca	~~~~~	DHMPSLSIVSPLDVLRDK	---	MMQDI IERSIKNKIQA	---NDKILKDLIG~~	
DH44_Apis	~~~~~	SRPSLSIVNSLDVLRQKL	---	MYEVARRHVDENQKVL	SQ--NHQILKNLIG~~	
DH44_Turt	~~~~~	GVSPRLSVTSPIAVLRDAL	---	MEEIKRKKIQETQAKIAL	--NEKILKEVIG~~	
DH44_Oarc	IPEILEQPVPDSSGSL	SIVGPLDVLRQNM	---	LMEMHKTRVRHAKNKIVES	-NREYLERIG~~	

8. Alignment of bilaterian Calcitonin/DH31 peptides (family 8 - bilaterian)

	*	20	*	40	*	60	*	80				
CGRP1_Hsap		MGFQKFS	PFLALSILVLLQAGSLHA	APFRSALESSPADPATLSEDEARLLLAALVQNYVQMKASELEQEQEREGSRI	IAQ							
Calc_Hsap		MGFQKFS	PFLALSILVLLQAGSLHA	APFRSALESSPADPATLSEDEARLLLAALVQNYVQMKASELEQEQEREGSSLDSP								
IAPP_Hsap		MGILKLQVFLIVLSVALNHLKATPIESHQVEK	-----									
ADML_Hsap		MKLVSV	ALMYLGLS	LAFLGADTARLDVASEFRKKWNKWALSRGKRELRMSSSYPTGLADV	KAGPAQTLIRPQDMKGASRSP							
ADM2_Hsap		MARIPTAALGCISLLCLQLPGSLS	RS	LGDP	RPVKPREPPARSPSSSLQPRHPAPRPVWKLHRALQAQRGAGLAPVMGQ							
Calc_Cint		MVMNTFC	SLLEFILLVFCVYNASTTGGIY	NRL	LHPRGTGRQQLLYHNFNRYGEVLKRNQPSRSDYDTHDEL	IKNVQPLQQ						
Calc1_Bflo		MMTTEVGRFLLCACVTF	SILLTTCTAAPT	TARGELPEASLRLSEEDVGRVVSAMAREVLQIVNENVDKLAQPNEFGYGLDG								
Calc2_Bflo		MLLGNMLVNTVAALTVCVVVFWGTDHVGAL	PRPADDGDNPLAMTNSDMRRI	V	SALIREVDQLAAEKLAQAQRVFGPGIR	--						
Calc3_Bflo		MRPCFALMVLAFFVLVHTNQLTASVIRRYDDD	MYDYDGDMEPLLALLGQQAGRVYHGLARELLDNI	EDNTNTQDNRF	SRT							
Calc_Spur		MKSTVIVTLTICCLLYQTTRAASLTNRDGLSRQDILDLLQLYE	EPIRQEGD-----									
Calc_Skow		MDRLIVASSAFLVILYITCFVDVTIAYDDSESE	EVVPPNYWSLQLAELTELVKLGEEVLAQKASAEMKAA-----									
DH31_1_Ctel		MYVQVLSLLLGCVLLGGR	ISEA	ADERE	SEDLQEALRVYQNLGETR	KGLTALKRVVSDLDGDILQKHDFHDLARKRKGLDI						
DH31_2_Ctel		MVSQFLIESELS	PRVLSIMNSAVMRFSLIAMASCIVIASLTSRAQATSLHRQRRDVTEPSLAI	AVLEDLIMELRDEI	HSK							
DH31_1_Lgig		MISTTPLYVTVSICLFYLT	TTTVYCR	TDFRFLMKRDTRNNINTDSLQETLKNLDDEYQRLQKRTCAFGINSHQCTLTSLNN								
DH31_2_Lgig		MGASILLGLTILLSYVNQVHLQMFHPRDISRGGQQQEEQLRRGYLIQILKSFLNRRQEDATEKR	-----									
DH31_Dpul		MSRFVMTIFFLLVACLALIVPGSA	APRRPMLVDLDDPDSVMEVITRLERSLLRNSDYEHQ-----									
DH31_Dmel		MTNRCACFALAFLLFCLLAISSIEA	APMPRYQSNGGYGGAGYNELEEVDDLLMELMTRFRGTIIRARNDLENS-----									
DH31_Cele		MSCSSSSMLFLVLIATTVLIAES	RVFYNRFDGGLSSDRFMEQKRDGAEASYDYDANQVIRNTM-----									
		<-- signal peptide -->										
	* <td>100 <td>* <td>120 <td>* <td>140 <td>* <td>160 </td></td></td></td></td></td></td>	100 <td>* <td>120 <td>* <td>140 <td>* <td>160 </td></td></td></td></td></td>	* <td>120 <td>* <td>140 <td>* <td>160 </td></td></td></td></td>	120 <td>* <td>140 <td>* <td>160 </td></td></td></td>	* <td>140 <td>* <td>160 </td></td></td>	140 <td>* <td>160 </td></td>	* <td>160 </td>	160				
CGRP1_Hsap		-----										
Calc_Hsap		RS	-----									
IAPP_Hsap		-----										
ADML_Hsap		EDSSPDAARIRV	-----						KRYRQSMN	NFQ		
ADM2_Hsap		PLRDGGRQHSGPRRHSGP	-----						RTQAQ			
Calc_Cint		RQEEKLNKLEKLFADIMLEDNSYKNVLF	S	KKQESNEIDIEPSMMRDTRNNFLEMLQLSNWIHRVLSRLAATPHEQQAAPV								
Calc1_Bflo		LPQGPVY	-----							K		
Calc2_Bflo		-----										
Calc3_Bflo		YEDMMDPMAM	-----									
Calc_Spur		-----										
Calc_Skow		-----							KRG			
DH31_1_Ctel		LRRILSEMEADLIYEQ	-----									
DH31_2_Ctel		K	-----									
DH31_1_Lgig		KMMSQAWLSDGMSPGKRSDLPNLT	PDGRTQ	RLLED	EMSNTKALLTVRDILTQADSPTAR	-----						
DH31_2_Lgig		-----										
DH31_Dpul		-----										
DH31_Dmel		-----										
DH31_Cele		-----										
	* <td>180 <td>* <td>200 <td>* <td>220 <td>* <td>240 </td></td></td></td></td></td></td>	180 <td>* <td>200 <td>* <td>220 <td>* <td>240 </td></td></td></td></td></td>	* <td>200 <td>* <td>220 <td>* <td>240 </td></td></td></td></td>	200 <td>* <td>220 <td>* <td>240 </td></td></td></td>	* <td>220 <td>* <td>240 </td></td></td>	220 <td>* <td>240 </td></td>	* <td>240 </td>	240				
CGRP1_Hsap		KRAC	DTAT	CVTHRLAGLLSRS	GGVVKNNFVPTNVGSKAF	GRRRR	DLQA	~~~~~				
Calc_Hsap		KRC	GNLST	CMLGTYTQDFNKF	HTFPQTAIGVGAP	GKKR	DMSSDLERDHRPHVSMPQ	NAN-----				
IAPP_Hsap		KRC	NTAT	CATQRLANFLVHS	SNNFGAILSSTNVGSNTY	GKR	NAVEVLKREPLNYLPL	~~~~~				
ADML_Hsap		LRSFGC	RFGT	CTVQKLAHQIYQFTDKDKDNVAPRSKISPQGY	GRRRR	SLPEAGPGRTLVS	SKPQAHGAPAPPSG					
ADM2_Hsap		LLRVGC	VLGT	CQVQNL	SHRLWQL	MG	FAGRQ	DSAPVDPSSPHSYG-----				
Calc_Cint		TGKR	C	DGVSTCWLHEL	GNSVHAT	AAGKQNVGFG	BGRK	~~~~~				
Calc1_Bflo		KGKIAC	KTAW	CMNRLSHNLS	SSL	DNPTDTGVGAP	GKRKR	DTS~~~~~				
Calc2_Bflo		KRDC	STLT	CFNQKLAHEL	AMD	NQRTDTANPYS	GKRKR	SAEEDDH~~~~~				
Calc3_Bflo		RVRKRC	ESGT	CVQMH	LADRLRLG	LGHNMFTNTGPES	GKRKR	SLGASRRAARL~~~~~				
Calc_Spur		KRSKGC	GSFSG	CMQMEVAKNRVAA	LLRNSNAHLFGLNG	GKRKR	SVDDL	PQVNDAEETE~~~~~				
Calc_Skow		RGTSAC	GGFAT	CKQLEYGRKYATS	KADLSHF	GATS	GKRKR	TTNSELDKQA~~~~~				
DH31_1_Ctel		KRTC	QFNLGGH	CATE	SAASVADHW	HYLNSPLS	GKRKR	DTGLYKAVVSGRIFKDSKH~~~~~				
DH31_2_Ctel		KRC	RFDAGYGSRYGVAQSVGSKLMAL	-----				KQAADWNG	GKRKR	EAEEEA~~~~~		
DH31_1_Lgig		KRSC	SLRLGGM	CLTENL	NAAANQY	EYLSSGLS	GKRKR	SLRHILLNRXH~~~~~				
DH31_2_Lgig		KRSC	NLNLGFH	CQTDEYSS	IADMY	DFLQSALS	GKRKR	NVKIVSIEGS~~~~~				
DH31_Dpul		KRC	GVDFGLGRGYSGSQA	AKHLMGLA	-----				AANYAIG	GKRKR	DTTESTPEDVKTGAIN~~~~~	
DH31_Dmel		KRC	TVDFGLARGYSGTQEA	KHRMGLA	-----				AANFAGG	GRRRR	SETDV~~~~~	
DH31_Cele		KRNRQC	LLNAGLSQGC	DFSDLL	HAQTQA	-----				RKFMSFAG	GK	-----
		<----- calcitonin peptide ----->										

9. Alignment of deuterostomian Hypocretin(HCRT)/Orexin-like peptides (family 9 - deuterostomian)

	*	20	*	40	*
OxA_Hsap	~QPLPD CCRQ -----	K TCS CRL YELL -----			HGAGN HAAG GIL TL G
OxB_Hsap	~~~~~ RS GP-----	PGL QGR L QRL L-----			QASGN HAAG GIL TM G
OxA_Drer	~~~~~ S CC AR -----	APGS CKL Y EM L-----	CRAGRRNDSSVARHLVHLNNDAAV GIL TL G		
OxB_Drer	~~~~~ KV GE-----	SRV HD RL QQL L-----			HNSRN QAAG GIL TM G
Ox1_Bflo	SWAF PR CC WR -----	RTC NC PH FRR L-----			FGPRN HGH GIL TV G
Ox2_Bflo	~~ QK PACC ES -----	G SC IC PY VS RL -----			HSPGN HGY GIL TT G
Ox_Skow	~~~ QP CC- RG VG CK IP PN CK CP F Q SI I -----				CDN P TK N V L T A G
Ox1_Spur	~~~ Q SP CC RR AK G CS F PP G CH CP L K MS F-----				CGD P SR G L Q IV G
Ox2_Spur	~~~ D RA CC K R TV GC N L R SD CT CR I R E I T-----				CTD P SL G L Q NY G

