

Supplementary Information

Global map of oxytocin/vasopressin-like neuropeptide signalling in insects

Zita Liutkeviciute^{1,2}, Johannes Koehbach², Thomas Eder^{3,4}, Esther Gil-Mansilla¹ and Christian W. Gruber^{1,2}

¹*Medical University of Vienna, Center for Physiology and Pharmacology, Vienna, 1090, Austria*

²*The University of Queensland, School of Biomedical Sciences, St Lucia, 4072, Australia*

³*University of Vienna, CUBE-Division of Computational Systems Biology, Department of Microbiology and Ecosystem Science, Vienna, 1090, Austria*

⁴*Ludwig Boltzmann Institute for Cancer Research, Medical University of Vienna, 1090 Vienna, Austria*

Table of Contents

Supplementary Figure S1. Alignment of inotocin precursors	S2
Supplementary Figure S2. Alignment of multiple copies of inotocin precursors and receptors.	S13
Supplementary Figure S3.....	S18
Supplementary Figure S4. Discrimination between oxytocin/vasopressin-like and crustacean cardioactive peptide receptors.....	S43
Supplementary Figure S5. Phylogenetic tree of inotocin receptors.....	S46
Supplementary Figure S6. Alignment of selected inotocin-like receptors and precursors.	S48
Supplementary Data S1. Putative inotocin precursors.....	S50
Supplementary Data S2. Putative inotocin receptors.....	S59
Supplementary Table S1. List of analysed arthropod species	S82
Supplementary Table S2. List of species and accession numbers used to prepare dataset	S90
Supplementary References.....	S94

Supplementary Figure S1. Alignment of inotocin precursors. Putative mature inotocin peptide sequences are highlighted in green; amidation sequences are shown in grey; conserved vicinal cysteine pairs of the neurophysin domain are highlighted in magenta; additional C-terminal residues of decapeptides as well as ambiguous C-terminal peptide sequences are highlighted in red. (A) Alignment of 110 inotocin precursor sequences encoding for putative inotocin and inotocin-like peptides. (B) Alignment of 23 inotocin precursors containing neurophysin domains but lacking inotocin peptide domains.

(A)	1	50
Calanus_finmarchicus1	MITSWKILDPRIRRSWSFLIILLAQTMSASHG	CFISNCPVSGKKRSVSGEE
Calanus_finmarchicus3	MITSLKILDPSIRRSWRFLMILLAHTIPDSHG	CFISNCPVSGKKRSVSGEE
Daphnia_pulex	-----MAGLWTFCLIALSMTEMI IPLTAKP	CFITNCPVSGKKRSSQLVE
Daphnia_magna	-----MAALWTLCLIAFSILEMTMPSSAAKP	CFITNCPVSGKKRSGHVSE
Lepeophtheirus_salmonis	-----MAFGYPLITLTLIFQIANAC	CFITNCPVSGKKKSGSGST
Caligus_rogercresseyi	-----MALCLLQVTES	CFITNCPVSGGRKRPADPG
Dermatophagoides_farina	--MFRRESFSMMKIIILVLCIWIICLFNDVRG	CFITNCPVSGKKRSIMTES
Sarcoptes_scabiei	--MLFQQTNYLFRSISILVMIVLIVEN-VRG	CFITNCPVSGKKRSMIAAI
Symphylella_vulgaris	-----MSSGKSDITNAFVLLTFVSTVSA	CFITNCPVSGKKRS-----
Tigriopus_californicus	-----MQITFDRRCFIVLGLLSLLKAVSVNS	CFITNCPVSGKKR-----
Metaseiulus_occidentalis	-----MKLVALYFLSVSSLSWA	CFITNCPVSGKKRS-----
Varroa_destructor	-----MKLHVVLVLANIVGLSLT	CFITNCPVSGKKRSD----
Gryllotalpa_sp	-----MKVYYLLVFIISLIVLNTA	CMINCPVSGKKR-AMKIN
Teleogryllus_commodus	-----MAQFKLYSNIIVLMMILTFSCA	CMINCPVSGKKRSAMENN
Haploembia_palau	-----MINFRFARFIIITLAAVCTA	CLITNCPVSGKKRSLHLHG-
Aposthonia_japonica	-----MVNFRFARFIIITLAVVCTG	CLITNCPVSGKKRSLAHG-
Zootermopsis_nevadensis	-----MKMQLGTATLLAVFISLCTA	CLITNCPVSGKKRAGTHSQ
Blattella_germanica	-----MQLALVFLVFCAVCRA	CLITNCPVSGKKRAGVQSQ
Galloisiana_yuasai	-----MRLKQCLRMLALLVAVVGISSA	CLITNCPVSGKKRALNHS-
Locusta_migratoria_manilensis	-----MKPQLAVLLALVVSLAAA	CLITNCPVSGKKR-----
Nilaparvata_lugens	-----MKNTTSIGIMLFYAVGLAAG	CLITNCPVSGKKRGLHSYM
Halyomorpha_halys	-----MYRALLFLTALCLVQS	CLITNCPVSGKKRSLRPG
Homalodisca_vitripennis	-----MRGAVLTVCSLATA	CLITNCPVSGKKRSQSTID
Gynaikothrips_ficorum	-----MICVKIPIFLLLLAMTSA	CLITNCPVSGKKRNGARPP
Cotesia_vestalis	-----MMHKFLLVFFFITSSFA	CLITNCPVSGKKRSGES---
Microplitis_demolitor	-----MNLPGTMIRKIFAVVFLSTSA	CLITNCPVSGKKRSGES---
Fopius_arisanus	-----MSKIIILIMSALICMSSA	CLITNCPVSGKKRGEN---
Diachasma_alloem	-----MSKIIILISALVCVSCA	CLITNCPVSGKKRGEN---
Telenomus_podisi	-----MIAWVIVLVSIIFSLSSA	CLITNCPVSGKKRADQ---
Nasonia_giraulti	-----MSKVIIVLTTLVLSYSG	CLITNCPVSGKKRSGD---
Nasonia_vitripennis	-----MSKVIIVLTTLVLSYSG	CLITNCPVSGKKRSGD---
Copidosoma_floridanum	-----MLKVSIVLLALVSVAYS	CLITNCPVSGKKRSGD---
Trichogramma_pretiosum	-----MLKVIIVFVFMVFLSLSHC	CLITNCPVSGKKRSGD---
Brachycystis_timberlakei	-----MLKKFILIAILISLSYSG	CLITNCPVSGKKRSGE---
Crioscolia_alcione	-----YG	CLITNCPVSGKKRSGE---
Chrysis_viridula	-----MQYKMLTKLILFASMFVAVYG	CLITNCPVSGKKRSGD---
Trachymyrmex_septentrionalis	-----MLKELIVFASLIFLSYA	CLITNCPVSGKKRSD---
Trachymyrmex_cornetzi	-----MLKELIVFASLIFLSYA	CLITNCPVSGKKRSD---
Atta_cephalotes	-----MLKELIVFASLIFLSYA	CLITNCPVSGKKRSD---
Trachymyrmex_zeteki	-----MLKELIVFASLIFLSYA	CLITNCPVSGKKRSD---
Acromyrmex_echinator	-----MLKELIVFASLIFLSYA	CLITNCPVSGKKRSD---
Vollenhovia_emoryi	-----MLKEFVIFASLIFLSYA	CLITNCPVSGKKRSGD---
Solenopsis_invicta	-----MLKELVVLASLIFLSYA	CLITNCPVSGKKRSGD---
Monomorium_sp	-----MLKEFVVFASLIFFSYSG	CLITNCPVSGKKRSGD---
Wasmannia_auropunctata	-----MLKELVVLMSLIFLSYA	CLITNCPVSGKKRNN---
Harpegnathos_saltator	-----MLRELVVVFASLIFLSYA	CLITNCPVSGKKRSGD---
Dinoponera_quadriceps	-----MLRELVVLASLIFLSYA	CLITNCPVSGKKRSGD---
Cerapachys_biroi	-----MLKKLVVFATLIFLSYA	CLITNCPVSGKKRSGD---
Linepithema_humile	-----MLKELIVFANLILLSYA	CLITNCPVSGKKRSGD---
Pogonomyrmex_barbatus	-----MLKKIVVFASLIFLSYA	CLITNCPVSGKKRSD---
Camponotus_floridanus	-----MLKQLVICASLIFLSHA	CLIVNCPVSGKKRSD---
Pseudomasaris_vespoides	-----MAKELIVLIAIVVLSASA	CLITNCPVSGKKRG---
Chyphotes_mellipes	-----MAKELVFVAALLVVAYG	CLITNCPVSGKKRGGGKHG
Athalia_rosae	-----MFQKTAIILLVSSALG	CLINCPVSGKKRNGA---
Neodiprion_lecontei	-----MFRKIVVILFVSSTLG	CLINCPVSGKKRGGG---
Cephus_cinctus	-----MLKCLTVIMVIFISISFA	CLITNCPVSGKKRSGA---
Polistes_canadensis	-----MTKKILIFTSFIFISSA	CLITNCPVSGKKRSGD---
Polistes_metricus	-----MTKKILIFTSFIFISSA	CLITNCPVSGKKRSGD---
Polistes_dominula	-----MTKKILIFTSFIFITSA	CLITNCPVSGKKRSGD---
Mischocyttarus_flavitaris	-----MTKQILVIFITSFILISSA	CLITNCPVSGKKRVNDKV-
Corydalus_cornutus	-----MYPVVKYFVLVIVLVSVMIDS	CLITNCPVSGKKRNGSDRI
Onthophagus_taurus	-----MVKLIIFTLILCIIQDQLSHG	CLITNCPVSGKKRNGR-IN
Aleochara_curtula	-----MFSSKCLLIVGLACVVLQAVDG	CLITNCPVSGKKRSGKYL

Nicrophorus_vespilloides --MHSPSTMFILKSSALLLVAVVFLGDCSCLITNCPRGGKR---AMQ
Oryctes_borbonicus -----MNSLLLIGVFCIAGDQLEIEGCLITNCPRGGKRS GKMSH
Anoplophora_glabripennis -----MFKNILLLVLLVVFGEIFVNCCLITNCPRGGKRS GKFGA
Leptinotarsa_decemlineata1 -----MVRSVPLTIIYLFIFVMYVESCLITNCPKGGKRGGEFST
Leptinotarsa_decemlineata2 -----MSKTVSLFTLFLSVFVIFVESCLITNCPGIGGKRS GKFSL
Priacma_serrata -----AFFVLNSFLADSCLITNCPRGGKRS--RYN
Gyrinus_marinus -----ALLDICDSCLITNCPRGGKRSGRSQH
Dendroctonus_ponderosae ---MTRSRSKIAKMISQILMFILLSNILVSGCLITNCPRGGKRS GKGYL
Meloe_violaceus -----ATNKFLLVLIIVLTIPTNYFINGCLITNCPRGGKRG NTRYL
Tribolium_castaneum -----MSTIITSIILLVLSSELSVSGCLITNCPRGGKR--SKFA
Hypothenemus_hampeii ---MVSKRNLICTAGSNSTKLSIFMACLITVSGCLITNCPRGGKRS GKFLA
Agrilus_planipennis -----MYTNVCLVFVIVLVCYSLVFGCLITNCPRGGKRS GKME
Arachnocampa_luminosa MNENFLMMNLNDKKNLILFLLVVINLVINACYITNCPWG GKRSPQFLD
Tetranychus_urticae -----MLASFILLTFILNFHSSQACFITNCPGGKRS--HGD
Scolopendra_subspinipes1 -----HWLLFFYVIGMTSSCFITNCPGGKRS GKFE--
Scolopendra_subspinipes2 -----MRSSTCHWILYLSLVGLVSAICYIINCIDN GKRKRSIDH
Strigamia_maritima -----MKSTHFVNIIFYSVFIIMADGCYITNCPGGKRS GKNEK--
Limulus_polyphemus -----MHWTSFIMILGFCLAVTIKGCYITNCPGGKRS IGTF--
Litopenaeus_vannamei -----MQISAVVAMALLLGSGTACFITNCPGGKRS SPFAQ
Homarus_americanus -----MQLGVVVVMTVVVVGSTACFITNCPGGKRS GMSTAQ
Occasjapyx_japonicus -----MSSPVRIHPRLLALACVFCISSACFITNCPGGKRS QQAHY
Catajapyx_aquilonaris -----MSPFRVHQTLLAVACIFCITSACFITNCPGGKRS Q--SHY
Lithobius_forficatus -----MASHAAQSSVFLVLLCVFHIITLACFITNCPGGKRS LKGDQ
Meinertellus_cundinamarcensis -----MKSSMSTPAALFALLFVVSITSSCFITNCPGGKRS RAGAPG
Machilis_hrabei -----MSADMTNSASSTFALFTLLLFVGCVTS CFITNCPGGKRS LKSPG
Tricholepidion_gertschii -----MVARKNPQTVVICLMAAMSAATA CFITNCPGGKRS MGQVG
Atelura_formicaria -----ACFITNCPGGKRS MGQMG
Atelura_formicaria2 -----SLSKGILSVTIFFLAVISVTTACFITNCPGGKRS MGQMG
Speleonectes_cf_tumulensis -----MHLRPMDVLLSALCVLHVAGISTACFITNCPGGKRS LKRTVRTL
Anurida_maritima -----MRKYHTSIIICLVWLVSVSAAF CFITNCPGGKRS--SGP
Pogonognathellus_sp -----MIQFVTYNLWLVVLSVFAASGCFITNCPGGKRS--SGT
Folsomia_candida -----MKTSLLFAGFIVMVESLVLVSGCFITNCPGGKRS--SG-
Sminthurus_viridis -----MINLNCGICLFLITLSVVTGCFITNCPGGKRS--SG-
Ephemera_danica -----MHRKYEMATKVYLLTALIIIVQVTTACFITNCPGGKRS SAVVS
Triops_cancriformis -----IHSAPCFITNCPGGKRS-----
Eurylophella_sp -----MVHRRGATLSAMLIVHVVSACFITNCPGGKRS-----
Ixodes_scapularis -----MALSHMLLLAVVGGTSA CFITNCPGGKRS SEPS-
Ixodes_ricinus -----MALSHMLLLAVVGGTSA CFITNCPGGKRS SEPS-
Ladona_fulva ---MYSRQGM SMDQRQWLLVAVIFALLGLTSA CFITNCPGGKRS DVAFG
Menopon_gallinae -----MYNIFQQLRLGLLVATFGLVVSCLITNCPRGGKRS LKSLD
Pseudomallada_prasinus -----MNNNSLKATIVTFVIFTLLVHSCCLITNCPRGGKRS--NLLD
Liposcelis_bostrychophila -----MNTFQFVVLYIFVNSVNSCLITNCPRGGKRS DGSENN
Diaphorina_citri -----MYAMISRLLVCLVGYWYFFGSTWCCLINCPG GKR SALLMAL
Apachyus_sp -----MSFSLRFFAIFTLLCLGTGCLITNCPKGGKRS-----
Pachyphylla_venusta -----MIPKIFFFLIFLCLNFSFSCLISNCPKGGKRS-----
Cryptocercus_wrightii -----QLGTLATLAILLIGVCTACCLITNCPKGGKRS-----
Orussus_abietinus -----MKELLALYVLISAGYC--CLITNCPRGGKRSHHSES
* * :*

51

100

Calanus_finmarchicus1 QMVSFQAR-----EEVLACPS-NPAGLCYSPGLCC-VQGGCYADK
Calanus_finmarchicus3 QLVSFQAR-----EEVLACPS-NPAGLCYSPGLCC-IQGACYADM
Daphnia_pulex -----PSSYLECAPCGP-AGKGTCLGANLCCGSHFGCFFKT
Daphnia_magna DPSSFQGVA--EERPLLHQASCAGP-GGKGT CFGASLCCGSEFGCFFKT
Lepeophtheirus_salmonis NLGFLNSSF-----QYQCSSCGP-NNTGRCFGPRLCCSSEFGCFVYS
Caligus_rogercresseyi -LFSPKNRR-----QLDECSPCGP-SNEGRCYGNLCCGSTFGCFVYA
Dermatophagoides_farina NLGSNHKKK-----IKIKCTRCPG-SLSGRCYGNICCSPLTGNVGG
Sarcoptes_scabiei GSSTQTRR-----ECIRCPG-GLSGRCYGPSICCSPLFGCNVGG
Symphylella_vulgaris -----GHSLSSSVALRQCSPCGP-GGAGRCFGKSACCVPMGMGCFLGP
Tigriopus_californicus -----SELLT--VASRKCPCPGP-LGMGQCFGSPMCCGQYIGCHLNT
Metaseiulus_occidentalis -----AAFGLQLYSNEYRRCPPCGP-GSSGQCFGPGICCTPDY-CVLDP
Varroa_destructor -----TGFGVLQFSSDFRKCPCPGP-GSTGQCFGPNICCNSES-CLIDA
Gryllotalpa_sp E-----ISSIRSCARCGL-NNAGHCYGPDI CCAPELGCLLIAT
Teleogryllus_commodus E-----ILPIRNCARCAGP-NNTGHCYGPSTCCAEELGCLMGG
Haploembia_palaui -----TESVRQPCRCGP-AKLGHCFGPTICCGHEIGCLINT
Aposthonia_japonica -----SESLRQCPCRCGP-AKLGHCFGPTICCGHEIGCLINT
Zootermopsis_nevadensis EL-----HT-IRQCARCAGP-AKLGHCYGPDI CCAPELGCLLIAT
Blattella_germanica DS-----TVSIRQCARCAGP-AKLGHCYGPDI CCAPELGCLLIAT
Galloisiana_yuasai -----KDSVRQPCRCGP-AKLGHCYGPDI CCAPELGCLLIAT
Locusta_migratoria_manilensis -----ASLQHRCAACGP-GGQGVCLGPHICCGPRMGCRLAS
Nilaparvata_lugens KKLAEKMA----LAQVPLQCARCAGP-EGEGYCMGPSICCGPQLGCLLAS
Halyomorpha_halys RDP-----DCRRCGP-GLEGRCVGTVC CGPRLIGCLIGT
Homalodisca_vitripennis NTLGTE-----IVSLVACLRCGP-GLQGRCLGPAVCCGPRLGLCLVAT
Gynaikothrips_ficorum TKG-----SIEELPFCTLCGPPELGGLCFGPTMCCSPTGGCELGE
Cotesia_vestalis ---PLLS-----MPSLIKECSSCGP-GDQGCFCGPHICCGASIGCYIRS
Microplitis_demolitor ---PLLS-----MPSLIKECSSCGP-NDQGCFCGPHICCGATIGCYIKG
Fopius_arisanus ---PLLS-----LHSLAAECPSCGP-GHQGCFCGPNICCGTIGCFIGT
Diachasma_alloeuum ---PLLS-----LHSLAAECPSCGP-GHQGCFCGPNICCGTIGCFIGT

Telenomus_podisi ---SLML-----METSIRECTSCGR-DGSGRCFGPYICCGSTIGCFIGT
Nasonia_giraulti ---PTFL-----LENIARECPACGR-EEQGRFCFGPHICCSPSMGCLIGT
Nasonia_vitripennis ---PTFL-----LENIARECPACGR-EEQGRFCFGPHICCSPSMGCLIGT
Copidosoma_floridanum ---PTFL-----LENIARECPACGH-EEQGRFCFGPHICCGPSMGCHIGT
Trichogramma_pretiosum ---PTFF-----LENIARECPVCGH-EEQGHFCFGPHICCSPSMGCLIGT
Brachycistis_timberlakei ---AVVS-----LETIARECPSCGP-NRAGQCFGPHICCGPTIGCFIGT
Crioscobia_alcione ---IAPL-----LESVARECPSCGP-NHSGQCFGPHICCGPNIGCFIRT
Chrysis_viridula ---SAVT-----LDHLARECPSCGP-NRLGQCFGPHICCGPSIGCFIGT
Trachymyrmex_septentrionalis ---VASS-----LKTVIRECPSCGP-NHLGQCFGPHYICCGPSIGCFIGT
Trachymyrmex_cornetzi ---IASS-----FKTVIRECPSCGP-NHLGQCFGPHYICCGPSIGCFIGT
Atta_cephalotes ---VASS-----LRTVIRECPSCGP-NHLGQCFGPHYICCGPSIGCFIGT
Trachymyrmex_zeteki ---IASS-----LRTVIRECPSCGP-NHLGQCFGPHYICCGPSIGCFIGT
Acromyrmex_echinator ---IAS-----LKTVIRECPSCGP-NHLGQCFGPHYICCGPSIGCFIGT
Vollenhovia_emoryi ---IAPS-----LGTVVRECPSCGP-NRLGQCFGPHYICCGPSIGCFIGT
Solenopsis_invicta ---IAPS-----LGTVERECPSCGP-NRLGQCFGPHICCGPSIGCFIGT
Monomorium_sp ---IVPS-----LGTVARECSSCGP-NRLGQCFGPHICCGPSIGCFIGT
Wasmannia_auropunctata ---IASS-----LETVARECPSCGP-NHQGQCFGPHYICCGPSIGCFIGT
Harpegnathos_saltator ---IIPS-----LGTVTRECPSCGP-NHLGQCFGPHICCGPTIGCFIGT
Dinoponera_quadriceps ---IAPS-----LGVVTRECLCGP-NHLGQCFGPHICCGPSIGCFIGT
Cerapachys_biroi ---IAPS-----LGTVARECPSCGP-NHLGQCFGPHICCGPSIGCFIGT
Linepithema_humile ---IAP-----LETIARECPSCGP-NHLGQCFGPHICCGPSIGCFIGT
Pogonomyrmex_barbatus ---LAP-----LGNVVRECPSCGP-NHLGQCFGPHICCGPNIGCFIGT
Camponotus_floridanus ---IASF-----LKTVTRECPSCGP-NHMGQCFGPHICCGPNIGCFIGT
Pseudomasaris_vespoides ---DIAA-----LESVVRECPACGP-NRSGQCFGPHICCGPTIGCYIGT
Chyphotes_mellipes EVVPAFE-----DVRVTRECPSCGP-NRLGRCFGPHICCGPTIGCFIGT
Athalia_rosae ---LLP-----LKNPIRECPACGP-EMQGQCFGPKICCGPSIGCFEFGT
Neodiprion_lecontei ---FNP-----FKYQVRECSTCGP-DRQGQCFGPKICCGPSIGCFEFGT
Cephus_cinctus ---ITS-----LENIVRECPSCGA-DKQGQCFGPHICCGPSIGCLIGT
Polistes_canadensis ---IEV-----PESPIRECLPCGP-SQLGQCFGPHICCGPTFGCHIGT
Polistes_metricus ---IEV-----PESPIRECLPCGP-SQLGQCFGPHICCGPTFGCHIGT
Polistes_dominula ---IEV-----PES-IRECLPCGP-NQLGQCFGPKICCGPTFGCHIGT
Mischocyttarus_flavitaris ---PLVTT-----TEYPVKDCISCGP-NGQGQCFGPHICCGPTFGCHMGT
Corydalus_cornutus SNEQFIK-----QCISCGP-QRSGQCFGPHICCGS-FGCLVGT
Onthophagus_taurus SLDTNIK-----QCISCGP-ARSGQCFGPHICCGP-FGCLIGT
Aleochara_curtula DNNIKP-----CIACGP-GHSGQCFGPHICCGP-FGCLLGT
Microphorus_vespilloides DNTQIQ-----CITCGP-GRSGQCFGPHICCGP-FGCLLGT
Oryctes_borbonicus LAAAN-----QCVSCGP-GHTGQCFGPHICCGP-FGCLVGT
Anoplophora_glabripennis LEANIK-----FQCVSCGP-GHSGQCFGPHICCGP-FGCLMGT
Leptinotarsa_decemlineata1 SESNIKTVSNLNKYKHILQCISCGP-GHTGKCFGPHICCGP-FGCLLGS
Leptinotarsa_decemlineata2 TESNIK-----QCISCGP-GHTGQCFGPHICCGP-FGCLMGS
Priacma_serrata EEN-----IKQCISCGP-AHSGQCFGPHICCGP-FGCLLGT
Gyrinus_marinus ENN-----IKQCISCGP-GRSGQCFGPHICCGP-FGCLMGT
Dendroctonus_ponderosae STSNNIKQVIQFSLI---QCICPCGP-GGAGQCFGPHICCGP-FGCLLGT
Meloe_violaceus KQDTQIK-----QCINCGP-GNNGQCFGPHICCGP-FGCLFNT
Tribolium_castaneum ISENAVK-----PCVSCGP-GQSGQCFGPHICCGP-FGCLVGT
Hypothenemus_hampe AVVLFK-----CIPC GP-GGTGQCFGPHICCGP-FGCLLDT
Agrilus_planipennis GDIQP-----VCTSCGP-GLTGQCFGPHICCGP-FGCLLGT
Arachnocampa_luminosa SE-----NAHQCRKAS-G-LGMCFGPHICCGPDMGCLIDT
Tetranychus_urticae VD-----HMRELCRCGP-DNRGHCVSPNICCGTEFGCLINN
Scolopendra_subspinipes1 HKRTLRL-----QCTACGP-GSQGRFCGPHICCGEFGCYLKT
Scolopendra_subspinipes2 QKKAIR-----QCMSCGP-GMKGRFCGPHICCGEFGCYLKT
Strigamia_maritima SGRGVR-----QCTPCGP-GGIGRCYGPDICCGANVCFVGT
Limulus_polyphemus ATHYTR-----ECGQCGP-GGMGQCFGPHICCGSDIFGCFIKT
Litopenaeus_vannamei LG-----SVRTCAQCGP-GLQGRCMGPHICCGPEIGCYMGT
Homarus_americanus LG-----RTRTCTACGP-GLQGRCLGPHICCGVLGIGCFI
Occasjapyx_japonicus KPQAS-----RQCAVCGP-NGQGRFCGPHICCGPEIGCYMRT
Catajapyx_aquilonaris KPQAIRQ-----VSSAQCAVCGP-NGQGRFCGPHICCGPEIGCYLRT
Lithobius_forficatus G-----TTRQCTACGP-GGLGHCFGPHICCGPQIGCFLHT
Meinertellus_cundinamarcensis PRGVQR-----QCPSCGP-HRSGRCFGPHICCGEFGCHLGG
Machilis_hrabei PRGEPR-----QCPSCGP-RHSGRCFGPHICCGEFGCHLGA
Tricholepidion_gertschi -THATR-----ECTSCGP-AKLGRCYGPDICCGPQIGCLVGT
Atelura_formicarial -LHVNK-----QCTSCGP-ARTGRCYGPDICCGPRFGCLVGT
Atelura_formicaria2 -LHANK-----QCTSCGP-ARMGRCYGPDICCGPRFGCLVGT
Speleonectes_cf_tumulensis KSSTR-----QCTSCGPDLLG-RCYSPNICCGPES-----
Anurida_maritima LSTQAR-----QCESCGPEGSGRCYGPDICCSPGSGCLIGT
Pogonognathellus_sp TALTVR-----QCERCPPGMMGRCFGPHICCSPEFGCFST
Folsomia_candida ADTKIR-----QCEQCPPGMMGLCYGPHICCSSELGLCFGT
Sminthurus_viridis IERKTR-----QCEQCPPGAGGRCYGPDICCSPELGLCIAT
Ephemera_danica ETQPKSVIRQFPITCSSYFVQCARCGPGLTGRCFGPHICCESRGLLGS
Triops_cancriformis -----FPMSQQHFL-----
Eurylophella_sp -----SSITTVNARQCSRCGPGLSGRCFGPHICCDSTRRCMLAS
Ixodes_scapularis -----PARLCPRCGPAGRGVCYSADVCCAGSMCILNDALATLSCRAE
Ixodes_ricinus -----PARLVS-----SQFRSSLTVSWC
Ladona_fulva R-----IPLRQVMVSSVLSFKCSRCGFGRCFGPHICCSLKTGCLLAE
Menopon_gallinae KTSS-YP-----DTNYCIPC GP-DDQGVCLGNVCC-SREGCTTRS
Pseudomallada_prasinus S-----
Liposcelis_bostrychophila LIEAPRS-----DIKTCTPCGP-NNQVCIGRDICCCKHLGLCLISS

Diaphorina_citri
Apachyus_sp
Pachypsylla_venusta
Cryptocercus_wrighti
Orussus_abietinus

EERRQSHQKR--AKLWNRNIISCNAWGAEGVCVGLCCDPSRSEGDPGS
-----TSITVFSILKF-----
-----FDKKFPQNKKEIFDKSKVSTLYI
-----AGSHSQDHPHQVFLGYLTLTYQLL
PETTIEK-----FPLAGLYDQSRYPSSLHVYNDQFIDSYARS

Calanus_finmarchicus1
Calanus_finmarchicus3
Daphnia_pulex
Daphnia_magna
Lepeophtheirus_salmonis
Caligus_rogercresseyi
Dermatophagoides_farina
Sarcoptes_scabiei
Symphylella_vulgaris
Tigriopus_californicus
Metaseiulus_occidentalis
Varroa_destructor
Gryllotalpa_sp
Teleogryllus_commodus
Haploembia_palau
Aposthonia_japonica
Zootermopsis_nevadensis
Blattella_germanica
Galloisiana_yuasai
Locusta_migratoria_manilensis
Nilaparvata_lugens
Halyomorpha_halys
Homalodisca_vitripennis
Gynaikothrips_ficorum
Cotesia_vestalis
Microplitis_demolitor
Fopius_arisanus
Diachasma_alloenum
Telenomus_podisi
Nasonia_giraulti
Nasonia_vitripennis
Copidosoma_floridanum
Trichogramma_pretiosum
Brachycistis_timberlakei
Crioscolia_alcione
Chrysis_viridula
Trachymyrmex_septentrionalis
Trachymyrmex_cornetzi
Atta_cephalotes
Trachymyrmex_zeteki
Acromyrmex_echinator
Vollenhovia_emeryi
Solenopsis_invicta
Monomorium_sp
Wasmannia_aeropunctata
Harpegnathos_saltator
Dinoponera_quadricaps
Cerapachys_biroi
Linepithema_humile
Pogonomyrmex_barbatus
Camponotus_floridanus
Pseudomasaris_vespoides
Chyphotes_mellipes
Athalia_rosae
Neodiprion_lecontei
Cephus_cinctus
Polistes_canadensis
Polistes_metricus
Polistes_dominula
Mischocyttarus_flavivittatus
Corydalus_cornutus
Onthophagus_taurus
Aleochara_curtula
Microphorus_vespilloides
Oryctes_borbonicus
Anoplophora_glabripennis
Leptinotarsa_decemlineata1
Leptinotarsa_decemlineata2
Priaema_serrata
Gyrinus_marinus

101 150
GCLPQMEESRENREPRNLNRDL-----RFLYGWAPAHEKMFQQTG

-----EETN
-----NETN
NDIAKN-PCQTEAYDPVPCQ-----NNVKSCSSVLKNG
KSLQHQNPCLEARLPLPCR-----NKGSGCSGILENG
---FTAARCSLEAYHPILCT-----NPGTVCGPNKG-G
---FASSRCALEAFNPMLCS-----NPGSACGNKG-G
AHT---ATCRLEHSYP-----VPCDNGTPACGENGNG
PDT---QVCKTENSNP-----IPCDNDVPRCQSVRRG
VG---LSTCKSEALKM-----TPCNINRPRCGAENKG
GDSPHLRSCKREALKL-----KPCNTNTGMRCGSENKG
PETVPCQEEESQSPD-----PCIDTDLGPACHNGK--G
PEAKPCEAEALSPD-----PCVEPALGPRCFGQ--G
PDTLVCLKEHLSPD-----PCVGPATATNCGNRK--G
PDTLVCLKEHLSPD-----PCVGPSASNCGNRK--G
PDTARCLSEAAASPV-----PCTAPTGAQCCEGKFA-G
PETTRCLSEAAASPS-----PCTTPSGAPCGSGKNA-G
ADTAICQGESLYPE-----PCAN-TMPASSCRGEA-G
-ADADAACRAAPP-----CPLDSEPMRCAAGRGR--
PATLNQCAGSVLPP-----QSPNSPAPTCYMPDGY-G
PAVLSQCAAEPMLQ-----RGGQR-----CSI-G
PGIVRQCAGAAEGP-----SPHGKP---CITPSGL-G
PHVASCLGVHTVPPPLCRLPPQSMPLNGPYSAPSQTRATSLVTTCSG-G
PETYKCRKE-SLHSH-----PCVSGFAMCRDNT-A
PETYKCRKE-SLYSH-----PCVSGFAMCRDNT-A
PETYKCRTE-SLYSR-----PCIAGFAMCRDNT-G
PETYKCRTE-SLYSR-----PCIAGFAMCRDNT-G
PETYKCRKE-SLYSK-----PCIAGFAMCRDNT-G
PETLRCRKE-SLYSR-----PCVAGFAMCQGN-G
PETLRCRKE-SLYSR-----PCVAGFAMCQGN-G
LETLRCRKE-SLYSR-----PCVAGFAMCQGN-G
SETLRCRKE-SLYSR-----PCVAGFAMCQNNN-G
PETYRCRKE-SLFSR-----PCIAGYAMCRGNT-A
PETYRCRKE-SLFSR-----PCIAGYAMCRGNT-A
PETYKCRKE-SLFSR-----PCVAGYAMCRGNS-A
PETYQCRKE-SLYTR-----PCIAGYAMCRGNT-A
PETFRCRKE-SLYTR-----PCIAGYAMCRGNT-A
PETFRCRKE-SLYTR-----PCIAGYAMCRGNT-A
PETSRCRKE-SLYTR-----PCIAGYAMCRGNT-A
PETFRCRKE-SLYTR-----PCIAGYAMCRGNT-A
PETYRCRKE-SLYTR-----PCVAGYAMCRGNT-A
PETYRCRKE-SLYTR-----PCIAGYAMCRGNT-A
PETYRCRKE-SLYTR-----PCIAGYAMCRGNT-A
PETYRCRKE-SLYTR-----PCIAGYAMCRGNT-A
PETYRCRKE-SLYTR-----PCIAGYAMCRGNT-A
PETYRCRKE-SLYTR-----PCIAGYAMCRGNT-A
PETYRCRKE-SLYTR-----PCIAGYAMCRGNT-A
PETHKCRKE-SLFSR-----PCIAGYAMCRGNT-G
SQTQKCRKE-QFDSS-----PCMAGFAMCNGNK-G
SQTQKCRKE-QFDSS-----PCMAGFAMCNGNK-G
SQTQKCRKE-QFDTS-----PCLAGFAMCNGNK-G
SYTKKCRKE-FSDQI-----SCLSGFAMCSGNV-G
PETVRCARGGFHEPE-----PCIAGQASCRGDS-G
PDTLKLCKEGQFHENE-----PCIAGNSSCRNS-G
HETARCRRDGNFLEPE-----PCIAGNASCRNS-G
QETVKCQREGFFHGFE-----PCIAGSAPCRKNT-G
AETLRCQKDGFFHEAE-----PCIAGNSPCRNT-G
PETLRCQREGFFHERE-----PCIAGGASCRKNT-G
PETERCHKEGLFQETE-----PCIAGFSTCRKNT-G
HETFGCQRG-GFHESE-----PCIAGFSSCRKNT-G
SETIRQCQREGFFHERE-----PCIAGNAFCRKKH-R
SDTIRCHREGYFDSE-----PC-----

Dendroctonus_ponderosae
 Meloe_violaceus
 Tribolium_castaneum
 Hypothenemus_hampeii
 Agrilus_planipennis
 Arachnocampa_luminosa
 Tetranychus_urticae
 Scolopendra_subspinipes1
 Scolopendra_subspinipes2
 Strigamia_maritima
 Limulus_polyphemus
 Litopenaeus_vannamei
 Homarus_americanus
 Occasjapyx_japonicus
 Catajapyx_aquilonaris
 Lithobius_forficatus
 Meinertellus_cundinamarcensis
 Machilis_hrabei
 Tricholepidion_gertschi
 Atelura_formicaria1
 Atelura_formicaria2
 Speleonectes_cf_tumulensis
 Anurida_maritima
 Pogonognathellus_sp
 Folsomia_candida
 Sminthurus_viridis
 Ephemera_danica
 Triops_cancriciformis
 Eurylophella_sp
 Ixodes_scapularis
 Ixodes_ricinus
 Ladona_fulva
 Menopon_gallinae
 Pseudomallada_prasinus
 Liposcelis_bostrychophila
 Diaphorina_citri
 Apachyus_sp
 Pachypsylla_venusta
 Cryptocercus_wrighti
 Orussus_abietinus

PETIRCQREGMFHESE-----PCIAGNSN-----
 IDTVRCQKDGNFHQHE-----PCIAGFMNCHHYN-G
 PETLRCQREGFFHERE-----PCIAGSAPCRKNT-G
 PDSIHCQNEGMFYDLE-----PCTAGTMNCRKNT-G
 SDSLKCKYEGLFNGPE-----PCIAGNSSCRWKH-G
 KETSVCQLEDLKSNVPCQP-----YGKICDKVEF-G
 HYSSPCRAENLIP-TPCKI-----PGKLCSSGE--G
 RESAICRFENLSPIPCDND-----VLSCGP-----DGA
 PESAVCHLENLSPVPCDND-----TPSCG-----LGA
 RESAICRLENLYSLPCQNE-----GRACG-----TDG
 RESVICRYENLQVIPCCKK-----GKICETV-----PHG
 REAFLCRSENLVPTVCSNDD-----LKACGRQ-----REG
 REARMCHAENLVPVTCANRD-----LKSCGRM-----QEG
 RESSSCRAENLFPVQCENR-----ARPCGSE-----RSG
 REASACRAENLFPVQCENK-----ARPCGSE-----RSG
 R-----G
 RD-PVCRGEMSAAPGLCTNP-----GRPCG-----VG
 RD-ASCRREMSAPGLCINQ-----GRPCG-----VG
 REAAVCQENFYPVPCANR-----GGQCGG-----ESG
 RDTAVCQTEFNTPVPCGNR-----GPSCG-----ESG
 RDTAVCQ-----

 PETVACRSEARFS-TPCLNP-----GISCSG-SGSLSIK
 AETFVCQLENRFP-TPCHNP-----GSSCSGNGDTGLING
 SETLTCFQENLMYNTPCQNP-----GESCSGNDATNPING
 PETYSCQLENRHT-TLCQNP-----GATCAGPNGD-ISGG
 PLEVFMPLCLVESLQPTP-----CRNQAASNCGLTGDE

 STEPSLLPCLAESMQTTP-----CRNRAASCGQSGAG
 ALHGVACHVPGKRCGTDR-----CAIRGYCCGPDGCT
 SLLGVDFQRMSFYRMPDY-----
 KSNLPLLRPCAIEAGLPG-----ACISGSKRCGNSGG
 RYTDPCRSIQNTRIS-----CLSEVNVQTCGDKG

 PSTKICRRVREFPES-----CLSSFN--PCNGG
 KCGVDYKTCGSSRE-----VMEEYALCLSKGL

 GD-----
 SL-----
 ADTTKSATEACWENKEFL-----NDNGNQRKMKMLT

Calanus_finmarchicus1
 Calanus_finmarchicus3
 Daphnia_pulex
 Daphnia_magna
 Lepeophtheirus_salmonis
 Caligus_rogercresseyi
 Dermatophagoides_farina
 Sarcoptes_scabiei
 Symphylella_vulgaris
 Tigrionus_californicus
 Metaseiulus_occidentalis
 Varroa_destructor
 Gryllotalpa_sp
 Teleogryllus_commodus
 Haploembia_palau
 Aposthonia_japonica
 Zootermopsis_nevadensis
 Blattella_germanica
 Galloisiana_yuasai
 Locusta_migratoria_manilensis
 Nilaparvata_lugens
 Halyomorpha_halys
 Homalodisca_vitripennis
 Gynaikothrips_ficorum
 Cotesia_vestalis
 Microplitis_demolitor
 Fopius_arisanus
 Diachasma_alloem
 Telenomus_podisi
 Nasonia_giraulti
 Nasonia_vitripennis
 Copidosoma_floridanum
 Trichogramma_pretiosum
 Brachyistis_timberlakei
 Crioscilia_alcione

151 200
 FSIPICIGPYCNGNEKIMIRKEKQSQEKKSDDKVLDGSSNYDSLVIYNNLS

 VCLLTNLKSTQICNQHFWKTDLKSASCSLNGDKIDGICVADLLCCSLGNL
 ICLLTNLKSRSRSCDERFWQYFKSAPCSLNGDKLDGICVADRLCCSLGQC
 QCVFDNYCCNSSSGTCRFVVEELICSVSDDKKNYEKEKELVDDLQKNMIYI
 QCVFENYCCSPSGTCRFVDESICSNSTVPLGDS---DFMEDFRRLFLA
 VCALNATCCCTNG---KYFICFFYCKKN-----
 ICAINSTCCTDS---KI-----
 RCAVEGLCCCTGDG-CFYEDTCRDS-----SLLTSSLHHSSTLEDET
 FCATNGFCNDQGECTPEEKCLVENLSDFPSPFILRRHLSSASLASRPT
 YCALNRLCCCTSDS-CTLDESCSSAKDRDILRESLMLN-----
 HCALNRFCCCTS-----
 HCGANNICCTQDS-CYSDQTCQFGFPVE-----
 FCATSTLCCCTQVS-CHTDPSQCFVAVAGHKVSGATDLALPHRSYVYSLLN
 KCAADGVCCCTPES-CEID-----
 KCAADSI CCTPDS-CEIDASCRFGS--PQHFRNVGIYPQVVE-----
 RCTANGVCCCTHES-CHIDITCQLTT--SDAPELIDVSADQTNPLYSLYS-
 RCAANGVCCCTHES-CHIDVSCHPA--TDIAIGNTDQLNSFYNLNVISS
 KCAANGICCTSES-CHVDMSCRLTSRGEDDVIQFPDLSSDAKGVFLFSN
 -CSAPGVCCSQDS-CHIDPSCVADTEPADRYALDIFAVNDGDRDDMRI-
 VCSTDGVCCNSSES-CRIDPTCEVDPDHNVCNVWTEPKNMAL-----
 VCLADGVCCSPDG-CKMDMSCEVEQSVDVCSLAEQVY-----
 VCATDGVCCNSGG-LYFPS---PQIRHIYRNFEISQY-----
 ICAANGLCCTSDW-CRADDRLSSASQSNLVIPDHNL PANTRQEPQAEF
 RCAANGICCSQES-CFLDSSCKIGDEFL-----SDRKIDQEF SRLIGEN
 RCAANGICCSQES-CHVDPSCRVGEYFL-----SERKISQEF SRLIADN
 RCAANGICCSQEN-CHADSSCRVGEFES-----DRKIVQEYSRLSPEN
 RCAANGICCSQEN-CHVDSSCRISDEFN-----DRKIQEYSRLSPEN
 RCAANGICCSQEA-CYAD-----
 RCAANGICCSQES-CFIDSACKLVDETG-----NDRKIGAEFGAFLLN
 RCAANGICCSQES-CFIDSACKLVDETG-----NDRKIGAEFGAFLLN
 RCAANGICCSQES-CFTDSACKLVDESG-----NDRKIGAEFGAFLLN
 RCAANGICCSQES-CFIDPACKLVDEN-----NDRKIGAEFGAFLLN
 RCAANGICCSQES-CSMDAMCKIPDALR-----HDRKFD-SDVSSILSE

Chrysis_viridula RCAANGICCSQET-CHMDSTCRISDVDT-----RDRKEEGVDVAAVLSD
 Trachymyrmex_septentrionalis RCASNGICCSQAS-CHMDTSCKISDVG-----NDRKLD-DNVNVILPG
 Trachymyrmex_cornetzi RCASNGICCSQAS-CHMDTSCKISDVG-----NDRKLD-DNVNVILPG
 Atta_cephalotes RCASNGICCSQAF-CHMDTSCKISDVG-----NDRKLD-DNVNVILPG
 Trachymyrmex_zeteki RCASNGICCSQAS-CHMDTSCKISDVG-----NDRKLD-DNVNVILPG
 Acromyrmex_echinator RCASDGI CCSQAS-CHMDTSCKISDVG-----NDRNLD-DNVNVILPG
 Vollenhovia_emoryi RCASSGICCSQES-CHMDTSCRIPDVVG-----NDKKLD-ANLNVILPG
 Solenopsis_invicta RCASNGICCSQES-CHMDTSCRISDVVG-----NDRKLD-ANLNVIFPD
 Monomorium_sp RCALNGICCSQES-CHMDTSCKISNVVG-----NNQKLD-DNLNVILSG
 Wasmannia_auropunctata RCASNGICCSQES-CNMDTSCKISDVG-----NDRKLD-ANLNVILSG
 Harpegnathos_saltator RCATNGICCSQDS-CHMDTSCRISDVVS-----NDRKMD-ADLSAILSS
 Dinoponera_quadriceps RCATNGICCSQES-CHMDTSCRISDVVG-----NDRKMD-TDLNVILSS
 Cerapachys_biroi RCATNGICCSQES-CHMDTSCRISDVG-----NDRKID-ADLNVMFPG
 Linepithema_humile RCATNGICCSQES-CHMDTSCRISNVD-----NNRKID-TDLNMIIPG
 Pogonomyrmex_barbatus RCASNGICCSQES-CYIDSSCRISNAV-----SDRKLD-ADLNVLPG
 Camponotus_floridanus RCAANGICCSQ-----
 Pseudomasaris_vespoides RCAANGICCSQES-CFIDNTRIPDIMA-----KDQKID-SDINMIFGE
 Chyphotes_mellipes RCAAAGICCSQES-CHIDASCRLETSDDGGGNGHERRFSDLSAILSEN
 Athalia_roseae RCAAAGICCSQES-CHADSCKVTDNFAN-NQGISFDLNTLFSNTSLN
 Neodiprion_lecontei RCAANGICCSQES-CYVDPNCKVRSDI IQMSKQVTSFDMDKIYSESNLN
 Cephus_cinctus RCAANGICCTQES-CYVDDTCRITDDVNDHRIIS--ELNGFLNEGNVLA
 Polistes_canadensis RCGAGGICCSQDS-CFIDPSCRFTVDSS-FRRSIDSCLKAIASEIILK
 Polistes_metricus RCGAGGICCSQDS-CFIDPSCRFTVDSP-FRRSIDSCLKAIASEIILK
 Polistes_dominula RCGAAGICCSQNS-CFIDPSCRFPFDDWPGRQKIDSCLKAIASEIILKEE
 Mischoctytarus_flavitaris RCAAIGICCSQES-CFLDPICRSLDNLVGRKFNT-----
 Corydalus_cornutus RCAAADGICCTQES-CHTDSSCAFDEERHRSNGRPAIPIESIFSVLSPY
 Onthophagus_taurus RCASEGICCTQGN-F-----
 Aleochara_curtula RCAAEGICCSQ-----
 Nicrophorus_vespilloides RCAAEGLCSSQGI-I IQLLLLLHLRLTHRLHHPMMI-----
 Oryctes_borbonicus RCATDGVCCSQGI-RYIDS-----
 Anoplophora_glabripennis RCAAIDGICCSQGN-NSGFLKLLKNNLFLSLQILVMSTNNARWKTGAGFFP
 Leptinotarsa_decemlineata1 RCAAEEKICCTQGI-WTFFLVSN-----
 Leptinotarsa_decemlineata2 RCATENICCTQGI-FKIRSYT-----
 Priacma_serrata TMCQRGHMLHARL-LPHRQNYAHLTTNKQN-----
 Gyrimus_marinus -----
 Dendroctonus_ponderosae -----
 Meloe_violaceus RCATDGI CCNQDS-CHIDKTCISITTTIGFIENEKTRNFLETSPADLYNFI
 Tribolium_castaneum RCAFDPGICCSQDS-CHADKSCASD-----DKSPIDLYTLI
 Hypothenemus_hampeii RCATNGICCSQGK-RTVLVNSSSVYN-----
 Agrilus_planipennis RCATQGVCCNQGK-CFTSFYLLLNVLDISPYQGI IRRKVLLNKNLTMVGT
 Arachnocampa_luminosa RCATSNLCCNPEH-CLEDSTCVSEENDYSEYKEIDTKLLKALKRLISKK
 Tetranychus_urticae VCTSNGICCSNSDG-CFNDSTCENDK-----LSNMQRIFTSD
 Scolopendra_subspinipes1 KCAAADGLCCSSDQ-CKMEERC-----
 Scolopendra_subspinipes2 NCAVDGLCCNTSQ-CKRDERC-----
 Strigamia_maritima TCSADGFCSTDQ-CKADESCRGVHHTN-----NLQRVL
 Limulus_polyphemus YCAAAPGICCSAIQ-CAVDDECPTGVLDKG-----VAYKYD
 Litopenaeus_vannamei RCASSGVCCTEVK-CEFDINCVIEG-----VDRHRY
 Homarus_americanus RCAAAGLCCCTEMK-CEFDSSCTVEGREERVGKQ-----RAERQHL
 Occasjapyx_japonicus KCAAAVGICCTEDS--CTSDQTCRASPGKEAVAAVLPGRGSRPQLPSDLV
 Catajapyx_aquilonaris KCAAAMGLCCCTEAD-SCTSDSACRGAPSKEVVAASRGQR---PQQLPSDLV
 Lithobius_forficatus KCHLFP-----
 Meinertellus_cundinamarcensis KCAAQGVCCSETA-CALDSMCLDSWPS-----RNVVQ-----MNSGLA
 Machilis_hrabei VCAAQGVCCSETS-CALDASCMDSWSP-----RQLVP-----VNGLS
 Tricholepidion_gertschi RCAAATGVCCTEES-CSIDPSCHVTPOETILTPVSRQMYP-----INSAMN
 Atelura_formicarial RCAAANGVCCTEET-CTIDPSCRISNED--ISSSRQMFP-----ITNSVS
 Atelura_formicaria2 -----
 Speleonectes_cf_tumulensis -----AATSAP
 Anurida_maritima QCTGDGICCSSET-CTHDENCWERSMT-----SGTGDSQE
 Pogonognathellus_sp QCG-----
 Folsomia_candida QCATLGVCCSSDT-CTIDNCHKKDEQQNVSGHSRSTVAMDGSHTKHEHAT
 Sminthurus_viridis QCGAEGICCSNET-CTMDETCHEASVTRES-----VAKLSGL
 Ephemera_danica LCAAAPGICCSQGK-----
 Triops_cancriformis -----
 Eurylophella_sp QCASQGICCLQDSCHADVCKHENYD-----
 Ixodes_scapularis KDSSCSGGVPTDQFGSAVDILEYGMSE-----
 Ixodes_ricinus -----
 Ladona_fulva RCASDGI CCNDGKRN-----
 Menopon_gallinae RCKAKFICCSRDQCVMDLSCKSMPPAKYRDVNE-----
 Pseudomallada_prasinus -----KISTDSIKP-----
 Liposcelis_bostrychophila LCVARNVCCPKNLCRIDDTCKTIPYVDLGYRLGTSIDLNRLSSYSVDYPL
 Diaphorina_citri ACIDLNTLKC CNMYA IKVPTEVKLQLHQ-----
 Apachyus_sp -----
 Pachyphylla_venusta -----
 Cryptocercus_wrighti -----
 Orussus_abietinus ELFKRRRCKSKFINDTSIPSPNILI-----

Calanus_finmarchicus1
 Calanus_finmarchicus3
 Daphnia_pulex
 Daphnia_magna
 Lepeophtheirus_salmonis
 Caligus_rogercresseyi
 Dermatophagoides_farina
 Sarcoptes_scabiei
 Symphylella_vulgaris
 Tigriopus_californicus
 Metaseiulus_occidentalis
 Varroa_destructor
 Gryllotalpa_sp
 Teleogryllus_commodus
 Haploembia_palau
 Aposthonia_japonica
 Zootermopsis_nevadensis
 Blattella_germanica
 Galloisiana_yuasai
 Locusta_migratoria_manilensis
 Nilaparvata_lugens
 Halyomorpha_halys
 Homalodisca_vitripennis
 Gynaikothrips_ficorum
 Cotesia_vestalis
 Microplitis_demolitor
 Fopius_arisanus
 Diachasma_alloeum
 Telenomus_podisi
 Nasonia_giraulti
 Nasonia_vitripennis
 Copidosoma_floridanum
 Trichogramma_pretiosum
 Brachycistis_timberlakei
 Crioscobia_alcione
 Chrysis_viridula
 Trachymyrmex_septentrionalis
 Trachymyrmex_cornetzi
 Atta_cephalotes
 Trachymyrmex_zeteki
 Acromyrmex_echinatior
 Vollenhovia_emeryi
 Solenopsis_invicta
 Monomorium_sp
 Wasmannia_auropunctata
 Harpegnathos_saltator
 Dinoponera_quadriceps
 Cerapachys_biroi
 Linepithema_humile
 Pogonomyrmex_barbatus
 Camponotus_floridanus
 Pseudomasaris_vespoides
 Chyphotes_mellipes
 Athalia_rosae
 Neodiprion_lecontei
 Cephus_cinctus
 Polistes_canadensis
 Polistes_metricus
 Polistes_dominula
 Mischocyttarus_flavitaris
 Corydalus_cornutus
 Onthophagus_taurus
 Aleochara_curtula
 Nicrophorus_vespilloides
 Oryctes_borbonicus
 Anoplophora_glabripennis
 Leptinotarsa_decemlineata1
 Leptinotarsa_decemlineata2
 Priacma_serrata
 Gyrinus_marinus
 Dendroctonus_ponderosae
 Meloe_violaceus
 Tribolium_castaneum
 Hypothenemus_hampe
 Agrilus_planipennis
 Arachnocampa_luminosa

201
 NQRCNWMDLYLAR-----

 PQDDL-----
 KQNFAC-----
 RRQAYLGNQVPRLQQLNINDLEQ-----
 RELHSL-----

 TQ-----
 VEKAMITIPQPNKAYQEALNMQIIPKSNLSALNKYLSRHGDVK-----

 ALAKNQDHNPNQNNVE-----

 SYQQENPGLGLSE-----
 AYQQENP-----
 LGSYEPDHQAYRLPSNVERD-----

 NDWHS-----
 DQMIN-----
 DQLIN-----
 E-----
 EQ-----

 AGTNEHIL-----
 AGTNEHIL-----
 AGANERILR-----
 SGRNEHIL-----
 SEISNEII-----

 NELSADSVQ-----
 NEVSNEILQ-----
 NEVSNEILQ-----
 -EVSNEILQ-----
 NEVSNEILQ-----
 NEVSNEILQ-----
 SEVSSEILQ-----
 NEVSSDILQ-----
 NEISSEIPQ-----
 NEVSSDLF-----
 NEASHEIIQ-----
 NEVSHEILQ-----
 NEASSETFP-----
 NEVSSEILQ-----
 NEVSNEMFQ-----

 NEISNELTQ-----
 VGTSVEMVR-----
 DQ-----
 DE-----
 DHNQ-----
 EEAK-----
 EEAK-----
 AM-----

 RS-----

 ITLWEWICII-----

 NYQSELNSE-----
 NYQAEALAGDK-----

 LNIE-----
 RQKNENYKSHNIDNYQS-----

Tetranychus_urticae	-----
Scolopendra_subspinipes1	-----
Scolopendra_subspinipes2	-----
Strigamia_maritima	DGEIDLNDVMGPQR-----
Limulus_polyphemus	HLRFVLLPWNMNGKLPD-----
Litopenaeus_vannamei	SLLDRTLTEAQWRI-----
Homarus_americanus	TFLSSLPEDQWNL-----
Occasjapyx_japonicus	SFLEEVVDNMAPASGSEV-----
Catajapyx_aquilonaris	SFLEEVVENIAPASAPEV-----
Lithobius_forficatus	-----
Meinertellus_cundinamarcensis	SVLENMLEEVPSENGDDKK-----
Machilis_hrabei	SVLENMLEDIPMESGDDRR-----
Tricholepidion_gertschi	NYLEEAVDALPSHVILENRR-----
Atelura_formicaria1	MYLEELNDDLPARVGSDDR-----
Atelura_formicaria2	-----
Speleonectes_cf_tumulensis	KNRRLPVRE---LLPCL-----
Anurida_maritima	FNQDLPLREDRFLIPLPATHEKFRSFPISQIRVGRKKNQFEDLRNHLH-----
Pogonognathellus_sp	-----
Folsomia_candida	TMFQNLDRWIPRRFGLGRPTGQRKHVRIGVKPDAQILAPENSLMDRLVI-----
Sminthurus_viridis	YHHRYPDLVVFRFVDGQHSQHRLPARLPLPTQSSSSSNDY-----
Ephemera_danica	-----
Triops_cancriformis	-----
Eurylophella_sp	-----
Ixodes_scapularis	-----
Ixodes_ricinus	-----
Ladona_fulva	-----
Menopon_gallinae	-----
Pseudomallada_prasinus	-----
Liposcelis_bostrychophila	ELPSNMPIGSTSLDEVWGSKEDSIVPNYNFKIEAS-----
Diaphorina_citri	-----
Apachyus_sp	-----
Pachyphylla_venusta	-----
Cryptocercus_wrighti	-----
Orussus_abietinus	-----

251

Calanus_finmarchicus1	-----
Calanus_finmarchicus3	-----
Daphnia_pulex	-----
Daphnia_magna	-----
Lepeophtheirus_salmonis	-----
Caligus_rogercresseyi	-----
Dermatophagoides_farina	-----
Sarcoptes_scabiei	-----
Symphylella_vulgaris	-----
Tigriopus_californicus	-----
Metaseiulus_occidentalis	-----
Varroa_destructor	-----
Grylotalpa_sp	-----
Teleogryllus_commodus	-----
Haploembia_palau	-----
Aposthonia_japonica	-----
Zootermopsis_nevadensis	-----
Blattella_germanica	-----
Galloisiana_yuasai	-----
Locusta_migratoria_manilensis	-----
Nilaparvata_lugens	-----
Halyomorpha_halys	-----
Homalodisca_vitripennis	-----
Gynaikothrips_ficorum	-----
Cotesia_vestalis	-----
Microplitis_demolitor	-----
Fopius_arisanus	-----
Diachasma_alloeum	-----
Telenomus_podisi	-----
Nasonia_giraulti	-----
Nasonia_vitripennis	-----
Copidosoma_floridanum	-----
Trichogramma_pretiosum	-----
Brachycistis_timberlakei	-----
Crioscolia_alcione	-----
Chrysis_viridula	-----
Trachymyrmex_septentrionalis	-----
Trachymyrmex_cornetzi	-----
Atta_cephalotes	-----
Trachymyrmex_zeteki	-----
Acromyrmex_echinatior	-----

Vollenhovia_emeryi	-----
Solenopsis_invicta	-----
Monomorium_sp	-----
Wasmannia_auropunctata	-----
Harpegnathos_saltator	-----
Dinoponera_quadriceps	-----
Cerapachys_biroi	-----
Linepithema_humile	-----
Pogonomyrmex_barbatus	-----
Camponotus_floridanus	-----
Pseudomasaris_vespoides	-----
Chyphotes_mellipes	-----
Athalia_rosae	-----
Neodiprion_lecontei	-----
Cephus_cinctus	-----
Polistes-c_canadensis	-----
Polistes-m_metricus	-----
Polistes_dominula	-----
Mischocyttarus_flavitaris	-----
Corydalus_cornutus	-----
Onthophagus_taurus	-----
Aleochara_curtula	-----
Nicrophorus_vespilloides	-----
Oryctes_borbonicus	-----
Anoplophora_glabripennis	-----
Leptinotarsa_decemlineata1	-----
Leptinotarsa_decemlineata2	-----
Priacma_serrata	-----
Gyrinus_marinus	-----
Dendroctonus_ponderosae	-----
Meloe_violaceus	-----
Tribolium_castaneum	-----
Hypothenemus_hampeii	-----
Agrilus_planipennis	-----
Arachnocampa_luminosa	-----
Tetranychus_urticae	-----
Scolopendra_subspinipes1	-----
Scolopendra_subspinipes2	-----
Strigamia_maritima	-----
Limulus_polyphemus	-----
Litopenaeus_vannamei	-----
Homarus_americanus	-----
Occasjapyx_japonicus	-----
Catajapyx_aquilonaris	-----
Lithobius_forficatus	-----
Meinertellus_cundinamarcensis	-----
Machilis_hrabei	-----
Tricholepidion_gertschi	-----
Atelura_formicaria1	-----
Atelura_formicaria2	-----
Speleonectes_cf_tumulensis	-----
Anurida_maritima	RPQMDFQPPISSTESLYP-
Pogonognathellus_sp	-----
Folsomia_candida	FPDTSGRISSEY-----
Sminthurus_viridis	-----
Ephemera_danica	-----
Triops_cancriformis	-----
Eurylophella_sp	-----
Ixodes_scapularis	-----
Ixodes_ricinus	-----
Ladona_fulva	-----
Menopon_gallinae	-----
Pseudomallada_prasinus	-----
Liposcelis_bostrychophila	-----
Diaphorina_citri	-----
Apachyus_sp	-----
Pachypsylla_venusta	-----
Cryptocercus_wrighti	-----
Orussus_abietinus	-----

(B)

	1	50
Tenthredo_koehleri	-----CPACGPD-RQGQCFGPKI	CCGPS---
Tetramorium_bicarinaratum	-----GDIAPLGTIVRECPSCGPN-HLGQCFGPHI	CCGPS---
Ceratosolen_solmsi_marchali	MTNYPRGGKR-----AMFANPTFLLD-KIAREFGPHI	CCGPT---
Lepicerus_sp	-VNCPRGGKRGELPFLSIQGLVKECQSCGPG-HQGQCFGPNI	CCGTN---
Inocellia_crassicornis	-----	-----
Osmylus_fulvicephalus	-----SVYFFGKSMYTLQCIISCGPQ-RSGQCFGPAI	CCGP---
Aethina_tumida	-----CVSCGPG-HTGQCFGPSI	CCGP---
Pogonus_chalceus	-----CIACGPG-HSGQCFGPNI	CCGP---
Dastarcus_helophoroides	-----QCIPCGPA-RTGQCFGPNI	CCGP---
Diabrotica_virgifera_virgifera	-----GQCFGPNI	CCGP---
Prorhinotermes_simplex	-----QCARC GPA-KLEHCYGP	CCGPQ---
Periplaneta_americana	-----	-----
Ceuthophilus_sp	-----CARCGPA-KLGHCYGP	CCAPQ---
Blaberus_atropos	---IFFLCNVDIKIMHLKYLDTKQCARC GPA-KLGHCYGP	CCGPQ---
Medauroidea_extradentata	-----VTHFNSSPGFKHKKCPRCGPA-KLGHCYGDNI	CCGVE---
Oncopeltus_fasciatus	-----FLLLFKCKIYFFQQAFFRCEPD-REGRLGRAI	CCGPK---
Scylla_paramamosain	-----GRCVGPDI	CCGAR---
Campodea_augens	-----GRCFSPDL	CCGPE---
Baetis_sp	-----	-----
Isonychia_bicolor	-----ACLQCARC GF-LAGRCFGPRI	CCDTR---
Tetradontophora_bielanensis	-----IPEQHNTNKVRE CASCGPVGQGRCYGPET	CCGPN---
Frankliniella_occidentalis	-----QCTPCGPG-GEGLCVGPGI	CCSPV---
Calanus_finmarchicus2	-----PVSGKKRSLHVGEEQVRD GELT C P S N P A G L C Y S P L C	CCVQGGCY

	51	100
Tenthredo_koehleri	--IGCFID-----TAETHKCRKESLYS--RPCTAGFA-	
Tetramorium_bicarinaratum	--IGCFIG-----TSETYRCRKESLYT--RPCVAGYA-	
Ceratosolen_solmsi_marchali	--MGCLLG-----TPEAHCQKESLYS--QPYVAGFA-	
Lepicerus_sp	--IGCFIG-----TPETYKCKMESLYS--RPCIAGFS-	
Inocellia_crassicornis	--FGCLVG-----TPETIRCERDGA FQEREPCIAGRS-	
Osmylus_fulvicephalus	--FGCLIA-----TAETTRCERDGA FHEREPICAGKS-	
Aethina_tumida	--FGCLMG-----TSETIRCQREGFFQEREPCIAGSS-	
Pogonus_chalceus	--FGCLIG-----TSETLKCQREGFFQEP EPCIAGNG-	
Dastarcus_helophoroides	--FGCLVG-----TPDTIKCQREGFFHERDPC IAGNS-	
Diabrotica_virgifera_virgifera	--FGCLLG-----SPETVRCQREGSFHEREPIC IAGSG-	
Prorhinotermes_simplex	--IGCLVA-----TPETARCLTEAASP--VPCIAPTGV	
Periplaneta_americana	---GCLIA-----TPDTARCLSEASP--VPCIAPTGA	
Ceuthophilus_sp	--FGCLIG-----TPDTPCQREDQSP--IPCIGTG--	
Blaberus_atropos	--IGCLIA-----TPDTARCLNEASP--IPCTA--	
Medauroidea_extradentata	--IGCLLA-----TPDQVCQRESMTP--DPCVGP I G-	
Oncopeltus_fasciatus	--IGCLVG-----TPAILSQCS EQPPE--LPYSKPYS-	
Scylla_paramamosain	--IGCF LG-----SRETRMCR TENMVPITCYN S D L K P C-	
Campodea_augens	--IGCYFR-----TKESSVCKSENLFVPVPCEN-PAKSC	
Baetis_sp	-----VAPAATA-----SNLALLPCVAESLFP EPCSNGPTVRC	
Isonychia_bicolor	--LGMVGSAMEP-----LQAE L L P C L A E S I F P A A C H N - H A A T C	
Tetradontophora_bielanensis	--FGCMVG-----TPETHCLIEDRIN--	
Frankliniella_occidentalis	--FGCVLTSRGGCGRGAVFAPRCSPSSAALAAASAAAVPLDAPCGADLTP	
Calanus_finmarchicus2	ADGGCLPG-----LTERGEEQIKTRESVSKRGLRFLY G	

	101	150
Tenthredo_koehleri	--MCRGNTGRCAADGICCSQESQVDPNCKITDDSITS-----	
Tetramorium_bicarinaratum	--MCRGNTARCASNGICCSQDSCYVDASCNSD GVRNDQKFDANLNEVLP	
Ceratosolen_solmsi_marchali	--MCRGNSGRCAANGIMNIPKNHVSLIHHAN-----	
Lepicerus_sp	--MCRDNNRC-----	
Inocellia_crassicornis	--NCRGDTGRCAADGICCTQGNYE-----	
Osmylus_fulvicephalus	--SCRGDTGRCAF D G I C C T Q G M C T V Q L K L G L K S L P N A I R L I -----	
Aethina_tumida	--FCRKNTGRCAIDGICCNQESCHVDKHC SLDEKKSSENLMGMEL-----	
Pogonus_chalceus	--YCRKNTGRCAADGVCC T Q-----	
Dastarcus_helophoroides	--SCRKNTGRCAADGICCS-----	
Diabrotica_virgifera_virgifera	--FCRKNTGRCATDNI C C D Q D S C Y T D R Q C S S D E K L K A E A L S G L D I Y N F L N	
Prorhinotermes_simplex	QCGEGKLAGRCTANGVCC THGKQSS T M Y C L Y V F N Q A Q V Q L -----	
Periplaneta_americana	QCGEGKSAGRCTANGVCC THGEASQNIYNLQYSFITSTTFLLPYLLEILK	
Ceuthophilus_sp	SGPRCQE QHCTANEVCC T Q E S C H I D P T C R L T L P A E G G L P D G P D A T T D L S	
Blaberus_atropos	-----	
Medauroidea_extradentata	-GAPCGNSGKCAAPGVCC T P D S C T I D P T C H Q T L S Q E M A S L Y L Y N A G N A R G	
Oncopeltus_fasciatus	-----IGVCLSDGGLLFIG-----	
Scylla_paramamosain	G---RMQEGRCGAPGICCTENKCEMNDDCVAEDTQGE-----	
Campodea_augens	G---TDRNGK CAGQGLCC TEDSCTVDSSCHVILKDLPPPPAAVAPPSPW	
Baetis_sp	G---RGAKGVCAAPGVCC F H N S C E T D A S C A K M R R -----	
Isonychia_bicolor	G---RMA T G Q C A A T G L C C Y Q D S C H P D M T C R G R S E -----	
Tetradontophora_bielanensis	-----SVCHNPGIPCTVNV D N G N I N G F C A T G -----	
Frankliniella_occidentalis	D---GSAPGRCAAQGVCC TH-----	
Calanus_finmarchicus2	MAPSQMNLFGQEGMAIPCIGPYCNGKGARSHGKQKQRKRKQSQEHVNRDQ	

151

Tenthredo_koehleri	-----
Tetramorium_bicarinatum	GNFESREIM-----
Ceratosolen_solmsi_marchali	-----
Lepicerus_sp	-----
Inocellia_crassicornis	-----
Osmylus_fulvicephalus	-----
Aethina_tumida	-----
Pogonus_chalceus	-----
Dastarcus_helophoroides	-----
Diabrotica_virgifera_virgifera	TY-----
Prorhinotermes_simplex	-----
Periplaneta_americana	YISQ-----
Ceuthophilus_sp	DRNLVYSLFNAISTYQ-----
Blaberus_atropos	-----
Medauroidea_extradentata	VSQISDVDDK-----
Oncopeltus_fasciatus	-----
Scylla_paramamosain	-----VEESQRGGRPRDLLAAARDRWEEQ--
Campodea_augens	LKYPSVFRVLQQQQPNTDLSSATGALWDDMLE
Baetis_sp	-----VNAIARESNAFA-----
Isonychia_bicolor	-----
Tetradontophora_bielanensis	-----
Frankliniella_occidentalis	-----
Calanus_finmarchicus2	ALLGSSNYDSAVSDDQFLKHNCWMDLYLAR--

Supplementary Figure S2. Alignment of multiple copies of inotocin precursors and receptors. Relevant parts of the sequences (inotocin peptides and transmembrane domain; TM) are highlighted in yellow. Transmembrane domains were assigned according to the human neuropeptide S receptor (GeneBank: NP_997055)¹ after alignment with the receptors. (A) Inotocin precursors and (B) inotocin receptors. Multiple copies of precursors were only found in 4 species; multiple copies of receptors were only found in eight species.

