

Supplementary Materials: Venom Gland Transcriptomic and Proteomic Analyses of the Enigmatic Scorpion *Superstitionia donensis* (Scorpiones: Superstitioniidae), with Insights on the Evolution of Its Venom Components

Carlos E. Santibáñez-López, Jimena I. Cid-Urbe, Cesar V. F. Batista, Ernesto Ortiz and Lourival D. Possani

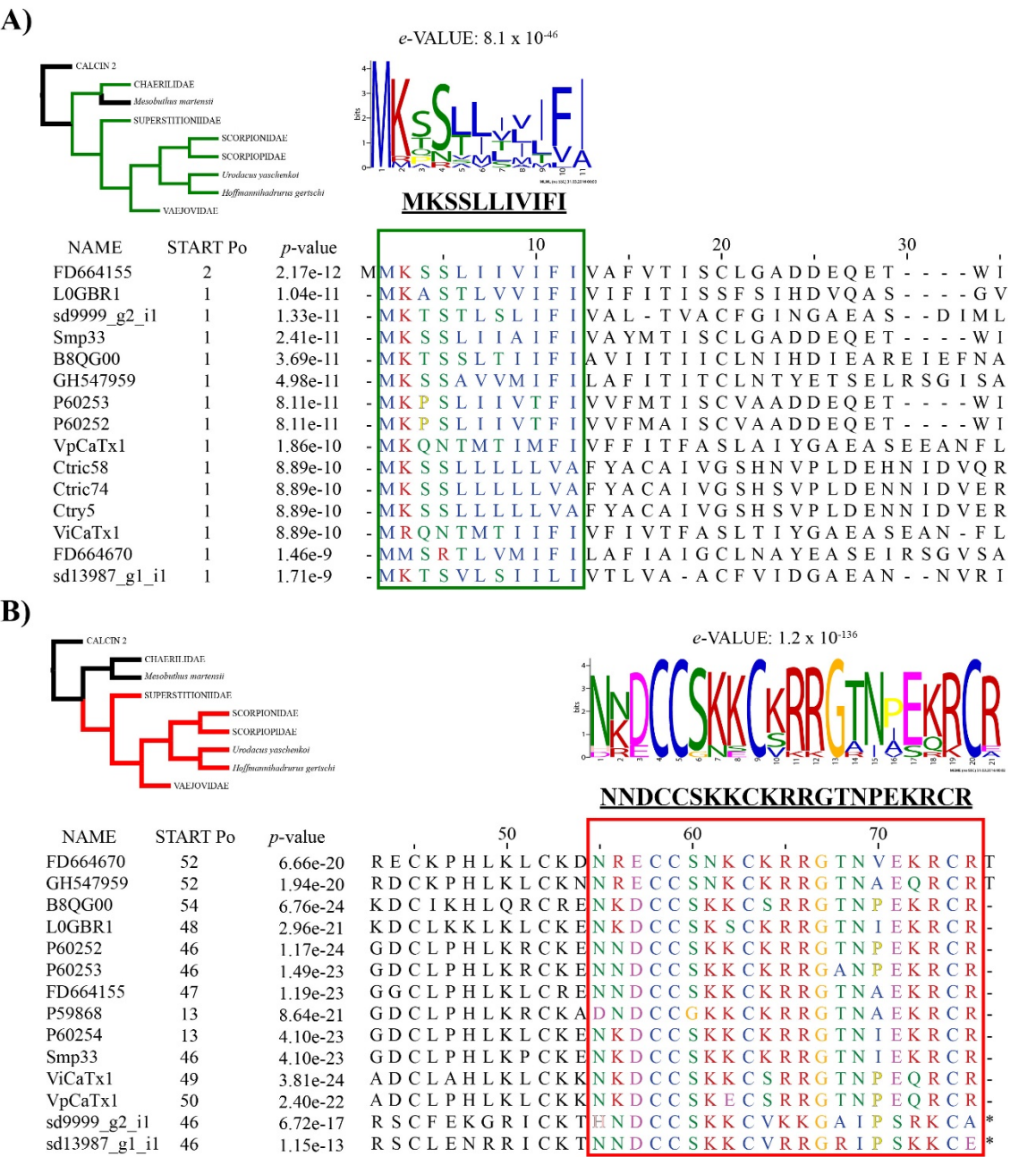


Figure S1. Amino acid sequence alignment of true calcins (Figure 8), retrieved from MAFFT's analysis; showing the two motifs found with MEME, along with a cladogram with branches with the Motifs colored. *e*-values above MEME's logo. Consensus sequence underlined. (A) Motif 1, missing in the Buthidae branch; (B) Motif 2, missing in the Chaerilidae and Buthidae clade.

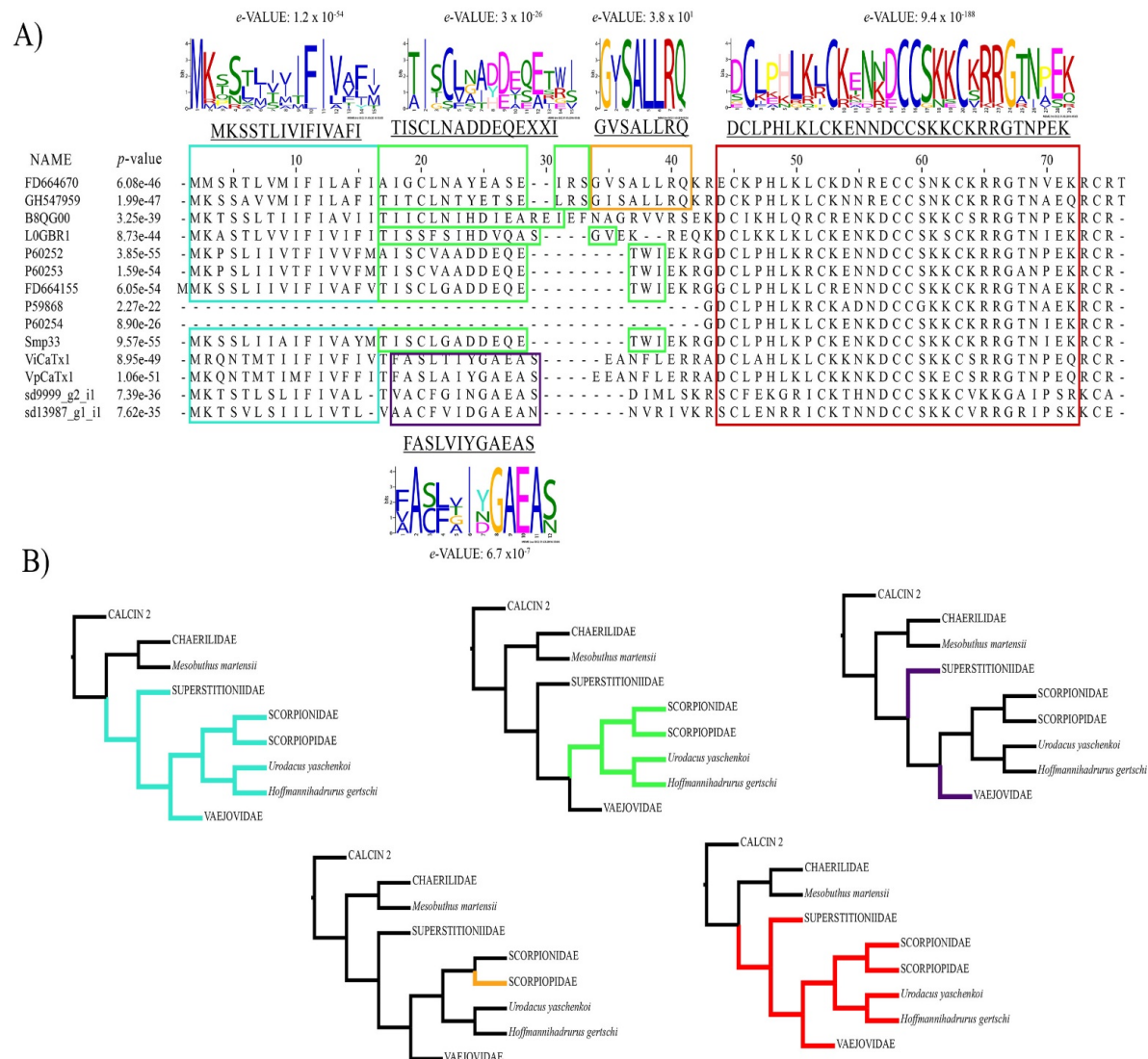


Figure S2. (A) Amino acid sequence alignment of true calcins (Figure 8), retrieved from MAFFT's analysis, from scorpion species of the Parvorder Iuroida showing five plausible motifs found with MEME; *e*-values above MEME's logo; consensus sequence underlined; (B) Cladograms colored accordingly to the colors of the motifs where they are present.

