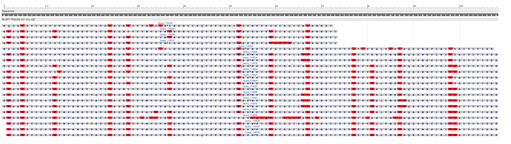
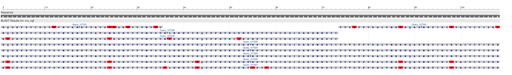
Fig. S7: A larger pool of sequences available from various snakes and other reptile groups (Colubridae, Boidae, Pythonidae, Acrochordidae, Lizards, Crocodiles and Testudines) were compared with the sequence of Russell's viper for putative homologs of NGF, PDGF, Kunitz BPTI, CAP and CRISP domains.

A *NGF*

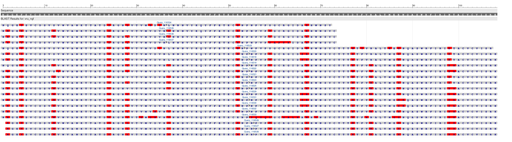
Crotalines



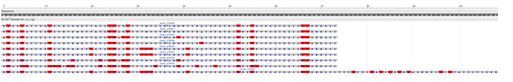
Viperines



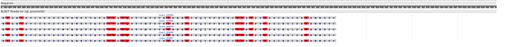
Elapids



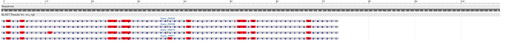
Colubrids



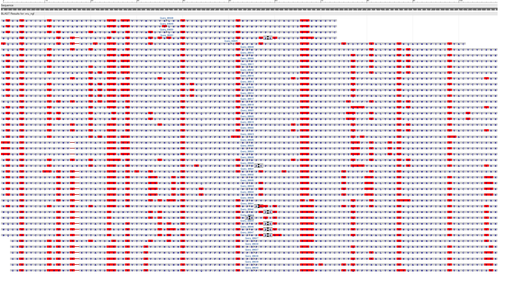
Acrochordids



Boids

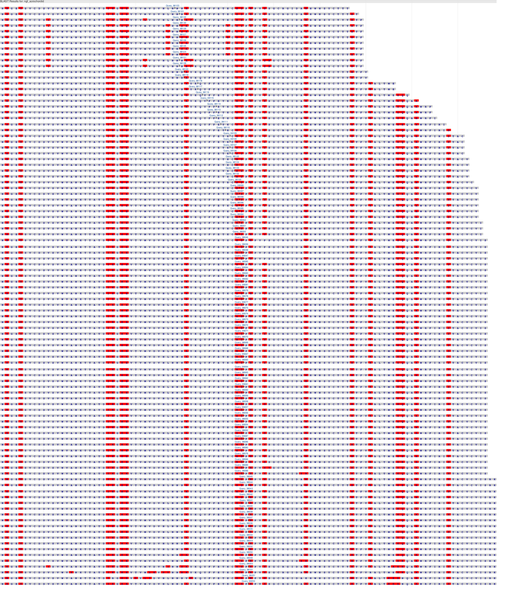


Elapids

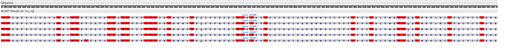


Pythonids

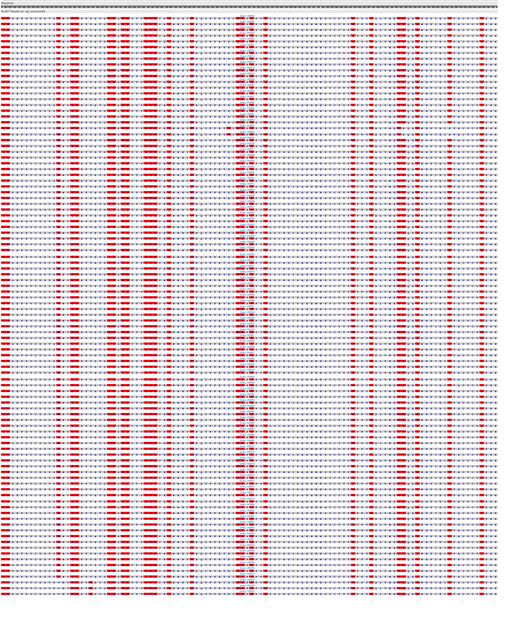
Lizards



Crocodiles

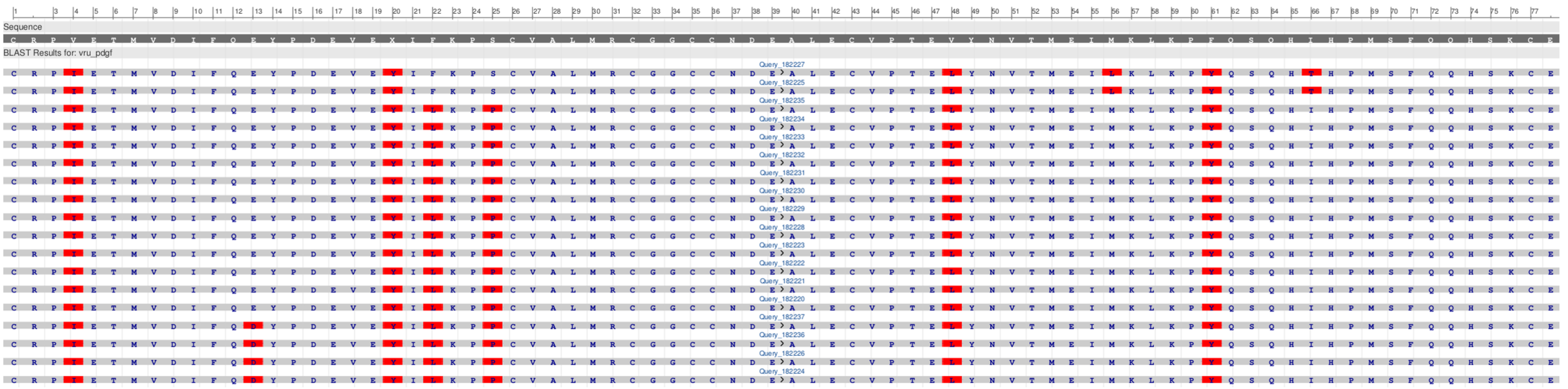


Testudines

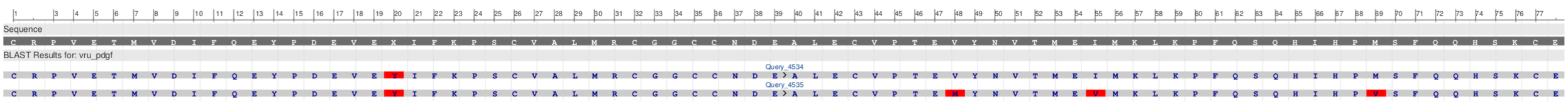


B PDGF domain

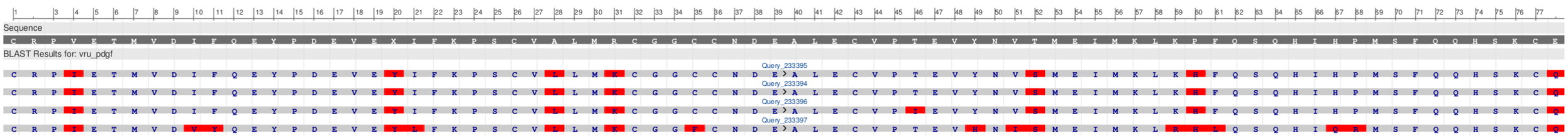
Crotalines



