

Supplementary Materials: Investigation of Peptide Toxins Diversity in Ribbon Worms (Nemertea) Using Transcriptomic Approach

Anna E. Vlasenko, Vasiliy G. Kuznetsov and Timur Yu. Magarlamov*

Table S1. Toxin transcripts of *Carinoma hamanako*.

Protein family	Transcript ID	Uniprot accession	Description	e-value	Expression, TPM
Neurotoxins					
Neurotoxin 20 family	Gene.29146_r_16340_g.29146_m.29146	TXCA_CAEEX	U3-aranetoxin-Ce1a OS=Caerostris extrusa OX=172846 PE=2 SV=1	7.4E-06	39.36
Pore-forming toxins					
Actinoporin family. Conoidea subfamily	Gene.23587_r_11081_g.23587_m.23587	ACTP_CONCN	Conoporin-Cn1 OS=Conus consors OX=101297 PE=1 SV=1	5.1E-09	7.21
Enzymes					
5'- nucleotidase family	Gene.35055_r_23242_g.35055_m.35055	V5NTD_NAJAT	Snake venom 5'-nucleotidase (Fragment) OS=Naja atra OX=8656 PE=1 SV=1	1.5E-46	2.84
Arthropod phospholipase D family. Class II subfamily	Gene.22051_r_9780_g.22051_m.22051	B1R2_LOXSN	Dermonecrotic toxin LspiSicTox-betaIE1ii (Fragment) OS=Loxosceles spinulosa OX=571532 PE=2 SV=1	1.2E-40	45.45
Dnase II family	Gene.12683_r_4081_g.12683_m.12683	DNA2_ACAPL	Plancitoxin-1 OS=Acanthaster planci OX=133434 PE=1 SV=1	1.8E-74	10.12
Nucleotide pyrophosphatase/phosphodiesterase family	Gene.26217_r_13397_g.26217_m.26217	PDE_MACLB	Venom phosphodiesterase OS=Macrovipera lebetina OX=8709 PE=1 SV=1	7.6E-36	4.58
Phospholipase A2 family. Group I subfamily. D49 sub-subfamily	Gene.30711_r_18012_g.30711_m.30711	PA2A_BUNMU	Acidic phospholipase A2 OS=Bungarus multicinctus OX=8616 PE=1 SV=2	1.1E-24	7.95
Phospholipase A2 family. Group III subfamily	Gene.30102_r_17363_g.30102_m.30102	PA23_HELSU	Phospholipase A2 isozymes PA3A/PA3B/PA5 OS=Heloderma	7.5E-30	144.13

suspectum OX=8554 PE=1 SV=3					
Phospholipase B-like family	Gene.12079_r_3800_g.12079_m.12079	PLB_DRYCN	Phospholipase-B 81 OS=Drysdalia coronoides OX=66186 PE=1 SV=1	0	11.45
Venom metallo-proteinase (M12B) family. P-III subfamily. P-iiia sub-subfamily	Gene.13186_r_4338_g.13186_m.13186	VM3K_NAJKA	Hemorrhagic metalloproteinase-disintegrin-like kaouthiagin OS=Naja kaouthia OX=8649 PE=1 SV=1	1.4E-29	83.90
Proteinase inhibitors					
Venom Kunitz-type family	Gene.32798_r_20368_g.32798_m.32798	VKT2_BITGA	Kunitz-type serine protease inhibitor bitisilin-2 OS=Bitis gabonica OX=8694 PE=1 SV=1	5.9E-20	38.81
Ion channel inhibitors					
CRISP family	Gene.16102_r_5875_g.16102_m.16102	CRVP_LATSE	Cysteine-rich venom protein latisemin OS=Laticauda semifasciata OX=8631 PE=2 SV=1	1.3E-26	12.67
	Gene.11853_r_3703_g.11853_m.11853	CRVP_HOPST	Cysteine-rich venom protein pseudochetoxin-like OS=Hoplocephalus stephensii OX=196418 PE=2 SV=1	3.6E-29	9.52
	Gene.9077_r_2517_g.9077_m.9077	CRVP_LEIMD	Cysteine-rich venom protein LEI1 (Fragment) OS=Leioheterodon madagascariensis OX=46577 PE=1 SV=1	2.5E-30	9.87
	Gene.21131_r_9101_g.21131_m.21131	CRVP_TRILK	CRISP/Allergen/PR-1 OS=Tritame loki OX=1295018 PE=1 SV=1	1.4E-33	464.73
	Gene.22696_r_10292_g.22696_m.22696	CRVP2_NAJKA	Cysteine-rich venom protein kaouthin-2 OS=Naja kaouthia OX=8649 PE=1 SV=2	2.7E-40	10.31
	Gene.26019_r_13221_g.26019_m.26019	CRVP_TELDH	Cysteine-rich venom protein TEL1 (Fragment) OS=Telescopus dhara OX=338837 PE=2 SV=1	1.6E-28	6.49
CRISP family. Venom allergen 5-like subfamily	Gene.44110_r_37299_g.44110_m.44110	VA543_SCODE	Scoloptoxin SSD43 OS=Scolopendra dehaani OX=2609776 PE=1 SV=1	2.4E-12	20.57
	Gene.33252_r_20934_g.33252_m.33252	VA5_VESVI	Venom allergen 5 OS=Urospora vidua OX=30215 PE=1 SV=1	2.4E-27	6.97

Scoloptoxin-05 family	Gene.14011_r_4742_g.14011_m.14011	TX51A_SCOMO	U-scoloptoxin(05)-Sm1a OS=Scolopendra morsi-tans OX=943129 PE=2 SV=1	8.6E-07	6.63
Scoloptoxin-11 family	Gene.38036_r_27351_g.38036_m.38036	TX14B_SCODE	Scoloptoxin SSD20 (Frag-ment) OS=Scolopendra dehaani OX=2609776 PE=1 SV=1	2.4E-27	7.46
Venom Kunitz-type family. Sea anemone type 2 potassium channel toxin subfamily	Gene.48512_r_45419_g.48512_m.48512	VKT1A_ANEVI	U-actitoxin-Avd3f OS=Anemonia viridis OX=51769 PE=3 SV=15,	1E-09	57.06
	Gene.37015_r_25865_g.37015_m.37015	VKTB_ANEVI	U-actitoxin-Avd3n OS=Anemonia viridis OX=51769 PE=3 SV=1	3.5E-14	20.64
	Gene.35176_r_23397_g.35176_m.35176	VKT5_ANEVI	U-actitoxin-Avd3h OS=Anemonia viridis OX=51769 PE=3 SV=14,	9E-20	7.23
Other toxins candidates					
AVIT (prokineticin) family	Gene.32199_r_19665_g.32199_m.32199	BO8_BOMOR	Prokineticin Bo8 OS=Bom-bina orientalis OX=8346 PE=1 SV=1	6.5E-07	76.69
EGF-like, Sushi, TSP type-1, LDL-receptor class A	Gene.17457_r_6644_g.17457_m.17457	CTX_SEPES	SE-cephalotoxin OS=Sepia esculenta OX=31210 PE=1 SV=1	1.1E-07	16.51
Elevenin - like	Gene.38214_r_27621_g.38214_m.38214	CELE_CONV	Elevenin-Vc1 OS=Conus victoriae OX=319920 PE=1 SV=1	1.3E-06	11.90
Glycoprotein hormones subunit alpha family	Gene.21463_r_9336_g.21463_m.21463	CTHA2_CONV C	Thyrostimulin alpha-2 subunit OS=Conus victo-riae OX=319920 PE=1 SV=1	4.9E-31	9.14
Glycoprotein hormones subunit beta family	Gene.35802_r_24219_g.35802_m.35802	CTHB5_CONV	Thyrostimulin beta-5 sub-unit OS=Conus victoriae OX=319920 PE=2 SV=1	3E-17	3.73
IGFBP N-termi-nal, Kazal-like, Ig-like C2-type	Gene.20580_r_8675_g.20580_m.20580	IGFBP_CUPSA	Insulin-like growth factor-binding protein-related protein 1 OS=Cupiennius salei OX=6928 PE=2 SV=1	4.4E-68	42.79
TCTP family	Gene.14168_r_4820_g.14168_m.14168	TCTP_BRABE	Translationally-controlled tumor protein homolog OS=Branchiostoma belch-eri OX=7741 PE=2 SV=1	2.2E-19	7.96
	Gene.16043_r_5846_g.16043_m.16043	TCTP_BRAOL	Translationally-controlled tumor protein homolog OS=Brassica oleracea OX=3712 GN=TCTP PE=2 SV=1	7.1E-23	325.64

Table S2. Toxin transcripts of *Cephalothrix hongkongiensis*. Unique toxins families are shown in bold.

Protein family	Transcript ID	Uniprot accession	Description	E-value	Expression, TPM
Neurotoxins					
Neurotoxin 20 family	Gene.34245_c_hong_26879_g.34245_m.34245	TXCA_CAEEX	U3-aranetoxin-Ce1a OS=Caerostris extrusa OX=172846 PE=2 SV=1	4E-06	199.67
Pore-forming toxins					
Actinoporin family. Conoidea subfamily	Gene.11883_c_hong_4214_g.11883_m.11883	ACTP1_TERAN	Tereporin-Ca1 (Fragment) OS=Ter-ebra anilis OX=553697 PE=2 SV=1	1.8E-25	16.88
Actinoporin family. Sea anemone subfamily	Gene.26045_c_hong_15774_g.26045_m.26045	ACTP2_PHYSE	DELTA-alicitoxin-Pse1b OS=Phyllo-discus semoni OX=163701 PE=2 SV=1	4.9E-13	36.99
	Gene.35099_c_hong_28188_g.35099_m.35099	ACTP1_SAGRO	DELTA-sagatoxin-Srs1a OS=Sagartia rosea OX=396345 PE=1 SV=1	8.5E-19	1.96
MACPF domain	Gene.18196_c_hong_8305_g.18196_m.18196	TX60A_ACTVL	DELTA-thalatoxin-Avl2a OS=ActinERIA villosa OX=227975 PE=1 SV=1	9E-59	16.88
	Gene.5492_c_hong_1368_g.5492_m.5492	TX60B_PHYSE	DELTA-alicitoxin-Pse2b OS=Phyllo-discus semoni OX=163701 PE=1 SV=21,2	1E-65	14.88
	Gene.6822_c_hong_1836_g.6822_m.6822	TX60A_PHYSE	DELTA-alicitoxin-Pse2a OS=Phyllo-discus semoni OX=163701 PE=1 SV=1	7.5E-77	113.04
Enzymes					
5'- nucleotidase family	Gene.8680_c_hong_2612_g.8680_m.8680	V5NTD_NAJAT	Snake venom 5'-nucleotidase (Fragment) OS=Naja atra OX=8656 PE=1 SV=1	8E-153	5.61
Arthropod phospholipase D family. Class II subfamily	Gene.31998_c_hong_23588_g.31998_m.31998	A1LB2_LOXAR	Dermonecrotic toxin larsictox-alphaib2bii (Fragment) OS=Loxosceles arizonica OX=196454 PE=2 SV=1	6.9E-26	5.62

	Gene.18047_c_hong_8189_g.18047_m.18047	A1I1_LOXSP	Dermonecrotic toxin Ispasictox-alpha2i (Fragment) OS=Loxosceles spadicca OX=571530 PE=2 SV=1	3.9E-47	14.08
Dnase II family	Gene.10361_c_hong_3406_g.10361_m.10361	DNA2_ACAPL	Plancitoxin-1 OS=Acanthaster planci OX=133434 PE=1 SV=1	2.4E-71	3.65
Flavin mono-amine oxidase family. FIG1 subfamily	Gene.29350_c_hong_19924_g.29350_m.29350	OXLA_CROAT	L-amino-acid oxidase apoxin-1 OS=Crotalus atrox OX=8730 PE=1 SV=2	2.9E-20	3.10
Glycosyl hydrolase 56 family	Gene.17971_c_hong_8131_g.17971_m.17971	HYAL1_MESMA	Hyaluronidase-1 OS=Mesobuthus martensii OX=34649 PE=1 SV=2	1.1E-54	5.89
Nucleotide pyrophosphatase/phosphodiesterase family	Gene.11880_c_hong_4213_g.11880_m.11880	PDE_CRODO	Venom phosphodiesterase cdcpde OS=Crotalus durissus collilineatus OX=221569 PE=1 SV=1	2.1E-66	3.74
	Gene.27311_c_hong_17262_g.27311_m.27311	PDE1_CROAD	Venom phosphodiesterase 1 OS=Crotalus adamanteus OX=8729 PE=1 SV=2	1.7E-66	3.62
Phospholipase A2 family	Gene.24117_c_hong_13701_g.24117_m.24117	PA21_SCODE	Phospholipase A2 SSD387 OS=Scolopendra dehaani OX=2609776 PE=1 SV=1	1.8E-25	5.78
Phospholipase A2 family. Group III subfamily	Gene.17905_c_hong_8085_g.17905_m.17905	PA23_HELSU	Phospholipase A2 isozymes PA3A/PA3B/PA5 OS=Heloderma suspectum OX=8554 PE=1 SV=3	1.4E-20	39.35
	Gene.16417_c_hong_7078_g.16417_m.16417	PA2A2_HELSU	Acidic phospholipase A2 PA4 OS=Heloderma suspectum OX=8554 PE=1 SV=2	3.2E-36	8.47

Venom metalloproteinase (M12B) family. P-III subfamily. P-iiia sub-subfamily	Gene.47013_c_hong_50313_g.47013_m.47013	VM3_CERRY	Zinc metalloproteinase-disintegrin-like OS=Cerberus rynchops OX=46267 PE=1 SV=1	6.6E-14	6.06
Venom metalloproteinase (M12B) family. P-II subfamily. P-iiid sub-subfamily	Gene.32433_c_hong_24210_g.32433_m.32433	VM2SA_GLOSA	Zinc metalloproteinase/disintegrin OS=Gloydus saxatilis OX=92067 PE=2 SV=1	1.4E-11	3.58
Ion channel inhibitor activity					
CRISP family	Gene.21111_c_hong_10759_g.21111_m.21111	CRVP_OXYMI	Cysteine-rich venom protein pseudochetoxin-like OS=Oxyuranus microlepidotus OX=111177 PE=2 SV=1	6.4E-30	4.19
	Gene.749_c_hong_89_g.749_m.749	CRVP_HOPST	Cysteine-rich venom protein pseudochetoxin-like OS=Hoplocephalus stephensii OX=196418 PE=2 SV=1	2.7E-30	27.92
	Gene.22720_c_hong_12307_g.22720_m.22720	CRVP_AUSSU	Cysteine-rich venom protein OS=Austrelaps superbis OX=29156 PE=2 SV=1	9.2E-36	3.07
	Gene.6717_c_hong_1800_g.6717_m.6717	CRVP_ERYPO	Cysteine-rich venom protein LIO1 (Fragment) OS=Erythrolamprus poecilogyrus OX=338838 PE=2 SV=1	7.4E-37	4.53
	Gene.12301_c_hong_4442_g.12301_m.12301	MR30_CONMR	Cysteine-rich venom protein Mr30 OS=Conus marmoreus OX=42752 PE=1 SV=1	2.1E-39	5.22
CRISP family. Venom allergen 5-like subfamily	Gene.38009_c_hong_33066_g.38009_m.38009	VA51_VESCR	Venom allergen 5.01 OS=Vespa crabro OX=7445 PE=1 SV=1	7.5E-15	1.45

	Gene.15844_c_hong_6675_g.15844_m.15844	VA576_SCODE	Scoloptoxin SSD976 OS=Scolopendra dehaani OX=2609776 PE=1 SV=1	3.2E-25	6.48
Scoloptoxin-05 family	Gene.29823_c_hong_20580_g.29823_m.29823	TX51A_ETHRU	U-scoloptoxin(05)-Er1a OS=Eth-mostigmus rubripes OX=62613 PE=2 SV=1	1E-06	2.87
Sea anemone type 5 potassium channel toxin family	Gene.30277_c_hong_21219_g.30277_m.30277	KV53_BUNCI	Kappa-actitoxin-Bcs4a OS=Bunodosoma caesarum OX=31165 PE=1 SV=1	2.6E-19	9.35
Hemostasis impairing toxin					
Snaclec family	Gene.43733_c_hong_43800_g.43733_m.43733	SLUA_DEIAC	Snaclec agkisacutacin subunit A OS=Deinagkistrodon acutus OX=36307 PE=1 SV=2	1.7E-09	4.39
	Gene.48482_c_hong_53305_g.48482_m.48482	VA5_VESPE	Venom allergen 5 OS=Vespula pennsylvanica OX=30213 PE=1 SV=1	5E-10	3.00
	Gene.7929_c_hong_2279_g.7929_m.7929	SLLC2_DABSI	Snaclec coagulation factor X-activating enzyme light chain 2 OS=Daboia siamensis OX=343250 GN=LC2 PE=1 SV=1	8.1E-09	14.65
SNTX/VTX toxin family	Gene.32124_c_hong_23751_g.32124_m.32124	CTXB_SCOPL	Cytolytic toxin-beta OS=Scorpaena plumieri OX=274700 PE=1 SV=1	4.5E-19	1.96
	Gene.938_c_hong_118_g.938_m.938	CTXA_SCOPL	Cytolytic toxin-alpha OS=Scorpaena plumieri OX=274700 PE=1 SV=1	4.1E-52	27.73
Other toxins candidates					
Conotoxin-like	Gene.35778_c_hong_29319_g.35778_m.35778	CXE3_CONIM	Conotoxin Im14.3 OS=Conus imperialis OX=35631 PE=1 SV=1	1E-07	2.98
EGF-like, Sushi, TSP type-1,	Gene.12659_c_hong_4652_g.12659_m.4652	CTX_SEPES	SE-cephalotoxin OS=Sepia esculenta	4.7E-73	8.01

LDL-receptor class A	g.12659_m.12659		OX=31210 PE=1 SV=1		
Elevenin-like	Gene.46986_c_hong_50253_g.46986_m.46986	CELE_CONVC	Elevenin-Vc1 OS=Conus victoriae OX=319920 PE=1 SV=1	2E-07	5.19
IGFBP N-terminal domain, Kazal-like, Ig-like C2-type	Gene.20111_c_hong_9872_g.20111_m.20111	IGFBP_CUPSA	Insulin-like growth factor-binding protein-related protein 1 OS=Cupiennius salei OX=6928 PE=2 SV=1	4.6E-62	14.00
Vasopressin/oxytocin family	Gene.40543_c_hong_37563_g.40543_m.40543	CESS2_CONMO	Conopresin/conophysin, isoform 2 (Fragment) OS=Conus monile OX=351660 PE=2 SV=1	2.6E-24	3.22

Table S3. Toxin transcripts of *Cephalothrix cf. simula*. Unique toxins families are shown in bold. The expression might be quantified using Illumina reads only. No expression values were obtained for toxins transcripts from MinIon Oxford nanopore sequencing; they were assigned as NA.

