Supplementary document: Multiple sequence alignment of Gryllus Bimaculatus neuropeptide and their candidate sequence

Adipokinetic hormone (AKH)

```
CLUSTAL format alignment by MAFFT FFT-NS-2 (v7.490)


AKH             ------------------------MSRGTLVLVLAGLLLNFASAQVNFSTGWGKRSGTQDG
4202_c0_g1_i2.m MWFTKGPQCTGSYSNFITDIVDIMSRGTLVLVLAGLLLTFASAQVNFSTGWGKRSGTQDG
4202_c0_g1_i1.m MWFTKGPQCTGSYSNFITDIVDIMSRGTLVLVLAGLLLTFASAQV---------------
4202_c0_g1_i3.m MWFTKGPQCTGSYSNFITDIVDIMSRGTLVLVLAGLLLTFASAQV---------------
                                         ***************.******

AKH             CNSSMDSLMYIYKLIQMEAQK---------
4202_c0_g1_i2.m CKSSMDSLMYIYKLIQMEAQKIIECEKFAN
4202_c0_g1_i1.m ------SSHAINQVLNNN------------
4202_c0_g1_i3.m ------SSHAINQVLNNN------------
                      *   * :::: :
```

AKH/Corazonin-related peptide (ACP)

```
CLUSTAL format alignment by MAFFT FFT-NS-1 (v7.490)


AKH/Corazonin-r MASWGRPLGRALLCGAAVLLVLACAARAQITFSRDWNAGKRAGPAPGPAPAPPLADQCGP
11870_c1_g1_i1. MASWGRPLGRALLCGAAVLLVLACAARAQITFSRDWNAGKRAGPAPGPAPAPPLGDQCGP
                ******************************************************.*****

AKH/Corazonin-r VAKSASALCQMLLSEIRQMASCELRSLLHYSSDENSNPSDLFMDLHGRR
11870_c1_g1_i1. VAKSASALCQMLLSEIRQMASCELRSLLHYSSDENSNPSDLFMDLHGRR
                **************************************************
```

Allatotropin

```
CLUSTAL format alignment by MAFFT FFT-NS-2 (v7.490)


Allatotropin    -------------------------------YQGRSKPRTIRGFKNVALSTARGFGKRAG
12736_c4_g1_i1. PTMRRPCVSSMCAAAALLCLLACVAGGASAGYQGRSKPRTIRGFKNVALSTARGFGKRAG
12736_c2_g1_i1. --MRRPCVSSMCAAAALLCLLACVAGGASAGYQGRSKPRTIRGFKNVALSTARGFGKRAG
                                             ****************************

Allatotropin    GA-AAAQGPGEAVPASALDLLAAAPPAAADAFAQHDSFPVEWFVEEMQSNPELARVIVHK
12736_c4_g1_i1. GA-AAAQGPGEAVPASALDLLAAAPPAAADAFAQHDSFPVEWFVEEMQSNPELARVIVHK
12736_c2_g1_i1. GGVTAAQGPGEAVPASALDLLAAAPPAAADAFAQHDSFPVEWFVEEMQSNPELARVIVHK
                *. :*******************************************************

Allatotropin    FVDANQDGELSPEELLRPLY
12736_c4_g1_i1. FVDANQDGELSPEELLRPLY
12736_c2_g1_i1. FVDANQDGELSPEELLRPLY
                ********************
```

Allatostatin A (Ast A)

```
CLUSTAL format alignment by MAFFT FFT-NS-2 (v7.490)


Allatostatin    ALLGGAAPGVSASDAAAAQEAAGELLERLENEAGSGATPDDELEFYKRLYDFGVGKRAYS
797_c0_g1_i3.p1 ------------------------------------------------------------
797_c0_g1_i5.p1 ------------------------------------------------------------
GBI_04463-RA    ------------------------------------------------------------


Allatostatin    YVSEYKRLPVYNFGLGKRAGGRQYGFGLGKRAGGRQYGFGLGKRTPGDEDDYYFPDEEEE
797_c0_g1_i3.p1 YVSEYKRLPVYNFGLGKRAGGRQYGFGLGKRAGGRQYGFGLGKRTPGDEDDYYFPDEEEE
797_c0_g1_i5.p1 YVSEYKRLPVYNFGLGKRAGGRQYGFGLGKRAGGRQYGFGLGKRTPGDEDDYYFPDEEEE
GBI_04463-RA    ------------------------------------------------------------


Allatostatin    DVPEDNLEDSDSVDKRDRLYSFGLGKRSRPFGFGLGKRAGMYSFGLGKRAQHQYSFGLGK
797_c0_g1_i3.p1 DVPEDNFEDSDSVDKRDRLYSFGLGKRSRPFGFGLGKRAGMYSFGLGKRAQHQYSFGLGK
797_c0_g1_i5.p1 DVPEDNFEDSDSVDKRDRLYSFGLGKRSRPFGFGLGKRAGMYSFGLGKRAQHQYSFGLGK
GBI_04463-RA    ----------------------------------------MYSFGLGKRAQHQYSFGLGK
                                                        ********************

Allatostatin    RGEGRMYSFGLGKRPNYERMAGSRFNFGLGKRADANPAYLLSDLGEEKRGPDHRFAFGLG
797_c0_g1_i3.p1 RGEGRMYSFGLGKRPNYERMAGSRFNFGLGKRADANPAYLLSDLGEEKRGPDHRFAFGLG
797_c0_g1_i5.p1 RGEGRMYSFGLGKRPNYERMAGSRFNFGLGKRADANPAYLLSDLGEEKRGPDHRFAFGLG
GBI_04463-RA    RGEGRMYSFGLGKRPNYERMAGSRFNFGLGKRADANPAYLLSDLGEEKRGPDHRFAFGLG
                ************************************************************

Allatostatin    KREVSPNELEAVREEQLHHDQEAQQHELAEAAPAPEREPNDAHANGKHAVKRSLHYGFGI
797_c0_g1_i3.p1 KREVSPNELEAVREEQLHHDKEAQQHELAEAAPAPEREPNDAHANGKHAVKRSLHYGFGI
797_c0_g1_i5.p1 KREVSPNELEAVREEQLHHDKEAQQHELAEAAPAPEREPNDAHANGKHAVKRSLHYGFGI
GBI_04463-RA    KREVSPNELEAVREEQLHHDQEAQQHELAEAAPAPERQPNDAHANGKHAVKRSLHYGFGI
                ********************:***************:**********************

Allatostatin    GKRTSDAFGLDVDPEEDDRDAISEDFTRYIRRPYSFGLGKRVPMYDFGIGKRADR
797_c0_g1_i3.p1 GKRTSDAFGLDVEPEEDDRDAISEDFTRYIRRPYSFGLGKRVPMYDFGIGKRADR
797_c0_g1_i5.p1 GKRTSDAFGLDVDPEEDDRDAISEDFTRYIRRPYSFGLGKRVPMYDFGIGKRADR
GBI_04463-RA    GKRTSDAFGLDVEPEEDDRDAISEDFTRYIRRPYSFGLGKRVPMYDFGIGKRADR
                ************:***********************************
```

Allatostatin B (Ast B)

```
CLUSTAL format alignment by MAFFT FFT-NS-2 (v7.490)


ASTB_tsukamoto  -----MLPSAAAAGVLGLLLLAWAGPSCQGDPLPEGQSPSGAVAP----ASGPAAGPAPS
STRG.5257.1.p1  SPPHTMLPSAAAAGVLGLLLLAWAGPSCQGDPLPEGQSPSGAVAP----ASGPAAGPAPS
GBI_04462-RA    ---------------MGL------------------HPPTPPFVPHYHHRSTTHAPPRPK
                               :**                  :.*: ...*     * . * * *.

ASTB_tsukamoto  DSVVAADDDKRAWRDLSGGWGKRAWNNLGSAWGKRGWRDLNGGWGKRGWQDLNGGWGKRG
STRG.5257.1.p1  DSVVAADEDKRAWRDLSGGWGKRAWNNLGSAWGKRGWRDLNGGWGKRGWQDLNGGWGKRG
GBI_04462-RA    ------------------------------------------------------------


ASTB_tsukamoto  WQNLQGSWGKRAWDQLRPGWGKRAWERFHGSWGKRDGVGAGAAGDELSGEGALDLGLADP
STRG.5257.1.p1  WQNLQGSWGKRAWDQLRPGWGKRAWERFHGSWGKRDGVGAGAAGDELSGEGALDLGLADP
GBI_04462-RA    ------------------------------------------------------------


ASTB_tsukamoto  AAAAALEAEAEAEVARALGLDEDTASPSAAAAAAALLAAEGGSAPLQLAALGDAGPEREI
STRG.5257.1.p1  AAAAALEAEAEAEVARALGLDEDTASPSAAAAAAALLAAEGGSAPLQLAALGDAGPEREI
GBI_04462-RA    ------------------------ASPSAAAAAAALLAAEGGSAPLQLAALGDAGPEREI
                                         ************************************
```

```
ASTB_tsukamoto  EGQYEDKRAWKNLGSAWGKRGDWASFRG----------SWGKRDPGWNNLKGLWGKRVEA
STRG.5257.1.p1  EGQYEDKRAWKNLGSAWGKRGDWASFRG----------SWGKRDPGWNNLKGLWGKRVEA
GBI_04462-RA    EGQYEDKRAWKNLGSAWGKRGDWASFRGIHIPILPLAAAEAEEAEAVEVVEAVEARSERA
                ****************************          : .:.  . : ::.: .:  .*

ASTB_tsukamoto  NKWNRLSAVWGKRSVGDASGMKEEPATSSAEE
STRG.5257.1.p1  NKWNRLSAVWGKRSVGDASGMKEEPATSSAEE
GBI_04462-RA    SAWRLLQ----------GRGASETLAGTT---
                . *. *.          . * .*  * ::
```