(A)

Alignment of 2 inotocin precursor sequences of *Scolopendra subspinipes*:
 mature peptide
 Scolopendra_subspinipes1 -----HWLLFFYVIGMTSSCFITNCPE--GKRSLGEHKRTLROCTACGPGSQGRCFGP
 Scolopendra_subspinipes2 MRSSTCHWILYLSLVGLVSAFYIINCIDNDGRKRSIDHQKKAIRQCMSCGPGMKGRCFGP
 **::: :*: :*: :*: :* * * * * : :*: :*: :*: :*: :* * * * *
 Scolopendra_subspinipes1 DLCCGEFFGCVLKTRESAICRFENLSPICDNDVLSGPDGAKAADGLCCSSDQKMEE
 Scolopendra_subspinipes2 DLCCIESFGCFQTQTPESAVCHLENLSPVPCDNDTPSCGL-GANCAVDGLCCNTSQCKRDE
 * * * * * : * * * * * : * * * * * : * * * * * : * * * * * : * * * * * : * * * * * : * * * * *
 Scolopendra_subspinipes1 RCR
 Scolopendra_subspinipes2 RC-
 **

Alignment of 3 inotocin precursor sequences of *Calanus finmarchicus*:
 mature peptide
 Calanus_finmarchicus2 -----PVSQKRLSHVG---EEQVRDG
 Calanus_finmarchicus1 MITSWKILDPRIRRSWFLIILLAQTMSASHGCFISNCPVSGKRSVGEQMVFSQAREE
 Calanus_finmarchicus3 MITSLKILDPSIRRSWFLMILLAHTIPDSHGCFISNCPVSGKRSVGEQVLSFQAREE
 * * * * * : : * * * * * : * * * * * : * * * * * : * * * * * : * * * * *
 Calanus_finmarchicus2 ELTCPSPNAGLCYSPGLCCVQGGCYADGGCLPGLTERGEEQIKRESVSKRGLRFLYGMA
 Calanus_finmarchicus1 VLACPSNPAGLCYSPGLCCVQGGCYADKGLPQMEESRENVEP--RLNKRDLRFLYGWA
 Calanus_finmarchicus3 VLACPSNPAGLCYSPGLCCIQAACYADM-----
 * : * * * * * : * * * * * : * * * * * : * * * * * : * * * * * : * * * * * : * * * * *
 Calanus_finmarchicus2 PSQMNLFQGEAIPICIGPYCNGK GARSHGKQKQKRKQSQEHVNRDQALLGSSNYDSAV
 Calanus_finmarchicus1 PAHEKMFQGTGF SIPCIGPYCNGNEKMI-----MRKEKQSQEKSSDDKVLGDSSNYDSL
 Calanus_finmarchicus3 -----
 Calanus_finmarchicus2 SDDQFLKHNCDWMDLYLAR
 Calanus_finmarchicus1 YNENLSNQR CNWMDLYLAR
 Calanus_finmarchicus3 -----

Alignment of 2 inotocin precursor sequences of *Atelura formicaria*:
 mature peptide
 Atelura_formicaria1 -----ACFITNCPPGKRSMGQMLHVNKQCTSCGPARTGRCYG
 Atelura_formicaria2 SLSKGILSVTIFFLAVISVTTACFITNCPPGKRSMGQMLHANKQCTSCGPARGRCYG
 * * * * * : * * * * * : * * * * * : * * * * * : * * * * * : * * * * * : * * * * *
 Atelura_formicaria1 PAICCGPRFGCLVGRDITAVCQTE NFTPVPVCGNRGPSCGESGRCAANGVCCTEETCTIDP
 Atelura_formicaria2 PAICCGPRFGCLVGRDITAVCQ-----
 * * * * * : * * * * * : * * * * * : * * * * * : * * * * * : * * * * * : * * * * *
 Atelura_formicaria1 SCRISNEDISSSRQMPFITNSVSMYLEELNDDLPARVGSDDR
 Atelura_formicaria2 -----

Alignment of 2 inotocin precursor sequences of *Leptinotarsa decemlineata*:
 mature peptide
 Leptinotarsa_decemlineata1 MVRSVPLTIIYLFIFVMYVESCLITNCPGGKRGGEFSTSESNIKTIVSINLNNYKHILQC
 Leptinotarsa_decemlineata2 MSKTVSLFTLFLSVFVIFVESCLITNCPIGGKRSGKFSLTESNI-----KQC
 * : * * * : * * * * : * * * * * : * * * * * : * * * * * : * * * * * : * * * * *
 Leptinotarsa_decemlineata1 ISCGPGHTGKCFGNICCGPFGCLLGSPE TERCHKEGLFQETEPICIAGFSTCRKNTGRCA
 Leptinotarsa_decemlineata2 ISCGPGHTGQCFGNICCGPFGCLMGSHE TFGQRGG-FHESEPCIAGFSSCRKNTGRCA
 * * * * * : * * * * * : * * * * * : * * * * * : * * * * * : * * * * * : * * * * *
 Leptinotarsa_decemlineata1 AEKICCTQG IWTFFLVSN
 Leptinotarsa_decemlineata2 TENICCTQGIKIRSYT-
 : * : * * * * * : : :

(B)

Alignment of 3 inotocin receptor sequences of *Limulus polyphemus*:

```

                                          TM1
Limulus_polyphemus3  MSSLKKEEQTELTNASFVNFSPIENITV-GDTQRDETIARIEVGVGLAIIFFLLTIGNTCV
Limulus_polyphemus1  MSTLDLPGETPEILNVFSFMNSSTLINNTKDKGIQRDETIARIEVGVGLASIFLLTILGNMCV
Limulus_polyphemus2  MSTLAKGETTGFNLNLSFVNLSTITNNTKADVQRDETVARIEVAVLATIFLLTIVIGNTIV
           :* : * ** : * * * * * : * : * : * : * : * : * : * : * : *

                                          TM2
Limulus_polyphemus3  LVALAVRRTNMTIMYYFLLHLCSLDLITAFFHVLPLQLAWDAARFYGGNVLCVVKYLQI
Limulus_polyphemus1  LVALAVRRIKMAIMYYFLLHLCSLDLITAFFNLPQLAWDVTYRFYGGNILCKVIRYLQI
Limulus_polyphemus2  LVALAVRRIKMTIMYYFLLHLCSLDLITAFFHVLPLQLAWDVTYRFYGGNVLCIVKYMQI
           ***** : * : * : * : * : * : * : * : * : * : * : * : *

                                          TM3
Limulus_polyphemus3  LGPYLSSYVLMVTAIDRYQAICFPLTRCTWTPRHSKLMIVGAWIISILCCSQAFIFSYQ
Limulus_polyphemus1  LGPYLSSYVLMVTAIDRYHAICFPLRNCVWTPRHSKLMIIAAWTISMLCCVPQVFIQSYQ
Limulus_polyphemus2  LGPYLSSYVLLVTAIDRYQAICFPLTSCVWTPRHSKLMIANAWIISILCCFPQIFIFSYQ
           ***** : * : * : * : * : * : * : * : * : * : * : * : *

                                          TM4

Limulus_polyphemus3  QVSSDPLVFDWGTFIQPWGEKVVYVLWYTISSQFFIPLLVIITFTYVNVTKTVWNNYLRKK
Limulus_polyphemus1  KVLIEPITFDCWGVFIQPWGEKVVYVLWYALSQFFIPLIVITFTCVIICKNVWYNFHLRGK
Limulus_polyphemus2  KVSDEDVTFDCWGVFIQPWGEKVVYVLWYAVSQFFIPLVIAFTYIICKSVWYNLQMRRO
           :* : * : * : * : * : * : * : * : * : * : * : * : * : * : *

                                          TM5

Limulus_polyphemus3  NF-----IHCRSVPDLSRAKVTITITIVVIACYIICSTPPFLAVQLWAYWSPYQNSP
Limulus_polyphemus1  NS-----SRSHSMRGLSRAKVTITVVVVIACYIICSTPPIVQLWAYWSPYQNTSP
Limulus_polyphemus2  ASNCEFTTVPRSHCMRGLSRAKVTITVVVITCYIICSTPPIIQLWAYWSPNAKNSS
           : : : * : * : * : * : * : * : * : * : * : * : * : * : *

                                          TM6

Limulus_polyphemus3  IWGPTVAIIMLLASLNSCVNPWIYLAFNHNLIITALKQLCCRSVLQDYMAQSTEATSNNN
Limulus_polyphemus1  IWGPTVAIIMLLASLNSCVNPWIYLAFNHNLVITALKHICCHERSQGYSPQVVENIN-N
Limulus_polyphemus2  IWGPTVAIIMLLASLNSCVNPWIYLAFNYNLVITALEVCCQTSKSFSSQVPENTDN-N
           ***** : * : * : * : * : * : * : * : * : * : * : * : *

Limulus_polyphemus3  NANSYPTENEVNSSYPLSFFIAQEEPVMLRNLKQKQ-----DEAETFS
Limulus_polyphemus1  TTSRSTQDNEICTSYPLSLRCGVHYTSSFRLLKKTITIGCRPCPNIQDLH---DEAETFS
Limulus_polyphemus2  TFSR----SERCSSYPLSVRTGSRHKFP--DGSTTRTRKRLCRELGSKNESTDVGENRG
           : . * : * : * : * : * : * : * : * : * : * : * : * : * : *

Limulus_polyphemus3  -----
Limulus_polyphemus1  A-----
Limulus_polyphemus2  SVTQTETTSEPGKRVTRDKDKTLIC

```

Alignment of 3 inotocin receptor sequences of *Ixodes scapularis*:

```

                                          TM1
Ixodes_scapularis2  ----- --QVEVAVLTFIFGFITVLGNTCV
Ixodes_scapularis1  MDV-PSNQKPEFAASVPTVLNFASTNLTAETREDES LALVELAVLTLIFAFITVMGNSTV
Ixodes_scapularis3  MDLVANQDQPAFSTSLPDSLDDVPVNETFWGTREDES LAQIELGVLTAIFTFVIGNTIV
           : * : * * * * * : * : * : * : * : * : * : * : * : *

                                          TM2
Ixodes_scapularis2  LVALAARRSKMTIMYYFLLHLCSLDLITAFLSVLPQLGWDATHFRFGGNLVCVAVKFGQL
Ixodes_scapularis1  LLALATRRSKMTIMYYFLLHLCSLDLITAFLLVLPQLGWDATHFRFGGNLACKAVKFGQL
Ixodes_scapularis3  LAALAAARRSKMIMYYFLLHLCSLDLITAFFTVLPQLGWDATHFRFGGNLACKTVKFGQL
           * : * : * : * : * : * : * : * : * : * : * : * : * : * : *

                                          TM3
Ixodes_scapularis2  LGPYLSSYVLVVTAVDRYQAICFPLSNCSWSPTECKLLIAGAWVAALVCCVPQVFIQSYQ
Ixodes_scapularis1  LGPYLSSYVLVVTAVDRYQAICFPLSNCSWTPTECKLLIAGAWVAALVCCVPQVFIQSYQ
Ixodes_scapularis3  LGPYLSSYVLVVTAADRYQAICFPLSNCSWTPTECKLLISAAWVAALVCCVPQVFIQSYQ
           ***** : * : * : * : * : * : * : * : * : * : * : * : *

                                          TM4

Ixodes_scapularis2  EVAPGVFDCWGTFAQPWGLEAYVTWYSVSVFFVPLAVLSFTYVCI CRSIWRNLYLKRKSS
Ixodes_scapularis1  EVSPEVFDWGTYVESWGLEAYVTWYGMSVFFVPLMLVLTFTYVCI CRSIWRNLYLKRKSS
Ixodes_scapularis3  EISPKVFDWGTYVEPWGLEAYVTWYGVSVFFVPLVLSFTYVCI CRSIWRNLYLKRKSS
           :* : * : * : * : * : * : * : * : * : * : * : * : * : * : *

                                          TM5

Ixodes_scapularis2  DA-----DHSVRGMSRAKVTITVVVIALYIVCS
Ixodes_scapularis1  DAESWKGERAYRFRGLAHNGTKQDSSVFPGRSHSVRGLSRAKVTITVVVIALYIVCS
Ixodes_scapularis3  DAESWKGSRAIRFKGTAQNGTKQDSSF-----TVKITVVVIALYIVCS
           * * * * * : * : * : * : * : * : * : * : * : * : * : * : *

                                          TM6
Ixodes_scapularis2  SPFICVQMMWYWSPDVDLADVWVINAIVTILMLLNS- - - - - NSCVNPNWYLFVFNRSLVH
Ixodes_scapularis1  SPFICVQMMWYWSPHVDMANPWISE-----
Ixodes_scapularis3  SPFICVQMMWYWSPDAD-----
           ***** : * : * : * : * : * : * : * : * : * : * : * : *

Ixodes_scapularis2  TLRHQICRCPDAKNVSSGIAGTGSCPSAVILADLTTQGTAEQSVLSYKSSPTDTSARLAT
Ixodes_scapularis1  -----
Ixodes_scapularis3  -----

```

Ixodes_scapularis2 AVVGKRGATDVEEDLQCSLEKTS
 Ixodes_scapularis1 -----
 Ixodes_scapularis3 -----

Alignment of 2 inotocin receptor sequences of *Metaseiulus occidentalis*:

```

                                TM1                                TM2
Metaseiulus_occidentalis1  --MNSSAGNFGDARDETIAHVRITVLCFCLELFTLGGNLFVFLLVTRNRPKSVHQLHIYHF
Metaseiulus_occidentalis2  MEYNITDTDFVPQENNWLSVKCATLVIIFFLTLSSNLFVLHAVLLRNRQNRRPLSRVQLF
                                * : : * : : : * : : * : : : * : : * : : : * : : * : : : * : : *
                                TM2                                TM3
Metaseiulus_occidentalis1  MVHLSLADMLVGVFNILPQIVWEIYFRFRWGNIACKFVKFMQIFVLYLSTYTLVGLSLNS
Metaseiulus_occidentalis2  MLHLTVADILVALLNILPQLAWDLTIQFRGGAVLCKLVFAQVYVLYLSTYILTGMSLDF
                                * : : * : : * : : * : : * : : * : : * : : * : : * : : * : : *
                                ICL2                                TM4
Metaseiulus_occidentalis1  SLVVRSGSSST-----S-----SLWVILGAGWFLS
Metaseiulus_occidentalis2  LITRAIESQWQTASLRSRDHDQSSDKSPQSHKIKFNNHRCRVGYRKFAKLIVFAWFLA
                                : : * : * : : : * : : * : : * : : * : : * : : * : : * : : *
                                ECL2                                TM5
Metaseiulus_occidentalis1  ALLASPQVYIFSFKQLSN--GVYDCWGTFDPP-LTSVYVYFIAMALIVPALIMGACYS
Metaseiulus_occidentalis2  AALSIPQLLFFSYTRIHDHGSWYDCKANFSWHRFGQYITTYFVVLILGVPVVMMLFCYI
                                * * : : * : : * : : * : : * : : * : : * : : * : : * : : * : : *
                                ICL3                                TM6
Metaseiulus_occidentalis1  YLCRAS-----SKRLMSDAKLTIRMTMVMLVLVFLCW
Metaseiulus_occidentalis2  QICLIIVRIQRHMTKTTSAPANFGVNTAGFFESNRRITKAVMVMMTFTVVLCFIVCW
                                : * : : * : : * : : * : : * : : * : : * : : * : : * : : * : : *
                                TM7
Metaseiulus_occidentalis1  TPFCCAQLYL---VFGGEEASTFVTMCLMVPNLNSCANPWVLSFSTDLRRRLVNF-CSL
Metaseiulus_occidentalis2  SPYSIAELLLLAYKIAGGEHVSPPFMVFLLLASLNSAVNPWIYTAFTNSFACKSLRTLKPE
                                : * : * : * : * : : * : : * : : * : : * : : * : : * : : * : :
Metaseiulus_occidentalis1  IHLRGNRYGEESRKPCTRANAIVCEKPARQLRGYRIS
Metaseiulus_occidentalis2  VHLITV-----
                                : * :
  
```

Alignment of 2 inotocin receptor sequences of *Varroa destructor*:

```

                                TM1                                TM2
Varroa_destructor1  MAGNIVVLVVLQSPKSAHLSRIYYFLLHLSIADILVGIFNISPQLVWDIYFRFPLGNF
Varroa_destructor2  -----EARRSSSLRVQLFMMHLSIADILVALLNILPQLAWDITARFYGGAL
                                : : * : : * : : * : : * : : * : : * : : * : : * : : * : : *
                                TM3                                TM4
Varroa_destructor1  ACKIVKFLQVFLYLSTYVLAGMAVDYLAIRSGINRPVVVRTILSVSWLVAAVLASPQ
Varroa_destructor2  LCKFVKYAQVLVLYLSTYILTGMSLDLVSM-----
                                * : : * : : * : : * : : * : : * : : * : : * : : * : : * : :
                                TM5
Varroa_destructor1  LYIFSFQKLPNGAHDCWATFEPPITSFYVLFFFITAVLFIPVTLMALCYTYLSWIISKRS
Varroa_destructor2  -----
                                TM6                                TM7
Varroa_destructor1  LSHTLNPIMTMVMVIVFVLCWTFPCCAQLYLESTGQVPSIFITFLLVPNLNSCANFW
Varroa_destructor2  -----
Varroa_destructor1  VCLTFSTTLRRKLDALSFFGFCEHLSVYRSKNAITISILQYPPNRSKRQPRAYRGA
Varroa_destructor2  -----
  
```

Alignment of 2 inotocin receptor sequences of *Achipteria coleoptrata*:

```

                                TM1
Achipteria_coleoptrata2  MSSDSSDMSVENISQTIIFQIINDDNMTANTSLAVKRNELVLLEIGILLIFLLIFVFGN
Achipteria_coleoptrata1  -----EN-----ITEELKNNTVSDTRDEHLAIFEIATLSLLFVLILIFGN
                                * : : * : : * : : * : : * : : * : : * : : * : : * : : * : : *
                                TM1                                TM2                                TM3
Achipteria_coleoptrata2  SCVLIALQINKLKMNMYYFLQHSISDMITAFFNVLPQLAWEITHRFYGGNILCTIY
Achipteria_coleoptrata1  SCVLLLALLMKIKMNMYYFLLHLIIADYLVAFFNVLPQLIWDITYRFYGGNLLCKVIY
                                * : : * : : * : : * : : * : : * : : * : : * : : * : : * : : *
                                TM3                                TM4
Achipteria_coleoptrata2  LQIFGPYLSSYVLVMTAIDHYQAICNPLSNCKWTPGSLMITIAWIVTSFCCSPQIFIFF
Achipteria_coleoptrata1  LQILGPYLSSYVLVMTSIDHYQAICYPLTNCQWTPTSQLMITLAWIALLCCIPQVLIF
                                * : : * : : * : : * : : * : : * : : * : : * : : * : : * : : *
                                TM5
Achipteria_coleoptrata2  SYQQIPGTDAIYDCWGTFQKPWGEIYVTWYAVSVFIIPFIIVVTHYHICREIWLNLH
Achipteria_coleoptrata1  SYQQIPGTDIYDCWGTFPLQPYGEIYVTWYAVSFFFIIPFILLTATHVQICREIW----
                                * : : * : : * : : * : : * : : * : : * : : * : : * : : * : : *
                                TM6
Achipteria_coleoptrata2  KKRKSFKLNKNRVGKSYRFKSRGKLEVSVDKDFKEDFSPRTHSIHGLSRAINTVITTV
Achipteria_coleoptrata1  -----
                                TM6                                TM7
Achipteria_coleoptrata2  IILCYIMCSTPPICVQLWAYWVPTAQKSHIWNVKYTYNIYLMFFSIIDVTIAFKILYSE
Achipteria_coleoptrata1  -----
  
```

Alignment of 5 inotocin receptor sequences of *Platynothrus peltifer*:

```

                                TM1
Platynothrus_peltifer5    METVSDLITFSRREQEFDPELLNDSNNVKNSSFEIRDSRNESLAIEIESLLTFMFSILIG
Platynothrus_peltifer3    -----M-----TGNGSLTVKRDEWVLLLEIGILSLIFILIVFG
Platynothrus_peltifer1    MEEIGTTVTLEELEDKLPET-----IIANVTKDSRDEHLAVFEIATLGLIFLLIVFG
Platynothrus_peltifer2    ME-VSTAIS-EETDGIFFET-----SSIKPNITGRNENLALIEVGTLTGTFVLLIVFG
Platynothrus_peltifer4    MSNVIMSI--NNTTSVLYN-----ISGDKRDENLAIMEVSILALIFILIIIG
                                *****
                                TM1          TM2          TM3
Platynothrus_peltifer5    NIFVLTALIVRDSKMNMYFFLPHLCIADLITAFFNVLPQLIWDITYRFYGGNVLCRLIK
Platynothrus_peltifer3    NSCVLIALQVRKLKMNMYFFLLHLCIADLITAFFNVLPQLAWEITHRFYGGNFLCWTIK
Platynothrus_peltifer1    NSCVLIALIMRKLKMNMYFFLLHLCIADLITAFFNVLPQLAWDITYRFYGGNILCWTIK
Platynothrus_peltifer2    NCCVLLALALRRLKMTMYFFLLHLCISDLMTGFFTVLPQLAWDITYRFNGGNILCRAVK
Platynothrus_peltifer4    NLCVLILALAVRFKMTMYFFLLHLCISDIITGCFVTMPQLAWDITHRFNGGNILCLVK
                                *****
                                TM3          TM4
Platynothrus_peltifer5    YLQILGPYLSSYILVITTAIDRYQAICFPPLSNCSWTPKRSQLMISIAWVLSLIFCAPQLFI
Platynothrus_peltifer3    YLQILGPYLSSYVLVMTTAIDRYQAICYPLSNCAWTPSLSLMILMAMIVSLLCCAPQII
Platynothrus_peltifer1    YLQILGPYLSSYVLVMTSIDRYQAICYPLSNCAWTPKRSQLMISFAWIIALLCCIPQVII
Platynothrus_peltifer2    SMQILGPYLSSYVLVMTTAIDRYQAICFPPLSNCSWTPRRALMISCAWIIISIVCSLPQAFI
Platynothrus_peltifer4    CLQLFGPYLSSYVLVMTTAIDRYQAICFPPLTNCHWTSRKSLMITIAWIIISILCSAPQAFI
                                *****
                                TM5
Platynothrus_peltifer5    FSYQQIPGTLGNVYDCWGIFPPQYGERIYVTWYAITVFVIPCIIIILFAHVCICREICNNL
Platynothrus_peltifer3    FSYQEI-GS--QIFDCWGTFSQPYGERIYVTWYAVSVFIIPFILLTFTHVHCICREIWNL
Platynothrus_peltifer1    FSYQQIPGY--DIIDCWGTFFPQFGERIYVSWYAISFFFVPFILLTFTHVHCICREIWRNV
Platynothrus_peltifer2    FSYQVEPETN-HYDCWGTFFPQWGERIYVTWYAISVFFIPLVLTFTTHVICREIWNL
Platynothrus_peltifer4    FSYQEIPRTN-GVRDCWGTFFPQYGERIYVTWYAITVFFIPLIIIITYTYVICREIWNV
                                *****
                                ICL3
Platynothrus_peltifer5    HRKRESIEEIKNCIHYSFKRNKFS-TSSLKSTSLTSFSGPIKSPI-----TYSIRPSK
Platynothrus_peltifer3    HKRKSFKINRNKSSSSCNRNDKLDCDSVNSPETSE--HRSGTRLLVTVGKSYRFKGKG
Platynothrus_peltifer1    HQRRKSVKMEQNKIIQNDDS-DRVSSCS---TNDS--IARSTNLLVTVGRSYRFKGKG
Platynothrus_peltifer2    NLKRQTGRRETQTINQIDSNSY-----STRKCLLIALNRVYRLRRQ
Platynothrus_peltifer4    RRRKRTLKPEISLIEVRKNW-----G-----KLKSS
                                *****
                                ICL3          TM6
Platynothrus_peltifer5    RLRRIHSQIDLKDLRNSLNLSVKVNDLNSTPRSHSLRLVSRAKIKTVITIVIMLCYV
Platynothrus_peltifer3    QVEVSVEK-DC-----GKEDYNSPRTHSIHGLTRAKIKTVITIVIMLCYI
Platynothrus_peltifer1    RVVSVVDG-PK-----SRGTY-NPRSHLNGLSRAKIKTVITIVVILCYI
Platynothrus_peltifer2    DTETAEIQICNDNQEVRPLHTVVTFQESVSSSPRVNTFNRLSRAKIKTVITVVVILCYV
Platynothrus_peltifer4    DDKSRLQSDRC-----LANNLLNPRSHSIYRISKAKIKTVVTVVVILCYI
                                *****
                                TM6
Platynothrus_peltifer5    ICSMPFISVQLWVYWFPSAQSFFQTSE---LSNIY-----
Platynothrus_peltifer3    FCSTPFICVQLWAYWWPNAQQSPIWNKYTYLSNNFA-----
Platynothrus_peltifer1    ICSSPFICVQLWAYWWPNAQNSTFWGKCSENSFIIQFRYSFQ
Platynothrus_peltifer2    ICSSPFICVQLWAYWWPNASTTFWNGMFSLFII-----
Platynothrus_peltifer4    VCSSPFICVQVWAYWYPSAQETSFWTGKH
                                *****

```

Alignment of 2 inotocin receptor sequences of *Strigamia maritima*:

```

Strigamia_maritima1    MSNESHWEDDLTMDNATSNAPPQS-----S--AIADAKL----TVL
Strigamia_maritima2    MA--THAE---GDSYTRTNPPTKTIPMDDNPNYNNKTTDGIMDIRDNLASIEIAVQ
                                *****
                                TM1          TM2
Strigamia_maritima1    ALMFATIMLGNTIVITSLL--IRRKKLTMYFFILHLCIADLIVAFLHVLPQLCWDVTHR
Strigamia_maritima2    SIILVVAIISNSFVFAALCCQRFRPTSMYLFMLHLSVADLVAFLSLLPQLIWDVTFR
                                *****
                                TM3          TM4
Strigamia_maritima1    FQGNDFLCKVIFGQLLGPYLSSYILVGMAIDYLAICFPLN-SWAATRS-KGMVCVAWV
Strigamia_maritima2    FQGSDILCVVVYLQVMVLYLSTYILVMMAVDCRAVCWSITGHWNSLAAKLMIVGAWV
                                *****
                                TM4          TM5
Strigamia_maritima1    VSVVFSSPQMFSYKYVSVLKYWECWVDFTLE-EEFAYVTWYFVANTFVPLLVLVYTS
Strigamia_maritima2    LAFLAIPQAIIFGKMEI-RPGVHDCWAHFEQPWGEFAYVTWFVLSIFIPLIVIAASYG
                                *****
                                ICL3
Strigamia_maritima1    AICWAVWRNFRHKKNSPKGDFSAASSPTATHLSVPQVNHIQRNGSCRFKASESVNP
Strigamia_maritima2    FICYTLWIYDEEHGR--SGDVIALRAVGNGTG-----GGDTVTDSCRLYSRRVA--
                                *****
                                TM6          TM7
Strigamia_maritima1    RSHGLQRISRAKIKTVLTVVVITCYLLCSMPYTCAMMWVAYDKRAQETAFYKGLPPVL
Strigamia_maritima2    GVSNPNPISEAVTLLTFLVVVCFFVCWSPFCITQLVLTFNPPSPDA--QIGSVEVIL
                                *****
                                TM7
Strigamia_maritima1    VLVASLNSCVNPVYLLFNKNLVHTLRHYLCCSKENEMKSHRTLATTSRTSFSESVGPR
Strigamia_maritima2    LLLASLNSCTNPWIYVAFSGSLLNQLRMCLGLGLTRPK---DIASIGDEEPQPQQQP-

```



```

Strigamia_maritima1  :*:*****.***:*. * .*. ** * . . . . . :*: . . . :. *
Strigamia_maritima2 VALQSLPPSSNNFLRVNDNKLNVRVAAVSDSALYSCEKRHSSPNLNVKSAASTLVLCSSQ
--TNKLPSTKSEMV-----
:.* * :. . . :
Strigamia_maritima1  HHHDTQNHLKDGVTMETQCA
Strigamia_maritima2 -----

```

Alignment of 4 different splicing variants of inotocin receptor sequences of *Daphnia magna*:

TM1

```

Daphnia_magna4  MASSSLLSNVTNVTTTELASSSRDE LASIEIGTLSFILLAVTSNLTMLIAIWRQRNRNP
Daphnia_magna3  MASSSLLSNVTNVTTTELASSSRDE LASIEIGTLSFILLAVTSNLTMLIAIWRQRNRNP
Daphnia_magna1  MASSSLLSNVTNVTTTELASSSRDE LASIEIGTLSFILLAVTSNLTMLIAIWRQRNRNP
Daphnia_magna2  MASSSLLSNVTNVTTTELASSSRDE LASIEIGTLSFILLAVTSNLTMLIAIWRQRNRNP
*****

```

TM2 **TM3**

```

Daphnia_magna4  LSRMYFFMMHLSLADLLVALFNILPQLAWDI TYRFHGGDVLCHFVY YTQIMTLYLSTYLL
Daphnia_magna3  LSRMYFFMMHLSLADLLVALFNILPQLAWDI TYRFHGGDVLCHFVY -----
Daphnia_magna1  LSRMYFFMMHLSLADLLVALFNILPQLAWDI TYRFHGGDVLCHFVY YTQIMTLYLSTYLL
Daphnia_magna2  LSRMYFFMMHLSLADLLVALFNILPQLAWDI TYRFHGGDVLCHFVY YTQIMTLYLSTYLL
*****

```

TM4

```

Daphnia_magna4  MFMAVDYRAYCCRNLHWNLSLVA CFVAASWVMSMLFAIPQAV IFHEEEISVGVTDWCWV
Daphnia_magna3  -----TNSRFLVA CFVAASWVMSMLFAIPQAV IFHEEEISVGVTDWCWV
Daphnia_magna1  MFMAVDYRAYCCRNLHWNLSLVA CFVAASWVMSMLFAIPQAV IFHEEEISVGVTDWCWV
Daphnia_magna2  MFMAVDYRAYCCRNLHWNLSLVA CFVAASWVMSMLFAIPQAV IFHEEEISVGVTDWCWV
*****

```

```

Daphnia_magna4  QFAEPWGAAYVTFV-----VS
Daphnia_magna3  QFAEPWGAAYVTFV-----VS
Daphnia_magna1  QFAEPWGAAYVTFV-----VS
Daphnia_magna2  QFAEPWGAAYVTFVVSIFGAPLLVVAVCYXXXXXXXXXWVQFAEPWGAAYVTFVVS
*****

```

TM5 **ICL3**

```

Daphnia_magna4  IFGAPLLVVAVCYGVICRQIWIYSQSAQPSLLPSDNSAIPSHSSITETGSTLSVMRRWFL
Daphnia_magna3  IFGAPLLVVAVCYGVICRQIWIYSQSAQPSLLPSDNSAIPSHSSITETGSTLSVMRRWFL
Daphnia_magna1  IFGAPLLVVAVCYGVICRQIWIYSQSAQPSLLPSDNSAIPSHSSITETGSTLSVMRRWFL
Daphnia_magna2  IFGAPLLVVAVCYGVICRQIWIYSQSAQPSLLPSDNSAIPSHSSITETGSTLSVMRRWFL
*****

```

ICL3

```

Daphnia_magna4  RAGMRWQKSRNSSNAIKNNSATASQLSDTIPMRSLATQQASNPLTTPDTIPMRSLATQQA
Daphnia_magna3  RAGMRWQKSRNSSNAIKNNSATASQLS-----ADPIPMSLATQQA
Daphnia_magna1  RAGMRWQKSRNSSNAIKNNSATASQLS-----DTIP-----
Daphnia_magna2  RAGMRWQKSRNSSNAIKNNSATASQLS-----DTIPMRSLATQQA
*****

```

ICL3 **TM6**

```

Daphnia_magna4  SNPLTTENKISPMPLQPPPAAPQR CQOMSLRRSNSNQNRITKAKMTI I LTLAVVLCFVA
Daphnia_magna3  SNPLTTENKISPMPLQPPPAAPQR CQOMSLRRSNSNQNRITKAKMTI I LTLAVVLCFVA
Daphnia_magna1  -----NKISPMPLQPPPAAPQR CQOMSLRRSNSNQNRITKAKMTI I LTLAVVLCFVA
Daphnia_magna2  SNPLSTENKISPMPLQPPPAAPQR CQOMSLRRSNSNQNRITKAKMTI I LTLAVVLCFVA
*****

```

TM6 **TM7**

```

Daphnia_magna4  CWAPFCITQLIMVYCPPTSQADVSPVAVIILLASLNSCSNPWIY LAFSGSLLNQMRVCL
Daphnia_magna3  CWAPFCITQLIMVYCPPTSQADVSPVAVIILLASLNSCSNPWIY LAFSGSLLNQMRVCL
Daphnia_magna1  CWAPFCITQLIMVYCPPTSQADVSPVAVIILLASLNSCSNPWIY LAFSGSLLNQMRVCL
Daphnia_magna2  CWAPFCITQLIMVYCPPTSQADVSPVAVIILLASLNSCSNPWIY LAFSGSLLNQMRVCL
*****

```

```

Daphnia_magna4  GLRWLRGQDKDSIGEDRRGAAGPAGGQPADTNHRFGRGPRRAQTRDQHRQV-----
Daphnia_magna3  GLRWLRGQDKDSIGEDRRGAAGPAGGQPADTNHRFGRGPRRAQTRDQHRQVMAEQQLLP
Daphnia_magna1  GLRWLRGQDKDSIGEDRRGAAGPAGGQPADTNHRFGRGPRRAQTRDQHRQVMAEQQLLP
Daphnia_magna2  GLRWLRGQDKDSIGEDRRGAAGPAGGQPADTNHRFGRGPRRAQTRDQHRQVMAEQQLLP
*****

```

```

Daphnia_magna4  -----
Daphnia_magna3  AGEQHPAMLATKCTRADIVTHLGNTKKLQFQQNHQHVEKIG
Daphnia_magna1  AGEQHPAMLATKCTRADIVTHLGNTKKLQFQQNHQHVEKIG
Daphnia_magna2  AGEQHPAMLATKCTRADIVTHLGNTKKLQFQQNHQHVEKIG

```

Supplementary Figure S3. Alignment of inotocin receptors. Alignment of 125 putative inotocin receptor sequences of arthropods. Conserved sequence motifs XPQX₂WX₅₋₆F and CXNPW are highlighted green and grey, respectively. Residues that diverge from the consensus of motif conservation are highlighted in red.

	1	60
Varroa_destructor1	-----	-----
Metaseiulus_occidentalis1	-----	-----
Metaseiulus_occidentalis2	-----	-----
Tigriopus_californicus	-----	MATLLSSDIEAKMDKEPQDNPYNSIP---DS
Anurida_maritima	-----	-----
Meinertellus_cundinamarcensis	-----	-----
Pogonognathellus_sp	-----	MATN-----SNTTNEI----S
Triops_cancriformis	-----	-----
Strigamia_maritima2	-----	MATH----AEGDSYTRTNPPTKTIP---MD
Catajapyx_aquilonaris	-----	-----
Daphnia_pulex	-----	-----
Daphnia_magna3	-----	-----MA---SS
Daphnia_magna2	-----	-----MA---SS
Daphnia_magna1	-----	-----MA---SS
Daphnia_magna4	-----	-----MA---SS
Arachnocampa_luminosa	-----	-----MTSYQENILP-N---YSEQD
Calanus_finmarchicus	-----	-----
Epiophlebia_superstes	-----	-----
Ladona_fulva	-----	-----
Cordulegaster_boltonii	-----	-----
Diaphorina_citri	-----	-----
Pachypsylla_venusta	-----	-----
Acanthocasuarina_muellerianae	-----	-----
Glomeris_pustulata	-----	-----
Frankliniella_cephalica	-----	-----
Machilis_hrabei	-----	-----
Carabus_granulatus	-----	-----
Dendroctonus_frontalis	-----	-----
Lepeophtheirus_salmonis	-----	-----
Caligus_rogercresseyi	-----	-----
Parhyale_hawaiensis	-----	-----MLDEPLPTMSEELVL-NVSVNA--SE
Hyalella_azteca	-----	-----
Strigamia_maritima1	-----	-----MSNE-----SHW---
Conwentzia_psociformis	-----	-----IPYKMNDFNATDQ-----NYGFEYF-----LNSTA---SD
Liposcelis_bostrychophila	-----	-----MNTKAREFGNKGKRKT-STRSQKHLSHNEKMDEEARQSSIPDINLT-----
Tetranychus_urticae	-----	-----MDLSSFGSLEF---STL--SVFSTNETSSTLPSLVLPFDVNLTSRRYL
Osmylus_fulvicephalus	-----	-----R---TTM--ALMNNSVGMGVPTPSLELVGVLAAGGGG
Ornithodoros_turicata	-----	-----
Acerentomon_sp	-----	-----M--ANQSLN-----VGDPWI--NETQVAEHVL
Ixodes_ricinus	-----	-----MDLV---A--NQDQPAF-ST
Folsomia_candida	-----	-----PLHED-NF
Limulus_polyphemus1	-----	-----MSTL---DF-GETPEIL-NV
Limulus_polyphemus3	-----	-----MSSL---KE-EQTTELT-NA
Platynoctrus_peltifer5	-----	-----METVSDLITF-SREQEF--DF
Platynoctrus_peltifer1	-----	-----MEEIGTTVTL-EE-----
Platynoctrus_peltifer3	-----	-----
Achipteria_coleoptrata2	-----	-----M--SSDSSDMSVENISQTIIF-QI-----
Platynoctrus_peltifer2	-----	-----ME-VSTAIS--EE-----
Platynoctrus_peltifer4	-----	-----MSNVIMSI--NN-----
Ixodes_scapularis2	-----	-----
Ixodes_scapularis1	-----	-----MDV-P--SNQKPEFAASVP-----
Ixodes_scapularis3	-----	-----MDLVA--NQDQPAFSTSLP-----
Cotesia_vestalis	-----	-----
Microplitis_demolitor	-----	-----
Zorotypus_caudelli	-----	-----
Nasonia_giraulti	-----	-----
Nasonia_vitripennis	-----	-----
Varroa_destructor2	-----	-----
Leuctra_sp	-----	-----
Tricholepidion_gertschi	-----	-----
Perla_marginata	-----	-----
Crioscolia_alcione	-----	-----ME-----
Mischocyttarus_flavitaris	-----	-----
Polistes_metricus	-----	-----
Polistes_canadensis	-----	-----
Chrysis_viridula	-----	-----
Argochrysis_armilla	-----	-----
Chyphotes_mellipes	-----	-----

Epiophlebia_superstes -----GGRDEELAKAEIATLAAMLAVSVIGNGAVLVA-LWVRPRPSP
 Ladona_fulva -----MATLAAMLVIVSIVGNVAVMVA-LWARPRPSP
 Cordulegaster_boltonii -----MATLAAMLVVSVVGNVAVLVA-LWARPRPSP
 Diaphorina_citri -----
 Pachypsylla_venusta --MDESNGTLVNYNDTSDSDEDEDLARVEILTLIIILVITIVGNIMVLFA-LYRRHFQK
 Acanthocasuarina_muellerianae -----
 Glomeris_pustulata -----
 Frankliniella_cephalica -----
 Machilis_hrabei -----
 Carabus_granulatus -----
 Dendroctonus_frontalis -----
 Lepeophtheirus_salmonis -----VSNTSLNTPSSPNSLLHTKLWVLGIIIVLTLGNISVILA-IATRF----
 Caligus_rogercresseyi -----EGNSLHQTKLWVLGIIIVLTLGNISVILA-IATRH----
 Parhyale_hawaiensis DAINFD--ILSVQNNTSFGSRDEVLAFAEVLTLASIFVVTIVGNCIVIFK-HFMRR----
 Hyalella_azteca -----
 Strigamia_maritima --EDDL--TMDNATSNAPPQSSAIADAKLTVLALMFATIMLGNTIVITS-LLIRR----
 Conwentzia_psociformis AVIEAG--TDLAAASDNGDERNEELAKIEIILIVIFNVTLIGNLVLLA-LSARKRYSG
 Liposcelis_bostrychophila --ADPTMELVVRKNDSTDDFRNEDLAQIEIGTLGVILIVTLGNGLVLLA-LYAKCKAG
 Tetranychus_urticae KAVSTGSPSASSLSSSAHSRDNLAILEIITLSAIFVMIVFGNTSVLLA-LILSR----
 Osmylus_fulvicephalus GLLLPVDPTSANSTAMHDYDRDEALAQVEIGTLALIFGVTLGNVAVLVA-LYIRRRYSG
 Ornithodoros_turicata -----
 Acerentomon_sp NVGDPWTNETQEAEDGFKYERNEDLARIEIAILAAIFCATVIGNVVLVA-LFNTK----
 Ixodes_ricinus SLPDPL-DDVPVNDTSWTGRDESLAQIELGVLTAIFFTVIGNNTVLLA-LAARR----
 Folsomia_candida SLTPNL-SL-VNTTLTPASPRDEFKAEIQSVLAIIFLITIVGNFLVLMG-IYFRK----
 Limulus_polyphemus1 SFMNSS-TI-INNTKDKGIQRDETIARIEVGLASIFTLTILGNMCLVLA-LAVRR----
 Limulus_polyphemus3 SFVNFSP-PI-E-NITVGDTRQDETIARVEVGLAIFLITLIGNTCVLA-LAVRR----
 Platynothrus_peltifer5 ELLNDS-NNVKNSSFEIRDSRNEISLAIIEISLLTFMFIISILIGNIFVLA-LIVRD----
 Platynothrus_peltifer1 --LEDK-LPETIIANVTKDSRDEHLAVFEIATLGLIFLIVFGNSCVLIA-LYMRK----
 Platynothrus_peltifer3 -----M--TGNGSLTVKRDEKWLLEIGILSLIFLIVFGNSCVLIA-LQVRK----
 Achipteria_coleoptrata2 --INDD-NM--TANTSLAVKRNEKLVLEIGILLIFLIVFGNSCVLIA-LQINK----
 Platynothrus_peltifer2 --TDGI-PFETSIIKPNITGRNENLALIEVGTGTIFVLIIVFGNCCVLLA-LALRR----
 Platynothrus_peltifer4 --TTSV-LYN----ISGSDKRDENLAIMEVSIILALIFLIIIGNLCLVLA-LAVKR----
 Ixodes_scapularis2 -----QVEVAVLTFIFGFTVLGNTCVLVA-LAAR----
 Ixodes_scapularis1 ----TVLNFASTNLTAETREDESALVELAVLTLIFAFVTMGNSTVLLA-LATR----
 Ixodes_scapularis3 ----DSLDDVPVNETFTWTRDESLAQIELGVLTAIFFTVIGNNTVLLA-LAAR----
 Cotesia_vestalis -----DNSTSLDTRDENLAFWEIIVLVINLIITLIGNCFIIFA-LYLRRYH--
 Microplitis_demolitor -----MMGNSTQPDTRDENLAIWEITVLAINLIITIGNCLIFFA-LYLRRYH--
 Zorotypus_caudelli -----LLVIILLVTLVGNVILVFA-IYVRRCR--
 Nasonia_giraulti ----MEESATSMIAVPAEDWRDESLAVWEIVLVILITTTLMGNVVLVA-IYLRKCR--
 Nasonia_vitripennis ----MEESATSMIAVPAEDWRDESLAVWEIVLALILITTTMGNVVLVA-IYLRKCR--
 Varroa_destructor2 -----E
 Leuctra_sp -----LVTAVVANLLVLTAL-LILRS----
 Tricholepidion_gertschi -----
 Perla_marginata -----EVTSLAAIFLTALAGNVCLVA-LYGHR----
 Crioscolia_alcione G-----MPEDQNSSEIDGRDEYLAKWEITVLTSLILLTLLGNTLVLS-LYIRKRY--
 Mischoctytarus_flavitaris ----MNETTNSSTFAANEEDIRDENLAKWEIVLLANILIFTIFGNLSVLLS-LYLRRYR--
 Polistes_metricus ----MNETTNSSTFVANEKDRDENLAKWEIVLLANILIFTIFGNLSVLLS-LYLRKRY--
 Polistes_canadensis -MSV---EQNLVTEETEEDVRDEYLAKWEIIVLATILYMTLVGNLSLLFA-LYLRKRR--
 Chrysis_viridula -----
 Argochrysis_armilla -----MYRDRNATARGCTAGERDERDEYLARWEIAVLVTLVVTILGNLVLLS-LHVRHR--
 Chyphotes_mellipes DMFADRNSSEVQTSDELDDERDEELAKWELVVLASILVITLVGNLVLLA-LYARRYH--
 Brachycistis_timberlakei -MYNDRNNT-TTLGEAKDDTRDEELAKWEIGVLTIFITILGNLSVLLA-LYIRRR--
 Sphaerophthalma_orestes ---MAND-LVFNSSLASDLERDEELARAEIAVLAVIVVVTVTGNTAVLVA-LYARRFC--
 Homalodisca_vitripennis ----FSTERVNESVAVSNGGDRDEDLARVEATLAAIATLGNSTVLLA-LYMRRTW--
 Cercopis_vulnerata ----ENITEELKNNTTVSDTRDEHLAIFEIATLSLLFVLILFGNSCVLLA-LLMR----
 Nilaparvata_lugens -----IATLAIIFGVTVLGNVCLVA-ISFR----
 Achipteria_coleoptrata2 -----
 Ephemera_danica -----
 Leptopilina_clavipes -----
 Ganaspis_sp -----MENGTLINDTRDEELAKWEIGILACFFVIIIGNSLVLLS-IYLRKY--
 Leptopilina_boulardi -----MENGTLINDTRDEELAKWEIGILACFFVIIIGNSLVLLS-IYLRKY--
 Mantis religiosa -----AILSTLFVIVLGNSSVLLA-LSSR----
 Blattella_germanica --MENASQAVNGSTTAEDLDRDEVLARAEIATLSVMFTVTVGNFVLLV-LSAR----
 Zootermopsis_nevadensis --EVSEACNLTANSTSGLDREDEALAEIATLATMLTIVTLGNFVLLA-LSAR----
 Stigmatomma_oregonense ---LSLSLSPSSSERTSNDARDEYLARWEIAVLTSIFLITLIGNLVLLA-LYVRRH--
 Dinoponera_quadriceps --STS--SPPSASEQTPVDGRNEDLAKWEIALTSIFLITLIGNLVLLA-LYARKR--
 Harpegnathos_saltator ---SSLSLP-PSEQKTSVDRDEYLAKWEIAVLTSIFLITLIGNLVLLA-LYVRRY--
 Cerapachys_biroi ---SSPSSSSPSSLEVSDDLREYLARWEIAVLTSIFLITLIGNLVLLA-LYARRCY--
 Monomorium_pharaonis ---SSPSSPSEWPLDDARDEYLARWEIAVLTSIFLITLIGNLVLLA-LYVRRY--
 Tetramorium_bicaratum ---SSSLTSPSPPLPDDARDEYLARWEIAVLTSIFLITLIGNLVLLA-LYARRY--
 Solenopsis_invicta ---SSS---SPPSSEWPPDDARDEYLARWEIAVLTSIFLITLIGNLVLLA-LYARRY--
 Atta_cephalotes ---SSS---SSEL---PLDDARDEYLARWEIAVLTSIFLITLIGNLVLLA-LYARRY--
 Acromyrmex_echinator ---SSS---SSEL---PLDDARDEYLARWEIAVLTSIFLITLIGNLVLLA-LYARRY--
 Pogonomyrmex_barbatus ---S-----S-LSSEWPPDDVRDEYLARWEIAVLTSIFLITLIGNLVLLA-LYTRRRY--
 Wasmannia_auropunctata ---SSSSP--LSSDRPQDDARDEYLARWEIAVLTSIFLITLIGNLVLLA-LYVRRY--
 Vollenhovia_emeryi ---SSSSTP-SLSEWPSNDARDEYLAKWEIAVLTSIFLITLIGNLVLLA-LYIRRRY--
 Orussus_abietinus -EDEMADPPPTTNPVEDFRSDLARWEIFTLAAIILLENLVA-LYLR----

Blaberus_atropos
Limulus_polyphemus2
Isonychia_bicolor
Occasjapyx_japonicus
Baetis_sp
Panonychus_ulmi
Frankliniella_occidentalis
Eurylophella_sp
Telenomus_podisi
Aposthonia_japonica
Haploembia_palau
Halyomorpha_halys
Stenobothrus_lineatus
Inocellia_crassicornis
Tenthredo_koehler
Corydalus_cornutus
Chrysopa_pallens
Meloe_violaceus
Aethina_tumida
Gyrinus_marinus
Tribolium_castaneum
Microphorus_vespilloides
Aleochara_curtula
Pogonus_chalceus
Sipyloidea_sipylus
Extatosoma_tiaratum
Aretaon_asperimus
Medauroidea_extradentata
Ramulus_artemis
Gallosiana_yuasai
Athalia_rosae

SF--VNLSTITNNTKADVQDETVARIEVAVLATIFTLTVIGNTVLVA-LVVR-----
-----VGNTCVLLA-IRHR-----
SPRMNASSNASATGGMNGYERNEDLAKVEIALLSTIFVLTVIGNSMLVA-IFLK-----
--MDSSVDNSTTTTVDVAVPTRDEQLARVEIATLAFIFAVTVIGNSLILSA-ILFRR-----
-----RDENLAIIEIITLSAIFVMIVFGNTSVLLA-LLSL-----
-----APQVEVAVLGVLLVLTVLGNNAVLLA-LYARRC-----
-----FVVTTIGNSCVLVA-LSLR-----
----MPVESQTVKNVTEDFRDESLAQWEVGLAAIFVITIIIGNSLVLLA-IYLRRYR-----
-----MNSSAEKSDGDRDEDLARVEVTLAIFAITLVGNLLVLLA-LLVL-----
-MVHRKRQNDVMNSSVADGRDEDLARVEVTLAIFAITLVGNLLVLLA-LLVL-----
-----PNDSINCSAVHERDEDLAKIEMATLAVMFVMTVVGNLVA-LFARRQS-----

--MNGTELKISAPETNGNERDEVLAQAEIITSAVIFVVTVIGNGTVLLA-LFARQKY--
SF--VESECNLTISSEIDDSRDEYLAWEVATLALIFVVAIAGNSLVLLA-FYFRRYD--

-----ILTLAIFVVTLLGNLVA-LYNRQKC-----
-SIENTTKSLRDDTEESPTDRDESLARIEIATLAVIFLITVIGNSTVLLA-LWARRRF-----
----TSTGETIEELERAAKERDESLAKIEVAVLAVIFVTVIGNSTVLLA-LWARRC-----
-----MNTTANATDQTFDRDENLAQFEIATLAVIFVVTVIGNGTVLLA-LWTRRR-----
DISENSTYLFDKHEDRNNDRDENLARVEVATLAIIFLVTVIGNSTVLLA-LWTRRRY--
SL--RGSPPSSEEREERSSSHRDCN-----FHHHSHHX-LWTRRRY--
-----RY-----

SVDNGNGNSNGSNSTSSGYDRDEDLARAEIATLAVMLLVTVIGNSCILYA-LCARR-----
-----AE--NSTNSSGGYDRDEDLARGEIATLAIMFIVTVGNLVA-LCARR-----
-----GSSANITNSTGGYDRDENLARAEIATLAVMFIITVIGNSCILYA-LCLR-----
-----VK--NSTNSTDGYDRDEDLAHAEIATLAVMFIITVGNLVA-LCARR-----
-----AENSSANSTYGYDRDENLAHAEIATLATMFAITLVGNFCILYA-LCARR-----

CA--TANEALKVDDGNDRDREDIANWEVATLAAMFVVAVFGNSLVVTA-LYLRRYGKT

Varroa_destructor1
Metaseiulus_occidentalis1
Metaseiulus_occidentalis2
Tigriopus_californicus
Anurida_maritima
Meinertellus_cundinamarcensis
Pogonognathellus_sp
Triops_cancriformis
Strigamia_maritima2
Catajapyx_aquilonaris
Daphnia_pulex
Daphnia_magna3
Daphnia_magna2
Daphnia_magna1
Daphnia_magna4
Arachnocampa_luminosa
Calanus_finmarchicus
Epiophlebia_superstes
Ladona_fulva
Cordulegaster_boltonii
Diaphorina_citri
Pachyphylla_venusta
Acanthocasuarina_muellerianae
Glomeris_pustulata
Frankliniella_cephalica
Machilis_hrabei
Carabus_granulatus
Dendroctonus_frontalis
Lepeophtheirus_salmonis
Caligus_rogercresseyi
Parhyale_hawaiensis
Hyalella_azteca
Strigamia_maritima1
Conwentzia_psociformis
Liposcelis_bostrychophila
Tetranychus_urticae
Osmylus_fulvicephalus
Ornithodoros_turicata
Acerentomon_sp
Ixodes_ricinus
Folsomia_candida
Limulus_polyphemus1
Limulus_polyphemus3

121
-----AHLRSRIYFLLHLSIADILVGFNI
-----VHQLHIYHFVHLSLADMLVGVFNI
-----RPLSRVQFLMHLTLVADILVALLNI
-----KPSRRMYRLMYHLSIADLLVAVLNVI
-----RPLSRMYFFMQQLSIADLMVAVFNV
-----RPMRMYFFMLNLSVADLMVAFGNI
-----RPLSRMYFFMLHLSLADVLVAVFNI
-----RPTSRMYFLMHLVADLLVAFVLSL
-----RPMRMYFFMLHLSVADLLVAVFNI
-----RPLSRMYFFMMHLSLADLLVALFNI
-----RPLSRMYFFMMHLSLADLLVALFNI
-----RPLSRMYFFMMHLSLADLLVALFNI
-----RPLSRMYFFMMHLSLADLLVALFNI
-----RPLSRMYFFMMHLSLADLLVALFNI
KRARWFKLNKNISRMSFYIIHLSIADFNVAFMSILPQLIWRQS-VVFNHS-HFLCKFVAF
-----ADILTAIFTLIP
-----RRRLSRMHLLVLYLCTADLITAAFTVLPQMAWEAT-YRFPQQAAPLCKPLKV
-----RRRLSRMHLLVHLCTADLITAAFTVLPQMAWEAT-YRFPQQAAPLCKPLKV
-----RRRLSRMHLLVHLCTADLITAAFTVLPQMAWEAT-YRFPQQAAPLCKPLKV
-----MV
-----QIKMPRMYFIFLHLSIADLITAFFNVLPQLIWDIT-YRFPGSSNWLCKLVKF

-----IKMTRMYFFILHLSIADVLTAFVTLPL
-----IKMTRMYFFILHLSIADVLTAFVTLPL
-----KKFRRMNYFIFALSLSLVTAMFNVL
-----SDLVTAAFNVFPQLMWDIT-FRFRGG-DFLCRSVKF
-----KKLTRMYFFILHLCIADLIVAFVHVL
-----HRKLRMYFFILHLSLADLISAFNLVLPQMIWK
-----KKTLSRMYFYIFHLVADLITAFVHVL
-----IKLRRMYFFLHLSIADLITAFVHVL
-----RKKLSRMYFFILHLSIADLITAFVHVL
-----KKMTRMYFFMMHLSIADLITAFVHVL
-----SKMSRMYFFLHLCVSDLITAFVHVL
-----QKMTRMYFYIAHLAIADLITAFVHVL
-----IKMARMYFFLHLCISDLITAFVHVL
-----TNMTRMYFFLHLCISDLITAFVHVL

XPQX₂WX₅₋₆F motif

180

Platynothrus_peltifer5 -----SKMNRMYFYLHLCIADLITAFFNVLPLQIWDIT-YRFYGG-NVLCKLIKY
 Platynothrus_peltifer1 -----LKMNRMYFLLHLCIADLITAFFNVLPLQAWDIT-YRFYGG-NILCKTIKY
 Platynothrus_peltifer3 -----LKMNRMYFLLHLCIADLITAFFNVLPLQAWDIT-YRFYGG-NFLCKTIKY
 Achipteria_coleoptrata2 -----LKMNRMYFYLQHLSDMI TAFFNVLPLQAWDIT-HRFYGG-NILCKTIKY
 Platynothrus_peltifer2 -----LKMTRMYFLLHLCISDLMTGFFTVLPLQAWDIT-YRFNGG-NILCKAVKS
 Platynothrus_peltifer4 -----FKMTRMYFLLHLCISDIITGCFTVMPQLAWDIT-HRFNGG-NILCKLVK
 Ixodes_scapularis2 -----RSKMTRMYFLLHLCVSDLITAFLSVLPQLGWDAT-YRFQGG-NLACKAVKF
 Ixodes_scapularis1 -----RSKMTRMYFLLHLCVSDLITAFLTVPQLGWDAT-YRFQGG-NLACKAVKF
 Ixodes_scapularis3 -----RSKMSRMYFLLHLCVSDLITAFFTVLPLQAWDIT-YRFQGG-NLACKTVKF
 Cotesia_vestalis -----GRQRKLTRMYFFMMHLSIADFITGIFNLPQLSWDIT-FRFQGG-PAMCKIVKF
 Microplitis_demolitor -----GRQRKLTRMYFFMHLHSIADFTVTGIFNVLPLQAWDIT-FRFQGG-YGLCKIKF
 Zorotypus_caudelli -----GRRHRLTRMHFFVMHLSIADLINGLLNVLPLQAWDIT-FRFQGG-QILCKMVKF
 Nasonia_giraulti -----GRRQLTRMHFFVMHLSVADLITGLLNVLPLQAWDVT-FRFQGG-PILCKLVKF
 Nasonia_vitripennis -----GKRQLTRMHFFVMHLSVADLITGLLNVLPLQAWDVT-FRFQGG-PILCKLVKF
 Varroa_destructor2 A-----RRSSLSRVQLFMMHLSIADILVALNLPQLAWDIT-ARFYGG-ALLCKFVKY
 Leuctra_sp -----RRQLARLHFFILHLSLADLVNALFNVLPLQVWKST-FRFVGG-TVLCCKLVKF
 Tricholepidion_gertschi -----
 Perla_marginata -----NRKLTRMHFFILHLTIADMTAVFSVMPQMLWKAT-YRFAGG-PTLCKVVKV
 Crioscobia_alcione -----ER-RKFTRMYFFIMHLSVADMLTGLLNVLPLQAWDIT-FRFQGG-ALLCKAVKF
 Mischocyttarus_flavitaris -----
 Polistes_metricus -----AH-KKLSRMYFFIMNLSIADLLTGLLDVLPQLAWDIT-FRFQGG-LVLCKLVKF
 Polistes_canadensis -----AH-KKLSRMYFFIMNLSIADLLTGLLDVLPQLAWDIT-FRFQGG-LVLCKLVKF
 Chrysis_viridula -----GRRRKFTRMHFFILHLSIADLITGLFNVLPLQAWDIT-FRFQGG-NILCKLVKF
 Argochrysis_armilla -----
 Chyphotes_mellipes -----QR-RKFTRMYFFIMHLSVADLLTGLLNVLPLQAWDIT-FRFKGG-PILCKLVKF
 Brachycistis_timberlakei -----CR-RKFTRMYFFIMHLSIADLLTGLLDVLPQLAWDIT-FRFQGG-PVLCKMVKF
 Sphaerophthalma_orestes -----GR-RKFTRMYFFIMHLSIADLITGLCDVLPQLAWDIT-FRFQGG-PMLCKIVKY
 Homalodisca_vitripennis -----TGNKLSRMYFFILHLCVADLITGLLNVLPLQAWDIT-YRFKGG-NLCKVVKY
 Cercopis_vulnerata -----GRRKLSRMYFFILHLCIADLVTALLNVLPLQIWDIT-FRFKGG-PFLCKLVKY
 Nilaparvata_lugens -----GRRKLSRMYFFILHLCIADLVTGLLNVLPLQIWDIT-YRFQGG-PLLCKLVKY
 Achipteria_coleoptrata1 -----KIKMNRMYFLLHLIADYLVAFNVLPLQIWDIT-YRFYGG-NLLCKVIKY
 Ephemera_danica -----RAKLSRMYFFIMHLSVADLITAFFNVLPLQAWDIT-YRFCLS--QLCRGVKF
 Leptopilina_clavipes -----VADLLTAVLNVLPLQAWKIT-FRFQGG-PFLCKLIK
 Ganaspis_sp -----SQRKKLTRMHFFIMNLSVADLLTAIILNVLPLQAWKIT-FRFQGG-PILCKLIK
 Leptopilina_boulardi -----GQRKKLTRMHFFIMNLSVADLLTAIILNVLPLQAWKIT-FRFQGG-QILCKLIK
 Mantis_religiosa -----RRKKLSRMYFFILHLSIADLITALLSVLPQLAWDIT-YRFHGG-NILCKLIKY
 Blattella_germanica -----PRKKLSRMYFFILHLSIADLCTAFLSILPLQAWDVT-YRFQGG-PIMCKVVKY
 Zootermopsis_nevadensis -----PRKKLSRMYFFILHLSVADLCTAFLSVLPQLAWDVT-YRFYGG-PLLCKIVKY
 Stigmatomma_oregonense -----QRRKFTRMYFFILHLCVADLLTDLNVLPLQAWDIT-FRFQGG-AVLCKLIK
 Dinoponera_quadricaps -----QRRKFTRMYFFILHLSIADLLTGLFDVLPQLAWDIT-FRFQGG-AVLCKLIK
 Harpegnathos_saltator -----QRHKFTRMYFFILHLSIADLLTGLLDVLPQLAWDIT-FRFQGG-AVLCKLIK
 Cerapachys_biroi -----QRRKFTRMYFFILHLSIADLLTGLLDVLPQLAWDIT-FRFQGG-AVLCKLIK
 Monomorium_pharaonis -----QRRKFTRMYFFILHLSVADLLTGLLDVLPQLAWDIT-FRFQGG-AVLCKLIK
 Tetramorium_bicarinarum -----QRRKFTRMYFFILHLSVADLLTGLLDVLPQLAWDIT-FRFQGG-AVLCKLIK
 Solenopsis_invicta -----QRRKFTRMYFFILHLSVADLLTGLLDVLPQLAWDIT-FRFQGG-AVLCKLIK
 Atta_cephalotes -----QRRKFTRMYFFIMHLSVADLLTGLFDVLPQLAWDIT-FRFQGG-AVLCKLIK
 Acromyrmex_echinator -----QRRKFTRMYFFIMHLSVADLLTGLFDVLPQLAWDIT-FRFQGG-AVLCKLIK
 Pogonomyrmex_barbatus -----QRRKFTRMYFFILHLSIADLLTGLLDVLPQLAWDIT-FRFQGG-AVLCKLIK
 Wasmannia_auropunctata -----QRRKFTRMYFFILHLSVADLLTGLLDVLPQLAWDIT-FRFQGG-AVLCKLIK
 Vollenhovia_emoryi -----QRRKFTRMYFFILHLSVADLLTGLLDVLPQLAWDIT-FRFQGG-AALCKLIKY
 Orussus_abietinus -----GRRKLSRIQFFILHLSIADLLTGLLNVLPLQAWDIT-FRFQGG-DLLCRLVKF
 Blaberus_atropis -----
 Limulus_polyphemus2 -----RIKTRMYFYLQHLCSIDLITAFFHVLPLQAWDVT-YRFYGG-NVLCKIVKY
 Isonychia_bicolor -----RSKLTRMYFYIFHLSIADLVTAFNVLPLQAWDIT-YRFKGG-DELCKIKF
 Occasjapyx_japonicus -----RKKMSRMYFFILHLSIADLITGFFNVLPLQAWDIT-YRFYGG-NFMCKFIKY
 Baetis_sp -----RVKLTRMYFYIFHLSIADLVTAFNVLPLQAWDIT-YRFKGG-NLCKGVKF
 Panonychus_ulmi -----RIKLRRMYFLLHLSIADLITAFNVLPLQIWEIT-EHFYGG-QILCKGIKY
 Frankliniella_occidentalis -----GRRKLSRMYFFILHLSVADMTAFFSVLPQLVW-VT-FRFHGG-NFLCKAVKF
 Eurylophella_sp -----RAKISRMYFYIFHLSIADLVTAFNVLPLQAWDIT-YRFQGG-DILCKAVKF
 Telenomus_podisi -----GRRKLSRMYFFILHLSVADLITAFFDVLPLQAWDIT-FRFQGG-PILCKLVK
 Aposthonia_japonica -----RRKKLSRMYFFIVHLSIADLITAFFNVLPLQAWDVT-YRFQGG-PILCKIKF
 Haploembia_palau -----RRKKLSRMYFFIVHLSIADLITAFFNVLPLQAWDVT-YRFQGG-PILCKIKF
 Halyomorpha_halys -----ATRTKVPVPRMFFMHLCSVADMTAWLNLPQLAWDIT-FRFKGG-EFLCKSVKF
 Stenobothrus_lineatus -----QLSVVDDLNGLLNVLPLQAWDIT-FRFQGG-AVLCKLVK
 Inocellia_crassicornis -----SGCRKLSRMYFFILHLSIADLVTAFNVLPLQAWDIT-FRFKGG-PLLCKAVKY
 Tenthredo_koehlerii -----APRKKLPRIYFFILHLSIADLLTALLNVLPLQIWEIT-FRFQGG-PVLCKVVKF
 Corydalus_cornutus -----VTAFNVLPLQIWEIT-YRFQGG-EILCKAVKF
 Chrysopa_pallens -----TGRKKLSRIYFFILHLSIADLVTAFNVLPLQAWDIT-YRFQGG-VLCKAVKF
 Meloe_violaceus -----AGRKKLSRMYFFILHLSVADLITAFLSVLPQLAWDIT-YRFYGG-YFLCKAIKY
 Aethina_tumida -----AGRKKLSRMYFFILHLSIADLITAFLSVLPQLAWDIT-YRFQGG-YILCKLVKF
 Gyrinus_marinus -----AGRKKLSRMYFFILHLSIADLVTAFNVLPLQAWDIT-YRFQGG-AVLCKLVKF
 Tribolium_castaneum -----AGRKKLSRMYFFILHLSIADLITAFNVLPLQAWDIT-YRFYGG-FLLCKVVKY
 Nicrophorus_vespilloides -----AGRKKLSRMYFFILHLSIADLITAFNVLPLQAWDIT-FRFQGG-EVLCKLVKF
 Aleochara_curtula -----AGRKKLSRMYFFILHLSIADLITAFNVLPLQAWDIT-YRFYGG-GALCKMVKF
 Pogonys_chalceus -----MYFFILHLSIADLVTAFNVLPLQAWDIT-YRFNGG-FLLCKIVKY
 Sipyloidea_sipylus -----RSKLTRMYFFILHLSIADLITGMCNVLPLQAWDIT-YRFKGG-PVLCKIVKF
 Extatosoma_tiaratum -----KRRKLSRMYFFILHLSIADLITGFLNVLPLQAWDIT-YRFQGG-PVLCKIKY

Aretaon_asperimus -----RKKKLTRMYFFILHLSIADLISGLLEVL**PQLAWDIT-YRF**QGG-PVLCKFVKY
 Medauroidea_extradentata -----RHKKLTRMYFFILHLSIADLITGLLNVL**PQLAWDIT-YRF**QGG-PVLCKIVKY
 Ramulus_arteris -----RRKKLTRMYFFILHLSIADLITGLLNVL**PQLAWDIT-YRF**QGG-PVLCKVVKF
 Galloisiana_yuasai -----ADLITAFNLV**PQLGWEIT-YRF**SGG-PVLCKAVKF
 Athalia_rosae P-----IRKKSSSRMYFFILHLSIADLITAFNLV**PQLGWEIT-YRF**QGG-PILCKLVKF

181

240

Varroa_destructor1 LQVFLVLYLSTYVLGMAVDRYLAIIRSGIN-----
 Metaseiulus_occidentalis1 MQIFVLYLSTYTLVGLSLNSSLVVRSGSS-----
 Metaseiulus_occidentalis2 AQVYVLYLSTYILTGMSLDRLITMRAIESQWQTASLRRSDHDQSSDKSPQSHKIKFNNHR
 Tigriopus_californicus GQVMPYLYSSFILTLMVAVDRVGVTKRHGS-----
 Anurida_maritima LQIFVLYLSTYILISMTLDRYLTVVCHHSF-----SR
 Meinertellus_cundinamarcensis FQVMPYLYGSTYVLMFLAVDRYRAVCSAGP-----
 Pogonognathellus_sp LQIFVLYLSTYVLTSMVDRYLTVVCHHSF-----TR
 Triops_cancriformis GQIMPLYLSTYLLMFALDRYRAVCSASN-----N
 Strigamia_maritima2 LQVMVLYLSTYILVMMVAVDRYRAVCSASN-----I
 Catajapyx_aquilonaris FQVMVLYLSSYILMFMAVDRYKALCCD-A-----F
 Daphnia_pulex AQVMTLYLSTYILMFMAVDRYRAVCCR-N-----L
 Daphnia_magna3 -----
 Daphnia_magna2 TQIMTLYLSTYILMFMAVDRYRAVCCR-N-----L
 Daphnia_magna1 TQIMTLYLSTYILMFMAVDRYRAVCCR-N-----L
 Daphnia_magna4 TQIMTLYLSTYILMFMAVDRYRAVCCR-N-----L
 Arachnocampa_luminosa SQVFSVYASTFLLIVMAIDRFRCICWPIK-----S
 Calanus_finmarchicus LQMLGPYLSSFLLCVTSMDRYQAICKPFK-----T
 Epiophlebia_superstes LQLLGPYLSSYLLVAMALDRHRAVCRPLS-----A
 Ladona_fulva LQLLGPYLSSYLLVAMALDRHRAVCRPLS-----V
 Cordulegaster_boltonii LQLLGPYLSSYLLVMAIDRHRVAVCRPLS-----V
 Diaphorina_citri VHNVGSFLSSYILMAIAIDRYAICHPLT-----Y
 Pachypsylla_venusta VQPSGSFLSSYILMAIAIDRYAICQPLT-----Y
 Acanthocasuarina_muellerianae -----
 Glomeris_pustulata -----
 Frankliniella_cephalica -----
 Machilis_hrabei -----
 Carabus_granulatus -----
 Dendroctonus_frontalis -----ICYPLT-----Y
 Lepeophtheirus_salmonis GQMIGPYLSSYVLMVTAIDRYHAICFPFS-----K
 Caligus_rogercresseyi CQMIGPYLSSYVLMVTAIDRYHAICNPLS-----K
 Parhyale_hawaiensis GQLVGPYLNAYILVVTVAIDRYQVICRPLS-----N
 Hyalella_azteca GQLVGPYMNSSYLLVVTVAIDRYQVICRPLS-----N
 Strigamia_maritima1 GQLLGPYLSSYILVGMALDRYLAICFPLN-----
 Conwentzia_psociformis -----
 Liposcelis_bostrychophila G-----
 Tetranychus_urticae LQILGPYLSSFTLCATAIDRYAICFPLE-----S
 Osmylus_fulvicephalus S-----
 Ornithodoros_turicata -----SYLVVTAIDRYQAICFPLS-----N
 Acerentomon_sp MQIFGPYLSSYILVVTVAIDRYAICFPLQ-----N
 Ixodes_ricinus GQLLGPYLSSYLLVVTVAIDRYQAICFPLS-----N
 Folsomia_candida -----
 Limulus_polyphemus1 LQILGPYLSSYVLMVTAIDRYHAICFPLR-----N
 Limulus_polyphemus3 LQILGPYLSSYVLMVTAIDRYQAICFPLT-----R
 Platynothrus_peltifer5 LQILGPYLSSYILVITAIDRYQAICFPLS-----N
 Platynothrus_peltifer1 LQILGPYLSSYVLMVTSIDRYQAICYPLS-----N
 Platynothrus_peltifer3 LQILGPYLSSYVLMVTAIDRYQAICYPLS-----N
 Achipteria_coleoptrata2 LQIFGPYLSSYVLMVTAIDRYQAICNPLS-----N
 Platynothrus_peltifer2 MQILGPYLSSYVLMVTAIDRYQAICFPLS-----N
 Platynothrus_peltifer4 LQLFGPYLSSYVLMVTAIDRYQAICFPLT-----N
 Ixodes_scapularis2 GQLLGPYLSSYVLMVTAIDRYQAICFPLS-----N
 Ixodes_scapularis1 GQLLGPYLSSYVLMVTAIDRYQAICFPLS-----N
 Ixodes_scapularis3 GQLLGPYLSSYVLMVTAIDRYQAICFPLS-----N
 Cotesia_vestalis LQPFNGYLSSYVLTATAIDRYQAICNPFPS-----Y
 Microplitis_demolitor LQPFNGYLSSYVLTATAIDRYQAICYPFN-----Y
 Zorotypus_caudelli -----
 Nasonia_giraulti CQPLGSYLSSYVLIATAVDRYHAICYPLS-----Y
 Nasonia_vitripennis CQPLGSYLSSYVLIATAVDRYHAICYPLS-----Y
 Varroa_destructor2 AQVLVLYLSTYILTGMSLDRLVSM-----
 Leuctra_sp GQTLGPHLTAFLVATLWDRTHAFCY-----
 Tricholepidion_gertschi -----
 Perla_marginata GQALG-----
 Crioscolia_alcione GQPLGHLSSYILTAAIDRYQAICHPLS-----Y
 Mischocyttarus_flavitaris FQPLGHLSSYILTATAIDRYHAICHPLS-----Y
 Polistes_metricus FQPFGLYSSYILTATAIDRYHAICHPLS-----Y
 Polistes_canadensis FQPFGLYSSYILTATAIDRYHAICHPLS-----Y
 Chrysis_viridula MQPLGPYLSSYVLMATAIDRYHAICHPLS-----Y
 Argochrysis_armilla IQPLGPYLSSYV-MATAIDRYHAICHPLS-----Y
 Chyphotes_mellipes GQPLGPYLSSYVLMATAIDRYHAICHPLS-----Y
 Brachycistis_timberlakei GQPLGPYLSSYVLMATAIDRYHAICHPLS-----Y

Sphaerophthalma_orestes IQPIGPYLSSYVLTATAIDRYHAICHPLS-----Y
Homalodisca_vitripennis GQTMGPYLSSYILVATALDRYKAICEPLN-----Y
Cercopis_vulnerata GQTLGPYLSSYVLMSTAMDRYKAICHPLT-----Y
Nilaparvata_lugens GQTLGPYLSSYVLMATAMDRYKAICHPLT-----Y
Achipteria_coleoptratal LQILGPYLSSYVLMVMTSIDRYQAICYPLT-----N
Ephemera_danica SLLLGPYLSSFVLVLTAVDRYEAIICRPLT-----Y
Leptopilina_clavipes GQPIGPYLSSYILTATAIDRYHAICFPFS-----Y
Ganaspis_sp VQPIGPYLSSYILTATAIDRYHAICFPFS-----Y
Leptopilina_boulardi GQPIGPYLSSYILTATAIDRYHAICFPFS-----Y
Mantis_religiosa GQTL-----Y
Blattella_germanica GQTLGPYLSAYILMVTALDRYQAVCHPLA-----Y
Zootermopsis_nevadensis GQTLGPYLSAYILMATALDRYQAVCHPLA-----Y
Stigmatomma_oregonense GQPFGLYLSSYILTVTAMDRYQAICHFPFS-----Y
Dinoponera_quadriceps GQPFGLYLSSYILTVAAVDRYQAICHFPFS-----Y
Harpegnathos_saltator GQPFGLYLSSYILTVTAMDRYQAICHFPFS-----Y
Cerapachys_biroi GQPFGLYLSSYILTVTAMDRYQAICHFPFS-----Y
Monomorium_pharaonis GQPFGLYLSSYILTVTAFDRYQAICHFPFS-----Y
Tetramorium_bicarinatum GQPFGLYLSSYILTVTALDRYQAICHFPFS-----Y
Solenopsis_invicta GQPFGLYLSSYILTVTIDRYHAICHFPFS-----Y
Atta_cephalotes GQPFGLYLSSYILTVTIDRYHAICHFPFS-----Y
Acromyrmex_echinatior GQPFGLYLSSYILTVTAMDRYHAICHFPFS-----Y
Pogonomyrmex_barbatus GQPFGLYLSSYILTVTIDRYQAICYPFS-----Y
Wasmannia_auropunctata GQPFGLYLSSYILTVTIDRYQAICHFPFS-----Y
Vollenhovia_emeryi GQPFGLYLSSYILTVTAMDRYQAICHFPFS-----Y
Orussus_abietinus GQPFGLYLSSYVLTATAIDRYRAICKPLD-----S
Blaberus_atropes -----S
Limulus_polyphemus2 MQILGPYLSSYVLLVTAIDRYQAICFPLT-----S
Isonychia_bicolor LQLLGPYLSSYILVLTAVDRFHAICLPLS-----Y
Occasjapyx_japonicus MQILGPYLSSYVLMVMTAIDRYQAICFPLS-----N
Baetis_sp GQILGPYLSSYILVLTAVDRYQAICQPLA-----H
Panonychus_ulmi LQLLGPYLSSFTLCATAIDRYRAICYPLE-----S
Frankliniella_occidentalis GQPLGVYLSSYVLTATAIDRYRAICHPLT-----Y
Eurylophella_sp GQLLGPYLSSYVLTAVDRYFAICRPLS-----Y
Telenomus_podisi GQPFGLYLSSYVLTAVDRYHAICHPLN-----Y
Aposthonia_japonica CQTLGPYLSSYVLLATAVDRYRAICSPLV-----Y
Haploembia_palau CQTLGPYLSSYVLLATAVDRYRAICSPLV-----Y
Halyomorpha_halys GQTLGPYLSSYVLTAVTALDRYQAICHPLT-----Y
Stenobothrus_lineatus GQPLGPYLSSYVLTAVTALDRHQAVCRPLT-----Y
Inocellia_crassicornis NQLLGPYLSAYILSATAIDRHQAICYPLT-----Y
Tenthredo_koehleri GQTLGPYLSSYVLAATAIDRYQAVRHPLI-----Y
Corydalus_cornutus AQPVGPYLSSYVLTATAIDRHQAICHPLT-----Y
Chrysopa_pallens GQPLGTYLSSYILSATAIDRHQAICYPLT-----Y
Meloe_violaceus GQTLGPYLSSYVLMATAIDRHQAICYPLT-----Y
Aethina_tumida GQTLGPYLSSYVLMATAIDRHQAICYPLT-----Y
Gyrinus_marinus GQTLGPYLSSYVLMATAIDRHQAICYPLT-----Y
Tribolium_castaneum GQTLGPYLSSYVLMATAIDRHQAICYPLT-----Y
Microphorus_vespilloides GQTLGPYLSSYILMATAIDRHQAICYPLT-----Y
Aleochara_curtula GQTLGPYLSSYILMATAIDRHQAICYP-----Y
Pogonus_chalceus CQTLGPYLSSYILMATAIDRHQAICYPLT-----Y
Sipyloidea_sipylus IQPLGPYLSSYVLLATALDRYQAICHPMT-----Y
Extatosoma_tiaratum LQPLGPYLSSYVLLATALDRYQAICHPMT-----Y
Aretaon_asperrimus FQPLGPYLSSYVLLATALDRYQAICQPM-----Y
Medauroidea_extradentata FQPLGPYLSSYVLLATALDRYQAICQPM-----Y
Ramulus_artemis FQPLGPYLSSYVLIATALDRYQAICHPMT-----Y
Galloisiana_yuasai GQTLGPYLSSYVLLATALDRFQAICHPLT-----Y
Athalia_rosae GQPLGPYLSSYVLMVTALDRYQAICHPLN-----Y

