

Supplementary Materials: Serrulin: A Glycine-Rich Bioactive Peptide from the Hemolymph of the Yellow *Tityus serrulatus* Scorpion

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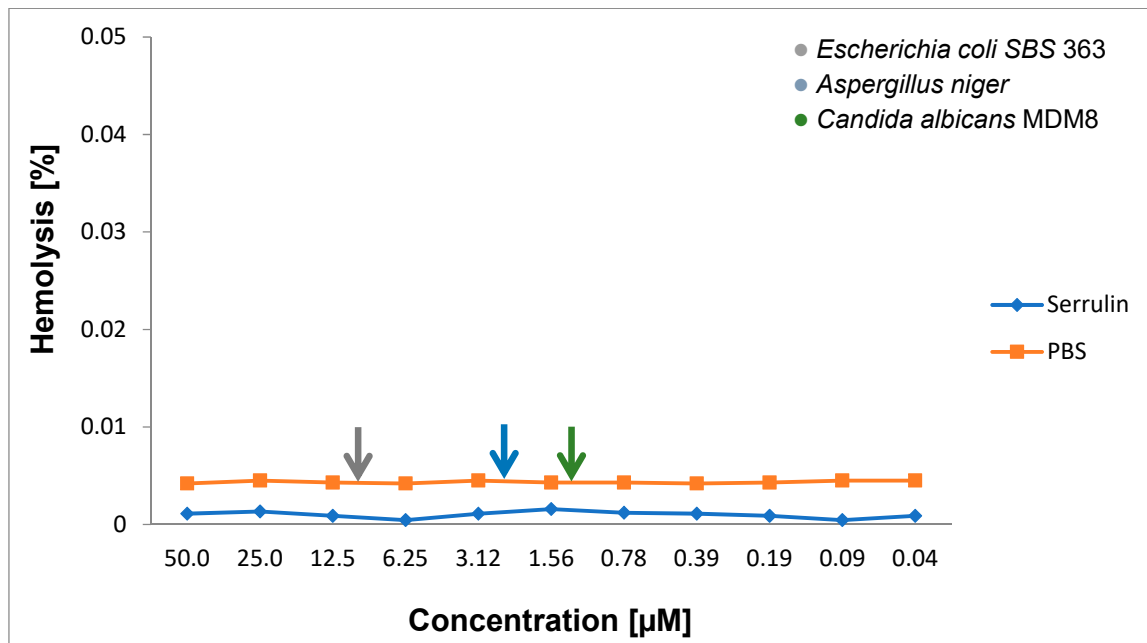


Figure S1. Hemolytic effects of serrulin on human erythrocytes. The concentration-response curve of the hemolytic activity of the peptide shows the maximum tested concentration (50 µM), which is very similar to that of the negative control (phosphate-buffered saline (PBS)).

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Number of amino acids: 37
Molecular weight: 3048.29
Theoretical pI: 11.10

Amino acid composition: 
Ala (A) 0 0.0%
Arg (R) 2 5.4%
Asn (N) 0 0.0%
Asp (D) 0 0.0%
Cys (C) 0 0.0%
Gln (Q) 0 0.0%
Glu (E) 0 0.0%
Gly (G) 26 70.3%
His (H) 0 0.0%
Ile (I) 2 5.4%
Leu (L) 0 0.0%
Lys (K) 2 5.4%
Met (M) 0 0.0%
Phe (F) 4 10.8%
Pro (P) 0 0.0%
Ser (S) 0 0.0%
Thr (T) 0 0.0%
Trp (W) 0 0.0%
Tyr (Y) 1 2.7%
Val (V) 0 0.0%
Pyl (O) 0 0.0%
Sec (U) 0 0.0%

(O) 0 0.0%
(Z) 0 0.0%
(X) 0 0.0%

Total number of negatively charged residues (Asp + Glu): 0
Total number of positively charged residues (Arg + Lys): 4

Atomic composition:
Carbon C 133
Hydrogen H 195
Nitrogen N 45
Oxygen O 39
Sulfur S 0

Formula: C133H195N45O39
Total number of atoms: 412

Extinction coefficients:
This protein does not contain any Trp residues. Experience shows that
this could result in more than 10% error in the computed extinction coefficient.

Extinction coefficients are in units of M-1 cm2, at 280 nm measured in water.

Ext. coefficient 1490
Abs 0.1% (=1 g/l) 0.489

Estimated half-life:
The N-terminal of the sequence considered is G (Gly).

The estimated half-life is: 30 hours (mammalian reticulocytes, in vitro).
>20 hours (yeast, in vivo).
>10 hours (Escherichia coli, in vivo).
    
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Figure S2. Physico-chemical parameters of serrulin. Data obtained by the sequence analysis, "GFGGGRGGFGGGRGGFGGGGIGGGFGGGYGGGKIKG," in ExPASy ProtParam. Information on the following is provided: The theoretical pI, molecular weight, total number of negatively and positively charged residues, atomic composition, extinction coefficients and percentage of amino acids found in the sample.

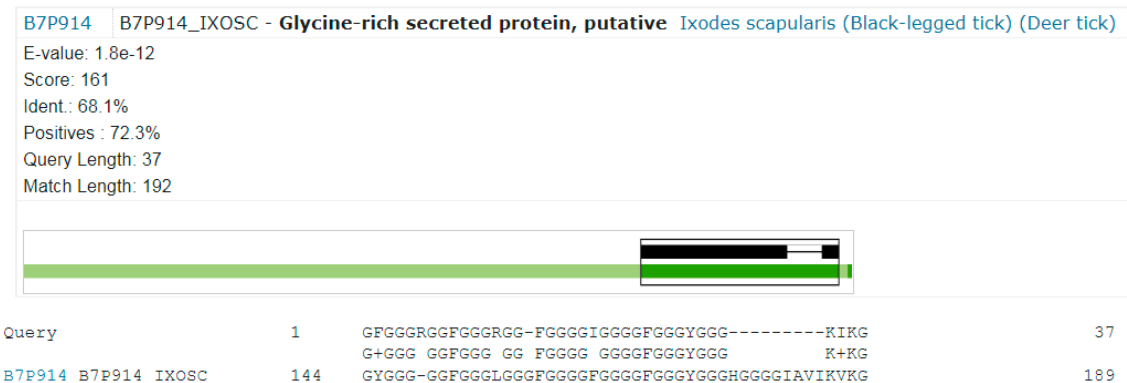


Figure S3. Results obtained by searching with BLAST (Basic Local Alignment Search Tool) using Uniprot (Universal Protein resource). The amino acid sequence of serrulin had a similarity of 68% to a protein found in the tick transcriptome of the species, *Ixodes scapularis*.