10. Alignment of deuterostomian Allatotropin-like peptides (family 9 - protostomian)

*

AT_Mgal	G	F	L	A	G	V	H	D	R	M	G	H	G	F	G
AT_Lsta	G	F	R	A	N	S	A	S	R	V	A	H	G	Y	G
AT_Acal	G	F	R	L	N	S	A	S	R	V	A	H	G	Y	G
AT_Lgig	G	F	K	A	N	S	A	S	R	V	A	H	G	Y	G
AT_Ctel	G	E	R	M	G	A	A	D	R	F	S	H	G	F	G
AT_Apom	G	E	R	L	G	A	A	D	R	F	S	H	G	F	G
AT_Hrob	S	E	K	L	Y	D	N	S	R	Y	A	H	G	Y	G
AT_Bmor	G	F	K	-	N	V	E	M	M	T	A	R	G	F	G
AT_Rpro	G	F	K	-	N	V	Q	L	S	T	A	R	G	F	G
AT_Apis	G	F	K	-	N	M	D	L	S	T	A	R	G	F	G
AT_Dpul	G	F	K	-	T	V	G	L	A	T	A	R	G	F	G
AT_Hvit	G	F	K	-	N	H	A	L	S	T	A	R	G	F	G

11. Alignment of protostomian Allatotropin-like precursors with Saccoglossus orexin-like precursor (family 9 - bilaterian)

		*	20	*	40	*	60	*		
AT_Rpro	---	MMRWSSLLVLVALAS	I	INCIKAGSPSSALYSSAARASGR	RTI	RGFK	-NVQLSTARGE	GKR	TYPDSQLQP----	
AT_Hvit	-----	MRVYTL	LLLVLLMSVTANS	VPVYL	LRDKP	RSI	RGFK	-NHALSTARGE	GKR	SDSELSSE----
AT_Apis	MAVNN	NIMVRL	LVIETFLILAVVNSYPAFEDSEFKHKHRDKG	FTI	RGFK	-NMDL	STARGE	GKR	TDHYMNLMP----	
AT_Bmor	-----	MNLTMQ	LEVIVAVCLVLAEG	APDVRL	VRTKQQ	RPT	RGFK	-NVEMMTARGE	GRR	DRPHPRAELYGLD
AT_Lsta	-----	MSRTSL	TLQVGVLLAICLFDITYADERIH	RQ	RGFRANSASRVAHGY	GKR	GYLSSNENLPTLS			
AT_Acal	-----	MLSAP	SIAHTGVALLVLMCLCPFSQSTEASLS	RA	KRGFRINSASRVAHGY	GKR	GYASSSGAVPYPE			
AT_Lgig	-----	MKLTL	VLVTVTLTITILANAYPQSPSLSHH	RS	KRGFKANSASRVAHGY	GKR	GFPSWKNY----			
AT_Ctel	-----	MKVSIC	FIVVALVVCIEVMTSHAANLS	RS	KRGFRMGAA	DRF	SHGE	GKR	G-----	
Ox_Skow	---	MRTTIM	LIFSAVLVAVLFTHTSA	QPQC	CRGVGCKIPPNCKCPFQSIIC	D	NPTKNVLT	A	GKR	NYLPISKSN----

<---Alt----->

<-----orexin----->

	80	*	100	*	120	*	140	*	
AT_Rpro	-----	DL	-IPADWMAEELSSNPELAREFI	I	RRFIDVDQDGLVSPVEILLRNTVCQEPN	~~~			
AT_Hvit	-----	TSQFTDR	-----	DS	-FPADWFASEVQNNGELARLVVHKFIDTNQD	GELSADELLRPLYGPPTTTYK			
AT_Apis	-----	LDLFVDNKEDSFNQNI	PMEVSLEKILKNKY	--	KHFIEKLI	DVNH	DGYISGEILL	SIDGES~~~~~	
AT_Bmor	NFWVMSEPSPEREVQEVDEKTFES	-I	PLDWFVNEMLNNPDEAREFVVEKFIDLNQD	GMLSSEELRN	V	~~~~~			
AT_Lsta	LDQLESSTGLMEEISDG	----	SL	-MTVNEFSQLLTSHPNLARALVKKFVDINGDDVISTDE	ELFRPILK	~~~~~			
AT_Acal	LAR--DVL	LDNLRAEEEEKELEWSI	-MSVDE	ELASLLQSHPKLARALVKKFVDINGDNLVTA	EELFRP	PTRK	~~~~~		
AT_Lgig	-----	FQD	GGS	---DV	-LSVEDMAELVAENPSLAKALLRK	FVD	TDNDGIISTTELLG	TKQMLK~~~~~	
AT_Ctel	-----	GDFNS	LIDGESD	---MV	-MSDEDL	TEIIRADARLAQTFVKRFIDTDGD	GEVSRQELFEA	~~~~~	
Ox_Skow	-----	ELSTY	QRPVSDAKT	---NV	-VTSDDIVNLI	RSSPSLIRKIVKA	-IDL	NGDDMISKAELQSLVYD	~~~~~

<-----cryptic peptide----->

13. Alignment of ambulacrarian and amphioxus NPS-like precursors (family 10 - deuterostomian)

```

      *           20           *           40           *           60           *
NPS_Bflo MMQTPIFLCSVVLVGAVCGQLSETNFPQNGNRRLSPERSATVLRQFLHLEGAVGSPVSPSDGRALETGD
NPS_Spur MGYERRILRTLILLSILIVLASFVTVYGERDSNFMQOKQFRNIVPSPLIQKWRENRMGPAAEKTSENEQWRDE
NPS_Skow MLRKINAVVFFLVAICTLSRATFGEDGMTEKQVLLKLHKYWPKEDISEIGSSSTS GDSGENEAVKMGFWAV
<--- Signal peptide --->

```

```

      80           *           100          *           120          *           140
NPS_Bflo KRSFRNGVGKRRDSEERLPQNRGATELKAEATIFSQNGDPHDEGAKAASEKRSFRNGVGKRRTHFRIVAD
NPS_Spur LLSNLRNVLVRKHNASPSSRSRDRDITAYGLQEPMQQLPADVTADQLFILEGAVNSPRENYEEETPIDED
NPS_Skow DGKRNNGFWNGKRNNGFWNGKRNFDLLRIFGTNKKHSSINNQKRNNGFWNGKRNFDLDFEIPKKEQPHWRDEK
      NPS-like                                NPS-like

```

```

      *           160          *           180          *           200          *
NPS_Bflo ASLGGLDEPEALRQTGGDANSPSLSRDLWAEVQKDDDEQ-----
NPS_Spur KRNGFFFKRNNGFFFKRRSDSDASSTKMDDRLPKYESSGSFDK-----
NPS_Skow KNGFWNDGKRNFDNFKTDLLQYPSIEDKRNNGFWNGKRNFMMSMNNKASASTESEKRNNGFYMGKRSVDNTM
      NPS-like                                NPS-like

```

```

      220          *           240          *           260          *           280
NPS_Bflo -----CPACGSDGSEVCVILKGVCCRLDSCG-VLRKDVCSLIPDRALCASLQYSATCRITD GKC
NPS_Spur -----CRPCGPGROGR CVMVGTCCSPLFGCYLFTPEAAACMTED-VSPCQLNAPS CGLAGKC
NPS_Skow NISSYHYKESAKKCTTCGPGGKGC CVMYGVCCSLEIGCSMLTKE TEECTTISPLVGE CGRSDVQCGNFFRC
<-----Neurophysin-like----->

```

```

      *           300
NPS_Bflo VAPGVCCRAADHSCFLDPECD-----
NPS_Spur VADGICCSAAEGACHLDPTCTSMSLN
NPS_Skow VANGVCCTKETQSCKIDQECNVRW~~
      ----->

```

also refer to:

Rowe ML, Elphick MR. (2012). "The neuropeptide transcriptome of a model echinoderm, the sea urchin *Strongylocentrotus purpuratus*." *Gen Comp Endocrinol*.179(3):331-44.

14. Alignment of protostomian CCAP-like peptides (family 10 - protostomian)

*

CCAP_Ctel	I	F	C	N	-	F	D	G	C	Y	N	~	~	~	~
CCAP_1_Lgig	V	F	C	N	G	F	T	G	C	G	G	R	H	R	G
CCAP_2_Lgig	P	F	C	N	N	W	-	G	C	G	N	G	~	~	~
CCAP_3_Lgig	L	F	C	N	N	Y	G	G	C	R	G	G	~	~	~
CCAP_1_Cgig	V	F	C	N	G	F	F	G	C	S	N	G	~	~	~
CCAP_2_Cgig	L	F	C	N	-	T	G	G	C	F	G	~	~	~	~
CCAP_1_Acal	V	F	C	N	G	F	T	G	C	G	G	R	F	R	G
CCAP_2_Acal	P	F	C	N	T	L	-	G	C	Y	N	G	G	~	~
CCAP_1_Ipar	V	F	C	N	S	F	G	G	C	R	S	L	~	~	~
CCAP_2_Ipar	V	F	C	N	S	Y	G	G	C	K	S	F	~	~	~
CCAP_Dpul	P	F	C	N	A	F	A	G	C	G	~	~	~	~	~
CCAP_Dmel	P	F	C	N	A	F	T	G	C	G	~	~	~	~	~

15. Alignment of deuterostomian NPS-like peptides with protostomian CCAP-like peptides
 (family 10 - bilaterian)

		*	20
NPS_Hsap	~SERNGV	-G	TGMKKTSEFQRAKS
NPS_Ggal	~SERNGV	-G	SGIKKTSFERRAKS
NPS_Skow	NGEWN	G	~::~::~::~::~::~
NPS_Bflo	~SERNGV	-G	~::~::~::~::~::~
CCAP_Lgig	~PECNNW	-G	CGNG~::~::~::~::~
CCAP_Dpul	~PECNAFAG	G	CG~::~::~::~::~

16. Alignment of chordate NPFF-like peptides (family 11 - deuterostomian)

	*	20	*
NPVF_3_Hsap	~~~~~	NMEVSLVRRVPNLP	QRF
NPFF_3_Hsap	~~~~~	SQFWSL	----AAPQRF
NPFF_2_Hsap	~~~~~	SQAFL	----FQPQRF
NPFF_1_Mmus	~~~~~	SPAFL	----FQPQRF
NPFF_2_Mmus	SAWGSWSKEQLNPQARQFWSL	----	AAPQRF
NPFF_1_Olat	~~~~~	ESVL	----HQPQRF
NPFF_1_Drer	~~~~~	PSVL	----HQPQRF
NPFF_2_Olat	~~~~~	DWEAAPGQIWSM	----AVPQRF
NPFF_2_Drer	~~~~~	DWETVPGQIWSM	----AVPQRF
NPFF_Trub	~~~~~	EGAPGQVWSM	----AVPQRF
NPFF_2_Pmar	~~~~~	AGPSSL	----FQPQRF
NPFF_3_Pmar	~~~~~	SWGAPAEKFWMR	----AMPQRF
NPFF_1_Pmar	~~~~~	LARAFMHFP	QRF
NPFF_4_Bflo	~~~~~	GFSLDS	----DVPRRF
NPFF_3_Bflo	~~~~~	SARFSVPF	----DIPRRF
NPFF_1_Bflo	~~~~~	AAAASLF	----RPPNRF
NPFF_2_Bflo	~~~~~	SPAVWL	----DSPNRF

