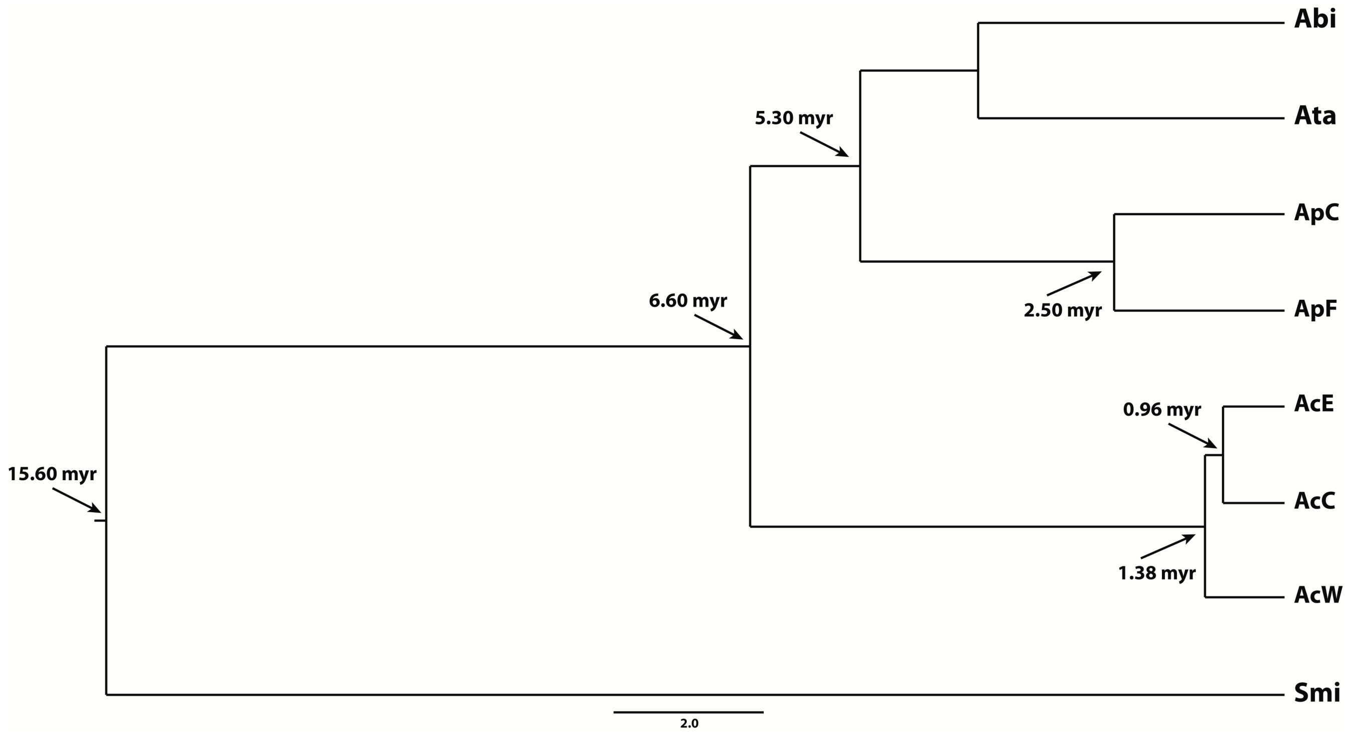


Figure S1

Phylogenetic tree used for comparative phylogenetic analysis of venom differentiation in *Agkistrodon*. Data and methods to generate tree are from Guiher and Burbrink [28]. Taxon abbreviations (and analyzed subspecies they represent) are as follows: Abi – *A. bilineatus* (*A. b. howardgloidi* and *A. b. bilineatus*); Ata – *A. taylori*; ApC – *A. piscivorus* Central mtDNA clade (*A. p. piscivorus* and *A. p. leucostoma*); *A. piscivourus* Florida mtDNA clade (*A. p. conanti*); AcE – *A. contortrix* Eastern mtDNA clade (*A. c. contortrix* and *A. c. mokasen*); AcC – *A. contortrix* Central mtDNA clade (*A. c. phaeogaster*); AcW - *A. contortrix* Western mtDNA clade (*A. c. pictigaster* and *A. c. laticinctus*). Divergence dates are from Table 1 in Guiher and Burbrink [28].

Figure 2A

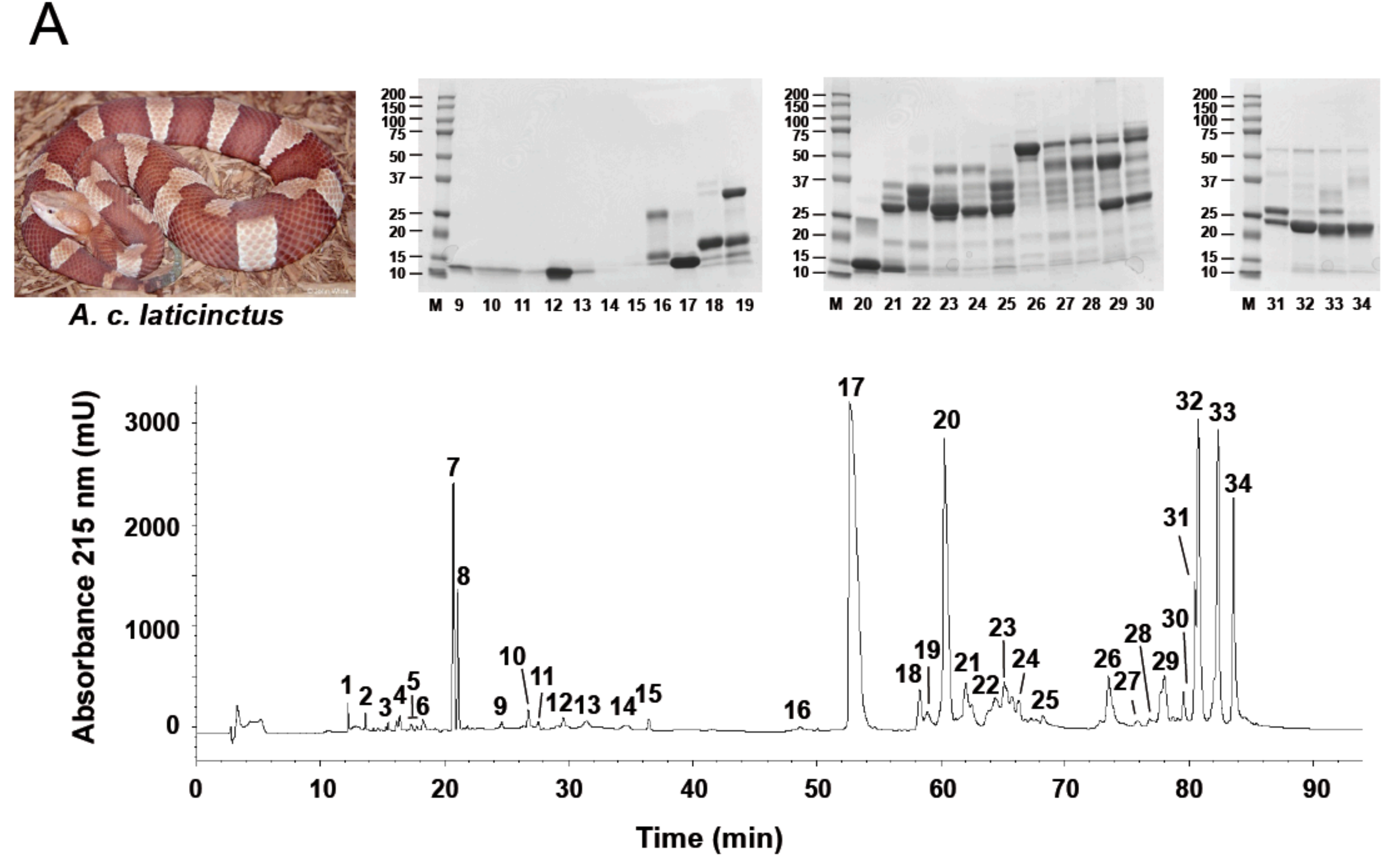

A
A. c. laticinctus
200
150
100
75
50
37
25
20
15
10
M 9 10 11 12 13 14 15 16 17 18 19
M 20 21 22 23 24 25 26 27 28 29 30
M 31 32 33 34
Absorbance 215 nm (mU)
0
1000
2000
3000
Time (min)
0 10 20 30 40 50 60 70 80 90
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34

Table S1: Assignment of the RP-HPLC isolated fractions of *Agkistrodon contortrix laticinctus* venom to protein families by MALDI-TOF-TOF or nESI-MS-MS of selected peptide ions from in-gel trypsin-digested protein bands from the SDS-PAGE shown in Fig.2A. * Cysteine residues are carbamidomethylated. X: Leu/Ile; B: Lys/Gln; Z, pyroglutamate (2-oxo-pyrrolidone carboxylic acid). ^{ox}: oxidized; ^{da}: deamidated; ^{cat}: cation; ^{kyn}: kynurenine. Mass estimations by SDS-PAGE (reducing conditions) are indicated in kDa. Confidence (Conf) and Score (Sc) values are calculated by the Paragon algorithm of ProteinPilot®.

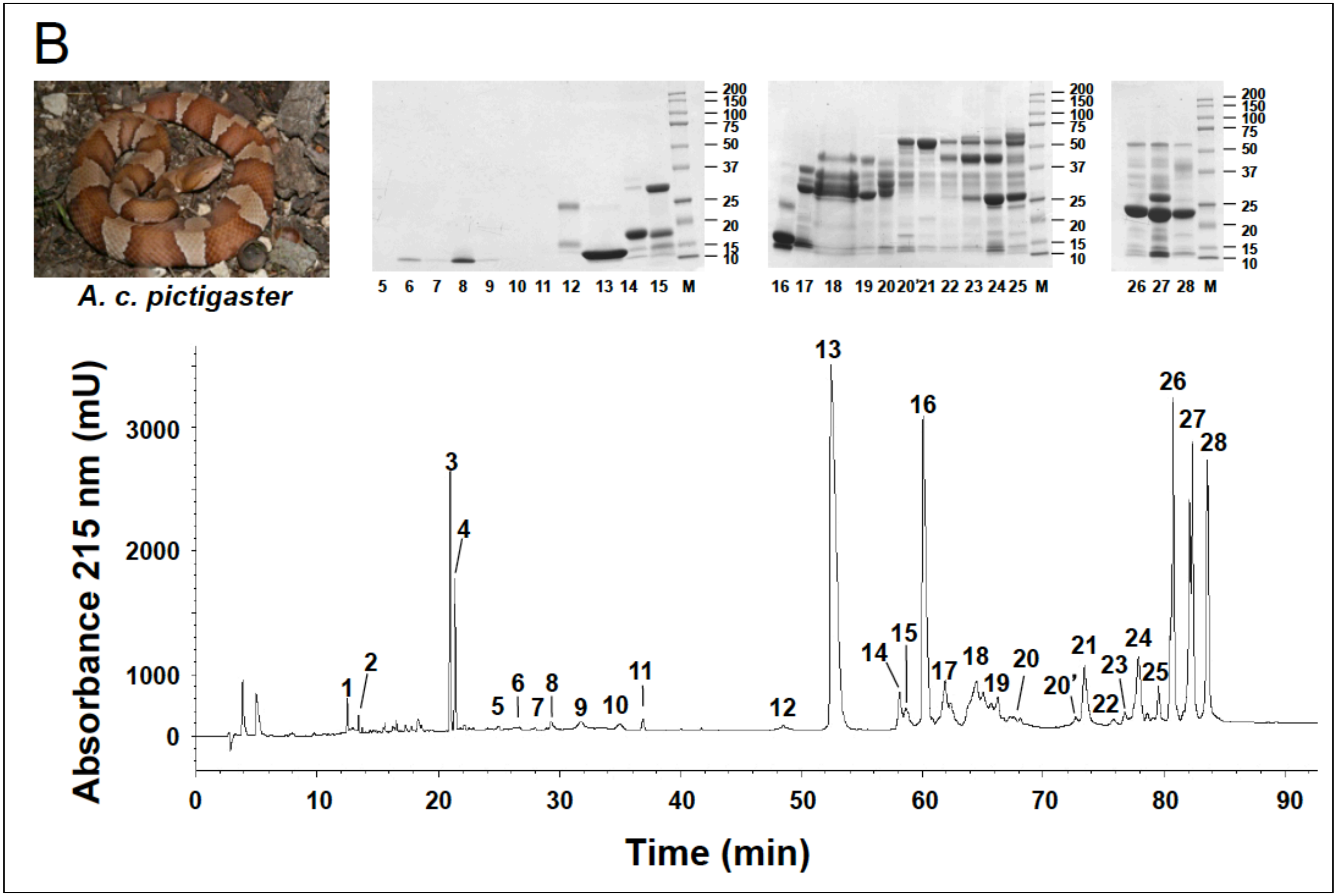
Peak	%	Mass, kDa	Peptide ion		MS/MS-derived or N-terminal (Nt) sequence	Conf (%)	Sc	Protein family; ~ related protein *
			m/z	z				
1	0.3	-	385.1	1	TPPA	-	-	Bradykinin-inhibitory peptide; P85025
2	0.2	-	449.3	1	ZBW^{kyn}	-	-	SVMP inhibitor; P01021
3	0.1	-	-	-	-	-	-	-
4	0.3	-	398.8	2	BVTPVPR	-	-	Fragment of PI-SVMP; ACV83930
5	0.3	-	-	-	-	-	-	-
6	0.3	-	865.4	1	PAGPDVGPR	-	-	Bradykinin-inhibitory peptide; P85025
			481.7	2	PPAGPDVGPR			Bradykinin-inhibitory peptide; P85025
			532.3	2	TPPAGPDVGPR			Bradykinin-inhibitory peptide; P85025
7	3.3	-	452.1	1	ZNW+Na	-	-	SVMP inhibitor; P01021
			430.2	1	ZNW			SVMP inhibitor; P01021
8	2.0	-	444.1	1	ZBW	-	-	SVMP inhibitor; P01021
9	0.2	11	1983.9	1	XTPGSBCAEGXCCDBCK	99.0	6	Disintegrin; ~ Q805F7
			1196.5	1	NPCCDAATCK	98.4	5	
10	0.5	11			unknown	-	-	-
11	0.2	10	1983.8	1	XTPGSBCAEGXCCDBCK	59.5	5	Disintegrin; ~ Q805F7
12	0.4	10	1196.5	1	NPCCDAATCK	99.0	10	Disintegrin; ~ Q805F7
			1983.9	1	XTPGSBCAEGXCCDBCK	99.0	18	
13	0.6	10	-	-	unknown	-	-	-
14	0.3	-	-	-	unknown	-	-	-
15	0.3	-	-	-	unknown	-	-	-
16a	0.1	24	1111.6	1	NPNPVPTGCR	86.7	6	Nerve growth factor; Q9DEZ9
			1427.7	1	CRNPNPVPTGCR	82.9	7	
16b		15	1111.6	1	NPNPVPTGCR	99.0	10	Nerve growth factor; Q9DEZ9
			1427.7	1	CRNPNPVPTGCR	99.0	10	

17	26.9	14	855.4	1	CCFVHK	97.8	7	Phospholipase A_2, K49; ~ P49121
			919.5	1	MXXBETGK	51.2	8	
18	1.5	17	1505.6	1	CCFVHDCCYGK	99.0	18	Phospholipase A_2, D49; ~ P51972
			2462.2	1	MDXYTYSVDNGNXVCGGTNPCK	99.0	19	
19a	0.5	32	1129.7	1	FXVAXYTFR	92.2	6	Serine proteinase; ~ Q9DF68
19b	0.5	18	1505.6	1	CCFVHDCCYGK	99.0	17	Phospholipase A_2, D49; ~ P51972
			2461.2	1	MDXYTYSVDNGN^{da}XVCGGTNPCK	99.0	13	
19c	0.1	15	2059.9	1	NAXTSYGSYGCNCGWGHR	99.0	8	Phospholipase A_2, D49; ~ P49121
			1505.6	1	CCFVHDCCYGK	99.0	15	
20a	3.8	24	2509.1	1	SGPPCGDCPSACVNGXCTNPCTK	99.0	10	Serine proteinase; ~ Q7ZTA0
20b	10.2	13	2175.9	1	N^{da}AXP^{ox}FYAFYGCYCGWGGR	99.0	12	Phospholipase A_2, D49; ~ P0C943
21a	0.3	34	1539.9	1	BVPNEDEBTRVPK	99.0	7	Serine proteinase; ~ Q91053
21b	0.3	30	1307.7	1	NFBMXFGVHSK	99.0	15	Serine proteinase; ~ Q9YGJ8
			1512.7	1	VXGGDECNXNEHR	99.0	10	
			2494.3	1	ETYPDVPHCANXNXXDHAVCR	99.0	13	
21c	1.1	26	1512.7	1	VXGGDECNXNEHR	99.0	9	Serine proteinase; ~ O93421
			1307.7	1	NFBMXFGVHSK	99.0	14	
21d	0.1	18	1641.9	1	XNXXDYAVCBAAYK	99.0	9	Serine proteinase; ~ P09872
21e	1.2	12	1241.6	1	DFSWEWTDR	52.8	7	C-type lectin/lectin-like; ~ AER27037
22a	1.2	32	1512.7	1	VXGGDECNXNEHR	99.0	7	Serine proteinase; ~ P09872
			3360.7	1	DTCBGDSGGPXXCNGBFBGXXSVGGNPCABPR	99.0	13	
			2250.2	1	NSAHXAPXSXPSNP^{ox}P^{ox}SVGSVCR	99.0	14	
			2856.4	1	GDSGGPXXCNGBFBGXXSVGGNPCABPR	99.0	18	
22b	1.6	28	1498.7	1	VVGGDECNXNEHR	99.0	12	Serine proteinase; ~ Q9PTL3
			1189.7	1	WDBDXMXXR	99.0	14	
			1097.6	1	FXAXVYTDR	98.9	11	
23a	0.6	40	2233.2	1	DSGGPXXCNGBFBGXVSWGP^{ox}K	99.0	11	Serine proteinase; ~ Q9PSN3
			1762.0	1	XXCAGVXEGGXDTCBR	99.0	15	
23b	2.1	26	1429.7	1	SXPSSPPSVGSVCR	99.0	12	Serine proteinase; ~ Q8QHK3
			1190.7	1	XMGWGTXSPTK	99.0	15	
			1824.0	1	XAPXSXPSSPPSVGSVCR	99.0	18	
			1498.7	1	VVGGDECNXNEHR	99.0	12	
			2900.6	1	XDRPVSNSAHXAPXSXPSSPPSVGSVCR	99.0	22	
			1097.6	1	FXAXVYTDR	99.0	13	
23c	0.6	24	1498.7	1	VVGGDECNXNEHR	99.0	6	Serine proteinase; ~ Q9YGJ8

24a	0.2	40	1762.0	1	XXCAGVXEGGXDTCBR	99.0	13	Serine proteinase; ~ Q9PSN3
24b	1.0	25	1596.9	1	BXXNEDEBXRNPK	99.0	9	Serine proteinase; ~ Q8AY79
			1468.8	1	XXNEDEBXRNPK	99.0	16	
			1498.7	1	VVGGDECNXNEHR	99.0	9	
25a	0.2	33	1512.7	1	VXGGDECNXNEHR	99.0	9	Serine proteinase; ~ P09872
			2857.4	1	GDSGGPXXCNGBFBGXXSVGGNPCABPR	99.0	15	
25b	0.1	29	2856.5	1	GDSGGPXXCNGBFBGXXSVGGNPCABPR	90.4	6	Serine proteinase; ~ P09872
25c	0.4	25	1427.4	1	APYPE^{cat}FGXPATSR	53.8	10	Serine proteinase; ~ Q91053
25d	0.1	12	1187.6	1	NAFXCBCBF	99.0	11	C-type lectin/lectin-like; ~ Q9PSN0
26	3.0	51	2347.2	1	XYFAGEYTABFHGWXDSTXK	99.0	22	L-amino acid oxidase; ~ Q6STF1
			1064.5	1	NPXEECFR	99.0	12	
			1594.8	1	DBEDWYANXGPMR	99.0	18	
			1513.8	1	ETNYEEFXEXAR	99.0	19	
27a	0.2	55	-	-	unknown	-	-	-
27b	0.2	42	1684.7	1	GABCAEGXCCDBCR	73.0	6	Metalloproteinase; ~ P21858
28a	0.3	57	-	-	unknown	-	-	-
28b	0.5	42	1183.7	1	BSNXTPEBBR	99.0	11	Metalloproteinase; ~ Q9DGB9
			1269.6	1	SAECTDRFBR	99.0	10	
			1684.7	1	GABCAEGXCCDBCR	99.0	12	
29a	0.1	250	1733.9	1	MYDXVNVXTPXYHR	99.0	9	Metalloproteinase; ~ Q9DGB9
			1803.8	1	YFVEVGEECDCGSPR	99.0	12	
			1368.6	1	XYCFPNSPENK	92.8	7	
29b	0.4	57	1594.7	1	DBEDWYANXGPMR	99.0	11	L-amino acid oxidase; ~ Q6STF1
			1064.5	1	NPXEECFR	99.0	9	
			1513.7	1	ETNYEEFXEXAR	99.0	15	
29c	1.7	42	1269.6	1	SAECTDRFBR	99.0	9	Metalloproteinase; ~ Q2LD49
			1684.7	1	GABCAEGXCCDBCR	99.0	17	
29d	1.2	26	2241.2	1	XNFXVAVTMAHEMGHNXGMR	99.0	9	Metalloproteinase; ~ Q92032
			1247.6	1	HTXDSFGEWR	99.0	15	
			1532.8	1	HTXDSFGEWRER	99.0	17	
30a	0.6	58	1983.8	1	XTPGSBCADGVCCDBCR	95.4	8	Metalloproteinase; ~ O42138
30b	0.2	44	1983.8	1	XTPGSBCADGVCCDBCR	62.2	6	Metalloproteinase; ~ O42138
30c	0.6	27	1247.6	1	HTXDSFGEWR	99.0	12	Metalloproteinase; ~ Q92032
31a	1.5	26	1313.8	1	YVEXVXVADHR	99.0	14	Metalloproteinase; ~ Q92043

31b	1.4	23	1187.6	1	TPEBBGFPBR	99.0	14	Metalloproteinase; ~ Q92031
			2235.2	1	DXXTVTSVSHDTXASFGNWR	91.6	7	
32a	0.8	55	1064.5	1	NPXEECFR	99.0	8	L-amino acid oxidase; ~ P0C2D6
			1513.8	1	ETNYEEFXEXAR	99.0	15	
32b	7.7	22	2563.5	1	XSHDNABXXTAXEXDGETXGXANR	99.0	12	Metalloproteinase; ~ P28891
			3122.6	1	HDNABXXTAXDFDGDTVGXAYVGGMCBXK	99.0	26	
			2165.1	1	DYBTFXTVNNPBCXXNBP	99.0	14	
			1313.8	1	YVEXVXVADHR	99.0	15	
			2506.5	1	BWVHBXVNTXNEXYRPXNXR	99.0	16	
33a	0.5	55	1064.5	1	NPXEECFR	99.0	8	L-amino acid oxidase; ~ P0C2D6
			1513.8	1	ETNYEEFXEXAR	98.9	7	
33b	1.6	26	1187.6	1	TPEBBGFPBR	99.0	10	Metalloproteinase; ~ Q9IAB0
33c	6.9	21	2297.3	1	BSHDNABXXTAXVFDEGXXGR	99.0	27	Metalloproteinase; ~ B7U492
			2169.2	1	SHDNABXXTAXVFDEGXXGR	99.0	27	
34a	0.2	55	1513.8	1	ETNYEEFXEXAR	99.0	10	L-amino acid oxidase; ~ P0C2D6
34b	6.5	21	1201.6	1	APXAGMCDPNR	67.4	6	Metalloproteinase; ~ B7U492

Figure 2B


B
A. c. pictigaster
5 6 7 8 9 10 11 12 13 14 15 M
16 17 18 19 20 20' 21 22 23 24 25 M
26 27 28 M
200
150
100
75
50
37
25
20
15
10
Absorbance 215 nm (mU)
0
1000
2000
3000
Time (min)
0
10
20
30
40
50
60
70
80
90
1
2
3
4
5
6
7
8
9
10
11
12
13
14
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16
17
18
19
20
20'
21
22
23
24
25
26
27
28

Table S2: Assignment of the RP-HPLC isolated fractions of *Agkistrodon contortrix pictigaster* venom to protein families by MALDI-TOF-TOF or nESI-MS-MS of selected peptide ions from in-gel trypsin-digested protein bands from the SDS-PAGE shown in Fig.2B. * Cysteine residues are carbamidomethylated. X: Leu/Ile; B: Lys/Gln; Z, pyroglutamate (2-oxo-pyrrolidone carboxylic acid). ^{ox}: oxidized; ^{da}: deamidated; ^{dh}: dehydrated; ^{py}: pyroglutamic; ^{kyn}: kynurenine. Mass estimations by SDS-PAGE (reducing conditions) are indicated in kDa. Confidence (Conf) and Score (Sc) values are calculated by the Paragon algorithm of ProteinPilot®.