Protein family	Transcript ID	Uniprot accession	Description	E-value	Expression, TPM
Neurotoxins					
Neurotoxin 20 family	Gene.485063_csim_min-ion_347459_g.485063_m.485063	TXCA_CAEEX	U3-aranetoxin-Ce1a OS=Caerostris extrusa OX=172846 PE=2 SV=1	4E-06	30.77
Pore-forming toxins					
Actinoporin family. Conoidea subfamily	Gene.35246_csim_min-ion_9736_g.35246_m.35246	ACTP1_TERSU	Tereporin-Ts1 (Fragment) OS=Ter-ebr subulata OX=89435 PE=2 SV=1	2.9E-13	NA
	Gene.335613_csim_min-ion_180378_g.335613_m.335613	ACTP1_TERAN	Tereporin-Ca1 (Fragment) OS=Ter-ebr anilis OX=553697 PE=2 SV=1	2.9E-26	NA
Actinoporin family. Sea anemone subfamily	Gene.474824_csim_min-ion_331394_g.474824_m.474824	ACTP5_ACTEQ	DELTA-actitoxin-Aeq1b OS=Actinia equina OX=6106 PE=2 SV=1	1.4E-09	NA
	Gene.407909_csim_min-ion_249004_g	ACTP2_PHYSE	DELTA-alicitoxin-Pse1b OS=Phyllo-discus semoni	2E-15	NA

	.407909_m.407909		OX=163701 PE=2 SV=1		
MACPF domain	Gene.301043 _csim_min-ion_153953_g .301043_m.301043	TX60A_ACTVL	DELTA-thalatoxin-Avl2a OS=Actinervilla villosa OX=227975 PE=1 SV=1	4.6E-66	31.85
	Gene.273396 _csim_min-ion_135569_g .273396_m.273396	TX60A_PHYSE	DELTA-alicitoxin-Pse2a OS=Phyllo-discus semoni OX=163701 PE=1 SV=1	4.3E-77	115.63
	Gene.293181 _csim_min-ion_148573_g .293181_m.293181	TX60B_PHYSE	DELTA-alicitoxin-Pse2b OS=Phyllo-discus semoni OX=163701 PE=1 SV=2	1.2E-80	0.58
Enzymes					
5'- nucleotidase family	Gene.197718 _csim_min-ion_86712_g .197718_m.197718	V5NTD_GLOBR	Snake venom 5'-nucleotidase OS=Gloydus brevicaudus OX=259325 PE=2 SV=1	3.2E-22	NA
Arthropod phospholipase D family. Class II subfamily	Gene.464893 _csim_min-ion_317229_g .464893_m.464893	A21_LOXVA	Dermonecrotic toxin lvsictox-alpha1i1 (Fragment) OS=Loxosceles variegata OX=571533 PE=2 SV=1	7.1E-11	NA
	Gene.510941 _csim_min-ion_397287_g .510941_m.510941	B1R_LOXAS	Dermonecrotic toxin lfsictox-beta1e1 (Fragment) OS=Loxosceles aff. Spinulosa (strain GJB-2008) OX=575951 PE=2 SV=1	8.6E-12	NA
	Gene.403668 _csim_min-ion_244462_g .403668_m.403668	A1O_LOXGA	Dermonecrotic toxin lgsictox-alpha1c1 OS=Loxosceles gaucho OX=58216 PE=1 SV=1	1.5E-14	NA
	Gene.381627 _csim_min-ion_221329_g .381627_m.381627	B1H2_LOXIN	Dermonecrotic toxin lisictox-beta1a1ii OS=Loxosceles intermedia OX=58218 PE=2 SV=1	4.7E-15	NA

	Gene.372490 _csim_min- ion_212540_g .372490_m.37 2490	A1OB3_LOXVA	Dermonecrotic toxin lvsictox-al- phaic1biii (Frag- ment) OS=Loxosce- les variegata OX=571533 PE=2 SV=1	4.2E-20	NA
	Gene.423589 _csim_min- ion_266101_g .423589_m.42 3589	A1IA3_LOXIN	Dermonecrotic toxin lisictox-al- phaia2aiii (Frag- ment) OS=Loxosce- les intermedia OX=58218 PE=2 SV=1	8.6E-21	NA
	Gene.380591 _csim_min- ion_220301_g .380591_m.38 0591	A411_LOXHI	Dermonecrotic toxin lhsictox-al- phaiv1i (Fragment) OS=Loxosceles hir- suta OX=571525 PE=2 SV=1	1.6E-21	NA
	Gene.503547 _csim_min- ion_382170_g .503547_m.50 3547	B1H_LOXLA	Dermonecrotic toxin llsictox-be- taia1 OS=Loxosce- les laeta OX=58217 PE=1 SV=1	1.7E-20	NA
	Gene.290660 _csim_min- ion_146874_g .290660_m.29 0660	A1I1_LOXSP	Dermonecrotic toxin lspasictox-al- phaia2i (Fragment) OS=Loxosceles spa- dicea OX=571530 PE=2 SV=1	4E-47	NA
	Gene.387485 _csim_min- ion_227187_g .387485_m.38 7485	A1IB1_LOXIN	Dermonecrotic toxin lisictox-al- phaia2bi OS=Lox- osceles intermedia OX=58218 PE=2 SV=1	5.4E-54	NA
Dnase II family	Gene.354317 _csim_min- ion_196206_g .354317_m.35 4317	DNA2_ACAPL	Plancitoxin-1 OS=Acanthaster planci OX=133434 PE=1 SV=1	1.3E-71	2.96
Flavin mono- amine oxidase family. FIG1 subfamily	Gene.138452 _csim_min- ion_54012_g .138452_m.13 8452	OXLA_MICMP	L-amino acid oxi- dase OS=Micrurus mipartitus OX=430902 PE=1 SV=1	2.3E-14	NA
Glycosyl hydro- lase 56 family	Gene.408049 _csim_min- ion_249149_g	HUGA_APIME	Hyaluronidase OS=Apis mellifera OX=7460 PE=1 SV=1	3.1E-18	NA

	.408049_m.408049				
	Gene.399637_csim_min-ion_239919_g.399637_m.399637	HYAL_LOXIN	Hyaluronidase OS=Loxosceles intermedia OX=58218 PE=2 SV=1	7E-23	NA
	Gene.342583_csim_min-ion_186216_g.342583_m.342583	HYAL1_MESMA	Hyaluronidase-1 OS=Mesobuthus martensii OX=34649 PE=1 SV=2	4.7E-51	NA
Nucleotide pyrophosphatase/phosphodiesterase family	Gene.10925_csim_min-ion_2435_g.10925_m.10925	PDE_MACLB	Venom phosphodiesterase OS=Macrovipera lebetina OX=8709 PE=1 SV=1	3.2E-60	0.45
Peptidase S1 family. Snake venom subfamily	Gene.450589_csim_min-ion_298071_g.450589_m.450589	VSPPA_GLOBR	Venom plasminogen activator Haly-PA OS=Gloydus brevicaudus OX=259325 PE=1 SV=2	2.5E-16	NA
Phospholipase A2 family	Gene.437846_csim_min-ion_282313_g.437846_m.437846	PA2_CONGI	Phospholipase A2 A2-actitoxin-Cgg2a OS=Condylactis gigantea OX=47073 PE=1 SV=1	2.5E-13	NA
	Gene.441169_csim_min-ion_286288_g.441169_m.441169	PA21_SCODE	Phospholipase A2 SSD387 OS=Scolopendra dehaani OX=2609776 PE=1 SV=1	3.9E-28	35.91
Phospholipase A2 family. Group I subfamily. D49 sub-subfamily	Gene.524403_csim_min-ion_430111_g.524403_m.524403	PA2A2_PSETE	Acidic phospholipase A2 2 OS=Pseudonaja textilis OX=8673 PE=1 SV=1	8E-07	NA
	Gene.518466_csim_min-ion_414418_g.518466_m.518466	PA2B2_BUNCE	Basic phospholipase A2 beta-bungarotoxin A2 chain OS=Bungarus caeruleus OX=132961 PE=2 SV=1	3E-08	NA
	Gene.466258_csim_min-ion_319116_g.466258_m.466258	PA2A1_PSETE	Acidic phospholipase A2 1 OS=Pseudonaja textilis OX=8673 PE=1 SV=1	2.9E-09	NA

Phospholipase A2 family. Group III subfamily	Gene.436441_csim_min-ion_280594_g.436441_m.436441	PA23_HELSU	Phospholipase A2 isozymes PA3A/PA3B/PA5 OS=Heloderma suspectum OX=8554 PE=1 SV=3	8.4E-30	2.50
Phospholipase B-like family	Gene.90104_csim_min-ion_31095_g.90104_m.90104	PLB_DRYCN	Phospholipase-B 81 OS=Drysdalia coronoides OX=66186 PE=1 SV=1	5.3E-170	42.77
Venom metalloproteinase (M12B) family. P-III subfamily. P-iiiia sub-subfamily	Gene.518063_csim_min-ion_413463_g.518063_m.518063	VM3A_NAJAT	Zinc metalloproteinase-disintegrin-like atrase-A OS=Naja atra OX=8656 PE=2 SV=1	9.5E-38	1.11
Proteinase inhibitors					
Natriuretic peptide family	Gene.299081_csim_min-ion_152562_g.299081_m.299081	SVMII1_CERCE	Snake venom metalloprotease inhibitor 02A10 OS=Cerastes cerastes OX=8697 GN=Svmpi-Cce12 PE=1 SV=1	5E-07	226.81
Venom Kunitz-type family	Gene.217819_csim_min-ion_99052_g.217819_m.217819	VKT_ERIMA	Kunitz-type serine protease inhibitor OS=Eristicophis macmahoni OX=110227 PE=1 SV=1	5E-06	NA
	Gene.217316_csim_min-ion_98765_g.217316_m.217316	VKTCL_OPHHA	Kunitz-type serine protease inhibitor OS=Ophiophagus hannah OX=8665 PE=1 SV=2	2.4E-09	2.95
	Gene.4163_csim_min-ion_791_g.4163_m.4163	VKT2_BITGA	Kunitz-type serine protease inhibitor bitisilin-2 OS=Bitis gabonica OX=8694 PE=1 SV=1	3.8E-19	1.14
Venom Kunitz-type family. 03 (sub-Kunitz) subfamily	Gene.520922_csim_min-ion_420428_g.520922_m.520922	VKT76_CYRHA	Kunitz-type serine protease inhibitor HNTX-0109076 (Fragment) OS=Cyriopagopus hainanus OX=209901 PE=2 SV=1	1.2E-12	0.15

Venom Kunitz-type family. Sea anemone type 2 potassium channel toxin subfamily	Gene.133532 _csim_min-ion_51501_g.133532_m.133532	VKT1_ANTAF	PI-actitoxin-Axm2a OS=Anthopleura aff. Xanthogrammica OX=152178 PE=1 SV=1	2E-07	NA
Ion channel inhibitor activity					
CRISP family	Gene.212790 _csim_min-ion_95926_g.212790_m.212790	CRVP_LEIMD	Cysteine-rich venom protein LEI1 (Fragment) OS=Leioheterodon mada-gascariensis OX=46577 PE=1 SV=1	5.3E-09	NA
	Gene.430137 _csim_min-ion_273348_g.430137_m.430137	VA3_DINQU	Venom allergen 3 homolog OS=Dinoponera quadriceps OX=609295 PE=2 SV=1	1E-08	NA
	Gene.405636 _csim_min-ion_246603_g.405636_m.405636	CRVP_DEMVE	Cysteine-rich venom protein OS=Demansia vestigiata OX=412038 PE=2 SV=1	1.5E-12	NA
	Gene.260819 _csim_min-ion_127234_g.260819_m.260819	CRVP_PSETE	Cysteine-rich venom protein pseudochetoxin-like OS=Pseudonaja textilis OX=8673 PE=1 SV=1	1.7E-12	NA
	Gene.435671 _csim_min-ion_279641_g.435671_m.435671	CRVP_TRILK	CRISP/Allergen/PR-1 OS=Tritame loki OX=1295018 PE=1 SV=1	8.4E-15	NA
	Gene.15278_csim_min-ion_3622_g.15278_m.15278	CRVP_DRYCN	Cysteine-rich venom protein OS=Drysdalia coronoides OX=66186 PE=1 SV=1	5E-19	NA
	Gene.527762 _csim_min-ion_440812_g.527762_m.527762	CRVP_PSEAU	Cysteine-rich venom protein pseudochetoxin OS=Pseudechis australis OX=8670 PE=1 SV=1	3.1E-24	NA
	Gene.298733 _csim_min-ion_152323_g.298733_m.298733	VA576_SCODE	Scoloptoxin SSD976 OS=Scolopendra dehaani OX=2609776 PE=1 SV=1	4.5E-29	73.35

	Gene.164601 _csim_min- ion_67500_g. 164601_m.16 4601	CRVP2_NAJKA	Cysteine-rich venom protein kaouthin-2 OS=Naja kaouthia OX=8649 PE=1 SV=2	3.4E-31	5.50
	Gene.178202 _csim_min- ion_75128_g. 178202_m.17 8202	MR30_CONMR	Cysteine-rich venom protein Mr30 OS=Conus marmoreus OX=42752 PE=1 SV=1	4.4E-28	2.02
	Gene.10434_c sim_min- ion_2310_g.1 0434_m.1043 4	CRVP_HOPST	Cysteine-rich venom protein pseudechetoxin- like OS=Hop- locephalus ste- phensii OX=196418 PE=2 SV=1	4.3E-30	16.04
	Gene.353457 _csim_min- ion_195465_g .353457_m.35 3457	TX31_CONTE	Cysteine-rich venom protein OS=Conus textile OX=6494 PE=1 SV=1	2.7E-31	1.36
	Gene.305948 _csim_min- ion_157402_g .305948_m.30 5948	CRVP_CERRY	Cysteine-rich venom protein OS=Cerberus ryn- chops OX=46267 PE=1 SV=1	1.8E-34	1.57
	Gene.321837 _csim_min- ion_169492_g .321837_m.32 1837	CRVP_ERYPO	Cysteine-rich venom protein LIO1 (Fragment) OS=Erythrolampru s poecilogyrus OX=338838 PE=2 SV=1	1.2E-36	21.73
CRISP fam- ily. Venom al- lergen 5-like subfamily	Gene.418340 _csim_min- ion_260429_g .418340_m.41 8340	VA5_LYCSI	Venom allergen 5 OS=Lycosa singoriensis OX=434756 PE=2 SV=1	4E-11	NA
	Gene.363965 _csim_min- ion_204653_g .363965_m.36 3965	VA5_POLFU	Venom allergen 5 OS=Polistes fusca- tus OX=30207 PE=1 SV=1	6.1E-09	NA
	Gene.147066 _csim_min- ion_58363_g.	VA53_DOLMA	Venom allergen 5.02 (Fragment) OS=Dolichovespula	6.3E-15	0.15

	147066_m.14 7066		maculata OX=7441 PE=1 SV=3		
Jellyfish toxin family. Type II subfamily	Gene.464452 _csim_min- ion_316670_g .464452_m.46 4452	JTX1_CARRA	Toxin crtX-A OS=Carybdea rastonii OX=78582 PE=1 SV=1	1.7E-21	NA
	Gene.216327 _csim_min- ion_98149_g. 216327_m.21 6327	JTX1_CARRA	Toxin crtX-A OS=Carybdea rastonii OX=78582 PE=1 SV=1	2.7E-12	NA
Scoloptoxin-05 family	Gene.197801 _csim_min- ion_86749_g. 197801_m.19 7801	TX51A_ETHRU	U-scoloptoxin(05)- Er1a OS=Eth- mostigmus ru- bripes OX=62613 PE=2 SV=1	6E-08	3.99
Scoloptoxin-11 family	Gene.397028 _csim_min- ion_237164_g .397028_m.39 7028	TXB3A_SCODE	U-scoloptoxin(11)- Ssd3a OS=Scolo- pendra dehaani OX=2609776 PE=1 SV=1	3E-07	0.09
Sea anemone type 5 potassium channel toxin family	Gene.517497 _csim_min- ion_412076_g .517497_m.51 7497	KV51_METSE	U-metritoxin- Msn2a OS=Metrid- ium senile OX=6116 PE=3 SV=1	1.1E-15	66.35
	Gene.496728 _csim_min- ion_368326_g .496728_m.49 6728	KV53_BUNCI	Kappa-actitoxin- Bcs4a OS=Bu- nodosoma cais- sarum OX=31165 PE=1 SV=1	2.4E-19	1.41
Venom Kunitz-type family. Sea anemone type 2 potassium channel toxin subfamily	Gene.323953 _csim_min- ion_171126_g .323953_m.32 3953	VKTG_ANEVI	U-actitoxin-Avd3s (Fragment) OS=Anemonia vi- ridis OX=51769 PE=2 SV=1	2.8E-10	NA
Hemostasis impairing toxin					
Ficolin lectin family. Veficolin subfamily	Gene.445543 _csim_min- ion_291627_g .445543_m.4 45543	FCNV3_CERRY	Ryncolin-3 OS=Cerberus ryn- chops OX=46267 PE=1 SV=1	8.4E-33	1.11
Snaclec family	Gene.355855 _csim_min- ion_197543_g .355855_m.35 5855	SLAB3_TRIST	Snaclec stejaggre- gin-A subunit beta- 3 OS=Trimeresurus stejnegeri OX=39682 PE=2 SV=1	2.9E-12	NA

	Gene.14062_c sim_min- ion_3288_g.1 4062_m.1406 2	SLEB_CALRH	Snaclec rhodocetin subunit beta OS=Calloselasma rhodostoma OX=8717 PE=1 SV=1	3E-06	0.11
	Gene.424617 _csim_min- ion_267267_g .424617_m.42 4617	SLB2_MACLB	Snaclec B2 OS=Macrovipera le- betina OX=8709 PE=2 SV=1	4E-07	1.25
	Gene.96560_c sim_min- ion_33927_g. 96560_m.965 60	SLLC2_MACLB	Snaclec coagulation factor X-activating enzyme light chain 2 OS=Macrovipera lebetina OX=8709 GN=LC2 PE=1 SV=1	3E-08	4.44
	Gene.67427_c sim_min- ion_21579_g. 67427_m.674 27	SLLC2_DABSI	Snaclec coagulation factor X-activating enzyme light chain 2 OS=Daboia sia- mensis OX=343250 GN=LC2 PE=1 SV=1	8.6E-09	NA
SNTX/VTX toxin family	Gene.45640_c sim_min- ion_13412_g. 45640_m.456 40	STXA_SYNVE	Neoverrucotoxin subunit alpha OS=Synanceia ver- rucosa OX=51996 PE=1 SV=1	7.2E-15	NA
	Gene.19568_c sim_min- ion_4884_g.1 9568_m.1956 8	CTXB_SCOPL	Cytolytic toxin-beta OS=Scorpaena plumieri OX=274700 PE=1 SV=1	1.4E-19	0.09
	Gene.429229 _csim_min- ion_272364_g .429229_m.42 9229	STXB_SYNVE	Neoverrucotoxin subunit beta OS=Synanceia ver- rucosa OX=51996 PE=1 SV=1	2.8E-27	1.56
	Gene.17739_c sim_min- ion_4362_g.1 7739_m.1773 9	CTXA_SCOPL	Cytolytic toxin-al- pha OS=Scorpaena plumieri OX=274700 PE=1 SV=1	3.7E-52	64.77
True venom lectin family	Gene.200635 _csim_min- ion_88492_g. 200635_m.20 0635	LECG1_BUNFA	C-type lectin bfl-1 OS=Bungarus fasci- atus OX=8613 PE=2 SV=1	6E-07	NA

	Gene.381021 _csim_min- ion_220751_g .381021_m.38 1021	LECM2_BUNMU	C-type lectin BML- 2 OS=Bungarus multicinctus OX=8616 PE=1 SV=1	5E-08	NA
	Gene.347148 _csim_min- ion_190074_g .347148_m.34 7148	LECM1_HYDHA	C-type lectin 1 OS=Hydrophis hardwickii OX=8781 PE=2 SV=1	2E-08	5.66
Other toxins candidates					
AVIT (prokinet- icin) family	Gene.306077 _csim_min- ion_157513_g .306077_m.30 6077	MIT1_DENPO	Toxin MIT1 OS=Dendroaspis polylepis polylepis OX=8620 PE=1 SV=3	1E-08	NA
EGF-like, Sushi, TSP type-1, LDL-receptor class A	Gene.154083 _csim_min- ion_61961_g. 154083_m.15 4083	CTX_SEPES	SE-cephalotoxin OS=Sepia esculenta OX=31210 PE=1 SV=1	1.6E-35	1.30
Elevenin-like	Gene.291057 _csim_min- ion_147124_g .291057_m.29 1057	CELE_CONVC	Elevenin-Vc1 OS=Conus victoriae OX=319920 PE=1 SV=1	3E-07	NA
IGFBP N-termi- nal, Kazal-like, Ig-like C2-type	Gene.254428 _csim_min- ion_123013_g .254428_m.25 4428	IGFBP_CUPSA	Insulin-like growth factor-binding pro- tein-related protein 1 OS=Cupiennius salei OX=6928 PE=2 SV=1	4.6E-62	15.78
Venom comple- ment C3 homo- log family	Gene.461311 _csim_min- ion_312333_g .461311_m.46 1311	VCO32_AUSSU	A.superbus venom factor 2 OS=Austre- laps superbus OX=29156 PE=2 SV=1	2.8E-13	NA

Table S4. Toxin transcripts of *Tubulanus polymorphus*. Unique toxins families are shown in bold.