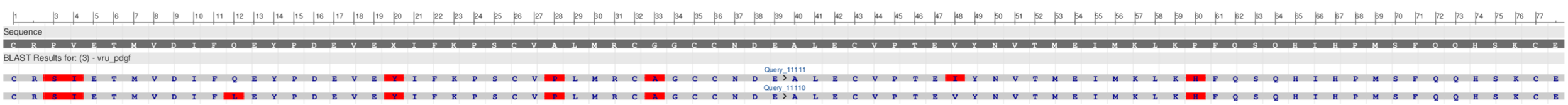
Viperines



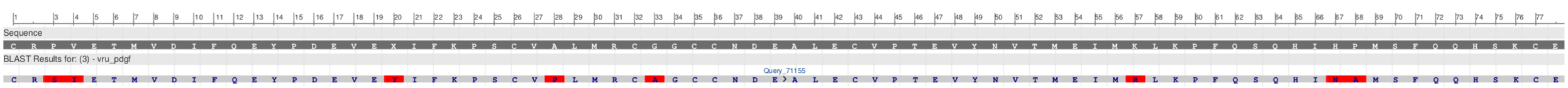
Elapids



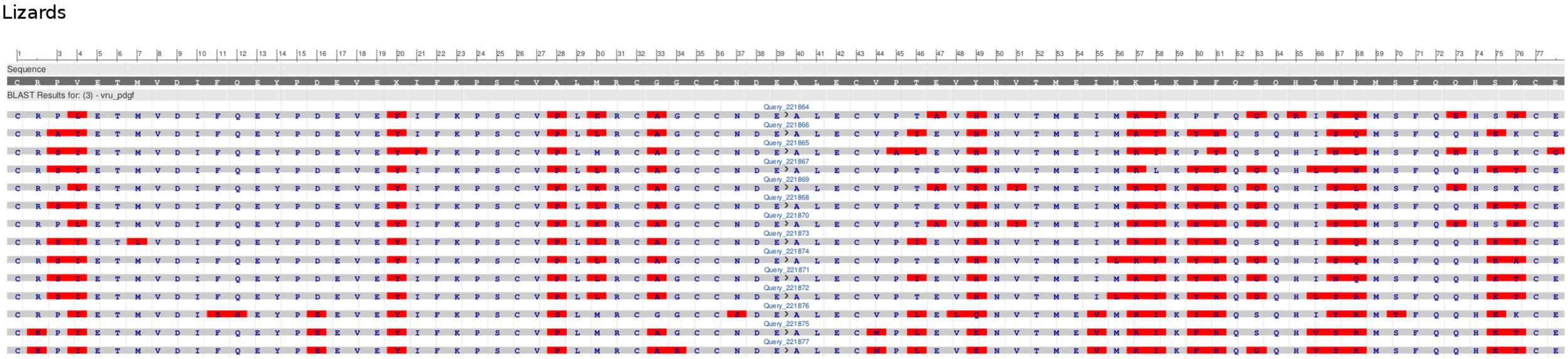
Colubrids



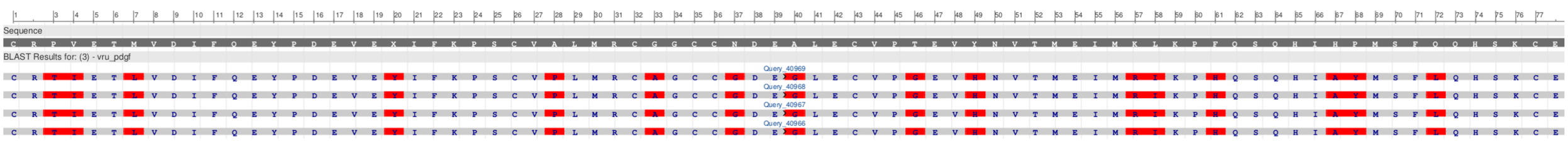
Pythonids



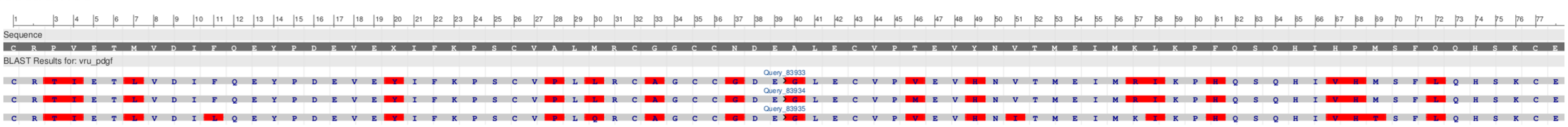
Lizards



Crocodiles



Testudines



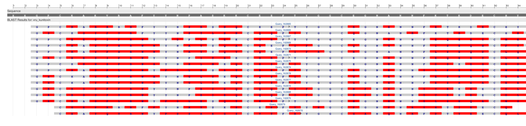
C kunitoxin

Crotalines

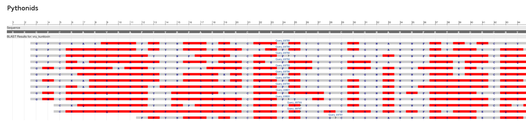
Viperines

Elapids

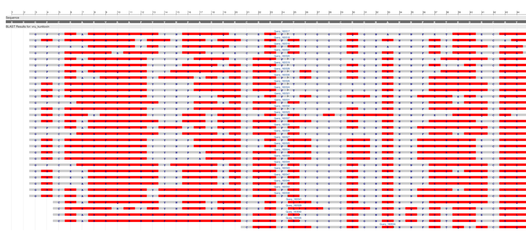
Colubrids



Pythonids



Lizards