Allatostatin C (Ast C)

```
CLUSTAL format alignment by MAFFT FFT-NS-2 (v7.490)


Allatostatin    -------------------------------------------------------GNAAD
STRG.23460.2.p1 ---------------MNPAKKGSVWSQTNIVKSLQAG-----EGGQTNTKRSIEKGNAAD
STRG.23460.1.p1 ---------------MNPAKKGSVWSQTNIVKSLQAG-----EGGQTNTKRSIEKGNAAD
STRG.23460.4.p1 LIHSLSFSPLPMAQRMDCSRRYKRLVHSFAFLALLAALLILQSSAMENEISSILKGNAAD
                                                                     *****

Allatostatin    RTLEYVNEDTHLDFNRKPYRLQEQSQYPSPEGQTSNEEWQSYNSLLPRFISTAAVKRQIR
STRG.23460.2.p1 RTLEYVNEDTHLDFNRKPYRLQEQSQYPSPEGQTSNEEWQSYNSLLPRFISTAAVKRQIR
STRG.23460.1.p1 RTLEYVNEDTHLDFNRKPYRLQEQSQYPSPEGQTSNEEWQSYNSLLPRFISTAAVKRQIR
STRG.23460.4.p1 RTLEYVNEDTHLDFNRKPYRLQEQSQYPSPEGQTSNEEWQSYNSLLPRFISTAAVKRQIR
                ************************************************************

Allatostatin    FHQCYFNPISCFKKRNKIQVQRNEIKQKPAHQHEN
STRG.23460.2.p1 FHQCYFNPISCFKKRNKI-----------------
STRG.23460.1.p1 FHQCYFNPISCFKKRNKI-----------------
STRG.23460.4.p1 FHQCYFNPISCFKKRNKI-----------------
                ******************
```

Allatostatin CC (Ast CC)

```
CLUSTAL format alignment by MAFFT FFT-NS-2 (v7.490)


Allatostatin    ------------------------------------------------RFDEYPVVVPKRT
78939_c0_g1_i1. ---------AAAAAAAAPAGGAPLDIDKRSVSAATADFGASDYPDYQRFDEYPVVVPKRT
82217_c0_g1_i1. AASTALVAPAAAAAAAAPAGGAPLDIDKRSVSAATADFGASDYPDYQRFDEYPVVVPKRT
                                                             *************

Allatostatin    AMLLDRIMTELQHAMGEGGSAAGGGSAGPSSSKAPVVDLPDTMDLQRRGQQKGSRVYWRC
78939_c0_g1_i1. AMLLDRIMTELQHAMGEGGSAAGGGSAGPSSSKAPVVDLPDTMDLQRRGQQKGSRVYWRC
82217_c0_g1_i1. AMLLDRIMTELQHAMGEGGSAAGGGSAGPSSSKAPVVDLPDTMDLQRRGQQKGSRVYWRC
                ************************************************************

Allatostatin    YFNAVTCFRRK
78939_c0_g1_i1. YFNAVTCFRRK
82217_c0_g1_i1. YFNAVTCFRRK
                ***********
```

Allatostatin CCC (Ast CCC)

```
CLUSTAL format alignment by MAFFT FFT-NS-2 (v7.490)


Allatostatin    PAAEAAISPVIHAPAASLLQATPPQPQTPTLSRPPLPAPVIHAPAASLLQATPPQPQTPT
GBI_09174-RA    ------------------------------------------------------------
GBI_09174-RB    ------------------------------------------------------------


Allatostatin    LSRPPLPAPVPRRKLLALRSGKMAASAASSAGASAAAARASLALLLLLGALGWAAGKTLG
GBI_09174-RA    -----------------------MAASAASSAGASAAAARASLALLLLLGALGWAAGKTLG
GBI_09174-RB    -----------------------MAASAASSAGASAAAARASLALLLLLGALGWAAGKTLG
                                       **************************************

Allatostatin    SPADKERLLSELDQLVDDDGSVETALINYLFAKQVVNRLRSQMDVSDLQRKRSYWKQCAF
GBI_09174-RA    SPADKERLLSELDQLVDDDGSVETALINYLFAKQVVNRLRSQMDVSDLQRKRSYWKQCAF
GBI_09174-RB    SPADKERLLSELDQLVDDDGSVETALINYLFAKQVVNRLRSQMDVSDLQRKRSYWKQCAF
                ************************************************************

Allatostatin    NAVSCFGK
GBI_09174-RA    NAVSCFGK
GBI_09174-RB    NAVSCFGK
                ********
```

Bursicon-alpha

```
CLUSTAL format alignment by MAFFT FFT-NS-1 (v7.490)


Bursicon-alpha  MLHDKAVATVTLLFLGSCGILLTCALETTAPIADECQVTPVIHVLQYPGCVPKPIPSFAC
GBI_18108-RA    MLHDKAVATVTLLFLGSCGILLTCALETTAPIADECQVTPVIHVLQYPGCVPKPIPSFAC
                ************************************************************

Bursicon-alpha  TGRCSSYLQVSGSKIWQMERSCMCCQESGEREASVSLFCPKAKPGERKFRKVTTKAPLEC
GBI_18108-RA    TGRCSSYLQVSGSKIWQMERSCMCCQESGEREASVSLFCPKAKPGERKFRKVTTKAPLEC
                ************************************************************

Bursicon-alpha  MCRPCTGVEESAVIPQEIAGYADESTLTSHFRKSQ
GBI_18108-RA    MCRPCTGVEESAVIPQEIAGYADESTLTSHFRKSQ
                **********************************
```

Bursicon-beta

```
CLUSTAL format alignment by MAFFT FFT-NS-1 (v7.490)


Bmori_pburs     ------------------------------------------------------------
GBI_18109-RA    AGEGEVSPSPSQQLSAGEECETWLYKRTAAREAHHCYLSGDSVNIHKFSASGAAFGHHFI


Bmori_pburs     ----------MNIMITKIFFLVQLFYI---VVSKSSAEENCETVASEVHVTKEEYDEMGR
GBI_18109-RA    THYQASSMSQSSVMVLTAFVILHMTGIANHVYANSDNPEACETLPSEIHLIKEEFDELGR
                           .:*: . *.::::  *   * ::*.  * ***:.**:*: ***:**:**

Bmori_pburs     LLRSCSGEVSVNKCEGMCNSQVHPSISSPTGFQKECFCCREKFLRERLVTLTHCYDPDGI
GBI_18109-RA    LQRTCTSEVGVNKCEGACNSQVQPSVVTPTGFLKECYCCRESFLRERTITLTHCYNPDGV
                * *:*:.**.****** *****:**: :**** ***:****.***** :******:***:

Bmori_pburs     RFEDEENALMEVRLREPDECECYKCGDFSR
GBI_18109-RA    RLVQEGQATMDIKLREPAECKCYKCGDFSR
                *: :* :* *:::**** **:*********
```

CAPA

```
CLUSTAL format alignment by MAFFT FFT-NS-1 (v7.490)


CAPA            MNEAAACVALAMLVFLSACHGTGAFKAFPRVGRSGDLTWDYENDALKPKRQAGLFPFPRV
GBI_04457-RB    MNEAAACVALAMLVFLSACHGTGAFKAFPRVGRSGDLTWDYENDALKPKRQAGLFPFPRV
                ************************************************************

CAPA            GRSGDLTWEFA-------------PEGKRQG----------LIPFPRVGRSGPAGAAAAA
GBI_04457-RB    GRSGDLTWEFAPGAPGYVCPTCFGPRGRVSGAPPDSLRVENVVPSRRIASQSNAGEGKRQ
                ***********             *.*: .*          ::*  *:. .. ** .

CAPA            GLIPFPRVGRSGPAGAAAAA
GBI_04457-RB    GLIPF-RAWRVGPAGRRRRR
                ***** *. * ****
```

Crustacean cardioactive peptide (CCAP)

```
CLUSTAL format alignment by MAFFT FFT-NS-1 (v7.490)

CCAP            ------------------PLRGAPALRDPLASCGGVGRDRTPAAAAPAAPAPSDHAPRLH
GBI_09648-RA    MQLAQMLVGTSLLLALALPL-GAPSAAAAAA----------PAAAAPAAPAPSDHAPRLH
                                 ** ***:   . *          ******************

CCAP            KR----------------------QADPAELERLAAEPKRKRPFCNAFTGCGKKRADESL
GBI_09648-RA    KRVTDVKPSLVCLRPNAADLPLLQQADPAELERLAAEPKRKRPFCNAFTGCGKKRADESL
                **                      ***********************************

CCAP            GTLVELNSEPAVAELSRQILSEAKLWEAIQEARAELLRRRQQ-----QLQTNRIAADGPL
GBI_09648-RA    GTLVELNSEPAVAELSRQILSEAKLWEAIQEARAELLRRRQQQRAMLQLQTNRIAADGPL
                ****************************************     *************

CCAP            PLPLTSFRKRRAALAAPEAAPAAA------
GBI_09648-RA    PLPLTSFRKRRAALAAPEAAPAADAAPAPQ
                ***********************
```

CCHamide-1

```
CLUSTAL format alignment by MAFFT FFT-NS-1 (v7.490)


CCHamide-1      YLGGPSWLRLGQSAAARRVSHQPSRSPAPAAARMSAPATRGAAGGGAGGGGVGSLLSLPL
15771_c0_g2_i1. ------------SAAARRVSHQPSRSPAPAAARMSAPATRGAAGGGAGGGG-GSLLSLPL
                             ************************************** ********

CCHamide-1      LLLAALVLLAGPARGSCLSYGHSCWGAHGKRSGVGSVGGGX--------------------
15771_c0_g2_i1. LLLAALVLLAGPARGSCLSYGHSCWGAHGKRSGVGSVGGVGGVGAGASAAVGDAASAGRG
                **************************************

CCHamide-1      ------------------------------------------------------------
15771_c0_g2_i1. RGLLAAPEDARWVLSRVALPPPPDDVWRHLDARALRAAAAQAAAEAEAAAAAADDGGG
```

