

Supplementary Materials: Proteomic Characterization of the Venom of Five *Bombus* (*Thoracobombus*) Species

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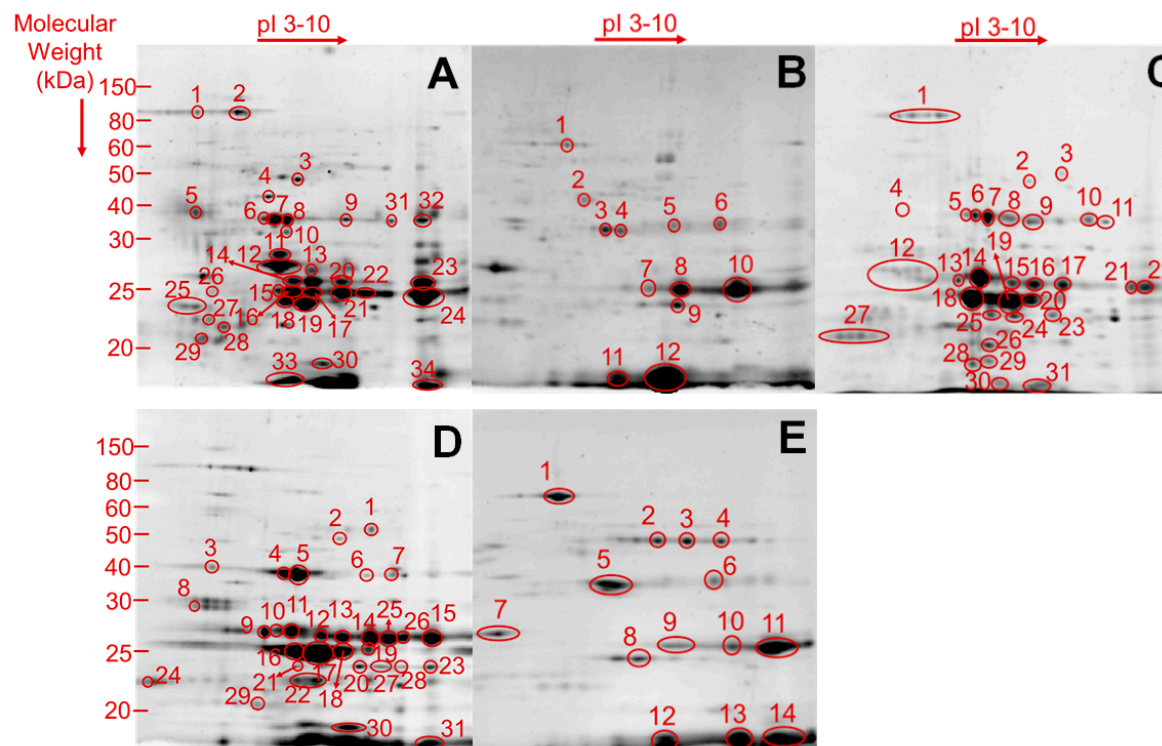


Figure S1. 2DE gel images of *Thoracobombus* venom. Representative images of venom profile of (A) *B. humilis*, (B) *B. pascuorum*, (C) *B. ruderarius*, (D) *B. sylvarum*, and (E) *B. zonatus*. Gel analyses were conducted in triplicates. Marked spots are spectrometrically identified (See: Tables S3–S7).

Table S1. Sample Collection. Locations, number of specimens, and plants species where the bumble bee species are collected from.