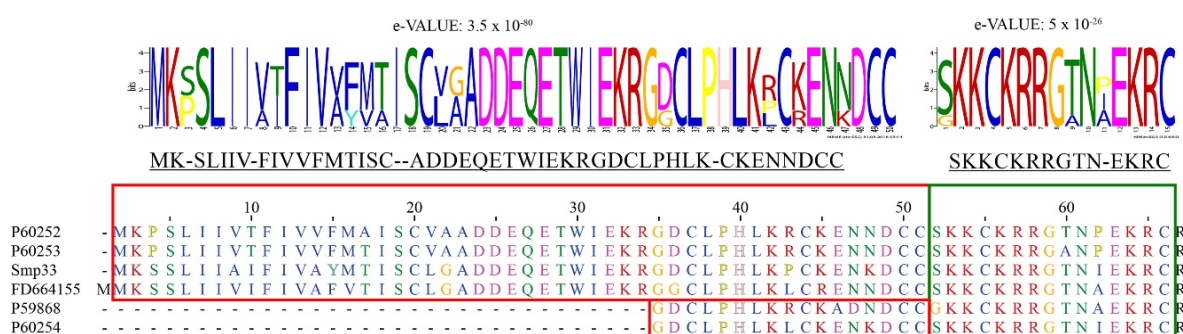


Figure S3. Motifs found in the amino acid sequences alignment of the six Calcins (Figure 8), retrieved from MAFFT's analysis, found in the venom of scorpion species of family Scorpionidae. *e*-values above MEME's logo. Consensus sequence underlined.

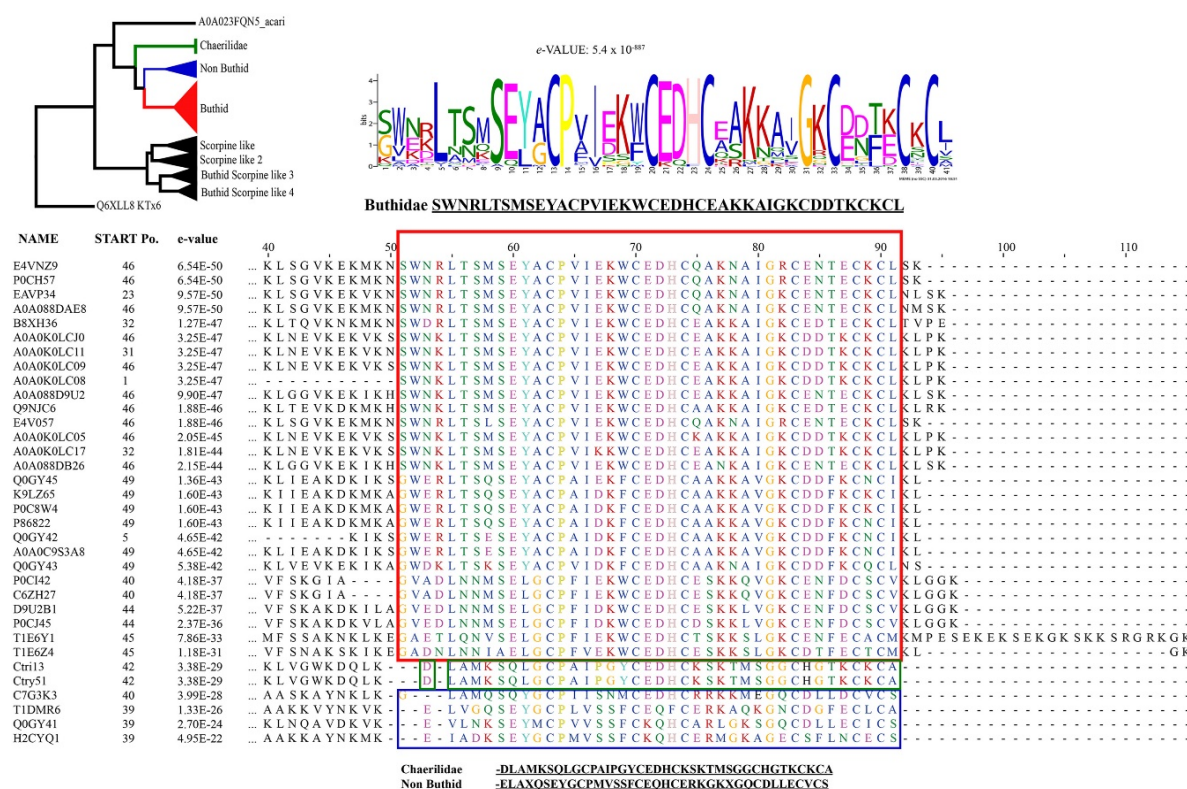


Figure S4. Amino acid sequence alignment of β KTx used in this study (Figure 9), retrieved from MAFFT's analysis, showing the motif found with MEME, along with a cladogram with branches with the Motif colored. ϵ -value above MEME's logo. Consensus sequence underlined.

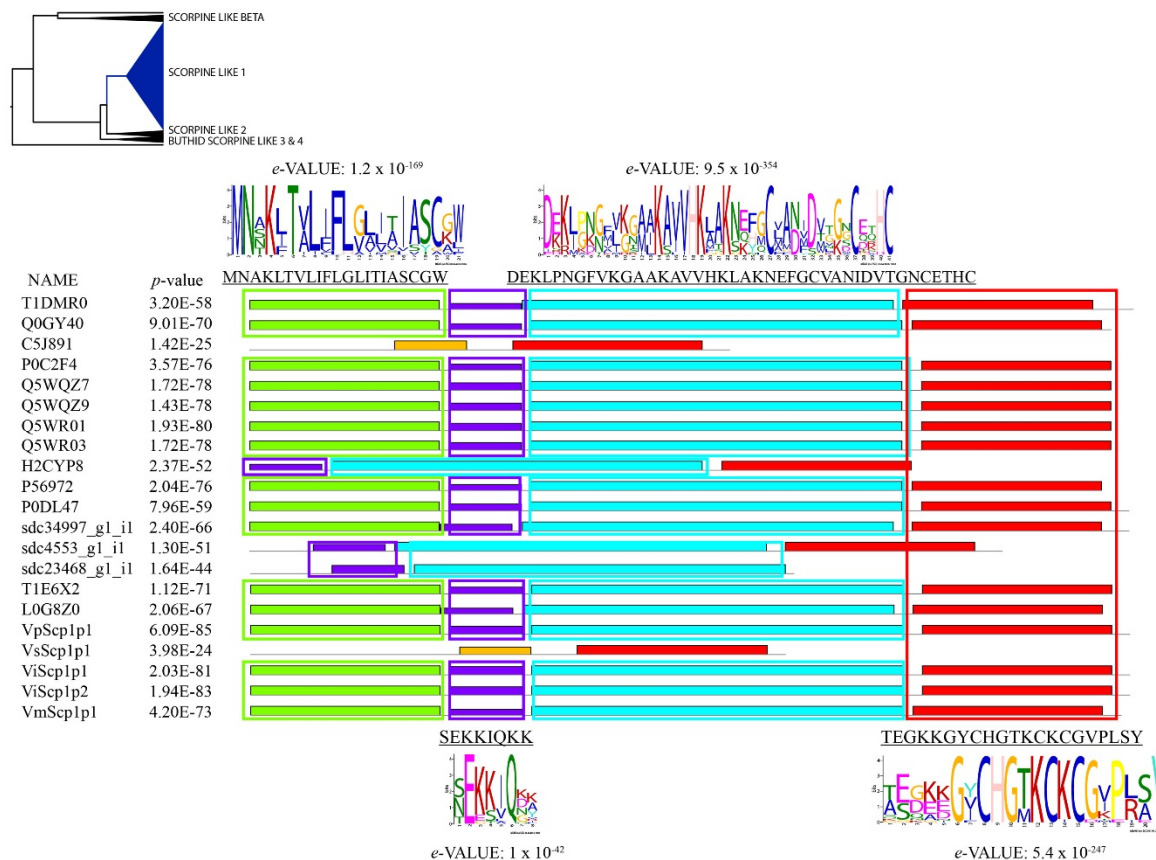


Figure S5. Amino acid sequence alignment of Scorpine like 1 (Figure 9), retrieved from MEME's analysis, showing the motifs found with MEME. Consensus sequence underlined.

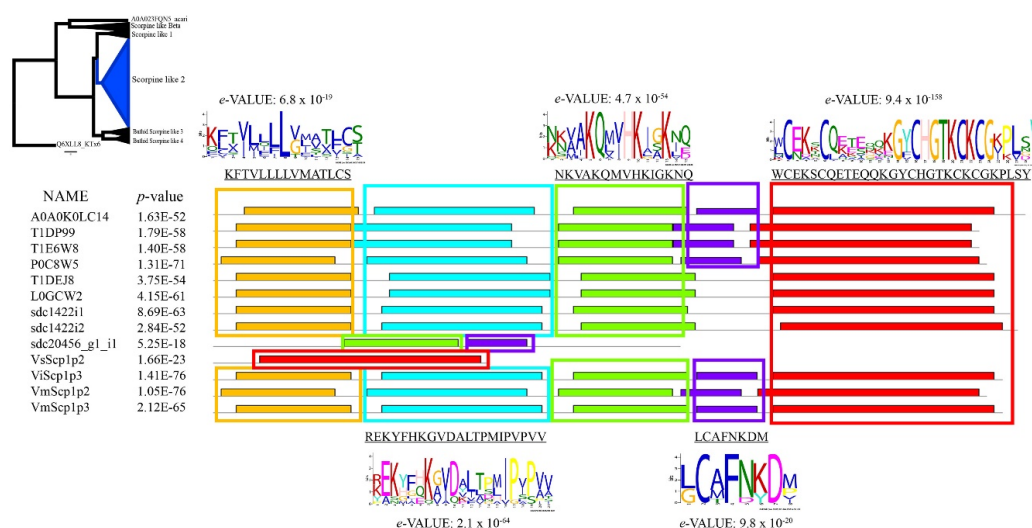


Figure S6. Amino acid sequence alignment of Scorpine like 2 (Figure 9) retrieved from MEME's analysis, showing the motifs found with MEME. Consensus sequence underlined.