17. Alignment of protostomian SIF-amide-like peptides (family 11 - protostomian)

*

SIF_1_Lgig	~~~~~QVPVANPLLEFC
SIF_2_Lgig	~~~~GINPDMSSLEFC
SIF_1_Hasi	~~NLNRLVGQQPLLEFC
SIF_2_Hasi	~~~~GVNPNMNSLEFC
SIF_1_Cgig	~~GLTRLVGQQPLLEFC
SIF_2_Cgig	~~~~GMNPNMNSLEFC
SIF_Ipar	~~~~GLNPNVNSLEFC
SIF2_1_Lgig	~QSARGNGRQRPLLEFC
SIF2_2_Lgig	~~~HGVRPGMNGLVFC
SIF_1_Ctel	DPLEDHLPETSGLLEFC
SIF_2_Ctel	~~~~SSHPNMNNLEFC
SIF_1_Apom	DPLRDQLPDTTGLLEFC
SIF_2_Apom	~~~~GSHPNMNNLEFC
SIF_1_Ecom	EPLEDQLPEDTGLLEFC
SIF_2_Ecom	~~~TSHNPNMNNLVFC
SIF_Tcas	~~~TYRKPPFNCSIIFC
SIF_Agam	~~~GYRKPPFNCSIIFC
SIF_Dmel	~~~AYRKPPFNCSIIFC
SIF_Dpul	~~~~TRKLPFNCSIIFC
SIF_1_Cele	~~~~~AIPFSGGMYG
SIF_2_Cele	~~~~~STMPFSGGMYG
SIF_3_Cele	~~~~~AAIPFSGGMYG
SIF_4_Cele	~~~~~GAMPFSGGMYG
SIF_1_Ppac	~~~~~GPVMFSGGMYG
SIF_2_Ppac	~~~~~AAPSQFSGGMYG
SIF_3_Ppac	~~~~~AVPMTFSGGMYG
SIF_4_Ppac	~~~ASSPMMFGGMYG
SIF_5_Ppac	~~~~~APMPYSGGMYG

18. Alignment of protostomian SIF-amide-like precursors (family 11 - protostomian)

```

                *           20           *           40           *           60           *
SIFa_Ctel      ~~~~~--MDCRLVTFVALFCSMLLVQQVLSDPLEDHLPETSGLEFFGKRSSHPN--MNNLLFGRRSYAQM
SIFa_1_Lgig    ~~~~~--MNRCTACLVLVLVILTVNAVQVSARGNGRQRPLFRHGVRPG--MNLVFR-----
SIFa_2_Lgig    ~~~~~--MVAKGTVGILIVLFNTICANIDLNYNQVPVANPLFRGINPD--MSSFRGKR-SGNS
SIFa_Cgig      ~~~-MKIYSIISIVIALVAVIVLKTSASKENSRGLTRLVGGQPLFRGMNPN--MNSFRGKR-AVDR
SIFa_Hasi      ~~~~~--MNCKIPCLLLVLTFCIMSFTHAQANPRNLNRLVGGQPLFRGVNPN--MNSFRGKR----A
SIFa_Ipar      MSGRNLLVPASLVLILSAILFFGHETQQVEAAYSPTRGQQNTHSFRGLNPN--VNSFRGKRGGSEQ
SIFa_Dpul      ~~~~~--MRSSEFIVVMVCVVVLTFWGQVAEATRKLFRFNGSFRSNQ-----GTD
SIFa_Tcas      ~~~~~--MQLALAKVFSVCIVVILTSWIEMTEATYRKPPFNGSFRGATIGKLIFRFLSKIIISSE
SIFa_Agam      ~~~~~--MAAFKVLGSLIVVLLVLLALSGHAEAGYRKPPFNGSFRNGN-----SVD
    <--- signal peptide --->   <- SIFa ->   <--- SIFa --->

```

```

                80           *           100           *
SIFa_Ctel      AANYQVEEARQGICKSMKETCGKWGFDVEN~~~~~
SIFa_1_Lgig    -NSESEQEQQ--DCWSSLNLCLKVILNNGDMEEV~~~~~
SIFa_2_Lgig    DHRDLRKMKD--TCKAVLSSCKILFSDYEDDCTVRNKVQDGFGRFK-
SIFa_Cgig      PTLDDI-IVE--KCSRIMAACREYCAHERMGEDDI~~~~~
SIFa_Hasi      PSMNNDVCVRT--MCNAVLSACAAWCQADMTDN~~~~~
SIFa_Ipar      EALSNTCEMGR--KCLAAMSMCNMCYFETNTINES~~~~~
SIFa_Dpul      KLESCPSNCQL--LCDAAMNACSDCWLPCIGSK~~~~~
SIFa_Tcas      YDSASKACLSA--MCEIACSECACQTCWFCPSCQCEK~~~~~
SIFa_Agam      YEGNAKCVLST--MCEIACACECACQCSWCFTCQCECQK~~~~~
    <-----> conserved cysteines

```

19. Alignment of chordate Gastrin-Releasing peptide (GRP) precursors (family 12 - deuterostomian)

```

                *           20           *           40           *           60           *
NMB_Hsap      ~~~-MARRAGGARMFGSLLLFALLAAGVAPLSWDLPEPRSRASKIRVHSRGNLWATGHFMGKKSLEPSSP
NMB_Drer      ~~~-MADDGHCKYTLFLFALIMLFNVSLSTSLSLDLTELNRNKVSKIKVHPRGNLWATGHFMGKKSISNSQL
NMB2_Drer     MSSPSVSRFCCCGFLTLYLVLFYISKTSSVSLDLTELNRNKVAKIKVNPRGNLWATGHFMGKKSVVDSKH
GRP_Hsap      ~~~~~--MRGRELPLVLLALVLCCLAPRGRAVPLPAGGGTVLTKMYPRGNHWAVGHLMGKKSTGESSS
Bombesin_Bvar  ----MSAIPLNRIPLGLFLLIFSFISLSSCMFVEDPNNQGGLNLQQRLLGNQWAVGHLMGKKSLQDTDF
GRP_Bflo      ~~~~~~MKSGWYVAFVLFVAGLLAPSRA-----DKGQEHWQYGHWYGKRDPSDVNN
                <--- signal peptide --->                <---- GRP ---->

```

```

                80           *           100           *           120           *           140
NMB_Hsap      SPLGTAPHTSLRDQRLQLSHDLLGILLKAL-GVSLSRPAPQIQYRLLVQILQK~~~~~-----
NMB_Drer      QDSPFPVKPDRNIMGESGSSDLKELITQEMLKIALQAQLEDPKRTRDVYNQVIREIFKELANRM~~~~~
NMB2_Drer     LPTEDESTMTAVEAALNARQVEPEDVFQEMLRVALQTHLDTRHIRPNVPETAILMKILES YIQDNK~~~~~
GRP_Hsap      VSERGSLKQQLREYIRWEEAARNLLGLIEAKENRNHQPPQPKAL-GNQQPSWDSSEDSSNFKVDVGSKGKGS
Bombesin_Bvar  EEMESFAKRNVENMKAESERELRHAQLVVRNILEQYLKNMQN~~~~~-----
GRP_Bflo      AQIDDVLRSHPELQQLLNKLMELPRRPKASSQMYTKYDDDYPDGDVSDSTKRVLEEPGSPYWKRVNEHVD

```

```

                *           160           *           180
NMB_Hsap      -----
NMB_Drer      ~-----
NMB2_Drer     ~~-----
GRP_Hsap      QREG RNPQLNQQ~~~~~-----
Bombesin_Bvar  -----
GRP_Bflo      RDYTSIIQRSAKNPRVVQGHKVLKPKTNSFKRTIWDRFMARI F PAGED

```

20. Alignment of protostomian CCH-amide-like precursors (family 12 - protostomian)

	*	20	*	40	*	60	*
CCHa_Ctel	~	MLSVRSVGVLVGIAVLFSLQSFVQAK	C	GGSWAIHACAG	GN	KRSEGSAGARAPPALCRATR	
CCHa_Lgig	-	MEVRCTTLFAVTSLLYLTVSVSLVSGK	C	SGRWAIHACFG	GN	KRSDPSLTDNTENSRQETLL	
CCHa_Acal	-	MELTFGSSFTVALLSCLYISLITCPVVTAK	C	HGRWAIHACFG	GN	KRSDPNMSPSTDELPTLLR	
CCHa_Cgig	-	MRNPSSFVLFSATLCVYFTVQISSVSASK	C	KGPWANHMC	GN	KRSDSWSPPVQEPENNRKDEL	
CCHa_Dpul	-	MHIFFYVIHVTAMLAIVSGNC	-	NKYGNAC	FG	AHGKRSDFKRTSAVDLSDQIWPV	
CCHa_Bmor	-	MAQICLAVSIAVLLMMSQGVSAKRGC	-	SAFGHSC	FG	GHGKRSGEPAPMDMANQDMVRH	
CCHa_Tcas	-	MNCWSTQVLLAFVMAFVLAEEAKRGC	-	ATFGHSC	YG	GMGKRRTENNNEELLQDVQSEENP	
CCHa1_Amel	M	KNNATSGLPLSVCASICALIILIFFTDNSYAKRGC	-	SAFGHSC	FG	GHGKRFDPNIREKILQDDDTITN	
CCHa2_Amel	-	MAITSVNSQSVTVLIRTWIFMIIFCFAGGVAGS	C	LSYGHSC	WG	AHGKRNGGHNNGYLVP SKTINEQ	
CCHa_Agam	-	MHQLSTICFTLVIVSVLVQSTNGKRGC	-	AAFHAC	YG	GHGKRSGSSASTLYPDGLDPSMV	
CCHa1_Dmel	-	MKSTISLLLVICTVVLAAQQSQAKKGC	-	QAYGHVC	YG	GHGKRSLSPGSGSGTGVGGGMGE	
CCHa2_Dmel	-	MWYSKCSWTLVVLVALFALVTGSC	-	LEYGHSC	WG	AHGKRSGGKAVIDAKQHPLPNSY	
		<--- signal peptide --->		<--- CCHa --->			
	80	*	100	*	120	*	140
CCHa_Ctel	ARRSTEATLP	AIHREFCRGT	SERPNN	~	~	~	~
CCHa_Lgig	RQILLPQTYEYHKSNDALLQDDDINTYEKSHEESQRM	DLRALNILLK	TLMMEQK	V	R	TENS	VMA
CCHa_Acal	QLLVSDVQRLSRL	LLREPEAPVEDADL	SPNPGFEPGHPNEQLMPRLAAQKPVD	~	~	~	~
CCHa_Cgig	GRTMLRN	VLLKRLNTYPSMSSYYS	SDSQSFYPMGSD	FTEEGDSMSRENE	LRQLLKEQ	ILRKEMAAL	VGDDD
CCHa_Dpul	AANWNPTRPDEPIQERRQMKPLPALQLESVLVYNDIP	PSAEHSRYLNQEDYNN	~	~	~	~	~
CCHa_Bmor	QLGQEETPPHPGYPHSSYNVLQPGDDIIP	IRDGGVYDHDAARDVMKYKLRNIFKH	WMDNYRRSQNTNDE				
CCHa_Tcas	AFVFTGPRSENQOKLTPEQYDNISRVIRQWILSYRRAQEMRPDYN	~	~	~	~	~	~
CCHa1_Amel	REIEDLNSRNEFDVSEKKFGGQTEILSSQSRHQDSSRFNPFALS	FIVRQWLTSHRLHQ	PDME	L	N	NK	~
CCHa2_Amel	GVPYLTKDQFILSRLIGRPLVSNKYKGRWDR	LFKIKASFPEHWNDELDTHLINNEPIRDQNNNENMNQN					
CCHa_Agam	GLEVLPI	PYSKLALDKSRSMDS	SAPEGMRLTNVYGF	VPAASTHRTET	TRPGELKYAIYAML	RQLMDEAA	IN
CCHa1_Dmel	AASGGQEPDYVRPNGLLPMMA	PNEQVPLEGDFNDY	PARQVLYKIMKSWFNRRPRPASRLGELDY	PLANS	A		
CCHa2_Dmel	GLDSVVEQLYN	NNNNNNQNNQ	DDDDNDDSNRNTNANSANNIPLAAPAIISRRESEDRRIGGLKWAQLMRQ				

