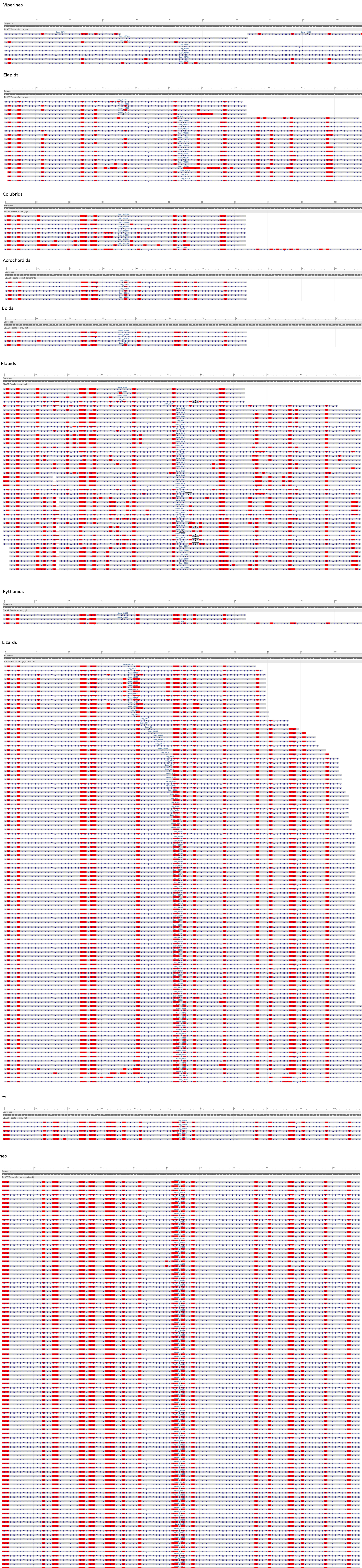


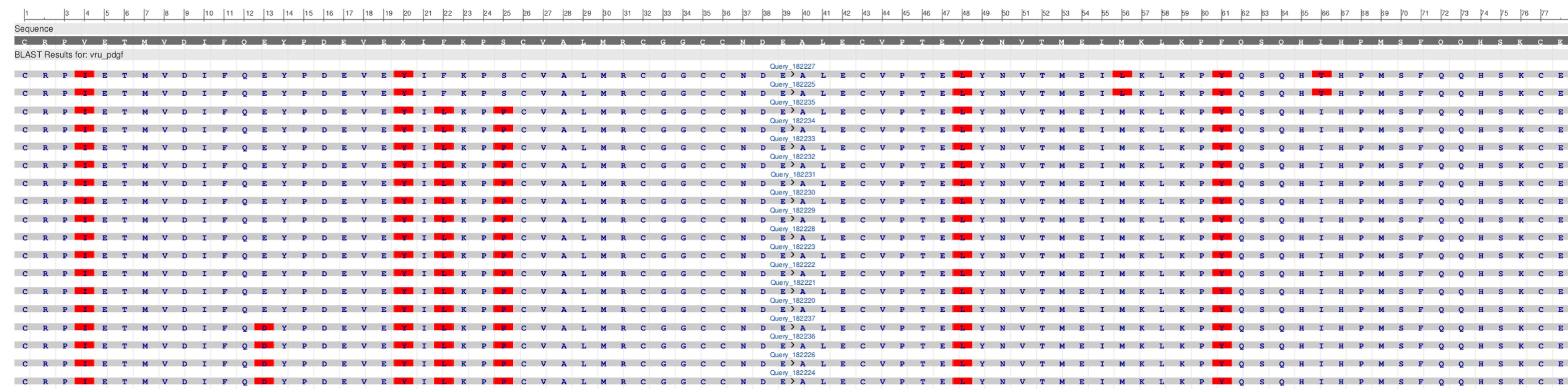
Fig. 37. A larger pool of sequences available from various snakes and other reptile groups (Colubridae, Boidae, Pythonidae, Acrochordidae, Lizards, Crocodiles and Testudines) were compared with the sequence of Russell's viper for putative homologs of NGF, PDGF, Kunitz BPTI, CAP and CRISP domains.