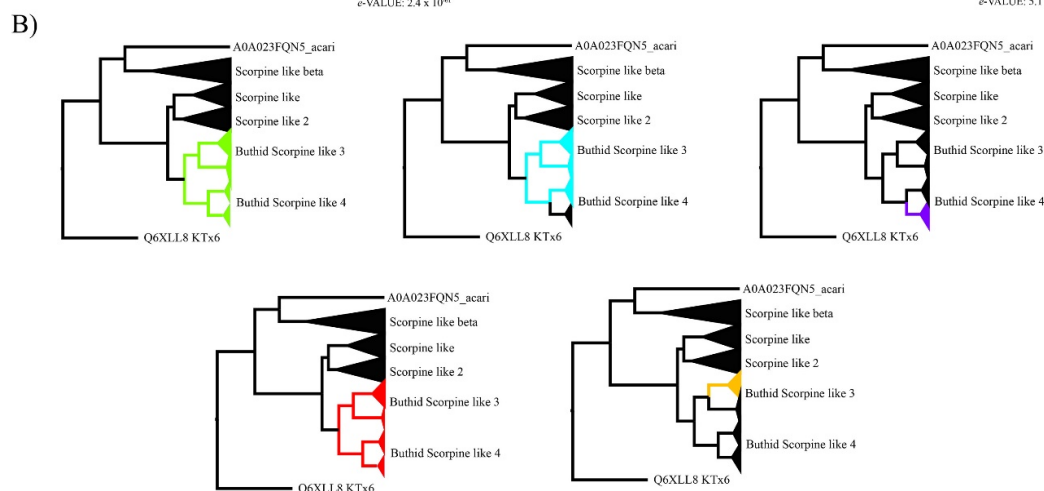
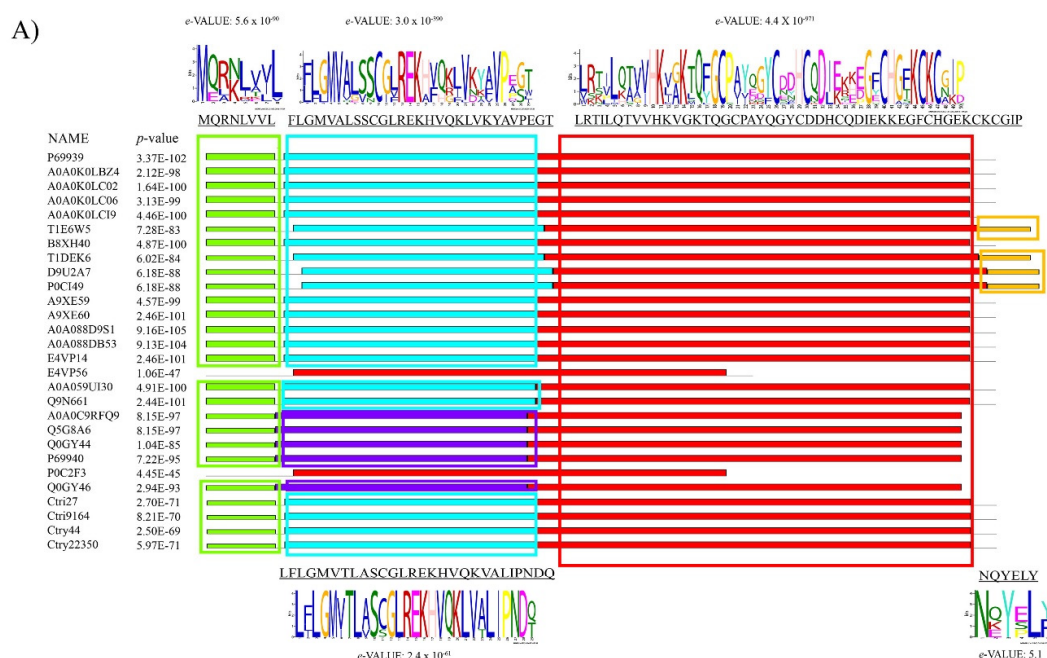


Figure S7. (A) Amino acid sequence alignment of Buthid Scorpine like clades 1-2 (Figure 9), retrieved from MEME's analysis, showing the motifs found with MEME. Consensus sequence underlined; (B) Cladograms colored according to the colors of the Motifs showing their presence in each clade.

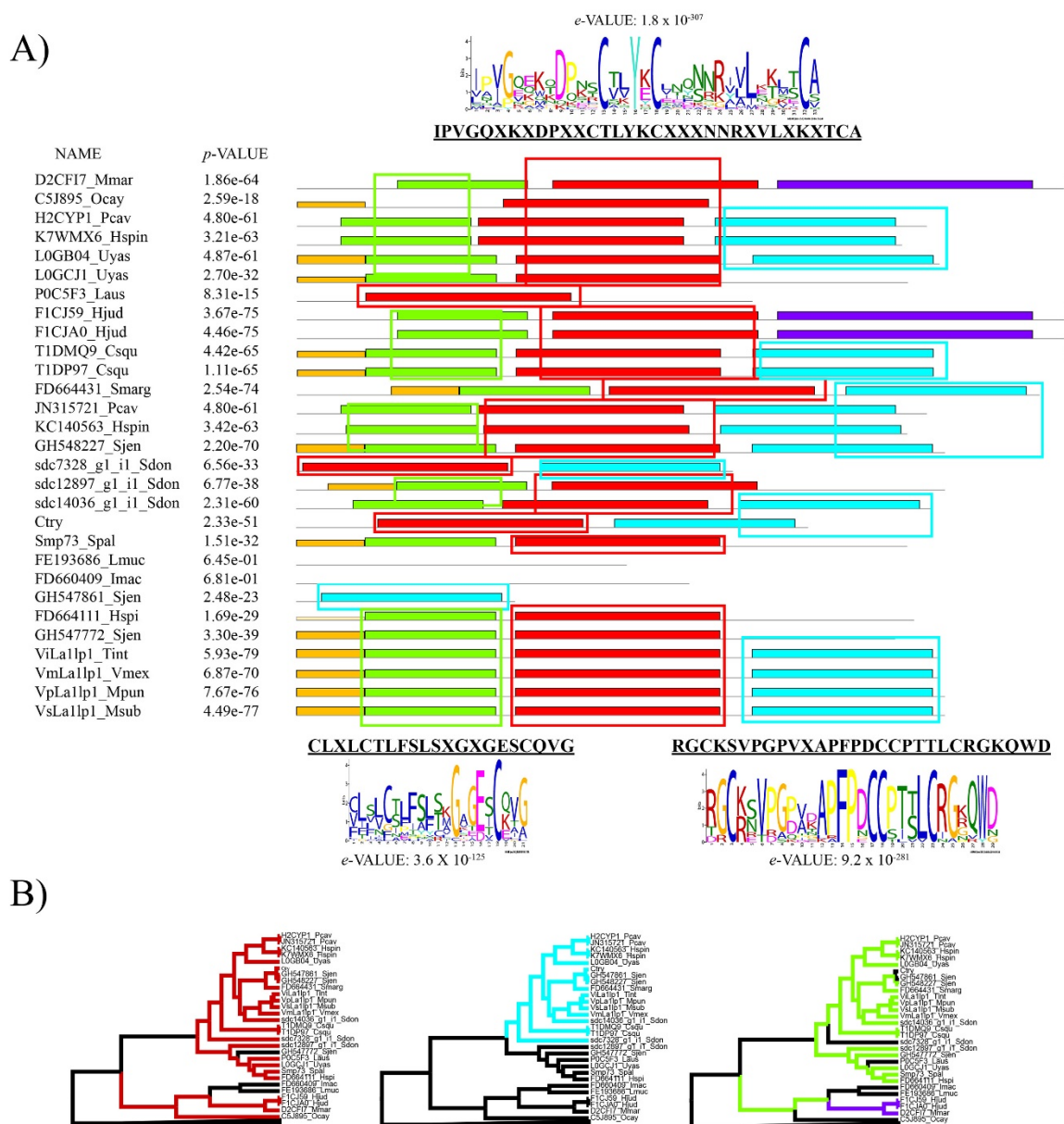


Figure S8. (A) Amino acid sequence alignment of La1 like peptide (Figure 10), retrieved from MEME's analysis, showing the motifs found with MEME. Consensus sequence underlined; (B) Cladograms colored accordingly to the colors of the Motifs showing their presence in each clade.

