

Supplementary table 1 Assignment of the reverse-phase chromatographic fractions from *Protobothrops cornutus* venom to protein families by nESI-MS/MS of selected peptide ions from in-gel digested protein bands separated by SDS-PAGE.

Peak	%	MW (kDa)	Peptide Ion		Score	MS/MS-derived sequence	Protein family/species/accession
			m/z	z			
1	0.03	de novo	255.7	2	55	PPPIS	BPP/CNP; <i>Protobothrops jerdonii</i> ; ~PJD c31701
2	0.75	de novo	248.6	2	71	QSKPG	BPP/CNP; <i>Protobothrops flavoviridis</i> ; ~P0C7P5
		de novo	255.7	2	59	PPISP	
3	3.05	-	622.3	2	104	QSKPGRPPPISP	BPP/CNP; <i>P. jerdonii</i> ; ~PJD c31701
		-	475.8	2	47	RPPHHIPP	
4	2.75	de novo	241.1	2	80	QSKPG	BPP/CNP; <i>P. flavoviridis</i> ; ~P0C7P5
		de novo	255.7	2	60	PPISP	
5	0.18	-	670.6	3	79	GDWNDDRCTGQSADCPR	Disintegrin; <i>Protobothrops mucrosquamatus</i> ; ~E9NW26
6	1.90	14.5	1005.4	2	79	GDWNDDRCTGQSADCPR	Disintegrin; <i>P. mucrosquamatus</i> ; ~E9NW26
7	0.98	11.9	670.6	3	64	GDWNDDRCTGQSADCPR	Disintegrin; <i>P. mucrosquamatus</i> ; ~E9NW26
			984.4	2	49	LSPGAQCADGLCCDQCR	
8	0.44	-	576.2	2	58	CTGQSADCPR	Disintegrin; <i>P. mucrosquamatus</i> ; ~E9NW26
			984.4	2	55	LSPGAQCADGLCCDQCR	
9	0.12	32.5	978.7	3	66	AAESECDAESCTGQSAECPTDDFQR	SVMP-fragment; <i>P. mucrosquamatus</i> ; ~XP_015682631
			801.3	3	57	LRPGTQCEDGECCEQCQFK	
			559.8	2	53	LFCVQGPIGK	
			623.9	2	52	LFCVQGPIGKK	
			514.3	2	43	IPCAPQDVK	
			467.6	3	42	IPCAPQDVKCGR	
			578.3	2	42	KIPCAPQDVK	
10	0.51	16.0	456.8	2	36	ETLVPILK	VEGF; <i>P. jerdonii</i> ; ~PJD c48748_g1
11	0.75	17.4	502.5	3	54	CCFVHDCCYGK	PLA <sub>2</sub> ; <i>P. mucrosquamatus</i> ; ~Q90W39
			591.3	2	45	AAAVCLGHNLR	
12	0.01	28.9	-	-	-	-	Unknown
	2.72	17.3	657.1	4	95	KNAIPFYSSYGICYCGWGGQGKPK	PLA <sub>2</sub> ; <i>P. mucrosquamatus</i> ; ~Q90W39
			1249.1	2	87	NAIPFYSSYGICYCGWGGQGKPK	
			1019.1	3	86	NAIPFYSSYGICYCGWGGQGKPKDATDR	
			769.6	3	79	CCFVHDCCYGKLTDCSPK	
		12.8	838.7	3	69	TGVIIICGEGTECEKQICECDR	PLA <sub>2</sub> ; <i>P. flavoviridis</i> ; ~Q805A2
			776.9	2	57	TGVIIICGEGTECEK	
13	4.77	17.4	657.1	4	85	KNAIPFYSSYGICYCGWGGQGKPK	PLA <sub>2</sub> ; <i>P. mucrosquamatus</i> ; ~Q90W39
			833.0	3	80	NAIPFYSSYGICYCGWGGQGKPK	
			764.6	4	67	NAIPFYSSYGICYCGWGGQGKPKDATDR	
			577.5	4	63	CCFVHDCCYGKLTDCSPK	
			591.3	2	57	AAAVCLGHNLR	

Peak	%	MW (kDa)	Peptide Ion		Score	MS/MS-derived sequence	Protein family/species/accession
			m/z	z			
14	8.75	13.1	838.7	3	102	TGVIIICGEGTECEKQICECDR	PLA <sub>2</sub> ; <i>P. flavoviridis</i> ; ~Q805A2
			776.9	2	66	TGVIIICGEGTECEK	
		17.4	1019.1	3	127	NAIPFYSSYGICYCGWGGQGKPKDATDR	PLA <sub>2</sub> ; <i>P. mucrosquamatus</i> ; ~Q90W39
			657.1	4	91	KNAIPFYSSYGICYCGWGGQGKPK	
			833.0	3	86	NAIPFYSSYGICYCGWGGQGKPK	
			769.6	3	83	CCFVHDCCYGKLTDCSPK	
			591.3	2	81	AAAVCLGHNLR	
			591.3	2	69	AAAVCLGHNLR	
		13.1	1032.4	2	73	DATDRCCFVHDCCYGK	PLA <sub>2</sub> ; <i>P. mucrosquamatus</i> ; ~Q90W39
			577.5	4	49	CCFVHDCCYGKLTDCSPK	
			502.5	3	44	CCFVHDCCYGK	
		11.2	591.3	2	72	AAAVCLGHNLR	PLA <sub>2</sub> ; <i>P. mucrosquamatus</i> ; ~Q90W39
			657.1	4	60	KNAIPFYSSYGICYCGWGGQGKPK	
			502.5	3	50	CCFVHDCCYGK	
			833.0	3	43	NAIPFYSSYGICYCGWGGQGKPK	
15	3.73	28.4	1722.7	1	86	TNCPASCFCHNEII	CRISP; <i>P. jerdonii</i> ; ~Q7ZZN9
		21.2	583.3	2	51	NVDFDSESPR	CRISP; <i>P. flavoviridis</i> ; ~1WVR_A
	0.25	17.3	591.3	2	68	AAAVCLGHNLR	PLA <sub>2</sub> ; <i>P. mucrosquamatus</i> ; ~Q90W39
			577.5	4	67	CCFVHDCCYGKLTDCSPK	
			657.1	4	58	KNAIPFYSSYGICYCGWGGQGKPK	
			833.0	3	46	NAIPFYSSYGICYCGWGGQGKPK	
16	0.46	50.1	596.8	2	42	IMGWGTTPTK	SVSP; <i>Crotalus scutulatus</i> ; ~AUS82544
		42.9	756.8	2	72	VIGGDECNINEHR	SVSP; <i>Gloydus blomhoffii</i> ; ~Q9PT51
	0.04	31.1	777.3	2	57	MEWYPEAAANAER	CRISP; <i>P. flavoviridis</i> ; ~1WVR_A
			583.3	2	49	NVDFDSESPR	
			769.3	2	46	MEWYPEAAANAER	
			589.3	2	41	SVNPTASNMLK	
			611.8	2	49	GNVDFDSESPR	
			560.6	3	78	FIRIDAACVCVISR	
	0.05	19.9	556.3	2	72	NPNPVPTGCR	NGF; <i>P. mucrosquamatus</i> ; ~XP_015667549
			632.3	2	72	IDAACVCVISR	
			697.3	2	59	ALTM <del>E</del> GKQASWR	
			714.3	2	54	CRNPNPVPTGCR	
			594.6	3	41	HWNSYCTTTHTFVK	
			962.5	1	39	QYFFETK	
			591.3	2	71	AAAVCLGHNLR	
			559.8	2	35	TLCAGILEGGK	
17	0.28	17.4	591.3	2	71	AAAVCLGHNLR	PLA <sub>2</sub> ; <i>P. mucrosquamatus</i> ; ~Q90W39
	0.22	33.9	559.8	2	35	TLCAGILEGGK	SVSP; <i>P. mucrosquamatus</i> ; ~PMR c29163_g4
	19.07	18.9	1505.5	1	91	CCFVHDCCYGK	PLA <sub>2</sub> ; <i>Trimeresurus stejnegeri</i> ; ~P82896

Peak	%	MW (kDa)	Peptide Ion		Score	MS/MS-derived sequence	Protein family/species/accession
			m/z	z			
18	0.15	15.7	871.9	2	82	EICECDKAAAICFR	PLA <sub>2</sub> ; <i>P. flavoviridis</i> ; ~Q805A2
			838.7	3	83	TGVIIICGEGTECEKQICECDR	
			776.9	2	80	TGVIIICGEGTECEK	
		57.9	565.3	2	51	ILCAGILQGGK	SVSP; <i>P. flavoviridis</i> ; ~BAN82037
			423.2	2	47	RMPAQSR	
			46.4	2	72	VIGGDECNINEHR	
19	0.02	28.4	611.8	2	55	GNVDFDSESPR	SVSP; <i>Agkistrodon contortrix contortrix</i> ; ~P09872
			19.4	2	61	EICECDKAAAICFR	
			19.4	2	61	EICECDKAAAICFR	
	2.52	57.4	550.8	2	50	NVPNEDEQR	CRISP; <i>V. berus nikolskii</i> ; ~B7FD10
			419.5	3	49	NVPNEDEQRR	
			50.5	3	61	SAHIAPLSLPSNPPSVGSVCR	
20	5.61	34.8	679.3	2	37	EWVLTAAHCDR	PLA <sub>2</sub> ; <i>T. stejnegeri</i> ; ~P82896
			559.3	2	48	TLCAGILQGGK	
			33.9	2	58	DDENDKDIMLIR	
		32.0	498.2	3	46	DDENDKDIMLIR	SVSP; <i>T. stejnegeri</i> ; ~Q8AY80
			492.9	3	81	DDENDKDIMLIR	
			498.2	3	57	DDENDKDIMLIR	
21	1.70	19.4	492.9	3	60	DDENDKDIMLIR	SVSP; <i>A. contortrix contortrix</i> ; ~JAV51428
			722.4	2	39	VLNEDEQTRDPK	
			16.0	2	62	VIGGDECNINEHR	
	0.89	16.2	58.4	2	56	VIGGDECNINEHR	SVSP; <i>P. jerdonii</i> ; ~Q9DF66
			35.7	2	77	IIGGDECNINEHR	
			573.3	2	48	EKFFCLSSK	
22	0.44	33.9	749.8	2	79	VVGGDECNINEHR	SVSP; <i>C. atrox</i> ; ~AUS82489
			811.0	3	65	VFQQQM <sup>N</sup> WADA EK FCTQQR	
			805.7	3	65	VFQQQM <sup>N</sup> WADA EK FCTQQR	
	0.60	17.9	829.8	2	57	TTDNQWWSMDCSK	SVSP; <i>G. blomhoffii</i> ; ~AAP20637
			808.4	2	49	YNAWSAESECIASK	
			756.8	2	66	VIGGDECNINEHR	
23	0.79	76.2	42.7	2	81	VVGGDECNINEHR	SVSP; <i>G. blomhoffii</i> ; ~CAB65936
			33.9	3	61	VVGGDECNINEHR	
			500.2	3	61	VVGGDECNINEHR	
	0.60	17.9	811.0	3	63	VFQQQM <sup>N</sup> WADA EK FCTQQR	SVSP; <i>Ovophis okinavensis</i> ; ~AAB34084
			829.8	2	48	TTDNQWWSMDCSK	
			797.9	2	43	VFQQQM <sup>N</sup> WADA EK	
	0.79	76.2	808.4	2	40	YNAWSAESECIASK	SVSP; <i>A. contortrix contortrix</i> ; ~P82981
			674.8	4	82	SEC DIAESCTGQSADCPDTHYHR	
			577.3	3	80	YSEDLDYGMVDHGK	
			742.6	3	73	LHSWVECESGECCEQCR	

Peak	%	MW (kDa)	Peptide Ion		Score	MS/MS-derived sequence	Protein family/species/accession
			m/z	z			
24	0.60	56.5	1013.4	2	63	LTPGSQCAEGLCCEQCR	SVMP; <i>P. mucrosquamatus</i> ; ~XP_029142018
			549.3	2	48	FSTEGKLCR	
			664.4	2	44	YIELVIVADHR	
		43.8	734.7	3	92	HDNAQLLTGMIFNEKIEGR	SVMP; <i>P. mucrosquamatus</i> ; ~XP_029142018
			1013.4	2	73	LTPGSQCAEGLCCEQCR	
			643.0	4	71	FSDCSLNQYSNEIIHNHFTSR	
			556.1	4	65	IYETANDLNEIYRPLKIR	
			729.4	3	63	HDNAQLLTGMIFNEKIEGR	
			664.4	2	61	YIELVIVADHR	
			549.3	2	56	FSTEGKLCR	
			583.0	3	56	HDNAQLLTGMIFNEK	
			532.3	2	50	TRPHLVANR	
			651.3	3	46	IYETANDLNEIYRPLK	
			414.9	3	37	YDGDKTEISSK	
	0.89	38.7	1013.4	2	70	LTPGSQCAEGLCCEQCR	SVMP; <i>T. stejnegeri</i> ; ~P0DM87
			549.3	2	51	FSTEGKLCR	
		33.2	718.4	3	97	IMGWGTISSTKETYPNVPR	SVSP; <i>Gloydus intermedius</i> ; ~ASX97880
			713.0	3	76	IMGWGTISSTKETYPNVPR	
		18.2	591.3	2	57	FCSEQVKGAR	CTL; <i>P. jerdonii</i> ; ~D1MGU0
			618.8	2	77	SAGQLFEESLR	
	3.99	-	455.6	3	61	SAGQLFEESLRK	LAAO; <i>P. mucrosquamatus</i> ; ~XP_015673892
			583.4	2	54	ITFRPPLPPK	
			618.4	2	70	KVTVTYQTPAK	
		-	554.3	2	65	VTVTYQTPAK	LAAO; <i>P. flavoviridis</i> ; ~BAN82013
			725.4	2	95	VVSLNVLCTECR	
			653.9	2	86	QVPVVQAYAFGK	
		-	640.2	3	70	DCPSDWSSYEGHCYR	CTL; <i>Trimeresurus albolabris</i> ; ~P81114
			584.3	2	52	EQFECLVSR	
			545.8	2	59	YGPVSGEIR	
	0.94	110.0	746.8	2	48	SVQPQAQSWSCSK	PDE; <i>Protobothrops elegans</i> ; ~BAP39928
			782.4	2	60	CSSITELEKVNQR	
			561.3	2	48	NPFYTPSPAK	
		81.9	545.8	2	46	YGPVSGEIR	PDE; <i>P. elegans</i> ; ~BAP39928
			516.8	2	38	YCLLHQAQ	
			403.2	2	38	ALEMADR	
			457.8	2	35	LNLNNQAQ	
			678.3	2	33	AATYFWPGSEVK	
			618.8	2	64	SAGQLFEESLR	
	0.17	59.7	618.8	2	64	SAGQLFEESLR	LAAO; <i>P. mucrosquamatus</i> ; ~XP_015673893
			618.8	2	64	SAGQLFEESLR	