21. Alignment of chordate galanin-like peptides (family 13 – deuterostomian)

	*	20	*	40	*	60	*																																																									
Gal_Hsap	M	A	R	G	S	A	L	L	L	A	A	A	L	S	A	S	A	---	---	---	---	G	L	W	S	P	A	K	E	K	R	G	W	T	L	N	S	A	G	Y	L	L	G	P	H	A	V	G	N	H	R	S	-	F	S	D	K	N	G	L	T	S		
GalP_Hsap	M	A	P	P	S	V	P	L	V	L	L	V	L	L	L	S	L	A	---	---	---	---	E	T	P	A	S	A	P	A	H	R	G	R	G	G	W	T	L	N	S	A	G	Y	L	L	G	P	---	V	L	H	L	P	Q	-	M	G	D	Q	D	G	---	---
Gal_Cint	M	N	S	F	G	R	Y	T	F	S	L	A	V	V	L	Y	I	S	I	V	L	C	A	E	N	S	E	A	A	T	A	K	R	P	F	R	G	Q	G	G	W	T	L	N	S	V	G	Y	N	A	G	---	L	G	A	L	R	K	L	F	E	---	---	---
	<-- signal peptide -->															<-- galanin-like -->																																																

	80	*	100	*	120	*																																																													
Gal_Hsap	K	R	E	L	R	P	E	---	D	D	M	K	P	-	G	S	F	D	R	S	I	P	E	N	N	I	M	R	T	I	E	F	L	S	-	F	L	H	L	K	E	A	G	A	L	D	R	L	I	D	L	P	A	A	A	S	S	E	D	I	E	R	S	---	---	---	---
GalP_Hsap	K	R	E	T	A	L	E	I	L	D	L	W	K	A	I	D	G	L	P	Y	S	H	P	P	Q	P	S	K	R	N	V	M	E	T	F	A	-	K	P	E	I	G	D	L	G	M	L	S	---	M	K	I	P	---	K	E	E	D	V	L	K	S	---	---	---	---	
Gal_Cint	K	R	D	G	S	S	L	D	V	E	S	M	P	L	---	---	---	---	---	---	D	N	E	E	M	E	N	L	A	K	D	F	A	L	F	L	E	V	K	E	S	G	L	L	G	P	R	M	L	R	C	I	L	S	R	N	D	Q	V	M	D	S	M	S	E	M	

also refer to:

Kawada, T et al. (2011). "Peptidomic analysis of the central nervous system of the protochordate, *Ciona intestinalis*: homologs and prototypes of vertebrate peptides and novel peptides." *Endocrinology* 152(6): 2416-27.

22. Alignment of protostomian Allatostatin-A/Buccalin peptides (family 13-protostomian)

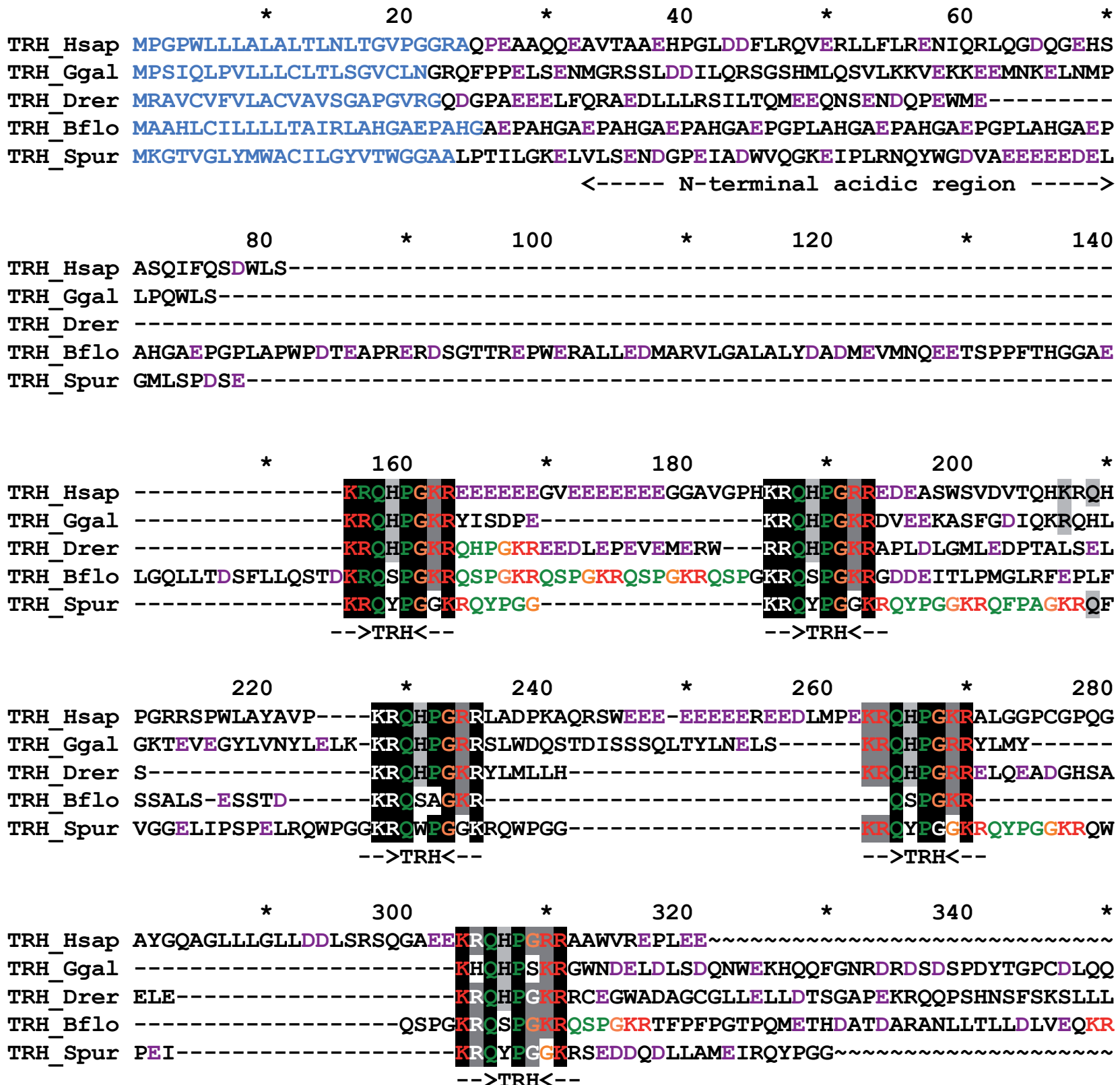
*

```

Buc_1_Acal    ~~~GMDSLAFAGGLG
Buc_2_Acal    ~~~~MDSFAFAPGLG
Buc_3_Acal    ~~~GLDRYGFVGGIG
Buc_4_Acal    ~~~GMDHFAFTGGIG
Buc_5_Acal    ~~~GLDAYSFTGALG
Buc_6_Acal    ~~~GMDDFAFSPGLG
Buc_7_Acal    ~~~RMDSEFMFGSRLG
Buc_8_Acal    ~~~GMDRFSEFSGHLG
Buc_9_Acal    ~~~KMDQFSEFGPGLG
Buc_10_Acal   ~~~GFDHYGFTGGIG
Buc_11_Acal   ~~~QLDPMLFSGRLG
Buc_1_Lgig    ~~~GMDKFGFAGGVC
Buc_2_Lgig    ~~~GLDKFGFTGQLG
Buc_3_Lgig    ~~~DMDSEGFAGQLG
Buc_4_Lgig    ~~~GLDQYGFETGQLG
Buc_5_Lgig    ~~~GLDQLGFETGQLG
Buc_6_Lgig    ~~~QMDIFGYRGQLG
Buc_1_Ctel    ~~~YSNPSMKFAGIG
Buc_2_Ctel    ~~~AMDPSMKFAGIG
Buc_3_Ctel    ~~~SMDPSMKFAGIG
Buc_4_Ctel    ~~~YSNPSMQFAGIG
Buc_5_Ctel    ~~~~STDRMMLAGIG
Buc_6_Ctel    ~~ISIDPGIKYFGLG
Buc_7_Ctel    ~~~SFDPTYSHIGIG
Asta_1_Dmel   ~~~~~~VERYAFGLG
Asta_2_Dmel   ~~~~~~LPVYNFGLG
Asta_3_Dmel   ~~~~~~SRPYSFGLG
Asta_4_Dmel   ~~~TTRPQPFNFGIG
Asta_5_Apis   ~~~~~~AHKQYGFGLG
Asta_6_Apis   ~~~~~~LYRQYEFGLG
Asta_7_Apis   ~~~~~~SASKQYGFGLG
Asta_8_Apis   ~~~~~~AALKQYEFGLG
Asta_9_Apis   ~~~~~~ASPTFYSFGLG
Asta_10_Apis  ~~~~~~ASPQYSFGLG
Asta_1_Dpul   TSRSYSINPYSFGLG
Asta_2_Dpul   ~~~~~~NPTKYNFGLG
Asta_3_Dpul   ~~~~~~PDRFGFGLG
Asta_4_Dpul   ~~~~~~LPVYNFGLG
Asta_1_Cele   ~~~MAAPKQMVFGFG
Asta_2_Cele   ~~~~~~YKPRSEAMGFG
Asta_3_Cele   ~~~~~~AAMRSENMGFG
Asta_1_Ppac   ~~~~~~SDPRMESAAGFG
Asta_2_Ppac   ~~~~~~GDPRMESAAGFG

```


23. Alignment of deuterostomian TRH precursors (family 14- deuterostomian)



also refer to:

Rowe ML, Elphick MR. (2012). "The neuropeptide transcriptome of a model echinoderm, the sea urchin *Strongylocentrotus purpuratus*." *Gen Comp Endocrinol.*179(3):331-44.