CCHamide-2

```
CLUSTAL format alignment by MAFFT FFT-NS-1 (v7.490)


CCHamide-2      GAAAAPAGSSASAATSSAASASSERFPWPPKHEWPNAEQPRLAAARGASAARRARAARRA
5060_c0_g3_i2.p ----------------------------------------RVAAGQ--------------
                                                        *:**.:

CCHamide-2      RAAGPRGRWAREGADQAMELLVLLLLLLLLLLVRQTPRRRRPAHTTPHHTPAAAGSSSSS
5060_c0_g3_i2.p ---------------------------------------------PTPHHTPAAG--SSSS
```

```
                                                        .********.  ****

CCHamide-2      SSSAPALHAPAPRPRRTSSSSTSSSMAWSAPSRAQRPRGPAALALLAALALLAADAPLAA
5060_c0_g3_i2.p SSSAPALHAPAPRPRRTSSSSTSSSMAWSAPSRAQRPRGPAALALLAALALLAADAPLAA
                ************************************************************

CCHamide-2      AKRGCSAFGHSCFGGHGKRSDEALAALDVAALAEEPAGAAAAADDX--------------
5060_c0_g3_i2.p AKRGCSAFGHSCFGGHGKRSDEALAALDVAALAEEPAGAAAAAADDAAAAAAAAASAAAA
                ****************************************** *
```

Corazonin

```
CLUSTAL format alignment by MAFFT FFT-NS-1 (v7.490)


Corazonin       CPAYEGSPTDAAYRHSSSFNISSASLTYLQNMLTWRCVLLLSLCCGTLLAQTFQYSRGWT
STRG.10676.1.p1 --------------HSSSFNISSASLTYLQNMLTWRCVLLLSLCCGTLLAQTFQYSRGWT
                               **********************************************

Corazonin       NGRKRAGSPVPPGAPGLCGRLQHQRLLLLLSGRATPELLVACGGWRGADLEDSAAPX---
STRG.10676.1.p1 NGRKRAGSPVPPGAPGLCGRLQHQRLLLLLSGRATPELLVACGGWRGADLEDSAAPEEYS
                *******************************************************

Corazonin       -----------------------
STRG.10676.1.p1 SLLRPRPDAAGFHDAPRADLEV
```

Diapause hormone (DH/PBAN-like peptide)

```
CLUSTAL format alignment by MAFFT FFT-NS-1 (v7.490)


Bmori_PBAN      -----------MYKTNIVFNVLAL-----ALFSIFFA------------------------
STRG.20898.1.p1 ATAADGRQCGKMFNAATTTRLLVLLHLGAAVLTAVQAAGPTAAASARAPAPPAKRAAGVD
                           *:::  . .:*.*     *::: . *

Bmori_PBAN      ------------SCTDMKDESD---------------------------------RGAHS
STRG.20898.1.p1 PADAPSRTPPVDATVDAEDTGDAADADGDDTQLSAPSRADVLLLLDRDAEKSPVKRDGAS
                             : .* :* .*                                 *.. *

Bmori_PBAN      ERGALWFGPRLGK---------------RSMKPSTEDNRQTFL------RLLEAADALKF
STRG.20898.1.p1 AAGGMWFGPRMGRASDDQNVSPGMWFGPRMGRAAGEDRNQASSGMWFGPRMGRATSA---
                  *.:*****:*:               *  :.: **..*:        *: .*:.*

Bmori_PBAN      YYDQLPY------------ERQADEPETKVTKKIIFTPKLGRS--------VAKPQTHE-
STRG.20898.1.p1 --EEQPFSPGMWFGPRMGRSTATDEQNRQLAAGMWFGPRMGRSGRVTAGAGDAARREHDL
                  :: *:            .  :** : :::  : * *::***         *  : *:

Bmori_PBAN      --SLEFIPRL------------GRRLSEDM-----PATPADQEIYQPD-----PEEMESR
STRG.20898.1.p1 SSGMWFGPRMGRSAAASGEALGGRRGADDVLLVFRRRQPADQ---APGAGLQRPQELAS-
                  .: * **:            *** ::*:        ****    *.     *:*: *

Bmori_PBAN      TRYFSPRLGRT----------------MSFSPRLGRELSYDYPTKYRVARSVNKTMDN
STRG.20898.1.p1 GMWFGPRMGRRRDADWAGKRGPDSPEGMWFGPRLG-----------------------
                  :*.**:**                 * *.****
```

Diuretic hormone 31 (CT/DH)

```
CLUSTAL format alignment by MAFFT FFT-NS-2 (v7.490)


Diuretic_hormon PPPTPTDARRRRSRPSSAMPSCSAMVSCALLLGVALLLAVSRSTHASPLSRYQSYLPAMD
STRG.10008.1.p1 ------------------MPSCSAMVSCALLLGVALLLAVSRSTHASPLSRYQSYLPAMD
STRG.10008.2.p1 ------------------MPSCSAMVSCALLLGVALLLAVSRSTHASPLSRYQSYLPAMD
                                  ****************************************
```

```
Diuretic_hormon PEPDSEYMLEMLARMARLGQSLITPNDVEN-KRALDLGLSRGFSGSQAAKHLMGLAAANY
STRG.10008.1.p1 PEPDSEYMLEMLARMARLGQSLITPNDVEN-KRALDLGLSRGFSGSQAAKHLMGLAAANY
STRG.10008.2.p1 PEPDSEYMLEMLARMARLGQSLITPNDVENSKRALDLGLSRGFSGSQAAKHLMGLAAANY
                ****************************** ****************************

Diuretic_hormon A------------
STRG.10008.1.p1 AGGPGRRRRSPAL
STRG.10008.2.p1 AGGPGRRRRSPAL
                *
```

Corticotropin releasing factor-like diuretic hormone (CRF/DH)

```
CLUSTAL format alignment by MAFFT FFT-NS-1 (v7.490)


Diuretic_hormon --------------PSQ------------WEASPAAAATALLLAPEDLDAQEALAARRVK
2611_c0_g1_i1.p DDDAVEAEAGAAGGPAEGAAPALLARLRAWEASPAAAATALLLAPEDLDAQEALAARRVK
                              *::            ******************************

Diuretic_hormon RTGAQSLSIVAPLDVLRQRLMNELNRRRMRELQGNRIQQNRQLLTSIGKRLDARLPPAVA
2611_c0_g1_i1.p RTGAQSLSIVAPLDVLRQRLMNELNRRRMRELQGNRIQQNRQLLTSIGKRLDARLPPAVA
                ************************************************************

Diuretic_hormon LWGSWDDRLAAEQA
2611_c0_g1_i1.p LWGSWDDRLAAEQA
                **************
```

Ecdysis triggering hormone (ETH)

```
CLUSTAL format alignment by MAFFT FFT-NS-1 (v7.490)


Ecdysis_trigger MATGNLGCLLVLLVLLAAVASADDSGPFFIKASKSVPRIGRRGDFYIKAASKSVPRMGKK
GBI_07130-RA    MATGNLGCLLVLLVLLAAVASADDSGPFFIKASKSVPRIGRRGDFYIKAASKSVPRMGKK
                ************************************************************

Ecdysis_trigger SEDGLLENSGATAPVENPKPVYLVRYARRGPAETPGAGSAVVPLNGKRDDPWGTEDLSWK
GBI_07130-RA    SEDGLLENSGATAPVENPKPVYLVRYARRGPAETPGAGSAVVPLNGKRDDPWGTEDLSWK
                ************************************************************

Ecdysis_trigger DIDRLMEERPDLWRRMLEAPAPPATGDADADAPWRRHFE-
GBI_07130-RA    DIDRLMEERPDLWRRMLEAPAPPATGDADADAPWRRHFEE
                ****************************************
```

Eclosion hormone

```
CLUSTAL format alignment by MAFFT FFT-NS-1 (v7.490)


Eclosion_hormon -------------------------MAPLLSRSGLALAALLLLLAGLGAPGAHADPAAAA
GBI_03726-RA    PHIPQQLALRNRLSSAQSLLSRTPAMAPLLSRSGLALAALLLLLAGLGAPGAHADPAAAA
                                         ***********************************

Eclosion_hormon AVGLCVRNCAQCKKMFGPYFEGQLCADSCVKFKGKLVPDCEDFASIAPFFNKLE
GBI_03726-RA    AVGLCVRNCAQCKKMFGPYFEGQLCADSCVKFKGKLVPDCEDFASIAPFFNKLE
                ******************************************************
```

Elevenin

```
CLUSTAL format alignment by MAFFT FFT-NS-2 (v7.490)


Elevenin        ------------------------------------------------------------
STRG.16982.3.p3 ------------------------------------------------------------
STRG.16982.1.p1 FNRARPRLHLLIPRAFIMKRTAPTAPEQSLSAAATASPGRRAWVAAGAAAQPAPEALRAA
STRG.16982.2.p3 ------------------RR------------GAEGSGVRRTREISTQTSFP---ILKAA


Elevenin        --MAPPCRRSSPRPRRRSRPAPAALLLALLAACTVAAEAAKRVDCRKFVFAPMCRGVAAK
STRG.16982.3.p3 --MAPPCRRSSPRPRRRSRPAPAALLLALLAACTVAAEAAKRVDCRKFVFAPMCRGVAAK
STRG.16982.1.p1 ISMAPPCRRSSPRPRRRSRPAPAALLLALLAACTVAAEAAKRVDCRKFVFAPMCRGVAAK
STRG.16982.2.p3 ISMAPPCRRSSPRPRRRSRPAPAALLLALLAACTVAAEAAKRVDCRKFVFAPMCRGVAAK
                  ************************************************************

Elevenin        RASAPVLLPDAARSQLGTLEQVLGLGTVPPPPGAGPGDLVWGPPEPPRRTQQQALYDLLA
STRG.16982.3.p3 RASAPVLLPDAARSQLGTLEQVLGLGTVPPPPGAGPGDLVWGPPEPPRRTQQQALYDLLA
STRG.16982.1.p1 RASAPVLLPDAARSQLGTLEQVLGLGTVPPPPGAGPGDLVWGPPEPPRRTQQQALYDLLA
STRG.16982.2.p3 RASAPVLLPDAARSQLGTLEQVLGLGTVPPPPGAGPGDLVWGPPEPPRRTQQQALYDLLA
                ************************************************************

Elevenin        AAAVAPATSPGDYDY
STRG.16982.3.p3 AAAVAPATSPGDYDY
STRG.16982.1.p1 AAAVAPATSPGDYDY
STRG.16982.2.p3 AAAVAPATSPGDYDY
                ***************
```

