

Table S1. Assignment of the RP-HPLC fractions from Sichuan *Azemiops feae* venom to protein families by MALDI-TOF-MS/MS and nESI-MS/MS of selected peptide ions from in-gel digested protein bands separated by SDS-PAGE. CNP: C-type natriuretic peptide; CRISP, cysteine-rich secretory protein; HA: Hyaluronidase; LAAO: L-amino acid oxidase; NGF: nerve growth factor; PLA₂, phospholipase A₂; PLB: phospholipase B; SVMP: snake venom metalloproteinase; SVSP: snake venom serine proteinase; Unknown: unidentified components.

Peak	%	MW (kDa)	Peptide Ion		Score	MS/MS-derived sequence	Protein family/species/accession
			m/z	z			
1	2.16	-	581.0	3	84	AAATPQKLAKGRGAAATSA	CNP; <i>Azemiops feae</i> ; K4IT20
			610.0	3	71	SDSKAAATPQKLAKGRGAA	
			633.7	3	68	SDSKAAATPQKLAKGRGAAA	
			608.8	2	66	SDSKAAATPQKL	
			556.9	2	50	RLKGLAKKGAA	
			627.8	2	47	SLRPEAASGPAAAAG	
			599.4	2	45	PRPPRPRPKP	
			682.4	2	44	KPPHQGPRPPRP	
			458.8	2	43	KPPHQGPR	
			857.5	2	42	PPHQGPRPPRPRPKP	
			357.9	3	42	RGVGGGGSRL	
			521.3	2	37	HQGPRPPRP	
			367.6	3	36	RPPRPRPKP	
			409.2	2	35	GAAATSARL	
			1041.7	1	34	RLKGLAKKGA	
			614.7	3	33	KPPHQGPRPPRPRPKP	
			760.4	2	32	HQGPRPPRPRPKP	
2	1.12	-	720.1	3	93	SDSKAAATPQKLAKGRGAAATSA	CNP; <i>A. feae</i> ; K4IT20
			371.6	3	52	RLKGLAKKGAA	
			682.4	2	49	KPPHQGPRPPRP	
			410.6	3	46	AKGRGAAATSARL	
3	1.21	-	633.7	3	46	SDSKAAATPQKLAKGRGAAA	CNP; <i>A. feae</i> ; K4IT20
			430.7	2	64	LPPHPHY	
4	0.10	-	645.4	2	65	KGRGAAATSARLM	CNP; <i>A. feae</i> ; K4IT20
			552.8	2	59	RGAAATSARLM	
			680.9	2	48	AKGRGAAATSARLM	
			637.8	2	47	DLRTDGKQWR	

Peak	%	MW (kDa)	Peptide Ion		Score	MS/MS-derived sequence	Protein family/species/accession
			m/z	z			
5	2.07	-	637.8	2	54	DLRTDGKQWR	CNP; <i>A. feae</i> ; K4IT20
			509.3	2	39	KPPGVYYPP	
			750.4	2	38	QKWGRMVPPKGES	
			454.3	3	34	AKGRGAAATSARLM	
6	2.40	-	491.9	3	54	LAKGRGAAATSARLM	CNP; <i>A. feae</i> ; K4IT20
			557.3	2	51	GPAAAGVGDGWR	
			750.4	2	49	QKWGRMVPPKGES	
			509.3	2	41	KPPGVYYPP	
			600.8	2	40	SGPAAAGVGDGWR	
			636.3	2	40	ASGPAAAGVGDGWR	
			671.8	2	39	AASGPAAAGVGDGWR	
			460.7	2	25	KPGVYYPP	
7	7.41	-	575.6	3	63	RPEAASGPAAAGVGDGWR	CNP; <i>A. feae</i> ; K4IT20
			613.3	3	63	LRPEAASGPAAAGVGDGWR	
			736.4	2	50	EAASGPAAAGVGDGWR	
			552.0	3	47	REELSLRPEAASGPAA	
			748.9	2	41	ELSLRPEAASGPAAAG	
			588.3	2	40	KPVQYLPPHP	
			600.8	2	39	SGPAAAGVGDGWR	
			684.9	2	38	ELSLRPEAASGPAA	
			400.6	3	37	REELSLRPEA	
			509.3	2	36	KPPGVYYPP	
			813.4	2	35	EELSLRPEAASGPAAAG	
			473.9	3	35	DEKPVQYLPPHP	
			594.6	3	35	REELSLRPEAASGPAAAG	
			460.7	2	34	KPPGVYYPP	
8	36.52	4.7	388.7	2	67	VTGCDPK	PLA ₂ ; <i>A. feae</i> ; A0A0D3N8V5
9	0.12	10.0	403.7	2	15	AAAICFR	PLA ₂ ; <i>A. feae</i> ; A7X4P4
	0.27	4.0	1138.5	1	15	SVDFDSESPR	CRISP; <i>Crotalus horridus</i> ; ~F2Q6E7
10	0.18	25.4	1905.0	1	78	KPEIQNEIVDLHNSLR	SVMP; <i>Trimeresurus stejnegeri</i> ; ~Q2LD49
			634.3	2	67	LYCIDSSPANK	
			423.9	3	53	SAECTDRFQR	
			634.3	2	70	LYCIDSSPANK	
	0.04	13.9					SVMP; <i>T. stejnegeri</i> ; ~Q2LD49