Species	Location	Date	Altitude (m)	Specimens	Foraged plant species
<i>B. humilis</i>	Ankara-Çerkeş Road, Kızılcahamam-ANKARA 40°33.535'K 32°39.026'D	02/07/2014	1120	16	<i>Anchusa leptophylla</i> ROEMER ET SCHULTES subsp. <i>incana</i> (LEDEB.) CHAMB., <i>Stachys byzantina</i> C. KOCH
	Ankara-Çerkeş Road, Kızılcahamam-ANKARA 40°33.535'K 32°39.026'D	17/07/2014	1120	34	<i>Anchusa leptophylla</i> ROEMER ET SCHULTES subsp. <i>incana</i> (LEDEB.) CHAMB., <i>Melilotus officinalis</i> (L.) DESR., <i>Nepeta nuda</i> L. subsp. <i>nuda</i> L., <i>Stachys byzantina</i> C. KOCH, <i>Nepeta nuda</i> L. subsp. <i>nuda</i> L.
	Soğuk Su National Park, Kızılcahamam-ANKARA 40°27.113'K 32°37.355'D	04/07/2014	1216	15	<i>Trifolium</i> sp., <i>Lathyrus incurvus</i> (ROTH.) WILLD.
<i>B. pascuorum</i>	Abant Lake Natural Park-BOLU 40°36'K 31°16'D	09/08/2013	1350	10	<i>Carduus nutans</i>
	Soğuk Su National Park, Kızılcahamam-ANKARA 40°27.113'K 32°37.355'D	04/07/2014	1216	22	<i>Trifolium</i> sp., <i>Lathyrus incurvus</i> (ROTH.) WILLD.
	Ankara-Çerkeş Road, Kızılcahamam-ANKARA 40°33.535'K 32°39.026'D	02/07/2014	1120	6	<i>Anchusa leptophylla</i> ROEMER ET SCHULTES subsp. <i>incana</i> (LEDEB.) CHAMB., <i>Melilotus officinalis</i> (L.) DESR., <i>Nepeta nuda</i> L. subsp. <i>nuda</i> L., <i>Stachys byzantina</i> C. KOCH, <i>Nepeta nuda</i> L. subsp. <i>nuda</i> L.
	Ankara-Çerkeş Road, Kızılcahamam-ANKARA 40°33.535'K 32°39.026'D	17/07/2014	1120	3	<i>Anchusa leptophylla</i> ROEMER ET SCHULTES subsp. <i>incana</i> (LEDEB.) CHAMB., <i>Melilotus officinalis</i> (L.) DESR., <i>Nepeta nuda</i> L. subsp. <i>nuda</i> L., <i>Stachys byzantina</i> C. KOCH,
	Ilgaz Mountain National Park-ÇANKIRI 41°4.306'K 33°43.815'D	19/07/2014	1857	19	<i>Allium</i> sp., <i>Trifolium</i> sp.
Ilgaz Mountain National Park-ÇANKIRI 41°4.306'K 33°43.815'D	30/08/2014	1857	7	<i>Epilobium angustifolium</i> L.	
<i>B. ruderarius</i>	Erciyes Mountain-KAYSERİ 38°32.807'K 35°31.427'D	28/07/2014	2177	35	<i>Carduus</i> sp.
<i>B. sylvarum</i>	Erciyes Mountain-KAYSERİ 38°32.807'K 35°31.427'D	28/07/2014	2177	43	<i>Carduus</i> sp.
<i>B. zonatus</i>	H. U. Beytepe Campus, ANKARA 39°52.321'K 32°44.168'D	24/07/2014	1038	23	<i>Syringia</i> sp.
	Ankara-Çerkeş Road, Kızılcahamam-ANKARA 40°20.442'K 32°41.731'D	02/07/2014	991	2	<i>Salvia candidissima</i> VAHL subsp. <i>candidissima</i> VAHL.
	H. U. Beytepe Campus, ANKARA 39°52.265'K 32°43.844'D	14/07/2014	1017	4	<i>Consolida regalis</i> S. F. GRAY subsp. <i>paniculata</i> (HOST) SOO var. <i>paniculata</i> (HOST) SOO

Table S2. Common and differentially expressed protein spots in *Thoracobombus venom*. Spots intensities are compared in *B. humilis*, *B. pascuorum*, *B. ruderarius*, *B. sylvarum*, and *B. zonatus* venom.

Species	Number of common protein spots	Number of differentially expressed protein spots ($p < 0.05$)
<i>B. humilis/B. pascuorum</i>	56	15
<i>B. humilis/B. sylvarum</i>	67	19
<i>B. humilis/B. ruderarius</i>	66	22
<i>B. humilis/B. zonatus</i>	45	23
<i>B. pascuorum/B. sylvarum</i>	48	14
<i>B. pascuorum/B. ruderarius</i>	46	21
<i>B. pascuorum/B. zonatus</i>	31	16
<i>B. sylvarum/B. ruderarius</i>	61	19
<i>B. sylvarum/B. zonatus</i>	46	18
<i>B. ruderarius/B. zonatus</i>	44	19

Table S3. List of identified proteins in *B. humilis* venom.

