

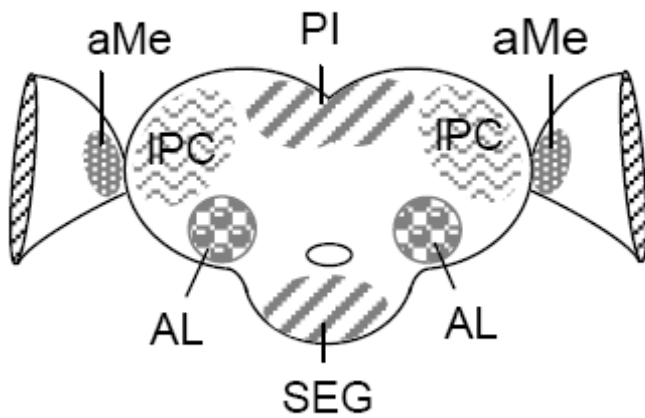


Figure S1:

For direct tissue peptide profiling, distinct parts of the brain/subesophageal ganglion of *Nasonia* were dissected, which are marked in grey. AL, antennal lobe; aMe, accessory medulla; PI, *pars intercerebralis*; IPC, laterale protocerebellum; SEG, subesophageal ganglion (ventral part).

Fig. S2: Annotated or cloned *Nasonia vitripennis* neuropeptide preprohormones

The putative signal peptides (predicted by SignalP) are boxed, the putative active neuropeptides or protein hormones (based on similarity to neuropeptides or protein hormones identified in other insects and the peptides found with mass spectrometry) are marked in yellow. Green indicates putative basic cleavage sites; glycines used for amidation are shown in blue. Dots indicate missing N- or C-termini. Underlined cysteine residues are proposed to be involved in cystine bridges.

It is not certain if the identified ITG-like and NVP-like sequences are neuropeptide precursors, although both have orthologues in the honeybee (9).

>AKH (NV_13000); **cloned cDNA** (see Fig. S3)

MNCRSLLALGLCLCVVLVQTRAAEG**QLNFSTGW****GKR**SSHLLQPARASSSSSS
SSSSSSTSAAAAAASSGIGRPRQQADLDYFLQRYRRLRKIEAQRLANSQV

>ACP (NV_30201)

MGRRLSIGLAAAAILFSCMLHFALA**QVTFSKGWGP****GKR**SALYETDCSRVNYK
SLALLFHTLLAEVKHLMACDHQATVNYLQSVVERQ

>Allatostatin A (NV_13011)

MSSSNLSGTAMSLTIFCVLSILGGTSVA**MDEQPSASSSSGVSSSSSSSSSHGPHFS**
PLVDPREQIVG**GKR**AYTYRSEY**KRLPIYQFGL****GKR**WVDD**KRSQPFSGFL****GKR**
TRPYSFGL**GKR**SSYSEDDDSRYGLDLSYLIQPSDLYEQLAQDALENYLQQQ
QAI**KRTGGFNFG****L****GKR**DAEMNEGMMREDGLHEKVPVKHS**RD****KYLFGL****GKR**
FYEPATMQDDEDEEMLEDA

>Allatostatin C (NV_30011); **cloned cDNA** (see Fig. S4)

MMSLRIAVCTAVALVVLVDWSTA**LPAGDKEALMNGLNMMGDEEGA**VER
DLLNYLVGRRFVKRLRNQADVDDLQ**RKR**NYWRQ**CAFNAVSCF****GK**

>Allatostatin CC (NV_30012); **cloned cDNA** (see Fig. S5)

MTSSGCRTFLALATALTILGTVSG**SPRGHALAKRSADANVIEYPDYEYQ**RVM
PKRAALLLDRLVALQKAVENDDVGKENSNSYVRS�PNFSDMPDSQRMQLS
NEKTMDLQ**RRGQAKGRVYWR**CYFNAVTC**FKRK**

>Bursicon-alpha (NV_13010)