241

300

Varroa_destructor1 ----RPIVVVRTILSVSWLVAAVLSPQL---YIFSFQKL----PNG----AH-DCWA
Metaseiulus_occidentalis1 ----STSSRLWVILGAGWFLSALLASPQV---YIFSFQKL----SNG----VY-DCWG
Metaseiulus_occidentalis2 CRV--GYRKFAKKLIVFAWFLAALSIPQL---FLFSYTRI----HDH--GSWY-DCKA
Tigriopus_californicus ----VEPKPLRPLIQGVWLVAAILCALPQP---FIFSIKDI----DDK---GIY-DCWA
Anurida_maritima NHY--GGLKSPKVMVAISWILSLIFASPQA---VIFSQSEI----RPG----VF-DCWT
Meinertellus_cundinamarcensis SPQ--AALKEARLMVCAAWILSIILAIPQA---LVFTHREI----APG----IQ-DCWA
Pogonognathellus_sp NHY--GGLRGPKILVILSWILSFIFASPQA---FIFSEKEL----TMNDQTKVY-DCWS
Triops_cancriformis LHW--NSLKVAKMMVTSAWVLSLLLAIPQA---IIFSEQYI----NPDGTTTET-DCWV
Strigamia_maritima2 GHW--NSLRAAKLMIVGAWVLAFLAAIPQA---IIFGKMEI----RPG----VH-DCWA
Catajapyx_aquilonaris SPW--NSLLAAKIMVASAWVMAFGFATPQA---VIFTLKKI----SPG----VQ-DCWG
Daphnia_pulex -HW--NSLKVAKCFVAASWVMALLFSIPQA---VIFHEEEI----SVG----VT-DCWV
Daphnia_magna3 -TW--NSRKVAKCFVAASWVMSMLFAIPQA---VIFHEEEI----SVG----VT-DCWV
Daphnia_magna2 -HW--NSLKVAKCFVAASWVMSMLFAIPQA---VIFHEEEI----SVG----VT-DCWV
Daphnia_magna1 -HW--NSLKVAKCFVAASWVMSMLFAIPQA---VIFHEEEI----SVG----VT-DCWV
Daphnia_magna4 -HW--NSLKVAKCFVAASWVMSMLFAIPQA---VIFHEEEI----SVG----VT-DCWV
Arachnocampa_luminosa CSW--NYR-HALVPVFFSWILAAVSSPQL---FLFKIQHM----SVQHY--TVETCSV
Calanus_finmarchicus CSW--EPK-NSDKLVGGAWVLAALCCIPQL---LIFNTSSQ----IGCNSGEMFEKQCT
Epiophlebia_superstes RVF--LPR-SPRRLVAIAWALSFLFSLPQA---FVFSYRRA----TE----TEW-DCWA

Ladona_fulva RAF--LPR-SPRRLVAIAWALSALFSLPQA---FVFSYQKA-----TE----TEW--CWA
 Cordulegaster_boltonii RAF--LPR-SPRRLVAIAWALSFLFSLPQA---FIFSYRKA-----TE----TEW-DCWA
 Diaphorina_citri HTW--NSR-RSRIMITAWSTAFTCIPQI---TIFSYQEV-----KP----GIY-DCWA
 Pachypsylla_venusta HSW--NSR-RSRIMILIAWSAAFTFCIPQV-QISIFSYQEI-----KP----GVY-DCWA
 Acanthocasuarina_muellerianae -----
 Glomeris_pustulata -----
 Frankliniella_cephalica -----SIEP-----VE----GGY-DCWA
 Machilis_hrabei -----
 Carabus_granulatus -----
 Dendroctonus_frontalis CSW--TSR-RSKFMMYVAWIASLLCCIPQV---IIFSFQEV-----EP----RVY-DCWA
 Lepeophtheirus_salmonis CTW--TPK-RSNIMIGLAWLVSLALCVPQI---IIFGSGE-----KSH-SCSA
 Caligus_rogercresseyi CTW--TPK-RSNIMIGLAWLVSFALCIPQA---IIFGSSE-----AKY-SCSA
 Parhyale_hawaiiensis CRW--RPG-HSIRLIGAAATFLSLWLSVPQL---FIFSLRSK-----NG----IQ-DCWA
 Hyalella_azteca CRW--TPG-HSIRLISCATAISLLFSIPQL---FNFSFREK-----NG----IY-DCWA
 Strigamia_maritima1 -SW--AAT-RSKGMVCVAVVSVVFSPPQM---FLFSYKYV-----SV--L-KYW-ECWV
 Conwentzia_psociformis -----
 Liposcelis_bostrychophila -----
 Tetranychus_urticae RS---ALN-RSKLKVSIWGLLALICCLPQL---FIFSYRQI-----PN--SPGVY-ECWG
 Osmylus_fulvicephalus -----
 Ornithodoros_turicata CSW--TPT-KSKLMIAFAWVSLCCVPQL---FIFSYQQV-----EN----GVY-DCWG
 Acerentomon_sp SRW--TER-RYKAMIAVAWTATLCLCSPQV---FIFSYMKV-----GTNQSGDIY-DCWA
 Ixodes_ricinus CSW--TPT-KSKLLISAQVAVSLCCVPQV---FIFSYQEI-----SP----RVF-DCWG
 Folsomia_candida -----
 Limulus_polyphemus1 CVW--TPR-KSKLMIIAAWTISMLCCVPQV---FIFSYQKV-----LI-EP-ITF-DCWG
 Limulus_polyphemus3 CTW--TPR-RSKLMIVGAWIISILCCSPQA---FIFSYQQV-----SS-DP-LVF-DCWG
 Platynothrus_peltifer5 CSW--TPK-RSQLMISIAWVLSLIFCAPQL---FIFSYQQI-----PG-TLGNVY-DCWG
 Platynothrus_peltifer1 CAW--TPK-RSQLMISFAWIIALLCCIPQV---IIFSYQQI-----PG-YD--II-DCWG
 Platynothrus_peltifer3 CAW--SPT-RSKLMILMAWIVSLCCAPQI---IIFSYQEI-----G---S-QIF-DCWG
 Achipteria_coleoptrata2 CKW--TPG-RSKLMITIAWIVTSFCCSPQI---FIFSYQQI-----PG-TD-AIY-DCWG
 Platynothrus_peltifer2 CSW--TPR-RAKLMISCAWIIISIVCSLPQA---FIFSYQEV-----PE-TN-HIY-DCWG
 Platynothrus_peltifer4 CHW--TSR-KSKLMITIAWIIISILCSAPQA---FIFSYQEI-----PR-TN-GVR-DCWG
 Ixodes_scapularis2 CSW--SPT-RSKLMIVSAWAVTLCCVPQV---FIFSYQEI-----APGV-----F-DCWG
 Ixodes_scapularis1 CSW--TPT-KSKLLICAQVAVALLCCVPQV---FIFSYQEV-----SPEV----F-DCWG
 Ixodes_scapularis3 CSW--TPT-KSKLLISAQVAVSLCCVPQV---FIFSYQEI-----SPKV----F-DCWG
 Cotesia_vestalis CR-----
 Microplitis_demolitor CRT--SSL-KSRVMVYGAWSLSFVLCIPQV---IVFSYQEI-----SPGV----W-DCWA
 Zorotypus_caudelli -----
 Nasonia_giraulti CRT--TSR-RSRITVYVAVLLALLFCLPQV---FIFSYQEI-----SAGV----W-DCWA
 Nasonia_vitripennis CRT--TSR-RSRITVYVAVLLALLFCLPQV---FIFSYQEI-----SAGV----W-DCWA
 Varroa_destructor2 -----
 Leuctra_sp -----
 Tricholepidion_gertschi -----
 Perla_marginata -----
 Crioscobia_alcione -----
 Mischocyttarus_flavitaris -----
 Polistes_metricus CSS--TSR-KARIMLYSAWVVALVFCIPQI---FIFSYREI-----SPNV----W-DCWA
 Polistes_canadensis CSV--TSR-KSRIMVYCAWLSLILCIPQL---FVFSYQEI-----TPNI----W-DCWA
 Chrysis_viridula CSV--TSR-KSRIMVYCAWVSLILCIPQL---FVFSYQEV-----MPRI----W-DCWA
 Argochrysis_armilla CGS--SLK-RSKIMVYSAWAVTLILCIPQV---IVFSYQEV-----TPKV----W-DCWA
 Chyphotes_mellipes CGS--SLK-RSKIMVYSAWVALILCIPQV---VFSYQEV-----TPKV----W-DCWA
 Brachycistis_timberlakei CRT--TSK-RSRVMVYGAWIITLFLCIPQV---FIFSYQEI-----MPSV----W-DCWA
 Sphaerophthalma_orestes CST--TSR-RSRIMVYGAWVLLALLCIPQV---IVFSYKEV-----EQVQ----W-DCWA
 Homalodisca_vitripennis CST--TSR-RSRIMVYGAWVLLALLCIPQV---YVFSYEEI-----MPNV----W-DCWA
 Cercopis_vulnerata SNW--TSR-RSALTVSAWVSLTLLFCIPQVSVIIFSYQEI-----APGV----Y-DCWA
 Nilaparvata_lugens CSW--TSR-RSRMVRVAVIVSLILCIPQV---NIFSYQEI-----APGI----Y-DCWA
 Achipteria_coleoptrata1 CSW--TSH-HARSMVQCAWATALLFCIPQV---TIFSYMEVPG---SPGD----Y-DCWA
 Ephemera_danica CQW--TPT-RSKLMITLAWIIALLCCIPQV---LIFSYQQIP---GT----DIY-DCWG
 Leptopilina_clavipes CTW--PAR-RAWFLVAGAWTLALLCCAPQL---FVFSYRPVQQ---QPDV----F-DCWA
 Ganaspis_sp CRT--TSR-RSRIMVYSAWIIALLILCTPQV---FVFSYQLI-----SPGI----W-DCWA
 Leptopilina_boulardi CRT--TSR-RSRIMVYSAWIIALLILCTPQI---FIFSYQLI-----SPGV----W-DCWA
 Mantis_religiosa -----
 Blattella_germanica CSW--TSR-RSKFMVWTAWVVALGFCVPQ-----S-----
 Zootermopsis_nevadensis CSW--TSR-RSRAMVMAWVVALIFCIPQV-----S-----
 Stigmatomma_oregonense CRV--TSR-RSRMMVYGAWTLATILCIPQV---FIFSYQEI-----STGV----W-ECWA
 Dinoponera_quadriceps CSV--TSR-RSKMMVYVWVLLAVVLCVPQV---FIFSYQEI-----SPNV----W-DCWA
 Harpegnathos_saltator CNV--TSR-RSKMMVYAAWTLAVVLCVPQI---FIFSYQEI-----SPNV----W-ECWA
 Cerapachys_biroi CAV--TSR-RSKMMVYGAWVLAALILCVPQV---FVFSYKEI-----SPGV----W-ECWA
 Monomorium_pharaonis CGV--TSQ-RSKMMVYGAWVLAALILCVPQI---FIFSYMEI-----APDI----W-ECWA
 Tetramorium_bicarinarum CSV--TSR-RSKMMVYGAWVLSVALSVPQI---FIFSYTEI-----APGV----W-ECWA
 Solenopsis_invicta CGV--TSR-RSKMMVYGAWVLAALILCVPQI---FIFSYMEI-----SPGV----W-ECWA
 Atta_cephalotes CSV--TSR-RSKMMVYGTWMLAAMLCVPQI---FIFSYMEI-----SPGV----W-ECWA
 Acromyrmex_echinaior CSV--TSR-RSKMMVYGTWMLAAMLCVPQI---FIFSYMEI-----SPGV----W-ECWA
 Pogonomyrmex_barbatus CGI--TSR-RSKMMVYGAWMLAVILCIPQI---FIFSYTEI-----SPGV----W-ECWA
 Wasmannia_auropunctata CGV--TSR-RSKMMVYGAWMLAALCVPQI---FIFSYTEI-----SPGV----W-ECWA
 Vollenhovia_emoryi CGI--TSR-RSKMMVYGAWMLAALCVPQI---FIFSYTEI-----SPGV----W-ECWA
 Orussus_abietinus LDHRICTL-QSRNMIRCSWCLALLFSLPQV---FVFSYKEI-----SPGV----W-DCWA
 Blaberus_atropos -----

Limulus_polyphemus2
Isonychia_bicolor
Occasjapyx_japonicus
Baetis_sp
Panonychus_ulmi
Frankliniella_occidentalis
Eurylophella_sp
Telenomus_podisi
Aposthonia_japonica
Haploembia_palau
Halyomorpha_halys
Stenobothrus_lineatus
Inocellia_crassicornis
Tenthredo_koehleri
Corydalus_cornutus
Chrysopa_pallens
Meloe_violaceus
Aethina_tumida
Gyrinus_marinus
Tribolium_castaneum
Nicrophorus_vespilloides
Aleochara_curtula
Pogonus_chalceus
Sipyloidea_sipylus
Extatosoma_tiaratum
Aretaon_asperimus
Medauroidea_extradentata
Ramulus_artemis
Gallosiana_yuasai
Athalia_rosae

CVW--TPR-KSKIMIANAWIISILCCFPQI---FIFSYQKVSE---DPVT----F-DCWG
CTW--PAK-KAKLLVSGAWVLALLCCLPQV---LIFSYQPI-----TPGG--DVF-DCWA
CSW--TPK-RSKVMGILSWVLSLMLFCAP-----
CTW--PVR-RARALVCVAWALALACCTPQV---FIFSYQPIG-----DTY-DCWG
RSR---LN-RSNLKVSIWGLLALICCLPQL---LIFSYHQIPN---NPQV----Y-ECWG
CSW--TSR-RAKTMVAAWVAICFSAPQV---RSEGYTAGQRQTLEANSV-PCV-NCCN
CTW--PAR-RARLLVSTWVLLALLFCLPQL---AVFSYQRVQNAPDKQDQ----Y-DCWA
CRT--TSR-RSRFMVYAAWILAFLLCTPQA---YVFSFQEV-----WPGV----S-DCWA
HSW--SFR-RAKIMVLIWIIISLWFCVPQA---VVFSYQEL-----EPGV----W-DCWA
HSW--SFG-RAKVMVFIWITISLLFCLPQS---IIFSYQEL-----KPGV----W-DCWA
CSW--SSK-RARGMIMGAWALSITFCTPQL---TIFSYQEV-----APGV----F-DCWA
CSW--TYR-RSRAMQVAV-----
CSW--TSR-CSRAMIWMAWASLAFCLPQL---IIFSYQEI-----EPNV----W-DCWG
CSI--TSR-RSKMTVYPAWCLSLLLCVPQT---LVFSYKEV-----SSGV----W-DCWA
CSW--TSR-RSKGMVYLAWLCSLIFCIPQV---FIFSYQIVP---DAPGV----Y-DCWA
CSW--TSQ-RSQVMVTAWIIISLIFCIPQL---FIFSYQEV-----SPGI----W-DCWG
CSW--TSR-RSKVMVYIAWCTSLIFCLPQL---FIFRYKEL-----SDGI----Y-DCWA
CSW--TSR-RSKFMVYIAWITSLVFCIPQL---TIFSYQEV-----DDGE----F-DCWA
CSW--TSR-RSKVMVYIAWVAALAFCLPQL---NIFSYQEI-----APGV----Y-DCWA
CSW--TSR-RSKVMVYLAWCVSLAFCLPQL---TIFTYTSV-----GEDE----Y-DCWA
CSW--TSR-RSRVMVYIAWVLSLAFCLPQI---TIFSYQHV-----ENEE----Y-DCWA

CSW--TSR-RSKVMVYLAWATSLAFCLPQV---TIFAYQEV-----APGI----N-DCWA
CSS--DSR-RSRVMIWMAWCVSLAFCLPQV---IIFSYQET-----VPGV----Y-DCWG
CST--DSR-RSRVMVMAWCVSLAFCLPQV---IIFSYQET-----APGV----Y-DCWA
CSS--DSR-RSRVMVMAWCVSLVFCIPQV---IIFSYQET-----EPGV----H-DCWA
CST--DSR-RSRAMIWLAWCVSLVFCIPQV---IIFSYQET-----APGV----F-DCWA
CST--DSR-RSRMIWLAWCVSLGFCIPQV---IIFSYQET-----ASGV----Y-DCWA
CSW--TSR-RSRMTVWLAWAFS-----
CSV--TSR-RSKIMVYLAWGLSLALCLPQL---VVFSYQEA-----SPGV----W-DCWG

Varroa_destructor1
Metaseiulus_occidentalis1
Metaseiulus_occidentalis2
Tigriopus_californicus
Anurida_maritima
Meinertellus_cundinamarcensis
Pogonognathellus_sp
Triops_cancriformis
Strigamia_maritima2
Catajapyx_aquilonaris
Daphnia_pulex
Daphnia_magna3
Daphnia_magna2
Daphnia_magna1
Daphnia_magna4
Arachnocampa_luminosa
Calanus_finmarchicus
Epiophlebia_superstes
Ladona_fulva
Cordulegaster_boltonii
Diaphorina_citri
Pachypsylla_venusta
Acanthocasuarina_muellerianae
Glomeris_pustulata
Frankliniella_cephalica
Machilis_hrabei
Carabus_granulatus
Dendroctonus_frontalis
Lepeophtheirus_salmonis
Caligus_rogercresseyi
Parhyale_hawaiensis
Hyalabella_azteca
Strigamia_maritima1
Conwentzia_psociformis
Liposcelis_bostrychophila
Tetranychus_urticae
Osmylus_fulvicephalus
Ornithodoros_turicata
Acerentomon_sp
Ixodes_ricinus
Folsomia_candida
Limulus_polyphemus1
Limulus_polyphemus3
Platynothrus_peltifer5

301

360

TFEP-PITFRYVLFITAV-----
TFDP-PLTSVRVYVFIAMA-----
NFSWHRFQRIYTYFVLI-----
DFGGEKWEKGYVVTFLFTV-----
FL--GPSGVKAYVTWVVISV-----
DFPGGQQGAKIYVLFVVIWV-----
TFIE-PWGVRYVTWVVCV-----
RFIE-PWGAKEYVTWVVISI-----
HFEQ-PWGEKAYVTWVLSI-----
TFVE-PWGTKAYVTWVVISI-----
QFVE-PWGAKAYVTWV-----V
QFAE-PWGAKEYVTWV-----V
QFAE-PWGAKEYVTWVVSIFGAPLLVVAVCYXXXXXXXXXXWVQFAEPWGAKEYVTWV-----V
QFAE-PWGAKEYVTWV-----V
QFAE-PWGAKEYVTWV-----V
KWLS-KKHEGLYLLFHMSTQ-----
NFPT-WVTPSQYILYFSFAN-----
TFEP-PWTQKAYVTWYGISV-----
TFDP-PWTQKAYVTWYGISV-----
TFDP-PWTQKAYVTWYGISV-----
SWDQ-EWGERAYVTWFSITV-----
SWDQ-EWGERIYITWFSVSV-----

TFVP-EWGQRAYVTWYTCV-----

TFDN-EWGEQAYVVCYSVTV-----
TFAQ-DWGQKAYVTWFAVSN-----
SFVV-DWGQKAYVTWFAVSN-----
SFIQ-PWGVVAYVTWYFYSIAV-----
DFIP-GWGVTAAYVTWYIAV-----
DFTL--EEERAYVTWYFVAN-----

TFIQ-PYGERLYVTWYALTS-----

TYAE-PWGVTAAYVTWYGVSV-----
TFIE-PWGAKEYVTWYAFVI-----
TYVE-PWGLRAYVTWYGVSV-----

VFIQ-PWGEKAYVVLWYALSQ-----
TFIQ-PWGEKAYVVLWYALSQ-----
IFPQ-PYGERIYVTWYAITV-----

Platynothrus_peltifer1	TFPQ-PFGERIYVSWYAISF-----
Platynothrus_peltifer3	TFSQ-PYGERIYVTWYAVSV-----
Achipteria_coleoptrata2	TFQK-PWGERIYVTWYAVSV-----
Platynothrus_peltifer2	TFPQ-PWGERIYVTWYAISV-----
Platynothrus_peltifer4	TFPQ-PYGERIYVTWYAITV-----
Ixodes_scapularis2	TFA-QPWGLRAYVTWYSVSV-----
Ixodes_scapularis1	TYV-ESWGLRAYVTWYGMSV-----
Ixodes_scapularis3	TYV-EPWGLRAYVTWYGVS-----
Cotesia_vestalis	-----
Microplitis_demolitor	SFS-LPYGERIYVTWYSITI-----
Zorotypus_caudelli	-----
Nasonia_giraulti	TFT-VPYGERAYVTWYSVTV-----
Nasonia_vitripennis	TFT-VPYGERAYVTWYSVTV-----
Varroa_destructor2	-----
Leuctra_sp	-----
Tricholepidion_gertschi	-----
Perla_marginata	-----
Crioscolia_alcione	TFD-LPYGERAYVTWYAVTV-----
Mischocyttarus_flavitaris	TFD-IKFGERAYVTWYSLMV-----
Polistes_metricus	TFD-IKFGEKAYVTWYSLMV-----
Polistes_canadensis	TFD-IQFGEKAYVTWYSLMV-----
Chrysis_viridula	VFN-VAYGERIYVTWYSTMV-----
Argochrysis_armilla	VFD-VAYGERIYVTWYSTMV-----
Chyphotes_mellipes	TFD-PTYGEKAYVTWYSITV-----
Brachycistis_timberlakei	TFD-LEYGERAYVTWYSVTV-----
Sphaerophthalma_orestes	TFG-LHYGERAYVTWYSVTV-----
Homalodisca_vitripennis	TFP-FPWGERVYVTWYSVSV-----
Cercopis_vulnerata	TFP-EPWGEKLYVTWYSVSV-----
Nilaparvata_lugens	TFP-RDWGERAYVTWYSVSV-----
Achipteria_coleoptrata1	TFPLQPYGERIYVTWYAISF-----
Ephemera_danica	TFE-PWGERAYVSWYATS-----
Leptopilina_clavipes	TFT-VPYQEAAYVTWYSISV-----
Ganaspis_sp	TFK-MPYQEAAYVTWYSISV-----
Leptopilina_boulardi	TFT-VPYQEAAYVTWYSISV-----
Mantis_religiosa	-----
Blattella_germanica	-----
Zootermopsis_nevadensis	-----
Stigmatomma_oregonense	IFY-LKYGERAYITWYSVTQ-----
Dinoponera_quadriceps	TFN-VKYGERSYVTWYSVTQ-----
Harpegnathos_saltator	TFH-LKYGERAYITWYSVTQ-----
Cerapachys_biroi	TFY-LKYGERAYITWYSVTQ-----
Monomorium_pharaonis	TFY-MPYGERAYITWYSVTQ-----
Tetramorium_bicarinarum	TFY-LKYGERAYITWYSVMQ-----
Solenopsis_invicta	TFY-LKYGERAYITWYSVTQ-----
Atta_cephalotes	IFY-LKYGERAYITWYSVMQ-----
Acromyrmex_echinator	TFY-LKYGERAYITWYSVMQ-----
Pogonomyrmex_barbatus	TFY-LKYGERAYITWYSIMQ-----
Wasmannia_aurouncata	TFY-LKYGERAYITWYSVTQ-----
Vollenhovia_emoryi	TFN-LKYGERAYITWYSVTQ-----
Orussus_abietinus	TFE-LSYGERAYVTWYCLAV-----
Blaberus_atropos	-----
Limulus_polyphemus2	IFI-QPWGEKVYVVLWYAVSQ-----
Isonychia_bicolor	TFP-PYWGERAYVSWYTVSV-----
Occasjapyx_japonicus	-----
Baetis_sp	TFP-EGWGERAYVTWYSGSV-----
Panonychus_ulmi	TFI-QPYGERLYVTWYAFSS-----
Frankliniella_occidentalis	LFI-----
Eurylophella_sp	TFQ-PAWGERAYVTWYAGSV-----
Telenomus_podisi	TFN-LPYGERIYVTWYSVTV-----
Aposthonia_japonica	TFI-KPWGERAYVTWYSVFS-----
Haploembia_palaui	TFI-QPWGERTYITWYSVFA-----
Halyomorpha_halys	VFS-EPYGERVYVTWYSISV-----
Stenobothrus_lineatus	-----
Inocellia_crassicornis	TFP-EPWGAQAYVTWYSLSI-----
Tenthredo_koehleri	TFDLTPYQQTYVTWYSISV-----
Corydalus_cornutus	TFS-ETWGEKAYVTWY-----
Chrysopa_pallens	TFP-EKWGEKTYVTWYSISV-----
Meloe_violaceus	VFE-EPWGAQAYVTWYSISV-----
Aethina_tumida	TFQ-EPWQKAYVIWYCVSV-----
Gyrinus_marinus	TFP-QAWGQKAYVTWYGLSV-----
Tribolium_castaneum	TFQ-EPWQKAYVTWYSISV-----
Nicrophorus_vespilloides	TFL-PAWGEKAYVTWYGISV-----
Aleochara_curtula	-----
Pogonus_chalceus	TFP-QPWGARAYVTWYSISV-----
Sipyloidea_sipylus	TFA-SDWGETTYVTWYSVSV-----
Extatosoma_tiaratum	TFA-GHWGERTYVTWYSVSV-----
Aretaon_asperimus	TFV-EKWGERTYVTWYSISV-----

Medauroidea_extradentata
Ramulus_artemis
Gallosiana_yuasai
Athalia_rosae

TFP-EAWGEKTYVTWYSVSV-----
TFS-GAWGETTYVTWYSVSV-----

TFY-SPLGERAYVTWFSISA-----

361

420

Varroa_destructor1
Metaseiulus_occidentalis1
Metaseiulus_occidentalis2
Tigriopus_californicus
Anurida_maritima
Meinertellus_cundinamarcensis
Pogonognathellus_sp
Triops_cancriformis
Strigamia_maritima2
Catajapyx_aquilonaris
Daphnia_pulex
Daphnia_magna3
Daphnia_magna2
Daphnia_magna1
Daphnia_magna4
Arachnocampa_luminosa
Calanus_finmarchicus
Epiophlebia_superstes
Ladona_fulva
Cordulegaster_boltonii
Diaphorina_citri
Pachypsylla_venusta
Acanthocasuarina_muellerianae
Glomeris_pustulata
Frankliniella_cephalica
Machilis_hrabei
Carabus_granulatus
Dendroctonus_frontalis
Lepeophtheirus_salmonis
Caligus_rogercresseyi
Parhyale_hawaiensis
Hyaella_azteca
Strigamia_maritima1
Conwentzia_psociformis
Liposcelis_bostrychophila
Tetranychus_urticae
Osmylus_fulvicephalus
Ornithodoros_turicata
Acerentomon_sp
Ixodes_ricinus
Folsomia_candida
Limulus_polyphemus1
Limulus_polyphemus3
Platynothis_peltifer5
Platynothis_peltifer1
Platynothis_peltifer3
Achipteria_coleoptrata2
Platynothis_peltifer2
Platynothis_peltifer4
Ixodes_scapularis2
Ixodes_scapularis1
Ixodes_scapularis3
Cotesia_vestalis
Microplitis_demolitor
Zorotypus_caudelli
Nasonia_giraulti
Nasonia_vitripennis
Varroa_destructor2
Leuctra_sp
Tricholepidion_gertschi
Perla_marginata
Crioscolia_alcione
Mischoctytarus_flavitaris
Polistes_metricus
Polistes_canadensis
Chrysis_viridula
Argochrysis_armilla
Chyphotus_mellipes
Brachycistis_timberlakei
Sphaerophthalma_orestes

--LFIPVTLMLALCYTYLSWII-----
--LIVPALIMGACYSYLCRAS-----
--LGVVVMMLFCYIQICLIIVRIQRHH--MTKTTTAPAN-----
--FFLPFIVITSSYCIYTYRIWYSYRAT--QGSKASPQMSLAS-----NR-VVLSS
--FLLPLLICGYSYGAICFKVVSFSLHE--SNNRKLNEV-SR-----
--FMAPLTVIAACYGIIISLKVWFSSPQ--STTAEPLAA-----
--FILPLVIIGASYGAICCKVVSFNLPN--ES-----
--FALPLLIIGISYGAISLRLWRYSQEA--HRSEEMTRGHKRT-----IGLP-AGA
--FIIPLLIVIAASYGFCYTLWIYDEEH--GRSGDVI-----AL-----R-----
--FVMPLLVISSSYGAIYRIWYTNSEP--RCWT-----
SIFGAPLLVIGVYCYGVICRQIWIYSQSA--LPSSQQPPTSSAY-----P--ALTSE
SIFGAPLLVVAVCYGVICRQIWIYSQSA--QPSLLPS-DNSAI-----PSHSSITE
SIFGAPLLVVAVCYGVICRQIWIYSQSA--QPSLLPS-DNSAI-----PSHSSITE
SIFGAPLLVVAVCYGVICRQIWIYSQSA--QPSLLPS-DNSAI-----PSHSSITE
SIFGAPLLVVAVCYGVICRQIWIYSQSA--QPSLLPS-DNSAI-----PSHSSITE
--FLIPLFVLTFLYSRIFMTVSKNIKQK--HASIRFERESSKTATEINQLNQENSLNTQ
--FFIPLLILLFSNCFICKTIWASSNLLNWNRRRTTKENKM-----
--FAVPLVLLLAYAGICSVLRRNHREK--TRPHDERFLS-----RG-----
--FAVPLVLLLAYAGICRALRRNHREK--LRPQEDGLIP-----RG-----
--FAVPLVLLLAYAGICRALRRNHREK--MRPQQDGIIP-----RG-----
--FIIPFLVLYTYTTCICVALWQNTTYP-----
--FIIPLICLIYTYTTCICLAL--KNTAYP-----

--FMIPLTVLLFTYSRICCEIWRSSASK--HAPALVDGTC-----KTCPHV-----

--FIIPFLVLYTYTTCICREIWRCSOSS--LRPRSM-----
--FFLPLIILICYGICICKCIWDFNSK--IPLNPGVEVR-----SITCKNKGRAE
--FFFPLIILICYGRICKTIWDFNSK--VPMSSD--AG-----GVTCCGNRGRAE
--FFVPLIILVFFSVCIATLLRHNQV--PIQCNYIRQSYST--TSVHCLHHSPL--
--FFIPLVLLIFFSGCICCALLRYNFQV--PNQSSYVSRSHSQ--AGQESPNNETTS--
--TFVPLLVLYTYSAICWAVWRNFRHK--KNSPKGDFDS-----AASSPPT-----

--FFIPFVILIFTFSNICLELWRNGRI--KK-----

--FFVPLAVLTFTYIYICRAIWHNLYLK--RKSSEGSRDK-----
--FIIPLLVLIYTYFNICRTIWRSKNWI--STKVSPVKRC-----VKVSQLYEDGGA--
--FFVPLAVLSFTYVVICRSIWRNLYLK--RKSSDAESWK-----

--FFIPLIVITFTCVRICKNVWYFNHLR--GK-----
--FFIPLLVITFTYVNVTKTVWNNYLR--KK-----
--FVIPCIIILFAHVCICREICNNLHRK--RESIEEIKNC-----IHYSFKRN-----
--FFVFPILLTFTYVICREIWRNVHQK--RKSVMKQNK-----IIQNDDS-----
--FIIPFIILTFTYVICREIWLNLHKK--RKSFKINRNK-----SSSSCNNR-----
--FIIPFIIIVTTHYHICREIWLNLHKK--RKSFKLNKNR-----
--FFIPLVILTFTYIYICREIWRNLYLK--RQTGRRETQT-----INQIDNS-----
--FFIPLIIITTYVYICREIWRNVRRK--RQTLKPEISL-----IEVRKNW-----
--FFVPLAVLSFTYVVICRSIWRNLYLK--RKSSDAD-----
--FFVPLMVLFTYVVICRSIWRNLYLK--RKSSDAES-----
--FFVPLVLSFTYVVICRSIWRNLYLK--RKSSDAES-----

--FLLPFLVLLTYASICANIRRNTEIS--DRFDHVN-----

--FLLPFCVLTFTYAEICCSIWRNREVM--VLASHER-----
--FLLPFCVLTFTYAEICCSIWRNREVM--VLASHER-----

-----TRGRP--VIHQGAT-----

--FLLPFAILLTYVVICIGIWRSSNIL--GATDNRK-----
--FLLPFIIVLVTYVVICVGVWQSNKMS--DAVDDRK-----
--FLLPFIIVLVTYVVICVGVWQSNKMS--GAVDDRT-----
--FLLPFIIVLVTYVVICVGVWQSNKMS--GAVDDRA-----
--FLLPFTVLLTYTGTICIGIWRSNKMS--GVEDWRK-----
--FLLPFTVLLTYTGTICIGIWRSNKMT--SAENWRK-----
--FLLPLIVLTYTGTICIGIYKSNRMS--GVNDVRK-----
--FLLPLIVLTYVVICVGVWQSNKMT--GMVDVIG-----
--FLLPLVLLTYTGTICIGIWRSNKMT--GIMDVKI-----

Homalodisca_vitripennis --FLVPLFVLIYTYFCICWTLWRYSGLP--DS-S-----
Cercopis_vulnerata --FLIPLCVLIYTYTTCICRELRNAGFP--ESTS-----
Nilaparvata_lugens --FILPLIVLIYTYWCICRELRNAGFP--VTKA-----
Achipteria_coleoptrata --FFIFPILLTATHVCICREIW-----
Ephemera_danica --FLVPLMVLVYAYFRICQALWRNYNLK--QRAQONGL-----
Leptopilina_clavipes --FLLPFTVLVYTYTGICIGVWKNNGSVS--DPLEIGYK-----
Ganaspis_sp --FLLPFTVLIYTYTGICIGVWKNNGSVS--DPLEIGFA-----
Leptopilina_boulardi --FLLPFTVLVYTYTGICIGVWKNNGSVS--DPLEIGYK-----
Mantis religiosa -----
Blattella_germanica -----
Zootermopsis_nevadensis -----
Stigmatomma_oregonense --FLLPFAVLVYTYVRCISVWTSNKMS--RVIDL-----
Dinoponera_quadriceps --FLLPFIVLVYTYTRICITIWTSNKMS--GVVDL-----
Harpegnathos_saltator --FLLPFIVLAYTYMRCISIWASSKIS--GVVDF-----
Cerapachys_biroi --FLLPFIVLVYTYTQICRSIWTSNKMS--GVVDF-----
Monomorium_pharaonis --FLIPFIVLIYTYTKICVSIWTSNKIS--GIVDF-----
Tetramorium_bicarinarum --FLLPFVLVLYTYTKICMAIWTSNKMS--GVVDL-----
Solenopsis_invicta --FLIPFIALTYTYTKICVSIWTSNKMS--GVIDL-----
Atta_cephalotes --FLLPFIVLVYTYTRICISIWRSKLS--GLIDL-----
Acromyrmex_echinator --FLLPFIVLVYTYTRICISIWRSKLS--GLIDL-----
Pogonomyrmex_barbatus --FLLPFIVLVYTYTRICMSIWTSNKMS--GVVDL-----
Wasmannia_auropunctata --FLLPFMVLVYTYTRICLSIWRSKMS--GVVEL-----
Vollenhovia_emoryi --FLLPFIVLVYTYTRICMSIWTSNKMS--GVVDL-----
Orussus_abietinus --FLLPLCVLVYTYSGICRVRRRSEVG--VATSKS-----
Blaberus_atropos -----
Limulus_polyphemus2 --FFIPLVVIIFTYIRICKSVWYNLQMR--RQASNC-----
Isonychia_bicolor --FLAPLLILFPTYTCICRAIWHNYNAK--KIASDGFT-----
Occasjapyx_japonicus -----
Baetis_sp --FLIPLLILIFTYTCICQAIWRNYNAK--KESVAGLP-----
Panonychus_ulmi --FFIPFTIIIFTFSNICSELWKN-----
Frankliniella_occidentalis -----
Eurylophella_sp --FLVPLAILVYAYLVCICFAIWRNYNNK--KQFSAQGI-----
Telenomus_podisi --FVLPYCVLIYTYTGICIGIWNNGLS--GLPNSS-----
Aposthonia_japonica --FIIPLSVLTYTYSCICRKIWRNTGAG--FHII-----
Haploembia_palaui --FIIPLSVLTYTYSCICRKIWRNTGAG--FHII-----
Halyomorpha_halys --FVVPLVSLIYTYTICLTIWHNTGPL--SASA-----
Stenobothrus_lineatus -----
Inocellia_crassicornis --FIIPLCVLVFTYTCICREIWRNTARHG--ILRPATP-----
Tenthredo_koehlerii --FILPLIILVYTYTSCICIVIWNNGIV--GEAR--S-----
Corydalus_cornutus -----
Chrysopa_pallens --FIIPLSILVFTYTRICCEIWRNANIG--MPLR--A-----
Melo_violaceus --FIVPLIVLVYTYTSCIEIWHSSSESS--L--R--P-----
Aethina_tumida --FIVPLIVLVYTYTCKDIWHSSSEIS--M--R--P-----
Gyrinus_marinus --FIVPLTVLTYTYGICREIWHSSAAAG--DLGG--P-----
Tribolium_castaneum --FMVPLVLLIFTYTYTSCIEIWHSSSESS--L--R--P-----
Microphorus_vespilloides --FIIPLVLLVYTYTSCICREIWHSAVGE--LGMR--P-----
Aleochara_curtula -----
Pogonus_chalceus --FIVPLIVLIFTYGAICRVIWQSAGGE--LGLR--S-----
Sipyloidea_sipylus --FIVPLCVLVYTYSCICHEIWEKSGFR--AAHA-----
Extatosoma_tiaratum --FIVPLCVLVFTYTRICHEIWEKSGFR--AAHA-----
Aretaon_asperimus --FVIPLCVLVYTYSCICREIWEKSGFR--AAHA-----
Medauroidea_extradentata --FIIPLCVLVYTYTRICHEIWEKSGFR--AAHA-----
Ramulus_artemis --FIIPLCVLVYTYSCICHEIWEKSGFR--AAHA-----
Galloisiana_yuasai -----
Athalia_rosae --FILPLLVLGYTNVSICLAIWRNTGIA--GEAR--G-----

421

480

Varroa_destructor1 -----
Metaseiulus_occidentalis1 -----
Metaseiulus_occidentalis2 -----FG-----
Tigriopus_californicus VGDGS-----KNE-----
Anurida_maritima -----YSKNRSR-----
Meinertellus_cundinamarcensis -----ICCARCKRSSK-----
Pogonognathellus_sp -----
Triops_cancriformis AGAAL--RPTSQRWRRASRLGRFFLQRER-----AT--HQRNCS-----G-----
Strigamia_maritima2 -----A-----VGNGTGG-----
Catajapyx_aquilonaris -----ASKWK-----WL--DLKKCLCCTRKESGR-----
Daphnia_pulex TGSTL-----SVMRRWILRASLR-----WQ--KSRSSSNGTKNHSIAI-----
Daphnia_magna3 TGSTL-----SVMRRWFLRAGMR-----WQ--KSRNSNSNAIKNNS-----
Daphnia_magna2 TGSTL-----SVMRRWFLRAGMR-----WQ--KSRNSNSNAIKNNS-----
Daphnia_magna1 TGSTL-----SVMRRWFLRAGMR-----WQ--KSRNSNSNAIKNNS-----
Daphnia_magna4 TGSTL-----SVMRRWFLRAGMR-----WQ--KSRNSNSNAIKNNS-----
Arachnocampa_luminosa NGLITEVKHSDNSIFRDKKFGILWWIRSRFNKGIHKLIFTS'TKKRGNKIKFGKTGNFL-----
Calanus_finmarchicus -----
Epiophlebia_superstes -----
Ladona_fulva -----

Cordulegaster_boltonii	-----	-----	-----
Diaphorina_citri	-----	-----	-----
Pachypsylla_venusta	-----	-----	-----
Acanthocasuarina_muellerianae	-----	-----	-----
Glomeris_pustulata	-----	-----	-----
Frankliniella_cephalica	-----	-----	-----
Machilis_hrabei	-----	-----	-----
Carabus_granulatus	-----	-----	-----
Dendroctonus_frontalis	-----	-----	-----
Lepeophtheirus_salmonis	EGTIR-----	YR-WKSTK-----	RALGSTAEYSKRNDTI
Caligus_rogercresseyi	EGMIR-----	YR-WKSSK-----	RSRNNQNEV--HQNTE
Parhyale_hawaiensis	-----	K-----	V-----YHHRGNM
Hyaella_azteca	-----	R-----	K-----YGRTLDDT
Strigamia_maritima1	-----	-----	-----
Conwentzia_psociformis	-----	-----	-----
Liposcelis_bostrychophila	-----	-----	-----
Tetranychus_urticae	-----	-----	-----
Osmylus_fulvicephalus	-----	-----	-----
Ornithodoros_turicata	-----	-----	-----
Acerentomon_sp	-----	K-----	KHRGCNGFY--
Ixodes_ricinus	-----	-----	-----
Folsomia_candida	-----	-----	-----
Limulus_polyphemus1	-----	-----	-----
Limulus_polyphemus3	-----	-----	-----
Platynothrus_peltifer5	-----	K-----	EFSTS-SLKSTSLTSTF
Platynothrus_peltifer1	-----	D-----	RVSSCS----STNDSI
Platynothrus_peltifer3	-----	N-----	DKLDCSVNSPETSEH
Achipteria_coleoptrata2	-----	-----	-----
Platynothrus_peltifer2	-----	N-----	SY-----S
Platynothrus_peltifer4	-----	-----	-----G
Ixodes_scapularis2	-----	-----	-----
Ixodes_scapularis1	-----	WKGER-----	-----
Ixodes_scapularis3	-----	WKGSR-----	-----
Cotesia_vestalis	-----	-----	-----
Microplitis_demolitor	-----	-----	-----
Zorotypus_caudelli	-----	-----	-----
Nasonia_giraulti	-----	-----	-----
Nasonia_vitripennis	-----	-----	-----
Varroa_destructor2	-----	-----	-----
Leuctra_sp	-----	-----	-----
Tricholepidion_gertschi	-----	-----	-----
Perla_marginata	-----	-----	-----
Crioscolia_alcione	-----	-----	-----
Mischocyttarus_flavitaris	-----	-----	-----
Polistes_metricus	-----	-----	-----
Polistes_canadensis	-----	-----	-----
Chrysis_viridula	-----	-----	-----
Argochrysis_armilla	-----	-----	-----
Chyphotes_mellipes	-----	-----	-----
Brachycistis_timberlakei	-----	-----	-----
Sphaerophthalma_orestes	-----	-----	-----
Homalodisca_vitripennis	-----	-----	-----
Cercopis_vulnerata	-----	-----	-----
Nilaparvata_lugens	-----	-----	-----
Achipteria_coleoptrata1	-----	-----	-----
Ephemera_danica	-----	-----	-----
Leptopilina_clavipes	-----	-----	-----
Ganaspis_sp	-----	-----	-----
Leptopilina_boulardi	-----	-----	-----
Mantis_religiosa	-----	-----	-----
Blattella_germanica	-----	-----	-----
Zootermopsis_nevadensis	-----	-----	-----
Stigmatomma_oregonense	-----	-----	-----
Dinoponera_quadriceps	-----	-----	-----
Harpegnathos_saltator	-----	-----	-----
Cerapachys_biroi	-----	-----	-----
Monomorium_pharaonis	-----	-----	-----
Tetramorium_bicarinatum	-----	-----	-----
Solenopsis_invicta	-----	-----	-----
Atta_cephalotes	-----	-----	-----
Acromyrmex_echinatior	-----	-----	-----
Pogonomyrmex_barbatus	-----	-----	-----
Wasmannia_auropunctata	-----	-----	-----
Vollenhovia_emoryi	-----	-----	-----
Orussus_abietinus	-----	-----	-----
Blaberus_atropos	-----	-----	-----
Limulus_polyphemus2	-----	-----	-----

Platynothis peltifer3	--RSGTRLLVTVGKS--YRFKGGQVEVSVE-----K----
Achipteria coleoptrata2	-----VGKS--YRFKSRGKLEVSVD-----K----
Platynothis peltifer2	--RTRKCLLIALLNRV---YRLGRRQDTETAEIQI-----NCDNQEVRLHTVV-----
Platynothis peltifer4	-----KLSKSSDDKSRLQSD-----RC-----
Ixodes scapularis2	-----
Ixodes scapularis1	-----AYRFRGLAHN-----
Ixodes scapularis3	-----AYRFGTAQN-----
Cotesia vestalis	-----
Microplitis demolitor	-----
Zorotypus caudelli	-----
Nasonia giraulti	-----
Nasonia vitripennis	-----
Varroa destructor2	-----
Leuctra sp	-----
Tricholepidion gertschi	-----VGQ-----
Perla marginata	-----
Crioscolia alcione	-----
Mischocyttarus flavitarsis	-----
Polistes metricus	-----
Polistes canadensis	-----
Chrysis viridula	-----
Argochrysis armilla	-----
Chyphotes mellipes	-----
Brachycistis timberlakei	-----
Sphaerophthalma orestes	-----
Homalodisca vitripennis	-----
Cercopis vulnerata	-----
Nilaparvata lugens	-----
Achipteria coleoptrata1	-----
Ephemera danica	-----LQP-N-----
Leptopilina clavipes	-----
Ganaspis sp	-----
Leptopilina boulandi	-----
Mantis religiosa	-----
Blattella germanica	-----
Zootermopsis nevadensis	-----
Stigmatomma oregonense	-----
Dinoponera quadriceps	-----
Harpegnathos saltator	-----
Cerapachys biroi	-----
Monomorium pharaonis	-----
Tetramorium bicarinatum	-----
Solenopsis invicta	-----
Atta cephalotes	-----
Acromyrmex echinatior	-----
Pogonomyrmex barbatus	-----
Wasmannia auropunctata	-----
Vollenhovia emeryi	-----
Orussus abietinus	-----
Blaberus atropos	-----
Limulus polyphemus2	-----
Isonychia bicolor	-----TK-----
Occasjapyx japonicus	-----
Baetis sp	-----PTDSK-----
Panonychus ulmi	-----
Frankliniella occidentalis	-----
Eurylophella sp	-----HHQH-----
Telenomus podisi	-----
Aposthonia japonica	-----
Haploembia palaui	-----
Halyomorpha halys	-----
Stenobothrus lineatus	-----
Inocellia crassicornis	-----PMSV-----
Tenthredo koehleri	-----
Corydalus cornutus	-----
Chrysopa pallens	-----MS-----
Meloe violaceus	-----RS-----
Aethina tumida	-----RNSL-----
Gyrinus marinus	-----
Tribolium castaneum	-----RS-----
Nicrophorus vespilloides	-----RNVQ-----
Aleochara curtula	-----
Pogonus chalceus	-----PRLA-----
Sipyloidea sipyulus	-----
Extatosoma tiaratum	-----
Aretaon asperimus	-----
Medauroidea extradentata	-----

Ramulus_artemis
Gallosiana_yuasai
Athalia_rosae

Varroa_destructor1
Metaseiulus_occidentalis1
Metaseiulus_occidentalis2
Tigriopus_californicus
Anurida_maritima
Meinertellus_cundinamarcensis
Pogonognathellus_sp
Triops_cancriformis
Strigamia_maritima2
Catajapyx_aquilonaris
Daphnia_pulex
Daphnia_magna3
Daphnia_magna2
Daphnia_magna1
Daphnia_magna4
Arachnocampa_luminosa
Calanus_finmarchicus
Epiophlebia_superstis
Ladona_fulva
Cordulegaster_boltonii
Diaphorina_citri
Pachyphylla_venusta
Acanthocasuarina_muellerianae
Glomeris_pustulata
Frankliniella_cephalica
Machilis_hrabei
Carabus_granulatus
Dendroctonus_frontalis
Lepeophtheirus_salmonis
Caligus_rogercresseyi
Parhyale_hawaiiensis
Hyalella_azteca
Strigamia_maritima1
Conwentzia_psociformis
Liposcelis_bostrychophila
Tetranychus_urticae
Osmylus_fulvicephalus
Ornithodoros_turicata
Acerentomon_sp
Ixodes_ricinus
Folsomia_candida
Limulus_polyphemus1
Limulus_polyphemus3
Platynocheilus_peltifer5
Platynocheilus_peltifer1
Platynocheilus_peltifer3
Achiapteria_coleoptrata2
Platynocheilus_peltifer2
Platynocheilus_peltifer4
Ixodes_scapularis2
Ixodes_scapularis1
Ixodes_scapularis3
Cotesia_vestalis
Microplitis_demolitor
Zorotypus_caudelli
Nasonia_giraulti
Nasonia_vitripennis
Varroa_destructor2
Leuctra_sp
Tricholepidion_gertschi
Perla_marginata
Crioscobia_alcione
Mischocyttarus_flavitaris
Polistes_metricus
Polistes_canadensis
Chrysis_viridula
Argochrysis_armilla
Chyphotus_mellipes
Brachycystis_timberlakei
Sphaerophthalma_orestes
Homalodisca_vitripennis

541

600

-----SKRSLSHTKLNPTRMTMVMVIVFLCWTPFCCAQLY
-----SKRLMSDAKLKTRMTMVMVIVFLCWTPFCCAQLY
-----VN----TAGFFESNRRITKAKVRMVKMTFTVVLCFVWSPYSIAELL
RP---NLAHNSHAPTGGFVRVQTEQIVLLSKAKRKSLSMTAIVSVCFAVCWLPWCVTMLL
APTPK-----DVGSRRLAQQISEVKIKTLKLTLLVVLCCFFVWSPFCVTLQLI
RP-----IQSRNTSQRSSARLSRARMRTLRLTLAVVACFIICWAPFCVSQLV
-----GK-KIKMEFPPLRRSNSHRITRAKIKTIQTLTLLVVISFVVCWAPFCITQLV
-----TDS-CRLYSRRVAGVSNPNP ISEAKVKTLKLTFLVVVCFVWSPFCITQLV
-----AGRL-KSKVG-CNVQKRKSMISDAKIKTLQTLVAVVICFFVWAPFCIAQLI
RSLPPPLSPQC-CQQMP-LRRSNSNQNRITKAKMKTIKLTLAVVLCFVACWAPFCITQLI
LPQPPPAAPQR-CQQMS-LRRSNSNQNRITKAKMKTIKLTLAVVLCFVACWAPFCITQLI
LPQPPPAAPQR-CQQMS-LRRSNSNQNRITKAKMKTIKLTLAVVLCFVACWAPFCITQLI
LPQPPPAAPQR-CQQMS-LRRSNSNQNRITKAKMKTIKLTLAVVLCFVACWAPFCITQLI
LPQPPPAAPQR-CQQMS-LRRSNSNQNRITKAKMKTIKLTLAVVLCFVACWAPFCITQLI
-----S---KSFKSNFPIRQTFSGKALTRSKIKTLKLTLLVTVVITYVMCSLPHYVCTFI
-----KSKLSVQNLFRSTSVMSRAKIKSVKLTLLV IACYILCSPFIVGQLL
-----APPRTHSVGTISKAKMKTLLRITVAVACYILCSPFVLSQLW
-----APPRTHSMGTISRAKMRTLRLITVAVACYILCSPFVLSQLW
-----APLRTHSMGTISRAKMRTLRLITVAVACYILCSPFVLSQLW
-----TTSPHKIISRAKINTIKQTIIVAVITLYIVCSLPIFVQLW
-----APSPHKIISRAKINTVKQTIIVAVITLYIICSLPIFAQLW
-----KIISRAKINTVKQTIIVAVITLYIICSLPIFAQLW
-----KTVKLTVVVILSYIACSMPYISAMLW
-----FAYARSQQQATQRTNPLISRAKINTVKQTVLVIAIYIICSAFPIVQLW
-----GISRAKIKTVKLTVVVIVGYIACSAPFICAEWL
-----SRAKINTVKQTIIVAVITLYIICSAFPIVQLW
-----SKQSTKRDRVPLISRAKINTVKQTIIVAVITLYIICSAFPIVQLW
-----QTKNKKSLKPRTHSIQGISRAKIKTIKLTVVVIAGYIACSAPFICVQLW
-----QKQKRSLKPRSHSIQGISRAKIKTIKLTVVVIVGYIACSAPFICVQLW
-----QKMKQNSLSMKKQVRVSRIMSPISRAKIKTVKLTLLVIFVACSAFPIVQLW
-----CR----YRFQKTPGAKTVMSPIISRAKIKTIKLTLLVIFVACSAFPIVQLW
-----RF----KASESVNPRSHGLQRISRAKIKTVKLTVVVITCYILCSPMYTCAMMW
-----ANLSQSHSTAYFSKAKIKTVKLTVTIIICYICSSPFFNVQIW
-----ANGSFVAPRSHSVRGLSRAKIKTVKITVVVIVGYIACSAPFICVQMW
-----EN----SEILDMAMRST-----IVPV-----TEPQPVTQQS
-----TK----QDSSFVGPVGRSHSVRGLSRAKIKTVKITVVVIALYVVCSSPFFICVQMW
-----NSSRSHSMRGLSRAKIKTVKITVVVIVGYIACSAPFICVQMW
-----NFIHCRSVPDLISRAKIKTVKITVVVIVGYIACSAPFICVQMW
-----VK----VNLDNSTPRSHSLRFVSRAKIKTVKITVVVILCYIICSSPFFICVQMW
-----PK----SR-GTYNPRSHSLNGLSRAKIKTVKITVVVILCYIICSSPFFICVQMW
-----DC----GKEDYNPRSHSLNGLSRAKIKTVKITVVVILCYIICSSPFFICVQMW
-----DF----KE--DFSPRTHSIHGLSRAKIKTVKITVVVILCYIICSSPFFICVQMW
-----TF----QESVSSSPRVNTFNRLSRAKIKTVKITVVVILCYIICSSPFFICVQMW
-----LANNLLNPRSHSIYRISRAKIKTVKITVVVIVGYIACSAPFICVQMW
-----HSVRGMSRAKIKTVKITVVVIALYVVCSSPFFICVQMW
-----GTKQDSSFVGPVGRSHSVRGLSRAKIKTVKITVVVIALYVVCSSPFFICVQMW
-----GTKQDSSF-----TVKITVVVIALYVVCSSPFFICVQMW
-----NNKKINFNNKNRQPLISRAKIKTVKITVVVIVGYIACSAPFICVQMW
-----QQALTKEGRSQTTLISRAKIKTVKITVVVIVGYIACSAPFICVQMW
-----QQALTKEGRSQTTLISRAKIKTVKITVVVIVGYIACSAPFICVQMW
-----ADVRPAPVNPRTSHSMKGISRAKIKTVKITVVVIVGYIACSAPFICVQMW
-----IKG--DVFEKNRSTFVSKALISSVKQTIIVVTVLTVGSPFICGQLW
-----YIRS-ISSCTRNRSFISKAMINTVKQTIIVAVITLYAITSPFICGELW
-----YIRS-ISNYSRNRSSFISKAMINTVKQTIIVAVITLYAITSPFICGELW
-----YIRS-ISNYSRNRSSFISKAMINTVKQTIIVAVITLYAITSPFICGELW
-----KVRNNGNFLERNRSPFISKAMINTMRQTIIVVIVGYIACSAPFICGQLW
-----KSRNSVNLERNRSPFISKAMINTMRQTIIVVIVGYIACSAPFICGQLW
-----SVKG-KKSFQNRTPLVSKAMINTVKQTIIVAVITLYAITSPFICGQLW
-----RGGKSGKLEGNRSPFISKAMINTVRQTIIVAVITLYAITSPFICGQLW
-----RAKG-SNLPNRNRSPFISRAMINTVKQTIIVAVITLYAITSPFICGQLW
-----SPHLLISRAKINTIKQTVAVILLYIACSAPFICVQLW

Cercopis_vulnerata -----SPHRLISRAKINTIKQTVAVIALYISCSSPFICAQLW
Nilaparvata_lugens -----SPHRLISRAKVNTVKQTVAVIALYVACSSPFIVAQLW
Achipteria_coleoptratal -----
Ephemera_danica -----FHFYPRIPMEPRTHSLRGISRAKLRSIKLTIIVVIACVVICSTPFIGAQLW
Leptopilina_clavipes -----KNSNI IKKKAKS INNKGSKYDETNCCC-----
Ganaspis_sp -----KNSHFTKKKQSPLITKARVNTMKQTIIVVVTLYFLTWSPFIGCELW
Leptopilina_boulardi -----KNSNI IKKKQSPLITKARVNTMKQTIIVVVTLYFLTWSPFIGCELW
Mantis_religiosa -----
Blattella_germanica -----
Zootermopsis_nevadensis -----
Stigmatomma_oregonense -----KKGSKDNFLQRNRDPFISNALINTVKQTIIVVVTLYIVTSPFIGCELW
Dinoponera_quadriceps -----RKGNKASFSQRNRDPFISKALINTVKQTIIVVILYIVTSTPFIGCQLW
Harpegnathos_saltator -----KK---ASFSQRNRDPFISKALINTVKQTIIVVVTLYIVTSPFIGCQLW
Cerapachys_biroi -----KQGNKASFSLRNRDPFISKALINTIKQTIIVVVSPLYIITSIPFIGCELW
Monomorium_pharaonis -----KKGNKANFSQRNRDPLISKAMINTIKQMIIVVVTLYIITNTPFIGCELW
Tetramorium_bicarinarum -----KKNRASFQRNRDPLISKAMINTVKQMIIVVVTLYIITNTPFIGCELW
Solenopsis_invicta -----KKGNKASFCQRNRDPLISKAMINTVKQMIIVVVTLYIITNTPFIGCELW
Atta_cephalotes -----KKS NKVSFCQRNRDPLISKAMINTVKQMIIVVVTLYIVTNTPFIGCELW
Acromyrmex_echinator -----KRSNKISFCQRNRDPLISKAMINTVKQMIIVVVTLYIVTNTPFIGCELW
Pogonomyrmex_barbatus -----KRRNKASFSQRNRDPLISKAMINTVKQMIIVVVTLYIITNTPFIGCELW
Wasmannia_auropunctata -----KRDNKASFCQRNRDPLISKAMINTVKQMIIVVVTLYIVTNIPIFIGCELW
Vollenhovia_emoryi -----KRSNKASFFQRNRDPLISKAMINTVKQTIIVVVTLYILTNSPFIGCELW
Orussus_abietinus -----PRGDIRAPATISRAKIRTAWQTIIVVVTLYIASSTPFIGCELW
Blaberus_atropos -----NTVKQMVAVLFLYVACSAFPIISAQLW
Limulus_polyphemus2 -----ETFTVPRSHCMRGLSRSKVKTFKITVVTITCYIICSTPFIIVQLW
Isonychia_bicolor -----QTNIQPRVHSIRGISRAKIKTVKLTVVVIACVVIACSSPFISAQLW
Occasjapyx_japonicus -----
Baetis_sp -----VLGNG-RVMHPRVHSMRGISRAKMKTIKLTVVVIACVVICSTPFIGAQLW
Panonychus_ulmi -----
Frankliniella_occidentalis -----
Eurylophella_sp -----I--VRNMNPRVHSIRGISRAKMKTIKLTVVVIACVVICSTPFIGAQLW
Telenomus_podisi -----KNANFRGDNANLITKARIKTVKQTIIVVVTLYIITNTPFIGCELW
Aposthonia_japonica -----QTSPVISRAKINTVKQMVIVILFYIICSTPFTFSLW
Haploembia_palaui -----KSSPVISRAKINTVKQMVIVIFFYIICSTPFTC----
Halyomorpha_halys -----PHKVVSRAKINTIKQTVAVIALYIACSLPFIISAQLW
Stenobothrus_lineatus -----
Inocellia_crassicornis -----TTAPTHGVPVRGRRTQPFVSRKINTVKQTVAVIVTVIVCSMPFIISAQLW
Tenthredo_koehlerii -----T--HGGLLRQRTVISRAKINSIKQMIIVVVTLYIITNTPFIGCELW
Corydalus_cornutus -----
Chrysopa_pallens -----SP--PCTPKRRAPLISRAKINTVKQTVAVIILYIACSSPFISAQLW
Meloe_violaceus -----SQKAGKRTPLISRAKINTVKQTIIVVVTLYIITNTPFIGCELW
Aethina_tumida -----VKG-----KRTKMPLISRAKINTVKQTIIVVVTLYIITNTPFIGCELW
Gyrinus_marinus -----
Tribolium_castaneum -----SQ--KSAPGKRTPLISRAKINTVKQTIIVVVTLYIITNTPFIGCELW
Microphorus_vespilloides -----TGNGK--SQQTGKRAPLISRAKINTVKQTIIVVVTLYIITNTPFIGCELW
Aleochara_curtula -----
Pogonus_chalceus -----PDSPP--RCARSRRAPLISRAKINTVKQTVAVIAMIACSTPFIGAQLW
Sipylloidea_sipylus -----A--RSSPLKMNPTISRAKINTVKQTVAVIVLYIACSSPFISAQLW
Extatosoma_tiaratum -----A--RSSPLKMNPTISRAKINTVKQTVSVIVLYIACSSPFISAQLW
Aretaon_asperimus -----A--RSSPLKMNPTISRAKINTVKQTVAVIVLYIACSSPFISAQLW
Medauroidea_extradentata -----A--RSSPLKINPTISRAKINTVKQTVAVIVLYIACSSPFISAQLW
Ramulus_artemis -----A--RSSPLKMNPTISRAKINTVKQTVAVIMLYIACSSPFISAQLW
Gallosiana_yuasai -----
Athalia_rosae -----T--DGTLRLRQGSVISRAKINSIKQMVAVISFYAASSPFIIVQLW

	601	CXNPW motif	660
Varroa_destructor1	LES-T----	GQ--VPSIFITLFL--VPNL-----	NSCANPWVCLTFSTTLRRLKLTDA
Metaseiulus_occidentalis1	LVF-G----	GE--EASTFVTMCLM--VPNL-----	NSCANPWVYLSFSTDLRRLVNF
Metaseiulus_occidentalis2	LAY-KIAG--	GE--HVSPPFMVFL--LASL-----	NSVNPWIYTAFTNSF----
Tigriopus_californicus	MSF-DIQV--	GGD--KVHPLMVFAL--LASL-----	NSITNPNWIYLCFSSAVLQVVKHL
Anurida_maritima	LVY-NPTL--	-----PVGPGNVIILL--LPSL-----	NSCTNPWIYLAFAFSELCNQLRVF
Meinertellus_cundinamarcensis	YNF-NPPT--	DQK--QMSGVTVI--LASL-----	NSCTNPWLYLAFSGSLLNHLRVC
Pogonognathellus_sp	-----	-----	-----
Triops_cancriformis	LVY-DPPS--	N-----	-----
Strigamia_maritima2	LTF-NPPS--	PDA---QTGSVEVILL--LASL-----	NSCTNPWIYVAFSGSLLNQLRMC
Catajapyx_aquilonaris	LVY-NPPE--	DR---DVDPVTVILL--LASL-----	NSCTNPWIYVAFSGSLLNQLRV
Daphnia_pulex	MVY-CPPT--	SQA---DVSPVAVILL--LASL-----	NSCSNPWIYLAFAFSGSLLNQMRC
Daphnia_magna3	MVY-CPPT--	SQA---DVSPVAVILL--LASL-----	NSCSNPWIYLAFAFSGSLLNQMRC
Daphnia_magna2	MVY-CPPT--	SQA---DVSPVAVILL--LASL-----	NSCSNPWIYLAFAFSGSLLNQMRC
Daphnia_magna1	MVY-CPPT--	SQA---DVSPVAVILL--LASL-----	NSCSNPWIYLAFAFSGSLLNQMRC
Daphnia_magna4	MVY-CPPT--	SQA---DVSPVAVILL--LASL-----	NSCSNPWIYLAFAFSGSLLNQMRC
Arachnocampa_luminosa	HFLGLSAHNHSSLFTK--	TLVYI--TISTNMLFQLNSCANP	IIYLFNNGICKLAKRL
Calanus_finmarchicus	ATL-GPPH--	IRSKIGLQ--MEPLFW--LMTL-----	NSVNPWIYIWFNRNRLFVRQTS
Epiophlebia_superstes	VTW-YPGA--	TESSFWRG--AAFTILSL--MSCL-----	NSCVNPWIYMAFNEDIRVALKER
Ladona_fulva	ATW-YPGA--	TESSFWRG--AAFTILSL--LPCL-----	NSCVNPWIYMAFNEDIRVALKER
Cordulegaster_boltonii	ATW-YPGA--	TESPFWRG--AAFTILSL--LPCL-----	NSCVNPWIYMAFNEDIRVALKER

Diaphorina_citri QTW-NLNQ-TVYPVFQDNAVLTIIML-LSSL-----NSCVNPWIYLVSNRELI AALRTL
 Pachypsylla_venusta ETW-NLNQ-TVYPVFQDSA-LTIIML-LSSL-----NSCVNPWIYLVSNRELITALWTL
 Acanthocasuarina_muellerianae QTW-NLNE-SFYPVFQDNAVLTIIML-LSSL-----NSCVNPWIYLFNSRKLITALRTL
 Glomeris_pustulata LVW-YPEA-RNTPFGRS-AAFTILAL-LASL-----NSCANPWIYLCFNENVAQTLGDV
 Frankliniella_cephalica AAW-GNA---DNPFFQG-RYMTILTL-LFSL-----NSCVNPWIYLA FNNDLVRMLWLL
 Machilis_hrabei AAW-DPNA-VHSSFWQG-PAFTILTL-LASL-----NSCVNPWLYLVFNPNLVRDRFRHG
 Carabus_granulatus ATW-DPE----STFLNG-AAYTILTL-LYSL-----NSCVNPWIYLA FNRELPRLLLRH
 Dendroctonus_frontalis ATF-DPK----SAFLEG-STFTILTL-LYSL-----NSCVNPWIYLFNRELPRLLLRH
 Lepeophtheirus_salmonis VTF-GTVT-ESIRK-----
 Caligus_rogercresseyi -----
 Parhyale_hawaiensis SVW-DPNA-KNSPFSSG-E-----
 Hyalella_azteca SVW-DP-----
 Strigamia_maritima1 VAY-DKRA-QETAFYKG-GLFPVLVL-VASL-----NSCVNPWVYLLFNKNLVTLRHY
 Conwentzia_psociformis -----
 Liposcelis_bostrychophila -----
 Tetranychus_urticae AYW-APGA-QESSLWRG-PLITIAML-LPSL-----NSCVNPWIYLFNRLNLLSTLDKL
 Osmylus_fulvicephalus -----
 Ornithodoros_turicata MYW-SPDA-ESSELWSS-STVTILML-LNSL-----NSCVNPWIYLA FNKNLLNALRTA
 Acerentomon_sp ISF-FQSV-SS-----TSS-A-LPVTRTTSNTSSCESTSVH-----
 Ixodes_ricinus MYW-SPDA-DMADTWTN-TAGSSVTQ-AEGSYIRCGKTKCRNVFSSLLSTSNV---GKQF
 Folsomia_candida -----
 Limulus_polyphemus1 AYW-SPYA-QTSPWKG-PTVAILML-LASL-----NSCVNPWIYLA FNHNLTALKHI
 Limulus_polyphemus3 AYW-SPYA-QNSPIWKG-PTVAILML-LASL-----NSCVNPWIYLA FNHNLTALKQL
 Platynothrus_peltifer5 VYW-FPSA-QSFFQTS---ELSNII-----
 Platynothrus_peltifer1 AYW-WPNA-QNSTFWG-KCSENSFI-IQFR-----YS----FQ-----
 Platynothrus_peltifer3 AYW-WPNA-QQSPIWNV-KYTYSNN-FA-----
 Achipteria_coleoptrata2 AYW-VPTA-QKSHIWNV-KYTYNIYL-MFFS-----IIDVTIAFKILYSE-----
 Platynothrus_peltifer2 AYW-WPNA-STTFWNG-MFSLFII-----
 Platynothrus_peltifer4 AYW-YPSA-QETSFWTG-KH-----
 Ixodes_scapularis2 MYW-SPD-VDLADVWIN-ATVTILML-LNSL-----NSCVNPWVYLLFNRLVHTLRHQ
 Ixodes_scapularis1 MYW-SPH-VDANPWIS-E-----
 Ixodes_scapularis3 MYW-SPD-AD-----
 Cotesia_vestalis -----
 Microplitis_demolitor ATW-DPQ-AANSSIFNG-PAFTILTL-MSSL-----TSCVNPWIYLFNRELRLNLSNY
 Zorotypus_caudelli -----
 Nasonia_giraulti ATW-DPF-ASSSAFFDG-PIFTILSL-LSSL-----TSCVNPWIYLFNRELRAALTKF
 Nasonia_vitripennis ATW-DPF-ASSSAFFDG-PIFTILSL-LSSL-----TSCVNPWIYLFNRELRAALTKF
 Varroa_destructor2 -----
 Leuctra_sp -----
 Tricholepidion_gertschi ATW-DPN-ASKSPFWTG-TTFTIFTL-LASL-----NSCVNPWIYLFNRLVRLNQQV
 Perla_marginata -----
 Crioscolia_alcione ATW-DPR-AISSPFFSG-AAFTILTL-LSSL-----TSCVNPWIYLFNRELRAALTDY
 Mischocyttarus_flavitaris1 VTW-DTE-AIKSSFANG-PAFTILTL-LNSL-----TSCVNPWIYLFNRELRLQNLNMY
 Polistes_metricus ISW-DPE-APKSSFANG-PAFTILAL-LNSL-----TSCVNPWIYLFNRELRLQNLNMY
 Polistes_canadensis VSW-DTK-AFESSFANG-PAFTILAL-LNSL-----TSCVNPWIYLFNRELRLQNLNMY
 Chrysis_viridula ATW-DPS-ASSSFING-PAFTILSL-LSSL-----TSCVNPWIYLFNRELRAVLKDN
 Argochrysis_armilla ATW-DPS-ASSSPFITG-PAFTILSL-LSSL-----TSCVNPWIYLFNRELRSALKDN
 Chyphotes_mellipes ATW-YPK-ATVSPFFSG-ATFTILAL-LSSL-----TSCVNPWIYLFNRELRLVTDY
 Brachycistis_timberlakei ATW-DPK-AAFSPFFTG-AAFTILAL-LSSL-----TSCVNPWIYLFNRELRLALKEY
 Sphaerophthalma_orestes ATW-DPK-ASSPFFSG-PAFTILAL-LSSL-----TSCVNPWIYLFNRELRLALMDY
 Homalodisca_vitripennis ASW-GPR---QPFFDG-AAFTILSL-LSSL-----NSCVNPWIYLFNRELRLSLWRA
 Cercopis_vulnerata ASW-DPN-ALSSPFFLG-ATFTILTL-LS-----
 Nilaparvata_lugens AVW-DPG-AVHSPFFQG-ATFTILSL-LSSL-----NSCVNPWIYLVSNKELMRGLRQL
 Achipteria_coleoptrata1 -----
 Ephemera_danica ATW-DPE-AMQSPFWG-PTFTIVTL-LASL-----NSCVNPWIYLA FNPELARLLITR
 Leptopilina_clavipes -----
 Ganaspis_sp MAW-DPIRANSSIFDG-PLFTVLSL-LSCL-----TSCVNPWIYMAFNSELRIILLNF
 Leptopilina_boulardi MAW-DPVRANSSIFDG-PLFTVLSL-LSCL-----TSCVNPWIYIAFNSELRIILLNF
 Mantis_religiosa -----
 Blattella_germanica -----
 Zootermopsis_nevadensis -----
 Stigmatomma_oregonense ATW-DPK-ASTSPFFSG-ATFTILSL-LNSL-----TSCVNPWIYFTFNSELRLVAVTNF
 Dinoponera_quadriceps ATW-DPG-AATSPFHT--AAFTILCL-LNSL-----TSCINPWIYFAFNRELRSALTNL
 Harpegnathos_saltator ATW-DRP-AAISPFLLTG-AAFTILCL-LNSL-----TSCVNPWIYFAFNRELRLVAVTNF
 Cerapachys_biroi ATW-DPK-ASTSPFFTG-AAFTILSL-LNSL-----TSCVNPWIYFAFNRELRAALTNF
 Monomorium_pharaonis ATW-DPK-ASSPFFTG-AAFTILSL-LNSL-----TSCVNPWIYFAFNKELRMALINF
 Tetramorium_bicarinatum ATW-DPT-ASSPFFSG-AAFTILSL-LNSL-----TSCVNPWIYFAFNKELRGALTSS
 Solenopsis_invicta ATW-NPK-ASSSPFITG-AAFTILSL-LNSL-----TSCVNPWIYFAFNKELRALTNF
 Atta_cephalotes ATW-DPK-ASTSPFFTG-AAFTILSL-LNSL-----TSCVNPWIYFAFNKELRVALTCF
 Acromyrmex_echinatior ATW-DPK-ASTSPFFTG-AAFTILSL-LNSL-----TSCVNPWIYFAFNKELRVALTCF
 Pogonomyrmex_barbatus ATW-DPK-ASTSPFFTG-AAFTILSL-LNSL-----TSCVNPWIYFAFNKELRTALTNF
 Wasmannia_auropunctata ATW-DPK-ASTSPFFTG-AAFTILSL-LNSL-----TSCVNPWIYFAFNKELRAALTNF
 Vollenhovia_emoryi ATW-DPT-ASSPFFTG-AAFTILSL-LNSL-----TSCVNPWIYFAFNKELRAALTNF
 Orussus_abietinus ATW-DPG-ASSSAFLNG-PAFTILAL-LSSL-----NSCVNPWVHLGFDPELREVILRH
 Blaberus_atropos ATW-DDL-AHTRPFFSG-TAFTILAL-LYSL-----NSCMNPWIYLFNRELIRFLTQQ
 Limulus_polyphemus2 AYW-SPN-AKNSSIWKG-PTVAILML-LASL-----NSCVNPWIYLA FNYNLVTALREV
 Isonychia_bicolor ATW-DPM-AMHS-----

Occasjapyx_japonicus	-----
Baetis_sp	ATW-DPD-AMQSPFWG-TQPTTHLSMFLL-----HHAR-----
Panonychus_ulmi	-----
Frankliniella_occidentalis	-----
Eurylophella_sp	-----
Telenomus_podisi	AVW-SDT-AASSPFITG-PAFTILSL-LSSL-----TSCVNPWIYLTFFNYELRKILLKR
Aposthonia_japonica	ATW-DVT-AVELPFFFG-PAFTILTTL-LSSL-----NSCVNPWIYLTFNKELIALLVNC
Haploembia_palau	-----
Halyomorpha_halys	ATW-DPH-ATSSPFLSG-GTFTILTTL-LSSL-----NSCVNPWIYLTNSQDLMEALWET
Stenobothrus_lineatus	-----
Inocellia_crassicornis	VTW-YPH-AMESPFFSG-STFTILTTL-LSSL-----NSCVNPWIFLLFNKDLFRLLKRL
Tenthredo_koehler	VTW-DRN-ASASPFYSG-AAFTILTTL-LSSL-----NSCVNPWIYLTNLRDLRSLINR
Corydalus_cornutus	-----
Chrysopa_pallens	ATW-DPY-AYKSPFWTG-ATFTILTTL-LSSL-----NSCVNPWIYLSFNKELRKLKHI
Meloe_violaceus	ATW-DPQ----NPFSEG-PVFVILAL-LYSL-----NSCVNPWIYLTFNRELPRLLVKH
Aethina_tumida	ATW-DPT----NPFQFG-PIFTILTTL-LYSL-----NSCVNPWIYLAFNRELPKYLLRH
Gyrinus_marinus	-----
Tribolium_castaneum	ATW-DPQ----SPFIDG-PVFVILTL-LYSL-----NSCVNPWIYLAFNRELPRLLLRH
Nicrophorus_vespilloides	ATW-DPE-AVNSPFLNG-PVFTIVSL-LYSL-----NSCFNPWIYLAFNRELPRLLLRH
Aleochara_curtula	-----
Pogonus_chalceus	ATW-DPE-ANESAFFNG-AAFTILTTL-LSSL-----NSCVNPWIYLAFNRELPRLLLRH
Sipyloidea_sipylus	ATW-DPH-ASDSPFFTG-AAFTILTTL-LSSL-----NSCVNPWIYLAFNTELVQLLAR
Extatosoma_tiaratum	ATW-DPH-ATESPFFTG-AAFTILAL-LSSL-----NSCVNPWIYLAFNTELVHLLATC
Aretaon_asperrimus	ATW-DPH-AAQSAFFTG-AAFTILAL-LSSL-----NSCVNPWIYLAFNTELVHLLTNR
Medauroidea_extradentata	ATW-DPH-ASESAFLTG-AAFTILAL-LSSL-----NSCVNPWIYLAFNTELVRLLLKK
Ramulus_artemis	ATW-DPH-ASESAFFTG-AAFTILAL-LSSL-----NSCVNPWIYLAFNTELVRLLVKR
Galloisiana_yuasai	-----
Athalia_rosae	VTW-DPG-AVNSPFFEG-AAFAILTL-MSSL-----NSCVNPWIYLTNRELPRTLFAR