Protein family	Transcript ID	Uniprot accession	Description	E-value	Expression, TPM
Pore-forming toxins					
Actinoporin fam- ily. Conoidea subfamily	Gene.32873_r _15596_g.328 73_m.32873	ACTP1_TERAN	Tereporin-Ca1 (Fragment) OS=Ter- ebra anilis OX=553697 PE=2 SV=1	5.4E-36	62.64
Enzymes					

Arthropod phospholipase D family. Class II subfamily	Gene.48334_r_35867_g.48334_m.48334	B1T1_LOXSN	Dermonecrotic toxin Ispisictox-betaie3i (Fragment) OS=Loxosceles spinulosa OX=571532 PE=2 SV=1	4.5E-12	13.49
	Gene.40754_r_23774_g.40754_m.40754	B1R2_LOXSN	Dermonecrotic toxin Ispisictox-betaie1ii (Fragment) OS=Loxosceles spinulosa OX=571532 PE=2 SV=1	7.3E-15	9.10
	Gene.31713_r_14663_g.31713_m.31713	A412_LOXHI	Dermonecrotic toxin Ihsictox-alphaiv1ii (Fragment) OS=Loxosceles hirsuta OX=571525 PE=2 SV=1	1.2E-41	6.59
	Gene.27650_r_11664_g.27650_m.27650	A1O_LOXGA	Dermonecrotic toxin Igsictox-alphaic1 OS=Loxosceles gaucho OX=58216 PE=1 SV=1	4.8E-48	4.84
Arthropod phospholipase D family. Class II subfamily. Class iia sub-subfamily	Gene.20564_r_7470_g.20564_m.20564	A51_LOXIN	Dermonecrotic toxin Iisictox-alphaiv1 OS=Loxosceles intermedia OX=58218 PE=1 SV=1	3.6E-48	375.93
Dnase II family	Gene.21807_r_8136_g.21807_m.21807	DNA2_ACAPL	Plancitoxin-1 OS=Acanthaster planci OX=133434 PE=1 SV=1	3.2E-70	22.11
GGT_peptidase domain	Gene.7717_r_1895_g.7717_m.7717	TX14A_SCODE	Scoloptoxin SSD14 OS=Scolopendra dehaani OX=2609776 PE=1 SV=1	2.2E-154	4.21
Glutaminyl-peptide cyclotransferase family	Gene.45237_r_30379_g.45237_m.45237	QPCT_BOIDE	Glutaminyl-peptide cyclotransferase OS=Boiga dendrophila OX=46286 GN=QPCT PE=2 SV=1	4.4E-10	8.08
Natterin family	Gene.36879_r_19297_g.36879_m.36879	NATT3_THANI	Natterin-3 OS=Thalasophryne nattereri OX=289382 PE=1 SV=1	3E-12	4.58

	Gene.25133_r _10065_g.251 33_m.25133	NATT4_THANI	Natterin-4 OS=Thalas- sophryne nattereri OX=289382 PE=2 SV=1	6E-16	6.23
Phospholipase A2 family	Gene.36857_r _19278_g.368 57_m.36857	PA2_URTCR	Phospholipase A2 A2-actitoxin-Ucs2a OS=Urticina crassi- cornis OX=45621 PE=1 SV=1	7.1E-22	57.12
	Gene.11763_r _3435_g.1176 3_m.11763	PA2_SCOVI	Phospholipase A2 Scol/Pla OS=Scolo- pendra viridis OX=118503 PE=1 SV=1	1.2E-23	17.73
	Gene.34244_r _16760_g.342 44_m.34244	PA21_SCODE	Phospholipase A2 SSD387 OS=Scolo- pendra dehaani OX=2609776 PE=1 SV=1	2.1E-29	9.31
Phospholipase A2 fam- ily. Group I subfamily. D49 sub-subfamily	Gene.20339_r _7345_g.2033 9_m.20339	PA2HB_OXYSC	Neutral phospho- lipase A2 homolog taipoxin beta chain 1 OS=Oxyuranus scutellatus scutella- tus OX=8667 PE=1 SV=2	6.3E-19	40.41
	Gene.38345_r _20954_g.383 45_m.38345	PA2A6_TROCA	Acidic phospho- lipase A2 6 OS=Tropidechis carinatus OX=100989 PE=2 SV=1	2E-21	35.95
	Gene.37234_r _19686_g.372 34_m.37234	PA22_OXYSC	Phospholipase A2 OS2 OS=Oxyuranus scutellatus scutella- tus OX=8667 PE=1 SV=2	4.3E-23	35.72
	Gene.26820_r _11136_g.268 20_m.26820	PA2B_MICCO	Basic phospho- lipase A2 OS=Mi- crurus corallinus OX=54390 PE=1 SV=1	4.8E-25	27.75
Phospholipase A2 fam- ily. Group II subfamily. D49 sub-subfamily	Gene.33600_r _16227_g.336 00_m.33600	PA2BA_CRODU	Phospholipase A2 crotoxin basic chain cba2 OS=Crotalus durissus terrificus OX=8732 PE=1 SV=1	8.3E-17	24.36

	Gene.40578_r_23581_g.40578_m.40578	PA2B2_DABRR	Basic phospholipase A2 Drk-b2 OS=Daboia russelii OX=8707 PE=1 SV=1	4E-21	16.13
Phospholipase A2 family. Group III subfamily	Gene.9410_r_2486_g.9410_m.9410	PA23_HELSU	Phospholipase A2 isozymes PA3A/PA3B/PA5 OS=Heloderma suspectum OX=8554 PE=1 SV=3	1.1E-19	23.19
Phospholipase B-like family	Gene.7245_r_1736_g.7245_m.7245	PLB_DRYCN	Phospholipase-B 81 OS=Drysdalia coronoides OX=66186 PE=1 SV=1	0	12.37
Venom metalloproteinase (M12B) family. P-III subfamily	Gene.8763_r_2255_g.8763_m.8763	VM38_DRYCN	Zinc metalloproteinase-disintegrin-like MTP8 OS=Drysdalia coronoides OX=66186 PE=1 SV=1	4.4E-70	15.46
Venom metalloproteinase (M12B) family. P-III subfamily. P-iiia sub-subfamily	Gene.15411_r_4963_g.15411_m.15411	VM3K_NAJKA	Hemorrhagic metalloproteinase-disintegrin-like kaouthiagin OS=Naja kaouthia OX=8649 PE=1 SV=1	1.8E-33	150.29
Proteinase inhibitors					
Venom Kunitz-type family	Gene.40270_r_23201_g.40270_m.40270	VKT3_PSETT	Kunitz-type serine protease inhibitor textilinin-3 OS=Pseudonaja textilis textilis OX=169397 PE=2 SV=1	1.2E-12	10.68
	Gene.46405_r_32385_g.46405_m.46405	VKT1_VIPAA	Kunitz-type serine protease inhibitor 1 OS=Vipera ammodytes ammodytes OX=8705 PE=1 SV=2	2.2E-18	41.66
Ion channel inhibitor activity					
CRISP family	Gene.53044_r_45762_g.53044_m.53044	CRVP_OPHHA	Cysteine-rich venom protein ophanin OS=Ophiophagus hannah OX=8665 PE=1 SV=1	5.9E-06	15.44

	Gene.33069_r _15764_g.33069_m.33069	VA3_SOLIN	Venom allergen 3 OS=Solenopsis invicta OX=13686 PE=1 SV=2	2.7E-31	32.60
	Gene.22507_r _8513_g.22507_m.22507	MR30_CONMR	Cysteine-rich venom protein Mr30 OS=Conus marmoreus OX=42752 PE=1 SV=1	1.3E-33	15.77
	Gene.25045_r _10009_g.25045_m.25045	CRVP_TRILK	CRISP/Aller- gen/PR-1 OS=Trit- tame loki OX=1295018 PE=1 SV=1	1.4E-35	19.85
CRISP fam- ily. Venom al- lergen 5-like subfamily	Gene.44509_r _29206_g.44509_m.44509	VA5_POLDO	Venom allergen 5 OS=Polistes domi- nula OX=743375 PE=1 SV=2	3.9E-08	20.85
	Gene.44041_r _28460_g.44041_m.44041	VA5_VESMG	Venom allergen 5 OS=Vespa mag- nifica OX=202807 PE=1 SV=2	1.4E-08	4.36
	Gene.21335_r _7884_g.21335_m.21335	VA576_SCODE	Scoloptoxin SSD976 OS=Scolopendra dehaani OX=2609776 PE=1 SV=1	1.9E-26	63.60
Venom Kunitz- type family. Sea anemone type 2 potassium channel toxin subfamily	Gene.37385_r _19844_g.37385_m.37385	VKT9_ANEVI	U-actitoxin-Avd3l OS=Anemonia vi- ridis OX=51769 PE=3 SV=1	8E-15	151.04
	Gene.35073_r _17541_g.35073_m.35073	VKT7_ANEVI	U-actitoxin-Avd3j OS=Anemonia vi- ridis OX=51769 PE=3 SV=1	2.5E-16	8.85
Sea anemone type 5 potas- sium channel toxin family	Gene.48662_r _36543_g.48662_m.48662	KV51_METSE	U-metritoxin- Msn2a OS=Metrid- ium senile OX=6116 PE=3 SV=1	2.1E-07	76.57
Scoloptoxin-11 family	Gene.47169_r _33709_g.47169_m.47169	TX14B_SCODE	Scoloptoxin SSD20 (Fragment) OS=Scolopendra dehaani OX=2609776 PE=1 SV=1	1.9E-20	16.02
Hemostasis impairing toxin					
Snaclec family	Gene.46142_r _31919_g.46142_m.46142	SLB9_MACLB	Snaclec B9 OS=Macrovipera le- betina OX=8709 PE=2 SV=1	6.1E-09	8.78

	Gene.36055_r _18475_g.36055_m.36055	SL3_SISCA	Snaclec 3 OS=Sistrurus catenatus edwardsii OX=8762 PE=2 SV=1	4.1E-11	356.96
SNTX/VTX toxin family	Gene.34675_r _17159_g.34675_m.34675	CTXB_SCOPL	Cytolytic toxin-beta OS=Scorpaena plumieri OX=274700 PE=1 SV=1	1.9E-21	8.53
Other toxins					
AVIT (prokineticin) family	Gene.36658_r _19081_g.36658_m.36658	VP164_LYCMC	Venom protein 164 OS=Lychas mucronatus OX=172552 PE=3 SV=1	3.9E-06	6.71
	Gene.28814_r _12460_g.28814_m.28814	BM8D_BOMMX	Prokineticin Bm8-d OS=Bombina maxima OX=161274 PE=2 SV=1	1.6E-06	19.34
Conocap-like	Gene.27537_r _11591_g.27537_m.27537	CCAP_CONVL	Conocap OS=Conus viliepinii OX=257347 GN=conocap PE=1 SV=1	1.1E-06	4.01
Endothelin/sarafotoxin family	Gene.8413_r _2134_g.8413_m.8413	SRTX_ATREN	Sarafotoxins=At-ractaspis en-gaddensis OX=1343144 PE=1 SV=2	8.5E-09	53.05
IGFBP N-terminal domain, Kazal-like, Ig-like C2-type	Gene.26911_r _11196_g.26911_m.26911	IGFBP_CUPSA	Insulin-like growth factor-binding protein-related protein 1 OS=Cupiennius salei OX=6928 PE=2 SV=1	1.1E-60	281.21
PDGF/VEGF growth factor family	Gene.10036_r _2731_g.10036_m.10036	VEGFA_BITGA	Vascular endothelial growth factor A OS=Bitis gabonica OX=8694 PE=1 SV=1	1.2E-08	32.39
Venom complement C3 homolog family	Gene.48677_r _36574_g.48677_m.48677	VCO3_OPHHA	Ophiophagus venom factor OS=Ophiophagus hannah OX=8665 PE=1 SV=1	5.6E-15	12.49

Table S5. Toxin transcripts of *Baseodiscus unicolor*. Unique toxins families are shown in bold.

Protein family	Transcript ID	Uniprot accession	Description	E-value	Expression, TPM
Pore-forming toxins					

MACPF domain	Gene.67601_B_uni-color_11432_g.67601_m.67601	PV21_POMMA	Perivitellin-2 67 kda subunit OS=Pomacea maculata OX=1245466 PE=1 SV=1	5.6E-90	12.26
Enzymes					
Arthropod phospholipase D family. Class II subfamily	Gene.134482_B_uni-color_60655_g.134482_m.134482	A411_LOXLA	Dermonecrotic toxin IIsictox-alphaiv1i (Fragment) OS=Loxosceles laeta OX=58217 PE=2 SV=1	5.5E-23	2.46
	Gene.121778_B_uni-color_43745_g.121778_m.121778	A4A1_LOXIN	Dermonecrotic toxin IIsictox-alphaiva1 OS=Loxosceles intermedia OX=58218 PE=1 SV=1	1E-24	22.20
	Gene.105966_B_uni-color_29654_g.105966_m.105966	A51_LOXIN	Dermonecrotic toxin IIsictox-alphaiv1 OS=Loxosceles intermedia OX=58218 PE=1 SV=1	6.5E-45	143.78
Dnase II family	Gene.74427_B_uni-color_13659_g.74427_m.74427	DNA2_ACAPL	Plancitoxin-1 OS=Acanthaster planci OX=133434 PE=1 SV=1	2.5E-89	3.00
Flavin monoamine oxidase family. FIG1 subfamily	Gene.49406_B_uni-color_6706_g.49406_m.49406	OXLA_VIPAA	L-amino-acid oxidase OS=Vipera ammodytes ammodytes OX=8705 PE=1 SV=1	2.2E-44	5.69
Natterin family	Gene.90302_B_uni-color_20347_g.90302_m.90302	NATT3_THANI	Natterin-3 OS=Thalasiosophryne nattereri OX=289382 PE=1 SV=1	3.9E-06	1.84
Phospholipase A2 family	Gene.124081_B_uni-color_46290_g.124081_m.124081	PA21_SCODE	Phospholipase A2 SSD387 OS=Scolopendra dehaani OX=2609776 PE=1 SV=1	2.3E-23	8.12
Phospholipase A2 family. Group II subfamily. D49 sub-subfamily	Gene.155914_B_uni-color_110324_g.155914_m.155914	PA2B_VIPAZ	Basic phospholipase A2 B chain OS=Vipera aspis zinnikeri OX=55427 PE=1 SV=1	6.6E-16	1.36

Phospholipase A2 family. Group III subfamily	Gene.67828_B_uni-color_11496_g.67828_m.67828	PA23_HELSEU	Phospholipase A2 isozymes PA3A/PA3B/PA5 OS=Heloderma suspectum OX=8554 PE=1 SV=3	1.8E-34	5.25
Phospholipase B-like family	Gene.41256_B_uni-color_5044_g.41256_m.41256	PLB_DRYCN	Phospholipase-B 81 OS=Drysdalia coronoides OX=66186 PE=1 SV=1	0	1.32
Proteinase inhibitors					
Venom Kunitz-type family	Gene.116042_B_uni-color_37940_g.116042_m.116042	VKT1B_CONCL	Kunitz-type serine protease inhibitor conotoxin Cal9.1b (Fragment) OS=Californiconus californicus OX=1736779 PE=2 SV=1	5.5E-17	9.08
	Gene.112285_B_uni-color_34627_g.112285_m.112285	VKT1_WALAE	Protease inhibitor 1 OS=Walterinnesia aegyptia OX=64182 PE=1 SV=1	2.2E-14	28.02
	Gene.128801_B_uni-color_52271_g.128801_m.128801	VKT_BOMTE	Kunitz-type serine protease inhibitor Bt-KTI OS=Bombus terrestris OX=30195 PE=2 SV=1	3.2E-16	11.22
	Gene.135598_B_uni-color_62534_g.135598_m.135598	VKT1A_CONCL	Kunitz-type serine protease inhibitor conotoxin Cal9.1a OS=Californiconus californicus OX=1736779 PE=2 SV=1	5.8E-16	87.26
	Gene.67501_B_uni-color_11401_g.67501_m.67501	VKT2_BITGA	Kunitz-type serine protease inhibitor bitisilin-2 OS=Bitis gabonica OX=8694 PE=1 SV=1	2.7E-14	31.10
	Gene.134404_B_uni-color_60534_g.134404_m.134404	VKT1C_CONCL	Kunitz-type serine protease inhibitor conotoxin Cal9.1c (Fragment) OS=Californiconus californicus OX=1736779 PE=2 SV=1	3.5E-17	10.94

Venom Kunitz-type family. Sea anemone type 2 potassium channel toxin subfamily	Gene.110156_B_uni-color_32810_g.110156_m.110156	ATPI1_ACTTE	Actinia tenebrosa protease inhibitors OS=Actinia tenebrosa OX=6105 PE=1 SV=1	3.3E-48	129.66
Ion channel inhibitor activity					
CRISP family	Gene.68366_B_uni-color_11667_g.68366_m.68366	CRVP_LATSE	Cysteine-rich venom protein latisemin OS=Latisemina semifasciata OX=8631 PE=2 SV=1	6.6E-26	0.82
	Gene.48770_B_uni-color_6564_g.48770_m.48770	CRVP_OPHHA	Cysteine-rich venom protein ophanin OS=Ophiophagus hannah OX=8665 PE=1 SV=1	2.9E-18	2.02
CRISP family. Venom allergen 5-like subfamily	Gene.53702_B_uni-color_7686_g.53702_m.53702	VA576_SCODE	Scoloptoxin SSD976 OS=Scolopendra dehaani OX=2609776 PE=1 SV=1	2.8E-27	2.07
Scoloptoxin-11 family	Gene.59910_B_uni-color_9247_g.59910_m.59910	TX14B_SCODE	Scoloptoxin SSD20 (Fragment) OS=Scolopendra dehaani OX=2609776 PE=1 SV=1	1.6E-11	1.39
	Gene.75161_B_uni-color_13935_g.75161_m.75161	TXB3A_SCODE	U-scoloptoxin(11)-Ssd3a OS=Scolopendra dehaani OX=2609776 PE=1 SV=1	6.2E-06	2.85
Hemostasis impairing toxin					
Snaclec family	Gene.158425_B_uni-color_118108_g.158425_m.158425	SL6_DABSI	Snaclec 6 OS=Daboia siamensis OX=343250 PE=2 SV=1	2.2E-09	1.90
	Gene.148898_B_uni-color_90567_g.148898_m.148898	SLRB_BITRH	Snaclec rhinocetin subunit beta OS=Bitis rhinoceros OX=715877 PE=1 SV=1	5.7E-12	1.02
	Gene.72526_B_uni-color_13001_g.72526_m.72526	SLAB_BOTJA	Snaclec bothrojaracin subunit beta OS=Bothrops jararaca OX=8724 PE=1 SV=1	4.3E-10	3.63

SNTX/VTX toxin family	Gene.30482_B_uni-color_3180_g.30482_m.30482	STXA_SYNHO	Stonustoxin subunit alpha OS=Synanceia horrida OX=13279 PE=1 SV=3	6.2E-87	1.31
	Gene.132857_B_uni-color_58073_g.132857_m.132857	STXB_SYNVE	Neoverrucotoxin subunit beta OS=Synanceia verrucosa OX=51996 PE=1 SV=1	4.9E-53	0.95
True venom lectin family	Gene.124185_B_uni-color_46399_g.124185_m.124185	LECM1_HYDHA	C-type lectin 1 OS=Hydrophis hardwickii OX=8781 PE=2 SV=1	1.1E-11	1.15
Other toxins candidates					
IGFBP N-terminal domain, Kazal-like, Ig-like C2-type	Gene.73465_B_uni-color_13314_g.73465_m.73465	IGFBP_CUPSA	Insulin-like growth factor-binding protein-related protein 1 OS=Cupiennius salei OX=6928 PE=2 SV=1	2E-56	47.56
Insulin-like growth factor binding	Gene.133104_B_uni-color_58427_g.133104_m.133104	VP302_LYCMC	Venom protein 302 OS=Lychas mucronatus OX=172552 PE=2 SV=1	1.2E-12	1.74
Glycoprotein hormones subunit alpha family	Gene.161711_B_uni-color_129356_g.161711_m.161711	CTHA2_CONVC	Thyrostimulin alpha-2 subunit OS=Conus victoriae OX=319920 PE=1 SV=1	9.3E-12	2.69
LDL-receptor class A domain	Gene.79949_B_uni-color_15712_g.79949_m.79949	CPROH_CONVC	Neuropeptide prohormone-4 OS=Conus victoriae OX=319920 PE=1 SV=1	4.1E-24	15.45

Table S6. Toxin transcripts of *Hubrechtella iijimai*. Unique toxins families are shown in bold.

