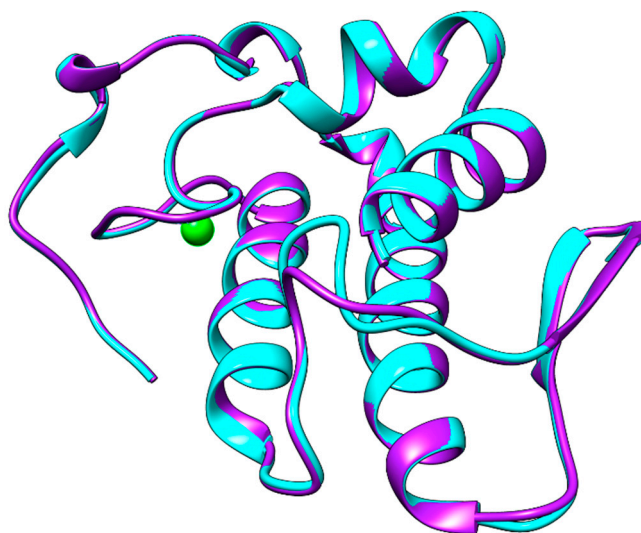
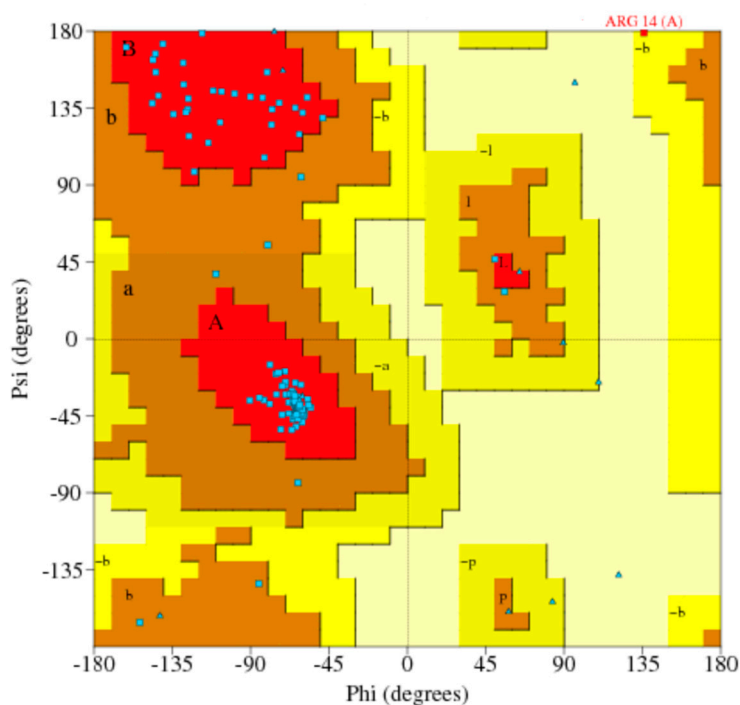


## Supplementary Materials: Isolation and functional characterization of an acidic myotoxic phospholipase A<sub>2</sub> from Colombian *Bothrops asper* venom