Peak	%	MW (kDa)	Peptide Ion		Score	MS/MS-derived sequence	Protein family/species/accession
			m/z	z			
26	5.37 1.18	27.0 17.3	438.7	2	61	STTDLP <sup>SR</sup>	SVMP; <i>P. jerdonii</i> ; ~Q7ZZS9 CTL; <i>P. jerdonii</i> ; ~D1MGU1
			501.2	2	46	DVNRASENP	
			474.8	2	35	IVREYIR	
			655.4	2	46	KPQCILNAPLR	
			829.8	2	53	TTDNQWW <sup>SMDCSK</sup>	
			808.4	2	53	YNAWSAESECIASK	
	0.05	112.0	811.0	3	47	VFQQQM <sup>NWADA</sup> EKFCTQQR	CTL; <i>P. mucrosquamatus</i> ; ~XP_015671571
			805.9	2	43	VFQQQM <sup>NWADA</sup> EK	
			591.3	2	55	WVNVYCGQR	
			655.3	2	53	KWVNVYCGQR	
			466.2	3	52	TCLGLEKGTDFR	
			457.2	2	40	FCMEQAK	
	1.06	77.6	545.8	2	59	YGPVSGEIR	PDE; <i>P. elegans</i> ; ~BAP39928 SVMP; <i>P. mucrosquamatus</i> ; ~XP_029142019
			746.8	2	47	SVQPQAQSWSCSK	
			899.4	3	89	SECDAIESCTGQSAD <sup>CPTDHYHR</sup>	
			577.3	3	71	YSEDLDYGMVDHGTK	
			587.8	2	47	MIPCAPQDVK	
			552.3	2	43	CGKLYCFR	
	0.11	57.4	412.6	3	58	K.KVTVTYQTPAK.D	LAAO; <i>P. flavoviridis</i> ; ~BAN82013
			626.8	2	49	K.SAGQLYEESLR.K	
			597.8	2	69	TPVPAGCYDSK	
			450.9	3	57	RTPVPAGCYDSK	
			453.2	2	52	VADISMAAK	
			555.3	2	48	YSDQTNILR	
	0.98	17.9	811.0	3	96	VFQQQM <sup>NWADA</sup> EKFCTQQR	CTL; <i>P. jerdonii</i> ; ~D1MGU1
			805.7	3	78	VFQQQM <sup>NWADA</sup> EKFCTQQR	
			829.8	2	66	TTDNQWW <sup>SMDCSK</sup>	
			808.4	2	59	YNAWSAESECIASK	
			532.2	3	46	VFQQQM <sup>NWADA</sup> EK	
			805.9	2	44	VFQQQM <sup>NWADA</sup> EK	
27	0.26	-	591.3	2	66	WVNVYCGQR	CTL; <i>P. mucrosquamatus</i> ; ~XP_015671571
			466.2	3	52	TCLGLEKGTDFR	
			555.3	2	63	YSDQTNILR	
			597.8	2	63	TPVPAGCYDSK	
	2.88	-	640.2	3	100	DCPSDWSSYEGHCYR	CTL; <i>T. albolabris</i> ; ~P81114
			584.3	2	58	EQFECLVSR	
			808.4	2	63	YNAWSAESECIASK	
			805.9	2	49	VFQQQM <sup>NWADA</sup> EK	

Peak	%	MW (kDa)	Peptide Ion		Score	MS/MS-derived sequence	Protein family/species/accession
			m/z	z			
28	1.74	64.4	559.8	2	50	LFCVQGPIGK	SVMP; <i>P. mucrosquamatus</i> ; ~XP_015682631
			623.9	2	45	LFCVQGPIGKK	
			514.3	2	44	IPCAPQDVK	
	2.31	54.7	1467.6	2	37	AAESECDAESC TGQAECPTDDFQR	SVMP; <i>P. flavoviridis</i> ; ~Q90ZI3
			520.3	2	45	FKAAGTECR	
			816.3	3	38	AAGTECRAATDECDMADLCTGR	
		17.9	1216.1	2	83	VFQQQMNWADA EK FCTQQR	CTL; <i>P. jerdonii</i> ; ~D1MGU1
			829.8	2	63	TTDNQWWSMDCSK	
			808.4	2	54	YNAWSAESECIASK	
		16.3	532.2	3	43	VFQQQMNWADA EK	CTL; <i>P. jerdonii</i> ; ~D1MGU1
			805.9	2	42	VFQQQMNWADA EK	
			811.0	3	75	VFQQQMNWADA EK FCTQQR	
			829.8	2	48	TTDNQWWSMDCSK	
			805.9	2	41	VFQQQMNWADA EK	
			539.2	3	35	YNAWSAESECIASK	
29	5.82	63.4	978.7	3	79	AAESECDAESC TGQAECPTDDFQR	SVMP; <i>P. mucrosquamatus</i> ; ~XP_015682631
			559.8	2	64	LFCVQGPIGK	
			623.9	2	62	LFCVQGPIGKK	
		53.8	843.3	2	65	AATDECDMADLCTGR	SVMP; <i>P. flavoviridis</i> ; ~Q90ZI3
			567.9	3	55	AATDECDMADLCTGR	
		43.4	843.3	2	60	AATDECDMADLCTGR	SVMP; <i>P. flavoviridis</i> ; ~Q90ZI3
			851.3	2	47	AATDECDMADLCTGR	
		34.6	843.3	2	62	AATDECDMADLCTGR	SVMP; <i>P. flavoviridis</i> ; ~Q90ZI3
			567.9	3	50	AATDECDMADLCTGR	
		33.2	843.3	2	61	AATDECDMADLCTGR	SVMP; <i>P. flavoviridis</i> ; ~Q90ZI3
			567.9	3	44	AATDECDMADLCTGR	
		29.1	559.8	2	60	LFCVQGPIGK	SVMP; <i>P. mucrosquamatus</i> ; ~XP_015682631
			623.9	2	54	LFCVQGPIGKK	
		22.8	532.6	3	62	YIPCAQEDVKCGR	SVMP; <i>Bothrops jararacussu</i> ; ~Q1PHZ4
			574.9	3	58	ENEKYIPCAQEDVK	
	3.52	17.8	1208.1	2	110	VFQQQMNWADA EK FCTQQR	CTL; <i>P. jerdonii</i> ; ~D1MGU1
			1216.1	2	98	VFQQQMNWADA EK FCTQQR	
			1658.7	1	71	TTDNQWWSMDCSK	
			571.3	4	61	KESHLVSFESSEEVDFVVS	
			808.4	2	61	YNAWSAESECIASK	
			532.2	3	49	VFQQQMNWADA EK	
			805.9	2	47	VFQQQMNWADA EK	
		16.2	805.7	3	82	VFQQQMNWADA EK FCTQQR	CTL; <i>P. jerdonii</i> ; ~D1MGU1

Peak	%	MW (kDa)	Peptide Ion		Score	MS/MS-derived sequence	Protein family/species/accession
			m/z	z			
30	0.32	84.7	811.0	3	80	VFQQQM <u>N</u> WADA EK FCTQQR	SVMP; <i>P. mucrosquamatus</i> ; ~XP_015685802
			829.8	2	56	TTDNQWW SMDCSK	
			808.4	2	51	YNAWSAESECIASK	
			805.9	2	39	VFQQQM <u>N</u> WADA EK	
			797.9	2	35	VFQQQM <u>N</u> WADA EK	
			823.3	3	78	RSECDIAESCTGHSDDCPTDR	
			551.2	5	72	SECDIAESCTGHSDDCPTDRFHR	
	0.64	70.5	771.3	3	67	SECDIAESCTGHSDDCPTDR	SVMP; <i>P. mucrosquamatus</i> ; ~XP_015685802
			742.6	3	69	LHSWVECESGECCEQCR	
			617.7	4	62	RSECDIAESCTGHSDDCPTDR	
			771.3	3	60	SECDIAESCTGHSDDCPTDR	
			551.2	5	60	SECDIAESCTGHSDDCPTDRFHR	
			467.6	3	49	IPCAPQDVKCGR	
			811.0	3	82	VFQQQM <u>N</u> WADA EK FCTQQR	CTL; <i>P. jerdonii</i> ; ~D1MGU1
31	0.48	17.4	805.7	3	61	VFQQQM <u>N</u> WADA EK FCTQQR	
			797.9	2	42	VFQQQM <u>N</u> WADA EK	
			539.2	3	40	YNAWSAESECIASK	
			640.2	3	49	DCPSDWSSYEGHCYR	
			52.4	2	43	SVCDLPEQCTGQSADCPTDR	
			805.7	3	58	VFQQQM <u>N</u> WADA EK FCTQQR	CTL; <i>P. jerdonii</i> ; ~D1MGU1
	0.24	17.4	811.0	3	57	VFQQQM <u>N</u> WADA EK FCTQQR	
			808.4	2	51	YNAWSAESECIASK	
			829.8	2	47	TTDNQWW SMDCSK	
			797.9	2	40	VFQQQM <u>N</u> WADA EK	
			805.9	2	38	VFQQQM <u>N</u> WADA EK	
			811.0	3	62	VFQQQM <u>N</u> WADA EK FCTQQR	CTL; <i>P. jerdonii</i> ; ~D1MGU1
32	0.46	64.8	808.4	2	55	YNAWSAESECIASK	
			551.3	4	98	HDNAQLLTGMIFNEKIEGR	SVMP; <i>P. mucrosquamatus</i> ; ~XP_015681821
			583.0	3	64	HDNAQLLTGMIFNEK	
			769.4	2	62	IYESVNALNVIFR	
			729.4	3	50	HDNAQLLTGMIFNEKIEGR	
			453.7	2	50	YHFVANR	
			505.8	2	46	SVGIVQDHR	
	0.46	63.0	734.7	3	80	HDNAQLLTGMIFNEKIEGR	SVMP; <i>P. mucrosquamatus</i> ; ~XP_015681821
			769.4	2	64	IYESVNALNVIFR	
			583.0	3	64	HDNAQLLTGMIFNEK	
			851.0	3	62	DSCSCGANSCIMSETVSNPSSR	
			505.8	2	49	SVGIVQDHR	

Peak	%	MW (kDa)	Peptide Ion		Score	MS/MS-derived sequence	Protein family/species/accession
			m/z	z			
			453.7	2	47	YHFVANR	
			437.9	3	46	FIELVIVADHR	
			575.3	2	36	SRYHFVANR	
			729.4	3	35	HDNAQLLTGMIFNEKIEGR	
		58.8	734.7	3	91	HDNAQLLTGMIFNEKIEGR	SVMP; <i>P. mucrosquamatus</i> ; ~XP_015681821
			729.4	3	76	HDNAQLLTGMIFNEKIEGR	
			577.6	3	65	HDNAQLLTGMIFNEK	
			583.0	3	61	HDNAQLLTGMIFNEK	
			769.4	2	60	IYESVNALNVIFR	
			453.7	2	49	YHFVANR	
			656.4	2	49	FIELVIVADHR	
			575.3	2	48	SRYHFVANR	
			505.8	2	45	SVGIVQDHR	
		54.7	851.0	3	42	DSCSCGANSCIMSETVSNEPSSR	
			551.3	4	89	HDNAQLLTGMIFNEKIEGR	SVMP; <i>P. mucrosquamatus</i> ; ~XP_015681821
			547.3	4	80	HDNAQLLTGMIFNEKIEGR	
			851.0	3	69	DSCSCGANSCIMSETVSNEPSSR	
			577.6	3	68	HDNAQLLTGMIFNEK	
			583.0	3	65	HDNAQLLTGMIFNEK	
			656.4	2	62	FIELVIVADHR	
			629.7	3	61	RHDNAQLLTGMIFNEK	
			453.7	2	58	YHFVANR	
			505.8	2	56	SVGIVQDHR	
			635.0	3	56	RHDNAQLLTGMIFNEK	
			845.7	3	46	DSCSCGANSCIMSETVSNEPSSR	
			583.8	2	44	RSVGIVQDHR	
		43.4	729.4	3	111	HDNAQLLTGMIFNEKIEGR	SVMP; <i>P. mucrosquamatus</i> ; ~XP_015681821
			734.7	3	94	HDNAQLLTGMIFNEKIEGR	
			684.3	3	85	LRPGAQCAEGLCCDQCR	
			629.7	3	74	RHDNAQLLTGMIFNEK	
			865.9	2	74	HDNAQLLTGMIFNEK	
			769.4	2	70	IYESVNALNVIFR	
			476.5	4	68	RHDNAQLLTGMIFNEK	
			851.0	3	68	DSCSCGANSCIMSETVSNEPSSR	
			579.6	3	66	MAHELGHNLGLHHDR	
			873.9	2	64	HDNAQLLTGMIFNEK	
			585.0	3	63	MAHELGHNLGLHHDR	
			656.4	2	59	FIELVIVADHR	