Spot #	Access #	Identified protein	Score	Theoretical pI/Mw (kDa)	Observed pI/Mw (kDa)	Sequence coverage (%)	Matched/unmatched peptides
1	XP_013164724	Neurexin-4 isoform X2	55	5.83/144.4	5.63/153.32	8	9/1
2	Q10737	Aminopeptidase N	37	6.47/111.2	6.26/151.29	8	7/2
2	Q01202	Paramyosin	20	5.80/101.9	6.26/151.29	7	5/3
3	XP_003694643	Malate dehydrogenase, cytoplasmic	45	6.92/35.9	7.27/56.08	19	5/5
4	EKC41389	39S ribosomal protein L47, mitochondrial	40	9.55/47.9	6.78/49.48	17	6/3
5	XP_008477265	Mitotic checkpoint serine/threonine-protein kinase BUB1-like	56	8.71/35.3	5.64/45.78	23	7/5
6	XP_003486583	Venom acid phosphatase Acph-1-like isoform X3	96	6.84/46.9	6.86/42.39	18	8/5
7	XP_003486583	Venom acid phosphatase Acph-1-like isoform X3	99	6.84/46.9	6.88/42.39	17	8/4
8	XP_003486583	Venom acid phosphatase Acph-1-like isoform X3	95	6.84/46.9	6.90/42.38	16	8/5
9	P85841	Hyaluronidase 1 (Fragment)	43	8.75/45.2	6.82/42.37	10	3/5
10	XP_011559125	L-lactate dehydrogenase isoform X2	62	6.45/37.6	6.86/42.39	21	7/3
11	XP_011184077	Tropomyosin-1, isoforms 33/34 isoform X26	62	4.74/32.7	6.95/33.79	27	7/1
11	LOC100118569	phytanoyl-CoA dioxygenase, peroxisomal-like	44	5.95/32.6	6.95/33.79	20	4/1
12	LOC102680781	TNF receptor-associated factor 4-like	54	8.33/42.5	6.95/31.21	19	7/4
13	XP_005187259	NADH dehydrogenase [ubiquinone] iron-sulfur protein 3, mitochondrial	43	6.97/30	7.51/30.74	13	4/1
13	XP_005175580	Alpha-tocopherol transfer protein-like	52	5.97/20.5	7.51/30.74	18	4/1
14	P00630	Phospholipase A2	35	7.05/19.6	7.18/28.42	13	5/9
15	P43689	Tropomyosin-2	49	4.58/32.6	7.04/24.78	26	6/5
16	P14208	Arginine kinase	32	6.05/40.3	7.2/26.36	28	8/14
17	Q7M4I3	Venom protease	23	8.85/27.6	7.53/26.58	23	3/7
18	P00630	Phospholipase A2	29	7.05/19.6	7.2/26.36	29	5/17
19	P00630	Phospholipase A2	40	7.05/19.6	7.18/28.42	13	5/9
20	Q9U9J4	Arginine kinase	44	6.39/40.5	7.99/28.25	32	9/11

21	KHJ85713	Triose-phosphate isomerase	53	8.18/27.6	7.99/28.25	31	8/13
22	Q9U9J4	Arginine kinase	44	6.39/40.5	7.99/28.25	13	3/7
23	P00630	Phospholipase A2	22	7.05/19.6	9.40/28.20	15	5/7
23	XP_013096194	Centrosomal protein of 290 kDa-like	56	9.04/27.7	9.40/28.20	34	7/5
23	XP_011493908	Cyclin-dependent kinase inhibitor 1C-like	44	11.15/28.9	9.40/28.20	31	5/7
23	XP_012525274	Phosphoserine phosphatase isoform X1	37	8.26/28	9.87/25.84	31	5/9
24	P00630	Phospholipase A2	42	7.05/19.6	9.87/25.84	14	2/2
25	XP_013309262	Ankyrin repeat protein	66	5.30/28.2	5.44/25.16	32	7/4
25	XP_013147109	Adenylate kinase isoenzyme 1 isoform X2	42	6.64/25.8	5.44/25.16	23	5/6
26	AJO64864	Arginine kinase, partial	40	6.78/22.7	5.88/27.80	26	5/6
27	XP_014236257	Ribose-5-phosphate isomerase	40	5.96/25.9	5.7/22.9	25	5/6
28	AGB85951	Triosephosphate isomerase, partial	66	5.07/15.9	6.08/21.7	36	7/7
29	XP_011191994	Peroxioredoxin-6-like	42	6.30/25.4	5.8/20.03	21	4/2
30	P48816	Lysozyme	34	8.99/16.1	7.65/16.53	29	4/6
30	XP_013144263	probable maleylacetoacetate isomerase 1, partial	52	8.57/25.3	7.65/16.53	25	6/4
31	CEF63756	3-hydroxyacyl-CoA dehydrogenase, C-terminal domain	45	9.05/50.1	8.84/42.25	16	7/4
31	XP_011639815	Bystin	50	8.63/50.4	8.84/42.25	17	8/3
32	O76756	40S ribosomal protein S8	37	10.58/24.1	9.89/42.70	31	5/7
32	P00630	Phospholipase A2	35	7.05/19.6	9.89/42.70	11	4/8
33	XP_012798920	25 kDa integral membrane protein	61	8.47/15.5	7.45/15.21	39	5/3
34	Q56FG8	60S ribosomal protein L18	37	11.45/21.8	9.88/15.52	21	4