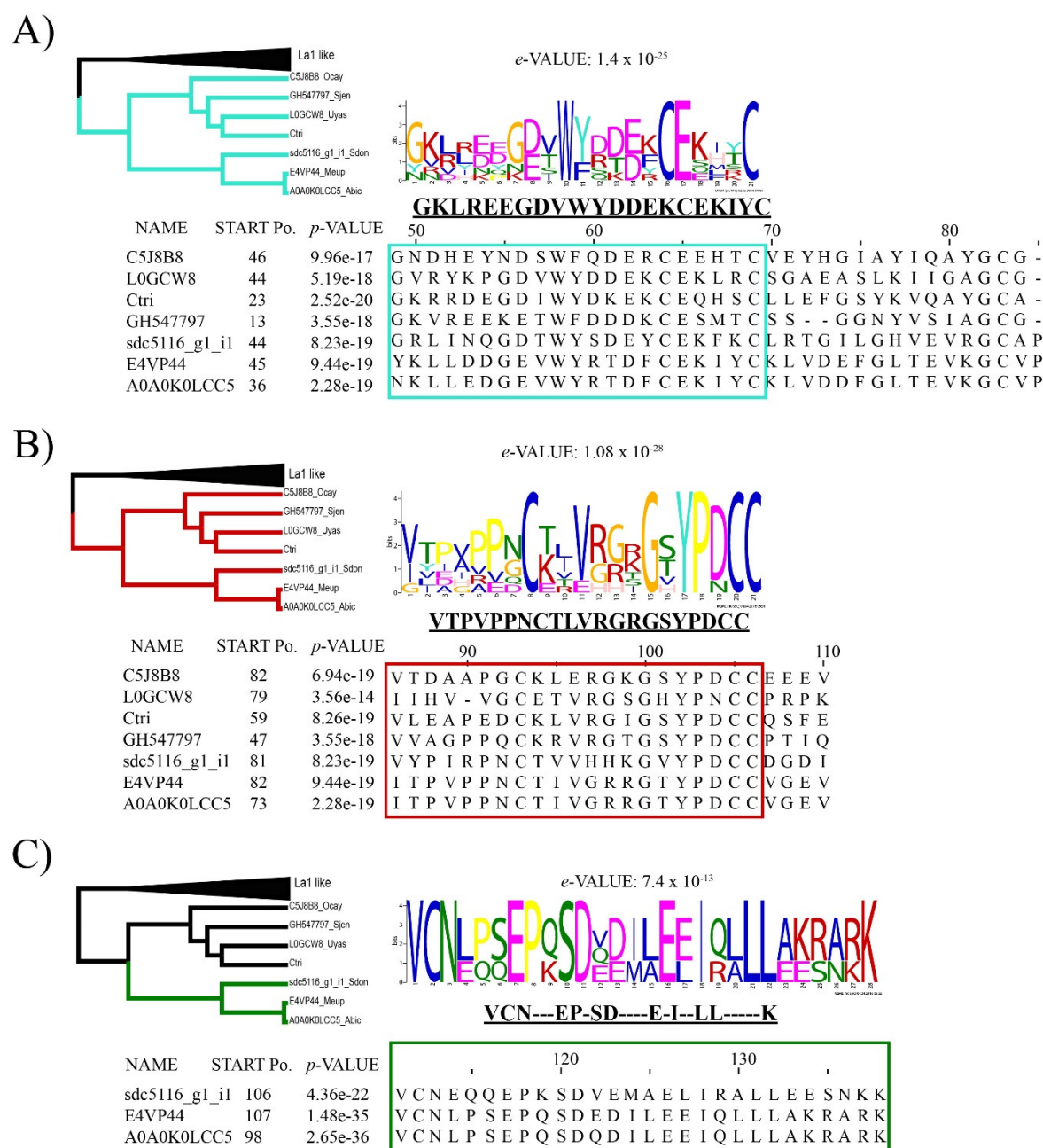


Figure S9. Amino acid sequence alignment of SVWC Scorpion like peptides (Figure 10), retrieved from MAFFT's analysis, showing the motifs found with MEME. Consensus sequence underlined. Cladograms colored accordingly to the colors of the Motifs showing their presence in each clade. (A,B) Motif for all SVWC Scorpion like peptides; (C) Motif only for three sequences including two buthid SVWC Scorpion like peptides and one superstitioniid.

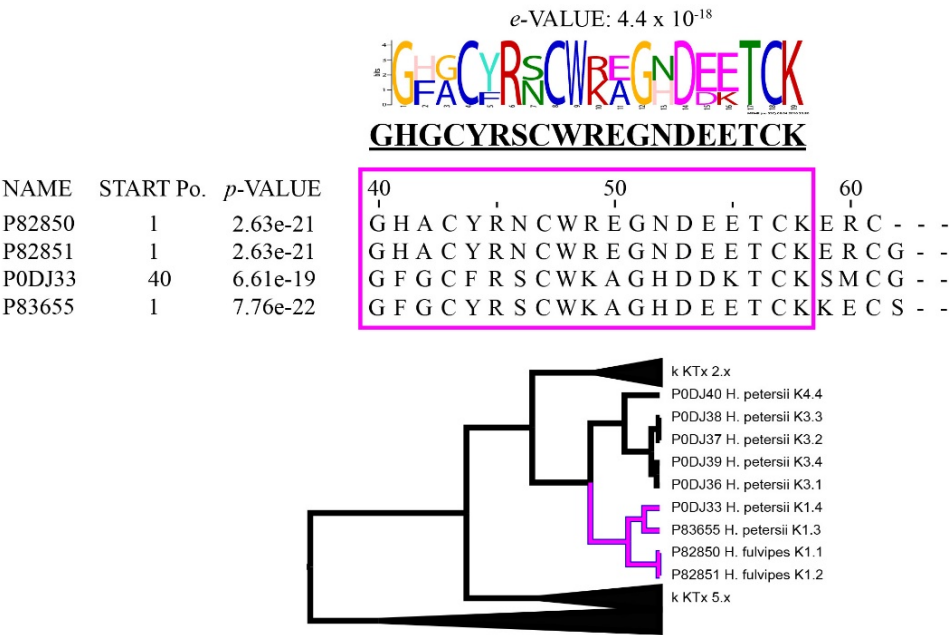


Figure S10. Amino acid sequence alignment of κ KTx subfamily 1 (Figure 11), retrieved from MAFFT's analysis, showing the motif found with MEME. Consensus sequence underlined. E-value above MEME's logo. Cladogram colored accordingly to the presence of the motif.

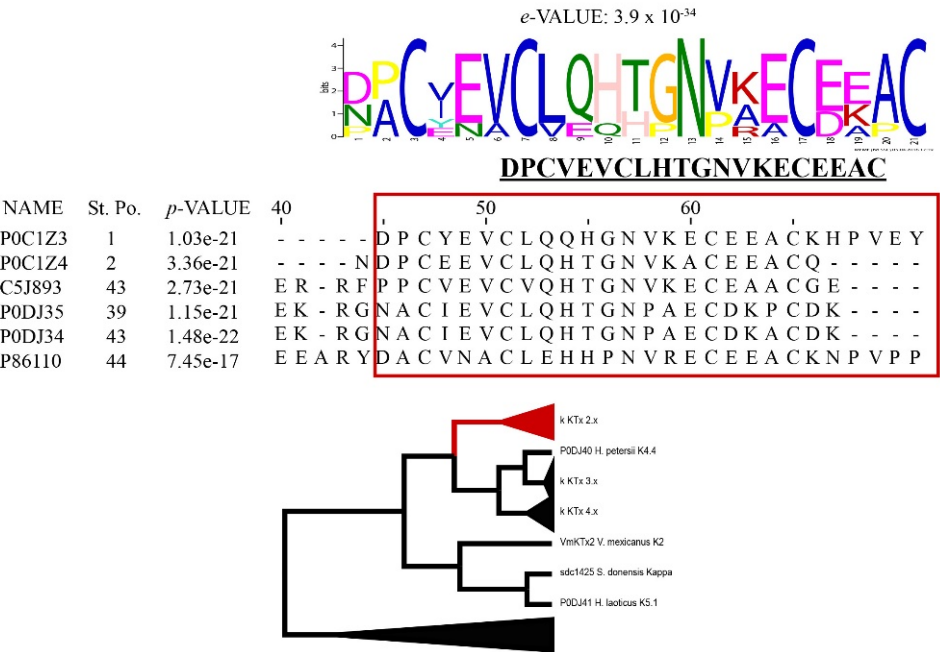


Figure S11. Amino acid sequence alignment of κ KTx subfamily 2 (Figure 11), retrieved from MAFFT's analysis, showing the motif found with MEME. Consensus sequence underlined. E-value above MEME's logo. Cladogram colored accordingly to the presence of the motif.