Peak	%	MW (kDa)	Peptide Ion		Score	MS/MS-derived sequence	Protein family/species/accession
			m/z	z			
			575.3	2	58	SRYHFVANR	
			453.7	2	58	YHFVANR	
			845.7	3	54	DSCSCGANSCIMSETVSNEPSSR	
			490.0	3	53	RFIELVIVADHR	
			505.8	2	47	SVGIVQDHR	
			583.8	2	42	RSVGIVQDHR	
		19.0	684.3	3	115	LRPGAQCAEGLCCDQCR	SVMP; <i>P. mucrosquamatus</i> ; ~XP_015681821
			551.3	4	102	HDNAQLLTGMIFNEKIEGR	
			769.4	2	71	IYESVNALNVIFR	
			583.0	3	65	HDNAQLLTGMIFNEK	
			577.6	3	58	HDNAQLLTGMIFNEK	
			729.4	3	52	HDNAQLLTGMIFNEKIEGR	
			505.8	2	51	SVGIVQDHR	
			437.9	3	47	FIELVIVADHR	
			453.7	2	44	YHFVANR	

Methionine oxidation is underlined.

Supplementary table 2 Assignment of the reverse-phase chromatographic fractions from *Protobothrops jerdonii* 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.

Peak	%	MW (kDa)	Peptide Ion		Score	MS/MS-derived sequence	Protein family/species/accession
			m/z	z			
1	0.09	-	422.0	4	69	RLPKSKGASATSAASRP	BPP/CNP; <i>Protobothrops flavoviridis</i> ; ~P0C7P5
			493.0	4	63	HRLPKSKGASATSAASRPM	
			687.7	3	59	AAPHRLPKSKGASATSAASRP	
			456.3	4	56	HRLPKSKGASATSAASRP	
			981.5	2	49	ASGPAAPHRLPKSKGASATSA	
			401.2	3	45	ASGPAAPHRLPK	
2	0.18	-	406.6	3	41	SGPAAPHRLPKS	BPP/CNP; <i>Protobothrops mucrosquamatus</i> ; ~XP_05680879
			410.7	2	40	GRPPPISP	
			655.4	3	25	HHIPPLLVQQAQGSPP	
			566.8	2	30	SKPGRPPPISP	
			367.2	3	20	LKGLGKKAVGE	
			523.3	2	28	KPGRPPPISP	
			699.4	2	40	HQSKPGRPPPISP	
			529.3	2	44	QQAQGSPP	
3	1.34	-	459.3	2	22	PGRPPPISP	BPP/CNP; <i>Protobothrops elegans</i> ; ~M5A7M5
			523.3	2	34	KPGRPPPISP	
			410.7	2	34	GRPPPISP	
4	5.32	-	835.4	3	101	ASGPAAPHRLPKSKGASATSAASRPM	BPP/CNP; <i>P. flavoviridis</i> ; ~BAP39952
			811.8	3	94	SGPAAPHRLPKSKGASATSAASRPM	
			676.9	4	62	SGPAAPHRLPKSKGASATSAASRPMRD	
			676.9	4	58	EAASGPAAPHRLPKSKGASATSAASRPM	
5	0.76	18.7	548.8	4	42	AAPHRLPKSKGASATSAASRPM	Disintegrin; <i>Protobothrops jerdonii</i> ; Q7ZZS9
			1151.4	1	5	CTGQSADCPR	
			1920.7	1	83	GDNPDRCCTGQSADCPR	
6	0.44	19.0	1967.8	1	85	LSPGAQCADGLCCDQCR	Disintegrin; <i>P. jerdonii</i> ; Q7ZZS9
			1015.4	1	36	ARGDNPDDR	
			1151.5	1	66	CTGQSADCPR	
			1920.7	1	68	GDNPDRCCTGQSADCPR	
7	5.09	9.4	1967.8	1	139	LSPGAQCADGLCCDQCR	VEGF; <i>Bitis gabonica</i> ; ~AAR06855
			451.2	2	38	QLELNER	
8	5.20	9.4	2011.8	1	73	LTPGSQCAEGLCCDQCR	Disintegrin; <i>P. jerdonii</i> ; P0C6E4
9	2.09	18.9	1180.5	1	13	CTGLSDDCPR	Disintegrin; <i>P. flavoviridis</i> ; ~P23323
			2011.8	1	88	LTPGSQCAEGLCCDQCR	
10	3.53	19.3	1180.5	1	51	CTGLSDDCPR	Disintegrin; <i>P. jerdonii</i> ; P0C6E4
			1211.5	1	39	FARGDYPDDR	

Peak	%	MW (kDa)	Peptide Ion		Score	MS/MS-derived sequence	Protein family/species/accession
			m/z	z			
11	2.10	19.2	1998.8	1	90	GDYPDDRCTGLSDDCPR	Disintegrin; <i>P. jerdonii</i> ; P0C6E4
			2011.8	1	106	LTPGSQCAEGLCCDQCR	
			666.9	3	83	GDYPDDRCTGLSDDCPR	
			404.5	3	58	FARGDYPDDR	
12	0.51	19.4	666.9	3	81	GDYPDDRCTGLSDDCPR	Disintegrin; <i>P. jerdonii</i> ; P0C6E4
			404.5	3	55	FARGDYPDDR	
13	0.01	14.4	2011.8	1	110	LTPGSQCAEGLCCDQCR	Disintegrin; <i>P. flavoviridis</i> ; ~P23323
			10.9	1	113	LTPGSQCAEGLCCDQCR	Disintegrin; <i>P. flavoviridis</i> ; ~P23323
			31.3	1	42	GNDYGYCR	SVMP fragment; <i>P. elegans</i> ; ~BAP39935
		0.62	1083.5	1	35	DSCFKGNQK	
			1132.5	1	25	GNDYGYCRK	
			666.9	3	68	GDYPDDRCTGLSDDCPR	Disintegrin; <i>P. jerdonii</i> ; P0C6E4
14	0.12	19.0	606.3	2	52	FARGDYPDDR	Disintegrin; <i>P. jerdonii</i> ; P0C6E4
			14.7	2	56	LTPGSQCAEGLCCDQCR	
			666.9	3	40	GDYPDDRCTGLSDDCPR	
			1004.4	1	49	GNDYGYCR	
		32.3	1004.4	1	49	GNDYGYCR	SVMP fragment; <i>P. elegans</i> ; ~BAP39935
			1083.5	1	36	DSCFKGNQK	
			1132.5	1	24	GNDYGYCRK	
			1058.5	1	56	IACEPQNVK	
		29.7	1812.7	1	134	QGAQCAEGLCCDQCR	SVMP fragment; <i>Deinagkistrodon acutus</i> ; ~ALE20769
			2053.8	1	125	LKQGAQCAEGLCCDQCR	
			1025.5	1	55	FKGAGTECR	
			1058.5	1	38	IACEPQNVK	
		0.02	1269.5	1	37	SAECTDRFQR	SVMP fragment; <i>Gloydus halys</i> ; ~Q8AW15
			1812.7	1	96	QGAQCAEGLCCDQCR	
			1116.5	1	54	LDIYSYSQK	
			1505.5	1	69	CCFVHDCCYGK	
15	0.09	28.0	1567.6	1	77	NEDIVCGGGTECEK	SVMP fragment; <i>P. mucrosquamatus</i> ; ~XP_0568263
			2063.8	1	49	DATDRCCFVHDCCYGK	
			1001.4	1	48	GKGNFYCR	
			1118.6	1	38	LFCVQGPIGK	
			1155.6	1	30	KIPCAPQDVK	
			2401.9	1	31	LRPGTQCEDGECCEQCQFK	
			2934.1	1	215	AAESECDAESCTGQSAECPTDDFQR	
16	0.18	20.5	962.4	1	56	QYFFETK	NGF; <i>Gloydus intermedius</i> ; ~ALB06112
			1003.4	1	60	EDHPVHNR	
			1111.5	1	73	NPNPVPTGCR	
			1263.6	1	83	IDAACVCVISR	

Peak	%	MW (kDa)	Peptide Ion		Score	MS/MS-derived sequence	Protein family/species/accession
			m/z	z			
17	0.08	16.1	1427.6	1	27	CRNPNPVPTGCR	VEGF; <i>P. mucrosquamatus</i> ; ~Q330K6
			1781.8	1	120	HWNSYCTTHTFVK	
			910.5	1	37	IEVMQFK	
			1315.6	1	35	EHTACECRPR	
			2207.0	1	48	IEVMQFKEHTACECRPR	
	0.02	11.0	1505.5	1	35	CCFVHDCCYGK	PLA <sub>2</sub> ; <i>Crotalus durissus cumanensis</i> ; ~P86805
	8.11	16.7	1741.8	1	117	QICECDKAAAICFR	PLA <sub>2</sub> ; <i>Trimeresurus stejnegeri</i> ; ~Q6H3C5
	0.16	12.1	910.5	1	20	IEVMQFK	VEGF; <i>P. mucrosquamatus</i> ; ~Q330K6
			1315.5	1	17	EHTACECRPR	
18	0.44	21.3	1116.5	1	61	LDIYSYSQK	PLA <sub>2</sub> ; <i>P. jerdonii</i> ; Q8JIY9
			1505.5	1	73	CCFVHDCCYGK	
			1567.6	1	99	NEDIVCGGGTECEK	
			2063.8	1	61	DATDRCCFVHDCCYGK	
			2665.2	1	129	LDIYSYSQKNEDIVCGGGTECEK	PLA <sub>2</sub> ; <i>P. jerdonii</i> ; Q8JIY9
		16.7	1116.6	1	30	LDIYSYSQK	
			1505.5	1	56	CCFVHDCCYGK	
			1670.8	1	79	AAAICFLDNLGTYNK	
			2214.0	1	8	EPLTTYLFYACYCGWGGR	
			2700.2	1	38	EATGKEPLTTYLFYACYCGWGGR	
			-	-	-	-	Unknown
19	0.01	10.4	-	-	-	-	Unknown
	6.92	15.8	1116.5	1	66	LDIYSYSQK	PLA <sub>2</sub> ; <i>P. jerdonii</i> ; Q8JIY9
			1505.5	1	74	CCFVHDCCYGK	
			1567.6	1	92	NEDIVCGGGTECEK	
20	0.70	34.8	1670.8	1	89	AAAICFLDNLGTYNK	PLA <sub>2</sub> ; <i>P. flavoviridis</i> ; ~BAP39949
			980.4	1	44	QICECDR	
			1148.5	1	40	SDIYSYSWK	
			1206.6	1	88	AAAVCFGQNLRL	
			1552.7	1	96	TGVIICGEGTECEK	
			1577.6	1	68	CCFVHDCCYEK	
			2514.1	1	180	TGVIICGEGTECEKQICECDR	
		28.8	980.4	1	21	QICECDR	PLA <sub>2</sub> ; <i>P. flavoviridis</i> ; ~S6BAM8
			1148.5	1	5	SDIYSYSWK	
			1206.6	1	61	AAAVCFGQNLRL	
			1552.7	1	79	TGVIICGEGTECEK	
			1577.6	1	65	CCFVHDCCYEK	
			1577.6	1	65	CCFVHDCCYEK	
		21.5	980.4	1	43	QICECDR	PLA <sub>2</sub> ; <i>P. flavoviridis</i> ; ~BAP39949
			1148.5	1	46	SDIYSYSWK	