Peak	%	Mass, kDa	Peptide ion		MS/MS-derived sequence	Conf (%)	Sc	Protein family; ~ related protein *
			m/z	z				
1	0.3	-	385.3	1	TPPA	-	-	Bradykinin-inhibitory peptide; P85025
			470.2	1	ZSPR	-	-	Fragment of NGF-β; ACC85799
2	0.2	-	532.3	2	TPPAGPDVGPR	-	-	Bradykinin-inhibitory peptide; P85025
3	3.8	-	430.1	1	ZNW	-	-	SVMP inhibitor; P01021
			449.3	1	ZBW^{kyn}	-	-	SVMP inhibitor; P01021
			624.4	2	BSGPBNDTAA(278.2)	-	-	Fragment of PLA$_2$; ~ AAP48902
3b		-	468.3	1	PVPR	-	-	Fragment of PI-SVMP; ACV83930
			569.2	1	TPVPR	-	-	Fragment of PI-SVMP; ACV83930
			668.5	1	VTPVPR	-	-	Fragment of PI-SVMP; ACV83930
			398.8	2	KVTPVPR	-	-	Fragment of PI-SVMP; ACV83930
3c,d		-	532.3	2	TPPAGPDVGPR	-	-	Bradykinin-inhibitory peptide; P85025
4	2.4	-	444.1	1	ZBW	-	-	SVMP inhibitor; P01021
			466.1	1	ZBW + Na	-	-	SVMP inhibitor; P01021
5	0.2	-	638.8	2	ZBWPPGHHIPP	-	-	Bradykinin-potentiating peptide; ~ P0C7J9
5c			534.8	2	ZNXPHPWPP	-	-	Bradykinin-potentiating peptide; ~ Q27J49
6	0.4	9	1196.5	1	NPCCDAATCK	99.0	6	Disintegrin; ~ P16338
			2098.0	1	ARGDDVN^{da}DYCNGXSAGCPR	99.0	9	
			1870.9	1	GDDVN^{da}DYCNGXSAGCPR	99.0	8	
			1967.9	1	XTPGABCAEGXCCDBCK	99.0	8	
7	0.2	-	-	-	unknown	-	-	
8	0.4	9	1196.5	1	NPCCDAATCK	99.0	10	Disintegrin; ~ P16338
			1870.9	1	GDDVN^{da}DYCNGXSAGCPR	99.0	8	
			2098.0	1	ARGDDVN^{da}DYCNGXSAGCPR	99.0	13	
			1983.9	1	XTPGSBCAEGXCCDBCK	99.0	9	
9	0.6	-	-	-	unknown	-	-	-

10	0.4	-	-	-	unknown	-	-	-
11	0.3	-	-	-	unknown	-	-	-
12a	0.1	23	1111.6	1	NPNPVPTGCR	99.0	8	Nerve growth factor; ~ Q90W38
			1758.9	1	HWNSYCTTTNTFVK	99.0	20	
			1363.7	1	AXTMEGNBASWR	99.0	11	
12b	0.1	15	1111.6	1	NPNPVPTGCR	99.0	9	Nerve growth factor; ~ Q90W38
			1992.1	1	GNVVTVMVDVNXNNNVYK	99.0	7	
			1758.9	1	HWNSYCTTTNTFVK	99.0	18	
			1363.7	1	AXTMEGNBASWR	99.0	10	
			962.5	1	BYFFETK	98.9	6	
13	24.9	13	1474.8	1	AXXCEEBNPCXK	99.0	17	Phospholipase A$_2$, K49; ~ P49121
			1754.9	1	EMCECDBAVAXCXR	99.0	17	
			1205.6	1	TDRYSYSWK	99.0	14	
			2060.0	1	NAXTSYGSYGCNCGWGHR	99.0	20	
			919.5	1	MXXBETGK	97.3	9	
			850.4	1	CCFVHK	97.3	7	
			1408.7	1	DATDRCCFVHK	95.5	6	
14	1.5	17	1505.6	1	CCFVHDCCYGK	99.0	15	Phospholipase A$_2$, D49; ~ P51972
			2461.2	1	MD^{dh}XYTYSVDNGN^{da}XVCGGTNPCK	99.0	16	
			2589.3	1	MD^{dh}XYTYSVDNGN^{da}XVCGGTNPCBK	99.0	20	
15a	0.6	29	1683.0	1	TYTBWDBDXMXXR	99.0	12	Serine proteinase; ~ Q7T229
			1526.8	1	XXGGDECNXNEHR	99.0	9	
			2515.3	1	FHCSGTXXNBEWVXTAANCDR	99.0	10	
			1975.1	1	HXAPXSXPSSPPTVGSVCR	99.0	18	
			2135.2	1	SAHXAP^{ox}XSXPSSPPSVGSVCR	99.0	14	
			1129.7	1	FXVAXYTFR	99.0	12	
			1189.7	1	WDBDXMXXR	98.1	12	
15b	0.4	17	1505.6	1	CCFVHDCCYGK	99.0	14	Phospholipase A$_2$, D49; ~ P51972
			2461.2	1	MD^{dh}XYTYSVDNGN^{da}XVCGGTNPCK	99.0	12	
			2589.3	1	MD^{dh}XYTYSVDNGN^{da}XVCGGTNPCBK	99.0	16	
15c	0.2	14	1505.6	1	CCFVHDCCYGK	99.0	11	Phospholipase A$_2$, D49; ~ P86169
16a	2.0	23	1325.6	1	SXVBBYGCBDK	99.0	7	CRISP; ~ Q7ZTA0
			1976.0	1	SVDFDSESPRBPEXBNK	99.0	4	
			1537.7	1	MEWYPEAAANAER	99.0	10	
			1066.6	1	XVDXHNSXR	98.9	10	
16b	7.9	15	1505.6	1	CCFVHDCCYGK	99.0	18	Phospholipase A$_2$, D49; ~ P51972
			2461.2	1	MD^{dh}XYTYSVDNGN^{da}XVCGGTNPCK	99.0	14	
			2589.3	1	MD^{dh}XYTYSVDNGN^{da}XVCGGTNPCBK	99.0	16	
			2176.0	1	N^{da}AXP^{ox}FYAFYGCYCGWGGR	99.0	12	

16c	3.3	12	1505.6	1	CCFVHDCCYGK	99.0	18	Phospholipase A_2, D49; ~ P51972
			1859.9	1	AAAXCFRDNXDTYN^{da}SK	99.0	19	
			2589.3	1	MD^{dh}XYTYSVDNGN^{da}XVCGGTNPCBK	99.0	17	
			2176.0	1	N^{da}AXP^{ox}FYAFYGCYCGWGGR	99.0	13	
17a	2.4	28	1585.9	1	BXXNEDEBTRDPK	99.0	11	Serine proteinase; ~ Q9YGJ8
			2508.3	1	ETYPDVPHCANXNXXDHAVCR	99.0	17	
			1747.0	1	BBDDEBDBDXMXXR	99.0	18	
			1323.7	1	NFBM^{ox}XFGVHSK	99.0	18	
			1512.8	1	VXGGDECNXNEHR	99.0	9	
			1307.7	1	NFBMXFGVHSK	99.0	18	
17b	1.3	15	2413.2	1	SCTDYXTWDBNBPDHYBNK	99.0	14	C-type lectin/lectin-like; ~ Q9PSN0
			3342.7	1	YBPGCHXASFHBYGESXEXAEYXSDYHK	99.0	16	
			1278.6	1	XWNDBVCESK	99.0	15	
			1401.8	1	GBAEVWXGXWDK	99.0	19	
			1572.8	1	EFCVEXVSXTGYR	99.0	18	
			1241.6	1	DFSWEWTDR	99.0	13	
			1519.8	1	NVGVPBVVPDNPER	99.0	12	Ohanin-like; ~ Q27J48
18a	0.9	42	2317.3	1	NSEHXAPXSXPSSPPXVGSVCR	99.0	15	Serine proteinase; ~ Q9PSN3
			1512.7	1	VXGGDECNXNEHR	99.0	9	
			2217.1	1	DSGGPXXCNGBFBGXVSWGPK	99.0	8	
			1762.0	1	XXCAGVXEGGXDTCBR	99.0	9	
			1189.7	1	WDBDXMXXR	99.0	11	
18b	1.1	33	1512.7	1	VXGGDECNXNEHR	99.0	8	Serine proteinase; ~ P09872
			2856.5	1	GDSGGPXXCNGBFBGXXSVGGNPCABPR	99.0	15	
18c	2.1	28	1189.7	1	WDBDXMXXR	99.0	13	Serine proteinase; ~ Q71QI3
			1097.7	1	FXAXVYTDR	99.0	9	
18d	0.5	13	1278.6	1	XWNDBVCESK	99.0	7	C-type lectin/lectin-like; ~ Q9PSM4
			1401.8	1	GBAEVWXGXWDK	99.0	14	
			1572.8	1	EFCVEXVSXTGYR	99.0	14	
			1241.6	1	DFSWEWTDR	96.0	7	
19a	0.5	42	1512.7	1	VXGGDECNXNEHR	99.0	11	Serine proteinase; ~ Q9PSN3
			1762.0	1	XXCAGVXEGGXDTCBR	99.0	11	
			2217.2	1	DSGGPXXCNGBFBGXVSWGPK	99.0	16	
			2317.3	1	NSEHXAPXSXPSSPPXVGSVCR	99.0	19	
19b	1.0	27	1468.8	1	XXNEDEBXRNPK	99.0	15	Serine proteinase; ~ Q8AY79
			1596.9	1	BXXNEDEBXRNPK	99.0	17	
			1498.7	1	VVGGDECNXNEHR	99.0	11	
			2866.6	1	FXAXVYANGSXCGGTXXNBEWVXTAR	99.0	12	

20	0.6	13	1401.8	1	GBAEVWXGXWDK	99.0	13	C-type lectin/lectin-like; ~ Q9PSM4
			1572.8	1	EFCVEXVSXTGYR	99.0	14	
			1241.6	1	DFSWEWTDR	99.0	10	
			1278.6	1	XWNDBVCESK	98.6	7	
			2169.2	1	SHDNABXXTAXVFDEGXXGR	99.0	12	Metalloproteinase; ~ B7U492
20'a	0.1	54	1165.7	1	XBFEPPXPPK	99.0	10	L-amino acid oxidase; ~ Q6STF1
			1064.5	1	NPXEECFR	99.0	11	
			2347.2	1	XYFAGEYTABFHGWXDSTXK	99.0	15	
			1594.8	1	DBEDWYANXGPMR	99.0	12	
20'b	<	38	1123.5	1	HDDXFGYEK	99.0	10	L-amino acid oxidase; ~ P56742
			2347.2	1	XYFAGEYTABFHGWXDSTXK	99.0	7	
20'c	0.1	34	1064.5	1	NPXEECFR	97.1	7	L-amino acid oxidase; ~ Q90W54
			2856.4	1	GDSGGPXXCNGBFBGXXSVGGNPCABPR	99.0	15	Serine proteinase; ~ P09872
20'd	0.1	30	1064.5	1	NPXEECFR	99.0	8	L-amino acid oxidase; ~P0C2D6
			1513.7	1	ETNYEEFXEXAR	99.0	16	
20'e	0.1	17	1507.8	1	VVGGRPCNXNEHR	99.0	11	Serine proteinase; ~ Q9YGJ8
			1498.7	1	VVGGDECNXNEHR	99.0	9	
20'f	0.1	13	1401.7	1	GBAEVWXGXWDK	99.0	16	C-type lectin/lectin-like; ~ Q9PSM4
			1572.8	1	EFCVEXVSXTGYR	99.0	10	
			1241.5	1	DFSWEWTDR	99.0	12	
			1064.5	1	NPXEECFR	99.0	7	L-amino acid oxidase; ~ P0C2D6
			1513.7	1	ETNYEEFXEXAR	99.0	10	
21	3.0	52	2953.5	1	YAMGGXTTFTPYBFBHFSEAXTAPFK	99.0	8	L-amino acid oxidase; ~ P56742
			1064.5	1	NPXEECFR	99.0	10	
			1594.8	1	DBEDWYANXGPMR	99.0	15	
			2347.2	1	XYFAGEYTABFHGWXDSTXK	99.0	20	
			1513.7	1	ETNYEEFXEXAR	99.0	19	
22a	0.1	54	2347.2	1	XYFAGEYTABFHGWXDSTXK	99.0	8	L-amino acid oxidase; ~ P56742
			1513.8	1	ETNYEEFXEXAR	99.0	9	
22b	0.3	42	1368.7	1	XYCFPNSPENK	99.0	7	Metalloproteinase; ~ Q9DGB9
			1684.7	1	GABCAEGXCCDBCR	99.0	8	
			2929.4	1	TDVVSPAVCGNYFVEVGEECDCGSPR	99.0	12	
			1137.5	1	E^{py}GNHYGYCR	99.0	8	
			1734.0	1	MYDXVNVXTPXYHR	99.0	11	
23a	0.4	54	1594.8	1	DBEDWYANXGPMR	99.0	10	L-amino acid oxidase; ~ Q6STF1
			2347.2	1	XYFAGEYTABFHGWXDSTXK	99.0	13	

			1513.7	1	ETNYEEFXEXAR	99.0	10	
			1064.5	1	NPXEECFR	98.6	7	
23b	0.2	42	1733.9	1	MYDXVNVXTPXYHR	99.0	18	Metalloproteinase; ~ Q9DGB9
24a	0.6	54	2347.2	1	XYFAGEYTABFHGWXDSTXK	99.0	10	L-amino acid oxidase; ~ P56742
			1513.8	1	ETNYEEFXEXAR	99.0	14	
			1064.5	1	NPXEECFR	95.2	7	
24b	1.4	42	1368.7	1	XYCFPNSPENK	99.0	8	Metalloproteinase; ~ Q9DGB9
			1734.0	1	MYDXVNVXTPXYHR	99.0	16	
			1684.7	1	GABCAEGXCCDBCR	99.0	11	
			1440.8	1	XVXVADYXM^{ox}FXK	99.0	14	
			2929.4	1	TDVVSPAVCGNYFVEVGEECDCGSPR	99.0	14	
			1137.5	1	E^{py}GNHYGYCR	96.5	7	
24c	1.7	26	1401.7	1	BWVHBMVNTMK	99.0	11	Metalloproteinase; ~ Q92032
			1097.6	1	DXXDVBPAAR	99.0	10	
			3337.8	1	XSHDNABXXTSTDFDGPTXGXAYVGTMCDPK	99.0	21	
			2717.2	1	HDTGSCSCGGYSCXMSPVXSDDSPK	99.0	18	
			3080.7	1	YMYXDXSXAGVEXWSNBDXXDVBPAAR	99.0	15	
			2257.2	1	XNFXVAVTM^{ox}AHEMGHNXGMR	99.0	19	
			1754.0	1	YVEXVTVVDHGMYTK	99.0	22	
			2241.2	1	XNFXVAVTMAHEMGHNXGMR	99.0	12	
			1247.6	1	HTXDSFGEWR	99.0	17	
24d	0.2	12	3080.7	1	YMYXDXSXAGVEXWSNBDXXDVBPAAR	99.0	13	Metalloproteinase; ~ Q92032
			2002.0	1	YMYXDXSXAGVEXWSNK	99.0	10	
			1753.9	1	YVEXVTVVDHGMYTK	99.0	18	
			1247.6	1	HTXDSFGEWR	99.0	17	
			1097.6	1	DXXDVBPAAR	96.5	10	
			1572.8	1	EFCVEXVSXTGYR	99.0	9	C-type lectin/lectin-like; ~ Q9PSN0
25a	0.3	60	1800.0	1	YVEFVVVXDHGMYTK	99.0	6	Metalloproteinase; ~ O42138
			2141.2	1	SHDNABXXTVXDFDGPTXGK	99.0	17	
			1714.9	1	Q^{py}XNXTPEBBAYXDAK	99.0	13	
25b	0.2	53	1064.5	1	NPXEECFR	99.0	7	L-amino acid oxidase; ~ Q6STF1
			2347.2	1	XYFAGEYTABFHGWXDSTXK	99.0	10	
			1594.8	1	DBEDWYANXGPMR	99.0	13	
			1513.8	1	ETNYEEFXEXAR	99.0	7	
25c	0.2	41	2856.4	1	GDSGGPXXCNGBFBGXXSVGGNPCABPR	99.0	11	Serine proteinase; ~ P09872
			1512.7	1	VXGGDECNXNEHR	99.0	6	
25d	0.4	26	1384.7	1	Q^{py}WVHBMVNTMK	99.0	11	Metalloproteinase; ~ Q92032
			1401.7	1	BWVHBMVNTMK	99.0	8	

			1247.6	1	HTXDSFGEWR	99.0	7	
			1313.8	1	YVEXVXVADHR	99.0	11	
26a	2.0	57	2347.2	1	XYFAGEYTABFHGWXDSTXK	99.0	9	L-amino acid oxidase; ~ P56742
			1513.7	1	ETNYEEFXEXAR	99.0	10	
26b	6.3	24	3122.6	1	HDNABXXTAXDFDGDTVGXAYVGGMCBXK	99.0	25	Metalloproteinase; ~ Q92031
			2564.4	1	XSHDNABXXTAXEXDGETXGXANR	99.0	13	
			1067.5	1	YNGDSDBXR	99.0	9	
			1187.6	1	TPEBBGFPBR	99.0	14	
			2219.2	1	DXXTVTSVSHDTXASFGNWR	99.0	16	
			2293.3	1	BDYBTFXTVNNPBCXXNBP	99.0	17	
			2165.1	1	DYBTFXTVNNPBCXXNBP	99.0	16	
			2489.5	1	Q^{py}WVHBXVNTXNEXYRPXNXR	99.0	11	
			2506.5	1	BWVHBXVNTXNEXYRPXNXR	99.0	14	
			1313.8	1	YVEXVXVADHR	99.0	15	
26c	1.4	12	1313.8	1	YVEXVXVADHR	99.0	9	Metalloproteinase; ~ Q92043
27a	2.2	56	1165.7	1	XBFEPPXPPK	99.0	6	L-amino acid oxidase; ~ Q6STF1
			1064.5	1	NPXEECFR	99.0	7	
			1594.8	1	DBEDWYANXGPMR	99.0	12	
			2347.2	1	XYFAGEYTABFHGWXDSTXK	99.0	12	
			1513.7	1	ETNYEEFXEXAR	99.0	10	
27b	2.8	28	1187.6	1	TPEBBGFPBR	99.0	15	Metalloproteinase; ~ Q92031
			1313.7	1	YVEXVXVADHR	99.0	14	
27c	4.4	23	1187.6	1	TPEBBGFPBR	99.0	12	Metalloproteinase; ~ Q92031
			1313.8	1	YVEXVXVADHR	99.0	15	
			2297.3	1	BSHDNABXXTAXVFDEGXXGR	99.0	34	
			2169.2	1	SHDNABXXTAXVFDEGXXGR	99.0	34	
			1083.6	1	NPBCXXNBP	98.5	9	
27d	3.1	12	2297.3	1	BSHDNABXXTAXVFDEGXXGR	99.0	23	Metalloproteinase: ~ B7U492
			2169.2	1	SHDNABXXTAXVFDEGXXGR	99.0	30	
28a	1.8	40	3432.6	1	NEPSGTDXVSPPVCGNDXXEVGEECDCGCPR	99.0	9	Metalloproteinase; ~ P0C6E3
			1801.0	1	TSHDNABXXTAXVFNR	99.0	16	
			1463.8	1	VAXVGXEFWCNK	99.0	14	
			1651.9	1	XYEXVNXXNEXYR	99.0	14	
			1380.8	1	YXEXFXVVDNR	99.0	14	
			2123.8	1	YSWVBCESGECCDBCR	95.0	6	
28b	4.4	24	3786.9	1	VAXXMAHEXGHNXGMGHDDNSCTCGGYSCXMXP	99.0	8	Metalloproteinase: ~ B7U492
					R	99.0	12	
			1201.6	1	APXAGMCDPNR			
			1327.8	1	YVEXVXXADHR	99.0	14	

28c	1.5	12	1327.8	1	YVEXVXXADHR	99.0	12	Metalloproteinase; ~ B7U492

Figure 2C

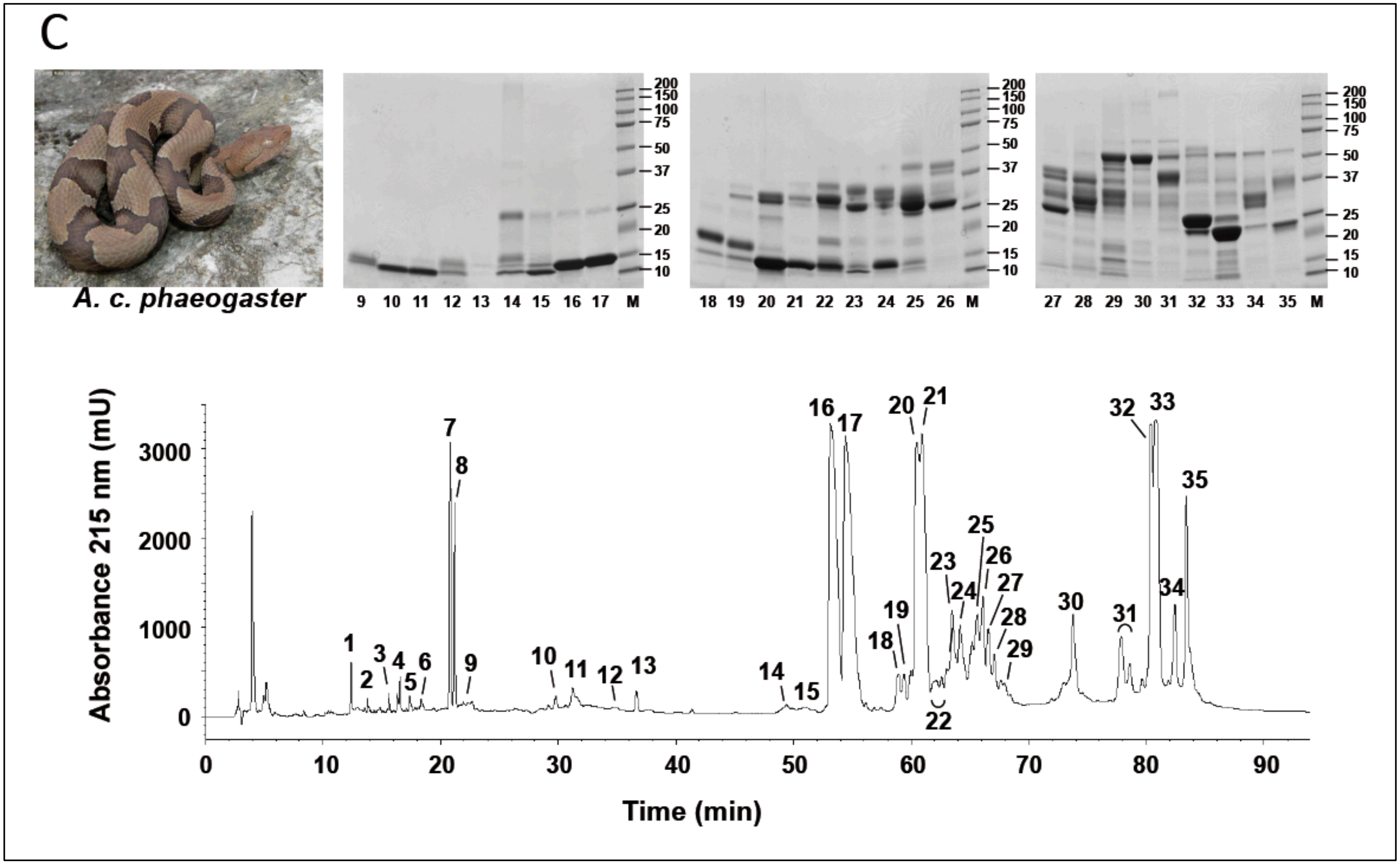
C
A. c. phaeogaster
9 10 11 12 13 14 15 16 17 M
18 19 20 21 22 23 24 25 26 M
27 28 29 30 31 32 33 34 35 M
200
150
100
75
50
37
25
20
15
10
Absorbance 215 nm (mU)
0
1000
2000
3000
Time (min)
0 10 20 30 40 50 60 70 80 90
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35

Table S3: Assignment of the RP-HPLC isolated fractions of *Agkistrodon contortrix phaeogaster* venom to protein families by MALDI-TOF-TOF or nESI-MS-MS of selected peptide ions from in-gel trypsin-digested protein bands from the SDS-PAGE shown in Fig.2C. * Cysteine residues are carbamidomethylated. X: Leu/Ile; B: Lys/Gln; Z, pyroglutamate (2-oxo-pyrrolidone carboxylic acid). ^{da}: deamidated; ^{ca}: carbamidomethyl; ^{kyn}: kynurenine. Mass estimations by SDS-PAGE (reducing conditions) are indicated in kDa. Confidence (Conf) and Score (Sc) values are calculated by the Paragon algorithm of ProteinPilot®.