MAHYRCKEYFFITNYFNISL**GWFILFINGLSA****IVHIDE****C**EVTPVIHVLQYT**G****C**VP
KPIPSFA**C****GKR****C**SSYLQVSGSKIWQMERS**C****M****C****C**QESGEREASVSL**F****C**PKTKAG
DRKFRKVITKAPLD**C****M****C****R****P****C**TSIEERIVIPQEIAGLSNNGPLSNSAHFRNTFKLT

>Bursicon-beta (NV_03820)

MRLIVSLLIAMFLKKIVLA**NALVNEN****C**EKLDSEIRITKDEYSETGKLFRT**C****S**DEI
QVSK**C****E****G****Y****C****D****S****Q****V****Q****P****S****I****V****T****S****T****G****F****T****K****E****C****S****C****C**REEFLEERTVYLN**N****C**YDSNGK**Q****F**
SLLDNSNMAIKIREPTN**C****K****C****I****K****C****G****F****L**

>CCAP (NV_04678)

MPDGSIKEQVLKLVLSLLIIESVEIARA**DDGLEIVAM****KRP****F****C****N****A****F****T****G****C****G****R****K**RD
PSYASGLQLPIPLYRALLRLSSLRNGAAAEVRMRQRPLGLIGPENLVQLGPQA
PRLMAAPVVVPSLY

CCHamide-1 (scaffold176)

M^RG^NP^EL^VA^PR^NV^YC^WA^GI^LI^LI^SS^FA^GC^AA^GSCLSYGHSCWGAHGKRSGV
V^RP^VD^SL^MP^SD^LS^LK^HP^AA^GQ^RV^VS^PS^FG^ER^WL^LS^RL^VN^RQ^LM^QV^PL^RG^RM^I
L^TQ^PL^GD^EL^PE^VT^SL^AK^HR^CV^FA^FL^YT^YP^AI^S

CCHamide-2 (scaffold218)

...GCSAFGHSCYGGHGKRSYSESVDLDLARNKEGTQQNDYDLSRSNAESVAL
V^PS^QG^YN^RQ^EQ^RS^IH^SI^HE^RP^NT^NS^WS^LF^IR^KL^VN^YF^KF^L

>Corazonin (NV_09278)

M^IR^GL^TI^AL^VT^VA^LV^SL^AT^CQTFQYSRGWTNGKRAETSPLASILDYRAAMAG
A^GG^RM^ND^LQ^MA^RC^AN^LL^KW^KM^FL^LS^SG^DN^EE^VC^RV^PC^EF^LD^VL^RQ^CL^IR^Q
D^KA^SP^ND^LS^DF^RR^PS^AP^AE^TS^SS^LS^Y

>Diuretic hormone (DH44/CRF-like) (NV_13001)

...GKRIGSLSVVNSVDVLRERVLELARRKAMENQQQLGENQYVFKSVGKR...

>Diuretic hormone (DH31-like) (NV_02135)

M^QR^EI^AL^SW^LL^LA^TE^AA^LA^IS^NR^VE^AL^PF^IS^RS^LW^NQ^FQ^ED^YP^EA^AQ^EL^LD^RI^E
N^FA^VY^AQ^PD^NAKRGLDLGLNRGFSGSQAAKHLMGLAANYAGGPGRRS
E^QA

>EH (NV_08338)

M^VL^SK^RL^LV^VL^LM^SY^LV^FL^TV^AA^AHPSVGTCFRNCSQSKKFLGIYFDVQLCD
EYCVKFKGKMTPDVEDPDSLAPITNLNEVQ

>ETH (NV_01589)

M^KR^LV^NT^FI^SR^NY^IL^SA^IF^IV^AV^LA^IE^NK^IV^AADEPPAFFLKIAKNIPRIGRSEPY
D^EY^AI^KN^SN^VK^DD^IP^WH^KG^EI^SKRRVGFSPESNTYAWQHFPLAIEGPPELWRT
L^AG^YS^HD^PL^YK^TT^DD^FN^NE^LW^SR^DKRTNNPEA

