

A comparative *in silico* characterization of functional and physicochemical properties of 3FTx (three finger toxin) proteins from four venomous snakes

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Abstract:

Snake venom is an abundant resource of diverse pharmacologically bioactive proteins and peptides and a good natural source of drug lead compounds and used as important research tools in the field of toxicology, pharmacology and neuroscience. Three finger toxins (3FTx) is an important super-family of snake venom proteins which has a conserved three finger like appearance in three dimensional structures. Members of 3FTx family show a wide array of pharmacological effects by targeting different receptors and ion channels with high specificity and many of them are being investigated as potential drug target. Therefore, with a vision to verdict a new edge and attempt we determined the amino acid compositional (%) profile, physicochemical properties, secondary structural and functional analysis and phylogenetic relationship of three finger toxins present in four different elapid snake species namely, *Naja naja*, *Astrotia stokesii*, *Hydrophis cyanocinctus* and *Pelamis platura* using different bioinformatics tools. From the outcome of the current studies, it will be possible to know about a range of biological functions which are responsible mainly for the glowing amino acid composition profile of these proteins. Amino acid composition (%) profile although represents differential amount of different amino acid residues which encompasses a family precise model but all the protein sequence have a conserved amount of cysteine. The analysis of physicochemical properties can be used as a basic approach to contribute in developing rational drug through protein engineering and understanding different physiological function which will be beneficial for the welfare of human being.

Keywords: Snake venom, Neurotoxin, Cardiotoxin, Physicochemical properties.

Background:

Snakes are a group of amazing reptiles which have fascinated human being since beginning of mankind. Venomous snakes are regarded as most frightening animals with awesome striking power combined with lethal venoms. Venom from a single venomous snake species may contain 50-200 different venom components which are proteins or peptides [1]. Each of these proteins and peptides has profound effect on various physiological systems of the victim or prey [2, 3]. These venom

toxins are of biological interest due to their diverse and selective pharmacological and physiological effects through their interaction with different molecular targets. They play significant role in the development of therapeutic agents. For example, Captopril®, the most extensively used drug to control the blood pressure and cardiac disease was developed from one of the venom component of pit viper snake (*Bothrops jararaca*) [4]. Moreover, for the diagnosis of several diseases snake venom proteins are used as pharmacological probes. For example,

thrombin-like enzymes from snake venom are used for fibrinogen and fibrinogen-breakdown product assays as well as detecting dysfibrinogenaemias [5].

Snake venom proteins are classified into a small number of superfamilies. Among these, one of the most abundant and well characterized groups of non-enzymatic polypeptides is the three-finger toxin family which containing 60–74 amino-acid residues and confers lethality to Elapidae and Hydrophidae venoms [6]. Members of this superfamily illustrate resemblance in their primary, secondary and tertiary structures but, at times, they show vivid diversification in their biological functions [7]. All 3FTXs have three beta stranded loops resembling three-fingers, emerging from a globular core and stabilized by four conserved disulfide bridges. Members of 3FTXs have a molecular mass within the range of 6000- 8000 Da with high affinity and specificity for different receptors and ion channels. Due to their pin point accuracy of targeting capability they confer a wide array of specific pharmacological effects. Postsynaptic neurotoxins, cardiotoxins, cytotoxins, fasciculins, platelet -aggregation inhibitors and specific ion-channel blockers are included in this family A large number of members of 3FTXs are neurotoxins. They interfere with cholinergic transmission at post synaptic sites in the peripheral and central nervous systems. Snake venom neurotoxins are exploited for the identification and characterization of membrane ion channels and receptors in vertebrate cells, including human neurons [8].