Peak	%	Mass, kDa	Peptide ion		MS/MS-derived sequence	Conf (%)	Sc	Protein family; ~ related protein *
			m/z	z				
1	0.4	-	470.3	1	ZSPR	-	-	peptidic fragment
		-	642.1	2	[NeuAc-Hex-HexNAc]-(626.4)	-	-	glycan
2	0.1	-	440.3	1	PARP			peptidic fragment
3	0.2	-	473.5	3	DGGRS(473.5)	-	-	Bradykinin-potentiating peptide fragment; ~ P01021
			539.3	1	TPPAGP	-	-	Bradykinin-inhibitory peptide fragment; ~ P85025
4	0.4	-	449.2	1	ZBW^{kyn}	-	-	SVMP inhibitor; P01021
5	0.2	-	668.6	1	VTPVPR	-	-	Metalloproteinase fragment; ~ Q92031
6	0.3	-	532.4	2	TPPAGPDVGPR	-	-	Bradykinin-inhibitory peptide; ~ P85025
		-	865.6	1	PAGPDVGPR	-	-	Bradykinin-inhibitory peptide fragments; ~ P85025
			636.5	1	TPPAGPP	-	-	
7	2.1	-	430.3	1	ZNW	-	-	SVMP inhibitor; P01021
8	1.7	-	444.2	1	ZBW	-	-	SVMP inhibitor; P01021
9	0.6	12	2124.0	1	YSWVBCESGECCDBCR	95.2	6	Disintegrin; ~ P0C6E3
10	0.4	11	1550.7	1	DAPANPCCDAATCK	99.0	13	Disintegrin; ~ Q805F4
			1967.9	1	XTPGABCAEGXCCDBCK	99.0	14	
			1196.5	1	NPCCDAATCK	99.0	14	
			2098.1	1	ARGDDVN^{da}DYCNGXSAGCPR	99.0	10	
11	1.0	10	1063.5	1	ARGDNPDYR	99.0	9	Disintegrin; ~ P0C6E3
			1983.9	1	XTPGSBCAEGXCCDBCK	99.0	9	
12a	0.2	11	2123.9	1	YSWVBCESGECCDBCR	96.7	6	Disintegrin; ~ P0C6E3
12b	0.1	10	-	-	unknown	-	-	-
13	0.4	-	-	-	unknown	-	-	-
14a	0.2	22	1111.5	1	NPNPVPTGCR	99.0	10	Nerve growth factor; ~ Q9DEZ9
			1758.8	1	HWNSYCTTTNTFVK	99.0	15	
14b	0.1	13	1111.5	1	NPNPVPTGCR	99.0	9	Nerve growth factor; ~ Q9DEZ9

			1758.7	1	HWNSYCTTTNTFVK	99.0	19	
			1363.6	1	AXTMEGNBASWR	99.0	8	
14c	0.2	10	-	1	unknown	-	-	-
15a	0.2	12	1992.2	1	GNVVTVMVDVNXNNNVYK	99.0	10	Nerve growth factor; ~ B8QCI0
			2272.4	1	ETXVSXXEEHPD^{ca}EVSHXFR	99.0	10	svVEGF: ~ Q90X24
			2060.0	1	NAXTSYGSYGCNCGWGHR	99.0	10	Phospholipase A_2, K49; ~ P49121
15b	0.4	10	1460.7	1	TEHTDCECRPR	72.9	-	svVEGF
16	12.8	13	1474.7	1	AXXCEEBNPCXK	99.0	16	Phospholipase A_2, K49; ~ P49121
17	13.5	13	1754.9	1	EMCECDBAVAXCXR	99.0	14	Phospholipase A_2, K49; ~ P49121
			1104.6	1	DRYSYSWK	99.0	9	
18	1.0	16	1505.6	1	CCFVHDCCYGK	99.0	18	Phospholipase A_2, D49; ~ P51972
			1070.5	1	DNXDTYN^{da}SK	97.0	9	
19a	0.3	28	1526.8	1	XXGGDECNXNEHR	98.3	7	Serine proteinase; ~ Q9DF68
			1129.7	1	FXVAXYTFR	76.3	6	
19b	0.6	16	1505.6	1	CCFVHDCCYGK	99.0	17	Phospholipase A_2, D49; ~ P51972
			1070.5	1	DNXDTYN^{da}SK	96.9	10	
20a	2.0	28	1498.9	1	VVGGDECNXNEHR	95.2	6	Serine proteinase; ~ Q9YGJ8
20b	2.5	26	1129.7	1	FXVAXYTFR	99.0	10	Serine proteinase; ~ Q9DF68
			1526.8	1	XXGGDECNXNEHR	76.6	7	
20c	3.6	13	1505.6	1	CCFVHDCCYGK	99.0	16	Phospholipase A_2, D49; ~ P51972
21	6.9	13	980.5	1	BXCECDR	88.5	-	Phospholipase A_2, D49; ~ Q90W39
22a	0.4	31	1526.9	1	XXGGDECNXNEHR	99.0	9	Serine proteinase; ~ P81176
22b	0.6	26	1189.7	1	WDBDXMXXR	99.0	7	Serine proteinase; ~ P09872
			1531.9	1	GXAATTXCAGXXEGGK	99.0	18	
22c	0.2	17	1531.9	1	GXAATTXCAGXXEGGK	99.0	12	Serine proteinase; ~ P09872
			1498.8	1	VVGGDECNXNEHR	99.0	8	
22d	0.6	13	980.5	1	BXCECDR	88.5	-	Phospholipase A_2, D49; ~ Q90W39
23a	0.8	29	1531.9	1	GXAATTXCAGXXEGGK	99.0	10	Serine proteinase; ~ P09872
			2260.3	1	NSAHXAPXSXPSNPPSVGSVCR	99.0	12	
			2578.4	1	ETYPDVPHCANXNXXDYEVCR	99.0	12	
			2562.4	1	TFXCGGTXXNBEWVXTAAHCDR	99.0	10	
			2856.6	1	GDSGGPXXCNGBFBGXXSVGGNPCABPR	99.0	8	
23b	1.4	25	1457.9	1	XXNEDEBTRDPK	99.0	9	Serine proteinase; ~ Q9YGJ8
			1512.8	1	VXGGDECNXNEHR	99.0	10	

23c	1.1	11	1202.7	1	XWBTGXWWX	99.0	10	Ohanin-like; ~ Q27J48
			2073.1	1	ADVTFDSNTAFSSXVVSANK	99.0	22	
			1241.6	1	DFSWEWTDR	99.0	8	C-type lectin/lectin-like; ~ G8FML6
			1401.8	1	GBAEVWXGXWDK	99.0	14	
			1572.8	1	EFCVEXVSXTGYR	99.0	13	
24a	0.9	29	1512.7	1	VXGGDECNXNEHR	99.0	10	Serine proteinase; ~ Q9PTL3
			2260.1	1	NSAHXAPXSXPSNPPSVGSVCR	99.0	10	
24b	1.0	26	1512.8	1	VXGGDECNXNEHR	99.0	7	Serine proteinase; ~ Q9PTL3
			2260.3	1	NSAHXAPXSXPSNPPSVGSVCR	99.0	10	
24c	1.2	13	1112.5	1	DNBDTYDNK	99.0	12	Phospholipase A_2, D49; ~ Q7SID6
			2217.1	1	SGXWYYGSYGCYCGAGGBGR	99.0	9	
			1505.6	1	CCFVHDCCYGK	99.0	17	
			981.4	1	EXCECDR	99.0	9	
25a	0.5	39	1605.8	1	XXCAGVXEGGXDTCK	99.0	14	Serine proteinase; ~ Q9PSN3
			1277.8	1	XAXDXEXATYR	99.0	11	
			1512.7	1	VXGGDECNXNEHR	99.0	8	
			1189.7	1	WDBDXMXXR	99.0	7	
			1762.0	1	XXCAGVXEGGXDTCBR	99.0	11	
			2317.3	1	NSEHXAPXSXPSSPPXVGSVCR	99.0	20	
			2218.1	1	DSGGPXXCNGBFBGXVSWGPK	99.0	23	
25b	1.0	28	1097.7	1	FXAXVYTDR	99.0	9	Serine proteinase; ~ Q71QI3
			1498.8	1	VVGGDECNXNEHR	92.0	6	
25c	1.5	25	2900.7	1	XDRPVSNSAHXAPXSXPSSPPSVGSVCR	99.0	12	Serine proteinase; ~ Q9YGJ9
			1824.1	1	XAPXSXPSSPPSVGSVCR	99.0	10	
			1512.8	1	VXGGDECNXNEHR	99.0	8	
			1190.7	1	XMGWGTXSPTK	99.0	12	
			1097.7	1	FXAXVYTDR	99.0	13	
25d	0.9	23	1498.6	1	VVGGDECNXNEHR	99.0	9	Serine proteinase; ~ Q9YGJ8
26a	0.6	40	1762.0	1	XXCAGVXEGGXDTCBR	99.0	12	Serine proteinase; ~ Q9PSN3
			2317.4	1	NSEHXAPXSXPSSPPXVGSVCR	99.0	16	
			1512.8	1	VXGGDECNXNEHR	99.0	8	
26b	0.3	37	-	1	unknown	-	-	-
26c	1.3	25	1597.0	1	BXXNEDEBXRNPK	99.0	8	Serine proteinase; ~ Q8AY79
			1498.8	1	VVGGDECNXNEHR	99.0	7	
27a	1.0	41	1747.1	1	BBDDEBDBDXMXXR	99.0	10	Serine proteinase; ~ Q2QA04
			1512.8	1	VXGGDECNXNEHR	99.0	10	
27b	0.3	37	1514.7	1	ETDYEEFXEXAR	99.0	9	L-amino acid oxidase; ~ Q90W54

27c	0.3	31	1514.7	1	ETDYEEFXEXAR	99.0	9	L-amino acid oxidase; ~ Q90W54
			1165.7	1	XBFEPPXPPK	99.0	9	
			1123.5	1	HDDXFGYEK	99.0	11	
			1711.9	1	DCGDXVXNDXSXXHB	99.0	14	
27d	0.6	26	2857.6	1	GDSGGPXXCNGBFBGXXSVGGNPCABPR	99.0	10	Serine proteinase; ~ E5L0E6
			2260.4	1	NSAHXAPXSXPSNPPSVGSVCR	95.0	6	
28a	0.3	36	1498.7	1	VVGGDECNXNEHR	99.0	9	Serine proteinase; ~ Q71QJ1
28b	0.4	29	1514.8	1	ETDYEEFXEXAR	99.0	11	L-amino acid oxidase; ~ Q90W54
			2523.4	1	FGXEXNEFFBENDNAWYFXK	99.0	8	
			2953.7	1	YAMGGXTTFTPYBFBHFSEAXTAPFK	99.0	9	
			2347.4	1	XYFAGEYTABFHGWXDSTXK	99.0	21	
28c	0.3	26	1762.1	1	XXCAGVXEGGXDTCBR	99.0	8	Serine proteinase; ~ Q9PSN3
			3363.8	1	SSCDGDSGGPXXCNGEXBGXVSWGGDXCABPR	99.0	12	
			2317.4	1	NSEHXAPXSXPSSPPXVGSVCR	99.0	13	
			2218.3	1	DSGGPXXCNGBFBGXVSWGPK	99.0	18	
29a	0.4	48	1514.8	1	ETDYEEFXEXAR	99.0	8	L-amino acid oxidase; ~ Q90W54
			2347.4	1	XYFAGEYTABFHGWXDSTXK	99.0	10	
29b	0.2	41	2856.6	1	GDSGGPXXCNGBFBGXXSVGGNPCABPR	99.0	13	Serine proteinase; ~ P09872
			1531.9	1	GXAATTXCAGXXEGGK	99.0	7	
			3362.9	1	SSCDGDSGGPXXCNGEXBGXVSWGGDXCABPR	99.0	15	
29c	0.2	31	1468.8	1	XXNEDEBXRNPK	99.0	8	Serine proteinase; ~ Q8AY79
			1596.9	1	BXXNEDEBXRNPK	99.0	9	
29d	0.2	28	1526.6	1	XXGGDECNXNEHR	91.0	7	Serine proteinase; ~ Q9YGJ9
29'e	0.1	15	1327.8	1	YVEXVXXADHR	99.0	9	Metalloproteinase; ~ B7U492
29"f	0.1	10	1594.7	1	DBEDWYANXGPMR	99.0	11	L-amino acid oxidase; ~ Q90W54
			1514.7	1	ETDYEEFXEXAR	99.0	15	
			1220.6	1	RNPXEECFR	97.5	8	
30	4.0	47	3362.9	1	SSCDGDSGGPXXCNGEXBGXVSWGGDXCABPR	99.0	13	Serine proteinase; ~ B0VXT7
31a	0.3	210	-	1	unknown	-	-	-
31b	1.4	48	1123.5	1	HDDXFGYEK	99.0	12	L-amino acid oxidase; ~ Q90W54
			1064.5	1	NPXEECFR	99.0	11	
			1514.7	1	ETDYEEFXEXAR	99.0	11	
31c	2.1	37	1733.9	1	MYDXVNVXTPXYHR	99.0	10	Metalloproteinase; ~ Q9DGB9
			2929.2	1	TDVVSPAVCGNYFVEVGEECDCGSPR	99.0	12	
			1368.6	1	XYCFPNSPENK	98.9	6	
32a	0.8	49	1514.7	1	ETDYEEFXEXAR	99.0	11	L-amino acid oxidase; ~ Q90W54

32b	3.2	23	1313.9	1	YVEXVXVADHR	99.0	14	Metalloproteinase; ~ Q92031
32c	2.6	20	1067.5	1	YNGDSDBXR	96.1	6	Metalloproteinase; ~ P28891
33a	1.7	50	1514.7	1	ETDYEEFXEXAR	99.0	10	L-amino acid oxidase; ~ Q90W54
33b	2.0	23	1310.7	1	SHDNABXXTAXK	99.0	15	Metalloproteinase; ~ P84035
33c	4.3	20	1312.9	1	YVBXVXVADHR	99.0	14	Metalloproteinase; ~ P28891
			2564.6	1	XSHDNABXXTAXEXDGETXGXANR	99.0	12	
			3407.0	1	BRHDNABXXTAXDFDGDTVGXAYVGGMCBXK	99.0	11	
			3122.8	1	HDNABXXTAXDFDGDTVGXAYVGGMCBXK	99.0	25	
			2169.3	1	SHDNABXXTAXVFDEGXXGR	99.0	26	
34a	0.5	51	2169.1	1	SHDNABXXTAXVFDEGXXGR	99.0	27	Metalloproteinase; ~ B7U492
			1312.7	1	YVBXVXVADHR	99.0	11	
34b	0.8	30	1380.9	1	YXEXFXVVDNR	99.0	9	Metalloproteinase; ~ P0C6E3
			1313.8	1	YVEXVXVADHR	99.0	12	
34c	0.8	28	1380.9	1	YXEXFXVVDNR	99.0	11	Metalloproteinase; ~ P0C6E3
			1652.0	1	XYEXVNXXNEXYR	99.0	13	
			1313.8	1	YVEXVXVADHR	99.0	15	
34d	0.3	21	1313.8	1	YVEXVXVADHR	99.0	15	Metalloproteinase; ~ P0C6E3
			1801.1	1	TSHDNABXXTAXVFNR	99.0	7	
35a	1.7	36	3432.8	1	NEPSGTDXVSPPVCGNDXXEVGEECDCGCPR	99.0	16	Metalloproteinase; ~ P0C6E3
			2564.6	1	XSHDNABXXTAXEXDGETXGXANR	99.0	17	
			1327.8	1	YVEXVXXADHR	99.0	9	
			1652.0	1	XYEXVNXXNEXYR	99.0	14	
			1312.8	1	YVBXVXVADHR	99.0	13	
35b	3.0	22	1327.8	1	YVEXVXXADHR	99.0	8	Metalloproteinase; ~ P0C6E3
			3432.8	1	NEPSGTDXVSPPVCGNDXXEVGEECDCGCPR	99.0	18	
			2124.0	1	YSWVBCESGECCDBCR	99.0	11	
			1652.0	1	XYEXVNXXNEXYR	99.0	15	

Figure 2E

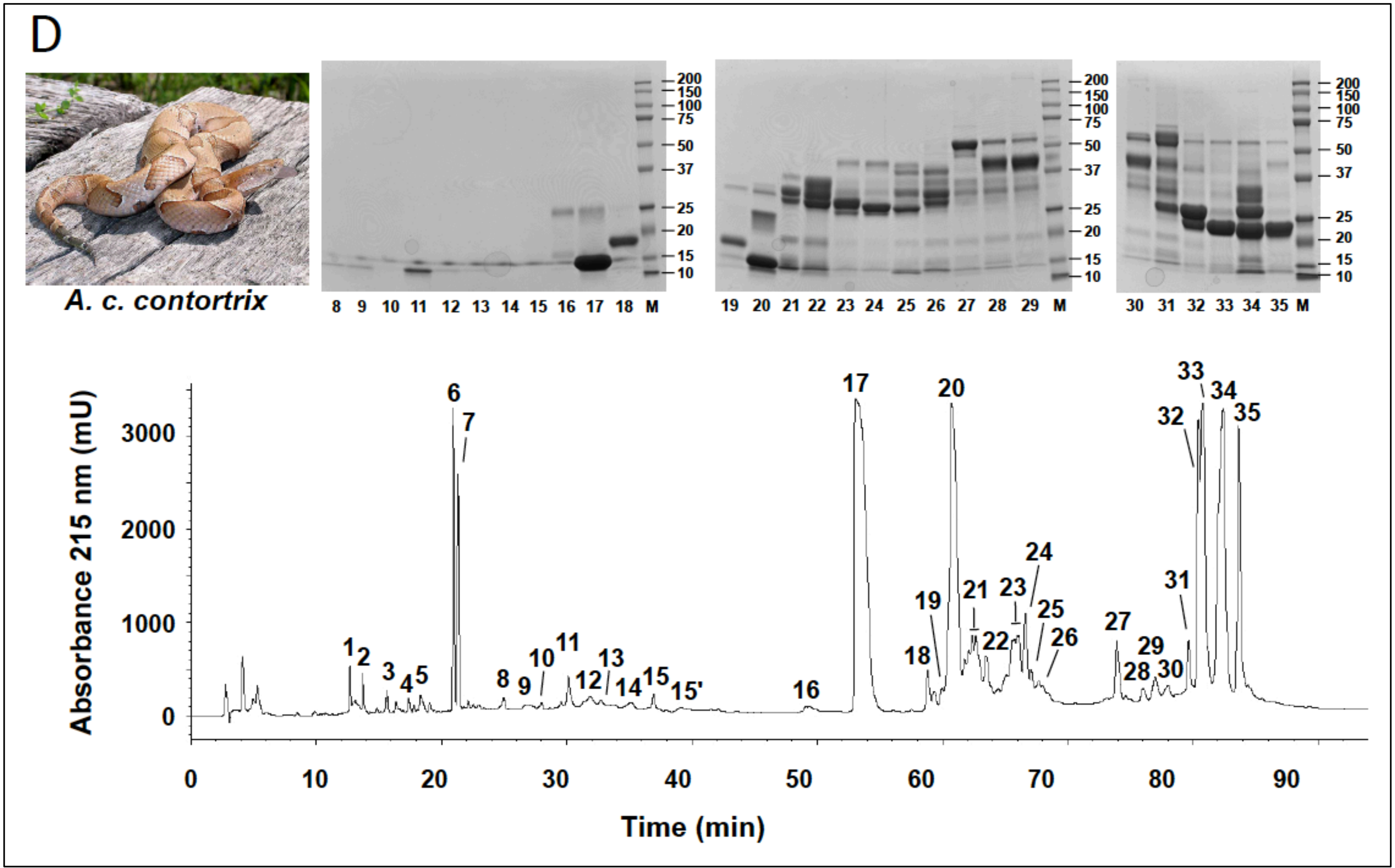
D
A. c. contortrix
8 9 10 11 12 13 14 15 16 17 18 M
19 20 21 22 23 24 25 26 27 28 29 M
30 31 32 33 34 35 M
200
150
100
75
50
37
25
20
15
10
Absorbance 215 nm (mU)
0
1000
2000
3000
Time (min)
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Table S4: Assignment of the RP-HPLC isolated fractions of *Agkistrodon contortrix contortrix* venom to protein families by MALDI-TOF-TOF or nESI-MS-MS of selected peptide ions from in-gel trypsin-digested protein bands from the SDS-PAGE shown in Fig.2D. * Cysteine residues are carbamidomethylated. X: Leu/Ile; B: Lys/Gln; Z, pyroglutamate (2-oxo-pyrrolidone carboxylic acid). ^{ox}: oxidized; ^{da}: deamidated; ^{ca}: carbamidomethyl; Mass estimations by SDS-PAGE (reducing conditions) are indicated in kDa, or in parentheses when determined by ESI-MS. Confidence (Conf) and Score (Sc) values are calculated by the Paragon algorithm of ProteinPilot®.