24. Alignment of chordate Kiss1 precursors (family 15- deuterostomian)

```

                *           20           *           40           *           60           *
Kiss1_Hsap  MNSLVSWQLLFLCATHFGEPLEKVASVGNSRPTGQQLESLGLLAPGEQSLPCTERKPAATARLSRRGTSLSPPP
Kiss1_1_Drer MLLTVILMLSVARVHTNPSGHFQYLEDETPEETSLRVLRGTDTRPTDGSPSKLSALFSMGAGPQKNTWWWSP
Kiss1_2_Drer MNTRALILFMSAMVSQSTAMRAILTDMDTPEPMPDPKPRFLSMERR-----
Kiss1_Pmar  MTPACSLAALLAVCVFGGGAVAARTDRYGASPDSNHARRARSSEEIVTGDLRASPLRLFGAVCRHAAETPRLLRL
Kiss1_1_Bflo MRTTAFLLASLLVLLHTILPSTVDSLALGGREAQHRQDCGGRIRSRVPVGLKRAWPDRRGLNSDDIFWEDTLP
Kiss1_2_Bflo MSPHIPGKTMVALLLILAAVASESRFAHLKLPSFPGLQQTSGPYGPREPATPLRSFTQESRWQPWKPAGVVQTSE
Kiss1_3_Bflo MAVEAQMTSRAVVAVLLVSMATSHPAAAHHLVSWAVPAKIEAQPAPQYEDVADSNSLALEAHEPLLEALSPESQ
Kiss1_4_Bflo MMKRRLLVAVLLVACSMGCRGTQRDILLPHGAREDTAKSGDGRAVHDAVLLREVLTHGPTIEALVRSTMTTVLV
<-- Signal peptide -->

                80           *           100           *           120           *           140           *
Kiss1_Hsap  ESSGSPQQPGLSAPHSR-----
Kiss1_1_Drer ESPYTKR-----
Kiss1_2_Drer -----QFEEPSASDDASLCFFIQEKDETSQISCK
Kiss1_Pmar  RALRGGHDLDAGLTDGEALPRS-----
Kiss1_1_Bflo NSIERR-----QPSTEIDDEEVVDS
Kiss1_2_Bflo GSSAGFGLLHEWFRIGSKR-----SGGAWV
Kiss1_3_Bflo PRHPASQPDSYRPLLIRLPWPLARALSKR-----
Kiss1_4_Bflo ATGWYKMMHGKVPGLDGSRRGLQQGRRQGEEASTLHGILTSNIATTEQNSTSTARQTTEVSTSHTARSGWE

                160           *           180           *           200           *           220
Kiss1_Hsap  REKDLPNYNWNSFGLRFGKREAAPGNHGRSAGRGGAGAGQ-----
Kiss1_1_Drer -RQNVAYYNLNSFGLRYGKREQDMLTRLKQKSPVK-----
Kiss1_2_Drer HRLARSKEFNYNPEFGLRFGKRNEATTSDSRLKHKHLLPMMLYLRKQLETS-----
Kiss1_Pmar  AEQDVTEFNYNPEFGLRFGRRSGAQSSTAATRSRAEAACAPGKRGCRLVISKFKLRF-----
Kiss1_1_Bflo ADPDRVQYNPNAWS-RFGRSMCP-----
Kiss1_2_Bflo ADTNMDDISPNMFS-LHGKRNVS-----
Kiss1_3_Bflo ---ARKPPNMNAWGQPWGKRDLSLVN-----
Kiss1_4_Bflo YENEPPEYNPNSWS-VEGRMVSPQASPAPEQDDEPGVPGMPVLAEMPPKAAANLNMWSSFGRRSAADRIPERTR
<--Kiss1 peptide-->                                     <-- Kiss1-->

                *           240           *           260           *           280           *
Kiss1_Hsap  -----
Kiss1_1_Drer -----
Kiss1_2_Drer -----
Kiss1_Pmar  -----
Kiss1_1_Bflo -----
Kiss1_2_Bflo -----
Kiss1_3_Bflo -----
Kiss1_4_Bflo DGSPVRSSVNPAFFLTPFGDQTDKQRSIEERQVKQTGDAAASHKRTPDPRVYPPNARPTLQPDWTKIPFFG
<-- Kiss1 -->

```

25. Alignment of chordate Ox26/QRFP precursors (family 16 - deuterostomian)

```

                *           20           *           40           *           60           *           80
QRFP_Hsap  MVRPYPLIYFLFLPLGAC-----FPLDDRREPTDAMGGLGAGERWADLAMGPRPHSVWGSSRWLRASQPQALLVIARGL
QRFP_Trub  MTTAFHLGASHLLFFTLCPIPRSIMPSPHFPSILLPFEDLSELQQHQQDHCLLQQVTRAGSGDQPHVTLLQPKQSRLRR
QRFP1_Bf1o MSRILAVLLAVLATTAAT-----ANLPSPHRLVRRSAPSEDEVRMQRRANLLALLEDDDDNETREPSEAQGAGLSKEEA
QRFP2_Bf1o MSRMLAVLLAVLVTTAATTNPSPHRLARRSAPSEDEVRLQRRANLMALLEDDDDNGASEATDTPVPGLSLTEEEADALVKC
QRFP3_Bf1o MGVRVMRSRICVIGLLVLMLTQSEA-----YSFREKSWRTSPYYRQYGGYFRRRRDGGDQAPSFTS
<--- signal peptide --->

```

```

                *           100           *           120           *           140           *
QRFP_Hsap  QTSGREHAGCRFRFRGRQDEGSEATGFLPAAGEKTSGPLNLAEELNGYSRKKGGFSSRFGRR~~~~~
QRFP_Trub  AQRDALATRILTPLTGGPSVSFRERRQGENGGKKNEALTSIAGEIQAVSREKGGFGFRFGKRRWTDWRRKSLRQN~
QRFP1_Bf1o EALVKYLQEPVGGLRRPAINVYRPDVEEVEREKKTRLLSWAAEMLRMMSTKGGFGQFRFGKREAAEGKER~~~~~
QRFP2_Bf1o LVDPVGGLRGPLHTGGGFHRPRSGRGERGDREKKALDLSSLAQSLRTMGSRKAGIILRFGGKRDEDEGENTSLAANI
QRFP3_Bf1o TGNGEDVSNGLDDDAGIYLSDQAGDDGISPADKRSAMLQQLAQQLKNRPREKGGFTFRFGKRESRRSFGSD~----
<----- Ox26/QRFP peptide ----->

```

26. Alignment of chordate Parathyroid hormone (PTH) peptides (family 17 - bilaterian)

		*		20		*		40	
PTH_Hsap	~~SVSEIQ	L	MHNLGKHLNSMER	VEWLRKKLQDV	-----	HNF	~~		
PTHrP1_Hsap	~~AVSEHQ	L	LHDKGKSIQDLRRR	FFLHHLIAEI	-----	HTAEI			
PTH1_Drer	~~SVTHAQ	L	MHDKGRTLQDFKRR	MWLQELLHEV	-----	HTAEI			
PTH2_Drer	~~SVGHAQ	M	HDRSRSLHDRKRR	MWLQDLLQV	-----	HTAQV			
PTH3_Drer	~~SISEVQ	L	MHNVREHKEMLD	RQDWLQLKLNNI	-----	IIPSV			
PTH4_Drer	~~AVNEVQ	L	MHNLGVHKKHVEL	RQDWLQMKLRGI	-----	HTASV			
TIP39_Hsap	SLALADDA	A	FRERARLLAALERR	HWLNSYMHKI	-----	LVL			
TIP39_Drer	NIVVADDA	A	FREKSKLLTAMER	QKWLNSYMQKI	-----	LVV			
PTH_Cint	~QSNADLN	L	QNKKTRHMNELIR	QYYISSILNEI	-----	KG	~~~		
PTH1_1_Bflo	~~SITDVT	M	TEERTRDMISRAR	QAWLTALVDEI	-----	LLPEGANS			
PTH1_3_Bflo	~~QITDR	T	MTEERSRDLVDR	ARQAWISSLVDEI	-----	VEASGTS			
PTH1_4_Bflo	~~QITD	V	DTSDHSKAFTDR	ERTAWLHRLNAV	-----	QGQ	~~		
PTH2_Bflo	~TGLTDV	T	LLNERHGDLNER	ARVAWLRFLGGID	PDASEALASEED				

27. Alignment of chordate (Glucagon+PACAP)-like peptides (family 17 - bilaterian)

	*	20	*
Hsap_GIP	~YAEGTFTISDYSIAMDKIHQQDFVNW~~~~~		
Hsap_PACAP	~HSDGIFTDSYSRYRKQMAVKKYLAAVLG~~~~~		
Hsap_VIP	~HSDAVFTDNYTRLRKQMAVKKYIENSILNG~~~~~		
Hsap_PHM	~HADGVFTSDFSKLIGQLSAKKYTESLMG~~~~~		
Hsap_sec	~HSDGTFTESELSRLREGARLQRLIQG~~~~~		
Hsap_GLP1	~HAEGTFTSDVSSYLEGQAAKEFLAWLVKGRG~~~		
Hsap_Gluc	~HSQGTFTSDYSKYLDSTRRAQDFVQWLMNT~~~~~		
Hsap_GLP2	~HADGSFSDEMNTILDNLAARDFLNWLIQTKITD		
Cint	~YAESAFTSMAAKQMDHAAFQQLIRG~~~~~		
Csav	~YVENAFTSYTAKQLDRAAYQHLLIRG~~~~~		
Bflo_95424	QLGDQGVTSALAAARLEQAEARQYIKDLLAQAVG~		
Bflo_96553	QLGDQGVTSALAAARLEQAEARQYIKDLLAQAVG~		
Bflo_95424_2	ALGDQGFTSDLASKLSEAEARRMIQTLMAQAIG~		
Bflo_96553_2	ALGDQGFTSDLASKLSEAEARRMIQTLMAQAIG~		
Bflo_96553_3	QLGDQSITSEMSVRLREAEARRLIQSLMAKQG~~~		

28. Alignment of protostomian Leucokinin peptides (family 18 - protostomian)

```
Lk_1_Ctel ~AFSAWGE
Lk_2_Ctel ~GFHAWGE
Lk_3_Ctel ~AFNPWGE
Lk_4_Ctel ~QFGPWGE
Lk_5_Ctel ~AFNPWGE
Lk_6_Ctel ~SFNPWGE
Lk_1_Lgig AAFAAWGE
Lk_2_Lgig APFSVWNG
Lk_3_Lgig AAFTSWGE
Lk_4_Lgig ~AFTSWGE
Lk_5_Lgig PAFSSWNG
Lk_6_Lgig ~SFSAWKE
Lk_1_Acal AGFAPWAG
Lk_2_Acal PAFHAWSE
Lk_1_Ipar ~KFSPWAG
Lk_2_Ipar SRFSPWHG
Lk_3_Ipar ~GFNPWAG
Lk_1_Llon IKFHSWGE
Lk_2_Llon TPFHSWGE
Lk_Dmel QRFHSWGE
Lk_Cele KQFYAWAG
Lk_1_Xind ~KFYAWAG
Lk_2_Xind ~RFYAWAG
Lk_3_Xind ~KFYQWAG
Lk_Tspi ~KFYPWAG
```

