c l e i n f o

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a b s t r a c t

The snake venom may be considered as a potent source of untapped therapeutic proteins and peptides. The peptide mass “ngerprinting and N-terminal sequence alignment of a 6.9 kDa peptide named Rusvikunin from Daboia russelii russelii venom show the presence of putative conserved domains of the KU superfamily. Further, BLASTanalysis of two of the de novo peptide sequences of Rusvikunin demonstrates signi“cant sequence homology with serine proteases reported in the NCBI database. Rusvikunin possesses conserved

(5 mol/l trypsin or Russelobin; 0.5 mol/l plasmin, thrombin or t-PA; 0.15 mol/l FXa) was pre-incubated with

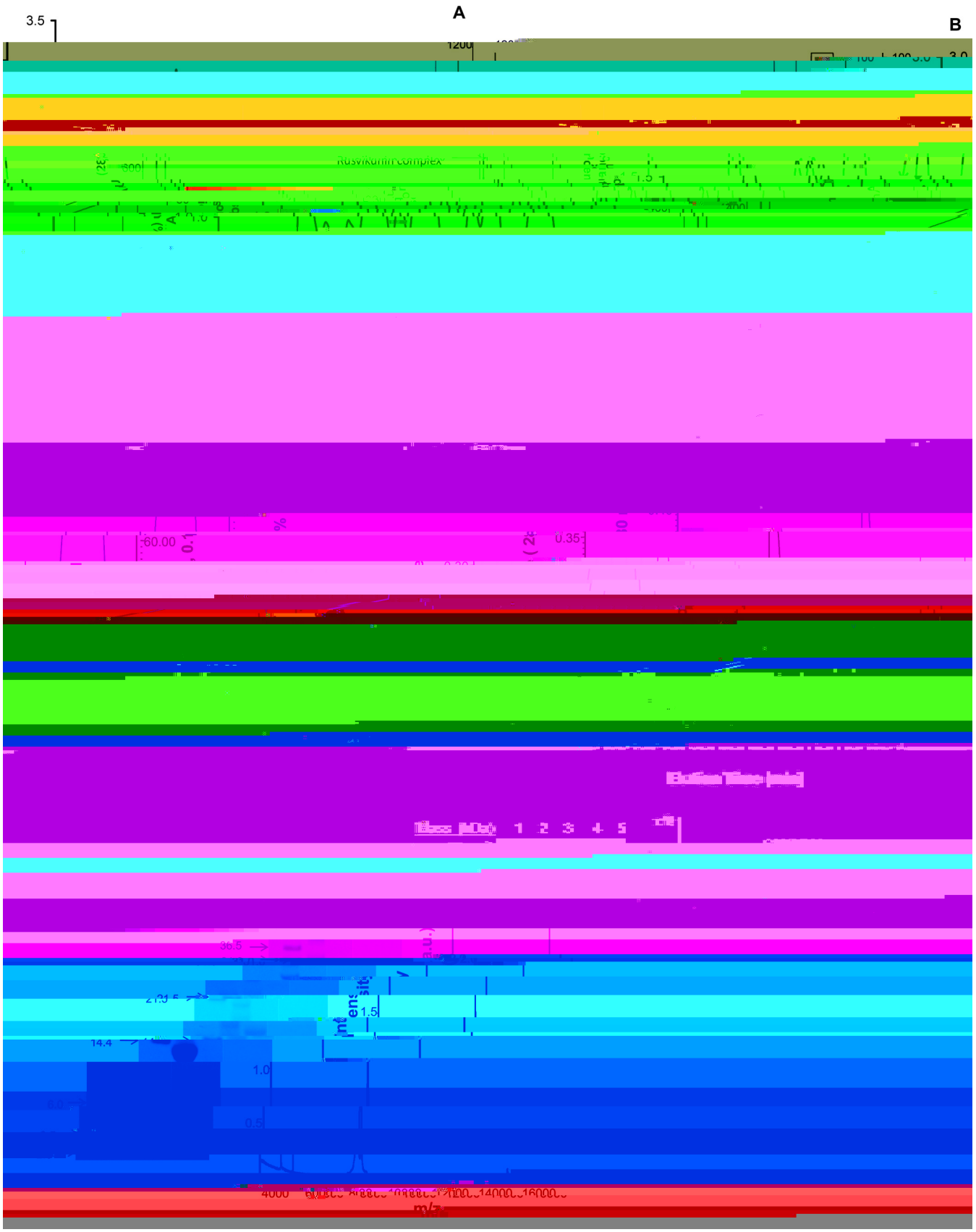
A
B
3.5
1200
Rusvikunin complex
60.00
0.35
1 2 3 4 5
36.5
21.5
14.4
1.5
1.0
0.5
4000
m/z

Fig. 1. (A)

Table 1
Multiple sequence alignment of N-terminal sequence of RP-44 with other known protease inhibitors from snake venom. *Sequence of mature peptide.

Accession/Reference	Description	Species	N-terminal sequence	Residues
This work	Rusvikunin	Daboia russelii russelii	HDRPTFCNLAPESGR	1…15
P00990.1	Venom basic protease inhibitor II	D. russelii siamensis	HDRPTFCNLAPESGR	1…15
Q2ES50.1	Kunitz protease inhibitor 1	D. russelii russelli	HDRPTFCNLAPESGR	1…15
AFE83617.1	Kunitz-type protease inhibitor	D. russelii russelii	HDRPTFCNLAPESGR	1…15*
AFB74192.1	Protease inhibitor	D. russelii russelii	HDRPTFCNLAPESGR	1…15*
A8Y7P4.1	Trypsin inhibitor B4	Daboia russelii siamensis