Peak	%	MW (kDa)	Peptide Ion		Score	MS/MS-derived sequence	Protein family/species/accession
			m/z	z			
21	0.44	20.5	1206.6	1	88	AAAVCFGQNLR	PLA <sub>2</sub> ; <i>P. flavoviridis</i> ; ~Q805A2
			1552.7	1	100	TGVIICGEGTECEK	
			1577.6	1	75	CCFVHDCCYEK	
			2135.8	1	57	DATDRCCFVHDCCYEK	
			2514.1	1	160	TGVIICGEGTECEKQICECDR	
			799.9	2	106	AAAVCFGQNLRTYK	
			723.3	3	103	QICECDRAAAVCFGQNLR	
			402.9	3	86	AAAVCFGQNLR	
			629.3	4	84	TGVIICGEGTECEKQICECDR	
			776.9	2	76	TGVIICGEGTECEK	
	0.29	15.0	980.4	1	43	QICECDR	PLA <sub>2</sub> ; <i>P. flavoviridis</i> ; ~BAP39949
			1206.6	1	88	AAAVCFGQNLR	
			1552.7	1	96	TGVIICGEGTECEK	
			1577.5	1	57	CCFVHDCCYEK	
			929.5	1	56	LQFGLHSK	
			1117.6	1	64	TLCAGILQGGK	
			637.9	3	49	VHDCCYEKLTDSPK	
			784.3	2	80	NEDIVCGGGTECEK	
			1333.1	2	67	LDIYSYSQKNEDIVCGGGTECEK	
			835.9	2	66	AAAICFLDNLGTYNK	
22	0.71	51.0	1285.1	2	53	AAAICFLDNLGTYNKEYNNYSK	SVSP; <i>T. stejnegeri</i> ; ~Q7QI7
			929.5	1	62	LQFGLHSK	
			1117.6	1	45	TLCAGILQGGK	
			929.5	1	59	LQFGLHSK	
			1189.6	1	38	WDKDIMLIR	
			1205.6	1	22	WDKDIMLIR	
	1.45	28.7	1165.5	1	94	NVDFDSESPR	CRISP; <i>Echis coloratus</i> ; ~P0DMT4
			1537.6	1	61	MEWYPEAAANAER	
			1553.6	1	52	MEWYPEAAANAER	
			2075.1	1	127	KPEIQNEIIDLHNSLR	
23	0.75	39.0	583.3	2	56	NVDFDSESPR	CRISP; <i>P. flavoviridis</i> ; ~6IMF_A
			581.3	2	45	SVNPTASNMLK	
			769.3	2	42	MEWYPEAAANAER	
			781.4	4	90	GNVDFDSESPRKPEIQNEIIDLHNSLR	
		28.8	611.8	2	64	GNVDFDSESPR	CRISP; <i>Vipera berus nikolskii</i> ; ~B7FDI0
			1505.5	1	51	CCFVHDCCYGK	
			1741.8	1	65	QICECDKAAAICFR	
			2063.8	1	46	DATDRCCFVHDCCYGK	

Peak	%	MW (kDa)	Peptide Ion		Score	MS/MS-derived sequence	Protein family/species/accession
			m/z	z			
24	0.50	45.0	929.5	1	54	LQFGLHSK	SVSP; <i>P. flavoviridis</i> ; ~A0A077LD42
			1129.6	1	68	FLVALYTFR	
			1188.6	1	51	WNKDIMLIR	
			1204.6	1	21	MKLQFGLHSK	
25	2.43	19.9	1505.5	1	73	CCFVHDCCYGK	PLA <sub>2</sub> ; <i>Trimeresurus hageni</i> ; ~A0A0H3UX6
			1728.7	1	125	EVCECDKAAAICFR	
			929.5	1	53	LQFGLHSK	
			1204.7	1	15	MKLQFGLHSK	
	1.89	49.6	1722.8	1	134	TLCAGVLQGGTDCNR	SVSP; <i>P. flavoviridis</i> ; ~A0A077LD42
			929.5	1	54	LQFGLHSK	
			1129.6	1	69	FLVALYTFR	
			1188.7	1	55	WNKDIMLIR	
			1204.6	1	33	WNKDIMLIR	
		31.5	1129.6	1	63	FLVALYTFR	
			1172.6	1	46	VFDHLDWIK	
			1188.6	1	59	WNKDIMLIR	
			1204.6	1	5	WNKDIMLIR	
	0.39	16.1	2055.0	1	137	IQLGMHSTNVINEDVQTR	PLA <sub>2</sub> ; <i>P. flavoviridis</i> ; ~T2HPU3
			2071.0	1	82	IQLGMHSTNVINEDVQTR	
			967.4	1	42	EVCECDR	
			1505.6	1	61	CCFVHDCCYGK	
			2063.8	1	71	DATDRCCFVHDCCYGK	
			-	-	-	-	
			968.5	1	15	FFCPNRK	
			1097.5	1	30	EKFFCPNR	
26	0.02	57.4	-	-	-	-	Unknown
			-	-	-	-	
	0.36	38.6	968.5	1	15	FFCPNRK	SVSP; <i>P. flavoviridis</i> ; ~U3TAG3
			1097.5	1	30	EKFFCPNR	
			1129.6	1	40	FLVALYTFR	
			2055.0	1	5	IQLGMHSTNVINEDVQTR	
		27.3	2071.0	1	77	IQLGMHSTNVINEDVQTR	SVSP; <i>P. jerdonii</i> ; B0ZT25
			2536.2	1	85	ETHPDVPYCANINILDYSVCR	
			-	-	-	-	
			-	-	-	-	
27	6.06	20.7	-	-	-	-	Unknown
		34.3	968.4	1	18	FFCPNRK	SVSP; <i>T. stejnegeri</i> ; ~Q91516
			1097.5	1	44	EKFFCPNR	
			2506.1	1	134	EIYPDVPHCANINILDHAVCR	
			2879.4	1	189	LDSSVSNSEHIAPLSLPSSPPSVGSVCR	
			3046.4	1	122	TIPTKEIYPDVPHCANINILDHAVCR	
		29.7	1204.6	1	10	WNKDIMLIR	SVSP; <i>P. elegans</i> ; ~P84788
			2119.1	1	158	SAHIAPLSLPSSPPSVGSVCR	
			1188.6	1	53	WNKDIMLIR	
		26.8	-	-	-	-	SVSP; <i>P. mucrosquamatus</i> ; ~Q91510
			-	-	-	-	

Peak	%	MW (kDa)	Peptide Ion		Score	MS/MS-derived sequence	Protein family/species/accession
			m/z	z			
28	6.89	49.6	1204.6	1	36	WNKDIMLIR	SVSP; <i>P. mucrosquamatus</i> ; ~Q91508 SVSP; <i>P. elegans</i> ; ~P84788
			2054.1	1	139	VMGWGTITSPQVTLPDVPR	
			2119.1	1	141	SAHIAPLSLPSSPPSVGSVCR	
			2247.2	1	141	KSAHIAPLSLPSSPPSVGSVCR	
			1035.5	2	35	VMGWGTITSPQVTLPDVPR	
			436.2	3	53	NMEIYLGVHSK	
			645.8	2	51	NMEIYLGVHSK	
			820.4	2	80	CANINLLDYEVC	
			690.7	3	66	VMGWGTITSPQVTLPDVPR	
			685.4	3	48	VMGWGTITSPQVTLPDVPR	
		30.7	1188.6	1	67	WNKDIMLIR	SVSP; <i>D. acutus</i> ; ~Q918X0
			2119.0	1	152	SAHIAPLSLPSSPPSVGSVCR	
			2247.1	1	164	KSAHIAPLSLPSSPPSVGSVCR	
			645.8	2	59	NMEIYLGVHSK	
		28.8	653.8	2	59	NMEIYLGVHSK	SVSP; <i>P. elegans</i> ; ~P84788
			641.8	2	48	INLLDYSECR	
			1035.5	2	94	VMGWGTITSPQVTLPDVPR	
			1027.5	2	75	VMGWGTITSPQVTLPDVPR	
		27.2	646.3	2	59	DMEIYLGVHSK	SVSP; <i>P. mucrosquamatus</i> ; ~Q9508
			436.5	3	54	DMEIYLGVHSK	
			820.4	2	43	CANINLLDYEVC	
29	3.68	56.5	1152.7	1	83	AAKPELPAISR	SVSP; <i>P. flavoviridis</i> ; ~T2HQA7
			2119.2	1	165	SAHIAPLSLPSSPPSVGSVCR	
			1037.5	1	82	GAHAGLPATSR	
			1189.6	1	75	WDKDIMLIR	
			968.5	1	23	FFCPNRK	
		33.2	1097.5	1	27	EKFFCPNR	SVSP; <i>P. flavoviridis</i> ; ~U3TAG3
			1205.6	1	54	WDKDIMLIR	
			1512.7	1	92	VIGGDECNINEHR	
			2903.5	1	193	LDSPVSNSEHIAPLSLPSSPPSVGSICR	
			42.1	-	-	-	
30	0.33	63.0	22.8	-	-	-	Unknown
			14.7	-	-	-	Unknown
			618.8	2	68	SAGQLFEESLR	LAAO; <i>P. elegans</i> ; ~BAP3995
			682.9	2	67	SAGQLFEESLRK	
			490.3	2	46	EYLIKEGK	
		55.6	618.8	2	70	SAGQLFEESLR	LAAO; <i>P. elegans</i> ; ~BAP3995
			682.9	2	67	SAGQLFEESLRK	

Peak	%	MW (kDa)	Peptide Ion		Score	MS/MS-derived sequence	Protein family/species/accession
			m/z	z			
			490.3	2	52	EYLIKEGK	
		48.2	588.6	4	42	YPVKPSEEGKSAGQLFEESLR	
			618.8	2	61	SAGQLFEESLR	LAAO; <i>P. elegans</i> ; ~BAP3995
			682.9	2	60	SAGQLFEESLRK	
		28.2	490.3	2	50	EYLIKEGK	
			1058.0	2	82	RFDEIVGGMDQLPTSMYR	LAAO; <i>P. elegans</i> ; ~BAP3995
			588.6	4	73	YPVKPSEEGKSAGQLFEESLR	
			711.0	3	68	RFDEIVGGMDQLPTSMYR	
			682.9	2	59	SAGQLFEESLRK	
			653.6	3	57	FDEIVGGMDQLPTSMYR	
			711.0	3	54	RFDEIVGGMDQLPTSMYR	
			988.0	2	48	FDEIVGGMDQLPTSMYR	
			716.3	3	44	RFDEIVGGMDQLPTSMYR	
		25.3	490.3	2	41	EYLIKEGK	
			711.0	3	76	RFDEIVGGMDQLPTSMYR	LAAO; <i>P. elegans</i> ; ~BAP3995
			705.7	3	75	RFDEIVGGMDQLPTSMYR	
			711.0	3	62	RFDEIVGGMDQLPTSMYR	
			618.8	2	62	SAGQLFEESLR	
			682.9	2	57	SAGQLFEESLRK	
			988.0	2	49	FDEIVGGMDQLPTSMYR	
			716.3	3	46	RFDEIVGGMDQLPTSMYR	
		21.9	490.3	2	45	EYLIKEGK	
			618.8	2	74	SAGQLFEESLR	LAAO; <i>P. elegans</i> ; ~BAP3995
			682.9	2	70	SAGQLFEESLRK	
			784.4	3	67	YPVKPSEEGKSAGQLFEESLR	
			716.3	3	63	RFDEIVGGMDQLPTSMYR	
			988.0	2	60	FDEIVGGMDQLPTSMYR	
			490.3	2	47	EYLIKEGK	
0.37		41.9	1512.7	1	58	VIGGDECNINEHR	SVSP; <i>G. brevicaudus</i> ; ~P85109
		34.2	2506.2	1	114	EIYPDVPHCANINILDHAVCR	SVSP; <i>T. stejnegeri</i> ; ~Q91516
			2879.4	1	110	LDSSVSNSEHIAPLSLPSSPPSVGSVCR	
		30.7	2119.1	1	122	SAHIAPLSLPSSPPSVGSVCR	SVSP; <i>P. mucrosquamatus</i> ; ~Q91509
		22.7	987.5	1	45	EIYPNVPR	SVSP; <i>C. oreganus helleri</i> ; ~TDE97
			1347.7	1	11	AAYPWWPVTTTR	
		21.2	987.5	1	22	EIYPNVPR	SVSP; <i>C. oreganus helleri</i> ; ~TDE97
0.27		13.3	666.9	3	74	GDYPDDRCTGLSDDCPR	SVMP; <i>P. jerdonii</i> ; P0C6E4
			590.7	2	55	CTGLSDDCPR	



Peak	%	MW (kDa)	Peptide Ion		Score	MS/MS-derived sequence	Protein family/species/accession
			m/z	z			
31	0.38	10.7	604.8	2	52	LSVGLVQDYSK	SVMP; <i>P. jerdonii</i> ; P0C6E4
			1006.4	2	47	LTPGSQCAEGLCCDQCR	
			625.6	3	37	IHNDAADSTASISACDGLK	
		65.3	1449.7	1	101	VVSLNVLCTECR	5'NT; <i>P. flavoviridis</i> ; ~T2HRS9
			1555.8	1	119	IILGHSGFLEDQR	
			1577.9	1	98	HANFPILSANIRPK	
			2421.2	1	155	FHECNLGNLICDAVIYNNVR	5'NT; <i>P. elegans</i> ; ~BAP39925
			3125.6	1	136	ETPVLSNPGPYLEFRDEVEELQNHANK	
		22.8	725.4	2	63	VVSLNVLCTECR	
			573.6	3	54	ETPVLSNPGPYLEFR	
			526.6	3	53	HANFPILSANIRPK	
			653.9	2	47	QVPVVQAYAFGK	
			513.2	2	44	QDCYGGVAR	
	0.31	56.1	430.2	2	42	IINVGSEK	LAAO; <i>P. elegans</i> ; ~A0A077L6L4
			948.6	1	29	IVREYIR	
			1178.7	1	42	INFRPPLPPK	
			1236.6	1	94	SAGQLFEESLR	
			1306.8	1	37	INFRPPLPPKK	
			1334.8	1	36	RINFRPPLPPK	
		45.0	1176.1	2	75	YPVKPSEEGKSAGQLFEESLR	LAAO; <i>P. elegans</i> ; ~BAP3995
			634.8	2	70	SGTKIFLTCNK	
			557.0	4	68	NCADIVMNDLSLIHQPKK	
			412.9	3	68	SAGQLFEESLR	LAAO; <i>P. elegans</i> ; ~BAP3995
			682.9	2	61	SAGQLFEESLRK	
			699.7	3	53	NCADIVMNDLSLIHQPK	
		41.4	490.3	2	46	EYLIKEGK	
			431.9	3	57	HDDIFAYEKR	
			705.7	3	47	RFDEIVGGMDQLPTSMYR	
			711.0	3	47	RFDEIVGGMDQLPTSMYR	
			581.6	3	43	DPGVLYKYPVKPSEEGK	
			716.3	3	30	RFDEIVGGMDQLPTSMYR	
			582.3	3	30	KDIQAFCYPSMIQK	
			634.3	3	29	DTSLVTADYVIVCTTSR	
			618.8	2	29	SAGQLFEESLR	
			711.0	3	28	RFDEIVGGMDQLPTSMYR	
			757.9	2	28	ETDYEEFLEIAR	
			577.0	3	27	KDIQAFCYPSMIQK	
			699.7	3	27	NCADIVMNDLSLIHQPK	