Table S4. List of identified proteins in *B. pascuorum* venom.

Spot #	Access #	Identified protein	Score	Theoretical pI/Mw (kDa)	Observed pI/Mw (kDa)	Sequence coverage (%)	Matched/ unmatched peptides
1	WP_022965612	nitrogen regulation protein NR(I)	80	5.56/20	6.26/151.29	20	10/3
2	XP_005077830	PREDICTED: kelch-like protein 25	79	6.27/66.8	6.78/49.48	28	13/6
2	P21879	Inosine-5'-monophosphate dehydrogenase	50	6.18/53.1	6.78/49.48	26	10/9
2	Q8Z2E5	L-lactate dehydrogenase	34	6.25/42.9	6.78/49.48	15	4/4
3	XP_003486583	Venom acid phosphatase AcpH-1-like isoform X3	88	6.84/46.9	6.86/42.39	18	8/5
4	XP_003486583	Venom acid phosphatase AcpH-1-like isoform X3	80	6.84/46.9	6.92/42.38	18	8/5
5	Q8LPJ5	Isocitrate dehydrogenase [NADP], chloroplastic/mitochondrial	50	8.05/54.5	7.09/42.37	15	7/4
5	WP_034695000	transporter	63	6.08/46.8	7.09/42.37	28	9/7
5	WP_023383864	peptide ABC transporter ATP-binding protein	64	9.01/37.4	7.09/42.37	34	9/8
5	P49597	Protein phosphatase 2C 56	38	5.81/47.9	7.09/42.37	13	5/3
5	Q8IY84	Serine/threonine-protein kinase NIM1	59	8.53/49.9	7.09/42.37	20	6/2
5	Q9ZKU5	Acetate kinase	48	6.47/44.9	7.09/42.37	22	7/10
6	P85841	Hyaluronidase 1 (Fragment)	62	8.75/45.2	8.84/42.25	24	6/5
7	Q9U9J4	Arginine kinase	36	6.39/40.5	7.2/26.36	20	6/4

8	Q7M4I3	Venom protease	40	8.85/27.6	7.62/26.58	23	6/4
9	Q6VU70	Apolipoprotein-3	23	8.71/20.7	7.88/24.25	24	3/8
9	BAH86593	farnesoic acid O-methyltransferase	60	5.86/31.1	7.88/24.25	23	6/4
10	P00630	Phospholipase A2	20	7.05/19.6	9.88/25.84	17	5/6
11	P55948	Metallothionein	20	8.07/7.2	7.07/15.44	37	2/9
11	P31824	Acyl-CoA-binding protein homolog	19	6.56/9.7	7.07/15.44	34	2/9
12	P55928	Potassium channel toxin alpha-KTx 7.2	21	9.24/4.4	7.45/15.21	77	2/13
12	O96669	Putative potassium channel blocker (Fragment)	20	8.68/5.7	7.07/15.44	31	2/13
12	Q10745	Defensin	21	8.70/4.8	7.07/15.44	58	2/13
12	P41965	4 kDa defensin	25	9.69/4.6	7.07/15.44	42	2/11
12	B8XH50	Amphipathic peptide Tx348	21	9.16/7.7	7.07/15.44	25	2/11
12	Q6JQN2	Peptide BmKn2	21	9.10/7.9	7.07/15.44	24	2/11
12	E4VP07	Venom antimicrobial peptide-6	21	9.10/7.9	7.07/15.44	24	2/11

Table S5. List of identified proteins in *B. ruderarius* venom.