Varroa_destructor1	661	720
Metaseiulus_occidentalis1	LSFFGF-----CEHLS-----	
Metaseiulus_occidentalis2	CSLIHL-----RGNRY-----	
Tigriopus_californicus	-SLRTL-----KPEVH-----	
Anurida_maritima	VGMRST-----IGGPD-----	
Meinertellus_cundinamarcensis	LGIGLR-----RGSSE-----	
Pogonognathellus_sp	LGLGIG-----RAQGD-----	
Triops_cancriformis	-----	
Strigamia_maritima2	LGLGLT-----RPKDIA-----	
Catajapyx_aquilonaris	-----	
Daphnia_pulex	SILLLR-----STHLF-----	
Daphnia_magna3	LGLRWL-----RGQDK-----	
Daphnia_magna2	LGLRWL-----RGQDK-----	
Daphnia_magna1	LGLRWL-----RGQDK-----	
Daphnia_magna4	LGLRWL-----RGQDK-----	
Arachnocampa_luminosa	KTKV-----	
Calanus_finmarchicus	NENTTA-LQLSQMNEVFSPS-----	
Epiophlebia_superstes	LSARVR----YLLRPSFRPD-----	
Ladona_fulva	LPGRVR----DAVRSLFRFN-----	
Cordulegaster_boltonii	LPGRVR----DLLRPIFHPD-----	
Diaphorina_citri	CSNLR-----SD-----	
Pachypsylla_venusta	CFNINV-----KE-----	
Acanthocasuarina_muelleriana	CVNLVL-----SE-----	
Glomeris_pustulata	ICCRK-----RN-----	
Frankliniella_cephalica	V----S-----CQ-----	
Machilis_hrabei	LKKLM-----CG-----	
Carabus_granulatus	Y--AA-----TS-----	
Dendroctonus_frontalis	F--LA-----SN-----	
Lepeophtheirus_salmonis	-----	
Caligus_rogercresseyi	-----	
Parhyale_hawaiiensis	-----	
Hyaella_azteca	-----	
Strigamia_maritima1	LCCSKE----NEMKSHRTL-----	
Conwentzia_psociformis	-----	
Liposcelis_bostrychophila	-----	
Tetranychus_urticae	FCYCST----NTNINAGN-----	
Osmylus_fulvicephalus	-----	
Ornithodoros_turicata	CCLAKV----SGRGCSYLA-----	
Acerentomon_sp	-----	
Ixodes_ricinus	NCSIML----R-----	
Folsomia_candida	-----	
Limulus_polyphemus1	CCHERS----QGYSQVPV-----	
Limulus_polyphemus3	CCRSVL----QDYMAQSTE-----	
Platynothis_peltifer5	-----	
Platynothis_peltifer1	-----	
Platynothis_peltifer3	-----	

Achipteria_coleoptrata2	-----
Platynothrus_peltifer2	-----
Platynothrus_peltifer4	-----
Ixodes_scapularis2	ICRCPDAKNVSSGIAGTGSCPSAVI-----
Ixodes_scapularis1	-----
Ixodes_scapularis3	-----
Cotesia_vestalis	-----
Microplitis_demolitor	LKLLLC-KQNVINYDI-----
Zorotypus_caudelli	-----
Nasonia_giraulti	LRSLIK-RDRTSRFGK-----
Nasonia_vitripennis	LRSLIK-RDRTSRFER-----
Varroa_destructor2	-----
Leuctra_sp	-----
Tricholepidion_gertschi	L-----
Perla_marginata	-----
Crioscolia_alcione	FFTSNDEYSLTYD-----
Mischocyttarus_flavitaris	FYNRNDEYSQTYYGQR-----
Polistes_metricus	FCNHNE-HSQKYYGQR-----
Polistes_canadensis	FCNRNE-HSQKYYGQR-----
Chrysis_viridula	LCCRSYD-YSTTYD-----
Argochrysis_armilla	LWCRNN-YSPTYD-----
Chyphotes_mellipes	LCRRQD-YSLTYG-----
Brachycistis_timberlakei	FFRED-YSLAYD-----
Sphaerophthalma_orestes	FCNSHD-YLPTYD-----
Homalodisca_vitripennis	SICTGS-PRHRNLRGS-----
Cercopis_vulnerata	-----
Nilaparvata_lugens	LGCKYA-LS-SDYRGN-----
Achipteria_coleoptrata1	-----
Ephemera_danica	GRV-----
Leptopilina_clavipes	-----
Ganaspis_sp	LRKITR-HKYSPPAS-----
Leptopilina_boulardi	LRKITR-HKYSPTS-----
Mantis_religiosa	-----
Blattella_germanica	-----
Zootermopsis_nevadensis	-----
Stigmatomma_oregonense	FYNKRD-YSLTHGNC-----
Dinoponera_quadriceps	FFKRKD-YSPAY-----
Harpegnathos_saltator	FCKRKD-YSLAY-----
Cerapachys_biroi	FCKRKD-YSLTY-----
Monomorium_pharaonis	LCGKKD-YSLTYGNHNVSL-----
Tetramorium_bicaratum	FCKRKD-YSLTY-----
Solenopsis_invicta	FYRKKD-YSLTY-----
Atta_cephalotes	FYRKKD-YSLTY-----
Acromyrmex_echinator	FCKRKD-YSLTYGNHNLSTLSTLSTLYIYIYISSSHVCICLIPSNIWITRINIVIFIC
Pogonomyrmex_barbatus	FCKRKD-YSLTY-----
Wasmannia_auropunctata	FCKRKD-YSLTY-----
Vollenhovia_emeryi	FCSKKD-YSLTY-----
Orussus_abietinus	LQAPTR-SK---QEADRKP-----
Blaberus_atropos	LFCRTQ-----
Limulus_polyphemus2	CCQTSS-KSFSSQVPE-----
Isonychia_bicolor	-----
Occasjapyx_japonicus	-----
Baetis_sp	-----
Panonychus_ulmi	-----
Frankliniella_occidentalis	-----
Eurylophella_sp	-----
Telenomus_podisi	FGRLFY-YNAYSIDR-----
Aposthonia_japonica	GASDLH-----YRGS-----
Haploembia_palau	-----
Halyomorpha_halys	IICRKN-KDRPENVG---SG-----
Stenobothrus_lineatus	-----
Inocellia_crassicornis	FVNNLD-SSKT-KYTR--GG-----
Tenthredo_koehler	LYPTRG-SSIKSQEN---P-----RQSI-----
Corydalus_cornutus	-----
Chrysopa_pallens	ICSKTY-KNKNYSTA-----I-----
Meloe_violaceus	CT---A-SSKNYKSA-----N-----
Aethina_tumida	YT---A-TNKKLKSS-----SM-----
Gyrinus_marinus	-----
Tribolium_castaneum	YT---A-SSKNYRSA-----T-----
Nicrophorus_vespilloides	YT---S-N-RNYREA-----
Aleochara_curtula	-----
Pogonus_chalceus	YAATS----KNYRSA--GTGN-----
Sipyloidea_sipylus	-----
Extatosoma_tiaratum	GNPRA----NADLIG-----
Aretaon_asperimus	ASAGA----HADLVS-----
Medauroidea_extradentata	GDPRT----NADLFG-----
Ramulus_artemis	GDPRT----NADLFG-----

Galloisiana_yuasai
Athalia_rosae

IYSSG---RSASYARTREGR-----RRCV-----

Varroa_destructor1
Metaseiulus_occidentalis1
Metaseiulus_occidentalis2
Tigriopus_californicus
Anurida_maritima
Meinertellus_cundinamarcensis
Pogonognathellus_sp
Triops_cancriformis
Strigamia_maritima2
Catajapyx_aquilonaris
Daphnia_pulex
Daphnia_magna3
Daphnia_magna2
Daphnia_magna1
Daphnia_magna4
Arachnocampa_luminosa
Calanus_finmarchicus
Epiophlebia_superstes
Ladona_fulva
Cordulegaster_boltonii
Diaphorina_citri
Pachypsylla_venusta
Acanthocasuarina_muellerianae
Glomeris_pustulata
Frankliniella_cephalica
Machilis_hrabei
Carabus_granulatus
Dendroctonus_frontalis
Lepeophtheirus_salmonis
Caligus_rogercresseyi
Parhyale_hawaiensis
Hyalella_azteca
Strigamia_maritima1
Conwentzia_psociformis
Liposcelis_bostrychophila
Tetranychus_urticae
Osmylus_fulvicephalus
Ornithodoros_turicata
Acerentomon_sp
Ixodes_ricinus
Folsomia_candida
Limulus_polyphemus1
Limulus_polyphemus3
Platynothrus_peltifer5
Platynothrus_peltifer1
Platynothrus_peltifer3
Achipteria_coleoptrata2
Platynothrus_peltifer2
Platynothrus_peltifer4
Ixodes_scapularis2
Ixodes_scapularis1
Ixodes_scapularis3
Cotesia_vestalis
Microplitis_demolitor
Zorotypus_caudelli
Nasonia_giraulti
Nasonia_vitripennis
Varroa_destructor2
Leuctra_sp
Tricholepidion_gertschi
Perla_marginata
Crioscolia_alcione
Mischocyttarus_flavitaris
Polistes_metricus
Polistes_canadensis
Chrysis_viridula
Argochrysis_armilla
Chyphotes_mellipes
Brachycistis_timberlakei
Sphaerophthalma_orestes
Homalodisca_vitripennis
Cercopis_vulnerata

721

780

-----VYRSKNA-ITIS-----
-----GEESRKPCTRAN-----
-----LI-----TV-----
-----LG-----GADADRPEPQT-----HHRTKR
-----SI-----GAEQDIILRTKKFKTPRPDTRPHQDK
-----SI-----GDEPEG-KTPPP-----IQKQTNQDG

-----SI-----GDEEPQPQQQP-----TNKLPSTKS

-----I-----EQ-----L
-----SI-----GEDDRRGAAGP-----AGGQPADTN
-----SI-----GEDDRRGAAGP-----AGGQPADTN
-----SI-----GEDDRRGAAGP-----AGGQPADTN
-----SI-----GEDDRRGAAGP-----AGGQPADTN

-----SPTPTR-----LRR---NLSKNSVLRES-----SFIEVV-----
-----TTKRVRHQEASMSAS---SSSRG-----SSQPKIRANSEEGRN-----G
-----TSKRLRHNDAITYAS---SSSRTR---SS---RESPQMEIKTLNSPVKDDPPS-----
-----TNKRARHHDATASAS---LSSRTR---SS---RESPQPEVKATAESSKDEER---DG
-----DTELT-MDTASAS---G--S-----KECGRRTESDLTF-
-----ENRTV--DTASGN---SSSA-----RECCRRTDSNVTMG
-----EAKVA-MDTASGM---SSS-----RERRNESEMTLG
-----SSATNEHGAPIVG---VFSRSSL-----SDTNQRSTHVHTLAHQGG-----
-----TGHPSGS---VLSA-----HSGGSGSSQSNTTQHRTCFTD-----
-----GDYLNHNSGIPSGG---GFDRGTLFRSSSTSDSKAPSANQNKIAVTRTSVSSQSG
-----KNYR---SAGTGN---SASN-----SSGGV-----ESTS-----
-----KSYR---GAPDQG---TLSN-----SSGEQ-----VTSCLKLTRAS-----

-----ATTYSRT---SFSE-----S-----VGPRVALQSLPPSSN-----

-----RSKT---LDDS-----S-----VNI-----
-----RDTTDGT---NDSN-----A-----HSV-----

-----ENI-NNT---TSRS-----S-----QTD-----
-----ATSNNNN---ANRS-----Y-----PTE-----

-----LADLTT-QGT-EAQSVL---SYKSSPTDTSARLATAV-----VGKR-----

-----D---TSYVNSNGS---STKSSIIVTMF-RFAGSMYH-----R-QT-YQERS---

-----Y---QFYFLCQY-----
-----A---SSNANSNETRSSKRSSFISRMS-RYTSFIIY-----G-PMRTIEIV-----

-----QSMRRSDSFETSTR-----STLFSRIS-RLTGSA-----MFR-----
-----GMMRRSDSNDTSTR-----ASLMSRIS-RYASSI-----IPR-----
-----MMRRSDSNDTSTR-----TSLMSRIS-RYTSSI-----IPR-----
-----MMRRSDSNDTSTR-----ISLMSRIS-RYTSSI-----IRR-----
-----QELHPANSTETSTR-----SSFISRIF-WYAGSM-----IFR-----
-----QELHPANSNETSTR-----SSLISRIS-RYAGSM-----IFR-----
-----RNTHRSNSHENSTR-----SSLISRIS-RYAGTA-----IFR-----
-----RDMQRSWNEASTR-----SSLISRIS-RYANSV-----ISH-----
-----RDVRRGNSDETSTR-----SSLISRIS-RYAGSV-----IFR-----
-----A-----SSCR-----

Nilaparvata_lugens -----NSAAESGSSGCGAGSCSKRSEVTNTTSL-----LPRK-PLVAEQ-----
 Achipteria_coleoptratal -----
 Ephemera_danica -----
 Leptopilina_clavipes -----
 Ganaspis_sp -----DEASKNDHSNEPSTTS-----SLISKVSV-Y--PN-V--R-----PNYSEA-----
 Leptopilina_boulardi -----DDNSKIGHSNEPSTTS-----SLISKVST-C--PTTV--K-----PIYTEV-----
 Mantis religiosa -----
 Blattella_germanica -----
 Zootermopsis_nevadensis -----
 Stigmatomma_oregonense -----
 Dinoponera_quadriceps -----DAVAQONASDAASTT-----SSFISRIS-RL-----
 Harpegnathos_saltator -----DVIARQNTSDAPSIT-----SSFISRIS-RL-----
 Cerapachys_biroi -----DIDAHQNASDVPSTT-----SSFISRIS-RL-----
 Monomorium_pharaonis -----
 Tetramorium_bicarinatum -----DIDARQNASDVPSTT-----SSFISRIS-RL-----
 Solenopsis_invicta -----DIDARQNASDVPSTT-----SSFISRIS-RL-----
 Atta_cephalotes -----DIDARQNASDVPSTT-----SSFISRIS-RL-----
 Acromyrmex_echinatior HFLSDIDARQNTSDVPSTT-----SSFISRIS-RL-----
 Pogonomyrmex_barbatus -----DIDARQNALDVPSTT-----SPFISRIS-RL-----
 Wasmannia_auropunctata -----DIDVRQNASDVPSTT-----SSFISRIS-RL-----
 Vollenhovia_emoryi -----DIDVRQNASDVPSTT-----SSFISRIS-RL-----
 Orussus_abietinus -----
 Blaberus_atropos -----
 Limulus_polyphemus2 -----NTDNNTFSRSERCSSYPLSVRTGSRHKFPDGTTRTRK-RLCRELGSK--
 Isonychia_bicolor -----
 Occasjapyx_japonicus -----
 Baetis_sp -----
 Panonychus_ulmi -----
 Frankliniella_occidentalis -----
 Eurylophella_sp -----
 Telenomus_podisi -----STRSGSSNENSTR-----SSFISRIS-RYAS-----F-VMHGPA-----
 Aposthonia_japonica -----SSSKERSRLSKLVSWRST-----
 Haploembia_palau -----
 Halyomorpha_halys -----GSSGRPHQS---CTLAGQHTH-----
 Stenobothrus_lineatus -----
 Inocellia_crassicornis -----MSKASNSSTVETAVGRLSWLSKSFSS-KASF-----
 Tenthredo_koehler -----EI-IRWGSSASSSGT---SIRSYASRMS-RYAN-----S-VLRRSSDSS--
 Corydalus_cornutus -----
 Chrysopa_pallens -----TNSGGSNSQGVST---TVRVPL---RISF-----YTRNDGG--
 Meloe_violaceus -----AGNSGNSSSGEPQST---SLRPFS---KWSF-----CNSPKSN--
 Aethina_tumida -----GNSGNSSSGEIQST---SLRTLS---RLSR-----NNSGRL--
 Gyrinus_marinus -----
 Tribolium_castaneum -----GGNSASNSGDAQST---SLRPFS---RWSL-----CNSARS--
 Nicrophorus_vespilloides -----AGNSTSNSSGGVEST---SLRPFT---RWSF-----CNGNRA--
 Aleochara_curtula -----
 Pogonus_chalceus -----SASNSSSGGVEST---SLRPFS---KWSL-----CASAKSS--
 Sipyloidea_sipylus -----
 Extatosoma_tiaratum -----GSGS-STT---SWRNSK---VYRL-----V-----
 Aretaon_asperimus -----GSGS-SST---SWRNSR---TYRL-----V-----
 Medauroidea_extradentata -----GSGS-STT---SWRNSK---VYRL-----V-----
 Ramulus_artemis -----GSGS-STT---SWRNSK---VYRL-----V-----
 Galloisiana_yuasai -----
 Athalia_rosae -----STETPCNSSGS-STG---TSVESY-----

781

840

Varroa_destructor1 ILQYRPPNRSKRQPRAYRGA-----
 Metaseiulus_occidentalis1 AIVCE---KPARQLRGYRIS-----
 Metaseiulus_occidentalis2 -----
 Tigrionus_californicus ILFTRKAEPLKGNPLGARPHPLFALQDQE-IVRA---GIRSEPMLS-SHHR---PNV--K
 Anurida_maritima SR-----TMKQVS-TLDA---IENQGAFLQLETK---SEV--L
 Meinertellus_cundinamarcensis G---GGGGTK---SDL---V-----
 Pogonognathellus_sp -----
 Triops_cancriformis -----
 Strigamia_maritima2 EMV-----
 Catajapyx_aquilonaris -----
 Daphnia_pulex LFFIRVSRK---SRN-----I-----
 Daphnia_magna3 HRFGRGPRR---AQT---RDQHRQVMAEQQ-LLPA---GEQHPAMLATKCTR---ADI--V
 Daphnia_magna2 HRFGRGPRR---AQT---RDQHRQVMAEQQ-LLPA---GEQHPAMLATKCTR---ADI--V
 Daphnia_magna1 HRFGRGPRR---AQT---RDQHRQVMAEQQ-LLPA---GEQHPAMLATKCTR---ADI--V
 Daphnia_magna4 HRFGRGPRR---AQT---RDQHRQVMAEQQ-LLPA---GEQHPAMLATKCTR---ADI--V
 Arachnocampa_luminosa -----
 Calanus_finmarchicus ---GL-----QE-----
 Epiophlebia_superstes GR-----
 Ladona_fulva VKKNGVVAEPKTEK-----
 Cordulegaster_boltonii CRMIGLADRTKEEK-----AVKESAVLLSN-----A-----
 Diaphorina_citri ---LNRRTYSNPDEN-----GALIPLIILTF-----AYTCIC---RAI--I

Pachyphylla_venusta	TYLNRQSCNDD--T-----YVSEDNLI-----
Acanthocasuarina_muellerianae	TFLNRHEDT-----GM-SDDSL-----
Glomeris_pustulata	-----
Frankliniella_cephalica	-----
Machilis_hrabei	VLLKRRRTLNGDKQP-----T-----
Carabus_granulatus	-----
Dendroctonus_frontalis	-----PGRDR-----H-----
Lepeophtheirus_salmonis	-----
Caligus_rogercresseyi	-----
Parhyale_hawaiensis	-----
Hyalessa_azteca	-----
Strigamia_maritima1	N-FLRVNDNK--L-----NVRVAAVSDSA-----LYSCEK-----R
Conwentzia_psociformis	-----
Liposcelis_bostrychophila	-----
Tetranychus_urticae	-----EPHCSS-----IN--R
Osmylus_fulvicephalus	-----
Ornithodoros_turicata	-----VSHCEGDHA-----RIKCSP--SKR--R
Acerentomon_sp	-----
Ixodes_ricinus	-----
Folsomia_candida	-----
Limulus_polyphemus1	-----NEICTSYPL-----SLRCGV--HY----
Limulus_polyphemus3	-----NEVNSSYPL-----SFFIAQ--EE----
Platynothrus_peltifer5	-----
Platynothrus_peltifer1	-----
Platynothrus_peltifer3	-----
Achipteria_coleoptrata2	-----
Platynothrus_peltifer2	-----
Platynothrus_peltifer4	-----
Ixodes_scapularis2	---GATDVEEDL-----QC
Ixodes_scapularis1	-----
Ixodes_scapularis3	-----
Cotesia_vestalis	-----
Microplitis_demolitor	---TDFILT-----R
Zorotypus_caudelli	-----
Nasonia_giraulti	-----
Nasonia_vitripennis	-----NKLYI-----
Varroa_destructor2	-----
Leuctra_sp	-----
Tricholepidion_gertschi	-----
Perla_marginata	-----
Crioscolia_alcione	-----
Mischocyttarus_flavitaris	-----
Polistes_metricus	-----
Polistes_canadensis	-----
Chrysis_viridula	-----
Argochrysis_armilla	-----
Chyphotes_mellipes	-----
Brachycistis_timberlakei	-----
Sphaerophthalma_orestes	-----
Homalodisca_vitripennis	-----
Cercopis_vulnerata	-----
Nilaparvata_lugens	-----PLPEVTPIRRWVVTIPPVNSREERECLQLFSGLNNERILPR
Achipteria_coleoptrata1	-----
Ephemera_danica	-----
Leptopilina_clavipes	-----
Ganaspis_sp	-----RERNIS-----
Leptopilina_boulardi	-----RERNIS-----
Mantis religiosa	-----
Blattella_germanica	-----
Zootermopsis_nevadensis	-----
Stigmatomma_oregonense	-----
Dinoponera_quadriceps	-----
Harpegnathos_saltator	-----
Cerapachys_biroi	-----
Monomorium_pharaonis	-----
Tetramorium_bicaratum	-----
Solenopsis_invicta	-----
Atta_cephalotes	-----
Acromyrmex_echinatior	-----
Pogonomyrmex_barbatus	-----
Wasmannia_auropunctata	-----
Vollenhovia_emoryi	-----
Orussus_abietinus	-----
Blaberus_atropos	-----
Limulus_polyphemus2	---NESTDVGE--NRGSVTQTETT-----S-----
Isonychia_bicolor	-----
Occasjapyx_japonicus	-----

Baetis_sp -----
 Panonychus_ulmi -----
 Frankliniella_occidentalis -----
 Eurylophella_sp -----
 Telenomus_podisi -----TK-----ERISR-----
 Aposthonia_japonica -----
 Haploembia_palaui -----YAKWVVALPPNLSSEDKTMLRL-----FR
 Halyomorpha_halys -----
 Stenobothrus_lineatus -----
 Inocellia_crassicornis ---QVHVN---NI---IQS-----
 Tenthredo_koehlerii ---SNKE-----LQPSNRIR-----
 Corydalus_cornutus -----
 Chrysopa_pallens ---ANG-----KQ-----TY
 Meloe_violaceus ---GNK-----YT-----SR
 Aethina_tumida ---NR-----CS-----VR
 Gyrinus_marinus -----
 Tribolium_castaneum ---NK-----YP-----TR
 Nicrophorus_vespilloides ---AAK-----FN-----PR
 Aleochara_curtula -----
 Pogonus_chalceus ---SAINHNGNNTNGHAIGSGD---FRARYPAPPASSAASTLIRLPAPAHSPQQLM
 Sipyloidea_sipylus -----
 Extatosoma_tiaratum -----SGSVFKQRDAVRERRSAPLRTIYGSLDLELL-----
 Aretaon_asperirum -----SGSMFKSRDSVRERRWAMAMPTKIPIATALMAGRDLDPSTSEEV-AS
 Medauroidea_extradentata -----NGSAFKQRDAVRERRWAMAMPTKIPIATALMAGRDPSTSQDV-A-
 Ramulus_artemis -----SGSAFKQRDSVRERRWAMAMPTKIPIATALMVGRDIPSTSQDA-A-
 Galloisiana_yuasai -----
 Athalia_rosae -----ASRMSRYAYAI-----LGKSDTANSKEF-HC

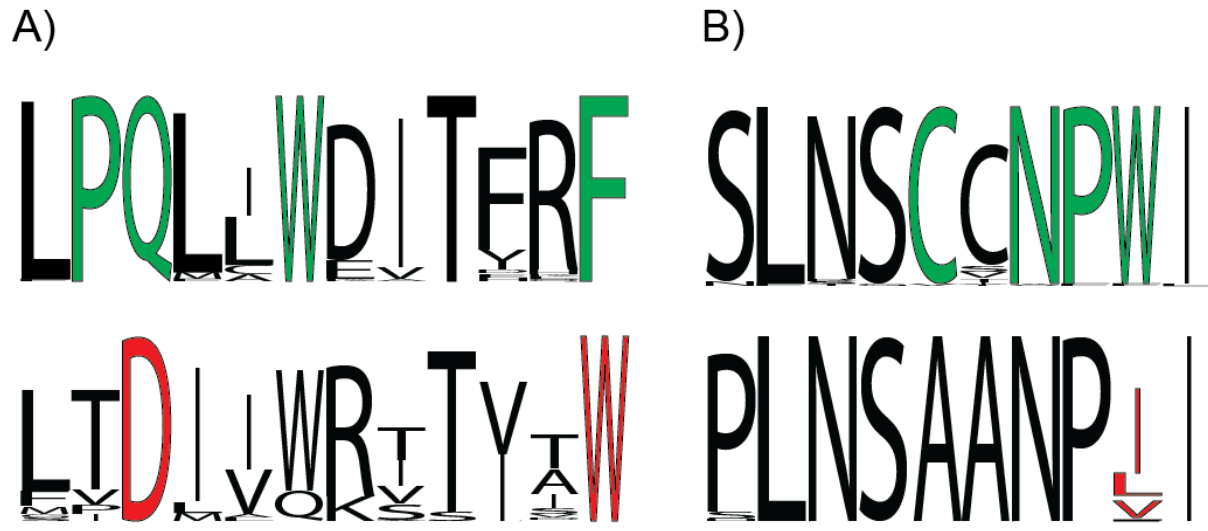
841

885

Varroa_destructor1 -----
 Metaseiulus_occidentalis1 -----
 Metaseiulus_occidentalis2 -----
 Tigriopus_californicus NPLPA-----S-----NQNK---SWT-KT---
 Anurida_maritima -----
 Meinertellus_cundinamarcensis -----
 Pogonognathellus_sp -----
 Triops_cancriformis -----
 Strigamia_maritima2 -----
 Catajapyx_aquilonaris -----
 Daphnia_pulex -----
 Daphnia_magna3 THLGN-----TKKLQFQQNH---QHVEKIG--
 Daphnia_magna2 THLGN-----TKKLQFQQNH---QHVEKIG--
 Daphnia_magna1 THLGN-----TKKLQFQQNH---QHVEKIG--
 Daphnia_magna4 THLGN-----TKKLQFQQNH---QHVEKIG--
 Arachnocampa_luminosa -----
 Calanus_finmarchicus -----
 Epiophlebia_superstes -----
 Ladona_fulva -----
 Cordulegaster_boltonii ---PV-----
 Diaphorina_citri N--FSMKNSIRRHQFSRSSRSTRDS---ETENELCHTIVDSG--
 Pachypsylla_venusta ---VSRPRQWVVSVPDG-----
 Acanthocasuarina_muellerianae ---TLRSRQWVTLPDANQT---R-----
 Glomeris_pustulata -----
 Frankliniella_cephalica -----
 Machilis_hrabei ---AVEMRNWKDETNRPLPLLAETSDFIQCAIGENE---
 Carabus_granulatus ---LRPFSKWSLCASTKSTPRY-----
 Dendroctonus_frontalis ---LTNGRQWMVTAT-----
 Lepeophtheirus_salmonis -----
 Caligus_rogercresseyi -----
 Parhyale_hawaiiensis -----
 Hyalella_azteca -----
 Strigamia_maritima1 HSSPNLNVKSAASTLVLCSQ---QHHHDTQNHKLDGVTMETQCA
 Conwentzia_psociformis -----
 Liposcelis_bostrychophila -----
 Tetranychus_urticae NGSRTIFVSQKMSKYSDDKPSVEAHG---
 Osmylus_fulvicephalus -----
 Ornithodoros_turicata NGFRS-STDVEMRTAQDCGADT-----
 Acerentomon_sp -----
 Ixodes_ricinus -----
 Folsomia_candida -----
 Limulus_polyphemus1 ---TS-SFRLKTKITGCRPCPNIQDLHDEAETFSA---
 Limulus_polyphemus3 ---PV-MLRNRLKKKQ-----
 Platynothis_peltifer5 -----
 Platynothis_peltifer1 -----
 Platynothis_peltifer3 -----
 Achipteria_coleoptrata2 -----
 Platynothis_peltifer2 -----

Platynothis_peltifer4	-----
Ixodes_scapularis2	S-----LEKTS-----
Ixodes_scapularis1	-----
Ixodes_scapularis3	-----
Cotesia_vestalis	-----
Microplitis_demolitor	RQS-----
Zorotypus_caudelli	-----
Nasonia_giraulti	-----
Nasonia_vitripennis	-----
Varroa_destructor2	-----
Leuctra_sp	-----
Tricholepidion_gertschi	-----
Perla_marginata	-----
Crioscolia_alcione	-----
Mischocyttarus-_flavitaris	-----
Polistes_metricus	-----
Polistes_canadensis	-----
Chrysis_viridula	-----
Argochrysis_armilla	-----
Chyphotes_mellipes	-----
Brachycistis_timberlakei	-----
Sphaerophthalma_orestes	-----
Homalodisca_vitripennis	-----
Cercopis_vulnerata	-----
Nilaparvata_lugens	SQQQQ---HNQQRAIR-TSSSPCR-AARCRLDL-----
Achipteria_coleoptrata1	-----
Ephemera_danica	-----
Leptopilina_clavipes	-----
Ganaspis_sp	-----
Leptopilina_boulardi	-----
Mantis_religiosa	-----
Blattella_germanica	-----
Zootermopsis_nevadensis	-----
Stigmatomma_oregonense	-----
Dinoponera_quadriceps	-ASSKIFG-----
Harpegnathos_saltator	-ASSKIFG-----
Cerapachys_biroi	-ASSKIFG-----
Monomorium_pharaonis	-----
Tetramorium_bicarinarum	-ASSKIFG-----
Solenopsis_invicta	-ASSKIFG-----
Atta_cephalotes	-ASSKIFG-----
Acromyrmex_echinatior	-ASSKIFG-----
Pogonomyrmex_barbatus	-ISSKIFE-----
Wasmannia_auropunctata	-ASSKIFG-----
Vollenhovia_emoryi	-ASSKIFG-----
Orussus_abietinus	-----
Blaberus_atropos	-----
Limulus_polyphemus2	-EPGKFVTRDKDKTLC-----
Isonychia_bicolor	-----
Occasjapyx_japonicus	-----
Baetis_sp	-----
Panonychus_ulmi	-----
Frankliniella_occidentalis	-----
Eurylophella_sp	-----
Telenomus_podisi	-----
Aposthonia_japonica	-----
Haploembia_palau	-----
Halyomorpha_halys	TPNRNVWSS-LEAKYETTDSKLSPE-L-----
Stenobothrus_lineatus	-----
Inocellia_crassicornis	-----
Tenthredo_koehleri	-----
Corydalus_cornutus	-----
Chrysopa_pallens	TTNYHPSVRYTPKKWTVAIEELPP-----
Meloe_violaceus	LTQRPYDAQSNTRRWIVTTTT-----
Aethina_tumida	TANQNYITKYDAKDWIVATAT-----
Gyrinus_marinus	-----
Tribolium_castaneum	VPHRPYVAQYNARRWIVTTTT-----
Nicrophorus_vespilloides	QPQRQYVTQYNARRWIVTTTT-----
Aleochara_curtula	-----
Pogonus_chalceus	QQPSPFLGRYHARRWIVTTSA-----
Sipyloidea_sipylus	-----
Extatosoma_tiaratum	-----
Aretaon_asperimus	-----
Medauroidea_extradentata	-----
Ramulus_artemis	-----
Galloisiana_yuasai	-----
Athalia_rosae	LQSSSLRGIRNELE-----

Supplementary Figure S4. Discrimination between oxytocin/vasopressin-like and crustacean cardioactive peptide receptors. Sequence logo frequency plots and alignments of sequence stretches used to distinguish oxytocin/vasopressin-like from closely related crustacean cardioactive peptide (CCAP) receptors. (A) Sequence logo of the end of transmembrane domain 2 and the beginning of extracellular loop 1 of 68 oxytocin/vasopressin-like receptors (upper panel) and 68 CCAP receptors (lower panel). (B) Sequence logo of transmembrane domain 7 of 68 oxytocin-like receptors (upper panel) and 68 CCAP receptors (lower panel). Individual sequences and of those conserved motifs are shown for oxytocin/vasopressin-like (C) and CCAP receptors (D). Conserved residues are highlighted in green. Major differences of oxytocin/vasopressin-like to CCAP receptor sequences are shown in red.



(C)

Transmembrane domain 2/extracellular loop 1 (XPQX₂WX_{5,6}F)

Transmembrane domain 7 (CXNPW)

tr Q6Q4A4 Q6Q4A4_THETS	LPQLLDITEK	tr Q6Q4A4 Q6Q4A4_THETS	SLNSCVNPI
tr B1NWW5 B1NWW5_TRICA	LPQLADITFR	tr B1NWW5 B1NWW5_TRICA	SLNSCVNPWI
gi 332020179 gb EGI60623.1	LPQLADITFR	gi 332020179 gb EGI60623.1	SLTSCVNPWI
sp Q75W84 ANR_EISFO	LPQLLDVTHRF	sp Q75W84 ANR_EISFO	SLNSCINPWI
sp Q7YW31 CTR1_OCTVU	LPQLMDITFL	sp Q7YW31 CTR1_OCTVU	SLNSCTNPWI
tr K9JBV2 K9JBV2_DAPPU	LPQLADITFR	tr K9JBV2 K9JBV2_DAPPU	SLNSCSNPWI
sp P30518 V2R_HUMAN	LPQLAKATDRF	sp P30518 V2R_HUMAN	SLNSCTNPWI
tr B3XZZ4 B3XZZ4_PROAN	LPQLLDVTDQF	tr B3XZZ4 B3XZZ4_PROAN	SLNSCSNPWI
tr Q25397 Q25397_LYMST	LPQLWDITERF	tr Q25397 Q25397_LYMST	SLNSCCNPWI
tr H7CEK0 H7CEK0_TRISC	LPQLWEITFR	tr H7CEK0 H7CEK0_TRISC	SLNSCCNPWI
tr H3K0J0 H3K0J0_CALMI	LPQLWEITFR	tr H3K0J0 H3K0J0_CALMI	SLNSCCNPWI
tr H2T2H1 H2T2H1_TAKRU	FPQLWDITFR	tr H2T2H1 H2T2H1_TAKRU	SLNSCCNPWI
tr DOUYC9 DOUYC9_CYPNE	LPQLWDITFR	tr DOUYC9 DOUYC9_CYPNE	SLNSCCNPWI
tr H1ADE8 H1ADE8_ORYLA	LPQLWDITFR	tr H1ADE8 H1ADE8_ORYLA	SLNSCCNPWI
tr H2LDT4 H2LDT4_ORYLA	LPQLWDITFR	tr H2LDT4 H2LDT4_ORYLA	SLNSCCNPWI
tr E4W698 E4W698_DANRE	LPQLWDITFR	tr E4W698 E4W698_DANRE	SLNSCCNPWI
sp Q90334 ITR_CATCO	LPQLWDITFR	sp Q90334 ITR_CATCO	SLNSCCNPWI
tr E4W699 E4W699_DANRE	LPQLWDITFR	tr E4W699 E4W699_DANRE	SLNSCCNPWI
tr G3N7A8 G3N7A8_GASAC	LPQLWDITFR	tr G3N7A8 G3N7A8_GASAC	SLNSCCNPWI
tr H7CEB8 H7CEB8_AMPOC	LPQLWDITFR	tr H7CEB8 H7CEB8_AMPOC	SLNSCCNPWI
tr H1ADE9 H1ADE9_ORYLA	LPQLWDITFR	tr H1ADE9 H1ADE9_ORYLA	SLNSCCNPWI
tr H3DAW1 H3DAW1_TETNG	LPQLWDITFR	tr H3DAW1 H3DAW1_TETNG	SLNSCCNPWI
tr H2S576 H2S576_TAKRU	LPQLWDITFR	tr H2S576 H2S576_TAKRU	SLNSCCNPWI
tr H2S575 H2S575_TAKRU	LPQLWDITFR	tr H2S575 H2S575_TAKRU	SLNSCCNPWI
tr G3WCZ9 G3WCZ9_SARHA	LPQLWDITFR	tr G3WCZ9 G3WCZ9_SARHA	SLNSCCNPWI
tr F6U716 F6U716_MONDO	LPQLLDITFR	tr F6U716 F6U716_MONDO	SLNSCCNPWI
tr G5BX96 G5BX96_HETGA	LPQLWDITFR	tr G5BX96 G5BX96_HETGA	SLNSCCNPWI
sp Q28756 OXYR_SHEEP	LPQLWDITFR	sp Q28756 OXYR_SHEEP	SLNSCCNPWI
sp P56449 OXYR_BOVIN	LPQLWDITFR	sp P56449 OXYR_BOVIN	SLNSCCNPWI
tr C4PD02 C4PD02_BUBBU	LPQLWDITFR	tr C4PD02 C4PD02_BUBBU	SLNSCCNPWI
tr G1SQ05 G1SQ05_RABIT	LPQLWDITFR	tr G1SQ05 G1SQ05_RABIT	SLNSCCNPWI
tr H0VZP0 H0VZP0_CAVPO	LPQLWDITFR	tr H0VZP0 H0VZP0_CAVPO	SLNSCCNPWI
tr G1PUQ9 G1PUQ9_MYOLU	LPQLWDITFR	tr G1PUQ9 G1PUQ9_MYOLU	SLNSCCNPWI
tr G3TTL6 G3TTL6_LOXAF	LPQLWDITFR	tr G3TTL6 G3TTL6_LOXAF	SLNSCCNPWI

tr	G3UGJ6	G3UGJ6_LOXAF	LPOLLNDITFRF	tr	G3UGJ6	G3UGJ6_LOXAF	SLNSCCNPWI
sp	P32306	OXYR_PIG	LPOLLNDITFRF	sp	P32306	OXYR_PIG	SLNSCCNPWI
tr	E3V2E5	E3V2E5_CANFA	LPOLLNDITFRF	tr	E3V2E5	E3V2E5_CANFA	SLNSCCNPWI
tr	G1M104	G1M104_AILME	LPOLLNDITFRF	tr	G1M104	G1M104_AILME	SLNSCCNPWI
tr	G3H112	G3H112_CRIGR	LPOLLNDITFRF	tr	G3H112	G3H112_CRIGR	SLNSCCNPWI
tr	E0V872	E0V872_MICOH	LPOLLNDITFRF	tr	E0V872	E0V872_MICOH	SLNSCCNPWI
sp	P97926	OXYR_MOUSE	LPOLLNDITFRF	sp	P97926	OXYR_MOUSE	SLNSCCNPWI
sp	P70536	OXYR_RAT	LPOLLNDITFRF	sp	P70536	OXYR_RAT	SLNSCCNPWI
tr	F2YMM4	F2YMM4_SAISS	LPOLLNDITYRF	tr	F2YMM4	F2YMM4_SAISS	SLNSCCNPWI
tr	F7ILY7	F7ILY7_CALJA	LPOLLNDITFRF	tr	F7ILY7	F7ILY7_CALJA	SLNSCCNPWI
tr	H0WII7	H0WII7_OTOGA	LPOLLNDITFRF	tr	H0WII7	H0WII7_OTOGA	SLNSCCNPWI
sp	P56494	OXYR_MACMU	LPOLLNDITFRF	sp	P56494	OXYR_MACMU	SLNSCCNPWI
tr	E3V2E7	E3V2E7_MACFA	LPOLLNDITFRF	tr	E3V2E7	E3V2E7_MACFA	SLNSCCNPWI
sp	P30559	OXYR_HUMAN	LPOLLNDITFRF	sp	P30559	OXYR_HUMAN	SLNSCCNPWI
tr	G1QUE2	G1QUE2_NOMLE	LPOLLNDITFRF	tr	G1QUE2	G1QUE2_NOMLE	SLNSCCNPWI
tr	G3R8I4	G3R8I4_GORGO	LPOLLNDITFRF	tr	G3R8I4	G3R8I4_GORGO	SLNSCCNPWI
tr	Q5D7U5	Q5D7U5_CHICK	LPOLLNDITFRF	tr	Q5D7U5	Q5D7U5_CHICK	SLNSCCNPWI
tr	G3USG7	G3USG7_MELGA	LPOLLNDITFRF	tr	G3USG7	G3USG7_MELGA	SFRGVSAPWL
tr	Q3LRX3	Q3LRX3_TARGR	LPOLLNDITFRF	tr	Q3LRX3	Q3LRX3_TARGR	SLNSCCNPWI
tr	F7C7K9	F7C7K9_XENTR	LPOLLNDITFRF	tr	F7C7K9	F7C7K9_XENTR	SLNSCCNPWI
tr	Q6WNV4	Q6WNV4_LITCT	LPOLLNDITFRF	tr	Q6WNV4	Q6WNV4_LITCT	SLNSCCNPWI
sp	Q90252	MTR_BUFMA	LPOLLNDITFRF	sp	Q90252	MTR_BUFMA	SLNSCCNPWI
tr	Q8AYS5	Q8AYS5_HYLJA	LPOLLNDITFRF	tr	Q8AYS5	Q8AYS5_HYLJA	SLNSCCNPWI
tr	H7CE74	H7CE74_PROAN	LPOLLNDITFRF	tr	H7CE74	H7CE74_PROAN	SLNSCCNPWI
tr	H3BG77	H3BG77_LATCH	LPOLLNDITFRF	tr	H3BG77	H3BG77_LATCH	SLNSCCNPWI
sp	P37288	V1AR_HUMAN	LPQMCNDITYRF	sp	P37288	V1AR_HUMAN	SLNSCCNPWI
tr	A8CWP8	A8CWP8_CHICK	LPQLCNEVTHRF	tr	A8CWP8	A8CWP8_CHICK	SLNSCCNPWI
tr	H3K0J2	H3K0J2_CALMI	LPQFNDITYRF	tr	H3K0J2	H3K0J2_CALMI	SLNSCCNPWI
sp	Q90352	AVT_CATCO	LPQLCNEITFRF	sp	Q90352	AVT_CATCO	SLNSCCNPWI
tr	Q6WNV5	Q6WNV5_LITCT	LPQLCNEITYRF	tr	Q6WNV5	Q6WNV5_LITCT	SLNSCCNPWI
tr	B3XZZ3	B3XZZ3_PROAN	LPQLCNEVTYRF	tr	B3XZZ3	B3XZZ3_PROAN	SLNSCCNPWI
tr	H7CEB4	H7CEB4_PROAN	LPQMIWEVTYRF	tr	H7CEB4	H7CEB4_PROAN	SLNSCCNPWI
sp	P47901	V1BR_HUMAN	LPOLLNDITYRF	sp	P47901	V1BR_HUMAN	NLNSCCNPWI
tr	H3K0J1	H3K0J1_CALMI	LPQLCNEITYRF	tr	H3K0J1	H3K0J1_CALMI	NLNSCCNPWI

(D)

Transmembrane domain 2/extracellular loop1 (X₂DX₈W)

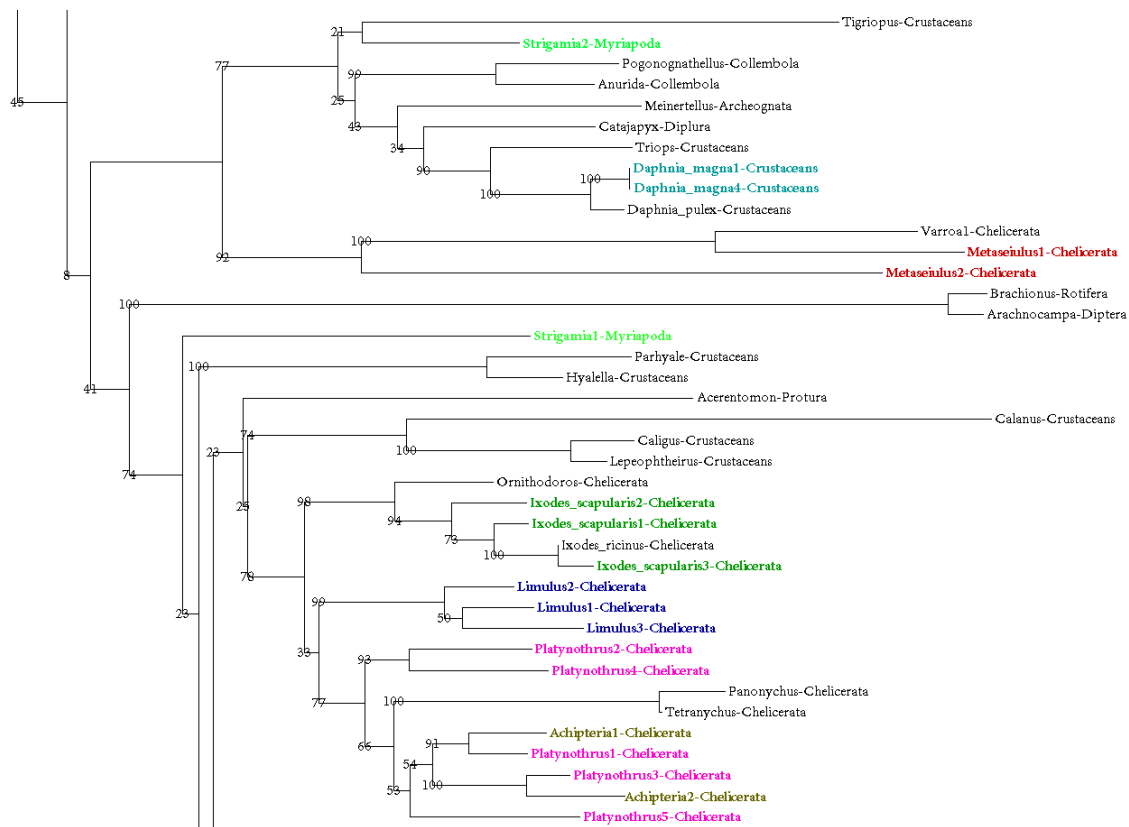
Transmembrane domain 7 (AXNPV/L/F)

gi	768420480	ref	XP_011551009.1	LPQLIQRTITISW	gi	768420480	ref	XP_011551009.1	PLNSANPVI
gi	913307839	ref	XP_013184425.1	LPQLIQRTITITW	gi	913307839	ref	XP_013184425.1	PLNSANPVI
gi	909558612	ref	XP_013134323.1	LPQLIQRTITISW	gi	909558612	ref	XP_013134323.1	PLNSANPVI
gi	943960983	ref	XP_014363004.1	LPQLIQRTITISW	gi	943960983	ref	XP_014363004.1	PLNSANPVI
gi	910347322	ref	XP_013177593.1	LPQLIQRTITISW	gi	910347322	ref	XP_013177593.1	PLNSANPVI
gi	913307945	ref	XP_013184483.1	FVILQKITTIAN	gi	913307945	ref	XP_013184483.1	PLNSANPLII
gi	913307943	ref	XP_013184481.1	FVILQKITTIAN	gi	913307943	ref	XP_013184481.1	PLNSANPLII
gi	943960974	ref	XP_014363000.1	FVILQKITTITW	gi	943960974	ref	XP_014363000.1	PLNSANPLII
gi	910348561	ref	XP_013178264.1	FVILQKITTITW	gi	910348561	ref	XP_013178264.1	PLNSANPLII
gi	910348559	ref	XP_013178263.1	FVILQKITTITW	gi	910348559	ref	XP_013178263.1	PLNSANPLII
gi	909558903	ref	XP_013134477.1	FVILQKITTIAN	gi	909558903	ref	XP_013134477.1	PLNSANPLII
gi	909558901	ref	XP_013134476.1	FVILQKITTIAN	gi	909558901	ref	XP_013134476.1	PLNSANPLII
gi	909558899	ref	XP_013134475.1	FVILQKITTIAN	gi	909558899	ref	XP_013134475.1	PLNSANPLII
gi	817089496	ref	XP_012267616.1	GTIARSTVDW	gi	817089496	ref	XP_012267616.1	PLNSANPLII
gi	817089494	ref	XP_012267615.1	GTIARSTVDW	gi	817089494	ref	XP_012267615.1	PLNSANPLII
gi	936698029	ref	XP_014226999.1	LTIIVRSTVAN	gi	936698029	ref	XP_014226999.1	HLNSANPLII
gi	939636316	ref	XP_014294173.1	LTIIVRVTIAN	gi	939636316	ref	XP_014294173.1	PLNSANPLII
gi	939636313	ref	XP_014294172.1	LTIIVRVTIAN	gi	939636313	ref	XP_014294172.1	PLNSANPLII
gi	939276044	ref	XP_014258479.1	STIIVRITITW	gi	939276044	ref	XP_014258479.1	PLNSANPLII
gi	641666914	ref	XP_008183896.1	MIMMIWRITVAV	gi	641666914	ref	XP_008183896.1	PLNSANPLII
gi	641666912	ref	XP_008183895.1	MIMMIWRITVAV	gi	641666912	ref	XP_008183895.1	PLNSANPLII
gi	641666910	ref	XP_008183894.1	MIMMIWRITVAV	gi	641666910	ref	XP_008183894.1	PLNSANPLII
gi	328713510	ref	XP_003245097.1	MIMMIWRITVAV	gi	328713510	ref	XP_003245097.1	PLNSANPLII
gi	662202708	ref	XP_008474661.1	LTIIVWRSSVTW	gi	662202708	ref	XP_008474661.1	PLNSANPLII
gi	939631611	ref	XP_014282181.1	STIIVRITVAN	gi	939631611	ref	XP_014282181.1	PLNSANPVI
gi	939258178	ref	XP_014248905.1	LTIIVRITVAN	gi	939258178	ref	XP_014248905.1	PLNSANPVI
gi	939258176	ref	XP_014248904.1	LTIIVRITVAN	gi	939258176	ref	XP_014248904.1	PLNSANPVI
gi	939258174	ref	XP_014248903.1	LTIIVRITVAN	gi	939258174	ref	XP_014248903.1	PLNSANPVI
gi	929381616	ref	XP_014101257.1	LTIIVRITVAN	gi	929381616	ref	XP_014101257.1	PLNSANPLII
gi	939259418	ref	XP_014249533.1	LTIIVRSTVEW	gi	939259418	ref	XP_014249533.1	PLNSANPVI
gi	817085633	ref	XP_012265516.1	LTIIVWRSTITW	gi	817085633	ref	XP_012265516.1	PLNSANPLII
gi	817085631	ref	XP_012265515.1	LTIIVWRSTITW	gi	817085631	ref	XP_012265515.1	PLNSANPLII
gi	665804934	ref	XP_008550635.1	LTIIVRVTIIN	gi	665804934	ref	XP_008550635.1	PLNSANPLII
gi	665804932	ref	XP_008550634.1	LTIIVRVTIIN	gi	665804932	ref	XP_008550634.1	PLNSANPLII
gi	665804930	ref	XP_008550633.1	LTIIVRVTIIN	gi	665804930	ref	XP_008550633.1	PLNSANPLII
gi	665804928	ref	XP_008550632.1	LTIIVRVTIIN	gi	665804928	ref	XP_008550632.1	PLNSANPLII
gi	665804926	ref	XP_008550631.1	LTIIVRVTIIN	gi	665804926	ref	XP_008550631.1	PLNSANPLII
gi	665804924	ref	XP_008550630.1	LTIIVRVTIIN	gi	665804924	ref	XP_008550630.1	PLNSANPLII
gi	665804922	ref	XP_008550629.1	LTIIVRVTIIN	gi	665804922	ref	XP_008550629.1	PLNSANPLII
gi	665804920	ref	XP_008550628.1	LTIIVRVTIIN	gi	665804920	ref	XP_008550628.1	PLNSANPLII
gi	665804918	ref	XP_008550627.1	LTIIVRVTIIN	gi	665804918	ref	XP_008550627.1	PLNSANPLII
gi	665804916	ref	XP_008550626.1	LTIIVRVTIIN	gi	665804916	ref	XP_008550626.1	PLNSANPLII
gi	665804914	ref	XP_008550625.1	LTIIVRVTIIN	gi	665804914	ref	XP_008550625.1	PLNSANPLII
gi	755928159	ref	XP_011306641.1	LTIIVRSTVTW	gi	755928159	ref	XP_011306641.1	PLNSANPLII
gi	755928161	ref	XP_011306649.1	LTIIVRSTVTW	gi	755928161	ref	XP_011306649.1	PLNSANPLII

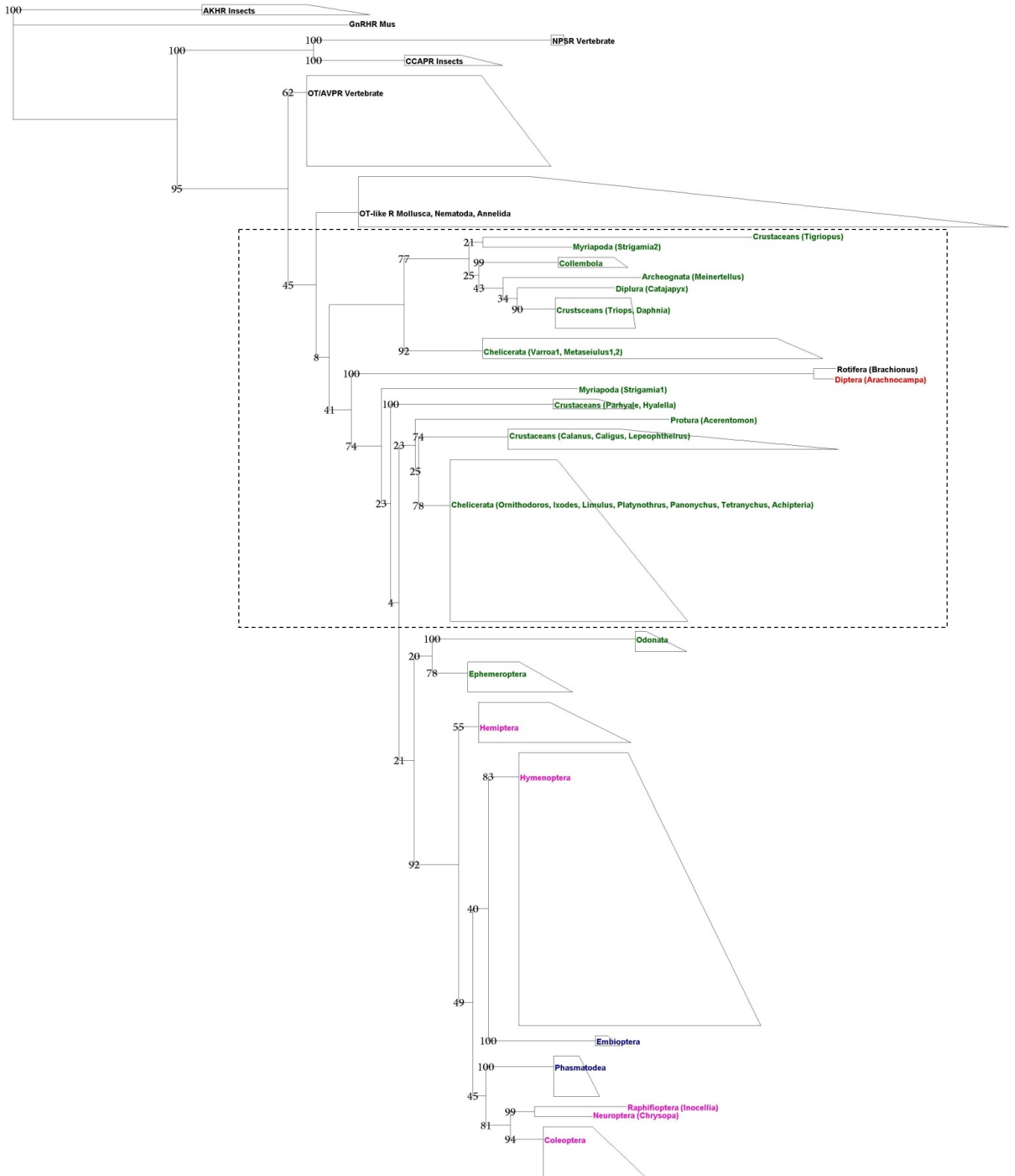
gi	755928156	ref	XP_011306628.1	LTIIVWRSTVTM	gi	755928156	ref	XP_011306628.1	PLNSANPTI
gi	755928154	ref	XP_011306619.1	LTIIVWRSTVTM	gi	755928154	ref	XP_011306619.1	PLNSANPTI
gi	755928151	ref	XP_011306611.1	LTIIVWRSTVTM	gi	755928151	ref	XP_011306611.1	PLNSANPTI
gi	954560085	ref	XP_014603803.1	LTIIWRTTVM	gi	954560085	ref	XP_014603803.1	PLNSANPTI
gi	954560083	ref	XP_014603802.1	LTIIWRTTVM	gi	954560083	ref	XP_014603802.1	PLNSANPTI
gi	951561515	ref	XP_014479680.1	LTIIWRATVM	gi	951561515	ref	XP_014479680.1	PLNSANPTI
gi	746852311	ref	XP_011056707.1	LTIIWRTTVM	gi	746852311	ref	XP_011056707.1	PLNSANPTI
gi	746852309	ref	XP_011056706.1	LTIIWRTTVM	gi	746852309	ref	XP_011056706.1	PLNSANPTI
gi	746852307	ref	XP_011056705.1	LTIIWRTTVM	gi	746852307	ref	XP_011056705.1	PLNSANPTI
gi	746852305	ref	XP_011056704.1	LTIIWRTTVM	gi	746852305	ref	XP_011056704.1	PLNSANPTI
gi	826496319	ref	XP_012541117.1	LTIIWRTTVM	gi	826496319	ref	XP_012541117.1	SLNSANPTI
gi	826496313	ref	XP_012541116.1	LTIIWRTTVM	gi	826496313	ref	XP_012541116.1	SLNSANPTI
gi	826496307	ref	XP_012541114.1	LTIIWRTTVM	gi	826496307	ref	XP_012541114.1	SLNSANPTI
gi	759077735	ref	XP_011348644.1	LTIIWRTTVM	gi	759077735	ref	XP_011348644.1	PLNSANPTI
gi	759077733	ref	XP_011348643.1	LTIIWRTTVM	gi	759077733	ref	XP_011348643.1	PLNSANPTI
gi	759077731	ref	XP_011348642.1	LTIIWRTTVM	gi	759077731	ref	XP_011348642.1	PLNSANPTI
gi	759077729	ref	XP_011348641.1	LTIIWRTTVM	gi	759077729	ref	XP_011348641.1	PLNSANPTI
gi	759077727	ref	XP_011348640.1	LTIIWRTTVM	gi	759077727	ref	XP_011348640.1	PLNSANPTI
gi	759077725	ref	XP_011348639.1	LTIIWRTTVM	gi	759077725	ref	XP_011348639.1	PLNSANPTI
gi	752886184	ref	XP_011260909.1	LTIIWRTTVM	gi	752886184	ref	XP_011260909.1	PLNSANPTI
gi	795082282	ref	XP_011877638.1	LTIIWRTTVM	gi	795082277	ref	XP_011877637.1	PLNSANPTI
gi	795082287	ref	XP_011877639.1	LTIIWRTTVM	gi	795082272	ref	XP_011877636.1	PLNSANPTI
gi	795082277	ref	XP_011877637.1	LTIIWRTTVM	gi	768420480	ref	XP_011551009.1	PLNSANPTI

Supplementary Figure S5. Phylogenetic tree of inotocin receptors. (A) Enlarged view early-diverging lineages of Arthropoda (Chelicerata, Myriapoda and Crustaceans) (enlarged view of dashed rectangle in B). The same colour is used for one species. Full species name is shown only for genus, which represent more than one species (*Daphnia* and *Ixodes*). Receptor sequence numbers are the same as in Supplementary Data S2. (B) Entire phylogenetic tree of inotocin receptors. Partial sequences shorter than 200 residues were excluded, giving a total of 93 receptors that were selected for analyses. Vertebrate and invertebrate oxytocin/vasopressin-like receptors (OT/AVPR) as well as vertebrate neuropeptide S receptor (NPSR)/invertebrate crustacean cardioactive peptide receptor (CCAPR) and adipokinetic hormone receptor (AKHR) were also included in the analyses. According to the study of Pitti and Manoj¹ the mouse gonadotropin-releasing hormone receptor (GnRHR) was used as outgroup. In most of the cases sequences of species within the same insect order are clustering together with high confidence values, i.e. Collembola (99% confidence value), Odonata (100%), Ephemeroptera (78%), Hemiptera (55%), Hymenoptera (83%), Embioptera (100%), Phasmatodea (100%), and Coleoptera (94%). However, the tree topology is not well-resolved regarding early diverging lineages, namely the Chelicerata, Myriapoda and Crustacean receptor sequences. Phylogeny supports lineage-specific duplication of inotocin receptor for some of the species (e.g. *Limulus polyphemus*). Some of similar species could share the same WGD or large scale duplication event (*Platynothrus peltifer* and *Achipteria coleoptrata*; *Ixodes scapularis* and *Ixodes ricinus*; possibly *Metaseiulus occidentalis* and *Varroa destructor* - only one inotocin receptor of *V. destructor* was analysed; the second one is a very short partial sequence and was not included into analyses), but phylogeny does not support the duplication event at the base of Chelicerata. Two inotocin receptors of *Strigamia maritima* are very different from each other, but unfortunately it is the only species of Myriapoda in our list having two copies of receptors, hence it would be too far-fetched to draw any conclusions based on this result.

(A)



(B)



Supplementary Figure S6. Alignment of selected inotocin-like receptors and precursors. *Arachnocampa luminosa*^{2,3} (New Zealand glowworm) is the only exception among numerous transcriptomes and genomes within Diptera, where both an inotocin-like receptor (A) and precursor (B) were identified. The sequences are shown as alignment in comparison to *Tribolium castaneum* and *Brachionus koreanus*. Two hypotheses could explain why *A. luminosa* stands out of this group: (i) the inotocin signalling system was re-acquired through horizontal (lateral) gene transfer; or (ii) there has been a sample contamination during the production of the *A. luminosa* datasets. Utilizing the phylogenetic tree of inotocin receptors, it is evident that *A. luminosa* is forming on a separate branch distinct from other insects receptors with a 100% confidence value (Supplementary Figure S5). Therefore we performed tblastn searches against the eukaryotes Transcriptome Shotgun Assembly database at NCBI and the first hits for both oxytocin-like peptide and receptor were from *Brachionus koreanus*, a planktonic microorganism, which belongs to the class Rotifera⁴. Although evolutionary distantly related to insects, the observed identity and similarity is between 81-91% for both peptide and receptor, but the identity and similarity to *Tribolium castaneum* sequences are only 27-37%. To verify if the putstive inotocin precursor and receptor are unique among other *A. luminosa* genes we performed a pairwise blast between *A. luminosa* and *B. koreanus* transcriptomes. We have found 11106 hits (out of 196675 contigs/transcripts; 5.6%) *A. luminosa* versus *B. koreanus* and 8455 hits (out of 28660 contigs/transcripts; 29.5%) *B. koreanus* versus *A. luminosa* with a very high bit score (>400). Moreover after checking the *A. luminosa* transcriptome for universal single copy genes on metazoa level we discovered that the glowworm transcriptome contains a very high number of duplications (82%), which has been illustrated by genome and transcriptome parameters of *A. luminosa* and *B. koreanus* transcriptomes on metazoa level (C). These findings strongly suggest a contamination of the *A. luminosa* sample; however horizontal gene transfer of large amounts of genetic information from some *Brachionus* species cannot be completely excluded because (i) the main cause for both to occur is the same: two species should meet each other physically (which could happen between *A. luminosa* and *Brachionus* species because the latter species is spread all over the world in fresh and semi-fresh water⁴); (ii) contamination of the samples especially of transcriptomes is a common problem in horizontal gene transfer studies⁵; (iii) the big transfers between species are reported before (entire *Wolbachia* genome >1 Mb was transferred to *Drosophila ananassae*⁶) as well as more and more evidence of horizontal gene transfer in insects accumulated during the last years⁷⁻¹⁰. Therefore the question remains open if the inotocin signalling system identified in *A. luminosa* is due to horizontal gene transfer from some *Brachionus* species (Rotifera), or it is an artefact due to sample contamination.

(A)

```

Tribolium      ---MY---TPKLSQMDISENS--TYLFDKHE--DRNNTDRDENLARVEVATLAIIFLVTV
Arachnocampa  -MTSYQENILPNYSEQDKFEN--SNVSLNNSNSVQQFQLNSSLLTKIEVFLLSLFLLTV
Brachionus     MTSSYQENMLLDYSEQKKSEELQNLSPNNSDSSEQFQINNKLTLQIEVFLLSCLFVLTV
               *      . * : . * : . : : : . : . . . * : : * * * * * * : : : : * *
Tribolium      IGNSTVLLALWTRR-----RYAGRKKLSRMFYFFILHLSIADLITAFLSVLPQLAWDI
Arachnocampa  IGNLIVILIIILLYRNMSPKRARWFKLNKNI SRMSFYIIHLSIADFNVAFMSILPQLIWRQ
Brachionus     IGNLTVILIIILLYRNMSKRRARWFKLNKNI SRMSFYIIHLSIADLNVAFMSILPQLIWRQ
               *** * : * : *      : . : * : * * * * * * : * * * : * * * * * *
Tribolium      TYRFYGGFLLCKVVKYQTLGPYLSSVLMATAIDRHQAICYPLTYCSWTSRRSKVMVYL
Arachnocampa  SVVFNHSHFLCKFVAFSQVFSVYASTFLLIVMAYDRFKCICWPIKSCSWNRRHALVPVFF
Brachionus     SVVFNHSHFLCKFVAFSQVFSVYASTFLLIVMAYDRFKCICWPIKSCSWNCRHALIGIFV
               : * . : * * * * * : * : . : * * : * : * : * * * * * * * * * * : : :
Tribolium      AWWASLAFICIPQLTIFTYTSVGEDEYDC---WATFQEPWGRAYVTWYSISVFMVPLVVL
Arachnocampa  SWLIAAVVSSPQLFLFKIQHMSVQHYTVETCSVKWLSKKEGLYLLPHMSTQFLIPLFVL
Brachionus     AWLIAATISSPQLFLFKIQHMNAHVYTVETCSVKWMSKRHEGLYLLPHMSTHFLIIPFVL
               : * : . . . * * * * * : . : *      . . . : . : * : : : * : * : * *
Tribolium      IFTYTSICIEIWQSSSESS--LR-PRSSQK-----
Arachnocampa  TFLYSRIFMTVSNIKQKHASIRFERESSKTATEINQLNRENSLNTQNGLITEVKHDSDN
Brachionus     TYLYSRIFLTVSRNISRKHASVRFERESSKTGTEINQLNRENSLNTQNGLITEIKNESEN
               : * : * : : : . . . : * * * * *
Tribolium      -----SA-----

```



```

Arachnocampa      SIFRDKKFGILWWIRSRFNKIRHKILFTSTKKRGKNIKFGKTGNFLMNDQTMPKEYEMR
Brachionus        SIFRDKKKTGLIILWLRSHFNKIRHKILYLTSTKSGKNIKFRSQNFSLNN-SLPKEYEMK
:
Tribolium         -----P---GKRTPLISRKINTVKQTIAVI
Arachnocampa     LMLKRKETSLSDS-EKYSMRLDKNSVYKSPKSNFPPIRQTFSGKALTRSKIKTLKLTITVV
Brachionus       LMLKKNDPLESNDNRYSMRDLKNSVYKSPKKNFPPIRQTFGKALTRSKIKTLKLTITVV
:
Tribolium         VMYIACSTPFILAQWLWDP-----QSPFIDGPVF--VILTLLYSLNSCVNPWIYLA
Arachnocampa     ITYVMCSLPFYVCTFIHFLGLSAHNHSSLFTKTLVYITISTNMLFQLNSCANPFIYLPF
Brachionus       ITYVMCSLPFYVCTFIHFLGLSAHNHSLFTKILVFATISTNMLFQLNSC-----
:
Tribolium         NRELPRLLLRHYTASSKNYRSATGGNSASNSGDAQSTSLRPFRRWSLCNSARSNKYPTR
Arachnocampa     NGNICLAKRLKTKV-----
Brachionus       -----

Tribolium         VPHRPYVAQYNARRWIVTTTT
Arachnocampa     -----
Brachionus       -----

```

	Identity ^a %				Similarity ^b %		
Tribolium	100			Tribolium	100		
Arachnocampa	27.5	100		Arachnocampa	28.5	100	
Brachionus	24.3	81.3	100	Brachionus	26.2	85.2	100
	Tribolium	Arachnocampa	Brachionus		Tribolium	Arachnocampa	Brachionus

^acalculated using BLOSUM62 matrix using alignment above at <http://imed.med.ucm.es/Tools/sias.html>

(B)

mature peptide

```

Tribolium         -----MSTIITSIILLVLSSELVSGCLITNCPGGKRSKFAISENAVKPCVSC
Arachnocampa     MNENFLMMNLNDKKNLILFIVINLNVINACYITNCPWGGKRSQPFLDSENAHQCRKC
Brachionus       MNENNIMNLSDRKNLILFIVINLNVINACYITNCPWGGKRSQPFLDFENAHQCRKC
:
Tribolium         GPGQSGQCFGPSICCGP-FGCLVGTPELRCQREGFFHEREPCAGS-APCRKNTGRCAF
Arachnocampa     ASG-LGMCFGPRIICCGPDMGCLIDTKETSVCQLEDLKS-VPCQPYGKICDKVEFGRCAT
Brachionus       ASG-LGMCFGPKICCGPDMGCLVDTKESSVCQLEDLKS-VPCQPYGKICDKVEYGRCAT
:
Tribolium         DGICCSQDSCHADKSCASDDKSPIDLTYTLINQAEIAGDK-----
Arachnocampa     SNLCCNPEHCLEDSTCVSEENDYSEYKEIDTKLLKALKRLISKRRQKNEENYKSHNI-DN
Brachionus       SNLCCNPEHCLEDSTCASDDIDYSEYKEIDAKVLKAIKRLISKRRERNEKYDEGHISDK
:
Tribolium         -----
Arachnocampa     YQS--
Brachionus       YQSNF

```

	Identity ^a %				Similarity ^a %		
Tribolium	100			Tribolium	100		
Arachnocampa	34.9	100		Arachnocampa	37.3	100	
Brachionus	37.7	84.4	100	Brachionus	26.2	90.8	100
	Tribolium	Arachnocampa	Brachionus		Tribolium	Arachnocampa	Brachionus

^acalculated using BLOSUM62 matrix using alignment above at <http://imed.med.ucm.es/Tools/sias.html>

(C)

File	Complete Single-copy BUSCOs	Complete Duplicated BUSCO	Fragmented BUSCOs	Missing BUSCOs	Total BUSCO groups searched
short_summary_arachnocampa_luminosa_met	67%	38%	5.2%	27%	843
short_summary_arachnocampa_luminosa_trans_met	98%	82%	1.0%	0.3%	843
short_summary_brachionus_koreanus_met	57%	10%	10%	32%	843
short_summary_brachionus_koreanus_trans_met	70%	15%	13%	16%	843

Supplementary Data S1. Putative inotocin precursors. Sequences of 144 novel inotocin precursor sequences from Arthropoda are shown. Inotocin-like peptides are highlighted in yellow. (A) 75 newly annotated precursor sequences containing the inotocin-like peptide domain. (B) 35 deposited inotocin precursor sequences derived from NCBI containing the inotocin-like peptide domain. (C) 23 newly annotated inotocin precursor sequences containing the neurophysin domain but lacking the inotocin-like peptide domain (the first sequence of *Ceratosolen solmsi marchali* is from NCBI). (D) 11 non-annotated inotocin precursor sequences presented as BLAST search results. Sequences from (A) and (B) were used to prepare the alignment illustrated in Supplementary Figure S1.