Based on their receptor selectivity, they can be generally classified as α -neurotoxins (curaremimetic), κ -neurotoxins and muscarinic toxins that target muscle n- AChR, neuronal nAChR and various subtypes of muscarinic receptors, respectively. Another member of 3FTXs is cardiotoxin which is the second-largest group of this toxin superfamily and only found in cobra venoms. At lower concentrations, they are responsible to increase heart rate while, at higher concentrations, kill the animal by cardiac arrest [9]. Acetylcholine receptors are blocked by α -neurotoxin [10], cardiotoxins (cytotoxins) that exert their toxicity by forming pores in cell membranes [11], acetylcholine esterase and L-type calcium-channel blockers are inhibited by fasciculins [12]. The aim of this present study is to carry out an *in silico* comparative characterization and analysis of three finger toxin proteins from four venomous snake species (*Naja naja*, *Astrotia stokesii*, *Hydrophis cyanocintus* and *Pelamis platura*) using various bio-computational tools which are related to their physico-chemical, structural and functional properties. From the perspective of application, the results will provide significant information in developing rational drug through protein engineering and understanding different physiological function. Moreover, this would set a guideline for comparative characterization studies of other large protein families.

Methodology:

Sequence retrieval of three finger proteins

A total of nineteen protein sequences of long neurotoxin, short neurotoxin and cardiotoxin from *Naja naja*, *Astrotia stokesii*, *Hydrophis cyanocintus* and *Pelamis platura* reported so far were retrieved from the national center for biotechnology information (NCBI: <http://ncbi.nlm.nih.gov>) source in FASTA format.

Physico-chemical properties analysis

The protein sequence was used as the input data type to compute the amino acid composition (%), molecular weight, theoretical isoelectric point (pI), and number of positively and negatively charged residues, extinction coefficient, instability and aliphatic index, Grand Average of Hydropathy (GRAVY) using Expsy Protparam tool (<http://web.expsy.org/protparam>).

Secondary structure analysis

To analyze the secondary structural features of amino acid sequences, SOPMA tool (Self- Optimized Prediction Method with Alignment) of NPS (Network Protein Sequence Analysis, <http://npsapbil.ibcp.fr> /cgibin/cgibin/npsa_automat.pl?page=/NPSA/npsa_sopma.html) server was used to illustrate alpha helix, 3_{10} helix, Pi helix, beta bridge, extended strand, beta turns, bend region, random coil, ambiguous states and other states [13].

Functional properties analysis

The analysis of the selected three finger toxins is done with the help of Motif scan (http://myhits.isb-sib.ch/cgi-bin/motif_scan) tool [14]. The input data type was in FASTA format and scanned against 'PROSITE Patterns' which is a selected protein profile database.

Phylogenetic analysis

Phylogenetic analysis of three finger toxin protein sequences was done by two software namely, ClustalX and TreeView. All the sequences were aligned by using the clustalx version 2.1 and phylogenetic tree was constructed using NJ (Neighbor Joining) method. Phylogenetic tree was viewed by TreeView in Phylip format.

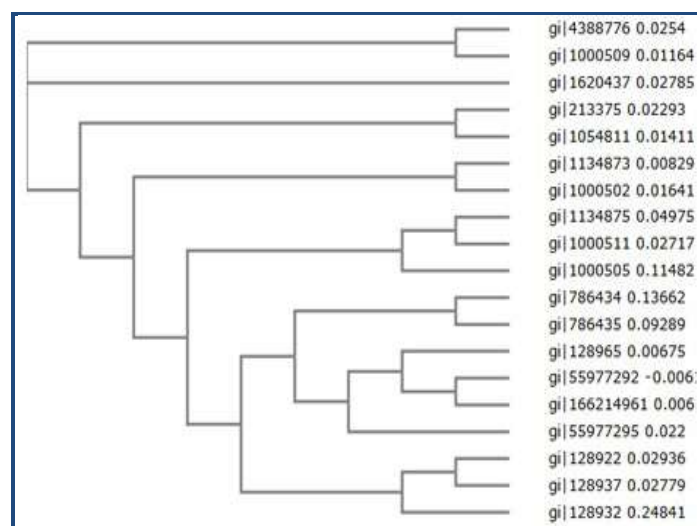


Figure 1: Phylogenetic tree of three finger toxin protein sequences by using Neighbor- Joining Method.

