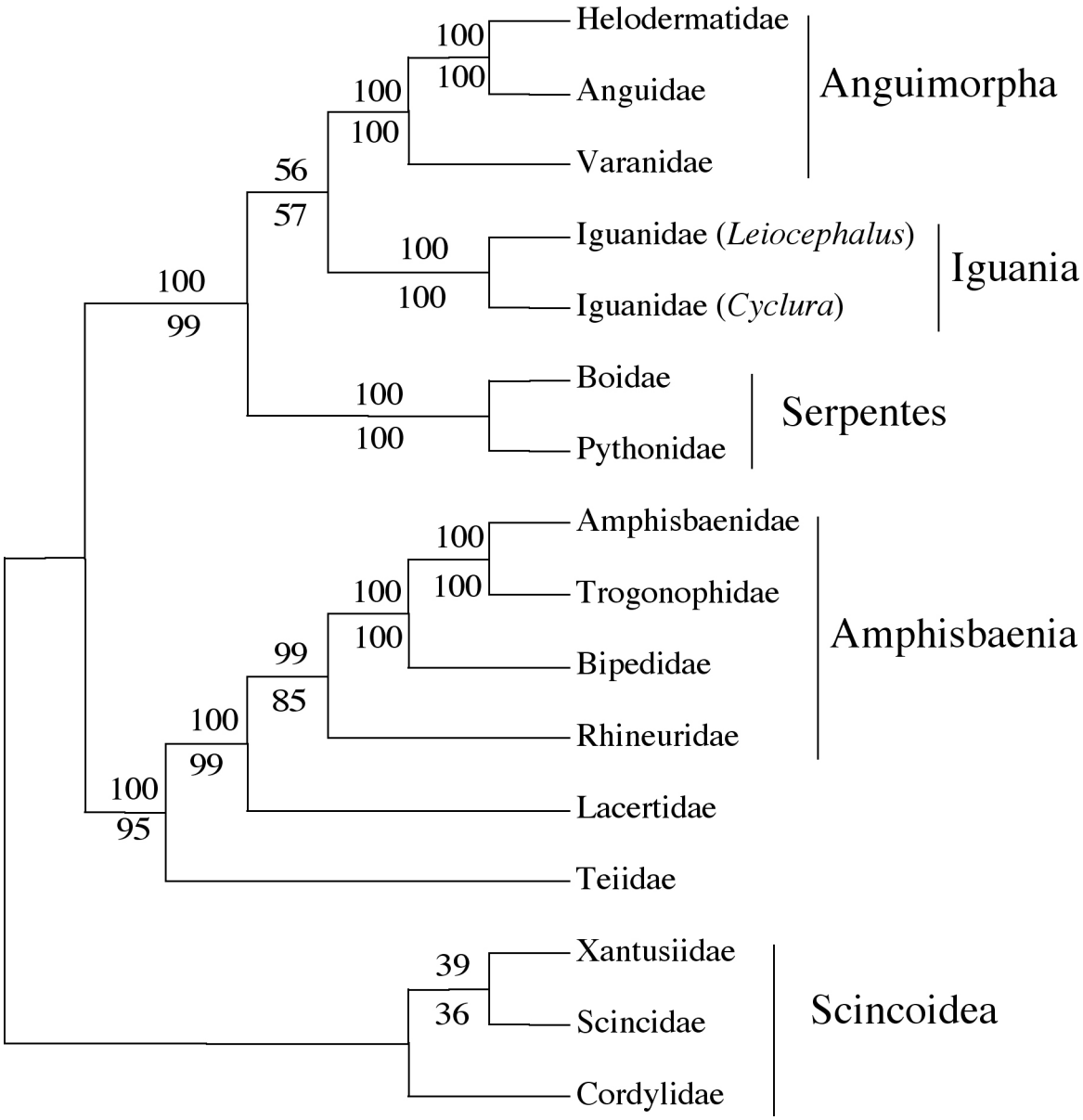
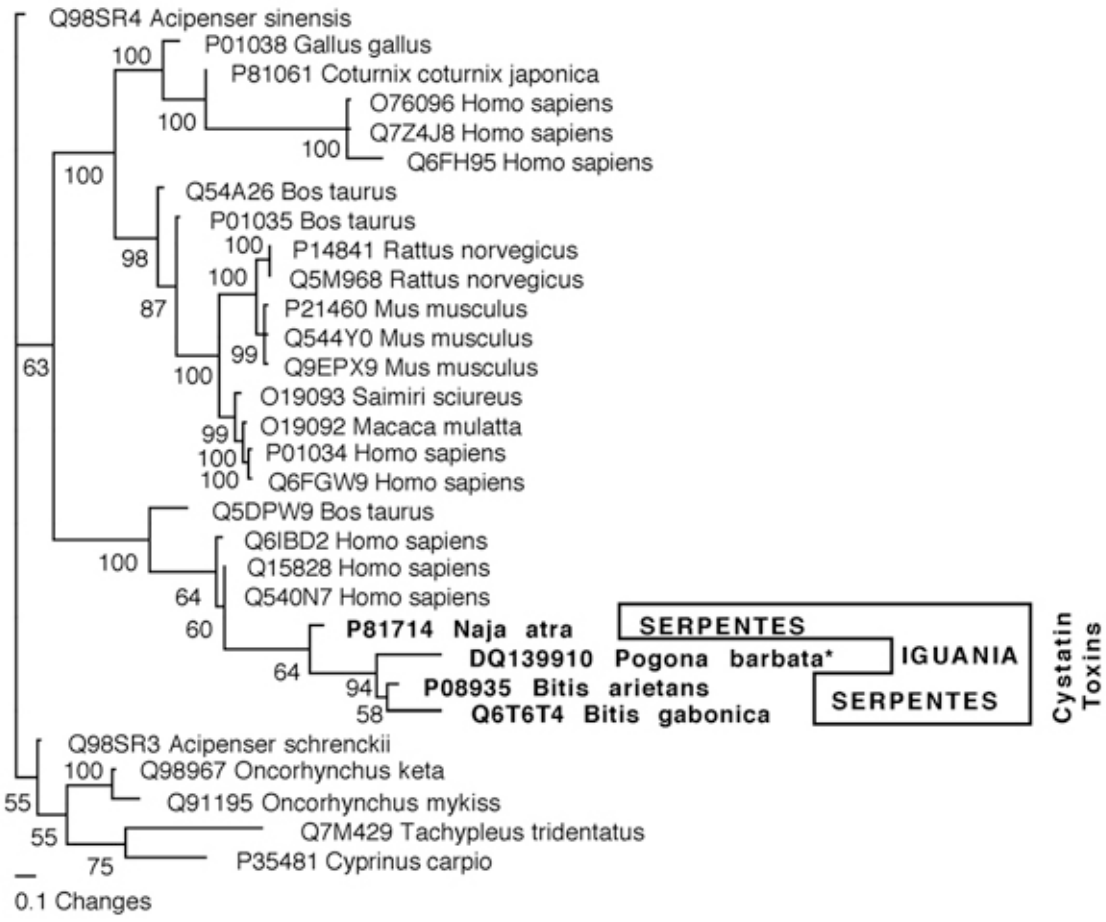
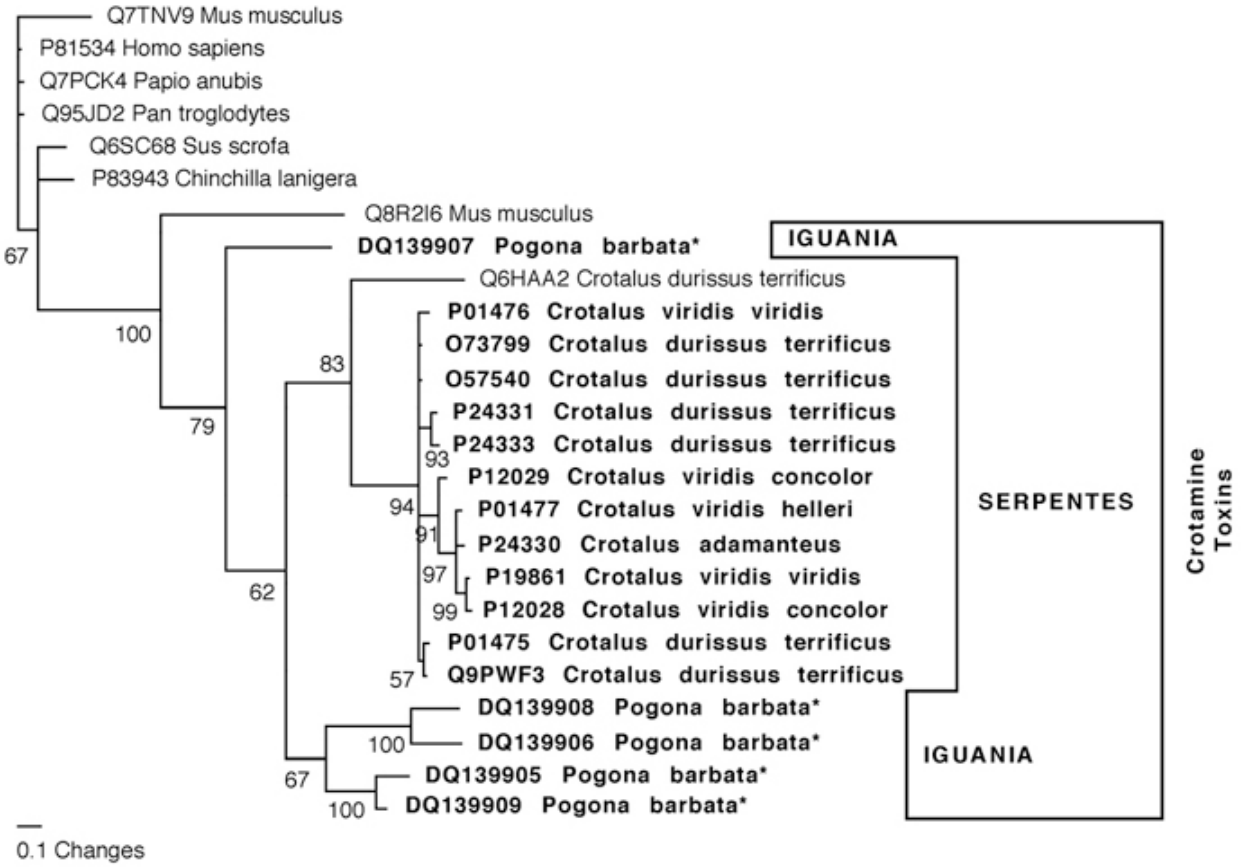


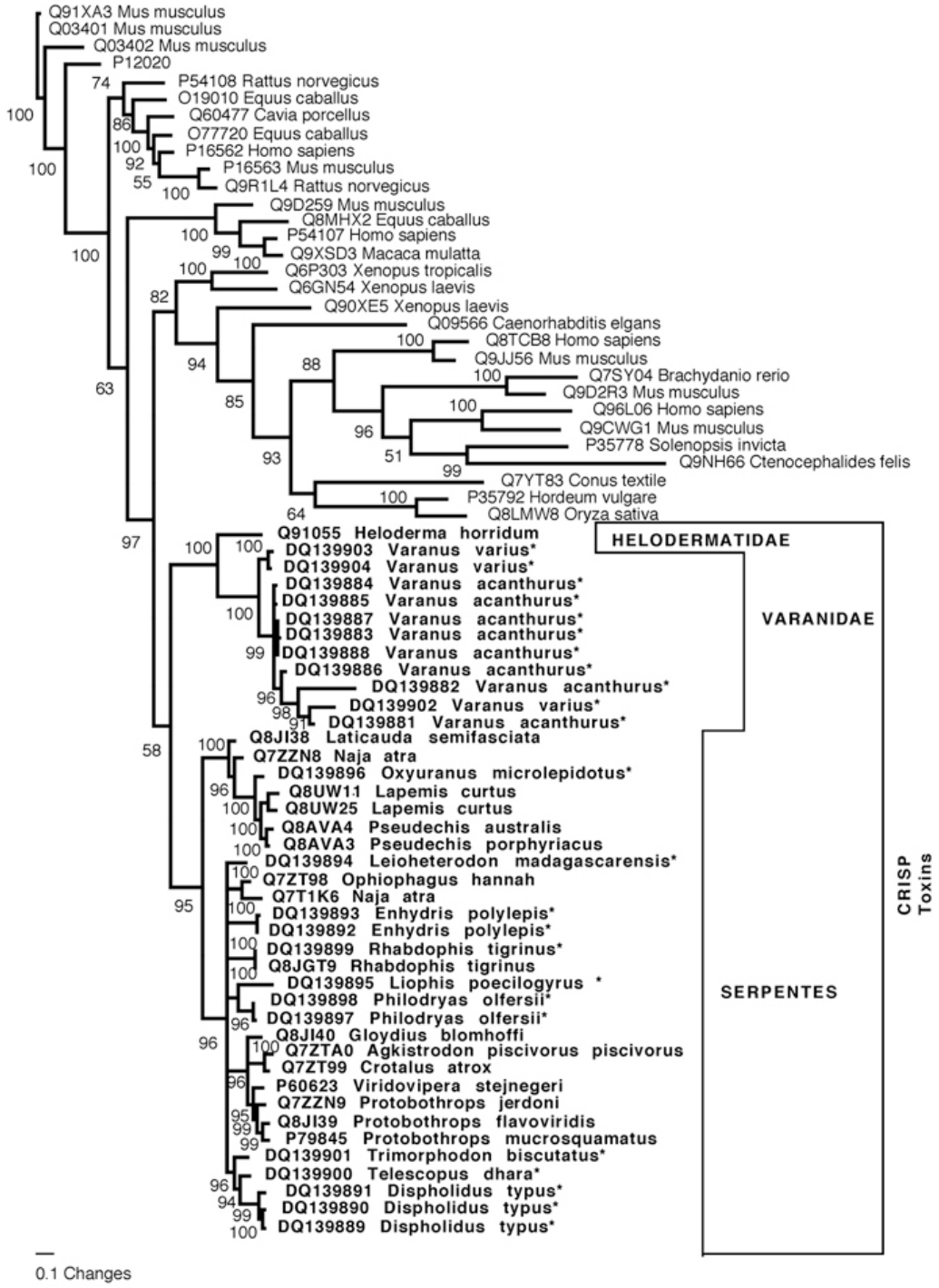
Supplementary Figure 1: Squamate molecular phylogeny. Values