

Comprehensive Snake Venomomics of the Okinawa Habu Pit Viper, *Protobothrops Flavoviridis*, by Complementary Mass Spectrometry-Guided Approaches

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Supplementary Materials: The following are available online at www.mdpi.com/xxx/s1, Figure S1-S5: Annotated MS2 spectra of BPP-RP, Figure S6-S9: Annotated MS2 spectra of tripeptidic svMP-i, Figure S101: *P. flavoviridis* reduced venom MS TIC for IMP and TD, Figure S11: *P. flavoviridis* venom tested for cytotoxicity against different human cell lines, Figure S12: SH-SY5Y cells after 48 h treatment with different *P. flavoviridis* venom fractions.

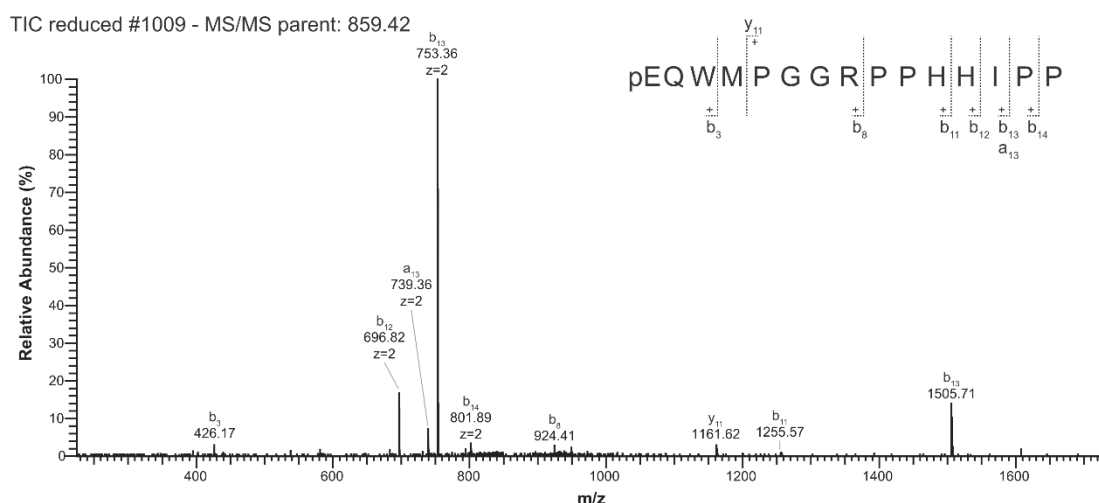


Figure S1. MS2 spectra of pEQWMPGGRPPHHIPP. Representative MS/MS spectra of the m/z 859.42 ($z=2$) precursor ion for the top-down annotation of a BPP.

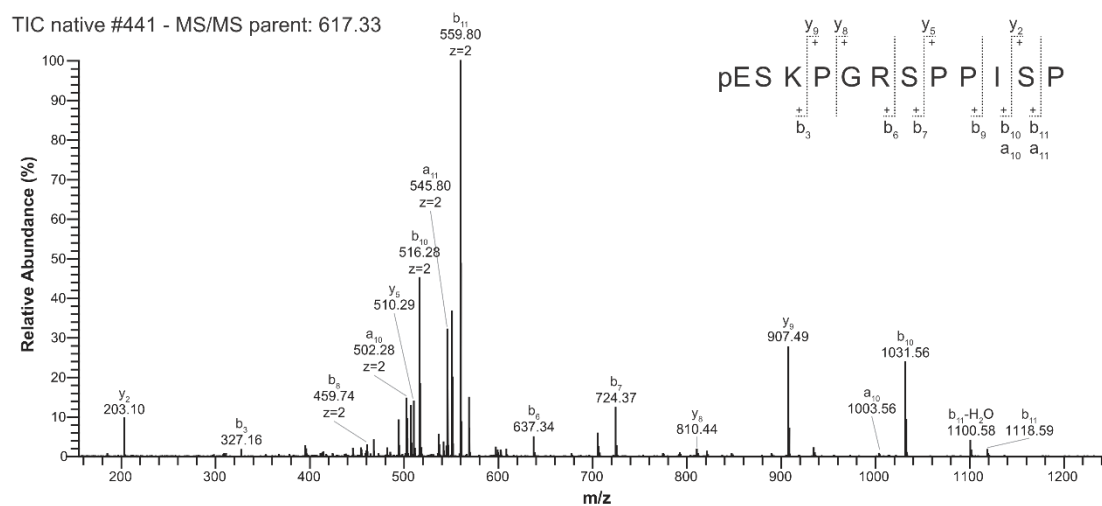


Figure S2. MS2 spectra of pESKPGRRSPPIISP. Representative MS/MS spectra of the m/z 617.33 ($z=2$) precursor ion for the top-down annotation of a BPP.

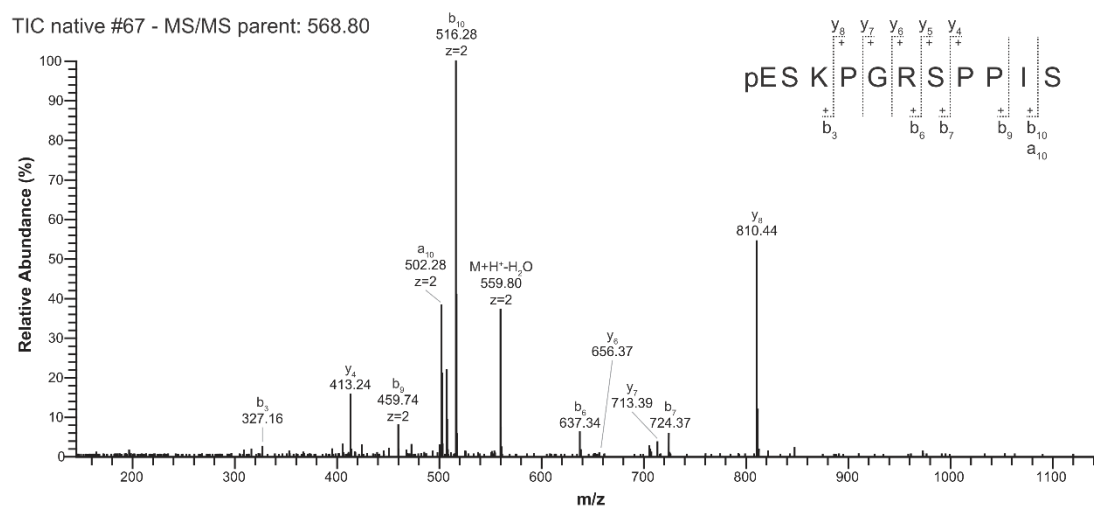


Figure S3. MS2 spectra of pESKPGRSPPIS. Representative MS/MS spectra of the m/z 568.80 ($z=2$) precursor ion for the top-down annotation of a BPP.

