

A

AaegDH31	- - T V D F G L S R G Y S G A Q E A K H R M A M A V A N F A G G P	31
AgamDH31	- - T V D F G L S R G Y S G A Q E A K H R M A M A V A N F A G G P	31
DmeDH31	- - T V D F G L A R G Y S G I Q E A K H R M G L A A A N F A G G P	31
RproDH31	- - G L D L G L S R G F S G S Q A A K H L M G L A A A N Y A G G P	31
BmorDH31	- - A F D L G L S R G Y S G A Q A K H L M G L A A A N F A G G P	31
AmelDH31	- - G L D L G L S R G F S G S Q A A K H L M G L A A A N Y A G G P	31
NvitDH31	- - G L D L G L I R G F S G S Q A A K H L M G L A A A N Y A G G P	31
TcasDH31	- - G L D L G L I R G F S G S Q A A K H L M G L A A A N F A G G P	31
DpunDH31	- - G L D L G L S R G F S G S Q A A K H L M G L A A A N Y A G G P	31
ApisDH31	- - G L D L G L S R G Y S G I Q A A K H L M G M A A A N F A G G P	31
HsapCT	C G N L S T C M L G T Y T Q D F N K F H T F P Q T A I G - V G A P	32
RnorCT	C G N L S T C M L G T Y T Q D L N K F H T F P Q T S I G - V G A P	32
GgalCT	C A S L S T C V L G K L S Q E L H K L Q T Y P R T D V G - A G I P	32
SsalCT	C S N L S T C V L G K L S Q E L H K L Q T Y P R T N T G - S G I P	32

B

AaegDH31	T V D F G L S R G Y S G A Q E A K H R M A M A V A N F A G - - G P	31
AgamDH31	T V D F G L S R G Y S G A Q E A K H R M A M A V A N F A G - - G P	31
DmeDH31	T V D F G L A R G Y S G I Q E A K H R M G L A A A N F A G - - G P	31
RproDH31	G L D L G L S R G F S G S Q A A K H L M G L A A A N Y A G - - G P	31
BmorDH31	A F D L G L S R G Y S G A Q A K H L M G L A A A N F A G - - G P	31
AmelDH31	G L D L G L S R G F S G S Q A A K H L M G L A A A N Y A G - - G P	31
NvitDH31	G L D L G L I R G F S G S Q A A K H L M G L A A A N Y A G - - G P	31
TcasDH31	G L D L G L I R G F S G S Q A A K H L M G L A A A N F A G - - G P	31
DpunDH31	G L D L G L S R G F S G S Q A A K H L M G L A A A N Y A G - - G P	31
ApisDH31	G L D L G L S R G Y S G I Q A A K H L M G M A A A N F A G - - G P	31
HsapCGRP	A C D T A T C V T H R L A G L L S R S G G V V K N N F V P T N V G S K A F	37
RnorCGRP	S C N T A T C V T H R L A G L L R R S G G V V K D N F V P T N V G S K A F	37
GgalCGRP	A C N T A T C V T H R L A D F L S R S G G V G K N N F V P T N V G S K A F	37
SsalCGRP	A C N T A T C V T H R L A D F L S R S G G M G N S N F V P T N V G S K A F	37

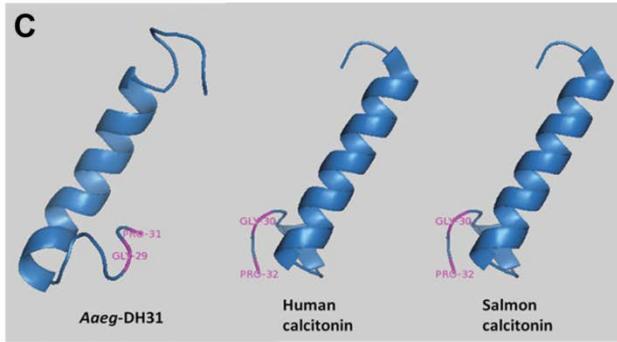
C

Figure S4. Amino acid sequence alignment of calcitonins (CTs) and calcitonin gene related peptides (CGRPs). (A) The *A. aegypti* diuretic hormone 31 (Aaeg-DH₃₁) sequence was aligned with those of other arthropod DH₃₁ and CTs and in (B) with CGRPs. In (A) and (B), GenBank accession numbers: 1. *A. aegypti* DH₃₁ (EAT40182). 2. *A. gambiae* DH₃₁ (XP_321755). 3. *D. melanogaster* (AAF52685). 4. *R. prolixus* DH₃₁ (ACX47068). 5. *Bombyx mori* DH₃₁ (NP_001124379). 6. *Apis mellifera* DH₃₁ (P85830). 7. *N. vitripennis* DH₃₁ (XP_001599948). 8. *T. castaneum* DH₃₁ (EEZ99367). 9. *D. punctata* DH₃₁ (P82372). 10. *Acyrthosiphon pisum* DH₃₁ (XP_001945901). 11. hCT (AAA58403). 12. hCGRP (1005250A). 13. *R. norvegicus* CT (AAA40849). 14. *R. norvegicus* CGRP (NP_612522). 15. *G. gallus* CT (ABY65359) 16. *G. gallus* CGRP (P10286). 17. *Samo salar* CT (NP_001135058). 18. *S. salar* CGRP (NP_001140052). Predicted hormone sequences: 2-3, 6-8 and 10; translated from cloned cDNAs: 1, 4-5, 9, 11-18. (C) Predicted protein structure of the Aaeg-DH₃₁. Amino acid residues in pink are conserved in human CT.