Peak	%	MW (kDa)	Peptide Ion		Score	MS/MS-derived sequence	Protein family/species/accession
			m/z	z			
11	0.04	10.5	1535.5	1	35	CCFEHDCCYGK	PLA ₂ ; <i>Bothriechis nigroviridis</i> ; ~C0HJL8
	0.20	4.6	517.8	2	43	GCFGLPLDR	CNP; <i>A. feae</i> ; K4IT20
	0.20		404.7	2	34	AAAICFR	PLA ₂ ; <i>Protobothrops flavoviridis</i> ; ~S6B451
	0.44	23.3	647.3	2	42	IDTACVCVISR	NGF; <i>A. feae</i> ; Q2XXL6
			549.3	2	38	NPNPVPSGCR	
	0.10	16.6	1097.5	1	42	NPNPVPSGCR	NGF; <i>A. feae</i> ; Q2XXL6
			1293.6	1	80	IDTACVCVISR	
			1413.6	1	11	CRNPNPVPSGCR	
			1825.8	1	57	HWNSYCTTTHTYVR	
	0.52	14.4	403.7	2	29	AAAICFR	PLA ₂ ; <i>A. feae</i> ; A7X4P4
			440.2	2	19	AVCECDK	
			436.7	2	17	NNVIVCR	
12	0.04	9.3	-	-	-	-	Unknown
	0.46	16.4	947.4	1	49	EGNQASWR	NGF; <i>A. feae</i> ; Q2XXL6
			1097.5	1	80	NPNPVPSGCR	
			1293.6	1	78	IDTACVCVISR	
			1413.6	1	28	CRNPNPVPSGCR	
13			1825.8	1	77	HWNSYCTTTHTYVR	
	0.04	27.5	1369.6	1	60	CQFKTAGELCR	PLA ₂ ; <i>Protobothrops mucrosquamatus</i> ; ~XP_015683146
			1737.8	1	78	DGHPCQNNLGycFR	
	0.56	16.6	947.4	1	54	EGNQASWR	NGF; <i>A. feae</i> ; Q2XXL6
			1097.5	1	79	NPNPVPSGCR	
14			1293.6	1	81	IDTACVCVISR	
			1413.6	1	32	CRNPNPVPSGCR	
			1825.8	1	25	HWNSYCTTTHTYVR	
	0.03	50.8	1148.6	1	29	MIPCAAKDVK	SVMP; <i>Hoplocephalus bungaroides</i> ; ~R4FIL3
	0.11	40.5	1259.6	1	76	YSVGIVQDHNK	SVMP; <i>Echis coloratus</i> ; ~A0A0A1WCK4
	0.01	29.6	1905.1	1	42	KPEIQNEIVDLHNSLR	CRISP; <i>A. feae</i> ; F2Q6E3
	0.01	26.3	1138.5	1	34	SVDfDSESPR	CRISP; <i>Deinagkistrodon acutus</i> ; ~F2Q6G1
			1553.7	1	10	MEWYPEAAANAER	
			1905.0	1	22	KPEIQNEIVDLHNSLR	
	0.04	19.3	947.4	1	28	EGNQASWR	NGF; <i>A. feae</i> ; Q2XXL6
			1097.5	1	20	NPNPVPSGCR	