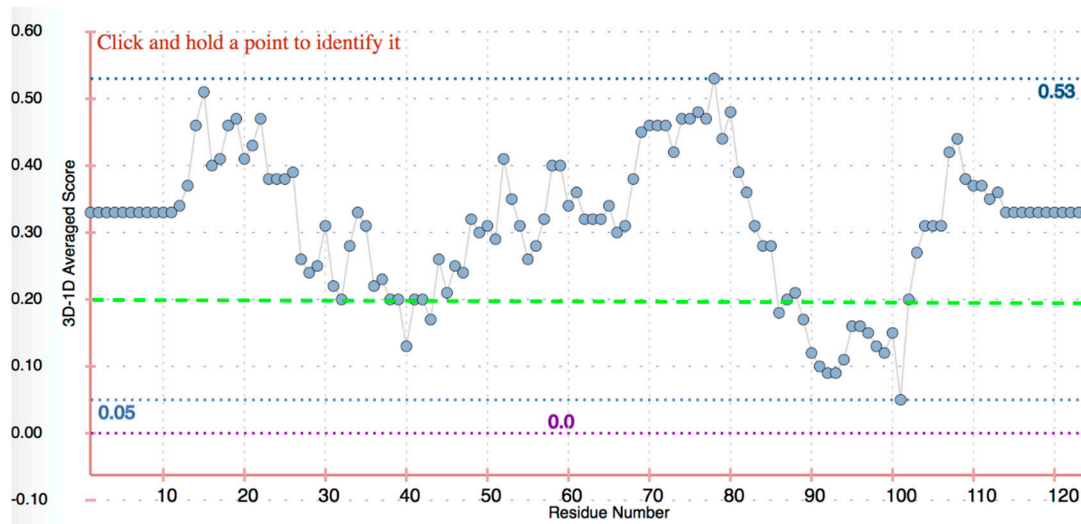
Silvia Posada Arias, Paola Rey-Suárez, Andrés Pereáñez J, Cristian Acosta, Mauricio Rojas, Lucilene Delazari dos Santos, Rui Seabra Ferreira Jr and Vitelbina Núñez



**Figure S1.** Overlay of the proposed structure of BaCol PLA<sub>2</sub> (Cyan) with the template structure (PDB ID: 1UMV\_X, Purple). Green sphere represents a Ca<sup>2+</sup> ion.



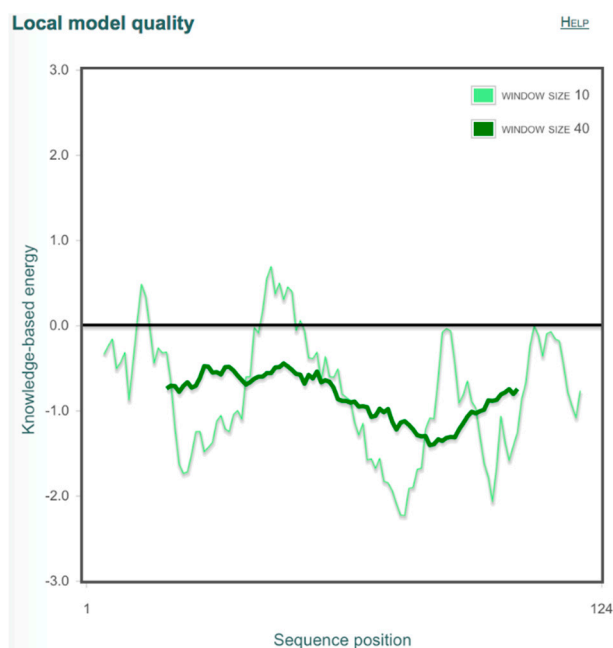
**Figure S2.** Ramachandran plot of modeled BaCol PLA<sub>2</sub>. The favored and most favored region is red and brown respectively. Yellow is the generally allowed and disallowed regions is pale yellow.



**Figure S3.** Verify-3D analysis. Green-dashed line represents the limit score of 0.2. Positive scores suggest that the residues are compatible with their environments in the model build for BaCol PLA<sub>2</sub>. The lowest and the highest values are shown.

**Table S1.** Residues with a score under 0.2.

Residues	3D-1D	Average Scores
avg C	43	0.17
avg E	89	0.17
avg C	90	0.12
avg D	91	0.10
avg R	92	0.09
avg V	93	0.09
avg A	94	0.11
avg A	95	0.16
avg I	96	0.16
avg C	97	0.15
avg F	98	0.13
avg R	99	0.12
avg D	100	0.15
avg N	101	0.05



**Figure S4.** ProSA energy plot calculated for the BaCol PLA<sub>2</sub> homology model. The energy plot displayed by ProSA shows the local model quality by plotting energies in function of the amino acid sequence position. Positive values correspond to problematic or erroneous parts of a model. When the fragment of 10 residues was evaluated, most of them were in the negative region. However, when a fragment of 40 residues was evaluated none of the residues is outside of the negative region.