N R G E Y S

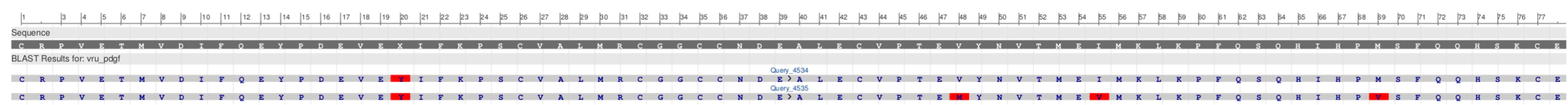


B PDGF domain

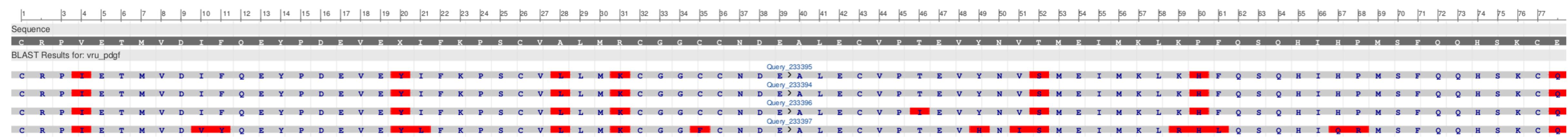
Crotalines



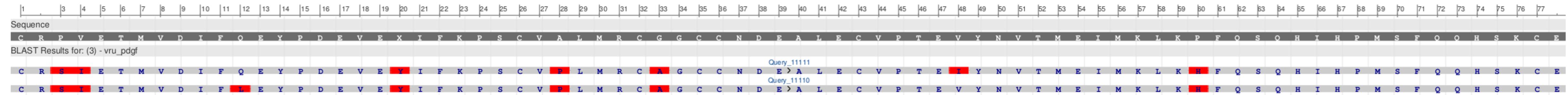
Viperines



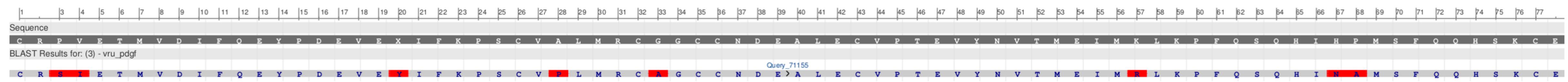
Elapids



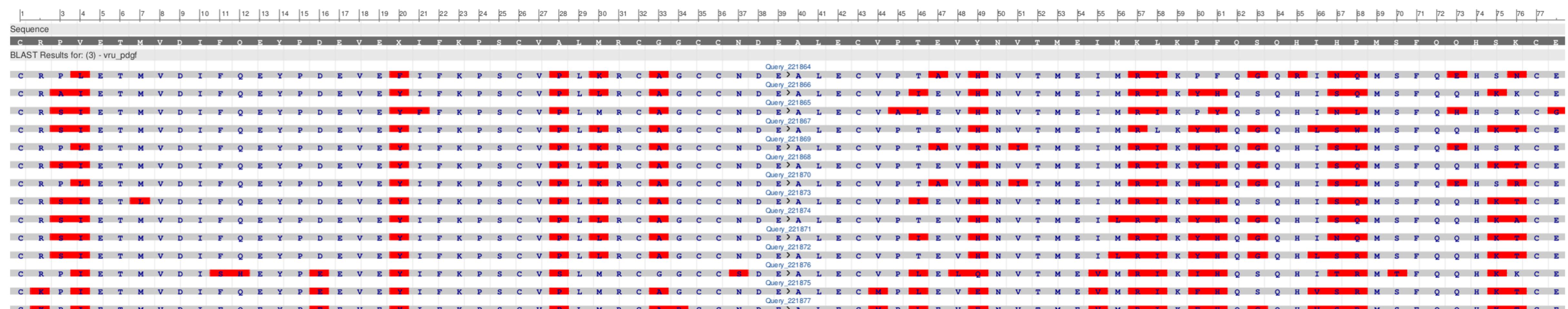
Colubrids



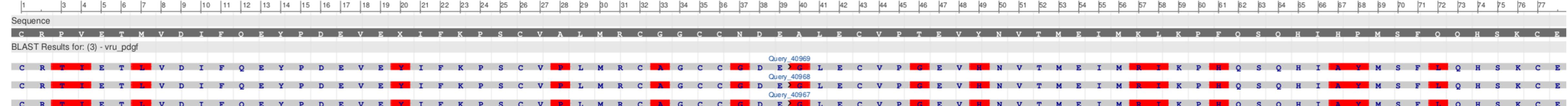
Pythonids



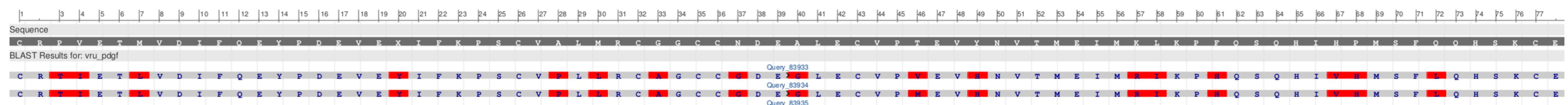
Lizards



Crocodiles



Testudines



C kunitoxin


Crotalines



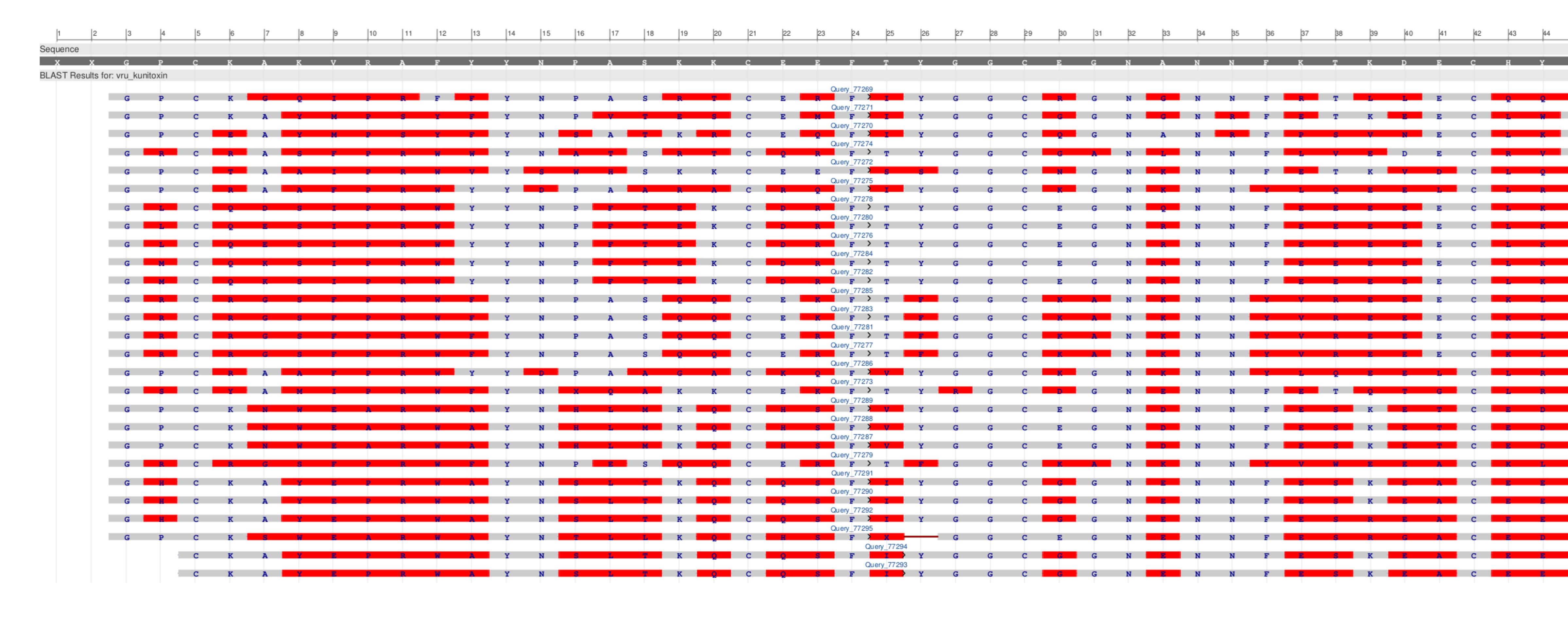
Viperines



Elapids



Colubrids



Pythonids

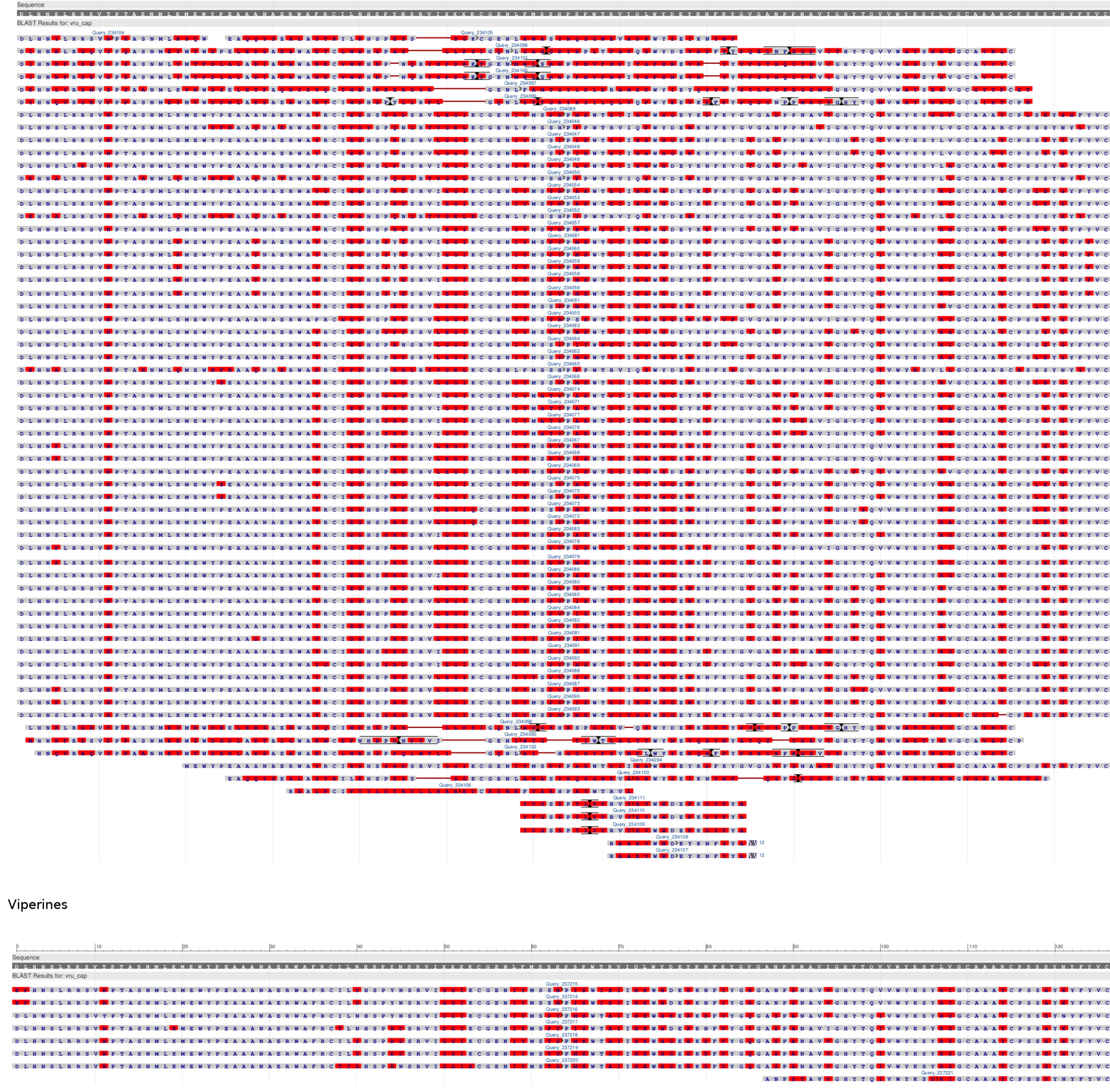
Lizards

Crocodiles

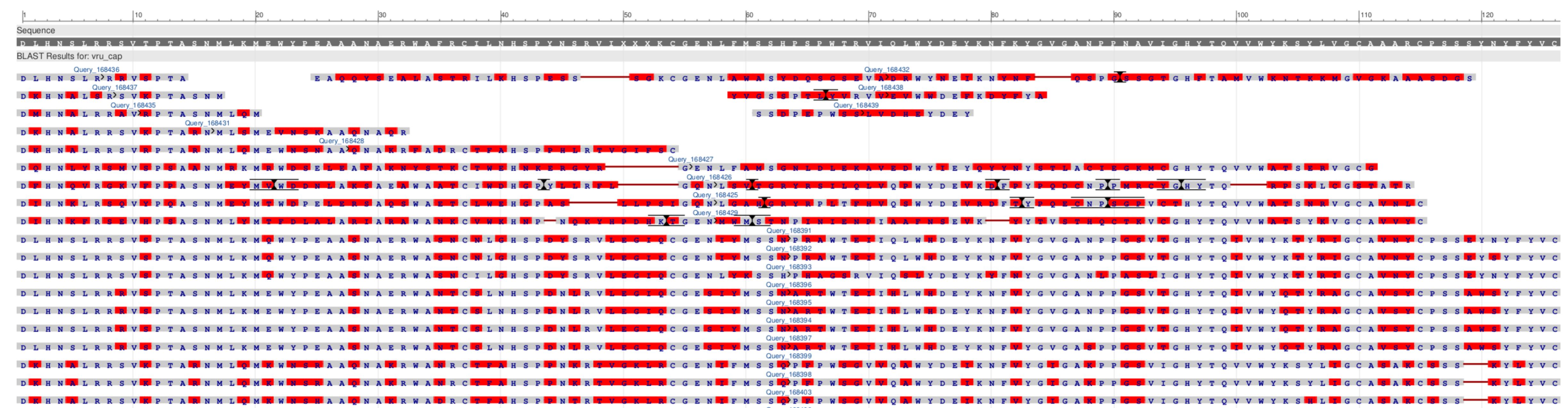
Testudines

DCAP domain

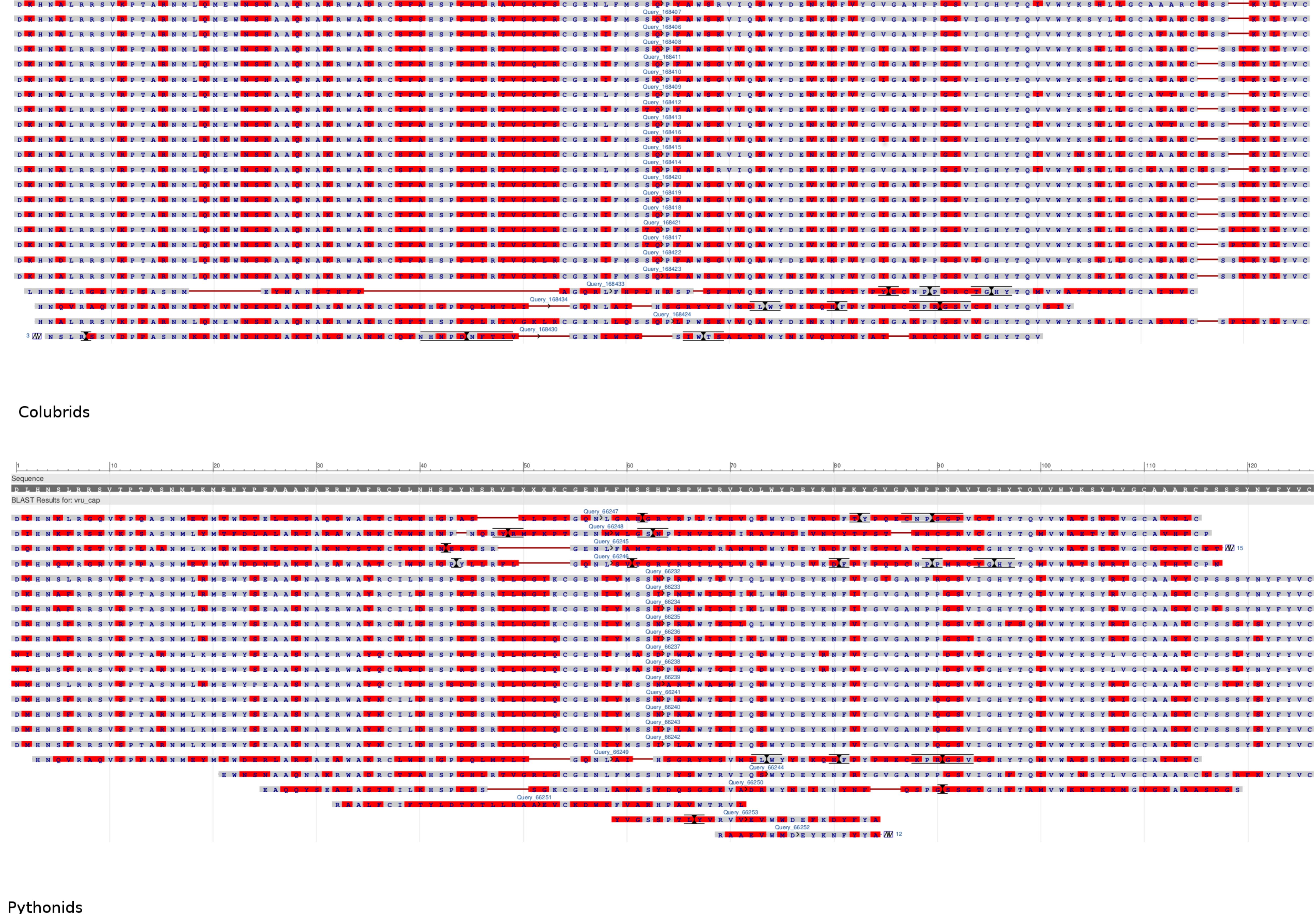
Crotalines



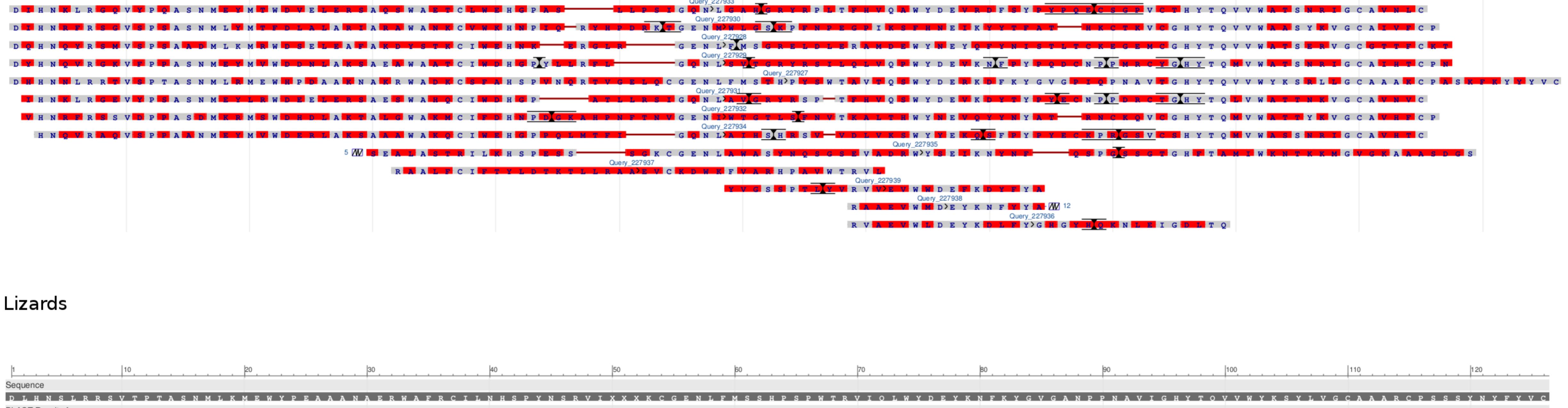
Viperines



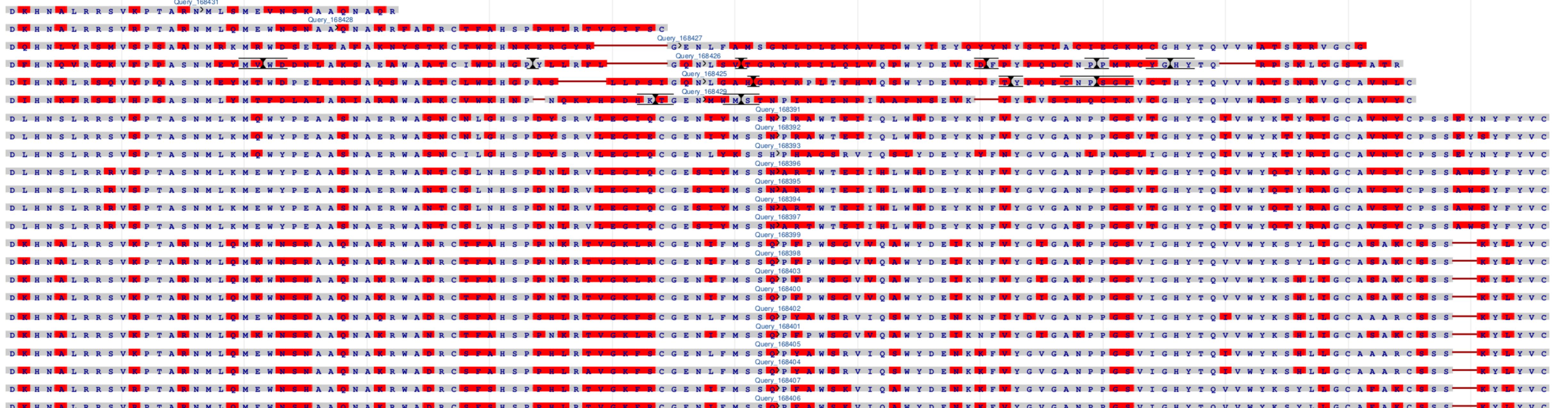
Elapids



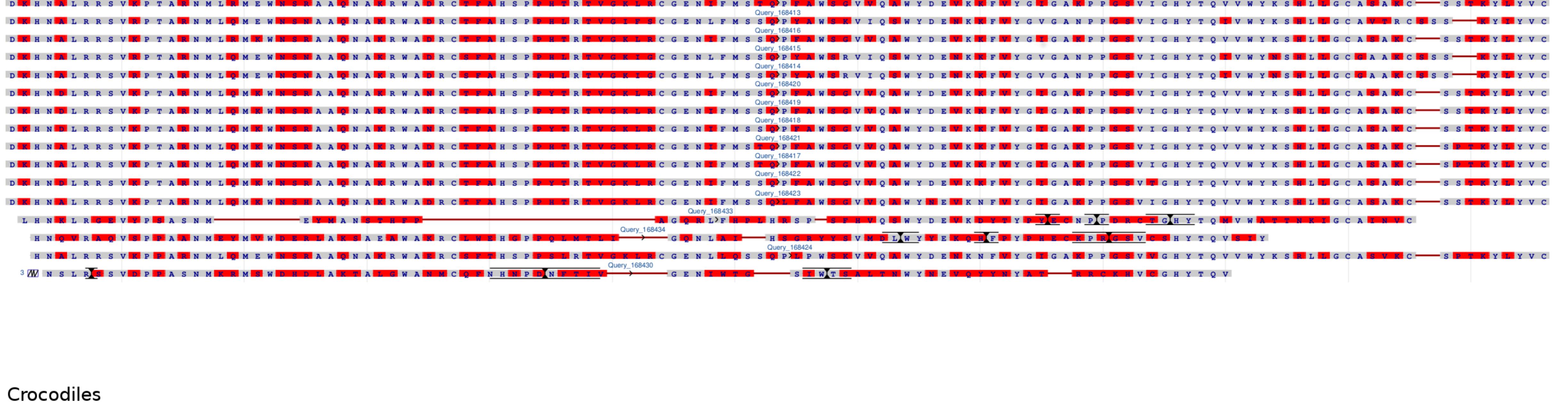
Colubrids



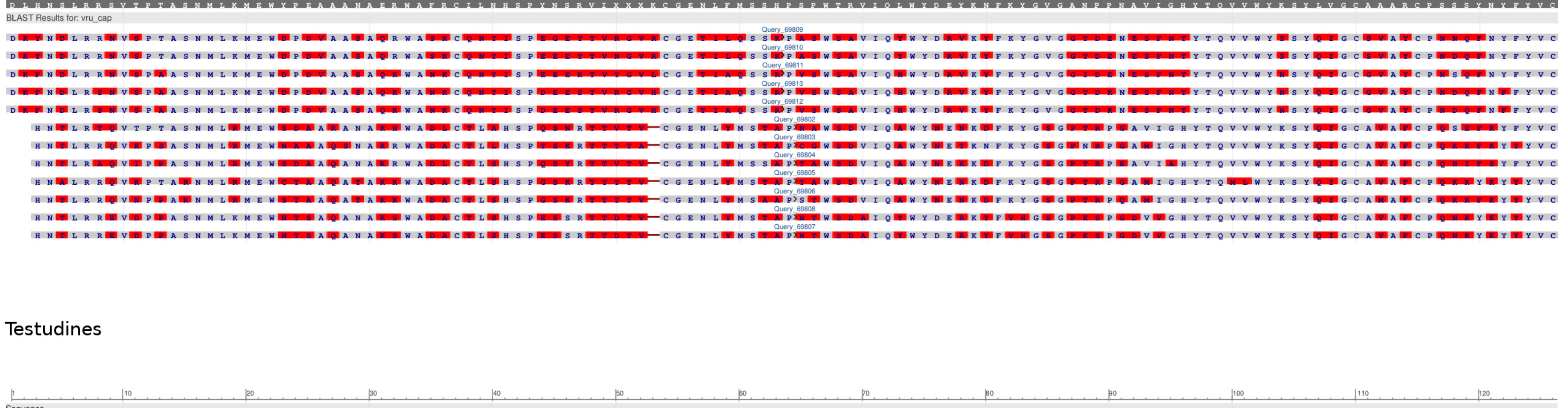
Pythonids



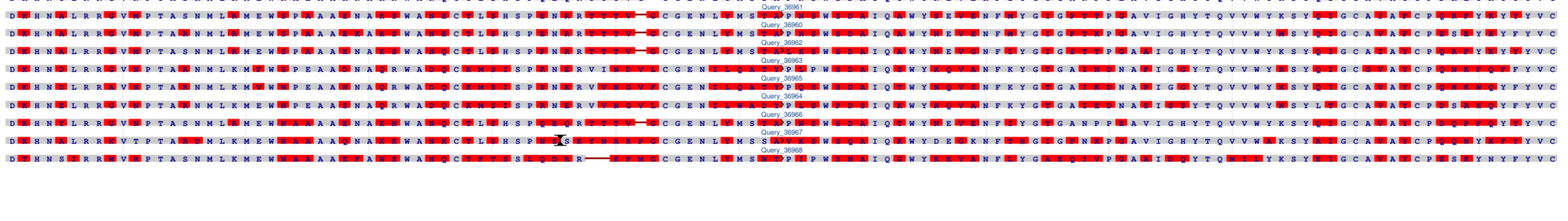
Lizards



Crocodiles



Testudines



E CRISP domain

Crotalines

Sequence

N	P	C	R	H	E	N	V	F	S	N	C	N	D	L	V	K	H	O	G	C	O	N	N	N	M	K	S	N	C	P	G	S	C	F	C	R	N	E	