Peak	%	MW (kDa)	Peptide Ion		Score	MS/MS-derived sequence	Protein family/species/accession
			m/z	z			
15	0.01	16.6	1293.6	1	66	IDTACVVCVISR	PLA ₂ ; <i>A. feae</i> ; A7X4P4
			403.7	2	53	AAAICFR	
	0.04	48.0	1537.7	1	14	MEWYPEAAANAER	CRISP; <i>A. feae</i> ; F2Q6E3
			1905.0	1	32	KPEIQNEIVDLHNSLR	
	5.24	26.1	1537.7	1	33	MEWYPEAAANAER	CRISP; <i>A. feae</i> ; F2Q6E3
			1553.7	1	17	MEWYPEAAANAER	
	0.36	20.2	1905.1	1	95	KPEIQNEIVDLHNSLR	CRISP; <i>C. horridus</i> ; ~F2Q6E5
			1138.5	1	50	SVDFDSESPR	
			1553.6	1	31	MEWYPEAAANAER	
			1905.0	1	134	KPEIQNEIVDLHNSLR	
16	0.15	26.6	1535.5	1	40	CCFEHDCCYGK	PLA ₂ ; <i>B. nigroviridis</i> ; ~C0HJL8
	0.49	31.3	1304.6	1	57	NFQMQLGVHSK	SVSP; <i>A. feae</i> ; A0A1Y0DIB6
			1429.7	1	32	VLNDDEQTRDPK	
	0.32	25.3	2929.5	1	138	LNSPVHESTHIAPLSLSPSSPTVGSVCR	SVSP; <i>A. feae</i> ; A0A1Y0DIC1
17	0.01	19.2	2929.5	1	108	LNSPVHESTHIAPLSLSPSSPTVGSVCR	SVSP; <i>A. feae</i> ; A0A1Y0DIC1
	0.32	16.6	1535.5	1	44	CCFEHDCCYGK	PLA ₂ ; <i>B. nigroviridis</i> ; ~C0HJL8
	0.08	56.1	494.5	3	82	VVGGDCECNINDHR	SVSP; <i>Trimeresurus purpureomaculatus</i> ; ~P0DJF7
			741.8	2	85	VVGGDCECNINDHR	
	0.59	31.6	1288.6	1	42	NFQMQLGVHSK	SVSP; <i>A. feae</i> ; A0A1Y0DIB6
			1304.6	1	56	NFQMQLGVHSK	
	0.74	25.8	1304.6	1	35	NFQMQLGVHSK	SVSP; <i>A. feae</i> ; A0A1Y0DIB6
	0.94	16.8	1535.5	1	55	CCFEHDCCYGK	PLA ₂ ; <i>B. nigroviridis</i> ; ~C0HJL8
	0.88	55.3	1594.7	1	80	TLCAGILQGGTDTCK	SVSP; <i>A. feae</i> ; A0A1Y0DIB5
			1003.6	1	46	ALYPGLLEK	
18	1.11	44.3	1095.7	1	57	FLVALYTLR	SVSP; <i>A. feae</i> ; A0A1Y0DIB4
			2233.2	1	63	NSAHIAPLSLPSSPPSVGSVCR	
			2480.2	1	20	ETYPDVPHCANINIVDHAVCR	
			2929.5	1	148	LNSPVHESTHIAPLSLSPSSPTVGSVCR	
	0.88	31.4	2929.5	1	174	LNSPVHESTHIAPLSLSPSSPTVGSVCR	SVSP; <i>A. feae</i> ; A0A1Y0DIC1
	0.83	26.2	2929.5	1	174	LNSPVHESTHIAPLSLSPSSPTVGSVCR	SVSP; <i>A. feae</i> ; A0A1Y0DIC1
	2.32	16.9	1535.5	1	45	CCFEHDCCYGK	PLA ₂ ; <i>B. nigroviridis</i> ; ~C0HJL8
			2093.8	1	36	DATDRCCFEHDCCYGK	
	7.74	19.2	1505.6	1	6	CCFVHDCCYGK	PLA ₂ ; <i>A. feae</i> ; A0A0D3N8V5
			1728.8	1	49	EVCECDKAAAICFR	