29. Alignment of protostomian Ecdysis-Triggering Hormone (ETH) peptides (family 19 - protostomian)

	*	20
Pleurin_Ctel	~~~~~IF	YTN SKENDY PRLG
Pleurin_Apom	~~~~~FY	AQNEGNDF PRIG
Pleurin_1_Lgig	~~~~~VF	YTSSKANDY PRIG
Pleurin_2_Lgig	~~~~~FF	TSSKENTY PRMG
Pleurin_3_Lgig	~~~~~FT	AGDSASY PRLG
Pleurin_4_Lgig	~~~~~AG	YFTKGAASY PRLG
Pleurin_Vdec	~~~~~FW	TNSKDSDY PRIG
ETH_Dpul	~~~~~GS	LSNFFLKASKAV PRLG
ETH_1_Tcas	~~~~~EN	YVLKAAKNV PRIG
ETH_2_Tcas	~~~~~FF	MKASKSV PRIG
ETH_Apis	~~~~~GF	AGEEFFLKASKSV PRIG
ETH_Nvit	~~~~~DE	PPAFFLKIAKNI PRIG
ETH_Amel	~~~~~DE	VPAFFLKIAKNI PRVG
ETH_1_Bmor	~~~~~GL	DGSFIK-PNNV PRVG
ETH_2_Bmor	SNEAF	DEDVMGYVIKSNKNI PRMG
ETH_Lmig	~~~~~SD	FFLKTAKSV PRIG
ETH_1_Dmel	~~~~~DD	SSPGFFLKITKNV PRLG
ETH_2_Dmel	~~~~~GE	NEFAIKNLKTI PRIG

30. Alignment of lophotrochozoan luqin and arthropod RYamide peptides (family 20 - protostomian)

```

                *           20           *           40           *           60           *
Lq_Lgig      MKLSEMIMCIMAVLLVTITLGNG-----
Lq_Lstag     MISTCCVLSVIFSLCYA-----
Lq_Apom      MATFRAIVMGLASLILSLLILTQPSEQ-----
lq_Iobs      MMELMLVACVLVVMTSLLQPTAA-----TPSWKPGQRFGRGGPS--
RYa_Dpul     MARKESVFWLFC TLALMMSVVLVDA--QTFFTNGRYGKRSEVRSRVASRSADERFFGGPRFGRSGNGGIV
RYa_Tcas     MHARKLIVVLVYILTVLVSVAVS-----KRYTSEKRVQNLATFKTMMRYGRGGPSPNN
RYa_Dpon     MLVRKVPVIFVFLVSIFITVNA-----DMESIKRIPSHSFKQMMRYGRSSANN--
RYa_Isca     MLHCRAWAVALIALLVLSVASA-----
Luqin_Tspi   MDLKIKIRIIFFLIGMALFSEA-----
Luqin_Cele   MLTRVPVLILAVIVMLALC-----QEPE
<-- Signal peptide -->
    
```

```

                80           *           100           *           120           *           140
Lq_Lgig      -----APQWRPQGRFGKRVNPTLSLLLHGDQEKQFLNHEKPFISEDKPYIPEVTDEISVERLTS
Lq_Lstag     -----TPHWRPQGRFGKRTTEDDNPVDFGISRPQDIPIELMF'SKNELSRNSKPRL-----
Lq_Apom      -----QYAWRPQGRFGKRDNYLARGILSGPSLDTSNKIKMLSTHMFESNGVL-----
lq_Iobs      --DYLGIQKKPHGWRPQGRFGKRSLASSSSPSSSSFEQSIDAELLKSAAVSGAIEVPVELLSTGENGM--
RYa_Dpul     LGNSELDARNPERFFIGSRYGKRSEMEQIVPSPQVDESTSNSQEKETFLE-----
RYa_Tcas     KENKVNIRPRADAFFLGPRYGKRSGWSPNASLVYPVSTPLCGLDED-----
RYa_Dpon     --EKINVNPRADLFYLGRYGKRAGPTLAKLDTVYDSTF-----
RYa_Isca     -----AKGTPQFVPNGRYGRRSVTPPLAGVSKDITVNFEGDST-----
Luqin_Tspi   ----KPASLARYGRAALPRYGKRAELISGLDAMRDEVTEFKNSP-----
Luqin_Cele   KPEKRPALLSRYGRAVLPRYGKRSGNLMESSQNSLTEESSDVV-----
<--Luqin/NepY-->
    
```

```

                *           160           *           180           *           200           *
Lq_Lgig      ARDNLKFLHRLCSESGLENVPRCSWSRKTSESSDP-----
Lq_Lstag     -----CSTSGVAGYPPCDAQVNAMQVATLG-----
Lq_Apom      -----CVSAGSRGLRYCFTV-----NPVPGSSSPVSMANTPFIEVGDVLCVSVAEIGAYRCFQ
lq_Iobs      ----FLRLGVKPCSITGMDGIPPC-----TGASEGASETF~
RYa_Dpul     -----CNPIGIEQLYHC-----IERLKSAAHFDLMQHQQV~
RYa_Tcas     -----LSCAYTGISDLYRC-----TPRKGESEEFTSSN~
RYa_Dpon     -----MPCTYTGVADLYRC-----DTSRSTMREDRRK~
RYa_Isca     -----ISCHTHGFADIYRC-----TRKTSDDYKDSSFE~
Luqin_Tspi   -----CVYTGYEDLYRCSSMT~
Luqin_Cele   -----CQL--IDGKYICLPVDAGFLGEVNGSIKQNSKTKCPAFFKNVSFSLFFRAFYLTVPAC
<- Conserved Cys ->
    
```


31. Alignment of protostomian Allatostatin B peptides (family 21 - protostomian)

*

```

AstB_Ipar      ~~NGDTWDSM--SAWG
AstB1_1_Ctel  ~~~~~GWKNNNMRVWG
AstB1_2_Ctel  ~~~~~KWGSNSMRVWG
AstB1_3_Ctel  ~~~~~WGGNDRVWG
AstB1_4_Ctel  ~~~~~SWKTNVMRVWG
AstB1_5_Ctel  ~~~~~GWADNNMRVWG
AstB1_6_Ctel  ~~~~~AWVGDKSLSWG
AstB2_1_Ctel  ~~~~~KWSNNMGMWG
AstB2_2_Ctel  ~~~~~AWSSNKMMWG
AstB2_3_Ctel  ~~~~~EWASNYMGMWG
AstB2_4_Ctel  ~~~~SKWGSKMMMWG
AstB_1_Lgig   ~~~~~AWKSSYLNTWG
AstB_2_Lgig   ~~~~~~WTNSGLITWG
AstB_3_Lgig   ~~~~~KWNQF--ITWG
AstB_4_Lgig   ~ASDKGWNGF--TTWG
AstB_5_Lgig   ~~ANKDWSSL--STWG
AstB_6_Lgig   ~GQNKDWSSL--TTWG
AstB_7_Lgig   ~GHDRDWSL--TTWG
AstB_8_Lgig   ~ARENDWSAL--STWG
AstB_9_Lgig   ~ANNKDWASL--TTWG
AstB_10_Lgig  ~ANDRDWSL--TTWG
AstB_11_Lgig  ~AKGNNWSGL--TTWG
AstB_12_Lgig  ~~ANKDWSL--TTWG
AstB_13_Lgig  ~~ANKDWSGL--TTWG
AstB_14_Lgig  ~~GNKDWSGL--TTWG
AstB_1_Apis   ~~~~~AWRDLQTAGWG
AstB_2_Apis   ~~~~~GWQNLK-TTWG
AstB_3_Apis   ~~~AQDWQNLH-SSWG
AstB_4_Apis   ~~~~QGQQLH-GGWG
AstB_5_Apis   ~~~~~GWKDMQSGGWG
AstB_6_Apis   ~~~~~SWDNFQ-GSWG
AstB_7_Apis   ~~~AADWTSFR-GSWG
AstB_1_Hvir   ~~~~~GWNDMS-SAWG
AstB_2_Hvir   ~~~~~AWQDLN-SAWG
AstB_3_Hvir   ~~~~~AWRDMSQSPWG
AstB_4_Hvir   ~~~~~GWQDMS-SAWG
AstB_5_Hvir   ~~GPEKWANFH-GSWG
AstB_1_Tcas   ~~~~~DWNKDL-HIWG
AstB_2_Tcas   ~~~~~GWNNLH-EGWG
AstB_3_Tcas   ~~~~~AWQSLQ-SGWG
AstB_4_Tcas   ~~~~~NWGQFH-GGWG
AstB_5_Tcas   ~~~~SKWDFR-GSWG
AstB_6_Tcas   ~~~EPAWSNLK-GIWG
AstB_1_Cele   DDRVLGWNKAH-GLWG
AstB_2_Cele   ~~TPQNWKNLN-SLWG
AstB_3_Cele   ~~SPAQWQRAN-GLWG
AstB_Ppac     QEEPRGWNKAY-GLWG

```

32. Alignment of protostomian proctolin precursors (family 21 - protostomian)

```

          *          20          *          40          *          60          *          80
Prct_Dmel MGVPRSHGTGIGCGSGHRWLLVWMTVLLLVPVPHLVDG-----RYLPTRSHGDDLDKI-REIMLQILELSN
Prct_Tcas MFDRKLVFALVFVVFATLAVEG-----RYLPTRSNGDRIEKI-REILKDIFFENEV
Prct_Apis MAGKFSALFLVGFVAADVVPYMAEA-----RYLPTRGNDRLTRI-KELITDILLDSGA
Prct_Dpul MLKSTSLKALVTLVVSFVLMASSPRAADA-----RYLMTRGKDPREFRI-YDIITKILLQNGG
Prct_Ctel MEIRLTLVLALLVAALGVVANALSIPSDALKDNQMDVADKGDQS---RRATWLETRDLEDDFKELVYLTIEELVNEGR
Prct_Apom MDMCRLSAILVILYGTLCAVTNAMSIPASQLKDSGVELDSSENTALDEGRRASWLETRDLENDFKDIVFLTIQETAQEGR
Prct_Lgig MRSSTILSLLVLLLAAPTFCCLPPDQGSEIDDL-----KRPKYMDTREELSVLKDMVYIVLQELAEDGK
Prct_Acal MELQACNIFALFVVVVTLSVASSLPASRTDDVLQEASGLALN-----KRPKYMDTRRDLDVFKDIVLISIQEIVDENR
<--- signal peptide --->          <-----> <-----...----->
                                proctolin  conserved domain

          *          100          *          120          *          140          *
Prct_Dmel EDPQQQQ-QQQQQQQH--PQLRLHNEATGGSSSSSNINNPRVSNNGNSNAAWLQKLSAMGALDELGGDGAREFGPNYGRY
Prct_Tcas EKEEYQADAPPRWHPESKLFYKREAPAH~::~::~::~::~::~::~::~::~::~::~::~::~::~::~::~::~::~
Prct_Apis QPNLEMERPYVDVNGDFSRLRPREYNIPEKSIMELFNPTVPHHQRPRES~::~::~::~::~::~::~::~::~::~::~::~
Prct_Dpul GDLEYQIKSQLDSGP~::~::~::~::~::~::~::~::~::~::~::~::~::~::~::~::~::~
Prct_Ctel MDPRVLS-KEENEVKE--KRGRWQGFCFKRTRSGRFLPYICWKGDGRK~::~::~::~::~::~::~::~::~::~::~::~
Prct_Apom IDPRVIVEENSLDTKE--KRGRWQGFCFRRTKTGRFLPYICWKGDGRK~::~::~::~::~::~::~::~::~::~::~::~
Prct_Lgig INPELFT-IHDQKAVV--KRMKYMIGICMRRTKYNAVVPYPCLRSGR~::~::~::~::~::~::~::~::~::~::~::~
Prct_Acal LNPALLPEEDAPKPVE--KRMRYMIGICMKK-QYNNFIPFPCLRSGR~::~::~::~::~::~::~::~::~::~::~::~
>

```

also refer to:
 Veenstra, JA. (2010). "Neurohormones and neuropeptides encoded by the genome of *Lottia gigantea*, with reference to other mollusks and insects."
 Gen Comp Endocrinol.167(1):86-103.