EFLamide: Not detected

FMRFamide

```
CLUSTAL format alignment by MAFFT FFT-NS-1 (v7.490)


FMRFamide       ----------------------------------------APSASPGQLPPSPGLGDRED
GBI_14002-RA    MSLRKGAPPPPWRLLPVALLAAACALAAAASDGAGAAPDAAPSASPGQLPPSPGLGDRED
                                                        ********************

FMRFamide       DDAAGDADAALDELLLPRQGRAARDNFLRFGKAARDNFLRFGRAPRDNFLRF--------
GBI_14002-RA    DDAAGDADAALDELLLPRQGRAARDNFLRFGKAARDNFLRFGRAPRDNFLRFGKASRDNF
                **************************************************

FMRFamide       ------------------------------------------------------------
GBI_14002-RA    LRFGRAPRDNFVRAASNFFRLGRPDPDAQVSLEEEALAARLAREDGEADSEAEAEADGLG


FMRFamide       ------------------------------------------------------------
GBI_14002-RA    AEEEPSLERLLRFARDRNFLRFGRGRPDNFVRFGRGGDDGSGDDDNDDRDGSQAPTHLGQ


FMRFamide       ------------------------------------------------------------
GBI_14002-RA    EEAAAAAAASAAAVAAAAEAESEASTEGARAAEEGAEAADEHLQRVGRAARTRNLFGRWK


FMRFamide       ------------------------------------------------------------
GBI_14002-RA    MADLNFIRLGRSASAGAAGPAGALLPAPAKRSGTPPRPGRSQVGRTAGHVDNFLRLGNGK


FMRFamide       ------------------------------------------------------------
GBI_14002-RA    RAKRSAGASARPACAPRRPASLLGDLPLAPLTYYSPLAVGLPNYLLAPELGLLPAAAAAA

FMRFamide       ------------------
GBI_14002-RA    PAKRGPADRQGSNFIRLG
```

Glycoprotein hormone subunit A2 (GPA2)

```
CLUSTAL format alignment by MAFFT FFT-NS-2 (v7.490)


Bmori_gpa       -----------------MLLRFIVTLMFLCQIF--AAESWRKPGCHRIGHTRNISIPDCV
STRG.7443.1.p1  MTTTTTTTVAAAAGGAPRRLLLVASALLLGAVLADARDPWQRPGCHMIGHTRTVSIPDCV
STRG.7443.2.p1  MTTTTTTTVAAAAGGAPRRLLLVASALLLGAVLADARDPWQRPGCHMIGHTRTVSIPDCV
STRG.7443.4.p1  MTTTTTTTVAAAAGGAPRRLLLVASALLLGAVLADARDPWQRPGCHMIGHTRTVSIPDCV
                                  * ::.: ::*  ::  * :.*::**** *****.:******

Bmori_gpa       EFKITTNACRGYCESWSLPSIMLGFKRHP---VTSLGQCCNIMEAEDVPVKVLCLDGERN
STRG.7443.1.p1  QFDVETNACRGYCESWAVPSAPNTLRINPHQAITSVGQCCNMMETEDVEVRVMCLGGPRD
STRG.7443.2.p1  QFDVETNACRGYCESWAVPSAPNTLRINPHQAITSVGQCCNMMETEDVEVRVMCLGGPRD
STRG.7443.4.p1  QFDVETNACRGYCESWAVPSAPNTLRINPHQAITSVGQCCNMMETEDVEVRVMCLGGPRD
                :*.: ***********::**    :: :*   :**:*****:**:*** *:*:**.* *:

Bmori_gpa       LIFKSAVSCACYHCQKE
STRG.7443.1.p1  LVFKSAKSCSCYHCKKE
STRG.7443.2.p1  LVFKSAKSCSCYHCKKE
STRG.7443.4.p1  LVFKSAKSCSCYHCKKE
                *:**** **:****:**
```

Glycoprotein hormone subunit B5 (GPB5)

```
CLUSTAL format alignment by MAFFT FFT-NS-1 (v7.490)


Bmori_gpb  BAG  MLNKINRLSMMTVGLMACICWAFFCVDASMSVRCKLKRHSHKVMQTDLNSRRCWDDVKIV
STRG.8674.2.p1  -------------------------------------KYSYKVVKADSAGRQCWDLVGVN
                                                     ::*:**:::*  .*:*** * :

Bmori_gpb  BAG  SCWGYCLSYEISDWQFPYKESHHPVCVHGERRHASVKLRNCDPGVEPGTEIYHYVEAVNC
STRG.8674.2.p1  ACWGRCDSREISDWRFPNKRAYHPVCLHAAREASAVTLRHCDPDAEPGTERYEFMQALSC
                :*** * * *****:** *.::****:*. *. ::*.**:***..***** *.:::*:.*

Bmori_gpb  BAG  RCQVCSSEDTSCE-------WLPPDSSLLGGLILKEELEEELE-----------------
STRG.8674.2.p1  RCSVCKSSEASCESARFKXXXXXPSTEL--HRLLHRSLQLSLSCFVSSLALHARSKCPHS
                **.**.*.::***          *.:.*    :*:..*: .*.

Bmori_gpb  BAG  ---------------------------
STRG.8674.2.p1  LRSTSVLRGHRALALVFLFAHLFTSPQ
```

Insulin-like peptide

```
CLUSTAL format alignment by MAFFT FFT-NS-1 (v7.490)


Insulin-like_pe MWTVCLRLLLLTAVCLCVITHAQRDIFHAQTDIFQVPKRGNEVRLCGRYLSNMLHVVCNG
GBI_11105-RA    MWAVCLRLLLLTAVCLCVITHAQRDIFHAQTDIFQVPKRGNEVRLCGRYLSNMLHVVCNG
                **:*********************************************************

Insulin-like_pe LYNPMFKKAEKEPEPEFWLNEPASVEEQLPYPLKSLPKASSFLRSSNRQKRQGIYDECCR
GBI_11105-RA    LYNPMFKKAEKEPEPEFWLNEPASVEEQLPYPLKSLPKASSFLRSSNRQKRQGIYDECCR
                ************************************************************

Insulin-like_pe KSCAIAELRSYCAGS
GBI_11105-RA    KSCAIAELRSYCAGS
                ***************
```