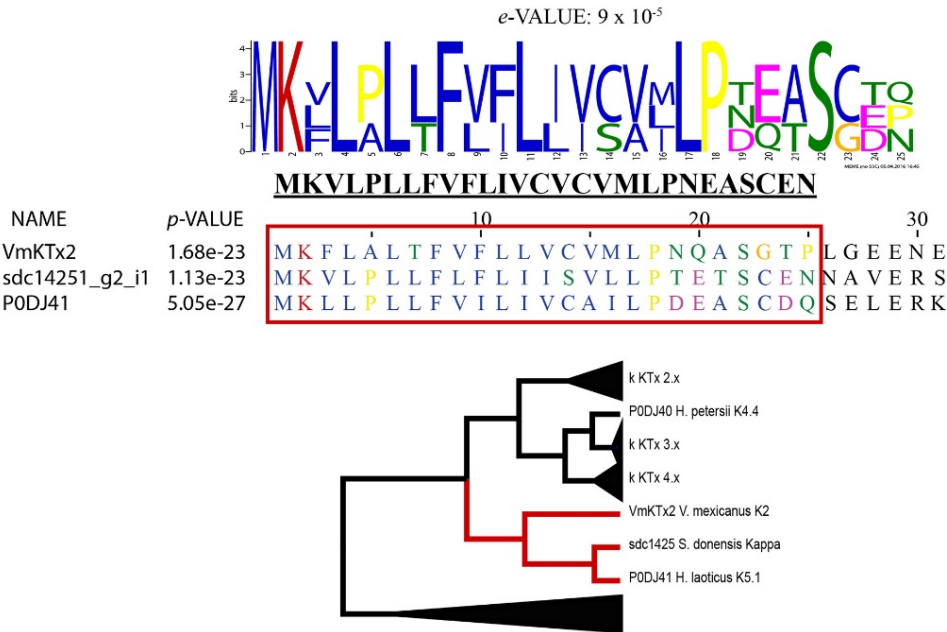


Figure S12. Amino acid sequence alignment of κ KTx subfamily 2 (Figure 11), retrieved from MAFFT's analysis, showing the motif found with MEME. Consensus sequence underlined. E-value above MEME's logo. Cladogram colored accordingly to the presence of the motif.

Table S1. Unique sequences encoded by 135 transcripts of the *Superstitionia donensis* venom transcriptome. In underlined: Signal peptide. In bold: propeptide cut. In brackets, the GI number from GenBank accession number; in asterisk terminal stop codon.

TOXINS		
SODIUM CHANNEL TOXINS		
sdc14319_g1_i1	<u>MNNCTCFILCLVALIYEF</u> <u>GNAQ</u> <u>G</u> KDGYPLNDMGNTIFCVMVQSGNEKCEKNCKERGGHGYCYALRCYCKGMK NNVKIWE *	Csab Cer 2 (522802561)
sdc14462_g1_i1	<u>MKTAFLSIVVFLMLHLD</u> <u>TVLL</u> QIYDGDLYKKGGSTIPCLKHGGDSYCVDVCAKHGAHGGSCYSIPSRCWCEGLDI RKHGGYPKNEKGDYVWCGLPGGENKECEDVCRKQEAGYGYCYDRYCWCEGK *	Lipolysis activating peptide 1 alpha chain (93140443)
sdc14462_g1_i2	<u>MKTAFLSIVVFLMLHLD</u> <u>TVLL</u> QIYDGDLYTKDGSIPCLKHGQDKYCKRICAEHGAHGGSCHGLPSRCWCEGLDI RKHGGYPKNEKGDYVWCGLPGGENKDCQDVCKKKGSGYGYCYDRYCWCEAPQ *	Altitoxin (116241245)
sdc14462_g2_i2	<u>MMKTAVLSIVGILL</u> <u>LNLDIV</u> <u>VL</u> QMYDGYIYDDDGTHYPCRRIGHKYCEELCKDVGAGEGWCKAFPSGCFRCRL DIRKHGGYPRDKNGDWIWCGLPGGKNKECENVCTEQGAGYGYCYDRYCWCEAP *	Birtoxin (20137305)
sdc15193_g1_i1	<u>MKRLALLILGFIVLDVIDA</u> <u>EEEGGYPLREGEPAVY</u> <u>NCAEGGTEYCIK</u> <u>VCRKIDAGYGYCYGLIR</u> <u>TCYCEGLTITKH</u> RGYPN	Toxin CII7 (31376362)
sdc16570_g1_i1	<u>MGKVALRIVGIIIFHIDRIFS</u> <u>YEGGY</u> <u>PVLINGADLYYGCSP</u> <u>NDYCNKLCLAMDAGEGYCIDNC</u> <u>FCKGLHVS</u> <u>KHA</u> AYPKTDGGDYIWCDNRQNNRYCEQVCKRYKGGPGICALNYHVCYCWDVPVLEMGEFTIPESLYE *	Toxin TdNa8 (294863151)
sdc21236_g1_i1	<u>MEGVSTLLIIVTIAISRLSSV</u> <u>ASYE</u> <u>GLIVKGT</u> <u>DNYNCDIRGNGNVYCRQICHKFDAGD</u> <u>GHCQGIYSQ</u> <u>SCWCKNLR</u> ISKHGGYPKQSNGLYSCWKDEYCEGICKQHDAAYGYCYASSCYE *	Neurotoxin LmNaTx30 (317412111)
sdc10528_g1_i1	<u>MKSVVLSIIWVLVLLLOD</u> <u>TVVLQ</u> <u>KYDGYLYHKN</u> <u>GSYYQCYRATVSN</u> <u>CPSVCHKYGAYGGECHGTPAGCFCKGLEI</u> KKHGGYPMENGEYVWC GGDDMCDDVCKRQEAESGYCYSSRYCWCVPV *	Toxin Pg8 (187763642)
POTASSIUM CHANNEL TOXINS		
sdc10141_g1_i1	<u>MNKTLIFSMLLLITIMMTIGDADGERCS</u> <u>SSTYCNSYCWKKAKCTR</u> <u>GKCINKECKCYNCGRGD</u> *	Potassium channel alpha KTx 6.10 (74838001)
sdc13949_g1_i1	MRAPTGGCPFSDALCANYCKKNKFGKGGKCDGPKCKCSIKMAPFDAKVPLTE *	Toxin KTx 8 (159146538)
sdc26193_g1_i1	<u>MNKVHCTILLVVL</u> <u>VMVFAVSVLP</u> <u>IEGVPTGGCP</u> <u>SDALCAKYCKSNKYGSTGKCDNTNCKCSVG</u> *	Toxin KTx 8 (159146538)
sdc14251_g2_i1	<u>MKVLPLLFLFLIISVLLPTETSC</u> <u>ENNAVERS</u> <u>GDSFAELSR</u> <u>SIVKR</u> <u>SCKRVC</u> <u>SGNRRSKQCMQKCKNGR</u> *	Potassium channel alpha KTx 5.1 (384950677)
sdc14273_g1_i1	<u>MRKLLIVFLVLT</u> <u>VL</u> <u>LEMAIVPOVDA</u> <u>SGEPC</u> <u>STSKQCTAPCRAGG</u> <u>SHGKCMNRRCKCYG</u> *	Potassium channel toxin alpha KTx 12.5 (302425088)
sdc14273_g1_i2	<u>MRKFLIVLLVLT</u> <u>VL</u> <u>LEMAIVPOVDA</u> <u>SGE</u> <u>EPPIWPCRTSKQCTDPCRAGG</u> <u>SHGKCMNGKCR</u> <u>CY</u> *	Potassium channel toxin alpha KTx 6.7 (74838004)
sdc13860_g1_i2	<u>MTKLFIVLLVSTVIAMTIVPKVDA</u> <u>SGE</u> <u>KCRNSAQCKDICRAETGGQGR</u> <u>CMNSKCKCFVG</u> *	Potassium channel toxin alpha KTx 6.7