(A)

```
>Symphylella_vulgaris
MSSGKSDITNAFVLLTFVSTVSACFITNCPIGGKRSSGHSLSSSVALRQCSPCGPGGAGRCFGKSACCVPGMGCFLGPAHTATCRLEHSYPVPCDNGTPACG
ENGNGRCAVEGLCCTGDGCFYEDTCRDSLLTSSLHHSGSTLEDETTQ-
>Strigamia_maritima
MKSTHFVNIIFYSVFIFIMADGCYITNCPPGGKRSSGNEKSGRGRVQCTPCGPGGIGRCYGPDICCGANVGCVFVTRESAICRLENLYSLPCQNEGRACGTD
GTCSADGFCCSTDQCKADESCRGVVHTNLQRVLDGEIDLNDVMGPQR
>Litopenaeus_vannamei
MQISAVVAMALLLGSGTACFITNCPPGGKRSSSPAQLGSVRTCAQCGPGLQGRCMGPDICCGPEIGCYMGTTREAFLCRSENLVPVTCSNDDLKACGRQREG
RCASSGVCCEVKECFDINCVIEGVDRHRYSLDLTLEAQWRI-
>Lepeophtheirus_salmonis
MAFGYPLITLLLIFQIANACFITNCPVGGGKKGSGSTNLGFLNSSFQYKQCSSCGPNNTGRCFGPRLCCSSEFGCFVYSNDIAKNPCQTEAYDPVPCQNNV
KCSSSVLKNGQCVFDNYCNSSGTCRFVEEELICSVSDDKKNYEKEKELVDDLQKNMIYIRRQAYLGNGPRLQQLNINDLEQ-
>Calanus1_finmarchicus
MITSWKILDPRIRRSWSFLILLAQTMSASHGCFISNCPVSGKKRSVGEEQMVSFQAREEVLACPSNPAGLCYSPGLCCVQGGCYADKGCLPQMEESRENR
VEPRLNKRDLRFLYGWAPAHEKMFGQTGFSIPCIGPYCNGNEKMIRKEKQSQEKKSDDKVLDGSSNYDSLVYNENLSNQRCNWMDLYLAR
>Caligus_rogercresseyi
MALCLLQVTESCFITNCPVGSGRKRADPGLFSPKNRRQLDECSPCGPSNEGRCYGNLCCGSTFGCFVYAKSLQHQNPCLTEARLPPCRNKGSGCSGILE
NGQCVFFENYCCSPSGTCRFVDESICSNSTVPQLGSDDFMEDFRRLFLARELHSL
>Tigriopus_californicus
MQITFDRRCFIVLGLLSLLKAVSVNSCFITNCPSGGKRSELLTVASRKCPCGPGLMGQCFGPSMCCGQYIGCHLNTPDTQVCKTENSNPIPCDNDVPRC
QSVRRGFCATNGFCNDQGECTPEEKVENLSDFPSPFILRRHLSSASLASRPTVEKAMITIPQPNKAYQEALNLMQIIPKSNALNKYLSRHGDVK
>Speleonectes_cf_tumulensis
MHLRPMDVLLSALCVLHVAGISTACFILDCPLMIRNRTVRTLKSSTRQCTSCGPDDLGRCYSPNICCGPESAATSAPKNRRLPVRELLPCSL-
>Sminthurus_viridis
MINLNCGICLFLITLSVVTGCFITNCPPGGKRSGIERKTRQCEQCGPPGAGRCYGPSICCSPELGCLIATPETYSCOLENRHTTLCQNPGATCAGPNGDI
SGGQCGAEGICCNSETCTMDETCHDEASVTRESVAKLSGLYHHRYPLDVVFQRFVDGQHSQHHRLPARLPLPTQSSSSSNDY-
>Anurida_maritima
MRKYHTSIICLVWLISVSAAFGCFITNCPPGGKRSGPLSTQARQCESCGPEGSGRCYGNICCSPSGCLIGTPETVACRSEARFSTPCLNPGISCSGSG
SLSIKGQCTGDGICCSSETCHDENCWERSMTSGTGSQEFNQDLPLREDRFLIPLPATHEKFRSFPISQIIRVGRRKNQFEDLRNHLLHRPQMDFQPPIS
STESLYP-
>Pogonognathellus_sp
MIQFVTYNLWLGLLVSFVAASGCFITNCPPGGKRSGTALTVRQCERCGPPGMGRCFGPQICCSPEFGCFFSTAETFVCLENRFPTPCHNPGSSCSGN
GDTGLINGQCG
>Folsomia_candida
MKTSLLFAFGIVMVESLLVSGCFITNCPPGGKRSGADTKIRQCEQCGPPGMNGLCYGPHICCSSELGCLFGTSETLTCFQENLMYNTPQNPGESCSGNDA
TNPINGQCATLGVCCSSDCTTIDDNCHKKDEQQVNSGHSRSTVAMDGSHTKEHATTMFQNPLDRWIPRRFGLGRPTQRKHVRIGVKPDAQILAPENSLMD
RLVIFPDTSGRISSDEY-
>Occasjapyx_japonicus
MSSPVRIHPRLLALACVFCISSACFITNCPPGGKRSQAHYKPQASRQCAVCGPNGQGRCFGPELCCGPEIGCYMRTRESSCRAENLFPVQCENRARPCG
SERSGKCAAVGICCTEDSCTSDQTCRASPGKEAVAAVLPRGPSRPQLPSDLVSFLEEVDNMAPASGSEV-
>Meinertellus_cundinamarcensis
MKSSMSTPAALFALLFVSITSSCFITNCPPGGKRAMGAPGRVQRQCPSCGPHRSGRCFGPDLCCGEGFCHLGRDPVCRGEMSAPGLCTNPGRPCGVG
KCAAQGVCCSETACALDSMCLDSWPSRNVVQMNSGLASVLENMLEEVPSENGDDK-
>Machilis_hrabei
MSADMTNSASSTFALFTLLLVGCVTSCFITNCPPGGKRGLSGPGRGEPRQCPSCGPHRSGRCFGPDLCCGDFGCRLGARDASCREMSAPGLCINQGRP
CGVGVCAAQGVCCSETSCALDASCMDSWSPRQLVPVNNGLSSVLENMLEDIPMESGDDRR-
>Tricholepidion_gertschi
MVARKNPQTVVICLMAAMSAATACFITNCPPGGKRSMGQVGTHATRECTSCGPAKLGRCYGAICCGPQIGCLVGTREAAVCQTENFYVPPCANRGGQCGG
ESGRCAATGVCCTEESCSIDPSCHVTPQETILTPVSRQMYPINSAMNNYLEAVDALPSHVILENRR-
>Eurylophella_sp
MVHRRGATLSAMLIVHVSACFITNCPPGGKRSSITTVNARQCSRCGPGLSGRCFGARICCDSRRGCMLASSTEPSLLPCLAESMQTTPCRNRAASCGQS
GAGQCASQGICCLQDSCHADVKCHENYD
>Apachyus
MSFSLRFFAIFLLLCLGTGCLITNCPKGKRTSITVSFILKF
>Gryllotalpa_sp
MKVYLLVFISLIVLNTACMINCPRGKRAMKINEISSIRSCARCGLNNAGHCYGPDICCAPELGCLIATPETVPCQEESSQSPDPCIDTDLGPACHNGK
HCGANNICTQDSCYSDQTCFGFPVE
>Teleogryllus_commodus
MAQFKLYSNIIVLMMILTFSCACMINCPRGKRSAMENNEILPIRNCARCGPNNTGHCYGPSTCCAEELGCLMGGPEAKPCEAEALSPDPCVEPALGPRC
FGGQGFCATSTLCTQVSCHTDPSCQFAVAGHKSVGATDLALPHRSYVYSLLNALAKNQDHNPQNVE-
>Locusta_migratoria_manilensis
```

MKPQLAVLLALVVSLAAA **CLITNCPRG**GKRASLQHRCAACGPGQGVCLGPHICCGPRMGCRLASADADSAACRAAPPCLDSEMERCAAGRGRCSAPGVC
CSQDSCHIDPSCVADTTEPADRYALDIFAVNDGDRDDMRI-
>Galloisiana_yuasai
MRLKQCLRMLALLVAVVGISSA **CLITNCPKG**GKRALNHSKDSVRQCPRCGPAKLGHYGPAAICCATQFGCLVATADTAICQGESLYPEPCANTMPASSCRG
EAGKCAANGICTSESCHVDMSCLRTSRGEDDVIQFPDLSSDAKGVFSLFNLGSYEPDHQAYRLPSNVERD-
>Haploemia_palau
MINFRFARFILLITLAAVCTA **CLITNCPIG**GKRSLHLGTESVRQCPRCGPAKLGHCFGPTICCGHEIGCLINTPDLVCLKEHLSPPDCVGPATATNCGNRK
GKCAADGVCCTPESCEID
>Aposthonia_japonica
MVNFRFARFILLITLAVVCTG **CLITNCPKG**GKRSLAHGSESLRQCPRCGPAKLGHCFGPTICCGHEIGCLINTPDLVCLKEHLSPPDCVGPASASNCGNRK
GKCAADSI CCTPDSCEIDASCRFGSPQHFRNVGIYPQYVE
>Cryptocercus_wrighti
QLGTLATLAILLIGVCTA **CLITNCPKG**GKRAGSHSQDSHPIRQVFLGYLTTLTYQLLSL
>Zootheropsis_nevadensis
MKMQLGTATLLAVFISLCTA **CLITNCPKG**GKRAGTHSQELHTIRQCARGPAKLGHYGPAAICCGPQIGCLVATPDTARCLSEAASVPCTAPTGAQCCEG
KFAGRCTANGVCCTHE SCHIDITCQLTTSDAPELIDVSADQTNPLYSLYSSYQENPGLGLSE-
>Gynaikothrips_ficorum
MICVKIPSI FLLLAMTSA **CLITNCPRG**GKRNGARPPTKGSIEELPFCTLCGPPGLGGLCFGPTMCCSPTGGCELGEPHVASCLGVHTVPPCLRLPPQSM
LNGPYSAPSQTRATSLVTTTCGSGICAANGLCCTSDWCRADDRCLSSASQSNLVI PDHNL PANTRQEPQQA EFNWDHWS-
>Halyomorpha_halys
MYRALLFLTALCLVQSC **CLITNCPRG**GKRSLRPLGRDPDCRRCGPLEGRVCGKTVCCGPRIGCLIGTPAVLSQCAA EPMQLRGGQRCSIGVCLADGVCCSP
DGCKMMSCEVEQSV DVC SLAEQQVY-
>Diaphorina_citri
MYAMISRLVVCLVGVYFFGSTW **CLINNCPTG**GKR SALMALEERRQSHQKRAKLWNRNI ISCNAWGAEGVCGPLCCDPSRSEGDGPKSGVDYKTCGS
SREVMEEYALCLSKGLACDLNLTLCNMYAIKVPTEVKLQLHQ-
>Liposcelis_bostrychophila
MNTFQFVVLYIFVNSVNS **CLITNCPRG**GKRGDSENNLIEAPRSDIKTCTPCGPNNQVGCIGRDI CCGKHLGCLISSPSTKICRRVREFPESCLSSFNPCGN
GGLCVARNVCCFKNLCRIDDTCTIPYVDLGYRLGTSDILNRLSSYSVDYPLELPSNMPIGSTSLDEVWGSKEDSIVPNYNFKIEAS-
>Menopon_gallinae
MYNIFQFQLRLGLLVATFGLVVS **CLITNCPRG**GKRGDNSLDKTSYSPDTNYCIPCGPDDQVCLGKNVCCSREGCTTRSRYTDP CRSIQNTRISCLSEVNV
QTCGDKGRCKAKFICCSRQCVMDLSCKSMPPAKYRDVNE
>Cotesia_vestalis
MMHKFLLVFFFITSSFA **CLITNCPRG**GKRGESPLLSMPSLIKECSSCGPDQGCQFGPHICCGASIGCYIRSPETYKCRKESLHSHPCVSGFAMCRDNTAR
CAANGICCSQESCFDSSCKIGDEFSLDRKIDQEF SRLIGENDQMIN-
>Nasonia_giraulti
MSKVIIVLTTLVLSYSG **CLITNCPRG**GKRGDPTFLENIARECPACGREGQRCFGPHICCSPSMGCLIGTPETLRCRKESSLYRSPCVAGFAMCQNGSGRC
AANGICCSQESCFIDSACKLVDETGNDRI GA EFGAFLEENAGTNEHIL-
>Chrysis_viridula
MQYKMLTKLILFASMFVYVYG **CLITNCPRG**GKRGD SAVTLDHLARECPSCGNRLGQC FGFPHICCGPSIGCFIGTPETYKCRKESLFSRSPCVAGYAMCRGN
SARCAANGICCSQETCHMDSTCRISD VDRDRKEEGVDVA AVLSDNELSADSVQ-
>Polistes_metricus
MTKILIFTSFIFISSA **CLITNCPRG**GKRGDIEVPESPIRECLPGPSQLGQC FGFPHICCGPTFGCHIGTSQTQKCRKEQFDSSPCMAGFAMCNGKGRCG
AGGICCSQDSCFIDPSCRFSTVDSPPFRSIDS DLKAIASEIEILKEAK-
>Mischoyctarus_flavitaris
MTKQILVITSFILISSA **CLITNCPRG**GKRVDNKVPLVTTTEYPVKDCISCGPNQGQC FGSNICC GPTFGCHMGTSYTKCRKEFS DQISCLSGFAMCSG
NVGRCAAIGICCSQESCFLDPICRLSDNLPVGRKFNT
>Chyphotes_mellipes
MAKELFVFAALLVVAYG **CLITNCPRG**GKRGGGKHGEVVP AFEDVRVTR ECPSCGNRLGRFCGPRICCGPTIGCFIGTPETYGCRGEGSPFSKPCVAGYAM
CRRNTARCAASGICCSQESCHIDASCRLSETSDGGGGNGHERRFSDLSAILSENVGTSVEMVR-
>Pseudomasaris_vespoides
MAKELIVLIAIVVLASA **CLITNCPRG**GKRGDIAALESVVRECPACGNRSQC FGFPHICCGRTIGCYIGTPETYRKRKESLFSRSPCIAGYAMCRGNTARCA
ANGICCSQESCFIDNTCRIPDIMAKDQKIDSDINMIFGENEISNELTQ-
>Brachycistis_timberlakei
MLKKFILIAILISLSYSG **CLITNCPRG**GKRGEAVVSLETIARECPSCGNRAGQC FGFPHICCGPTIGCFIGTPETYRKRKESLFSRSPCIAGYAMCRGNTAR
AANGICCSQESCSMDAMCKIPDALRHDRKFDSDVSSILSEISEISNEII
>Crioscobia_alcione
YGC **CLITNCPRG**GKRGEIAPLLESVARECPSCGNHSGQC FGFPHICCGPNIGCFIRTPETYRKRKESLFS
>Telenomus_podisi
MIAWVIVLVSIFSLSSA **CLITNCPRG**GKRADQSLMLMETSIRECTSGRDGSGRCFGPYICCGSTIGCFIGTPETYKCRKESLYSKPCIAGFAMCRGNKGR
CAANGICCSQEACYAD
>Corydalus_cornutus
MYPVVKYFVLVIVLVSVMIDS **CLITNCPRG**GKRNGSDRI SNEQFIKQCISCGPQRSQC FGFPSICCGSFGCLVGT PETVR CARDGGFHEPEPCIAGQASCR
GDSGRCAADGICCTQESCHTDSSCAFDEERHDSHNGRPAIPIESIFSVLSPYRS-
>Aleochara_curtula
MFSSKCLLIVGLACVVLQAVDG **CLITNCPRG**GKRSGKYLDPNNIKPCIACGPGHSGQC FGFDPICCGPFGCLLGTHTETARCRDGNFLEPEPCIAGNASCR
RNSGRCAAEGICCSQ
>Meloe_violaceus
ATNKFLLVLI VLTIFTNYFING **CLITNCPRG**GKRGNTRYLQKDTQIKQCINCGPNNGQC FGPQICCGPFGCLFNTIDTVRCQKDNFHFQHEPEPCIAGFMNC
HHYNGRCATDGI CCNQDSCHIDKTC SITTTFIGFIENEKTRNFLETSPADLYNFINYQSELNSE-
>Priaema_serrata
AFFVLNSFLADS **CLITNCPRG**GKRSRNYEENIKQCISCGPAHSGQC FGFPNICCGLFGCLIGTSETIR CQREGFFHEREPCIAGNAFCRKKHRTMCQRGHML
HARLLPHRQNYAHLTTNKQN-
>Gyrinus_marinus
ALLDICDS **CLITNCPRG**GKRSGRSQHENNIKQCISCGPGRSGQC FGSNICC GPFGLMGTSDTIRCHREGYFQDSEPC
>Arachnocampa_luminosa
MNLNDKKNLKI LFLVIVLNLVINA **CYITNCPWG**GKR SQPFLDSENAHQCRK CASGLGMCFGPRICCGPDMGCLIDTKETSVCQLEDLKS NVPCQPYGKI
CDKVEFGRCATSNLCCNPEHCELDSTCVSEENDYSEDYKEIDTKLLKALKRLISKKRQKNENYKSHNIDNYQS-

>**Pseudomallada prasinus**
MNNNSLKATIVTFVIFTTLVHS**CLITNCPRG**GKRSNLLDSKISTDSIKP

>**Atelura formicarial**
ACFITNCPGGGKRSMGQMLHVNKQCTSCGPARTGRCYGPAICCGPRFGCLVGRDTRAVCQTFENFTVPVPCGNRGPSCGESGRCAANGVCTEETCTIDPSC
RISNEDISSSRQMFPIITNSVSMYLEELNDDLPARVGSDDR-

>**Atelura formicaria2**
SLSKGILSVTIFFLAVISVTTA**CFITNCPGG**GKRSMGQMLHANKQCTSCGPARGRCYGPAICCGPRFGCLVGRDTRAVCQ

>**Solenopsis invicta**
MLKELVVLASLI FLSYA**CLITNCPRG**GKRSDIAPSLGTVERECPSCGPNRLGQCFGPHICCGPSIGCFIGTPETYRCRKEISLYTRPCIAGYAMCHGNTARC
ASNGICCSQESCHMDTSCRISDVVGNDRKLDANLNVIIFPDNEVSSDILQ-

>**Ixodes ricinus**
MALSHMLLLAVVGGTSA**CFITNCPGG**GKRSSESPARLVSSQFRSSLTVSWCSLLGVDFQRMSFYRMPDY

>**Scolopendra subspinipes1**
HWLLFFYYIGMTSS**CFITNCPGG**GKRSLEGEHKRTLQCTACGPGSQGRFCGPDLCCEFFGCGYKLTRESAICRFENLSPICDNDVLSGPDGAKCAADGL
CCSSDQCKMEERCR

>**Scolopendra subspinipes2**
MRSSTCHWILYLSLVGLVSA**CYIINCIDNDG**RKRSIDHQKKAIRQCMSCGPGMKGRFCGPDLCCEFFGCGYKLTRESAICRFENLSPICDNDVLSGPDGAKCAADGL
NCAVDGLCCNTSQCKRDERC

>**Lithobius forficatus**
MASHAAQSSVFLVLLCVFHITLA**CFITNCPGG**GKRSLEGDQKGTTRQCTACGPGGLGHCFCGPNLCCGPQIGCFLHTRGKCHLPF-

>**Homarus americanus**
MQLGVVVVMTVVVGGSTTA**CFITNCPGG**GKRSGPATAQLGRTRTCTACGPGLOGRCLGPEICCVLIGICFLGTREARMCHAENLVPTCANRDLKSCGRMQE
GRCAAAGLCCTEMKCEFDSSCTVEGREERVGKQRAERQHLTFLSSLPEQWNL-

>**Calanus finmarchicus3**
MITSLKILDPSIRRSWRFLMILLAHTIIPDSHG**CFISNCPVS**GKKRSVGEQQLVSFQAREEVLACPSNPAGLCYSPGLCCIQGACYADM

>**Dermatophagoides farina**
MFRRESFSMMKIILVLCIWIICLFNDVRCFITNCPRAGKRSIMTESNLGNSHKKKIKIKCTRCGSPLSGRCYGPNICCSPLTGCNVGGFTAARCSLEAYH
PILCTNPGTVCGPNGKGVCALNATCCTNGKYFICFFYCKKN

>**Onthophagus taurus**
MVKLIIFTLILCIIQDQLSHG**CLITNCPRG**GKRNGRINSLDTNLIKQICISGPARSGQCFGPGICCGPFGLIGTPDTLCKLKEGQFHENEPCIAGNSSCR
NSGRCASEGICCTQGNF-

>**Nicrophorus vespilloides**
MHSPPSTMFILKSSALLVLAVVFLGLD**CLITNCPRG**GKRAMQDNTIQICITCGPGRSGQCFGPGICCGPFGLIGTQETVKCQREGFFHGREPCIAGS
APCRKNTGRCAAELCCSQGIIQLLLLLHLRLTHRLHHPMMI-

>**Oryctes borbonicus**
MNSLLLIQVFCIAGDQLIEG**CLITNCPRG**GKRSKGMSHLAAANQCVSCGPGHTGQCFGPNICCGPFGLVGTAEHLRCQKDGFFHEAEPCIAGNSPCCRNT
GRCATDGVCCSQGIRYIDS

>**Dendroctonus ponderosae**
MTRSSSSKIAKMISQILMFILLSNILVSG**CLITNCPRG**GKRSKGKYLSTSNNIKQVIQFSLIQICICPCGPGGAGQCFGSPICCGPFGLIGTQETVKCQREGFFHGREPCIAGS
EGMFHESEPCIAGNNS

>**Leptinotarsa decemlineata1**
MVRSVPLTIIYLFIFVMYVES**CLITNCPRG**GKRGGEFSTSESNIKTVSINLNMYKHILQCISCGPGHTGKCFGPNICCGPFGLIGTQETVKCQREGFFHGREPCIAGS
TEPCIAGFSTCRKNTGRCAAEEKICCTQGIWTFVFLVSN-

>**Leptinotarsa decemlineata2**
MSKTVSLFTFLVSVFVIFVES**CLITNCPIG**GKRSKGKFLSTESNIKQICISCGPGHTGQCFGPNICCGPFGLIGTQETVKCQREGFFHGREPCIAGS
TGRCATENICCTQGIKIRSYT-

>**Hypothenemus hampei**
MVKRNQLICTAGSNSTKLSIFMACLITVSG**CLITNCPRG**GKRSKGKFLAVVLFKICPCGPGGTGQCFGPKICCGPFGLIGTQETVKCQREGFFHGREPCIAGS
TAGTMNCRKNTGRCATNGICCSQKRTVLVNSSSVYN-

>**Anoplophora glabripennis**
MFKNILLVSLVVFGEIFVNC**CLITNCPRG**GKRSKGKFGALEANIKFQCVSCGPGHSGQCFGSPICCGPFGLIGTQETVKCQREGFFHGREPCIAGS
RKNTRCAIDGICCSQGNNSGFLKLNFLSLQILVMSTNNARWTKAGFFPITLWEWICII-

>**Agrilus planipennis**
MYTNVCLVFVIVLVCYSLVFG**CLITNCPRG**GRKRNGKMEGDIQPVCTSCGPGLTQCFGPNICCGPFGLIGTQETVKCQREGFFHGREPCIAGS
GRCATQGVCCNQKCFSTFYLLLNVLDISPYQGIIRKVVLLNKNLTVNGTLNIE

>**Homalodisca vitripennis**
MRGAVVLTVCSLATA**CLITNCPRG**GKRSQSTIDNTLGTIVSLVACLRCGPGQLGRCLGPAVCCGPRGLVATPGIVRQCAGAAEGSPHKGKPCITPSGL
GVCATDGVCCNSGGLYFSPQIRHIYRNFESISQY

>**Varroa destructor**
MKLHVLVLANIVGLSLT**CFITNCPIG**GKRSDTGFLVQFSSDFRKCPCGPGSTGQCFGPNICCNSESLIDAGDSPHLRSCKREALKLPCTNTGMRCGS
ENKGHCALNRFCCTS

>**Ephemera danica**
MHRKYEMATKVYLTALIIVQVTTA**CFITNCPGG**GKRSSAVVSETQPKSVIRQFPITCSSYFVQCARGPGLTGRFCGPRICCESSRGCLLGSPLVFMFL
PCLVESLQPTPCRNASNCGTDELCAAPGICCSQGK

>**Ladona fulva**
MYSRQMSMDQRQWLLVAVIFALLGLTSA**CFITNCPGG**GKRSVAVFGRIPLRQVMVSSVLSFKCSRFCGGRFCGPAICCSLKTGCILAEKSNLPLLRP
CAIEAGLPGACISGSKRCGNSGGRCASDGICCNDRKRN

>**Catajapyx aquilonaris**
MSPFRVHQTLAVACIFCITSA**CFITNCPGG**GKRSQSHYKPAIRQVSSAQCAVCGPNGQGRFCGPELCCGPEIGCYLRTREASACRAENLFPVQCENKAR
PCGSERSGKCAAMGLCCTEADSDTSACRGAPEVVAASRGQRQQLPSDLVSLFEEVVENIAPASAPEV

>**Blattella germanica**
MQLALVFLVFCVACRA**CLITNCPRG**GKRAGVQSQDSTVSIQCARCGPAKLGHCYGPAICCGPQIGCLIAETPETTRCLSEAAASPSPTTPSGAPCGSGKNA
GRCAANGVCTHESCHIDVSHPSATDIAIGNTDQLNSFYNLVNISSAYQENP

>**Pachypsylla venusta**
MIPKIFFFLIFLFLNFSFS**CLISNCPKG**GKRFDKFKPQNKKEIFDKSKVSTLYIGD

>**Triops cancriformis**
IHSAP**CFITNCPGG**GKRSFPMSSSQHFL

>**Brachionus_koreanus** gb|GBXV01012066.1| TSA: Brachionus sp. 'koreanus' Rotifer_07959 transcribed RNA sequence
MNENNIMNLSDRKNLIILFILIVINLNVINA**CYITNCPWG**GKRSQPFLLDFENAHQCRKASGLMCFGPKICCGPDMGCLVDTKESSVCQLEDLKSINVPC
QPYGKICDKVEYGRCATSNLCCNPEHCLEDSTCASDDIDYSEYKEIDAKVLKAIKRLISKRRERNEKYDEGHISDKYQSNF

(B)

>**Camponotus_floridanus** Gruber, C. W. & Muttenthaler, M. PLoS One 7, e32559 (2012)
MLKQLVICASLIFLSHA**CLIVNCPRG**GKRSDIASFLKTVTRECPTCGPNHMQCFGPRICCGPNIGCFIGTPETYRCRKEISLYTKPCIAGYAMCRGNTARC
AANGICCSQ
>**Limulus_polyphemus** gi|926609726|ref|XP_013784878.1| PREDICTED: conopressin/neurophysin-like [Limulus polyphemus]
MHWTSFIMILGFCLAVTIK**CFITNCPGG**GKRSIGTFATHYTRECQCGPGGMGQCQGPDIICCSDFGCF
IKTRESVICRYENLQVIPCNNKKGICETVPHGYCAAPGICCSAIQCAVDDCEPTGVLDKGVAYKYDHLRF
VLLPWNMNGKLPD
>**Ixodes_scapularis** gi|506953581|gb|AGM20426.1| inotocin preproprotein [Ixodes scapularis]
MALSHMLLLAVVGGTSA**CFITNCPGG**GKRSSESPARLCPRCPAGRGVCYSADVCCAGSMCILNDALAT
LSCRAEALHGVAHVPGKRCGTDRCAIRGYCCGPDGCTKDSSCSGGVPTDQFGSAVDILEYGMSE
>**Metaseiulus_occidentalis** gi|391348425|ref|XP_003748448.1| PREDICTED: isotocin-neurophysin IT 1-like
[Metaseiulus occidentalis]
MKLVALYFLSVSSLSWA**CFITNCPGG**GKRSAAFGQLYSNEYRRCPPCGPSSGQCFGPGICCTPDYCVL
DPVGLSTCKSEALKMTPCNINRPRCGAENKGYCALNRLCCTSDSCTLDESSAKDRDILRESMLN
>**Tetranychus_urticae** gi|1005954275|ref|XP_015785540.1| PREDICTED: neurophysin 1-like [Tetranychus urticae]
MLASFIILLTFILNFHSSQA**CFITNCPGG**GKRSHGVDVDMRECLRCGPDNRGHCVSPNICCGTEFGCLINN
HYSRPCRAENLIPTPCKIPGKLCSSGEGVCTSNIGCCNSDGCNDSTCENDKLSNMQRIFTS
>**Nilaparvata_lugens** gi|411530692|gb|AFW19795.1| arginine vasopressin-like peptide [Nilaparvata lugens]
MKNTTISIGIMLFYAVGLAAG**CLITNCPRG**GKRGHLHSYMKKLAEEKMALAQVPLQCARCGPEGEGYCMGSP
ICCGPQLGCLLASPATLNQCAGSVLPQSPNSPAPTCTYMPDGYGVCTDGVCCNSESCRIDPTCEVDPPH
NVCNVWTEPKNMAL
>**Dinoponera_quadriceps** gi|951576040|ref|XP_014485987.1| PREDICTED: neurophysin 1-like [Dinoponera quadriceps]
MLRELVVLASLIFLSYA**CLITNCPHG**GKRGDIAPSLGVVTRCPLCGPNHLGQCFGPHICCGPSIGCFIG
TPETYRCRKEISLYARPCIAGYAMCRGNTARCATNGICCSQESCHMDTSCRISDVVGNDRKMDTDLNVILS
SNEVSHEILQ
>**Monomorium_pharaonis** gi|826427284|ref|XP_012527594.1| PREDICTED: neurophysin 1-like [Monomorium pharaonis]
MLKEFVVAFASLIFFSYGLITNCPRGGKRGDIVPSLGTVARECSSCGPNRLGQCFGPHICCGPSIGCFIG
TPETYRCRKEISLYTRPCIAGYAMCRGNTARCALNGICCSQESCHMDTSCRISNVVGNQKLDLNLNVILS
GNEISSEIPQ
>**Vollenhovia_emeryi** gi|795056828|ref|XP_011871987.1| PREDICTED: neurophysin 1-like [Vollenhovia emeryi]
MLKEFVIFASLIFLSYA**CLITNCPHG**GKRGDIAPSLGTVVRECPSCGPNRLGQCFGPHYICCGPSIGCFIG
TPETYRCRKEISLYTRPCVAGYAMCRGNTARCASSGICCSQESCHMDTSCRIPDVVGNDRKLDANLNVILP
GSEVSSEILQ
>**Linepithema_humile** gi|815804199|ref|XP_012222809.1| PREDICTED: neurophysin 1-like [Linepithema humile]
MLKELIVFANLILLSYA**CLITNCPHG**GKRGDIAPLETIARECPSCGPNHLGQCFGPHICCGPSIGCFIG
TPETYRCRKEISLYTRPCIAGYAMCRGNTARCATNGICCSQESCHMDTSCRISNIVDNRKIDTDLNMIIPG
NEVSSEILQ
>**Atta_cephalotes** gi|801367097|ref|XP_012061245.1| PREDICTED: neurophysin 1-like [Atta cephalotes]
MLKELIVFASLIFLSYA**CLITNCPHG**GKRSVAVSLRTVIRECPSCGPNHLGQCFGPHYICCGPSIGCFIG
TPETFRCKESLYTRPCIAGYAMCRGNTARCASNGICCSQAFCHMDTSCRISDVVGNDRKLDLNVNVILPG
EVSNEILQ
>**Wasmannia_auropunctata** gi|780704521|ref|XP_011702880.1| PREDICTED: neurophysin 1-like [Wasmannia auropunctata]
MLKELVVLMSLIFLSYA**CLITNCPHG**GKRNNIASLETVARECPSCGPNHQGQCFGPHYICCGPSIGCFIG
TPETYRCRKEISLYTRPCIAGYAMCRGNTARCASNGICCSQESCNMDTSCRISDVVGNDRKLDANLNVILSG
NEVSSDLF
>**Pogonomyrmex_barbatus** gi|769867110|ref|XP_011645557.1| PREDICTED: neurophysin 1-like [Pogonomyrmex barbatus]
MLKKIVVFASLIFLSYA**CLITNCPHG**GKRSDLAPLGNVRECPSCGPNHLGQCFGPHICCGPNIGCFIG
SETYRCRKEISLYTRPCIAGYAMCRGNTARCASNGICCSQESCYIDSSCRISNAVGSDRKLDADLNVILPG
NEVSNEMFQ
>**Cerapachys_biroi** gi|759033592|ref|XP_011329433.1| PREDICTED: neurophysin 1-like [Cerapachys biroi]
MLKELVVFATLIFLSYA**CLITNCPHG**GKRGDIAPSLGTVARECPSCGPNHLGQCFGPHICCGPSIGCFIG
TSETYRCRKEISLYTRPCVAGYAMCRGNTARCATNGICCSQESCHMDTSCRISDVVGNDRKIDADLNVMFPG
NEASSETFP
>**Harpegnathos_saltator** gi|749788059|ref|XP_011147500.1| PREDICTED: neurophysin 1-like [Harpegnathos saltator]
MLRELVVFASLIFLSYA**CLITNCPHG**GKRGDIIPSLGTVTRECPCGPNHLGQCFGPHICCGPTIGCFIG
TPETYRCRKEISLYTRPCIAGYAMCRGNTARCATNGICCSQESCHMDTSCRISDVVSNDRKMDADLSAILS
SNEASHEILQ
>**Acromyrmex_echinatior** gi|746868398|ref|XP_011065328.1| PREDICTED: neurophysin 1-like [Acromyrmex echinatior]

MLKELIVFASLIFLSYA **CLITNCPRG**GKRSDIASLKTIVIRECPSCGPNHLGQCFFPYICCGPSIGCFIGT
PETFRRCRKEISLYTRPCIAGYAMCRGKTARCASDGISSQASCHMDTSCKISDVGNDRNLDDNVNVLPGN
EVSNEILQ
>**Polistes canadensis** gi|954542367|ref|XP_014601007.1| PREDICTED: neurophysin 1-like [Polistes canadensis]
MTKKILIFTSFIFISSA **CLITNCPRG**GKRGDIEVPESPIRECLPCGSQLGQCFFGNICCGPTFGCHIGT
SQTQKCRKEQFDSSPCMAGFAMCNGNKGRCGAGGICCSQDSCFIDPSCRFTVDSFRRSIDSIDLKAIAS
EIEILKEEAK
>**Microplitis demolitor** gi|665817708|ref|XP_008557637.1| PREDICTED: neurophysin 1 [Microplitis demolitor]
MNLPGTMIRKIFAVVFLSTSFAC **CLITNCPRG**GKRGESPLLSMPSLIKESSCGPNDQGCFFGNICCGPTFGCHIGT
TIGCYIKGPETYKCRKESLYSHPCVSGFAMCRDNTARCAANGICCSQESCHVDPSCRVRGDEYLSERKISQ
EFSRLIADNDQLIN
>**Trichogramma pretiosum** gi|936696156|ref|XP_014226062.1| PREDICTED: neurophysin 1-like [Trichogramma pretiosum]
MLKVIVFVFMFLSLSHC **CLITNCPRG**GKRGDPTFFLENIARECPVCGHEEQGHCFGPHICCSPSMGCLI
GTSETLSRCKESLYSRPCVAGFAMCQNNNGRCAANGICCSQESCFIDPACKLVDENNDRKIGAEFGAFLL
ENSGRNEHIL
>**Copidosoma floridanum** gi|936606102|ref|XP_014216967.1| PREDICTED: neurophysin 1-like [Copidosoma floridanum]
MLKVSLVLLALVSVAYS **CLITNCPRG**GKRGDPTFFLENIARECPACGHEEQGRFCGPHICCGPSMGCHIG
TLETLRCKESLYSRPCVAGFAMCQNSGRCAANGICCSQESCFIDSACKLVDESGNDRKIGAEFGAFLL
ENAGANERILR
>**Athalia rosae** gi|817077789|ref|XP_012261240.1| PREDICTED: neurophysin 1-like [Athalia rosae]
MFQKTAIIILLVSSALG **CLITNCPRG**GKRNAGALLPLKNPIRECPACGPEMQGQCFFGNICCGPSIGCFIFG
TAETHNCRKESLYSRPCIAGFAMCRGNTGRCAANGICCSQESCHADSNCVTDFFNANNQGISFDLNTLF
SENTSLNDQ
>**Fopius arisanus** gi|755956374|ref|XP_011303419.1| PREDICTED: neurophysin 1-like [Fopius arisanus]
MSKIIILMSALICMSSA **CLITNCPRG**GKRGENPLLSLHSLAAECPSCGPHGQGCFFGNICCGPTTIGCFI
GTPETKYCRTESLYSRPCIAGFAMCRDNTGRCAANGICCSQENCHADSSCRVGEFSDRKIVQEYSRLSP
ENE
>**Nasonia vitripennis** gi|156543816|ref|XP_001606547.1| PREDICTED: neurophysin 1 [Nasonia vitripennis]
MSKVIIVLTTLVALSYG **CLITNCPRG**GKRGDPTFFLENIARECPACGHEEQGRFCGPHICCSPSMGCLIG
TPETLRCKESLYSRPCVAGFAMCQNSGRCAANGICCSQESCFIDSACKLVDESGNDRKIGAEFGAFLL
ENAGTNEHIL
>**Orussus abietinus** gi|817209540|ref|XP_012280828.1| PREDICTED: uncharacterized protein LOC105699950
[Orussus abietinus]
MKELLALYVLISAGYCC **CLITNCPRG**GKRSHHSESPETTIEKFFLAGLYDQSRYPVSLHVNVDQFIDSYARS
ADTTKSATEACWENKEFLNDNGNQRKMKLTELFRKRRCKSKFINDTSPNLI
>**Cephus cinctus** gi|1000762296|ref|XP_015604200.1| PREDICTED: neurophysin 1-like [Cephus cinctus]
MLKLCTVIMVFISISFA **CLITNCPRG**GKRSGAITSLENIVRECPSCGADKQGCFFGNICCGPSILGCLIG
TPETHKCRKESLYSRPCIAGYAMCRGNTGRCAANGICCTQESCVDDTCRITDDVNDHRIISELNGFLN
EGNVLADHNQ
>**Neodiprion lecontei** gi|998512075|ref|XP_015516596.1| PREDICTED: neurophysin 1-like [Neodiprion lecontei]
MFRKIVVILFLVSSTLG **CLITNCPRG**GKRDGGFNFYQVRECSCTGPDQGCFFGNICCGPSIGCFIFG
TAETHKCRKESLYSRPCVAGFAMCRGNTGRCAANGICCSQESCVDPNCKVRSDIQMSKQVTSFDMDKI
YSESNLNDE
>**Diachasma alloeum** gi|970901303|ref|XP_015116397.1| PREDICTED: neurophysin 1-like [Diachasma alloeum]
MSKIIILISALVCVSCA **CLITNCPRG**GKRGENPLLSLHSLAAECPSCGPHGQGCFFGNICCGTAIGCFI
GTPETKYCRTESLYSRPCIAGFAMCRDNTGRCAANGICCSQENCHVDSSCRISDEFNDRKIQEYSRLSP
ENEQ
>**Polistes dominula** gi|972190475|ref|XP_015176922.1| PREDICTED: oxytocin-neurophysin 1-like [Polistes dominula]
MTKKILIFTSFIFITSA **CLITNCPRG**GKRGDIEVPESPIRECLPCGPNQLGQCFFGNICCGPTFGCHIGTS
QTQKCRKEQFDTSPLAGFSMCGNKGRCGAAGICCSQNSCFIDPSCRFTFFDDWPGRQKIDSIDLKTIAS
EILKEEAM
>**Daphnia pulex** gi|321460843|gb|EFX71881.1| putative vasopressin-like neuropeptide preprohormone
[Daphnia pulex]
MAGLWTFCLIALSMTEMIPLTAKP **CFITNCPG**GKRSSQLVEPSSYLECAPCPGAGKGTCLGANLCCGS
HFGCFFKTEETNVCLLTLNKSTQICNQHFWKTDLKSASCSLNGDKIDGICVADLLCCSLGNLPQDDL
>**Tribolium castaneum** gi|145651811|ref|NP_001078831.1| oxytocin/vasopressin-like peptide precursor
[Tribolium castaneum]
MSTIIITSIILLVLSLSESLVSG **CLITNCPRG**GKRSKFAISENAVKPCVSCGPGQSGQCFFGNICCGPFGCLV
GTPETLRQREGFFHEREPCIAGSAPCRKNTGRCAFDGICCSQDSCHADKSCASDDKSPIDLTYTLINYQA
ELAGDK
>**Sarcoptes scabiei** gi|934146681|gb|KPL97556.1| vasopressin-like protein [Sarcoptes scabiei]
MLFQQTNYLFRSISILVMIIVLIVENVRG **CFITNCPG**AGKRSMLAAIGSSTQTRRECIRCGPGLSGRCYGP
SICCSPLFGCNVGGFASSRCALEAFNPMLCSNPGSACGPNKGKICAINSTCCTDSKI
>**Daphnia magna** gi|941105145|gb|JAK93241.1| Oxytocin/vasopressin peptide precursor, partial [Daphnia magna]
VKDVQSRVLFQDGLTTLPIKFKFLSSTCVKTKYIVLIMAALWTLCLIAFSILEMTMPSAAKP **CFITNCP**
PGGKRSGHVSEDPSSFQVAEERPLLSHQCASCGPGGKGTFCFASLCCGSEFGCFKTNETNICLLTLNLK
SSRSCDERFWQIYFKSAPCSLNGDKLDGICVADRLCCSLGQCKQNFAC
>**Trachymyrmex zeteki** gi|1012971628|gb|KYQ46204.1| Vasotocin-neurophysin VT [Trachymyrmex zeteki]
MLKELIVFASLIFLSYALITNCPRGGKRSDIASLRTVIRECPSCGPNHLGQCFFPYICCGPSIGCFIG
TPETSRCKESLYTRPCIAGYAMCRGNTARCAANGICCSQASCHMDTSCKISDVGNDRKLLDDNVNVLPG

NEVSNEILQ
 >**Trachymyrmex septentrionalis** gi|1009421053|gb|KYN39529.1| Vasotocin-neurophysin VT 1 [Trachymyrmex septentrionalis]
 MLKELIVFASLIIFLSYA**CLITNCPRG**GKRSDVASSLKTIVIRECPSCGPNHLGQCFGPYICCGPSIGCFIG
 TPETFQCRKESLYTRPCIAGYAMCRGNTARCASNGICCSQASCHMDTSCKISDVGNDRKLDNDNVNVLPG
 NEVSNEILQ
 >**Trachymyrmex cornetzi** gi|1009399678|gb|KYN19822.1| Vasotocin-neurophysin VT [Trachymyrmex cornetzi]
 MLKELIVFASLIIFLSYA**CLITNCPRG**GKRSDIASSFKTVIRECPSCGPNHLGQCFGPYICCGPSIGCFIG
 TPETFRCRKEKESLYTRPCIAGYAMCRGNTARCASNGICCSQASCHMDTSCKISDVGNDRKLDNDNVNVLPG
 NEVSNEILQ

(C)

>**Ceratosolen solmsi marchali** gi|766922501|ref|XP_011505828.1| PREDICTED: isotocin-neurophysin IT 2-like [Ceratosolen solmsi marchali]
 MTNYPRGGKRAMFANPTFLLDKIAREFGPHICCGPTMGCLLGTPEAHHCQKESLYSQPYVAGFAMCRGNS
 GRCAANGIMNIPKNHVSLIHAN
 >**Frankliniella occidentalis**
 QCTPCGPGGEGLCVGPICCSVFGCVLTSRGGCGRGAVFAPRCSPSSAALAAASAAVPLDAPCGADLTPDGSAPGRCAAQGVCTH
 >**Oncopeltus fasciatus**
 FLLLFKCKIYFFQQAFFPRCEPDEGRCLGRAICCGPKIGCLVGTTPAILSQCEQPPELPYSKPYSIGVCLSDGGLLFIG
 >**Calanus finmarchicus2**
PVSGKKRSLHVGEQVRDGLTCSNPAGLCYSPGLCCVQGGCYADGGCLPGLTERGEEQIKTRESVSKRGLRFLYGMAPSQMNLFQEGMAIPCIGPYCN
 GKGARSHGKQKQRKRKQSQEHVNRDQALLGSSNYDSAVSDDQFLKHNCDDWMDLYLAR
 >**Prorhinotermes simplex**
 QCARCGPAKLEHCYGPVPAICCGPQIGCLVATPETARCLTEAASPVPCIAPTGVQCGEGKLAGRGTANGVCCTHKGQSSTMYCLYVFNQAQVQL-
 >**Scylla paramamosain** gi|957760967|gb|ALQ28600.1| vasotocin-neurophysin, partial [Scylla paramamosain]
 GRCVGPDIICGARIGCFGLSRETRMCRTEMVPICTYNSDLKPCGRMQEGRGAPGICCTENKCEMNDDCVAEDTQGEVEEESQRGGRPRLLDAAARDRW
 EEQ
 >**Ceuthophilus sp**
 CARCGPAKLGHCYGAICCAPQFGCLIGTPTDTPCQREDQSPICIGTGSGPCRGEQGHCTANEVCCTQESCHIDPTCRLTLPAGGLPDGPDATTDLSDR
 NLVYSLFNAISTYQ
 >**Tentredo koehleri**
 CPACGPDRCQCFGPKICCGPSIGCFIDTAETHKCRKESLYSRPCTAGFAMCRGNTGRCAADGICCSQESCQVDPNCKITDDSITS
 >**Tetradontophora bielanensis**
 IPEQHNTNKVRECASCSPVGGRCYGPETCCSPNFGCMVGTPTHTCLIEDRINSVCHNPGIPCTVNVNDNGNINGFCATG
 >**Campodea augens**
 GRCFSPDLCCGPEIGCYFRTEKSSVCKSENLFVPCENPAKSCGTRDRNGKAGQGLCCTEDSCTVDSSCHVILKDLPPPPAAVAPPSPWLKYPSVFRVLQ
 QQQQPNTDLSATGALWDDMLE
 >**Medauroidea extradentata**
 VTHFNSSPGFKHKKPCRCGPAKLGHCYGDNICCGVEIGCLLATPDTQVCQRESMTPDPCVGPPIGGAPCGNSGKCAAPGVCCTPDSCTIDPTCHQTLISQEMA
 SLYLYNAGNARGVSQISDVDDK-
 >**Blaberus atropos**
 IFFLCNVDIKIMHLKYLDTKQCRCGPAKLGHCYGPAVCCGPGQIGCLIATPDTARCLNEAASPIPCTA
 >**Periplaneta americana**
 GCLIATPDTARCLSEAASPVPCIAPTGAQCCEGKSAGRCTANGVCCTHGEASQNIYNLQYSFITSTTFLLPYLLEILKYISQ
 >**Tetramorium bicarinatum**
 GDIAPLGTIVRECPSCGPNHLGQCFGPHICCGPSIGCFIGTSETYRCRKEKESLYTRPCVAGYAMCRGNTARCASNGICCSQDSCYVDASCKNSDGVNRDQKF
 DANLNEVLPGNEFSREIM-
 >**Inocellia crassicornis**
 FGCLVGTPTETIRCERDGAFFQEREPCIAGRSNCRGDTGRCAADGICCTQGNYE-
 >**Osmylus fulvicephalus**
 SVYFFGKSMYTLQICISCGPQRSQCFGPAICCGPFGCLIATAETTRCERDGAFFHEREPCIAGKSSCRGDTGRCAFDGICCTQGMCTVQLKGLKSLPNAIR
 LI-
 >**Lepicerus sp**
VNCPRGGKRGELPFLSIQGLVKECQSCGPGHQGQCFGNICCGTNIGCFIGTPETYKCKMESLYSRPCIAGFSMCRDNNGR
 >**Aethina tumida**
 CVSCGPGHTGQCFGPSICCGPFGCLMGTSETIRCQREGFFQEREPCIAGSSFCRKNTRCAIDGICCNQESCHVDKHCLEKSSSENLMGMEL
 >**Pogonus chalceus**
 CIACGPGHSGQCFGNICCGPFGCLIGTSETLTKQREGFFQEPPEPCIAANGYCRKNTGRCAADGVCCTQ
 >**Dastarcus helophoroides**
 QCIPCGPARTGQCFGNICCGPFGCLVGTPTDIKQREGFFHERDPCIAGNSSCRKNTGRCAADGICCS
 >**Diabrotica virgifera virgifera**
 GQCFGNICCGPFGCLLSPETVRCQREGSHEREPCIAAGSFCRKNTRCATDNICCDQDSCYTRDQCSSDEKLKAEALSGLDIYNFLNTY
 >**Baetis sp**
 VAPAATASNLALLPCVAESLFPEPCSNPTVRCGRGAKGVCAAPGVCCFHNSCETDASCAKMRRVNIAIARESNAFA
 >**Isonychia bicolor**
 ACLQCRCGFLAGRCFGPRICCDTRLGCMVGSAMEPLQAEELLPCLAESIFPAACHNHAATCGRMATGQCAATGLCCYQDSCHPDMTCRGRSE

(D)**Atta colombica** contig16192, whole genome shotgun sequenceSequence ID: [gb|LKEW01016192.1](#)|Length: 13960

Number of Matches: 2

Range 1: 8764 to 8997[GenBankGraphics](#)

Query: Polistes dominula gi|972190475|ref|XP_015176922.1|

Alignment statistics for match #1

Score	Expect	Method	Identities	Positives	Gaps	Frame
96.3 bits(238)	6e-23	Compositional matrix adjust.	47/78(60%)	56/78(71%)	4/78(5%)	-2
Query 41	CLPCGPNQLGQCFGPKICCGPTFGCHIGTSQTQKCRKEQFDTSPLAGFSMCNGMKGRCG	100				
Sbjct 8997	C CGPN LGQCQFPG ICCGP+ GC IGT +T +CRKE T PC+AG++MC GN RC					
Query 101	AAGICCSQ----NSCFID 114					
Sbjct 8817	+ GICCSQ NSC ++					
Query 101	AAGICCSQ----NSCFID 114					
Sbjct 8817	SNGICCSQGKLNKNSCKLE 8764					

Range 2: 9826 to 9873[GenBankGraphics](#)

Alignment statistics for match #2

Score	Expect	Method	Identities	Positives	Gaps	Frame
37.0 bits(84)	0.025	Composition-based stats.	14/16(88%)	15/16(93%)	0/16(0%)	-2
Query 17	ACLITNCPRGGRGDI 32					
Sbjct 9873	ACLITNCPRGGRK D+					
Query 17	ACLITNCPRGGRGDI 32					
Sbjct 9873	ACLITNCPRGGRKSDV 9826					

Lasius niger Lnig_2.1_6499, whole genome shotgun sequenceSequence ID: [gb|LBM01006435.1](#)|Length: 10190

Number of Matches: 3

Range 1: 5184 to 5393[GenBankGraphics](#)

Query: Atta cephalotes gi|801367097|ref|XP_012061245.1|

Alignment statistics for match #1

Score	Expect	Method	Identities	Positives	Gaps	Frame
133 bits(335)	4e-36	Compositional matrix adjust.	60/70(86%)	67/70(95%)	0/70(0%)	+3
Query 42	ECPCGPNHLGQCFGPYICCGPSIGCFIGTPTFRCKRSLYTRPCIAGYAMCRGNTARCA	101				
Sbjct 5184	+CPCGPNHLGQCFGP+ICCG +IGCFIGTPT+ CRKESLYT+PC+AGYAMCRGNTARCA					
Query 102	ASNGICCSQA 111					
Sbjct 5364	A+NGICCSQ					
Query 102	ASNGICCSQA 111					
Sbjct 5364	ATNGICCSQG 5393					

Range 2: 4298 to 4423[GenBankGraphics](#)

Alignment statistics for match #2

Score	Expect	Method	Identities	Positives	Gaps	Frame
74.7 bits(182)	2e-15	Compositional matrix adjust.	34/42(81%)	39/42(92%)	0/42(0%)	+2
Query 1	MLKELIVFASLIFLSYAACLITNCPRGGRSDVASSLRTVIRE 42					
Sbjct 4298	MLK+L++FASLIFLSYAACLITNCPRGGRSD+A SL T +RE					
Query 1	MLKELIVFASLIFLSYAACLITNCPRGGRSDVASSLRTVIRE 42					
Sbjct 4298	MLKELIVFASLIFLSYAACLITNCPRGGRSDIAPSLTALRE 4423					

Range 3: 5551 to 5664[GenBankGraphics](#)

Alignment statistics for match #3

Score	Expect	Method	Identities	Positives	Gaps	Frame
45.8 bits(107)	2e-05	Compositional matrix adjust.	24/38(63%)	33/38(86%)	2/38(5%)	+1
Query 113	CHMDTSCKISDV-DNDRKLDNVDNVLPG-EVSNELIQ 148					
Sbjct 5551	C++D+SCKISDV NDRK+D ++N+I PG EVS+E+LQ					
Query 113	CHMDTSCKISDV-DNDRKLDNVDNVLPG-EVSNELIQ 148					
Sbjct 5551	CYIDSSCKISDVVANDRKIDADLNMIFFGNEVSSLELQ 5664					

Cyphomyrmex costatus contig18246, whole genome shotgun sequenceSequence ID: [gb|LKE01018246.1](#)|Length: 14919

Number of Matches: 1

Range 1: 12261 to 12491[GenBankGraphics](#)

Query: Atta cephalotes gi|801367097|ref|XP_012061245.1|

Alignment statistics for match #1

Score	Expect	Method	Identities	Positives	Gaps	Frame
136 bits(343)	4e-37	Compositional matrix adjust.	66/79(84%)	71/79(89%)	2/79(2%)	-2
Query 43	CPCGPNHLGQCFGPYICCGPSIGCFIGTPTFRCKRSLYTRPCIAGYAMCRGNTARCA	102				
Sbjct 12491	CPCGPNHLGQCFGPYICCGPSIGCFIGTPTFRCKRSLYTRPCIAGYAMCR NTARCA					
Query 103	SNGICCSQAFCHMDTCKI 121					
Sbjct 12311	SNGICCSQ + SC+					
Query 103	SNGICCSQAFCHMDTCKI 121					
Sbjct 12311	SNGICCSQ--KLKNSCRF 12261					

Cyphomyrmex costatus contig15288, whole genome shotgun sequenceSequence ID: [gb|LKE01015288.1](#)|Length: 17512

Number of Matches: 1

Range 1: 12730 to 12858[GenBankGraphics](#)

Query: Atta cephalotes gi|801367097|ref|XP_012061245.1|

Alignment statistics for match #1

Score	Expect	Method	Identities	Positives	Gaps	Frame
75.1 bits(183)	1e-15	Compositional matrix adjust.	37/43(86%)	38/43(88%)	0/43(0%)	+1
Query 1	MLKELIVFASLIFLSYAACLITNCPRGGRSDVASSLRTVIRE 43					
Sbjct 12730	MLKE IVFASLIFLS ACLITNCPRGGRSD+ SSLRT IRE					
Query 1	MLKELIVFASLIFLSYAACLITNCPRGGRSDVASSLRTVIRE 43					
Sbjct 12730	MLKEIVFASLIFLSSAACLITNCPRGGRSDISSLRTDIREV 12858					

Nasonia longicornis strain IV7(U) Contig18019, whole genome shotgun sequence

Sequence ID: [gb|ADAP01018019.1](#)|Length: 7333

Number of Matches: 2

Range 1: 6887 to 7273[GenBankGraphics](#)

Query: Monomorium pharaonis gi|826427284|ref|XP_012527594.1|

Alignment statistics for match #1

Score	Expect	Method	Identities	Positives	Gaps	Frame
126 bits(316)	6e-39	Compositional matrix adjust.	62/129(48%)	81/129(62%)	23/129(17%)	+2
Query 42	ECSSCGPNRLGQCFCGPHICCGPSIGCFIGTPEYRCRKRKESLYRPCIAGYAMCRGNTARC +C +CG G+CFGPHICC PS+GC IGTPEY RCRKRKESLY+RPC+AG+AMC+GN+ RC		101			
Sbjct 6887	QCPACGREEQRCFCGPHICCSPSMGCLIGTPEYRRCRKRKESLYRCPVAGFAMCQNGSGRC		7066			
Query 102	ALNGICCSQ-----ESCHMDTSCKISNVVGNQKLDLNLNVI A NGICCSQ ESC +D++CK+ + GN++K+		138			
Sbjct 7067	AANGICCSQKRTSVINMFVKQEKYF*FP*IFLESQFIDSACKLVDEGTGDRKIGAEFGAF		7246			
Query 139	LSGNEISSE 147 L N ++E					
Sbjct 7247	LLENAGTNE 7273					

Range 2: 6694 to 6825[GenBankGraphics](#)

Alignment statistics for match #2

Score	Expect	Method	Identities	Positives	Gaps	Frame
54.3 bits(129)	6e-39	Compositional matrix adjust.	26/44(59%)	30/44(68%)	0/44(0%)	+1
Query 1	MLKEFVVFASLIFFSYGCLITNCPRGGKRGDIVPSLGTVARECS 44 M K +V +L+ SYGCLITNCPRGGKRGD L +ARE S					
Sbjct 6694	MSKVIIVLTTLVLSYGCCLITNCPRGGKRGDPTFLENIAREVS 6825					

Steganacarus magnus, whole genome shotgun sequence

Sequence ID: [gb|BFN01029022.1](#)|Length: 1266

Number of Matches: 1

Range 1: 516 to 923[GenBankGraphics](#)

Query: Ixodes scapularis gi|506953581|gb|AGM20426.1|

Alignment statistics for match #1

Score	Expect	Method	Identities	Positives	Gaps	Frame
68.6 bits(166)	4e-13	Compositional matrix adjust.	49/137(36%)	67/137(48%)	26/137(18%)	-2
Query 1	MALSHMLLLAVVGG-TSACFITNCPPGGKRSSESPARL----- + LS + L+A++ G T+ACFITNCPPGGKRS+		38			
Sbjct 923	LNLSILTLIALIFGLTTACFITNCPPGGKRSFAFIKNNQKQVI*KTINGFLIRNYNRCVI*		744			
Query 39	-CPRCPAGRGVCYSADVCCAGSM-CILNDALATLSCRAEALHGVACHVPGKRCGT-DGR C RCGP G G C+ AD+CC ++ C +L + C E + C + GK C +G		95			
Sbjct 743	*CSRCPGPGVGRFCFGADICCGGATIGCHFKNRLTEV-CLTENYNPHPCIDGKSCDNGNGV		567			
Query 96	CAIRGYCCGPDGCTKDS 112 CA+ CC P CT +S					
Sbjct 566	CALNSTCCTPGKCTLNS 516					

Hypochthonius rufulus scaffold114652_cov135, whole genome shotgun sequence

Sequence ID: [gb|LBF01028909.1](#)|Length: 27086

Number of Matches: 2

Range 1: 2097 to 2183[GenBankGraphics](#)

Query: Ixodes scapularis gi|506953581|gb|AGM20426.1|

Alignment statistics for match #1

Score	Expect	Method	Identities	Positives	Gaps	Frame
43.5 bits(101)	7e-11	Composition-based stats.	20/29(69%)	25/29(86%)	1/29(3%)	-1
Query 3	LSHMLLLAVVGG-TSACFITNCPPGGKRS 30 +S + +LAV+ G T+ACFITNCPPGGKRS					
Sbjct 2183	MSILTILAVIFGITTA CFITNCPPGGKRS 2097					

Range 2: 1763 to 1984[GenBankGraphics](#)

Alignment statistics for match #2

Score	Expect	Method	Identities	Positives	Gaps	Frame
42.4 bits(98)	7e-11	Compositional matrix adjust.	26/75(35%)	36/75(48%)	3/75(4%)	-2
Query 39	CPRCPAGRGVCYSADVCCAGSM-CILNDALATLSCRAEALHGVACHVPGKRCGT-DGR C RCGP+G G C+ D+CC + C + + T+ CR E + C G+ C G C		96			
Sbjct 1984	CTRCPGSLGRFCFGDICCCEIEIGCHFKNQITTI-CRTENISPRLCRNEGRTCNNGKIGC		1808			
Query 97	AIRGYCCGPDGCTKD 111 AI CC C +					
Sbjct 1807	AIDSVCCSTSKCHNN 1763					

Platynothrus peltifer, whole genome shotgun sequence

Sequence ID: [gb|LBF001089471.1](#)|Length: 3080

Number of Matches: 2

Range 1: 990 to 1037[GenBankGraphics](#)

Query: Ixodes scapularis gi|506953581|gb|AGM20426.1|

Alignment statistics for match #1

Score	Expect	Method	Identities	Positives	Gaps	Frame
39.7 bits(91)	3e-08	Composition-based stats.	15/16(94%)	16/16(100%)	0/16(0%)	-1
Query 15	TSACFITNCPPGGKRS 30 T+ACFITNCPPGGKRS					
Sbjct 1037	TTA CFITNCPPGGKRS 990					

Range 2: 674 to 880[GenBankGraphics](#)

Alignment statistics for match #2

Score	Expect	Method	Identities	Positives	Gaps	Frame
37.7 bits(86)	3e-08	Compositional matrix adjust.	25/69(36%)	31/69(44%)	1/69(1%)	-2
Query 36	ARLCPRCGPAGRGVCYSADVCCAGSMCILNDALATLS CRAEALHGVACHVPGKRCGT-DG		94			
	A+ C RCGPAG G C+ D+CC ++ T C E C GK C G					
Sbjct 880	AQKCIRCGPAGIGRCFDPDICCCEAIGCHFKNRFTAVCSTEDYSPHPQNDGKTCANGKG		701			
Query 95	RCAIRGYCC 103					
	CA+ CC					
Sbjct 700	VCALDSTCC 674					

Achipteria coleoptrata scaffold1020_cov175, whole genome shotgun sequence

Sequence ID: [gb|LBFM01000221.1](#)|Length: 64589

Number of Matches: 2

Range 1: 14022 to 14162[GenBankGraphics](#)

Query: Ixodes scapularis gi|506953581|gb|AGM20426.1|

Alignment statistics for match #1

Score	Expect	Method	Identities	Positives	Gaps	Frame
44.3 bits(103)	1e-04	Compositional matrix adjust.	28/55(51%)	34/55(61%)	8/55(14%)	+3
Query 1	MALSHMLLAVVGGTSACFITNCPGGKRSSEPSPARLCPRCGPAGRGVCYSADV		55			
	M LS M L+ V+ TSACFITNCPGGKR S+PS R GP + + D+					
Sbjct 14022	MILSIIMTLIVLV--TSA CFITNCPGG GKR--SDPS-----LRDGPKKQVILLFNDL		14162			

Range 2: 14197 to 14394[GenBankGraphics](#)

Alignment statistics for match #2

Score	Expect	Method	Identities	Positives	Gaps	Frame
41.6 bits(96)	0.001	Compositional matrix adjust.	28/67(42%)	34/67(50%)	3/67(4%)	+1
Query 39	CPRCGPAGRGVCYSADVCCAGSM-CILNDALATLS CRAEALHGVACHVPGKRCGT-DGRC		96			
	C RCGP+G G C+ D+CC S+ C LN+ T C E CH GK C G C					
Sbjct 14197	CTRCPGSPGIGHCFDPDICCCEAIGCHFKNRFTAVCSTEDYSPHPCHNEGLKANGKGC		14373			
Query 97	AIRGYCC 103					
	A+ CC					
Sbjct 14374	ALESTCC 14394					

Rhipicephalus microplus strain Deutsch Ctg100269, whole genome shotgun sequence

Sequence ID: [gb|ADMZ02000298.1](#)|Length: 711

Number of Matches: 1

Range 1: 221 to 313[GenBankGraphics](#)

Query: Metaseiulus occidentalis gi|391348425|ref|XP_003748448.1|

Alignment statistics for match #1

Score	Expect	Method	Identities	Positives	Gaps	Frame
33.1 bits(74)	2.3	Compositional matrix adjust.	15/31(48%)	20/31(64%)	0/31(0%)	+2
Query 1	MKLVALYFLSVSSLSWACFITNCPGGKRS+ 31					
	M + L + ++ ACFITNCP GKR+S					
Sbjct 221	MTPLNFLMLGLVGMTSA CFITNCPGG GKRSS 313					

Centruroides exilicauda breed non domesticated species of scorpion Contig13139, whole genome shotgun sequence

Sequence ID: [gb|AXZI01013139.1](#)|Length: 1479

Number of Matches: 2

Range 1: 1049 to 1120[GenBankGraphics](#)

Query: Limulus polyphemus gi|926609726|ref|XP_013784878.1|

Alignment statistics for match #1

Score	Expect	Method	Identities	Positives	Gaps	Frame
36.6 bits(83)	0.17	Compositional matrix adjust.	16/24(67%)	17/24(70%)	0/24(0%)	+2
Query 14	LAVTIKGCFITNCPGGKRSIGTF 37					
	L V CFITNCPGGKRS+ T					
Sbjct 1049	LIVLTS CFITNCPGG GKRSLHTI 1120					

Range 2: 1323 to 1466[GenBankGraphics](#)

Alignment statistics for match #2

Score	Expect	Method	Identities	Positives	Gaps	Frame
31.6 bits(70)	8.8	Compositional matrix adjust.	19/51(37%)	24/51(47%)	3/51(5%)	+3
Query 61	ICCSDIFGCFIKTRESVICRYENLQVIPCNNKKGKICETVPHGYCAAPGICC 111					
	+CC GC I IC+ ++ C K G+IC HG C GICC					
Sbjct 1323	LCCGSTVGCIINEEGIPICQ-QSFDYHHCCKNGRICRL--HGICTTNGICC 1466					

Mesobuthus martensii Contig352499, whole genome shotgun sequence

Sequence ID: [gb|AYEL01091269.1](#)|Length: 16655

Number of Matches: 1

Range 1: 9791 to 9898[GenBankGraphics](#)

Query: Limulus polyphemus gi|926609726|ref|XP_013784878.1|

Alignment statistics for match #1

Score	Expect	Method	Identities	Positives	Gaps	Frame
36.6 bits(83)	0.19	Compositional matrix adjust.	18/36(50%)	23/36(63%)	5/36(13%)	+2
Query 7	IMILGFCLA-----VTIKGCFITNCPGGKRSIGTF 37					
	+M+ F L+ V CFITNCPGGKRS+ T					
Sbjct 9791	LMVMHFPLSFATLIVLTNA CFITNCPGG GKRSLHTI 9898					

Supplementary Data S2. Putative inotocin receptors. Sequences of 120 novel and 33 previously annotated inotocin receptor sequences from arthropods. (A) 92 newly annotated putative inotocin receptor sequences. (B) 33 deposited inotocin receptor sequences derived from NCBI. (C) 28 non-annotated inotocin receptors are presented as BLAST search results. Conserved motifs (XPQX₂WX₅-₆F at the end of transmembrane domain 2 and the beginning of extracellular loop 1, and CXNPW in transmembrane domain 7) are highlighted in yellow; see also Supplementary Figure S6. Sequences from (A) and (B) were used to prepare the alignment illustrated in Supplementary Figure S3.