above branches: Bayesian posterior probabilities Values below branches: Maximum Likelihood bootstrap values.



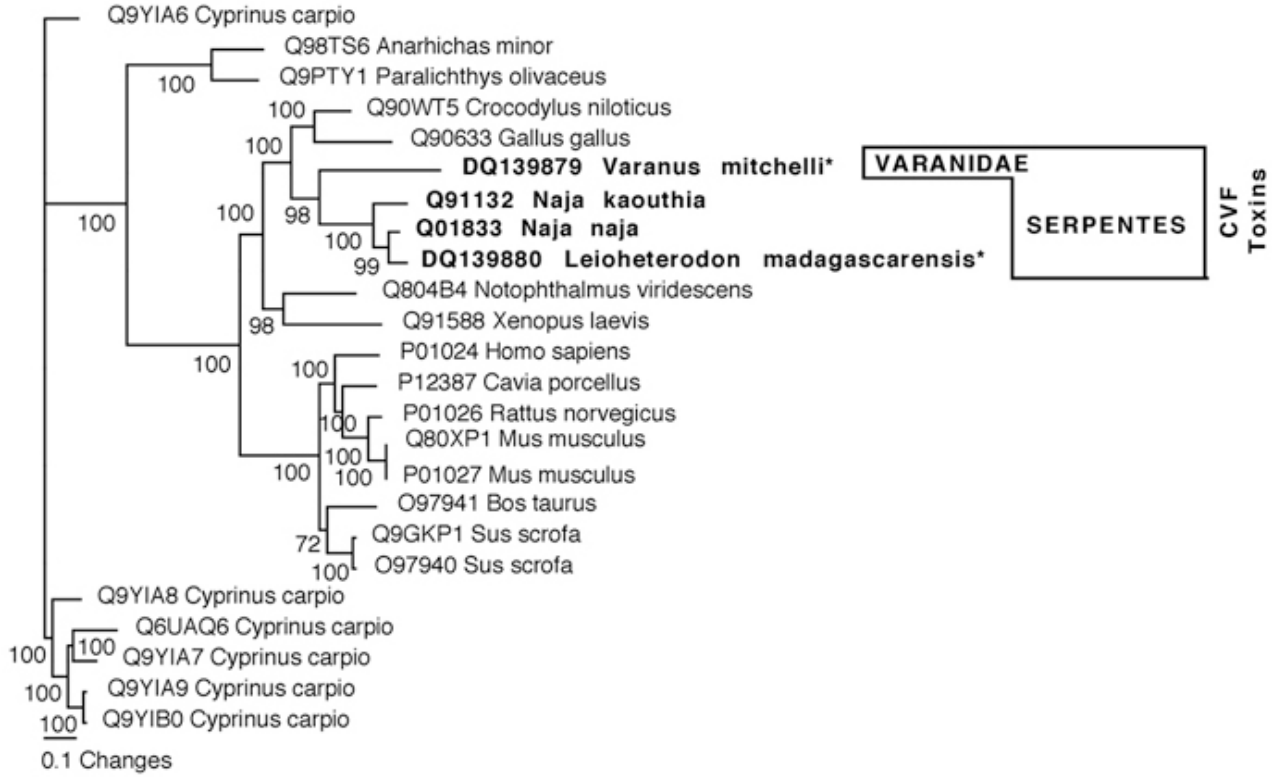
Supplementary Figure 2: Bayesian analysis of representative Cystatin-related sequences. In order to minimize confusion, all sequences are referred to by their SWISS-PROT accession numbers (http://www.expasy.org/cgi-bin/sprot-search-ful). * Designates transcripts obtained in this study.