Peak	%	Mass, kDa	Peptide ion		MS/MS-derived or N-terminal (Nt) sequence	Conf (%)	Sc	Protein family; ~ related protein *
		(ESI-MS)	m/z	z				
1	0.3		385.3	1	TPPA			Bradykinin-inhibitory peptide; P85025
2	0.2		539.2	1	TPPAGP			Bradykinin-inhibitory peptide; P85025
3	0.2		865.4	1	PAGPDVGPR			Bradykinin-inhibitory peptide; P85025
			481.7	2	PPAGPDVGPR			Bradykinin-inhibitory peptide; P85025
			532.3	2	TPPAGPDVGPR			Bradykinin-inhibitory peptide; P85025
4	0.2		592.2	2	TPNXTPEBBR			N-t fragment of PII-SVMP; ACJ61245
5	0.3		398.8	2	BVTPVPR			Fragment of PI-SVMP; ACV83930
6	3.0		452.1	1	ZNW+Na			SVMP inhibitor; P01021
			430.2	1	ZNW			SVMP inhibitor; P01021
7	2.2		444.1	1	ZBW			SVMP inhibitor; P01021
8	0.4	12	-	-	Nt: DAPANPCCDAATCKL			Disintegrin, acostatin β; Q805F6
9	0.4	12	1967.8	1	XTPGABCAEGXCCDBCK	99.0	7	Disintegrin; ~ C9E1S2
10	0.2	(13508)	-	-	Nt: IAPANPCCDAATCKL	-	-	Disintegrin, acostatin αβ; PDB 3C05
11	0.9	11	1870.8	1	GDDVNDYCNGXSAGCPR	99.0	13	Disintegrin; ~ P16338
			1967.8	1	XTPGABCAEGXCCDBCK	99.0	12	
12	1.0	13	2059.9	1	NAXTSYGSYGCNCGWGHR	99.0	7	Phospholipase A$_2$, K49: ~ P49121
13	0.4	13	2059.9	1	NAXTSYGSYGCNCGWGHR	99.0	6	Phospholipase A$_2$, K49: ~ P49121
14	0.4		2015.8	1	Nt: GQGCFGLKLDRIGSMSGMGC	-	-	C-natriuretic peptide; ~ P0CV87
15	0.2	13	2059.9	1	NAXTSYGSYGCNCGWGHR	99.0	7	Phospholipase A$_2$, K49; ~ P49121
	0.2				Nt: DIVSPPVCGNDILEV			Long disintegrin bilitoxin; P0C6E3
15'	<0.1				Nt: DIVSPPVCGNEVLEVG	-	-	DC fragment of metalloproteinase; ~ AEJ31992
16a	0.3	24	1420.7	1	A^{ca}XTMEGNBASWR	99.0	9	Nerve growth factor; ~ Q9DEZ9
			1815.9	1	H^{ca}WNSYCTTTNTFVK	99.0	11	
			1111.6	1	NPNPVPTGCR	99.0	7	

16b	0.1	13	-	-	Nt: SPPGIWKRADVTFASNTA	-	-	Ohanin-like/vespryn; AEJ32004
17a	2.0	(13993)			Nt: SLLELGKMILQETGKNAITSYGSYG			Phospholipase A$_2$, K49; ~ P49121
			2059.9	1	NAXTSYGSYGCNCGWGHR	95.1	7	
17b	18.1	13			Nt: SLLELGKMILQETGKNAITSYGSYG			Phospholipase A$_2$, K49; ~ P49121
			2059.9	1	NAXTSYGSYGCNCGWGHR	99.0	13	
18	0.8	17	1505.6	1	CCFVHDCCYGK	99.0	12	Phospholipase A$_2$, D49: ~ Q91506
			1292.5	1	Y^{ca}GCYCGWGGR	98.4	10	
19a	0.1	31	1186.8	1	FXVAXYTFR	97.7	8	Serine proteinase; ~ P0CV90
19b	0.3	18	1562.6	1	CCFVH^{ca}DCCYGK	99.0	11	Phospholipase A$_2$, D49; ~ Q91506
20a	1.2	30	1597.8	1	CANXNXXDYSVCR	99.0	9	Serine proteinase; ~ Q9DF68
			1186.7	1	F^{ca}XVAXYTFR	82.8	7	
20b	3.7	24	1537.7	1	MEWYPEAAANAER	99.0	9	CRISP; ~ Q7ZTA0
			1195.6	1	SVDFDSESPR	95.7	9	
20c	8.7	(14038)	-	-	Nt: NVYDFEKLIQKIVGR	-	-	Phospholipase A$_2$, D49; ~ P59265
			1562.6	1	CCFVH^{ca}DCCYGK	99.0	11	
			865.5	1	BAAXCFR	66.5	8	
21a	0.3	35	-	-	Nt: VVGGDECNINEHRFL	-	-	Serine proteinase; ~ P82981
21b	1.4	29	1498.7	1	VVGGDECNXNEHR	93.0	7	Serine proteinase; ~ Q71QJ1
			1189.7	1	WDBDXMXXR	59.7	8	
21c	1.0	27	1307.7	1	NFBMXFGVHSK	99.0	12	Serine proteinase; ~ Q9YGJ8
			2494.2	1	ETYPDVPHCANXNXXDHAVCR	99.0	14	
			2888.6	1	XDSPVSDSEHXAPXSXPSSPPSVGSVCR	99.0	14	
21d	0.4	18	1641.8	1	XNXXDYAVCBAAYK	99.0	10	Serine proteinase; ~ P09872
			1531.8	1	GXAATTXCAGXXEGGK	99.0	6	
21e	1.6	12	1206.6	1	XWNDBVCGSK	99.0	9	C-type lectin/lectin-like: ~ Q9PSN0
			1401.7	1	GBAEVWXGXWDK	99.0	10	
			1572.8	1	EFCVEXVSXTGYR	99.0	14	
			1241.5	1	DFSWEWTDR	99.0	14	
22a	0.5	32	2562.3	1	TFXCGGTXXNBEWVXTAAHCDR	99.0	7	Serine proteinase; ~ P09872
			2857.4	1	GDSGGPXXCNGBFBGXXSVGGNPCABPR	99.0	15	
			2260.2	1	NSAHXAPXSXPSNPPSVGSVCR	99.0	11	
22b	0.5	29	2856.4	1	GDSGGPXXCNGBFBGXXSVGGNPCABPR	99.0	14	Serine proteinase; ~ P09872
			1097.6	1	FXAXVYTDR	99.0	10	
			2260.2	1	NSAHXAPXSXPSNPPSVGSVCR	99.0	14	
22c	0.4	26	2494.2	1	ETYPDVPHCANXNXXDHAVCR	99.0	11	Serine proteinase; ~ Q072L6
			2888.5	1	XDSP^{ox}VSDSEHXAPXSXPSSPPSVGSVCR	99.0	18	

			1097.7	1	FXAXVYTDR	97.6	7	
22d	0.1	18	1824.0	1	XAPXSXPSSPPSVGSVCR	99.0	10	Serine proteinase; ~ Q9YGI6
			1097.6	1	FXAXVYTDR	98.7	10	
22e	0.1	12	1369.7	1	BDFSWEWTDR	99.0	9	C-type lectin/lectin-like: ~ Q9PSN0
			1401.8	1	GBAEVWXGXWDK	99.0	13	
			1572.8	1	EFCVEXVSXTGYR	99.0	15	
			1241.6	1	DFSWEWTDR	99.0	13	
23a	0.7	40	-	-	unknown	-	-	
23b	3.3	26	2119.2	1	SAHXAPXSXPSSPPSVGSVCR	99.0	12	Serine proteinase; ~ Q9YGJ9
			1824.0	1	XAPXSXPSSPPSVGSVCR	99.0	13	
			1097.6	1	FXAXVYTDR	98.9	11	
23c	1.0	24	2206.1	1	XXDDAACBPGYPEVXPEYR	99.0	9	Serine proteinase; ~ P82981
			2433.3	1	XNXXDDAACBPGYPEVXPEYR	99.0	10	
			1097.6	1	FXAXVYTDR	97.9	7	
23d	0.3	12	1401.8	1	GBAEVWXGXWDK	99.0	13	C-type lectin/lectin-like: ~ Q9PSN0
			1572.8	1	EFCVEXVSXTGYR	99.0	12	
			1241.6	1	DFSWEWTDR	99.0	11	
			1288.6	1	SCTDYXTWDK	96.7	7	
24a	0.4	40	1605.8	1	XXCAGVXEGGXDTCK	99.0	11	Serine proteinase; ~ Q9PSN3
			2218.1	1	DSGGPXXCN^{da}GBFBGXVSWGPK	99.0	13	
			2317.3	1	NSEHXAPXSXPSSPPXVGSVCR	99.0	16	
24b	1.3	25	1097.6	1	FXAXVYTDR	97.9	8	Serine proteinase; ~ Q8AY79
			2451.3	1	AVGXXGEFVDGHPYSDXDXDYR	97.2	10	
			1257.7	1	BXXNEDEBXR	95.4	7	
			1498.7	1	VVGGDECNXNEHR	94.2	6	
24c	0.1	12	1572.8	1	EFCVEXVSXTGYR	99.0	11	C-type lectin/lectin-like: ~ Q9PSN0
			1241.6	1	DFSWEWTDR	99.0	10	
			1401.8	1	GBAEVWXGXWDK	98.8	9	
25a	0.1	39	1605.8	1	XXCAGVXEGGXDTCK	99.0	13	Serine proteinase; ~ Q9PSN3
			1512.7	1	VXGGDECNXNEHR	99.0	8	
			2218.1	1	DSGGPXXCN^{da}GBFBGXVSWGPK	99.0	14	
			2317.3	1	NSEHXAPXSXPSSPPXVGSVCR	99.0	16	
25b	0.1	36	2218.1	1	DSGGPXXCN^{da}GBFBGXVSWGPK	99.0	6	Serine proteinase; ~ Q9PSN3
			2317.3	1	NSEHXAPXSXPSSPPXVGSVCR	99.0	14	
25c	0.1	29	1294.7	1	XNXXDYEVCR	98.2	7	Serine proteinase; ~ Q8UUJ1
25d	0.2	25	1498.7	1	VVGGDECNXNEHR	81.8	6	Serine proteinase; ~ Q8AY79
25e	0.1	11	1401.8	1	GBAEVWXGXWDK	99.0	12	C-type lectin/lectin-like: ~ Q9PSN0

			1572.8	1	EFCVEXVSXTGYR	99.0	15	
			1241.6	1	DFSWEWTDR	99.0	11	
26a	0.4	37	2218.1	1	DSGGPXXCN^{da}GBFBGXVSWGPK	99.0	11	Serine proteinase; ~ Q9PSN3
			2317.2	1	NSEHXAPXSXPSSPPXVGSVCR	99.0	12	
26b	0.2	33	2608.2	1	XVNNVVSDXVBXXEDTBVEPEVR	99.0	8	Serine proteinase; ~ P09872
			2857.4	1	GDSGGPXXCN^{da}GBFBGXXSVGGNPCABPR	99.0	12	
			2260.2	1	NSAHXAPXSXPSNPPSVGSVCR	99.0	14	
26c	0.7	29	1639.8	1	CANXNXXDYEVCR	99.0	13	Serine proteinase; ~ Q9DG84
			1294.6	1	XNXXDYEVCR	94.6	8	
26d	0.3	27	1639.8	1	CANXNXXDYEVCR	99.0	14	Serine proteinase; ~ Q9DG84
			1294.6	1	XNXXDYEVCR	99.0	13	
26e	0.1	12	1401.8	1	GBAEVWXGXWDK	99.0	11	C-type lectin/lectin-like; ~ Q9PSN0
			1572.8	1	EFCVEXVSXTGYR	99.0	13	
			1241.6	1	DFSWEWTDR	99.0	13	
			1369.7	1	BDFSWEWTDR	98.5	9	
27a	1.1	52			Nt: ADSRNPXEECFR			L-amino acid oxidase; ~ Q6STF1
			1064.5	1	NPXEECFR	99.0	11	
			1594.8	1	DBEDWYANXGPMR	99.0	17	
			1513.7	1	ETNYEEFXEXAR	99.0	18	
			2347.2	1	XYFAGEYTABFHGWXDSTXK	96.5	6	
27b	0.3	33	2260.2	1	NSAHXAPXSXPSNPPSVGSVCR	99.0	9	Serine proteinase; ~ P09872
27c	0.3	29	1581.8	1	CANXNXXDHAVCR	99.0	9	Serine proteinase; ~ ADP88561
27d	0.1	18	-	-	unknown	-	-	
28a	0.2	52	1594.8	1	DBEDWYANXGPMR	99.0	12	L-amino acid oxidase; ~ Q6STF1
			1513.8	1	ETNYEEFXEXAR	99.0	13	
			1064.5	1	NPXEECFR	98.1	8	
28b	0.3	40	1442.6	1	DECDMADXCTGR	99.0	14	Metalloproteinase; ~ Q9DGB9
			1368.7	1	XYCFPNSPENK	99.0	10	
			1734.0	1	MYDXVNVXTPXYHR	99.0	14	
			1803.8	1	YFVEVGEECDCGSPR	99.0	13	
			1684.7	1	GABCAEGXCCDBCR	99.0	13	
28c	0.2	31	1803.7	1	YFVEVGEECDCGSPR	99.0	11	Metalloproteinase; ~ Q9DGB9
28d	0.1	19	-	-	unknown	-	-	
29a	0.1	250	-	-	unknown	-	-	
29b	0.2	54	1064.5	1	NPXEECFR	99.0	10	L-amino acid oxidase; ~ P0C2D6
			1513.8	1	ETNYEEFXEXAR	99.0	12	

29c	0.9	41	1734.0	1	MYDXVNVXTPXYHR	99.0	18	Metalloproteinase; ~ Q9DGB9
			1803.8	1	YFVEVGEECDCGSPR	99.0	14	
			1684.7	1	GABCAEGXCCDBCR	99.0	17	
			1368.7	1	XYCFPNSPENK	99.0	10	
29d	0.1	31	1803.8	1	YFVEVGEECDCGSPR	99.0	11	Metalloproteinase; ~ Q9DGB9
			1684.7	1	GABCAEGXCCDBCR			
30a	0.1	64	-	-	unknown	-	-	
30b	0.2	61	1064.5	1	NPXEECFR	99.0	8	L-amino acid oxidase; ~ P0C2D6
			1513.8	1	ETNYEEFXEXAR	99.0	16	
30c	0.6	45	1442.6	1	DECDMADXCTGR	99.0	15	Metalloproteinase; ~ Q9DGB9
			1368.7	1	XYCFPNSPENK	99.0	11	
			1734.0	1	MYDXVNVXTPXYHR	99.0	15	
			1803.8	1	YFVEVGEECDCGSPR	99.0	13	
			1684.7	1	GABCAEGXCCDBCR	99.0	13	
30d	0.2	35	1803.8	1	YFVEVGEECDCGSPR	99.0	9	Metalloproteinase; ~ Q9DGB9
31a	0.1	72	1983.9	1	XTPGSBCADGVCCDBCR	94.2	6	Metalloproteinase; ~ O42138
31b	0.4	62	1699.9	1	NBCXYFFGPNAAVAK	99.0	12	Metalloproteinase; ~ O42138
			2316.9	1	DDCDMADXCTGBSAECPTDR	99.0	12	
			1983.8	1	XTPGSBCADGVCCDBCR	98.9	9	
31c	0.3	57	1514.7	1	ETDYEEFXEXAR	99.0	11	L-amino acid oxidase; ~ Q90W54
			1064.5	1	NPXEECFR	98.0	7	
31d	0.3	44	1734.0	1	MYDXVNVXTPXYHR	99.0	10	Metalloproteinase; ~ Q9DGB9
			1684.7	1	GABCAEGXCCDBCR	99.0	9	
			1803.8	1	YFVEVGEECDCGSPR	99.0	12	
			1368.7	1	XYCFPNSPENK	97.6	7	
31e	0.2	33	1512.7	1	VXGGDECNXNEHR	99.0	9	Serine proteinase; ~ P09872
			2856.4	1	GDSGGPXXCNGBFBGXXSVGGNPCABPR	99.0	12	
			2258.1	1	NSAHXAPXSXPSNPPSVGSVCR	99.0	13	
			1189.6	1	WDBDXMXXR	96.0	10	
31f	0.4	28	1401.7	1	BWVHBMVNTMK	99.0	13	Metalloproteinase; ~ Q92032
			1313.7	1	YVEXVXVADHR	99.0	10	
			1384.7	1	Q^{py}WVHBMVNTMK	97.1	5	
31g	0.1	16	1401.7	1	GBAEVWXGXWDK	99.0	14	C-type lectin/lectin-like; ~ Q9PSN0
			1572.8	1	EFCVEXVSXTGYR	99.0	15	
			1241.6	1	DFSWEWTDR	99.0	11	
32a	0.2	58	1513.8	1	ETDYEEFXEXAR	99.0	14	L-amino acid oxidase; ~ Q90W54
32b	0.3	41	-	-	unknown	-	-	

32c	2.8	26	1187.6	1	TPEBBGFPBR	99.0	11	Metalloproteinase; ~ Q92031
			1313.8	1	YVEXVXVADHR	99.0	13	
			1638.9	1	BXNXTPEBBGFPBR	96.6	9	
32d	1.4	24	1913.1	1	BWVHBXVNTXNEXYR	99.0	14	Metalloproteinase; ~ P28891
			3122.6	1	HDNABXXTAXDFDGDTVGXAYVGGMCBXK	99.0	12	
			1576.8	1	SVSHDTXASFGNWR	99.0	12	
			1312.8	1	YVBXVXVADHR	99.0	12	
			1187.6	1	TPEBBGFPBR	99.0	14	
33a	0.6	57	1513.8	1	ETNYEEFXEXAR	99.0	14	L-amino acid oxidase; ~ P0C2D6
33b	7.2	23	2564.4	1	XSHDNABXXTAXEXDGETXGXANR	99.0	17	Metalloproteinase; ~ P28891
			1576.8	1	SVSHDTXASFGNWR	99.0	14	
			2506.5	1	BWVHBXVNTXNEXYRPXNXR	99.0	12	
			2165.1	1	DYBTFXTVNNPBCXXNBP	99.0	16	
			1312.8	1	YVBXVXVADHR	99.0	13	
34a	0.9	57	1064.5	1	NPXEECFR	99.0	8	L-amino acid oxidase; ~ P0C2D6
			1513.8	1	ETNYEEFXEXAR	99.0	14	
34b	2.3	33	1187.6	1	TPEBBGFPBR	99.0	11	Metalloproteinase; ~ Q9IAB0
34c	2.4	26	1187.6	1	TPEBBGFPBR	99.0	13	Metalloproteinase; ~ Q92031
			3786.9	1	VAXXMAHEXGHNXGMGHDDNSCTCGGYSCXMX	99.0	8	
			1313.8	1	PR	99.0	13	
					YVEXVXVADHR			
34d	4.6	22	1313.8	1	YVEXVXVADHR	99.0	10	Metalloproteinase; ~ B7U492
			2297.3	1	BSHDNABXXTAXVFDEGXXGR	99.0	15	
			2169.2	1	SHDNABXXTAXVFDEGXXGR	99.0	29	
34e	1.1	17	1313.8	1	YVEXVXVADHR	99.0	7	Metalloproteinase; ~ Q92031
			1187.6	1	TPEBBGFPBR	99.0	11	
34f	1.6	14	1313.8	1	YVEXVXVADHR	99.0	11	Metalloproteinase; ~ B7U492
			2169.3	1	SHDNABXXTAXVFDEGXXGR	99.0	15	
			1187.6	1	TPEBBGFPBR	98.8	9	
35a	0.3	57	1514.8	1	ETDYEEFXEXAR	99.0	7	L-amino acid oxidase; ~ Q90W54
35b	0.4	44	1514.8	1	ETDYEEFXEXAR	99.0	7	L-amino acid oxidase; ~ Q90W54
35c	5.1	23	1327.8	1	YVEXVXXADHR	99.0	11	Metalloproteinase; ~ B7U492
			1201.6	1	APXAGMCDPNR	99.0	8	
35d	0.5	12	1327.8	1	YVEXVXXADHR	97.1	8	Metalloproteinase; ~ B7U492

Figure 2E

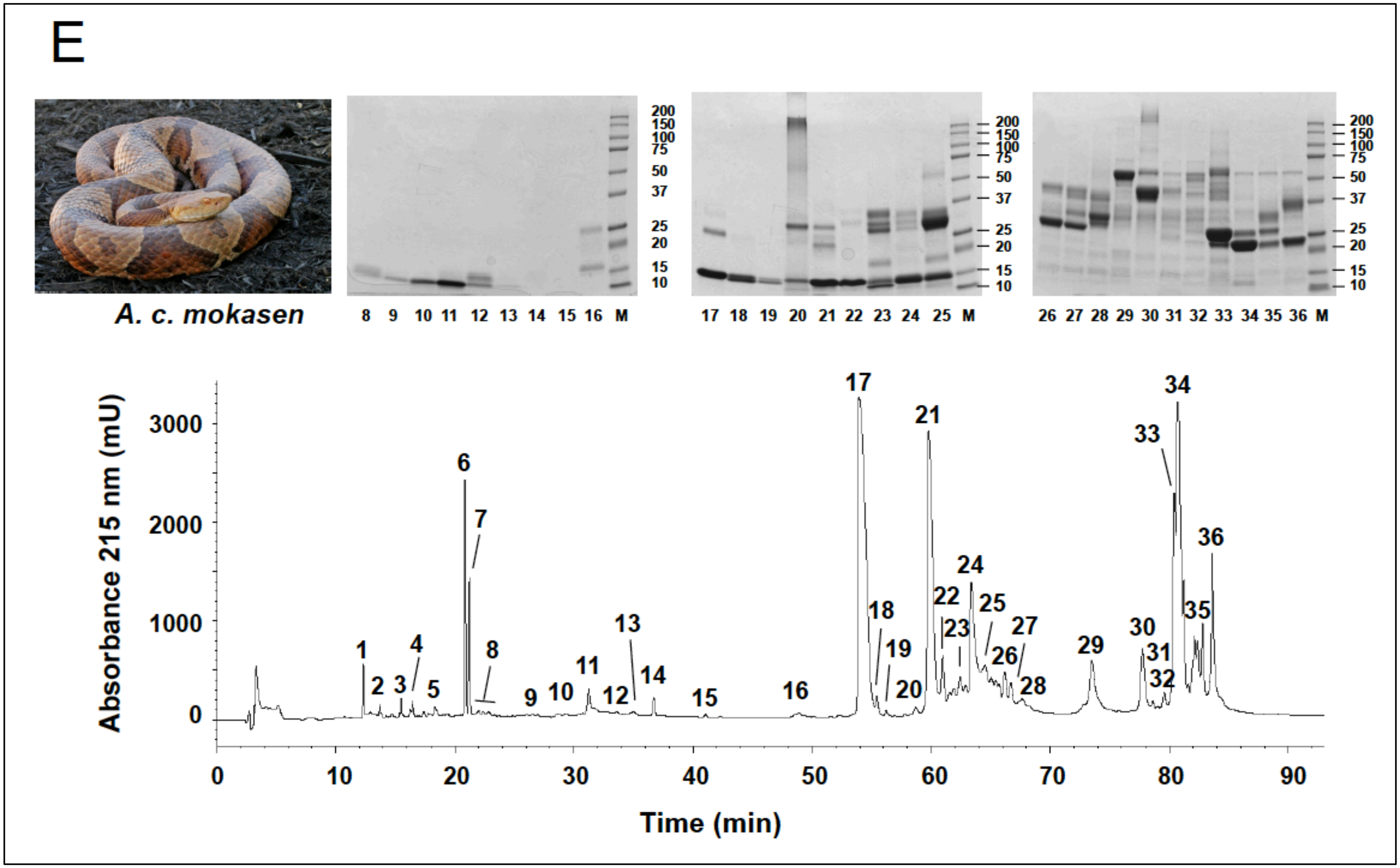

E
A. c. mokasen
8 9 10 11 12 13 14 15 16 M
17 18 19 20 21 22 23 24 25 M
26 27 28 29 30 31 32 33 34 35 36 M
200 150 100 75 50 37 25 20 15 10
Absorbance 215 nm (mU)
0 1000 2000 3000
Time (min)
0 10 20 30 40 50 60 70 80 90
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36

Table S5: Assignment of the RP-HPLC isolated fractions of *Agkistrodon contortrix mokasen* venom to protein families by MALDI-TOF-TOF or nESI-MS-MS of selected peptide ions from in-gel trypsin-digested protein bands from the SDS-PAGE shown in Fig.2E. * Cysteine residues are carbamidomethylated. X: Leu/Ile; B: Lys/Gln; Z, pyroglutamate (2-oxo-pyrrolidone carboxylic acid). ^{ox}: oxidized; ^{da}: deamidated; ^{kyn}: kynurenine. Mass estimations by SDS-PAGE (reducing conditions) are indicated in kDa. Confidence (Conf) and Score (Sc) values are calculated by the Paragon algorithm of ProteinPilot®.