>ILP-B (NV_03688)

M^SN^MS^TS^RL^SG^LV^TL^TF^AI^LL^LL^LQ^LV^QAQSDVYQYEQKRQGASKYCGQQLS
NALQLVCHGRYNPMFKKSVGQGMEMDDYPFNYDDSYPFRSRAVANAMMG
R^FG^AG^RFRRDSRGVHDECCLKSCTMNEMRSYCAIPQ

>ILP-C (NV_30146)

M^YP^SD^SD^RT^TS^TT^RS^IG^SR^CW^WL^CL^LV^LL^VL^SL^EL^TR^HQ^AE^ANNIHRRFYR
RAVRLCSRSLSDALYLLCKDRGYNEPTSSETVRHTTGPGLVEECCYNSCSI
EQMEQYCKPRNKA

>Inotocin (NV_08469)

M^SK^VI^IV^LT^TL^VA^LS^YGCLITNCPRGGKRGDPTFLLENIARECPACGREEQGRC
F^GP^HI^CC^SP^MG^CL^IG^TP^ET^LR^CR^KE^SL^YS^RP^CV^AG^FA^MC^QG^NS^GR^CA^AN^GI^C
C^SQ^ES^CF^ID^SA^CK^LV^DE^TG^ND^RK^IG^AE^FG^AF^LL^EN^AG^TN^EH^IL

>ITG-like putative neuropeptide (NV_06225)

M^LL^AV^LA^LM^NC^GA^DAWGGLFNRFSPEMLSNMGYGSHGGYLGRSSAFLQHG
S^SF^SD^NG^LD^DG^AD^EP^CYERRCNTNEDCCPGSVCMNPEGEWPEGRCMFIYGLK
Q^GE^LCRRDNDCETGLMCAEVAGSDSLSCQPPVTSNKYSETCSMSSECDISR

GLCCQLQRRHRQTPRKMC SYFKDPLVCIGPVAADQVKHVVQYTSGEKRITG
KNNRLYKRGFA

>Ion transporting peptide ITP (NV_07921)

MASVVGVLCA RCSETIMIVFLSLLPLPSVDPDHDVLADKRSFMDIQCKGVYDK
ALFARLDRI CEDCYNLFREPQLHTLCRKNCFTSDYFKGCCLDVLLLQDEMEWI
QTSIKQLHGADPGV

>Myosuppressin (NV_09202)

MLKYSSSRSNVAMLTLLCLCAVLATLCGEAHGMPPAQCS PGLLDEVPPRIRK
VCAALSTIYELGSAMENYINDKVLREDIPLPDSGVKRQDVDHVFLRFGRR

>Neuroparsin (NV_03041)

MASDTLYIFCMATLILLRQVLNELAGGIKPAGGTATPPQRPQHRRTAPGLDSS
DQKNDVLSADRFLGHPTIIERAVQRSECEGCGANCKQCKYGSAYSLWCGLDE
CLKGPGEMCGGVRNKYGE CGDGMYCRCNKCTGCSIDTLECFSGF CPILEQQ
MQLRHQDHSMHGLQLDK

>NPF (NV_13002)

MRVSLAMMHLTYLTTLTVLALGSVSVQSEPEPMARPTRPKVFESPEELRQYLD
LVKEYYSLSGKARYGKRAEPYAMQQGYEHPLNFLRMLLA FSRQKQELVDKD
ERSKLQIMQPYDRVARYYEIME

>NVP-like putative neuropeptide (NV_30009)

MLSDWLWLLAFGAMLVAVQSLPAGLSTSSGSSSADETKKTEQTMRPKVKR
AQEMLMFGNQNRQQA TAESNNAANNYSPPAEKR TLNSGLDDVSSALSDV
EQQQQQQQA AIMANSNNHPKALPSGYMMDQPGYAAAREELREPRYKRELD
LDPEDLITFLTLYDNERRNRQNW RNYGNEEYEGADDDSNMIGLDDDEDPRGSS
WLDSQQYGQPQQAQHHYLSGEPLLSSELAALARNRPSASSGYDQYLGGQ
YGTAGQQYETAPQVQYGTPQYGLPYLQQHASYY SPEKRFMVARKRSQNYDS
YGGRSGLLNSRGYPSYQHRLLY