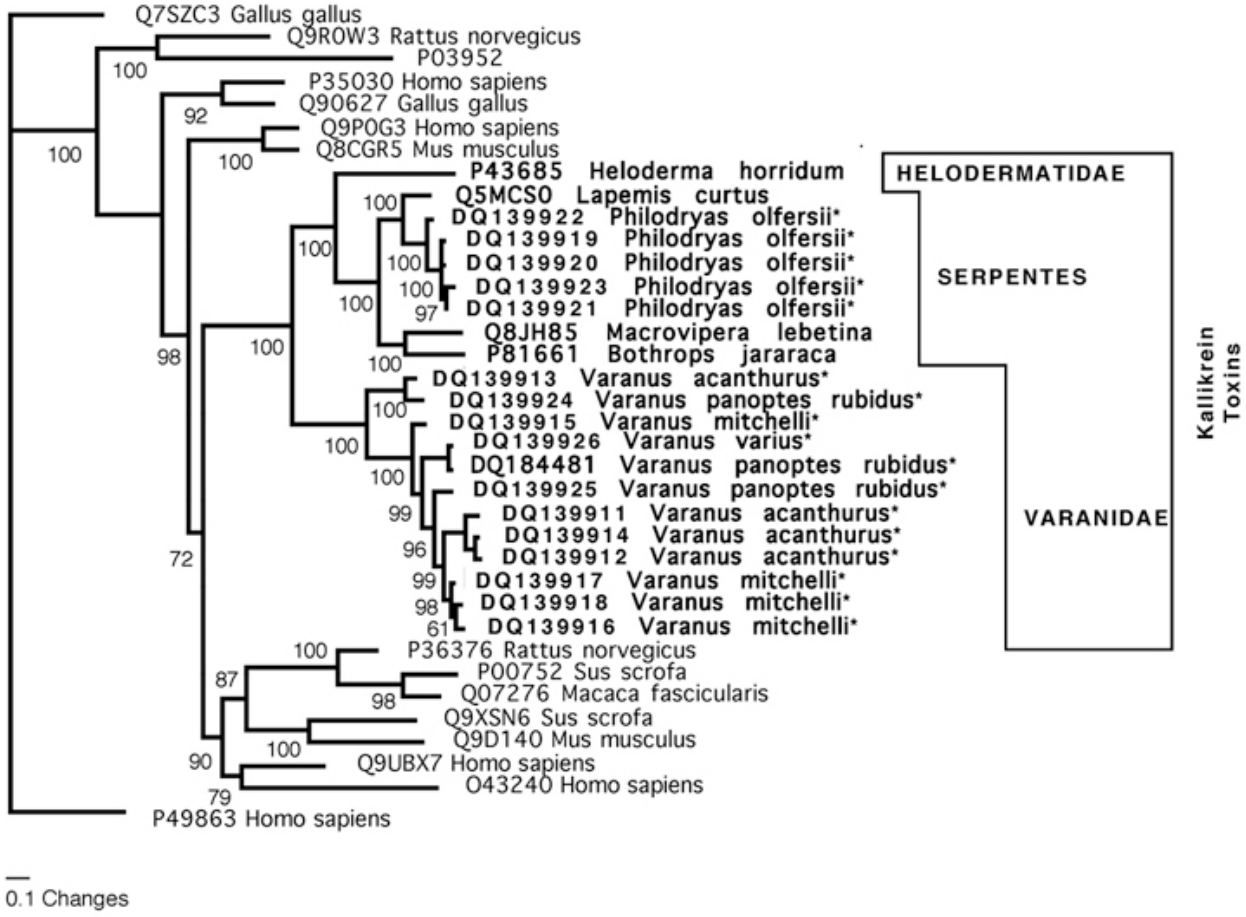
Supplementary Figure 3: Bayesian analysis of representative Crotamine-related sequences. In order to minimize confusion, all sequences are referred to by their SWISS-PROT accession numbers (http://www.expasy.org/cgi-bin/sprot-search-ful). * Designates transcripts obtained in this study. UPP and LOW respectively refer to transcripts from the maxillary and mandibular glands of *Pogona barbata*.



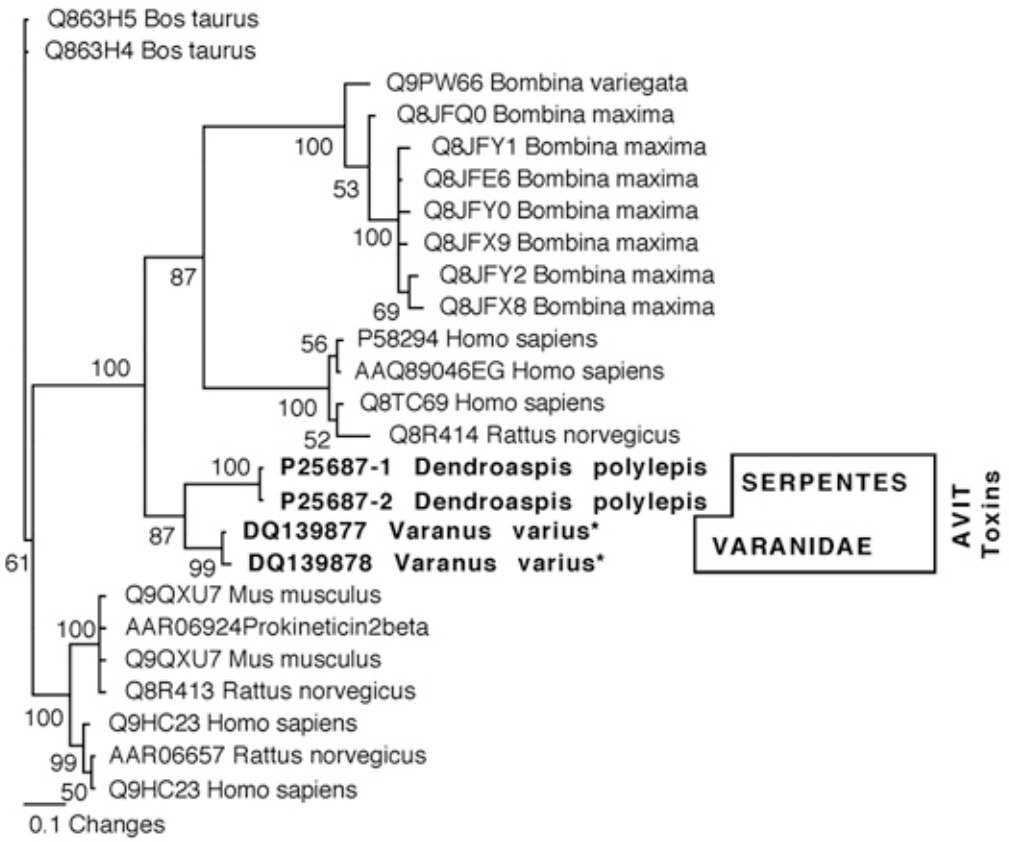
Supplementary Figure 4: Bayesian analysis of representative CRISP-related sequences. In order to minimize confusion, all sequences are referred to by their SWISS-PROT accession numbers (http://www.expasy.org/cgi-bin/sprot-search-ful). * Designates transcripts obtained in this study.