Protein family	Transcript ID	Uniprot accession	Description	E-value	Expression, TPM
Neurotoxins					
Conopeptide P-like superfamily	Gene.85849_h_iijimai_63935_g.85849_m.85849	TU92_POLAB	Turriptide Pal9.2 OS=Polystira albida OX=394106 PE=2 SV=1	5.3E-10	1.66
Pore-forming toxins					

Actinoporin family. Conoidea subfamily	Gene.48764_h_ijimai_18798_g.48764_m.48764	ACTP_CONCN	Conoporin-Cn1 OS=Conus consors OX=101297 PE=1 SV=1	4.7E-06	4.42
Cytotoxin A-III - like	Gene.57253_h_ijimai_26396_g.57253_m.57253	CXA3_CERLA	Cytotoxin A-III OS=Cerebratulus lacteus OX=6221 PE=1 SV=1	4.9E-09	9.23
MACPF domain	Gene.16805_h_ijimai_3077_g.16805_m.16805	PV21_POMMA	Perivitellin-2 67 kda subunit OS=Pomacea maculata OX=1245466 PE=1 SV=1	3E-74	8.88
Enzymes					
Arthropod phospholipase D family. Class II subfamily	Gene.38018_h_ijimai_11669_g.38018_m.38018	A1H2_LOXHI	Dermonecrotic toxin lhsictox-alpha1ii (Fragment) OS=Loxosceles hirsuta OX=571525 PE=2 SV=1	1.3E-47	50.05
Arthropod phospholipase D family. Class II subfamily. Class iia sub-subfamily	Gene.53539_h_ijimai_22853_g.53539_m.53539	A51_LOXIN	Dermonecrotic toxin lisictox-alpha1 OS=Loxosceles intermedia OX=58218 PE=1 SV=1	2.7E-14	11.19
	Gene.43821_h_ijimai_15293_g.43821_m.43821	BIB11_SICTE	Dermonecrotic toxin stsictox-beta1i OS=Sicarius terrosus OX=571544 PE=1 SV=1	2.4E-43	2.04
Glycosyl hydrolase 37 family	Gene.84678_h_ijimai_62109_g.84678_m.84678	TREA_PIMHY	Trehalase OS=Pimpla hypochondriaca OX=135724 GN=tre1 PE=1 SV=1	1.7E-26	1.74
Nucleotide pyrophosphatase/phosphodiesterase family	Gene.42207_h_ijimai_14250_g.42207_m.42207	PDE_NAJAT	Venom phosphodiesterase OS=Naja atra OX=8656 PE=1 SV=1	1E-89	1.64
	Gene.19434_h_ijimai_3830_g.19434_m.19434	PDE2_CROAD	Venom phosphodiesterase 2 OS=Crotalus adamanteus OX=8729 PE=1 SV=1	3.1E-21	2.91
Phospholipase A2 family	Gene.59761_h_ijimai_289	PA2_URTCR	Phospholipase A2 A2-actitoxin-Ucs2a OS=Urticina	5.7E-21	4.81

	83_g.59761_ m.59761		crassicornis OX=45621 PE=1 SV=1		
Phospholipase A2 fam- ily. Group I subfamily. D49 sub-subfamily	Gene.67873_ h_ijimai_382 75_g.67873_ m.67873	PA2B_BUNCE	Basic phospho- lipase A2 KPA2 OS=Bungarus caer- uleus OX=132961 PE=1 SV=1	3.1E-14	0.81
	Gene.96797_ h_ijimai_818 89_g.96797_ m.96797	PA2B1_ACAAN	Basic phospho- lipase A2 acanthin- 1 OS=Acanthophis antarcticus OX=8605 PE=1 SV=1	2.1E-17	1.69
Phospholipase A2 fam- ily. Group II subfamily. D49 sub-subfamily	Gene.93238_ h_ijimai_758 56_g.93238_ m.93238	PA2B_DABRR	Basic phospho- lipase A2 RVV-VD OS=Daboia russelii OX=8707 PE=1 SV=1	1.3E-15	1.94
	Gene.40461_ h_ijimai_131 61_g.40461_ m.40461	PA2BB_TRIST	Basic phospho- lipase A2 Ts-G6D49 OS=Trimeresurus stejnegeri OX=39682 PE=1 SV=2	1.4E-19	6.17
Phospholipase A2 fam- ily. Group III subfamily	Gene.61429_ h_ijimai_307 14_g.61429_ m.61429	PA2A2_HELSU	Acidic phospho- lipase A2 PA4 OS=Heloderma suspectum OX=8554 PE=1 SV=2	2.4E-30	4.40
	Gene.94293_ h_ijimai_776 73_g.94293_ m.94293	HEMI1_HEMLE	Phospholipase A2 hemilipin OS=Hemiscorpius lepturus OX=520031 PE=1 SV=1	3.8E-07	3.24
Venom metallo- proteinase (M12B) fam- ily. P-III sub- family. P-iiia sub-subfamily	Gene.78870_ h_ijimai_532 64_g.78870_ m.78870	VM3_NAJAT	Zinc metallopro- teinase-disintegrin- like namp OS=Naja atra OX=8656 PE=2 SV=1	7.8E-10	1.29
Venom metallo- proteinase (M12B) fam- ily. P-II subfam- ily. P-iib sub- subfamily	Gene.79950_ h_ijimai_548 68_g.79950_ m.79950	VM2AG_GLOHA	Zinc metallopro- teinase-disintegrin agkistin OS=Gloydus halys OX=8714 PE=2 SV=1	5.6E-19	2.33
Proteinase inhibitors					

Serine protease inhibitor-like (TIL domain-containing) family	Gene.55378_h_ijimai_245_27_g.55378_m.55378	ALL6_APICE	Venom serine protease inhibitor OS=Apis cerana OX=7461 PE=2 SV=1	1.3E-06	1.03
Venom Kunitz-type family	Gene.54210_h_ijimai_234_59_g.54210_m.54210	VKT2_NAJNI	Kunitz-type serine protease inhibitor 2 OS=Naja nivea OX=8655 PE=1 SV=1	1.5E-13	1.47
	Gene.39354_h_ijimai_124_94_g.39354_m.39354	VKT2_BITGA	Kunitz-type serine protease inhibitor bitisilin-2 OS=Bitis gabonica OX=8694 PE=1 SV=1	9.4E-15	2.65
	Gene.76307_h_ijimai_495_75_g.76307_m.76307	VKT1_BITGA	Kunitz-type serine protease inhibitor bitisilin-1 OS=Bitis gabonica OX=8694 PE=1 SV=1	1.5E-19	3.42
Venom Kunitz-type family. Sea anemone type 2 potassium channel toxin subfamily	Gene.46349_h_ijimai_170_45_g.46349_m.46349	ATPI1_ACTTE	Actinia tenebrosa protease inhibitors OS=Actinia tenebrosa OX=6105 PE=1 SV=1	4.7E-36	52.76
Ion channel inhibitor activity					
CRISP family	Gene.24894_h_ijimai_565_2_g.24894_m.24894	MR30_CONMR	Cysteine-rich venom protein Mr30 OS=Conus marmoreus OX=42752 PE=1 SV=1	1.9E-34	3.10
	Gene.49571_h_ijimai_194_58_g.49571_m.49571	CRVP1_PSEPL	Cysteine-rich venom protein ENH1 OS=Pseudoferania polylepis OX=338839 PE=2 SV=1	9E-39	3.33
	Gene.54175_h_ijimai_234_30_g.54175_m.54175	CRVP2_HYDHA	Cysteine-rich venom protein 2 OS=Hydrophis hardwickii OX=8781 PE=2 SV=2	2.6E-19	2.60
	Gene.39233_h_ijimai_124_25_g.39233_m.39233	CRVP_AUSSU	Cysteine-rich venom protein OS=Austrelaps superbus OX=29156 PE=2 SV=1	1E-18	15.81

	Gene.33916_ h_ijimai_946 5_g.33916_m. 33916	CRVP_LATSE	Cysteine-rich venom protein latisemin OS=Lati- cauda semifasciata OX=8631 PE=2 SV=1	6.3E-19	3.17
	Gene.48497_ h_ijimai_185 87_g.48497_ m.48497	TX31_CONTE	Cysteine-rich venom protein OS=Conus textile OX=6494 PE=1 SV=1	1.8E-23	2.45
CRISP fam- ily. Venom al- lergen 5-like subfamily	Gene.41400_ h_ijimai_137 75_g.41400_ m.41400	VA576_SCODE	Scoloptoxin SSD976 OS=Scolopendra dehaani OX=2609776 PE=1 SV=1	1.3E-26	22.85
	Gene.78783_ h_ijimai_531 31_g.78783_ m.78783	VA5_TITSE	Venom allergen 5 (Fragments) OS=Ti- tyus serrulatus OX=6887 PE=1 SV=1	1.4E-07	0.77
Hemostasis impairing toxin					
Snaclec family	Gene.76159_ h_ijimai_493 80_g.76159_ m.76159	SL124_ECHOC	Snaclec CTL- Eoc124 OS=Echis ocellatus OX=99586 PE=2 SV=1	3.5E-06	0.56
	Gene.93937_ h_ijimai_770 05_g.93937_ m.93937	SLAD_MACLB	Snaclec A13 OS=Macrovipera le- betina OX=8709 PE=2 SV=1	2E-08	1.73
	Gene.87733_ h_ijimai_669 57_g.87733_ m.87733	SLA_PROFL	Snaclec coagulation factor IX-binding protein subunit A OS=Protobothrops flavoviridis OX=88087 PE=1 SV=1	3.1E-09	0.82
	Gene.54259_ h_ijimai_235 03_g.54259_ m.54259	SLBB_TRIAB	Snaclec alboaggre- gin-B subunit beta OS=Trimeresurus albolabris OX=8765 PE=1 SV=2	1.7E-11	0.60
	Gene.15901_ h_ijimai_284 5_g.15901_m. 15901	STXB_SYNVE	Neoverrucotoxin subunit beta OS=Synanceia ver- rucosa OX=51996 PE=1 SV=1	2.1E-96	3.48
SNTX/VTX toxin family	Gene.62213_ h_ijimai_315 69_g.62213_ m.62213	CTXA_SCOPL	Cytolytic toxin-al- pha OS=Scorpaena plumieri	1.6E-31	2.57

OX=274700 PE=1 SV=1					
True venom lectin family	Gene.88129_h_ijimai_67546_g.88129_m.88129	LEC1_LEIMD	C-type lectin lecto-toxin-Lei1 OS=Leioheterodon mada-gascariensis OX=46577 PE=2 SV=1	2.6E-06	2.10
	Gene.72600_h_ijimai_44478_g.72600_m.72600	LECM1_HYDHA	C-type lectin 1 OS=Hydrophis hardwickii OX=8781 PE=2 SV=1	1.8E-09	0.28
Other toxins candidates					
AVIT (prokineticin) family	Gene.57892_h_ijimai_27009_g.57892_m.57892	BM8E_BOMMX	Prokineticin Bm8-e OS=Bombina maxima OX=161274 PE=2 SV=1	2.9E-06	6.50
EGF-like, Sushi, TSP type-1, LDL-receptor class A	Gene.62342_h_ijimai_31711_g.62342_m.62342	CTX_SEPES	SE-cephalotoxin OS=Sepia esculenta OX=31210 PE=1 SV=1	1.8E-28	0.96
IGFBP N-terminal, Kazal-like, Ig-like C2-type	Gene.33729_h_ijimai_9376_g.33729_m.33729	IGFBP_CUPSA	Insulin-like growth factor-binding protein-related protein 1 OS=Cupiennius salei OX=6928 PE=2 SV=1	2.1E-53	24.19

Table S7. Toxin transcripts of *Lineus longissimus*. Unique toxins families are shown in bold.

Protein family	Transcript ID	Uniprot accession	Description	E-value	Expression, TPM
Neurotoxins					
Neurotoxin 02 (plectoxin) family. 02 (plectoxin) subfamily.	Gene.137391_1_long35194_g.137391_m.137391	TX22A_PLETR	Omega-plectoxin-Pt1a OS=Plectreuryts tristis OX=33319 PE=1 SV=1	2.5E-06	152.67
Pore-forming toxins					
Cytotoxin A-III-like	Gene.136669_1_long34583_g.136669_m.136669	CXA3_CERLA	Cytotoxin A-III OS=Cerebratulus lacteus OX=6221 PE=1 SV=1	2E-45	0.24
MACPF domain	Gene.63359_1_long8572_g.63359_m.63359	PV21_POMMA	Perivitellin-2 67 kda subunit OS=Pomacea	2.4E-89	6.78

maculata OX=1245466 PE=1 SV=1					
Enzymes					
Arthropod phospholipase D family. Class II subfamily	Gene.130745 _l_long30563 _g.130745_m.130745	A1L1_LOXSA	Dermonecrotic toxin Isasictox-alphaib2i (Fragment) OS=Loxosceles sabina OX=571529 PE=2 SV=1	4.7E-35	1.83
Dnase II family	Gene.110707 _l_long21360 _g.110707_m.110707	DNA2_ACAPL	Plancitoxin-1 OS=Acanthaster planci OX=133434 PE=1 SV=1	4.2E-94	8.26
Flavin mono-amine oxidase family. FIG1 subfamily	Gene.48707_1 _long5836_g.48707_m.48707	OXLA_CALRH	L-amino-acid oxidase OS=Calloselasma rhodostoma OX=8717 PE=1 SV=2	3E-44	1.90
Multicopper oxidase family	Gene.125889 _l_long27832 _g.125889_m.125889	FA5_PSETE	Coagulation factor V OS=Pseudonaja textilis OX=8673 GN=F5 PE=1 SV=1	2.5E-24	0.59
Natterin family	Gene.131057 _l_long30751 _g.131057_m.131057	NATT4_THANI	Natterin-4 OS=Thalas-sophryne nattereri OX=289382 PE=2 SV=1	1.5E-07	0.80
Phospholipase A2 family. Group I subfamily. D49 sub-subfamily	Gene.107060 _l_long20049 _g.107060_m.107060	PA2B_MICCO	Basic phospholipase A2 OS=Micrurus corallinus OX=54390 PE=1 SV=1	1.2E-19	15.88
Phospholipase A2 family. Group III subfamily	Gene.139946 _l_long37449 _g.139946_m.139946	PA2A2_HELSU	Acidic phospholipase A2 PA4 OS=Heloderma suspectum OX=8554 PE=1 SV=2	4.2E-30	0.23
	Gene.100331 _l_long17837 _g.100331_m.100331	PA23_HELSU	Phospholipase A2 isozymes PA3A/PA3B/PA5 OS=Heloderma suspectum OX=8554 PE=1 SV=3	8.4E-33	17.55
Venom metalloproteinase (M12B) family. P-III	Gene.17811_1 _long1502_g.17811_m.17811	VM3_BUNMU	Zinc metalloproteinase-disintegrin-like bmbp OS=Bungarus	1.3E-53	0.42

subfamily. P-iiiia sub-subfamily		multicinctus OX=8616 PE=1 SV=1			
Proteinase inhibitors					
Cystatin family	Gene.144061 _l_long42022 _g.144061_m. 144061	CYT_CHIGU	Cystatin-1 OS=Chilobrachys guangxiensis OX=278060 PE=2 SV=1	3.3E-09	19.40
Kazal-like	Gene.141669 _l_long39209 _g.141669_m. 141669	IELA_ANESU	PI-actitoxin-Avd5a OS=Anemonia sul- cata OX=6108 PE=1 SV=1	1.6E-09	0.97
Natriuretic pep- tide family	Gene.101475 _l_long18215 _g.101475_m. 101475	SVM11_CERCE	Snake venom met- alloprotease inhibi- tor 02A10 OS=Ce- rastes cerastes OX=8697 GN=Svmpti-Cce12 PE=1 SV=1	4.3E-09	0.29
Venom Kunitz- type family	Gene.147661 _l_long47205 _g.147661_m. 147661	VKT2_BITGA	Kunitz-type serine protease inhibitor bitisilin-2 OS=Bitis gabonica OX=8694 PE=1 SV=1	1.6E-14	0.42
	Gene.143563 _l_long41377 _g.143563_m. 143563	VKT1D_CONCL	Kunitz-type serine protease inhibitor conotoxin Cal9.1d (Fragment) OS=Cal- iforniconus califor- nicus OX=1736779 PE=2 SV=1	1.5E-17	21.65
	Gene.138804 _l_long36403 _g.138804_m. 138804	VKT1A_CONCL	Kunitz-type serine protease inhibitor conotoxin Cal9.1a OS=Californiconus californicus OX=1736779 PE=2 SV=1	2.2E-17	13.22
Venom Kunitz- type family. Sea anemone type 2 potassium channel toxin subfamily	Gene.87468_l _long14140_ g.87468_m.87 468	VKT2H_HETCR	PI-stichotoxin- Hcr2h OS=Heter- actis crispa OX=175771 PE=3 SV=1	4.4E-16	1.79
Venom Kunitz- type fam- ily. Scorpion delta-Ktx sub- family. Delta-	Gene.127205 _l_long28520 _g.127205_m. 127205	VKT12_MESMA	Kunitz-type serine protease inhibitor bmktt-3 OS=Meso- buthus martensii OX=34649 PE=2 SV=1	6.7E-15	0.78