33. Alignment of protostomian Pigment-Dispersing Factor (PDF) precursors (family 22 - bilaterian)

```

                *           20           *           40           *           60           *
PDF_Dmel  MARYTYLVALVLLAICCGWGYCGA--MAMPDEERYVVRKEYNRDLLDFNNGVGVGQFSPGQVATLCRYPLI
PDF_Pmon  MCRVAMLLVVLAVTAVVVTEA-----QREPAASKCQAATELAIQIILQAV
PDF_Psed  MNSIIIVLSLAVLAIFTSSIQS-----SPLNRAEDLQPVERQIIAEMASK
PDF_Hduj  MDVKAFLFAVAMSTFLTSSSA-----IWVFLEPRFDAEFISRNSEMVGVQEVYSQFSPGSEGPAQLLSQG
PDF_Cele  MNRFIISMIALLAVFCAVSTA-----SPLLYRAPQYQMYDDVQFVKRSNAELINGL
Cere_Ctel MRNSIMLNLTVVVCIISLTVFQVCA-----RPYDTQLSEKDRQEIMHYAASILK
Cere_Lgig MVALSPEMNSCTKCLLLLTVFGLTVLVKLSSES-----SPLRPYQTQIEEKSRQDIITLAARVIK
PDF_Skow  MASYKSMMVIYCVFLLVADIEG-----FLKVVAKKSGRIQREVAEKRDLLRD
<--- signal peptide --->

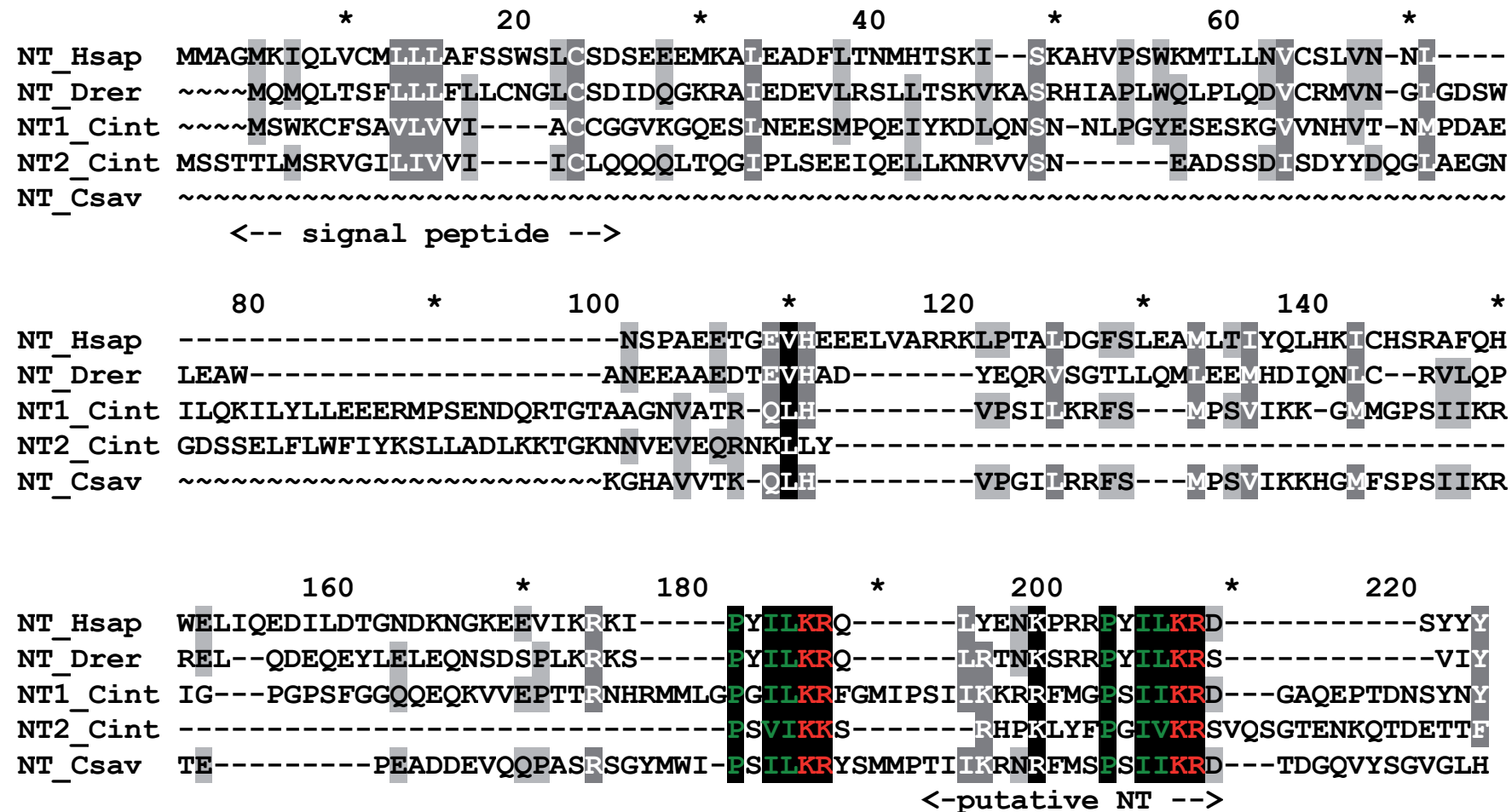
```

```

                80           *           100           *           120
PDF_Dmel  LENS LGPSVPIRKRN-SELINSLIISLP-KNMNDAGGR~-----
PDF_Pmon  KGAHPGVAVGPHKRN-SELINSLIIGLP-KFMIDAGGR-----
PDF_Psed  ILKVAEDGLVYSKRN-AELINSLIIGLP-KMMNDAGGR-----
PDF_Hduj  YQPVELTRIPIRKRN-SEILNTIIGLP-NKLRQRG-----
PDF_Cele  IGMDLGKLSAVGRSNAELINGLISMNLNKLSGAGGR-----
Cere_Ctel IAFGQGYLPTQEKRN-SGMLDAVINMP--DLFKAGRK-----
Cere_Lgig IAMYGSNQYDVIKRN-AGTVDHLLNFP---DLSVGR~-----
PDF_Skow  KEIEKRPHGERDLRN-YGNTKQEVDIP--RHMVLGR~-----
<--- PDF peptide --->

```

34. Alignment of chordate Neurotensin precursors - putative neurotensin-like peptides in Ciona



also refer to:
 Kawada, T et al. (2011). "Peptidomic analysis of the central nervous system of the protochordate, Ciona intestinalis: homologs and prototypes of vertebrate peptides and novel peptides." Endocrinology 152(6): 2416-27.

35. Alignment of putative chordate Opioid precursors - putative opioid-like peptides in *Ciona*

*
20
*
40
*
60
*

PENK_Hsap MA-RELTICTWLLLLGPGLLATVRAECSQDCATCSYRLVR-PADINFLACVMECEGKLPS-LKIWETCKE
 PDYN_Hsap MAWQGLVLAACILL-----MFPSTTADCLSRCSLCAVKTQDGPKPINPLICSLQCQAALLP-SEEWERCQS
 Op-like_Cint MK---LVKKFSILL-----AAIVVCYFGCIADAVP-VDTVE--KQ
 Op-like_Csav MY---SIQACILL-----LSILFNPDSIIVKAVPAIDAIE--RE

80
*
100
*
120
*
140

PENK_Hsap LIQ---LSKPELPQDGTSTIRENSKPE--ESHLL-----
 PDYN_Hsap FLS---FFTP-----STIGLNDKEDLGSKSVG-----
 Op-like_Cint LIQREGTGNPENFLDWINQINST--DDAEDNPEL-----AENR
 Op-like_Csav LISKQINKEEVNFIDFTKAINSTALDDMSDELWMLGOMIQPIQESTSVNDEEQLSGIDDIEEIDKEQG

*
160
*
180
*
200
*

PENK_Hsap -----A-----KRYGGFMKRYG-----GFMKKMDE--LYPMEPE--EEAN
 PDYN_Hsap -----E-----GPYSELAKLSG-----SFLKELEKSKFLPSIST--KENT
 Op-like_Cint NSDEENNDYSPGQAESIQSD-----KRFQSLFKRYP-----GFQGLFKR--HNPHLPDFLKRYN
 Op-like_Csav TNDELNLGKGDQONQAYFSPQMKRHFGLFKRMRGLFKRAPNAPLKRGLSGLFRDPNTEGEPDARKVSD

220
*
240
*
260
*
280

PENK_Hsap GSEILAKRYGCFMKKDAE-----EDDSIANSDDLKELLETCDNRERSHHQDGSNDEEIVSKRY
 PDYN_Hsap LKSLEEKLRGLSDGFRE-----GAESEIMRDAQLNDGAMETG-----TLYLAEEDPKEQV-KRY
 Op-like_Cint S-----MGLFKRSPG-----MLGLFKRG-----LLGLEKRS
 Op-like_Csav GGRTDTRGMQGLFKREPAFPVDADNSYDGKSHQVKLDRRRMPGLFKRC-----LONLEKRA

*
300
*
320
*
340
*

PENK_Hsap GGFMRGL-KRSPQLE-----DEA-----KEIQKRYGGEMRRVGRPEWMDYQKRYGGFLKR-FA
 PDYN_Hsap GGFIRKYPKRSSEVA-----GEGDGD SMGHEDLYKRYGGELRRI-RPKLKWDNQKRYGGELRRQFK
 Op-like_Cint DARLQGLFKRDSATQ--GSFKRSSEA-----QALPKRYPNEQ-----GLFKR-LS
 Op-like_Csav GG-ANSLFKREDGIENEVGARNRKS DL-----QEIFKR--GIQ-----GLFKR-MT