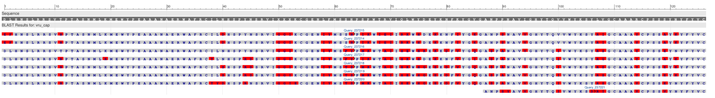
Crocodiles

Testudines

DCAP domain

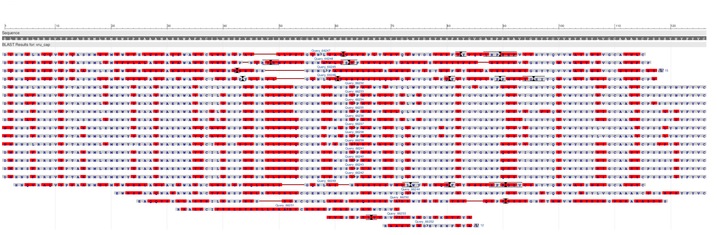
Crotalines

Viperines

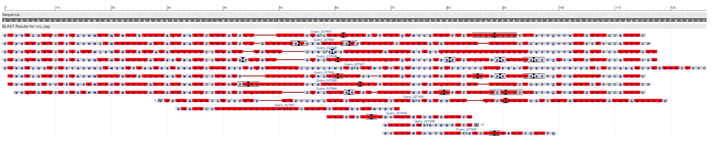


Elapids

Colubrids

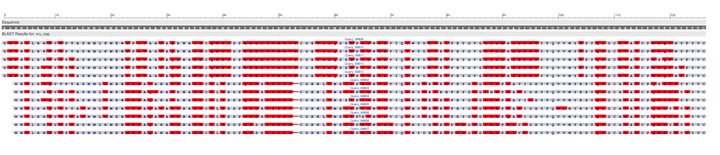


Pythonids

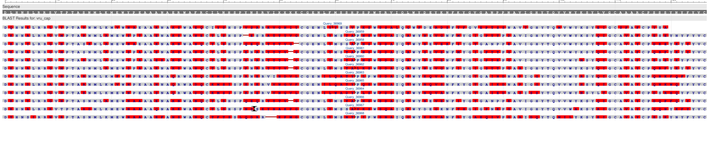


Lizards

Crocodiles



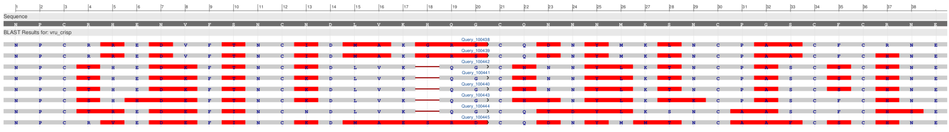
Testudines



E CRISP domain

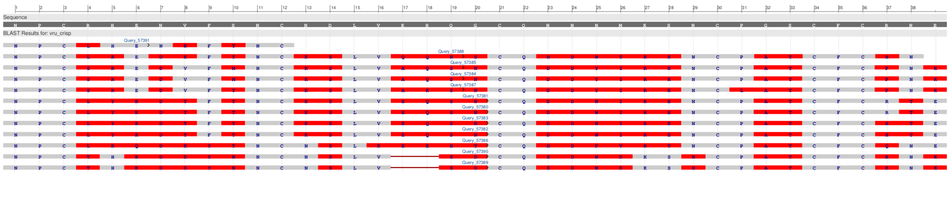
Crotalines

Viperines

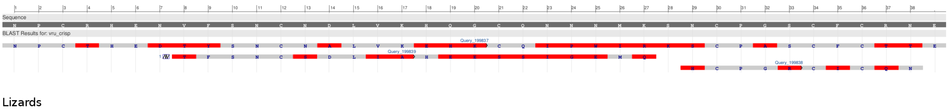


