

Supplementary Materials: A deeper examination of Thorellius atrox scorpion venom components with omic technologies

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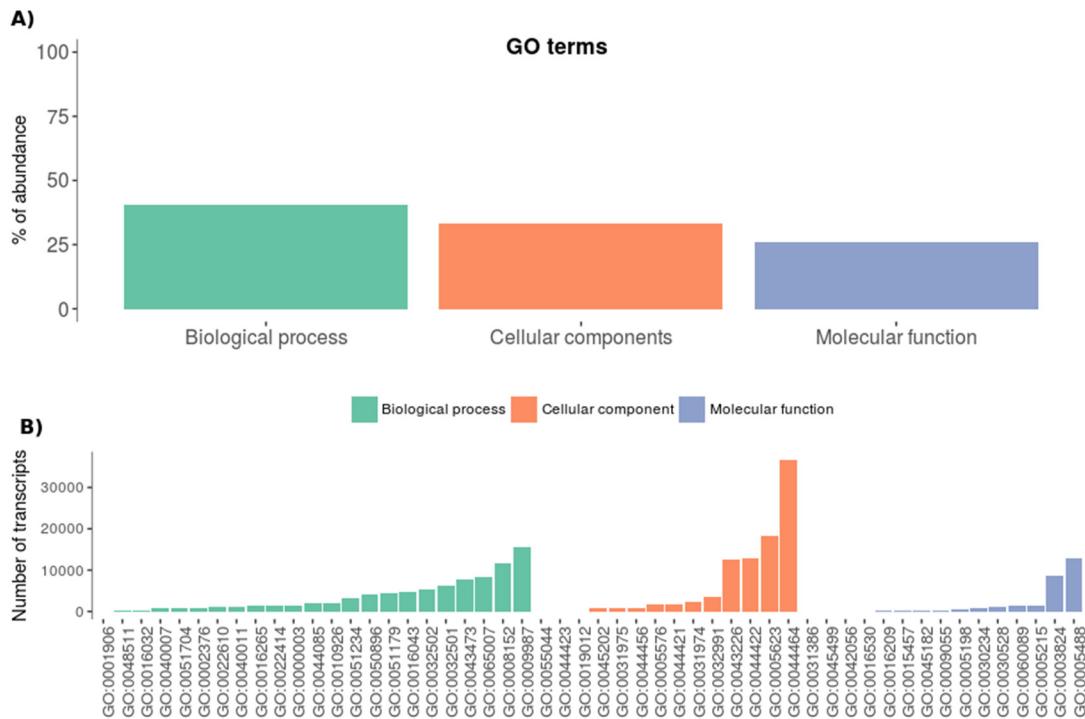


Figure S1. Distribution of the GO terms for the annotated *T. atrox* transcripts. (A) Distribution in accordance to the main three Gene Ontology (GO) ‘root’ nodes: Cellular Component, Molecular Function or Biological Process. (B) Assignment of the transcripts to the first level of ‘child’ terms of the GO hierarchy. The IDs of the GO terms are shown in the x-axis.

1 FWNTLLSVGK SLL 13

Sequence: FWNTLLSVGK, Charge: +2, Monoisotopic m/z: 582.8 Da (+0.76 mmu/+1.31 ppm),
 MH⁺: 1164.6 Da, RT: 91.93 min, Identified with: Sequest HT (v1.3); XCorr:3.18,
 Fragment match tolerance used for search: 0.6 Da

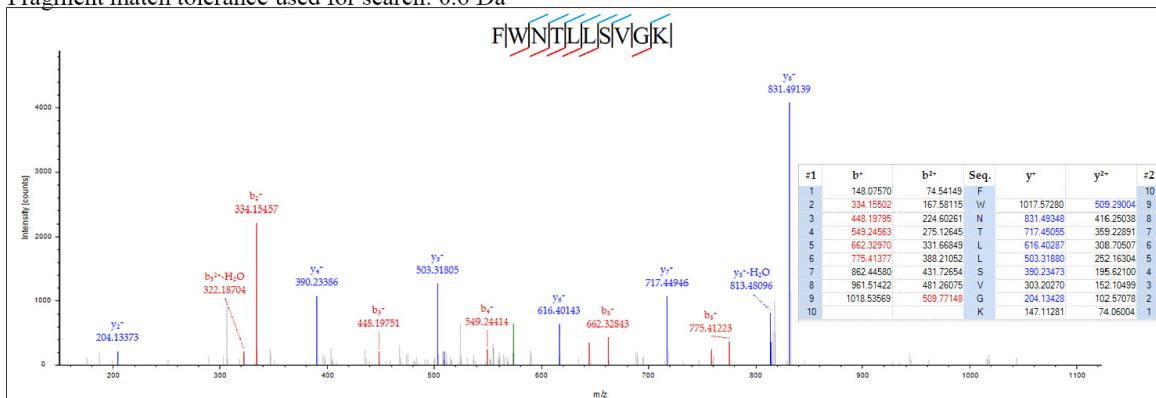


Figure S2. Sequence coverage and MS/MS spectrum of TatHDPND403