>orcokinin (NV-30010)

...MQEWKSPKQYHYS GGNLDHIGGGNLLRKKVVKIPNEYFTETTTTSVPVET
TTSDLKADRR LIGVAELKSQA EERQTRNARN DYDSPDYGHGQKFTGHRKRPDS
THRLINKGFSETIIPSDIIEYTNQKRN FDEIDRSGFSGFSKRN FDEIDRSGFSGF
NKKRN FDEIDRTGFSGFNKRN FDEIDRSGFSGFNKRN FDEIDRSGFSGFNKRN
FDEIDRSGFSGFNKRN FDEIDRTGFSGFNKRN FDEIDRSGFSGFNKRN FDEIDRS
GFSGFNKRN FDEIDRSGVPGFAKR SIASSRSDRIFCISIIYHAQDI

>PDF (NV_15000)

MRSWVSHLIRAFFVFGAILCASASMEDTSHMIMNNPYGRSLDAELITRLLLAP
QRLCHPKRNSELINSLSLPKNMNNA GK

>PTTH (NV_30191)

MKLQTFVLVLLTVQHRAKQQL ESYSDDFSDVELPTDERDDCSDGT CYAEKRII
LPEKIVEHRQLMPRFATKLQSVNLAESFPQPQWRPVCGC V TQHKLVNLGEGH
YPRYITTARCKSKTVANRFYQCKYYDYRVHVLVKRGLNSIPKNADEL DVRD
VEELPLPESLHANWQLFALS VSVACVAVERV

>Pyrokinin (NV_30144)

MELARLINGARTKAILCALLVIVLMANRVAGQYDGRGSDMVEGPRVERMHP
ETSGGCVGAHCLTQNSEGPVGAMWFGPRLGRRRRSDKFTPKKIEALSEMLGS
PNWNLVITPGGEDKRQETTTFTPRLGRELENAISVYDLVRGLVSSVDDQNGKD
RDQQAPPPMFPPRLGR TLLTPRLEHELRLNLLRKLQMQ

RYamide (NV_30121)

MISSSRKIRRVSDYLKLDKLVWLWISGIFLTLVSSQDNFYASGRFGKRYALS
MSQIPLCSKFDRESEDRSAGNSLKDSSLFSSARFGRSEDRNTGNSLRDSSSFPA
RYGRSEDRSTGNSLRDSSSFPAARFGRSEDRSTGNSLKDSSSFSPARYGRSEDR
SSGNSLKESFFSPGRYGRSEGHKNPKELPKFFEIKPRVDQFFIGSRYGKRSL
MLEPQPPEALHNQRFEAAIDYLDRIKQNLAEAEIEDETRDASRDDELVEAI
YPNDYTGLSKI

>sNPF (NV_13003)

...LIDESPNSEKSANLRELYRMLVQRSVDDSGSLRDLAEHLQPRAA
ERSPSLRLRFGRSYPKYPVSRTHA

>SIFamide (NV_30008)

MSAARFALVLMVVLAVAILNVDAAYRKPPFNGSIFGKRANSVSDYDYASRA
MDAICEIAKTNCNAYYGPQDSN

>Tachykinin (NV_03478)

MTSPAAARLRATTMLLTLLTLGVSAQHSMTTIRGQTDRDSEIILETKAPQQL
PPQLAYVREPEELDGYQALDSTKHLREPSSSYLERLLLTEELDKRASMRGFQG
MRGKKSVDPTSSFLAGYSSPEELQYYEAYEHEKRAPMGFQGMRGKSSAD
LEEDAYYKRAPMGFQGMRGKSAIEEVLEELEKRAMMGGFQGMRGKKSPE
PSVWNKRAPMGFQGMRGKSSFLDELDELEKRALLGFHGMRGKKNVVAEL
AYEPADMMDGYVEKRPMMMGFHGMRGKSASFYGVGERYEKRSPYRFFGTR
GKKNPRWEMRGKFVGVRGKWSLAPRMPYDELLRH