Peak	%	MW (kDa)	Peptide Ion		Score	MS/MS-derived sequence	Protein family/species/accession
			m/z	z			
20	0.15	27.0	918.5	1	35	VYPGLLEK	SVSP; <i>A. feae</i> ; A0A1Y0DIC1
			5.97	21.2	34	TDPYPYSR	PLA ₂ ; <i>A. feae</i> ; A0A0D3N944
			1534.5	1	43	CCFEHNCCYGK	
			2330.0	1	117	IAFDTYTFYGCNCGWEGLR	
21	0.54	27.9	1003.6	1	49	ALYPGLLEK	SVSP; <i>A. feae</i> ; A0A1Y0DIB4
			1095.7	1	54	FLVALYTLR	
			2233.1	1	145	NSAHIAPLSLPSSPPSVGSVCR	
			2480.1	1	98	ETYPDVPHCANINIVDHAVCR	
	0.66	21.9	1095.7	1	36	FLVALYTLR	SVSP; <i>A. feae</i> ; A0A1Y0DIB4
			2233.2	1	70	NSAHIAPLSLPSSPPSVGSVCR	
	0.16	17.8	1003.6	1	42	ALYPGLLEK	SVSP; <i>A. feae</i> ; A0A1Y0DIB4
			2233.2	1	104	NSAHIAPLSLPSSPPSVGSVCR	
22	0.32	31.8	2480.2	1	103	ETYPDVPHCANINIVDHAVCR	
			1138.5	1	38	SVDFDSESPR	CRISP; <i>C. horridus</i> ; ~F2Q6E5
			1553.7	1	4	MEWYPEAAANAER	
			1905.1	1	50	KPEIQNEIVDLHNSLR	
	1.66	16.8	1022.5	1	58	TLHYIYGR	PLA ₂ ; <i>A. feae</i> ; A7X4P4
			1488.7	1	95	IGLQFYVDAFCR	
			1533.6	1	73	CCFVHDCCYGR	
			1967.9	1	171	NPVTSYSAYGCYCGVGGR	
23	0.77	69.2	1127.6	1	48	AHGWIDSTIK	LAAO; <i>Demansia vestigiata</i> ; ~A6MFL0
			2.31	57.6	17	ITFEPPLPPK	LAAO; <i>Bothrops pictus</i> ; ~X2L4E2
			1294.8	1	35	RITFEPPLPPK	
			1388.7	1	42	KFWEDDGIHGGK	
	0.27	40.3	1138.6	1	10	ITFEPPLPPK	LAAO; <i>Lachesis muta</i> ; ~J7H670
			1266.8	1	22	ITFEPPLPPK	
	0.81	37.0	1137.5	1	30	HDDIFAYEK	LAAO; <i>B. pictus</i> ; ~X2L4E2
			1266.7	1	17	ITFEPPLPPK	
24	1.13	63.7	1294.7	1	18	RITFEPPLPPK	
			1852.0	1	140	DSTALFPNIYLETVLR	HA; <i>Agkistrodon piscivorus</i> ; ~A0A194ART0
			1889.9	1	103	HSDSNAFLHLFPDSFR	
25	1.01	65.4	2018.0	1	92	KHSDSNAFLHLFPDSFR	
			1615.5	1	32	ECEIGECCDQCR	SVMP; <i>E. coloratus</i> ; ~E9JG68

Peak	%	MW (kDa)	Peptide Ion		Score	MS/MS-derived sequence	Protein family/species/accession
			m/z	z			
26	0.23	48.4	1069.4	3	4	KYPCHYDYSEDPDYGM <u>V</u> VDHGTICADGK	SVMP; <i>Bothrops atrox</i> ; ~A0A1L8D666
	0.18	98.5	567.3	2	38	YPVKPSEEGK	LAAO; <i>L. muta</i> ; ~J7H670
			422.7	2	36	VAEELKR	
	0.43	41.6	438.7	2	41	STTDLPSR	LAAO; <i>Gloydus blomhoffii</i> ; ~Q90W54
			567.3	2	33	YPVKPSEEGK	
	0.09	35.5	438.7	2	34	STTDLPSR	LAAO; <i>Oxyuranus scutellatus scutellatus</i> ; ~Q4JHE3
	0.80	61.1	594.2	2	51	DSCCDAATCK	SVMP; <i>Gloydus halysi</i> ; ~Q8AWI5
			634.3	2	43	LYCIDSSPANK	
			529.8	2	35	IACEPQNVK	
			402.7	2	32	SAADVTLK	
	0.47	45.6	535.2	2	45	IAN <u>MM</u> ADSGK	PLB; <i>Crotalus adamanteus</i> ; ~F8S101
			527.2	2	43	IAN <u>MM</u> ADSGK	
			700.8	2	38	DQGKVTDM <u>ESMK</u>	
	0.23	37.3	535.2	2	60	IAN <u>MM</u> ADSGK	PLB; <i>C. adamanteus</i> ; ~F8S101
	0.25	32.2	756.3	2	63	SGPTCGDCPSACDK	CRISP; <i>A. feae</i> ; F2Q6E3
			569.8	2	43	SVDFDSESPR	
			507.7	2	42	CNEDHSPR	
	0.44	24.7	555.8	2	52	DNLDTYQNK	PLA ₂ ; <i>Protobothrops mangshanensis</i> ; ~A0A0H3U271
	0.20	20.3	437.7	2	42	NNVIVCR	PLA ₂ ; <i>A. feae</i> ; A7X4P4
27			472.7	2	35	CPEGQKEP	
	0.26	44.0	1259.6	1	59	YSVGIVQDHNK	SVMP; <i>E. coloratus</i> ; ~E9JGA2
	0.32	40.2	1259.6	1	64	YSVGIVQDHNK	SVMP; <i>E. coloratus</i> ; ~A0A0A1WCK4
28	0.41	42.4	1259.6	1	130	YSVGIVQDHNK	SVMP; <i>E. coloratus</i> ; ~E9JGA2
29	0.14	47.3	569.3	2	58	HDDIFAYEK	LAAO; <i>G. halys</i> ; ~Q6STF1
			567.3	2	53	YPVKPSEEGK	
			438.7	2	48	STTDLPSR	
30	0.32	44.7	569.3	2	74	HDDIFAYEK	LAAO; <i>Vipera ammodytes ammodytes</i> ; ~P0DI84
			630.8	2	46	FWEDDGIHGGK	
			438.7	2	44	STTDLPSR	