Elapids

Colubrids

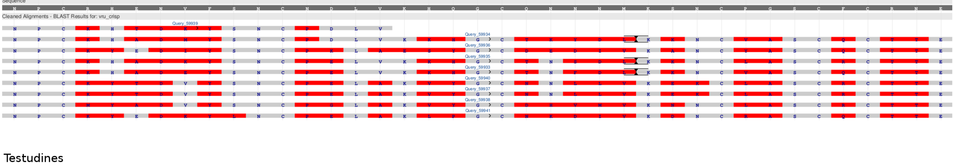


Pythonids



Lizards

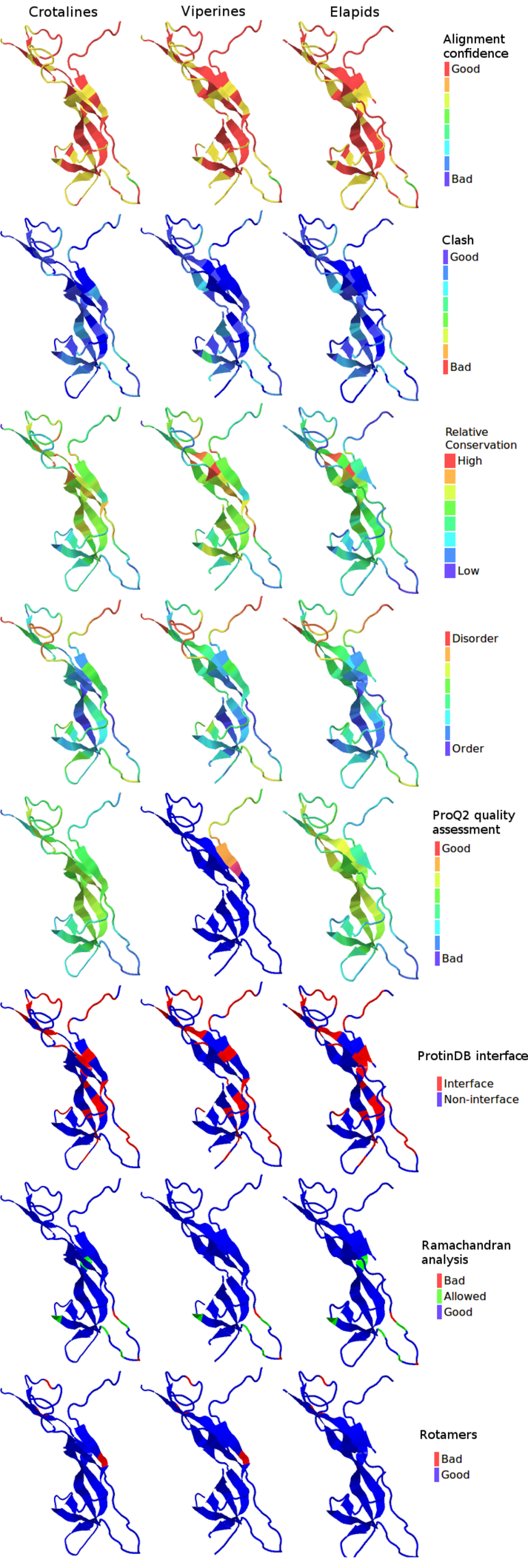
Crocodiles



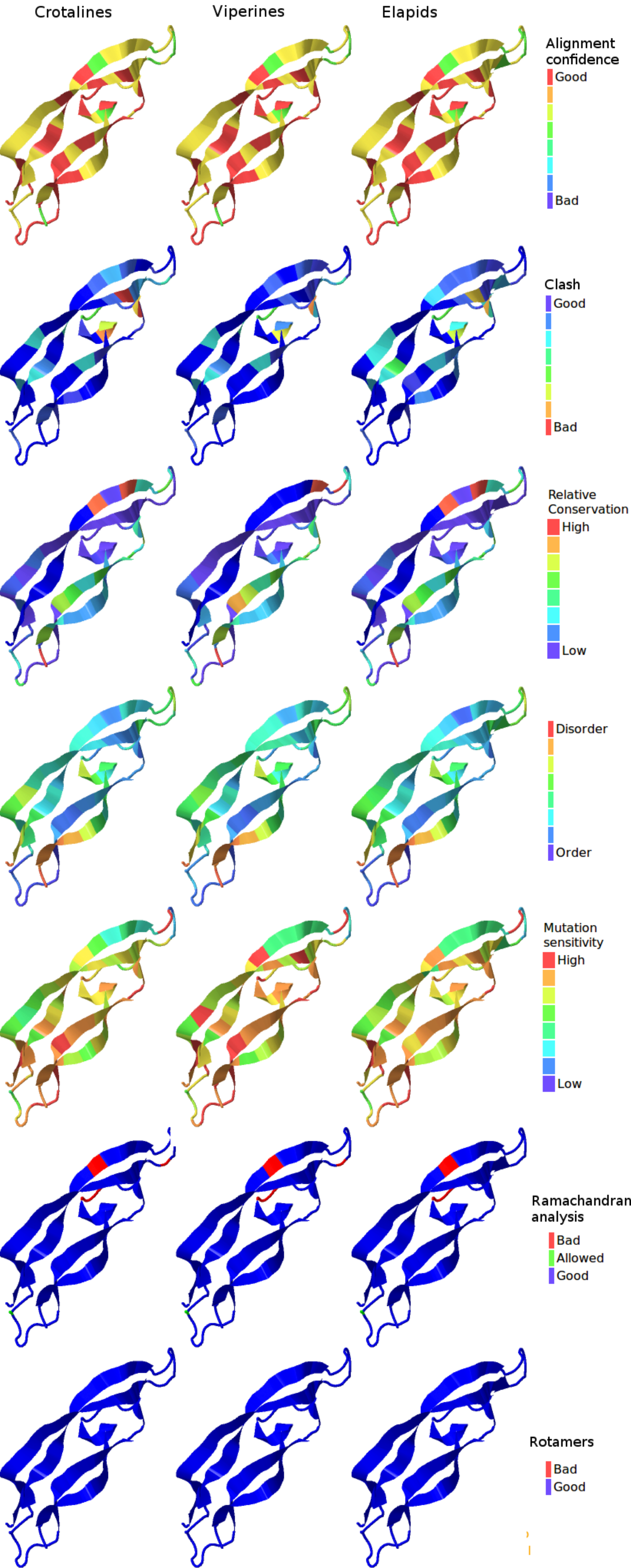
Testudines

Fig. S8: 3D protein structural model quality and function measuring parameter comparison across crotalines (CR), viperines (VP) and elapids in NGF,PDGF, Kunitz BPTI, CAP and CRISP domains. The status of the parameters being investigated using Phyre2 are indicated in the color legends on the side.