(A)

```
>Catajapyx_aquilonaris
LRDNVSGLVEQDSRDETLAAVEIATLAIILLVAIILGNMFMVVGIIWRQLQFRPMSRMYYFMLHLSVADLLVAVFNILPQLLWDITYRFQGS DALCRTVKYFQ
VMVLYLSSYILMFMAVDYKALCCDAFSPWNSLLAAKIMVASAWVMAFGFATPQAVIFTLKKISPGVQDCWGT FVEPWGTKAYVTWVVISIFVMPLLVISS
SYGAI SYRIWYNS EPRCWTASKWKWLDLKKCLCCTRKESEGRQSPSSVEDNDVLEQAESSPLPQKATQLELAGRLKSKVGCNVKQKRKSMISDAKIKTLQL
TLAVVICFFVCWAFPCIAQLILVYNPPEDRDVDPVTVILLLLASLNSCTNPWIIYTLFSGSLLNQLRV
>Blattella_germanica
MENASQAVNGSTTAEDLDRDEVLARAEIATLSVMFVTVTVGNFAVLLVLSARPRKLLSRMYFIFILHLSIADLCTAFLSILPQLAWDVTYRFRGGPIMCKVV
KYQOTLGPYLSAYILMVTALDRYQAVCHPLAYCSWTSRRSKFMVWTAWVFALGFCVPO
>Parhyale_hawaiensis
MLDEPLPTMSEELVLNVSVNASEDAINFIDILSVQNNTSFGSRDEVLAAFEVLTLASIFVVTIVGNCIVIFKHFMRKKFRMNYFIFALSLS
LVTAMFNVLPLQLIWDVTFRFKGGNVLCKCVKFGQLVGPYLNAYILVVTADRYQVICRPLSNCRWRP GHSIRLIGAATFSLWLSVPLQFIFSLR SKNGIQ
DCWASFIQPGWVAVYVTFYSIAVFPVPLILLVFFSVCI IATLLRHNFQVPIQCNIYRQSYSTTSVHCLHHSPhKVYHHRGNSMNLSCPTVYRSKPIGSLPH
CSLHSRSLSEKAFGQKMKQNSLSMVKQVRSRIMSPISRAKIKTVKLTIVIFFVACSAFFISVQLWSVWDPNAKNSPFSSE-
>Frankliniella_occidentalis
APQVEVAVLGVLLVLTVLGNVALLALYARRRCGRRKLSRMFYFILHLSVADMVTAFFSVLPQLVWVTFRFHGGNFLCKAVKFGQPLGVYLSYVLTATA
CDRYRAICHPLTYCSWTSRRAKTMVWAAGVAICFSAPQVRSEGYTAGQRQTLEANSVPCVNCNLF I
>Ephemera_danica
IATLAIIFGVTVLGNLVAIAISFRRAKISRMYFYIMHLSVADLITAFFNVLPQLAWEITYRYCLSQLCRGVKFSQQLLGPYLSYVLTAVDRYEAI CRP
LTYCTWPARRAWFLVAGAWTLALLCCAPQLFVFSYRVPVQQPDVFDCAWTFEPGWERAYVSWYATSVFLVPLMVLVAVYFRICQALWRNYNLKQRAQQNG
LLQPNFHFYPRIMEPRTHSLRGISRAKLRSIKLTIVVIACYVICSTPFI GAQLWATWDEAMQSPFWSGPTFTTIVTLLASLNSCVNPWIIYLA FNPELARL
LITRGRV
>Ladona_fulva
MATLAAMLVIVSIVGNAMVALWARPRSSPRRRLSRMHLVLHLCTADLITAAFTVLPQMAWEVYRFAQAAPLCKPLKVLQQLLGPYLSYLLVAMAIDR
HRAVCRPLSVRAF LPRSPRRLVAIAWALSALFSLPQAFVFSYQKATETEWCAWTFDPPWTKAYVTWYGISVFAVPLVLLLYAYAGICRALRRNHREKLRP
QEDGLIPRGAPPRTHSMGTISRAKMTRLRLTIVAVACYILCSCPFLVSLWATWYPGATESSFWRGAFTILSLLPCLNSCVNPWIIYMAFNEEIRVALRER
LPGRVRDAVRSLFRFNTSKRLRHNDAITYASSSSRTRSSRESPQMEIKTLNSPVKDPSPVKKNGVVAEPKTEK
>Platynothis_peltifer3
MTGNGSLTVKRDEKWLLEIGILSLIFILIVFGNSCVLIALQVRKLMNRMYYFLLHLCIADLITAFFNVIPQLAWEITHRFYGGNFKCTIKYLQILGPY
LSSYVLMVTAIDRYQAICYPLSNCAWTPSRSKLMILMAWIVSLLCCAPQIIIFSYQEIGSQIFDCWGTFSQPYGERIYVTVYAVSVFIPFIIILTFTHVHI
CREIWLNLHKKRKSFKINRNKSSSSCNRNDKLD CDSVNSPETSEHRSGTRLLVTVGKSYRFGKQVEVSVKEDCKGKEDYNSPRTHSIHGLTRAKIKTVK
ITIVIIMCYIFCSTPFIICVQLWAYWPNQAQSP IWNV KYTYLSNNA
>Platynothis_peltifer2
MEVSTAI SEETDGI PFETSSIKPNI TGRNENLALIEVGLTGI FVLIVFGNCCVLLALALRRLKMTMYFLLHLCISDLMTGFFTVLPQLAWDITYRFNG
GNILCKAVKSMQILGPYLSYVLVVTAIDRYQAICFPLSNCSWTPRRAKLMISCAWIIISIVCSLPQAFIFSYQVEPETNHIYDCWGTFFQPWGERIYVTWY
AISVFFIPLVILTFTHIYICREIWNVNLKRQTGRRETQINQINIDNSNSYSRTRKCLLIALNRVYRLGRQRDTEAEIQINCDNQEVRPLHTVVTQFQESV
SSSPRVNTFNRLSRAKIKTVKITVVVILCYVICSSPFIICVQLWAYWPNASTTTFWNGMFLSFI I
>Platynothis_peltifer1
MEEIGTTVLEELDKLPETIIANVTKDSRDEHLAVFEIATLGLIFLLIVFGNSCVLIALIMRKLKMNRMYYFLLHLCIADLITAFFNVLPQLAWDITYRF
YGNILCKTIKYLQILGPYLSYVLMVTSIDRYQAICYPLSNCAWTPKRSQMLISFAWIIALLCCIPQVIFSYQQIPGYDIIDCWGTFFQPWGERIYVSW
YAI SFFFVFPFILLTFTHVICREIWRNVHQKRSVKMEQNKIIQNDDSDRVSSCSSTNDSIARSTNLLVTVGRSYRFGKGRGRVEVSDGPKSRGTYNPRSH
SLNGLSRAKIKTVKITVVVILCYIICSSPFIICVQLWAYWPNQNSTFWGSKCSENSFI IQFRYSFQ
>Platynothis_peltifer4
MSNVIMSINNTTSVLYNISGSDKRDENLAIMEVSI LALIFILIIIGNL CVLIALAVKRFKMTMYFLLHLCISDIITGCFTVMPQLAWDITHRFNGGNIL
CKLVKCLQFGPYLSYVLVVTAIDRYQAICFPLTNCHWTSRKS KLMITIAWIIISILCSAPQAFIFSYQEI PRNTRNGVRDCWGTFFQPWGERIYVTVYAITV
FFIPLIIITTYTYVICREIWANVRKRQTLKPEISLIEVRKNWGKLSKSSDDKSRQLQSDRCLANNLLNPRSHSIYRISKAKIKTVKVTVVVICYIVCSSP
FICVQVWAYWYPSAQETSFWTGKH
>Platynothis_peltifer5
METVSDLITFSREQEFDFELLNDSNVNKSSFEIRDSRNE SLAIEISLTFMFISILIGNIFVLTALIVRDSKMNRMYYFLFHLHCIADLITAFFNVLPQL
IWDITYRFYGGNVLCKLIKYLQILGPYLSYVILVITADRYKAI CFPLSNCSWTPKRSQMLISIAWVLSLIFCAPQLFIFSYQQIPGTLGNVYDCWGFPPQ
PYGERIYVTVYAITV FVIPCIIILFAHVCI CREICNNLHRKRESIEEIKNCIHYSFKRNKEFSTSSLKSTSLTSFSGPIKSPITYSIRPSKRLRR IHSQID
LKKDLRNSLTNLSVKVNDLNSTPRSHSLRFVSRAKIKTVKITIVIMLCYVICSMPIFISVQLWVYWFPSAQSFQTSSELSNIY-
>Achipteria_coleoptrata2
MSSDSSMSVENISQTIIFQIINDNMTANTSLAVKRNEKLVLEIGILLIFLLIVFGNSCVLIALQINKLMNRMYYFLQHLISIDMITAFFNVLPQLA
WEITHRFYGGNILCKTIKYLQIFGPYLSYVLMVTAIDRYQAICNPLSNCKWTPGRSKLMTIAWIVTSFCCSPQIFIFSYQQIPGTDAIYDCWGTFFQKPW
GERIYVTVYAVSVFIPFIIIVVTHYHICREIWLNLHKKRKSFKLNKNRVGKSYRFSKRGKLEVSVDKDFKEDFSRTHSIHGLSRAKIKTVKITVVIIIC
YIMCSTPFIICVQLWAYWVPTAQKSHIWNV KYTYNIYLMFFSIIIDVTIAFKILYSE
>Achipteria_coleoptrata1
ENITEELKNNTTSDTRDEHLAIFEIATLSLFLVILFGNSCVLIALLMRKIKMNRMYYFLLHLIIADYLVAVFNVLPLQLIWDITYRFYGGNLLCKVIKYL
QILGPYLSYVLMVTSIDRYQAICYPLTNCQWTPTRSQLMITLAWIIALLCCIPQVIFSYQQIPGTDIYDCWGTFFLPQYGERIYVTVYAI SFFFIPFII
LTATHVICREIWI
```

>Varroa_destructor1
MAGNIVLVLVLQSKPKSAHLSRIYFFLLHLSIADILVGFNISPQLVWDIYFRFPLGNFACKIVKFLQVFLVYLSTYVLAGMAVDRYLAIRSGINRPVIV
VRTLLSVSWLVAASVLPQYIFSFQKLNPAHDCWATFEPPIITSFYRVLFFITAVLFIPTLMLALCYTYSWIISKRSLSHTKLNPIRMTMVMVIVFVLC
WTPFCCAQLYLESTGQVPSIFITLFLVLPNLNSCANPWVCLTFSTTLRRLKTDALSFFGFCEHLSVYRSKNAITISILQYRPPNRSKRQPRAYRGA
>Varroa_destructor2
EARRSSLSRVQLFMMHLSIADILVALLNLPQLAWDITARFYGGALLCKFVKYAQVLVLYLSTYILTGMSLDRLVSM
>Ornithodoros_turicata
SYVLVVTAVDRYQAI CFP LSNCSWPTPKSKLMI AF AWAVSLLCCVPQLFISYQQVENGVDWGTYAEPWGVTA YVTWYGVSVFVPLAVLTFTTYIYICR
AIWHNLYLKRSSEGRSDKELSSRRTYRFAGRQRKMSSANGS FVAPRSHSVRGLSRAKIKTVKIVVVI VYVVCSSPFCVQMMWYWSPDAESSELWSSS
TVTILMLLNSLNSCVNPIYLA FNKNLLNALRTACCLAKVSGRGC SYLARDTTDGTNDSNAHSVSHCEGDHARIKCSPSKRRNGFRSSTDVEMRTAQDCG
ADT
>Panonychus_ulmi
RDENLAIIEIITLSAIFVMIVFGNTSVLLALILSRIKLRRMYFFLLHLSIADLITAFNTVLPQLIWEITEHFYGGQILCKGIKYLQLLGPYLSSTFLCATA
IDRYRAICYPLESRRLNRSNLKVSIAWGLALICCLPQLLIFSYHQIPNPNQVYECWGTFIQPYGERLYVTWYAFSSFFIIFTIIIFTFSNICSELWKN
>Hyaella_azteca
SDLVTA AFNVFPQLMWDITFRFRGGDFLCRSVKFGQLVGPYMNSYILVVT AIDRYQVICQPLSNCRWTPGHSIRLISCATAISLFLSIPQLFNFSFREKNG
IYDCWADFI PGWGTAYVWYAI AVFFIPLVLLIFFSGCICCALLRYNFQVNPQSSYVSRSHSQAGQESPNNETTSRKYGRITLDDTTGSSSTVNDVNYGN
AVRILSYSSATNKARNTVIEHGCRYRFQKTPGAKTVMSPISRAKIKTIKLTMIVIFFFIVCSAPFITSLMWSVWDP
>Lepeophtheirus_salmonis
VSNTSLNTPSSSPNSLHHTKLWVLGIIIVLTILGNSIVILAIATRFIKMTRMYFFILHLSIADVLTAFLTLLPELIWYTSNPNFYGGAFCKAVKFGQ
MIGPYLSSYVLIIMTAIDRYHAICFPFSKCTWTPKRSNIMIGLAWLVSALCVPQIIIFGSGEKSHSCSATFAQDWGQKAYVTWFAVSNFFLPLIILYCYG
CICKIWDNFNSKIPLNPGVEVRSITCCKNKGRAEETIRYRWKSTKRALGSTAEYSKRNDTIEEVMMNLTLSVSNNDQNDPNQIQAASSFTFDRCGKLR
KSKNKVLIDLSDPTQTKNKKSLKPRTHSIQGISRAKIKTIKLTVVVIAGYIACSAPFICVQLWVTFGTVTSIRK-
>Triops_cancriformis
SARDEKLAIAEIA TLAVIFLLALSNNVFMVAIWRQRQYRPLSRMYFFMLHLSLADVLVAVFNILPQLLWDITYRFLGGDLLCRFVKYQGIMPLYLSTYLL
MFMALDRYRAVCSASNHLWNSLKVAKMMVTSAWVLSLLAIPQAIIFSEQYINPDGTTTETDCWVRFIEPWGAKAYVTWVISIFALPLLIIGISYGAIS
LRLWRYSQEAHRSEEMTRGHKRTIGLPAGAAGALRPTSRWRRASRLGRFFLQRERATHQRNSCGDLEEDFPATTHVILVESQSSSSGSKPVAESLPL
RESDTASSTKSSSHGKIKMPEPFLRRNSHRITRAKIKTIQLTLVVISFVVCWAPFCITQLVLVYDPPSN
>Caligus_rogercresseyi
EGNSLHQTKLWVLGIIIVLTILGNSIVILAIATRHIKMTMYFFILHLSIADVLTAFLTLLPELIWYTSNPNFYGGALCKIVKFCQMIGPYLSSYVLIIMT
AIDRYHAICNPLSKCTWTPKRSNIMIGLAWLVSFALCIPQAIIFGSSEAKYSCSASFVVDWGQKAYVTWFAVSNFFLPLIILYCYGRICKTIWDNFNSKV
PMSDAGGVTCCGNRGRAEEMIRYRWKSSKRSRNNQNEVHQNTENEMMDNFSLVSNQGTDRDNPQIKNATSFTFDTFHVQKGNKRVIIDLSSPVQKQK
RKS LKPRSHSIQGISRAKIKTIKLTVVVIAGYIACSAPFICVQL
>Pachypsylla_venusta
MDESNGTLVNYNDTSDERDEDLARVEILTLIIIVLITIVGNIMVLFALYSRRHFQKQIKMPRMYFFILHLSIADLITAFNVLPQLLWWDINRYRFPSSNW
LCKLVKFVQPSGFLSSYILMAIAIDRYRAICQPLTYHSWNSRRSRIMILLI AWAFAFTFCIPQVQISIFSYQEIKPGVYDCWASWDQEWGERIYITWFSVS
VFIIPLICLIYTYTCICLALKNTAYPAPSPHKIISRAKINTVKQTITVITLYIICSLPFIQAQLWETWNLNQTVYPVQDSALTIIMLLSSLNSCVNPIY
LVSNRELITALWTLCFNINVKENRTVDTASGNSSSARECCRRTDSNVTMGTYLNRQSCNDDTYVSEDNLIVSRPQWVVSVPDG
>Homalodisca_vitripennis
MANDLVFNSSLASDLRDEELARAEIAVLAVIFVVTVTGNTAVLVALYARRFCTGNKKLPRMYFFILHLCVADLTGLLNVFPQLCWKITRYFKGGMPLCK
VVKYQGTMGPYLSSYILVATALDRYKAICEPLNYSNWTSSRSALTVSAAWSLTLFCIPQVQVIFSYQEIAPGVYDCWATFPFPWGERVYVTWYSVSVF
LVPLFVLITYTYFCICWTLWRYSLGPDSSPHHLISRAKINTIKQTVAVILLYISCSSPFIQAQLWASWGPQPFFDGAFTILSLLSSLNSCVNPIYLSF
NRELLRSLWRASICTGSPRHRNLRGSASSCR
>Acerentomon_sp
MANQSLNVGDPWINETQVAEHLVNVGDPWTNETQEAEDGFKYERNEDLARIEIAILAAIFCATVIGNVLVVALFNTKKMTRMYFFMMHLSIADLFTAFF
NVLTLQIWEITEYRAGGNYLCKFKYMQIFGPYLSYIITVLTALDRYRAICFPQNSRWTERRYKAMIAVAWATLCLCSPQVFIYSYKMGVTNQSGDIYD
CWATFIEPWGAKTYVTWYAFITFIIPLLVLIYTYFNICRTIWRSKNWI STKVSPVKRCVKVSQLYEDGGAKKHRGNGFYRERRSLWKRMSMSNSQSMTN
SNVSAETIKLTLDEIDELSTVNSEIILDMAMRSTIVPVTPEPQVPTQQSISFFQSVSSTSSALPVRTTNTSSTSESTSVH
>Polistes_metricus
MNETTNSFTAANEEEDIRDENLAKWEIVLLANILIFTIPGNSLVLLSLYLRRAHKKLSRMYFFIMNLSIADLLTGLLDVLPQLAWDITFRFQGLVLC
LKVKFFQPPGLYLSYIITATAIDRYHAICHPLSYCSVTSRKRIMVYCAWSFALILCIPQLFVFSYQEVMPRIWDCWATFDIKFGEKAYVTWYSMLVFL
PFIVLVYTYVVICVGVWQSNKMSGAVDDRTYIRISINSYRNRSSIFSKAMINTVKQTI AVITLYAITSPIIGCELWISWDPEAPKSSFANGPAFTILALL
NSLTSCVNPIYLSFNRELRLQTLMNFCNHNEHSQKYYGQRMRRSDSNDTSTRTSLMSRISRYTSSIIPR-
>Wasmannia_auropunctata
MSHDLNSSSSPPLSSDRPQDDARDEDLARWEIAVLTSIFLVTLIGNALILLALYVRRYQRKFRTRMYFFILHLSVADLLTGLLDVLPQLAWDITFRFQ
GAVLCKLIKFGQPPGLYLSYIITVTAIDRYQAICHPFYSYCVTSRRSKMMVYGAWTLAAALCVPQIVIFSYTEISPGVWECWATFYLYKGERAYITWYSV
TQFLLPFVVLVYTYTRICLSIWRSSKMSGVVELKRDNKASFQQRNRDPLISKAMINTVKQMIIVTLYIVTNIPIGCELWATWDPKASTSPFFSGAAFTI
LSLLNSLTSCVNPIYFANFKELRAALINFFCRKDYSLTYDIDVRQNASDVPSTSSFISRI
SRLASSKIFG-
>Aethina_tumida
MYGLKMNVTSTGETIEELERAAKERDESLAKIEVAVLAVIFIVTVIGNSTVILALWARRRCAGRKKLSRMYFFILHLSIADLITAFSLVLAQLAWDITYRF
RGYIILCKLVKFGQTLGPYLSYVLMATAIDRHQAICYPLTYCSWTSRRSKFMVYIAWITSLVFCIPQLTIFSYQEIVDDGEFDCWATFQEPWQKAYVIWY
CVSVFIVPLIVLVYTYTCICKDIWHSSEISMRRNSLVGKRTKMP LISRAKINTVKQTI AVIFMYIICSSPFMFVQLWATVDPNPFQGPIFTIITLTL
SLNSCVNPIYLA FNRELRLQTLMNFCNHNEHSQKYYGQRMRRSDSNDTSTRTSLMSRISRYTSSIIPR-
>Pogonus_chalceus
MYFFILHLSIADLITAFNLTPQLGWDITYRFNGGFLCKIVKYCQTLGPYLSYILMATAIDRHQAICYPLTYCSWTSRRSKVMVWLAWATSLAFICPQV
TIFAYQEVAPGINDCWATFPQPWGARAYVTWYSISVFIIVPLIVLIFTYGAICRVIWQSAGGELGLRSPRLAPDPPRCARSRRAPLISRAKINTVKQTVAV
IAMYIACSTPFIQAQLWATWDPANESAFNGAAFTILTLSSLNSCVNPIYLA FNRELRLLLRHAYAATSKNYRSAGTGNASNSGGVESTSLRPFSSK
WSLCASAKSSSAINHNGNNTNGHAIGSGDFRFRYPAPPASSAASTLIRLPHAPAHSPQQLMQPSPFLGRYHARRWIVTSTA-
>Medauroidea_extradentata
MGDGRNCSLATSEDCQLPNMLVANHSVKNSTNDGYDRDEDLAHAEIATLAVMFIITMVGNSCIIYALCARMRHKLTMYFFILHLSIADLITGLLNV
LPQLAWDITYRFQGGPVLCKIVKYFQPLGPYLSYVLLATALDRYQAICQPMTYCSTDSRRSRAMWLAWCVSLVFCIPQVIFSYQETAPGVFDCWATFP
EAWGKTYVTWYSVSVFIIPCLVLYTYSRICHEIWEKSGFRAAHAARSSPLKINPTISRAKINTVKQTVAVIVLYISCSSPFIQAQLWATWDPHASESAF
LTGAAFTILALLSSLNSCVNPIYLA FNTELVRLLKKGDPRTNADLFGSGSSTSWRNSKVYRLVNGSAFKQRDAVRERRWAMAMPTKPIIATALMAGR
DAPSTSQDVA-

ILALLYSLNSVCNVPWIYLTFTNRELPRLLVKHCTASSKNYKSANAGNSGNSSSGEPQSTSLRPFKWSFCNSPKSNGNKYTSRLTQRPHYDAQSNTRRWIVTT
TT-
>Inocellia_crassicornis
MNGTELIKSAPEPNGNERDEVLAQAEIITS AVIFVVTVIGNGTVLLALFARQKYSGCRKLSRMYFFILHLSIADLVTAFFNVLPQLSWDITFRFKGGPLLC
KAVKYNQLLGPYLSAYILSATAIDRHQAI CYPLTYCSWTSRCSRAMIWMAWAASLAFICPQLIIFSYQIEPNVWDCWGTFFPEPWGAQAYVTWYLSLFI
PLCVLVFTYTCICREIWR TARHGILRPATTPMVSVTAPTHGPVRRRTQPFVSRKINTVKQTAVIVTYIVCSMPFISAQLWVTWYPHAMESPFFSGST
FTILTLLSSLNSVCNVPWIFLLFNKDLFRLLKRLFVNLDSSKTKYTRGGMSKASNSSTVETAVGRLSWLSKSFRRSSKASFQHVHNNIIQS-
>Cercopis_vulnerata
EELARAEIAVLA AIFVITVTGNTVVLVALYGRFFCGGRKLSRMYFFILHL CIADLV TALLNVFPQLIWDITFRFKGGPFLCKLVKYGQTLGPYLSYVLM
STAMDRYKAI CHPLTYCSWTSRRSRTMVRVAVIVSLILCIPQVNI FSYQEIAPGIYDCWATFPEPWGEKLYVTWYSVSVFLIPLCVLIYTYTCICRELWRN
AGFPESTSSPHRLISRAKINTIKQTVAVIALYISCSPPFICAQLWASWDPNALSSPFLQATFTILTLLS
>Aposthonia_japonica
MNSAEKSDGRDEDLARVEVTVLAIIFAITLVGNLLVLLVLRKRLSRMYFFIVHLSIADLITAFFNVLPQLGWDVTYRFIGGPI LCKI IKFCQTLG
PYLSYVLLATAVDRYRAICSPLYVHSWFRRAKIMVLIAWIISLWFCVPAQVVFYSYQIELEPGVWDCWATFIKPGGERAYVTWYSVFSFIIPLSVLTYS
CICRKIWRNTGAGFHI IQTSPVISRAKINTVKQMVIVILFYI ICSTPFTFSLWATWDTAVELPFKGAFTILTLLSSLNSVCNVPWIYLT FNKELIALL
VNCGASDLHYRGSSSSKERSLSKLVSWRST-
>Tenthredo_koehlerii
MSNSTAENRSFVESECNLTISSEIDDSRDEYLAWEVATLALIFVVAIAGNSLVLTAFYFRYDAPRKKLPRIYFFILHLSIADLITAFFNVLPQLGWDVTYRFIGGPI LCKI IKFCQTLG
FRFQGGPVLCKFVKFGQTLGPYLSYVLAATALDRYQAVRHPLIYCSITSRRSKMTVYFAWCLSLLLCVPQTLVFSYKEVSSGVWDCWATFDLTPYQOQTY
VTWYSISVFLPLIILVYTYTICIVIWNNGI VGEARSTHGGLLRQRTVISRKINSIKQMIAVISLYAASSPFIASLLWVTWRNASASPFFYSGAAFT
ILTLLSSLNSVCNVPWIYLTNRLDLSRALINRLYPTRGSSIKSQENPRQSI EIRWGSSASSSGTSIRSYASRMSRYANSVLRSSDSSSNKELQPSNRIR-
>Gyrinus_marinus
MNTTANADQTFDRDENLAQFEIATLAVIFVVTVIGNGTVLLALWTRRRACAGRKKLSRMYFFILHLSIADLVTAFLNVLPQLAWEVTYRFRGGAVLCKLVK
GQTLGPYLSYVLMATAIDRHQAI CYPLTYCSWTSRRSKVMVYTAWAALAFICPQLNIFSYQIEIAPGVYDCWATFPQAWGQKAYVTWYGISVFLVPLTY
LTTTYGCI CREIWOQSAAGDLGGP
>Chrysis_viridula
MSVEQNLNVTETEEDVRDEYLAKWEIIVLATILYMTLVGNLSLLFALYLRHRGRRRKFTRMHFFILHLSIADLITGLFNVLPQLAWDITFRFQGGNILLK
LVKFMQPLGPYLSYVLMATAIDRYHAICHPLSYCGSSLRKSKIMVYSAWAVTLLCIPQVIVFSYQEVTPKVWDCWAVFNVA YGERIYVTWYSTMVFLLP
FTVLLYTYTGICIGIWRSNKMSGVEDWRKVRNNGNFLERNRSPFISKAMINTMRQTI VVISLYAITSIPFICGQLWATWDPASSSSSFINGPAFTILTLL
SLLTSCVNPWIYLSFNRELRAVLKDNLCRSDYSTTYDQELHPANSTETSTRSSFISRIFWYAGSMIFR-
>Baetis_sp
MDSVDNSTTTTVDVAVPTRDEQLARVEIATLAFI FAVTVIGNSLILSAILFRRRVKITRMFYFIHLSIADLVTAFFNVLPQLAWELTYRFGGNLLCKGV
KFGQILGPYLSIIILVLT AIDRYAICQPLAHCTWPVRRARALCVAWALALACCTPQVIFSYQPIGDTYDCWGTFFPEGWGERAYVTWYSGSVFLIPLLI
LIFTYTCIQAIWRNYNAKKE SVAGLPPTDSKVLGNRVMHPRVHSMRGISRAKMKTIKLTVVVIACVYVVCSTPFI CAQLWATWDPDAMQSPFFWSGQPTT
HLHSMFLLHHAR
>Haploembia_palaui
MVHRKRQNDVMNSVASDGRDEDLARVEVTVLAIIFAITLVGNLLVLLALVLRKRLSRMYFFIVHLSIADLITAFFNVLPQLGWDVTYRFIGGPI LCKV
IKFCQTLGPYLSYVLLATAVDRYRAICSPLYVHSWFRGRAKVMVFIAWTISLLFCVPSIIFSYQELKPGVWDCWATFIQPWGERTYITWYSVFAFIPL
SVLTYTYTICICRKIWRNTGAGFHI IKSSPVISRAKINTVKQMVIVIFFYI ICSTPFTC
>Cordulegaster_boltonii
MATLAAMLVSVVGN GAVLIALWARPRSPRRRLSRMHLLVHLCTADLITAAFTVLPQMAWEATYRFAPAEAPLCKPLKVLQLLGPYLSYLLVAMAI DR
HRAVCRPLSVRAF LPRSPRRLVAIAWALSFLFSLPQAFIFS YRKATETEWDCWATFDPPWTQKAYVTWYGISVFAVPLVLLLYAYAGICRALRRNHREKMR
PQQDGIIPRGAPLRTHSMGTISRKMTLRLTIVAVACYILCSCPFLVLSQLWATWYPGATESPFWRGAAFTILSLLPCLNSVCNVPWIYMAFNEDIRIALKE
RLPGRVRLDLRPIFHPDITNKRRHHDATASASLSRTRSRRESPQPEVKATAESSKDEERDGC RMIGLADR TKEEKAVKESAVLLSNAPV-
>Isonychia_bicolor
VGNTCVLI AIRHRRSKITRMFYFIHLSIADLVTAFFNVIPQLAWEITYRFGGDELCKI IKFLQLLGPYLSFIVLVTAVDRFHAICLPLSYCTWPAKKA
KLLVSGAWVALLCCLPQVLI FSYQPI TPGGDVDFDCWATFPYWGGERAYVSVVTVSFLAPLLILFFTYTCICRAIWHNYNAKIASDGGFTTKQNTIQPRV
HSIRGISRAKIKTVKLTVVVIACVYVVCSTPFI CAQLWATWDPAMMHS
>Aretaon_asperimus
MDVSRNCSAAPEEGDQHS LQILDEIVGNCSSSANITNSTGGYDRDENLAEIATLAVMFIITVIGNSCILYALCLRKRKLLTRMYFFILHLSIADLI
SGLLEVLPLQAWDITFRFQGGPVLCKFVKYFQPLGPYLSYVLLATAALDRYQAI CQPMTYCSSDSRRSRVMVMAWCISLVFCIPQVIFSYQETEPGVHD
CWATFVEKWGERTYVTWYSISVFLIPLCVLVYTYSCICREIWEKSGFRAAHAARSSPLKMNPTISRKINTVKQTAVIVLYISCSLPPFIQAQLWATWDPH
AAQSAFFTGAFTILALLSSLNSVCNVPWIYLA FNTELVLHLLTNRASAGAHADLVSGSGSSSTSWRNSRTRYRLVSGSMFKSRDSVRERRWAMAMPTKIP
IATALMAGRDLPTSEEVAS-
>Epiophlebia_superstes
GGRDEELAKAEIATLAAMLAVSVIGNAVLVALVWRPRSPRRRLSRMHLLVLYLCTADLITAAFTVLPQMAWEATYRFAPQAAPLCKPLKVLQLLGPYLS
SYLLVAMALDRHRAVCRPLSARVFLPRSPRRLVAIAWALSFLFSLPQAFVFSYRRATETEWDCWATFEPWPWTQKAYVTWYGISVFAVPLVLLLYAYAGICS
VLRRNHREKTRPHDERFLSRGAPRTHSVGTISKAKMKT LRLTIVAVACYILCSCPFLVLSQLWVTWYPGATESSFWKGAFTILSLMSCLNSVCNVPWIYMA
FNEDIRVALKERLSARVRYLLRPSFRPDITKRVRHQEASMSASSSRGSSQPKIRANSEEGRNGGR-
>Eurylophella_sp
FVVTIGNSCVLLVALSLRRAKISRMYFFILHLSIADLVTAFFNVIPQLAWEVTYRFRGGDILCKAVKFGQLLGPYLSYVLLVLTAVDRYFAICRPLSYCTW
PARRARLLVSFTWVLLALFCLPQLAVFSYQRVQNPADKQDYDCWATFPQAWGERAYVTWYAGSVFLVPLAILVYAYLCIFAIWRNYNNKQFSAQGIH
QHIVRNMNPRVHSIRGISRAKMTVKTLLVVIACVYVVCSTPFI CAQLWATWDPAMMHS
>Pogonognathellus_sp
MATNSNTTNEISEFPENKSA AAVPDSGRNESLANIEIAVLSVILFFAVVGNGLMLLALRRLQFRPMSRMYFFMLNLSVADLMVAFGNILPQLAWDITYRF
KGNLDCRVVFKLQIFVLVLYSTYVLTSMADVRYLVVCHHSFTRNHYGGLRGPKILVILSWILSFIFASPQAFIFSPKELTMDQTKVYDCWSTFIEPWGVR
AYVTWFVCAFILPLVIGASYGAI CCKVISFNLPNES
>Meinertellus_cundinamarcensis
LAIVEVTVLAVVLFVALAGNTMALFSLRLLRRLRPLSRMYFFMQQLSIADLMVAVFNVLPQLIWDITYRFGGDLVLCRLVFFQVMPLYGTYVLMFLAVD
RYRAVCSAGPSPQAAKKEARLMVCAAWILSII LAIPQALVFTHREIAPGIQDCWADFPGGQGAKIYVLFVIAVFMAPLTVIAACYGIIISLKVWQFSSPQ
STTAEPLAII CCARCRSSKSSSDRDTVLLRPIQSRNTSQRSSARLSRARMRTLRLTAVVACFIICWAPFCVSLVYNFNPTDQKQMSGVTVIFL LLA
SLNSCTNPWLYLAFSGSLNLHLRVCLGLGIGRAQDGDSDIGDEPEKTPPPPIQKQTNQDGGGGGGTKSDLV-
>Chrysopa_pallens
ILT LAIIFVVTLLGN GAVLALYNRQKCTGRKLSRIYFFILHLSIADLVTAFLNVLPQLAWEITYRFGGDPVLCKAVKFGQPLGTYLSSYILSATAIDRH
QAI CYPLTYCSWTSQRSQVMVWTAWII SLIFCIPQLFIFSYQEVSPGIWDCWGTFFPEKWEKTYVTWYSISVFIIPLSILVFTYTRICCEIWRNANIGMPL
RAMSSPCTPKRRAPLISRKINTVKQTVAVIILYIASSPFI SAQLWATWDPYAYKSPFWTGAFTILTLLSSLNSVCNVPWIYLSFNKELRKLKHIICS
KTYKNKNYSTAITNSGSSSQGVESTTVRVPLRISFYTRNDGGANGKQYTTNYHPSVRYTPKKWTVAI EELPP-

>Corydalus_cornutus
VTAFNVLPQLIWEVTYFRGGEILCKAVKFAQVGPYLSYVLTATAIDRHQAICHPLTYCSWTSRRSKGMVYLAWLCSLIFCIPQVVFISYQIVPDAPG
VYDCWATFSETWGEKAYVTWY
>Aleochara_curtula
RYAGRKKLSRMYYFIFLHLSIADLITAFSLDPLQLGWEVTYRFGGALCKMVKFQQTLPYLSYILMATAIDRHQAICY
>Cotesia_vestalis
DNSTSLDRDENLAFWEIIVLVINLIITLIGNCFIFFALYLRRYHGRQRKLRMYFFMMHLSIADFITGIFNILPQLSWDITFRFQGGPAMCKIVKFLQPF
GNLSSYVLTATAIDRYQAICNPFYSYCR
>Galloisiana_yuasai
ADLITALFNVLPQLGWEITRFRSFGPVLCKAVKFGQTLGPLYSSYVLLATALDRFQAICHPLTYCSWTSRRSRTMVWLAWAFS
>Liposcelis_bostrychophila
MNTKAREFGNKGKRTSTRSQKHLSHNEKMEEARQSSIPDINLTADPTMELVRKNDSTDDFRGNEDLAQIEIGTLGVILIVTILGNGLVLLALYAKKCKA
GKKTLSRMYYFIFHLCAVDLITAFNLVLPQLFWDITRFRKGNQFLCKSVKYG
>Zootermopsis_nevadensis
EVSEACNLTTANSTSGLDRDEALQAEIATLATMLTVTVLGNFAVLLALSARPRKLSRMYYFIFLHLSVADLCTAFSLVLPQLAWDVTYRFGGPLLCKIV
KYGQTLGPLYLSAYILMATALDRYQAVCHPLAYCSWTSRRSRAMVMAWVAFALIFCIPQVS
>Conwentzia_psociformis
IPYKMNDFNATDQNYGFYFLNSTASDAVIEAGTDLAAASDNGDERNEELAKIEILILIVIFNVTLIGNLVLLALSARKRYSGHRKLRMFFFIHLHSLA
DLISAFNLVLPQMIWK
>Stenobothrus_lineatus
QLSVVDLLNGLLNVLPQLAWEVTRFRWGGAVLCKLVKFGQPLGPLYSSSVLVVLTALDRHQAVCRPLTYCSWTYRRSRAMQVAV
>Leptopilina_clavipes
VDLLTAVLNVLPMQAWKITFRFQGGPFLCKLIKFGQPIGPLYSSYILTATAIDRYHAICFPFSYCRTRRSRIMVYSAWIIALILCTPQVVFVSYQLIS
PGIWDCAWTFVTPYQGEAYVTWYSISVFLPFTVLVYTYTGICIGVWKNKSGVSDPLEIGYKKNINIKKAKSINNKGKSKYDETNNCCC-
>Folsomia_candida
PLHEDNFSLTPNLSLVNTTLTPASPRDEFLEAKIEQSVLAIIFILITVGNFLVLMGIYFRKQKMRMYFIAHLAIADLTTAFFQVLTQLAWEVTYRFGG
>Occasjapyx_japonicus
LESFRMNASSNASATGGMNGYERNEDLAKVEIAILSTIFVLTIVIGNSMVLAIFLKRKMSRMYYFIFLHLSIADLITGFFNVLTQLCWEVTYRFGGNFMC
KFIKYMQLGPLYSSYVLMATAIDRYQAICFPLSNCSWTPKRSKVMIGISWVISLWFCAP
>Zorotypus_caudelli
LLVILLVTLVGNLIVLFAIYVRRRCRGRHRLTRMHFFVMHLSIADLINGLLNVLPQLAWDITFRFQGGQILCKMVKF
>Perla_marginata
EVTSLAAIFLTALAGNVCLLALYGHNRKLRMHFFILHLTIADMVTAVFSVMPQLWKATYRFAAGPTLCKVVKVQALG
>Osmylus_fulvicephalus
RTTMALMNSVGMGVPPTPSLELVGVLAAGGGGGLLPVDPSTANSTAMHDYDRDEALQVEIGTLALIFGVTLGNGAVLIALYIRRRYSGRKKLSRMYY
FILHLSIADLVTAFNVLPQLAWEVTYRFRGGVLCCKAVKFS
>Leuctra_sp
LVTAVVANLLVLTALILRSRRQLARLHFFILHLSLADLVNLFNVLPQLVWVKSTFRFVGGTVLCKLVKFGQTLGPHLTAFILVATLWDRTHAFYCY
>Mantis religiosa
AILSTLFFVIVLGNSSVLLALSSRRRKLRSMYFIFLHLSIADLITALLSVLPQLAWDITRFRHGGPGLLCKLIKYGQTL
>Arachnocampa_luminosa
MYSYQENILPNYSEQDKFENSNSVSLNNSNSVQQFQNLNSLLTKIEVFLLSLFLTLVIGNLIVILIIILYRNMSPKRARWFKLNKNISRMSFYIIHLSIAD
FNVAFMSILPQLIWRQSVFVFNHSHFLCKFVAFSQQVFSVYASTFLLIVMAVDRFKCICWP IKSCSWNYRHALVPVFFSWILAAVSSPQLFLFKIQHMSVQH
YTVETCSVKWLSKKEGLYLLFHMSTQFLIPLFVLTFLYSRIFMTVSKNIKQKHASIRFERESSKTATEINQLNQENSLNTQNGLI TEVKHSDNSIFRDK
KFGILWWRSRFNKGRIRKILFTSTKKGKNIKFGKGTGNFLMNDQTMPKEYEMRLMLKRKETSLSDEKYSMLDKNSVYSKSFKNFP IRQTFSGKALTRS
KIKTLKLLTIVVITYVMCSLPHYVCTFIHFLGLLSAHNHSSLFKTLVYITISTNMLFQLNSCANPFIYLFNGNICKLAKRLKTKV-
>Diaphorina_citri
MUVHNVGSFLSSYILMAIAIDRYRAICHPLTYHTWNSRRSRIMIMTAWSTAFTFCIPQITIFSYQEVEKPGIYDCWASWDQEWGERAYVTWFSITVFIIPLF
CLVYTYTCICVALWQNTTYPTTSPHKIISRAKINTIKQTIIVITLYIVCSLPIFTQLWQTNWLNQTVYVQDNVLTIIIMLLSLNSCVNPWIIYLVNSR
ELIAALRTLCSNLRFSDDTELMTDASASGSKECGRRTESDLTFLNRTTYSNPDENGLIPLIILTFAYTICRAIINFMSKNSIRRHQFSRSRSTRDSE
TENELCHTIVDSG
>Blaberus_atropos
NTVKQMVAVLFLYVACSAPFISAQLWATWDDLAHTRPFFSGTAFTILALLYSLNSCMNPWIIYLFNRELIRFLTQQLFCRTQ
>Frankliniella_cephalica
SIEPVEGGYDCWATFVPEWQRAYVTWYTCVFMIPLTVLLFTYSRICCEIWRSSASKHAPALVDGCTKCPHVHAYAYRFAPHQQPAPVSSNSFAYARSQ
QQATQRTNPLISRAKINTVKQTVLVIAYIIICSAFFICVQLWAAWGNADNPFQGRYMTILTLLFSLNSCVNPWIIYLAFNNDLVRMLWLLVSCQTGHPSGS
VLSAHSGGSSQSNTTQHRTCTFD
>Tricholepidion_gertschi
TRGRPVIIHQGATVQADVPRPAPVNPRTSMKGISRAKIKTVKLTVVVIACYIFCSPFISVQLWATWDPNASKSPFWTGTFTTIFTLASLNSCVNPWIIY
LTFNRDLVRLNQL
>Carabus_granulatus
SRAKINTVKQTIIVIAMYIICSTPFICAQLWATWDPSTFLNGAAYTILTLNLSLNSCVNPWIIYLAFNRELPRLLLRHYAATSKNYRSAGTNSASNSGG
VESTSLRPFKWSLCASTKSTPRY
>Acanthocasuarina_muellerianae
KIISRAKINTVKQTVAVITLYIICSLPFIQAQLWQTNWLNESFYVQDNVLTIIIMLLSLNSCVNPWIIYLVSNRKLITALRTLVCNVLVSEAKVAM
DTASGMSSSRERNESEMGLTFLNRHEDTGMSDDLTLRSRQVWVTLDPANQTR-
>Anurida_maritima
SDFLCRLIKFLQIFVLYLSTYIILSMTLDRYLTVVCHHSFNRNHYGGLKSPKVMVAISWILSLIFASPAVIFSQSEIRPGVDFCWTFLGPGSVKAYVTWFW
ISVFLPLLLICGISYGAICFKVVSFSLHESNNRKLNEVSRYSKNSRSVSSSPETQSEVVEEAPTPKDVGSRRLAQQISEVKIKTLKTLVVVLCFFVCWS
PFCVTQLILVYNPTLPVPGNVILLLLPSLNSCTNPWIIYLAFASESLCNQRLVFLGIGLRRGSSGESIGAEQDIILRTKFKTPRPDTRPHQDKSRMTMKQVS
TLDAIENQGAFLQLLETKSEVL-
>Machilis_hrabei
GISRAKIKTVKLTVVVIACYVTCSTPFICAELWAADPNVHSSFWQGAFTILTLLASLNSCVNPWIIYLVFNPNLVRDFRHLKLMCCGGDYLHNSGIP
SGGGFDRGTLFRSSSTSDSKAPSANQNKIAVTRTSVSSQSGVLLKRRTLNGDKQPTAVEMRNWKCDETNRPLLAETSDFIQCAIGENE
>Glomeris_pustulata
KTVKLTVVVILSYIACSMPIISAMLWLVWYPEARNTPFGRSAAFTILALLASLNSCANPWIYLCFNENVAQTLGDVICCRKCRNSSATNEHGAPIVGVFSR
SSLSDTNQRSTHVHTLAHQG-

>Dendroctonus_frontalis
 ICYPLTYCSWTSRRSKFMVYVIAWIASLLCCIPQVIIFSFQEVPRVYDCWATFDNEWGEQAYVVCYSVTVFIIPLFVLVYTYTTCICREIWRCSDSLRRPS
 MSKQSTKRDRVPLISRAKICIGIWRSNKMTSAENWRKKSRSNRSVNIERNRSPFISKAMINTMRQTIIVVISLYAITSIPFIGCELWVTDTEAIKSSFANGPA
 GAPDQGTLSNNSGQVTSKLRTRASPRGRDRLHTNQRQWMTAT-
 >Mischocyttarus-_flavitaris
 QGGMVLCKLVKFFQPLGLYLSSYILTATAIDRYHAICHPLSYCSVTSRKRIRIMVYCAWSLSLILCIPQLFVFSYQEIPTNIWDCWATFDIKFGERAYVTWY
 SLMVFLLPFIVLVYTYGICVGVWQSNKMSDAVDDRKYIRSISSTCRNRSSFISKAMINTVQTIIVVISLYAITSIPFIGCELWVTDTEAIKSSFANGPA
 FTILTLLNSLTSCVNPWIYLSFNRELRQNLNMYFYNRNDEYSQTYYGQRGMRRSDSNDTSTRASLMSRISRYASSIIPR-
 >Argochrysis_armilla
 GGNVLCVLKVKFIQPLGPLYSSYVMATAIDRYHAICHPLSYCGSSSLKRSKIMVYSAWAVALILCIPQVVVFSYQEVTPKVVDCWAVFDVAYGERIYVTWYST
 MVFLLPFTVLLYTYGICVGVWQSNKMSDAVDDRKYIRSISSTCRNRSSFISKAMINTMRQTIIVVISLYAITSIPFIGCELWVTDTEAIKSSFANGPA
 TILSLSSLTSCVNPWIYLSFNRELRQNLNMYFYNRNDEYSQTYYGQRGMRRSDSNDTSTRASLMSRISRYAGSMIFR-
 >Calanus_finmarchicus
 ADILTAIFTLIPEIAWTTLPAFWGGDAVCKIIKFLQMLGPLYSSFLLCVTSMDRYQAICKPFKTCSEPKNSDKLVGGAVLAILCCIPQLLIFNTSSQ
 IGCNSGEMFEKQTNFPTWTPSQYILYFSANFFIPLILLFSNCFICKTIWASSNLNWNRRTTKKENKMDSPKLYITMANGPKSKLSVQNRSTSV
 VSRKIKSVKLTIVIIACYILCSAPFIVGQLLATLGPPIHRSKIGLQMEPLFWMTLNLSLVNPIYIWFNRNTLFRVQTSNENTTALQLSQMEVFPSSP
 TPTRLRRLNSKNSVLRSSFIIEVVGLE-
 >Tigriopus_californicus
 MATLLSSDIEAKMDKEPDNPNYSIPDSNETKGSGLDLNFTDGGPDFSRDQDLATAEVVVQAVIFVLALVGNGLVVALIRQLRRKPSRRMYRLMYHLSI
 ADLLVAVLNVLPLIWDITHRFHGPDILCRLVKFGQVMPYIYLSFILTMAVDRVGVTKRHGSVEPKPLRPLIQGVVLAIALCALPQPFIFSIKIDDDKGI
 YDCWADFGGEKWKLEKGVVTFVFLVFFLPFIVITSSYCIYTYRISYSRATQGSKASPQMSLASNRVVLSSVGDGSKNEDDDGATMETAVYEMKVINGRN
 GSSSSHRSSCKSTTRSINTSCTIYRPNLAHNSHAPTGGFVRVQTEQIVLLSKAKRKSLSMTAIVSVCFVAVCWLPWCVTMLLMSFDIQVGGDKVHPLMVIFA
 LLASLNSTNPNWIYLCFSAVQLQVVKHLVGMRSITGGPDSLGGADADRPQTHHRTKRILFTRKAEPLKGNPLGARPHPLFALQDQEIIVRAGIRSEPNLS
 SHRPNVKNPLPASNQNKSWTKT
 >Atta_cephalotes
 MSHDLNSSSSSELPLDDARDEYLARWEIAVLTSIFLITIIIGNVLVLLALYARRRYQRRKFTRMVFFIMHLSVADLLTGLFDVLPQLAWDITFRFQGGAVL
 CKLIKFGQPFGLYSSYILTATAIDRYHAICHPLSYCSVTSRKRIRIMVYCAWSLSLILCIPQLFVFSYQEIPTNIWDCWATFDIKFGERAYVTWY
 LFPFIVLVYTYGICVGVWQSNKMSDAVDDRKYIRSISSTCRNRSSFISKAMINTVQTIIVVISLYAITSIPFIGCELWVTDTEAIKSSFANGPA
 NSLTSCVNPWIYFAFNKELRVALTCFFYRKKDYSLTYDIDARQNASDVPSTSSFSRISRLASSKIFG-
 >Brachionus_koreanus gb|GBXV01023685.1| TSA: Brachionus sp. 'koreanus' Rotifer_01189 transcribed RNA
 sequence
 MTSYQENMLLDYSEQKKSEELQNSFNNSDSSEQFQINNKLLTQIEVFLSCLFVLTIVIGNLTVILIIILYRNMSSKRARWFKLNKNISRMSFYIHL
 IADLNVAFMSILPQLIWRQSVVFNHSHFLCKFVAFSQVFSVYASTFLLIVMAYDRFKCICWPIKCSWNCRHALIGIFVAWIIAATISSPQLFLFKIQHMN
 AHVYTVETCSVKWMSKRHEGLYLLFHMSTHFLIPFFVLTLYLSRIFLTVSRNISRKHASVRFERESSKTGTEINQLNRENSLNTQNGLITEIKNESENSIF
 RDKKTGIIWLRSFNKSIRHKILYTSKKSQKNIKFSRQNFSLNNSLPKEYEMKMLKKNPDSSEDRYSRMLDKNSVYSKSFKNFPIRQTFGKAL
 TKSIIKTLKLTTLTVVITYVMCSLFPYVCTFIHFLGLSAHNNSLFTFKILVFATISTNMLFQNLNSC

(B)

>Tetranychus_urticae gi|1005961572|ref|XP_015789083.1| PREDICTED: isotocin receptor-like
 RMLSSFGSLFSTLSVFNSTNETSSTLPSLVLPFDVNLTSRYLKAIVSTGSPASLSSSSAHSRDNLALEIITLSAIFVMIVFNSTVLLALILSRIKL
 RMYFFLLHLSIADLITAFANVLPQLIWEITERFYGGNVLCKGKYLQILGPLYSSFTLCATAIDRYRAICFPLESRSALNRSKLKVSIWGLALICCLPQ
 LFIFSYRQIPNSPGVYECWGTFIQPYGERLYVTWYALTSFFIPIFVILIFTSNICLELWRNGRRIKKANLSQSHSTAYFSKAKIKTKVLTVTIIICYICCS
 SPFNVVQIWAYWAPGAQESSLWRGPLITIAMLLPSLNSCVNPWIYLFNFRNLLSTLTKLFCYCSNTNINAGNRSKTLDDSSVNIPEHCSSINRNGSRTIF
 VSQMSKYSDDKPSVEAHS
 >Nasonia_vitripennis gi|288558761|ref|NM_001172274.1| Nasonia vitripennis neuropeptide receptor
 (ITR), mRNA
 MEESATSMIAAPAEWRDES LAVWEVIVLALILTTTFMGNVLVLFVFAIYLKRCRGRQRRLTRMHFFVMHLSVADLITGLLNVLPLQLAWDVTFRFQGGPILCK
 LVKFCQPLGSLYSSYILTATAIDRYHAICHPLSYCYRTTSRKRIRIMVYCAWSLSLILCIPQLFVFSYQEIPTNIWDCWATFDIKFGERAYVTWY
 FCVLTFTYAEICCSIWRNREVMVLASHERQALTKEGRSQTTLSKAKINTVQTIIVVISLYAITSIPFIGCELWVTDTEAIKSSFANGPAFTILALL
 LTSCVNPWIYLFVSYELRAALTKFLRSLIKRDRSRFERASSNANSNETRSSKRSFISRMSRYTSFIIYGPMTIEIVNKLYI-
 >Orussus_abietinus gi|817193573|ref|XP_012272252.1| PREDICTED: vasopressin V1b receptor-like
 MIHEDMDAEDPPTTNPVEDFRDSDLARWEIFTLAAILLALLENLVLALYRGRRLSRIQFIFILHLSIADLITGLLNVLPLQLAWDVTFRFQGGDLL
 CRLVKFGQPFGLYSSYILTATAIDRYHAICHPLSYCYRTTSRKRIRIMVYCAWSLSLILCIPQLFVFSYQEIPTNIWDCWATFDIKFGERAYVTWY
 FLLPLCVLVYTYGICVGVWQSNKMSDAVDDRKYIRSISSTCRNRSSFISKAMINTVQTIIVVISLYAITSIPFIGCELWVTDTEAIKSSFANGPAFTILALL
 NGCVNPVHLGFDPELREVILRHLQAPTRSKQEADRKP
 >Polistes_canadensis gi|954548184|ref|XP_014616661.1| PREDICTED: vasopressin V1a receptor-like
 MNETTNSSTVANEEKDTRDENLAKWEIVLLANILIFTIFGNSLVLLSLYLRKYRAHKKLSRMVFFIMNLSIADLITGLLDVLPQLAWDITFRFQGGVLVLC
 KLVKFFQPFGLYSSYILTATAIDRYHAICHPLSYCSVTSRQRIRIMVYCAWSLSLILCIPQLFVFSYQEIPTNIWDCWATFDIKFGERAYVTWY
 PFIVLVYTYGICVGVWQSNKMSDAVDDRKYIRSISSTCRNRSSFISKAMINTVQTIIVVISLYAITSIPFIGCELWVTDTEAIKSSFANGPAFTILALL
 NSLTSCVNPWIYLSFNRELRQNLNMYFYNRNDEYSQTYYGQRGMRRSDSNDTSTRISLMSRISRYTSSIIIR
 >Metaseiulus_occidentalis1 gi|391341506|ref|XP_003745071.1| PREDICTED: oxytocin receptor-like
 MNSSAGNFGDARDETIAHVRITVLCFCLLFTLGGNLFVFLVTRNRPKSVHQLHIYHFMVHLSLADMLVGVFNILPQIVWEIYFRFRWGNIAACKFVKFMQI
 FVLVYTYGICVGVWQSNKMSDAVDDRKYIRSISSTCRNRSSFISKAMINTVQTIIVVISLYAITSIPFIGCELWVTDTEAIKSSFANGPAFTILALL
 LCRASSKRLMSDAKLTIRMTVMVVLVFLVLCWTPFCCAQLYLVFGGEEASTFVTMCLMVPNLNSCANPWWYLSFSTDLRRLVNFCSLIHLRGNRYGEE
 KPCSTRANAIVCEKPARQLRGYRIS
 >Metaseiulus_occidentalis2 gi|391328891|ref|XP_003738916.1| PREDICTED: vasopressin V1a receptor-like
 MEYNTDITDFVQPENWVLSVKCATLVIIFFLTLSSNLFVLAHLLRNQRPLSRVQLFMLHLTVADILVALLNLPQLAWDLTIQFRGAVLCKLVKFA
 QVYVLYLSTYILTGMSLDRLITMRAIESQWQTASLRSDHQSSDKSPQSHKIKFNHRCRVGYRKFVAKKLVFAWFLAALSIPQLFLFSYTRIHDHGSW
 YDCKANFSWHRFGQRIYTYFYVVLILGVVVMMLFQIQLIIRQHMTTTSAPANFGVNTAGFFESNRRIKAKVIRVMKMTFTVTKLFCIVCWSPY
 SIAELLLAYKIAGGEHVSPFVFMVLLASLNSAVNPWIYTAFTNSFACKSLRTLKPEVHLITV
 >Strigamia_maritima Chipman AD et al. PLoS Biol. 2014 Nov 25;12(11):e1002005. doi:
 10.1371/journal.pbio.1002005. eCollection 2014
 MSNESHWEDDLTDNATSNAPPQSSAIADAKLTVLALMFATIMLGNTIVITSLIRKRLTRMYFFILHLCIADLIVAFVLPQLCWDVTHRFQGNDFL
 CKVIKFGQLGPLYSSYILVGMADRYLAICFPLNSWAATRSGKMGVCVAVVSVVSSPQMFVLSYKYVSVLKYWECWVDFLEERAYVTWYFVANTFVP
 LLVLVYTYSAICWAVWRNFRHKKNSPKGDFDSAASSPTTATHLSVQNVNHIQRNGSCRFKASESVNPRSHGLQRISRAKIKTKVLTVVVITCYILCSMP

YTCAMMWVAYDKRAQETAIFYKGGFLFPVLLVASLNSCVNPWVYLLFNKNLVHTLRLHYLCCSKENEMKSHRTLATYTSRSTFSESVGPVALQSLPSSNNF
 LRVDNKNLNVRAVAVSDSALYSCEKRHSSPNLNVKSAASTLVLCSSQHHHTDQNHKLDGVTMETQCA
 >Strigamia_maritima_2 Chipman AD et al. PLoS Biol. 2014 Nov 25;12(11):e1002005. doi:
 10.1371/journal.pbio.1002005. eCollection 2014
 MATHAEGDSYTRNPPPTKIPMDNNPNYNNKTTDGMIRDENLASIEIAVQSIILVVAIISNSFVFAALCCQRRFRPTSRMYLFMLHLSVADLLVAFLL
 SLLPQLIWDVTRFRQGSIDLRCVVKYLQVMVYLSTYILVMMAVDRCAVCSWITGHWNSLRAAKLMIVGAWLAFVLAIPQAIIFGKMEIRPGVHDCWAH
 FEQPWGEKAYVTFWVLSFIIPILVIAAASYGFCYTLWIYDEEHGRSGDVIALRAVGNVTGGGDDTVDTSCLRSYRVRVAGVSNPNPISEAKVTKLTLFLV
 VCFVVCWSPFCITQLVLTFFNPSPDAQIGSVEVILLLLASLNSCTNPWIYVAFSGSLLNQLRMCLGLGLTRPKDIASIGDEEPQPPQPPQNTKLPSTKSEM
 V
 >Ixodes_scapularis1 gi|215501697|gb|EEC11191.1| vasopressin v1a recpetor, putative
 MDVPSNQPEFAASVPTVLFNFASTNLASTETRDESLALVELAVLTLIFAFVTVMGNSTVLLALATRSMKTRMYFLLHLCSVDLITAFVTLVLPQLGWDAT
 YRFQGGNLACKAVKFGQLLGPYLSYVLLVAVDQYQAI CFPLSNCSWPTPKSKLLICAAWVAALLCCVPQVFI FSYQEIVSPEVDFCWGTYVESWGLRAYV
 TWYGMSVFFVPLMVLTFYVICRSIWRNLYLKRKSSDAESWKGERRAYRFRGLAHNGTKQDSSFFVGRSHSVRGLSRAKIKTVKITVVVIALYVVCSSPFI
 CVQMMWYSPHVDMANPWISE
 >Ixodes_scapularis3 gi|215501196|gb|EEC10690.1| vasopressin v1a recpetor, putative, partial
 MDLVANQDQPAFSTSLPDLDDVPVNETFWTGTREDESLAQIELGLVTAIFFTFTVIGNTTVAALAARRSKMSRMYFLLHLCSVDLITAFVTLVLPQLGWD
 TYRFRGGNLACKTKVFGQLLGPYLSYVLLVAVDQYQAI CFPLSNCSWPTPKSKLLISAAWVASLLCCVPQVFI FSYQEI SPKVFDCWGTVEPVGWGLRAY
 VTYWGVSVFFVPLVLLSFTYVICRSIWRNLYLKRKSSDAESWKGERRAYRFRKGTAGNGTKQDSSFTVKITVVVIALYVVCSSPFI CVQMMWYSPDAD
 >Ixodes_scapularis2 gi|215493320|gb|EEC02961.1| vasopressin v1a recpetor, putative, partial
 QVEVAVLTFIFGFTVLGNTCVLVALAARRSKMTRMYFLLHLCSVDLITAFVTLVLPQLGWDATHRFRGGNLVCKAVKFGQLLGPYLSYVLLVAVDQYQ
 AICFPLSNCSWSPCKKLLIAGAWVAALVCCVPQVFI FSYQEVAPGVDFCWGTFQAPWGLRAYVTVSVSVFFVPLAVLSFTYVICRSIWRNLYLKRKSS
 ADHSVRGMSRAKVKTVKITVVVIALYVVCSSPFI CVQMMWYSPDADVLDVWINATVITLMLLNSLNSCVNPWVYLLFNRSILVHTLRLHQICRCPDAKNVSS
 GIAGTGSQPSAVILADLTQTEAQSVLSYKSSPTDTSARLATAVVGKRGATDVEEDLQCSLEKTS
 >Ixodes_ricinus gi|1016843980|gb|JAR88791.1| putative vasopressin v1a receptor
 MDLVANQDQPAFSTSLPDLDDVPVNDTSWTGTREDESLAQIELGLVTAIFFTFTVIGNTTVAALAARRSKMSRMYFLLHLCSVDLITAFVTLVLPQLGWD
 TYRFRGGNLACKTKVFGQLLGPYLSYVLLVAVDQYQAI CFPLSNCSWPTPKSKLLISAAWVASLLCCVPQVFI FSYQEI SPRVDFCWGTVEPVGWGLRAY
 VTYWGVSVFFVPLAVLSFTYVICRSIWRNLYLKRKSSDAESWKGERRAYRFRKGTAGNGTKQDSSFFVGRSHSVRGLSRAKIKTVKITVVVIALYVVCSSPFI
 CVQMMWYSPDADMTYVNTICRSITWRNLYLKRKSSDAESWKGERRAYRFRKGTAGNGTKQDSSFFVGRSHSVRGLSRAKIKTVKITVVVIALYVVCSSPFI
 ICVQMMWYSPDADMTYVNTICRSITWRNLYLKRKSSDAESWKGERRAYRFRKGTAGNGTKQDSSFFVGRSHSVRGLSRAKIKTVKITVVVIALYVVCSSPFI
 >Limulus_polyphemus1 gi|926615389|ref|XP_013772773.1| PREDICTED: oxytocin receptor-like
 MSTLDFGETPEILNVFNMNSTIINNTKDKGIQRDETIARIEVGLASIFTLTILGNMCLVALAVRRIKMARMYFLLHLCSVDLITAFVTLVLPQLAWDV
 TYRFYGGNVLCKVIKYLQILGPYLSYVLLVMTAIDRYQAI CFPLRNCVWTPRKSCLMIAAWTISMLCCVPQVFI FSYQKVLIEPI FDCWGVFIQPWGK
 VYLVWYALSQFFIPLVITFTTCVRI CKNVVYVNFHLRGNKSSRSRSHMSRAKVKTVRITVVVIAICYI ICSTPFIIVQLWAYWSPYAQTSPIWKGPVAIL
 MLLASLNSCVNPWIYLAFNHNLVLTALKHICCHERSQGYSPQVVENINNTTSRSQTDNEICTSYPLSLRCGVHYTSSFRLLKTKITGCRPCPNIQDLHDE
 AETESA
 >Limulus_polyphemus2 gi|926636334|ref|XP_013784095.1| PREDICTED: oxytocin receptor-like
 MSTLAKGETTGFLNLSFVNLSTIINNTKADVQRDETVARIEVAVLATIFTLTILGNITVLLVALVRRRIKMARMYFLLHLCSVDLITAFVTLVLPQLAWDV
 TYRFYGGNVLCKVIKYMQLGPYLSYVLLVMTAIDRYQAI CFPLRNCVWTPRKSCLMIAAWTISMLCCVPQVFI FSYQKVSDEPVTDFCWGFIQPWGK
 VYLVWYAVSQFFIPLVIAFTYIIRICKSVVYVNLQMRQASNCETFTVPSRSHCMRGLSRSKVKTFKITVVVITCYI ICSTPFIIVQLWAYWSPYAKNSIWK
 GPTVAIIMLLASLNSCVNPWIYLAFNHNLVLTALREVCCQTSKFSFSSQVPENTDNTFSRSECSYPLSVRVTGSRHKFPDGGSTTRTRKRLCRELGSKNES
 DTVGENRGSVQTQFETTSEPGKFFVTRDKDKTLC
 >Limulus_polyphemus3 gi|926627326|ref|XP_013779233.1| PREDICTED: oxytocin receptor-like
 MSSLKEEQTELTNASFVNFSPINENITVGDTRDETIARIEVAVLATIFTLTILGNITVLLVALVRRRIKMARMYFLLHLCSVDLITAFVTLVLPQLAWDAA
 HRFYGGNVLCKVVKYLQILGPYLSYVLLVMTAIDRYQAI CFPLRTRCTWTPRKSCLMIVGAWIISILCCFPQVFI FSYQKVSDDPLVDFCWGTFI QPWGK
 VYLVWYALSQFFIPLVITFTYVNTVKNVYLRKKNFICRVSVPDLRSLAKVKTVRITVVVIAICYI ICSTPFIIVQLWAYWSPYAKNSIWKGPVAILM
 LLASLNSCVNPWIYLAFNHNLITALKQLCCRSVLQDYMAQSTEATSNNNANRSYPTENEVNSYPLSFFIAQEEPVMLRNLKKKQ
 >Daphnia_magna1 gi|940945035|gb|JAK30878.1| Vasopressin V2 receptor
 MASSSLLSNVTNVTTELASSRDEKLASIEIGTLSFILLAVTNSLNTMLIAIWRQRNRPLSRMYFFMMHLSLADLLVALFNILPQLAWDITYRFHGGDVL
 CRFVKYQIMTLYLSTYILMFMVAVDRYRAVCCRNHLHWSLKVAKCFVAASWVMSMLFAIPQAVIFHEEEISVGVTDWCWQFAEPWGAAYVTFVVSIFGA
 PLLVVAVCYGVICRQIWIYYSQSAQPSLLPSDNSAIPSHSITETGSTLSVMRRWFLRAGMRWQKSRNSNAIKNNSATASQLSDTIPNKISPMLPQPPAA
 PQRCCQMSLRRSNQNRITKAKMKTIKLTLAVVLCFVACWAPFCITQLIMVYCPPTSQADVSPVAVI ILLASLNSCVNPWIYLAFFSGSLLNQMRVCLGL
 RWRGQDKDSIGEDDRRGAAGPAGGQPADTNHRFGRGPRRAQTRDQHRQVMAEQQLLPAGEQHPAMPLATKCTRADIVTHLGNTKKQLQFQQNHQHVKEIG
 >Daphnia_magna2 gi|942393099|gb|JAN7849.1| Vasopressin V2 receptor
 MASSSLLSNVTNVTTELASSRDEKLASIEIGTLSFILLAVTNSLNTMLIAIWRQRNRPLSRMYFFMMHLSLADLLVALFNILPQLAWDITYRFHGGDVL
 CRFVKYQIMTLYLSTYILMFMVAVDRYRAVCCRNHLHWSLKVAKCFVAASWVMSMLFAIPQAVIFHEEEISVGVTDWCWQFAEPWGAAYVTFVVSIFGA
 PLLVVAVCYXXXXXXXXXVQFAEPWGAAYVTFVVSIFGAPLLVVAVCYGVICRQIWIYYSQSAQPSLLPSDNSAIPSHSITETGSTLSVMRRWFLRAG
 MRWQKSRNSNAIKNNSATASQLSDTIPMRSLATQQASNPLTTEENKISPMLPQPPAAPQRCCQMSLRRSNQNRITKAKMKTIKLTLAVVLCFVACWAP
 FCITQLIMVYCPPTSQADVSPVAVI ILLASLNSCVNPWIYLAFFSGSLLNQMRVCLGLRWRGQDKDSIGEDDRRGAAGPAGGQPADTNHRFGRGPRRAQ
 RDQHRQVMAEQQLLPAGEQHPAMPLATKCTRADIVTHLGNTKKQLQFQQNHQHVKEIG
 >Daphnia_magna3 gi|939881383|gb|JAJ41077.1| Vasopressin V2 receptor
 MASSSLLSNVTNVTTELASSRDEKLASIEIGTLSFILLAVTNSLNTMLIAIWRQRNRPLSRMYFFMMHLSLADLLVALFNILPQLAWDITYRFHGGDVL
 CRFVKYQIMTLYLSTYILMFMVAVDRYRAVCCRNHLHWSLKVAKCFVAASWVMSMLFAIPQAVIFHEEEISVGVTDWCWQFAEPWGAAYVTFVVSIFGA
 PLLVVAVCYGVICRQIWIYYSQSAQPSLLPSDNSAIPSHSITETGSTLSVMRRWFLRAGMRWQKSRNSNAIKNNSATASQLSDTIPMRSLATQQASNPL
 TTEENKISPMLPQPPAAPQRCCQMSLRRSNQNRITKAKMKTIKLTLAVVLCFVACWAPFCITQLIMVYCPPTSQADVSPVAVI ILLASLNSCVNPWIYLA
 FSGSLLNQMRVCLGLRWRGQDKDSIGEDDRRGAAGPAGGQPADTNHRFGRGPRRAQTRDQHRQVMAEQQLLPAGEQHPAMPLATKCTRADIVTHLGN
 TKKQLQFQQNHQHVKEIG
 >Daphnia_magna4 gi|942156180|gb|JAM92944.1| Vasopressin V2 receptor
 MASSSLLSNVTNVTTELASSRDEKLASIEIGTLSFILLAVTNSLNTMLIAIWRQRNRPLSRMYFFMMHLSLADLLVALFNILPQLAWDITYRFHGGDVL
 CRFVKYQIMTLYLSTYILMFMVAVDRYRAVCCRNHLHWSLKVAKCFVAASWVMSMLFAIPQAVIFHEEEISVGVTDWCWQFAEPWGAAYVTFVVSIFGA
 PLLVVAVCYGVICRQIWIYYSQSAQPSLLPSDNSAIPSHSITETGSTLSVMRRWFLRAGMRWQKSRNSNAIKNNSATASQLSDTIPMRSLATQQASNPL
 TPDTIPMRSLATQQASNPLTTEENKISPMLPQPPAAPQRCCQMSLRRSNQNRITKAKMKTIKLTLAVVLCFVACWAPFCITQLIMVYCPPTSQADVSP
 AVI ILLASLNSCVNPWIYLAFFSGSLLNQMRVCLGLRWRGQDKDSIGEDDRRGAAGPAGGQPADTNHRFGRGPRRAQTRDQHRQVMAEQQLLPAGEQHP
 MLATKCTRADIVTHLGNTKKQLQFQQNHQHVKEIG
 >Daphnia_pulex tr|K9JBV2|K9JBV2_DAPPU Oxytocin/vasopressin receptor-like protein OS=Daphnia pulex
 PE=2 SV=1
 MSTNMSNATEEPSSSLRDEKLASVEISTLSVILVAVTNSLNTMLIAIWRQRNRPLSRMYFFMMHLSLADLLVALFNILPQLAWDITYRFQGGDVL
 YAVMTLYLSTYILMFMVAVDRYRAVCCRNHLHWSLKVAKCFVAASWVMAIFSIQAVIFHEEEISVGVTDWCWQFAEPWGAAYVTFVVSIFGAPLLVI
 GVCYGVICRQIWIYYSQSAQPSLLPSDNSAIPSHSITETGSTLSVMRRWFLRAGMRWQKSRNSNAIKNNSATASQLSDTIPMRSLATQQASNPLT
 SAEA

KVIRSLPPLSPQCCQOMPLRRSNSNQNRITKAKMKTIKLTLAVVLCFVACWAPFCITQLIMVYCPPTSQADVSPVAVIILLASLNSCSNPWIYLAFFSGS
LLNQMRVCSILLRSTHLEFIEQLLFFIRVSRKSRNI
>Microplitis_demolitor gi|665813630|ref|XP_008555379.1| PREDICTED: vasopressin V1a receptor-like
MMGNSTQPDTRDENLAIWEITVLAJNLIITIGNCLIFFALYLRHYGRQRKLTMRMYFFMLHLSIADFTVIGFVNLVLPQLAWDITFRFQGGYGLCKI IKFLQ
PFGNYLSSVLTATAIDRYQAICYPFNYCRTSSLSKSRVMVYGAWLSFVLCIPQVIVFVSYQEISPGVWDCWASFSLPYGERIYVTVYSITIFLLPFLVLLY
TYASICANIRNTEISDRPDHVNKNKINFNKNRQPLISRAKIKTVKQMITVSVLSVMTSSPFIGCQLWATWDPQAANSSFIGPAFTILTLMSSLTSCV
NPWIYLGFNRELRNLISNYLKLKCKQNVINYDIDTSYVNSNGSSTKSSIVTMFVAGSMYHRQTYQERSTDFILTRRQS
>Vollenhovia_emoryi gi|795106077|ref|XP_011881673.1| PREDICTED: vasopressin V1a receptor-like
MSRDLNSSSSTSPSLSEWPSNDARDEYLAKWEIAVLTSIFLVTLLIGNALVLLALYIRRRYQRRKFTRMVFFILHLSVADLLTGLLDVLPQLAWDITFRFQ
GAALCKLIKYGQPFGLYLSSYILTVAIDRYAICHFPFSYCGITSRSSKMMVYGAWLAATLVCVPQIFIFSYTEISPGVWECWATFNLKYGERAYITWYSV
TQFLLPFIVLVYTYTRICMSIWTSSKMSGVVDLKRNSKASFFQRNRDPIISKAMINTVKQTIIVVVTLYIITNIPFIGELWATWDPATSSPFFTGAAFTI
LSLLNSLTSCVNPWIYFAFNKELRAALTNFFCSKDYSLTYDIDVRQNASDVPSSSTSSFSRISRLASSKIFG
>Cerapachys_biroi gi|759037579|ref|XP_011350516.1| PREDICTED: vasopressin V1a receptor-like
MSYDLSSSLPLSLSPSSPSSSSPSSLEVSDDLREYLAWEIAVLTSIFLITIGNGLVLFALYARRCYQRRKFTRMVFFILHLSIADLLTGLLDVLP
QLAWDITFRFQGGAVLCKLIFGQYFGLYSSYILTVAIDRYAICHFPFSYCAVTSRRSKMMVYGAWLAAILCVPQVVFVSYKEISPGVWECWATFYLK
YGERAYITWYSVTQFLLPFIVLVYTYTRICMSIWTSSKMSGVVDLKRNSKASFFQRNRDPIISKALINTVKQTIIVVVTLYIITNIPFIGELWATWDPKAS
TSPFFTGAAFTILSLLNSLTSCVNPWIYFAFNRELRRAALTNFFCRKDYSLTYDIDAHQNASDVPSTTSSFSRISRLASSKIFG
>Harpegnathos_saltator gi|749796630|ref|XP_011151734.1| PREDICTED: vasopressin V1a receptor-like
MSYDLNSSLPLSPSEWPSNDARDEYLAKWEIAVLTSIFLITLIGNALVLFALYVRRYQRRKFTRMVFFILHLSIADLLTGLLDVLPQLAWDITFRFQ
GAVLCKLIKYGQPFGLYLSSYILTVAIDRYAICHFPFSYCNVTSRRSKMMVYAATLAVVLCVPQIFIFSYQEISPNVWECWATFHLKYGERAYITWYSV
TQFLLPFIVLVYTYTRICMSIWTSSKMSGVVDLKRNSKASFFQRNRDPIISKALINTVKQTIIVVVTLYIITNIPFIGELWATWDPRAAISPFILTGAAFTILCL
LNSLTSCVNPWIYFAFNRELRVALTNFFCRKDYSLAYDVIARQNTSDAPISITSSFSRISRLASSKIFG
>Dinoponera_quadriceps gi|951533502|ref|XP_014470481.1| PREDICTED: vasopressin V1a receptor-like
isoform X2
MSDDLNSTSSPPSASEQTPVDGRNEDLAKWEIALTSIFLITLIGNTLVLLALYARRRQRRKFTRMVFFILHLCIADLLTGLFDVLPQLAWDITFRFQGG
AVLCKLIKFGQPFGLYLSSYILTVAADRYAICHFPFSYCVTSRRSKMMVYVWVLLAVVLCVPQVIFISYQEISPNVWDCWATFNVKYGERSYVTVYSVT
QFLLPFIVLVYTYTRICITITWTSNKMSGVVDLKRNSKASFFQRNRDPIISKALINTVKQTIIVVVTLYIITNIPFIGELWATWDPGAATSPFHTAAFTILC
LNSLTSCVNPWIYFAFNRELRVALTNFFCRKDYSPAYDAVAQNASDAASTSSFSRISRLASSKIFG
>Monomorium_pharaonis gi|826425402|ref|XP_012527228.1| PREDICTED: vasopressin V1a receptor-like
isoform X2
MSRDLNSSSPSEWPLDDARDEYLARWEIAVLTSIFLITLIGNTLVLLALYVRRYQRRKFTRMVFFILHLSVADLLTGLLDVLPQLAWDITFRFQGGAVL
CKLIKFGQPFGLYLSSYILTVAADRYAICHFPFSYCVTSRRSKMMVYGAWLAAILCVPQVIFISYMEIAPDIWECWATFVMPYGERAYITWYSVTQFL
IPFIVLYTYTKICVSIWTSNKISGIVDFKKGKANSFQRNRDPIISKAMINTVKQTIIVVVTLYIITNIPFIGELWATWDPKASSPFFTGAAFTILSLL
NSLTSCVNPWIYFAFNKELRMLINFLCGKDYSLTYGNHNVSL
>Athalia_roseae gi|817066760|ref|XP_012255235.1| PREDICTED: vasopressin V1a receptor-like isoform X2
MLCGSGMCATANEALKVDGDRDTRDEDIANWEVATLAAMFVAVFGNSLVVTVLALYLRVYQRRKFTRMVFFILHLSIADLLTGLLDVLPQLFWEI
TYRFQGGPILCKLVKFGQPLGPLYLSSYVLMVMTALDRYQAICHPLNYCSVTSRRSKIMVYLAWGLSLALCIPQLVVFVSYQEASPGVWDCWGTFFYSPLGERAY
VTWFSISAFILPLLVLYTNVSICLAIRWNTGIAAGEARTDGTLLRQGSVISRKINSIKQMVAVISFYAASSPFFVASLLVWTPDGAVNSPFFEGAAFA
ILTLMSLNSCNPWIYLTNRELPRTLFARIYSSGRSASARTREGRRRCVSTETPCNSSGSGSTGTSVESYASRMSRYAYAILGKSDTANSKEFHCLQSS
SLRGIRNELE
>Pogonomyrmex_barbatus gi|769855843|ref|XP_011639495.1| PREDICTED: vasopressin V1a receptor-like
isoform X1
MSHDLNSSLSEWPPDDARDEYLARWEIAVLTSIFLITLIGNSLVLLALYTRRRYQRRKFTRMVFFILHLSIADLLTGLLDVLPQLAWDITFRFQGGAVL
CKLIKFGQPFGLYLSSYILTVAIDRYAICHFPFSYCVTSRRSKMMVYGAWMLAVILCVPQVIFISYMEISPGVWECWATFYLYGERAYITWYSIMQFLL
PFIVLVYTYTRICMSIWTSSKMSGVVDLKRNSKASFFQRNRDPIISKAMINTVKQTIIVVVTLYIITNIPFIGELWATWDPKASTSPFFTGAAFTILSLL
SLTSCVNPWIYFAFNKELRVALTNFFCRKDYSLTYDIDARQNALDVPSSSTSSFSRISRLASSKIFG
>Solenopsis_invicta gi|751213591|ref|XP_011159612.1| PREDICTED: vasopressin V1a receptor-like isoform
X1
MSHDLNSSLSSSEWPPDDARDEYLARWEIAVLTSIFLITLIGNSLVLLALYTRRRYQRRKFTRMVFFILHLSVADLLTGLLDVLPQLAWDITFRFQGG
AVLCKLIKFGQPFGLYLSSYILTVAIDRYAICHFPFSYCVTSRRSKMMVYGAWMLAVILCVPQVIFISYMEISPGVWECWATFYLYGERAYITWYSIMQFLL
QFLIPFIALTYTYTKICVSIWTSNKMSGVVDLKRNSKASFFQRNRDPIISKAMINTVKQTIIVVVTLYIITNIPFIGELWATWDPKASSPFIGAAFTIL
SLLNSLTSCVNPWIYFAFNKELRAALTNFFCRKDYSLTYDIDARQNASDVPSSSTSSFSRISRLASSKIFG
>Nilaparvata_lugens gi|549137481|dbj|BA001091.1| neuropeptide GPCR A41
MIBANYTFSTERNVESVAVSNGRDEDLARVEATLAAITLAIILAGNSTVVLVALYMRRTWGGRRKLSRMVFFILHLCIADLVTLGLLVFPQLIWDITYRF
RGGPLCKLVKYGQTLGPLYLSSYVLMATAMDRYKAICHPLTYCSWTSHHARVQCAWATALLFCIPQVTFISYMEVPGSPGDYDCWATFRDWRGERAYVT
WYSVSVFLPVLIVLYTYTRICMSIWTSSKMSGVVDLKRNSKASFFQRNRDPIISKAMINTVKQTIIVVVTLYIITNIPFIGELWATWDPKASTSPFFTGAAFTILSLL
SCVNPWIYLVSNKELMRGLRQLLGGCKYALSSDYRGNSAAESGSGCGAGSCSKRSEVTNTTSLPRKPLVAEQPLPEVTPIRRWVVTIPPNVREERECL
QLFSGLNNERILPRSQQQHQQRAIRTSPPCRAARCRDL
>Halyomorpha_halys gi|939664743|ref|XP_014279829.1| PREDICTED: oxytocin receptor-like
MFLYFRSLYETRMVAFSSMGDASYSYADKDNITSTVPSRVLCPNDSINCSAVHERDEDLAKIEMATLAVFMVMTVVGNAGVLAALFARRQSATRTRKVP
MNFVFLHLCVADMCTAWNLILPQLAWEVTFRFKGGFELCKSVKFGQTLGPLYLSSYVLTVAIDRYAICHPLTYCSWSSKRARGMIMGAWALSITFCTPQL
TIFSYQEVAPGVDFCWA VSEP YGERVYVTVNSVVFVPLVSLIYTYTCICLTIWHNTGPLSASAPHKVVSRAKINTIKQTVAVIALYIACSLPFI SAQL
WATWDPHATSSPFLSGGTFTILTLLSSLNSCNPWIYLTNSQDLMEALWETIICRKNKDRPENVTGSGGSSGRPHQSQCTLAGQHTHYAKVVALPPNLS
KTMRLRFRTPNRRNVWSSLEAKYETDTSKLSPEL
>Acromyrmex_echinator gi|332020179|gb|EGI60623.1| [Arg8]-vasotocin receptor
MSHDLNSSLSSSELPLDDARDEYLARWEIAVLTSIFLITLIGNVILLALYARRRYQRRKFTRMVFFIMHLSVADLLTGLFDVLPQLAWDITFRFQGGAVL
CKLIKFGQPFGLYLSSYILTVAIDRYAICHFPFSYCVTSRRSKMMVYGTWTLAAMLCVPQVIFISYMEISPGVWECWATFYLYGERAYITWYSVMQFL
LPFIVLVYTYTRICMSIWTSSKMSGVVDLKRNSKASFFQRNRDPIISKAMINTVKQTIIVVVTLYIITNIPFIGELWATWDPKASTSPFFTGAAFTILSLL
NSLTSCVNPWIYFAFNKELRVALTCFFCRKDYSLTYGNHNSLFLSLSLSLYIYIYISSHVCICIIPSNWIITRNINIVIFICHFLSDIDARQNTSDVP
SSTSSFSRISRLASSKIFG
>Tribolium_castaneum tr|A3RE84|A3RE84_TRICA Arginine vasopressin receptor OS=Tribolium castaneum
GN=avpr PE=2 SV=2
MYTPKLSQMDISENSTYLFDKHEDRNTDRDENLARVEATLAIIFLVTVIGNSTVLLALWTRRRYAGRRKLSRMVFFILHLSIADLLTGLFDVLPQLAWD
ITYRFYGGFLLCKVVKYQTLGPLYLSSYVLMATAIDRYQAICYPLTYCSWTSRRSKMMVYLAWVSLAFCIPQLTIFTYTSVGEDEYDCWATFQEPWPKRA
YVTVYSISVFMVPLVVLIFTYTSICIEIYWQSSSESLRPRSSQKSAPGKRTPLISRAKINTVKQTIIVVVTLYIITNIPFIGELWATWDPQSPFIDGPVFI
LTLVYSLNSCNPWIYLAFNRELRLLRHYTASSKNYRATGGSANVSGDAQVSTSLRPF SRWSLCSNARSNKYPTRPVPHRPFVAQYNARRWIVTTTT

(C)

Polistes dominula PdomSCFr1.2-0007, whole genome shotgun sequence

Sequence ID: [gb|LMBU0100007.1](#)|Length: 3730956

Number of Matches: 4

Range 1: 2381887 to 2382378 [GenBankGraphics](#)