Peak	%	Mass, kDa	Peptide ion		MS/MS-derived sequence	Conf (%)	Sc	Protein family; ~ related protein *
			m/z	z				
1	0.5	-	385.3	1	TPPA	-	-	BIP; P85025
			470.2	1	ZSPR			Fragment NGF-β; ACC85799
2	0.1	-	440.2	1	PARP	-	-	Fragment 3FTx; ~ ABG27005
3	0.1	-	539.3	1	TAGP	-	-	-
			556.2	1	NPXTPE			
4	0.2	-	449.3	1	ZBW^{kyn}	-	-	SVMP inhibitor; P01021
5	0.3	-	532.3	2	TPPAGPDVGPR	-	-	BIP; P85025
6	2.8	-	430.1	1	ZNW	-	-	SVMP inhibitor; P01021
7	1.8	-	444.1	1	ZBW	-	-	SVMP inhibitor; P01021
			466.1	1	ZBW+Na			SVMP inhibitor; P01021
8	0.2	11	-	-	unknown	-	-	-
9	0.3	10	1884.8	1	GDDXDDYCNGXSAGCPR	99.0	7	Disintegrin; ~ Q9IAB0
			2111.9	1	ARGDDXDDYCNGXSAGCPR	99.0	10	
			1983.8	1	XTPGSBCAEGXCCDBCK	99.0	12	
10	0.4	10	1983.8	1	XTPGSBCAEGXCCDBCK	99.0	18	Disintegrin; ~ Q805F4
			1884.8	1	GDDXDDYCNGXSAGCPR	99.0	13	
			2111.9	1	ARGDDXDDYCNGXSAGCPR	99.0	16	
11	0.9	10	1550.6	1	DAPANPCCDAATCK	99.0	10	Disintegrin; ~ Q9IAB0
			1973.8	1	XTTGSBCADGXCCDBCK	99.0	16	
			1884.7	1	GDDXDDYCNGXSAGCPR	99.0	20	
			2111.9	1	ARGDDXDDYCNGXSAGCPR	99.0	19	
			1196.4	1	NPCCDAATCK	99.0	12	
			1137.4	1	CTGBSGDCPR	99.0	12	
			1983.8	1	XTPGSBCAEGXCCDBCK	99.0	27	
12a	0.3	12	2123.7	1	YSWVBCESGECCDBCR	99.0	8	Disintegrin; ~ P0C6E3
12b	0.3	9	2520.0	1	SPPVCGNDXXEVGEECDCGCPR	99.0	12	Disintegrin; ~ P0C6E3

			2123.8	1	YSWVBCESGECCDBCR	99.0	10	
			1983.8	1	XTPGSBCAEGXCCDBCK	99.0	10	
			1884.8	1	GDDXDDYCNGXSAGCPR	97.1	6	
			2111.9	1	ARGDDXDDYCNGXSAGCPR	99.0	14	
13	0.3	9	-	-	unknown	-	-	-
14	0.5	-	-	-	unknown	-	-	-
15	0.1	-	-	-	unknown	-	-	-
16a	0.2	25	1695.8	1	FXRXDSACVCVXSR	99.0	9	Nerve growth factor; ~ Q9DEZ9
			1111.5	1	NPNPVPTGCR	99.0	9	
			1363.6	1	AXTMEGNBASWR	99.0	11	
			1758.8	1	HWNSYCTTTNTFVK	99.0	21	
16b	0.2	15	1111.5	1	NPNPVPTGCR	99.0	11	Nerve growth factor; ~ Q9DEZ9
			1363.6	1	AXTMEGNBASWR	99.0	14	
			1758.8	1	HWNSYCTTTNTFVK	99.0	21	
17a	4.7	25	850.3	1	CCFVHK	86.3	7	Phospholipase A$_2$, K49; ~P49121
17b	16.7	14	2732.1	1	EMCECDBAVAXCXRENXDTYNK	99.0	9	Phospholipase A$_2$, K49; ~P49121
			2860.3	1	EMCECDBAVAXCXRENXDTYNBK	99.0	9	
			1104.5	1	DRYSYSWK	99.0	13	
			1754.7	1	EMCECDBAVAXCXR	99.0	19	
			1408.6	1	DATDRCCFVHK	99.0	10	
			2003.8	1	NAXTSYGSYGCNCGWGHR	98.4	10	
18a	0.1	13	1754.7	1	EMCECDBAVAXCXR	99.0	12	Phospholipase A$_2$, K49; ~P49121
			1104.5	1	DRYSYSWK	99.0	13	
			1408.6	1	DATDRCCFVHK	99.0	11	
			850.3	1	CCFVHK	98.3	7	
18b	0.4	12	1754.7	1	EMCECDBAVAXCXR	99.0	12	Phospholipase A$_2$, K49; ~P49121
			1408.6	1	DATDRCCFVHK	99.0	6	
			1104.5	1	DRYSYSWK	99.0	11	
			850.3	1	CCFVHK	98.0	7	
19	0.3	13	1754.7	1	EMCECDBAVAXCXR	99.0	8	Phospholipase A$_2$, K49; ~P49121
			1408.6	1	DATDRCCFVHK	99.0	7	
			1104.5	1	DRYSYSWK	99.0	11	
			850.3	1	CCFVHK	95.2	7	
20a	0.2	250	1479.8	1	XGEYGFBNAXXVR	99.0	10	Serum albumin (mammalian - contaminant)
			1609.7	1	DVFXGTFXYEYSR	99.0	16	
			1910.9	1	RPCFSAXEVDETYVPK	96.9	7	
20b	0.2	27	2135.0	1	SAHXAP^{ox}XSXPSSPPSVGSVCR	99.0	13	Serine proteinase; ~ Q7T229
			2515.1	1	FHCSGTXXNBEWVXTAAN^{da}CDR	99.0	11	

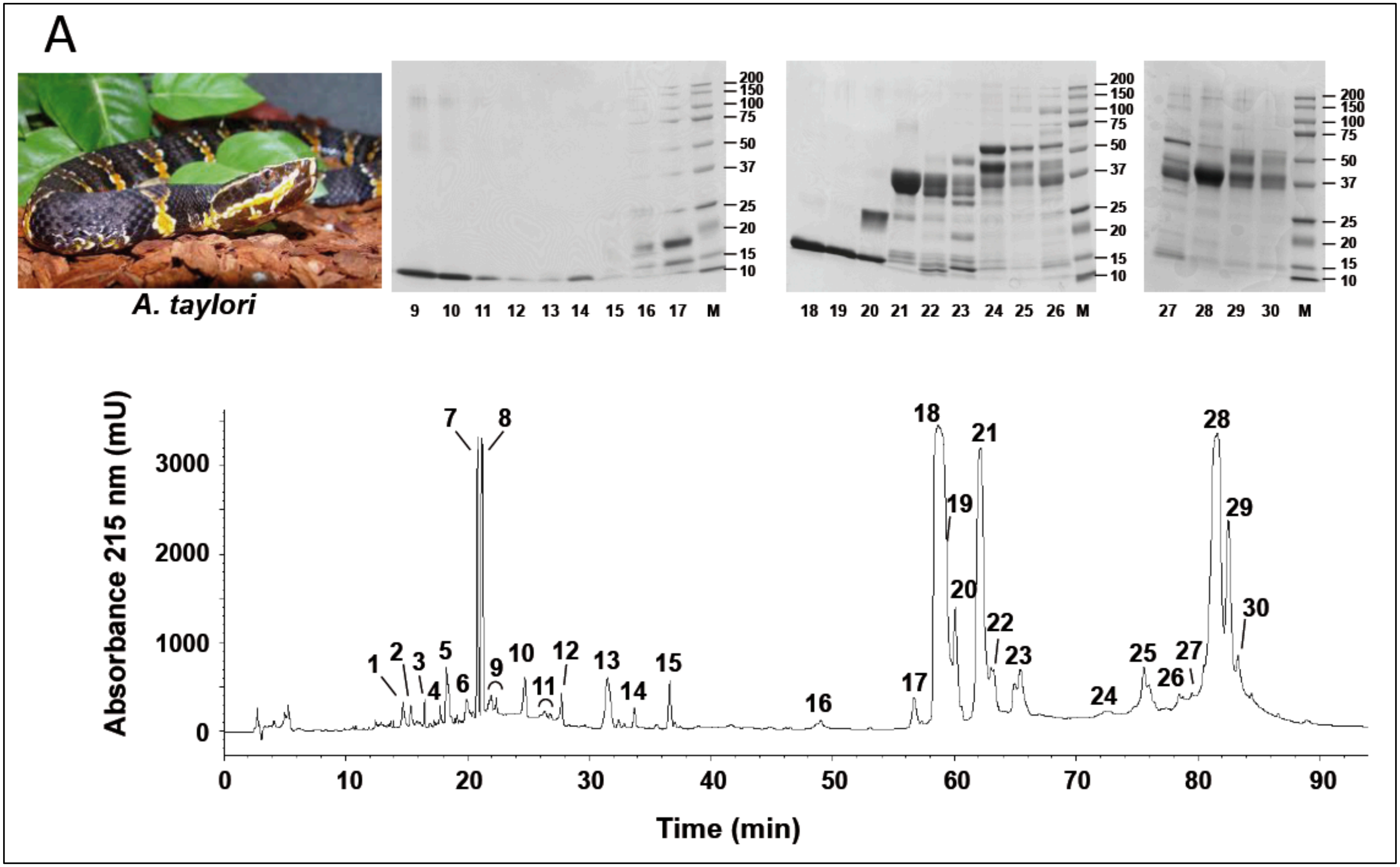
			1189.6	1	WDBDXMXXR	98.9	10	
			1526.6	1	XXGGDECNXNEHR	99.0	15	
			1129.6	1	FXVAXYTFR	98.8	10	
20c	0.1	13	1505.5	1	CCFVHDCCYGK	99.0	15	Phospholipase A$_2$; ~ Q9PVF2
21a	1.9	27	1129.6	1	FXVAXYTFR	98.6	9	Serine proteinase; ~ Q9DF68
21b	1.9	20	2446.1	1	YGXGADPPNAVXGHFTBXVWYK	99.0	10	CRISP; ~ Q7ZT99
			1325.5	1	SXVBBYGCBDK	99.0	6	Serine proteinase; ~ Q7ZT99
			2508.9	1	SGPPCGDCPSACVNGXCTNPCTK	99.0	13	
			1066.6	1	XVDXHNSXR	99.0	8	
			1537.6	1	MEWYPEAAANAER	99.0	13	
			1975.9	1	SVDFDSESPRBPEXBNK	99.0	13	
21c	9.9	12	2283.9	1	EAVHSYAXYGCYCGWGGBGR	99.0	8	Phospholipase A$_2$; ~ A60512
			1505.5	1	CCFVHDCCYGK	99.0	14	
22	1.8	12	1859.8	1	AAAXCFRDNXDTYNSK	99.0	20	Phospholipase A$_2$; ~ P00625
			1505.5	1	CCFVHDCCYGK	99.0	17	
23a	0.4	31	2562.2	1	TFXCGGTXXNBEWVXTAAHCDR	99.0	13	Serine proteinase; ~ P85109
			1512.7	1	VXGGDECNXNEHR	99.0	10	
			2856.4	1	GDSGGPXXCNGBFBGXXSVGGNPCABPR	99.0	25	
			1526.7	1	XXGGDECNXNEHR	99.0	9	
			2578.2	1	ETYPDVPHCANXNXXDYEVCR	99.0	18	
23b	0.1	27	1189.6	1	WDBDXMXXR	99.0	10	Serine proteinase; ~ Q71QJ1
			1498.7	1	VVGGDECNXNEHR	96.0	6	
23c	0.4	25	1512.7	1	VXGGDECNXNEHR	99.0	12	Serine proteinase; ~ Q072L6
			2494.1	1	ETYPDVPHCANXNXXDHAVCR	99.0	19	
			1498.7	1	VVGGDECNXNEHR	99.0	8	
			1307.6	1	NFBMXFGVHSK	99.0	18	
23d	0.1	17	1189.7	1	WDBDXMXXR	99.0	12	Serine proteinase; ~ P09872
			2258.1	1	NSAHXAPXSXPS^{dh}NP^{ox}PSVGSVCR	99.0	14	
23e	0.4	13	1241.5	1	DFSWEWTDR	99.0	8	C-type lectin/lectin-like; ~ Q9YGP1
			1498.7	1	VVGGDECNXNEHR	99.0	9	Serine proteinase; ~ Q9YGJ8
			1505.5	1	CCFVHDCCYGK	99.0	13	Phospholipase A$_2$, D49; ~ Q9PVF2
23f	0.4	10	3026.5	1	NVGVPBVVPDNPERFN^{da}SSPCVXGSPGFR	99.0	17	Ohanin-like; ~ Q27J48
			2201.1	1	ADVTFDSNTAFSSXVVSANBK	99.0	23	
			2357.2	1	RADVTFDSNTAFSSXVVSANBK	99.0	20	
			1525.7	1	FN^{da}SSPCVXGSPGFR	99.0	17	

24	6.1	13	2216.9	1	SGXWYYGSYGCYCGAGGBGR	99.0	13	Phospholipase A_2, D49; ~ Q7SID6
			1505.5	1	CCFVHDCCYGK	99.0	15	
25a	1.7	28	1189.6	1	WDBDXMXXR	99.0	10	Serine proteinase; ~ P09872
			1498.7	1	VVGGDECNXNEHR	99.0	12	
25b	0.2	18	1097.6	1	FXAXVYTDR	99.0	8	Serine proteinase; ~ Q71QI3
25c	1.1	13	1505.5	1	CCFVHDCCYGK	99.0	18	Phospholipase A_2, D49; ~ Q7SID6
			2216.9	1	SGXWYYGSYGCYCGAGGBGR	99.0	12	
26a	0.5	44	1761.9	1	XXCAGVXEGGXDTCBR	99.0	19	Serine proteinase; ~ Q9PSN3
			2317.2	1	NSEHXAPXSXPSSPPXVGSVCR	99.0	24	
			1189.6	1	WDBDXMXXR	99.0	11	
			2217.0	1	DSGGPXXCNGBFBGXVSWGPK	99.0	23	
			1512.7	1	VXGGDECNXNEHR	99.0	24	
26b	1.1	29	1468.8	1	XXNEDEBXRNPK	99.0	17	Serine proteinase; ~ Q8AY79
			1596.8	1	BXXNEDEBXRNPK	99.0	16	
			1498.6	1	VVGGDECNXNEHR	99.0	18	
			1097.6	1	FXAXVYTDR	99.0	11	
27a	0.4	42	1761.8	1	XXCAGVXEGGXDTCBR	99.0	13	Serine proteinase; ~ Q9PSN3
			2317.1	1	NSEHXAPXSXPSSPPXVGSVCR	99.0	22	
			2217.0	1	DSGGPXXCNGBFBGXVSWGPK	99.0	25	
			1189.6	1	WDBDXMXXR	97.0	8	
			1512.6	1	VXGGDECNXNEHR	99.0	12	
27b	0.2	32	1746.9	1	BBDDEBDBDXMXXR	99.0	8	Serine proteinase; ~ Q2QA04
			1512.6	1	VXGGDECNXNEHR	99.0	9	
27c	0.6	27	1468.7	1	XXNEDEBXRNPK	99.0	17	Serine proteinase; ~ Q8AY79
			1596.8	1	BXXNEDEBXRNPK	99.0	18	
			1498.6	1	VVGGDECNXNEHR	99.0	15	
28a	0.1	39	-	-	unknown	-	-	-
28b	0.4	30	1746.8	1	BBDDEBDBDXMXXR	99.0	18	Serine proteinase; ~ Q2QA04
			1512.6	1	VXGGDECNXNEHR	99.0	15	
28c	0.3	28	2916.3	1	XDRPVSNSAHXAPXSXPSSPPSVGSVCR	99.0	11	Serine proteinase; ~ Q9YGJ9
29a	3.1	53	1514.6	1	ETDYEEFXEXAR	99.0	16	L-amino acid oxidase; ~ Q6STF1
			1594.7	1	DBEDWYANXGPMR	99.0	15	
			2560.1	1	NPXEECFRETDYEEFXEXAR	99.0	10	
			2347.1	1	XYFAGEYTABFHGWXDSTXK	99.0	13	
29b	0.5	30	1512.6	1	VXGGDECNXNEHR	98.9	7	Serine proteinase; ~ P09872
30a	0.2	250	1368.6	1	XYCFPNSPENK	95.7	5	Metalloproteinase; ~ Q9DGB9
30b	0.5	56	-	-	unknown	-	-	-

30c	1.9	40	1733.9	1	MYDXVNVXTPXYHR	99.0	13	Metalloproteinase; ~ Q9DGB9
			1137.4	1	E^{py}GNHYGYCR	99.0	9	
			1684.6	1	GABCAEGXCCDBCR	99.0	16	
			1269.5	1	SAECTDRFBR	99.0	9	
			1712.7	1	PASSECDMADXCTGR	99.0	11	
30d	0.2	31	1684.6	1	GABCAEGXCCDBCR	98.2	7	Metalloproteinase; ~ Q9DGB9
31a	0.1	55	1064.5	1	NPXEECFR	99.0	6	L-amino acid oxidase; ~ Q90W54
			1514.7	1	ETDYEEFXEXAR	99.0	8	
31b	0.1	42	1733.8	1	MYDXVNVXTPXYHR	99.0	9	Metalloproteinase; ~ Q9DGB9
			1684.6	1	GABCAEGXCCDBCR	99.0	11	
31c	0.2	30	1512.7	1	VXGGDECNXNEHR	99.0	7	Serine proteinase; ~ Q9PTL3
31d	0.1	24	-	-	unknown	-	-	-
32a	0.3	54	2347.1	1	XYFAGEYTABFHGWXDSTXK	99.0	11	L-amino acid oxidase; ~ P56742
			1514.6	1	ETDYEEFXEXAR	99.0	10	
32b	0.2	49	1503.6	1	YBEEFNNFXN^{da}K	96.7	12	Metalloproteinase; ~ Q92043
			2658.0	1	SECDXAESCTGBSADCPTDDFHR	99.0	16	
			2225.8	1	XHSWVECESGECCEBCR	99.0	15	
32c	0.1	40	-	-	unknown	-	-	-
32d	0.2	32	2856.3	1	GDSGGPXXCNGBFBGXXSVGGNPCABPR	99.0	11	Serine proteinase; ~ P09872
			1512.6	1	VXGGDECNXNEHR	99.0	9	
			2250.1	1	NSAHXAPXSXP^{ox}SNPPSVGSVCR	99.0	17	
32e	0.2	30	1498.6	1	VVGGDECNXNEHR	99.0	10	Serine proteinase; ~ P09872
33a	0.8	56	1815.8	1	YVEFVVVXDHGM^{ox}YTK	99.0	8	Metalloproteinase; ~ O42138
			1983.7	1	XTPGSBCADGVCCDBCR	99.0	10	
33b	0.4	42	1313.7	1	YVEXVXVADHR	99.0	14	Metalloproteinase; ~ Q92043
33c	2.7	24	1313.7	1	YVEXVXVADHR	99.0	15	Metalloproteinase; ~ Q92043
			1438.7	1	SHDNABXXTAXK	95.5	10	
33d	0.8	22	2202.0	1	DXXNVBPAAADTXEAFGDWR	99.0	13	Metalloproteinase; ~ Q805F6
			1418.7	1	VSXTDXEVWSNR	99.0	12	
			2564.3	1	XSHDNABXXTAXEXDGETXGXANR	99.0	23	
			2165.0	1	DYBTFXTVNNPBCXXNBP	99.0	10	
			2293.1	1	BDYBTFXTVNNPBCXXNBP	99.0	12	
			1312.7	1	YVBXVXVADHR	99.0	12	
34a	0.6	55	1514.6	1	ETDYEEFXEXAR	99.0	14	L-amino acid oxidase; ~ Q90W54
			1064.4	1	NPXEECFR	98.1	6	
34b	3.3	25	1313.7	1	YVEXVXVADHR	99.0	15	Metalloproteinase; ~ Q92043

34c	10.2	21	2165.0	1	DYBTFXTVNNPBCXXNBP	99.0	20	Metalloproteinase; ~ P28891
			2293.1	1	BDYBTFXTVNNPBCXXNBP	99.0	23	
			1312.7	1	YVBXVXVADHR	99.0	15	
			2564.2	1	XSHDNABXXTAXEXDGETXGXANR	99.0	10	
35a	1.7	56	1514.7	1	ETDYEEFXEXAR	99.0	8	L-amino acid oxidase; ~ Q90W54
35b	0.4	31	1313.7	1	YVEXVXVADHR	99.0	14	Metalloproteinase; ~ Q92043
35c	2.2	26	1313.7	1	YVEXVXVADHR	99.0	8	Metalloproteinase; ~ Q92043
			1120.6	1	GXSAXGP^{ox}AYBK	98.1	13	
35d	1.5	22	2297.1	1	BSHDNABXXTAXVFDEGXXGR	99.0	25	Metalloproteinase; ~ Q9IAB0
			2169.0	1	SHDNABXXTAXVFDEGXXGR	99.0	25	
			2564.2	1	XSHDNABXXTAXEXDGETXGXANR	99.0	7	
			1312.7	1	YVBXVXVADHR	99.0	13	
36a	0.3	56	1514.7	1	ETDYEEFXEXAR	99.0	7	L-amino acid oxidase; ~ Q90W54
			2347.1	1	XYFAGEYTABFHGWXDSTXK	99.0	7	
36b	2.3	36	2046.0	1	YNPYBYXEXFXVVDNR	99.0	7	Metalloproteinase; ~ P0C6E3
			1380.7	1	YXEXFXVVDNR	99.0	12	
			2123.7	1	YSWVBCESGECCDBCR	99.0	9	
			1651.9	1	XYEXVNXXNEXYR	99.0	10	
36c	2.6	23	1864.9	1	XFSDCSBBDYXTFXK	99.0	12	Metalloproteinase; ~ B7U492
			1327.7	1	YVEXVXXADHR	99.0	15	

Figure 3A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50
37
25
20
15
10
Absorbance 215 nm (mU)
0
1000
2000
3000
Time (min)
0
10
20
30
40
50
60
70
80
90
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30

Table S6: Assignment of the RP-HPLC isolated fractions of *Agkistrodon taylori* venom to protein families by MALDI-TOF-TOF or nESI-MS-MS of selected peptide ions from in-gel trypsin-digested protein bands from the SDS-PAGE shown in Fig.3A. * Cysteine residues are carbamidomethylated. X: Leu/Ile; B: Lys/Gln; Z: pyrrolidone carboxylic acid; Mass estimations by SDS-PAGE (reducing conditions) are indicated in kDa. Confidence (Conf) and Score (Sc) values are calculated by the Paragon algorithm of ProteinPilot®.