Spot #	Access #	Identified protein	Score	Theoretical pI/Mw (kDa)	Observed pI/Mw (kDa)	Sequence coverage (%)	Matched/ unmatched peptides
1	CEF69244	Globin, structural domain and GPCR, 7TM domain-containing protein	40	9.42/69.3	5.55/136.11	14	8/8
1	XP_001602327	PREDICTED: DNA mismatch repair protein Mlh1	52	6.79/80.8	5.55/136.11	16	9/4
2	KPJ17530	Serine protease snake	60	9.02/38.7	6.99/56.53	20	9/5
2	P29190	Phosphoenolpyruvate carboxykinase [GTP]	31	6.86/70.2	6.99/56.53	11	5/2
3	Q622Z7	G protein-coupled receptor kinase 1	32	8.31/74.2	7.21/56.71	9	5/2
3	H9IWW7	Inactive peptidyl-prolyl cis-trans isomerase shutdown	33	5.84/49.6	7.21/56.71	13	4/3
3	CDS26201	t complex protein 11 protein 1	55	5.30/64.4	7.21/56.71	15	8/3
4	XP_011139073	PREDICTED: glutathione synthetase-like	52	8.03/54.9	5.54/42.25	15	6/1
4	KOC67432	Integrin-linked protein kinase	41	6.86/51	5.54/42.25	14	5/2
5	XP_003486583	Venom acid phosphatase Acph-1-like isoform X3	96	6.84/46.9	6.52/42.15	16	8/3
6	Q5BLY5	Venom acid phosphatase Acph-1	23	5.63/45.5	6.8/41.76	7	3/3
7	XP_013390249	PREDICTED: methylmalonic aciduria type A homolog	75	8.79/48.1	6.7/41.39	25	10/2
7	KHN81636	17-beta-hydroxysteroid dehydrogenase type 6	45	7.82/38.8	6.7/41.39	18	5/3
7	XP_011269785	PREDICT: KH domain-containing...signal trans.-associated pr3-like	42	8.85/48	6.7/41.39	13	5/2
8	P85841	Hyaluronidase 1 (Fragment)	50	8.75/45.2	6.95/41.97	18	6/4
9	KHJ42768	intermediate filament tail domain protein	57	6.37/66.3	7.17/40.91	16	9/1
9	XP_003486187	PREDICT: probable serine/threonine-protein kinase DDB_G0282963	48	9.71/46.1	7.17/40.91	17	7/3
9	KMQ86823	dna primase small subunit	42	7.56/49.3	7.17/40.91	16	7/3
10	XP_013294625	peptidase dimerization domain protein	62	6.04/48.3	8.51/41.61	20	6/0
10	CDJ84573	PAK-box P21-Rho-bind / Ser/thr protein kin.-related dom containing...	42	7.59/65.8	8.51/41.61	13	5/1
10	XP_001120785	PREDICT: zinc finger protein 704-like isoform X1	41	8.45/63.8	8.51/41.61	13	5/1
10	XP_012252555	PREDICT: uncharacterized aarF domain-containing protein kinase 1	61	9.09/60	8.51/41.61	17	7/2