		(74838004)
sdc13860_g1_i1	<u>MTKLFIVLLVSTVIAMTIVPOVDA</u> SVGRCTASKQCTAHCRMRGESHGECENRRCKCY	Potassium channel toxin alpha KT α 6.10 (74838001)
sdc9772_g1_i1	<u>MLLVITFMMAFDEINADGKKCLVSSECHDYCWKGKCSRGKCINKRCKCYNCRG</u> *	Potassium channel toxin (585636477)
sdc9772_g1_i2	<u>MKKAIIFNMLLVITFMMAFDEINADGKKCLVSSECHDYCWKGKCSRGKCINKRCKCYNCRG</u> *	Potassium channel toxin (585636477)
sdc13973_g1_i2	<u>MKAVLIILVLAVLEVAIG</u> VPQAYAPGVRCRNNRICQEVCPRSTKCINGKCRCKYKG *	Tbah02745 (757181004)
SCORPINE-LIKE PEPTIDES		
sdc34997_g1_i1	<u>MNAKLTLFFLVLSIASAGL</u> TEKKVQGYLDKKLDGMVKTALKSIVHKFTKSQYGCAADMVDTGNCQKHCQEA EQADGICHGMKCKCGVPAYRK *	Hge scorpine (121953382)
sdc2871_g1_i1	DVLTPMIAVPVVGILNKVAKQMLHKIGKLDSPCIFGID *	Hg scorpine like 2 (224493299)
sdc14222_g4_i1	<u>MOIKLVVILFLGFATLSTGGFIKEKHFKHKAIDVLTPMIPVPVVGIVNKVAKQMVHKGKLDTPCIFGIDKKGNCEK</u> TCQETTHQKGYCHGTKCKCGKPLNYK *	Hg scorpine like 2 (224493299)
sdc14222_g4_i2	<u>MQIKLTVLLLLGCVTIIAAGILKEKHFKHKAIDFVPMIPVPPSVSGALQKAAKQMVHKAIAKL</u> DSSCILGHDRGGKC NKGCCQETVQQIGYCHGTKCKCGVPLGYR *	Hg scorpine like 2 (224493299)
sdc20456_g1_i1	VDALTPLIPVPVVGIVNKVAKQMIHKIGKIQSLCAFNKDMAGLCEKKCQETEKLGKGYCHG	Hg scorpine like 2 (224493299)
sdc4553_g1_i1	SIASAGLTEKKVQGYLDKKLDGMVKTALKSIVHKFTKSQYGCAADMVDTGNCQKHCQEAEQADGICHGMKC KCGVPAYRK *	Antimicrobial peptide scorpine like 1 (430802820)
sdc23468_g1_i1	ITIASCAWISEKKIQDAIDRKLPNGLVKNAIKAVVHKAANKHGLADFDVGGGCEQHCR	Csab Uro 4 (522802580)
CALCIN		
sdc9999_g2_i1	<u>MKTSTLSLIFIVALTIVACFGINGAEASDIMLSKRSCFEKGRICKTHNDCCSKKCVKKGAIPSRKCA</u> *	Ca like 20 (430802828)
sdc13987_g1_i1	<u>MKTSVLSIILIVTLVAACFVIDGAEANNVRIVKRSCLNRRICKTNNDCCSKKCVRRGRIPSKKCE</u> *	Opicalcin 1 (37539456)
SPIDER TOXIN		
sdc21328_g1_i1	<u>MKLLAIAFIGCLLLLLVNEARSEGGDSMIRVARQARRCIPKYRSCDHNSGCCDNASCRCNLFGTNCKCQRKGIF</u> QG *	U8 agatoxin Ao1a (675369705)
NON DISULFIDE BRIDGE PEPTIDES		
sdc30354_g1_i1	<u>MNAKVFLAVFIVAMFVTDQAEAG</u> FWKNVWNSDIAKNLRNKAVNWVQEIGAPQAAKLDEFLNSLYR *	Antimicrobial peptide Con22 (430802818)

sdc19033_g1_i1	<u>VTDEAEALWGFLAKMASKVLP</u> SLFSGGKKR *	Con10 (240247615)
sdc24668_g1_i1	<u>VVLLHLISQSEALWG</u> ALLGLGSTLLQKLGKRGAQNLDQFDDIFEPELSEADIRYLQDLLR *	Amphiphatic peptide CT1 (384382522)
sdc36542_g1_i1	<u>AHQHLVFTNSLYKMKTQLVV</u> LIVALVLMQLFAQSEAFWGALLNAASSFLGKR	Amphiphatic peptide CT1 (384382522)
sdc12611_g2_i1	<u>VAMFLQFVSQSDA</u> FLKGIFDTVSKWIGKRGLKNLDQYNDLFDGEISDADIKFLLDLMR *	Amphiphatic peptide CT2 (384382528)
sdc8130_g1_i1	<u>MYSGSDA</u> EGYWGLWSGDKSAASSIQGKRGLKNKDQYEDFYAPDLTAADLKLL	Amphiphatic peptide CT2 (403399470)
sdc14358_g5_i1	<u>MKTQFVILIVALVLMQMFAE</u> SEAIFGAIWNGIKSLFGKRGLRDLDLDDNMFDDMYEPELSAADLKMLQDLFR *	Amphiphatic peptide CT2 (384382524)
sdc14106_g1_i1	<u>MKLITLMPVFLCLLIV</u> VDYCQSPFFLASLIPSAINLVKKIGKRDADFQRYVDLKRRDLDELMSRLSEY *	Amp1 (932534523)
sdc28695_g1_i1	<u>LTMQFKKALLVIFISYLL</u> VTDEAEAFWGFLAKMAGKVLPSSLSSGKKDKRNREIEDFYDPNQRQ *	Amp2 (932534537)
sdc14244_g1_i1	<u>MQFKKALLVIFISYLL</u> VTDEAEAFWGFLAKMAGKVLPSSLSSGKKDKRKREIEDFYDPYQRQLDLENLLNQDLN *	Amp2 (932534537)
sdc9431_g1_i1	<u>TMQFKKALLVMFIAYLLVA</u> HEVEAFWGALAKVATSVLPSPFSKRSSLRNVRKREVGNNFFDPYQKDLDDLFLAQLDKY *	Amp2 (932534537)
sdc10966_g1_i1	<u>MKTQLVVLIVALVFVQL</u> FSGSDASFWGNLWGGMKSVVGSFLGKRGLKN	CYLIP Uro 1 (522802600)
sdc6540_g1_i1	<u>MKSQLVVMIVALVFMQM</u> FSESEAGFWGNVWEGIKSVGKNLLGKRGLRNMDQFDDLYEPDLSPAD	CYLIP Uro 3 (522802596)
sdc8996_g2_i1	MQMFSESAGFWANVWKGKISIGNLLGKRGLRNMDQFDD	CYLIP Uro 3 (522802596)
sdc13329_g1_i1	<u>MKTQLVFLIVALVLVQM</u> FSGSDAEGFWGKLWSGVKSAASSILGKRGLKNIDQYDDFYEPDLAADLKLLQELFR *	CYLIP Uro 3 (522802596)
sdc10003_g1_i1	<u>MKSQLVVLIVALVFMQM</u> FSESEAGFWGNVWEGIKSVGKNLLGKRGLRNMDQFDDLYEPDLSPADLKFLQELLR *	CYLIP Cer 2 (522802549)
sdc13462_g1_i1	<u>MKTQFLVILIVALVFTQIF</u> SEAEAGFWGKLWEGVKSGLLGKRGLRNVDQFDDLYEPDLSPADLKFLQELLR *	CYLIP Cer 2 (522802549)
sdc13544_g1_i1	<u>MKTQLVILAVLVYMQV</u> FTESDAYFWTYTFPKHLFTRTPSPSLLGKSKLRNWDQFNDLYESDLSSADLKFLQKLLR *	CYLIP Cer 2 (522802549)
sdc14358_g12_i1	<u>MKTQFVILIVALVFMQM</u> FSESEAGFWGVDVWGIKTVGKNLLGKRGLKKLDQYDDMYEPDLDAADLEFLKELLR *	CYLIP Cer 2

		(522802549)
sdc13245_g2_i1	<u>MKTQFVILTIALVLVQMFSESEAE</u> FHSKVWGD LVKSL LGK <u>REL</u> RSFDQFDDLYE	CYLIP Cer 3 (522802547)
sdc4010_g1_i1	<u>MNAKVFLVVFIVAMLVTDQAEAG</u> FWKNIWNSDIVKNLRNKAVNWWKEKVGAPQVAKLDEF LDSVYNS *	Heterin 1 (485896696)
sdc15372_g1_i1	<u>EILLDPLLLMQMYAQSEAIL</u> GANWNGIKTLLGKRSL	IsCT2 (22213544)
sdc16828_g1_i1	<u>KTQFVILFVALVLMQLFAESEAFF</u> GAIWNLKSLFGKR	IsCT2 (22213544)
sdc22496_g1_i1	<u>MMTQFVFLIVALVFLQMFSLSEAG</u> FWGVVWSGI *	IsCT2 (22213544)
sdc22251_g1_i1	<u>MKTQFVVLIVALVFMQMISESEAG</u> NWGDVWSG	NDBP 5.5 (152962885)
sdc37652_g1_i1	<u>FVILIVDHLVLMQMFEASEAI</u> GGHIKGKASLLGKRGLRDL	Peptide Hp1035 (347602456)
sdc39539_g1_i1	TQFVILIDDLVFKQMFSDSEDGFWGEVWRGIKSV	Peptide Hp1165 (614103404)
sdc12606_g1_i1	<u>MNAKIFLVLLVAAFMTEETEAG</u> FFGKIWNSDFVKNLRNKAVKFISDKIGTNPPQAATLDELLDALYS *	Vejovine (325515699)
sdc14749_g1_i1	<u>MNAKTIFAIVLIGMLVTEQAEAG</u> IWSTIKKYASKAWNSDIGKSLRNK	Vejovine (325515699)
sdc14209_g1_i1	<u>MNTKTFLLVFLFALIVTEQAEAG</u> LWGAIKSFAKNAWWSKLGRKLRTMASNALMPKPESVPMPVPVPEAVAEAVP SGSRLDFMY * *	Vejovine (325515699)
sdc4413_g1_i1	FAESEAIIGDIIIGNLTAQFGKRSLRDLELDNDMYEPELSAADLKM *	Venom antimicrobial peptide 6 (149134048)
PROTEASE INHIBITOR		
sdc12570_g1_i1	<u>KMIVSCIFLILVLNAVFAESSHHK</u> SVNCLLPKTPGCKGSFARYYFDIETRTCKAFIYGGCEPNTNNFAKRHHCEK RCKRFGARKYHGK *	Kunit type serine protease inhibitor (224493105)
sdc31500_g1_i1	<u>MMFLLAFVLMTSLNVLVYSQDR</u> CTLPPESGLCLAYFEKYYYDSNFRTCKMFVYGGCDGNDNRFDTECLAACA GSK *	HW11c39 (627610707)
sdc13156_g1_i1	<u>FILWVPISVATDLYNLQSRMKFA</u> IVALFVAITIIAQVTSQEPKCRKNEYTTTCGGCDGNCQEYVVPCTRMCHPPG CYCVENTVRGPNGDCIFTSECSGNEI *	Cysteine rich venom protein (366984639)
sdc13156_g2_i1	<u>QRLKMKFTIVAVFVAITIIAQVTS</u> QETNCPKNEYRTCGNCDGNCRKHVVPCTRICHYPAGCYCVGGTVRGPNGDC IFTNECP *	Cysteine rich venom protein (366984639)