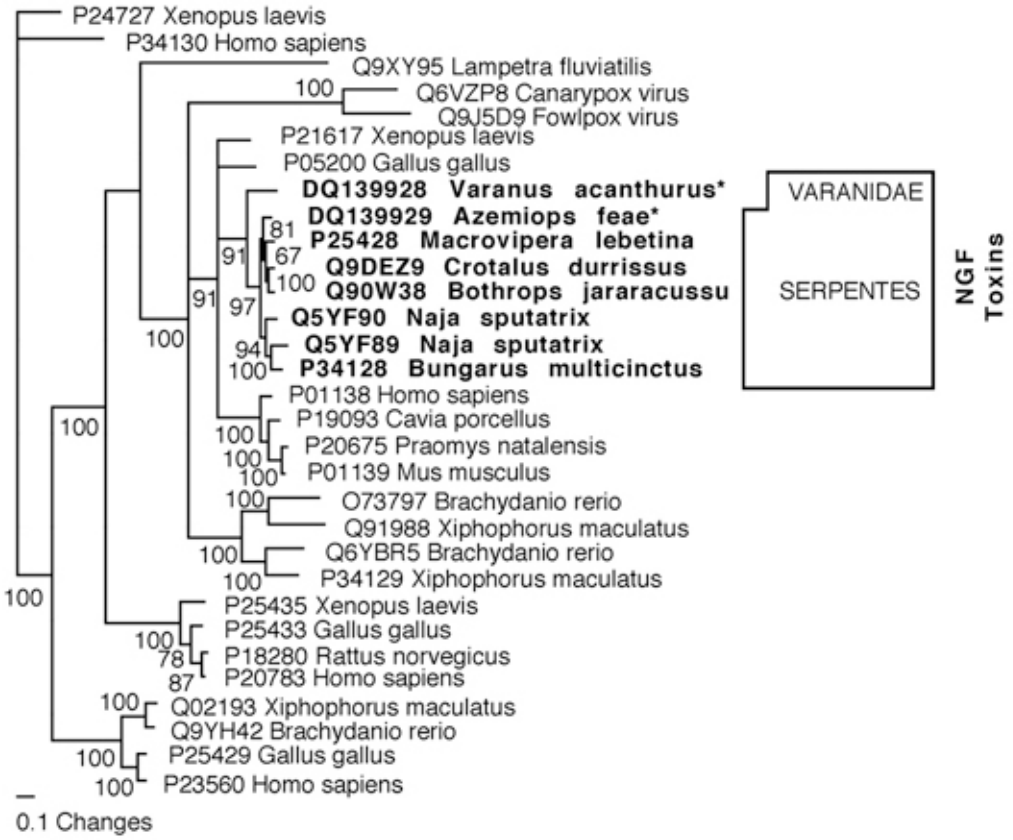
Supplementary Figure 5: Bayesian analysis of representative Cobra Venom Factor-related sequences. In order to minimize confusion, all sequences are referred to by their SWISS-PROT accession numbers (http://www.expasy.org/cgi-bin/sprot-search-ful). * Designates transcripts obtained in this study.



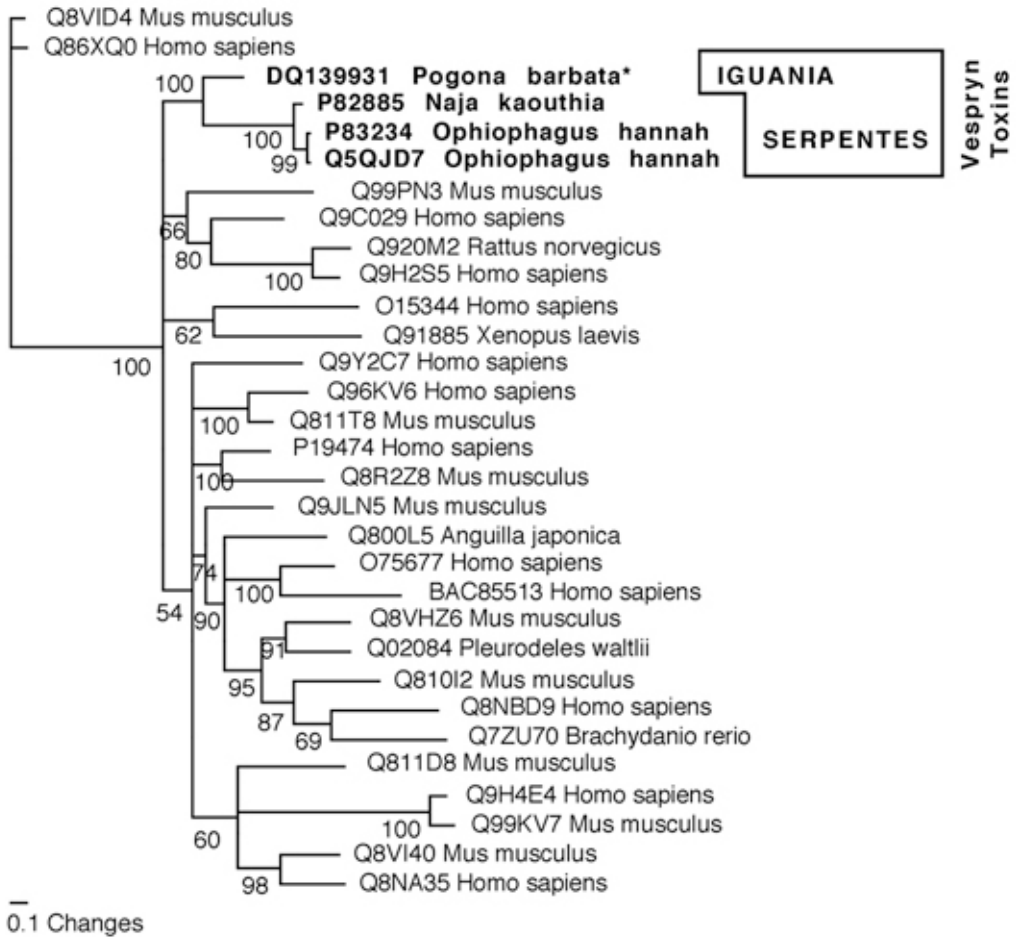
Supplementary Figure 6: Bayesian analysis of representative Kallkrein-related sequences. In order to minimize confusion, all sequences are referred to by their SWISS-PROT accession numbers (http://www.expasy.org/cgi-bin/sprot-search-ful). * Designates transcripts obtained in this study.