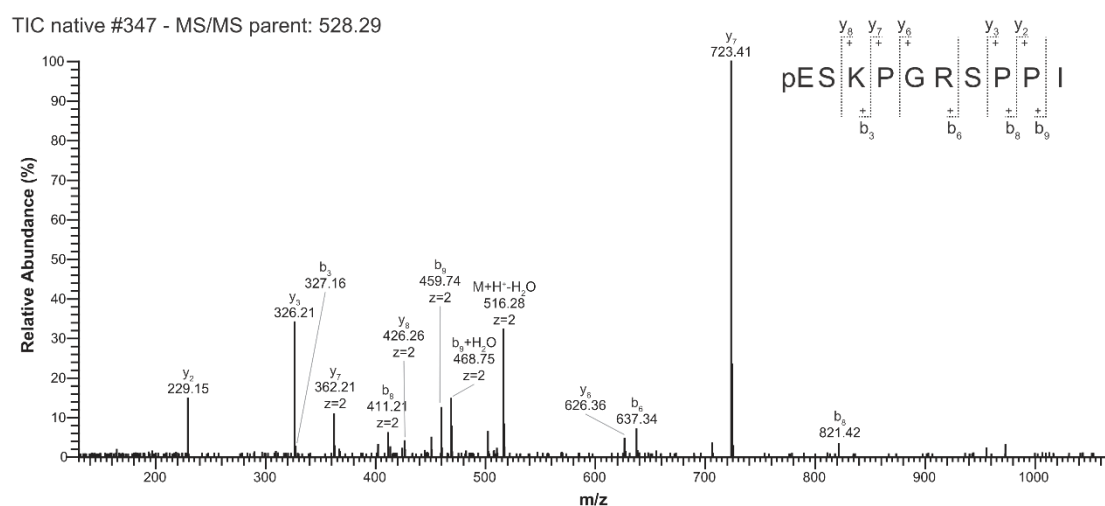


Figure S4. MS2 spectra of pESKPGRSPPPI. Representative MS/MS spectra of the m/z 528.29 ($z=2$) precursor ion for the top-down annotation of a BPP.

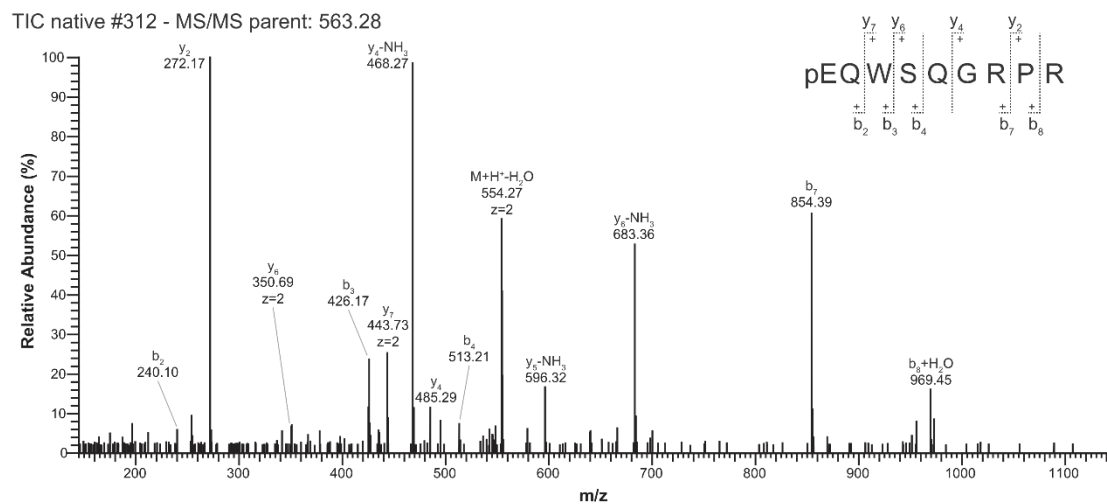


Figure S5. MS2 spectra of pEQWSQGRPR. Representative MS/MS spectra of the m/z 563.28 ($z=2$) precursor ion for the top-down annotation of a BPP.

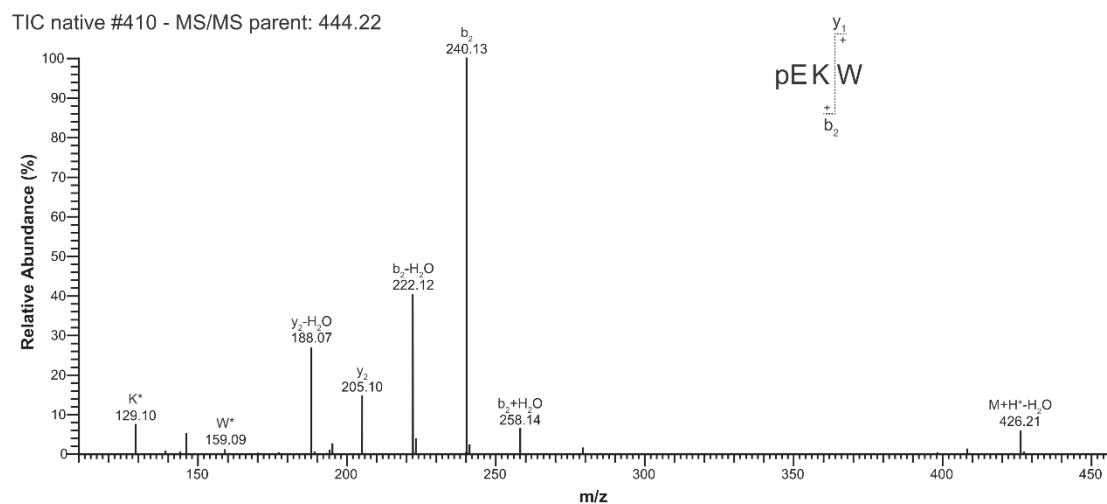


Figure S6. MS2 spectra of pEKW. Representative MS/MS spectra of the m/z 444.22 precursor ion for the de novo annotation of a small tripeptic svMP inhibitor.