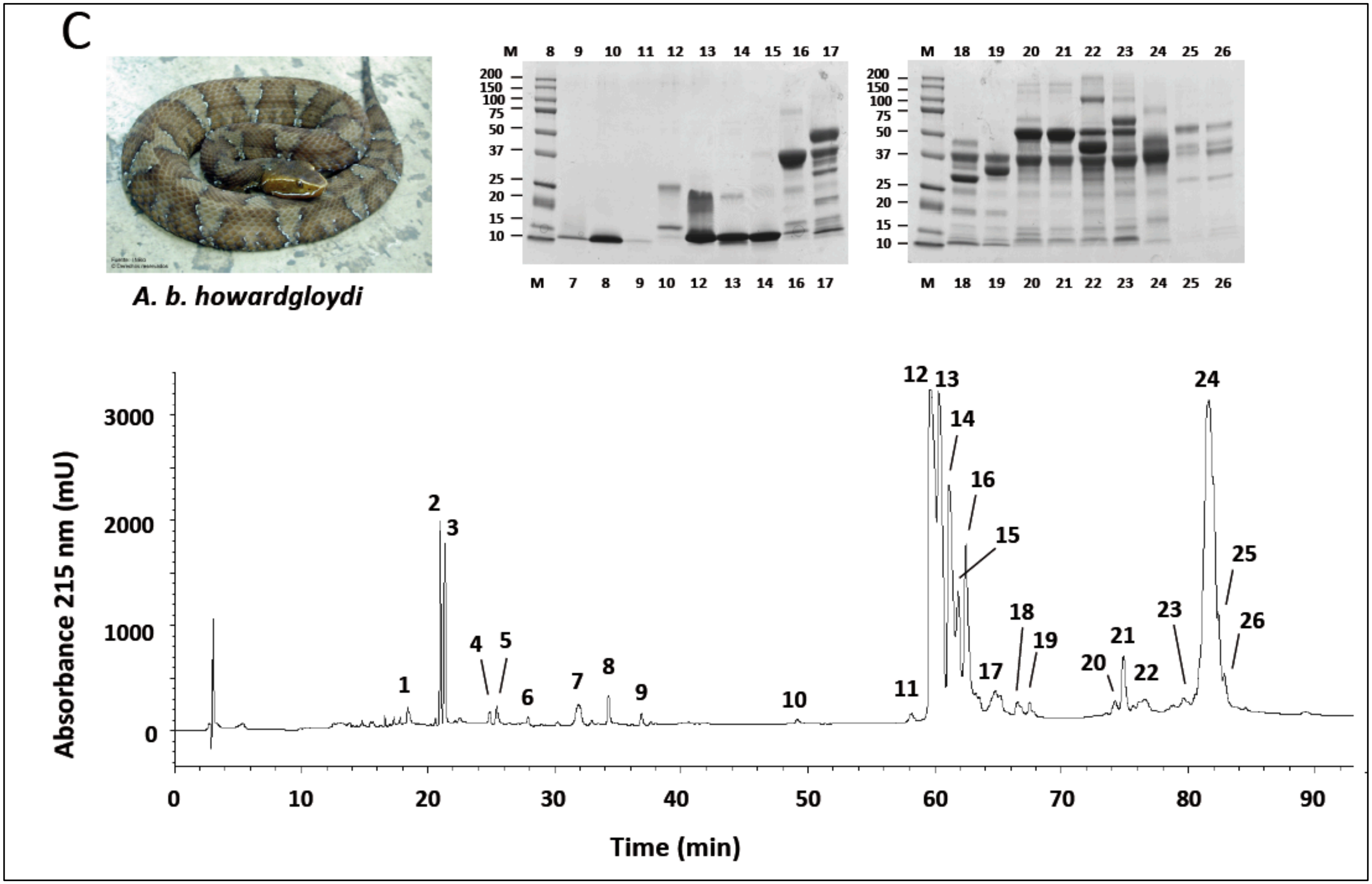
Peak	%	Mass, kDa	Peptide ion		MS/MS-derived sequence	Conf (%)	Sc	Protein family; ~ related protein *
			m/z	z				
1	0.3	-	731.5	1	RPPHPB	-	-	Bradykinin-potentiating peptide fragment; ~ P85167
			1333.8	1	DHHAGVGGGGGGGGGGA			C-type natriuretic peptide precursor; ~ P68515
2	0.2	-	731.5	1	RPPHPB	-	-	Bradykinin-potentiating peptide fragment; ~ P85167
3	0.1	-	-	-	unknown	-	-	-
4	0.3	-	1148.7	1	(SE)THYSDPGR	-	-	Metalloproteinase fragment; ~ Q92032
5	0.7	-	1063.7	1	TPPAGPDVGPR	-	-	Bradykinin-potentiating peptide; ~ P85025
6	0.4	-	-	-	unknown	-	-	-
7	3.0	-	430.5	1	ZNW	-	-	SVMP inhibitor; P01021
			520.1	2	RPPHPBXPP	-	-	Bradykinin-potentiating peptide; ~ P85167
8	3.0	-	444.2	1	ZBW	-	-	SVMP inhibitor; P01021
9	1.2	10	1983.8	1	XTPGSBCAEGXCCDBCK	99	7	Disintegrin; ~ Q805F7
10	1.1	10	1983.9	1	XTPGSBCAEGXCCDBCK	99	13	Disintegrin; ~ Q805F7
			1137.5	1	CTGBSGDCPR	95.4	8	
11	0.6	10	1276.8	1	ZBWPPGHHXPP	-	-	Bradykinin-potentiating peptide; ~ POC7J9
12	0.6	10	1276.8	1	ZBWPPGHHXPP	-	-	Bradykinin-potentiating peptide; ~ POC7J9
13	1.6	10	-	-	unknown	-	-	-
14	0.4	10	1196.5	1	NPCCDAATCK	99	10	Disintegrin; ~ Q805F7
			1983.9	1	XTPGSBCAEGXCCDBCK	99	10	
			2023.0	1	XRPGABCAEGXCCDBCK	99	11	
			1063.5	1	ARGDNPDYR	96.6	9	
15	0.7	10	-	-	unknown	-	-	-
16	0.4	16	1505.6	1	CCFVHDCCYGK	99	10	Phospholipase A_2, D49: ~ P51972
17	0.8	16	1505.6	1	CCFVHDCCYGK	99	10	Phospholipase A_2, D49: ~ P51972
18	23.1	16	1754.9	1	EMCECDBAVAXCXR	99	15	Phospholipase A_2, D49: ~ P51972
			1205.6	1	TDRYSYSWK	99	12	

			1505.6	1	CCFVHDCCYGK	99	18	
			2059.0	1	XAXTSYGSYGCNCGWGHR	99	21	
19	2.2	16	1505.6	1	CCFVHDCCYGK	99	16	Phospholipase A_2, D49: ~ P51972
			2059.0	1	XAXTSYGSYGCNCGWGHR	99	17	
20a	5.6	22	1196.5	1	SXVBBYGCBDK	99	12	CRISP; ~ Q7ZTA0
			1983.9	1	SVDFDSESPR	99	11	
			2023.0	1	MEWYPEAAANAER	99	12	
			1063.5	1	XVDXHNSXR	99	12	
20b	7.8	15	2059.0	1	XAXTSYGSYGCNCGWGHR	99	7	Phospholipase A_2, K49: ~ Q9PSF9
			850.4	1	CCFVHK	98.9	8	
21a	0.6	32	1088.7	1	XYXGMHNXK	79.1	5	Serine proteinase; ~ P09872
21b	0.1	16	1088.6	1	XYXGMHNXK	99	10	Serine proteinase; ~ P09872
			1498.7	1	VVGGDECNXNEHR	98.7	8	
21c	0.2	15	1088.5	1	XYXGMHNXK	99	8	Serine proteinase; ~ P09872
			1498.6	1	VVGGDECNXNEHR	88	8	
21d	0.2	14	-	-	unknown	-	-	-
22a	1.1	34	1088.6	1	XYXGMHNXK	99	11	Serine proteinase; ~ P09872
			1498.7	1	VVGGDECNXNEHR	99	14	
			2260.3	1	NSAHXAPXSXPSNPPSVGSVCR	99	26	
22b	1.2	30	1088.6	1	XYXGMHNXK	99	9	Serine proteinase; ~ P09872
			1498.7	1	VVGGDECNXNEHR	99	10	
			2260.3	1	NSAHXAPXSXPSNPPSVGSVCR	99	20	
22c	1.0	11	1519.8	1	NVGVPBVVPDNPER	99	11	Ohanin-like: ~ Q27J48
23a	0.2	43	1526.8	1	XXGGDECNXNEHR	99	14	Serine proteinase: ~ Q9PSN3
			2217.2	1	DSGGPXXCNGBFBGXVSWGPK	99	17	
			1762.0	1	XXCAGVXEGGXDTCBR	99	14	
			1605.9	1	XXCAGVXEGGXDTCK	99	18	
			2317.3	1	NSEHXAPXSXPSSPPXVGSVCR	99	24	
23b	0.2	34	1088.6	1	XYXGMHNXK	99	12	Serine proteinase; ~ P09872
			1456.8	1	SXPSNPPSVGSVCR	99	14	
			2260.2	1	NSAHXAPXSXPSNPPSVGSVCR	99	21	
			1498.7	1	VVGGDECNXNEHR	99	12	
23c	0.3	30	1498.7	1	VVGGDECNXNEHR	99	9	Serine proteinase; ~ Q71QJ1
			1189.7	1	WDBDXMXXR	94.6	6	
23d	0.2	27	2433.3	1	XNXXDDAACBPGYPEVXPEYR	99	7	Serine proteinase; ~ P82981
23e	0.1	18	-	-	unknown	-	-	-

23f	0.2	14	1498.7	1	VVGGDECNXNEHR	97.8	8	Serine proteinase; ~ Q9YGJ8
23g	0.3	13	1401.7	1	GBAEVWXGXWDK	99	12	C-type lectin/lectin-like; ~ Q9PSN0
			1241.5	1	DFSWEWTDR	99	13	
			1572.8	1	EFCVEXVSXTGYR	99	13	
			1206.6	1	XWNDBVCGSK	94.7	5	
24a	2.2	50	2560.1	1	NPXEECFRETDYEEFXEXAR	99	11	L-amino acid oxidase; ~ P56742
			2347.1	1	XYFAGEYTABFHGWXDSTXK	99	17	
			1514.7	1	ETDYEEFXEXAR	99	17	
24b	1.6	40	985.6	1	EHBAFXXK	99		Metalloproteinase; ~ Q9DGB9
			1733.9	1	MYDXVNVXTPXYHR	97.1		
24c	0.9	33	1498.7	1	VVGGDECNXNEHR	99	8	Serine proteinase; ~ P09872
			2260.2	1	NSAHXAPXSXPSNPPSVGSVCR	99	17	
			1088.6	1	XYXGMHNXK	98.8	6	
25a	1.1	51	1514.8	1	ETDYEEFXEXAR	60.7	6	L-amino acid oxidase; ~ Q90W54
25b	0.6	41	985.6	1	EHBAFXXK	99	10	Metalloproteinase; ~ Q8AWI5
26'	0.2	99	-	-	unknown	-	-	-
26a	0.4	53	1514.7	1	ETDYEEFXEXAR	99	13	L-amino acid oxidase; ~ Q90W54
26b	0.3	41	985.6	1	EHBAFXXK	99	11	Metalloproteinase; ~ Q9DGB9
			1368.7	1	XYCFPNSPENK	99	9	
			1734.0	1	MYDXVNVXTPXYHR	99	11	
26c	0.6	34	1088.6	1	XYXGMHNXK	99	11	Serine proteinase; ~ P09872
			2260.2	1	NSAHXAPXSXPSNPPSVGSVCR	99	21	
			1498.7	1	VVGGDECNXNEHR	99	12	
26d	0.3	13	1206.6	1	XWNDBVCGSK	99	7	C-type lectin/lectin-like; ~ Q9PSN0
			1401.7	1	GBAEVWXGXWDK	99	11	
			1572.8	1	EFCVEXVSXTGYR	99	12	
			1241.6	1	DFSWEWTDR	99	11	
27a	1.1	69	1514.8	1	ETDYEEFXEXAR	99	11	L-amino acid oxidase; ~ Q90W54
			1064.5	1	NPXEECFR	93.8	7	
27b	0.8	51	1380.7	1	YXEXFXVVDNR	90.2	5	Metalloproteinase; ~ P0C6E3
27c	1.8	42	1088.6	1	XYXGMHNXK	99	10	Serine proteinase; ~ P09872
			1498.7	1	VVGGDECNXNEHR	99	14	
			2260.2	1	NSAHXAPXSXPSNPPSVGSVCR	99	25	
27d	0.8	15	1621.9	1	XFDEXBAWEDAER	99	13	C-type lectin/lectin-like; ~ Q9PSN0
			1401.8	1	GBAEVWXGXWDK	99	14	
			1572.9	1	EFCVEXVSXTGYR	99	13	
			1206.6	1	XWNDBVCGSK	98	7	

			1241.6	1	DFSWEWTDR	96.1	8	
28	21.7	42	1598.7	1	NCBDPCCNAATCK	99	10	Metalloproteinase; ~ P0C6E3
			2252.0	1	BYSWVBCESGECCDBCR	99	9	
			1380.8	1	YXEXFXVVDNR	99	14	
			2123.9	1	YSWVBCESGECCDBCR	99	10	
			1664.8	1	GVXGSAYPAGMCDPNR	99	13	
			1800.0	1	TSHDNABXXTAXVFNR	99	25	
29a	1.4	52	1652.0	1	XYEXVNXXNEXYR	99	14	Metalloproteinase; ~ P0C6E3
29b	2.1	40	1652.0	1	XYEXVNXXNEXYR	99	15	Metalloproteinase; ~ P0C6E3
			2294.4	1	XYEXVNXXNEXYRPXYXR	99	13	
			1664.8	1	GVXGSAYPAGMCDPNR	99	14	
			2123.9	1	YSWVBCESGECCDBCR	99	14	
			1380.8	1	YXEXFXVVDNR	99	16	
			1800.0	1	TSHDNABXXTAXVFNR	99	26	
			2252.0	1	BYSWVBCESGECCDBCR	96.2	9	
30a	0.6	52	1652.0	1	XYEXVNXXNEXYR	99	11	Metalloproteinase; ~ P0C6E3
30b	1.5	40	2123.8	1	YSWVBCESGECCDBCR	99	8	Metalloproteinase; ~ P0C6E3
			1380.8	1	YXEXFXVVDNR	99	11	
			1800.0	1	TSHDNABXXTAXVFNR	99	14	

Figure 3C


C
A. b. howardgloydi
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150
100
75
50
37
25
20
15
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M 7 8 9 10 12 13 14 16 17
M 18 19 20 21 22 23 24 25 26
200
150
100
75
50
37
25
20
15
10
M 18 19 20 21 22 23 24 25 26
Absorbance 215 nm (mU)
3000
2000
1000
0
Time (min)
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Table S7: Assignment of the RP-HPLC isolated fractions of *Agkistrodon bilineatus howardgloydi* venom to protein families by MALDI-TOF-TOF or nESI-MS/MS of selected peptide ions from in-gel trypsin-digested protein bands from the SDS-PAGE shown in Fig.3C. * Cysteine residues are carbamidomethylated. X: Leu/Ile; B: Lys/Gln; Z, pyroglutamate (2-oxo-pyrrolidone carboxylic acid). ^{ox}: oxidized; ^{da}: deamidated; Mass estimations by SDS-PAGE (reducing conditions) are indicated in kDa, or in parentheses when determined by ESI-MS. (■): unreduced bands. Confidence (Conf) and Score (Sc) values are calculated by the Paragon algorithm of ProteinPilot®.

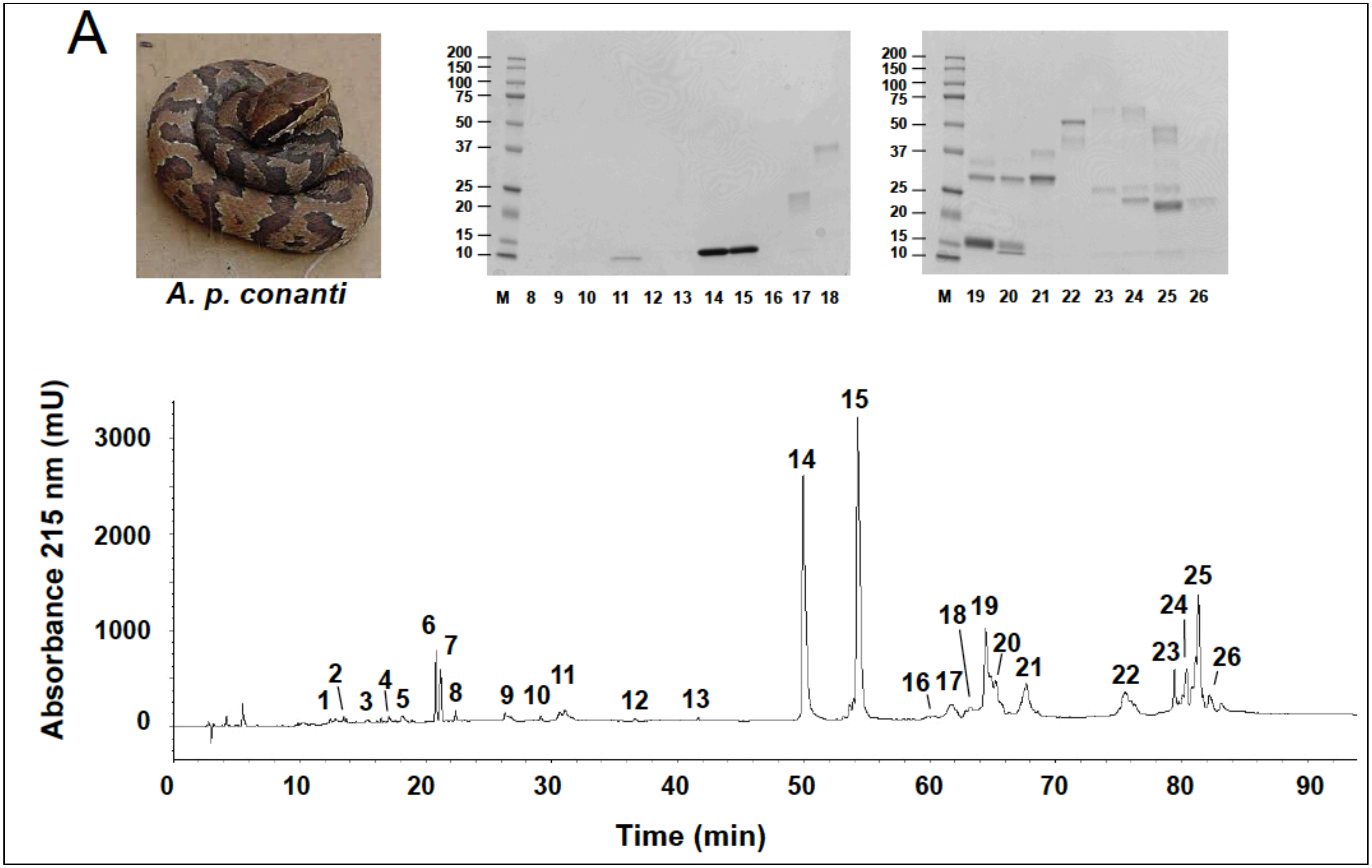
Peak	%	Mass, kDa	Peptide ion		MS/MS-derived or N-terminal (N-t) sequence	Conf (%)	Sc	Protein family; ~ related protein *
		(ESI-MS)	m/z	z				
1	0.4	-	610.4	2	(253.3)HAGVGGGGGGGGA	-	-	PolyHis-Gly peptide; ~ P0DL07
			539.3	1	TPPAGP			Bradykinin-inhibitory peptide
			532.3	2	TPPAGPDVGPR			Bradykinin-inhibitory peptide
2	2.3	-	430.2	1	ZNW	-	-	SVMP inhibitor; P01021
			452.1	1	ZNW+Na			
3	2.2	-	444.4	1	ZBW	-	-	SVMP inhibitor; P01021
4	0.3	-	724.4	2	ZBPWDPXPSPP + NAcHexN	-	-	Bradykinin-potentiating peptide
			805.4	2	ZBPWDPXPSPP + NAcHexN-Hex			Bradykinin-potentiating peptide
5	0.4	-	622.9	2	ZBPWDPXPSPP	-	-	Bradykinin-potentiating peptide
6	0.2	-	639.0	2	ZBWPPGHHXPP	-	-	Bradykinin-potentiating peptide
7	1.2	11	1063.4	1	ARGDNPDYR	95.5	8	Disintegrin; ~ Q805F7
			2022.8	1	XRPGABCAEGXCCDBCK	99.0	6	
			1608.5	1	DAPANPCCDAETCK	99.0	6	
8	0.7	10	2599.1	1	GDWNNDYCTGKSCDCPRNPWN	99.0	10	Disintegrin; ~ Q7SZE0
			2023.0	1	XRPGABCAEGXCCDBCK	97.6	7	
9	0.3	9	1063.4	1	ARGDNPDYR	73.1	6	Disintegrin; ~ Q805F7
10a	0.2	24	1758.7	1	HWNSYCTTTNTFVK	99.0	13	Nerve growth factor; ~ Q9DEZ9
			1363.6	1	AXTMEGNBASWR	98.7	7	
			962.4	1	BYFFETK	98.8	6	
10b		15	1758.9	1	HWNSYCTTTNTFVK	99.0	9	Nerve growth factor; ~ Q9DEZ9
			1696.0	1	FXRXDSACVCVXSR	97.2	6	
11	0.4	■ 20	1505.5	1	CCFVHDCCYGK	99.0	14	Phospholipase A_2, D49; ~ P51972
			2063.8	1	DATDRCCFVHDCCYGK	99.0	11	
12a	15.1	22	2059.1	1	XAXTSYGSYGCNCGWGHR	99.0	6	Phospholipase A_2, K49; Q9PSF9 (*Agkistrodon bilineatus*: PLA_2-II)
12b		12	2059.0	1	XAXTSYGSYGCNCGWGHR	99.0	11	Phospholipase A_2, K49; Q9PSF9
		(13996)	3700.1	1	SXXEXGBMXXBETGBXAXTSYGSYGCNCGWGHR	99.0	8	(*Agkistrodon bilineatus*: PLA_2-II)

			1205.7	1	TDRYSYSWK	99.0	9	
			1408.7	1	DATDRCCFVHK	96.5	11	
13	14.3	12 (14065)	2176.0	1	NAXPFYAFYGCYCGWGGR	95.6	7	Phospholipase A$_2$; ~ P86169
14	9.8	12 (14062)	1505.7	1	CCFVHDCCYGK	99.0	14	Phospholipase A$_2$, D49; ~ P86169
			3067.5	1	SGMXWYSAYGCYCGW^{ox}GGBGRPBDATDR	97.2	11	
			1859.0	1	AAAXCFRDNXDTYNSK	99.0	11	
15	4.6	■ 32	2036.0	1	GXAATTXCAGXXEGGBDTCK	99.0	11	Serine proteinase; ~ P09872
			1104.5	1	XYXGM^{ox}HNXK	99.0	6	
			2260.1	1	NSAHXAPXSXPSNPPSVGSVCR	99.0	12	
16a	5.4	35	2260.3	1	NSAHXAPXSXPSNPPSVGSVCR	99.0	10	Serine proteinase; ~ Q9PTL3
16b	0.7	16	1088.6	1	XYXGMHNXK	99.0	7	Serine proteinase; ~ P09872
			1498.8	1	VVGGDECNXNEHR	95.4	9	
16c	1.2	13	551.3	2	XDXYTYSVK	man	man	Phospholipase A$_2$, D49; ~ P84397
17a	2.3	48	2217.2	1	DSGGPXXCNGBFBGXVSWGPK	99.0	7	Serine proteinase; ~ Q9PSN3 (*Agkistrodon bilineatus*: bilineobin)
17b		38	1531.8	1	GXAATTXCAGXXEGGK	99.0	11	Serine proteinase; ~ P09872
			1088.6	1	XYXGMHNXK	99.0	12	
			1512.7	1	VXGGDECNXNEHR	99.0	7	
			2260.1	1	NSAHXAPXSXPSNPPSVGSVCR	99.0	19	
			1230.6	1	EBYFCXNTR	96.7	6	
17c		34	2260.1	1	NSAHXAPXSXPSNPPSVGSVCR	99.0	8	Serine proteinase; ~ P09872
			1498.6	1	VVGGDECNXNEHR	99.0	9	
17d		30	1561.7	1	NDEVXDBDXM^{ox}XXK	99.0	14	Serine proteinase; ~ P82981
			1582.8	1	BVXNEDEBXRNPK	99.0	11	
			1498.6	1	VVGGDECNXNEHR	99.0	8	
			1454.7	1	VXNEDEBXRNPK	99.0	12	
17e		21	1456.7	1	SXPSNPPSVGSVCR	99.0	8	Serine proteinase; ~ Q71QI4
			929.5	1	XBFGXHSK	93.5	6	
17f		17	1498.6	1	VVGGDECNXNEHR	99.0	8	Serine proteinase; ~ Q9YGJ8
17g	0.3	14	1401.8	1	GBAEVWXGXWDK	99.0	13	C-type lectin/lectin-like; ~ Q9PSN0
			1621.9	1	XFDEXBAWEDAER	99.0	9	
			1241.6	1	DFSWEWTDR	99.0	9	
18a	0.9	44	2217.0	1	DSGGPXXCNGBFBGXVSWGPK	99.0	11	Serine proteinase; ~ Q9PSN3 (*Agkistrodon bilineatus*: bilineobin)
			1761.8	1	XXCAGVXEGGXDTCBR	99.0	8	
			1526.7	1	XXGGDECNXNEHR	99.0	9	
			1655.7	1	CVNXNXFNYTVCR	99.0	9	