11	XP_013091290	PREDICT: cysteine and histidine-rich protein 1-like	43	6.50/40.5	9.01/40.80	14	5/2
12	P22311	Puff II/9-1 protein	38	5.27/33	5.56/30.42	22	5/5
13	P14208	Arginine kinase	32	6.05/40.3	7.2/26.36	28	8/14
14	P00630	Phospholipase A2	22	7.05/19.6	6.47/28.76	18	3/7
14	P00357	Glyceraldehyde-3-phosphate dehydrogenase	36	6.53/35.9	6.63/28.19	19	5/5
14	P56839	Phosphoenolpyruvate phosphomutase	24	5.51/33	6.63/28.19	15	4/6
15	P00630	Phospholipase A2	19	7.05/19.6	7.23/31.07	10	2/3
15	Q5TXB2	Structure-specific endonuclease subunit SLX1 homolog	24	5.76/32	7.23/31.07	12	3/2
16	P14208	Arginine kinase	37	6.05/40.3	7.78/31.06	20	9/12
16	Q27775	Triosephosphate isomerase	24	6.66/28	7.78/31.06	17	3/5
17	XP_002409028	tyrosine kinase, putative	54	6.05/43.9	8.52/31.06	16	5/0
17	XP_004535104	PREDICTED: dehydrogenase/reductase SDR family member 11	43	8.72/28.1	8.52/31.06	19	4/1
17	CDJ81617	dephospho-CoA kinase	43	8.92/26.7	8.52/31.06	21	4/1
17	P00630	Phospholipase A2	17	7.05/19.6	8.52/31.06	7	2/3
18	XP_013395969	PREDICTED: cytochrome P450 2D14-like	44	6.10/24.4	6.47/26.41	27	5/6
18	XP_013409932	PREDICTED: WD repeat-containing protein 92-like, partial	45	6.64/25.6	6.47/26.41	20	4/3
18	KFM60472	Transposable element Tcb1 transposase, partial	41	7.68/23.6	6.47/26.41	20	5/2
18	P00630	Phospholipase A2	16	7.05/19.6	6.47/26.41	10	2/5
18	A8Y461	Enolase-phosphatase E1	18	5.38/28.2	6.47/26.41	6	2/4
19	Q7M4I3	Venom protease	33	8.85/27.6	7.17/25.96	22	4/3
20	Q61D43	Mediator of RNA polymerase II transcription subunit 18	33	9.15/26.1	8.20/25.97	23	7/14
20	XP_003386765	PREDICTED: glutathione S-transferase-like	43	6.23/23.2	8.20/25.97	36	7/9
20	XP_005190650	PREDICTED: glutaredoxin 3	74	4.83/23.5	8.20/25.97	38	6/2
21	P00630	Phospholipase A2	21	7.05/19.6	9.20/25.97	13	3/7
21	P00630	Phospholipase A2	24	7.05/19.6	9.20/25.97	12	3/2
22	AKS40350	glutathione S-transferase theta 1 [Chilo suppressalis]	47	8.85/26.6	9.39/29.43	26	6/4
23	P00630	Phospholipase A2	37	7.05/19.6	8.41/25.96	20	4/3
23	P10737	Venom allergen 5.02 (Fragment)	17	9.13/24.7	8.41/25.96	13	2/4
24	EFN83275	Inositol monophosphatase	63	5.42/28.8	7.18/25.90	21	6/2
25	XP_011298725	PREDICTED: FK506-binding protein 2 isoform X1	54	4.67/24.6	6.90/25.92	26	6/5
26	A8XHX1	Tetratricopeptide repeat protein 36 homolog	20	5.26/19.8	6.88/24.85	22	3/11
26	Q16981	Neuronal calcium sensor 1	20	4.78/22.2	6.88/24.85	21	3/8
27	AGB86884	proteasome subunit, partial	42	4.42/19.6	4.22/24.90	24	4/4
28	E7CLP0	Putative alpha-neurotoxin RjAa9 (Fragment)	26	8.15/7.6	6.48/21.42	19	2/3
29	P86403	Neurotoxin MeuNaTx-2	23	8.19/7.6	6.85/21.45	21	2/6
30	KMQ93222	protein phosphatase 11-like protein, partial	55	5.63/12	6.87/18.72	55	5/6
31	KMQ93222	protein phosphatase 11-like protein, partial	74	5.63/12	7.78/18.70	55	5/1

Table S6. List of identified proteins in *B. sylvorum* venom.