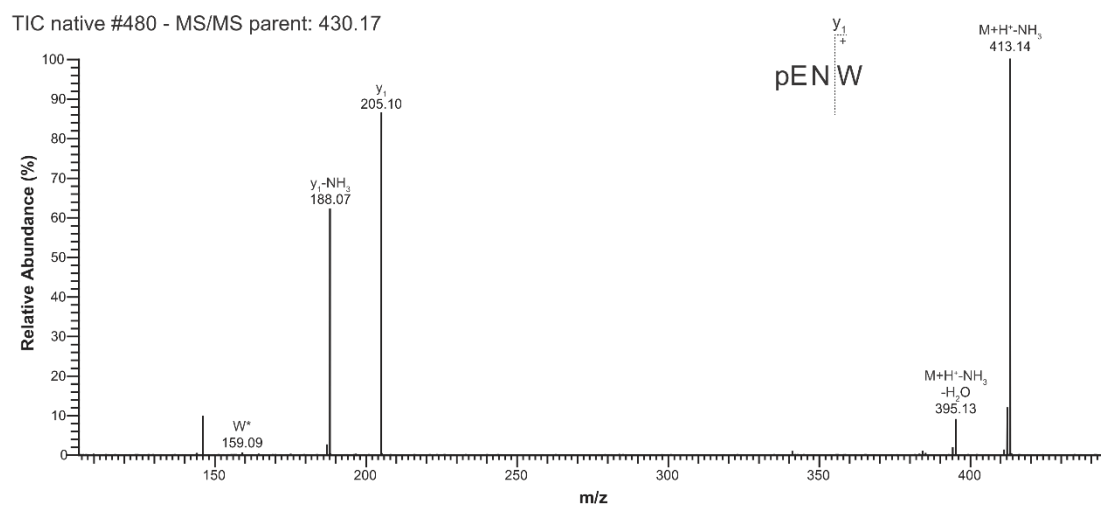


Figure S7. S2 spectra of pENW. Representative MS/MS spectra of the m/z 430.17 precursor ion for the de novo annotation of a small tripeptic svMP inhibitor.

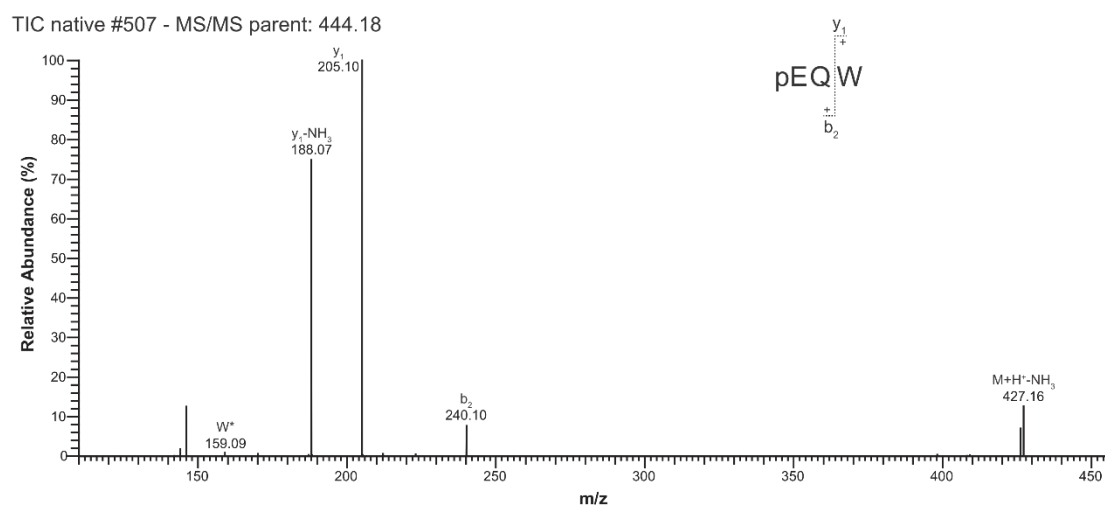


Figure S8. MS2 spectra of pEQW. Representative MS/MS spectra of the m/z 444.18 precursor ion for the de novo annotation of a small tripeptic svMP inhibitor.

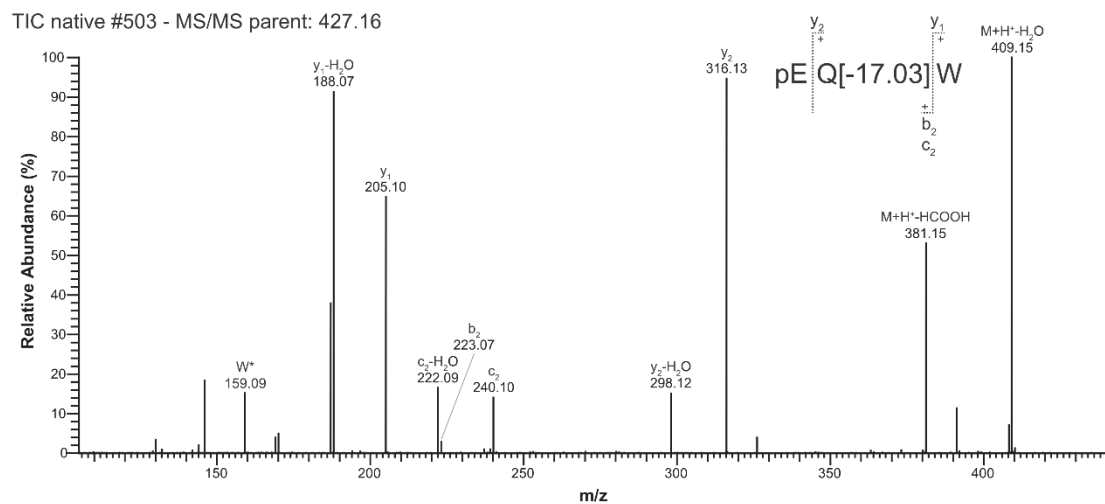


Figure S9. MS2 spectra of pEQ[-17.03]W/pEEW. Representative MS/MS spectra of the m/z 427.16 precursor ion for the de novo annotation of a small tripeptic svMP inhibitor.

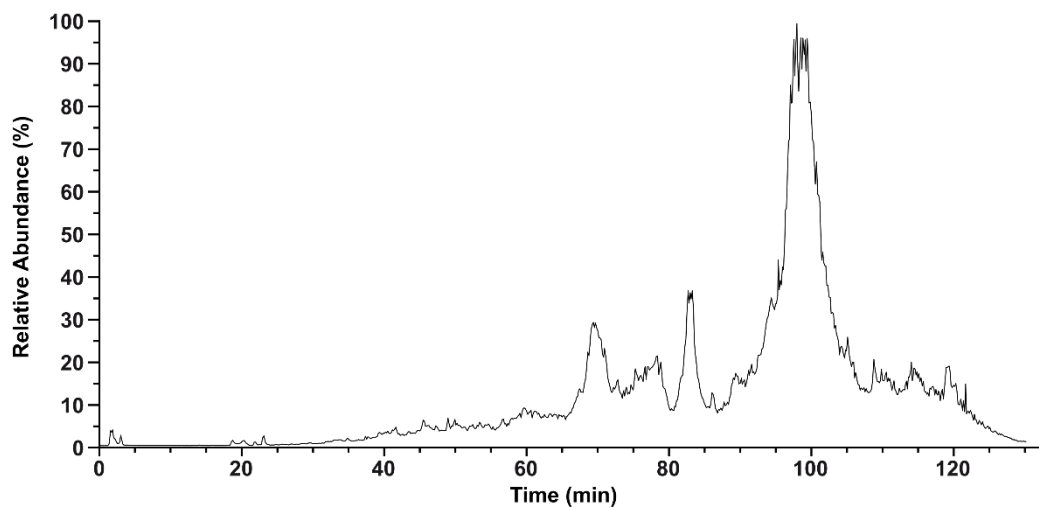


Figure S10. *P. flavoviridis* reduced venom MS TIC for IMP and TD. The total ion counts from *P. flavoviridis* crude venom were measured by an HPLC-ESI-MS of reduced crude venom. The relative abundance was set to 100% for the highest peak.