Methionine oxidation is underlined.

Table S2. Assignment of the RP-HPLC fractions from Zhejiang *Azemiops feae* venom to protein families by MALDI-TOF-MS/MS and nESI-MS/MS of selected peptide ions from in-gel digested protein bands separated by SDS-PAGE. CNP: C-type natriuretic peptide; CRISP, cysteine-rich secretory protein; HA: Hyaluronidase; LAAO: L-amino acid oxidase; NGF: nerve growth factor; PLA₂, phospholipase A₂; SVMP: snake venom metalloproteinase; SVSP: snake venom serine proteinase; Unknown: unidentified components.

Peak	%	MW (kDa)	Peptide Ion		Score	MS/MS-derived sequence	Protein family/species/accession
			m/z	z			
1	0.22	-	528.8	2	44	TDQHYPAPK	NGF; <i>Azemiops feae</i> ; B8QCH2
			462.2	2	38	TDQHYPAPKKAE	
			585.8	2	38	NTDQHYPAPK	
2	0.24	-	657.7	3	54	KTSRNTDQHYPAPKKAE	NGF; <i>A. feae</i> ; B8QCH2
			749.9	2	47	NTDQHYPAPKKAE	
			505.6	3	47	TSRNTDQHYPAPK	
			696.0	3	42	KTSRNTDQHYPAPKKAED	
			585.8	2	42	NTDQHYPAPK	
			692.8	2	42	TDQHYPAPKKAE	
			707.3	2	40	SRNTDQHYPAPK	
			821.9	2	40	KTSRNTDQHYPAPK	
			615.0	3	39	TSRNTDQHYPAPKKAE	
			528.8	2	38	TDQHYPAPK	
			442.9	3	37	RNTDQHYPAPK	
3	1.81	-	871.0	2	74	AAATPQKLAKGRGAAATSA	CNP; <i>A. feae</i> ; K4J3K2
			1044.1	2	64	SDSKAAATPQKLAKGRGAAATS	
			857.5	2	63	PPHQGPRPPRPRPKP	
			608.8	2	61	SDSKAAATPQKL	
			667.4	3	59	SDSKAAATPQKLAKGRGAAAT	
			543.6	3	58	SDSKAAATPQKLAKGR	
			633.7	3	57	SDSKAAATPQKLAKGRGAAA	
			494.6	3	57	AAATPQKLAKGRGAAA	
			586.3	3	54	SDSKAAATPQKLAKGRGA	
			1079.6	2	54	SDSKAAATPQKLAKGRGAAATSA	
			644.3	2	54	SDSKAAATPQKLA	
			809.0	2	53	PHQGPRPPRPRPKP	
			371.6	3	51	RLKGLAKKGAA	

Peak	%	MW (kDa)	Peptide Ion		Score	MS/MS-derived sequence	Protein family/species/accession
			m/z	z			
4	0.71	-	375.6	3	50	VPPKGESVGVR	CNP; <i>A. feae</i> ; K4J3K2
			627.8	2	50	SLRPEAASGPAAAG	
			682.4	2	50	KPPHQGPRPPRP	
			599.4	2	49	PRPPRPRPKP	
			565.3	2	48	DSKAAATPQKL	
			610.0	3	46	SDSKAAATPQKLAKGRGAA	
			563.8	2	45	SLRPEAASGPAA	
			529.3	2	45	GRMVPPKGES	
			492.8	2	42	SLRPEAASGP	
			528.3	2	41	SLRPEAASGPA	
			380.7	2	41	KPPHQGP	
			575.8	2	39	TDDTTALREE	
			557.3	3	38	AATPQKLAKGRGAAATSA	
			367.6	3	37	RPPRPRPKP	
			380.9	3	36	ZGPRPPRPRP	
			458.8	2	36	KPPHQGPR	
			921.5	2	35	KPPHQGPRPPRPRPKP	
			556.6	3	35	ZGPRPPRPRPKPSQS	
			455.9	3	34	ZGPRPPRPRPKP	
			600.8	2	34	DSKAAATPQKLA	
			760.4	2	34	HQGPRPPRPRPKP	
			720.1	3	90	SDSKAAATPQKLAKGRGAAATSA	
			627.8	2	51	SLRPEAASGPAAAG	
			682.4	2	49	KPPHQGPRPPRP	
			771.4	1	48	ZKPPGVY	
			410.6	3	48	AKGRGAAATSARL	
			515.8	2	48	GRGAAATSARL	
			371.6	3	43	RLKGLAKKGAA	
			422.7	2	41	PHPHYPP	
			563.8	2	38	SLRPEAASGPAA	
			579.8	2	38	KGRGAAATSARL	
5	0.39	-	380.7	2	37	KPPHQGP	CNP; <i>A. feae</i> ; K4IT20
			477.6	3	47	RDLRTDGKQWR	