Supplementary Figure 7: Bayesian analysis of representative AVIT-related sequences. In order to minimize confusion, all sequences are referred to by their SWISS-PROT accession numbers (http://www.expasy.org/cgi-bin/sprot-search-ful). * Designates transcripts obtained in this study.

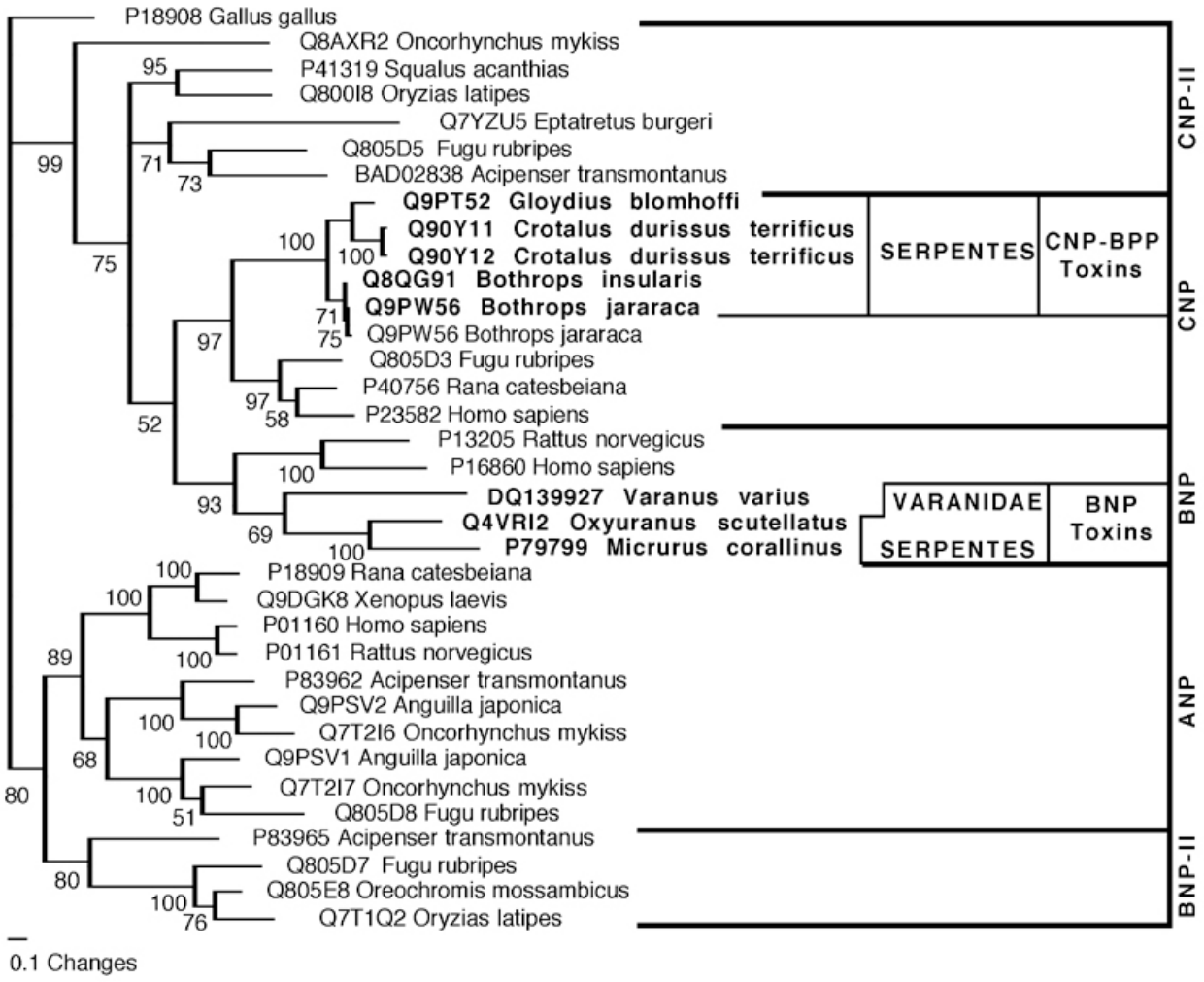


Supplementary Figure 8: Bayesian analysis of representative NGF-related sequences. In order to minimize confusion, all sequences are referred to by their SWISS-PROT accession numbers (http://www.expasy.org/cgi-bin/sprot-search-ful). * Designates transcripts obtained in this study.