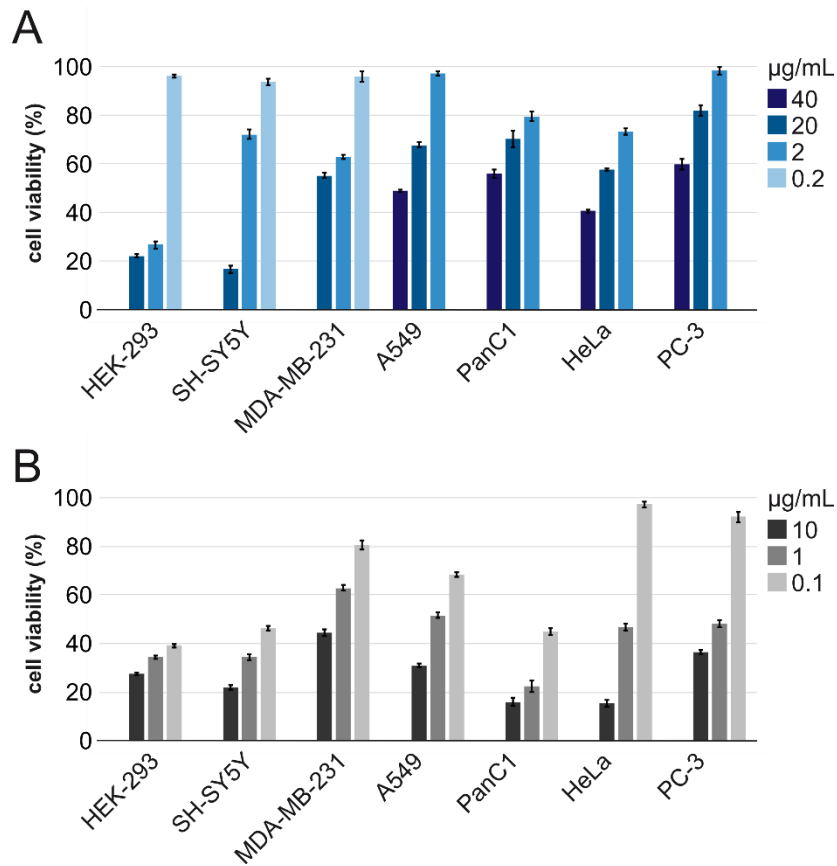


Figure S11. *P. flavoviridis* venom tested for cytotoxicity against different human cell lines. The effect on cell viability (%) of (A) *P. flavoviridis* crude venom was determined at various concentrations (0.2-40.0 µg/mL) and (B) Doxorubicin (0.1-10.0 µg/mL) as control after 48 h treatment by an MTT assay at 570 nm. One non-cancerous (HEK-293) and six cancerous human cell lines were tested. Error mean in $\pm$ SD.

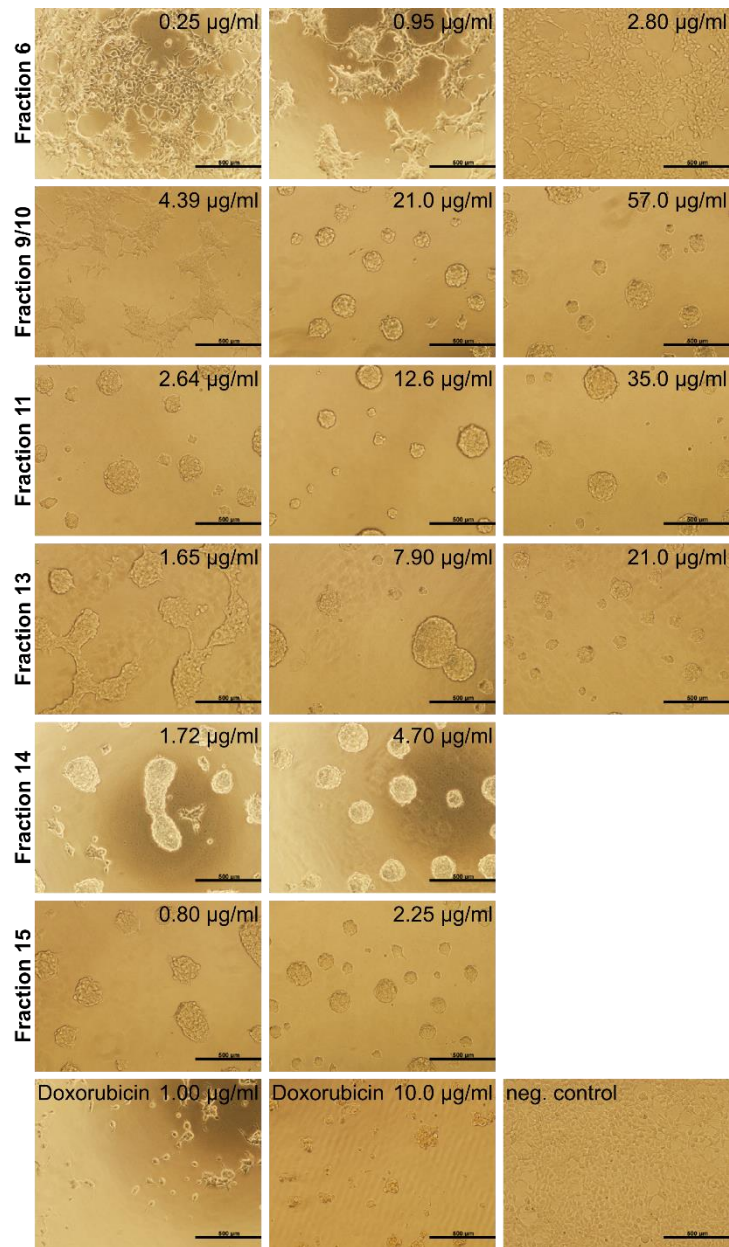


Figure S12. SH-SY5Y cells after 48 h treatment with different *P. flavoviridis* venom fractions. Single RP-HPLC venom fractions of *P. flavoviridis* with the mentioned concentration in µg/mL were tested against human neuroblastoma SH-SY5Y cells. Imaged were taken after 48 h treatment at 37 °C. Doxorubicin was used as positive cytotoxic control drug and no stimulation as negative control.