Discussion:

In the current study, the NCBI database was searched to retrieve the 3FTXs sequences from four specific snake species (*Naja naja*, *Astrotia stokesii*, *Hydrophis cyanocintus* and *Pelamis platura*). A total of 19 complete sequences (after removing the duplicates and partial sequences) were obtained from the selected four venomous snake species **Table 1 (see supplementary material)**. Amino acid composition analysis of

each sequence shows that the cysteine residues are highly conserved irrespective of snake species **Table 2 (see supplementary material)**. Cysteine residues play vital roles in protein structure and function by granting stability through disulfide bond formation, which maintaining proper maturation and localization during protein-protein intermolecular interactions [15]. Sequence analysis shows that high percentage of positively charged lysine residues is present in cardiotoxins and short chain neurotoxins. In short neurotoxins arginine is present in high quantity which is a positively charged amino acid responsible for the receptor binding mechanism. Both, Arginine and Lysine and their sufficient presence assist short neurotoxin to become an effective lethal bio-molecule. Moreover, short neurotoxins also manage well negatively charged amino acid than cardiotoxin. Both aspartic acid and glutamic acid are negatively charged which supported appropriate attachment to membrane receptor [16]. Nevertheless, the amount of negatively charged amino acid is very high in Long neurotoxin 1/ Toxin A which is contributed by the presence of Aspartic acid residues in the sequence. Other physico-chemical parameters also indicate the behavior of toxins in different conditions **Table 3 (See Supplementary material)**. pI values for all of toxins lie in the alkaline range (pH>7). Besides this, the instability index shows that Long neurotoxin 1, Cardiotoxin, Cardiotoxin 7, Cardiotoxin 8, Cardiotoxin I-like protein, Cardiotoxin V-like protein, Cardiotoxin 1, Cardiotoxin 3, Cardiotoxin 6, Cardiotoxin V, Cardiotoxin N and Long neurotoxin 2 are stable (Instability index <40) in nature. In the current study postsynaptic neurotoxin short chain/ toxin-3 is observed as the most thermostable toxin. Moreover, high extinction coefficients are observed for postsynaptic neurotoxin short chain /toxin-5 (*Naja naja*), Long neurotoxin 1/ Alpha-elapitoxin- Ast2a (*Astrotia stokesii*), Long neurotoxin 2/Alpha-elapitoxin-Ast2b (*Astrotia stokesii*) and Short neurotoxin 2/Hydrophitoxin b (*Hydrophis cyanocinctus*), which is associated with a high concentration of lysine, tryptophan and tyrosine residues in the sequence and may be valuable in protein-protein and protein ligand interaction studies in solution. In addition, aliphatic index, suggesting the relative volume of protein engaged by aliphatic side chains helps to study thermo stable properties of an enzyme. It is found to extent within a range of 23.55 to 112.96. Grand Average of Hydropathy (GRAVY) was computed for all the toxin proteins. A wide range of GRAVY value was found from -1.273 to 0.154 for all protein sequences. SOPMA analysis was done for all snake toxins and it displayed a high value for Random coil in all the toxin proteins **Table 4 (see supplementary material)**. The analysis of secondary structure signifies that values for extended strands were found higher than alpha helix in all members of protein family. High value for random coil allows important consequence in the study of protein tertiary structure and related functions. All three finger toxin members like Long neurotoxin, Cardiotoxin and short neurotoxin motifs were described as Snake toxins signature **Table 5 (see supplementary material)**. Three finger toxins are comprised of sixty to seventy five amino acids. Among the invariant residues are eight cysteines all involved in disulfide bonds and a signature pattern was developed which consist of four of these cysteines as well as a conserved proline thought to be significant for the maintenance of the tertiary structure. Using distance based Neighbor-Joining method Phylogenetic tree was made. Different clusters with close relationships were

identified including Cardiotoxin 8 (4388776) and Cardiotoxin N (1000509), Cardiotoxin (213375) and Cardiotoxin 3 (1054811), Cardiotoxin I-like protein (1134873) and Cardiotoxin 1 (1000502), Cardiotoxin V- like protein (1134875) and Cardiotoxin V (1000511) relating closely to Cardiotoxin 7 (1000505). Furthermore, Postsynaptic neurotoxin short chain/ toxin-3 (786434) and Postsynaptic neurotoxin short chain /toxin-5 (786435), Pelamitoxin a (55977292) and Short neurotoxin 2/Hydrophitoxin b (166214961) are closely related with Short neurotoxin 1/Hydrophitoxin a (128965) whereas, Long neurotoxin 1/ Alpha-elapitoxin-Ast2a (128922) and Long neurotoxin 2/Alpha-elapitoxin-Ast2b (128937) has close relation along with Long neurotoxin 1/ Toxin A (128932) (**Figure 1**). In close evolutionary relationship of Proteins may be investigated jointly for their contribution in related biological processes.

