Supplementary Material - file 4

The first venomous crustacean revealed by transcriptomics and functional morphology: remipede venom glands express a unique toxin cocktail dominated by enzymes and a neurotoxin

Research Article

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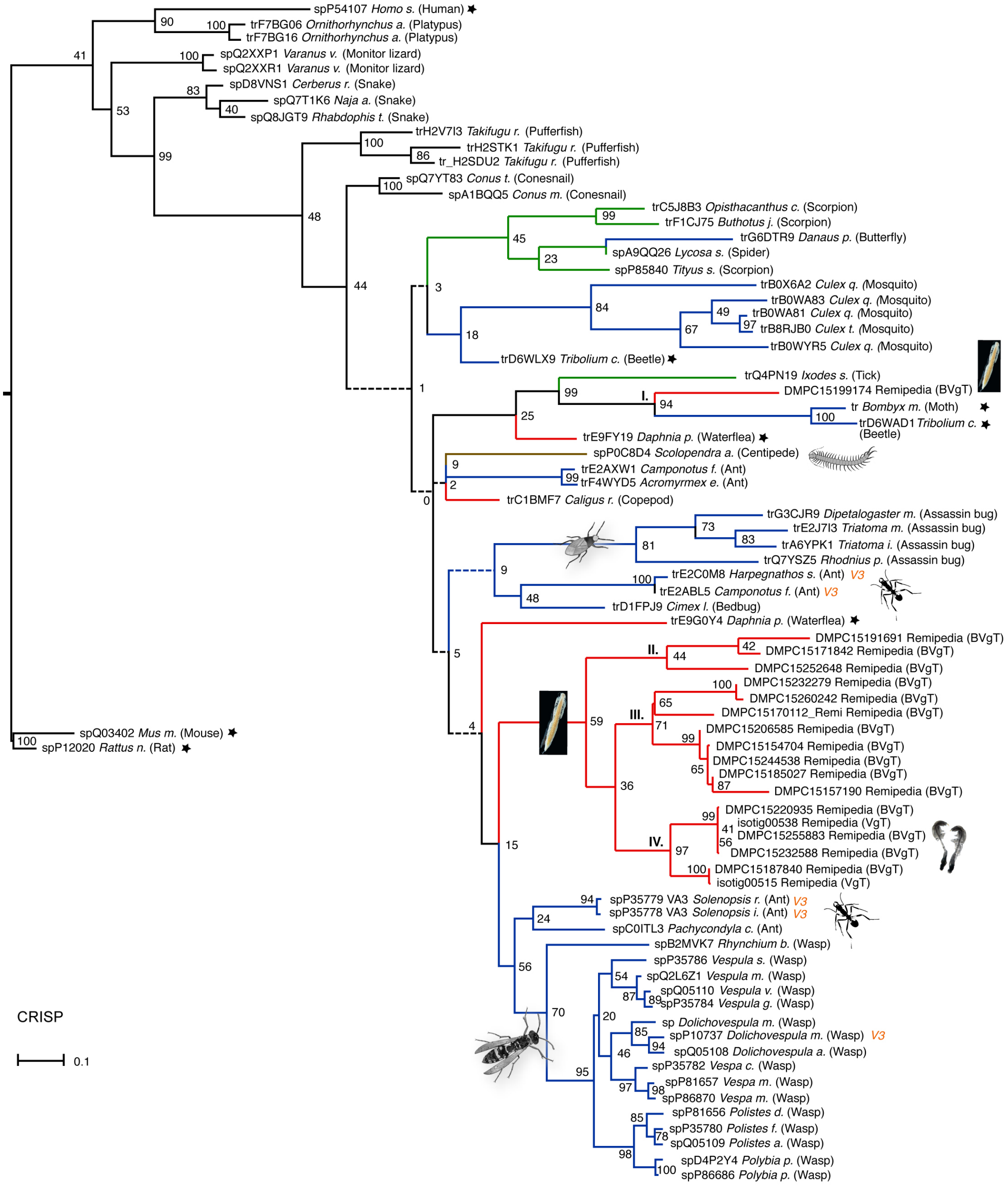
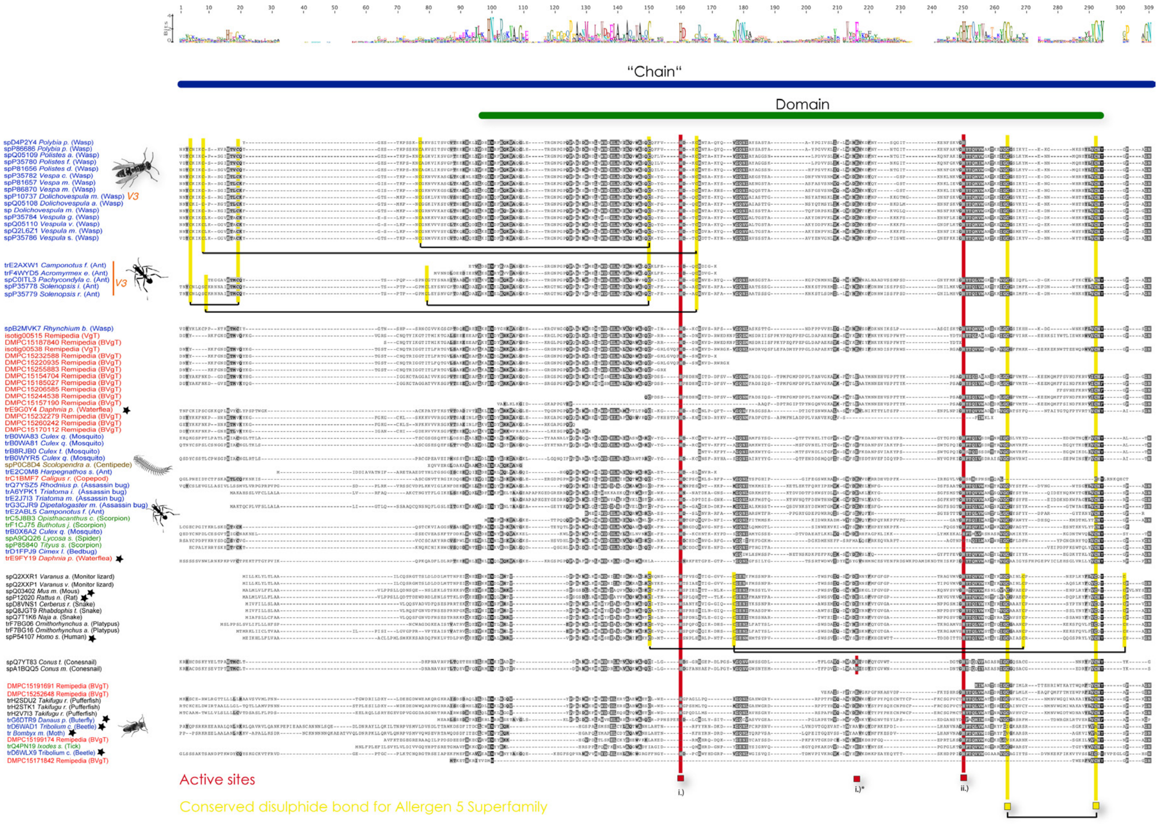
The supplementary PDF files include:

Supplementary_file1: Supplementary Text, Supplementary Figures 1-2
Supplementary_file2: Supplementary Figures 3
Supplementary_file3: Supplementary Figures 4-6
Supplementary_file4: Supplementary Figures 7-9
Supplementary_file5: Supplementary Tables 1 and 2



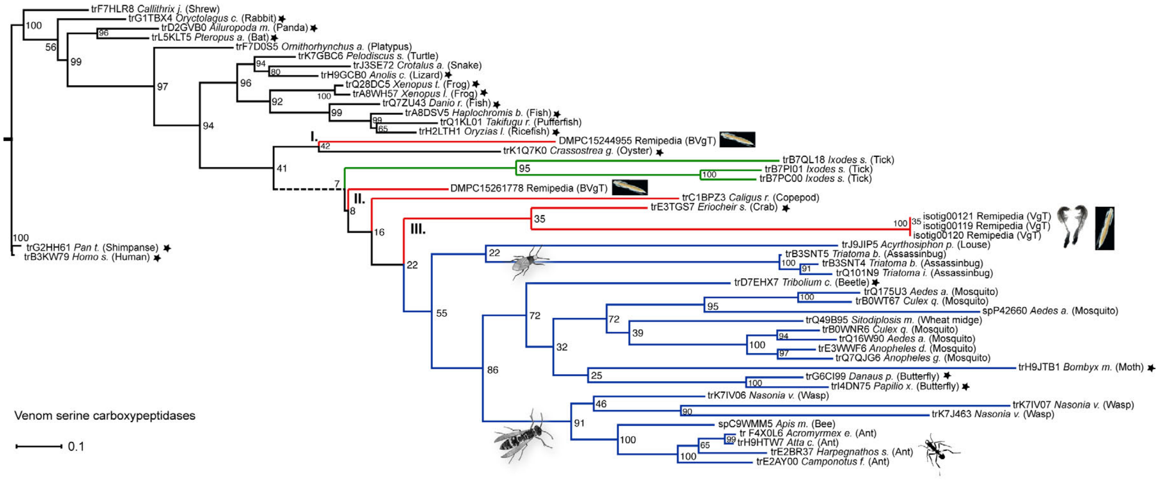
Supplementary Figure 7a

Phylogenetic tree of the CRISP sequences. The tree was reconstructed with RAxML (Stamatakis and Alachiotis 2010), -f a, PROTGAMMAIWAG, 10000 bootstraps. Sequences that were annotated in UniProt as venom allergen 3 sequences are labeled with V3. See previous figures for description.