Peak	%	MW (kDa)	Peptide Ion		Score	MS/MS-derived sequence	Protein family/species/accession
			m/z	z			
6	1.49	-	410.6	3	43	AKGRGAAATSARL	CNP; <i>A. feae</i> ; K4IT20
			424.6	3	39	MVPPKGESVGVR	
			459.6	3	39	AKGRGAAATSARLM	
			637.8	2	36	DLRTDGKQWR	
			459.6	3	35	AKGRGAAATSARLM	
7	0.59	-	482.7	2	33	GAAATSARLM	CNP; <i>A. feae</i> ; K4IT20
			509.3	2	32	KPPGVYYPP	
			425.6	3	32	DLRTDGKQWR	
8	3.66	-	460.7	2	26	KPGVYYPP	CNP; <i>A. feae</i> ; K4IT20
			600.8	2	46	SGPAAAGVGDGWR	
			491.9	3	42	LAKGRGAAATSARLM	
			557.3	2	42	GPAAAGVGDGWR	
			509.3	2	39	KPPGVYYPP	
9	2.33	-	440.2	3	48	AIVCGGDNPCKK	PLA ₂ ; <i>A. feae</i> ; A0A0D3N8V5
10	0.89	3.8	403.7	2	18	AAAICFR	PLA ₂ ; <i>A. feae</i> ; A0A0D3N8V5
11	35.00	5.0	403.7	2	29	AAAICFR	PLA ₂ ; <i>A. feae</i> ; A7X4P4
			440.2	2	21	AVCECDK	
			552.2	2	30	RQPMDATDR	
12	0.23	28.2	500.3	2	42	IACAPQDVK	SVMP; <i>Crotalus adamanteus</i> ; ~A0A1W7RB89
			564.3	2	54	KIACAPQDVK	
			376.2	3	31	KIACAPQDVK	
			494.7	2	46	TDSYPYSR	
13	0.10	-	494.7	2	46	TDSYPYSR	PLA ₂ ; <i>A. feae</i> ; A0A0D3N9P6
14	1.70	14.3	403.7	2	53	AAAICFR	PLA ₂ ; <i>A. feae</i> ; A7X4P4
			340.5	3	42	TLHYIYGR	
			510.8	2	35	TLHYIYGR	
15	0.53	12.7	403.7	2	35	AAAICFR	PLA ₂ ; <i>A. feae</i> ; A7X4P4
			436.7	2	30	NNVIVCR	
			552.2	2	22	RQPMDATDR	
			544.3	2	26	RQPMDATDR	
			1111.6	1	25	NPNPVPTGCR	
	0.69	16.2	1293.7	1	77	IDTACVCVISR	NGF; <i>Protobothrops flavoviridis</i> ; ~B1Q3K2
			1809.9	1	74	HWNSYCTTTHTFVR	
			340.5	3	42	TLHYIYGR	
			340.5	3	42	TLHYIYGR	
	0.58	14.4	340.5	3	42	TLHYIYGR	PLA ₂ ; <i>A. feae</i> ; A7X4P4
			340.5	3	42	TLHYIYGR	