Conclusion:

In this investigation, we reveal the buried information about three finger toxins of four venomous snake species by analyzing their structural features such as amino acid content, physico-chemical properties, secondary structural features and phylogenetic relationship classification. Snake venom toxin proteins facilitate to know what kind of compositional biasness and differences plays role for adaptation to different biological systems that are venom system, pheromone system, complement system and cellular communication system. Comparative analysis and intensive characterization of the three finger toxin family of proteins with the help of numerous bio-computational tools yielded latest insights and perspectives which can be used to identify changes in protein structure that can cause impairment of protein function and also responsible to develop many pathological conditions. The findings throughout this study may be used by researchers working on three finger toxins in context of any experimental system. The amino acid composition demonstrates a considerably high percentage of cysteine residues in Short neurotoxin 1/Toxin A (*Astrotia stokesii*), along with Short neurotoxin 1/Hydrophitoxin a (*Hydrophis cyanocinctus*) and Pelamitoxin a (*Pelamis platura*). In addition, Postsynaptic neurotoxin short chain/ toxin-3 are found to be the most thermo stable toxin protein. Physicochemical characterization of these toxin proteins depicts inside the Laboratory of Nature how proteins are engineered for modified biological necessities. To one side from these based on analyzing the evolutionary relationship it can be hypothesized that this in turn helps to generate therapeutic molecules of medicinal value for the treatment of snakebites. Furthermore, this investigation may be taken as an example for related *in silico* investigational studies to observe other large protein superfamilies.

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Supplementary material:

Table 1: The dataset of 3FTx used in the analysis. In total 19 3FTx sequences were collected from the protein sequence databases. The name of snake, NCBI-GI and the toxin name for each sequence are given in the table.

Name of Snake Species	NCBI-GI	Protein Name
<i>Naja naja</i>	128932	Long neurotoxin 1/ Toxin A
<i>Naja naja</i>	213375	Cardiotoxin
<i>Naja naja</i>	1000505	Cardiotoxin 7
<i>Naja naja</i>	4388776	Cardiotoxin 8
<i>Naja naja</i>	1134873	Cardiotoxin I-like protein
<i>Naja naja</i>	1134875	Cardiotoxin V-like protein
<i>Naja naja</i>	1000502	Cardiotoxin 1
<i>Naja naja</i>	1054811	Cardiotoxin 3
<i>Naja naja</i>	1620437	Cardiotoxin 6
<i>Naja naja</i>	1000511	Cardiotoxin V
<i>Naja naja</i>	1000509	Cardiotoxin N
<i>Naja naja</i>	786434	Postsynaptic neurotoxin short chain/ toxin-3
<i>Naja naja</i>	786435	Postsynaptic neurotoxin short chain /toxin-5
<i>Astrotia stokesii</i>	128922	Long neurotoxin 1/ Alpha-elapitoxin-Ast2a
<i>Astrotia stokesii</i>	128937	Long neurotoxin 2/Alpha-elapitoxin-Ast2b
<i>Astrotia stokesii</i>	55977295	Short neurotoxin 1/ Toxin A
<i>Hydrophis cyanocinctus</i>	128965	Short neurotoxin 1/Hydrophitoxin a
<i>Hydrophis cyanocinctus</i>	166214961	Short neurotoxin 2/Hydrophitoxin b
<i>Pelamis platura</i>	55977292	Pelamitoxin a

Table 2: Amino acid composition profile of four snake venom toxin proteins (in %)