Query: *Polistes canadensis* gi|954548184|ref|XP_014616661.1|

Alignment statistics for match #1

Score	Expect	Method	Identities	Positives	Gaps	Frame
196 bits(499)	2e-87	Compositional matrix adjust.	102/164(62%)	107/164(65%)	51/164(31%)	+1
Query 93	RFQGGVLVLCVKVFPFQFGLYLSSYILTATAIDRYHAI	CHPLSYCSVTSRKS	SRIMVYCAW	152		
Sbjct 2381887	RFQGGVLVLCVKVFPFQFGLYLSSYILTATAIDRYHAI	CHPLSYCSVTSRKS	SRIMVYCAW	2382066		
Query 153	SFALILCIP-----		161			
Sbjct 2382067	S ALILCIP					
Query 162	QLFVFSYQEVMPRIWDCWATFDIKFGEKAYVTWYSLMVFLPF		205			
Sbjct 2382247	QLFVFSYQEVMP+LWDCWATFDIKFGE+AYVTW ++ LL F+					
Sbjct 2382247	QLFVFSYQEVMPK1WDCWATFDIKFGERAYVTW*AIFRLLLSFL		2382378			

Range 2: 2381495 to 2381782 [GenBankGraphics](#)

Alignment statistics for match #2

Score	Expect	Method	Identities	Positives	Gaps	Frame
147 bits(372)	2e-87	Compositional matrix adjust.	89/96(93%)	90/96(93%)	2/96(2%)	+2
Query 1	MNETTNSSTAAAN--EEEDIRDENLAKWEIVLLANILIFTIFGNS	slvllslylrry	AHK	58		
Sbjct 2381495	MNETTNSST N EEED RDE LAKWEIVLLANILIFTIFGNS	slvllslylrry	AHK	2381674		
Query 59	KLSRMVFFIMNLSIADLLTGLLDVLPQLAWDITFRF		94			
Sbjct 2381675	KLSRMVFFIMNLSIADLLTGLLDVLPQLAWDITFR+					
Sbjct 2381675	KLSRMVFFIMNLSIADLLTGLLDVLPQLAWDITFRY		2381782			

Range 3: 2382545 to 2383084 [GenBankGraphics](#)

Alignment statistics for match #3

Score	Expect	Method	Identities	Positives	Gaps	Frame
236 bits(603)	1e-68	Compositional matrix adjust.	135/180(75%)	146/180(81%)	28/180(15%)	+2
Query 195	YSLMVFLPFIVLVYTYVVICVGVWQSNKMSGAVDDRTY	irsisnysrnrss	fiskAMIN	254		
Sbjct 2382545	YSLMVFLPFIVLVYTYVVICVGVW+SNKMSG +DD+ Y	IRSISNYSRNR	S+FISKAMIN	2382724		
Query 255	TVKQTIATIVITLYAITSIPFIGCELWISWDPEAPKSSFFAN		293			
Sbjct 2382725	TVKQTIATIVITLYA+TSIPFIGCELW++WD EA K+SFAN					
Query 294	-----GPAFTILALLNSLTSCVNPWYLSFNRELRQTL	MNYFCN	NEHSQKYYG	346		
Sbjct 2382905	FFVSPFSGPAFTILALLNSLTSCVNPWYLSFNRELRQTL	MNYFCN	NEHSQKYYG	2383084		

Range 4: 2383149 to 2383253 [GenBankGraphics](#)

Alignment statistics for match #4

Score	Expect	Method	Identities	Positives	Gaps	Frame
40.0 bits(92)	0.016	Compositional matrix adjust.	32/35(91%)	33/35(94%)	0/35(0%)	+3
Query 340	YYGQRMRRSDSNDTSTRSLMSRISRYTSSIIIPR		374			
Sbjct 2383149	+ GQRMRRSDSNDTSTR SLMSRISRYTSSIIIPR					
Sbjct 2383149	FTGQRMRRSDSNDTSTRISLMSRISRYTSSIIIPR		2383253			

Lasius niger Lnig_2.1_21704, whole genome shotgun sequence

Sequence ID: [gb|LBM01020432.1](#)|Length: 1899

Number of Matches: 2

Range 1: 1398 to 1694 [GenBankGraphics](#)

Query: *Monomorium pharaonis* gi|826425402|ref|XP_012527228.1|

Alignment statistics for match #1

Score	Expect	Method	Identities	Positives	Gaps	Frame
162 bits(409)	6e-44	Compositional matrix adjust.	73/99(74%)	89/99(89%)	0/99(0%)	-2
Query 196	YSVTQFLIPFIVLYTYTKICVSIWTSNKISGIVDFKKG	NKANFSQRNR	PLISKAMINT	255		
Sbjct 1694	YS+ QFL+PFIVL+YTYTKIC++IWTS+K+SG+VD	KK NKANFSQRNR	+PLISKAM+NT			
Sbjct 1694	YSIMQFLLPFIVLYTYTKICIAIWTSSKMSGVVDL	KNNKANFSQRNR	EPLISKAMNT	1515		
Query 256	IKQMIVVVTLYIITNTPFIGCELWATWDPKASSPPFFTG		294			
Sbjct 1514	++Q I+V+TLYI T+ PFIG LWATWDPKA + PFFTG					
Sbjct 1514	VRQTIIVITLYIATSPFFIGSMLWATWDPKAFTLPFFTG		1398			

Range 2: 938 to 1099 [GenBankGraphics](#)

Alignment statistics for match #2

Score	Expect	Method	Identities	Positives	Gaps	Frame
88.2 bits(217)	3e-18	Compositional matrix adjust.	45/55(82%)	46/55(83%)	1/55(1%)	-3
Query 292	FTGAAFTILSLNLSLTSCVNPWYFAPNKELRMALIN	FLOGKDYSLTYGNHNS	346			
Sbjct 1099	F GAAFTILSLNLSLTSCVNPWYFAPNKELR AL NF	KD SL YGNH+ S				
Sbjct 1099	FAGAAFTILSLNLSLTSCVNPWYFAPNKELRGAL	TNFPYRKKD-SLNYGNHDS	938			

Lasius niger Lnig_2.1_5428, whole genome shotgun sequence

Sequence ID: [gb|LBM01005371.1](#)|Length: 12101

Number of Matches: 3

Range 1: 11103 to 11315 [GenBankGraphics](#)

Query: Monomorium_pharaonis gi|826425402|ref|XP_012527228.1|

Alignment statistics for match #1

Score	Expect	Method	Identities	Positives	Gaps	Frame
135 bits(340)	4e-34	Compositional matrix adjust.	60/71(85%)	66/71(92%)	0/71(0%)	+3
Query 94	RFQGGAVLCKLIKFGQPFGLYLSSYILTVTAFDRYYAICHPPFSYCGVTSQRSKMMVYGAW		153			
	RFQGGAVLCKLIKFGQPFGLYLSSY+LTVTA DRYAICHPPF YC +TS+RSKMMVYGAW					
Sbjct 11103	RFQGGAVLCKLIKFGQPFGLYLSSYILTVTAMDRIYAICHPPFLYCSITSRRSKMMVYGAW		11282			
Query 154	ALAVILCVPQI 164					
	LA ILCVPQ+					
Sbjct 11283	TLAAILCVPQV 11315					

Range 2: 10003 to 10236 [GenBankGraphics](#)

Alignment statistics for match #2

Score	Expect	Method	Identities	Positives	Gaps	Frame
114 bits(285)	7e-27	Compositional matrix adjust.	69/78(88%)	73/78(93%)	0/78(0%)	+1
Query 17	DDARDEYLARWEIAVLTSIFLLTVIGNILvllalalyvrrryqrrKFTRMYFFILHLSVADL		76			
	DD RDEYLARWEIAVL T IFL+T+IGN L+L ALY RRRYQRRKFTRMYFFILHLS+ADL					
Sbjct 10003	DDTRDEYLARWEIAVLTIIFLVTLIGNTLILFALYARRRYQRRKFTRMYFFILHLSIADL		10182			
Query 77	LTGLLDVLPQLAWDITFR 94					
	LTGLLDVLPQLAWDITFR					
Sbjct 10183	LTGLLDVLPQLAWDITFR 10236					

Range 3: 11691 to 11780 [GenBankGraphics](#)

Alignment statistics for match #3

Score	Expect	Method	Identities	Positives	Gaps	Frame
58.5 bits(140)	2e-08	Compositional matrix adjust.	23/30(77%)	27/30(90%)	0/30(0%)	+3
Query 166	IFSYMEIAPDIWECWATFYMPYGERAYITW 195					
	IFSY EI+P +WECWATFY+ YGERAY+TW					
Sbjct 11691	IFSYQEISPGVWECWATFYLYKGERAYVTW 11780					

Cyphomyrmex costatus contig19312, whole genome shotgun sequence

Sequence ID: [gb|LKE01019312.1](#)|Length: 44936

Number of Matches: 5

Range 1: 27566 to 27862 [GenBankGraphics](#)

Query: Monomorium_pharaonis gi|826425402|ref|XP_012527228.1|

Alignment statistics for match #1

Score	Expect	Method	Identities	Positives	Gaps	Frame
171 bits(432)	5e-54	Compositional matrix adjust.	77/99(78%)	90/99(90%)	0/99(0%)	+2
Query 196	YSVTQFLIPFIVLYTYTKICVSIWTSNKISGIVDFKKGKANKANFSQRNRDPLISKAMINT		255			
	YSV QFL+PFIVL+YTY +IC+SIW S+K+SG++D KK N ++ QRNRDPLISKAMINT					
Sbjct 27566	YSVMQFLLPFIVLVYTYMRICISIWKSSKLSGLIDHKKSNVSYCQRNRDPLISKAMINT		27745			
Query 256	IKQMIIVVVTLYIITNTPFIGCELWATWDPKASSSPFFTG 294					
	+KQMI+VVTLYI TNTPFIGCELWATWDPKAS+SPFFTG					
Sbjct 27746	VKQMIIVVVTLYIATNTPFIGCELWATWDPKASTSPFFTG 27862					

Range 2: 27379 to 27489 [GenBankGraphics](#)

Alignment statistics for match #2

Score	Expect	Method	Identities	Positives	Gaps	Frame
59.7 bits(143)	5e-54	Compositional matrix adjust.	27/37(73%)	30/37(81%)	1/37(2%)	+1
Query 168	SYMEIAPDIWECWATFYMPYGERAYITW-YSVTQFLI 203					
	SYMEI+P +WECWATFY+ YGERAYITW YS F I					
Sbjct 27379	SYMEISPGVWECWATFYLYKGERAYITW*YSFIYFFI 27489					

Range 3: 26537 to 26758 [GenBankGraphics](#)

Alignment statistics for match #3

Score	Expect	Method	Identities	Positives	Gaps	Frame
134 bits(338)	1e-33	Compositional matrix adjust.	61/74(82%)	68/74(91%)	0/74(0%)	+2
Query 91	ITFRFQGGAVLCKLIKFGQPFGLYLSSYILTVTAFDRYYAICHPPFSYCGVTSQRSKMMVY		150			
	+ RFQGGAVLCKLIKFGQPFGLYLSSYILTVTA DRY+AIC+PFSYC +TS+RSKMMVY					
Sbjct 26537	MAVRPQGGAVLCKLIKFGQPFGLYLSSYILTVTAIDRYAICYPFSYCSITSRRSKMMVY		26716			
Query 151	GAWALAVILCVPQI 164					
	GAW LA +LCVPQ+					
Sbjct 26717	GAWTLAAMLCVPQV 26758					

Range 4: 23292 to 23573 [GenBankGraphics](#)

Alignment statistics for match #4

Score	Expect	Method	Identities	Positives	Gaps	Frame
125 bits(315)	1e-30	Compositional matrix adjust.	80/94(85%)	85/94(90%)	0/94(0%)	+3
Query 1	MSRDNLNSSSPSEWPLDDARDEYLARWEIAVLTSIFLLTVIGNILvllalalyvrrryqrrK		60			
	MS DLN SSS DDARDEYLARWEIAVLTSIFL+T+IGNIL+LLALYVRR YQ+RK					
Sbjct 23292	MSHDNLNSSSSSERPSSDDARDEYLARWEIAVLTSIFLITIIIGNILILLALYVRRCYQRRK		23471			
Query 61	FTRMYFFILHLSVADLLTGLLDVLPQLAWDITFR 94					
	FTRMYFFI+HLSVADLLTGLLDVLPQLAWDITFR					
Sbjct 23472	FTRMYFFIMHLSVADLLTGLLDVLPQLAWDITFR 23573					

Range 5: 28253 to 28411 [GenBankGraphics](#)

Alignment statistics for match #5

Score	Expect	Method	Identities	Positives	Gaps	Frame
97.8 bits(242)	3e-21	Compositional matrix adjust.	46/53(87%)	47/53(88%)	0/53(0%)	+2
Query 292	FTGAAFTILSLNLSLTSCVNPWYFAPFNKELRMALINFLCGKKDYSLTYGNNH		344			
	F GAAFTILSLNLSLTSC+NPWYFAPFNKELR AL F C KKDYSLTYGNNH					
Sbjct 28253	FAGAAFTILSLNLSLTSCINPWYFAPFNKELRAALTYFFCRKKDYSLTYGNNH		28411			

Atta colombica contig24766, whole genome shotgun sequence
Sequence ID: [gb|LKEW01024766.1](#) Length: 24004 Number of Matches: 4
Related Information
Range 1: 3747 to 4241 [GenBankGraphics](#)
Query: Monomorium_pharaonis gi|826425402|ref|XP_012527228.1|

Alignment statistics for match #1

Score	Expect	Method	Identities	Positives	Gaps	Frame
212 bits(539)	5e-60	Compositional matrix adjust.	102/165(62%)	117/165(70%)	38/165(23%)	-3
Query 169	YMEIAPDIWECWATFYMPYGERAYITW-----		195			
	YMEI+P +WECWATFY+ YGERAYITW					
Sbjct 4241	YMEISPGVWECWATFYLYKYGERAYITW*YPFYIFSLKNILFLYNI TFNNINRFKCCEMS		4062			
Query 196	-----YSVTQFLPIFFIVLIYTYTKICVSIWTSNKISGIVDFKKGKGNKANSQRNRDPLISK		250			
	YSV QFL+PFIIVL+YTYT+IC+SIW S+K+SG++D KK NK +F QRNRDPLISK					
Sbjct 4061	GFNRYYSVMQFLPFIIVLVYTYTRICISIWRSKSLGSLDLKSKNSVFCQRNRDPLISK		3882			
Query 251	AMINTIKQMIVVVTLIIITNTPFIGCELWATWDPKASSPFFTGA		295			
	AMINT+KQMIVVV LYI+TNTPFIGCELWATWDPKAS+SPFFTG					
Sbjct 3881	AMINTVKQMIVVVLIYIVTNTPFIGCELWATWDPKASTSPFFTGK		3747			

Range 2: 4891 to 5103 [GenBankGraphics](#)

Alignment statistics for match #2

Score	Expect	Method	Identities	Positives	Gaps	Frame
136 bits(343)	5e-34	Compositional matrix adjust.	62/71(87%)	66/71(92%)	0/71(0%)	-2
Query 94	RFQGGAVLCKLIKFGQPFGLYLYSSYILTVTAFDRYYAICHFPFSYCGVTSQRSKMMVYGAW		153			
	RFQGGAVLCKLIKFGQPFGLYLYSSYILTVTA DRY+AICHFPFSYC VTS+RSKMMVYG W					
Sbjct 5103	RFQGGAVLCKLIKFGQPFGLYLYSSYILTVTAIDRYHAICHFPFSYCVTSRRSKMMVYGTW		4924			
Query 154	ALAVILCVPOI 164					
	LA +LCVPQ+					
Sbjct 4923	MLAAMLCVPQV 4891					

Range 3: 6822 to 7103 [GenBankGraphics](#)

Alignment statistics for match #3

Score	Expect	Method	Identities	Positives	Gaps	Frame
125 bits(313)	5e-30	Compositional matrix adjust.	85/95(89%)	89/95(93%)	2/95(2%)	-3
Query 1	MSRDLNSSSSPSEWPLDD-ARDEYLARWEIAVLTSIFLLTVIGNILvllalalyvrrryqrr		59			
	MS DLNSSSS SE PLDD ARDEYLARWEIAVLTSIFL+T+IGN+LVLLALY RRRYQRR					
Sbjct 7103	MSHDLNSSSS-SEPLDDDDARDEYLARWEIAVLTSIFLITIIIGNVLVLLALYARRRYQRR		6927			
Query 60	KFTRMYFFILHLSVADLLTGLLDVLPQLAWDITFR 94					
	KFTRMYFFI+HLSVADLLTGL DVLPQLAWDITFR					
Sbjct 6926	KFTRMYFFIMHLSVADLLTGLFDVLPQLAWDITFR 6822					

Range 4: 3235 to 3387 [GenBankGraphics](#)

Alignment statistics for match #4

Score	Expect	Method	Identities	Positives	Gaps	Frame
96.7 bits(239)	2e-20	Compositional matrix adjust.	46/51(90%)	47/51(92%)	0/51(0%)	-2
Query 294	GAAFTILSLNLSLTSCVNPWYFAPFNKELRMALINFLCGKKDYSLTYGNNH		344			
	GAAFTILSLNLSLTSCVNPWYFAPFNKELR+AL F C KKDYSLTYGNNH					
Sbjct 3387	GAAFTILSLNLSLTSCVNPWYFAPFNKELRVALTCFFCRKKDYSLTYGNNH		3235			

Linepithema humile ctg7180000726062, whole genome shotgun sequence
Sequence ID: [gb|ADQO01003105.1](#) Length: 22838
Number of Matches: 5
Range 1: 12037 to 12333 [GenBankGraphics](#)
Query: Monomorium_pharaonis gi|826425402|ref|XP_012527228.1|

Alignment statistics for match #1

Score	Expect	Method	Identities	Positives	Gaps	Frame
173 bits(439)	1e-54	Compositional matrix adjust.	79/99(80%)	92/99(92%)	0/99(0%)	+1
Query 196	YSVTQFLPIFFIVLIYTYTKICVSIWTSNKISGIVDFKKGKGNKANSQRNRDPLISKAMINT		255			
	YSVTQFL+PFIIVL+YTYT+IC+SIWTSN +SG+V FKK +KA+F+ RNRDP ISKA+INT					
Sbjct 12037	YSVTQFLPFIIVLVYTYTRICISIWTSNMTMSGVGVGFKKSDKASFHRNRDPFISKALINT		12216			
Query 256	IKQMIVVVTLIIITNTPFIGCELWATWDPKASSPFFTGA 294					
	+KQ IVVVTLIIITN PFIGCELWATWDPKAS+SPFFT+G					
Sbjct 12217	VKQTIIVVTLIIITNIPFIGCELWATWDPKASTSPFFSG 12333					

Range 2: 11847 to 11957 [GenBankGraphics](#)

Alignment statistics for match #2

Score	Expect	Method	Identities	Positives	Gaps	Frame
59.3 bits(142)	1e-54	Compositional matrix adjust.	26/37(70%)	31/37(83%)	2/37(5%)	+3
Query 161	VPQ--IFIFSMEIAPDIWECWATFYMPYGERAYITW 195					
	VP+ +FIFSY EI+P +WECWATFY+ YGE AYITW					
Sbjct 11847	VPKL*VFIFSYPEISPGVWECWATFYLYKYGAAAYITW 11957					

Range 3: 11290 to 11502 [GenBankGraphics](#)

Alignment statistics for match #3

Score	Expect	Method	Identities	Positives	Gaps	Frame
135 bits(339)	5e-34	Compositional matrix adjust.	61/71(86%)	65/71(91%)	0/71(0%)	+1
Query 94	RFQGGAVLCKLIKFGQPFGLYLSSYILTVTAFDRYYAICHPPFSYCGVTSQRSKMMVYGAW		153			
Sbjct 11290	RFQGGAILCKLIKFGQPFGLYLSSYILTVTALDRYYAICHPPFSYCVTSRRSKMMVFAAW		11469			
Query 154	ALAVILCVPQI 164					
Sbjct 11470	AFAAILCVPQV 11502					

Range 4: 10330 to 10563 [GenBankGraphics](#)

Alignment statistics for match #4

Score	Expect	Method	Identities	Positives	Gaps	Frame
121 bits(303)	3e-29	Composition-based stats.	69/78(88%)	75/78(96%)	0/78(0%)	+1
Query 17	DDARDEYLARWEIAVLTISIFLLTVIGNIILVllalyvrrryqrKFTRMYYF ILHLSVADL		76			
Sbjct 10330	DDARDEYLARWEIAVLTISIFL+T+IGN+++L ALY RRRYQRRKFTRMYYF ILHLS+ADL		10509			
Query 77	LTGLLDVLPQLAWDITFR 94					
Sbjct 10510	LTGLFDVLPQLAWDITFR 10563					

Range 5: 12585 to 12746 [GenBankGraphics](#)

Alignment statistics for match #5

Score	Expect	Method	Identities	Positives	Gaps	Frame
92.4 bits(228)	2e-19	Compositional matrix adjust.	45/54(83%)	45/54(83%)	0/54(0%)	+3
Query 292	FTGAFTILSLNLSLTCVNPWIYFAPNKELRMALINFLCGKDKDYSLTNGNHN		345			
Sbjct 12585	FPGALFTILSLNLSLTCVNPWIYFAPNKELRALTNFFCRKDKDYSLTNGNRT		12746			

Camponotus floridanus CamFlo_1.0_4.contig5511, whole genome shotgun sequence

Sequence ID: [gb|AEAB01029474.1|](#)Length: 1857

Number of Matches: 2

Range 1: 520 to 816 [GenBankGraphics](#)

Query: Monomorium_pharaonis gi|826425402|ref|XP_012527228.1|

Alignment statistics for match #1

Score	Expect	Method	Identities	Positives	Gaps	Frame
159 bits(403)	4e-43	Compositional matrix adjust.	69/99(70%)	88/99(88%)	0/99(0%)	-1
Query 196	YSVTQFLPFIIVLYTYTKICVSIWTSNKISGIVDFKKNKANFSQRNRDPLISKAMINT		255			
Sbjct 816	YS+ QFL+PFIVL+YTY IC++IW SNK+SG++D KK NK NFSQ+NR+P +SKAM+NT		637			
Query 256	IKQIMVVVTLIIITNTPFIGCELWATWDPKASSPFFTG 294					
Sbjct 636	+Q I+V+TLYI+T++PFIGCELWATWDPKA S PFFTG		520			

Range 2: 88 to 240 [GenBankGraphics](#)

Alignment statistics for match #2

Score	Expect	Method	Identities	Positives	Gaps	Frame
84.0 bits(206)	8e-17	Compositional matrix adjust.	39/51(76%)	44/51(86%)	0/51(0%)	-1
Query 294	GAAPTILSLNLSLTCVNPWIYFAPNKELRMALINFLCGKDKDYSLTNGNHN		344			
Sbjct 240	GAAPTILSLNLSLTCVNPWIYFAPNK+LR AL F +K++SL YGNH+		88			

Camponotus floridanus CamFlo_1.0_4.contig5512, whole genome shotgun sequence

Sequence ID: [gb|AEAB01029475.1|](#)Length: 4331

Number of Matches: 3

Range 1: 1496 to 1714 [GenBankGraphics](#)

Query: Monomorium_pharaonis gi|826425402|ref|XP_012527228.1|

Alignment statistics for match #1

Score	Expect	Method	Identities	Positives	Gaps	Frame
130 bits(327)	2e-32	Compositional matrix adjust.	60/73(82%)	64/73(87%)	0/73(0%)	-2
Query 92	TFRQGGAVLCKLIKFGQPFGLYLSSYILTVTAFDRYYAICHPPFSYCGVTSQRSKMMVYG		151			
Sbjct 1714	T RFQGGAVLCKLIKFGQPFGLYLSSY+LTVTA DRY AICHPPFSYC TS+RSK+MVYG		1535			
Query 152	AWALAVILCVPQI 164					
Sbjct 1534	AWFAAILCVPQV 1496					

Range 2: 2836 to 3159 [GenBankGraphics](#) [Next Match](#) [Previous Match](#) [First Match](#)

Alignment statistics for match #2

Score	Expect	Method	Identities	Positives	Gaps	Frame
119 bits(298)	1e-28	Compositional matrix adjust.	77/108(71%)	87/108(80%)	10/108(9%)	-3
Query 8	SSSPSEWPLDDARDEYLARWEIAVLTISIFLLTVIGNIILVllalyvrrryqrKFTRMYYF		67			
Sbjct 3159	S SPS D+ RDEYLARWEIA+LTSIFL+T+IGN L+L ALYVRRRYQR+KFTRMYYF		2980			
Query 68	ILHLSVADLLTGLLDVLPQLAWDITFR----FQG----GAVLCKLI 105					
Sbjct 2979	ILHLSVADLLTGLLDVLPQLAWDITFR FQ ++C+L+		2836			

Range 3: 1016 to 1099 [GenBankGraphics](#)

Alignment statistics for match #3

Score	Expect	Method	Identities	Positives	Gaps	Frame
51.2 bits(121)	4e-06	Compositional matrix adjust.	19/28(68%)	24/28(85%)	0/28(0%)	-2
Query 168	SYMEIAPDIWECWATFYMPYGERAYITW	195				
	SY EI+PD+W+CWATF + YGER Y+TW					
Sbjct 1099	SYEISPDVWDCWATFNLYKGERVYVITW	1016				

Trachymyrmex septentrionalis contig23603, whole genome shotgun sequence

Sequence ID: [gb|LKEZ01023603.1](#) Length: 6298

Number of Matches: 4

Range 1: 5221 to 5724 [GenBankGraphics](#)

Query: Monomorium_pharaonis gi|826425402|ref|XP_012527228.1|

Alignment statistics for match #1

Score	Expect	Method	Identities	Positives	Gaps	Frame
222 bits(565)	2e-63	Compositional matrix adjust.	107/168(64%)	122/168(72%)	37/168(22%)	+1
Query 164	IFIFSYMEIAPDIWECWATFYMPYGERAYITW-----	195				
	IFIFSYMEI+P +WECWATFY+ YGERAYITW					
Sbjct 5221	IFIFSYMEISPGVWECWATFYLYKGERAYITW*DLFIYFFIQKYLIFIT*HLITLIRFKC	5400				
Query 196	-----YSVTQFLIPFIVLYTYTKICVSIWTSNKISGIVDFKKGKANKFSQRNRDP	246				
	YSV QFL+PFIVL+YTYT+IC+SIW S K+SG++D K+ NK +F QRNRDP					
Sbjct 5401	CKMSGFNRYRSMQFLPPFIVLVYTYTRICISIWRSKLSGLIDLKRSNKVSPFCQRNRDP	5580				
Query 247	LISKAMINTIKQMIWVVTLYIITNTPFIGCELWATWDPKASSPFFTG	294				
	LISKAMINT+KQMIWVVTLYI+TNTNTPFIGCELWATWDPKAS+SPFFTG					
Sbjct 5581	LISKAMINTVKQMIWVVTLYIVTNTNTPFIGCELWATWDPKASTSPFFTG	5724				

Range 2: 4405 to 4617 [GenBankGraphics](#)

Alignment statistics for match #2

Score	Expect	Method	Identities	Positives	Gaps	Frame
137 bits(345)	4e-34	Compositional matrix adjust.	62/71(87%)	66/71(92%)	0/71(0%)	+1
Query 94	RFQGGAVLCKLIKFGQPFGLYLSSYILTVTAFDRYYAICHPPFSYCGVTSQRSKMMVYGAW	153				
	RFQGGAVLCKLIKFGQPFGLYLSSYILTVTA DRY+AICHPPFSYC VTS+RSKMMVYG W					
Sbjct 4405	RFQGGAVLCKLIKFGQPFGLYLSSYILTVTAIDRYHAICHPPFSYCVTSRRSKMMVYGTW	4584				
Query 154	ALAVILCVPOI	164				
	LA +LCVPO+					
Sbjct 4585	TAAAMLCVPOV	4617				

Range 3: 2497 to 2769 [GenBankGraphics](#)

Alignment statistics for match #3

Score	Expect	Method	Identities	Positives	Gaps	Frame
131 bits(330)	4e-32	Compositional matrix adjust.	82/92(89%)	87/92(94%)	2/92(2%)	+1
Query 4	DLNSSSSPSEWPLDD-ARDEYLARWEIAVLTSIFLLTVIGNIvlilalyvrrryqrrKFT	62				
	DLNSSSS SE PLDD ARDEYLARWEIAVLTSIFL+T+GN+LVLALY RRRYQRRKFT					
Sbjct 2497	DLNSSSS-SELPLDDARDEYLARWEIAVLTSIFLITIVGNVLLALYARRRYQRRKFT	2673				
Query 63	RMYYFHLHLSVADLLTGLDVLPLQAWDITFR	94				
	RMYYFI+HLSVADLLTGL DVLPLQAWDITFR					
Sbjct 2674	RMYYFIMHLSVADLLTGLPDVLPQLAWDITFR	2769				

Range 4: 6089 to 6241 [GenBankGraphics](#)

Alignment statistics for match #4

Score	Expect	Method	Identities	Positives	Gaps	Frame
96.7 bits(239)	3e-20	Compositional matrix adjust.	46/51(90%)	47/51(92%)	0/51(0%)	+2
Query 294	GAAFTILSLNLSLTCVNPWIYFAPNKLRLMALINFLCGKDYSLTYGNHN	344				
	GAAFTILSLNLSLTCVNPWIYFAPNKLRL+AL F C KKDYSLTYGNHN					
Sbjct 6089	GAAFTILSLNLSLTCVNPWIYFAPNKLRLVALTCFFCRKDYSLTYGNHN	6241				

Trachymyrmex zeteki contig15596, whole genome shotgun sequence

Sequence ID: [gb|LKFA01015596.1](#) Length: 111526

Number of Matches: 5

Range 1: 16865 to 17161 [GenBankGraphics](#)

Query: Monomorium_pharaonis gi|826425402|ref|XP_012527228.1|

Alignment statistics for match #1

Score	Expect	Method	Identities	Positives	Gaps	Frame
175 bits(443)	3e-54	Compositional matrix adjust.	78/99(79%)	91/99(91%)	0/99(0%)	-1
Query 196	YSVTQFLIPFIVLYTYTKICVSIWTSNKISGIVDFKKGKANKFSQRNRDPLISKAMINT	255				
	YSV QFL+PFIVL+YTYT+IC+SIW S+K+SG++D K+ NK +F QRNRDPLISKAMINT					
Sbjct 17161	YSVMQFLPPFIVLVYTYTRICISIWRSKLSGLIDLKRSNKVSPFCQRNRDPLISKAMINT	16982				
Query 256	IKQMIWVVTLYIITNTPFIGCELWATWDPKASSPFFTG	294				
	+KQMIWVVTLYI+TN PFIGCELWATWDPKAS+SPFF G					
Sbjct 16981	VKQMIWVVTLYIVTNIPTFIGCELWATWDPKASNSPFFAG	16865				

Range 2: 17257 to 17337 [GenBankGraphics](#)

Alignment statistics for match #2

Score	Expect	Method	Identities	Positives	Gaps	Frame
57.8 bits(138)	3e-54	Compositional matrix adjust.	22/27(81%)	25/27(92%)	0/27(0%)	-2
Query 169	YMEIAPDIWECWATFYMPYGERAYITW	195				
	YMEI+P +WECWATFY+ YGERAYITW					
Sbjct 17337	YMEISPGVWECWATFYLYKGERAYITW	17257				

Range 3: 17954 to 18166[GenBankGraphics](#)

Alignment statistics for match #3

Score	Expect	Method	Identities	Positives	Gaps	Frame
138 bits(348)	2e-34	Compositional matrix adjust.	63/71(89%)	67/71(94%)	0/71(0%)	-1
Query 94	RFQGGAVLCKLIKFGQPFGLYLSSYILTVTAFDRYYAICHPPFSYCVTSQRSKMMVYGAW		153			
Sbjct 18166	RFQGGAVLCKLIKFGQPFGLYLSSYILTVTADRY+AICHPPFSYC VTS+RSKMMVYGAW		17987			
Query 154	ALAVILCVPQI 164					
Sbjct 17986	LA +LCVPQ+ TLAAMLCVPQV 17954					

Range 4: 19839 to 20126[GenBankGraphics](#)

Alignment statistics for match #4

Score	Expect	Method	Identities	Positives	Gaps	Frame
123 bits(308)	3e-29	Compositional matrix adjust.	83/96(86%)	88/96(91%)	2/96(2%)	-3
Query 1	MSRDLNSSSSPSEWPLDD-ARDEYLARWEIAVLTSIFLLTVIGNIlvllalyvrrryqrr		58			
Sbjct 20126	MS DLNSSSS E PLDD ARDE+LARWEIAVLTSIFL+T+IGN+LVLLALY RRRYQRR		19947			
Query 59	rKFRMYFFIHLHLSVADLLTGLLDVLPQLAWDITFR 94					
Sbjct 19946	RKFRMYFFI+HLSVADLLTGL DVLPQLAWDITFR RKFRMYFFIMHLSVADLLTGLFDVLPQLAWDITFR 19839					

Range 5: 16354 to 16515[GenBankGraphics](#)

Alignment statistics for match #5

Score	Expect	Method	Identities	Positives	Gaps	Frame
100 bits(249)	2e-21	Compositional matrix adjust.	48/54(89%)	49/54(90%)	0/54(0%)	-2
Query 294	GAAFTILSLNLSLTSCVNPWIYFAFNKELRMALINFLCGKDKDYSLTYGNNHNSL		347			
Sbjct 16515	GAAFTILSLNLSLTSCVNPWIYFAFNKELR AL +F C KKDYSLTYGNNH NSL		16354			

Trachymyrmex cornetzi contig27754, whole genome shotgun sequence

Sequence ID: [gb|LKEY01027754.1](#)|Length: 9614

Number of Matches: 5

Range 1: 8717 to 9013[GenBankGraphics](#)

Query: Monomorium_pharaonis gi|826425402|ref|XP_012527228.1|

Alignment statistics for match #1

Score	Expect	Method	Identities	Positives	Gaps	Frame
180 bits(456)	9e-49	Compositional matrix adjust.	81/99(82%)	93/99(93%)	0/99(0%)	+2
Query 196	YSVTQFLPFIVLIVTYTYTKICVSIWTSNKISGIVDFKKNKANFSQRNRDPLISKAMINT		255			
Sbjct 8717	YSV QEL+PFIVL+YTYT+IC+SIW SNK+SG+D K+ NK +F QRNRDPLISKAMINT		8896			
Query 256	IKQMIVVVTLYIITNTPFIGELWATWDPKASSPFFFTG 294					
Sbjct 8897	+KQMIVVVTLYI+TNTNTPFIGELWATWDPKAS+SPFFFTG VKQMIVVVTLYIVTNTNTPFIGELWATWDPKASTSPFFFTG 9013					

Range 2: 7686 to 7898[GenBankGraphics](#)

Alignment statistics for match #2

Score	Expect	Method	Identities	Positives	Gaps	Frame
138 bits(348)	2e-34	Compositional matrix adjust.	63/71(89%)	67/71(94%)	0/71(0%)	+3
Query 94	RFQGGAVLCKLIKFGQPFGLYLSSYILTVTAFDRYYAICHPPFSYCVTSQRSKMMVYGAW		153			
Sbjct 7686	RFQGGAVLCKLIKFGQPFGLYLSSYILTVTADRY+AICHPPFSYC VTS+RSKMMVYGAW		7865			
Query 154	ALAVILCVPQI 164					
Sbjct 7866	LA +LCVPQ+ TLAAMLCVPQV 7898					

Range 3: 5839 to 6120[GenBankGraphics](#)

Alignment statistics for match #3

Score	Expect	Method	Identities	Positives	Gaps	Frame
126 bits(316)	3e-30	Compositional matrix adjust.	85/95(89%)	89/95(93%)	2/95(2%)	+1
Query 1	MSRDLNSSSSPSEWPLDD-ARDEYLARWEIAVLTSIFLLTVIGNIlvllalyvrrryqrr		59			
Sbjct 5839	MS DLNSSSS SE PLDD ARDEYLARWEIAVLTSIFL+T+IGN+LVLLALY RRRYQRR		6015			
Query 60	KFRMYFFIHLHLSVADLLTGLLDVLPQLAWDITFR 94					
Sbjct 6016	KFRMYFFI+HLSVADLLTGL DVLPQLAWDITFR KFRMYFFIMHLSVADLLTGLFDVLPQLAWDITFR 6120					

Range 4: 9426 to 9578[GenBankGraphics](#)

Alignment statistics for match #4

Score	Expect	Method	Identities	Positives	Gaps	Frame
94.0 bits(232)	2e-19	Compositional matrix adjust.	45/51(88%)	47/51(92%)	0/51(0%)	+3
Query 294	GAAFTILSLNLSLTSCVNPWIYFAFNKELRMALINFLCGKDKDYSLTYGNNHNSL		344			
Sbjct 9426	GAAFTILSLNLSLTSCVNPWIYFAFNKELR+AL F C KKDYSLTYGNNHNSL		9578			

Range 5: 8524 to 8658 [GenBankGraphics](#) [Next Match](#) [Previous Match](#) [First Match](#)

Alignment statistics for match #5

Score	Expect	Method	Identities	Positives	Gaps	Frame
55.8 bits(133)	5e-07	Compositional matrix adjust.	27/45(60%)	32/45(71%)	1/45(2%)	+1
Query 169	YMEIAPDIWECWATFYMPYGERAYITW-YSVTQFLPFIIVLIYTY		212			
	YMEI+P+WECWATFY+YGERAYITW Y F I ++ TY					
Sbjct 8524	YMEISPGVWECWATFYLYKYGERAYITW*YPFYIYFFIKKYLIFITY		8658			

Nasonia longicornis strain IV7(U) Contig169224, whole genome shotgun sequence

Sequence ID: [gb|ADAP01169223.1|](#) Length: 6826

Number of Matches: 2

Range 1: 5931 to 6248 [GenBankGraphics](#)

Query: Monomorium_pharaonis gi|826425402|ref|XP_012527228.1|

Alignment statistics for match #1

Score	Expect	Method	Identities	Positives	Gaps	Frame
113 bits(282)	4e-26	Compositional matrix adjust.	53/106(50%)	72/106(67%)	0/106(0%)	-3
Query 189	ERAYITWYSVTQFLPFIIVLIYTYTKICVSIWTSNKISGIVDFKKNKANFQRNRDPLI		248			
	+AY+YSVTFL+PFLV+TY+ICSIW+++R++LI					
Sbjct 6248	DNAYLYRYSVTVFLPFCVLTFTYAEICCSIWRNRREVWVLAHERQALTKEGRSQTTLI		6069			
Query 249	SKAMINTIKQMIWVVTLYIITNTPFIGELWATWDPKASSSPFFTG		294			
	SKAINT+KQ+VVTLY++PF+GC+LWATWDPASSFFG					
Sbjct 6068	SKAKINTVKQTLAVVTLYAASSIPFVGCQLWATWDPFASSAFFDG		5931			

Range 2: 5200 to 5367 [GenBankGraphics](#)

Alignment statistics for match #2

Score	Expect	Method	Identities	Positives	Gaps	Frame
44.3 bits(103)	0.002	Compositional matrix adjust.	31/56(55%)	37/56(66%)	2/56(3%)	-2
Query 291	FFTGAFTILSLLSLTSCVNPWIYFAPNKELRMALINFLCG--KKDYSLTYGNNH		344			
	F G FTILSLL+SLTSCVNPWIY F+ELR AL FL K+D + +G +					
Sbjct 5367	FLLGPIFTILSLLSLTSCVNPWYLYLTFYSYELRAALTKFLRSLIKRDRTSRFGKYQ		5200			

Nasonia longicornis strain IV7(U) Contig169231, whole genome shotgun sequence

Sequence ID: [gb|ADAP01169230.1|](#) Length: 1848

Number of Matches: 1

Range 1: 602 to 919 [GenBankGraphics](#)

Query: Monomorium_pharaonis gi|826425402|ref|XP_012527228.1|

Alignment statistics for match #1

Score	Expect	Method	Identities	Positives	Gaps	Frame
89.7 bits(221)	2e-18	Compositional matrix adjust.	57/107(53%)	80/107(74%)	2/107(1%)	-3
Query 6	NSSSPSEWLPDDARDEYLARWEIAVLTSIFLLTVIGNIvl1alalyvrr-ryqrrKFTRM		64			
	S++S P+D RDE LA WE+ VL I T++GN+LVL A+Y++R R R++ TRM					
Sbjct 919	ESATSMVAAPAEDEWDESLAVWEVIVLVLILTTLMGNVVLVFAIYLRKCRGRQRRLTRM		740			
Query 65	YFFILHLSVADLLTGLLDVLPQLAWDITFRFQGGAVLCKLIKFGQPF		111			
	+FF++HLSVADL+TGLL+VLPQLAWD+TFR+ L ++IKF + F					
Sbjct 739	HFFVMHLSVADLITGLLNVLPQLAWDVTRVYVAHDL-QIIFKPKLF		602			

Neodiprion lecontei scaffold_555, whole genome shotgun sequence

Sequence ID: [gb|LGI01000555.1|](#) Length: 122789

Number of Matches: 4

Range 1: 54570 to 55106 [GenBankGraphics](#)

Query: Polistes_canadensis gi|954548184|ref|XP_014616661.1|

Alignment statistics for match #1

Score	Expect	Method	Identities	Positives	Gaps	Frame
108 bits(269)	2e-24	Compositional matrix adjust.	68/185(37%)	93/185(50%)	46/185(24%)	+3
Query 195	YSLMVFLLPFIIVLVVYTYGICVGVWQSNKMSGAVDDRAyirsisnysrnrresfisKAMIN		254			
	YS+ +F+LP+VLVYTY IC VW + + G D + + + IS+A IN					
Sbjct 54570	YSISIFILPPLVLVLYTYASICFAVWNTGIIGEAR-----TNGGPLRQRAIISRKIN		54731			
Query 255	TVKQTIATIVLYAITSIPFIGELWVSWDTKAFES-----		289			
	++KQ IAVI+ YA++S PFI LWV+WD A S					
Sbjct 54732	SIKQMIAVISFYAVSSPFIASLLWVTWDRNAPTSYFDGTLYSKL*FHWFNKLYL*YQK		54911			
Query 290	-----SPANGPAFTILALLNSLTSCVNPWIYLSFNRELRLQTLMNIFYC---NRN		334			
	+F G AF IL L++SL SCVNPWIYL+ NREL + L++ C NR+					
Sbjct 54912	VLRIASV*STNFIAGAAFAILTLMSSLNSCVNPWYLYLALNRELWRLALDRVCLRSRNRD		55091			
Query 335	EHSQK 339					
	E +					
Sbjct 55092	ETRKN 55106					

Range 2: 53667 to 53882 [GenBankGraphics](#)

Alignment statistics for match #2

Score	Expect	Method	Identities	Positives	Gaps	Frame
106 bits(265)	7e-24	Compositional matrix adjust.	49/72(68%)	58/72(80%)	0/72(0%)	+3
Query 92	FRFQGLVLCKLVKFPQFGLYSSYILTATAIDRYHAICHPLSYCVTSRQSRIMVYCA		151			
	+RFQGG +LCKLVKFP QP G Y SSYILTATA+DRY A+CHPL+Y S TSR+S+I V A					
Sbjct 53667	YRFQGGPILCKLVKFGQPLGYPSSYILTATALDRYKAVCHPLAYSSTSRRSKITVCLA		53846			
Query 152	WSFALILCIPQL 163					
	WS +L CIPQ+					
Sbjct 53847	WSLSLAFICIPQV 53882					

Range 3: 53329 to 53697 [GenBankGraphics](#)

Alignment statistics for match #3

Score	Expect	Method	Identities	Positives	Gaps	Frame
102 bits(253)	2e-22	Compositional matrix adjust.	59/130(45%)	84/130(64%)	8/130(6%)	+1
Query 1	MNETTNSFTVANEEKDTRDENLAKWEIVLLANILIFTIFGNSLVLLSLYLKRYRAHKK- +N TT ++ N++ D RDE LA WEI LA + + + GNSLVLL++YLR Y A KK		59			
Sbjct 53329	LNGTTENT---NKKDDPRDEYLAWEIATLAAMFLAALAGNSLVLLAIYLRGYDAPKKN		53496			
Query 60	LSRMYFFIMNLSIADLLTGLLDVLPQLAWDITFRFQGGVLCKLVKFFQPFGLYLSSYIL L+RM+ FL+LS+ADLLT +L+V PQLAW+ITFR+ + G YL+ +I+		119			
Sbjct 53497	LTRMHLFILHLSVADLLTALLNVFPQLAWELITFRYNN---INYTASIIHTTGFYLTRWIV		53667			
Query 120	TATAIDRYHA 129 T + R+ A					
Sbjct 53668	TGFKVGRFFA 53697					

Range 4: 54182 to 54316 [GenBankGraphics](#)

Alignment statistics for match #4

Score	Expect	Method	Identities	Positives	Gaps	Frame
65.9 bits(159)	1e-10	Compositional matrix adjust.	30/45(67%)	33/45(73%)	0/45(0%)	+2
Query 150	CAWSFALILCIPQLVFSYQEVMPRIWDCWATFDIQGKAYVTW 194 C +F LI I QL VFSYQEV P IWDCWATF+ GE+AYVTW					
Sbjct 54182	CRFTFPLITIIIRQLIVFSYQEVSPDIWDCWATFNPPSGERAYVTW 54316					

Diachasma alloeum Dall_scaffold_00798_contig13, whole genome shotgun sequence

Sequence ID: [gb|LDKA01015940.1](#)|Length: 53672|Number of Matches: 2

Related Information

Range 1: 50694 to 50906 [GenBankGraphics](#)

Query: Polistes_canadensis gi|954548184|ref|XP_014616661.1|

Alignment statistics for match #1

Score	Expect	Method	Identities	Positives	Gaps	Frame
106 bits(265)	9e-24	Compositional matrix adjust.	45/71(63%)	56/71(78%)	0/71(0%)	+3
Query 93	RFQGGVLVCKLVKFFQPFGLYLSSYILTATAIDRYHAICHPLSYCVTSRQSRIMVYCAW RFQGG VLCK+VKF QP G Y S+Y+L A AIDRYHAIC+P +YC T +Q+++MVY AW		152			
Sbjct 50694	RFQGGAVLCKMVKFGQPLGHYASTYVLIAGRIDRYHAICYPPNYCRTHKQAKVMVYIAW		50873			
Query 153	SFALILCIPQL 163 +L LCIPQ+					
Sbjct 50874	GISLALCIPQV 50906					

Range 2: 48177 to 48419 [GenBankGraphics](#)

Alignment statistics for match #2

Score	Expect	Method	Identities	Positives	Gaps	Frame
87.0 bits(214)	3e-17	Compositional matrix adjust.	51/81(63%)	65/81(80%)	1/81(1%)	+3
Query 12	ANEKDTDRDENLAKWEIVLLANILIFTIFGNSLVLLSLYLKRY-RAHKKLSRMYFFIMNL +N +D RDE LA WEIV+L IL+ T+ GN LVL +LYLR+Y +KL+RMYPF+M+L		70			
Sbjct 48177	SNMTEDPDRDEFILAVWEIVLILVILVITVVGNFVLFVLFALYLRYYCGRRRKLTRMYFFMMHL		48356			
Query 71	SIADLLTGLLDVLPQLAWDIT 91 SIADL+TG+L+VLPQL WDIT					
Sbjct 48357	SIADLMTGVLNVLPQLVWDIT 48419					

Diachasma alloeum Dall_scaffold_00798_contig14, whole genome shotgun sequence

Sequence ID: [gb|LDKA01015941.1](#)|Length: 26306

Number of Matches: 3

Range 1: 813 to 1109 [GenBankGraphics](#)

Query: Polistes_canadensis gi|954548184|ref|XP_014616661.1|

Alignment statistics for match #1

Score	Expect	Method	Identities	Positives	Gaps	Frame
83.6 bits(205)	5e-27	Compositional matrix adjust.	44/100(44%)	66/100(66%)	1/100(1%)	+3
Query 195	YSLMVFLLPFIVLVYTYVVICVGVNQSNKMSGAVDDRAYirsisnyernrssfiskAMIN YS+ V LLPF VLVYTYV +C +W++ +++ R ++ + + NR IS+A I		254			
Sbjct 813	YSITVLLLPFSVLVYTYVSVCAEIKWNTTEIT-VFGHRGEVVKRMSRENNREPVISRARIK		989			
Query 255	TVKQTIAVITLYAITSIPFIGCELWVSWDTKAFESSFANG 294 TVKQ I V++L+ ITS PF+GC+LW ++D A ++SF G					
Sbjct 990	TVKQMITVSLHVITSAPFVGCQLWAAFPDPAVKTSFYEG 1109					

Range 2: 625 to 723 [GenBankGraphics](#)

Alignment statistics for match #2

Score	Expect	Method	Identities	Positives	Gaps	Frame
57.0 bits(136)	5e-27	Compositional matrix adjust.	22/33(67%)	27/33(81%)	0/33(0%)	+1
Query 162	QLFVFSYQEVMPRIWDCWATFDIQGKAYVTW 194 Q+F+FSYQE+ PRIWDCWA F G++AYVTW					
Sbjct 625	QIFIFSYQEISPRIWDCWADFTPPHGQRAYVTW 723					

Range 3: 2519 to 2698 [GenBankGraphics](#)

Alignment statistics for match #3

Score	Expect	Method	Identities	Positives	Gaps	Frame
51.2 bits(121)	8e-06	Compositional matrix adjust.	32/60(53%)	38/60(63%)	0/60(0%)	+2
Query 294	GPAFTILALLNSLTSCVNPWIYLSFNRELRQTLMNIFCNRNEHSQKYYGQRMRRSDSDND GPAF IL+LL+SLTSCVNPWIY+ FNRELR TL Y +G+ + SD D		353			
Sbjct 2519	GPAFALLSLLSLTSCVNPWIYMGFNRELRSTLKKYIKKLLILGRSMTFGESKHQNSDITD		2698			

Cephus cinctus Ccin1_scaffold0013_contig28, whole genome shotgun sequence

Sequence ID: [ajb|AMWH01000205.1](#)|Length: 159119

Number of Matches: 4

Range 1: 118317 to 118703[GenBankGraphics](#)

Query: *Polistes canadensis* gi|954548184|ref|XP_014616661.1|

Alignment statistics for match #1

Score	Expect	Method	Identities	Positives	Gaps	Frame
158 bits(400)	6e-88	Compositional matrix adjust.	76/129(59%)	89/129(68%)	25/129(19%)	-1
Query 91	TFRFQGGVLCKLVKFPFGLYLSSYILTATAIDRYHAICHPLSYCSVTSRQSRIMVYC		150			
	+ RFQGG +LCKLVK+ QP G YLSSY+LT TA+DRYHAIC+PLSYC TSRQSR+MVYC					
Sbjct 118703	SIRFQGGALLCKLVKYGQPLGPLYLSSYVLTALDRYHAICYPLSYCGTTSRQSRVMVYC		118524			
Query 151	AWSFALILCIP-----QLFVFSYQEVMPRIWDCWATFDIQ		185			
	AW AL C P QQLFVFSYQEVMP ++DCWATF++					
Sbjct 118523	AWVIALTFCTPQVCQSF*VAF*FSIDISLELCPLCQLFVFSYQEVMPGVDFCWATFELS		118344			
Query 186	FGEKAYVTW 194					
	+GE+AYVTW					
Sbjct 118343	YGEQAYVTW 118317					

Range 2: 118784 to 119044[GenBankGraphics](#)

Alignment statistics for match #2

Score	Expect	Method	Identities	Positives	Gaps	Frame
112 bits(279)	6e-88	Compositional matrix adjust.	58/89(65%)	69/89(77%)	3/89(3%)	-2
Query 6	NSSFTVANEKEDTRDENLAKWEIVLLANILIFTIFGNSLVLLSLYLRKYR-AHKLSRMV		64			
	N +F NE DTRDE LA+WEI L++IL T+ GN VL +LYLR+Y + KKL+RMV					
Sbjct 119044	NKTFEEVNE--DTRDEYLAQWEITLSSILALTLVGNIFVLFPALYLRYSISKKLTRMY		118871			
Query 65	FFIMNLSIADLLTGLLDVLPQLAWDITFR 93					
	FPI++LSIADLLTGL VLPQLAWDITFR					
Sbjct 118870	FFIIHLSIADLLTGLFSVLPQLAWDITFR 118784					

Range 3: 117938 to 118246[GenBankGraphics](#)

Alignment statistics for match #3

Score	Expect	Method	Identities	Positives	Gaps	Frame
94.4 bits(233)	6e-88	Compositional matrix adjust.	53/103(51%)	72/103(69%)	3/103(2%)	-2
Query 195	YSLMVFLLPFIVLVYTYVVICVGVWQSNKMSGAVD--DRAYIRISISYRNRSSFISKA		251			
	YS VFLLP VL+YTY GIC+G+W+++ + G + + + + N+ RNR+ IS+A					
Sbjct 118246	YSFVFLPLCLVLLYTYTGICMGIWRNSNVLDGLTEIGANGSLEKQNHFRNRTLISRA		118067			
Query 252	MINTVKQTIATIVITLYAITSIPFIGCELWVSWDTKAFESSFANG 294					
	INT+KQTIAVI+LY I S PFIGC+LW SWD +A S F +G					
Sbjct 118066	RINTLKQTIATIVISLYIICSSPFIGCQLWASWDPQASSSPFYSG 117938					

Range 4: 117681 to 117782[GenBankGraphics](#)

Alignment statistics for match #4

Score	Expect	Method	Identities	Positives	Gaps	Frame
56.6 bits(135)	7e-08	Compositional matrix adjust.	26/34(76%)	30/34(88%)	0/34(0%)	-1
Query 294	GPAFTILALLNSLTCVNPWYILSFNRELRLTLM 327					
	G FTILALL+SL SCVNPWYIL+FN ELR+TL+					
Sbjct 117782	GTTFTILALLSSLNSCVNFWIYLAFFNRELRLTLI 117681					

Trichogramma pretiosum Contig3858, whole genome shotgun sequence

Sequence ID: [ajb|JARR01003858.1](#)|Length: 67335

Number of Matches: 4

Range 1: 28185 to 28532[GenBankGraphics](#)

Query: *Polistes canadensis* gi|954548184|ref|XP_014616661.1|

Alignment statistics for match #1

Score	Expect	Method	Identities	Positives	Gaps	Frame
163 bits(413)	8e-62	Compositional matrix adjust.	76/119(64%)	92/119(77%)	3/119(2%)	+3
Query 93	RFQGGVLCKLVKFPFGLYLSSYILTATAIDRYHAICHPLSYCSVTSRQSRIMVYCAW		152			
	RF GG +LCKLVK+ QP G YLSSY+L ATA DRYHAIC+PLSYC TSR+SRI VY AW					
Sbjct 28185	RFHGGEILCKLVKFGQPLGSLSSYVLMATAADRYHAICYPLSYCRTTSRRSRITVYTAW		28364			
Query 153	SFALILCIPQLFVFSYQEVMPRIWDCWATFDIQFGEKAYVTWYSLMVFLLPFIVLVYTY		211			
	+L+LC+PQ+F+FS QE+ P IWDWATFD+ +KAYVTW +VF F++ TY					
Sbjct 28365	ILSLLCLPQIFIFSIEIAPGIWDCWATFDLPYAKKAYVTW--LVFKKIFVIACNTY		28532			

Range 2: 27862 to 28101[GenBankGraphics](#)

Alignment statistics for match #2

Score	Expect	Method	Identities	Positives	Gaps	Frame
92.8 bits(229)	8e-62	Compositional matrix adjust.	48/80(60%)	67/80(83%)	1/80(1%)	+1
Query 15	EKDTRDENLAKWEIVLLANILIFTIFGNSLVLLSLYLRKYRAHKK--LSRMVFFIMNLSIA		73			
	E+D RD +L K E+++L+ I + T+ GNSLVL ++YLR+ R ++ L+RM+FF+M+LSIA					
Sbjct 27862	EEDERDNDLVKVELLVLSLIFLVTLMGNSLVLFVAILYLRRCRGRRLTRMHFVHMLSIA		28041			
Query 74	DLITGLLDVLPQLAWDITFR 93					
	DL+TGLL+VLPQLAWDITFR					
Sbjct 28042	DLITGLLNVLPQLAWDITFR 28101					

Range 3: 29159 to 29452 [GenBankGraphics](#)

Alignment statistics for match #3

Score	Expect	Method	Identities	Positives	Gaps	Frame
88.6 bits(218)	4e-18	Compositional matrix adjust.	48/100(48%)	69/100(69%)	2/100(2%)	+2
Query 195	YSLMVFLLPFIVLVYTYVVGICVGVWQSNKMSGAVDDRAyirsisnysrnrssfisKAMIN		254			
	+S+M+FLLPF VL +TYV IC+ +W + ++ A+ + +RN+ S ISKA IN					
Sbjct 29159	FSMIFLPLPFVSLTFTTYVEICLSIWHNREV--AMLESQQALQPQIRARNQGSLSKAKIN		29332			
Query 255	TVKQTIATIVITLYAITSIPFIGCELWVSWDTKAFESSFANG		294			
	T+KQT+AV+ LYA +S+PFIG +LW +WD A ES+F G					
Sbjct 29333	TIKQTLAVVILYAASSMPFIGQLWSAWDPYAAESAFFPKG		29452			

Range 4: 29709 to 29822 [GenBankGraphics](#)

Alignment statistics for match #4

Score	Expect	Method	Identities	Positives	Gaps	Frame
43.1 bits(100)	0.001	Compositional matrix adjust.	26/38(68%)	32/38(84%)	0/38(0%)	+3
Query 292	ANGPAFTLLALLNSLTSCVNPWYILSFNRELRLQTLNMY		329			
	+GP FTIL+LL+SLTSCVNPWYIL+F+ ELR LM +					
Sbjct 29709	CSGPTFTILSLLSSTSCVNPWYILYLFYSYELRIVLMKF		29822			

Copidosoma floridanum Contig51734, whole genome shotgun sequence

Sequence ID: [gb|JBOX01051729.1|](#) Length: 2154

Number of Matches: 4

Range 1: 1652 to 1864 [GenBankGraphics](#)

Query: Polistes_canadensis gi|954548184|ref|XP_014616661.1|

Alignment statistics for match #1

Score	Expect	Method	Identities	Positives	Gaps	Frame
116 bits(291)	3e-27	Compositional matrix adjust.	53/71(75%)	60/71(84%)	0/71(0%)	-3
Query 93	RFQGGVLVCKLVKFFQPFGLYLSYILTATAIDRYHAICHPLSYCSVTSRQSRIMVYCAW		152			
	RF+GG VLCK+VKF QP G YLSSYIL ATA+DRYHAIC PLSYC TSR+SR+MVY AW					
Sbjct 1864	RFKGGVDLVCKMVKFGQPLGSLYLSYILITAVDRYHAICFPLSYCRTTSSRRSRVMVYSAW		1685			
Query 153	SFALILCIPQL		163			
	ALILC+PQ+					
Sbjct 1684	VLALILCVPOV		1652			

Range 2: 980 to 1282 [GenBankGraphics](#)

Alignment statistics for match #2

Score	Expect	Method	Identities	Positives	Gaps	Frame
79.7 bits(195)	3e-22	Compositional matrix adjust.	47/101(47%)	70/101(69%)	1/101(0%)	-3
Query 195	YSLMVFLLPFIVLVYTYVVGICVGVWQSNKMSGAVD-DRAyirsisnysrnrssfisKAMI		253			
	YSL VFL+PF VL +TY IC +W++ + + ++ +++SN +RN+ + ISKA +					
Sbjct 1282	YSLTVFLVFPFVSLTFTTYTRICCSIWRNRDVLVLGNLEKQQQALSNQARNQHALISKAKM		1103			
Query 254	NTVKQTIATIVITLYAITSIPFIGCELWVSWDTKAFESSFANG		294			
	+TVKQT+AV+ LYA +S+PFIG+LW +W A ES F G					
Sbjct 1102	STVKQTLAVVILYAASSLPFIGQLWATWVPGAESPFYTG		980			

Range 3: 1404 to 1514 [GenBankGraphics](#)

Alignment statistics for match #3

Score	Expect	Method	Identities	Positives	Gaps	Frame
45.1 bits(105)	3e-22	Compositional matrix adjust.	20/38(53%)	27/38(71%)	1/38(2%)	-2
Query 157	IILCIPQLFVFSYQVEMPRWDWCATFDIQFGEKAYVTW		194			
	I+C+ Q+F+FS + V +WDCWATF G+K YVTW					
Sbjct 1514	IICVFQVFIFSLRIVSAGVWDCWATFT-GHGQKIYVTW		1404			

Range 4: 757 to 978 [GenBankGraphics](#)

Alignment statistics for match #4

Score	Expect	Method	Identities	Positives	Gaps	Frame
50.4 bits(119)	1e-05	Compositional matrix adjust.	36/74(49%)	48/74(64%)	9/74(12%)	-1
Query 276	CELWVSWDTKAFESSFAN---GPAFTLLALLNSLTSCVNPWYILSFNRELRLQTLNMYFC		331			
	C ++ ++ F S+A GPAFTIL+LL+SLTSCVNPWYIL F+RELR +L+ +					
Sbjct 978	CCVFSYQSRIFSIYARVLCAGPAFTILSLLSSTSCVNPWYILVFSRELRVSLIKFLH		799			
Query 332	-----NRNEHSQKY		340			
	NR+ S KY					
Sbjct 798	HLVKRNRSSSSGKY		757			

Copidosoma floridanum Contig51735, whole genome shotgun sequence

Sequence ID: [gb|JBOX01051730.1|](#) Length: 2519

Number of Matches: 1

Range 1: 182 to 430 [GenBankGraphics](#)

Query: Polistes_canadensis gi|954548184|ref|XP_014616661.1|

Alignment statistics for match #1

Score	Expect	Method	Identities	Positives	Gaps	Frame
82.0 bits(201)	1e-15	Compositional matrix adjust.	47/83(57%)	65/83(78%)	1/83(1%)	-2
Query 13	NEEKDRDENLAKWEIVLLANILIFTIFGNSLVLLSFLYLRKYRAHKKL-SRMVFFIMNLS		71			
	++ +D RDE+LA WE+ LL IL ++ N LVL ++YLR+YR + +RM+FF+M+LS					
Sbjct 430	SKGEDWRDEDLAFWEVALLGFILAVSVVSNGLVLFALYLRRYRGRHRLTRMHFFVMHLS		251			
Query 72	IADLLTGLLDVLPQLAWDITFRF		94			
	IADL TGLL+VLPQLAWDIT+R+					
Sbjct 250	IADLTTGLLNVLPLQLAWDITRW		182			

Fopius arisanus strain USDA-PBARC FA_bdor contig003174, whole genome shotgun sequence
 Sequence ID: [gb|JRKH01003174.1](#)|Length: 107392
 Number of Matches: 4
 Range 1: 6563 to 7036[GenBankGraphics](#)
 Query: Polistes_canadensis gi|954548184|ref|XP_014616661.1|

Alignment statistics for match #1

Score	Expect	Method	Identities	Positives	Gaps	Frame
117 bits(294)	1e-58	Compositional matrix adjust.	73/159(46%)	97/159(61%)	25/159(15%)	+2
Query 195	YSLMVFLLPFIVLVYTYVVICVGVNQSNKMSGAVDDRAYirsisnyernrsffisKAMIN		254			
Sbjct 6563	YSITVLMPLPFSVLVYTYVVICREIWKNTTEIT-VFGRHGEVVRMSRENNREPVISRARIK		6739			
Query 255	TVKQTIATIVITLYAITSIPFFIGCELWVSWDTKAFESSFANGP-----		295			
Sbjct 6740	TVKQ I V++L+ ITS PF+GC+LW +WD A ++ F GP		6919			
Query 296	-----AFTILALLNSLTCVNFWIYLSFNRELRQTLNMY 329					
Sbjct 6920	AFTIL+LL+SLTSCVNFWIY+ FNRELR TL NY		7036			

Range 2: 6057 to 6275[GenBankGraphics](#)

Alignment statistics for match #2

Score	Expect	Method	Identities	Positives	Gaps	Frame
105 bits(261)	1e-58	Compositional matrix adjust.	45/73(62%)	56/73(76%)	0/73(0%)	+3
Query 93	RFQGGVLVCKLVKFFQPFGLYSSYILTATAIDRYHAICHPLSYCSVTSRQSRIMVYCAW		152			
Sbjct 6057	RFQGG +LCKLVKF QP G Y S+Y+L A AIDRYHAIC+P +YC T RQ+R+MVY AW		6236			
Query 153	SFALILCIPQLFV 165					
Sbjct 6237	+ LC+PQ+ +		6275			

Range 3: 6385 to 6468[GenBankGraphics](#)

Alignment statistics for match #3

Score	Expect	Method	Identities	Positives	Gaps	Frame
43.1 bits(100)	1e-58	Compositional matrix adjust.	17/28(61%)	20/28(71%)	0/28(0%)	+1
Query 167	SYQEVMPRIWDCWATFDIQFGKAYVTW 194					
Sbjct 6385	SYQE+ P IWDCA F G++ YVTW		6468			

Range 4: 5664 to 5894[GenBankGraphics](#)

Alignment statistics for match #4

Score	Expect	Method	Identities	Positives	Gaps	Frame
99.0 bits(245)	1e-21	Compositional matrix adjust.	49/77(64%)	63/77(81%)	1/77(1%)	+3
Query 16	KDTRDENLAKWEIVLLANILIFTIFGNSLVLLSLYLRY-RAHKLSRMYFFIMNLSIAD		74			
Sbjct 5664	+D RDE LA WE+V+L IL+ T+ GN LVL +LYLR+Y +KL+RMYFF+M+LSIAD		5843			
Query 75	LLTGLLDVLPQLAWDIT 91					
Sbjct 5844	L+TG+L+VLPQL W DIT		5894			

Hypochthonius rufulus scaffold216102_cov125, whole genome shotgun sequence

Sequence ID: [gb|LBF01050327.1](#)|Length: 5802
 Number of Matches: 1
 Range 1: 339 to 1244[GenBankGraphics](#)
 Query: Daphnia_pulex tr|K9JBV2|K9JBV2_DAPPU

Alignment statistics for match #1

Score	Expect	Method	Identities	Positives	Gaps	Frame
240 bits(612)	2e-68	Compositional matrix adjust.	143/360(40%)	196/360(54%)	62/360(17%)	-2
Query 17	RDEKLASVEISTLSVILVAVTSLNLTMLIAIWRQRRNPLSRMYFFMMHLSLADLLVALF		76			
Sbjct 1244	RDE LA EI +IL+LA+ N +L + +QR+ RP SR+Y FM HLSLADLLVA+F		1065			
Query 77	NILPQLAWDITVRFQGGDVLCRFVKYAQVMTLYLSTYILMFMAVDRYRAV-CCRNLHWNS		135			
Sbjct 1064	NILPQL W DIT+RF+ GD +CR VKY QV LYLSTYI++ M++DRY + + HW +		885			
Query 136	LKVAKCFVAASVVMALFISIPQAVIFHEEEISV--GVTDCWQVPEWGAAYVTFVVS		193			
Sbjct 884	K K + +W+++ LFSIPQA+IF +E+ + GV DCW F W K YV+WFV S		708			
Query 194	IFGAPLLVIGVCYVICRQIMYISqsalpssqqpptsaypaLTSETGSTLSVMRRWILR		253			
Sbjct 707	+F PL++I CYG IC ++W Y+ S T +L V		606			
Query 254	ASLRWQKSRSSSNNNGTKNHSAIANTSQLSDTI-PMRSLATQPASNPLSAEAKVIRslppp		312			
Sbjct 605	R ++N+ + N + I R + + L+ E +		474			
Query 313	lspqccqmqmplRRNSNQNRITKAKMKTIKLTLAVLFCFVACWAPFCITQLIMVYCPPTS		372			
Sbjct 473	+ N I++AK+KTIKLT+ VV+CF CWAPFCITQL + + PP S		339			

Steganacarus magnus, whole genome shotgun sequence

Sequence ID: [gb|LBFN01047006.1](#)|Length: 3438
 Number of Matches: 1
 Range 1: 853 to 1449[GenBankGraphics](#)

Query: Daphnia_pulex tr|K9JBV2|K9JBV2_DAPPU

Alignment statistics for match #1

Score	Expect	Method	Identities	Positives	Gaps	Frame
187 bits(476)	2e-50	Compositional matrix adjust.	94/202(47%)	136/202(67%)	7/202(3%)	+1
Query 17	RDEKLASVEISTLSVILVAVTSNLTMLIAIWRQRNRPLSRMYFFMMHLSLADLLVALF		76			
	RDE LA +EI L +I +L + N +LIA+ +R ++RMY+F++HL ++DL+					
Sbjct 853	RDEDLAKMEIIVLILIFILIIIGNSCVLIALAAKRFK--MTRMYFLLHLICISDLITGCC		1026			
Query 77	NILPQLAWDITYRFQGGDVLRCRFVKYAQVMTLYLSTYILMFMAVDYRAVC--CRNLHWN		134			
	+LPQ+AWDITYRF+GG++LC+FKVQ Q++ YLS+Y+L+ A+DRY+A+C N W					
Sbjct 1027	TVLPQIAWDITYRFKGGGNILCKFVKTIQLLGPYLSYVLVVNAIDRYQAICFPLTNSQWT		1206			
Query 135	SLKVAKCFVAASWVMALLFSPQAVIFHEEEI--SVGVTDCWVQFVEPWGAKAYVTWVW		192			
	S + +K + +W +AI+FS PQA F +EI S G +DCW F EPWG K YVTW+ +					
Sbjct 1207	S-RQSKLMIATIAWCIAIVFSSPQAFPPSYQEIPNSSGESDCWGTFFPEPWGEKLYVTWYAI		1383			
Query 193	SIFGAPLLVIGVCYGVICRQIW 214					
	SIF PL +I Y ICR++W					
Sbjct 1384	SIFFIPLFIITYTYVYICREW 1449					

Dermatophagoides farinae contig5815, whole genome shotgun sequence

Sequence ID: gb|ASGP01005815.1|Length: 7082

Number of Matches: 1

Range 1: 3977 to 4369GenBankGraphics

Query: Daphnia_pulex tr|K9JBV2|K9JBV2_DAPPU

Alignment statistics for match #1

Score	Expect	Method	Identities	Positives	Gaps	Frame
122 bits(307)	2e-28	Compositional matrix adjust.	60/133(45%)	90/133(67%)	9/133(6%)	+2
Query 52	RNRPL--SRMYFFMMHLSLADLLVALFNILPQLAWDITYRFQGGDVLRCRFVKYAQVMTLY		109			
	+NR L +RMYFF+ HLS+ADL+ FN+LPQL W+I RF GG+VLC+ +K+ Q++ Y					
Sbjct 3977	KNRKLKRNMYFFLAHLSIADLVTGFFNVLPQLGWEIASRFYGGNVLCKMIKFLQILGPY		4156			
Query 110	LSTYILMFMAVDYRAVCCRNHLHNSL--KVAKCFVAASWVMALLFSPQAVIFHEEEI		166			
	LS+Y+L+ ++DRY+A+C + NSL + ++ VA +W+M++LF PQ IF ++I					
Sbjct 4157	LSSVVLVMTSIDRYQAIC--HPLSNSLAHTRRSRWMVAVAWIMSLFCTPQTFIFSQKI		4330			
Query 167	SVGVTD--CWVQF 177					
	S D CW F					
Sbjct 4331	SPTSDDYECWATF 4369					

Sarcoptes scabiei Contig17956, whole genome shotgun sequence

Sequence ID: gb|JXLN01017957.1|Length: 20533

Number of Matches: 3

Range 1: 20086 to 20493GenBankGraphics

Query: Daphnia_pulex tr|K9JBV2|K9JBV2_DAPPU

Alignment statistics for match #1

Score	Expect	Method	Identities	Positives	Gaps	Frame
111 bits(277)	1e-24	Compositional matrix adjust.	53/136(39%)	84/136(61%)	7/136(5%)	-2
Query 53	RNRPL--SRMYFFMMHLSLADLLVALFNILPQLAWDITYRFQGGDVLRCRFVKYAQVMTLYL		110			
	NR L +RMYFF+ HLS+ADL+ FN+LPQLAW+ RF GG+ LC+ +K+ Q++ YL					
Sbjct 20493	NRKLKRNMYFFLAHLSIADLVTGFFNVLPQLAWEAARFFYGGNVLCKTIKFLQILGPYL		20314			
Query 111	STYILMFMAVDYRAVCC--CRNLHNSLKVAKCFVAASWVMALLFSPQAVIFHEEEIS		167			
	S+Y+L+ A+DRY+A+C + + + ++ +A +W + ++ + PQ IF + +S					
Sbjct 20313	SSVVLVMTAIDRYQAICYPLSNSFATKNTRRSRWMIAIAWIFSLSYCTPQCFIFSQRVS		20134			
Query 168	VGVTD--CWVQFVEPW 181					
	D CW F W					
Sbjct 20133	YETDDYECWGTQVSW 20086					

Range 2: 14702 to 14812GenBankGraphics

Alignment statistics for match #2

Score	Expect	Method	Identities	Positives	Gaps	Frame
48.1 bits(113)	2e-04	Compositional matrix adjust.	17/37(46%)	26/37(70%)	0/37(0%)	-1
Query 179	EPWGAKAYVTWVVSIFGAPLLVIGVCYGVICRQIWI 215					
	+PW +K YVTW+ +S+F P L++ + ICR+IWI					
Sbjct 14812	QPWMSKVYVTWYAISVIFVPLILLWTHYFICREIWI 14702					

Range 3: 5948 to 6088GenBankGraphics

Alignment statistics for match #3

Score	Expect	Method	Identities	Positives	Gaps	Frame
41.6 bits(96)	0.020	Compositional matrix adjust.	21/49(43%)	31/49(63%)	2/49(4%)	-1
Query 372	SQADVSPVAVIILLASLNSCSNPWIYLFAGSLLNQMRVCSILLRST 420					
	S + PV I++LL SLNSC NPWIY+ F+ +L+ +C L+S+					
Sbjct 6088	SSISLGPVIAIIMLLPSLNSCVNPNWYIYFNPNI--ALLCQFPKPKSS 5948					

Centruroides exilicauda breed non domesticated species of scorpion Contig23310, whole genome shotgun sequence

Sequence ID: gb|AXZ101023310.1|Length: 1410

Number of Matches: 2

Range 1: 522 to 1058 [GenBankGraphics](#)
 Query: Caligus_rogercresseyi

Alignment statistics for match #1

Score	Expect	Method	Identities	Positives	Gaps	Frame
179 bits(453)	2e-50	Compositional matrix adjust.	88/180(49%)	125/180(69%)	6/180(3%)	-2
Query 24	NSIVILAIATRHIKMTMYFFILHLSIADVLTAPLTLLELIWYTSNPFYGGALCKIV		83			
	N +V+LA+ R I+MTRMY+F+ HL ++D++TAF+LP++ W T F GG LCK+V					
Sbjct 1058	NCLVLLALMGRRIQMTRMYFLFHLCLSDLVTAFLHVLPQIAWDITY-RFRGGYLLCKLV		882			
Query 84	KFCQMIGPYLSSYVIMTAIDRYHAICNPLSKCTWTPKRSNIMIGLAWLVSFALCIPQAI		143			
	K+ Q++GPYLSY+L++TAIDRY AIC PL+ +WTP R IM+ +AW++S CIPQ					
Sbjct 881	KYVQLGPLYLSSYILVITAIIDRYQAICPLTSFSWTPIRGKIMVLVAWIISLCCIPQLF		702			
Query 144	IFGSSEAK-----YSCSASFVVDWGQKAYVTWFAVSNFFPPLLILYCYGRICKTIWDF		198			
	IF + + C +F+ WG+KAYVTW+ +S FF P +I+ + Y RIC +W NF					
Sbjct 701	IFSYQDVLGSLGVKDCWGTFIQWGEKAYVTWYTIISVFFIPFIIITFTYTRICLAVWKNF		522			