CACATCTCGGCTCCACATAAGTAGCACACGCAGCTTCCTTCCTCGCCCCGAGACGCACC																	-1
ATG	AAC	TGC	AGG	AGC	CTG	CTC	GCG	CTG	GGA	CTC	TGT	CTG	TGC	GTC	GTC	CTG	51
M	N	C	R	S	L	L	A	L	G	L	C	L	C	V	V	L	17
CCG	CAG	ACT	CGG	GCC	GCC	GAG	GGT	CAG	TTG	AAC	TTC	TCC	ACC	GGC	TGG	GGC	102
V	Q	T	R	A	A	E	G	Q	L	N	F	S	T	G	W	G	34
AAG	CGA	AGC	AGT	CAT	CTG	CTC	CAG	CCG	GCG	CGC	GCT	TCG	TCA	TCC	TCG	TCC	153
K	R	S	S	H	L	L	Q	P	A	R	A	S	S	S	S	S	51
TCG	TCC	TCG	TCC	TCG	TCC	TCA	ACG	TCG	GCG	GCG	GCG	GCG	GCG	GCG	GCT	TCC	204
S	S	S	S	S	S	S	T	S	A	A	A	A	A	A	A	S	68
TCG	GGA	ATC	GGC	AGG	CCT	CGA	CAG	CAA	GCC	GAT	CTC	GAC	TAC	TTT	CTG	CAG	255
S	G	I	G	R	P	R	Q	Q	A	D	L	D	Y	F	L	Q	85
CGC	TAC	TAT	CGC	CGC	CTG	CGC	AAG	ATC	GAA	GCC	CAG	CGA	CTG	GCG	AAT	TCT	282
R	Y	Y	R	R	L	R	K	I	E	A	Q	R	L	A	N	S	102
CAG	GTG	TAA															
Q	V	*															
ATGGCGCTGATGGAAGCTCGTATAGTTAGAACAGAAGATTTGTATTTGTTTGTATTATACCGTATG																	333
AAGCTTATTTTAATAATAAAATTAAATATTCGATTGC(A) _N																	370

Figure S3:

cDNA and deduced amino acid sequence of the AKH preprohormone from *Nasonia vitripennis* (GenBank accession number HM461995). Nucleotides are numbered from 5' – to 3' –end. Amino acid residues are numbered from the first start (ATG) codon in the open reading frame. The signal peptide is highlighted in yellow, the immature AKH peptide in blue and the dibasic cleavage site in red. The stop codon is indicated by an asterisk. Exon-intron boundaries are highlighted in grey. The putative polyadenylation signal in the 3'-noncoding region is underlined.