Protein Name	Ala	Arg	Asn	Asp	Cys	Gln	Glu	Gly	His	Ile	Leu	Lys	Met	Phe	Pro	Ser	Thr	Trp	Tyr	Val
Long neurotoxin 1/ Toxin A	2.8	8.5	1.4	11.3	14.1	1.4	0.0	7.0	1.4	7.0	1.4	5.6	0.0	4.2	8.5	4.2	12.7	1.4	1.4	5.6
Cardiotoxin	2.5	2.5	4.9	3.7	11.1	0.0	1.2	2.5	0.0	2.5	13.6	12.3	3.7	2.5	6.2	2.5	9.9	0.0	4.9	13.6
Cardiotoxin 7	3.7	2.4	4.9	2.4	11.0	1.2	1.2	3.7	1.2	2.4	14.6	12.2	1.2	4.9	6.1	3.7	11.0	0.0	2.4	9.8
Cardiotoxin 8	6.2	2.5	3.7	3.7	11.1	1.2	0.0	3.7	0.0	3.7	13.6	11.1	3.7	2.5	6.2	3.7	6.2	0.0	4.9	12.3
Cardiotoxin I-like protein	2.5	2.5	6.2	4.9	11.1	0	0	3.7	0.0	6.2	14.8	11.1	4.9	1.2	3.7	3.7	9.9	0.0	3.7	9.9
Cardiotoxin V-like protein	3.6	1.2	6.0	3.6	10.8	1.2	1.2	3.6	1.2	2.4	14.5	14.5	2.4	4.8	6.0	3.6	8.4	0.0	3.6	7.2
Cardiotoxin 1	2.5	2.5	6.2	3.7	11.1	0.0	0.0	3.7	1.2	6.2	14.8	11.1	4.9	1.2	4.9	3.7	8.6	0.0	3.7	9.9
Cardiotoxin 3	2.5	3.7	4.9	3.7	9.9	0.0	0.0	3.7	0.0	2.5	14.8	12.3	3.7	2.5	6.2	2.5	8.6	0.0	4.9	13.6
Cardiotoxin 6	4.9	3.7	6.1	3.7	11.0	2.4	0.0	3.7	0.0	3.7	13.4	9.8	3.7	3.7	4.9	2.4	7.3	0.0	4.9	11.0
Cardiotoxin V	3.6	1.2	6.0	3.6	10.8	1.2	1.2	3.6	1.2	2.4	14.5	14.5	2.4	4.8	6.0	2.4	9.6	0.0	3.6	7.2
Cardiotoxin N	6.2	2.5	4.9	3.7	11.1	1.2	0.0	3.7	0.0	3.7	13.6	11.1	3.7	2.5	6.2	2.5	7.4	0.0	4.9	11.1
Postsynaptic neurotoxin short chain/ toxin-3	0.0	9.7	8.1	4.8	12.9	4.8	6.5	11.3	3.2	3.2	1.6	4.8	0.0	0.0	3.2	6.5	12.9	1.6	3.2	1.6
Postsynaptic neurotoxin short chain /toxin-5	1.6	4.9	8.2	3.3	13.1	4.9	4.9	8.2	3.3	3.3	3.3	9.8	0.0	0.0	4.9	6.6	11.5	3.3	1.6	3.3
Long neurotoxin 1/ Alpha-elapitoxin-Ast2a	7.1	2.9	5.7	2.9	14.3	1.4	2.9	10.0	2.9	5.7	2.9	5.7	1.4	2.9	4.3	7.1	8.6	2.9	4.3	4.3
Long neurotoxin 2/Alpha-elapitoxin-Ast2b	6.9	4.2	4.2	2.8	13.9	1.4	2.8	9.7	2.8	4.2	2.8	5.6	1.4	2.8	4.2	8.3	9.7	2.8	4.2	5.6
Short neurotoxin 1/ Toxin A	1.7	3.3	10.0	1.7	15.0	6.7	5.0	8.3	3.3	5.0	1.7	8.3	1.7	0.0	3.3	8.3	11.7	1.7	1.7	1.7
Short neurotoxin 1/Hydrophitoxin a	1.7	5.0	8.3	1.7	15.0	6.7	6.7	6.7	3.3	3.3	1.7	10.0	1.7	0.0	3.3	8.3	11.7	1.7	1.7	1.7
Short neurotoxin 2/Hydrophitoxin b	1.3	3.8	6.3	2.5	12.7	5.1	5.1	6.3	2.5	3.8	8.9	6.3	1.3	0.0	3.8	7.6	12.7	1.3	2.5	6.3
Pelamitoxin a	1.7	5.0	8.3	1.7	15.0	6.7	6.7	6.7	3.3	3.3	1.7	8.3	1.7	0.0	3.3	10.0	11.7	1.7	1.7	1.7