Ktx 1 sub-sub-family	Gene.140308 _l_long37783 _g.140308_m.140308	VKT11_HOFGE	Kunitz-type serine protease inhibitor Hg1 OS=Hoffman-nihadurus gertschi OX=380989 PE=1 SV=1	2.6E-15	0.42
Ion channel inhibitor activity					
CRISP family	Gene.157145 _l_long67833 _g.157145_m.157145	CRVP_VIPBN	Cysteine-rich venom protein (Fragment) OS=Vipera berus nikolskii OX=1808362 PE=2 SV=1	2.6E-13	0.32
	Gene.130943 _l_long30684 _g.130943_m.130943	CRVP_NOTSC	Cysteine-rich venom protein pseudetoxin-like OS=Notechis scutatus scutatus OX=70142 PE=2 SV=1	8E-18	0.36
	Gene.142151 _l_long39713 _g.142151_m.142151	CRIS3_HUMAN	Cysteine-rich secretory protein 3 OS=Homo sapiens OX=9606 GN=CRISP3 PE=1 SV=1	2.2E-30	54.62
	Gene.122600 _l_long26276 _g.122600_m.122600	CRVP_PSEPO	Cysteine-rich venom protein pseudocin OS=Pseudechis porphyriacus OX=8671 PE=1 SV=1	7.5E-33	10.34
	Gene.73577_1 _long10775_ g.73577_m.73577	CRVP_AUSSU	Cysteine-rich venom protein OS=Austrelaps superbus OX=29156 PE=2 SV=1	2.8E-36	0.07
	Gene.90326_1 _long14917_ g.90326_m.90326	CRVP_PSEAU	Cysteine-rich venom protein pseudetoxin OS=Pseudechis australis OX=8670 PE=1 SV=1	8.9E-38	1.61
	Gene.121444 _l_long25753 _g.121444_m.121444	MR30_CONMR	Cysteine-rich venom protein Mr30 OS=Conus marmoreus OX=42752 PE=1 SV=1	1.6E-37	0.15

	Gene.125968 _l_long27877 _g.125968_m. 125968	CRVP_LATSE	Cysteine-rich venom protein latisemin OS=Lati- cauda semifasciata OX=8631 PE=2 SV=1	1.7E-15	6.31
CRISP fam- ily. Venom al- lergen 5-like subfamily	Gene.123301 _l_long26609 _g.123301_m. 123301	VA543_SCODE	Scoloptoxin SSD43 OS=Scolopendra dehaani OX=2609776 PE=1 SV=1	6E-27	0.91
Scoloptoxin-11 family	Gene.119454 _l_long24839 _g.119454_m. 119454	TXB3A_SCODE	U-scoloptoxin(11)- Ssd3a OS=Scolo- pendra dehaani OX=2609776 PE=1 SV=1	2E-07	21.20
Hemostasis impairing toxin					
Snaclec family	Gene.141292 _l_long38803 _g.141292_m. 141292	SLCB_DEIAC	Snaclec agkicetin-C subunit beta OS=Deinagkistro- don acutus OX=36307 PE=1 SV=1	4.2E-08	15.18
	Gene.102923 _l_long18662 _g.102923_m. 102923	SLDB_TRIAB	Snaclec alboaggre- gin-D subunit beta OS=Trimeresurus albolabris OX=8765 PE=1 SV=1	3.6E-10	1.58
	Gene.112660 _l_long22103 _g.112660_m. 112660	SLLC1_MACLB	Snaclec coagulation factor X-activating enzyme light chain 1 OS=Macrovipera lebetina OX=8709 GN=LC1 PE=1 SV=1	1.9E-12	0.88
	Gene.9577_l_ long658_g.95 77_m.9577	SL3_SISCA	Snaclec 3 OS=Sis- trurus catenatus edwardsii OX=8762 PE=2 SV=1	2.4E-13	0.50
	Gene.67592_l_ long9457_g. 67592_m.675 92	SLA_BITAR	Snaclec bitiscetin subunit alpha OS=Bitis arietans OX=8692 PE=1 SV=1	3.3E-14	0.54
True venom lectin family	Gene.146352 _l_long45155 _g.146352_m. 146352	LECG1_BUNMU	C-type lectin BML- 1 OS=Bungarus multicinctus OX=8616 PE=2 SV=1	5.1E-09	0.28
	Gene.102764 _l_long18613	LEC1_MICCO	C-type lectin OS=Micrurus	7.8E-08	0.72

	_g.102764_m. 102764		corallinus OX=54390 PE=1 SV=1		
	Gene.99209_1 _long17495_ g.99209_m.99 209	LECM1_PHIOL	C-type lectin lec- toxin-Phi1 OS=Phil- odryas olfersii OX=120305 PE=2 SV=1	5E-10	0.18
Other toxins candidates					
Conocap - like	Gene.38449_1 _long4188_g. 38449_m.384 49	CCAP_CONVL	Conocap OS=Co- nus viliepinii OX=257347 GN=conocap PE=1 SV=1	8.7E-07	5.49
EGF domain peptide family	Gene.123598 _1_long26751 _g.123598_m. 123598	TX18A_MANRB	U18-myrmecitoxin- Mri1a OS=Manica rubida OX=219785 PE=1 SV=1	7.7E-07	1.34
Glycoprotein hormones sub- unit alpha family	Gene.117298 _1_long23931 _g.117298_m. 117298	CTHA2_CONVC	Thyrostimulin al- pha-2 subunit OS=Conus victoriae OX=319920 PE=1 SV=1	7.4E-19	7.02
Glycoprotein hormones sub- unit beta family	Gene.120462 _1_long25319 _g.120462_m. 120462	CTHB5_CONVC	Thyrostimulin beta- 5 subunit OS=Co- nus victoriae OX=319920 PE=2 SV=1	9.9E-19	11.19
IGFBP N-termi- nal domain	Gene.151742 _1_long54638 _g.151742_m. 151742	VP302_LYCMC	Venom protein 302 OS=Lychas mucro- natus OX=172552 PE=2 SV=1	1.8E-08	0.40
IGFBP N-termi- nal, Kazal-like, Ig-like C2-type	Gene.129083 _1_long29578 _g.129083_m. 129083	IGFBP_CUPSA	Insulin-like growth factor-binding pro- tein-related protein 1 OS=Cupiennius salei OX=6928 PE=2 SV=1	6.2E-52	9.67
Insulin family	Gene.100267 _1_long17817 _g.100267_m. 100267	INS2C_CONFO	Con-Ins F2c OS=Conus floridu- lus OX=97180 PE=1 SV=1	9.3E-09	2.85
	Gene.109882 _1_long21067 _g.109882_m. 109882	INS1_CONIM	Con-Ins Im1 OS=Conus imperi- alis OX=35631 PE=2 SV=1	2.6E-14	1.25
LDL-receptor class A domain	Gene.99182_1 _long17485_ g.99182_m.99 182	CPROH_CONVC	Neuropeptide pro- hormone-4 OS=Co- nus victoriae OX=319920 PE=1 SV=1	8.6E-24	11.07

NGF-beta family	Gene.71709_1_long10348_g.71709_m.71709	NGFV1_PSEAU	Venom nerve growth factor 1 OS=Pseudechis australis OX=8670 PE=2 SV=1	1.8E-12	0.43
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Table S8. Toxin transcripts of *Lineus ruber*.

Protein family	Transcript ID	Uniprot accession	Description	E-value	Expression, TPM
Pore-forming toxins					
Actinoporin family. Conoidea subfamily	Gene.59713_L_ruber_19170_g.59713_m.59713	ACTP1_TERAN	Tereporin-Ca1 (Fragment) OS=Ter-ebra anilis OX=553697 PE=2 SV=1	2.1E-28	45.91
Cytotoxin A-III-like	Gene.88551_L_ruber_53287_g.88551_m.88551	CXA3_CERLA	Cytotoxin A-III OS=Cerebratulus lacteus OX=6221 PE=1 SV=1	7.9E-42	63.10
MACPF domain	Gene.29509_L_ruber_5163_g.29509_m.29509	PV21_POMMA	Perivitellin-2 67 kda subunit OS=Pomacea maculata OX=1245466 PE=1 SV=1	3.9E-92	3.01
Enzymes					
Arthropod phospholipase D family. Class II subfamily	Gene.50684_L_ruber_13690_g.50684_m.50684	A1LB1_LOXAR	Dermonecrotic toxin larsictox-alphaib2bi (Fragment) OS=Loxosceles arizonica OX=196454 PE=1 SV=1	1.6E-29	7.57
Arthropod phospholipase D family. Class II subfamily. Class iia sub-subfamily	Gene.40924_L_ruber_9156_g.40924_m.40924	A4A1_LOXIN	Dermonecrotic toxin lisictox-alphaiva1 OS=Loxosceles intermedia OX=58218 PE=1 SV=1	1.7E-39	17.86
Arthropod phospholipase D family. Class II subfamily. Class iib sub-subfamily	Gene.95693_L_ruber_66547_g.95693_m.95693	B1Q_LOXIN	Dermonecrotic toxin lisictox-betaid1 OS=Loxosceles intermedia OX=58218 PE=1 SV=1	3.1E-13	0.50
	Gene.89353_L_ruber_547	B1H_LOXLA	Dermonecrotic toxin llsictox-	7E-22	0.51

	04_g.89353_m.89353		betaia1 OS=Loxosceles laeta OX=58217 PE=1 SV=1		
	Gene.41631_L_ruber_9450_g.41631_m.41631	B1HA_LOXBO	Dermonecrotic toxin lbsictox-betaia1a OS=Loxosceles boneti OX=283164 PE=1 SV=2	2.1E-41	6.18
Dnase II family	Gene.48438_L_ruber_12571_g.48438_m.48438	DNA2_ACAPL	Plancitoxin-1 OS=Acanthaster planci OX=133434 PE=1 SV=1	1.9E-91	0.98
Flavin monoamine oxidase family. FIG1 subfamily	Gene.23011_L_ruber_3399_g.23011_m.23011	OXLA_BOTAT	L-amino-acid oxidase OS=Bothrops atrox OX=8725 PE=1 SV=2	5.9E-48	1.84
Phospholipase A2 family. Group I subfamily. D49 sub-subfamily	Gene.45934_L_ruber_11378_g.45934_m.45934	PA2B_MICCO	Basic phospholipase A2 OS=Micrurus corallinus OX=54390 PE=1 SV=1	5E-20	4.17
Phospholipase A2 family. Group III subfamily	Gene.53961_L_ruber_15534_g.53961_m.53961	PA23_HELSU	Phospholipase A2 isozymes PA3A/PA3B/PA5 OS=Heloderma suspectum OX=8554 PE=1 SV=3	6.8E-30	7.76
	Gene.36510_L_ruber_7471_g.36510_m.36510	PA2A2_HELSU	Acidic phospholipase A2 PA4 OS=Heloderma suspectum OX=8554 PE=1 SV=2	1.5E-32	2.39
Proteinase inhibitors					
Venom Kunitz-type family. Scorpion delta-Ktx subfamily. Delta-Ktx 3 sub-subfamily	Gene.54609_L_ruber_15904_g.54609_m.54609	VKT31_MESMA	Kunitz-type serine protease inhibitor bmkt-2 OS=Mesobuthus martensii OX=34649 PE=2 SV=2	2.2E-15	35.16
Ion channel inhibitor activity					
CRISP family	Gene.48539_L_ruber_12613_g.48539_m.48539	CRVP_LATSE	Cysteine-rich venom protein latisemin OS=Laticauda semifasciata OX=8631 PE=2 SV=1	4.9E-23	2.40

	Gene.70348_ L_ruber_282 88_g.70348_ m.70348	GPRL1_BOVIN	GLIPR1-like pro- tein 1 OS=Bos tau- rus OX=9913 GN=GLIPR1L1 PE=1 SV=1	2.4E-25	6.97
	Gene.48775_ L_ruber_127 26_g.48775_ m.48775	CRVP_AUSSU	Cysteine-rich venom protein OS=Austrelaps su- perbus OX=29156 PE=2 SV=1	1.2E-28	2.48
	Gene.45105_ L_ruber_109 68_g.45105_ m.45105	CRVP_ERYPO	Cysteine-rich venom protein LIO1 (Fragment) OS=Erythrolampru s poecilogyrus OX=338838 PE=2 SV=1	2.5E-30	1.61
	Gene.47888_ L_ruber_123 10_g.47888_ m.47888	CRVP_PHIOL	Cysteine-rich venom protein OS=Philodryas olf- ersii OX=120305 PE=2 SV=1	2.7E-31	2.66
	Gene.50154_ L_ruber_134 16_g.50154_ m.50154	MR30_CONMR	Cysteine-rich venom protein Mr30 OS=Conus marmoreus OX=42752 PE=1 SV=1	6.9E-38	2.03
	Gene.57217_ L_ruber_175 56_g.57217_ m.57217	CRVP_PSEAU	Cysteine-rich venom protein pseudechetoxin OS=Pseudechis australis OX=8670 PE=1 SV=1	4.8E-40	0.44
CRISP fam- ily. Venom al- lergen 5-like subfamily	Gene.42835_ L_ruber_994 7_g.42835_m. 42835	VA576_SCODE	Scoloptoxin SSD976 OS=Scolopendra dehaani OX=2609776 PE=1 SV=1	1.1E-32	1.62
Nemertide fam- ily	Gene.99712_ L_ruber_746 18_g.99712_ m.99712	NEMA1_LINLO	Nemertide alpha-1 (Fragment) OS=Lineus longissi- mus OX=88925 PE=1 SV=1	1.4E-35	20.54
Venom Kunitz- type family. Sea anemone type 2 potassium channel toxin subfamily	Gene.87032_ L_ruber_505 99_g.87032_ m.87032	VKT5_ANEVI	U-actitoxin-Avd3h OS=Anemonia vi- ridis OX=51769 PE=3 SV=1	4.1E-16	140.87
Hemostasis impairing toxin					

Snaclec family	Gene.52300_ L_ruber_145 63_g.52300_ m.52300	SL3_SISCA	Snaclec 3 OS=Sis- trurus catenatus edwardsii OX=8762 PE=2 SV=1	3.6E-13	1.74
	Gene.50378_ L_ruber_135 34_g.50378_ m.50378	SLA_BITAR	Snaclec bitiscetin subunit alpha OS=Bitis arietans OX=8692 PE=1 SV=1	4.7E-15	0.00
SNTX/VTX toxin family	Gene.19632_ L_ruber_263 3_g.19632_m. 19632	STXB_SYNVE	Neoverrucotoxin subunit beta OS=Synanceia ver- rucosa OX=51996 PE=1 SV=1	2.5E-99	0.88
True venom lectin family	Gene.82960_ L_ruber_440 78_g.82960_ m.82960	LECM1_PHIOL	C-type lectin lec- toxin-Phi1 OS=Phil- odryas olfersii OX=120305 PE=2 SV=1	1.9E-15	0.53
Other toxins candidates					
Glycoprotein hormones subu- nit alpha family	Gene.62977_ L_ruber_216 77_g.62977_ m.62977	CTHA2_CONVC	Thyrostimulin al- pha-2 subunit OS=Conus victoriae OX=319920 PE=1 SV=1	6.6E-20	0.24
Glycoprotein hormones subu- nit beta family	Gene.64507_ L_ruber_229 03_g.64507_ m.64507	CTHB5_CONVC	Thyrostimulin beta- 5 subunit OS=Co- nus victoriae OX=319920 PE=2 SV=1	2.1E-18	0.60
IGFBP N-termi- nal, Kazal-like, Ig-like C2-type	Gene.22728_ L_ruber_333 0_g.22728_m. 22728	IGFBP_CUPSA	Insulin-like growth factor-binding pro- tein-related protein 1 OS=Cupiennius salei OX=6928 PE=2 SV=1	1.3E-51	3.45
LDL-receptor class A domain	Gene.29081_ L_ruber_503 5_g.29081_m. 29081	CPROH_CONVC	Neuropeptide pro- hormone-4 OS=Co- nus victoriae OX=319920 PE=1 SV=1	1.7E-24	8.09
Venom comple- ment C3 homo- log family	Gene.80447_ L_ruber_404 51_g.80447_ m.80447	VCO3_OPHHA	Ophiophagus venom factor OS=Ophiophagus hannah OX=8665 PE=1 SV=1	3E-19	1.52

Table S9. Toxin transcripts of *Lineus sanguineus*. Unique toxins families are shown in bold.

Protein family	Transcript ID	Uniprot accession	Description	E-value	Expression, TPM
Neurotoxins					
Conopeptide P-like superfamily	Gene.81947_ L_san-guineus_509 72_g.81947_ m.81947	TU91_LOPOL	Turriptide Lol9.1 OS=Lophiotoma olangoensis OX=2420066 PE=2 SV=1	2.5E-07	1.52
	Gene.86098_ L_san-guineus_566 33_g.86098_ m.86098	TU11_LOPAL	Turriptide OL11-like (Fragment) OS=Lophiotoma albina OX=1525239 PE=2 SV=1	3.1E-08	1.41
Neurotoxin 04 (omega-agtx) family. 02 (Tx1) subfamily	Gene.68419_ L_san-guineus_353 94_g.68419_ m.68419	TXL1_PHONI	Mu-ctenitoxin-Pn1a OS=Phoneutria nigriventer OX=6918 PE=1 SV=2	4.6E-06	185.65
Neurotoxin 10 (Hwtx-1) family. 15 (Hntx-3) subfamily	Gene.74066_ L_san-guineus_415 16_g.74066_ m.74066	H3A08_CYRHA	Hainantoxin-III 8 OS=Cyriopagopus hainanus OX=209901 PE=1 SV=1	1.2E-07	564.98
Pore-forming toxins					
Cytotoxin A-III-like	Gene.52528_ L_san-guineus_217 31_g.52528_ m.52528	CXA3_CERLA	Cytotoxin A-III OS=Cerebratulus lacteus OX=6221 PE=1 SV=1	2.9E-47	427.35
MACPF domain	Gene.82474_ L_san-guineus_516 62_g.82474_ m.82474	PV21_POMCA	Perivitellin-2 67 kda subunit OS=Pomacea canaliculata OX=400727 PE=1 SV=2	2.6E-15	1.38
	Gene.61455_ L_san-guineus_288 89_g.61455_ m.61455	PV21_POMMA	Perivitellin-2 67 kda subunit OS=Pomacea maculata OX=1245466 PE=1 SV=1	1.1E-24	2.77
Enzymes					
Arthropod phospholipase D family. Class II subfamily	Gene.94336_ L_san-guineus_693 30_g.94336_ m.94336	A1LB1_LOXAR	Dermonecrotic toxin larsictox-alphaib2bi (Fragment) OS=Loxosceles arizonica OX=196454 PE=1 SV=1	8.9E-07	1.44
	Gene.55261_ L_san-guineus_237	A1OC_LOXRU	Dermonecrotic toxin lrusictox-alphaic1c (Fragment)	1.9E-18	2.30

	98_g.55261_ m.55261		OS=Loxosceles ru- fescens OX=571528 PE=2 SV=1		
	Gene.40396_ L_san- guineus_140 37_g.40396_ m.40396	A11B1_LOXIN	Dermonecrotic toxin lisictox-al- phaia2bi OS=Lox- osceles intermedia OX=58218 PE=2 SV=1	2.4E-38	6.73
	Gene.37457_ L_san- guineus_124 69_g.37457_ m.37457	A21_LOXAR	Dermonecrotic toxin larsictox-al- phaii1 (Fragment) OS=Loxosceles ari- zonica OX=196454 PE=2 SV=1	1.8E-47	4.00
Arthropod phospholipase D family. Class II subfam- ily. Class iia sub-subfamily	Gene.29321_ L_san- guineus_861 9_g.29321_m. 29321	A51_LOXIN	Dermonecrotic toxin lisictox-al- phav1 OS=Loxosce- les intermedia OX=58218 PE=1 SV=1	4.3E-46	10.15
Dnase II family	Gene.59918_ L_san- guineus_275 83_g.59918_ m.59918	DNA2_ACAPL	Plancitoxin-1 OS=Acanthaster planci OX=133434 PE=1 SV=1	6.6E-56	3.10
Flavin mono- amine oxidase family. FIG1 subfamily	Gene.16674_ L_san- guineus_384 2_g.16674_m. 16674	OXLA_BOTPC	L-amino acid oxi- dase (Fragment) OS=Bothrops pictus OX=133440 PE=1 SV=1	1.2E-38	9.77
Natterin family	Gene.29078_ L_san- guineus_851 8_g.29078_m. 29078	NATT4_THANI	Natterin-4 OS=Thalas- sophryne nattereri OX=289382 PE=2 SV=1	1.1E-11	3.44
Nucleotide py- rophospha- tase/phos- phodiesterase family	Gene.16311_ L_san- guineus_372 7_g.16311_m. 16311	PDE2_CROAD	Venom phos- phodiesterase 2 OS=Crotalus ada- manteus OX=8729 PE=1 SV=1	4E-176	3.81
Peptidase M12A domain	Gene.56334_ L_san- guineus_246 34_g.56334_ m.56334	VMPA4_LOXLA	Astacin-like metal- loprotease toxin 4 (Fragment) OS=Loxosceles laeta OX=58217 PE=2 SV=1	5.9E-08	1.46