Peak	%	MW (kDa)	Peptide Ion		Score	MS/MS-derived sequence	Protein family/species/accession
			m/z	z			
	0.19	12.6	510.8	2	39	TLHYIYGR	PLA ₂ ; <i>A. feae</i> ; A7X4P4
			511.8	2	59	TLHYIYGR	
			511.9	3	58	CCFVHDCCYGR	
			437.7	2	49	NNVIVCR	
16	0.07	14.9	549.3	2	75	NPNPVPSGCR	NGF; <i>A. feae</i> ; Q2XXL6
			707.3	2	41	CRNPNPVPSGCR	
17	0.27	14.7	1096.5	1	38	DNLDITYSLR	PLA ₂ ; <i>A. feae</i> ; A0A0D3N9S4
			1475.6	1	20	CCFVHNCCYR	
18	0.21	15.3	1096.6	1	59	DNLDITYSLR	PLA ₂ ; <i>A. feae</i> ; A0A0D3N9S4
			1475.6	1	35	CCFVHNCCYR	
19	5.89	28.2	1489.6	1	10	CCFVHNCCYRK	CRISP; <i>Crotalus horridus</i> ; ~F2Q6E5
			1138.5	1	55	SVDFDSESPR	
			1537.7	1	15	MEWYPEAAANAER	
			1553.7	1	19	MEWYPEAAANAER	
			1905.1	1	121	KPEIQNEIVDLHNSLR	
			2061.2	1	4	KPEIQNEIVDLHNSLR	
			1138.5	1	21	SVDFDSESPR	
			1905.0	1	25	KPEIQNEIVDLHNSLR	
20	0.22	14.4	403.7	2	35	AAAICFR	CRISP; <i>C. horridus</i> ; ~F2Q6E7 PLA ₂ ; <i>A. feae</i> ; A0A0D3N8V5 SVSP; <i>A. feae</i> ; A0A1Y0DIB6
			1304.6	1	15	NFQMQLGVHSK	
			2599.2	1	11	ETYPDVPNCANINILDHAVCQR	
			1535.5	1	30	CCFEHDCCYGK	
21	2.82	32.2	1304.6	1	22	NFQMQLGVHSK	PLA ₂ ; <i>Bothriechis nigroviridis</i> ; ~C0HJL8 SVSP; <i>A. feae</i> ; A0A1Y0DIB6
			2599.2	1	63	ETYPDVPNCANINILDHAVCQR	
			2915.5	1	54	LNSPVHESTHIAPVSLPSSSPTVGSVCR	
			2599.3	1	50	ETYPDVPNCANINILDHAVCQR	
			2915.6	1	62	LNSPVHESTHIAPVSLPSSSPTVGSVCR	
22	0.07	18.7	403.7	2	53	AAAICFR	PLA ₂ ; <i>A. feae</i> ; A7X4P4 SVSP; <i>Bothrops jararaca</i> ; ~O13069 SVSP; <i>A. feae</i> ; A0A1Y0DIB6 SVSP; <i>A. feae</i> ; A0A1Y0DIB6
			558.3	2	67	TLCAGILQGGK	
			2599.2	1	31	ETYPDVPNCANINILDHAVCQR	
			1288.6	1	69	NFQMQLGVHSK	
			1304.6	1	34	NFQMQLGVHSK	
			2599.2	1	130	ETYPDVPNCANINILDHAVCQR	