Table S1. Venom proteins and peptides identified from *Protobothrops flavoviridis*. Assignment of venom components by crude venom intact mass profiling (IMP, method A), bottom-up (BU, method C) and top-down (TD, method D). Peak numbers are based on the RP-HPLC annotation (Figure 2) and low abundant peaks in the HPLC, but detectable in the IMP, are marked by #. Sequence tags were obtained *de novo* from MS/MS spectra and identified against a non-redundant *Protobothrops flavoviridis* protein database (taxid: 88087) by BLASTP. SDS-PAGE and intact mass profile analysis provided the average molecular weight. Most abundant mass in a IMP TIC are asterisked. Method B with no distinct R_T are marked by °. Monoisotopic TD masses are marked by an indexed m.

Peak	Method	M _{app}	Identification sequence tag	Species	Protein ID	E-value	NCBI accession	RT	Native intact mass
1	A				peptide			1.61	338.09, *407.04, 596.32, 636.49
2	A; D		Q[-17.03]SKPGRSPPIS	BPP-RP	Bradykinin-potentiating and C-type peptide	2.0E-07	BAP39952.1	2.88	1136.60 _m
#	D		Q[-17.03]QWSQGRPR	BPP-RP	Bradykinin-potentiating and C-type peptide	1.0E-06	P0C7P5.1	2.88	408.14, 665.01, *1136.60, 1150.59, 1307.72
#	D		Q[-17.03]SKPGRSPPI	BPP-RP	Bradykinin-potentiating and C-type peptide	1.0E-05	P0C7P5.1	15.28	1049.56 _m
3	A; C	15			peptide			15.45	723.41, 786.16, *1049.56
4	A; C; D	20	853.42-DGLCCDQCR	svMP/DI	zinc metalloproteinase/disintegrin	6.0E-07	P18619.2		
			VKQPQCADGLCCEQCR		zinc metalloproteinase/disintegrin	5.0E-09	P18619.2		
			pEKW	svMP-i	small tripeptic inhibitor			17.82	*444.22
					peptide			17.82	887.43
5	A; C; D	20	GDNPDDR	svMP/DI	zinc metalloproteinase/disintegrin	6.0E-04	P14530.3		
			RLQPQCADGLCCEQCGV		zinc metalloproteinase/disintegrin	5.0E-08	P18619.2		
			Q[-17.03]SKPGRSPPISP	BPP-RP	Bradykinin-potentiating and C-type peptide	9.0E-03	BAP39952.1	19.28	1233.64m
6	A; D		pENW	svMP-i	small tripeptic inhibitor			19.44	445.26, 1118.59, *1233.65
					unknown (peptide)			20.74	*430.17
7	A; D		pEQ[-17.03]W	svMP-i	small tripeptic inhibitor			20.74	376.14, 413.14, 859.33
			pEQW	svMP-i	small tripeptic inhibitor			21.88	427.16
					peptide			21.88	*444.18
8	A				peptide			21.88	316.13, 887.36
					peptide			24.90	374.22, 445.17, 828.28, 1105.54, 1233.60, 7349.03,
9	A; C	15			peptide			27.89	*7622.16, 7693.18
10	A; C	15	GDFPDDR	svMP/DI	metalloprotease P-IIa 1/disintegrin	4.0E-04	BAP39948.1		
					peptide			30.00	*7622.16, 7693.18

11a	A; C	22	GDFPDDR	svMP/DI	metalloprotease P-IIa 1/disintegrin peptide	4.0E-04	BAP39948.1	33.61	413.26, 1733.82, *748.4 nG
11b	C	20	VKQPQCADGLCCDQCR CTQSADCPR GDFPDDR	svMP/DI	zinc metalloproteinase/disintegrin metalloprotease P-II	6.0E-10 3.0E-07	P18619.2 BAN89392.1		
12a	A; C	20	GDFPDDR	svMP/DI	metalloprotease P-IIa 1/disintegrin	4.0E-04	BAP39948.1		
12b	C	10	GDFPDDR	svMP/DI	metalloprotease P-IIa 1/disintegrin peptide	4.0E-04	BAP39948.1	36.88	42949.50, 1161.62, 1717.87 7513.17 *7057.77
13a	A; C	20	GDFPDDR	svMP/DI	metalloprotease P-IIa 1/disintegrin peptide	4.0E-04	BAP39948.1	38.10	1161.62, 1406.70, 1717.83, *706.1 77
13b	C	10	GDFPDDR	svMP/DI	metalloprotease P-IIa 1/disintegrin	4.0E-04	BAP39948.1		
	D		TPEQQIFPQRY	svMP/DI	metalloprotease P-II	6.1E-07	BAN89360.1	38.39	1406.69 _m
14	A; D		SHNSDKIKVRVHQMVNHINEMYRP Q[-17.03]QWMPCGRPPHHPP	svMP/DI BPP-RP	metalloprotease P-IIa Bradykinin-potentiating and C-type natriuretic peptide	2.0E-04 1.6E-03	BAP39948.1 BAP39952.1	41.03 41.36	2932.45 _m 1717.82 _m
15a	C; D	20	RIARGDFPDDRCTGLSDDCPR)[-12.17] VNHIN IVVDHGMVKKYSHNSDKIKVRVHQM VNHINEMVPP ELLEGEDCYCHIPPNPCCDPATCKLT PGSQCAEGL(CCDQCRFKKGTICRIA RGDFPDDRCTGLSDDCPR)[-12.17]WN YTIYPKPF NYGLYGCVDDTGGV	svMP/DI	zinc metalloproteinase/disintegrin; metalloprotease P-IIa disintegrin CTF-II	3.0E-08 5.3E-04 2.9E-03	P18619.2 BAP39948.1 P23323.1	45.48 44.09 44.71	426.17, 949.50, 1161.62, 1717.87 *7042.76 8315.47 4294.11 _m
15b	C	15		PLA ₂	basic phospholipase A2 BP-II	8.0E-06 9.0E-04	PODJ19.1		
	A				peptide peptide			44.71 45.48	8316.49 1648.82, 4083.98, 8317.48, 12796.42