BLAST Results for: vru_crisp																																							
N	P	C	T	R	E	D	K	Y	T	N	C	R	S	L	V	Q	Q	> A	G	C	Q	D	R	Q	M	Q	S	D	C	P	A	I	C	F	C	Q	N	E	
N	P	C	T	R	E	D	K	Y	T	N	C	K	S	L	V	P	Q	> A	G	C	Q	D	R	Q	M	Q	S	D	C	P	A	I	C	F	C	Q	N	E	
N	P	C	R	H	E	D	V	Y	T	N	C	N	D	L	M	K	Q	L	S	C	Q	N	N	N	M	H	S	N	C	P	A	S	C	F	C	H	N	E	
N	P	C	R	Y	E	N	H	Y	T	N	C	D	S	L	A	Q	H	S	S	C	Q	N	N	N	M	K	S	N	C	P	A	S	C	F	C	H	N	E	
N	P	C	L	K	Y	E	D	R	F	S	N	C	N	D	L	V	K	Q	L	S	C	Q	N	N	N	I	K	S	S	C	P	A	S	C	F	C	H	N	E
N	P	C	R	Q	E	N	K	F	T	N	C	D	S	L	V	R	Q	S	S	C	Q	D	N	Y	M	K	T	N	C	P	A	S	C	F	C	H	N	E	
N	P	C	K	H	I	D	R	Y	T	N	C	D	S	L	V	Q	Q	I	G	> C	Q	N	N	N	M	K	S	D	C	P	A	S	C	F	C	H	N	E	
N	P	C	T	Q	E	N	T	Y	S	N	C	N	S	L	V	Q	Q	S	S	C	Q	D	N	N	M	K	T	K	C	P	A	S	C	F	C	Q	N	K	
N	P	C	T	Q	E	N	T	Y	S	N	C	N	S	L	V	Q	Q	S	S	C	Q	D	N	N	M	K	T	K	C	P	A	S	C	F	C	Q	N	K	
N	P	C	T	Q	E	N	T	Y	S	N	C	N	S	L	V	Q	Q	S	S	C	Q	D	N	N	M	K	T	K	C	P	A	S	C	F	C	Q	N	K	
N	P	C	T	Q	E	D	V	F	T	N	C	N	S	L	V	Q	Q	S	S	C	Q	H	N	Y	I	K	T	N	C	P	A	S	C	F	C	H	N	E	
N	P	C	T	Q	E	N	K	F	T	N	C	N	T	M	V	Q	Q	S	S	C	Q	D	N	Y	M	K	T	N	C	P	A	S	C	F	C	Q	N	K	
N	P	C	T	R	E	N	K	F	T	N	C	N	T	M	V	Q	Q	S	S	C	Q	D	N	Y	M	K	T	N	C	P	A	S	C	F	C	Q	N	K	
N	P	C	T	R	E	N	K	F	T	N	C	N	T	M	V	Q	Q	S	S	C	Q	D	N	Y	M	K	T	N	C	P	A	S	C	F	C	Q	N	K	