Peak	%	MW (kDa)	Peptide Ion		Score	MS/MS-derived sequence	Protein family/species/accession
			m/z	z			
			800.9	2	23	DIQAFCYPSMIQK	
			438.7	2	23	STTDLPSR	
			569.3	2	21	HDDIFAYEK	
			682.9	2	21	SAGQLFEESLRK	
		33.8	618.8	2	75	SAGQLFEESLR	LAAO; <i>P. elegans</i> ; ~BAP3995
			784.4	3	69	YPVKPSEEGKSAGQLFEESLR	
			682.9	2	63	SAGQLFEESLRK	
		30.7	711.0	3	70	RFDEIVGGMDQLPTSMYR	LAAO; <i>P. elegans</i> ; ~BAP3995
			682.9	2	67	SAGQLFEESLRK	
			711.0	3	67	RFDEIVGGMDQLPTSMYR	
			716.3	3	64	RFDEIVGGMDQLPTSMYR	
			490.3	2	50	EYLIKEGK	
			988.0	2	44	FDEIVGGMDQLPTSMYR	
			423.6	3	31	SGTKIFLTCNK	
			512.3	2	31	IFLTCNK	
			422.7	2	26	AIEEKVR	
			664.3	3	25	FDEIVGGMDQLPTSMYR	
			448.2	2	24	IFLTCNK	
			699.7	3	23	NCADIVMNDLSLIHQLPK	
		28.8	581.6	3	68	DPGVLYKYPVKPSEEGK	LAAO; <i>P. elegans</i> ; ~BAP3995
			618.8	2	68	SAGQLFEESLR	
			711.0	3	66	RFDEIVGGMDQLPTSMYR	
			757.9	2	52	ETDYEEFLEIAR	
			682.9	2	51	SAGQLFEESLRK	
			716.3	3	49	RFDEIVGGMDQLPTSMYR	
			784.4	3	46	YPVKPSEEGKSAGQLFEESLR	
			577.0	3	45	KDIQAFCYPSMIQK	
			438.7	2	42	STTDLPSR	
			532.7	2	41	NPLEECFR	
			550.9	3	37	NDKEGWYANLGPMR	
			490.3	2	37	EYLIKEGK	
			582.3	3	37	KDIQAFCYPSMIQK	
			705.7	3	35	RFDEIVGGMDQLPTSMYR	
			508.6	3	34	YDTYSTKEYLIK	
			634.3	3	33	DTSLV TADYVIVCTTSR	
			556.3	3	32	NDKEGWYANLGPMR	
			474.8	2	32	IVREYIR	
			988.0	2	28	FDEIVGGMDQLPTSMYR	

Peak	%	MW (kDa)	Peptide Ion		Score	MS/MS-derived sequence	Protein family/species/accession
			m/z	z			
32	0.02	21.6	567.3	2	27	YPVKPSEEGK	LAAO; <i>P. elegans</i> ; ~BAP3995
			422.7	2	26	AIEEKVR	
			501.2	2	25	DVNRASE	
			589.9	2	21	INFRPPLPPK	
			448.2	2	21	IFLTCNK	
			512.3	2	20	IFLTCNKK	
			808.9	2	15	DIQAFICYPSMIQK	
			711.0	3	74	RFDEIVGGMDQLPTSMYR	
			618.8	2	62	SAGQLFEESLR	
			682.9	2	60	SAGQLFEESLRK	
			577.0	3	56	KDIQAFICYPSMIQK	
			567.3	2	55	YPVKPSEEGK	
			423.6	3	53	SGTKIFLTCNK	
			463.6	3	49	KFWEDDGIHGGK	
			705.7	3	49	RFDEIVGGMDQLPTSMYR	
			438.7	2	49	STDLPSR	
	0.28	25.2	530.3	4	48	FWEDDGIHGGKSTDLPSR	SVSP; <i>P. elegans</i> ; ~P84788
			711.0	3	47	RFDEIVGGMDQLPTSMYR	
			716.3	3	46	RFDEIVGGMDQLPTSMYR	
			1290.7	1	51	NMEIYLGIVHVK	
			2119.1	1	129	SAHIAPLSLPSSPPSVGSVCR	
			2247.2	1	74	KSAHIAPLSLPSSPPSVGSVCR	
			1292.6	1	65	DYYQTFLTNK	
			1309.7	1	65	KPQCILNAPLR	SVMP; <i>P. jerdonii</i> ; Q7ZZS9
	0.09	16.1	2130.0	1	111	LFSDCSKDYYQTFLTNK	
			2147.1	1	64	DLITVQADAPTTAGLFGDWR	
			993.5	1	52	SYVWIGLR	
			1410.7	1	92	TCLGLEKETGFR	CTL; <i>P. flavoviridis</i> ; ~Q7LZ7
	0.14	10.7	-	-	-	-	
	0.15	109.1	540.9	3	65	KSVQPQAQSWSCSK	Unknown PDE; <i>P. elegans</i> ; ~BAP39928
			746.8	2	50	SVQPQAQSWSCSK	
	1.57	104.9	1180.5	2	40	EQSSPLSCFPVSPDVSGCR	PDE; <i>P. flavoviridis</i> ; ~BAN82023
		57.4	948.6	1	18	IVREYIR	LAAO; <i>P. elegans</i> ; ~A0A077L6L4
			1178.7	1	31	INFRPPLPPK	
			1236.6	1	92	SAGQLFEESLR	
			1306.8	1	14	INFRPPLPPKK	
			1334.8	1	17	RINFRPPLPPK	
			1364.7	1	10	SAGQLFEESLRK	

Peak	%	MW (kDa)	Peptide Ion		Score	MS/MS-derived sequence	Protein family/species/accession
			m/z	z			
33	0.03	55.1	711.0	3	72	RFDEIVGGMDQLPTSMYR	LAAO; <i>P. elegans</i> ; ~BAP3995
			618.8	2	64	SAGQLFEESLR	
			711.0	3	64	RFDEIVGGMDQLPTSMYR	
			682.9	2	52	SAGQLFEESLRK	
			490.3	2	45	EYLIKEGK	
		34.7	618.8	2	53	SAGQLFEESLR	LAAO; <i>P. mucrosquamatus</i> ; ~XP_05673893
			438.7	2	39	STTDLPSR	
			540.9	3	62	KSVQPQAQSWSCSK	
			746.8	2	53	SVQPQAQSWSCSK	
			705.7	3	71	RFDEIVGGMDQLPTSMYR	
	0.11	57.0	711.0	3	59	RFDEIVGGMDQLPTSMYR	LAAO; <i>P. elegans</i> ; ~BAP3995
			577.0	3	53	KDIQAFICYPSMIQK	
			682.9	2	52	SAGQLFEESLRK	
			423.6	3	49	SGTKIFLTCNK	
			711.0	3	46	RFDEIVGGMDQLPTSMYR	
		34.7	490.3	2	44	EYLIKEGK	SVMP; <i>P. jerdonii</i> ; P0C6E4
			604.8	2	57	LSVGLVQDYSK	
			686.9	2	51	LAIVVDYGYMYTK	
			590.7	2	49	CTGLSDDCPR	
			694.9	2	44	LAIVVDYGYMYTK	
	8.59	25.3	933.5	1	69	DSDKITVR	SVMP; <i>P. jerdonii</i> ; P0C6E4
			2569.3	1	120	NDYQTFLTNYKQCILNAPLR	
			3406.6	1	158	LFSDCSKNDYQTFLTNYKQCILNAPLR	
		16.7	694.9	2	41	LAIVVDYGYMYTK	SVMP; <i>P. jerdonii</i> ; P0C6E4
			604.8	2	37	LSVGLVQDYSK	
			1006.4	2	32	LTPGSQCAEGLCCDQCR	
			666.9	3	32	GDYPDDRCTGLSDDCPR	
			466.6	3	31	SHDCAHLLTDTK	
		11.0	590.7	2	28	CTGLSDDCPR	SVMP; <i>P. jerdonii</i> ; P0C6E4
			1006.4	2	66	LTPGSQCAEGLCCDQCR	
			666.9	3	64	GDYPDDRCTGLSDDCPR	
			604.8	2	60	LSVGLVQDYSK	
			686.9	2	59	LAIVVDYGYMYTK	
34	0.01	109.1	466.6	3	57	SHDCAHLLTDTK	PDE; <i>P. elegans</i> ; ~BAP39928
			590.7	2	55	CTGLSDDCPR	
			540.9	3	63	KSVQPQAQSWSCSK	
			596.1	4	61	AKRPDFYTLYIEEPDTTGHK	
			746.8	2	35	SVQPQAQSWSCSK	

Peak	%	MW (kDa)	Peptide Ion		Score	MS/MS-derived sequence	Protein family/species/accession
			m/z	z			
		102.2	1121.6	1	23	NPFYTPSPAK	PDE; <i>P. flavoviridis</i> ; ~T2HP62
			1355.7	1	10	AATYFWPGSEVK	
			1924.0	1	16	VRDVELLTGLNFYSGLK	
			2360.1	1	34	EQSSPLSCPFGVPVSPDVSQCR	
	0.02	67.6	2405.2	1	20	TESEAHNLPYGRPQVLQNHSK	5'NT; <i>P. elegans</i> ; ~BAP39925
			513.2	2	52	QDCYGGVAR	
			408.2	3	51	MGKVYPAVEGR	
			445.7	2	51	VYPAVEGR	
			513.2	2	46	NYSSQEIGK	5'NT; <i>P. elegans</i> ; ~BAP39925
		41.7	725.4	2	70	VVSLNVLCTECR	
			523.9	3	66	HGQGMGELLQVSGIK	
			519.3	3	63	IHALGHSGFLEDQR	
			513.2	2	51	QDCYGGVAR	
			653.9	2	47	QVPVVQAYAFQK	
			686.0	3	45	ASGNPILLNKDISEDQDVK	
			476.3	2	44	VGIIGYTTK	
	0.05	57.9	430.2	2	41	IINVGSEK	LAAO; <i>P. elegans</i> ; ~BAP3995
			423.6	3	67	SGTKIFLTCNK	
			699.7	3	59	NCADIVMNDLSLIHQLPK	
			557.0	4	58	NCADIVMNDLSLIHQLPK	
		55.1	784.4	3	104	YPVKPSEEGKSAGQLFEESLR	LAAO; <i>P. elegans</i> ; ~BAP3995
			618.8	2	66	SAGQLFEESLR	
			634.8	2	65	SGTKIFLTCNK	
			682.9	2	60	SAGQLFEESLRK	
			490.3	2	53	EYLIKEGK	LAAO; <i>P. elegans</i> ; ~BAP3995
			694.4	3	46	NCADIVMNDLSLIHQLPK	
			699.7	3	43	NCADIVMNDLSLIHQLPK	
		33.0	618.8	2	63	SAGQLFEESLR	
			634.3	3	54	DTSLVTADYVIVCTTSR	LAAO; <i>P. elegans</i> ; ~BAP3995
			682.9	2	53	SAGQLFEESLRK	
			582.3	3	48	KDIQAFCYPSMIQK	
		32.3	711.0	3	86	RFDEIVGGMDQLPTSMYR	
			618.8	2	63	SAGQLFEESLR	LAAO; <i>P. elegans</i> ; ~BAP3995
			951.0	2	61	DTSLVTADYVIVCTTSR	
			577.0	3	55	KDIQAFCYPSMIQK	
			757.9	2	53	ETDYEEFLEIAR	
			569.3	2	51	HDDIFAYEK	
			582.3	3	50	KDIQAFCYPSMIQK	