		peptide				46.95	1116.60, 1377.54, *1531.79,
#	A	peptide					2548.41, 3854.93, 4523.25,
#	D	L-amino acid oxidase					1403.73, *8298.47
16a	C; D	TAHAHGWDSTIKSGLTAARDVNRAS	LAAO	svMP/DI	metallopeptase P-III	1.6E-09	3075.50 _m
		YLCSLGNQLPCR		svMP/DI	metallopeptase P-IIa	4.0E-07	
16b	C	TPEQQIFPQRYIELA	PLA ₂	basic phospholipase A2 BP-II		9.9E-05	1832.94 _m
16c	C	YTIYPKPF	PLA ₂	basic phospholipase A2 BP-II		8.0E-06	
		MDSYSYSWK	PLA ₂	basic phospholipase A2 BP-II		3.0E-07	
		NYGLYGCNRGGCV				5.0E-05	
16d	A; C	NYGLYGCNCGVGR	PLA ₂	basic phospholipase A2 BP-II		1.0E-10	*13753.42
		MDSYSYSWK				3.0E-07	
		131.03-LFQETGKEAAK				3.0E-06	
16e	C	NYGLYGCNCGVGR	PLA ₂	basic phospholipase A2 BP-II		1.0E-10	
		YTIYPKPF				8.0E-06	
17a	C	CCFVHECCYEK	PLA ₂	basic phospholipase A2 PL-X'		3.0E-09	
		AAAVCFGQNLR		PLA-N(O)		1.0E-07	
		303.04-FVHDCCYEK				2.0E-07	
		AFYGCYCGK		phospholipase A2		9.0E-07	
		337.11-TFPDICTDSCK				2.0E-06	
17b	A; C	TGVHCGEGTECEK	PLA ₂	PLA-N(O)		4.0E-11	13753.43, *14021.19
		142.04-AAAVCFGQNLR				1.0E-07	
		AAAVCFGQNLR				1.0E-07	
		NYGLYGCNCGVGR		basic phospholipase A2 BP-II		1.0E-10	
17c	C	MDSYSYSWK	PLA ₂	basic phospholipase A2 BP-II		3.0E-07	
		YTIYPKPF				8.0E-06	
		CGDHLLQFR		basic phospholipase A2 PL-X'		8.0E-03	
D		HLLQFRKMIKMTGKEPIV(SYAFYGC	PLA ₂	basic phospholipase A2 PLA-B		7.6E-04	14013.19 _m
		YCGKGGRGKPKDATDRCCFVHDCCY					
		EKVTGCDPKWSYYTYSLENGDIVCEG					

18	A; C	15	HLLQFRKMIKMTGKEPIVSYAFYGC	PLA ₂	basic phospholipase A2 PL-Y	3.4E-04	Q90Y77.1	61.40	14013.14 _m
			YCGKGGRGPKKDATDRCCFVHDCCY						
			EKVTGCDPKWDYYTYS(LENGDIVCG						
			CNDCTVAVGCEGNYA A AICEDDNI I/T						
			AAAVCFGQNLRL	PLA ₂	PLA-N(O)	1.0E-07	BAC56893.1	63.51	*13945.26
D			MDSYSYSWK		basic phospholipase A2 BP-II	3.0E-07	P0DJ19.1		
			CCFLHDCHADEQ		phospholipase A2	2.0E-03	BAA01565.1		
			HLLQFRKMIKMTGKEPIVSYAFYGC	PLA ₂	basic phospholipase A2 PLA-B	8.5E-03	P59265.1	62.57	13937.22 _m
			YCGKGGRGPKKDATDRCCFVHDCCY						
			EKVTGCDPKWSYYTYSLENGDIVCEG						
19a	C	20	CNDCTVAVGCEGNYA A AICEDDNI I/T						
			HLLQFRKMIKMTGKEPIV(SYAFYGC	PLA ₂	basic phospholipase A2 PLA-B	1.1E-09	P59265.1	62.80	13937.24 _m
			YCGKGGRGPKKDATDRCCFVHDCCY						
			EKVTGCDPKWSYYTYSLENGDIVCEG						
			CNDCTVAVGCEGNYA A AICEDDNI I/T						
19b	C	15	YMTFPDICTDTEPK		phospholipase A2 precursor	8.0E-09	AJC52505.1		
			AAAVCFGQNLRL		PLA-N(O)	1.0E-07	BAC56893.1		
			CCFVHDCCYEK		phospholipase A2	3.0E-10	BAP39946.1		
			SAVIICGEGTECEK	PLA ₂	PLA-N(O)	3.0E-09	BAC56893.1		
			AAAVCFGQNLRL			1.0E-07			
20a	C	50	337.11-TFPDICTDPTFNR		phospholipase A2 precursor	1.0E-08	AJC52505.1		
			MEWYPEAANAER	CRISP	cysteine-rich venom protein	3.0E-11	BAP39957.1		
			NVDFDSESPR		Triflin	6.0E-07	Q8I139.1		
			VFDHLDWIK	svSP	snake venom serine protease 2	5.0E-07	O13057.1		
			FLVALYTFR			4.0E-06			
20b	C	35	PEKIQNEIIDLHNVEK	CRISP	Triflin	5.0E-08	Q8I139.1		
			NVDFDSESPR			6.0E-07			
			GCENIYMATYPAK	CRISP	Triflin	1.0E-08	Q8I139.1	70.26	*24768.2
			243.10-EFTNCDSLQK			3.0E-08			
			NVDFDSESPR			6.0E-07			

20d	C	24	MEWYPEAAAAAER YTQIVWYK	CRISP	cysteine-rich venom protein	3.0E-11	BAP39957.1
			174.02-GENIYMATYPAK		Triflin	3.0E-06	
			NVDFDSESPR			1.0E-09	Q8I139.1
20e	C	20	MEWYPEAAAAAER 346.10-NIYMATYPAK	CRISP	cysteine-rich venom protein	6.0E-07	
			NVDFDSESPR		Triflin	3.0E-11	BAP39957.1
			FLVALYTFR			1.0E-07	Q8I139.1
			MEWYPEAAAAAER		cysteine-rich venom protein 2	6.0E-07	
20f	C	17	KPENKAEIIDLHNSLGV	CRISP	cysteine-rich venom protein	4.0E-06	O13057.1
			NVDFDSESPR			3.0E-11	BAP39957.1
			AAVCFGQNLRL		Triflin	5.0E-07	
20g	C	15	SDIYSYSWK	PLA ₂	PLA-N(O)	6.0E-07	Q8I139.1
			VMGWGTISATK	CRISP	cysteine-rich venom protein	1.0E-07	BAC56893.1
21a	C	35	TLCAGILEGGK	svSP	Snake venom serine protease 2	9.0E-07	BAP39957.1
			ADSGGLPLCDGEIQKVSRL			4.0E-08	O13057.1
			542.29-HSTNVINEDVTKR			3.0E-07	
			VFDHLDWLK			5.0E-06	
21b	A; C	24	KMKAHNEIIDLHNSLR	CRISP	cysteine-rich venom protein	1.0E-05	
			276.08-WYPEAAANSLR			5.0E-08	BAP39957.1
			NVDFDSESPR		Triflin	71.00-	21723.77, 24766.14,
			218.11-QNLYMATYPAK			71.05	*27800.64
21c	C	20	MEWYPEAAAAAER	CRISP	cysteine-rich venom protein	3.0E-05	
			NVDFDSESPR		Triflin	6.0E-07	Q8I139.1
21d	C	17	MEWYPEAASYK	CRISP	cysteine-rich venom protein	2.0E-06	
			NVDFDSESPR		Triflin	3.0E-11	BAP39957.1
			FLVALYTFR		cysteine-rich venom protein	6.0E-07	Q8I139.1
			356.18-QFENMIK	svSP	snake venom serine protease 2	7.0E-06	BAP39957.1
21e	C	15	SLDLDSLADLK	PLA ₂	phospholipase A2	6.0E-07	Q8I139.1
					hypothetical protein	4.0E-06	O13057.1
						8.0E-06	BAA01565.1
						5.9E-02	BAN82053.1