Ion transport peptide (ITP) & Ion transport peptide-like (ITP-L)

```
CLUSTAL format alignment by MAFFT FFT-NS-2 (v7.490)


Ion_transport_p ----MR--------------------------------------RHS-------------
GBI_18262-RF    MSVGMRCLTVLFFGPFSEGFVAELSCIVIAVAEECLLVCSSVHARHSYVNEYSLSRRFYR
GBI_18262-RE    MSVGMRCLTVLFFGPFSEGFVAELSCIVIAVAEECLLVCSSVHARHSYVNEYSLSRRFYR
GBI_18262-RH    MSVGMRCLTVLFFGPFSEGFVAELSCIVIAVAEECLLVCSSVHARHSYVNEYSLSRRFYR
GBI_18262-RG    MSVGMRCLTVLFFGPFSEGFVAELSCIVIAVAEECLLVCSSVHARHSYVNEYSLSRRFYR
                    **                                      ***

Ion_transport_p ------------------------------------------------------------
GBI_18262-RF    ISRARTSKLSECKFGLQSLERSLEDVTALGTVFTQRVLRNVSWATRAVAAASRCAQLAAR
GBI_18262-RE    ISRARTSKLSECKFGLQSLERSLEDVTALGTVFTQRVLRNVSWATRAVAAASRCAQLAAR
GBI_18262-RH    ISRARTSKLSECKFGLQSLERSLEDVTALGTVFTQRVLRNVSWATRAVAAASRCAQLAAR
GBI_18262-RG    ISRARTSKLSECKFGLQSLERSLEDVTALGTVFTQRVLRNVSWATRAVAAASRCAQLAAR


Ion_transport_p -------------------------------------------------SLRSASLGAALA
GBI_18262-RF    GGGASGRTLESKLHIPVGCGQSSTRCSDGAEQCSSVLQIHHPSCYLPAAASSATAAAASA
GBI_18262-RE    GGGASGRTLESKLHIPVGCGQSSTRCSDGAEQCSSVLQIHHPSCYLPAAASSATAAAASA
GBI_18262-RH    GGGASGRTLESKLHIPVGCGQSSTRCSDGAEQCSSVLQIHHPSCYLPAAASSATAAAASA
GBI_18262-RG    GGGASGRTLESKLHIPVGCGQSSTRCSDGAEQCSSVLQIHHPSCYLPAAASSATAAAASA
                                                            :  **: .** *

Ion_transport_p LLALAALGALA-------------------------------------------------
GBI_18262-RF    SAAAAASAASAAAPPPSPPRAVPRQRCSRQSAAARRLGRWAERGEAALIYEQRRPWSHKI
GBI_18262-RE    SAAAAASAASAAAPPPSPPRAVPRQRCSRQSAAARRLGRWAERGEAALIYEQRRPWSHKI
GBI_18262-RH    SAAAAASAASAAAPPPSPPRAVPRQRCSRQSAAARRLGRWAERGEAALIYEQRRPWSHKI
GBI_18262-RG    SAAAAASAASAAAPPPSPPRAVPRQRCSRQSAAARRLGRWAERGEAALIYEQRRPWSHKI
                  * ** .* *

Ion_transport_p ------------------------------------------------------------
GBI_18262-RF    RALRAARHHLRRSCSAAVRSAPPALRRPDESPPPVHLCSLRAGQSAAVCVRAPVPPVLVW
GBI_18262-RE    RALRAARHHLRRSCSAAVRSAPPALRRPDESPPPVHLCSLRAGQSAAVCVRAPVPPVLVW
GBI_18262-RH    RALRAARHHLRRSCSAAVRSAPPALRRPDESPPPVHLCSLRAGQSAAVCVRAPVPPVLVW
GBI_18262-RG    RALRAARHHLRRSCSAAVRSAPPALRRPDESPPPVHLCSLRAGQSAAVCVRAPVPPVLVW


Ion_transport_p ------------------------------------------------------------
GBI_18262-RF    VAVAVSSPVLSVRSACSSFASVSVCLSSGRFHRNDAPPLVVLSRGGGWGGARAAGAGRPG
GBI_18262-RE    VAVAVSSPVLSVRSACSSFASVSVCLSSGRFHRNDAPPLVVLSRGGGWGGARAAGAGRPG
GBI_18262-RH    VAVAVSSPVLSVRSACSSFASVSVCLSSGRFHRNDAPPLVVLSRGGGWGGARAAGAGRPG
GBI_18262-RG    VAVAVSSPVLSVRSACSSFASVSVCLSSGRFHRNDAPPLVVLSRGGGWGGARAAGAGRPG


Ion_transport_p ----LAGRAAAGPTLAHPLSKRSFFDLQCKGVYDKSIFARLDRICEDCYNLFREPQLHSL
GBI_18262-RF    RWRQLAGRAAAGPTLAHPLSKRSFFDLQCKGVYDKSIFARLDRICEDCYNLFREPQLHSL
GBI_18262-RE    RWRQLAGRAAAGPTLAHPLSKRSFFDLQCKGVYDKSIFARLDRICEDCYNLFREPQLHSL
GBI_18262-RH    RWRQLAGRAAAGPTLAHPLSKRSFFDLQCKGVYDKSIFARLDRICEDCYNLFREPQLHSL
GBI_18262-RG    RWRQLAGRAAAGPTLAHPLSKRSFFDLQCKGVYDKSIFARLDRICEDCYNLFREPQLHSL
                    ******************************************************

Ion_transport_p C------------------------------------------------------------
GBI_18262-RF    CRSKCFTSPYFKGCIEALLLNEDEENLTQMEMDPILLQKQVRDNADELNSFLKELKSWEK
GBI_18262-RE    CR-------------------------IMQEMDPILLQKQVRDNADELNSFLKELKSWEK
GBI_18262-RH    CRKNCFTTDYFKGC-----------------LDVLLLQ-------DEMD----KIQTW--
GBI_18262-RG    CR-------------------------------------------------------
                *

Ion_transport_p ------------------------------------------------------------
GBI_18262-RF    DMKRKDQELINSATESVAVPPVRSKIKRKKVTDNSDKSPVVNEVKRISSYDYTAWDKFDV
GBI_18262-RE    DMKRKDQELINSATESVAVPPVRSKIKRKKVTDNSDKSPVVNEVKRISSYDYTAWDKFDV
GBI_18262-RH    ------------------------------------------------------------
GBI_18262-RG    ------------------------------------------------------------
```

```
Ion_transport_p ------------------------------------------------------------
GBI_18262-RF    EKACAEIDSKKKESEETDSETEEDLANGDVAQLKEQALYEKELGNQHVKEKRWKDAIDCY
GBI_18262-RE    EKACAEIDSKKKESEETDSETEEDLANGDVAQLKEQALYEKELGNQHVKEKRWKDAIDCY
GBI_18262-RH    ------------------------------------------------------------
GBI_18262-RG    ------------------------------------------------------------


Ion_transport_p ------------------------------------------------------------
GBI_18262-RF    SKAILYNPHDAIFYANRALCYLKTKRAKLAETDCTTALQLDSTYVKAYQRRALARIEIGL
GBI_18262-RE    SKAILYNPHDAIFYANRALCYLKTKRAKLAETDCTTALQLDSTYVKAYQRRALARIEIGL
GBI_18262-RH    ------------------------------------------------------------
GBI_18262-RG    ------------------------------------------------------------


Ion_transport_p ------------------------------------------------------------
GBI_18262-RF    KDDAKADFEKVLEFEPNNSAAKSELIKLEKQGSSAIKTRVKETKKNVERSESDQNIRKDY
GBI_18262-RE    KDDAKADFEKVLEFEPNNSAAKSELIKLEKQGSSAIKTRVKETKKNVERSESDQNIRKDY
GBI_18262-RH    ------------------------------------------------------------
GBI_18262-RG    ------------------------------------------------------------


Ion_transport_p ------------------------------------------------------------
GBI_18262-RF    SVLKEKSCSTSTTEEISVCTKRVGGAPDILGGGGDTGTVKVPCSFLQEGDEDIVPRPLRV
GBI_18262-RE    SVLKEKSCSTSTTEEISVCTKRVGGAPDILGGGGDTGTVKVPCSFLQEGDEDIVPRPLRV
GBI_18262-RH    --IKQSKCFTS-----------------------------------------------
GBI_18262-RG    -----SKCFTS-----------------------------------------------

Ion_transport_p ------------------------------------------------------------
GBI_18262-RF    VPVQEVETIGDLLKKNSKPKEMLDNSPKPKIVELESEATVTESVSVTEQISLPTSSAPAI
GBI_18262-RE    VPVQEVETIGDLLKKNSKPKEMLDNSPKPKIVELESEATVTESVSVTEQISLPTSSAPAI
GBI_18262-RH    ------------------------------------------------------------
GBI_18262-RG    ------------------------------------------------------------


Ion_transport_p ------------------------------------------------------------
GBI_18262-RF    KASVMKETKHQDTKSSELQTSNNKVDLPPVPKTSVQFLVSWKIVRYNSELRHQFLKQIPG
GBI_18262-RE    KASVMKETKHQDTKSSELQTSNNKVDLPPVPKTSVQFLVSWKIVRYNSELRHQFLKQIPG
GBI_18262-RH    ------------------------------------------------------------
GBI_18262-RG    ------------------------------------------------------------


Ion_transport_p ------------------------------------------------------------
GBI_18262-RF    NEFPQIFQESLESREFSEIISTLATEFLEKNDPVYPYLKGLSEVKRFSALVMFMSKTEKQ
GBI_18262-RE    NEFPQIFQESLESREFSEIISTLATEFLEKNDPVYPYLKGLSEVKRFSALVMFMSKTEKQ
GBI_18262-RH    -----------------------------------PYFKGCIE-----ALLL--------
GBI_18262-RG    -----------------------------------PYFKGCIE-----ALLL--------


Ion_transport_p ---------------------------------------------
GBI_18262-RF    VIKKLLQSCAENEECSKEDIAYLLKCYEINNVIASNRKSQQECYL
GBI_18262-RE    VIKKLLQSCAENEECSKEDIAYLLKCYEINNVIASNRKSQQECYL
GBI_18262-RH    ---------NEDEENLTQMVDFIGK--------------------
GBI_18262-RG    ---------NEDEENLTQMVDFIGK--------------------
```

Kinin (Leucokinin)

```
CLUSTAL format alignment by MAFFT FFT-NS-2 (v7.490)


Kinin           RDWRPCALPWAVAAGLAAAAAASDPDDEVLPGPDAVDLREAKRNFKFNPWGGKREQLPAA
110628_c0_g1_i1 ---------------LAAAAAASDPDDEVLPGPDAVDLREAKRNFKFNPWGGKREQLPAA
STRG.7466.1.p1  ---------------------------------DAVDLREAKRNFKFNPWGGKREQLPAA
                                                 ***************************
```

```
Kinin           KPRKAYFSPWGGKRSLPFSSWGGKRADSPASGPGAEDLPGDEDEQQAVGKRAFHSWGGKR
110628_c0_g1_i1 KPRKAYFSPWGGKRSLPFSSWGGKRADSPASGPGAEDLPGDEDEQQAVGKRAFHSWGGKR
STRG.7466.1.p1  KPRKAYFSPWGGKRSLPFSSWGGKRADSPASGPGAEDLPGDEDEQQAVGKRAFHSWGGKR
                ************************************************************

Kinin           VPEDAPAAAPDDALALFLEDGDDADAKRVFHSWGGKRRAEDGPRLAKRKTKFYPWGGKRA
110628_c0_g1_i1 VPEDAPAAAPDDALALFLEDGDDADAKRAFHSWGGKRRAEDGPRLAKRKTKFYPWGGKRA
STRG.7466.1.p1  VPEDAPAAAPDDALALFLEDGDDADAKRAFHSWGGKRRAEDGPRLAKRKTKFYP------
                ****************************.************************

Kinin           AAEDAAADQTAADAGVLRRSGADFYPWGGKRAGPAV
110628_c0_g1_i1 AAEDAAADQTAADAGVLRRSGADFYPWGGKRAGPAV
STRG.7466.1.p1  -------------------------------------
```

Myosupressin

```
CLUSTAL format alignment by MAFFT FFT-NS-1 (v7.490)


myosupressin    ------------------------------------------------------------
DN4455_c0_g1_i4 PLVHRMQPHTSVVVAVAAALCALLLLGSAGPGAAAPHPCDPDNLMVAPSQLREMCAALYK


myosupressin    ------------EYDGPVIKRQDVDHVFLRFGRRR
DN4455_c0_g1_i4 LSSAMQVYLEDREYDGPVIKRQDVDHVFLRFGRRR
                            ***********************
```