N	P	C	T	R	E	N	K	F	T	N	C	N	T	M	V	Q	Q	S	S	C	Q	D	N	Y	M	K	T	N	C	P	A	S	C	F	C	Q	N	K	
N	P	C	T	R	E	N	K	F	T	N	C	D	S	L	V	Q	Q	I	S	C	Q	S	N	N	M	H	T	D	C	P	A	S	C	F	C	H	N	E	
N	P	C	T	R	E	N	K	F	T	N	C	D	S	L	V	Q	Q	K	S	S	Q	D	N	Y	M	K	S	K	C	P	A	S	C	F	C	Q	N	K	
N	P	C	T	R	E	N	K	F	T	N	C	D	S	L	V	Q	Q	K	S	S	Q	D	N	Y	M	K	S	K	C	P	A	S	C	F	C	Q	N	K	
N	P	C	T	R	E	N	K	F	T	N	C	D	S	L	V	Q	Q	K	S	S	Q	D	N	Y	M	K	S	K	C	P	A	S	C	F	C	Q	N	K	
N	P	C	R	R	E	N	D	F	T	N	C	D	S	L	V	Q	Q	S	S	C	Q	D	N	Y	M	K	T	N	C	P	A	S	C	F	C	H	N	E	
N	P	C	T	E	E	N	M	F	T	N	C	D	S	M	V	Q	Q	K	R	S	C	Q	D	N	Y	I	K	S	K	C	P	A	S	C	F	C	Q	N	K
N	P	C	T	E	E	N	M	F	T	N	C	D	S	M	I	Q	K	R	S	C	Q	D	N	Y	I	K	S	K	C	P	A	S	C	F	C	Q	N	K	
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N	P	C	T	R	E	D	T	F	T	N	C	D	S	M	V	Q	Q	L	S	G	C	Q	D	R	Q	M	Q	S	E	C	P	A	T	C	F	C	Q	N	K
N	P	C	T	K	E	D	K	Y	T	N	C	K	S	L	V	Q	Q	Q	A	G	C	Q	D	K	Q	M	Q	S	D	C	P	A	I	C	F	C	Q	N	K
N	P	C	T	K	E	D	K	Y	T	N	C	K	S	L	V	Q	Q	Q	A	G	C	Q	D	K	Q	M	Q	S	D	C	P	A	I	C	F	C	Q	N	K
N	P	C	T	E	E	N	K	F	I	N	C	N	S	M	V	Q	Q	K	S	S	C	Q	D	N	Y	I	K	S	I	C	P	A	S	C	F	C	Q	N	K
N	P	C	T	V	E	N	K	Y	T	N	C	N	S	L	V	Q	Q	S	S	C	Q	D	E	E	I	Q	S	D	C	P	A	T	C	F	C	Q	N	K	