			2317.1	1	NSEHXAPXSXPSSPPXVGSVCR	99.0	12	
18b		36	2260.3	1	NSAHXAPXSXPSNPPSVGSVCR	93.3	6	Serine proteinase; ~ Q9PTL3
18c		28	1512.8	1	VXGGDECNXNEHR	99.0	8	Serine proteinase; ~ Q71QJ2
			929.6	1	XBFGXHSK	84.8	8	
18d		24	2260.3	1	NSAHXAPXSXPSNPPSVGSVCR	84.7	6	Serine proteinase; ~ Q9PTL3
18e		19	929.5	1	XBFGXHSK	84.6	6	Serine proteinase; ~ Q71QJ3
			1674.8	1	NYTXWDBDXMXXR	77.7	7	
18f		11	1512.6	1	VXGGDECNXNEHR	99.0	6	Serine proteinase; ~ Q9YGJ2
			888.4	1	FFCXSSK	85.4	7	
			1118.5	1	TXCAGXXEGGK	81.9	6	
19a	0.7	36	1498.8	1	VVGGDECNXNEHR	99.0	9	Serine proteinase; ~ P09872
			2260.3	1	NSAHXAPXSXPSNPPSVGSVCR	99.0	18	
			1104.7	1	XYXGM^{ox}HNXK	96.6	7	
19b		30	1746.8	1	BBDDEBDBDXMXXR	99.0	12	Serine proteinase: ~ Q2QA04
			1118.5	1	TXCAGXXEGGK	99.0	9	
			1498.6	1	VVGGDECNXNEHR	99.0	9	
19c		10	1512.6	1	VXGGDECNXNEHR	99.0	8	Serine proteinase; ~ Q71QJ2
			928.5	1	XBFGXHSK	93.3	9	
20a	0.3	50	2347.3	1	XYFAGEYTABFHGWXDSTXK	99.0	8	L-amino acid oxidase; ~ P56742
20b	0.4	35	1531.7	1	GXAATTXCAGXXEGGK	99.0	8	Serine proteinase; ~ P09872
			1230.5	1	EBYFCXNTR	99.0	7	
			1088.5	1	XYXGMHNXK	99.0	9	
			2260.0	1	NSAHXAPXSXPSNPPSVGSVCR	99.0	19	
			1512.6	1	VXGGDECNXNEHR	94.3	7	
20c	0.1	14	1507.7	1	VVGGDECNXNEHR	99.0	8	Serine proteinase; ~ Q9YGJ8
20d	0.1	12	-	-	unknown	-	-	-
21a	1.5	50	2347.3	1	XYFAGEYTABFHGWXDSTXK	99.0	13	L-amino acid oxidase; ~ P56742
21b	0.8	35	1088.6	1	XYXGMHNXK	99.0	9	Serine proteinase; ~ P09872
			1498.6	1	VVGGDECNXNEHR	99.0	9	
			2260.1	1	NSAHXAPXSXPSNPPSVGSVCR	99.0	18	
			1230.5	1	EBYFCXNTR	98.0	6	
22a	0.3	99	-	-	unknown	-	-	-
22b	0.3	51	2537.3	1	FDXBXN^{da}EFSQ^{da}ENENAWYFXK	93.2	7	L-amino acid oxidase;
22c	0.6	42	1456.9	1	XVXVADYXMFXK	99.0	11	Metalloproteinase; ~ Q4VM08
			1154.6	1	GNHYGYCR	83.4	8	

22d	0.2	34	1088.5	1	XYXGMHNXK	99.0	11	Serine proteinase; ~ P09872
			2260.1	1	NSAHXAPXSXPSNPPSVGSVCR	99.0	23	
			1498.6	1	VVGGDECNXNEHR	99.0	12	
			928.5	1	VXNBDAXR	94.6	8	
22e	0.1	12	-	-	unknown	-	-	-
23a	0.3	60	2347.3	1	XYFAGEYTABFHGWXDSTXK	99.0	8	L-amino acid oxidase; ~ P56742
			2537.4	1	FDXBXN^{da}EFSQ^{da}ENENAWYFXK	99.0	9	
23b	0.2	51	2347.3	1	XYFAGEYTABFHGWXDSTXK	99.0	8	L-amino acid oxidase; ~ P56742
			2537.4	1	FDXBXN^{da}EFSQ^{da}ENENAWYFXK	99.0	9	
23c	0.4	35	1088.5	1	XYXGMHNXK	99.0	9	Serine proteinase; ~ P09872
			2260.0	1	NSAHXAPXSXPSNPPSVGSVCR	99.0	18	
			1498.6	1	VVGGDECNXNEHR	99.0	10	
23d	0.1	13	1622.0	1	XFDEXBAWEDAER	97.5	6	C-type lectin/lectin-like; ~ Q9PSN0
			1241.6	1	DFSWEWTDR	68.8	4	
24a	9.4	44	702.8	2	FAXVGXEXWSNR	man	man	Metalloproteinase; ~ ACV83930
			1016.6	2	(1657.1)YNYXEXFXVVDNR			
24b	16.7	37	2252.1	1	BYSWVBCESGECCDBCR	99.0	8	Metalloproteinase; P0C6E3 (*Agkistrodon bilineatus*: bilitoxin)
			2124.0	1	YSWVBCESGECCDBCR	99.0	9	
			2294.5	1	XYEXVNXXNEXYRPXYXR	99.0	11	
			2046.3	1	YNPYBYXEXFXVVDNR	99.0	16	
			1380.9	1	YXEXFXVVDNR	99.0	14	
			1800.1	1	TSHDNABXXTAXVFNR	99.0	4	
			1726.8	1	NCBDPCCNAATCBK	99.0	9	
			1496.9	1	SASSVTXASFANWR	99.0	11	
25	2.8	54	1223.6	1	HDNABXXTAXK	99.0	7	Metalloproteinase; ~ P84035
26a	1.1	56	2032.1	1	(975.5)XFXVVDNR			Metalloproteinase; P0C6E3 (*Agkistrodon bilineatus*, bilitoxin)
26b		44	2124.0	1	YSWVBCESGECCDBCR	99.0	6	Metalloproteinase; P0C6E3 (*Agkistrodon bilineatus*, bilitoxin)
			2294.5	1	XYEXVNXXNEXYRPXYXR	99.0	9	
			2046.3	1	YNPYBYXEXFXVVDNR	99.0	10	
			1380.9	1	YXEXFXVVDNR	99.0	11	
			1800.1	1	TSHDNABXXTAXVFNR	99.0	9	
26c	0.4	40	2260.1	1	NSAHXAPXSXPSNPPSVGSVCR	99.0	5	Serine proteinase; ~ Q9PTL3
			1498.6	1	VVGGDECNXNEHR	98.8	4	
26d		28	3574.6	1	VSXTDXEVWSDBDXXNVBPAAADTXXEAFGDWR	80.2	7	Metalloproteinase; ~ C9E1S1

Figure 4A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Absorbance 215 nm (mU)
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0 10 20 30 40 50 60 70 80 90
Time (min)

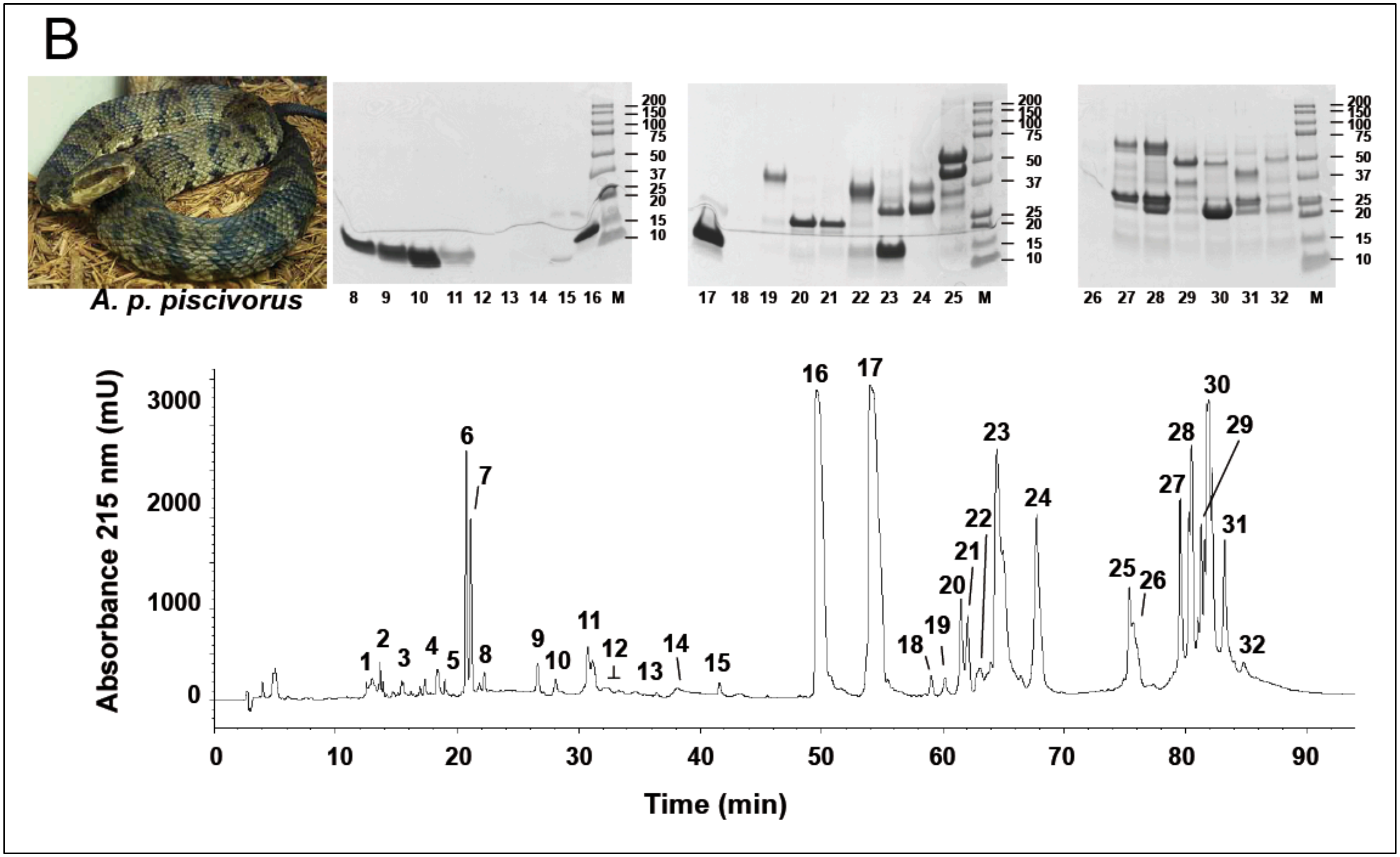
Table S8: Assignment of the RP-HPLC isolated fractions of *Agkistrodon piscivorus conanti* venom to protein families by MALDI-TOF-TOF or nESI-MS-MS of selected peptide ions from in-gel trypsin-digested protein bands from the SDS-PAGE shown in Fig.4A. * Cysteine residues are carbamidomethylated. X: Leu/Ile; B: Lys/Gln; Z, pyroglutamate (2-oxo-pyrrolidone carboxylic acid). ^{da}: deamidated; ^{kyn}: kynurenine. Mass estimations by SDS-PAGE (reducing conditions) are indicated in kDa. Confidence (Conf) and Score (Sc) values are calculated by the Paragon algorithm of ProteinPilot®.

Peak	%	Mass, kDa	Peptide ion		MS/MS-derived or N-terminal (Nt) sequence	Conf (%)	Sc	Protein family; ~ related protein *
			m/z	z				
1	0.2	-	385.3	1	TPPA	-	-	Bradykinin-inhibitory peptide; P85025
2	0.3	-	449.3	1	ZBW^{kyn}	-	-	SVMP inhibitor; P01021
			539.2	1	TPPAGP			Bradykinin-inhibitory peptide; P85025
3	0.2	-	-	-	unknown	-	-	-
4	0.3	-	398.8	2	BVTPVPR	-	-	Fragment of PI-SVMP; ACV83930
5	0.4	-	865.4	1	PAGPDVGPR	-	-	Bradykinin-inhibitory peptide; P85025
			481.7	2	PPAGPDVGPR			Bradykinin-inhibitory peptide; P85025
			532.3	2	TPPAGPDVGPR			Bradykinin-inhibitory peptide; P85025
6	2.1	-	452.1	1	ZNW +Na	-	-	SVMP inhibitor; P01021
			430.1	1	ZNW			SVMP inhibitor; P01021
7	1.8	-	488.1	1	WBPG	-	-	Fragment of C-type lectin; ~ ABP94108
8	0.4	-	467.3	1	BGVY	-	-	Peptide of SVMP; ~ Q0NZY0
9	0.6	-	-	-	unknown	-	-	-
10	0.5	-	-	-	unknown	-	-	-
11	2.2	9	1967.9	1	XTPGABCAEGXCCDBCK	99.0	6	Disintegrin; ~ Q805F4
			1884.8	1	GDDXDDYCNGXSAGCPR	99.0	8	
12	0.2	-	-	-	unknown	-	-	-
13	0.2	-	-	-	unknown	-	-	-
14	17.3	13	919.5	1	MXXBETGK	99.0	10	Phospholipase A$_2$, K49; ~ P49121
			2060.0	1	NAXTSYGSYGCNCGWGHR	99.0	21	
15	22.7	13	2316.1	1	SGMXWYSAYGCYCGWGGBGR	99.0	14	Phospholipase A$_2$, D49; ~ P51972
			1505.6	1	CCFVHDCCYGK	99.0	18	
			1578.7	1	SAYGCYCGWGGBGR	99.0	19	
			1257.6	1	GCYCGWGGBGR	98.7	9	
16	0.7	-	-	-	unknown	-	-	-

17	2.4	23	2510.1	1	SGPPCGDCPSACVN^{da}GXCTNPCTK	99.0	9	CRISP; ~ Q7ZTA0
			1138.6	1	SVDFDSESPR	99.0	9	
			1325.7	1	SXVBBYGCBDK	99.0	11	
			1890.9	1	BMBSECSAXCFCBNK	99.0	8	
			1620.9	1	WTEXXHAWHGENK	99.0	17	
			1537.8	1	MEWYPEAAANAER	99.0	14	
			1904.1	1	BPEXBNBXVDXHNSXR	99.0	20	
18	2.3	37	1512.7	1	VXGGDECNXNEHR	99.0	9	Serine proteinase; ~ P09872
			2856.5	1	GDSGGPXXCNGBFBGXXSVGGNPCABPR	99.0	12	
			2260.2	1	NSAHXAPXSXPSNPPSVGSVCR	99.0	18	
19a	2.9	33	1512.7	1	VXGGDECNXNEHR	99.0	7	Serine proteinase; ~ P0CG03
			1294.7	1	XNXXDYEVCR	99.0	8	
			1639.8	1	CANXNXXDYEVCR	99.0	10	
19b	1.4	28	1498.7	1	VVGGDECNXNEHR	99.0	8	Serine proteinase; ~ Q9YGJ8
			1307.7	1	NFBMXFGVHSK	99.0	12	
			2889.6	1	XDSPVSNSEHXAPXSXPSSPPSVGSVCR	99.0	17	
19c	4.5	15	1505.6	1	CCFVHDCCYGK	99.0	18	Phospholipase A$_2$, D49; ~ P51972
			1578.7	1	SAYGCYCGWGGBGR	99.0	14	
			1368.7	1	N^{da}XMBFETXXMK	99.0	15	
20a	1.9	28	1307.7	1	NFBMXFGVHSK	99.0	16	Serine proteinase; ~ Q9YGJ8
			1190.6	1	XMGWGTXSPTK	99.0	11	
			1498.7	1	VVGGDECNXNEHR	99.0	10	
			2889.5	1	XDSPVSNSEHXAPXSXPSSPPSVGSVCR	99.0	14	
20b	1.5	14	1505.5	1	CCFVHDCCYGK	99.0	15	Phospholipase A$_2$, D49; ~ P51972
			1578.6	1	SAYGCYCGWGGBGR	98.9	8	
20c	1.3	12	1369.7	1	BDFSWEWTDR	99.0	11	C-type lectin/lectin-like; ~ Q9PSN0
			1401.7	1	GBAEVWXGXWDK	99.0	18	
			1572.8	1	EFCVEXVSXTGYR	99.0	17	
			1241.5	1	DFSWEWTDR	99.0	13	
			1206.6	1	XWNDBVCGSK	96.4	9	
21a	0.8	36	-	-	unknown	-	-	
21b	5.4	28	1429.7	1	SXPSSPPSVGSVCR	99.0	12	Serine proteinase; ~ Q91053
			1639.8	1	CANXNXXDYEVCR	99.0	16	
			1294.7	1	XNXXDYEVCR	99.0	13	
			1512.7	1	VXGGDECNXNEHR	98.0	8	
22a	4.5	51	1594.8	1	DBEDWYANXGPMR	99.0	11	L-amino acid oxidase; ~ Q6STF1
			1064.5	1	NPXEECFR	99.0	9	
			1514.7	1	ETDYEEFXEXAR	99.0	18	

			1252.7	1	SAGBXYEESXR	98.6	9	
22b	1.1	41	1734.0	1	MYDXVNVXTPXYHR	99.0	10	Metalloproteinase; ~ Q9DGB9
			1475.8	1	WEXXBBVDTSTR	99.0	7	
			1368.7	1	XYCFPNSPENK	99.0	8	
			1803.8	1	YFVEVGEECDCGSPR	99.0	12	
			1994.0	1	THNXEPYFESFXNNXR	96.1	6	
23a	0.5	59	1983.9	1	XTPGSBCADGVCCDBCR	81.6	6	Metalloproteinase; ~ O42138
23b	1.9	25	1097.6	1	DXXDVBPAAR	99.0	8	Metalloproteinase; ~ Q92032
			1247.6	1	HTXDSFGEWR	99.0	14	
24a	1.3	58	1983.8	1	XTPGSBCADGVCCDBCR	96.7	7	Metalloproteinase; ~ O42138
24b	0.6	25	1313.8	1	YVEXVXVADHR	99.0	10	Metalloproteinase; ~ Q92043
24c	1.9	22	1065.6	1	YNGN^{da}XNTXR	99.0	8	Metalloproteinase; ~ Q9IAB0
			1921.0	1	XWVHEXVNTMNVFYR	99.0	11	
			1351.7	1	AADTXEAFGDWR	99.0	11	
			1313.8	1	YXEXVVVADHR	99.0	11	
			2564.4	1	XSHDNABXXTAXEXDGETXGXANR	99.0	25	
25a	2.5	45	2658.1	1	SECDXAESCTGBSADCPTDDFHR	99.0	8	Metalloproteinase; ~ Q92043
			2225.9	1	XHSWVECESGECCEBCR	99.0	8	
25b	1.2	25	1187.6	1	TPEBBGFPBR	99.0	9	Metalloproteinase; ~ Q92031
			1313.8	1	YVEXVXVADHR	99.0	12	
25c	7.4	21	2506.5	1	BWVHBXVNTXNEXYRPXNXR	99.0	8	Metalloproteinase; ~ Q92031
			1223.6	1	NTXNSFGEWR	99.0	9	
			1913.1	1	BWVHBXVNTXNEXYR	99.0	13	
			1187.6	1	TPEBBGFPBR	99.0	12	
			1313.8	1	YVEXVXVADHR	99.0	13	
26	2.6	22	1290.8	1	TAXVFDEGXXGR	99.0	9	Metalloproteinase; ~ B7U492
			2169.2	1	SHDNABXXTAXVFDEGXXGR	99.0	10	
			1327.8	1	YVEXVXXADHR	99.0	8	

Figure 4B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Time (min)
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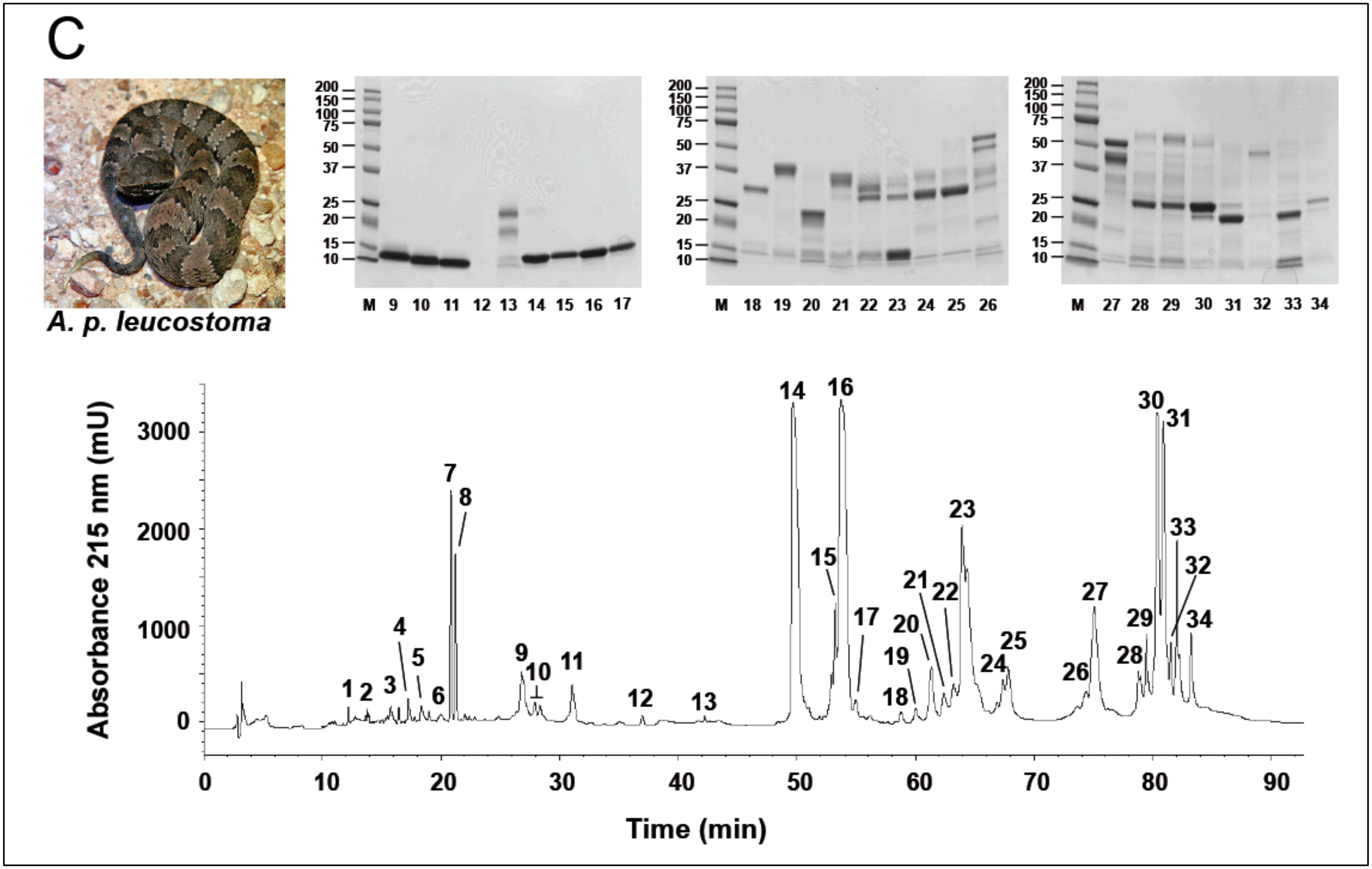
Table S9: Assignment of the RP-HPLC isolated fractions of *Agkistrodon piscivorus piscivorus* venom to protein families by MALDI-TOF-TOF or nESI-MS-MS of selected peptide ions from in-gel trypsin-digested protein bands from the SDS-PAGE shown in Fig.4B. * Cysteine residues are carbamidomethylated. X: Leu/Ile; B: Lys/Gln; Z, pyroglutamate (2-oxo-pyrrolidone carboxylic acid). ^{da}: deamidated; ^{py}: pyroglutamic; Mass estimations by SDS-PAGE (reducing conditions) are indicated in kDa, or in parentheses when determined by ESI-MS. Confidence (Conf) and Score (Sc) values are calculated by the Paragon algorithm of ProteinPilot®.