Natalisin

```
# Protein
CLUSTAL format alignment by MAFFT FFT-NS-1 (v7.490)

Natalisin       ---DPFWVARGRRRRDGASSGSSFEEPFWAARGRRYWPQPRETSIEEPFWAARGRRAPSE
STRG.7468.1.p4  SPSGPPGGGAPRPRTRGAAGDALGSTPRAGAAAR-----------SSPWRSPSGPRADAE
                   .*   .  * *  **:..:  . *  .* .*           ..*: :. * ** :*

Natalisin       DAW----SR-------GRRAGVDAPRWRRRQVESVEEP-----------FWAARGRRGPA
STRG.7468.1.p4  DPLTPSPSRSPSGRPGGRRA-----RW----LSKTSCPRCEIVLLYYFILFVSRSR----
                *.     **       ****     **    :.... *           ::.:*.*

Natalisin       DSLSVEEPFWAARGKKGALAFQDLLSKVRNRFALLFHPLCLPQPL
STRG.7468.1.p4  ---SSEE---ARRSRR-----------------------------
                   * **   * *.::

# cDNA
CLUSTAL format alignment by MAFFT FFT-NS-1 (v7.490)

Natalisin       gacccgttctgggtggcgcgcggccggcggcggcgcgacggcgcctcctcgggcagctcc
STRG.7468.1.p4  ------------------------------------------------------------


Natalisin       ttcgaagagcccttctgggcggccaggggccgccgctactggccgcagccccgggagacg
STRG.7468.1.p4  ------------------------------------------------------------


Natalisin       tccatcgaggagcccttctgggccgccagggggcggcgcgccccgtccgaggacgcgtgg
STRG.7468.1.p4  ----------agcccttctgggccgccagggggcggcgcgccccgtccgaggacgcgtgg
                           ************************************************

Natalisin       agccgcgggcgacgcgctggggtcgacgccccgcgctggcgccgccgccaggtcgagtcc
STRG.7468.1.p4  agccgcgggcgacgcgctggggtcgacgccccgcgctggcgccgccgccaggtcgagtcc
                ************************************************************

Natalisin       gtggaggagcccttctgggccgcgcgcggacgccgaggacccgctgactccctctccgtc
STRG.7468.1.p4  gtggaggagcccttctgggccgcgcgcggacgccgaggacccgctgactccctctccgtc
                ************************************************************
```

```
Natalisin       gaggagcccttctgggcggcccgggggaagaagggcgcgctggctttccaagacctcttg
STRG.7468.1.p4  gaggagcccttctgggcggcccgggggaagaagggcgcgctggctttccaagacctcttg
                ************************************************************

Natalisin       tccaaggtgcgaaatcgttttgctttattatttcatcctctttgtctcccgcagccg---
STRG.7468.1.p4  tccaaggtgcgaaatcgttttgctttattatttcatcctctttgtctcccgcagccgttc
                *********************************************************

Natalisin       ctctgaagaagcgaggaggtcgcgaaggtagattttgtaatctctggaattgacgaagga
STRG.7468.1.p4  ctctgaagaagcgaggaggtcgcgaaggtagattttgtaatctctggaattgacgaagga
                ************************************************************

Natalisin       cccttctggaccaccgtgaacgaagcatgagcttgcagccgagacggacatcccatggat
STRG.7468.1.p4  cccttctggaccaccgtgaacgaagcatgagcttgcagccgagacggacaccccatggat
                ************************************************.*********

Natalisin       tttttctggacatctaattggaatcttattggaagtccaggagaaaggccaatttccagg
STRG.7468.1.p4  tttttctggacatctaattggaatcttattggaagtccaggagaaaggccaatttccagg
                ************************************************************

Natalisin       aaaatatgctgtctattatacaaaatttctttgatatttttagcttccaaaactgaccct
STRG.7468.1.p4  aaaatatgctgtctattatacaaaatttctttgatatttttagcttccaaaactgaccct
                ************************************************************

Natalisin       aagaacggcttgctggattggcaaggcaaatttatgttatctttagcatcctttctcaag
STRG.7468.1.p4  aagaacggcttgctggattggcaaggcaaatttatgttatctttagcattctttctcaag
                ************************************************.**********

Natalisin       atcttctgtgcccactgcgccgtatgtccctcactgtggcgccatcattcatagacatat
STRG.7468.1.p4  gtcttctgtgcccactgcgccgtatgtccctca-tgaggcgccatcattcatagacatat
                .******************************** ** ************************

Natalisin       atgaccagcacatcgcacttttaacttctcatttcaccatatttattttgtttagcgtct
STRG.7468.1.p4  atgaccagcacatcgcacttttcacttatcatttcaccatatttattttgtttagcgtct
                ********************** **** ********************************

Natalisin       tcaacagttgccgacaccagtcgcgtgcttcttgaaggtaaggctcccgatgtttcaaat
STRG.7468.1.p4  tcaacagttgccgacaccagtcgcgtgcttcttgaaggtaaggctcccgatgtttcaaat
                ************************************************************

Natalisin       aggagtctttatccccatctgtggggcctggcaagaagggcgctctagctttcgaggacg
STRG.7468.1.p4  aggagtctttatccccatctgtgtggcctggcaagaagggcgctctagctttcgaggacg
                ********************** *************************************

Natalisin       tgttggcagaggtacgtgatagctacacagtattttacgagcctagagtattagtttgtt
STRG.7468.1.p4  tgttggcagaggtacgtgatagctacacagtattttacgagcctagagtattagtttgtt
                ************************************************************

Natalisin       tagtgcactctgcacttccttagatttcattcaagaggcg--------------------
STRG.7468.1.p4  tagtgcactctgcacttccttagatttcattcaagaggcgactcggattgtcgaagccac
                ****************************************

Natalisin       ------------------------------------------------------------
STRG.7468.1.p4  tatttcgagtacatagataatcatattttgacgtaacaagcttttaaggtacgggtaaaa

Natalisin       ------------------------------------------------------------
STRG.7468.1.p4  atgaataggtaaaatattcagaaactcctgtaatccttttccagatggtcttaattgtta

Natalisin       ------------------------------------------------------------
STRG.7468.1.p4  ctctcctgtagatgtcattgtttctaagtctgatgtgaaaatgttccatatcttctaact

Natalisin       ------------------------------------------------------------
STRG.7468.1.p4  tctgggggtgagtatcattttgtggttgtatcaattcctcaataagagcaaatatatata
```

```
Natalisin       ------------------------------------------------------------
STRG.7468.1.p4  gtgaatatatattggttcttcaagttcgaagtaatttcgcataagtaatgtataaaacat

Natalisin       ------------------------------------------------------------
STRG.7468.1.p4  ttacgcaagtactgtaggcttttatatgttcttcatgtattgatgataacgagcagcgct

Natalisin       ------------------------------------------------------------
STRG.7468.1.p4  acagacgaaagcgtttagaagactgccagctttaagaagagagtcggccctaccacaacc

Natalisin       ------------------------------------------------------------
STRG.7468.1.p4  tacagtaaaatgcgcggtaacagtttcaaaaatgtgttttagatcctttctaacaacagg

Natalisin       ------------------------------------------------------------
STRG.7468.1.p4  ttccagaggttctcgaaaatatctcgcaggttcgcctcgtcacaactgcattcggcgtgg

Natalisin       ------------------------------------------------------------
STRG.7468.1.p4  aaacgtacagctgaggcagcggccggttcctgcgtcgccgctgaggagtgattgtggtcc

Natalisin       ------------------------------------------------------------
STRG.7468.1.p4  tcgtttgatagcagttgcaatgggcgtcagcgggcaaggcgtttgcgccggaggggatgg

Natalisin       ------------------------------------------------------------
STRG.7468.1.p4  cgaaggcggaggcgcagctgggacgcggttgccgcgccgccccgcacgcccccgagcacg

Natalisin       ------------------------------------------------------------
STRG.7468.1.p4  ccttctgggagccctcggggcggcgggggaagagggggagtcaggagttccgcgacctgc

Natalisin       ------------------------------------------------------------
STRG.7468.1.p4  tctccaaggtgtggtaacgttcgcctcactccaactctcgccaatccggcccgggaggcg

Natalisin       ------------------------------------------------------------
STRG.7468.1.p4  cgggaagagcgactctctgcaaactgggcgcttgttgggaacgcagtaatgtttgtggga

Natalisin       ------------------------------------------------------------
STRG.7468.1.p4  agaacgttgcggatacgtgctctgttggtggttcttgtacacgtaacgaattcgccggtg

Natalisin       ------------------------------------------------------------
STRG.7468.1.p4  ttaattctaatatttagctggcgtagtcagggtggatcttggggaaactagaaacattgg

Natalisin       ------------------------------------------------------------
STRG.7468.1.p4  atgagtttatcattggataagtaaacctatggataagtttttgggtagataggtttttga

Natalisin       ------------------------------------------------------------
STRG.7468.1.p4  gataattttccaaaaaaaggagacatttccgcggattaaaataattttatttgaaatcaa

Natalisin       ------------------------------------------------------------
STRG.7468.1.p4  aaatgtaatagtgatccaaaacaagtaataaacacgagaataaaattaaataagctgaat

Natalisin       ------------------------------------------------------------
STRG.7468.1.p4  ggcattagagcctccttattcttttacgcttcctaattgtccttcttgacaatgtcgaac
```

```
Natalisin       ------------------------------------------------------------
STRG.7468.1.p4  tccgagatttcttctcttgtcggtttcgtcgagatgatactcaacaggagcgagatagta

Natalisin       ------------------------------------------------------------
STRG.7468.1.p4  ttccttttcactctcttcaatcccggtactataagttttgcattaaaaacttaagtaatt

Natalisin       ------------------------------------------------------------
STRG.7468.1.p4  actggacgggttagcgagagtatggtataattcaaatctaatctattacttttctatcaa

Natalisin       ------------------------------------------------------------
STRG.7468.1.p4  ttatgttaggttgtgctcccgtctgatgttcaggatacgcccagaagatcggagagaggt

Natalisin       ------------------------------------------------------------
STRG.7468.1.p4  aatgctaagtaattgttaacattttcagcgagacgacaccaaggtataaaccgaatagtg

Natalisin       ------------------------------------------------------------
STRG.7468.1.p4  tatttcttcaaagggatcactgagtagtagtttgtagtagatcgtgtagaactataatgc

Natalisin       ------------------------------------------------------------
STRG.7468.1.p4  ttttgggagtgtggtgcgattgttactcatttgtagaggcaaaataaataattctgttac

Natalisin       ------------------------------------------------------------
STRG.7468.1.p4  gatactactatttaagacggaaaattaattcgggttcagagacaacacgaattctatcac

Natalisin       ------------------------------------------------------------
STRG.7468.1.p4  ctatattctagtaaatcagtgtcataactattgaaacaatttggcttaaagagttctgaa

Natalisin       ------------------------------------------------------------
STRG.7468.1.p4  catattacaatttctttgcgaatactgtttagaacgagaaggaaaatgatatttgaaaat

Natalisin       ------------------------------------------------------------
STRG.7468.1.p4  tatcttccctttcagcttaaattaacactcgataaactaaattagcgtaataacgtcttc

Natalisin       ------------------------------------------------------------
STRG.7468.1.p4  attacaaaaattattatttcgtgaaaattatattaagatatttcgtatttaagtagtata

Natalisin       ------------------------------------------------------------
STRG.7468.1.p4  ggcttctatttgattaaaaaagttactaatcgaataagttttaatgattagttgggaact

Natalisin       ------------------------------------------------------------
STRG.7468.1.p4  ttttatctaaacggaatagaaggcgatgataataaactaaccaaaacattaattataatc

Natalisin       ------------------------------------------------------------
STRG.7468.1.p4  agattgtcacactacatgaaacataattttgaactttaataaatgtattaagttttcatt

Natalisin       ------------------------------------------------------------
STRG.7468.1.p4  tatgacgaatagaaataaacttaccaagattaaccctacatataaataagatattttttt

Natalisin       ------------------------------------------------------------
STRG.7468.1.p4  aaaaacttcatcattaaattattatgctctttaatgaacgggaacatttcatttaggaaa
```

```
Natalisin       ------------------------------------------------------------
STRG.7468.1.p4  acaatcacactaacagcaagcacaatgatattaacaaaaattcgactctaaatgtactaa

Natalisin       ------------------------------------------------------------
STRG.7468.1.p4  caataaacactaagagaaactgcaggaacaataacaacacttgggcaaattcagtacgta

Natalisin       ------------------------------------------------------------
STRG.7468.1.p4  agtgaacaaaaacgaaactaacaagggagagaaaataaagtttttctgtcgcgcacaca

Natalisin       ------------------------------------------------------------
STRG.7468.1.p4  ttcgagggcgcacacgttagcgtgttaaatatttatttcagcttaactcgtgataattat

Natalisin       ------------------------------------------------------------
STRG.7468.1.p4  tcacgtttctcaagttctcaaaatgcattggagaattgtgttttcaacgaatgttgcgtt

Natalisin       ------------------------------------------------------------
STRG.7468.1.p4  atcctacagaatactatcaaagaggtttaatttttctctgaatagcactcgaaaatata

Natalisin       ------------------------------------------------------------
STRG.7468.1.p4  gaaatcacttacaaaatacattaggtatttattacccacttcgttaatcgacatttaagc

Natalisin       ------------------------------------------------------------
STRG.7468.1.p4  ccatattagctattaatttaacggccattattaacattatcatcgctaataagttatata

Natalisin       ------------------------------------------------------------
STRG.7468.1.p4  gtatttgactggttcctctttctgcgttcggctggcttgcggattttcaataaccgatta

Natalisin       ------------------------------------------------------------
STRG.7468.1.p4  tgagcaaatcaacgataatacggacgttgtaatgggatgcttgtggtttgcctctacaat

Natalisin       ------------------------------------------------------------
STRG.7468.1.p4  attaatttgaaaatatcaaagcttcacgcaagttctgaatttacaacttatcgttttgcc

Natalisin       ------------------------------------------------------------
STRG.7468.1.p4  ttgagtggttgccattgcagtcgtttgcatttcgttcgcaatactaaaatgtattatcgc

Natalisin       ------------------------------------------------------------
STRG.7468.1.p4  attgctactcaaatgctagaactagggccaaaatgcccgtattgactctcgcttctggag

Natalisin       ------------------------------------------------------------
STRG.7468.1.p4  gtgcacgcgtgcctctcgcttttccctagattagaacccatcgcgaccgagcttctcatc

Natalisin       ------------------------------------------------------------
STRG.7468.1.p4  tctttcacccgttcggcaaactcaacaagcagcgggcaacatctgtggcccgaaggtaag

Natalisin       ------------------------------------------------------------
STRG.7468.1.p4  cgtcattcgcgaagtgagaagctttgcaccaccgctaatactattaaagatgccttagtt

Natalisin       ------------------------------------------------------------
STRG.7468.1.p4  agcagataatttttggtcggtgtgacacaggtggtcgcagataagtgttctgtcagggca
```

```
Natalisin       ------------------------------------------------------------
STRG.7468.1.p4  cgccaagtgagtcgcccacttgaactgccctgcactacctctaaaactactcaaaccacc


Natalisin       ------------------------------------------------------------
STRG.7468.1.p4  ttcatttgtactgcattgcgctttgtcagggtataccaagagggccgcccacttcatcag


Natalisin       ------------------------------------------------------------
STRG.7468.1.p4  attcgtcctcctcgtccttctcctcctcgttttcctcgtcctcctcctcctcgtcctcct


Natalisin       ----------------------------------
STRG.7468.1.p4  cctcctcgtcctcctcctcctcgtcctcctcctc
```