Table 3: Physico-chemical parameters of four snake venom toxin proteins

Protein Name	No. of A.A.	M.W (Da)	pI	"-" charged residues	"+" charged residues	Extinction coefficient	Instability index	Aliphatic index	GRAVY
Long neurotoxin 1/ Toxin A	71	7847.0	8.11	8	10	7615	22.66	52.11	-0.327
Cardiotoxin	81	9098.1	9.15	4	12	6460	32.82	104.44	0.459
Cardiotoxin 7	82	9086.0	9.30	3	12	3480	33.85	98.54	0.360

Cardiotoxin 8	81	8923.0	9.17	3	11	6460	34.04	109.38	0.632
Cardiotoxin I-like protein	81	8996.0	9.05	4	11	4970	25.29	112.96	0.552
Cardiotoxin V-like protein	83	9309.3	9.25	4	13	4970	26.86	90.36	0.154
Cardiotoxin 1	81	9014.1	9.18	3	11	4970	26.95	112.96	0.544
Cardiotoxin 3	81	9091.2	9.45	3	13	6460	31.77	109.26	0.467
Cardiotoxin 6	82	9201.2	9.18	3	11	6460	27.07	103.29	0.471
Cardiotoxin V	83	9323.3	9.25	4	13	4970	24.53	90.36	0.155
Cardiotoxin N	81	8952.0	9.17	3	11	6460	29.66	105.80	0.538
Postsynaptic neurotoxin short chain/ toxin-3	62	6957.6	8.20	7	9	8980	61.60	23.55	-1.273
Postsynaptic neurotoxin short chain /toxin-5	61	6817.6	8.71	5	9	12990	45.55	36.72	-0.984
Long neurotoxin 1/ Alpha-elapitoxin-Ast2a	70	7573.6	8.10	4	6	16095	40.24	53.00	-0.061
Long neurotoxin 2/ Alpha-elapitoxin-Ast2b	72	7789.9	8.39	4	7	16095	34.93	50.14	-0.099
Short neurotoxin 1/ Toxin A	60	6599.4	8.42	4	7	7490	46.62	32.50	-0.875
Short neurotoxin 1/Hydrophitoxin a	60	6728.5	8.64	5	9	7490	53.04	26.00	-1.083
Short neurotoxin 2/Hydrophitoxin b	79	8715.0	8.23	6	8	9105	41.91	68.99	-0.306
Pelamitoxin a	60	6687.4	8.42	5	8	7490	54.46	26.00	-1.032

Table 4: Secondary structural features of four snake venom toxin proteins (in %)

