

Supplementary file 2

The three-dimensional models presented in Fig 3 and illustrated by the crystallographic or NMR structures of some members of each protein family have been generated from the following spatial coordinates: 3DSL, PIII-snake venom metalloproteinase (SVMP) bothropasin from the jararaca, *Bothrops jararaca*; 1ND1, PI-SVMP BaP1 from the fer-de-lance *Bothrops asper*; 1TGM, monomeric snake venom phospholipase A₂ (PLA₂) from the Russell's viper *Daboia russelii*; 3R0L, heterodimeric β -neurotoxic PLA₂ crotoxin from the venom of the South American rattlesnake *Crotalus durissus terrificus*; 1OP0, snake venom serine protease (SVSP) Dav-PA from the Chinese moccasin *Deinagkistrodon acutus*; 1IJC, three-finger toxin (3FTx) bucandin from the venom of the Malayan krait (*Bungarus candidus*); 1DTX, dendrotoxin (DenTx) from the green mamba (*Dendroaspis angusticeps*); 1IXX, coagulation factors IX/X-binding C-type lectin-like (CTL) protein from the habu snake *Protobothrops flavoviridis*; 3MZ8, cysteine-rich secretory protein (CRISP) natrin from the Chinese cobra *Naja atra*; 2IID, L-amino acid oxidase (LAO) from the Malayan pitviper *Calloselasma rhodostoma*; 4GV5, myotoxin (Myo) crotamine from the South American rattlesnake *Crotalus durissus terrificus*. Structural models were rendered with UCSF Chimera¹.

1. Pettersen. E.F. *et al.* UCSF Chimera--a visualization system for exploratory research and analysis. *J. Comput. Chem.* **25**, 1605-1612 (2004).