21f	C	10	FLVALYTFR	svSP	snake venom serine protease 2	4.0E-06	O13057.1	
22a	C	30	VMGWGTISATK	svSP	snake venom serine protease 2	4.0E-08	O13057.1	
			FLVALYTFR			4.0E-06		
			TLCAGILENK			2.0E-04		
22b	C	25	DNLDITYDR	PLA ₂	phospholipase A2	2.0E-05	BAA01565.1	
22c	A; C	15	370.20-SYSAYGCYCGSVNR	PLA ₂	phospholipase A2	3.0E-07	BAA01565.1	*13764.96
			DNLDITYDR			2.0E-05		
			NLGEQFENMIHK			2.0E-05		
			AAALCFR		phospholipase A2 precursor	1.0E-03	AJC52507.1	
22d	C	12	GSILSYSGYCGWNR	PLA ₂	phospholipase A2	3.0E-11	BAA01565.1	
			QVWQFENMIHK			2.0E-07		
22e	C	10	QVWQFENMIHK	PLA ₂	phospholipase A2	2.0E-07	BAA01565.1	
			370.23-SYSAYGCYCQDNR			2.0E-06		
23a	C	50	FLVALYTFR	svSP	snake venom serine protease 2	4.0E-06	O13057.1	
23b	C	40			unknown (protein)			
23c	C	30	FLVALYTFR	svSP	snake venom serine protease 2	4.0E-06	O13057.1	
			508.18-EEFLEALR		hypothetical protein	4.0E-03	BAN82089.1	
24a	A; C	30	ETDYEEFLEIAR	LAAO	L-amino acid oxidase	5.0E-10	P0C2D5.2	*30384.71
			HDDIFAYEK			1.0E-06	BAN82013.1	0.4 nM
			SAGQLEYESLR			3.0E-03		
24b	A; C	15	ALSIQSSEEEAFVGK	CTL	C-type lectin beta subunit	4.0E-09	BAN82010.1	*13527.50
								0.4 nM
25a	C	60	EGWYANLGMPR	LAAO	L-amino acid oxidase	3.0E-05	BAN82013.1	
25b	C	35	ETDYEEFLEIAR	LAAO	L-amino acid oxidase	5.0E-10	P0C2D5.2	
25c	A; C	25	NDEVLDKDIMLIK	svSP	Thrombin-like enzyme Flavoxobin	1.0E-10	P05620.2	*25687.40
			VLNEDEQIRNPK			2.0E-09		
25d	C	20	TVLQIWSNK	svMP/DI	metalloprotease P-IIa 1	3.0E-04	BAP39948.1	
25e	C	15	271.06-LQSSEEEAFVGK	CTL	C-type lectin beta subunit	3.0E-07	BAN82010.1	
			STFQYVWIGLR		C-type lectin alpha subunit	7.0E-07	Q8AV97.1	
			356.19-QFENMIHK	PLA ₂	phospholipase A2	8.0E-06	BAA01565.1	

26a	C	70	VVSLNVLCTECR YLGYLEAG-1214.63	5-N	5-nucleotidase	3.0E-09	BAP39972.1
26b	C	60	LGDDANFFQALDFK SAGQLYEESLR KFWEDDKHNK ETDYEEFLEIAR	LAAO	L-amino acid oxidase	8.2E-02	
26c	C	25	FLVALYTFR VLNEDEQIR	svSP	Apoxin I-like protein OHAP-1 snake venom serine protease 2	5.0E-10 4.0E-06	BAN82013.1
26d	C	23	TPEQQIFPQR	svMP/DI	Thrombin-like enzyme Flavoxobin	4.0E-06	P05620.2
27a	C	110	TPEQQIFPQR 1309.70-LTTGQVIGLAYK NSVGIVK	svMP/DI	metalloprotease P-IIa 1 metalloprotease P-IIa 1	1.0E-07 1.0E-07 6.0E-04	BAP39948.1 BAP39948.1
27b	C	25	CEACIMSAVISDKPSK TPEQQIFPQR YIELAIVVDH-479.22	svMP/DI	zinc metalloproteinase/disintegrin zinc metalloproteinase/disintegrin metalloprotease P-IIa 1	3.0E-03 2.0E-13 1.0E-07 3.0E-07	P14530.3 P14530.3 BAP39948.1
27c	C	23	ASAPGLLNGTDIFNTGNIIGLAYK CEACIMSAVISDKPSK DYYQTFLTNKS	svMP/DI	metalloprotease P-II zinc metalloproteinase/disintegrin	1.0E-07 2.0E-13 1.0E-06	BAN81998.1 P14530.3
27d	C	15	DHGALGPGWGTDVNFTGKGIGLAYK VTDLDSILAEVK YIELAIVVDHMYGK TPEQQIFPQR STFQYVWIGLR 1398.64-FVAQLVGDR TLGMLMEKK VYRRHLTGLNFYSKK	svMP/DI	metalloprotease P-II hypothetical protein zinc metalloproteinase/disintegrin metalloprotease P-IIa 1 C-type lectin alpha subunit C-type lectin F IX/X A phosphodiesterase	2.0E-06 2.0E-03 9.0E-09 1.0E-07 7.0E-07 3.2E-02 3.0E-04 4.0E-04	BAN81998.1 BAN82044.1 P14530.3 BAP39948.1 BAN81988.1 BAP39954.1 BAN82022.1 BAN82023.1 Q90ZI3.1
28a	C	110	AAVSQDACFQFNR LYCIDSSPAK LLVQSVPDVTLK ETDYEEFLEIAR	svMP/DI	zinc metalloproteinase-DI-like HV1	3.0E-10 5.0E-07 3.0E-06	
28b	C	50		LAAO	Apoxin I-like protein OHAP-1	5.0E-10	POC2D5.2