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N	P	C	T	K	E	D	K	Y	T	N	C	K	S	L	V	Q	Q	A	G	C	Q	D	K	Q	M	Q	S	D	C	S	A	T	C	F	C	Q	N	K	
N	P	C	T	K	E	D	K	Y	T	N	C	K	S	L	V	Q	Q	A	G	C	Q	D	R	Q	M	Q	S	D	C	S	A	T	C	F	C	Q	N	K	
N	P	C	T	K	E	D	K	Y	T	N	C	K	S	L	V	Q	Q	A	G	C	Q	D	R	Q	M	Q	S	D	C	S	A	T	C	F	C	Q	N	K	
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N	P	C	T	K	E	D	K	Y	T	N	C	K	S	L	V	Q	Q	A	G	C	Q	D	R	Q	M	Q	S	D	C	S	A	I	C	F	C	Q	N	K	
N	P	C																																					

N P

Elapids

The figure displays a sequence alignment of Elapids. The top row shows the sequence with positions numbered 1 to 38. The second row shows the sequence with amino acid residues: N P C R H E N V F S N C N D L V K H Q G C Q N N M K S N C P G S C F C R N E. The third row is labeled "BLAST Results for: vru_crisp". Below it, seven horizontal rows represent different BLAST queries, each aligned with the sequence above. The queries are: Query_110308, Query_110310, Query_110309, Query_110313, Query_110324, Query_110316, and Query_110316 again. Each query row shows a red-highlighted segment corresponding to the alignment. The labels for the queries are placed to the right of their respective rows.