Spot #	Access #	Identified protein	Score	Theoretical pI/Mw (kDa)	Observed pI/Mw (kDa)	Sequence coverage (%)	Matched/unmatched peptides
1	CDJ88047	Dehydrogenase domain containing protein	42	6.08/48.3	8.1/63.38	10	4/7
1	XP_013391792	PREDICTED: uncharacterized protein LOC106159893	33	8.70/64	8.1/63.38	9	4/7
2	KPJ17530	Serine protease snake	30	9.02/38.7	7.27/56.08	9	3/7
2	XP_013081819	PREDICT: MAP kinase kinase kinase 1-like isoform X1	30	5.48/42.1	7.27/56.08	9	3/7
3	CAX82492	Malate dehydrogenase	31	7.59/42	5.64/45.78	12	3/8
4	XP_003486583	Venom acid phosphatase AcpH-1-like isoform X3	96	5.33/46.2	6.86/42.39	10	9/4
5	XP_003486583	PREDICTED: venom acid phosphatase AcpH-1-like isoform X3	86	6.84/46.9	7.52/42.64	18	9/15
6	P85841	Hyaluronidase 1 (Fragment)	55	8.75/45.2	8.06/42.37	10	3/5
7	EJW83419	hypothetical protein WUBG_05671	67	5.41/42.3	8.84/42.25	20	6/4
8	EGT37222	hypothetical protein CAEBREN_12699	50	6.65/40.2	5.33/30.08	20	6/3
9	P86699	Arginine kinase (Fragments)	19	7.74/25.4	6.66/27.01	6	2/12
10	XP_011873210	PREDICT: isochorismatase domain-containing pr. 2, mitochondrial-like	47	6.30/21.7	6.66/27.01	29	4/12
10	P86699	Arginine kinase (Fragments)	19	7.74/25.4	6.66/27.01	6	2/12
11	EFN72991	FAD synthetase	32	8.67/34.2	6.97/26.55	15	3/10
11	XP_011563998	PREDICTED: peroxisome biogenesis factor 10	33	8.23/30.8	6.97/26.55	17	3/10
12	Q7M4I3	Venom protease	33	8.85/27.6	7.45/26.02	25	3/6
13	KHN71023	Aspartyl protease inhibitor, partial	61	8.62/20.9	7.97/26.07	30	5/12
13	P30114	Glutathione S-transferase class-mu 28 kDa isozyme	17	6.56/24	7.97/26.07	13	2/18
13	P39673	Allergen Mag (Fragment)	23	6.92/39.6	7.97/26.07	11	3/12
14	Q1EIQ3	Peptidase 1	33	6.95/36.6	8.36/26.1	26	6/14
15	XP_011142752	PREDICTED: serine/threonine-protein kinase ICK isoform X2	65	9.34/66.2	9.89/25.84	20	7/11
15	P00630	Phospholipase A2	28	7.05/19.6	9.89/25.84	16	3/13
16	P00630	Phospholipase A2	31	7.05/19.6	7.04/24.78	25	5/10
17	P00630	Phospholipase A2	35	7.05/19.6	7.39/24.65	27	4/8
17	ACD01564	Dopa decarboxylase, partial	63	9.05/21.7	7.39/24.65	32	6/4
17	P00630	Phospholipase A2	35	7.05/19.6	7.39/24.65	31	5/10
18	P46419	Glutathione S-transferase	20	6.32/25.8	7.88/24.25	21	3/7
19	P00630	Phospholipase A2	21	7.05/19.6	8.34/24.77	15	3/6
19	XP_011564135	PREDICTED: transcription factor Sox-14	52	9.94/25.5	8.34/24.77	35	6/2
20	D2Y2Q2	Kunitz-type serine protease inhibitor hainantoxin-XI-13	27	9.36/10.1	8.21/22.04	36	3/8
20	P00630	Phospholipase A2	20	7.05/19.6	8.21/22.04	9	3/8
21	Q5MGE6	Defense protein 3	22	5.75/25	6.8/22.67	22	3/8
22	XP_011666262	PREDICTED: ankyrin-1-like	50	5.94/33	7.02/21.36	34	7/6
23	Q3YAU5	Phospholipase A2 large subunit (Fragment)	18	7.46/11.9	9.89/22.02	29	2/8
24	Q8T6C4	Thioredoxin peroxidase	44	5.78/21.7	4.94/20.63	41	5/8
25	Q1EIQ3	Peptidase 1	34	6.95/36.6	8.74/26.21	26	6/12
26	Q9NH49	Arginine kinase	35	6.19/40.6	9.03/26.14	23	6/7
27	KII66870	Serine/threonine-protein phosphatase 2B catalytic subunit y isoform	42	9.67/16.4	8.38/23.15	42	6/11

28	P51898	NADH-ubiquinone oxidoreductase chain 4 (Fragment)	31	8.92/25.1	8.51/23.95	24	4/7
29	KFM62790	Endoribonuclease Dicer, partial	40	6.32/20.8	5.94/18.19	29	5/5
30	P00630	Phospholipase A2	42	7.05/19.6	7.98/34	40	5/13
31	D2Y2Q2	Kunitz-type serine protease inhibitor hainantoxin-XI-13	67	9.36/10.1	9.89/15.37	27	3/4

Table S7. List of identified proteins in *B. zonatus* venom.