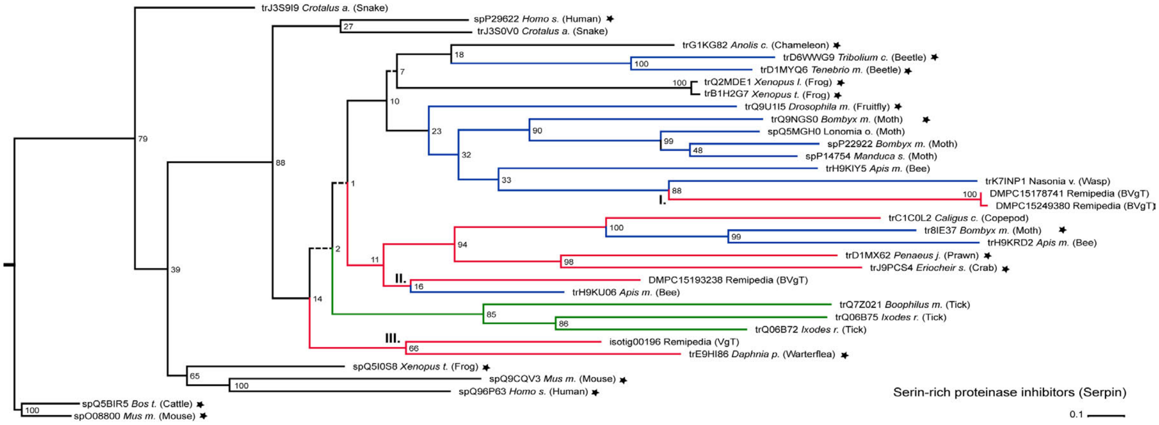
Supplementary Figure 7b

Alignment of the protein's chain region of the CRISP sequences. The chain of the mature protein is indicated by a blue, the domain region by a green bar. Disulphide bonds are pictured with black lines, the cysteine residue backbone by yellow squares. Active sites are marked by red bars and squares. The active site i.)* pictures the additional active site found in cone snail sequences. Sequences that were annotated in UniProt as venom allergen 3 sequences are labeled with V3.



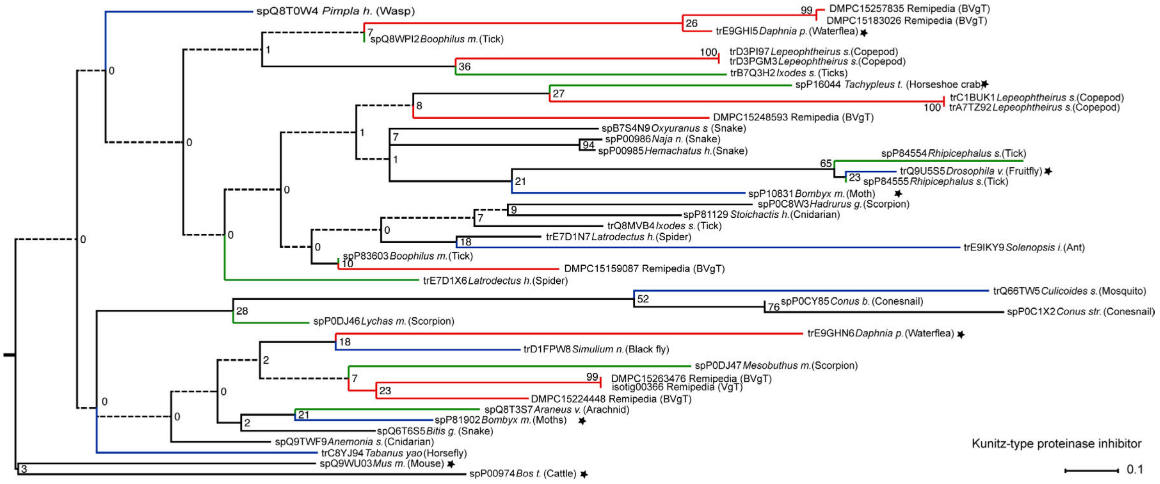
Supplementary Figure 8

Phylogenetic tree of the venom serine carboxypeptidase (VSC) sequences. The tree was reconstructed with RAxML (Stamatakis and Alachiotis 2010), -f a, PROTGAMMAILG, 1000 bootstraps. See previous figures for description.



Supplementary Figure 9a

Phylogenetic tree of the Serine-rich proteinase inhibitor (Serpin) sequences. The tree was reconstructed with RAxML (Stamatakis and Alachiotis 2010), -f a, PROTGAMMAIFLG, 1000 bootstraps. See previous figures for description.



Supplementary Figure 9b

Phylogenetic tree of the Kunitz-type proteinase inhibitor sequences. The tree was reconstructed with RAxML (Stamatakis and Alachiotis 2010), -f a, PROTGAMMAWAG, 10000 bootstraps. See previous figures for description.