N P
N P
N P

Colubrids

Sequence

N	P	C	R	H	E	N	V	F	S	N	C	N	D	L	V	K	H	O	G	C	O	N	N	M	K	S	N	C	P	G	S	C	F	C	R	N	E
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---

BLAST Results for: vru_crisp

Query_57391

Query_57388

Query_57385

Query_57384

Query_57387

Query_57381

Query_57380

Query_57383

N P

Pythonids

The figure displays sequence alignments between Pythonids and Lizards. The top part shows the Pythonid sequence from position 1 to 38, with gaps indicated by vertical lines. The bottom part shows the Lizard sequence from position 1 to 38, also with gaps. Three red horizontal bars represent BLAST results for vru_crisp, Query_199837, Query_199839, and Query_199838. The first bar (vru_crisp) covers positions 4-38. The second bar (Query_199837) covers positions 10-38. The third bar (Query_199839) covers positions 1-38. The fourth bar (Query_199838) covers positions 28-38. Red boxes highlight specific matches between the Pythonid and Lizard sequences.

Sequence

BLAST Results for: vru_crisp

Query_199837

Query_199839

Query_199838

Lizards

N P C

N A C P Y K N V Y S E C E K M K N L F S > C E S N V M V D N C Q A L C R C P D Q
 Query_112350
 N S C K Y A D R I T D C D V L L G M S S > C S E E L M K T N C K A T C T C K T E
 Query_112349
 N P C P G E D K I S N C L S L K K K H P > C T N P L L Q E M C P A S C H C E N K
 Query_112341
 N P C K Y R D R Q L N C A D T I R E Y G > C E Q D W V Q K D C K A S C E C Q T E
 Query_112342
 N P C K Q E D E F S N C V Q L K E I H T > C E H P F I K E N C P G C C Q C T T E
 Query_112334
 N P C K H M D Q Y G N C N D L A K M S G > C K D A K I M K Y C P A S C L C T T E
 Query_112331
 N P C L H N N Q Y S N C D P L T K Q W G > C N H P D L K E E C K A S C K C T T E
 Query_112332
 N P C K H N N I Y S N C P D L A R S H G > C D H P D V K E W C K A S C Q C K T E
 Query_112329
 N P C K H D D K Y S N C G S L A R Q P G > C S H G N M M E D C A A S C L C K T E
 Query_112328
 N P C P Q E D L L S N C A N L K K A H S > C E H P V M K Q N C R A S C L C V S E
 Query_112333
 N P C A Y N D D Y T S C P D L T K Q V G > C E H P V M K Q N C R A S C L C V S E
 Query_112344
 N P C N Y D D N Y T S C P D L T K Q V G > C E H P V M K Q N C R A S C L C V S E
 Query_112348
 N P C N Y D D N Y T S C P D L T K Q V G > C D T S I M V F H C E N K C T T E
 Query_112349

N P
N P
N P

Crocodiles

Sequence

N	P	C	R	H	E	N	V	F	S	N	C	N	D	L	V	K	H	Q	G	C	O	N	N	M	K	S	N	C	P	G	S	C	F	C	R	N	E
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---

Cleaned Alignments - BLAST Results for: vru_crisp

Query_59939

Sequence

N	P	C	K	H	T	D	K	>	Y	S	N	C	P	D	L	V	K	K	H	G	C	T	K	Y	D	L	K	K	N	C	V	A	S	C	Q	C	T	T	E
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---

BLAST Results for: vru_crisp

Query_207175

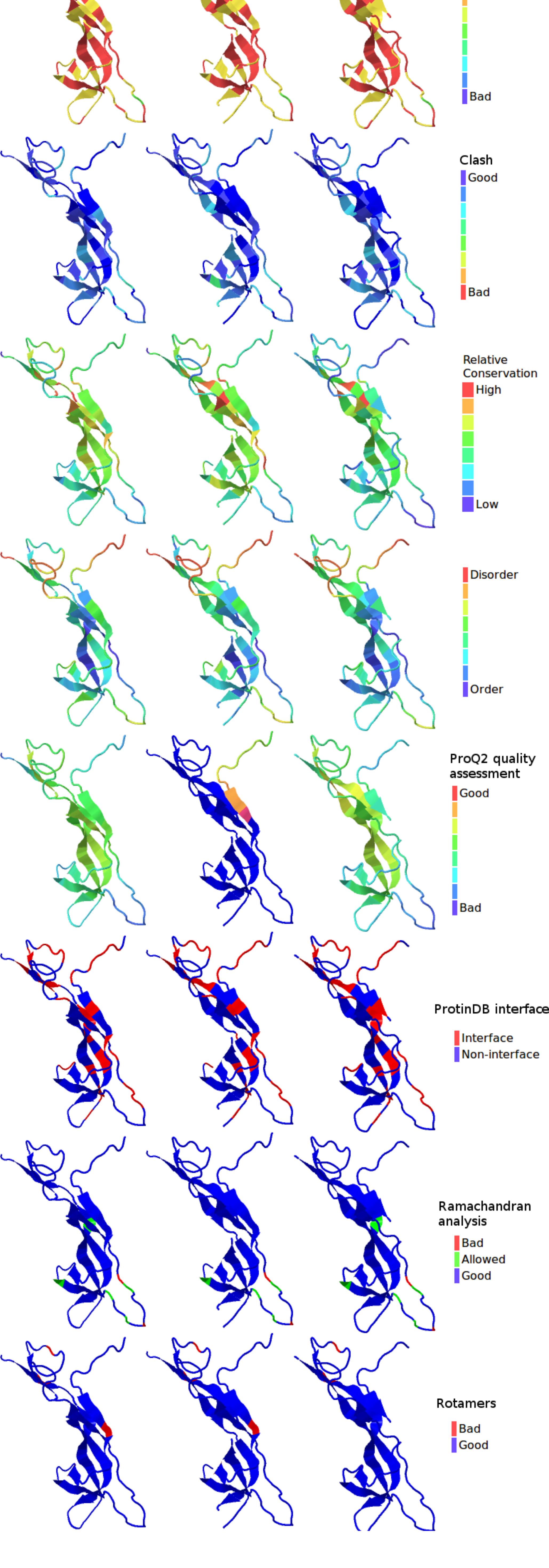
Sequence

N	P	C	K	Y	E	D	T	Y	A	N	C	G	Q	L	K	K	>	Q	Y	T	C	R	N	A	T	T	K	S	S	I	S	K	E	C	L	C	R	C	N	T	E
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---