CTCTGCTCTCTCTCTCTCTCT																	-135
CTCTGGCTTCTGCTCTTACCGTTTCGCTGTCGTCGGCCCTACCATCGCCGATTATCCGCCGCTAACT																	-68
CGAGCCACCTGTCAGATTGGAAATTTCCAGCCGCCAATTACACACAACTCACACCGAATCAGCAAA																	-1
ATG	ATG	TCT	TTA	AGA	ATT	GCC	GTT	TGC	ACA	GCA	GTA	GCG	CTC	GTA	GTG	CTC	51
M	M	S	L	R	I	A	V	C	T	A	V	A	L	V	V	L	17
GTC	GAC	TGG	TCG	ACG	GCA	CTT	CCA	GCT	GGG	GAT	AAG	GAG	GCG	CTC	ATG	AAC	102
V	D	W	S	T	A	L	P	A	G	D	K	E	A	L	M	N	34
GGG	CTT	AAT	ATG	ATG	GGT	GAC	GAG	GAA	GGG	GCA	GCA	GTA	GAG	AGG	GAC	CTG	153
G	L	N	M	M	G	D	E	E	G	A	A	V	E	R	D	L	51
CTC	AAC	TAC	CTC	GTA	GGC	AGA	AGG	TTC	GTT	AAA	CGC	CTA	CGC	AAC	CAA	GCC	204
L	N	Y	L	V	G	R	R	F	V	K	R	L	R	N	Q	A	68
GAC	GTC	GAC	GAT	CTG	CAG	CGC	AAG	CGA	AAC	TAC	TGG	AGG	CAG	TGC	GCT	TTT	255
D	V	D	D	L	Q	R	K	R	N	Y	W	R	Q	C	A	F	85
AAC	GCC	GTC	TCC	TGC	TTC	GGC	AAG	TAG									282
N	A	V	S	C	F	G	K	*									93
GCTGCGGCTGATGAATTAGATCGCTTCGCGGATGACTATGTGGGCCCGACGACGCGAATTATTAAT																	349
CTTAATAATATATTACGGCCCATTCGGAGCGACGTGATGACGACGCGCTATAATACACTGAATAGAA																	416
CAAACAATTTGCTTCCTGTGAACAGAAAAAACAAGCTTCGTTAACTAACTGTCATTCGATGTATA																	483
CCTCAGATATTCGATTTATTCATCGGACGCACACGTCTTATGTCTATATGAATTTTAATTGTTAGAT																	550
GATAGAGAGATGGTCGGTATACCACGCGCCAACAGTATTTTTATTTTTCTCTCTTTTTCTCTCGATG																	617
ATATTGTGTGTTTGTATACTTATAGCTTAGTTGGGAGTTGTCCTGGGATTATGTATGGTCGATGGCT																	684
TCTCATGCGGGTACTTGCGCATGCACAATTACCGGAAGTTAGCTTTGTTGGTAATTTTCGTTTATACC																	751
GTTATCGTGGCGAATTTTTTTTTTAATATTTATCTCGCGCAACTTACTGTACATATGCTAGTTGAGCT																	818
GGAAGAGATCAAGATAGAATAGATAATTATAGAAATTTTCGGCGATTTCGTTTTGTAATTTGAATTTTA																	885
TATTTAGATTTGACTTTACGTATCGACTTTACGACCGAGACGATTCTCCTATTAGTTTCATGTTTTT																	952
TAAGTTGATTTTCGCGAGTAAGCATTTTTTCGGCACTAAAAATTTACCAGTATCCTATG(A) _N																	1009

Figure S4:

cDNA and deduced amino acid sequence of the allatostatin C preprohormone from *Nasonia vitripennis* (GenBank accession number HM461994). Nucleotides are numbered from 5' – to 3' –end. Amino acid residues are numbered from the first start (ATG) codon in the open reading frame. The signal peptide is highlighted in yellow and the immature allatostatin C peptide in blue. The basic amino acid residues used for cleavage are shown in red. The stop codon is indicated by an asterisk. Exon-intron boundaries are highlighted in grey. An in frame stop codon in the 5'-untranslated region is underlined.