Protein Name	α Helix	3_{10} Helix	Pi Helix	β Bridge	Extended Strand	β Turn	Bend Region	Random Coil	Ambiguous States	Other States
Long neurotoxin 1	0.0	0.0	0.0	0.0	28.17	2.82	0.0	69.01	0.0	0.0
Cardiotoxin	12.35	0.0	0.0	0.0	38.27	7.41	0.0	41.98	0.0	0.0
Cardiotoxin 7	9.76	0.0	0.0	0.0	40.24	7.32	0.0	42.68	0.0	0.0
Cardiotoxin 8	9.88	0.0	0.0	0.0	41.98	7.41	0.0	40.74	0.0	0.0
Cardiotoxin I-like protein	9.88	0.0	0.0	0.0	40.74	7.41	0.0	41.98	0.0	0.0
Cardiotoxin V-like protein	10.84	0.0	0.0	0.0	37.35	4.82	0.0	46.99	0.0	0.0
Cardiotoxin 1	9.88	0.0	0.0	0.0	33.33	7.41	0.0	49.38	0.0	0.0
Cardiotoxin 3	9.88	0.0	0.0	0.0	40.74	2.47	0.0	46.91	0.0	0.0
Cardiotoxin 6	9.46	0.0	0.0	0.0	36.59	7.32	0.0	46.34	0.0	0.0
Cardiotoxin V	10.84	0.0	0.0	0.0	33.73	4.82	0.0	50.60	0.0	0.0
Cardiotoxin N	16.05	0.0	0.0	0.0	30.86	7.41	0.0	45.68	0.0	0.0
Postsynaptic neurotoxin short chain/ toxin-3	0.0	0.0	0.0	0.0	25.81	6.45	0.0	67.74	0.0	0.0
Postsynaptic neurotoxin short chain	1.64	0.0	0.0	0.0	29.51	8.20	0.0	60.66	0.0	0.0
Long neurotoxin 1	0.0	0.0	0.0	0.0	28.57	11.43	0.0	60.00	0.0	0.0
Long neurotoxin 2	5.56	0.0	0.0	0.0	30.56	2.78	0.0	61.11	0.0	0.0
Short neurotoxin 1	0.0	0.0	0.0	0.0	30.00	3.33	0.0	66.67	0.0	0.0
Short neurotoxin 1	1.67	0.0	0.0	0.0	30.00	6.67	0.0	61.67	0.0	0.0
Short neurotoxin 2	11.39	0.0	0.0	0.0	32.91	6.33	0.0	49.37	0.0	0.0
Pelamitoxin a	0.0	0.0	0.0	0.0	30.00	3.33	0.0	66.67	0.0	0.0

Table 5: Motifs in four snake venom toxin proteins (in %).

Protein Name	Motif found	Motif ID	Description	Start	End	Match Status	Significance
Long neurotoxin 1	SNAKE_TOXIN	PS00272	Snake toxins signature	40	60	Strong match;	not a false positive
Cardiotoxin	SNAKE_TOXIN	PS00272	Snake toxins signature	58	78	Strong match;	not a false positive
Cardiotoxin7	SNAKE_TOXIN	PS00272	Snake toxins signature	59	79	Strong match;	not a false positive
Cardiotoxin8	SNAKE_TOXIN	PS00272	Snake toxins signature	58	78	Strong match;	not a false positive
Cardiotoxin I-like protein	SNAKE_TOXIN	PS00272	Snake toxins signature	58	78	Strong match;	not a false positive

Cardiotoxin V-like protein	SNAKE_TOXIN	PS00272	Snake toxins signature	60	80	Strong match; not a false positive
Cardiotoxin6	SNAKE_TOXIN	PS00272	Snake toxins signature	58	78	Strong match; not a false positive
CardiotoxinV	SNAKE_TOXIN	PS00272	Snake toxins signature	60	80	Strong match; not a false positive
CardiotoxinN	SNAKE_TOXIN	PS00272	Snake toxins signature	58	78	Strong match; not a false positive
Postsynaptic neurotoxin short chain/toxin-3	SNAKE_TOXIN	PS00272	Snake toxins signature	40	58	Strong match; not a false positive
postsynaptic neurotoxin short chain	SNAKE_TOXIN	PS00272	Snake toxins signature	39	57	Strong match; not a false positive
Long neurotoxin 1	SNAKE_TOXIN	PS00272	Snake toxins signature	40	60	Strong match; not a false positive
Long neurotoxin 2	SNAKE_TOXIN	PS00272	Snake toxins signature	40	60	Strong match; not a false positive
Short neurotoxin 1	SNAKE_TOXIN	PS00272	Snake toxins signature	38	56	Strong match; not a false positive
Short neurotoxin 1	SNAKE_TOXIN	PS00272	Snake toxins signature	38	56	Strong match; not a false positive
Short neurotoxin 2	SNAKE_TOXIN	PS00272	Snake toxins signature	57	75	Strong match; not a false positive
Pelamitoxina	SNAKE_TOXIN	PS00272	Snake toxins signature	38	56	Strong match; not a false positive