Peak	%	Mass, kDa	Peptide ion		MS/MS-derived amino acid sequence	Conf (%)	Sc	Protein family; ~ related protein *
		(ESI-MS)	m/z	z				
1	0.5	-	-	-	unknown	-	-	-
2	0.3	-	539.2	1	TPPAGP	-	-	Bradykinin-inhibitory peptide; P85025
3	0.3	-	398.9	2	BVTPVPR	-	-	Fragment of PI-SVMP; ACV8393
4	0.5	-	532.3	2	TPPAGPDVGPR	-	-	Bradykinin-inhibitory peptide; P85025
5	0.2	-	865.4	1	PAGPDVGPR	-	-	Bradykinin-inhibitory peptide; P85025
6	2.5	-	430.1	1	ZNW	-	-	SVMP inhibitor; P01021
7	2.0	-	444.1	1	ZBW	-	-	SVMP inhibitor; P01021
			469.4	2	XXTXPSTPP			Bradykinin-inhibitory peptide
8	0.5	9	1869.9	1	GDDVNDYCNGXSAGCPR	99.0	10	Disintegrin; P16338
			2097.0	1	ARGDDVNDYCNGXSAGCPR	99.0	9	
			2023.0	1	XRPGABCAEGXCCDBCK	99.0	14	
			2517.0	1	EAGEECDCGSPENPCCDAATCK	93.1	6	
			519.5	2	RPPHPBXPP	-	-	Bradykinin-inhibitory peptide; ~ P85167
9	0.7	(7739.2)	2097.0	1	ARGDDVNDYCNGXSAGCPR	99.0	10	Disintegrin; P16338
			1869.9	1	GDDVNDYCNGXSAGCPR	99.0	8	
			2023.0	1	XRPGABCAEGXCCDBCK	99.0	8	
			1983.9	1	XTPGSBCAEGXCCDBCK	99.0	7	Disintegrin; Q805F5 [40-111]
10	0.5	(7667.8)	1984.0	1	XTPGSBCAEGXCCDBCK	99.0	8	Disintegrin; Q805F5 [40-110]
			2112.0	1	ARGDDXDDYCNGXSAGCPR	99.0	17	
			2041.0	1	ZCDCGSPGNPCCDAATCK	87.0	8	
11	1.9	9	2022.9	1	XRPGABCAEGXCCDBCK	99.0	8	Disintegrin; ~ P16338
			534.9	2	ZNXPHPWPP			Bradykinin-inhibitory peptide
12	1.1	-	-	-	unknown	-	-	-
13	0.2	-	-	-	unknown	-	-	-
14	0.8	-	-	-	unknown	-	-	-

15	0.2	8	-	-	unknown	-	-	-
16	12.8	(13949)	2060.0	1	NAXTSYGSYGCNCGWGHR	99.0	12	Phospholipase A_2, K49; P04361
			919.2	1	MXXBETGK	99.0	9	
			1474.4	1	AXXCEEBNPCXK	99.0	16	
			1751.7	1	BECECDBAVAXCXR	99.0	10	
			1204.5	1	TDRYSYSWK	99.0	13	
17	17.2	(13987)	2316.2	1	SGMXWYSAYGCYCGWGGBGR	99.0	17	Phospholipase A_2, D49: P51972
			1505.7	1	CCFVHDCCYGK	99.0	12	
			1278.5	1	AAAXCFRDNXK	99.0	12	
			925.3	1	NXFBFEK	99.0	11	
			2540.8	1	SGMXWYSAYGCYCGWGGBGRPK	99.0	19	
18	0.4	-	-	-	unknown	-	-	
19	0.5	39	1343.6	1	EWVVTAAHCDR	99.0	10	Serine proteinase; ~ P85109
			1189.6	1	WDBDXMXXR	99.0	10	
			2146.1	1	SAHXAPXSXPSNPPSVGSVCR	99.0	15	
20	1.9	21	1553.9	1	MEWYPEAAANAER	99.0	9	CRISP; ~ Q7ZTA0
			1904.3	1	BPEXBNBXVDXHNSXR	99.0	11	
			1138.6	1	SVDFDSESPR	93.0	5	
21	1.6	21	1553.8	1	MEWYPEAAANAER	99.0	9	CRISP; ~ Q7ZTA0
22a	1.2	33	3360.5	1	DTCBGDSGGPXXCNGBFBGXXSVGGNPCABPR	99.0	11	Serine proteinase; ~ P09872
			2260.1	1	NSAHXAPXSXPSNPPSVGSVCR	99.0	10	
			2856.3	1	GDSGGPXXCNGBFBGXXSVGGNPCABPR	99.0	19	
			2449.1	1	MTHPPBTPXXDBVXYPADXRK	95.8	10	
22b	0.4	13	1505.5	1	CCFVHDCCYGK	99.0	12	Phospholipase A_2, D49; ~ Q6H3D0
23a	5.1	25	2889.7	1	XDSPVSNSEHXAPXSXPSSPPSVGSVCR	99.0	12	Serine proteinase; ~ Q91053
			1190.7	1	XMGWGTXSPTK	87.0	5	
23b	6.4	13	1505.5	1	CCFVHDCCYGK	99.0	13	Phospholipase A_2, D49; ~ Q9PVF2
			1367.8	1	DXMBFETXXMK	99.0	18	
			1241.5	1	DFSWEWTDR	70.9	5	C-type lectin/lectin-like; ~ AER27037
			1650.0	1	VFBBXBTWEDAER	99.0	10	
24a	2.2	34	2608.2	1	ETYPDVPHCANXNXXDYEVCR	99.0	15	Serine proteinase; ~ P0DJG5
			2470.2	1	VFDHXDWXBSXXAGNTDATCPP	99.0	13	
			2574.3	1	GNFCGXTXXNBEWVXTAAHCDR	99.0	8	
24b	4.2	27	1512.7	1	VXGGDECNXNEHR	99.0	16	Serine proteinase; ~ Q91053
25a	0.8	51	1610.9	1	NEEAGWYANXGPMR	99.0	11	L-amino acid oxidase; ~ Q6STF1
			1064.6	1	NPXEECFR	72.3	6	

25b	0.7	41	1809.8	1	YFVEVGEECDCGSPR	99.0	10	Metalloproteinase; ~ Q9DGB9
			1712.8	1	AABDECDMADXCTGR	79.7	6	
25c	0.4	32	679.5	2	YEGDBTEXCSR	-	-	Metalloproteinase; ~ AEJ31986
26	2.5	37	2015.8	1	XTTGSBCAEGXCCDBCR	83.5	6	Metalloproteinase; ~ AAZ73489
27a	1.4	62	1983.8	1	XTPGSBCADGVCCDBCR	99.0	8	Metalloproteinase; ~ O42138
27b	2.1	26	1247.6	1	HTXDSFGEWR	99.0	7	Metalloproteinase; ~ Q92032
28a	1.7	61	1714.9	1	Q^{py}XNXTPEBBAYXDAK	99.0	10	Metalloproteinase; ~ O42138
			1983.8	1	XTPGSBCADGVCCDBCR	99.0	8	
			2316.9	1	DDCDMADXCTGBSAECPTDR	80.1	5	
28b	2.1	26	1751.9	1	VAVTMAHEXGHNXGMR	99.0	9	Metalloproteinase; ~ Q92032
			1313.8	1	SHDNABXXTAXK	99.0	7	
			1187.6	1	TPEBBGFPBR	99.0	9	
			1736.0	1	VAVTMAHEXGHNXGMR	79.0	6	
28c	2.1	16	2564.5	1	XSHDNABXXTAXEXDGETXGXANR	99.0	8	Metalloproteinase; ~ Q9IAB0
			2020.2	1	YXNXYDPBCXXNEPXR	76.9	7	
			2514.5	1	XWVHEXVNTMNVFYRPXNXR	66.3	6	
			1313.8	1	YXEXVVVADHR	51.8	5	
29a	2.1	46	2658.0	1	SECDXAESCTGBSADCPTDDFHR	99.0	6	Metalloproteinase; ~ Q92043
			2225.9	1	XHSWVECESGECCEBCR	99.0	7	
			1785.0	1	XVNTXNEXYXPXNXR	99.0	19	
			3234.4	1	TDXVSPPVCGNEXXEVGEECDCGSPANCR	99.0	12	
			2020.0	1	YXNXYDPBCXXNEPXR	99.0	13	
29b	1.2	33	1327.7	1	YXEXVXVADHR	99.0	10	Metalloproteinase; ~ Q8AWX7
30a	3.2	46	2531.0	1	XRPGTBCEDGECCEBCQ^{da}FBGA	92.7	8	Metalloproteinase; ~ P86092
30b	7.5	15	1327.8	1	YVEXVXXADHR	99.0	9	Metalloproteinase; ~ B7U492
			2168.6	1	SHDNABXXTAXVFDEGXXGR	99.0	27	
31a	1.3	40	1652.0	1	XYEXVNXXNEXYR	94.7	6	Metalloproteinase; ~ P0C6E3
31b	1.7	23	1313.8	1	YVEXVXVADHR	76.9	5	Metalloproteinase; ~ Q92043
31c	1.3	16	1327.9	1	YVEXVXXADHR	99.0	9	Metalloproteinase; ~ B7U492
32a	0.8	50	2688.4	1	SECDXAESCTGBSADCPMDDFHR	98.9	6	Metalloproteinase; ~ Q9PSN7
32b	1.0	18	1327.9	1	YVEXVXXADHR	98.0	7	Metalloproteinase; ~ B7U492

Figure 4C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M 9 10 11 12 13 14 15 16 17
M 18 19 20 21 22 23 24 25 26
M 27 28 29 30 31 32 33 34
Absorbance 215 nm (mU)
0
1000
2000
3000
Time (min)
0 10 20 30 40 50 60 70 80 90
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34

Table S10: Assignment of the RP-HPLC isolated fractions of *Agkistrodon contortrix leucostoma* venom to protein families by MALDI-TOF-TOF or nESI-MS-MS of selected peptide ions from in-gel trypsin-digested protein bands from the SDS-PAGE shown in Fig.4C. * Cysteine residues are carbamidomethylated. X: Leu/Ile; B: Lys/Gln; Z, pyroglutamate (2-oxo-pyrrolidone carboxylic acid). ^{ox}: oxidized; ^{da}: deamidated. Mass estimations by SDS-PAGE (reducing conditions) are indicated in kDa. Confidence (Conf) and Score (Sc) values are calculated by the Paragon algorithm of ProteinPilot®.

Peak	%	Mass, kDa	Peptide ion		MS/MS-derived or N-terminal (Nt) sequence	Conf (%)	Sc	Protein family; ~ related protein *
			m/z	z				
1	0.2	-	385.3	1	TPPA	-	-	Bradykinin-inhibitory peptide; P85025
			470.2	1	ZSPR			Fragment of NGF-β; ACC85799
2	0.2	-	440.2	1	PARP	-	-	Fragment of 3FTx; ~ ABG27005
3	0.5	-	603.4	1	DHPPH	-	-	Fragment of NGF-β; ACC85799
			506.4	1	HDPH			Fragment of NGF-β; ACC85799
			539.3	1	TAGP			Bradykinin-inhibitory peptide; P85025
			449.3	1	ZBW^{kyn}			SVMP inhibitor; P01021
4	0.4	-	398.8	2	BVTPVPR	-	-	Fragment of PI-SVMP; ACV83930
5	0.4	-	865.4	1	PAGPDVGPR	-	-	Bradykinin-inhibitory peptide; P85025
			481.7	2	PPAGPDVGPR			Bradykinin-inhibitory peptide; P85025
			532.3	2	TPPAGPDVGPR			Bradykinin-inhibitory peptide; P85025
6	0.3	-	519.7	2	RPPHPBXPP	-	-	Bradykinin-potentiating peptide; ~ P85167
7	2.2	-	452.1	1	ZNW +Na	-	-	SVMP inhibitor; P01021
			430.1	1	ZNW			SVMP inhibitor; P01021
			449.3	1	ZNW^{kyn}			SVMP inhibitor; P01021
8	1.7	-	444.1	1	ZBW	-	-	SVMP inhibitor; P01021
			466.1	1	ZBW + Na			SVMP inhibitor; P01021
9	2.2	10	2023.0	1	XRPGABCAEGXCCDBCK	99	12	Disintegrin; ~ P16338
			2097.0	1	ARGDDVNDYCNGXSAGCPR	99	12	
10	1.1	10	1968.0	1	XTPGABCAEGXCCDBCK	99	13	Disintegrin; ~ P16338
			1869.9	1	GDDVNDYCNGXSAGCPR	99	13	
			2097.1	1	ARGDDVNDYCNGXSAGCPR	99	16	
			2084.1	1	ABGDDXDDYCNGXSAGCPR	99	14	
11	1.4	10	1196.5	1	NPCCDAATCK	99	10	Disintegrin; ~ C9E1S1
			2023.0	1	XRPGABCAEGXCCDBCK	99	15	
			2084.0	1	ABGDDXDDYCNGXSAGCPR	99	16	
12	0.2	-	-	-	unknown	-	-	-

13a	0.2	21	1620.8	1	XXEVGEECDCGSPR	99	13	Disintegrin; ~ O42138
			1853.9	1	NGHPCXNDNGYCYNR	99	14	
13b		18	1812.8	1	BGABCAEGXCCDBCR	99	10	Disintegrin; ~ Q9DGB9
			1203.5	1	NNNGYCYNGK	99	10	
			1137.5	1	E^{py}GNHYGYCR	98.7	10	
			1025.5	1	FBGAGTECR	98.7	9	
			1368.7	1	XYCFPNSPENK	95.4	9	
13c		11	1505.6	1	CCFVHDCCYGK	97.9	7	Phospholipase A_2, D49; ~ Q9PVF2
14	14.6	11	2060.0	1	NAXTSYGSYGCNCGWGHR	99	9	Phospholipase A_2, K49: ~ P49121
15	2.6	11	1505.6	1	CCFVHDCCYGK	99	8	Phospholipase A_2, D49; ~ P51972
16	16.1	12	2316.1	1	SGMXWYSAYGCYCGWGGBGR	99	10	Phospholipase A_2, D49; ~ P51972
			2541.2	1	SGMXWYSAYGCYCGWGGBGRPK	99	13	
17	1.1	14	2316.0	1	SGMXWYSAYGCYCGWGGBGR	99	8	Phospholipase A_2, D49; ~ P51972
			2541.1	1	SGMXWYSAYGCYCGWGGBGRPK	94.6	8	
18a	0.4	29	1526.8	1	XXGGDECNXNEHR	99	8	Serine proteinase; ~ Q7T229
			1683.0	1	TYTBWDBDXMXXR	99	12	
			1129.7	1	FXVAXYTFR	97.9	10	
18b	0.1	13	-	-	unknown	-	-	-
19a	0.5	37	1189.7	1	WDBDXMXXR	81.5	6	Serine proteinase; ~ Q9PSN3
19b	0.1	12	1505.7	1	CCFVHDCCYGK	86.2	6	Phospholipase A_2, D49; ~ Q9PVF2
20a	2.0	22	3023.6	1	SVDFDSESPRBPEXBNBXVDXHNSXR	99	10	CRISP; ~ Q7ZTA0
			1537.7	1	MEWYPEAAANAER	99	14	
			2446.4	1	YGXGADPPNAVXGHFTBXVWYK	99	13	
20b		17	1620.8	1	WTEXXHAWHGENK	99	14	CRISP; ~ Q7ZTA0
			1537.7	1	MEWYPEAAANAER	99	12	
20c	0.2	12	-	-	unknown	-	-	-
20d		10	1904.1	1	BPEXBNBXVDXHNSXR	99	9	CRISP; ~ Q7ZTA0
			1537.8	1	MEWYPEAAANAER	99	10	
			1620.9	1	WTEXXHAWHGENK	98.9	8	
21a	1.0	33	1625.8	1	XVXGGDECNXNEHR	99	11	Serine proteinase; ~ P09872
			2036.1	1	GXAATTXCAGXXEGGBDTCK	99	15	
			1088.6	1	XYXGMHNXK	99	11	
			2856.5	1	GDSGGPXXCNGBFBGXXSVGGNPCABPR	99	18	
			1512.7	1	VXGGDECNXNEHR	99	11	
			2260.2	1	NSAHXAPXSXPSNPPSVGSVCR	99	23	
21b	0.2	12	-	-	unknown	-	-	-

22a	1.8	30	2867.6	1	FXAXVYAN^{da}GSXCGGTXXNBEWVXTAR	99	13	Serine proteinase; ~ P09872
22b		27	2889.8	1	XDSPVSNSEHXAPXSXPSSPPSVGSVCR	99	9	Serine proteinase; ~ ADP88561
22c	0.1	12	-	-	unknown	-	-	-
23a	0.5	31	-	-	unknown	-	-	-
23b	3.0	29	1498.7	1	VVGGDECNXNEHR	99	10	Serine proteinase; ~ Q91053
			1824.0	1	XAPXSXPSSPPSVGSVCR	99	14	
			1190.7	1	XMGWGTXSPTK	99	14	
			1307.7	1	NFBMXFGVHSK	99	18	
			2889.6	1	XDSPVSNSEHXAPXSXPSSPPSVGSVCR	99	21	
			1323.7	1	NFBM^{ox}XFGVHSK	95.5	8	
23c	8.7	12	1505.6	1	CCFVHDCCYGK	99	14	Phospholipase A_2,D49; ~ Q7SID6
			1368.7	1	N^{da}XMBFETXXMK	99	18	
			2577.2	1	TDSYTYSBENGDVVCGGDD^{da}PCBK	99	16	
24a	0.2	34	1512.7	1	VXGGDECNXNEHR	99	10	Serine proteinase; ~ O13063
			1858.0	1	YSXCR^{or}AVYXGMPVBSR	99	14	
24b	1.0	27	3465.9	1	SXAXVYXTSGFXCGGTXXNBEWVXTAAHCDR	99	14	Serine proteinase; ~ Q2QA04
			2919.6	1	N^{da}RSVRNSBH^{ox}XAPXSXPSSPPSVGSVCR	99	9	
24c	0.2	12	1401.8	1	GBAEVWXGXWDK	99	11	C-type lectin/lectin-like; ~ Q9PSN0
			1621.8	1	XFDEXBAWEDAER	99	15	
			1241.6	1	DFSWEWTDR	99	12	
25a	0.3	36	2856.5	1	GDSGGPXXCNGBFBGXXSVGGNPCABPR	99	10	Serine proteinase; ~ P09872
25b	1.7	28	1003.5	1	DBDXMXXR	99	10	Serine proteinase; ~ Q91053
			1294.6	1	XNXXDYEVCR	99	13	
			1512.6	1	VXGGDECNXNEHR	99	12	
			1639.7	1	CANXNXXDYEVCR	99	17	
			1429.6	1	SXPSSPPSVGSVCR	99	15	
25c	0.3	13	1572.8	1	EFCVEXVSXTGYR	99	9	C-type lectin/lectin-like; ~ Q9PSN0
			1621.8	1	XFDEXBAWEDAER	99	12	
26a	0.5	58	2347.3	1	XYFAGEYTABFHGWXDSTXK	99	10	L-amino acid oxidase; ~ P56742
26b	0.4	49	2347.1	1	XYFAGEYTABFHGWXDSTXK	99	14	L-amino acid oxidase; ~ P56742
26c	0.2	35	2260.3	1	NSAHXAPXSXPSNPPSVGSVCR	99	13	Serine proteinase; ~ P09872
26d	0.2	30	-	-	unknown	-	-	-
26e	0.1	20	2347.1	1	XYFAGEYTABFHGWXDSTXK	97.3	9	L-amino acid oxidase; ~ P56742
26f	0.1	15	-	-	unknown	-	-	-
26g	0.1	12	1594.8	1	DBEDWYANXGPMR	99	10	L-amino acid oxidase; ~ Q6STF1
			1514.7	1	ETDYEEFXEXAR	99	17	

27a	1.7	51	1594.8	1	DBEDWYANXGPMR	99	12	L-amino acid oxidase; ~ Q6STF1
			1514.7	1	ETDYEEFXEXAR	99	12	
			2347.2	1	XYFAGEYTABFHGWXDSTXK	99	10	
			1380.7	1	SAGBXYEESXRK	98.4	8	
27b	2.2	41	1733.9	1	MYDXVNVXTPXYHR	99	12	Metalloproteinase; ~ Q9DGB9
			1025.5	1	FBGAGTECR	99	11	
			1812.7	1	BGABCAEGXCCDBCR	99	12	
			1712.7	1	P^{ca}ASSECDMADXCTGR	99	16	
			1269.6	1	SAECTDRFBR	97.9	10	
27c	0.1	37	-	-	unknown	-	-	-
27d	0.6	35	985.6	1	EHBAFXXK	99	10	Metalloproteinase; ~ Q9DGB9
			1733.9	1	MYDXVNVXTPXYHR	99	12	
27e	0.2	18	-	-	unknown	-	-	-
27f	0.3	11	1621.8	1	XFDEXBAWEDAER	99	10	C-type lectin/lectin-like; ~ Q9PSN0
28a	0.3	57	1699.9	1	NBCXYFFGPNAAVAK	99	9	Metalloproteinase; ~ O42138
28b	1.3	24	3337.7	1	XSHDNABXXTSTDFDGPTXGXAYVGTMCDPK	99	13	Metalloproteinase; ~ Q92032
			3080.7	1	YMYXDXSXAGVEXWSNBDXXDVBPAAR	99	16	
			1532.7	1	HTXDSFGEWRER	99	14	
			1247.6	1	HTXDSFGEWR	99	16	
			1067.5	1	YNGDSDBXR	98.9	9	
28c	0.3	11	-	-	unknown	-	-	-
28d	0.3	10	1247.6	1	HTXDSFGEWR	99	13	Metalloproteinase; ~ Q92032
			3080.7	1	YMYXDXSXAGVEXWSNBDXXDVBPAAR	84.5	6	
29a	0.5	55	1699.9	1	NBCXYFFGPNAAVAK	99	11	Metalloproteinase; ~ O42138
29b	0.8	24	1401.7	1	BWVHBMVNTMK	99	13	Metalloproteinase; ~ Q92032
			3096.7	1	YMYXDXSXAGVEXWSNBDXXDVBPAAR	99	14	
			3337.7	1	XSHDNABXXTSTDFDGPTXGXAYVGTMCDPK	99	13	
			1247.6	1	HTXDSFGEWR	99	13	
			3080.7	1	YMYXDXSXAGVEXWSNBDXXDVBPAAR	99	13	
			1532.8	1	HTXDSFGEWRER	99	12	
29c	0.3	11	-	-	unknown	-	-	-
29d	0.2	10	1247.6	1	HTXDSFGEWR	99	11	Metalloproteinase; ~ Q92032
30a	0.4	52	-	-	unknown	-	-	-
30b	5.3	24	1735.9	1	VAVTMAHEXGHNXGMR	99	20	Metalloproteinase; ~ P84907
			1313.7	1	YVEXVXVADHR	99	13	
30c	2.4	21	1313.8	1	YXEXVVVADHR	99	11	Metalloproteinase; ~ Q9IAB0

			2564.4	1	XSHDNABXXTAXEXDGETXGXANR	99	16	
31a	0.7	24	-	-	unknown	-	-	-
31b	5.0	20	1083.5	1	NPBCXXNBP	99	12	Metalloproteinase; ~ Q92031
			1576.6	1	SVSHDTXASFGNWR	99	17	
			2347.0	1	BDXXTVTSVSHDTXASFGNWR	99	17	
			1313.6	1	YVEXVXVADHR	99	15	
32	1.2	44	2663.1	1	SECDXAESCTGBSAECPTDDFBR	99	12	Metalloproteinase; ~ C9E1S0
			1494.6	1	FSDCSRDEHWR	98.3	9	
33a	2.1	21	2169.2	1	SHDNABXXTAXVFDEGXXGR	99	13	Metalloproteinase; ~ B7U492
33b	1.0	12	2169.2	1	SHDNABXXTAXVFDEGXXGR	99	7	Metalloproteinase; ~ B7U492
33c	0.8	10	-	-	unknown	-	-	-
34	2.9	25	1313.8	1	YVEXVXVADHR	99	7	Metalloproteinase; ~ Q92043