CGCGGATCCGAACACTGCGTTTGCTGGC																	-470
TTTGATGAACATTGCGCCGGCCGACTACCGCTGGGGCTAACTTGCCCGTCGCTCGCGCGGCAACGCA																	-403
CACATACTCTCCTTTTGGCGCCGCATCAGCCCTAGCACCCAACCTGTTGCCGTCCTCCACCGCCGC																	-336
AGGACCTCCAGAGTAGCGCGCACCGATATACGCCATATACGCCGGGATTTCGCACAAGTTTGCAATTT																	-269
TTTTTCCAAACTGCAGTATGGGTGAAAATTGATTTCGTGCGGTCGACTGGAAAGAGTTTAAATGCGT																	-202
AGAGCGGTGAAACATTGCGAGGATTGACGCTTGC GCGAGGAGAAAAGATCGGAGAGAGGAAAAAGGCG																	-135
GGCCTCTAGTCGGAGCTTAGTCAGGTGCGCGCGCGCCGCTACGCACAGAGCTTCACGCAAGGCTTCG																	-68
CTCGAAAAGCAGCGAGTGGATTGTTTCGCCGTTGTTACCGTCAACCTTGTTGACTTGATCTTCGGG																	-1
ATG ACG AGC TCT GGC TGC CGT ACC TTC CTG GCG CTC GCA ACG GCG CTC ACG																	51
M T S S G C R T F L A L A T A L T																	17
ATC CTC GGC ACC GTC AGC GGC TCG CCG CGC GGA CAC GCG CTC GCC AAG AGA																	102
I L G T V S G S P R G H A L A K R																	34
AGC GCC GAT GCT AAC GTT ATC GAG TAT CCG GAT TAC GAG TAT CAG AGA GTT																	153
S A D A N V I E Y P D Y E Y Q R V																	51
ATG CCA AAA AGA GCA GCA CTT CTA CTA GAT CGA TTG TTA GTG GCT TTG CAA																	204
M P K R A A L L L D R L L V A L Q																	68
AAA GCA GTT GAA AAC GAT GAT GTA GGA AAA GAA AAC TCT AAC TCA TAC GTC																	255
K A V E N D D V G K E N S N S Y V																	85
AGG TCA CTA CCG AAC TTC TCA GAT ATG CCT GAT TCG CAG AGG ATG CAA CTT																	306
R S L P N F S D M P D S Q R M Q L																	102
TCT AAC GAA AAA ACG ATG GAT CTT CAA CGG CGA GGC CAA GCA AAA GGT CGC																	357
S N E K T M D L Q R R G Q A K G R																	117
GTT TAT TGG CGT TGT TAC TTT AAT GCT GTG ACA TGC TTT AAA AGG AAG TGA																	408
V Y W R C Y F N A V T C F K R K *																	133
TTATCCATTAGAAAAGACGAGGCATGGTGGTCTTTACTTTAAAAAATTGTTTTACTTCTTTCACTCAG																	481
TGTGGCTATAGTATTTTTCATACCATTATACGAAAAGAATGGAGTTGCTAAAAACAATTATCATAATAT																	548
CAGTAAATTTGAGAATATATTTTAATTTTATGTTTTATATTATATGTAATGATTTCCATAAAAAATA																	615
CACGAAATTATATTTAAGTCATGCTGTGAATAGATCC(A) _N																	652

Figure S5:

cDNA and deduced amino acid sequence of the allatostatin CC preprohormone from *Nasonia vitripennis* (GenBank accession number GU937435). Nucleotides are numbered from 5' – to 3' –end. Amino acid residues are numbered from the first start (ATG) codon in the open reading frame. The signal peptide is highlighted in yellow and the immature allatostatin CC peptide in blue. The basic amino acid residues used for cleavage are shown in red. The stop codon is indicated by an asterisk. Exon-intron boundaries are highlighted in grey.