Phospholipase A2 family	Gene.14943_L_san-guineus_3301_g.14943_m.14943	PA21_SCODE	Phospholipase A2 SSD387 OS=Scolopendra dehaani OX=2609776 PE=1 SV=1	6.9E-21	11.86
Phospholipase A2 family. Group I subfamily. D49 sub-subfamily	Gene.107532_L_san-guineus_92735_g.107532_m.107532	PA2B_MICCO	Basic phospholipase A2 OS=Micrurus corallinus OX=54390 PE=1 SV=1	2.6E-06	1.07
	Gene.15767_L_san-guineus_3556_g.15767_m.15767	PA2BA_BUNFA	Basic phospholipase A2 10 (Fragment) OS=Bungarus fasciatus OX=8613 PE=1 SV=2	1.6E-20	6.43
Phospholipase A2 family. Group III subfamily	Gene.39305_L_san-guineus_13431_g.39305_m.39305	HEMI1_HEMLE	Phospholipase A2 hemilipin OS=Hemiscorpius lepturus OX=520031 PE=1 SV=1	1.7E-17	29.62
	Gene.35790_L_san-guineus_11591_g.35790_m.35790	PA23_HELSU	Phospholipase A2 isozymes PA3A/PA3B/PA5 OS=Heloderma suspectum OX=8554 PE=1 SV=3	7E-29	5.67
	Gene.27806_L_san-guineus_7962_g.27806_m.27806	PA2A2_HELSU	Acidic phospholipase A2 PA4 OS=Heloderma suspectum OX=8554 PE=1 SV=2	1.2E-33	6.81
Type-B carboxylesterase/lipase family	Gene.23027_L_san-guineus_6063_g.23027_m.23027	ACES_BUNFA	Acetylcholinesterase OS=Bungarus fasciatus OX=8613 GN=ACHE PE=1 SV=2	1.3E-125	2.54
Venom metalloproteinase (M12B) family. P-I subfamily	Gene.78387_L_san-guineus_46574_g.78387_m.78387	VM1B2_BOTJR	Snake venom metalloproteinase bjsump-2 (Fragment) OS=Bothrops jararacussu OX=8726 PE=1 SV=1	7.3E-08	0.61
Venom metalloproteinase (M12B) family. P-II	Gene.86069_L_san-guineus_56583_g.86069_m.86069	VM2AB_AGKCO	Zinc metalloproteinase/disintegrin OS=Agkistrodon contortrix	8.4E-06	2.62

subfamily. P- ie sub-subfam- ily		contortrix OX=8713 PE=1 SV=1			
Proteinase inhibitors					
Venom Kunitz- type family	Gene.82424_ L_san- guineus_515 97_g.82424_ m.82424	VKT_BOMIG	Kunitz-type serine protease inhibitor Bi-KTI OS=Bombus ignitus OX=130704 PE=2 SV=1	2.8E-11	4.18
	Gene.85469_ L_san- guineus_556 87_g.85469_ m.85469	VKT_AUSLA	Putative Kunitz- type serine prote- ase inhibitor OS=Austrelaps la- bialis OX=471292 PE=2 SV=1	1.6E-12	1.32
	Gene.66438_ L_san- guineus_334 58_g.66438_ m.66438	VKT1A_CONCL	Kunitz-type serine protease inhibitor conotoxin Cal9.1a OS=Californiconus californicus OX=1736779 PE=2 SV=1	1.4E-16	1037.70
	Gene.66701_ L_san- guineus_337 10_g.66701_ m.66701	VKT3_BITGA	Kunitz-type serine protease inhibitor bitisilin-3 (Frag- ment) OS=Bitis ga- bonica OX=8694 PE=2 SV=1	1.2E-40	3.14
Ion channel inhibitor activity					
CRISP family	Gene.50968_ L_san- guineus_206 37_g.50968_ m.50968	CRVP_ERYPO	Cysteine-rich venom protein LIO1 (Fragment) OS=Erythrolampru s poecilogyrus OX=338838 PE=2 SV=1	1.5E-18	1.67
	Gene.35657_ L_san- guineus_115 30_g.35657_ m.35657	CRVP_LATSE	Cysteine-rich venom protein latisemin OS=Lati- cauda semifasciata OX=8631 PE=2 SV=1	1.9E-23	2.98
	Gene.19374_ L_san- guineus_475 0_g.19374_m. 19374	CRVP_PHIOL	Cysteine-rich venom protein OS=Philodryas olf- ersii OX=120305 PE=2 SV=1	1.3E-31	4.39
	Gene.45189_ L_san- guineus_168	MR30_CONMR	Cysteine-rich venom protein Mr30 OS=Conus	1.9E-40	20.41

	26_g.45189_ m.45189		marmoreus OX=42752 PE=1 SV=1		
CRISP fam- ily. Venom al- lergen 5-like subfamily	Gene.79573_ L_san- guineus_479 61_g.79573_ m.79573	VA543_SCODE	Scoloptoxin SSD43 OS=Scolopendra dehaani OX=2609776 PE=1 SV=1	3.3E-10	1.21
	Gene.88376_ L_san- guineus_599 69_g.88376_ m.88376	VA5_VESMA	Venom allergen 5 OS=Vespa manda- rinia OX=7446 PE=1 SV=1	8.1E-17	0.69
	Gene.68416_ L_san- guineus_353 92_g.68416_ m.68416	VA5_POLDO	Venom allergen 5 OS=Polistes domi- nula OX=743375 PE=1 SV=2	1.1E-19	1.61
	Gene.38598_ L_san- guineus_130 43_g.38598_ m.38598	VA576_SCODE	Scoloptoxin SSD976 OS=Scolopendra dehaani OX=2609776 PE=1 SV=1	4.3E-28	33.22
Nemertide fam- ily	Gene.54610_ L_san- guineus_233 00_g.54610_ m.54610	NEMA1_LINLO	Nemertide alpha-1 (Fragment) OS=Lineus longissi- mus OX=88925 PE=1 SV=1	1.8E-10	112.85
Hemostasis impairing toxin					
Snaclec family	Gene.97854_ L_san- guineus_752 37_g.97854_ m.97854	SLDA_TRIAB	Snaclec alboaggre- gin-D subunit al- pha OS=Tri- meresurus albo- labris OX=8765 PE=1 SV=1	3.9E-06	0.79
	Gene.92649_ L_san- guineus_664 72_g.92649_ m.92649	SL1_SISCA	Snaclec 1 OS=Sis- trurus catenatus edwardsii OX=8762 PE=2 SV=1	7.9E-09	2.22
	Gene.90645_ L_san- guineus_634 39_g.90645_ m.90645	SLB1_DEIAC	Snaclec agglucetin subunit beta-1 OS=Deinagkistro- don acutus OX=36307 PE=1 SV=1	4.6E-13	0.58
SNTX/VTX toxin family	Gene.97106_ L_san- guineus_740 35_g.97106_ m.97106	CTXA_SCOPL	Cytolytic toxin-al- pha OS=Scorpaena plumieri OX=274700 PE=1 SV=1	3.1E-13	0.77

	Gene.96616_ L_san- guineus_731 87_g.96616_ m.96616	CTXB_SCOPL	Cytolytic toxin-beta OS=Scorpaena plumieri OX=274700 PE=1 SV=1	3.5E-16	0.68
True venom lectin family	Gene.69521_ L_san- guineus_365 92_g.69521_ m.69521	LECM_THRJA	C-type lectin lec- toxin-Thr1 OS=Thrasops jack- sonii OX=186611 PE=2 SV=1	3.9E-08	1.31
Other toxins candidates					
Glycoprotein hormones subu- nit alpha family	Gene.62301_ L_san- guineus_296 40_g.62301_ m.62301	CTHA2_CONVC	Thyrostimulin al- pha-2 subunit OS=Conus victoriae OX=319920 PE=1 SV=1	1.9E-11	1.66
EGF domain peptide family	Gene.42600_ L_san- guineus_152 90_g.42600_ m.42600	TX18A_MANRB	U18-myrmecitoxin- Mri1a OS=Manica rubida OX=219785 PE=1 SV=1	4E-09	2.55
EGF-like, Sushi, TSP type-1, LDL-receptor class A	Gene.17262_ L_san- guineus_404 9_g.17262_m. 17262	CTX_SEPES	SE-cephalotoxin OS=Sepia esculenta OX=31210 PE=1 SV=1	1.9E-97	3.62
IGFBP N-termi- nal, Kazal-like, Ig-like C2-type	Gene.31441_ L_san- guineus_953 5_g.31441_m. 31441	IGFBP_CUPSA	Insulin-like growth factor-binding pro- tein-related protein 1 OS=Cupiennius salei OX=6928 PE=2 SV=1	2.2E-52	3.46
Insulin family	Gene.87792_ L_san- guineus_591 34_g.87792_ m.87792	INS1_CONIM	Con-Ins Im1 OS=Conus imperi- alis OX=35631 PE=2 SV=1	2.8E-06	1.14
LDL-receptor class A domain	Gene.18530_ L_san- guineus_446 2_g.18530_m. 18530	CPROH_CONVC	Neuropeptide pro- hormone-4 OS=Co- nus victoriae OX=319920 PE=1 SV=1	6.4E-23	11.06
Thyroglobu- lin_1,2 hits DOMAIN	Gene.64710_ L_san- guineus_318 21_g.64710_ m.64710	PN16_PHONI	U24-ctenitoxin- Pn1a OS=Phoneu- tria nigriventer OX=6918 PE=1 SV=1	6.6E-07	25.79

Table S10. Toxin transcripts of *Notospermus geniculatus*. Unique toxins families are shown in bold.

Protein family	Transcript ID	Uniprot accession	Description	E-value	Expression, TPM
Pore-forming toxins					
Cytotoxin A-III-like	Gene.128743_N_geniculatus_37710_g.128743_m.128743	CXA3_CERLA	Cytotoxin A-III OS=Cerebratulus lacteus OX=6221 PE=1 SV=1	1.2E-38	204.37
MACPF domain	Gene.146480_N_geniculatus_47623_g.146480_m.146480	PV21_POMCA	Perivitellin-2 67 kda subunit OS=Pomacea canaliculata OX=400727 PE=1 SV=2	6.8E-19	0.32
	Gene.44557_N_geniculatus_6765_g.44557_m.44557	PV21_POMMA	Perivitellin-2 67 kda subunit OS=Pomacea maculata OX=1245466 PE=1 SV=1	7.8E-89	6.82
Enzymes					
Arthropod phospholipase D family. Class II subfamily	Gene.147654_N_geniculatus_48338_g.147654_m.147654	B1O_LOXCS	Dermonecrotic toxin lcsictox-betaic1 (Fragment) OS=Loxosceles cf. Spinulosa (strain GJB-2008) OX=575952 PE=2 SV=1	1.9E-18	0.33
	Gene.73013_N_geniculatus_14545_g.73013_m.73013	A1O_LOXGA	Dermonecrotic toxin lgsictox-alphaic1 OS=Loxosceles gaucho OX=58216 PE=1 SV=1	5E-30	0.24
	Gene.74953_N_geniculatus_15169_g.74953_m.74953	B1T1_LOXSN	Dermonecrotic toxin lpsictox-betaie3i (Fragment) OS=Loxosceles spinulosa OX=571532 PE=2 SV=1	2.2E-38	0.17
Arthropod phospholipase D family. Class II subfamily. Class iia sub-subfamily	Gene.92607_N_geniculatus_21414_g.92607_m.92607	A51_LOXIN	Dermonecrotic toxin lisictox-alphav1 OS=Loxosceles intermedia OX=58218 PE=1 SV=1	2.3E-32	3.53
Arthropod phospholipase D family. Class II subfamily. Class iib sub-subfamily	Gene.87640_N_geniculatus_19525_g.87640_m.87640	B1Q_LOXIN	Dermonecrotic toxin lisictox-betaid1 OS=Loxosceles intermedia OX=58218 PE=1 SV=1	9.2E-42	2.74

Dnase II family	Gene.108701 _N_genicula- tus_28112_g. 108701_m.10 8701	DNA2_ACAPL	Plancitoxin-1 OS=Acanthaster planci OX=133434 PE=1 SV=1	3.2E-51	11.18
Glycosyl hydro- lase 56 family	Gene.176515 _N_genicula- tus_67089_g. 176515_m.17 6515	HYAL1_MESMA	Hyaluronidase-1 OS=Mesobuthus martensii OX=34649 PE=1 SV=2	2.3E-13	0.00
	Gene.143755 _N_genicula- tus_46005_g. 143755_m.14 3755	HYAL_ECHOC	Hyaluronidase OS=Echis ocellatus OX=99586 PE=2 SV=1	1.8E-15	0.00
	Gene.149563 _N_genicula- tus_49486_g. 149563_m.14 9563	HYAL_CONCN	Hyaluronidase con- ohyal-Cn1 OS=Co- nus consors OX=101297 PE=1 SV=1	9.3E-17	8.60
	Gene.88765_ N_genicula- tus_19933_g. 88765_m.887 65	HYAL_CONPU	Hyaluronidase con- ohyal-P1 OS=Conus purpurascens OX=41690 PE=1 SV=1	2.1E-40	0.21
	Gene.101095 _N_genicula- tus_24787_g. 101095_m.10 1095	HUGA_APIME	Hyaluronidase OS=Apis mellifera OX=7460 PE=1 SV=1	3.7E-60	0.00
Flavin monoam- ine oxidase fam- ily. FIG1 subfam- ily	Gene.46686_ N_genicula- tus_7256_g.4 6686_m.4668 6	OXLA_CALRH	L-amino-acid oxi- dase OS=Cal- loselasma rhodos- toma OX=8717 PE=1 SV=2	2.1E-46	0.27
Nucleotide pyro- phospha- tase/phos- phodiesterase family	Gene.32725_ N_genicula- tus_4280_g.3 2725_m.3272 5	PDE2_CROAD	Venom phos- phodiesterase 2 OS=Crotalus ada- manteus OX=8729 PE=1 SV=1	5.2E-129	4.33
Peptidase M12A domain	Gene.125887 _N_genicula- tus_36255_g. 125887_m.12 5887	VMPA4_LOXLA	Astacin-like metal- loprotease toxin 4 (Fragment) OS=Loxosceles laeta OX=58217 PE=2 SV=1	1.6E-06	0.00
Phospholipase A2 fam- ily. Group I sub- family	Gene.120949 _N_genicu- la- tus_33786_g.	PA22_ACAPL	Phospholipase A2 AP-PLA2-II OS=Acanthaster	4.3E-11	0.84

	120949_m.12 0949		planci OX=133434 PE=1 SV=1		
Phospholipase A2 family. Group I subfamily. D49 sub-subfamily	Gene.143594 _N_genicula- tus_45913_g. 143594_m.14 3594	PA2B_MICCO	Basic phospho- lipase A2 OS=Mi- crurus corallinus OX=54390 PE=1 SV=1	2E-12	0.00
Phospholipase A2 family. Group III subfamily	Gene.118636 _N_genicula- tus_32651_g. 118636_m.11 8636	HEMI1_HEMLE	Phospholipase A2 hemilipin OS=Hemiscorpius lepturus OX=520031 PE=1 SV=1	1.2E-24	2.78
	Gene.72635_ N_genicula- tus_14421_g. 72635_m.726 35	PA23_HELSU	Phospholipase A2 isozymes PA3A/PA3B/PA5 OS=Heloderma suspectum OX=8554 PE=1 SV=3	4.5E-37	24.90
Phospholipase A2 family. Group II subfamily. D49 sub-subfamily	Gene.90565_ N_genicula- tus_20610_g. 90565_m.905 65	PA2B1_VIPBN	Basic phospho- lipase A2 chain HDP-1P OS=Vipera berus nikolskii OX=1808362 PE=1 SV=1	1E-22	6.86
Phospholipase A2 family. Group III subfamily	Gene.91289_ N_genicula- tus_20900_g. 91289_m.912 89	PA2A2_HELSU	Acidic phospho- lipase A2 PA4 OS=Heloderma suspectum OX=8554 PE=1 SV=2	3.7E-29	20.81
Phospholipase B- like family	Gene.63302_ N_genicula- tus_11598_g. 63302_m.633 02	PLB_DRYCN	Phospholipase-B 81 OS=Drysdalia coro- noides OX=66186 PE=1 SV=1	0	11.03
Venom metallo- proteinase (M12B) family	Gene.106790 _N_genicula- tus_27259_g. 106790_m.10 6790	VMP03_EULPE	Venom metallopro- teinase 3 OS=Eulo- phus pennicornis OX=108749 PE=2 SV=1	3.1E-07	2.57
Venom metallo- proteinase (M12B) family. P- III subfamily	Gene.137591 _N_genicula- tus_42492_g. 137591_m.13 7591	VM34_DRYCN	Zinc metallopro- teinase-disintegrin- like MTP4 OS=Drysdalia coro- noides OX=66186 PE=1 SV=1	1.5E-23	0.00