Peak	%	MW (kDa)	Peptide Ion		Score	MS/MS-derived sequence	Protein family/species/accession
			m/z	z			
0.09		48.7	490.3	2	47	EYLIKEGK	SVSP; <i>Calloselasma rhodostoma</i> ; ~P26324 SVSP; <i>P. flavoviridis</i> ; ~T2HQA7 SVSP; <i>T. stejnegeri</i> ; ~Q91516
			659.0	3	45	FDEIVGGMDQLPTSMYR	
			1512.7	1	94	VIGGDECNINEHR	
			2119.1	1	34	SAHIAPLSLPSSPPSVGSVCR	
			968.5	1	16	FFCPNRK	
			1097.5	1	45	EKFFCPNR	
			2506.2	1	115	EIYPDVPHCANINILDHAVCR	
			2879.5	1	185	LDSSVSNSEHIAPLSLPSSPPSVGSVCR	
			3046.6	1	122	TIPTKEIYPDVPHCANINILDHAVCR	
			792.3	3	53	GAGTECRAASSECDMADLCTGR	
1.13		38.6	548.6	3	41	AASSECDMADLCTGR	SVMP; <i>P. mucrosquamatus</i> ; ~XP_02942320 SVMP; <i>P. flavoviridis</i> ; ~P20165 SVMP; <i>P. jerdonii</i> ; P0C6E4
			1129.5	1	51	NDYQTFLTK	
			1966.9	1	100	LFSDCSKNDYQTFLTK	
			933.5	1	26	DSDKITVR	
			1208.6	1	71	LSVGLVQDYSK	
			1388.7	1	4	LAIVVDYGM <sup>+</sup> YTK	
			2569.3	1	118	NDYQTFLTNYKPOCILNAPLR	
			609.9	3	60	CDTCIMSAVISDKPSK	
			604.6	3	53	CDTCIMSAVISDKPSK	
			647.6	4	49	SHDCAHLLTDTKLDDNTIGVAYK	
24.0			668.9	2	40	LDDNTIGVAYKK	SVMP; <i>P. jerdonii</i> ; PJD c52836_g4
			638.3	3	38	GMCDPKLSVGLVQDYSK	
			686.9	2	36	LAIVVDYGM <sup>+</sup> YTK	
			694.9	2	36	LAIVVDYGM <sup>+</sup> YTK	
			428.7	2	35	LFSDCSK	
			466.6	3	31	SHDCAHLLTDTK	
			608.0	3	28	LAIVVDYGM <sup>+</sup> YTKYNR	
			1006.4	2	82	LTPGSQCAEGLCCDQCR	
			666.9	3	69	GDYPDDRCTGLSDDCPR	
			466.6	3	63	SHDCAHLLTDTK	
16.4			604.8	2	61	LSVGLVQDYSK	SVMP; <i>P. jerdonii</i> ; P0C6E4
			590.7	2	58	CTGLSDDCPR	
			1006.4	2	75	LTPGSQCAEGLCCDQCR	
			699.3	2	74	SHDCAHLLTDTK	
			666.9	3	71	GDYPDDRCTGLSDDCPR	
			625.6	3	70	IHNDADSTASISACDGLK	
			604.8	2	68	LSVGLVQDYSK	
			590.7	2	56	CTGLSDDCPR	

Peak	%	MW (kDa)	Peptide Ion		Score	MS/MS-derived sequence	Protein family/species/accession
			m/z	z			
35	4.33	91.1	2225.8	1	121	LHSWVECESGECCEOCR	SVMP; <i>P. flavoviridis</i> ; ~A0A077LAC3
			57.9	1	92	IYACVNTLNLIYR	SVMP; <i>Crotalus adamanteus</i> ; ~J3SDW8
			2402.0	1	76	LRPGTQCEDGECCEQCQFK	
		49.1	1812.7	1	130	QGAQCAEGLCCDQCR	SVMP; <i>D. acutus</i> ; ~Q1PS45
			2053.9	1	150	LKQGAQCAEGLCCDQCR	
			2303.0	1	27	SCVMAGTLSCEASYLFSDCSR	
		25.2	1208.7	1	8	LSVGLVQDYSK	SVMP; <i>P. jerdonii</i> ; P0C6E4
			1388.7	1	5	LAIVVDYGYMYTK	
		11.3	666.9	3	59	GDYPDDRCTGLSDDCPR	SVMP; <i>P. jerdonii</i> ; P0C6E4
			1006.4	2	49	LTPGSQCAEGLCCDQCR	
	0.14	43.6	590.7	2	44	CTGLSDDCPR	
			746.7	3	60	HQGLPESYNFDFVTMKPVL	PLB; <i>P. elegans</i> ; ~BAP39922
			453.2	2	58	VADISMAAK	
			666.9	2	57	VVPESLFAWER	
			469.6	3	55	FTAYAINGPPVEK	
			682.6	3	52	IANMMADSGKTWAETFEK	
			487.6	3	47	KVVPESLFAWER	
			741.4	3	44	HQGLPESYNFDFVTMKPVL	
			684.8	2	44	DQGKVTDMESMK	
			468.9	3	44	YNNYKEDPYAK	
			470.7	2	41	VTDMESMK	
			481.6	3	41	HLDFKITDPQTK	
			401.7	2	40	ITDPQTK	
			682.6	3	38	IANMMADSGKTWAETFEK	
		34.5	666.9	2	63	VVPESLFAWER	PLB; <i>P. elegans</i> ; ~BAP39922
			453.2	2	59	VADISMAAK	
			450.9	3	56	RTPVPAGCYDSK	
			703.9	2	46	FTAYAINGPPVEK	
			555.3	2	46	YSDQTNILR	
0.04	0.04	40.2	448.2	3	68	HLVIACHYDSK	QC; <i>P. flavoviridis</i> ; ~BAN89376
			754.8	3	65	NTYQIQGIDLFVLLDLIGAR	
			591.0	3	62	NLYDLGLLNNYSSER	
			500.9	3	61	YPVEDDHIPFLR	
			561.0	3	60	MWQNDLHPILIER	
			553.0	3	54	RYPVEDDHIPFLR	
			515.0	3	53	GVPIHLIPSPFPR	
			513.3	3	53	NPVFPVYFLNTAR	
			713.4	3	52	VFVGATDSAVPCAMMLELAR	

Peak	%	MW (kDa)	Peptide Ion		Score	MS/MS-derived sequence	Protein family/species/accession
			m/z	z			
36	0.23	16.4	532.8	2	51	YFPPQLDGK	CTL; <i>P. flavoviridis</i> ; ~Q7LZ7
			627.8	2	47	WSPSDSLYGSR	
			481.6	3	47	LIFFDGEEAFVR	
			705.9	2	62	TCLGLEKETGFR	
			552.0	4	55	DCPSGWSSYEGHCYKPFK	
	3.69	63.4	432.9	3	47	LYKTWDDAER	SVMP; <i>Phalotris mertensi</i> ; ~A0A82C5Q9
			1025.5	1	51	FKGAGTECR	
			1830.0	1	34	KYIEFVIVVDNGMFR	
			694.6	3	77	LRQGAQCAEGLCCDQCR	
			843.3	2	50	AATDECDMADLCTGR	
			851.3	2	42	AATDECDMADLCTGR	
			694.6	3	59	LRQGAQCAEGLCCDQCR	
			25.8	1	67	DSDKITVR	
			1208.6	1	72	LSVGLVQDYSK	
			1397.6	1	56	SHDCAHLLTDTK	
	0.09	56.1	711.0	3	71	RFDEIVGGMDQLPTSMYR	LAAO; <i>P. elegans</i> ; ~BAP3995
			618.8	2	68	SAGQLFEESLR	
			711.0	3	60	RFDEIVGGMDQLPTSMYR	
			705.7	3	58	RFDEIVGGMDQLPTSMYR	
			682.9	2	53	SAGQLFEESLRK	
			490.3	2	48	EYLIKEGK	
			588.6	4	46	YPVKPSEEGKSAGQLFEESLR	
			716.3	3	45	RFDEIVGGMDQLPTSMYR	
			749.8	2	60	VVGGDCECNINEHR	
			993.5	1	48	SYVWIGLR	
37	0.06	34.5	1410.7	1	86	TCLGLEKETGFR	SVSP; <i>Agkistrodon contortrix contortrix</i> ; ~P8298
	0.41	16.4	905.4	1	15	STNNKWR	CTL; <i>P. flavoviridis</i> ; ~Q7LZ7
	0.31	11.0	-	-	-	-	CTL; <i>P. flavoviridis</i> ; ~T2HP57
		110.5	-	-	-	-	Unknown
	0.90	63.4	-	-	-	-	Unknown
		73.1	742.6	3	66	LHSWVECESGECCEQCR	SVMP; <i>P. mucrosquamatus</i> ; ~XP_05683679
		51.5	843.3	2	57	AATDECDMADLCTGR	SVMP; <i>P. flavoviridis</i> ; ~Q90ZI3
		26.3	567.9	3	42	AATDECDMADLCTGR	SVMP; <i>P. jerdonii</i> ; P0C6E4
			602.6	3	58	LAIVVDYGYMYTKYNR	
			466.6	3	55	SHDCAHLLTDTK	
			604.8	2	46	LSVGLVQDYSK	
		11.0	608.0	3	44	LAIVVDYGYMYTKYNR	SVMP; <i>P. jerdonii</i> ; P0C6E4
			1006.4	2	57	LTPGSQCAEGLCCDQCR	
			604.8	2	51	LSVGLVQDYSK	



Peak	%	MW (kDa)	Peptide Ion		Score	MS/MS-derived sequence	Protein family/species/accession
			m/z	z			
38	0.21	36.0	2879.4	1	86	LDSSVSNSEHIAPLSLPSSPPSVGSVCR	SVSP; <i>T. stejnegeri</i> ; ~Q91516
			3046.5	1	26	TIPTKEIYPDVPHCANINILDHAVCR	
	0.35	16.7	993.6	1	35	SYVWIGLR	CTL; <i>P. flavoviridis</i> ; ~Q7LZ7
			2204.9	1	66	DCPSGWSSYEGHCYKPFK	
	1.91	49.1	1174.6	1	38	IFPCAPQDVK	SVMP; <i>P. flavoviridis</i> ; ~G1UJB2
			1472.8	1	84	YLISHTPQCILK	
			1968.0	1	114	YLISHTPQCILKEPLR	
		26.3	933.5	1	55	DSDKITVR	SVMP; <i>P. jerdonii</i> ; P0C6E4
			1208.6	1	70	LSVGLVQDYSK	
	0.02	35.2	968.5	1	18	FFCPNRK	SVSP; <i>T. stejnegeri</i> ; ~Q91516
			1097.5	1	26	EKFFCPNR	
			2879.4	1	96	LDSSVSNSEHIAPLSLPSSPPSVGSVCR	
	0.51	16.7	993.5	1	51	SYVWIGLR	CTL; <i>P. flavoviridis</i> ; ~Q7LZ7
			1410.7	1	88	TCLGLEKETGFR	
			2204.9	1	92	DCPSGWSSYEGHCYKPFK	
		11.3	1843.8	1	47	YKAWAEESYCVYFK	CTL; <i>P. flavoviridis</i> ; ~A0A077LD73

Methionine oxidation is underlined.

Supplementary table 3 Assignment of the reverse-phase chromatographic fractions from *Protobothrops mangshanensis* venom to protein families by nESI-MS/MS of selected peptide ions from in-gel digested protein bands separated by SDS-PAGE.

Peak	%	MW (kDa)	Peptide Ion		Score	MS/MS-derived sequence	Protein family/species/accession
			m/z	z			
1	0.88	-	679.4	2	42	PPISPLSVQHWP	BPP/CNP; <i>Protobothrops jerdonii</i> ; ~PJD c31701
2	1.82	-	622.3	2	71	QSKPGRPPPISP	BPP/CNP; <i>P. jerdonii</i> ; ~PJD c31701
3	0.56	-	719.8	2	107	QPHEPAGGTTAFR	BPP/CNP; <i>P. jerdonii</i> ; ~PJD c31701
4	0.42	88.3	622.3	2	101	QSKPGRPPPISP	SVMP; <i>Protobothrops elegans</i> ; ~BAP39935
			530.3	2	43	QSKPGRPPPI	
			587.8	2	31	MIPCAPQDVK	
			502.7	2	51	GNDYGYCR	
			587.8	2	45	MIPCAPQDVK	
			579.8	2	38	MIPCAPQDVK	
	0.04	80.5	-	-	-	-	Unknown
		74.7	-	-	-	-	Unknown
5	0.06	27.8	906.8	2	79	QGAQCAEGLCCDQCR	Disintegrin; <i>Protobothrops flavoviridis</i> ; ~Q90ZI3
			529.8	2	43	IACEPQNVK	
6	0.17	5.8	-	-	-	-	Unknown
7	0.09	3.4	-	-	-	-	Unknown
8	0.11	-	-	-	-	-	Unknown
9	0.08	17.7	682.3	2	68	ALTMEGNQASWR	NGF; <i>P. flavoviridis</i> ; ~BAN82015
10	0.06	18.5	647.3	2	63	IDTACVCVISR	NGF; <i>P. flavoviridis</i> ; ~BAN82015
			855.4	2	53	FIRIDTACVCVISR	
			556.3	2	44	NPNPVPTGCR	
			570.6	3	61	FIRIDTACVCVISR	
			647.3	2	59	IDTACVCVISR	
			556.3	2	40	NPNPVPTGCR	
11	0.39	14.9	633.9	5	47	ETLVPIKEYPDEVSHLFKPCVPVLR	VEGF; <i>P. flavoviridis</i> ; ~P67862
	0.77	16.5	622.3	2	46	NLGTVDKNYR	PLA <sub>2</sub> ; <i>Protobothrops mangshanensis</i> ; P84776
			449.9	3	40	DRYSYSWENK	
			579.6	3	37	ELCECDKAVAICLR	
			401.7	2	34	AVAICLR	
			463.6	3	31	AIVCGEKNPCLK	
			470.2	2	30	MVFQETGK	
			583.3	2	41	NVDFDSESPR	
12	8.24	49.3	636.3	2	36	CPASCFCQNK	CRISP; <i>P. flavoviridis</i> ; ~1WVR_A
			743.8	2	51	SKCPASCFCQNK	CRISP; <i>P. flavoviridis</i> ; ~6IMF_A
			636.3	2	49	CPASCFCQNK	
			499.9	3	38	CPASCFCQNK	