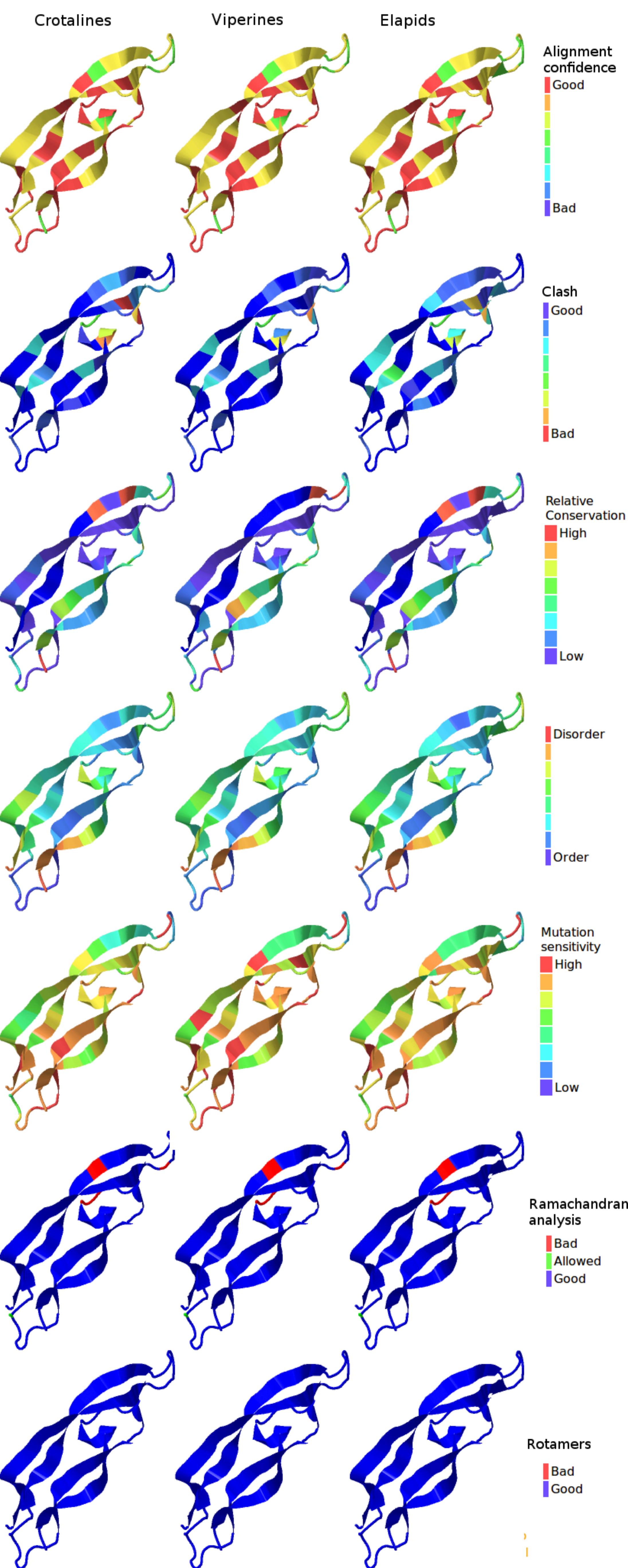
N P C
N P C
N P C

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.