Supplementary Figure 9: Bayesian analysis of representative Vespryn-related sequences. In order to minimize confusion, all sequences are referred to by their SWISS-PROT accession numbers (http://www.expasy.org/cgi-bin/sprot-search-ful). * Designates transcripts obtained in this study.

A)



B)

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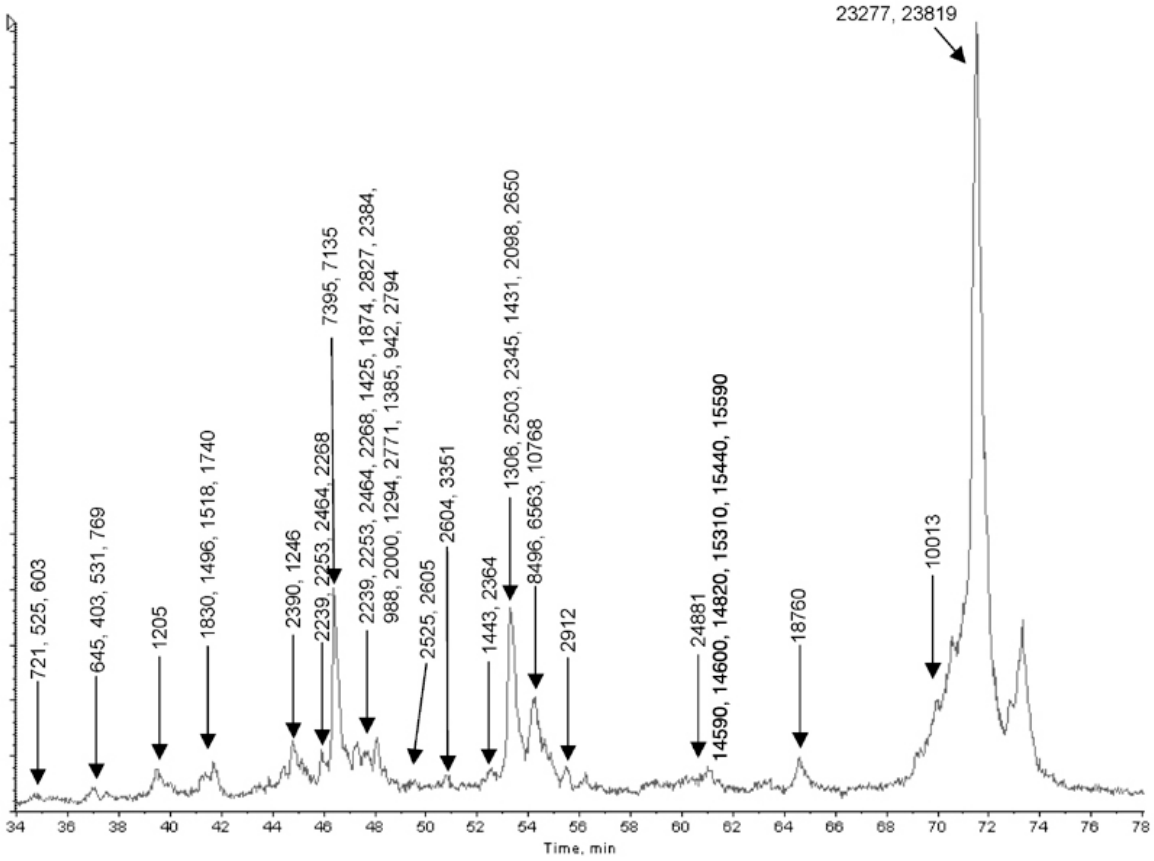
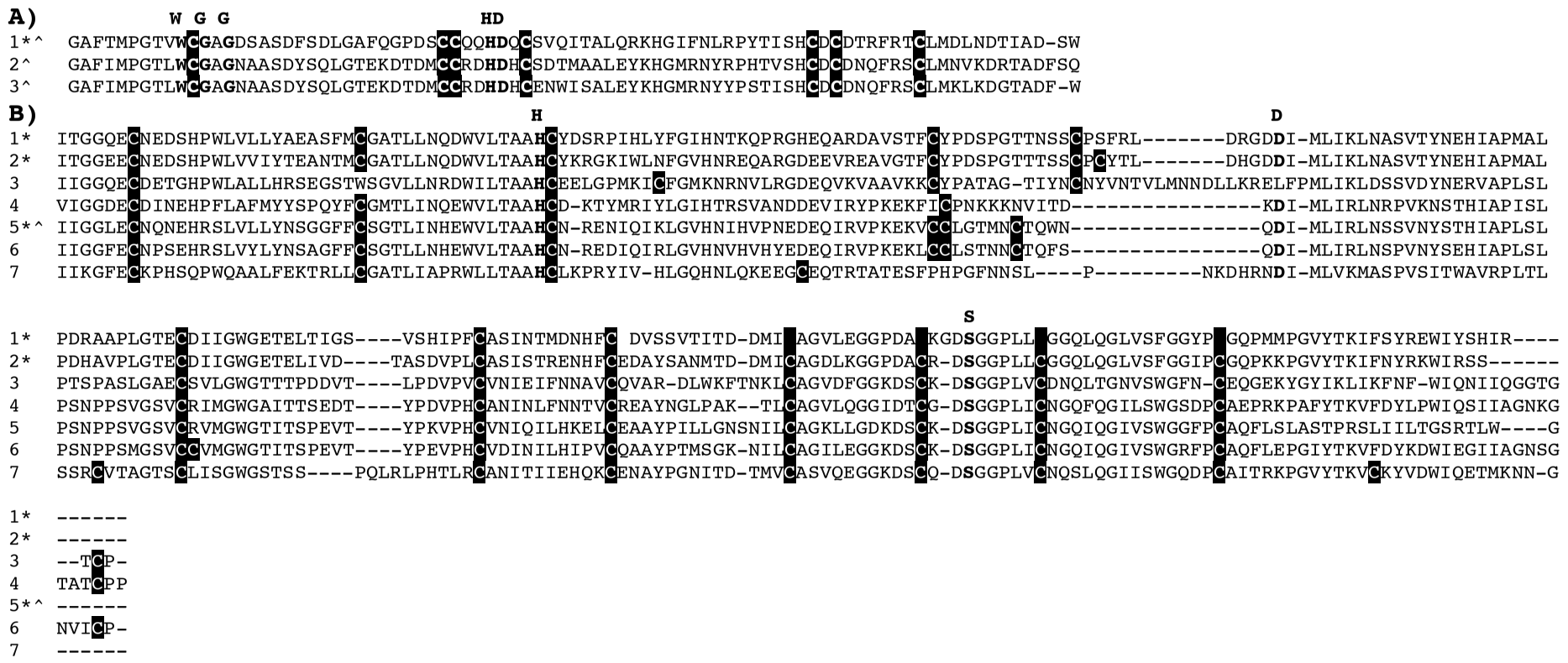
                                    ++    ++
1. GNP-1      ------EKRLQPEGSCFGQKMDRIGHVSGMGCNKFDPNKGSSSTGKK
2. TNP-c      -------SDSKIGNGCFGFPLDRIGSVSGLGCNRIMQNPPKKFSGE-
3. DNP        ---------EVKYDPCFGHKIDRINHVSNLGCPSLRDPRPNAPSTSA
4. Lebetin    -GDNKPPKKGPP-NGCFGHKIDRIGSHSGLGCNKVDDNKG-------
5. BNP Rat    IQERLRNSKMAHSSSCFGQKIDRIGAVSRLGCDGLRLF---------
```

Supplementary Figure 10: A) Bayesian analysis of representative full-length natriuretic toxins and related sequences. In order to minimize confusion, all sequences are referred to by their SWISS-PROT accession numbers (http://www.expasy.org/cgi-bin/sprot-search-ful). * Designates transcripts obtained in this study. B)) Sequence comparison of GNP-1 (DQ139927) from *V. varius* (Lace Monitor), 2) TNP-c (P83230) from *Oxyuranus microlepidotus* (Inland taipan), 3) DNP (P28374) from *Dendroaspis angusticeps* (Eastern Green Mamba), 4) Lebetin (Q7LZ09) from *Macrovipera lebetina* (Elephant snake) and 5) BNP from the rat (P13205) brain and atria. + designates conserved functional residues.