Range 2: 294 to 428 [GenBankGraphics](#)

Alignment statistics for match #2

Score	Expect	Method	Identities	Positives	Gaps	Frame
40.4 bits(93)	0.056	Compositional matrix adjust.	26/45(58%)	38/45(84%)	0/45(0%)	-2
Query 303	KRKSLKPRSHSIQGISRAKiktikltvvvivyGIACSAPPICVQL 347					
	+RK+ R H+++G+S+AK+KT+K+T+VVI+ YI CS PFICVQL					
Sbjct 428	RRKTPLSRRHNMKLSKAKVTKVITIVVIICIVCSPPICVQL 294					

Mesobuthus martensii Contig339050, whole genome shotgun sequence
 Sequence ID: [gb|AYEL01079865.1](#) Length: 43520

Number of Matches: 2

Range 1: 24252 to 24788 [GenBankGraphics](#)

Query: Caligus_rogercresseyi

Alignment statistics for match #1

Score	Expect	Method	Identities	Positives	Gaps	Frame
178 bits(451)	6e-48	Compositional matrix adjust.	89/180(49%)	123/180(68%)	6/180(3%)	+3
Query 24	NSIVILAIATRHIKMTMYFFILHLSIADVLTAFLLPELIWYTSNPFYGGALCKIV		83			
	N +V+LA+ R I+MTRMY+F+ HL I+D++TAF+LP++ W T F GG LCK V					
Sbjct 24252	NCLVLLALMGRRIQMTRMYFLFHLCLSDLVTAFLHVLPQIAWDITY-RFRGGYFLCKFV		24428			
Query 84	KFCQMIGPYLSSYVIMTAIDRYHAICNPLSKCTWTPKRSNIMIGLAWLVSFALCIPQAI		143			
	K+ Q++GPYLSY+L++TAIDRY AIC PL+ +WTP + IM+ +AW++S CIPQ					
Sbjct 24429	KYVQLGPLYLSSYILVITAIIDRYQAICPLASFSWTPKIGKIMVMVAWIISLCCIPQLF		24608			
Query 144	IFGSSEAK-----YSCSASFVVDWGQKAYVTWFAVSNFFPPLLILYCYGRICKTIWDF		198			
	IF E + C +F+ WG+KAYVTW+ +S FF P +I+ + Y RIC +W NF					
Sbjct 24609	IFSYQEIDDFSGVKDCWGTFIQWGEKAYVTWYTIISVFFIPFIIITFTYTRICIVVWKNF		24788			

Range 2: 24882 to 25016 [GenBankGraphics](#)

Alignment statistics for match #2

Score	Expect	Method	Identities	Positives	Gaps	Frame
39.3 bits(90)	0.17	Compositional matrix adjust.	24/45(53%)	38/45(84%)	0/45(0%)	+3
Query 303	KRKSLKPRSHSIQGISRAKiktikltvvvivyGIACSAPPICVQL 347					
	+RK+ + H+++G+S+AK+KT+K+T+VV++ YI CS PFICVQL					
Sbjct 24882	RRKTFLSQRHNLKLSKAKVTKVITIVVLCYIVCSPPICVQL 25016					

Oryctes borbonicus contig25461, whole genome shotgun sequence

Sequence ID: [gb|LJG01025627.1](#) Length: 62898

Number of Matches: 1

Range 1: 48816 to 49289 [GenBankGraphics](#)

Query: Tribolium_castaneum tr|A3RE84|A3RE84_TRICA

Alignment statistics for match #1

Score	Expect	Method	Identities	Positives	Gaps	Frame
280 bits(716)	5e-82	Compositional matrix adjust.	130/158(82%)	148/158(93%)	0/158(0%)	+3
Query 24	DRNNTDRDENLARVEVATLAIIFLVTVIGNSTVLLALWTRRRYAGRKKLSRMYFFILHLS		83			
	D N DRDENLA++E+ATLA+IFLVT+IGN VLLALWTR+RYAGRKKLSRMYFFILHLS					
Sbjct 48816	DENVLDRDENLAKIEIATLAVIFLVTIIGNCVLLALWTRKRYAGRKKLSRMYFFILHLS		48995			
Query 84	IADLITAFLSVLPQLAWDITYRFGYGFLLCKVVKYQTLGPLYLSSYVLMATAIDRHQAIC		143			
	IADLITAFLSVLPQLAW++T+RF GGF+LCKVVKYQTLGPLYLSSYV+ATAIDRHQAIC					
Sbjct 48996	IADLITAFLSVLPQLAWVTFRFGGFVLCVVKYQTLGPLYLSSYVLMATAIDRHQAIC		49175			
Query 144	YPLTYCSWTSRRSKVMVYLAWVASLAFQIPQLTIFTY 181					
	YPLTYCSWTSRRSKVMV++AW SL+FCIPQ++ F ++					
Sbjct 49176	YPLTYCSWTSRRSKVMVIAWVSLFQIPQVSNFCFS 49289					

Onthophagus taurus breed undomesticated insect ContigNC25934, whole genome shotgun sequence

Sequence ID: [gb|JHOM01025934.1](#) Length: 3568

Number of Matches: 1

Range 1: 1238 to 1732 [GenBankGraphics](#)

Query: Tribolium_castaneum tr|A3RE84|A3RE84_TRICA

Alignment statistics for match #1

Score	Expect	Method	Identities	Positives	Gaps	Frame
271 bits(694)	9e-80	Compositional matrix adjust.	128/165(78%)	150/165(90%)	2/165(1%)	-1
Query 14	NSTYLFDPKHEDR--NNTDRDENLARVEVATLAIIFLVTVIGNSTVLLALWTRRRYAGRKK		71			
	N+T L D E+ + +RDENLA++E+ATLAIIFLVT+IGN TVLLALWTRRRYAGRKK					
Sbjct 1732	NATPLNDTTEENVIDIVERDENLAKIEIATLAIIFLVTIIGNGTVLLALWTRRRYAGRKK		1553			
Query 72	LSRMYFFILHLSIADLITAFLSVLPQLAWDITYRFGYGFLLCKVVKYQTLGPLYLSSYV		131			
	LSRMYFFILHLS+ADLITAFLSVLPQL W++T+RF GGF+LCK+VK+QTLGPLYLSSY+L					
Sbjct 1552	LSRMYFFILHLSVADLITAFLSVLPQLIWEVTFRFGGFILCKLVKFGQTLGPLYLSSYIL		1373			

Query 132 MATAIDRHQAICYPLTYCSWTSRRSKVMVYLAWVASLAFQIPQLT 176
 +ATAIDRHQAICYPLTYCSWTSRRSK MV++AW SL+FCIPQ++
 Sbjct 1372 VATAIDRHQAICYPLTYCSWTSRRSKAMVWIAWGVSLSCIPQVS 1238

Agrilus planipennis Contig56141, whole genome shotgun sequence

Sequence ID: [gb|JENH01056123.1|](#)Length: 4939

Number of Matches: 1

Range 1: 4171 to 4683 [GenBankGraphics](#)

Query: Tribolium_castaneum tr|A3RE84|A3RE84_TRICA

Alignment statistics for match #1

Score	Expect	Method	Identities	Positives	Gaps	Frame
261 bits(668)	9e-76	Compositional matrix adjust.	124/171(73%)	148/171(86%)	2/171(1%)	+1
Query 8	QMDISENSTYLFDKHEDRNN--TDRDENLARVEVATLAIIFLVTVIGNSTVLLALWTRRR		65			
	+M+ S N+ L+ D N ++RDENLA++E+A L +IF+VTV+GNS VLLALWTRR					
Sbjct 4171	RMNFSVNNQSLYQPFQDVENVLSERDENLAKIEIAILIVIFIVTVLGNISVLLALWTRRI		4350			
Query 66	YAGRKKLSRMYFFILHLSIADLITAFLSVLPQLAWDITYRFYGGFLLCKVVKYQQTLPY		125			
	YAGRKKLSRMYFFILHLSIADL+TA LS LPQLAWDIT+RF GG+LLCK+VK+GQ LGPY					
Sbjct 4351	YAGRKKLSRMYFFILHLSIADLVTALLSDLPQLAWDITFRFKGGWLLCKIVKFGQLLPY		4530			
Query 126	LSSYVLMATAIDRHQAICYPLTYCSWTSRRSKVMVYLAWVASLAFQIPQLT 176					
	LSSY+LMATA+DR+QAICYPLTYCSWTSRRSK+MV+ AW+ SL FCIPQ+T					
Sbjct 4531	LSSYILMATAVDRYQAICYPLTYCSWTSRRSKLMVWTAWITSLIFCIPQVT 4683					

Anoplophora glabripennis Contig68241, whole genome shotgun sequence

Sequence ID: [gb|AQHT01068175.1|](#)Length: 5957

Number of Matches: 1

Range 1: 583 to 921 [GenBankGraphics](#)

Query: Tribolium_castaneum tr|A3RE84|A3RE84_TRICA

Alignment statistics for match #1

Score	Expect	Method	Identities	Positives	Gaps	Frame
214 bits(546)	2e-59	Compositional matrix adjust.	99/113(88%)	109/113(96%)	0/113(0%)	+1
Query 65	RYAGRKKLSRMYFFILHLSIADLITAFLSVLPQLAWDITYRFYGGFLLCKVVKYQQTLP		124			
	RYAGRKKLSRMYFFILHLSIADLITAF+ LPQLAWDIT+RF GGF +CKVVKYQQTLP					
Sbjct 583	RYAGRKKLSRMYFFILHLSIADLITAF+LPQLAWDITFRFQGGFFMCKVVKYQQTLP		762			
Query 125	YLSSYVLMATAIDRHQAICYPLTYCSWTSRRSKVMVYLAWVASLAFQIPQLTI 177					
	YLSSY+LMATA+DRHQAICYPLTYCSWTSRRSKVMVYLAW+L FCIPQ+++					
Sbjct 763	YLSSYILMATAVDRHQAICYPLTYCSWTSRRSKVMVYLAWMAALLFCIPQVSV 921					

Leptinotarsa decemlineata Contig191282, whole genome shotgun sequence

Sequence ID: [gb|AYNB01191279.1|](#)Length: 2693

Number of Matches: 1

Range 1: 387 to 725 [GenBankGraphics](#)

Query: Tribolium_castaneum tr|A3RE84|A3RE84_TRICA

Alignment statistics for match #1

Score	Expect	Method	Identities	Positives	Gaps	Frame
204 bits(520)	1e-56	Compositional matrix adjust.	97/113(86%)	103/113(91%)	0/113(0%)	-1
Query 65	RYAGRKKLSRMYFFILHLSIADLITAFLSVLPQLAWDITYRFYGGFLLCKVVKYQQTLP		124			
	RY GRKKLSRMYFFILHLSIADLITAF+L SVL QL WDITYRF GG LCK VKYQQTLP					
Sbjct 725	RYTGRKKLSRMYFFILHLSIADLITAF+L SVL TQLGWDITYRFKGGNFLLCKSVKYQQTLP		546			
Query 125	YLSSYVLMATAIDRHQAICYPLTYCSWTSRRSKVMVYLAWVASLAFQIPQLTI 177					
	YLSSY+L+ATA+DRHQAICYPLTYCSWTSRRSKVMVY+AW SL FCIPQ+++					
Sbjct 545	YLSSYILVATALDRHQAICYPLTYCSWTSRRSKVMVYIAWTVSLIFCIPQVSI 387					

Hypothenemus hampei scaffold1221, whole genome shotgun sequence

Sequence ID: [gb|LBGY01001191.1|](#)Length: 69032

Number of Matches: 5

Range 1: 61624 to 61809 [GenBankGraphics](#)

Query: Tribolium_castaneum tr|A3RE84|A3RE84_TRICA

Alignment statistics for match #1

Score	Expect	Method	Identities	Positives	Gaps	Frame
114 bits(286)	3e-25	Compositional matrix adjust.	52/62(84%)	57/62(91%)	0/62(0%)	-3
Query 117	KYGQTLGPYLSYVLMATAIDRHQAICYPLTYCSWTSRRSKVMVYLAWVASLAFQIPQLT		176			
	+YGQTLGPYLSYVLMATAIDRHQAICYPLTYCSWTSRRSKVM+Y+AW+ L CIPQ+					
Sbjct 61809	QYGQTLGPYLSYVLMATAIDRHQAICYPLTYCSWTSRRSKVMYVAVIVGLLCCIPQVN		61630			
Query 177	IF 178					
	IF					
Sbjct 61629	IF 61624					

Range 2: 59610 to 59918 [GenBankGraphics](#)

Alignment statistics for match #2

Score	Expect	Method	Identities	Positives	Gaps	Frame
112 bits(279)	2e-24	Compositional matrix adjust.	65/103(63%)	83/103(80%)	2/103(1%)	-1
Query 207	YSISVFMVPLVLIIFTYTSICIEIWqsesslrprssqksAPGKR--TPLISRAKINTVK		264			
	YS+++F++PL+VL++TY+ IC BIW+ S+SSLRPR+ K KR PLISRAKINTVK					
Sbjct 59918	YSLTIFIPLLVVYTYSCICREIWRCSDDSLRPRNMSKQIATKRDRVPLISRAKINTVK		59739			
Query 265	QTIIVIMYIACSTPPFILAQLWATWDPQSPFIDGPVVFVILTL 307					
	QT+AVIVMYI CSTPFI++QLWAT DP S F++G F + TLL					
Sbjct 59738	QTVAVIVMYIVCSTPFIIVSQLWATIDPTSSFFLEGKNFVFTLL 59610					

Range 3: 62170 to 62328[GenBankGraphics](#)

Alignment statistics for match #3

Score	Expect	Method	Identities	Positives	Gaps	Frame
96.7 bits(239)	2e-19	Compositional matrix adjust.	44/53(83%)	48/53(90%)	0/53(0%)	-3
Query 65	RYAGRKLSRMYFFILHLSIADLITAFLSVLPQLAWDITYRFYGGFLLCKVVK		117			
	RY GRKLSRMYFFILHLSIADLI AF SVLPQLAW++T+RF GGF+LCK VK					
Sbjct 62328	RYCGRKLSRMYFFILHLSIADLIVAFPSVLPQLANEVTFRFQGGFLLCKFVK		62170			

Range 4: 54000 to 54143[GenBankGraphics](#)

Alignment statistics for match #4

Score	Expect	Method	Identities	Positives	Gaps	Frame
77.4 bits(189)	5e-13	Compositional matrix adjust.	35/48(73%)	41/48(85%)	0/48(0%)	-1
Query 295	FIDGPFVILITLLYSLNSCVNPWIYLFNRELPRLLLRHYTASSKNYR		342			
	+ G F ILTLLYSLNSCVNPWIYLFNRELPRLLLRHYTASSKNYR					
Sbjct 54143	LLAGTFPFTILTLLYSLNSCVNPWIYLFNRELPRLLLRHYTASSKNYR		54000			

Range 5: 61006 to 61104[GenBankGraphics](#)

Alignment statistics for match #5

Score	Expect	Method	Identities	Positives	Gaps	Frame
45.1 bits(105)	0.007	Compositional matrix adjust.	17/33(52%)	23/33(69%)	0/33(0%)	-3
Query 175	LTIFTYTSVGEDEYDCWATFQEPWPKRAYVTWY		207			
	+ IF+Y V YDCWATF + WG++AYV W+					
Sbjct 61104	VIIFSYQEVAGHTYDCWATFNKEWGEQAYVIWF		61006			

Supplementary Table S1. List of analysed arthropod species

Subphylum or Order ^a	#	#	Species	Oxytocin-like peptide neurophysin domain (+)	Oxytocin-like precursor ID	Oxytocin-like receptor (+) ^b	Oxytocin-like receptor ID	Systematics (from NCBI)	Common name
Chelicerata	1	1	<i>Limulus polyphemus</i>	CFITNCPG	926609726	+++	926615389; 926636334; 926627326	Merostomata; Xiphosura; Limulidae	horseshoe crabs
	2	2	<i>Ixodes scapularis</i>	CFITNCPG	AGM20426.1	+++	215501697; 215501196; 215493320	Arachnida; Acari; Parasitiforme ; Ixodida; Ixodoidea; Ixodidae; Ixodinae	mites, ticks
	3	3	<i>Ixodes ricinus</i>	CFITNCPG	807918304	+	1016843980	Arachnida; Acari; Parasitiformes; Ixodida; Ixodoidea; Ixodidae; Ixodinae	
	4	4	<i>Rhipicephalus microplus</i>	CFITNCPG	ADMZ02000298.1			Arachnida; Acari; Parasitiformes; Ixodida; Ixodoidea; Ixodidae; Rhipicephalinae	
	5	5	<i>Ornithodoros turicata</i>			+	GDIE01074084.1	Arachnida; Acari; Parasitiformes; Ixodida; Ixodoidea; Argasidae	
	6	6	<i>Metaseiulus occidentalis</i>	CFITNCPG	391348425	++	391328891; 391341506	Arachnida; Acari; Parasitiformes; Mesostigmata; Gamasina; Phytoseioidea; Phytoseiidae; Typhlodrominae	
	7	7	<i>Varroa destructor</i>	CFITNCPG	ADDG01001370.1	++	ADDG01054890.1; ADDG01034892.1	Arachnida; Acari; Parasitiformes; Mesostigmata; Gamasina; Dermanysoidea; Varroidae	
	8	8	<i>Panonychus ulmi</i>			+	GCAC01000419.1	Arachnida; Acari; Acariiformes; Trombidiformes; Prostigmata; Eleutherengona; Raphignathae; Tetranychoidae; Tetranychidae	
	9	9	<i>Tetranychus urticae</i>	CFITNCPG	1005954275	+	1005961572	Arachnida; Acari; Acariiformes; Trombidiformes; Prostigmata; Eleutherengona; Raphignathae; Tetranychoidae; Tetranychidae	
	10	10	<i>Dermatophagoides farinae</i>	CFITNCPRA	ASGP01007982.1	+	ASGP01005815.1	Arachnida; Acari; Acariiformes; Sarcoptiformes; Astigmata; Psoroptidia; Analgoidea; Pyroglyphidae; Dermatophagoidinae	
	11	11	<i>Sarcoptes scabiei</i>	CFITNCPA	KPL97556.1	+	gbJXLN01017957.1	Arachnida; Acari; Acariiformes; Sarcoptiformes; Astigmata; Psoroptidia; Sarcoptoidea; Sarcoptidae; Sarcoptinae	
	12	12	<i>Hypochothonius rufulus</i>	CFITNCPG	LBFL01028909.1	+	LBFL01050327.1	Arachnida; Acari; Acariiformes; Sarcoptiformes; Oribatida; Enarthronota; Hypochothoidea; Hypochothoniidae	
	13	13	<i>Achipteria coleoptrata</i>	CFITNCPG	LBFM01000221.1	++	LBFM01000129.1; 5981-6625; LBFM01004763.1	Arachnida; Acari; Acariiformes; Sarcoptiformes; Oribatida; Brachypylina; Achipterioidea; Achipteriidae	
	14	14	<i>Platynothrus peltifer</i>	CFITNCPG	LBFO01089471.1	+++++	LBFO01084717.1; LBFO01069293.1; LBFO01087167.1; LBFO01104342.1, LBFO01089844.1	Arachnida; Acari; Acariiformes; Sarcoptiformes; Oribatida; Desmonomata; Crotonioidea; Camisiidae	
	15	15	<i>Steganacarus magnus</i>	CFITNCPG	LBFN01029022.1	+	LBFN01047006.1	Arachnida; Acari; Acariiformes; Sarcoptiformes; Oribatida; Mixonomata; Phthiracaroidae; Steganacaridae	
16	16	<i>Centruroides exilicauda</i>	CFITNCPG	AXZI01013139.1	+	AXZI01023310.1	Arachnida; Scorpiones; Buthida; Buthoidea; Buthidae	scorpions	
17	17	<i>Mesobuthus martensii</i>	CFITNCPG	AYEL01091269.1	+	AYEL01079865.1	Arachnida; Scorpiones; Buthida; Buthoidea; Buthidae		
18	18	<i>Loxosceles reclusa</i>					Arachnida; Araneae; Araneomorphae; Haplogynae; Sicariidae	spiders	
19	19	<i>Latrodectus hesperus</i>					Arachnida; Araneae; Araneomorphae; Entelegynae; Araneioidea; Theridiidae		
20	20	<i>Parasteatoda tepidariorum</i>					Arachnida; Araneae; Araneomorphae; Entelegynae; Araneioidea; Theridiidae		
21	21	<i>Stegodyphus mimosarum</i>					Arachnida; Araneae; Araneomorphae; Entelegynae; Eresoidea; Eresidae		
Myriapoda	22	1	<i>Symphylella vulgaris</i>	CFITNCPG	GAKX01066982.1			Symphyla; Scolopendrellidae	milipedes
	23	2	<i>Strigamia maritima</i>	CYITNCPG	AFFK01014417.1;1 57792-158367	++	AFFK01021536.1; 6079-6519;6079-	Chilopoda; Pleurostigmophora; Epimorpha; Geophilomorpha;	centipedes

					6519; AFFK01021536:22 344-23360;25188- 25421	Linotaeniidae	
	24	3	<i>Scolopendra subspinipes</i>	CFITNCPG CYIINCIDND	GBIM01005348.1; GBIM01002605.1	Chilopoda; Pleurostigmophora; Epimorpha; Scolopendromorpha; Scolopendridae	
	25	4	<i>Lithobius forficatus</i>	CFITNCPG	679426463	Chilopoda; Pleurostigmophora; Lithobiomorpha; Lithobiidae; Lithobius	
	26	5	<i>Glomeris pustulata</i>			Diplopoda; Pentazonia; Glomerida; Glomeridae	
Crustaceans	27	1	<i>Cypridina sp.</i>			Ostracoda; Myodocopa; Myodocopida; Cypridinoidea; Cypridinidae	mussels, shrimps crabs,
	28	2	<i>Sarsinebalia urgorrii</i>			Malacostraca; Phyllocarida; Leptostraca; Nebaliidae	lobsters, crayfish, shrimps,
	29	3	<i>Hyalella azteca</i>			Malacostraca; Eumalacostraca; Peracarida; Amphipoda; Senticaudata; Talitrida Talitroidea; Hyalellidae	krill, woodlice
	30	4	<i>Parhyale hawaiensis</i>			Malacostraca; Eumalacostraca; Peracarida; Amphipoda; Senticaudata; Talitrida Talitroidea; Hyalidae	
	31	5	<i>Litopenaeus vannamei</i>	CFITNCPG	JP362883.1	Malacostraca; Eumalacostraca; Eucarida; Decapoda; Dendrobranchiata; Penaeoidea Penaeidae	
	32	6	<i>Celuca pugilator</i>			Malacostraca; Eumalacostraca; Euc arida; Decapoda; Pleocyemata; Brachyura; Eubranchyura; Thoracotremata; Ocyropodoidea	
	33	7	<i>Scylla paramamosain</i>	+	ALQ28600.1	Malacostraca; Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura; Eubranchyura; Heterotremata; Portunoidea; Portunidae	
	34	8	<i>Homarus americanus</i>	CFITNCPG	GEBG01052869.1; GEBG01052869.1	Malacostraca; Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Astacidea; Nephropoidea; Nephropidae	
	35	9	<i>Triops cancriformis</i>	CFITNCPG	787010878:2475- 2558	Branchiopoda; Phyllopoidea; Notostraca; Triopsidae	shrimps
	36	10	<i>Daphnia magna</i>	CFITNCPG	JAK93241.1	Branchiopoda; Phyllopoidea; Diplostraca; Cladocera; Anomopoda; Daphniidae	
	37	11	<i>Daphnia pulex</i>	CFITNCPG	EFX71881.1	Branchiopoda; Phyllopoidea; Diplostraca; Cladocera; Anomopoda; Daphniidae	
	38	12	<i>Tigriopus californicus</i>	CFITNCPG	GBSZ01008472.1	Maxillopoidea; Copepoda; Neocopepoda; Podoplea; Harpacticoida; Harpacticidae	barnacles, copepods
	39	13	<i>Caligus rogercresseyi</i>	CFITNCPV S	GAZX01009828.1	Maxillopoidea; Copepoda; Neocopepoda; Sodoplea; Siphonostomatoida; Caligidae	
	40	14	<i>Lepeophtheirus salmonis</i>	CFITNCPV G	JAJ41077.1; JAN78479.1; JAK30878.1; JAM92944.1	Maxillopoidea; Copepoda; Neocopepoda; Podoplea; Siphonostomatoida; Caligidae	
	41	13	<i>Calanus finmarchicus</i>	CFISNCPV S	GAXK01089312.1; GAXK01048248.1; GBFB01189857.1	Maxillopoidea; Copepoda; Neocopepoda; Gymnople; Calanoida; Calanidae	
	42	14	<i>Eurytemora affinis</i>			Maxillopoidea; Copepoda; Neocopepoda; Gymnople; Calanoida; Temoridae	
	43	15	<i>Speleonectes cf. tulumensis</i>	CFILDCPLM	JL155260.1	Remipedia; Nectiopoidea; Speleonectidae	
Protura	44	1	<i>Acerentomon sp.</i>			Acerentomata; Acerentomidae	
Collembola	45	1	<i>Sminthurus viridis</i>	CFITNCPG	GATZ01101765.1	Symphyleona; Sminthuridae	
	46	2	<i>Tetradontophora bielensis</i>	+	GAXI01072001.1	Poduromorpha; Poduroidea; Onychiuridae; Tetradontophorinae	
	47	3	<i>Anurida maritima</i>	CFITNCPG	GAUE01051410.1	Poduromorpha; Poduroidea; Neanuridae; Pseudachorutinae	
	48	4	<i>Pogonognathellus sp.</i>	CFITNCPG	GATD01083368.1	Entomobryomorpha; Tomoceridae	
	49	5	<i>Folsomia candida</i>	CFITNCPG	GASX01087107.1	Entomobryomorpha; Isotomoidea; Isotomidae; Proisotominae	
Diplura	50	1	<i>Campodea augens</i>	+	GAYN01126761.1	Rhabdura; Campodeoidea; Campodeidae	

	51	2	<i>Catajapyx aquilonaris</i>	CFITNCPG	JYFJ01031256.1	+	JYFJ01023801.1	Dicellurata; Japygoidea; Japygidae; Japyginae
	52	3	<i>Occasjapyx japonicus</i>	CFITNCPG	GAXJ01105745.1	+	GAXJ01102351.1	Dicellurata; Japygoidea; Japygidae; Japyginae
Archaeognatha	53	1	<i>Meinertellus cundinamarcensis</i>	CFITNCPG	GAUG01237411.1	+	GAUG01249614.1	Meinertellidae
	54	2	<i>Machilis hrabei</i>	CFITNCPG	GAUM01180328.1	+	GAUM01006385.1	Machilidae
Zygentoma	55	1	<i>Tricholepidion gertschi</i>	CFITNCPG	GASO01245888.1	+	GASO01213666.1	Lepidotrichidae
	56	2	<i>Thermobia domestica</i>					Lepismatidae
	57	3	<i>Atelura formicaria</i>	CFITNCPG	GAYJ01010327.1; GAYJ01211146.1			Nicoletidae
Odonata	58	1	<i>Calopteryx splendens</i>					Zygoptera; Calopterygoidea; Calopterygidae; Calopteryx
	59	2	<i>Cordulegaster boltonii</i>			+	GAYO01131401.1	Anisoptera; Cavilabiata; Cordulegastridae
	60	3	<i>Ladona fulva</i>	CFITNCPG	APVN01010136.1	+	APVN01071783.1; APVN01071781.1	Anisoptera; Libellulidae
	61	4	<i>Epiophlebia superstes</i>			+	GAVW01126771.1	Anisozygoptera; Epiophlebiidae
Ephemeroptera	62	1	<i>Baetis sp.</i>	+	GATU01026804.1	+	GATU01012660.1	Pisciforma
	63	2	<i>Isonychia bicolor</i>	+	GAXA01082263.1	+	GAXA01009774.1	Setisura; Isonychiidae
	64	3	<i>Eurylophella sp.</i>	CFITNCPG	GAZG01089132.1	+	GAZG01097604.1	Furcatergalia; Pannota; Ephemerelloidea; Ephemerellidae
	65	4	<i>Ephemera danica</i>	CFITNCPG	AYNC01016661.1	+	AYNC01080313.1	Scaphodonta; Ephemeridae
Zoraptera	66	1	<i>Zorotypus caudelli</i>			+	GAYA01146842.1	Zorotypidae
Dermaptera	67	1	<i>Forficula auricularia</i>					Forficulina; Forficuloidea; Forficulidae
	68	2	<i>Apachys chartaceus</i>	CLITNCPKG	GAUW01104117.1	+		Forficulina; Apachyoidea; Apachyidae
Plecoptera	69	1	<i>Leuctra sp.</i>			+	GAUF01061620.1	Nemouroidea; Leuctridae
	70	2	<i>Perla marginata</i>			+	GATV01107607.1	Perloidea; Perlidae
	71	3	<i>Cosmioperla kuma</i>					Eusthenioidea; Eustheniidae
Orthoptera	72	1	<i>Gryllotalpa sp.</i>	CMIINCPRG	GAWZ01146014.1			Ensifera; Grylloidea; Gryllotalpidae
	73	2	<i>Teleogryllus commodus</i>	CMIINCPRG	GBHB01042598.1			Ensifera; Grylloidea; Gryllidae
	74	3	<i>Ceuthophilus sp.</i>	+	GAUX01264151.1			Ensifera; Rhaphidophoroidea; Rhaphidophoridae
	75	4	<i>Tetrix subulata</i>					Caelifera; Tetrigoidea; Tetrigidae
	76	5	<i>Prosarthria teretrirostris</i>					Caelifera; Acridomorpha; Eumastacoidea; Proscopiidae
	77	6	<i>Locusta migratoria manilensis</i>	CLITNCPRG	GCGJ01016197.1			Caelifera; Acridomorpha; Acridoidea; Acrididae
	78	7	<i>Stenobothrus lineatus</i>			+	GAUZ01276196.1	Caelifera; Acridomorpha; Acridoidea; Acrididae
Mantophasmatodea	79	1	<i>Tanzaniophasma sp.</i>					Tanzaniophasmatidae
Grylloblattodea	80	1	<i>Galloisiana yuasai</i>	CLITNCPKG	GAWN01176617.1	+	GAWN01106889.1	Grylloblattodea; Grylloblattidae
	81	2	<i>Grylloblatta bifratrilecta</i>					Grylloblattodea; Grylloblattidae
Embioptera	82	1	<i>Haploembia palaui</i>	CLITNCPG	GAZA01216527.1	+	GAZA01236978.1	Oligotomidae
	83	2	<i>Aposthonia japonica</i>	CLITNCPKG	GAWU01233766.1	+	GAWU01020812.1	Oligotomidae
Phasmatodea	84	1	<i>Timema cristinae</i>					Timematodea; Timematoidea; Timematidae
	85	2	<i>Peruphasma schultei</i>					Verophasmatodea; Areolatae; Pseudophasmatodea; Pseudophasmatidae
	86	3	<i>Aretaon asperimus</i>			+	GAWC01043798.1	Verophasmatodea; Areolatae; Bacilloidea; Heteropterygidae
	87	5	<i>Sipyloidea sipyulus</i>			+	GAWF01069276.1	Verophasmatodea; Anareolatae; Diapheromeridae
	88	4	<i>Ramulus artemis</i>			+	GAWE01092086.1	Verophasmatodea; Anareolatae; Phasmatidae
	89	6	<i>Extatosoma tiaratum</i>			+	GAWG01068689.1	Verophasmatodea; Anareolatae; Phasmatidae
	90	7	<i>Medauroidea extradentata</i>	+	GAWD01076003.1	+	GAWD01027027.1	Verophasmatodea; Anareolatae; Phasmatidae
Mantodea	91	1	<i>Metallyticus splendidus</i>					Metallyticidae
	92	2	<i>Empusa pennata</i>					Empusidae

	93	3	<i>Mantis religiosa</i>			+	GASW01107792.1	Mantidae			
Blattodea	94	1	<i>Blaberus atropos</i>	+			GAYD01152108.1	+	GAYD01167921.1	Blaberoidea; Blaberidae	
	95	3	<i>Blattella germanica</i>	CLITNCPKG	JPZV01163469.1; JPZV01163471.1	+			JPZV01131362.1; JPZV01131361.1	Blaberoidea; Ectobiidae	
	96	2	<i>Periplaneta americana</i>	+			GAWS01144903.1			Blattoidea; Blattidae	
	97	4	<i>Cryptocercus wrighti</i>	CLITNCPKG			GAZN01121910.1			Blattoidea; Cryptocercidae	
Isoptera	98	1	<i>Mastotermes darwiniensis</i>							Mastotermitidae	
	99	2	<i>Prorhinotermes simplex</i>	+			GASE02010515.1			Rhinotermitidae	
	100	3	<i>Nasutitermes exitiosus</i>							Termitidae	
	101	4	<i>Zootermopsis nevadensis</i>	CLITNCPKG	GCA_000696155.1 :scaffold412:22921: 25055:1 gene:L798_08907	+			KDQ65295:16-501	Termopsidae	
Thysanoptera	102	1	<i>Gynaikothrips ficorum</i>	CLITNCPKG			GAXG01236909.1			Tubulifera; Phlaeothripodea	
	103	2	<i>Frankliniella occidentalis</i>	+			JMDY01016652.1]; 503-766	+	JMDY01025147.1]	Terebrantia; Thripodea; Thripidae	
	104	3	<i>Frankliniella cephalica</i>					+	GAYE01097758.1	Terebrantia; Thripodea; Thripidae	
	105	4	<i>Thrips palmi</i>							Terebrantia; Thripodea;Thripidae	
Hemiptera	106	1	<i>Acanthosuarina muellerianae</i>					+	GAYY01128821.1	Sternorrhyncha; Psylliformes; Psylloidea; Psyllidae	jumping plant lice
	107	2	<i>Diaphorina citri</i>	CLINNCPTG	AWGM01069842.1	+			XM_008483692.1	Sternorrhyncha; Psylliformes; Psylloidea; Psyllidae	
	108	3	<i>Pachypsylla venusta</i>	CLISNCPKG	AZLD01215249.1	+			AZLD01271666.1; AZLD01292216.1; gb AZLD01271660 .1	Sternorrhyncha; Psylliformes; Psylloidea; Psyllidae	
	109	4	<i>Trialeurodes vaporariorum</i>							Sternorrhyncha; Aleyrodiformes; Aleyrodoidea; Aleyrodidae; Aleyrodinae	white flies
	110	5	<i>Bemisia tabaci</i>							Sternorrhyncha; Aleyrodiformes; Aleyrodoidea; Aleyrodidae; Aleyrodinae	
	111	6	<i>Pseudococcus longispinus</i>							Sternorrhyncha; Aphidiformes; Coccoidea; Pseudococcidae	scale insects
	112	7	<i>Maconellicoccus hirsutus</i>							Sternorrhyncha; Aphidiformes; Coccoidea; Pseudococcidae	
	113	8	<i>Ferrisia virgata</i>							Sternorrhyncha; Aphidiformes; Coccoidea; Pseudococcidae	
	114	9	<i>Trionymus perrisii</i>							Sternorrhyncha; Aphidiformes; Coccoidea; Pseudococcidae	
	115	10	<i>Paracoccus marginatus</i>							Sternorrhyncha; Aphidiformes; Coccoidea; Pseudococcidae	
	116	11	<i>Planococcus citri</i>							Sternorrhyncha; Aphidiformes; Coccoidea; Pseudococcidae	
	117	12	<i>Dactylopius coccus</i>							Sternorrhyncha; Aphidiformes; Coccoidea; Dactylopiidae	
118	13	<i>Essigella californica</i>							Sternorrhyncha; Aphidiformes; Aphidoidea; Lachnidae	aphids	
119	14	<i>Diuraphis noxia</i>							Sternorrhyncha; Aphidiformes; Aphidoidea; Aphididae; Macrosiphini		
120	15	<i>Acyrtosiphon pisum</i>							Sternorrhyncha; Aphidiformes; Aphidoidea; Aphididae; Macrosiphini		
121	16	<i>Aphis gossypii</i>							Sternorrhyncha; Aphidiformes; Aphidoidea; Aphididae; Aphidini		
122	17	<i>Velia caprai</i>							Heteroptera; Gerromorpha; Gerroidea; Veliidae; Veliinae	bugs	
123	18	<i>Gerris buenoi</i>							Heteroptera; Gerromorpha; Gerroidea; Gerridae; Gerrinae		
124	19	<i>Oncopeltus fasciatus</i>	+				JHQO01232535.1			Heteroptera; Panheteroptera; Pentatomomorpha; Lygaeoidea; Lygaeinae	
125	20	<i>Piezodorus guildinii</i>								Heteroptera; Panheteroptera; Pentatomomorpha; Pentamoidea; Pentatomidae; Pentatominae	
126	21	<i>Halyomorpha halys</i>	CLITNCPKG	JMPT01086066.1]; 13297-13677	+				XP_014279829.1	Heteroptera; Panheteroptera; Pentatomomorpha; Pentamoidea; Pentatomidae; Pentatominae	
127	22	<i>Acanthosoma haemorrhoidale</i>								Heteroptera; Panheteroptera; Pentatomomorpha; Pentamoidea; Acanthosomatidae	
128	23	<i>Cimex lectularius</i>								Heteroptera; Panheteroptera; Cimicomorpha; Cimicidae	
129	24	<i>Rhodnius prolixus</i>								Heteroptera; Panheteroptera; Cimicomorpha; Reduviidae;	

								Triatominae	
	130	25	<i>Notostira elongata</i>					Heteroptera; Panheteroptera; Cimicomorpha; Miridae; Stenodemiini	
	131	26	<i>Ranatra linearis</i>					Heteroptera; Panheteroptera; Nepomorpha; Nepidae; Ranatrinae	
	132	27	<i>Xenophysella greensladeae</i>					Coleorrhyncha; Peloridiomorpha; Peloridiidae	moss bugs
	133	28	<i>Nilaparvata lugens</i>	CLITNCPRG	AFW19795.1	+	BAO01091.1	Auchenorrhyncha; Fulgoroidea; Delphacidae; Delphacinae	planthopper
	134	29	<i>Homalodisca vitripennis</i>	CLITNCPKG	JJNS01285955.1; JJNS01158934.1	+	JJNS01062030.1; JJNS01434099.1	Auchenorrhyncha; Membracoidea; Cicadellidae; Cicadellinae; unclassified Cicadellinae	leafhoppers
	135	30	<i>Okanagana villosa</i>					Auchenorrhyncha; Cicadoidea; Cicadidae; Tibicininae; Tibicinini	cicadas
	136	31	<i>Cercopis vulnerata</i>			+	GAUN01111305.1	Auchenorrhyncha; Cercopoidea; Cercopidae;	frohoppers
Psocodea	137	1	<i>Ectopsocus briggsi</i>					Psocomorpha; Homilopsocidea; Lachesilloidea; Ectopsocidae	
	138	2	<i>Liposcelis bostrychophila</i>	CLITNCPRG	GAYV01106698.1	+	GAYV01018252.1	Troctomorpha; Nanopsocetae; Liposcelidae	
	139	3	<i>Menopon gallinae</i>	CLITNCPRG	GAWR01010043.1			Phthiraptera; Amblycera; Menoponidae	
	140	4	<i>Pediculus humanus corporis</i>					Phthiraptera; Anoplura; Pediculidae	
Hymenoptera	141	1	<i>Tenthredo koehleri</i>	+	GAWW01055882.1	+	GAWW01089352.1	Tenthredinoidea; Tenthredinidae; Tenthrediniinae	sawflies
	142	2	<i>Athalia rosae</i>	CLIINCPRG	XP_012261240.1	+	XP_012255235.1	Tenthredinoidea; Tenthredinidae; Allantinae	
	143	3	<i>Neodiprion lecontei</i>	CLIINCPRG	XP_015516596.1	+	LGIB01000555.1	Tenthredinoidea; Diprionidae; Diprioninae	
	144	4	<i>Orussus abietinus</i>	CLITNCPRG	XP_012280828.1	+	XP_012272252.1	Endopterygota; Hymenoptera; Orussoidea	
	145	5	<i>Ganaspis sp</i>			+	GAIW01017396.1	Symphyta; Cynipoidea; Figitidae; Eucoilinae	wasps
	146	6	<i>Leptopilina bouardi</i>			+	GAJA01004803.1	Symphyta; Cynipoidea; Figitidae; Eucoilinae	
	147	7	<i>Leptopilina clavipes</i>			+	GAXY01060534.1	Symphyta; Cynipoidea; Figitidae; Eucoilinae	
	148	8	<i>Nasonia giraulti</i>	CLITNCPRG	GBEC01021014.1	+	GBEC01022231.1	Apocrita; Chalcidoidea; Pteromalidae; Pteromalinae	
	149	9	<i>Nasonia vitripennis</i>	CLITNCPRG	XP_001606547.1	+	NM_001172274.1	Apocrita; Chalcidoidea; Pteromalidae; Pteromalinae	
	150	10	<i>Nasonia longicornis</i>	CLITNCPRG	ADAP01018019.1	+	ADAP01169230.1; ADAP01169223.1	Apocrita; Chalcidoidea; Pteromalidae; Pteromalinae	
	151	11	<i>Trichogramma pretiosum</i>	CLITNCPRG	XP_014226062.1	+	JARR01003858.1	Apocrita; Chalcidoidea; Trichogrammatidae	
	152	12	<i>Copidosoma floridanum</i>	CLITNCPRG	XP_014216967.1	+	JBOX01051729.1; JBOX01051730.1	Apocrita; Chalcidoidea; Encyrtidae; Encyrtinae	
	153	13	<i>Ceratosolen solmsi marchali</i>	+	XP_011505828.1			Apocrita; Chalcidoidea; Agaonidae; Agaoninae	
	154	14	<i>Cephus cinctus</i>	CLITNCPRG	XP_015604200.1	+	AMWH01000205.1	Apocrita; Cephoidea; Cephidae	
	155	15	<i>Diachasma alloeum</i>	CLITNCPRG	XP_015116397.1	+	LDKA01015940.1; LDKA01015941.1	Apocrita; Ichneumonoidea; Braconidae; Opiinae	
	156	16	<i>Fopius arisanus</i>	CLITNCPRG	XP_011303419.1	+	JRKH01003174.1	Apocrita; Ichneumonoidea; Braconidae; Opiinae	
	157	17	<i>Microplitis demolitor</i>	CLITNCPRG	XP_008557637.1	+	GAXO01007279.1	Apocrita; Ichneumonoidea; Braconidae; Microgastrinae	
	158	18	<i>Cotesia vestalis</i>	CLITNCPRG	GAUP01067026.1	+	GAUP01058790.1	Apocrita; Ichneumonoidea; Braconidae; Microgastrinae	
	159	19	<i>Telenomus podisi</i>	CLITNCPRG	GBEU01047114.1	+	GBEU01035833.1	Apocrita; Platygastridae; Scelionidae; Telenominae	
	160	20	<i>Chrysis viridula</i>	CLITNCPRG	GATY01003634.1	+	GATY01011771.1	Apocrita; Aculeata; Chrysididae; Chrysididae; Chrysidinae	
	161	21	<i>Argochrysis armilla</i>			+	GAXO01007279.1	Apocrita; Aculeata; Chrysididae; Chrysididae; Chrysidinae	
	162	22	<i>Sphaerophthalma orestes</i>			+	GAXP01010798.1	Apocrita; Aculeata; Pompiloidea; Mutillidae; Sphaerophthalminae	
	163	23	<i>Polistes dominula</i>	CLITNCPRG	XP_015176922.1	+	LMBU01000007.1	Apocrita; Aculeata; Vespoidea; Vespidae; Polistinae	
	164	24	<i>Polistes canadensis</i>	CLITNCPRG	XP_014601007.1	+	XP_014616661.1	Apocrita; Aculeata; Vespoidea; Vespidae; Polistinae	
	165	25	<i>Polistes metricus</i>	CLITNCPRG	GBGV01014087.1]; 870-1319	+	GBGV01009051.1	Apocrita; Aculeata; Vespoidea; Vespidae; Polistinae	
	166	26	<i>Mischocyttarus flavitarsis</i>	CLITNCPRG	GAXM01001949.1]; :391-804	+	GAXM01016032.1	Apocrita; Aculeata; Vespoidea; Vespidae; Polistinae	
	167	27	<i>Pseudomasaris vespoides</i>	CLITNCPRG	GAXQ01038846.1			Apocrita; Aculeata; Vespoidea; Vespidae; Masarinae	
	168	28	<i>Chyphotus mellipes</i>	CLITNCPRG	GAXL01043733.1	+	GAXL01018116.1	Apocrita; Aculeata; Vespoidea; Bradynobaenidae; Chyphotinae	
	169	29	<i>Brachycistis timberlakei</i>	CLITNCPRG	GAZU01023639.1]; 2211-2657	+	GAZU01029175.1	Apocrita; Aculeata; Vespoidea; Tiphidae; Brachycistidinae	

	170	30	<i>Crioscolia alcione</i>	CLITNCPRG	GAXT01010223.1 1-207	+	GAXT01013548.1	Apocrita; Aculeata; Vespoidea; Scoliidae	
	171	31	<i>Tetramorium bicarinatum</i>	+	GASM01006298.1	+	GASM01007371.1	Apocrita; Aculeata; Vespoidea; Formicidae; Myrmicinae	ants
	172	32	<i>Wasmannia auropunctata</i>	CLITNCPRG	XP_011702880.1	+	XM_011691615.1	Apocrita; Aculeata; Vespoidea; Formicidae; Myrmicinae	
	173	33	<i>Pogonomyrmex barbatus</i>	CLITNCPRG	XP_011645557.1	+	XP_011639495.1	Apocrita; Aculeata; Vespoidea; Formicidae; Myrmicinae	
	174	34	<i>Vollenhovia emeryi</i>	CLITNCPRG	XP_011871987.1	+	XP_011350516.1	Apocrita; Aculeata; Vespoidea; Formicidae; Myrmicinae	
	175	35	<i>Acromyrmex echinator</i>	CLITNCPRG	XP_011065328.1	+	EGI60623.1	Apocrita; Aculeata; Vespoidea; Formicidae; Myrmicinae	
	176	36	<i>Atta colombica</i>	CLITNCPRG	LKEW01016192.1	+	LKEW01024766.1	Apocrita; Aculeata; Vespoidea; Formicidae; Myrmicinae	
	177	37	<i>Atta cephalotes</i>	CLITNCPRG	XP_012061245.1	+	gb LKEW01024766 .1	Apocrita; Aculeata; Vespoidea; Formicidae; Myrmicinae	
	178	38	<i>Monomorium pharaonis</i>	CLITNCPRG	XP_012527594.1	+	XP_012527228.1	Apocrita; Aculeata; Vespoidea; Formicidae; Myrmicinae	
	179	39	<i>Trachymyrmex cornetzi</i>	CLITNCPRG	KYN19822.1	+	LKEY01027754.1	Apocrita; Aculeata; Vespoidea; Formicidae; Myrmicinae	
	180	40	<i>Trachymyrmex zeteki</i>	CLITNCPRG	KYQ46204.1	+	LKFA01015596.1	Apocrita; Aculeata; Vespoidea; Formicidae; Myrmicinae	
	181	41	<i>Trachymyrmex septentrionalis</i>	CLITNCPRG	KYN39529.1	+	LKEZ01023603.1	Apocrita; Aculeata; Vespoidea; Formicidae; Myrmicinae	
	182	42	<i>Solenopsis invicta</i>	CLITNCPRG	LJ563171.1	+	XP_011159612.1	Apocrita; Aculeata; Vespoidea; Formicidae; Myrmicinae	
	183	43	<i>Cyphomyrmex costatus</i>	CLITNCPRG	LKEX01018246.1; LKEX01015288.1; LKEX01011223.1	+	gb LKEX01019312 .1	Apocrita; Aculeata; Vespoidea; Formicidae; Myrmicinae	
	184	44	<i>Lasius niger</i>	CLITNCPRG	LBMM01006435.1	+	LBMM01005371.1.1; LBMM01020432.1	Apocrita; Aculeata; Vespoidea; Formicidae; Formicinae	
	185	45	<i>Camponotus floridanus</i>	CLIVNCPRG	gnl Cflo_3.3 CFLO 12125-RA; gnl Cflo_3.3 CFLO 19205-RA	+	AEAB01029474.1; AEAB01029475.1	Apocrita; Aculeata; Vespoidea; Formicidae; Formicinae	
	186	46	<i>Harpegnathos saltator</i>	CLITNCPRG	XP_011147500.1	+	XP_011151734.1	Apocrita; Aculeata; Vespoidea; Formicidae; Ponerinae	
	187	47	<i>Dinoponera quadriceps</i>	CLITNCPHG	XP_014485987.1	+	XP_014470481.1	Apocrita; Aculeata; Vespoidea; Formicidae; Ponerinae	
	188	48	<i>Linepithema humile</i>	CLITNCPRG	XP_012222809.1	+	ADOQ01003105.1	Apocrita; Aculeata; Vespoidea; Formicidae; Dolichoderinae	
	189	49	<i>Cerapachys biroi</i>	CLITNCPRG	XP_011329433.1	+	XP_011350516.1	Apocrita; Aculeata; Vespoidea; Formicidae; Cerapachyinae	
	190	50	<i>Stigmatomma oregonense</i>			+	GAXR01031290.1	Apocrita; Aculeata; Vespoidea; Formicidae; Amblyoponinae	
	191	51	<i>Exoneura robusta</i>					Apocrita; Aculeata; Apoidea; Apidae; Xylocopinae	bees
	192	52	<i>Habropoda laboriosa</i>					Apocrita; Aculeata; Apoidea; Apidae; Anthophorinae	
	193	53	<i>Melipona quadrifasciata</i>					Apocrita; Aculeata; Apoidea; Apidae; Meliponinae	
	194	54	<i>Apis mellifera</i>					Apocrita; Aculeata; Apoidea; Apidae; Apinae	
	195	55	<i>Apis dorsata</i>					Apocrita; Aculeata; Apoidea; Apidae; Apinae	
	196	56	<i>Apis florea</i>					Apocrita; Aculeata; Apoidea; Apidae; Apinae	
	197	57	<i>Apis cerana</i>					Apocrita; Aculeata; Apoidea; Apidae; Apinae	
	198	58	<i>Bombus impatiens</i>					Apocrita; Aculeata; Apoidea; Apidae; Bombinae	
	199	59	<i>Bombus terrestris</i>					Apocrita; Aculeata; Apoidea; Apidae; Bombinae	
	200	60	<i>Dufourea novaeangliae</i>					Apocrita; Aculeata; Apoidea; Halictidae; Rophitinae	
	201	61	<i>Lasioglossum albipes</i>					Apocrita; Aculeata; Apoidea; Halictidae; Halictinae	
	202	62	<i>Megachile rotundata</i>					Apocrita; Aculeata; Apoidea; Megachilidae; Megachilinae	
Raphidioptera	203	1	<i>Inocellia crassicornis</i>	+	GAZH01017073.1	+	GAZH01092118.1	Inocelliidae	
	204	2	<i>Xanthostigma xanthostigma</i>					Raphidiidae	
Megaloptera	205	1	<i>Corydalus cornutus</i>	CLITNCPRG	GATG01039646.1	+	GATG01035419.1	Corydalidae	
	206	2	<i>Sialis lutaria</i>					Sialidae	
Neuroptera	207	1	<i>Conwentzia psociformis</i>			+	GAYH01081470.1	Coniopterygidae	
	208	2	<i>Osmylus fulvicephalus</i>	+	GAYC01082079.1	+	GAYC01075986.1	Osmylidae	
	209	3	<i>Pseudomallada prasinus</i>	CLITNCPRG	GAVV02007136.1			Chrysopidae	
	210	4	<i>Chrysopa pallens</i>			+	GAGF01046297.1	Chrysopidae	

	211	5	<i>Euroleon nostras</i>						Myrmeleontidae
Strepsiptera	212	1	<i>Mengenilla moldrzyki</i>						Mengenillidia; Mengenilloidea; Mengenillidae
	213	2	<i>Stylops melittae</i>						Stylopidia; Stylopidae
Coleoptera	214	1	<i>Aleochara curtula</i>	CLITNCPRG	GATW01005644.1	+		GATW01023067.1	Polyphaga; Staphyliniformia; Staphylinioidea; Staphylinidae; Tachyporinae group; Aleocharinae
	215	2	<i>Nicrophorus vespilloides</i>	CLITNCPRG	LJCH01004160.1	+		GDKQ01006510.1	Polyphaga; Staphyliniformia; Staphylinioidea; Silphidae; Nicrophorinae
	216	3	<i>Dendroctonus frontalis</i>			+		GAFI01014329.1	Polyphaga; Cucujiformia; Curculionioidea; Curculionidae; Scolytinae
	217	4	<i>Dendroctonus ponderosae</i>	CLITNCPRG	APGL01028326.1; GAFX01014170.1				Polyphaga; Cucujiformia; Curculionioidea; Curculionidae; Scolytinae
	218	5	<i>Hypothenemus hampei</i>	CLITNCPRG	LBGY01005928.1	+		LBGY01001191.1	Polyphaga; Cucujiformia; Curculionioidea; Curculionidae; Scolytinae
	219	6	<i>Dastarcus helophoroides</i>	+	GBCX01024478.1; 5-211				Polyphaga; Cucujiformia; Cucujoidea; Bothrideridae
	220	7	<i>Aethina tumida</i>	+	GCKB01019799.1; 156-437	+		GCKB01003102.1	Polyphaga; Cucujiformia; Cucujoidea; Nitidulidae; Nitidulinae
	221	8	<i>Meloe violaceus</i>	CLITNCPRG	GATA01002325.1	+		GATA01005266.1	Polyphaga; Cucujiformia; Tenebrionoidea; Meloidae
	222	9	<i>Tribolium castaneum</i>	CLITNCPRG	NP_001078831.1	+		A3RE84	Polyphaga; Cucujiformia; Tenebrionoidea; Tenebrionidae
	223	10	<i>Anoplophora glabripennis</i>	CLITNCPRG	AQHT01068515.1	+		AQHT01068175.1	Polyphaga; Cucujiformia; Chrysomeloidea; Cerambycidae; Lamiinae
	224	11	<i>Diabrotica virgifera virgifera</i>	+	EW761630:18-293				Polyphaga; Cucujiformia; Chrysomeloidea; Chrysomelidae; Galerucinae
	225	12	<i>Leptinotarsa decemlineata</i>	CLITNCPKG CLITNCPIG	AYNB011151526.1	+		AYNB01191279.1	Polyphaga; Cucujiformia; Chrysomeloidea; Chrysomelidae; Chrysomelinae
	226	13	<i>Onthophagus taurus</i>	CLITNCPRG	JHOM01000375.1			JHOM01025934.1	Polyphaga; Scarabaeiformia; Scarabaeoidea; Scarabaeidae; Scarabaeinae; Scarabaeinae
	227	14	<i>Oryctes borbonicus</i>	CLITNCPRG	LJIG01009187.1	+		LJIG01025627.1	Polyphaga; Scarabaeiformia; Scarabaeoidea; Scarabaeidae; Dynastinae
	228	15	<i>Agrilus planipennis</i>	CLITNCPRG	JENH01072924.1	+		JENH01056123.1	Polyphaga; Elateriformia; Buprestoidea; Buprestidae; Agrilinae
	229	16	<i>Lepicerus sp.</i>	+	GAZB01101514.1; GAZB01008737.1; GAZB01008738.1				Myxophaga; Lepiceridae
	230	17	<i>Priacma serrata</i>	CLITNCPRG	GACO01007629.1				Archostemata; Cupedidae
231	18	<i>Gyrinus marinus</i>	CLITNCPRG	GAUY01035880.1	+		GAUY01010995.1	Adephaga; Gyrinoidea; Gyrinidae	
232	19	<i>Pogonus chalceus</i>	+	JU438286.1; 2-208	+		JU436954.1	Adephaga; Caraboidea; Carabidae; Trechinae	
233	20	<i>Carabus granulatus</i>			+		GACW01037691.1	Adephaga; Caraboidea; Carabidae; Carabinae	
Trichoptera	234	1	<i>Rhyacophila fasciata</i>						
	235	2	<i>Platycentropus radiatus</i>						
	236	3	<i>Hydroptila spp.</i>						
	237	4	<i>Philopotamus ludificatus</i>						
	238	5	<i>Annulipalpia sp.</i>						
Lepidoptera^c	239	1	<i>Micropterix calthella</i>						
	240	2	<i>Dyseriocrania subpurpurella</i>						
	241	3	<i>Triodia sylvina</i>						
	242	4	<i>Nemophora degeerella</i>						
	243	5	<i>Yponomeuta evonymella</i>						
	244	6	<i>Zygaena fausta</i>						
	245	7	<i>Polyommatus icarus</i>						
	246	8	<i>Parides eurimedes</i>						
	247	9	<i>Bombyx mori</i>						

	248	10	<i>Manduca sexta</i>				
Siphonaptera	249	1	<i>Ceratophyllus gallinae</i>				
	250	2	<i>Archaeopsylla erinacei</i>				
	251	3	<i>Ctenocephalides felis</i>				
Mecoptera	252	1	<i>Boreus hyemalis</i>				
	253	2	<i>Nannochorista philpotti</i>				
	254	3	<i>Bittacus pilicornis</i>				
	255	4	<i>Panorpa vulgaris</i>				
Diptera^c	256	1	<i>Anopheles gambiae</i>				
	257	2	<i>Aedes aegypti</i>				
	258	3	<i>Phlebotomus papatasi</i>				
	259	4	<i>Trichocera saltator</i>				
	260	5	<i>Tipula maxima</i>				
	261	6	<i>Bibio marci</i>				
	262	7	<i>Bombylius major</i>				
	263	8	<i>Drosophila melanogaster</i>				
	264	9	<i>Lipara lucens</i>				
	265	10	<i>Rhagoletis pomonella</i>				
	266	11	<i>Glossina morsitans morsitans</i>				
	267	12	<i>Sarcophaga crassipalpis</i>				
	268	13	<i>Arachnocampa luminosa</i>	CYITNCPWG	GDQV01021566.1	+	GDQV01043269.1
	269	14	<i>Triarthria setipennis</i>				

Colour codes: only oxytocin-like precursor or receptor both oxytocin-like precursor and receptor genomes available more than 1 receptor/precursor sequence not annotated

^aThree first groups of Arthropoda (Chelicerata, Myriapoda and Crustaceans, underlined) represent subphylum; all others are orders of the subphylum Hexapoda; the class Insecta comprises the orders from Archaeognatha to Diptera.

^bNumber of '+' shows the number of different found receptor copies.

^cNot all negative hits were included although 99 Diptera and 25 Lepidoptera species found in the NCBI genome database (13th of April 2016) were included in the analysis.

Supplementary Table S2. List of species and accession numbers used to prepare dataset

Organism^a	BioProject ID	BioSample Accession	Transcriptome Accession	Download source
Acanthocasuarina muellerianae	219519	SAMN02047100	GAYY00000000	NCBI, TSA
Acanthosoma haemorrhoidale	219520	SAMN02047154	GAUV00000000	NCBI, TSA
Acerentomon sp. AD-2013	219521	SAMN02047102	GAXE00000000	NCBI, TSA
Aleochara curtula	219522	SAMN02047128	GATW00000000	NCBI, TSA
Annulipalpia sp. AD-2013	219539	SAMN02047195	GATX00000000	NCBI, TSA
Anurida maritima	219523	SAMN02047180	GAUE00000000	NCBI, TSA
Apachyus charteceus	219524	SAMN02047175	GAUW00000000	NCBI, TSA
Aposthonia japonica	219525	SAMN02047170	GAWU00000000	NCBI, TSA
Aretaon asperimus	219526	SAMN02047129	GAZQ00000000	NCBI, TSA
Atelura formicaria	219527	SAMN02047107	GAYJ00000000	NCBI, TSA
Baetis sp. AD-2013	219528	SAMN02047149	GATU00000000	NCBI, TSA
Bibio marci	219529	SAMN02047144	GATJ00000000	NCBI, TSA
Bittacus pilicornis	219530	SAMN02047197	GATH00000000	NCBI, TSA
Blaberus atropos	219531	SAMN02047121	GAYD00000000	NCBI, TSA
Bombylius major	219532	SAMN02047145	GATI00000000	NCBI, TSA
Boreus hyemalis	219533	SAMN02047164	GAYK00000000	NCBI, TSA
Calopteryx splendens	219534	SAMN02047184	GAYM00000000	NCBI, TSA
Campodea augens	219535	SAMN02047108	GAYN00000000	NCBI, TSA
Ceratophyllus gallinae	219536	SAMN02047116	GAWK00000000	NCBI, TSA
Cercopis vulnerata	219537	SAMN02047155	GAUN00000000	NCBI, TSA
Ceuthophilus sp. AD-2013	219538	SAMN02047189	GAUX00000000	NCBI, TSA
Chrysis viridula	219540	SAMN02047158	GATY00000000	NCBI, TSA
Conwentzia psociformis	219541	SAMN02047147	GAYH00000000	NCBI, TSA
Cordulegaster boltonii	219542	SAMN02047156	GAYO00000000	NCBI, TSA
Corydalus cornutus	219543	SAMN02047201	GATG00000000	NCBI, TSA
Cosmioperla kuna	219544	SAMN02047101	GAYL00000000	NCBI, TSA
Cotesia vestalis	219545	SAMN02047178	GAUP00000000	NCBI, TSA
Cryptocercus wrighti	219546	SAMN02047199	GAZN00000000	NCBI, TSA
Ctenocephalides felis	219547	SAMN02047194	GAYP00000000	NCBI, TSA
Dyseriocrania subpurpurella	219549	SAMN02047140	GASY00000000	NCBI, TSA
Ectopsocus briggsi	219550	SAMN01801569	GAPT00000000	NCBI, TSA
Empusa pennata	219551	SAMN02047168	GAWT00000000	NCBI, TSA
Ephemera danica	219552	SAMN02047152	GAUK00000000	NCBI, TSA
Epiophlebia superstes	219553	SAMN02047171	GAVW00000000	NCBI, TSA
Essigella californica	219554	SAMN02047099	GAZF00000000	NCBI, TSA
Euroleon nostras	219555	SAMN02047165	GAXW00000000	NCBI, TSA
Eurylophella sp. AD-2013	219556	SAMN02047200	GAZG00000000	NCBI, TSA
Folsomia candida	219557	SAMN02047120	GASX00000000	NCBI, TSA
Forficula auricularia	219558	SAMN02047143	GAYQ00000000	NCBI, TSA
Frankliniella cephalica	219559	SAMN02047110	GAYE00000000	NCBI, TSA
Galloisiana yuasai	219560	SAMN02047172	GAWN00000000	NCBI, TSA
Grylloblatta	219561	SAMN02047192	GAWP00000000	NCBI, TSA

bifratrilecta

<i>Gryllotalpa</i> sp. AD-2013	219562	SAMN02047167	GAWZ00000000	NCBI, TSA
<i>Gynaikothrips ficorum</i>	219563	SAMN02047111	GAXG00000000	NCBI, TSA
<i>Gyrinus marinus</i>	219564	SAMN02047132	GAUY00000000	NCBI, TSA
<i>Haploembia palaui</i>	219565	SAMN02047183	GAZA00000000	NCBI, TSA
<i>Hydroptila</i> sp. AD-2013	219566	SAMN02047190	GAVM00000000	NCBI, TSA
<i>Inocellia crassicornis</i>	219567	SAMN02047103	GAZH00000000	NCBI, TSA
<i>Isonychia bicolor</i>	219568	SAMN02047198	GAXA00000000	NCBI, TSA
<i>Lepicerus</i> sp. AD-2013	219569	SAMN02047177	GAZB00000000	NCBI, TSA
<i>Leptopilina clavipes</i>	219570	SAMN02047179	GAXY00000000	NCBI, TSA
<i>Leuctra</i> sp. AD-2013	219571	SAMN02047153	GAUF00000000	NCBI, TSA
<i>Lipara lucens</i>	219572	SAMN02047130	GAZD00000000	NCBI, TSA
<i>Liposcelis bostrychophila</i>	219573	SAMN02047187	GAYV00000000	NCBI, TSA
<i>Machilis hrabei</i>	219574	SAMN02047109	GAUM00000000	NCBI, TSA
<i>Mantis religiosa</i>	219575	SAMN02047157	GASW00000000	NCBI, TSA
<i>Mastotermes darwiniensis</i>	219576	SAMN02047123	GAZE00000000	NCBI, TSA
<i>Meinertellus cundinamarcensis</i>	219577	SAMN02047182	GAUG00000000	NCBI, TSA
<i>Meloe violaceus</i>	219578	SAMN02047163	GATA00000000	NCBI, TSA
<i>Menopon gallinae</i>	219579	SAMN02047141	GAWR00000000	NCBI, TSA
<i>Metallyticus splendidus</i>	219580	SAMN02047174	GATB00000000	NCBI, TSA
<i>Nemophora degeerella</i>	219581	SAMN02047104	GATC00000000	NCBI, TSA
<i>Nilaparvata lugens</i>	219582	SAMN02047185	GAYF00000000	NCBI, TSA
<i>Notostira elongata</i>	219583	SAMN02047151	GASV00000000	NCBI, TSA
<i>Occasjapyx japonicus</i>	219584	SAMN02047169	GAXJ00000000	NCBI, TSA
<i>Okanagana villosa</i>	219585	SAMN02047193	GAWQ00000000	NCBI, TSA
<i>Orussus abietinus</i>	219586	SAMN02047118	GAUJ00000000	NCBI, TSA
<i>Osmylus fulvicephalus</i>	219587	SAMN02047166	GAYC00000000	NCBI, TSA
<i>Panorpa vulgaris</i>	219588	SAMN02047142	GAUH00000000	NCBI, TSA
<i>Parides eurimedes</i>	219589	SAMN02047186	GAXH00000000	NCBI, TSA
<i>Periplaneta americana</i>	219590	SAMN02047124	GAWS00000000	NCBI, TSA
<i>Perla marginata</i>	219591	SAMN02047115	GATV00000000	NCBI, TSA
<i>Peruphasma schultei</i>	219592	SAMN02047114	GAWJ00000000	NCBI, TSA
<i>Planococcus citri</i>	219593	SAMN02047127	GAXF00000000	NCBI, TSA
<i>Platycentropus radiatus</i>	219594	SAMN02047196	GASS00000000	NCBI, TSA
<i>Pogonognathellus</i> sp. AD-2013	219595	SAMN02047134	GATD00000000	NCBI, TSA
<i>Polyommatus icarus</i>	219596	SAMN02047136	GAST00000000	NCBI, TSA
<i>Prorhinotermes simplex</i>	219597	SAMN02047122	GASE00000000	NCBI, TSA
<i>Prosarthria teretirostris</i>	219598	SAMN02047125	GAZT00000000	NCBI, TSA
<i>Pseudomallada prasinus</i>	219548	SAMN02047105	GAVV00000000	NCBI, TSA
<i>Ranatra linearis</i>	219599	SAMN02047138	GAYZ00000000	NCBI, TSA
<i>Rhyacophila fasciata</i>	219600	SAMN02047161	GAXX00000000	NCBI, TSA
<i>Sminthurus viridis</i>	219601	SAMN02047148	GATZ00000000	NCBI, TSA
<i>Stenobothrus lineatus</i>	219602	SAMN02047137	GAUZ00000000	NCBI, TSA

<i>Stylops melittae</i>	219603	SAMN02047139	GAZM00000000	NCBI, TSA
<i>Tanzaniophasma</i> sp. AD-2013	219604	SAMN02047176	GAXB00000000	NCBI, TSA
<i>Tenthredo koehleri</i>	219605	SAMN02047159	GAWW00000000	NCBI, TSA
<i>Tetrix subulata</i>	219606	SAMN02047150	GASQ00000000	NCBI, TSA
<i>Tetrodontophora bielanensis</i>	219607	SAMN02047160	GAXI00000000	NCBI, TSA
<i>Thermobia domestica</i>	219608	SAMN02047119	GASN00000000	NCBI, TSA
<i>Thrips palmi</i>	219609	SAMN02047112	GAXC00000000	NCBI, TSA
<i>Timema cristinae</i>	219610	SAMN02047191	GAVX00000000	NCBI, TSA
<i>Trialeurodes vaporariorum</i>	219611	SAMN02047126	GAWX00000000	NCBI, TSA
<i>Triarthria setipennis</i>	219612	SAMN02047117	GAVA00000000	NCBI, TSA
<i>Trichocera saltator</i>	219613	SAMN02047162	GAXZ00000000	NCBI, TSA
<i>Tricholepidion gertschi</i>	219614	SAMN02047188	GASO00000000	NCBI, TSA
<i>Triodia sylvina</i>	219615	SAMN02047133	GAVB00000000	NCBI, TSA
<i>Velia caprai</i>	219616	SAMN02047131	GAUO00000000	NCBI, TSA
<i>Xanthostigma xanthostigma</i>	219617	SAMN02047106	GAUI00000000	NCBI, TSA
<i>Xenophysella greensladeae</i>	219618	SAMN02047181	GAYI00000000	NCBI, TSA
<i>Yponomeuta evonymellus</i>	219619	SAMN02047146	GASG00000000	NCBI, TSA
<i>Zorotypus caudelli</i>	219620	SAMN02047173	GAYA00000000	NCBI, TSA
<i>Zygaena fausta</i>	219621	SAMN02047113	GAYB00000000	NCBI, TSA

Organism^b	Download source	Accession / Version
<i>Acromyrmex echinator</i>	Hymenoptera genome database	Aech_2.0
<i>Acyrtosiphon pisum</i>	AphidBase	ACYPI v2.0
<i>Aedes aegypti</i>	VectorBase	AaegL3.3
<i>Anopheles gambiae</i>	VectorBase	AgamP4.3
<i>Aphis gossypii</i>	NCBI, TSA	GW572841.1
<i>Apis mellifera</i>	Hymenoptera genome database	Amel_4.5
<i>Archaeopsylla erinacei</i>	NCBI, TSA	GABB01000001.1
<i>Bemisia tabaci</i>	NCBI, TSA	GAPP01000001.1
<i>Bombus terrestris</i>	NCBI, TSA	JL856152.1
<i>Bombyx mori</i>	NCBI, TSA	EL645743.1
<i>Carabus granulatus</i>	NCBI, TSA	GACW01000001.1
<i>Celuca pugilator</i>	NCBI, TSA	JO494914.1
<i>Cyprinidinae</i> sp.	NCBI, TSA	JL207200.1
<i>Daphnia pulex</i>	NCBI, TSA	FE425512.1
<i>Dendroctonus ponderosae</i>	NCBI, TSA	GAFW01000001.1
<i>Drosophila melanogaster</i>	FlyBase	dmel_r6.03
<i>Exoneura robusta</i>	NCBI, TSA	HP931235.1
<i>Glomeris pustulata</i>	NCBI, TSA	GAKW01000001.1
<i>Glossina morsitans morsitans</i>	NCBI, TSA	DV619302.1
<i>Harpegnathos saltator</i>	Hymenoptera genome database	Hsal_3.3
<i>Ixodes scapularis</i>	VectorBase	IscaW1.4
<i>Lepeophtheirus</i>	NCBI, TSA	JP350109.1

salmonis

Litopenaeus vancouverensis	NCBI, TSA	JP403722.1
Manduca sexta	NCBI, TSA	JO840459.1
Mengenilla moldrzyki	NCBI, TSA	GACY01000001.1
Micropterix calthella	NCBI, TSA	GACP01000001.1
Nannochorista philpotti	NCBI, TSA	GADB01000001.1
Nasonia vitripennis	Hymenoptera genome database	Nvit_OGSv1.2
Pediculus humanus	VectorBase	PhumU2.1
Philopotamus ludificatus	NCBI, TSA	GACV01000001.1
Phlebotomus papatasi	NCBI, TSA	JP555361.1
Priacma serrata	NCBI, TSA	GACO01000001.1
Rhagoletis pomonella	NCBI, TSA	EZ140167.2
Sarcophaga crassipalpis	NCBI, TSA	EZ617705.1
Sarsinebalia urgorrii	NCBI, TSA	JL099665.1
Sialis lutaria	NCBI, TSA	GABK01000001.1
Speleonectes cf. tulumensis	NCBI, TSA	JL207199.1
Symphylella vulgaris	NCBI, TSA	GAKX01000001.1
Tipula maxima	NCBI, TSA	GACZ01000001.1
Tribolium castaneum	BeetleBase	Tcas_4.0
Zootermopsis nevadensis	Ensemblgenomes	GCA_000696155.1

Supplementary References

- 1 Pitti, T. & Manoj, N. Molecular evolution of the neuropeptide S receptor. *PLoS One* **7**, e34046, (2012).
- 2 Meyer-Rochow, V. B. Glowworms: a review of *Arachnocampa* spp. and kin. *Luminescence* **22**, 251-265, (2007).
- 3 Pugsley, C. W. Literature-Review of the New-Zealand Glowworm *Arachnocampa-Luminosa* (Diptera, Keroplatidae) and Related Cave-Dwelling Diptera. *N. Z. Entomol.* **7**, 419-424, (1983).
- 4 Lee, B. Y. *et al.* Whole transcriptome analysis of the monogonont rotifer *Brachionus koreanus* provides molecular resources for developing biomarkers of carbohydrate metabolism. *Comp. Biochem. Physiol., D: Genomics & Proteomics* **14**, 33-41, (2015).
- 5 Crisp, A., Boschetti, C., Perry, M., Tunnacliffe, A. & Micklem, G. Expression of multiple horizontally acquired genes is a hallmark of both vertebrate and invertebrate genomes. *Genome Biol.* **16**, 50, (2015).
- 6 Dunning Hotopp, J. C. *et al.* Widespread lateral gene transfer from intracellular bacteria to multicellular eukaryotes. *Science* **317**, 1753-1756, (2007).
- 7 Gasmi, L. *et al.* Recurrent Domestication by Lepidoptera of Genes from Their Parasites Mediated by Bracoviruses. *PLoS Genet.* **11**, e1005470, (2015).
- 8 Kirsch, R., Heckel, D. G. & Pauchet, Y. How the rice weevil breaks down the pectin network: Enzymatic synergism and sub-functionalization. *Insect Biochem. Mol. Biol.* **71**, 72-82, (2016).
- 9 Moran, N. A. & Jarvik, T. Lateral transfer of genes from fungi underlies carotenoid production in aphids. *Science* **328**, 624-627, (2010).
- 10 Zolfaghari Emameh, R., Barker, H. R., Tolvanen, M. E., Parkkila, S. & Hytonen, V. P. Horizontal transfer of beta-carbonic anhydrase genes from prokaryotes to protozoans, insects, and nematodes. *Parasit. Vectors* **9**, 152, (2016).