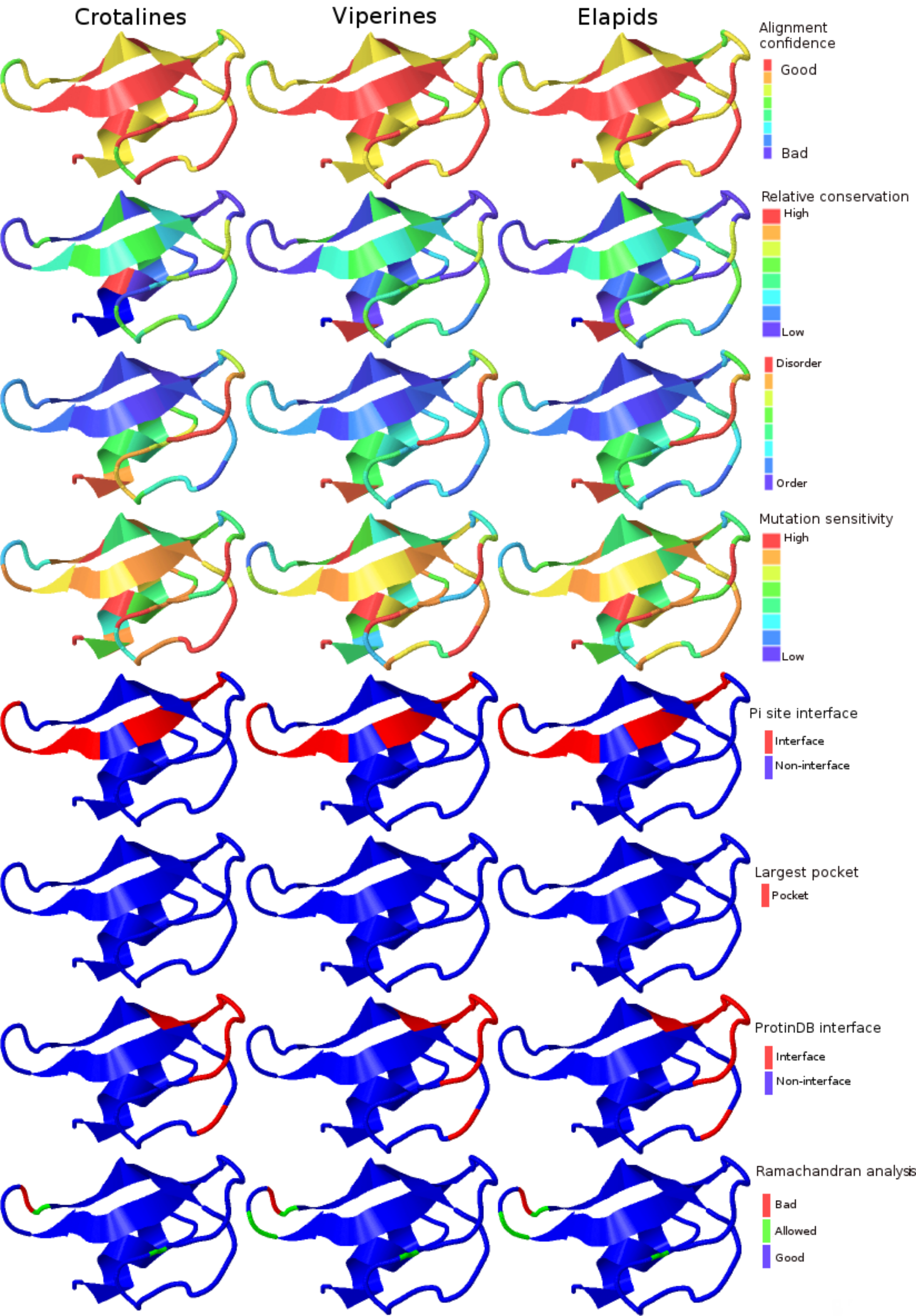
A. *NGF*



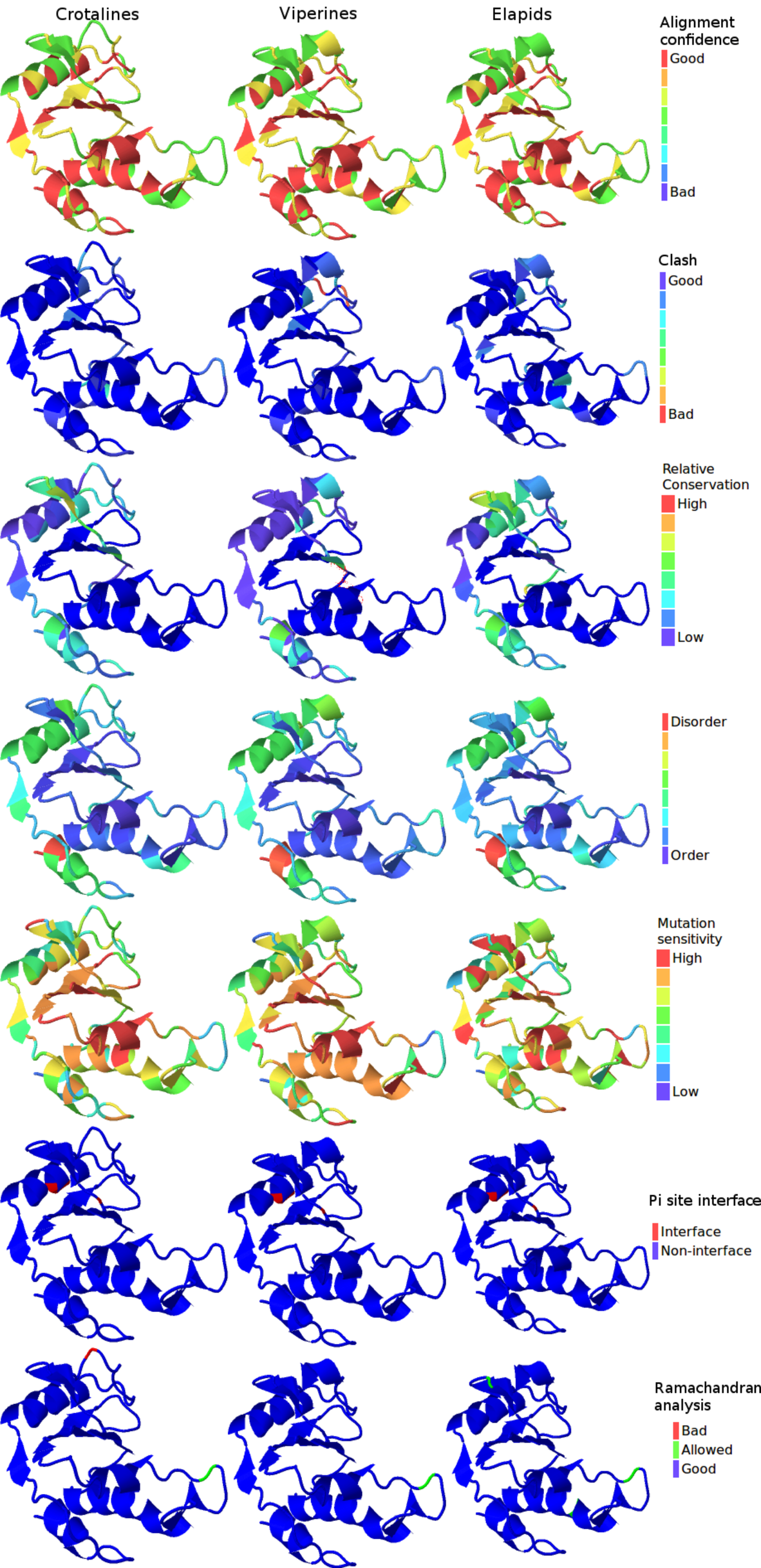
B. PDGF


Crotalines
Viperines
Elapids
Alignment confidence
Good
Bad
Clash
Good
Bad
Relative Conservation
High
Low
Disorder
Order
Mutation sensitivity
High
Low
Ramachandran analysis
Bad
Allowed
Good
Rotamers
Bad
Good

C. kunitoxin


Crotalines
Viperines
Elapids
Alignment confidence
Good
Bad
Relative conservation
High
Low
Disorder
Order
Mutation sensitivity
High
Low
Pi site interface
Interface
Non-interface
Largest pocket
Pocket
ProtinDB interface
Interface
Non-interface
Ramachandran analysis
Bad
Allowed
Good

D. CAP


Crotalines
Viperines
Elapids
Alignment confidence
Good
Bad
Clash
Good
Bad
Relative Conservation
High
Low
Disorder
Order
Mutation sensitivity
High
Low
Pi site interface
Interface
Non-interface
Ramachandran analysis
Bad
Allowed
Good