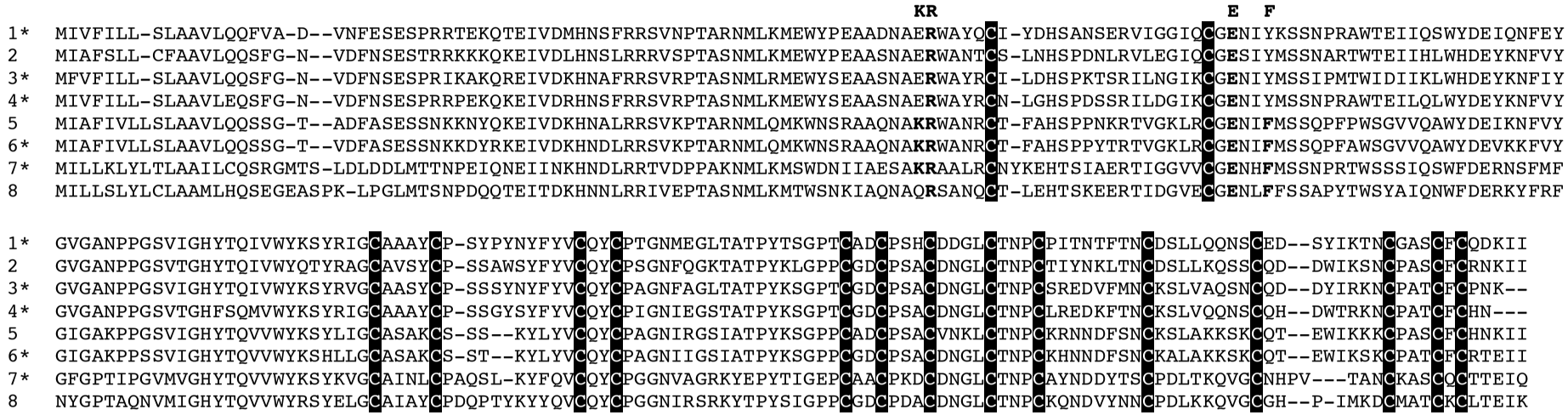
Varanus varius



Supplementary Figure 11: Liquid Chromatography/Mass Spectrometry analysis of crude mandibular secretions from *Varanus varius* (Lace Monitor). Reconstructed masses in Daltons are shown above each peak.



Supplemenary Figure 12: A) Alignment of Type III PLA_2: 1. *Varanus varius* (Lace Monitor) DQ139930 and *Heloderma suspectum* (Gila Monster) 2. P80003 and 3. P16354. B) Alignment of representative kallikrein (minus signal peptides): toxin forms 1. *Varanus mitchelli* (Mitchell's Water Monitor) DQ139915, 2. *Varanus acanthurus* (Spiny-tailed Monitor) DQ139914, 3. *Heloderma horridum* (Beaded Lizard) P43685, 4. *Bothrops jararaca* (Jararaca) P81661, 5. *Philodryas olfersii* (Argentine Racer) DQ139923, 6. *Lapemis curtus* (Spine-bellied Sea Snake) Q5MCS0 and tissue kallikrein 7. *Homo sapiens* (Human) Q9UBX7. * Designates transcripts obtained in this study. ^ Designates partial sequence.



Supplementary Figure 13: Sequence comparison of CRISP toxins: 1) DQ139892 *Enhydris polylepis* (Macleay's water snake), 2) Q7T1K6 *Naja atra* (Taiwanese cobra), 3) DQ139890 *Dispholidus typus* (Boomslang), 4) DQ139901 *Trimorphodon biscutatus* (Lyre snake), 5) Q8AVA4 *Pseudechis australis* (Mulga snake) , 6) DQ139896 *Oxyuranus microlepidotus* (Inland taipan), 7) DQ139904 *Varanus varius* (Lace monitor) and 8) Q91055 *Heloderma horridum* (Beaded lizard).