Venom metalloproteinase (M12B) family. P-III subfamily. P-iiib subfamily	Gene.133242_N_genicula-tus_40099_g.133242_m.133242	VM3HA_PROFL	Zinc metalloproteinase/disintegrin-like HR1a OS=Protobothrops flavoviridis OX=88087 PE=1 SV=1	4.6E-09	0.00
Proteinase inhibitors					
Venom Kunitz-type family	Gene.160680_N_genicula-tus_56483_g.160680_m.160680	VKTHD_DENAN	Kunitz-type serine protease inhibitor homolog delta-dendrotoxin OS=Dendroaspis angusticeps OX=8618 PE=1 SV=1	2.1E-09	0.00
	Gene.132845_N_genicula-tus_39889_g.132845_m.132845	VKT4_PSETT	Kunitz-type serine protease inhibitor textilinin-4 OS=Pseudonaja textilis textilis OX=169397 PE=2 SV=1	3E-09	3.55
	Gene.159195_N_genicula-tus_55539_g.159195_m.159195	VKTCT_OPHHA	Kunitz-type serine protease inhibitor TCI OS=Ophiophagus hannah OX=8665 PE=1 SV=1	3.2E-16	6.38
	Gene.123192_N_genicula-tus_34877_g.123192_m.123192	VKT1_TRILK	Kunitz-type U19-barytoxin-Tl1a OS=Trittame loki OX=1295018 PE=2 SV=2	8E-16	0.00
	Gene.147622_N_genicula-tus_48319_g.147622_m.147622	VKT1_OXYMI	Kunitz-type serine protease inhibitor microlepidin-1 OS=Oxyuranus microlepidotus OX=111177 PE=2 SV=1	1.4E-19	142.80
	Gene.142227_N_genicula-tus_45116_g.142227_m.142227	VKT3_BITGA	Kunitz-type serine protease inhibitor bitisilin-3 (Fragment) OS=Bitis gabonica OX=8694 PE=2 SV=1	1.9E-31	32.21
Venom Kunitz-type family. Sea anemone type 2 potassium	Gene.87698_N_genicula-tus_19544_g.87698_m.87698	VKT1_ANTAF	PI-actitoxin-Axm2a OS=Anthopleura aff. Xanthogrammica OX=152178 PE=1 SV=1	9.5E-20	0.00

channel toxin subfamily		Ion channel inhibitor activity			
Conotoxin I3 superfamily	Gene.158909_N_geniculus_55362_g.158909_m.158909	I3B2_CONPL	Conotoxin Pu11.2 OS=Conus pulicarius OX=93154 PE=3 SV=1	9.7E-06	3.61
CRISP family	Gene.178605_N_geniculus_68509_g.178605_m.178605	VA3_DINQU	Venom allergen 3 homolog OS=Dinoponera quadricaps OX=609295 PE=2 SV=1	2.4E-08	0.00
	Gene.43244_N_geniculus_6474_g.43244_m.43244	CRVP2_DISTY	Cysteine-rich venom protein DIS2 OS=Dispholidus typus OX=46295 PE=2 SV=1	9.2E-08	0.71
	Gene.71706_N_geniculus_14138_g.71706_m.71706	CRVP_CROAT	Cysteine-rich venom protein catrin OS=Crotalus atrox OX=8730 PE=1 SV=1	1.5E-24	0.16
	Gene.106517_N_geniculus_27136_g.106517_m.106517	CRVP_OXYMI	Cysteine-rich venom protein pseudochetoxin-like OS=Oxyuranus microlepidotus OX=111177 PE=2 SV=1	3.5E-30	0.87
	Gene.79877_N_geniculus_16779_g.79877_m.79877	CRVP_PHIOL	Cysteine-rich venom protein OS=Philodryas olfersii OX=120305 PE=2 SV=1	7E-34	2.01
	Gene.109329_N_geniculus_28397_g.109329_m.109329	CRVP_LEIMD	Cysteine-rich venom protein LEI1 (Fragment) OS=Leioheterodon mada-gascariensis OX=46577 PE=1 SV=1	1.6E-34	1.99
	Gene.110897_N_geniculus_29081_g.110897_m.110897	MR30_CONMR	Cysteine-rich venom protein Mr30 OS=Conus marmoreus OX=42752 PE=1 SV=1	2.2E-34	0.91

	Gene.71903_ N_genicula- tus_14199_g. 71903_m.719 03	CRVP_PSETE	Cysteine-rich venom protein pseudecheto- xin-like OS=Pseudonaja textilis OX=8673 PE=1 SV=1	3.5E-33	0.48
	Gene.92364_ N_genicula- tus_21318_g. 92364_m.923 64	TX31_CONTE	Cysteine-rich venom protein OS=Conus textile OX=6494 PE=1 SV=1	7.7E-34	2.06
	Gene.33460_ N_genicula- tus_4413_g.3 3460_m.3346 0	CRVP_AUSSU	Cysteine-rich venom protein OS=Austrelaps su- perbus OX=29156 PE=2 SV=1	3.2E-34	0.63
CRISP fam- ily. Venom aller- gen 5-like sub- family	Gene.111771_ N_genicula- tus_29480_g. 111771_m.11 1771	VA5_VESPE	Venom allergen 5 OS=Vespula pen- sylvanica OX=30213 PE=1 SV=1	4.5E-54	0.00
Sea anemone structural class 9a family	Gene.63263_ N_genicula- tus_11585_g. 63263_m.632 63	TX9A_ANTMC	Delta-actitoxin- Amc1a OS=Anthe- opsis maculata OX=280228 PE=1 SV=1	2.5E-11	19.21
Scoloptoxin-05 family	Gene.93901_ N_genicula- tus_21904_g. 93901_m.939 01	TX53A_ETHRU	U-scoloptoxin(05)- Er3a OS=Eth- mostigmus ru- bripes OX=62613 PE=2 SV=1	2.7E-06	0.47
Scoloptoxin-11 family	Gene.109455_ N_genicula- tus_28449_g. 109455_m.10 9455	TXB2A_SCOAL	U-scoloptoxin(11)- Sa2a OS=Scolopen- dra alternans OX=1329349 PE=2 SV=1	1.3E-06	2.36
Venom Kunitz- type family. Sea anemone type 2 potassium chan- nel toxin subfam- ily	Gene.155096_ N_genicula- tus_52945_g. 155096_m.15 5096	VKT7_ANEVI	U-actitoxin-Avd3j OS=Anemonia vi- ridis OX=51769 PE=3 SV=1	3.7E-19	4.04
Hemostasis impairing toxin					
Snaclec family	Gene.60567_ N_genicula- tus_10834_g. 60567_m.605 67	SLA4_TRIAB	Snaclec alboaggre- gin-A subunit beta' OS=Trimeresurus albolabris OX=8765 PE=1 SV=1	4E-06	1.01
	Gene.161623_ N_genicula- tus_57108_g.	SLA_BOTIN	Snaclec bothroin- sularin subunit al- pha OS=Bothrops	1.8E-13	0.00

	161623_m.16 1623		insularis OX=8723 PE=1 SV=1		
	Gene.85733_ N_genicula- tus_18850_g. 85733_m.857 33	SLCB_DEIAC	Snaclec agkicetin-C subunit beta OS=Deinagkistro- don acutus OX=36307 PE=1 SV=1	4.1E-12	13.03
	Gene.50710_ N_genicula- tus_8234_g.5 0710_m.5071 0	SLA_DABSI	Snaclec dabocetin subunit alpha OS=Daboia siamen- sis OX=343250 PE=1 SV=1	4.5E-15	0.36
SNTX/VTX toxin family	Gene.184803_ N_genicula- tus_72767_g. 184803_m.18 4803	VTXB_SYNVE	Verrucotoxin subu- nit beta OS=Synan- ceia verrucosa OX=51996 PE=1 SV=3	2.7E-22	0.00
	Gene.70470_ N_genicula- tus_13754_g. 70470_m.704 70	STXB_SYNHO	Stonustoxin subu- nit beta OS=Synan- ceia horrida OX=13279 PE=1 SV=3	1.3E-73	0.37
	Gene.83884_ N_genicula- tus_18187_g. 83884_m.838 84	CTXA_SCOPL	Cytolytic toxin-al- pha OS=Scorpaena plumieri OX=274700 PE=1 SV=1	2.9E-74	0.72
	Gene.58615_ N_genicula- tus_10309_g. 58615_m.586 15	STXA_SYNHO	Stonustoxin subu- nit alpha OS=Synanceia hor- rida OX=13279 PE=1 SV=3	9.2E-89	0.78
	Gene.49719_ N_genicula- tus_7994_g.4 9719_m.4971 9	STXA_SYNVE	Neoverrucotoxin subunit alpha OS=Synanceia ver- rucosa OX=51996 PE=1 SV=1	5.4E-97	3.16
	Gene.16256_ N_genicula- tus_1578_g.1 6256_m.1625 6	STXB_SYNVE	Neoverrucotoxin subunit beta OS=Synanceia ver- rucosa OX=51996 PE=1 SV=1	1.9E-93	3.89
	Gene.174251_ N_genicula- tus_65555_g. 174251_m.17 4251	LECM_NOTSC	C-type lectin man- nose-binding iso- form OS=Notechis scutatus scutatus OX=70142 PE=2 SV=1	2.7E-14	0.78
Other toxins candidates					

Elevenin-like	Gene.89934_ N_genicula- tus_20379_g. 89934_m.899 34	CELE_CONVC	Elevenin-Vc1 OS=Conus victoriae OX=319920 PE=1 SV=1	5.5E-06	1.26
IGFBP N-termi- nal, Kazal-like, Ig-like C2-type	Gene.67877_ N_genicula- tus_12957_g. 67877_m.678 77	IGFBP_CUPSA	Insulin-like growth factor-binding pro- tein-related protein 1 OS=Cupiennius salei OX=6928 PE=2 SV=1	4.4E-60	16.63
Insulin family	Gene.98850_ N_genicula- tus_23870_g. 98850_m.988 50	INS1_CONIM	Con-Ins Im1 OS=Conus imperi- alis OX=35631 PE=2 SV=1	3.2E-09	5.51
	Gene.86492_ N_genicula- tus_19114_g. 86492_m.864 92	INS2_CONIM	Con-Ins Im2 OS=Conus imperi- alis OX=35631 PE=2 SV=1	6.6E-15	1.98
	Gene.94322_ N_genicula- tus_22061_g. 94322_m.943 22	INS2C_CONFO	Con-Ins F2c OS=Conus floridu- lus OX=97180 PE=1 SV=1	6.1E-10	0.00
Glycoprotein hor- mones subunit al- pha family	Gene.96349_ N_genicula- tus_22878_g. 96349_m.963 49	CTHA2_CONVC	Thyrostimulin al- pha-2 subunit OS=Conus victoriae OX=319920 PE=1 SV=1	2.8E-17	2.97
Glycoprotein hor- mones subunit beta family	Gene.61031_ N_genicula- tus_10955_g. 61031_m.610 31	CTHB5_CONVC	Thyrostimulin beta- 5 subunit OS=Co- nus victoriae OX=319920 PE=2 SV=1	1.3E-22	1.49
LDL-receptor class A domain	Gene.107185_ N_genicula- tus_27436_g. 107185_m.10 7185	CPROH_CONVC	Neuropeptide pro- hormone-4 OS=Co- nus victoriae OX=319920 PE=1 SV=1	8E-25	5.63
NGF-beta family	Gene.108644_ N_genicula- tus_28085_g. 108644_m.10 8644	NGFV_NAJAT	Venom nerve growth factor OS=Naja atra OX=8656 PE=1 SV=1	4.7E-10	0.23
	Gene.122061_ N_genicula- tus_34320_g. 122061_m.12 2061	NGFV1_PSEAU	Venom nerve growth factor 1 OS=Pseudechis australis OX=8670 PE=2 SV=1	2.1E-10	0.19

	Gene.105448 _N_genicula- tus_26669_g. 105448_m.10 5448	NGFV_DRYCN	Venom nerve growth factor OS=Drysdalia coro- noides OX=66186 PE=2 SV=1	6.1E-13	3.83
	Gene.106335 _N_genicula- tus_27053_g. 106335_m.10 6335	NGFV_PSEPO	Venom nerve growth factor OS=Pseudechis porphyriacus OX=8671 PE=2 SV=1	4.6E-14	0.00
	Gene.108412 _N_genicula- tus_27983_g. 108412_m.10 8412	NGFV2_NAJSP	Venom nerve growth factor 2 OS=Naja sputatrix OX=33626 PE=2 SV=1	9.5E-18	0.29
PDGF/VEGF growth factor family	Gene.65140_ N_genicula- tus_12143_g. 65140_m.651 40	VEGFA_VIPAA	Vascular endothe- lial growth factor A OS=Vipera ammo- dytes ammodytes OX=8705 PE=2 SV=1	4.2E-09	3.28
Venom comple- ment C3 homolog family	Gene.113391 _N_genicula- tus_30216_g. 113391_m.11 3391	VCO3_NAJKA	Cobra venom factor OS=Naja kaouthia OX=8649 PE=1 SV=1	2.5E-24	0.48

Table S11. Toxin transcripts of *Riseriellus occultus*.

Protein family	Transcript ID	Uniprot accession	Description	E-value	Expression, TPM
Pore-forming toxins					
Cytotoxin A-III-like	Gene.68287_ R_occul- tus_26947_g. 68287_m.682 87	CXA3_CERLA	Cytotoxin A-III OS=Cerebratulus lacteus OX=6221 PE=1 SV=1	1.7E-44	57.67
MACPF domain	Gene.49434_ R_occul- tus_13168_g. 49434_m.494 34	PV21_POMMA	Perivitellin-2 67 kda subunit OS=Pomacea macu- lata OX=1245466 PE=1 SV=1	8.2E-59	8.34
Enzymes					
Arthropod phos- pholipase D fam- ily. Class II sub- family	Gene.90642_ R_occul- tus_56425_g. 90642_m.906 42	B1T1_LOXSN	Dermonecrotic toxin Ispisictox-be- taie3i (Fragment) OS=Loxosceles spi- nulosa OX=571532 PE=2 SV=1	1.1E-13	1.86

	Gene.72081_ R_occul- tus_30849_g. 72081_m.720 81	B1O_LOXCS	Dermonecrotic toxin lcsictox-be- taic1 (Fragment) OS=Loxosceles cf. Spinulosa (strain GJB-2008) OX=575952 PE=2 SV=1	2E-14	6.05
	Gene.75604_ R_occul- tus_34760_g. 75604_m.756 04	A1MA4_LOXDE	Dermonecrotic toxin ldsictox-al- phaib3aiv (Frag- ment) OS=Loxosce- les deserta OX=424440 PE=2 SV=1	3.6E-16	1.53
	Gene.91645_ R_occul- tus_58150_g. 91645_m.916 45	B1V_SICCD	Dermonecrotic toxin sdsictox-be- taif1 (Fragment) OS=Sicarius cf. Da- marensis (strain GJB-2008) OX=575956 PE=2 SV=1	1.4E-18	6.47
	Gene.56378_ R_occul- tus_17338_g. 56378_m.563 78	DTPLD_HEMLE	Dermonecrotic toxin HI-PLD1 OS=Hemiscorpius lepturus OX=520031 PE=1 SV=1	1.9E-22	7.64
Dnase II family	Gene.14621_ R_occul- tus_1659_g.1 4621_m.1462 1	DNA2_ACAPL	Plancitoxin-1 OS=Acanthaster planci OX=133434 PE=1 SV=1	1.6E-98	3.51
Flavin monoam- ine oxidase fam- ily. FIG1 subfam- ily	Gene.28153_ R_occul- tus_4706_g.2 8153_m.2815 3	OXLA_CALRH	L-amino-acid oxi- dase OS=Cal- loselasma rhodos- toma OX=8717 PE=1 SV=2	2.7E-44	16.20
Natterin family	Gene.59007_ R_occul- tus_19209_g. 59007_m.590 07	NATT4_THANI	Natterin-4 OS=Thalas- sophryne nattereri OX=289382 PE=2 SV=1	3.9E-14	7.80
Nucleotide pyro- phospha- tase/phos- phodiesterase family	Gene.28090_ R_occul- tus_4687_g.2 8090_m.2809 0	PDE2_CROAD	Venom phos- phodiesterase 2 OS=Crotalus ada- manteus OX=8729 PE=1 SV=1	8.9E-180	5.68

Phospholipase A2 family. Group I subfamily. D49 sub-subfamily	Gene.67220_R_occultus_25928_g.67220_m.67220	PA2TA_OXYSC	Basic phospholipase A2 taipoxin alpha chain OS=Oxyuranus scutellatus scutellatus OX=8667 PE=1 SV=1	6.3E-21	3.86
	Gene.34929_R_occultus_6835_g.34929_m.34929	PA2A2_NAJME	Acidic phospholipase A2 DE-II OS=Naja melanoleuca OX=8643 PE=1 SV=1	8.6E-25	40.35
Phospholipase A2 family. Group III subfamily	Gene.58712_R_occultus_19007_g.58712_m.58712	PA2_XYLAI	Phospholipase A(2) OS=Xylocopa appendiculata circumvolans OX=135722 GN=PLA2 PE=1 SV=1	9.9E-24	2.14
	Gene.13654_R_occultus_1496_g.13654_m.13654	PA2A2_HELSU	Acidic phospholipase A2 PA4 OS=Heloderma suspectum OX=8554 PE=1 SV=2	1.9E-32	3.84
Phospholipase B-like family	Gene.14123_R_occultus_1576_g.14123_m.14123	PLB_DRYCN	Phospholipase-B 81 OS=Drysdalia coronoides OX=66186 PE=1 SV=1	0	2.06
Venom metalloproteinase (M12B) family. P-I subfamily	Gene.88864_R_occultus_53388_g.88864_m.88864	VM1F_MACLB	Snake venom metalloproteinase fibrolase OS=Macrovipera lebetina OX=8709 PE=1 SV=1	1.2E-15	1.06
Proteinase inhibitors					
Venom Kunitz-type family	Gene.52630_R_occultus_14975_g.52630_m.52630	VKT2_BITGA	Kunitz-type serine protease inhibitor bitisilin-2 OS=Bitis gabonica OX=8694 PE=1 SV=1	1.1E-15	32.42
	Gene.83158_R_occultus_44528_g.83158_m.83158	VKT_BOMTE	Kunitz-type serine protease inhibitor Bt-KTI OS=Bombus terrestris OX=30195 PE=2 SV=1	6.5E-17	327.70

	Gene.71074_ R_occul- tus_29761_g. 71074_m.710 74	VKT3_BITGA	Kunitz-type serine protease inhibitor bitisilin-3 (Frag- ment) OS=Bitis ga- bonica OX=8694 PE=2 SV=1	3.5E-26	3.44
Venom Kunitz- type family. Sea anemone type 2 potassium chan- nel toxin subfam- ily	Gene.46126_ R_occul- tus_11483_g. 46126_m.461 26	ATPI1_ACTTE	Actinia tenebrosa protease inhibitors OS=Actinia tene- brosa OX=6105 PE=1 SV=1	9.8E-43	8.83
Ion channel inhibitor activity					
CRISP family	Gene.62190_ R_occul- tus_21590_g. 62190_m.621 90	CRVP_HOPST	Cysteine-rich venom protein pseudechetoxin- like OS=Hop- locephalus ste- phensii OX=196418 PE=2 SV=1	8E-14	314.25
	Gene.51903_ R_occul- tus_14556_g. 51903_m.519 03	TX31_CONTE	Cysteine-rich venom protein OS=Conus textile OX=6494 PE=1 SV=1	2.4E-26	331.75
	Gene.44413_ R_occul- tus_10655_g. 44413_m.444 13	MR30_CONMR	Cysteine-rich venom protein Mr30 OS=Conus marmoreus OX=42752 PE=1 SV=1	4.1E-32	54.22
	Gene.49813_ R_occul- tus_13368_g. 49813_m.498 13	CRVP_PSEAU	Cysteine-rich venom protein pseudechetoxin OS=Pseudechis australis OX=8670 PE=1 SV=1	1.9E-36	3.40
CRISP fam- ily. Venom aller- gen 5-like sub- family	Gene.59141_ R_occul- tus_19305_g. 59141_m.591 41	VA543_SCODE	Scoloptoxin SSD43 OS=Scolopendra dehaani OX=2609776 PE=1 SV=1	6E-30	113.83
Nemertide family	Gene.67160_ R_occul- tus_25870_g. 67160_m.671 60	NEMA1_LINLO	Nemertide alpha-1 (Fragment) OS=Lineus longissi- mus OX=88925 PE=1 SV=1	6.4E-12	2.02
Scoloptoxin-11 family	Gene.85657_ R_occul- tus_48208_g.	TX14B_SCODE	Scoloptoxin SSD20 (Fragment) OS=Scolopendra dehaani	3.7E-36	2.62