Peak	%	MW (kDa)	Peptide Ion		Score	MS/MS-derived sequence	Protein family/species/accession
			m/z	z			
23	0.05	18.4	2915.5	1	159	LNSPVHESTHIAPVSLPSSSPTVGSVCR	PLA ₂ ; <i>A. feae</i> ; A0A0D3N8V5
			753.3	2	75	CCFVHDCCYGK	
			659.8	2	69	AIVCGGDNPCCK	
			576.9	2	69	EVCECDKAAAICFR	
			595.8	2	66	AIVCGGDNPCCK	
			683.8	2	58	MDSYTYSEENK	
	0.38	15.0	404.7	2	57	AAAICFR	PLA ₂ ; <i>A. feae</i> ; A0A0D3N8V5
			690.8	2	64	MDSYTYSEENK	
			682.8	2	56	MDSYTYSEENK	
			1069.4	2	37	VTGCDPKMDSYTYSEENK	
			752.3	2	48	CCFVHDCCYGK	
	0.36	56.0	501.5	3	30	CCFVHDCCYGK	SVSP; <i>A. feae</i> ; A0A1Y0DIB5
			1513.7	1	200	IIGGDECDINDHR	
			1117.7	1	31	TLCAGILKGGK	
	0.19	48.6	572.3	2	56	EKFFCLSSK	SVSP; <i>A. feae</i> ; A0A1Y0DIB4
			443.7	2	31	FFCLSSK	
	0.05	32.7	1116.1	2	17	NSAHIAPLSLPSSPPSVGSVCR	SVSP; <i>A. feae</i> ; A0A1Y0DIB4
			1095.7	1	14	FLVALYTLR	
			1003.6	1	20	ALYPGLLEK	
			1095.7	1	38	FLVALYTLR	
			2233.2	1	8	NSAHIAPLSLPSSPPSVGSVCR	
	0.06	28.2	2480.2	1	9	ETYPDVPHCANINIVDHAVCR	SVSP; <i>A. feae</i> ; A0A1Y0DIB4
			1003.6	1	15	ALYPGLLEK	
			1003.6	1	12	ALYPGLLEK	
	0.28	15.9	2233.3	1	30	NSAHIAPLSLPSSPPSVGSVCR	SVSP; <i>A. feae</i> ; A0A1Y0DIB4
			2233.3	1	30	NSAHIAPLSLPSSPPSVGSVCR	
24	12.00	15.6	1505.5	1	10	CCFVHDCCYGK	PLA ₂ ; <i>A. feae</i> ; A0A0D3N8V5
25	5.56	19.7	998.5	1	29	TDPPYPYSR	PLA ₂ ; <i>A. feae</i> ; A0A0D3N944
26	0.07	42.3	1534.6	1	3	CCFEHNCCYGK	SVSP; <i>A. feae</i> ; A0A1Y0DIC1
			414.2	2	17	KVPNEDK	
			2929.5	1	99	LNSPVHESTHIAPLSLPSSSPTVGSVCR	
			918.5	1	45	VYPGLLEK	
			2537.3	1	64	VTHPDVPHCANINILNHAVCQK	
	0.14	28.9	2929.5	1	119	LNSPVHESTHIAPLSLPSSSPTVGSVCR	SVSP; <i>A. feae</i> ; A0A1Y0DIC1
			2929.5	1	119	LNSPVHESTHIAPLSLPSSSPTVGSVCR	

Peak	%	MW (kDa)	Peptide Ion		Score	MS/MS-derived sequence	Protein family/species/accession
			m/z	z			
27	0.52	16.9	1022.5	1	36	TLHYIYGR	PLA ₂ ; <i>A. feae</i> ; A7X4P4
			1488.7	1	29	IGLQFYVDAFCR	
			1533.6	1	36	CCFVHDCCYGR	
			1967.8	1	25	NPVTSYSAYGCYCGVGGR	
	0.63	15.6	1022.6	1	46	TLHYIYGR	PLA ₂ ; <i>A. feae</i> ; A7X4P4
			1488.8	1	18	IGLQFYVDAFCR	
			1533.7	1	12	CCFVHDCCYGR	
	0.43	16.9	1022.5	1	45	TLHYIYGR	PLA ₂ ; <i>A. feae</i> ; A7X4P4
			1488.8	1	50	IGLQFYVDAFCR	
			1533.6	1	42	CCFVHDCCYGR	
	0.68	15.6	1022.6	1	7	TLHYIYGR	PLA ₂ ; <i>A. feae</i> ; A7X4P4
			1488.8	1	3	IGLQFYVDAFCR	
28	3.64	67.9	439.2	2	48	YDTYSTK	LAAO; <i>Ovophis okinavensis</i> ; ~T2HQ57
			554.3	2	46	VTVTYQTPAK	
			567.3	2	35	YPVKPSEEGK	
29	0.09	156.0	-	-	-	-	Unknown
	1.69	86.0	1059.4	1	53	GQDNFYCR	SVMP; <i>Sistrurus tergeminus</i> ; ~A0A194ARR8
	0.46	55.9	1388.6	2	1	YSDDYSDDVLDDGMVDHG TK CAVGK	SVMP; <i>Agkistrodon piscivorus</i> ; ~A0A194ARK7
	0.17	65.9	1852.0	1	29	DSTALFPNIYLETVLR	HA; <i>A. piscivorus</i> ; ~A0A194ART0
			1889.9	1	6	HSDSNAFLHLFPDSFR	
30	0.15	97.3	2018.0	1	15	KHSDSNAFLHLFPDSFR	SVMP; <i>C. horridus</i> ; ~A0A0K8RYQ3
			836.8	2	46	GSQCADGVCCDQCR	
			449.2	2	40	TL SH QPSK	
	0.35	60.0	656.3	2	49	SADCPTDDFQR	SVMP; <i>S. tergeminus</i> ; ~A0A194ARL0
			425.2	2	37	RAGTEC	
31	2.31	-	1458.1	2	1	MARGDNMHDYCN G KTCDCPXNPYK	SVMP; <i>Echis ocellatus</i> ; ~E9KJX0
32	1.00	54.7	376.9	3	2	VHQM V NIM K	SVMP; <i>Crotalus atrox</i> ; ~P34182

Methionine oxidation is underlined.