sdc14810_g1_i1	<u>MNALTGLTFTFILLCVLHFNSFSVK</u> GDDNCEENEVYTKCGSICESCDDFITPRPCPEICFIGCACKEGYFRDTNEKCIP AEECKKQ *	Putative trypsin inhibitor like cysteine rich domain protein (604769033)
sdc3658_g1_i1	<u>MLLOKFNMNIFLVVLTAITIAVG</u> VRSDQCWLNEYYTECGGCDGTCDEPLVACPYICHYPAGCYCEYGTVRGPNG LCIAEEDCPKHK *	Putative salivary secreted serine protease inhibitor (366984585)
sdc6891_g1_i1	<u>MKFILAPMLMAILVQVKSQ</u> DKPCGENEYYTECGGCDGTCAEPVVQCTKNCHPAGCYCQQA VRGSDRKCILLE DC *	Putative salivary secreted serine protease inhibitor (366984585)
sdc13407_g1_i1	<u>MKAALVLLFAAVFLNFOVK</u> GHHVVGHEEGCASPDEVFDPCGPSCPPSCIGVIKPGTLCSTECVPGCYCRDGLVRT ARGTCVTPRACRNN *	Putative similar to chymotrypsin elastase inhibitor ixodidin (427777519)
sdc20776_g1_i1	MVTGTEVQCWWNESYTTCCGGCDGTCAEPMPICHTICHEPGCYCNSGTVRGPDGFCIPLESCPNHK	Putative salivary secreted serine protease inhibitor (366984585)
sdc27767_g1_i1	<u>MKFLLVAVFIVIIAIALVRS</u> QEPQCGNNAFYMECGGCDGTCEPLVACTMICHEPGCYCEWPNVRGPNGECIPRE QCP *	Putative salivary secreted serine protease inhibitor (366984585)
sdc12740_g1_i1	<u>MGKFILAVIVSMAVLVHA</u> FPQAHDLFRCDDEEMVTCLPPCPRSCSNLFPNRPCTVLLPTCRTGCSCCKGGKIRGN DGRCVFPADCPRRN *	TSA Tbah02514 mRNA (757180944)
sdc1626_g1_i1	<u>MKRNI VSGVFALAVLFIL</u> DNCD AQYNSVGRNCTNPDQVFTECASACSLTCDDYVNPKNWCTLQCIIGCICRPGY AFQTTFGTRCVPISDCRRK *	Venom peptide SjAPI (528050044)
sdc3980_g1_i1	<u>MKRNTILGVFALIVLFSIL</u> DKCEAEDLFEELSCKNPDEVFSQCFPICPLTCDDYVNPKPMCGLTDTCLFGVCVRRGY AFQNEIHSRCIPISDCKSG *	Venom peptide SjAPI (528050044)
sdc9177_g2_i1	ASPAAERCKKEGEEYDECGASCPETCENKGTGPGCFYVCLPGCLCK *	Venom peptide SjAPI (528050044)
sdc13359_g1_i1	<u>MMKCNVALSIFVVIVLCS</u> VFSGCVAQGNESRGRPCRSNNEEFTRCGTACPLTCQNYQNPPQVCTLQCVIGCVCKR GFIRENGVRSRCVRPQECRRY *	Venom peptide SjAPI (528050044)
sdc36886_g1_i1	<u>GFIGSLCRNTAF</u> CVLTILITCSVLESYMIQKNKSRNQCVLSGEEFTEKGSACPATCDNYQEVNKTCSVNSVIGCFCKT GLVRDVLNWRCVKPEEC *	Venom peptide SjAPI (528050044)
sdc13933_g2_i1	<u>MNKYVFLYVFALLTF</u> CCLHSSSGQRNGRPFNCNRPGEFFRRCGTACPLTCDNYRSPPKSCTRQCVIGCACKNGL VKDRNGSCVPPSQCLR *	Venom peptide SjAPI 2 (528050045)
sdc39356_g1_i1	NPNEVFTGCSSACTLTCDHYVNPPELCSLQCIIGCVCR	Venom peptide SjAPI 2 (528050045)
ENZYMES		

METALLOPROTEASES		
sdc14592_g1_i1	MEQRSYNTITGGRSVDLLTKDEDEVGFWAKRTRLEQALIVICSVLAIMA VCLIIAVVVISQKRNIDDVTSEAPPTTVTT SKPIVEKVCETEICKLADELKATINYSINPCEDFYSYVCSGWRRDNPIESMVTYTKFGLLDEKIKNELIEVLPNIDK YEDGDVRTKAKTFYTSCINTETREGKGVEGLKNVLKSVGGWPLLGENITEEYNWTDALVFSIRELGSSPIIAFAVGP DAKNTSDNIVQIDQTSLSIGRNELLNSNKSDEKVEIMAAYKNLVKQSAMLLGSKKTEDQLDNDINDMVEFERTL ATYTRSEEDRRDPNSLYKKMTIDGLQTGLNTEQIDILSFFNKIMANITELTNDTNIIVAEYDYLQYQCKLLGQNTTKP ETIANYIGWRIVQNYGTETTENTFTNTFLEFDKVTMGVEKSKPMNETCIDDANSLDFAFGNLFINHGFDVDTKTEI ENMIAELKTAFGELLKSNKWMDNNIKEKALNKLNEMFPMVAYPPWLNDTDKLNYYEKLGDIIEGSHLENVITIA KFHTQKQLNKINKSYNRTEEWASAPAVVNAFYDPSANTITFPAGILQPP	Neprilysin 1 (567441193)
sdc14619_g1_i1	MEQKSYNTLNGGGSVYQLIKGKYAGFRVKITKLEQTLIVVCWVLVIVANVTSHKLTAEKVCDTEVCKLAADKLKD TMNESINPCEDFYSYVCSGWKRDNPETMSALGNLHLLDENIKNELIEVLPKIVKYEEQDVRTKAKRFYTSCIDTE TRQSKGVEALKAVLKSLLGGWPLLGETIETGYDWDALAYAKRELANHVITFYVGPDDKNTSQNIKINQASFLK RDNFINKNRSEKVKKTMKAYKKLIKQSAKLLGSTKTEEELSDVDNMI EFERTLA EFSRSEEEKDLYSKYRKMTV GRLQLELNTKQIDILLNKNVMNITKLTNNTEVIVMELDYLKQTKCLLEQNNTKTETIANYIGWIIVRGYGEHTT KEFADAFEFDDKVTSGTAKAKPLNETCIKKANEYFRYALGNIFINNGFNDQTKTEIERMTVQLKTA FEELLQTNKW MDKETKESLNKLNEMIPMVAYPTWLNDTKKLNYYDKLGEIIEGSHLENVINIVKFIIRTRLNKNKPFNRTEKW GSGPAVANAFYSPNSNLRLPAGILQPPFYQVGLPALNFGGIGSIIGHEITHGFDNTGSQYDAQGNLKEWWTPEA RSRKFKNESKCFVEQYGSYKEPITGMNLNGNNTLGENIADNGGLRQAFKAYKSATSGIYSNMRLPGLDMTSDQLFF VGFAYAWCADARKEHLELALKYDAHSPPPFRIRGVLSNFEFKAFAKCP	Neprilysin 1 (567441193)
sdc14592_g3_i1	EQYGSYKDPITEMMLNGENTLGENIADNGGARESFKAYKSLTAVSEYNTRLPLGLDLTADQLFFVGFYSYVWCANER KEYLEKAIQYDPHSPPSFRVRGVFSNLEEFSEAFGCPPNSTLNPCHKCLLW *	Neprilysin 1 (567441193)
sdc14619_g1_i3	MIMKGVAKVEQKSHNPINWGSNVYHLIKYAGFRVKRTPVEQTLIVIVCVLAIMADVVTSRKLITEKVCDTEVCKL AADMLKATINDSINPCEDFHSHVCSGWKRDNPETMSALGNLHLLDENIKNELIEVLPKIVKYEEQDVRTKAKRF YTSCIDTETRQSKGVEALKAVLKSLLGGWPLLGETIKKGYDWDALAYAKRELARNAIKLYVGPDDKNTSQNIKV SDPSFGMKRDDFIDRSSEKVKRRIKAYKKLIKQSAKLLGSTKTEEELSDINDMVEFERTLAKFSRTVEEEKDLYSKY KKMTVGRLHLELNTEQIDILLNKNVMNITELTNSSEIIVMELDYLKRTCKLLEQNNTKTETIANYIGWTIVNGYG RQTTKEFADAFEFKRVSTGIVKATPLNITCIEKANYFYGLPLGNLFINNRFNVETKMEIENMVVQLKVA FEELLKT NEWMDNETKKKSLNKLNEMITLVAYPSWLNDTKKLNIFYEKIGEIIEGSYLENTITIAKFHVQTS LGRINKPNNRT KMWGNKIAGVEAYYDPKSNKIFLPAGVLQPPHYQVGLPALNFGAIGSIIGHEITHGFDN	Neprilysin 1 (567441193)
sdc14619_g1_i5	MADVVTSHKLITEKVCDTEVCKLAADMLKATINDSINPCEDFHSHVCSGWKKNPPIETMNLVGNLQMLNEKIK NELMEVLPNIVKYEEEDVRTKVKRFYTSCIDIETRQAKGVEGLKAVLKSLLGGWPLLGETIETGYDWDALAYATSE LAYNPISFSVGPDDKNTSQNIKVDEAKFGLKRDNLINTNRSNQKVRIMKAYAKLIKQSAKLLGSVKTENELDN DINDMIEFERTLAKFTRSEEEKRDLYSCYKKMTVDRLQLELNTEQIDILSLNKNVMKNITELTNTKIIVKELDYLKQ TCKLLEQNNTKTETIANYIGWIIVRGYGEHTTKEFADAFEFDDKVTSGTAKAKPLNETCIKKANEYFRYALGNIFIN NGFNDQTKTEIERMTVQLKTA FEELLQTNKWMDKETKESLNKLNEMIPLVAYPSWLNDTKKLNDFYEKLG NVI	Neprilysin 1 (567441193)