	85657_m.856 57		OX=2609776 PE=1 SV=1		
Venom Kunitz-type family. Sea anemone type 2 potassium channel toxin subfamily	Gene.45107_R_occul-tus_10986_g.45107_m.45107	VKT53_ANEVI	Kappapi-actitoxin-Avd3e OS=Anemonia viridis OX=51769 PE=3 SV=1	4.1E-18	168.01
Hemostasis impairing toxin					
Snaclec family	Gene.68472_R_occul-tus_27105_g.68472_m.68472	SL9A_CROAD	C-type lectin 9a OS=Crotalus adamanteus OX=8729 PE=1 SV=1	1.4E-08	89.97
	Gene.38071_R_occul-tus_7965_g.38071_m.38071	SLBB_TRIAB	Snaclec alboaggregin-B subunit beta OS=Trimeresurus albolabris OX=8765 PE=1 SV=2	2.5E-08	6.70
SNTX/VTX toxin family	Gene.24886_R_occul-tus_3814_g.24886_m.24886	STXA_SYNVE	Neoverrucotoxin subunit alpha OS=Synanceia verrucosa OX=51996 PE=1 SV=1	4.9E-42	5.02
	Gene.45481_R_occul-tus_11159_g.45481_m.45481	STXB_SYNVE	Neoverrucotoxin subunit beta OS=Synanceia verrucosa OX=51996 PE=1 SV=1	3.5E-78	4.53
	Gene.911_R_occul-tus_40_g.911_m.911	STXA_SYNHO	Stonustoxin subunit alpha OS=Synanceia horrida OX=13279 PE=1 SV=3	8.5E-88	6.48
	Gene.7321_R_occul-tus_590_g.7321_m.7321	CTXA_SCOPL	Cytolytic toxin-alpha OS=Scorpaena plumieri OX=274700 PE=1 SV=1	6.8E-95	4.72
True venom lectin family	Gene.91840_R_occul-tus_58524_g.91840_m.91840	LECG_THANI	Galactose-specific lectin nattererin OS=Thalassophryne nattereri OX=289382 PE=1 SV=1	4.5E-10	3.12
Other toxins candidates					
IGFBP N-terminal domain	Gene.96120_R_occul-tus_66363_g.	VP302_LYCMC	Venom protein 302 OS=Lychas mucronatus OX=172552 PE=2 SV=1	2E-06	1.61

96120_m.96120					
IGFBP N-terminal, Kazal-like, Ig-like C2-type	Gene.24185_R_occutus_3642_g.24185_m.24185_5	IGFBP_CUPSA	Insulin-like growth factor-binding protein-related protein 1 OS=Cupiennius salei OX=6928 PE=2 SV=1	1.8E-52	7.69
Insulin family	Gene.89464_R_occutus_54345_g.89464_m.89464_64	INS1_CONIM	Con-Ins Im1 OS=Conus imperialis OX=35631 PE=2 SV=1	7.8E-07	5.56
	Gene.47239_R_occutus_12039_g.47239_m.47239_39	INS1_CONFO	Con-Ins F1 OS=Conus floridulus OX=97180 PE=1 SV=1	9.9E-10	7.39
LDL-receptor class A domain	Gene.38355_R_occutus_8068_g.38355_m.38355_5	CPROH_CONVC	Neuropeptide pro-hormone-4 OS=Conus victoriae OX=319920 PE=1 SV=1	1.5E-24	28.02
-SE-CTX-like	Gene.14754_R_occutus_1682_g.14754_m.14754_4	CTXL_ACRMI	Cephalotoxin-like protein (Fragment) OS=Acropora millepora OX=45264 PE=1 SV=1	3.7E-144	46.79
Vasopressin/oxytocin family	Gene.65983_R_occutus_24746_g.65983_m.65983_83	CESS2_CONMO	Conopresin/conophysin, isoform 2 (Fragment) OS=Conus monile OX=351660 PE=2 SV=1	4.3E-24	3.06

Table S12. Toxin transcripts of *Amphiporous lactifloreus*.

Protein family	Transcript ID	Uniprot accession	Description	E-value	Expression, TPM
Pore-forming toxins					
MACPF domain	Gene.38401_Amphiporous_6886_g.38401_m.38401_01	PV21_POMCA	Perivitellin-2 67 kda subunit OS=Pomacea canaliculata OX=400727 PE=1 SV=2	8.7E-39	2.49
	Gene.31194_Amphiporous_4943_g.31194_m.31194_94	PV21_POMMA	Perivitellin-2 67 kda subunit OS=Pomacea maculata OX=1245466 PE=1 SV=1	1.2E-73	435.18

Enzymes					
Dnase II family	Gene.56234_ Amphipo- rous_13892_ g.56234_m.56 234	DNA2_ACAPL	Plancitoxin-1 OS=Acanthaster planci OX=133434 PE=1 SV=1	3.6E-36	2.00
Glycosyl hydro- lase 56 family	Gene.65205_ Amphipo- rous_20146_ g.65205_m.65 205	HUGA_APIME	Hyaluronidase OS=Apis mellifera OX=7460 PE=1 SV=1	8.9E-14	3.13
	Gene.65057_ Amphipo- rous_20037_ g.65057_m.65 057	HYAL_CONPU	Hyaluronidase con- ohyal-P1 OS=Conus purpurascens OX=41690 PE=1 SV=1	5.8E-12	2.47
	Gene.34524_ Amphipo- rous_5791_g. 34524_m.345 24	HYAL1_MESMA	Hyaluronidase-1 OS=Mesobuthus martensii OX=34649 PE=1 SV=2	2.4E-59	5.82
Peptidase M12A domain, Allrgn_V5/Tpx1_ CS, CAP_domain	Gene.50662_ Amphipo- rous_11207_ g.50662_m.50 662	VMPA2_LOXIN	Astacin-like metal- loprotease toxin 2 OS=Loxosceles in- termedia OX=58218 PE=2 SV=1	5.2E-32	260.11
Phospholipase A2 family. Group III subfamily	Gene.64909_ Amphipo- rous_19895_ g.64909_m.64 909	PA23_HELSU	Phospholipase A2 isozymes PA3A/PA3B/PA5 OS=Heloderma suspectum OX=8554 PE=1 SV=3	2E-19	1029.82
Type-B carboxy- lesterase/lipase family	Gene.23960_ Amphipo- rous_3328_g. 23960_m.239 60	ACES_BUNFA	Acetylcholinester- ase OS=Bungarus fasciatus OX=8613 GN=ACHE PE=1 SV=2	5.3E-126	15.33
Proteinase inhibitors					
Venom Kunitz- type family	Gene.41216_ Amphipo- rous_7730_g. 41216_m.412 16	VKT1D_CONCL	Kunitz-type serine protease inhibitor conotoxin Cal9.1d (Fragment) OS=Cal- iforniconus califor- nicus OX=1736779 PE=2 SV=1	1.1E-16	35.41

Venom Kunitz-type family. 02 (native) subfamily	Gene.52236_ Amphiporous_11892_ g.52236_m.52236	VKT1_ARAVE	Kunitz-type U1-aranetoxin-Av1a OS=Araneus ventricosus OX=182803 PE=2 SV=1	5.6E-8	10.78
Venom Kunitz-type family. Sea anemone type 2 potassium channel toxin subfamily	Gene.27479_ Amphiporous_4081_ g.27479_m.27479	VKT3C_ACTEQ	PI-actitoxin-Aeq3c OS=Actinia equina OX=6106 PE=1 SV=1	7.8E-14	129.20
Ion channel inhibitor activity					
CRISP family. Venom allergen 5-like subfamily	Gene.59180_ Amphiporous_15642_ g.59180_m.59180	VA552_SCODE	Scoloptoxin SSD552 OS=Scolopendra dehaani OX=2609776 PE=1 SV=1	7.3E-17	3.27
	Gene.49571_ Amphiporous_10741_ g.49571_m.49571	VA576_SCODE	Scoloptoxin SSD976 OS=Scolopendra dehaani OX=2609776 PE=1 SV=1	6.7E-23	30.43
Sea anemone structural class 9a family	Gene.21587_ Amphiporous_2850_ g.21587_m.21587	TX9A_ANTMC	Delta-actitoxin-Amc1a OS=Antheopsis maculata OX=280228 PE=1 SV=1	1.8E-6	114.61
Scoloptoxin-11 family	Gene.78441_ Amphiporous_37091_ g.78441_m.78441	TX14B_SCODE	Scoloptoxin SSD20 (Fragment) OS=Scolopendra dehaani OX=2609776 PE=1 SV=1	2E-10	2.80
Hemostasis impairing toxin					
Snaclec family	Gene.59882_ Amphiporous_16109_ g.59882_m.59882	SL9A_PROFL	Snaclec coagulation factor IX/factor X-binding protein subunit A OS=Protophthorops flavoviridis OX=88087 PE=1 SV=2	4.8E-6	1.89
	Gene.59450_ Amphiporous_15814_ g.59450_m.59450	SLA_BOTIN	Snaclec bothroinsularin subunit alpha OS=Bothrops insularis OX=8723 PE=1 SV=1	2E-6	1.91
	Gene.60327_ Amphiporous_16401_ g.60327_m.60327	SLA_GLOBR	Snaclec salmorin subunit A OS=Gloydus brevicaudus	4.9E-8	243.07

OX=259325 PE=1 SV=1					
	Gene.81843_ Amphipo- rous_42700_ g.81843_m.81 843	SLA1_DEIAC	Snaclec agglucetin subunit alpha-1 OS=Deinagkistro- don acutus OX=36307 PE=1 SV=1	1E-6	2.03
	Gene.58164_ Amphipo- rous_15029_ g.58164_m.58 164	SLRB_BITRH	Snaclec rhinocetin subunit beta OS=Bi- tis rhinoceros OX=715877 PE=1 SV=1	5.1E-6	4.70
	Gene.66006_ Amphipo- rous_20850_ g.66006_m.66 006	SLA_BITAR	Snaclec bitiscetin subunit alpha OS=Bitis arietans OX=8692 PE=1 SV=1	2.4E-6	3.02
True venom lec- tin family	Gene.66666_ Amphipo- rous_21506_ g.66666_m.66 666	LECM1_ERYPO	C-type lectin lec- toxin-Lio1 OS=Erythrolampru s poecilogyrus OX=338838 PE=2 SV=1	2.8E-09	2.49
	Gene.63849_ Amphipo- rous_18988_ g.63849_m.63 849	LECM1_HYDHA	C-type lectin 1 OS=Hydrophis hardwickii OX=8781 PE=2 SV=1	2.7E-07	1.82
Other toxins candidates					
Insulin family	Gene.56064_ Amphipo- rous_13794_ g.56064_m.56 064	INS1_CONTE	Con-Ins Tx1 OS=Conus textile OX=6494 PE=2 SV=1	6.8E-06	2.61
Insulin-like growth factor- binding protein domain, Kazal- type serine pro- tease inhibitor domain, Immu- noglobulin do- main	Gene.38477_ Amphipo- rous_6906_g. 38477_m.384 77	IGFBP_CUPSA	Insulin-like growth factor- binding protein-re- lated protein 1 OS=Cupiennius salei OX=6928 PE=2 SV=1	2.5E-46	67.34
LDL-receptor class A domain	Gene.44369_ Amphipo- rous_8766_g.	CPROH_CONVC	Neuropeptide pro- hormone-4 OS=Co- nus victoriae	2E-19	24.69

	44369_m.44369		OX=319920 PE=1 SV=1		
NGF-beta family	Gene.54049_Amphiporous_12770_g.54049_m.54049	NGFV_PSEPO	Venom nerve growth factor OS=Pseudechis porphyriacus OX=8671 PE=2 SV=1	3.4E-12	12.89
PDGF/VEGF growth factor family	Gene.37959_Amphiporous_6754_g.37959_m.37959	VEGFA_VIPAA	Vascular endothelial growth factor A OS=Vipera ammodytes ammodytes OX=8705 PE=2 SV=1	2.1E-10	7.12
TCTP family	Gene.54532_Amphiporous_13003_g.54532_m.54532	TCTP_BRABE	Translationally-controlled tumor protein homolog OS=Branchiostoma belcheri OX=7741 PE=2 SV=1	3.5E-27	2253.54

Table S13. Toxin transcripts of *Malacobdella grossa*.

Protein family	Transcript ID	Uniprot accession	Description	E-value	Expression, TPM
Pore-forming toxins					
MACPF domain	Gene.21779_M_grossa_5772_g.21779_m.21779	PV21_POMMA	Perivitellin-2 67 kda subunit OS=Pomacea maculata OX=1245466 PE=1 SV=1	5.6E-59	209.15
	Gene.37448_M_grossa_16878_g.37448_m.37448	PV21_POMCA	Perivitellin-2 67 kda subunit OS=Pomacea canaliculata OX=400727 PE=1 SV=2	1.9E-11	15.35
Enzymes					
Dnase II family	Gene.18803_M_grossa_4604_g.18803_m.18803	DNA2_ACAPL	Plancitoxin-1 OS=Acanthaster planci OX=133434 PE=1 SV=1	3.8E-74	13.52
Glycosyl hydrolase 56 family	Gene.25244_M_grossa_7377_g.25244_m.25244	HYAL1_MESMA	Hyaluronidase-1 OS=Mesobuthus martensii OX=34649 PE=1 SV=2	5.3E-70	5.02
Phospholipase A2 family. Group III subfamily	Gene.32339_M_grossa_11758_g.32339_m.32339	PA23_HELSU	Phospholipase A2 isozymes PA3A/PA3B/PA5 OS=Heloderma	1.7E-18	57.55

suspectum OX=8554 PE=1 SV=3					
Proteinase inhibitors					
Venom Kunitz-type family	Gene.26006_ M_grossa_77 64_g.26006_ m.26006	VKT1_OXYMI	Kunitz-type serine protease inhibitor microlepidin-1 OS=Oxyuranus mi- crolepidotus OX=111177 PE=2 SV=1	4.8E-11	64.37
	Gene.31449_ M_grossa_11 069_g.31449_ m.31449	VKT_PSEPC	Kunitz-type serine protease inhibitor PPTI OS=Pseu- docerastes persicus OX=47769 PE=1 SV=1	1.4E-14	10.66
Venom Kunitz-type family. 02 (native) subfam- ily	Gene.33811_ M_grossa_13 000_g.33811_ m.33811	VKT17_CYRHA	Kunitz-type serine protease inhibitor HNTX-03141017 (Fragment) OS=Cyriopagopus hainanus OX=209901 PE=2 SV=1	4.3E-12	8.67
Ion channel inhibitor activity					
CRISP family	Gene.14471_ M_grossa_31 36_g.14471_ m.14471	CRVP_LATSE	Cysteine-rich venom protein latisemin OS=Lati- cauda semifasciata OX=8631 PE=2 SV=1	4.8E-23	5.94
CRISP fam- ily. Venom aller- gen 5-like sub- family	Gene.20111_ M_grossa_51 18_g.20111_ m.20111	VA576_SCODE	Scoloptoxin SSD976 OS=Scolopendra dehaani OX=2609776 PE=1 SV=1	2.3E-26	5.64
Sea anemone structural class 9a family	Gene.29516_ M_grossa_97 55_g.29516_ m.29516	TX9A_ANTMC	Delta-actitoxin- Amc1a OS=Anthe- opsis maculata OX=280228 PE=1 SV=1	1.7E-14	174.77
Hemostasis impairing toxin					
SNTX/VTX toxin family	Gene.20782_ M_grossa_53 72_g.20782_ m.20782	VTXB_SYNVE	Verrucotoxin sub- unit beta OS=Synan- ceia verrucosa OX=51996 PE=1 SV=3	3.9E-06	6.41
True venom lec- tin family	Gene.31520_ M_grossa_11	LECM4_PSEPL	C-type lectin lec- toxin-Enh4 OS=Pseudoferania	6E-08	12.83

	121_g.31520_ m.31520		polylepis OX=338839 PE=2 SV=1		
Other toxins candidates					
IGFBP N-termi- nal, Kazal-like, Ig-like C2-type	Gene.23069_ M_grossa_63 46_g.23069_ m.23069	IGFBP_CUPSA	Insulin-like growth factor-binding pro- tein-related protein 1 OS=Cupiennius salei OX=6928 PE=2 SV=1	2E-47	8.91
LDL-receptor class A domain	Gene.30471_ M_grossa_10 361_g.30471_ m.30471	CPROH_CONVC	Neuropeptide pro- hormone-4 OS=Co- nus victoriae OX=319920 PE=1 SV=1	2.9E-21	26.05
PDGF/VEGF growth factor family	Gene.21287_ M_grossa_55 68_g.21287_ m.21287	VEGFA_VIPAA	Vascular endothe- lial growth factor A OS=Vipera ammo- dytes ammodytes OX=8705 PE=2 SV=1	6.7E-11	4.89

Table S14. Toxin transcripts of *Paranemertes peregrina*. Unique toxins families are shown in bold.

Protein family	Transcript ID	Uniprot accession	Description	E-value	Expression, TPM
Enzymes					
Glycosyl hydro- lase 56 family	Gene.13505_ P_pere- grina_2885_g .13505_m.135 05	HYAL1_MESMA	Hyaluronidase-1 OS=Mesobuthus martensii OX=34649 PE=1 SV=2	1.6E-59	4.15
Venom metal- loproteinase (M12B) fam- ily. P-II sub- family. P-iiia sub-subfamily	Gene.40257_ P_pere- grina_19132_ g.40257_m.40 257	VM2RH_CALRH	Zinc metallopro- teinase/disintegrin OS=Calloselasma rhodostoma OX=8717 PE=1 SV=2	3.3E-16	4.6
Proteinase inhibitors					
Venom Kunitz- type family	Gene.34086_ P_pere- grina_13107_ g.34086_m.34 086	VKT1D_CONCL	Kunitz-type serine protease inhibitor conotoxin Cal9.1d (Fragment) OS=Cal- iforniconus califor- nicus OX=1736779 PE=2 SV=1	7.9E-15	9.22
Venom Kunitz- type family. Sea anemone type 2	Gene.30860_ P_pere- grina_10693_	VKT3_ANTAF	PI-actitoxin-Axm2b OS=Anthopleura aff.	1.2E-15	110.86

potassium channel toxin subfamily	g.30860_m.30860		Xanthogrammica OX=152178 PE=1 SV=1		
Ion channel inhibitor activity					
CRISP family. Venom allergen 5-like subfamily	Gene.6371_P_pere-grina_1018_g.6371_m.6371	VA576_SCODE	Scoloptoxin SSD976 OS=Scolopendra dehaani OX=2609776 PE=1 SV=1	1.1E-28	11.64
Scoloptoxin-11 family	Gene.23106_P_pere-grina_6437_g.23106_m.23106	TX14B_SCODE	Scoloptoxin SSD20 (Fragment) OS=Scolopendra dehaani OX=2609776 PE=1 SV=1	2.2E-20	4.00
Hemostasis impairing toxin					
Snaclec family	Gene.34963_P_pere-grina_13832_g.34963_m.34963	SLAE_MACLB	Snaclec A14 OS=Macrovipera lebetina OX=8709 PE=2 SV=1	3.5E-6	3.00
	Gene.38662_P_pere-grina_17339_g.38662_m.38662	SLLC2_DABSI	Snaclec coagulation factor X-activating enzyme light chain 2 OS=Daboia siamensis OX=343250 GN=LC2 PE=1 SV=1	3.8E-10	8.49
SNTX/VTX toxin family	Gene.2895_P_pere-grina_341_g.2895_m.2895	STXA_SYNVE	Neoverrucotoxin subunit alpha OS=Synanceia verrucosa OX=51996 PE=1 SV=1	3.7E-13	14.73
	Gene.14425_P_pere-grina_3163_g.14425_m.14425	CTXA_SCOPL	Cytolytic toxin-alpha OS=Scorpaena plumieri OX=274700 PE=1 SV=1	8.7E-14	8.72
Other toxins candidates					
LDL-receptor class A domain	Gene.17193_P_pere-grina_4084_g.17193_m.17193	CPROH_CONVC	Neuropeptide pro-hormone-4 OS=Conus victoriae OX=319920 PE=1 SV=1	2.5E-19	8.15
Venom complement C3 homolog family	Gene.8194_P_pere-grina_1422_g.8194_m.8194	VCO31_AUSSU	A.superbus venom factor 1 OS=Austrelaps superbus OX=29156 PE=1 SV=1	5.2E-49	9.40