Peak	%	MW (kDa)	Peptide Ion		Score	MS/MS-derived sequence	Protein family/species/accession
			m/z	z			
13	0.49	22.3	512.3	4	38	WTDIIHAWHGEYKDFK	CRISP; <i>P. flavoviridis</i> ; ~Q8JI39
			777.3	2	94	MEWYPEAAANAER	
			581.3	2	63	SVNPTASNMLK	
			904.8	3	52	SVNPTASNMLKMEWYPEAAANAER	
		20.0	583.3	2	56	NVDFDSESPR	CRISP; <i>P. flavoviridis</i> ; ~6IMF_A
		23.8	-	-	-	-	Unknown
		0.46	581.6	3	71	EICECDKAAAICFR	PLA2; <i>P. mangshanensis</i> ; AHJ09547
			704.3	2	65	DIVCGEDNPCTK	
			730.7	3	52	VTGCNPKDDFYIYSLQNR	
			717.3	2	35	DDFYIYSLQNR	
			717.3	2	63	DDFYIYSLQNR	
			716.0	3	93	SAHIAPLSLPSNPPSVGSVCR	
	2.27	43.1	569.3	4	62	KSAHIAPLSLPSNPPSVGSVCR	SVSP; <i>Agkistrodon piscivorus conanti</i> ; ~JAS04401
			594.8	2	26	WNKDIMLR	
			536.9	3	49	TLCAGILEGGKDSCK	
			763.9	2	62	IIGGDECNINEHR	
			583.8	2	52	VMGWGTISATK	
			565.3	2	38	ILCAGILQGGK	
			647.3	2	56	IDTACVCVISR	
			565.3	2	50	ILCAGILQGGK	
			756.8	2	45	VIGGDECNINEHR	
			559.8	2	63	TLCAGILEGGK	
14	0.08	0.20	575.8	2	45	VMGWGTISATK	SVSP; <i>P. jerdonii</i> ; ~B0ZT25
			565.3	2	39	ILCAGILQGGK	
			411.2	3	49	KVLNEDEQTR	
			552.3	2	46	VLNEDEQTR	
			550.8	2	45	NVPNEDEQR	
			419.5	3	44	NVPNEDEQRR	
			473.3	2	37	EWVLTAAR	
			473.3	2	41	EWVLTAAR	
			411.2	3	55	KVLNEDEQTR	
			552.3	2	48	VLNEDEQTR	
15	1.20	1.20	411.2	3	46	KVLNEDEQTR	SVSP; <i>P. jerdonii</i> ; ~Q9DF66
			552.3	2	44	VLNEDEQTR	
			504.9	3	41	VIGGDECNINEHR	
			763.9	2	59	IIGGDECNINEHR	
			444.9	3	47	SKTLCAGILQGGK	
			582.8	2	31	IMGWGTISATK	
			504.9	3	41	VIGGDECNINEHR	
			763.9	2	59	IIGGDECNINEHR	
			444.9	3	47	SKTLCAGILQGGK	
			582.8	2	31	IMGWGTISATK	
16	2.48	2.48	504.9	3	41	VIGGDECNINEHR	SVSP; <i>Agkistrodon contortrix contortrix</i> ; ~2AIQ_A
			763.9	2	59	IIGGDECNINEHR	
			444.9	3	47	SKTLCAGILQGGK	
			582.8	2	31	IMGWGTISATK	
			504.9	3	41	VIGGDECNINEHR	
			763.9	2	59	IIGGDECNINEHR	
			444.9	3	47	SKTLCAGILQGGK	
			582.8	2	31	IMGWGTISATK	
			504.9	3	41	VIGGDECNINEHR	
			763.9	2	59	IIGGDECNINEHR	

Peak	%	MW (kDa)	Peptide Ion		Score	MS/MS-derived sequence	Protein family/species/accession
			m/z	z			
17	1.30	27.8	559.3	2	41	TLCAGILQGGK	SVSP; <i>P. jerdonii</i> ; ~AAG10790
			552.3	2	33	VLNEDEQTR	
		20.3	559.3	2	52	TLCAGILQGGK	SVSP; <i>P. jerdonii</i> ; ~AAG10790
			552.3	2	48	VLNEDEQTR	
			411.2	3	42	KVLNEDEQTR	
		19.2	552.3	2	47	VLNEDEQTR	SVSP; <i>P. jerdonii</i> ; ~AAG10790
			411.2	3	44	KVLNEDEQTR	
			559.3	2	42	TLCAGILQGGK	
		16.5	552.3	2	50	VLNEDEQTR	SVSP; <i>P. jerdonii</i> ; ~Q9DF66
			411.2	3	47	KVLNEDEQTR	
		15.0	411.2	3	54	KVLNEDEQTR	SVSP; <i>P. jerdonii</i> ; ~Q9DF66
			552.3	2	49	VLNEDEQTR	
		50.3	504.9	3	47	VIGGDECNINEHR	SVSP; <i>Gloydius blomhoffii</i> ; ~CAB65936
	3.28	45.4	590.8	2	49	IMGWGTISATK	SVSP; <i>P. flavoviridis</i> ; ~BAP39955
		33.5	588.3	2	50	AAYPELPATSR	SVSP; <i>P. mucrosquamatus</i> ; ~XP_015671560
			448.8	2	40	VTLPDVPR	
			820.4	2	35	CANINLLDYEVC	
		17.4	528.3	4	60	FCSEQVKGAHLVSIESYR	CTL; <i>P. mucrosquamatus</i> ; ~XP_015685588
		14.8	914.9	2	47	TTDNQWLSMDCSSKR	CTL; <i>P. mucrosquamatus</i> ; ~Q5FZI5
			922.9	2	38	TTDNQWLSMDCSSKR	
	4.24	107.4	442.2	3	58	CIELVIVADHR	SVMP; <i>Ovophis okinavensis</i> ; ~BAN82161
		44.1	1005.4	2	69	GDWNDDRCTGQSADCPR	SVMP; <i>P. mucrosquamatus</i> ; ~E9NW26
			576.2	2	58	CTGQSADCPR	
	0.98	85.1	-	-	-	-	Unknown
		18.2	-	-	-	-	Unknown
	2.74	56.8	754.1	3	50	NSAHIAPLSLPSNPPSVGSVCR	SVSP; <i>Gloydius brevicaudus</i> ; ~AAF25008
		49.3	559.8	2	55	TLCAGILEGGK	SVSP; <i>G. blomhoffii</i> ; ~CAB65936
			504.9	3	47	VIGGDECNINEHR	
		35.2	570.8	2	55	AAKPELPATSR	SVSP; <i>Crotalus adamanteus</i> ; ~J3SDW9
		33.5	588.3	2	42	AAYPELPATSR	SVSP; <i>P. mucrosquamatus</i> ; ~Q91508
		29.5	559.8	2	49	TLCAGILEGGK	SVSP; <i>Protobothrops elegans</i> ; ~P84787
		25.2	559.8	2	58	TLCAGILEGGK	SVSP; <i>P. mucrosquamatus</i> ; ~XP_015671557
		23.5	559.8	2	56	TLCAGILEGGK	SVSP; <i>P. mucrosquamatus</i> ; ~XP_015671557
		22.4	559.8	2	73	TLCAGILEGGK	SVSP; <i>P. mucrosquamatus</i> ; ~XP_015671557
	0.98	16.1	808.4	2	42	YNAWSAESECIASK	CTL; <i>P. jerdonii</i> ; ~D1MGU1
			588.8	2	40	LQWSDGTELK	
19	0.71	56.8	754.1	3	48	NSAHIAPLSLPSNPPSVGSVCR	SVSP; <i>Agkistrodon piscivorus leucostoma</i> ; ~ADP88562

Peak	%	MW (kDa)	Peptide Ion		Score	MS/MS-derived sequence	Protein family/species/accession	
			m/z	z				
20	0.48	49.3	562.3	2	48	SVQFDDEQR	SVSP; <i>Trimeresurus stejnegeri</i> ; ~AAN52347	
		43.7	562.3	2	27	SVQFDDEQR	SVSP; <i>Ovophis okinavensis</i> ; ~BAN82129	
		18.2	-	-	-	-	Unknown	
		0.40	16.0	797.9	2	46	LASIQSSEEEAFVGK	CTL; <i>P. flavoviridis</i> ; ~BAP39991
		0.12	44.3	626.8	2	55	SAGQLYEESLR	LAAO; <i>P. flavoviridis</i> ; ~BAN82013
	1.82			438.7	2	47	STTDLPSR	
		33.5	626.8	2	44	SAGQLYEESLR	LAAO; <i>P. flavoviridis</i> ; ~BAN82013	
			412.6	3	36	KVTVTYQTPAK		
			438.7	2	35	STTDLPSR		
		31.6	626.8	2	46	SAGQLYEESLR	LAAO; <i>P. flavoviridis</i> ; ~BAN82013	
			438.7	2	38	STTDLPSR		
			18.5	411.2	3	51	GAHLVSIESYR	CTL; <i>Trimeresurus purpureomaculatus</i> ; ~P0DJL2
			481.9	3	31	YHVGWGLSVQNK		
		15.6	420.7	2	31	TVSFCVK	CTL; <i>P. jerdonii</i> ; ~PJD c42983	
			797.9	2	28	LASIQSSEEEAFVGK		
	532.7	2	24	WEWSDDAR				
21	2.36	18.2	616.3	2	66	GAHLVSIESYR	CTL; <i>P. mucrosquamatus</i> ; ~XP_015685588	
			449.2	2	18	FCSEQVK		
		15.7	584.3	2	37	EQFECLVSR	CTL; <i>Trimeresurus albolabris</i> ; ~P81114	
			959.9	2	34	DCPSDWSSYEGHCYR		
22	5.38	17.4	411.2	3	66	GAHLVSIESYR	CTL; <i>Protobothrops elegans</i> ; ~BAP39929	
		15.5	616.3	2	52	GAHLVSIESYR	CTL; <i>P. elegans</i> ; ~BAP39929	
23	0.72	103.3	-	-	-	-	Unknown	
	0.16	66.2	782.4	2	65	CSSITELEKVNQR	PDE; <i>P. elegans</i> ; ~BAP39928	
			561.3	2	58	NPFYTPSPAK		
			787.9	2	51	STPTSVPPSASDCLR		
		57.4	782.4	2	68	CSSITELEKVNQR	PDE; <i>P. flavoviridis</i> ; ~BAN82021	
			787.9	2	59	STPTSVPPSASDCLR		
			561.3	2	49	NPFYTPSPAK		
			530.8	2	41	SVQPQVSCR		
		43.8	782.4	2	53	CSSITELEKVNQR	PDE; <i>P. flavoviridis</i> ; ~BAN82021	
			787.9	2	49	STPTSVPPSASDCLR		
			403.2	2	41	ALEMADR		
			457.8	2	39	LNLNNQAK		
			419.8	2	38	IQIHTAR		
		4.50	17.1	483.8	2	37	LVSIESYR	CTL; <i>P. jerdonii</i> ; ~D1MGU0
			15.0	959.9	2	80	DCPSDWSSYEGHCYR	CTL; <i>T. albolabris</i> ; ~P81114
				774.4	2	56	VFNEPQNWADA EK	

Peak	%	MW (kDa)	Peptide Ion		Score	MS/MS-derived sequence	Protein family/species/accession
			m/z	z			
24	0.12	103.3	826.4	3	53	VFNEPQNWADA EK FCTQQHK	PDE; <i>P. mucrosquamatus</i> ; ~PMR c20258
			787.9	2	35	STPTSVPPSASDCLR	
			561.3	2	33	NPFYTPSPAK	
	4.27	16.9	457.8	2	25	LNLNNQAK	CTL; <i>P. elegans</i> ; ~BAP39929
			411.2	3	70	GAHLVSIESYR	
			501.6	3	42	QYCYKPFKQLK	
		15.0	567.3	2	35	QYCYKPFK	CTL; <i>T. albolabris</i> ; ~P81114
			826.4	3	69	VFNEPQNWADA EK FCTQQHK	
			640.2	3	69	DCPSDWSSYEGHCYR	
25	0.04	99.4	584.3	2	52	EQFECLVSR	PDE; <i>P. elegans</i> ; ~BAP39928
			746.8	2	51	SVQPQAQSWSCSK	
			532.3	2	47	GETSWLKDK	
			410.2	2	38	SIPFEAR	
	0.33	58.6	403.2	2	36	ALEMADR	SVMP; <i>P. flavoviridis</i> ; ~Q90ZI3
			811.0	3	34	AAGTECRAATDECDMADLCTGR	
			656.4	2	34	IIVQSVDPVTLK	
			423.9	3	41	SAECTDRFQR	
		44.1	502.3	2	37	NMPQCILK	SVMP; <i>P. flavoviridis</i> ; ~Q90ZI3
			906.8	2	70	QGAQCAEGLCCDQCR	
			694.6	3	62	LRQGAQCAEGLCCDQCR	
			477.9	3	45	IACEPQNVKCGR	
	3.84	16.9	409.7	2	39	GMVLPGTK	CTL; <i>T. albolabris</i> ; ~P81114
			502.3	2	39	NMPQCILK	
			640.2	3	57	DCPSDWSSYEGHCYR	
			620.0	4	41	VFNEPQNWADA EK FCTQQHK	
			584.3	2	40	EQFECLVSR	
			774.4	2	37	VFNEPQNWADA EK	
		15.2	959.9	2	83	DCPSDWSSYEGHCYR	CTL; <i>T. albolabris</i> ; ~P81114
			1239.1	2	66	VFNEPQNWADA EK FCTQQHK	
			774.4	2	53	VFNEPQNWADA EK	
26	0.03	103.3	561.3	2	54	NPFYTPSPAK	PDE; <i>P. flavoviridis</i> ; ~BAN82023
			782.4	2	46	CSSITELEKVNQR	
			694.6	3	74	LRQGAQCAEGLCCDQCR	
	0.12	58.6	906.8	2	58	QGAQCAEGLCCDQCR	SVMP; <i>P. flavoviridis</i> ; ~Q90ZI3
			502.3	2	39	NMPQCILK	
			423.9	3	36	SAECTDRFQR	
			656.4	2	31	IIVQSVDPVTLK	
			666.9	2	69	VVPESLFAWER	
	0.10	43.7					PLB; <i>P. flavoviridis</i> ; ~BAN82026