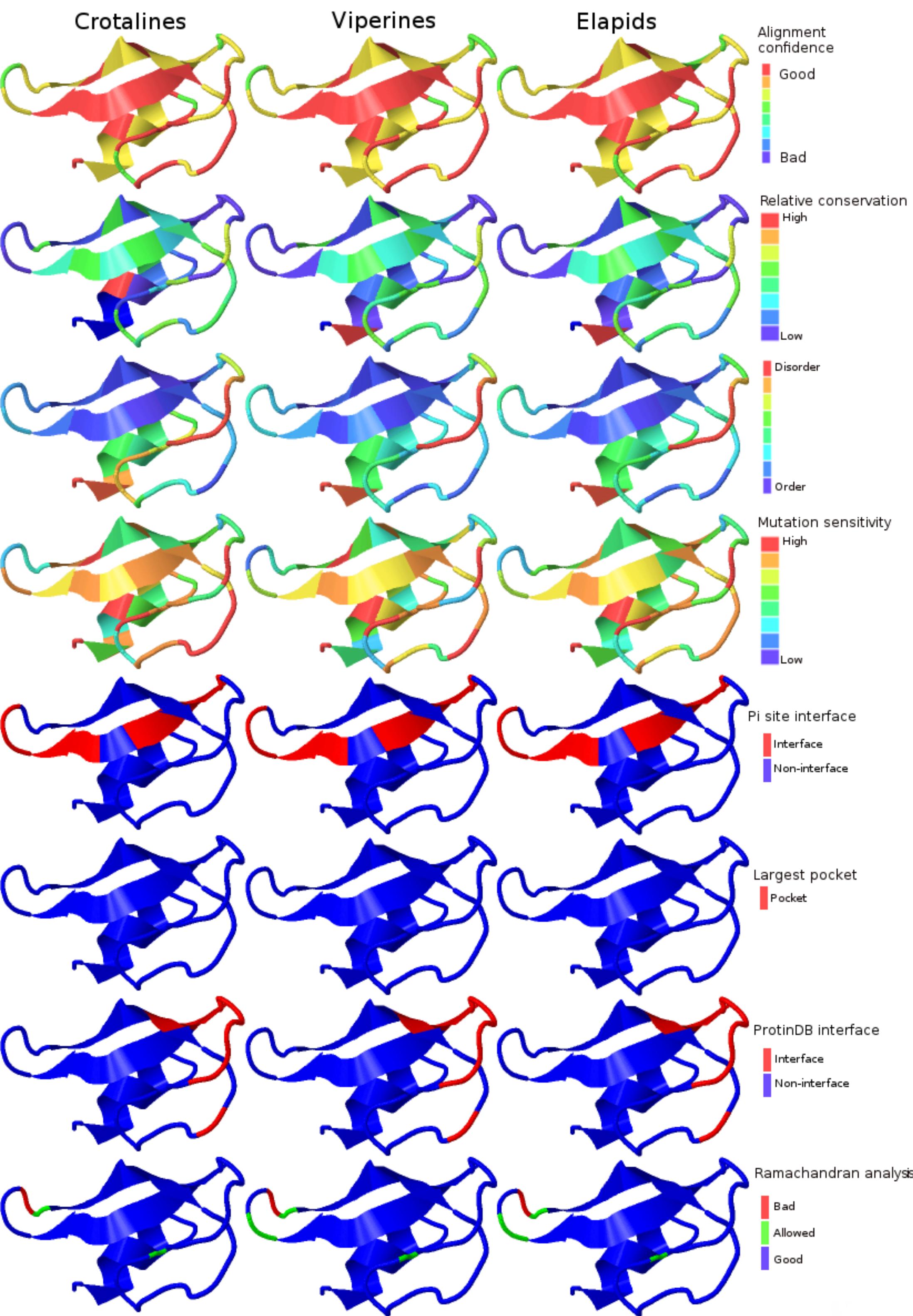
A. NGF



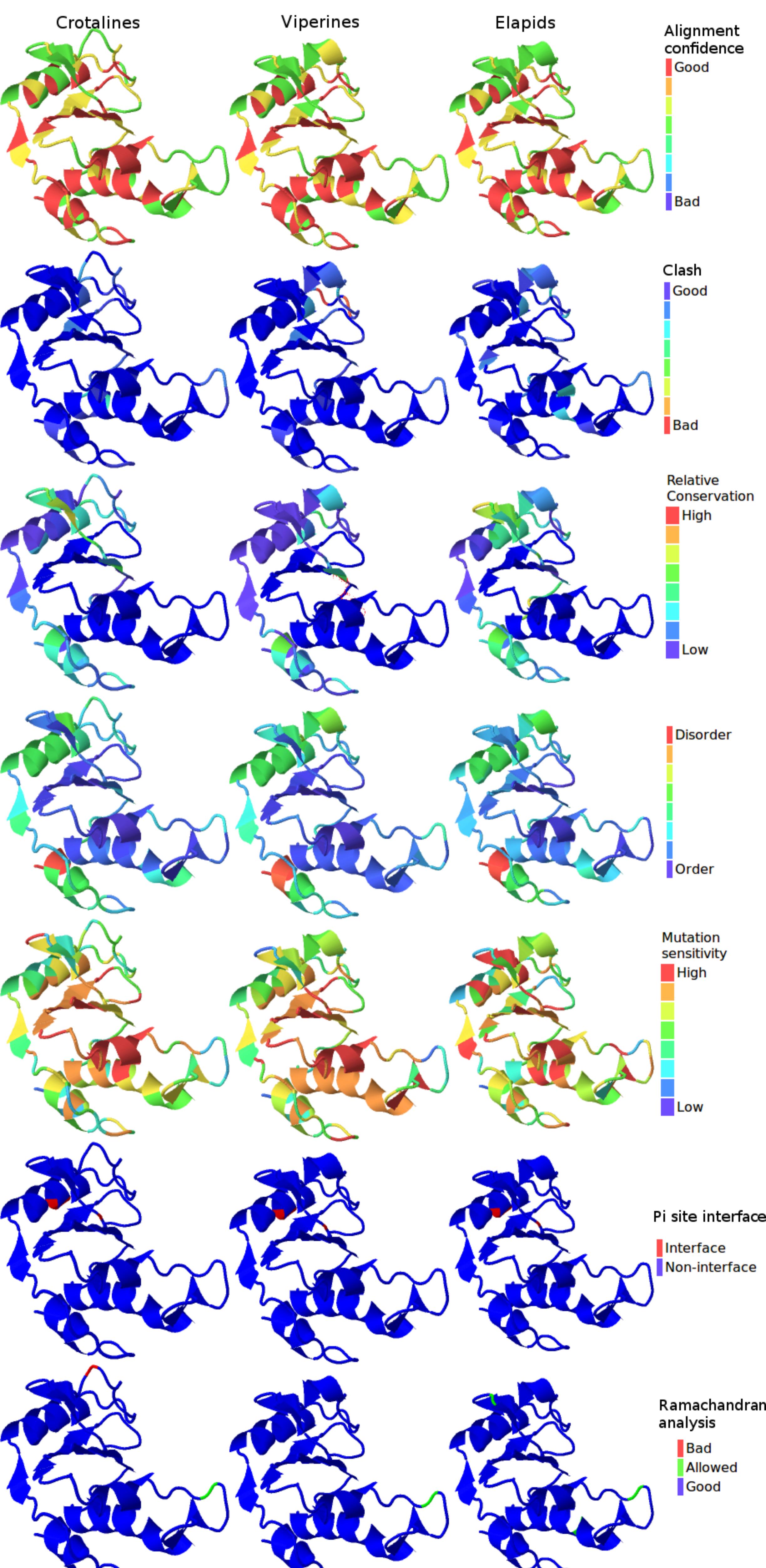
B. PDGF



C. kunitoxin



D. CAP



E. CRISP

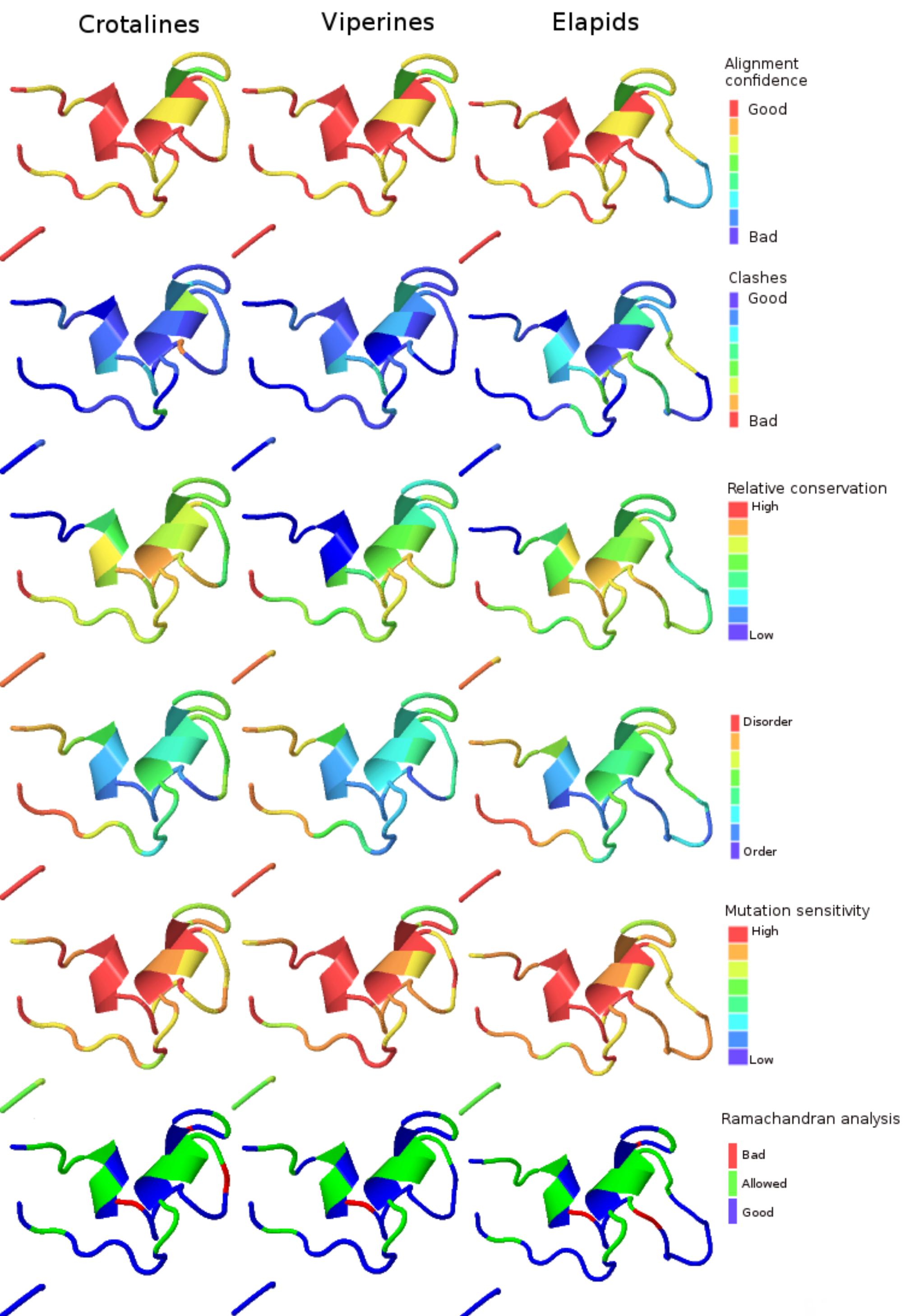
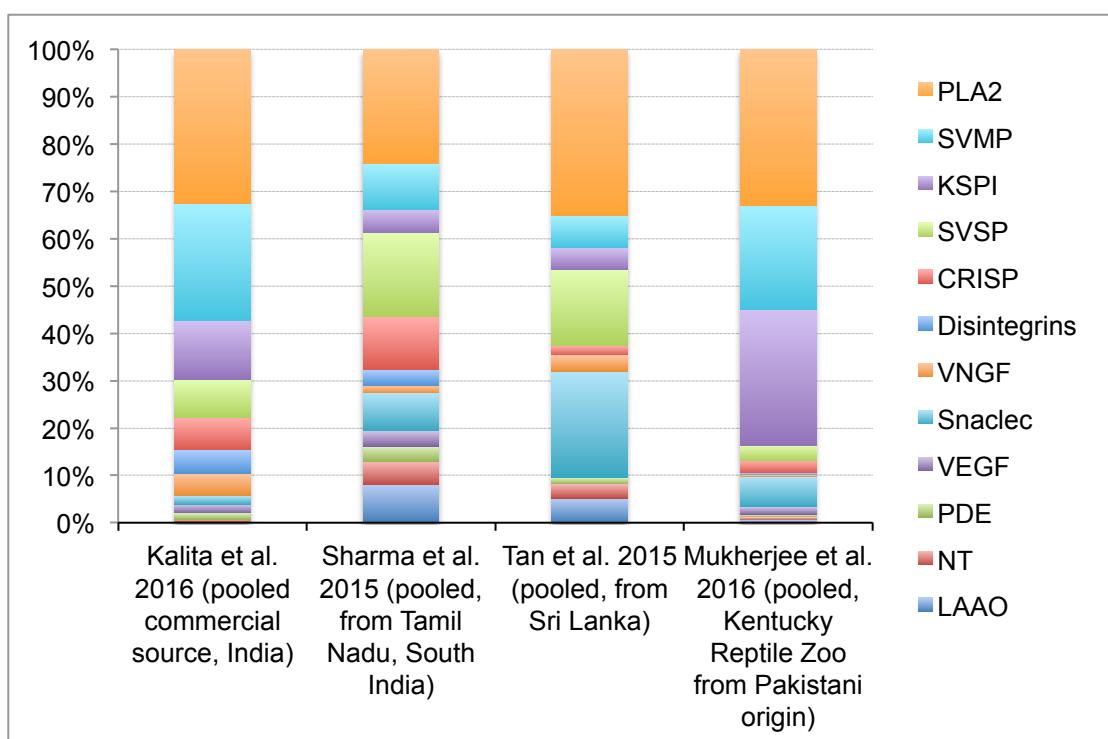


Fig. S9: A comparative compositional analysis of the major venom proteins in Russell's viper (A). Data from 4 past studies were compiled together for plotting. The actual data is shown in B.

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