Nv - NVP	MLSDWLWLLA-FGAMLVAVQSLPAGLSTSSGSSSSADETKKTEQTMRPKV KRAQ EMLMFGNQNRQQA TAE SNAA---NNYSPPAEK RTLS NS--GLDDVSSALSDVE-----	103
Am - NVP	MMCDWVWLLLTLCSSL MIVQ SLPTNL-----AEDTKKTEQTMRPKS KRAQ EMLMFGNQNHQ----PEN NP S---SSYSSTAE KRTLA AS--GLGGLKAALIEEEKPSRSNTLNNA	102
Tc - NVP	MELRWSIRWATLASCLALSFAIPASLVEEIKTNELRN NKV KRAHP QLNVGEHG REVP YYSKPTAI KRG AN N LKNPSPEQQSLSDWEQE QSL YQNPDSLADIQSSLYNAENP-----	111
Nv - NVP	-----Q-----Q-QQQQAAIMANSNNHPKALPSGYMMDQPGYAAAREELR-----EP RY KRELD DPEDLITFLTLYDN ERR NRQ NWR NYGN	180
Am - NVP	FYDRKNYDYGAVNELGYEIPQVWDNSPYSRYT NEDRRKRSEKSAVASGS STTIKPSTTSFQSPSTQQSVQTQ KRN VPIYQ EP RF KRELD IDPEDVLTLLSLWEN ERRKR -N WH KYMN	221
Tc - NVP	-----FDDKTIAEYEGGFHYGT NKE KLDEALENA VLK SELYGDP APLNQ YRYYGND DQRRRKR RDAR-K IRLDS RM KREVD LT PDE IFTILTLYENERNGYR PWG ----	210
Nv - NVP	EEYEGADDDSNMIGLDD ED PRGSS-WLDSQY Y GQPQQAQ HHY LSGEPLLSSELAALARNRPSASSGY YDQY LGQYGTAGQY ETAPQVQY GT PQYGLPY LQ QH ASY YSPE K R FMVARK	299
Am - NVP	EEYENVDDEDNLL--EEEDSRNIIPWMDSSVY-----PPRHYS LDS ---LSPSDIGI IRTH PS---YYEQYEN-QY G ---QY DT S---QY GSPQYGLVYPQ TY-Y SAPE K R FMISRK	320
Tc - NVP	--LEPEPSGD NLE --EEE---N--WLDAPVY-----PHATGHNDLAPSY---LM DEKRG -RWG---GFADS--- RKKR FMVAK KRNDP ---TRELR YL NGPN	285
Nv - NVP	RSQNYDSYGGRSGLLLNS --RGYPSYQHRLLY	329
Am - NVP	RSQAYDPYSNAAQFQLSSQSRGYP -YQHRLVY	351
Tc - NVP	KND---YYT LSQ LLSNQREPNVP-LYHRLVL	312

Figure S6:

Alignment of the NVP proteins from *N. vitripennis* (Nv-NVP), *A. mellifera* (Am-NVP) and *T. castaneum* (Tc-NVP). Amino acid residues that are common in at least two sequences are highlighted in grey. Blue letters indicate the signal peptides, putative basic cleavage sites are shown in bold. The *Nasonia* peptide identified by MS in this study is marked in green, the NVP peptide from *A. mellifera*⁹ is marked in red. In these three species, there is a moderate conservation of protein structure, but not of the NVP sequence. We could not find NVP proteins in other arthropods.

Table S1: PCR primers used to amplify *Nasonia* neuropeptide precursor cDNAs.

Gene	accession no.	technique	Sense Primer Sequence	Antisense Primer Sequence
AKH		PCR	5'-CACATCTCGGCTCCACATAAG	5'-TCAGCGCCATTACACCTGAG
		3'-RACE	5'-GAGGGTCAGTTGAACTTCTCC	
		3'-RACE	5'-CGAAGCAGTCATCTGCTCCAG	
		5'-RACE		N/A
		5'-RACE		N/A
Allatostatin C		PCR	5'-ATGATGTCTTTAAGAATTGCCGTTTG	5'-CTACTTGCCGAAGCAGGAG
		3'-RACE	5'-CTCGTAGGCAGAAGGTTTCGT	
		3'-RACE	5'-AAACGCCTACGCAACCAAGC	
		5'-RACE		5'-CGTTCATGAGCGCCTCCTTA
		5'-RACE		5'-GACCAGTCGACGAGCAC
Allatostatin CC	GU937435	PCR	5'-GAGCAGCACTTCTACTAG	5'-GCATGTCACAGCATTAAAGTAACAAC
		3'-RACE	5'-CGCGTTTATTGGCGTTGTTACTTTA	
		3'-RACE	5'-GTTGTTACTTTAATGCTGTGACATGC	
		5'-RACE		N/A
		5'-RACE		N/A