Spot #	Access #	Identified protein	Score	Theoretical pI/Mw (kDa)	Observed pI/Mw (kDa)	Sequence coverage (%)	Matched/unmatched peptides
1	A8XFM8	Lon protease homolog, mitochondrial	26	6.49/107.1	6.26/151.29	11	8/6
2	EFN76202	Arginyl-tRNA synthetase, cytoplasmic	44	6.85/78.8	7.26/49.41	9	6/0
2	XP_011050254	PREDICTED: putative glycerol kinase 5 isoform X3	55	8.71/52.6	7.26/49.41	14	6/0
2	XP_012150740	PREDICTED: zinc finger protein 37 homolog isoform X14	42	6.15/55	7.26/49.41	11	5/1
2	CDW54939	acyl coenzyme A dehydrogenase, C 4 to	42	8.38/46.8	7.26/49.41	13	5/1
2	XP_011699966	PREDICTED: catalase isoform X2	47	8.11/55.7	7.26/49.41	8	5/1
3	Q17GM7	Probable citrate synthase 1, mitochondrial	30	8.91/51.8	7.47/49.21	14	5/4
3	XP_012216101	PREDICTED: ribosomal RNA-processing protein 8	60	10.03/55.9	7.47/49.21	17	8/3
4	P85841	Hyaluronidase 1 (Fragment)	55	8.75/45.2	7.72/49.01	19	6/4
5	XP_003486583	Venom acid phosphatase AcpH-1-like isoform X3	78	6.84/46.9	6.95/33.79	15	3/5
6	Q6R7M4	Methyl farnesoate epoxidase	31	8.78/56.9	7.92/36.36	15	8/6
7	XP_011647527	PREDICTED: caspase-1-like	40	5.48/30.6	5.52/29.58	26	5/6
7	Q61UX1	Nascent polypeptide-associated complex subunit alpha	33	5.01/22	5.52/29.58	34	4/7
7	XP_002433504	protease m1 zinc metalloprotease, putative	41	5.50/26.3	5.52/29.58	24	4/4
7	O16127	Tropomyosin A (Fragment)	20	4.60/32.2	5.52/29.58	10	3/5
8	XP_008192565	PREDICTED: 39S ribosomal protein L28, mitochondrial	45	9.19/31.9	7.97/26.07	30	6/6
8	KKA73268	tRNA synthetase, partial	53	10.45/27.4	7.97/26.07	31	6/4
9	Q7M4I3	Venom protease	28	8.85/27.6	9.89/25.84	17	3/4
10	P86699	Arginine kinase (Fragments)	38	7.74/25.4	8.36/26.1	33	8/13
11	P00630	Phospholipase A2	20	7.05/19.6	9.89/25.84	13	3/8
12	M1J7U4	Putative sodium channel alpha-toxin Acra5	28	7.64/8.1	7.07/15.44	46	3/10
12	KFB53291	Methionine--tRNA ligase	59	9.34/9.7	7.07/15.44	53	5/8
12	Q1HPL8	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 10	31	5.93/19.2	7.07/15.44	27	4/9
12	P56219	Potassium channel toxin alpha-KTx 4.2	19	8.94/6.7	7.07/15.44	31	2/11
13	CDQ08235	Protein Bm12574, partial	72	4.78/6.9	7.45/15.21	90	6/6
13	P00038	Cytochrome c	23	9.50/12	7.45/15.21	33	3/9
13	Q8T3S7	Kunitz-type serine protease inhibitor U1-aranetoxin-Av1a	22	9.11/9.6	7.45/15.21	30	2/4
14	KFM80435	Coiled-coil-helix-coiled-coil-helix domain-containing protein 7, partial	50	8.84/12.5	9.89/15.37	44	4/2
14	XP_014253312	PREDICTED: leucine-rich repeat-containing protein 28 isoform X3	79	9.11/31.1	9.89/15.37	29	7/2