Neuropeptide F1a (NPF1a)

```
CLUSTAL format alignment by MAFFT FFT-NS-1 (v7.490)


Neuropeptide_F1 --------------------------------------MQAARPAALFGLLALSAVAALA
14629_c0_g1_i2. AVAVAAAAAAVVAAAPAAAAAAAPRPARVHLLLSRSLEMQAARPAALFGLLALSAVAALA
                                                      **********************

Neuropeptide_F1 LLATAAPAASAAPAAAPAQDIERAMEALKYLQELDRYYSQVARPRFGKRTEARSFSDDSL
14629_c0_g1_i2. LLATAAPAASAAPAAAPAQDIERAMEALKYLQELDRYYSQVARPRFGKRTEARPFSDDSL
                ****************************************************.******

Neuropeptide_F1 EEASNEKLWRRFSRRR
14629_c0_g1_i2. EEASNEKLWRRFSRRR
                ****************
```

Neuropeptide F1b (NPF1b)

```
CLUSTAL format alignment by MAFFT FFT-NS-1 (v7.490)


Neuropeptide_F1 --------------------------------------MQAARPAALFGLLALSAVAALA
14629_c0_g1_i6. AVAVAAAAAAVVAAAPAAAAAAAPRPARVHLLLSRSLEMQAARPAALFGLLALSAVAALA
                                                      **********************

Neuropeptide_F1 LLATAAPAASAAPVAAPAQDIERAMEALKYLQELDRYYSQVARPSPRSELTRSAETFKKD
14629_c0_g1_i6. LLATAAPAASAAPAAAPAQDIERAMEALKYLQELDRYYSQVARPSPRSELTRSAETFKKD
                *************.**********************************************

Neuropeptide_F1 NLYLKMLQLQTLDRIYAPRTRPRFGKRTEARPFSDDSLEEASNEKLWRRFSRRR
14629_c0_g1_i6. NLYLKMLQLQTLDRIYAPRTRPRFGKRTEARPFSDDSLEEASNEKLWRRFSRRR
                *****************************************************
```

Neuroparsin precursor (NPP) isoform 1 / Neuroparsin precursor (NPP) isoform 2

```
CLUSTAL format alignment by MAFFT FFT-NS-2 (v7.490)


NPP             ------------------------------------------------------------
NPP2            ---------------------------------------MATVVLLLSTRPLPVAANWY
STRG.2256.1.p1  --------------------MRAP----ASPAAASLSLLLMATVVLLLSTRPLPVAANWY
GBI_01783-RA    --------------------MRAP----ASPAAASLSLLLMATVVLLLSTRPLPVAANWY
GBI_06742-RA    MNRRRRRARQQLPSTADLRHAQPPPPRHAPPGECRAGRRTVARGDVCPAPSP-PSAADGC
GBI_06742-RB    ------------------------------------------------------------
```

```
NPP             -------------------------MLA---CPPCEADSCDVDPRTCEYGTDRDHCQRLV
NPP2            SE--------------------LTSMLA---CPPCEADSCDVDPLTCEHGTARDHCQRLV
STRG.2256.1.p1  SE--------------------LTSMLA---CPPCEADSCDVDPLTCEHGTARDHCQRLV
GBI_01783-RA    SE--------------------LTSMLA---CPPCEADSCDVDPLTCEHGTARDHCQRLV
GBI_06742-RA    SSRLNDDHDDDFEAAGRHSHRRLTRVAASPLCPPCEGGSCDVDPADCRHGVVRDHCGRQV
GBI_06742-RB    -----------------------MRRVAASPLCPPCEGGSCDVDPADCRHGVVRDHCGRQV
                                       : *   *****..******  *.:*. **** * *

NPP             CAKGPGERCGGTNDILGMCAKSLSCRCYRCTGCAGNPLQCFDIVGASCGI
NPP2            CAKGPGERCGGANGILGVCAESLSCRCYRCTGCAGNPLQCFRIVGASCGI
STRG.2256.1.p1  CAKGPGERCGGANGILGVCAESLSCRCYRCTGCAGNPLQCFRIVGASCGI
GBI_01783-RA    CAK-----------------------------------------------
GBI_06742-RA    CAKGPGQRCGGKGDLLGRCGEGMHCKCNRCAGCSLATLEC-DLSEFLCLS
GBI_06742-RB    CAKGPGQRCGGKGDLLGRCGEGMHCKCNRCAGCSLATLEC-DLSEFLCLS
                ***
```