28c	C	30	DNEVLDKDIMLIK	svSP	serine protease	8.0E-09	BAP39955.1
			LLVQSPDPVLTK	svMP/DI	zinc metalloproteinase-DI-like HV1	5.0E-03	Q90Z13.1
28d	C	25	YIELAIVVDHYMGK	svMP/DI	metalloprotease P-IIa 1	6.0E-07	BAP39948.1
			HDQWPLNGSDINFTGNIKAYK		metalloprotease P-II	4.0E-06	BAN81988.1
			616.2-MSAVISDGLNR		zinc metalloproteinase/DI-like HR1a	3.0E-03	Q8JIR2.1
28e	C	15	STFQYVWIGLR	CTL	C-type lectin alpha subunit	7.0E-07	BAN81988.1
			NWEDAESHEGEEPGK		C-type lectin A	1.0E-03	BAP39968.1
28f	C	12	AWAEESYCVYFK	CTL	C-type lectin F IX/X B	2.0E-10	BAP39964.1
			AWSGGSDCIVSK		C-type lectin beta subunit	9.0E-09	BAN82011.1
			384.23-QSSEEEAFVGK			2.0E-07	BAN82010.1
			WEWSDDAR			3.0E-06	
29a	C	110			unknown (protein)		
29b	C	50	LYCIDSSPAK	svMP/DI	zinc metalloproteinase-DI-like HV1	5.0E-07	Q90Z13.1
			LLVQSPDPDVTLK			3.0E-06	
29c	C	30	LLVQSPDPDVTLK	svMP/DI	zinc metalloproteinase-DI-like HV1	3.0E-06	Q90Z13.1
			FLVALYEFK	svSP	serine protease	1.0E-03	BAN82036.1
29d	C	25	LYCIDSSPAK	svMP/DI	zinc metalloproteinase-DI-like HV1	5.0E-07	Q90Z13.1
29e	C	15	TSFQYVWIGLR	CTL	C-type lectin alpha subunit	8.0E-09	BAN81988.1
			NWEDAESFMSSEGPk			5.0E-05	
			1226.58-GDFVAQLVTVK		C-type lectin F IX/X A	3.0E-04	BAP39954.1
29f	C	12	AWAEESYCVYFK	CTL	C-type lectin F IX/X B	2.0E-10	BAP39964.1
			384.24-GASSEEEAFVGK		C-type lectin beta subunit	5.0E-06	BAN82010.1
			186.7-EWSDDAR			2.0E-04	
30a	C	110	DFYTFDSEGIVK	PDE	phosphodiesterase	2.0E-09	BAN82022.1
			711.39-LTGLNFYSGLK			2.0E-07	
			LANVLCSCSDSWEK			2.0E-07	
			CSSITELEK			1.0E-05	
30b	C	70	LWYQLVNTINNIYR	svMP/DI	zinc metalloproteinase/DI-like HR1b	3.0E-10	P20164.4
			AIVVDHGIVTK			2.0E-07	

30c	C	60	KDGDANFFQALDFK	LAAO	L-amino acid oxidase	5.0E-08	BAN82013.1
			590.30-LVNTLNQVYR	svMP/DI	zinc metalloproteinase/DI-like HR1a	3.0E-04	Q8JIR2.1
30d	C	30	FLVALYTFR	svSP	snake venom serine protease 2	4.0E-06	O13057.1
			TSFQYVWLKR	CTL	Flavocetin-A alpha subunit	1.0E-04	Q8AV97.1
30e	C	25	SKNGHPLTAPPAQLFSDCSK	svMP/DI	metalloprotease P-II	3.0E-07	BAN81998.1
			1262.57-NFTGQVIGLAYK		metalloprotease P-IIa 1	2.0E-06	BAP39948.1
			TSFQYVWIGLR	CTL	Flavocetin-A alpha subunit	8.0E-09	Q8AV97.1
30f	C	15	434.20-NVYCGTENPFVCK	CTL	C-type lectin alpha subunit	4.0E-11	BAN81988.1
			188.08-FQYVWIGLR			5.0E-07	
			323.09-ICYQAFSKPK		Flavocetin-A alpha subunit	8.0E-08	AAB34807.1
			1226.57-FDGVAAQLVAEK			7.0E-04	Q8AV97.1
30g	C	12	231.79-STLQYTSMWIGLK	CTL	C-type lectin beta subunit	7.0E-10	BAN82010.1
			184.12-SIQSSEEEAFVGK			3.0E-09	
			257.11-AEESYCVYFK		C-type lectin F IX/X B	1.0E-07	BAP39964.1
30h	C	9	1432.74-LVAQLVTVK	CTL	C-type lectin F IX/X A	6.5E-02	BAP39954.1
31a	C	110	WCVKAAVAPDSGDFVAQLVAEK	CTL	C-type lectin A	2.0E-06	BAP39968.1
			STFQYVWLKR		Flavocetin-A alpha subunit	1.4E-02	Q8AV97.1
			508.18-EEFLEIAR	LAAO	L-amino acid oxidase	5.0E-05	BAN82013.1
			212.15-LVATEVMVR	svMP/DI	Flavorase	4.5E-02	BAK64383.1
31b	C	50	269.18-EDGLKDGGLCCYQCR	svMP/DI	Flavorase	8.0E-07	BAK64383.1
			FSIAGAEGR			1.0E-05	
			LVIVADDVHAPP			4.0E-04	
			SSKSLLNVLTLIYR			2.0E-04	
31c	C	25	335.15-QYVWLKR	CTL	C-type lectin alpha subunit	2.8E-02	BAN81988.1
31d	C	22			unknown (protein)		
31e	C	15	TSFQYVWIGLR	CTL	C-type lectin alpha subunit	8.0E-09	BAN81988.1
			1226.57-GDFVAQLVAEK		C-type lectin A	2.0E-06	BAP39968.1
32a	C	110	DFYTFDSEKVK	PDE	phosphodiesterase	3.0E-05	BAN82022.1
			711.38-LTGLNFYSKK			1.0E-04	

32b	C	70	TWVYEIVNTLNEIYR	svMP/DI	metalloprotease P-III	9.0E-14	BAN81999.1
32c	C	60	LYCSLGNQLPCR			1.0E-09	
			FNSNLNEVK			7.0E-06	
			TCTGLVQDYSSR			4.0E-05	
			LFELVIVADYR	LAAO	L-amino acid oxidase	2.0E-07	BAN82013.1
			ETDYEEFLEIAR	LAAO	Apoxin I-like protein OHAP-1	5.0E-10	POC2D5.2
32d	C	25	342.14-DANFFQALDFK		L-amino acid oxidase	3.0E-08	BAN82013.1
			820.38-VNLILQR	svMP/DI	metalloprotease P-III	9.0E-04	BAN82009.1
			1262.56-NFTGNIIGLAYK	svMP/DI	metalloprotease P-IIa 1	6.0E-09	BAP39948.1
32e	C	15	TSFQYVWIGLR	CTL	C-type lectin alpha subunit	8.0E-09	BAN81988.1
32f	C	12	HYEDAESF-716.31			1.8E-02	
			AWAEESYCVYFK	CTL	C-type lectin F IX/X B	2.0E-10	BAP39964.1
			ALSIQSSEEEAFVGK		C-type lectin beta subunit	4.0E-09	BAN82010.1
			TSFQYVWLKR		Flavocetin-A alpha subunit	1.0E-04	Q8AV97.1