<-opioid?->

360
*
380
*
400
*

PENK_Hsap EA--LPSDEEGESYSKEVPEMEKRYGG-----EMRF
 PDYN_Hsap VV--TRSQEDPNAYS GELFDA~
 Op-like_Cint EATEYPEDDSSNDDTKQ RGNLHSLFKRDTS-----AHYLEDRGESIPFLFRRS
 Op-like_Csav -TDDLNAENNLGEAPHYRRSFHSLFKRDLSLSWKNKSSGENKNKVHSLFKRGENIPFIFKRN

36. Presence of a common C-terminal domain in vertebrate ghrelin and motilin precursors

```

                *           20           *           40           *           60           *
ghrelin_Drer  MPLRCRASSMFLILLCVSLSLCLESVSGGTSFLSPT----QKPQG-----RRPPRVGRREAAD----
ghrelin_Asch  MFLKRNTYLLVFLFC-SLTIWCKSTSAGSSFLSPS----QKPQNRG-----KSSRVGRQVMQE----
ghrelin_Hsap  MPSPGTVCSILLII----GMFWLDLAMAGSSFLSPEHQRVQQRKESKKPPAKLQPRALAGWLRPEDGGQ--
ghrelin_Ajap  MRQMKRTAYIIILLVC-VLAIWMDSVQAGSSFLSPS----QRPQGD-----KKPPRVGRRDSDGILD
ghrelin_Ipun  MLGHGRVGHMILLIC-AFSTWAEIVMCGSSFLSPT----QKPQNRG-----DRKPPRVGRRTAEE----
motilin_Hsap  MVSARKAVAALLVVHV-AAMLASQTEAFVPIFTYGELQRMQEKERNKG-----QKKSLSVWQRSGEEGPVD
motilin_Oana  MVSARKAVAFLLVSV-AAMMA---EGFIPIFTHSDVQRMQERERNKG-----QKKSLLTVQQRSEQGLRT
Motilin_Ocun  MVSARKAVAALLLVHV-TAMLASQTEAFVPIFTYSELQRMQERERNRG-----HKKSLSVQQRSDAAAAPR
Motilin_Psin  MVSARKVVASLLVVYV-AAMLAGQTEGYLAFFTRSDIERMQERERNKA-----QKKSLLMQKRSESGDVTE
<--- signal peptide ---> <-- ghrelin/motilin -->

```

```

                80           *           100           *           120           *           140
ghrelin_Drer  -PEIPVIKED-DRFMMSAPFELSMSLSEAEYEKYGPVILQNLLENLIRDSSFEF~~~~~
ghrelin_Asch  ----PQQPTDDKHITISAPFEIGISMTEEDYDEYGVVLOEIIQRLIGGTEAAEGPPQL~~~~~
ghrelin_Hsap  ----AEGAEDELEVRFNAPFDVGIKISGVOYQQHSQALGKFIQDIIWEEAKEAPADK~~~~~
ghrelin_Ajap  FMRPPLQDEDIRHITFNTPEEIGITMTEELFQQYGEVMQKIMQD~~~~~
ghrelin_Ipun  -LEAPLPSE--EKIMVSAPFQLAVSLSDAEYEDYGPVILQRMILLDVLGDPPTLDGAN~~~~~
motilin_Hsap  -PAEPIREEENEMIKLTAPLEIGMRMNSROLEKYPATLEGLISEMIPQHAAK~~~~~
motilin_Oana  -LAEPNGEEEGEIIQLAAPVEIGLRMNSROLAKYRGILEELIMEALLSTQNGESNPDRGRGRCS~~~~~
Motilin_Ocun  -PAEPTLEEEENGRMQLTAPVEIGMRMNSROLEKYRAALEAAERAVHPDAPSRPCWPAGGESGWSGEPSP
Motilin_Psin  -LS-AESVAEAGEIVTLTAPGETSMRHSAGOLEKYQHVLKELLTEMLDAQNVN~~~~~
<----- obestatin domain ----->

```

37. Alignment of chordate somatostatin/cortistatin-like precursors

```

                *           20           *           40           *           60           *
SMS_Hsap  MLSCRLQCALAALSIVLALGCVTGAPSDPRLRQFLQKSLAAAAG-KQELAKYFL-A---ELLSEPNQTE-
Cort_Hsap MPLSPGLLLLLLISGAT----ATAALPLEGGPTGRDSEHMQEAAGIRKSSILTFE-A---WWFE--WTSQ-
SMS1_Trub MQLL--VVLAAALTGVLLSIRAAAVLPVEERSPVHLNRELSKE---RKELILKLV-S---GLLDGALDTN-
SMS2_Trub MQRHSSTIIMLTTLVL---CIQGVSSQPDRDLNQNQDLEMEVR-HHRLIQHVHGA---GLLSQEWKRA
SMS_Bflo  MKNLHAFLEFLSVLTLVVVWTSAEILPYQQSVDDMDRAQLDDEISPPYEDLAEAKEAAAYWIILRKALLEN-
<-- signal peptide -->

```

```

                80           *           100           *           120           *
SMS_Hsap  -----NDALEPEDLSQAAEQDEMRLLELQRSANSNPAMAPRERKAGCKNFFWKTFTSC~
Cort_Hsap -----ASA-GPL-----IGEEAREVARRQEGAPPQQSARRDRMPCRNFFWKTFSCK
SMS1_Trub -----MLPMETVDLEEPLESRLE-ERAVYNRLSLPQDRDRKAPCKNFFWKTFTSC~
SMS2_Trub VEDLIAQMSMPEGTGQRDTEVVSMATGGRMNLERSVDTTNNLSPPERKAGCKNFYWKGPTSC~
SMS_Bflo  -----PPGKPAHARNVMDTDEESRESLRTTVVQRLA---KRWKVKCNNAYWK-FCKG~
<-somatostatin->

```

38. Alignment of protostomian allatostatin C-like precursors

```

      *      20      *      40      *      60      *      80
AstC_Ctel  M-----VPSKSVCAIVVVMSCYVLCGFIVNAVPTQDGG-----SNLSHGYNE-----VSE
AstC_Hrob  M-----KNVTFLLAMSATILLLLASALPPRRRSL-----ISKNYIFPK-----THSKR
AstC_Lgig  M-----KSLPVTTLTLCICLNEVSSNKILPGEEH-----RQLVQITEE-----
AstC_Cgig  M-----ELTQSVFVLKLYAAVVAVLLVAEVHAQPQKF-----STEIQQTGD-----
AstC_Acal  MSVSVRTWRAVNTCLLTLTLWADVLVRAAVIPVSSP-----EPMEEASAL-----
AstC_Dpul  M-----MAKISAVVPVAIILLYLAASGAAKSTDREETE-----STDFGQDIE-----V
AstC_Tcas  M-----AAQLPRYTKTLFIFLIATLVVANARPNHFGDASQ-----NSISGLKFQ-----V
Ast-C_Dmel M-----MKFVQILLCYGLLLTFFFALSEARPSGAETG-----PDSGLDGDQDAEDVRGAYGGGYDMPAQA
Ast-CC_Dmel M-----VVPKRAALLDRIMVALHHALEQERSEQRIGEFFGDRNILSGKFGDSHNGMEHH-----QAREDMYSDDDAG
AstC1_Cele M-----VKFFVFLIFFAFLCSFTSAIPLRSLFL-----RSYDDINQE-----
AstC2_Cele M-----MAQKTLIAVMIVCSI-----
AstC3_Cele M-----RVLTEFLVTLF-ALANVMQAQRYDRAIYE-----ALLNDLERE-----
AstC4_Cele M-----KSSSVLSVALIVLVIVQLISASLASVPSS-----SAVSDGQID-----
AstC5_Cele M-----SSGKLFQFFIVFLATLLLLADAIPMVSSR-----DEDDQIIQK-----
<----- signal peptide ----->

```

```

      *      100      *      120      *      140      *
AstC_Ctel  MGLTDTKLAFLLEKKLREEIERDLADLLVMEHQHRH--NLNFIQEKKRQLEIKKREPV----QCLVNIVSCW----KRR
AstC_Hrob  FAKNDAEDPLYSSYPFEYNNNEPISMDSNKYANS--LNKEFPKAPKQVFKKAHV----PCLFSIISCW----K
AstC_Lgig  --SSNDRLLKRSTLQDAYESH LAMLMEAEQSLTK--QIEELKLRREELSNRKRSHV----MCLVNLISCF----RKR
AstC_Cgig  --ESSTDLNLFKMALREAYNRELEFYEQQEAQIVK--QLAALENDRNQIRERKRSHI----RCLVNVIIACY----RKK
AstC_Acal  ---QLLPGKIGRASLLREMERQLMILQAAEENIVS--GLQEELEERRVLSGRKRSHY---SSMOMFNVVACY---RKRK
AstC_Dpul  LGAVPDDGGSVETALLNYLFAKQIVARLRTNAN----PQDLMRKRSY-----WKQCAFNAVSCF----GK
AstC_Tcas  VGEPADGNNLLDSRLK-PWELEMLVQRLSEISSQT--GGDFAWDKSIRLPEAKRQSR---YRQCYFNPIISCF----RK
Ast-C_Dmel IYPNIPMDRLQMLFAQYRPTSYSAYLRSPTYGNVN--ELYRLPESKRQVR-----YRQCYFNPIISCF----RK
Ast-CC_Dmel TLLDYDFKDLNQINRATGETRRAGADRSQT----S--THSGSPAGSRRIQPSGSGGG-RAYWRCYFNNAVSCF~~~~~
AstC1_Cele -----SIARGYFAPQPVDDDNADNRPKR--GIDLLKRRVEIE-----RNRCLFFNPIITCY~~~~~
AstC2_Cele -----LQPMLALGSLTPSAAFRANMQQRERSPNTLFYMDGASKQYGDEIKDPYKRFKPCYYSPIQCL---IKRK
AstC3_Cele -----FVERELAQHVLKRELLRQDRQ--ELDRVRRASEKKS-----PRNCYFSPIQCL---FTRN
AstC4_Cele -----FDALAAKIEMLRPNRYWKRAHNIDTR--ALNQ-----FKNCYFSPIQCVLMERRRK
AstC5_Cele -----RLSNDALIRLLMRNRGTQ--TQLGLKRGVLVKKAEVERRSIDEDFSNCFLSPVQCM-LPSSRK
<- allatostatin C->

```

General references:

Petersen, T. N., Brunak S., et al. (2011). "SignalP 4.0: discriminating signal peptides from transmembrane regions." *Nat Methods* 8(10): 785-6.

Veenstra, JA. (2010). "Neurohormones and neuropeptides encoded by the genome of *Lottia gigantea*, with reference to other mollusks and insects." *Gen Comp Endocrinol.*167(1):86-103.

Veenstra, JA. (2011). "Neuropeptide evolution: neurohormones and neuropeptides predicted from the genomes of *Capitella teleta* and *Helobdella robusta*." *Gen Comp Endocrinol.*171(2):160-75.