E. CRISP

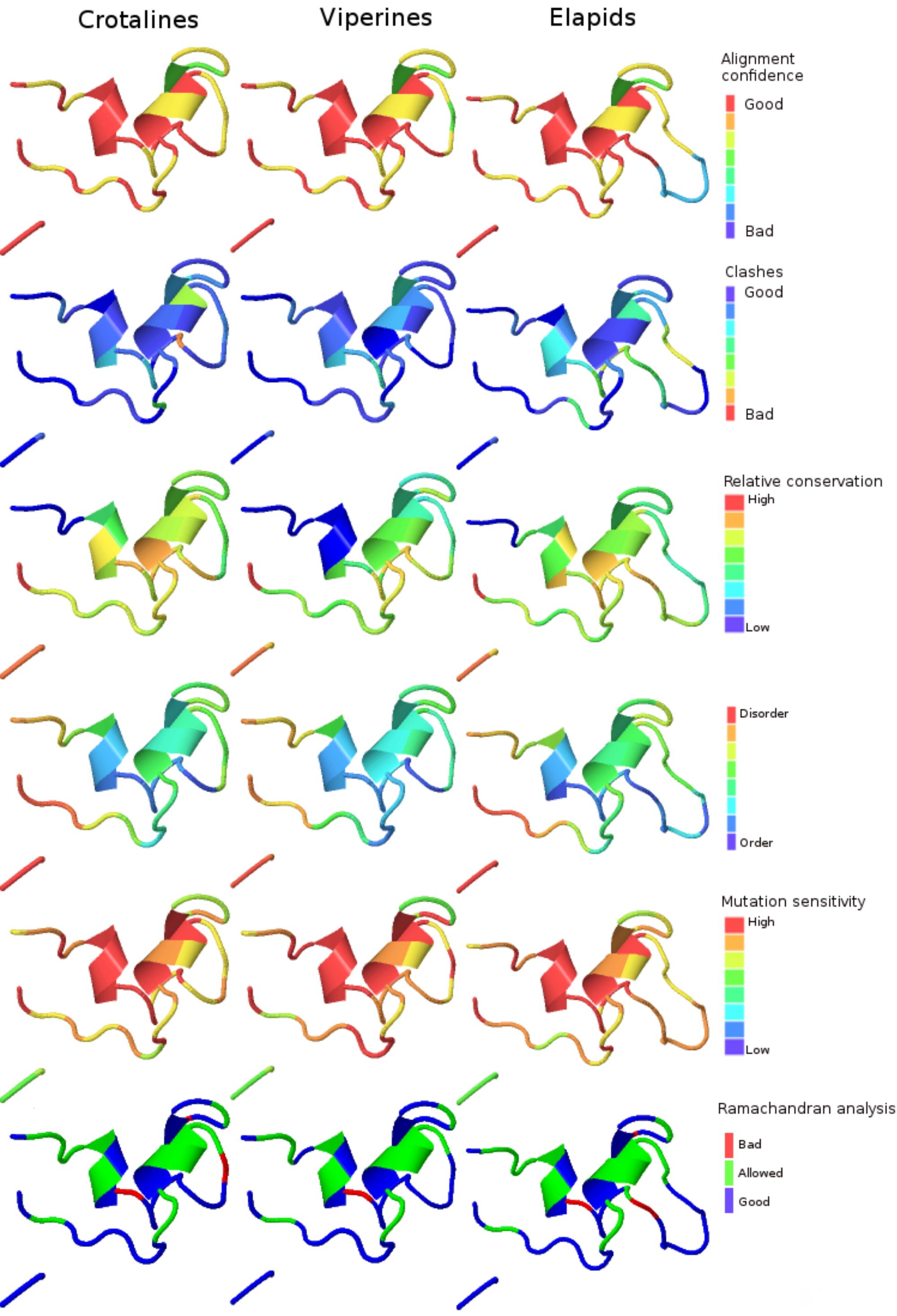
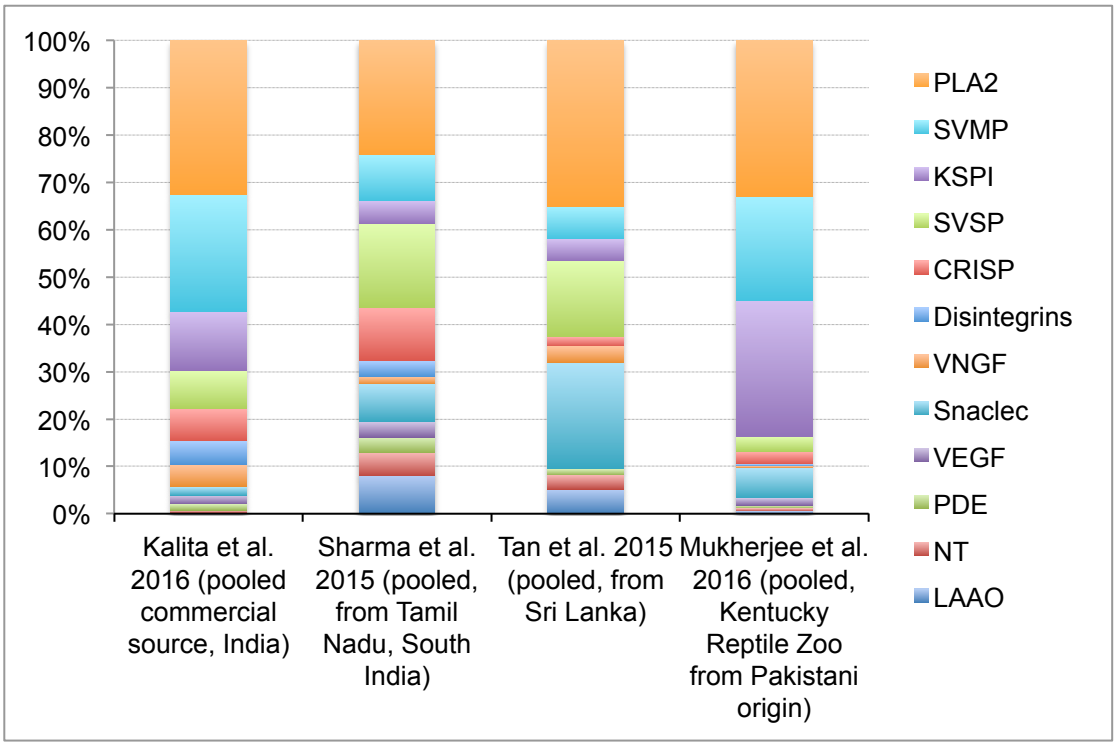

Crotalines
Viperines
Elapids
Alignment confidence
Good
Bad
Clashes
Good
Bad
Relative conservation
High
Low
Disorder
Order
Mutation sensitivity
High
Low
Ramachandran analysis
Bad
Allowed
Good

Fig. S9: A comparative compositional analysis of the major venom proteins in Russell's viper (A). Data from 4 past studies were compiled together for plotting. The actual data is shown in B.

A



B

	Kalita et al. 2016	Sharma et al. 2015	Tan et al. 2015	Mukherjee et al. 2016
LAAO	0.3	7.9	5.2	0.6
NT	0.4	4.8	3	0.6
PDE	1.4	3.2	1.3	0.6
VEGF	1.8	3.2	0	1.5
Snaclec	1.8	7.9	22.4	6.4
VNGF	4.8	1.6	3.5	0.4
Disintegrins	4.9	3.2	0	0.4
CRISP	6.8	11	2	2.6
SVSP	8	17.5	16	3.2
KSPI	12.5	4.8	4.6	28.4
SVMP	24.8	9.5	6.9	21.8
PLA2	32.5	23.8	35	32.8