Orcokinin

```
CLUSTAL format alignment by MAFFT FFT-NS-2 (v7.490)


Orcokinin       --------------MRPQQQHRSAAALATALLALLLVAGPAAALPAPQGDLREQVYRNFR
STRG.2901.1.p1  PPPPPLPPPPPASSMRPQQQHRSAAALATALLALLLVAGPAAALPAPQGDLREQVYRNFR
GBI_02308-RA    ------------------------------------------------GGALGNQ-KRTFD
                                                                 * * :*  *.*

Orcokinin       EDLEEAPIPRSLVAARSLANGRVRRP------------MPSGLDSLSGVTFGT-SKRLDP
STRG.2901.1.p1  EDLEEAPIPRSLVAARSLANGRVRRP------------MPSGLDSLSGVTFGT-SKRLDP
GBI_02308-RA    E------------IDRMGFNGFVKKNFDEIDRLGFNNFVKKNFDEIDRMGFGSFVKRNAP
                *              *   ** *::             : ..:*.:. : **:  **  *

Orcokinin       L----------SGGALGHQKRNFDKFDRLSLNSLVKKNFDEIDRTGFDSFVKRNFNEIDS
STRG.2901.1.p1  L----------SGGALGHQKRNFDKFDRLSLNSFVKKNFDEIDRTGFDSFVKRNFNEIDS
GBI_02308-RA    ALLARYYQMQEHGGALGHQKRNFDKFDRLSLNSFVKKNFDEIDRTGFDSFVKRNFNEIDS
                                    *********************:*************************

Orcokinin       TGFDNFIKRNAPALLWRYYRNHNH
STRG.2901.1.p1  TGFDNFIKRNAPALLWRYYRNHNH
GBI_02308-RA    TGFDNFIKRNAPALLWRYYRNHNH
                ************************
```

Pigment dispersing factor (PDF)

```
CLUSTAL format alignment by MAFFT FFT-NS-1 (v7.490)


Pigment_dispers ---------------------------------------MARRARFEANAAPSPLMCVHKR
4557_c4_g1_i1.m AALPRPAAAAADDDVAAAAAAAAAAKLLDKEVASWLLSMARRARFEANAAPSPLMCVHKR
                                                      **********************

Pigment_dispers NSEIINSLLGLPKVLNDAGRK
4557_c4_g1_i1.m NSEIINSLLGLPKVLNDAGRK
                *********************
```

Proctolin

```
CLUSTAL format alignment by MAFFT FFT-NS-1 (v7.490)

Proctolin       ----------------------------MGCPRRLALLLVVLLALHAQVGVDARYLPTRA
7875_c1_g1_i1.m PTKAPPPRRRRRKLAAQATHRPHSSASEMGCPRRLALLLVVLLALHAQVGVDARYLPTRA
                                             ********************************

Proctolin       QDDRLDRLRELIRDLLENEVDKYNNANVPADLFGPGDRAGFVFKQRQMPGRVMLADEDRK
7875_c1_g1_i1.m QDDRLDRLRELIRDLLENEVDKYNNANVPADLFGPGDRAGFVFKQRQMPGRVMLADEDRK
                ************************************************************
```

RYamide

```
CLUSTAL format alignment by MAFFT FFT-NS-1 (v7.490)


tr|M4QCG6|M4QCG ---------------MRGVLMCACVTLLGVLVLTGGEERTDMSPVPFVMGSRYGR-----
GBI_11027-RA    MAAEAVSAAAAGAGAGAGGRWCLC-ALLALAAAAAAAAAAAAGGPGAFYPSGRYGKRVETE
                                 *   * * :**.: . :..   :  .* .*  ..***:

tr|M4QCG6|M4QCG ---SPA-------------RLITPRNDRFFMGSRYGKRSDAG------------------
GBI_11027-RA    VPLAPAGRGGWAAGRFGRSGVMLPRADRFFMGSRYGKRAGGGPALPELAQLAQAAQQAQQ
                   :**              :: ** ************:..*

tr|M4QCG6|M4QCG ----REVRA-----LVCEYTGVG-------------------------------------
GBI_11027-RA    QQQQQQQQAPSAALLLAPRTGVGAGAGARGSPAAPAASSVAACGGERASVGAGATPPQPS
                    :: :*     *:.  ****

tr|M4QCG6|M4QCG ----PLYRCVNQ----NRRLYDKRSRSSEDVERGEQG-------------------
GBI_11027-RA    QQQPPAQQAAQQAAGRSRQRRRRRRTHAHGAGRGARGARPPAAPARPRPRSAALSL
                    *  :..:*    .*:   :*   :... ** :*
```

SIFamide

```
CLUSTAL format alignment by MAFFT FFT-NS-1 (v7.490)


SIFamide        MAGKSFAASRRSARPLAALLRAAAVLCVALLLVAASAPSASSYRKPPFNGSIFGKRAPAA
GBI_07129-RA    MAGKSFAASRRSARPLAALLRAAAVLCVALLLVAASAPSASSYRKPPFNGSIFGKRAPAA
                ************************************************************

SIFamide        AAA-----------------------------------------
GBI_07129-RA    AAAPAPAASAQDYEAAAAGKALSALCEVAAEACSAWFPQQNELN
                ***
```

Sulfakinin

```
CLUSTAL format alignment by MAFFT FFT-NS-1 (v7.490)


sulfakinin      -------------------------------------------------------RALVLG
GBI_05512-RA    MGCSMLTAAFFVVSVYLLVHHQHHAVSGHALPLPPSEGGAGGGAGGGAGGALRGRALVLG
                                                                      ******

sulfakinin      RRAPPVAPQLLRARLAVADDAAVQGLLGDFVVDDEELGEMSKRQSDDYGHMRFGKREPFD
GBI_05512-RA    RRAPPVAPQLLRARLAVADDAAVQGLLGDFVVDDEELGEMSKRQSDDYGHMRFGKREPFD
                ************************************************************
```

```
sulfakinin      DYGHMRFGRSA-
GBI_05512-RA    DYGHMRFGRSAE
                ***********
```

Short neuropeptide F (sNPF)

```
CLUSTAL format alignment by MAFFT FFT-NS-2 (v7.490)

short_neuropept -------------------------MARLPSVTCCCVALSLMLLLAHAAPSYGDYDSVRD
GBI_09088-RA    -------------------------MARLPSVTCCCVALSLMLLLAHAAPSYGDYDSVRD
GBI_09088-RC    -------------------------MARLPSVTCCCVALSLMLLLAHAAPSYGDYDSVRD
GBI_09088-RD    -------------------------MARLPSVTCCCVALSLMLLLAHAAPSYGDYDSVRD
GBI_09088-RB    MANPVTRNKGRPRKPLIMSHVEPGAMARLPSVTCCCVALSLMLLLAHAAPSYGDYDSVRD
                                         **********************************

short_neuropept LYELLLQKEALEGRLAPPQPQQAHELVRKSNRSPSLRLRFGRRADPLFTGSSFLDHSSVE
GBI_09088-RA    LYELLLQKEALEGRLAPPQPQQAHELVRKSNRSPSLRLRFGRRADPLFTGSSFLDHSSVE
GBI_09088-RC    LYELLLQKEALEGRLAPPQPQQAHELVRKSNRSPSLRLRFGRRADPLFTGSSFLDHSSVE
GBI_09088-RD    LYELLLQKEALEGRLAPPQPQQAHELVRKSNRSPSLRLRFGRRADPLFTGSSFLDHSSVE
GBI_09088-RB    LYELLLQKEALEGRLAPPQPQQAHELVRKSNRSPSLRLRFGRRADPLFTGSSFLDHSSVE
                ************************************************************

short_neuropept GPVEN
GBI_09088-RA    GPVEN
GBI_09088-RC    GPVEN
GBI_09088-RD    GPVEN
GBI_09088-RB    GPVEN
                *****
```

Tachykinin: Not detected

Trissin

```
CLUSTAL format alignment by MAFFT FFT-NS-2 (v7.490)


Dmel_trissin    ------------------------------------------------------------
GBI_01877-RB    MNSNDDLTDKSHKLVRQLHWKCDEQYTDCETSILRISAGSSAGGGAEAAWEACVGGEAWR
GBI_01877-RA    ------------------------------------------------------------


Dmel_trissin    --------------------------------------------------MTKTT-----
GBI_01877-RB    GREPVDVGAVPWRWMRRRPGELEERCVGVGSGVAALAGRGRRDDPGRSSSAGRTTRRPRD
GBI_01877-RA    ------------------------------------------------------------

Dmel_trissin    --------------MHWLAHFQIILLCIWLMCPPS--SQAIKCDTCGKECASACG-TKHF
GBI_01877-RB    SSDNRRPARSPPATMVHLSHFATLLSGLLLLAALGRLGGADACDICGRECMGSCGDTRTF
GBI_01877-RA    --------------MVHLSHFATLLSGLLLLAALGRLGGADACDICGRECMGSCGDTRTF
                              *  *:**  :*  : *:.. .  . *  ** **:** .:** *: *

Dmel_trissin    RTCCFNYLRKR--------------------SD-------PDALRQSSNRRLIDFIL----
GBI_01877-RB    VTCCYNYLRKRGVGPVGTAPLGLAPLAAAASDYAGPAPPPPALRP----RAAAFHLRPPS
GBI_01877-RA    VTCCYNYLRKRGVGPVGTAPLGLAPLAAAASDYAGPAPPPPALRP----RAAAFHLRPPS
                 ***:******                   **       * ***     *   * *

Dmel_trissin    ---LQGRALFTQELRERRHNGTLMDLGLNTYYP
GBI_01877-RB    PPAAAAVALYDD---------------------
GBI_01877-RA    PPAAAAVALYDD---------------------
                     . **: :
```