Peak	%	MW (kDa)	Peptide Ion		Score	MS/MS-derived sequence	Protein family/species/accession
			m/z	z			
27	0.05	31.7	479.6	3	51	HGLEFSYEMAPR	LAAO; <i>P. flavoviridis</i> ; ~BAP39950
			453.2	2	40	VADISMAAK	
			597.8	2	37	TPVPAGCYDSK	
			438.7	2	54	STTDLPSPR	
			626.8	2	49	SAGQLYEESLR	
	2.01	16..5	29.9	2	73	SAGQLYEESLR	LAAO; <i>P. flavoviridis</i> ; ~BAN82014 CTL; <i>P. elegans</i> ; ~BAP39929
			411.2	3	76	GAHLVSIESYR	
			567.3	2	39	QYCYKPFK	
			14.7	2	49	TTDNQWLSMDCSSKR	
			922.9	2	31	TTDNQWLSMDCSSKR	
	3.86	67.5	906.8	2	81	QGAQCAEGLCCDQCR	SVMP; <i>T. stejnegeri</i> ; ~ABC73079
			694.6	3	67	LRQGAQCAEGLCCDQCR	
			801.0	3	55	GAGTECRPASSECDMADLCTGR	
			502.3	2	47	NMPQCILK	
			423.9	3	47	SAECTDRFQR	
			59.2	3	47	IACEPQNVKCGR	
			529.8	2	43	IACEPQNVK	
			40.8	3	60	IACEPQNVKCGR	
			44.4	3	56	YNNYKEDPYAK	
			597.8	2	42	TPVPAGCYDSK	
			453.2	2	38	VADISMAAK	
			450.9	3	33	RTPVPAGCYDSK	
	1.92	16.5	-	-	-	-	Unknown
	2.78	14.7	584.3	2	52	EQFECLVSR	CTL; <i>T. albolabris</i> ; ~P81114
			640.2	3	60	DCPSDWSSYEGHCYR	
28	7.98	90.2	423.9	3	31	SAECTDRFQR	SVMP; <i>P. jerdonii</i> ; ~PJD c52836
			579.8	2	30	MIPCAPQDVK	
			587.8	2	30	MIPCAPQDVK	
			80.3	3	46	SAECTDRFQR	
			59.2	2	79	QGAQCAEGLCCDQCR	
			477.9	3	76	IACEPQNVKCGR	
			423.9	3	44	SAECTDRFQR	
			16.7	2	37	QCVDVNRAY	
	4.75	14.8	-	-	-	-	Unknown
	0.94	72.9	634.8	2	36	DESIGMVDVTGTK	SVMP; <i>P. mucrosquamatus</i> ; ~XP_015683679
29	6.17	17.6	-	-	-	-	Unknown
			-	-	-	-	Unknown
			-	-	-	-	Unknown
30	0.43	77.2	626.8	2	40	DESIGMVDVTGTK	SVMP; <i>P. mucrosquamatus</i> ; ~XP_015683679

Peak	%	MW (kDa)	Peptide Ion		Score	MS/MS-derived sequence	Protein family/species/accession
			m/z	z			
31	1.72	17.4	514.3	2	39	IPCAPQDVK	CTL; <i>P. flavoviridis</i> ; ~BAN81993
			634.8	2	36	DESIG <u>M</u> VDTGTK	
			410.7	2	29	TCLGLEK	
	1.98	50.3	584.3	2	55	EQFECLVSR	CTL; <i>T. albolabris</i> ; ~3023232 SVMP; <i>Sistrurus tergeminus</i> ; ~JAS05270
			700.3	3	68	LRPGAQCAEGLCCYQCR	
			587.8	2	33	IFPCAPQDVK	
32	3.07	16.8	584.3	2	40	EQFECLVSR	CTL; <i>T. albolabris</i> ; ~P81114
			584.3	2	38	EQFECLVSR	
	1.28	49.8	502.9	3	55	VCSNRQCVDVNR	SVMP; <i>Sistrurus tergeminus</i> ; ~JAS05269
	0.72	16.7	410.7	2	31	TCLGLEK	CTL; <i>P. flavoviridis</i> ; ~BAN81993
33	0.04	38.3	15.0	2	25	TCLGLEK	CTL; <i>P. jerdonii</i> ; ~PJD c52836 SVMP; <i>P. mucrosquamatus</i> ; ~XP_015681821
			453.7	2	45	YHFVANR	
			505.8	2	41	SVGIVQDHR	
	0.10	18.5	627.3	2	37	SVGIVQDHRSR	Unknown Unknown
			-	-	-	-	
			-	-	-	-	
	0.01	17.0	410.7	2	31	TCLGLEK	CTL; <i>P. jerdonii</i> ; ~PJD c52836

Methionine oxidation is underlined.



Supplementary table 4 Assignment of the reverse-phase chromatographic fractions from *Protobothrops mucrosquamatus* venom to protein families by nESI-MS/MS of selected peptide ions from in-gel digested protein bands separated by SDS-PAGE.

Peak	%	MW (kDa)	Peptide Ion		Score	MS/MS-derived sequence	Protein family/species/accession
			m/z	z			
1	2.06	-	458.8	4	61	RLPKSKGASATSAASRPM	BPP/CNP; <i>Protobothrops flavoviridis</i> ; ~P0C7P5
			657.0	3	60	HRLPKSKGASATSAASRPM	
			485.9	3	32	QPHESPAGGTAFR	
			615.8	2	29	HESPAGGTAFR	
2	2.67	-	523.3	2	46	KPGRPPPISP	BPP/CNP; <i>Protobothrops mucrosquamatus</i> ; XP_015680879
			485.9	3	40	QPHESPAGGTAFR	
			459.3	2	38	PGRPPPISP	
			466.6	3	33	HQSKPGRPPPISP	
			566.8	2	29	SKPGRPPPISP	
3	1.29	-	699.4	2	54	HQSKPGRPPPISP	BPP/CNP; <i>P. mucrosquamatus</i> ; XP_015680879
			630.9	2	46	QSKPGRPPPISP	
			523.3	2	43	KPGRPPPISP	
4	1.23	-	699.4	2	51	HQSKPGRPPPISP	BPP/CNP; <i>P. mucrosquamatus</i> ; XP_015680879
5	0.83	-	547.3	3	50	SGNVNDYEVVYPRK	Disintegrin; <i>P. mucrosquamatus</i> ; E9NW28
			520.8	2	37	DYEVVYPR	
6	0.38	13.8	1257.5	2	124	GDWNDDRCTGQSADCPNGLYG	Disintegrin; <i>P. mucrosquamatus</i> ; E9NW26
			784.0	3	112	IARGDWNDDRCTGQSADCPR	
7	0.19	4.1	616.8	2	70	GSGGGGGGLGSNSLR	BPP/CNP; <i>Bothrops jararaca</i> ; ~Q6LEM5
8	0.14	4.0	883.4	2	77	FSSCGGGGGSFGAGGGFGSR	BPP/CNP; <i>Gloydus blomhoffii</i> ; ~P01021
9	0.05	3.4	709.9	2	30	GGTAFREELSPGP	BPP/CNP; <i>P. flavoviridis</i> ; ~P0C7P5
			454.7	2	28	VHQSKPGR	
10	0.17	4.2	851.4	1	52	IGSTSGLGC	BPP/CNP; <i>P. mucrosquamatus</i> ; XP_015680879
11	0.06	-	801.3	3	82	LRPGTQCEDGECCEQCQFK	SVMP; <i>P. mucrosquamatus</i> ; XP_015682631
			1467.6	2	82	AAESEC DIAESCTGQSAECPTDDFQR	
			559.8	2	56	LFCVQGPIGK	
			936.9	2	48	NGQPCLNNGYCYNGK	
12	0.85	14.4	743.4	2	61	AIVCGEKNPPCLK	PLA <sub>2</sub> ; <i>P. mucrosquamatus</i> ; Q2PWA3
			861.9	2	60	AVAICLRENLTGYDK	
			881.4	3	54	QVCECDKAVAICLRENLTGYDK	
			848.4	3	54	YSYSWENKAIVCGEKNPPCLK	
			680.9	2	52	ENLTGYDKKHR	
13	15.19	26.6	880.4	2	79	QICECDKAAAMCFR	PLA <sub>2</sub> ; <i>P. mucrosquamatus</i> ; Q3HLQ4
			641.8	2	69	AAAMCFRDNVK	
			722.8	4	65	WDQYIYSWENGNIIVCGEKNPCKK	
			739.3	3	56	QICECDKAAAMCFRDNVK	

Peak	%	MW (kDa)	Peptide Ion		Score	MS/MS-derived sequence	Protein family/species/accession			
			m/z	z						
14	0.89	17.3	863.1	4	55	KMTGKEPILSYATYGCNCGMAGVGQPVDGTDR	PLA <sub>2</sub> ; <i>P. mucrosquamatus</i> ; Q3HLQ4			
			1145.2	3	109	KMTGKEPILSYATYGCNCGMAGVGQPVDGTDR				
			1150.5	3	108	KMTGKEPILSYATYGCNCGMAGVGQPVDGTDR				
			1150.5	3	107	KMTGKEPILSYATYGCNCGMAGVGQPVDGTDR				
			867.1	4	106	KMTGKEPILSYATYGCNCGMAGVGQPVDGTDR				
			1107.8	3	105	MTGKEPILSYATYGCNCGMAGVGQPVDGTDR				
			944.4	2	102	KQICECDKAAAMCFR				
			827.1	4	96	MTGKEPILSYATYGCNCGMAGVGQPVDGTDR				
			722.8	4	90	WDQYIYSWENGNIVCGEKNPCKK				
			880.4	2	88	QICECDKAAAMCFR				
			641.8	2	86	AAAMCFRDNVK				
			1108.5	2	79	QICECDKAAAMCFRDNVK				
			837.9	2	73	AAAMCFRDNVKTYK				
			1107.8	3	71	MTGKEPILSYATYGCNCGMAGVGQPVDGTDR				
			413.7	2	53	AAAMCFR				
			0.33	14.2	673.9	3		83	CGGCCDESILTCTATGKR	VEGF; <i>P. mucrosquamatus</i> ; Q330K6
					439.0	5		61	IEVMQFKEHTACECRPR	VEGF; <i>P. mucrosquamatus</i> ; XP_015676137
					757.7	3		55	EYPNEVSHLFKPSVPLR	
					471.8	2		43	EMLVPILK	
	0.33	16.5			787.0	3	45	KMTGKEPIVSYAFYGCYCGK	PLA <sub>2</sub> ; <i>P. flavoviridis</i> ; ~Q8JIG0	
					1116.0	2	42	MTGKEPIVSYAFYGCYCGK		
					1124.0	2	41	MTGKEPIVSYAFYGCYCGK		
	0.71	37.2			764.0	3	49	YRYFYVCQYCPAGNMIGK	CRISP; <i>P. mucrosquamatus</i> ; P79845	
			657.6	3	43	YFYVCQYCPAGNMIGK	CRISP; <i>P. mucrosquamatus</i> ; P79845			
			516.6	3	41	GGCAAAYCPSSKYR				
			27.5	765.3	2	63		CGENIYMSPYPAK		
			652.0	3	59	SYRGGCAAAYCPSSKYR				
614.8			2	57	GGCAAAYCPSSK					
750.8			2	56	TKCPASCFCQNK					
773.3			2	56	CGENIYMSPYPAK					
985.9			2	50	YFYVCQYCPAGNMIGK					
663.0			3	40	YFYVCQYCPAGNMIGK					
705.0			3	35	VIGGIKCGENIYMSPYPAK					
774.3			2	34	GGCAAAYCPSSKYR					
23.0			614.8	2	36	GGCAAAYCPSSK		CRISP; <i>P. mucrosquamatus</i> ; P79845		
				774.3	2	35		GGCAAAYCPSSKYR		
				20.4	545.6	3		56	SYRGGCAAAYCPSSK	CRISP; <i>P. mucrosquamatus</i> ; P79845