sdc14619_g1_i6	QGSHELENTITIAKFHTKRKLDKINKPYNRTEMWGSLVVANAYYAQKSNTIIFAGILQPPFYQVGLPPALNFGGI GSSIGHEITHGFDNQGGMYDAQGNLKEWWTPPEARNRFKYESKCFIEQYGSYREPKTGLMLNGKNTLGEN MEQKSYNTLNGGGSVYQLIKGKYAGFRVKITKLEQTLIVVCWVLVIVANVTSHKLTAEKVCDTEVCKLAADKLKD TMNESINPCEDFYSYVCSGWKRDNPETRAHYVNLLVEDKIINELIEALQNAGKYEEDVRTKVRFYTSIDDIET RQAKGVEGLKAVLKSLLGGWPLLGETIETGYDWDALAYATSELAYNPIISFSVGPDDKNTSQNIIVKDEAKFGLKR DNLINTNRSNQKVRIMKAYAKLIKQSAKLLGSVKTENELDNDINDMIEFERTLAKFTRSKEEKRDLYSCYKKMTV DRLQLELNTAQIDILSLLNKVMKNITELTNNTKIIVKELDYLKQTCCKLLEQNNTKTETIANYIGWKTVKRYGRQTTK EFGNAFFEFDKVSSGIVKAKPLNETCIQNANGYFDFALANLFINNRFNVEKTEVETMVAQLKLAFVELLKTNKW MDNKTKKESLNKLNEMIPLVAYPSWLNDDTKLNDIFYEKLGNVIQGSHELENTITIAKFHTKRKLDKINKPYNRTEM WGSLVVANAYYAQKSNTIIFAGILQPPFYQVGLPPALNFGGIGSSIGHEITHGFDNQGGMYDAQGNLKEWWTP EARNRFRKYESKCFIEQYGSYKEPKTGVMLNGKNTLGENIADNGGLRQAFKAYKSHTSGNDRNMRLPGLDLTSDQ LFFVGAYYVWCSNERKERLERDLKYGVHTPAFFRVRGTLSNSEEFA	Neprilysin 1 (567441193)
sdc13753_g1_i1	MLVFWTLTSIVLVFSVNGQFWDLRGDFCRTRKPQTCCPGRDDECTVPILDTLCYCDIFCNRTSGADCCPDFWPTCL GINPPGPIVTQQCFKDGSRYNVGESIKINCNKCTCRQSRPTNYDFVCEQNVCLVRPELIESINHGNYGWKASNYSL WGKTLLEGIQYRLGTFKPTVSTAMNEVKIKMRKELPENFDARQHWHLNLIHPVRDQGDGSSWAFSTTSLASDR LAIQSRGSMNMAISPOHLISCETRGQKGCDDGGHLDRAWFYLRHGVASEECYPYESGTSKENGRCRAVRKPRGRH GHILCTNGQEDMVHKSTPAYRIGPQEDLIRQEIFYNGPVQATFKVYNDFLYKGGVYRHTNLSDGKPEAYRLHGW HSVRIIGWIDRTGRRPVKYWLCDSWGRWGEDGYFRIIRGEDECDIEMFIIGVWANTNSNNMNGIGH *	Putative cysteine proteinase ixodes scapularis cysteine proteinase (604813376)
sdc14484_g1_i1	MNATRKFLLSICIVLASCNFSDLPGPYCRTRRPVDCCPGRDDSCAVPILGTLCYCDHFCNRRTYQDCCPDFLPHC LGITPPEPLVHRVCHHEGRTYQVGQTIRKNCNACTCRPTSATTFEFNNCEERVCLVRPELIDGINRGNYRWASNY TFLWGKSLDEGIRLRLGTFQPTQASRMTAIHQKGDPLPSSFDSSRRKWPNIQPVDRDQGNCGSSWAFSTTAVASDR LGIQSQGKERLSLSPQHLVSCQNRAQRGCHGGHIDRAWWFLRKRGVASESCYPYESGETGHKGTCLAKLSPNGN EPRIKCVSGGREDILHYSTPPYRIGRKEEDIMHEIFTNGPVQATFQVKEDFFLYKSGVYHHTPVSAHLPGKYRRSGW HSVRIIGWGVVDHSHGRPVNYWLCANSWGSRWGEDGYFRIIRGRNECDIENFVLATWGKRRTSNGRYYGRAGRRR RS *	Putative cysteine proteinase ixodes scapularis cysteine proteinase (604813376)
sdc4278_g1_i1	DRLPTFDVAVVITKLDMCRRQFNGGRCRGTAGFAYVGGACVVNKRLEKVNSVAIIEDSGGFSGIIVAAHEVGHL LGCVHDGSQPPSYLGGPGATNCPWEDGYIM	Uncharacterized protein like <i>Tetranychus</i> <i>urticae</i> (no GI available)
PHOSPHOLIPASES		
sdc12400_g1_i1	MALTFEVAVTMLLSLAYAHIAERELYVNFEPLPNQQDSWPVARAAIVTHRSEAGREFTECRMLGSIEELAREGRSL PEHLIKRTSKAEMDEFERICSAASEAERFMIVPGTKWCGPGNKAANESDLGWLAADKCCRAHDHCDISISQGKSK YGLKNEGEYTLNCDCEKAFHKCLTETADSQNWITSKPTQGIQIRYTYFTLYKPKCYKVS CGGGRSAIESRKCSNLVA TWKNSYLD *	Phospholipase A2 (218546750)

sdc14212_g1_i1	<u>MTFVFLTAIIALLSLAYSHTTERELYNFEPLPNQDDSWPAARAAIVSFRSEAGREFSECRMLNSVEELAREGINLPK</u> HMIKRASAEEMDDFERRCRSADRERFMIAPGTKWCGPGNKAANYSDLGSLEADKCCRTHDHCNIPKGKSKY GLTNDGEYTLNLCNCDKAFDSCLQNAANKEANSVDKATTNAIKFAYFTVYAPKCYRLSCGGGRSDMEGRACAN AVGTWKSSYLA *	Phospholipase A2 (218546750)
sdc14393_g1_i1	<u>MVFISLIIFTTFVWIGSTQNIQKELYVNFEPLPGQKDSWPIARAAIVSFDKSSEARRTLPECRMLHSLEEIAREGNYFSE</u> RMIKRVSKSEEMNTLERRCSRSSQEEERFSLTFIKWRDTKWCGPGNDAANETDFGLLEADKCCYAHDHCDSSISSES KYGLKNDEHITLLHCDCEEAFDKCLQDTANKVNSDYQKEQTQQLRHFYFVTIKHRCYRLYCENKRDNSTCRGYW RKDYKDEDYD *	Phospholipase A2 (218546750)
sdc14634_g4_i1	<u>MGMQNLI FVITFTLVSMAWAQ</u> SSSEKELYLNFEPLPGQRDGPVVRVAVRMLYQKRSEGGRELRTFDGCQILDSITEI SREAYRMPRHSMKRISKEEMKSFEGRCERSGEVERTFLGTKWCGAGNTSTSYSDLGTLNNIDSCCRDHDHCDIAA GETKYGLKNKGENSELMNCDCEVAFAACLDEVPSKTYWFLSKATEKLSIPAIAKKFYFDWYGNSCYNLTCSGRSLSN NECTNPVAEYNGPTGFFNPLFNG *	Phospholipase A2 (218546750)
sdc14634_g4_i2	<u>MONLIFVVFTLVSVAWAQ</u> SSSEKELYLNFEPLPGQRDGPVVRVAVRMLYQKRSEGGRELRTFDGCQILDSITEISRE AYRMPRHSMKRISKEEMKSFEGRCERSGEVERTFLGTKWCGAGNTSTSYSDLGTLNNIDSCCRDHDHCDIAAGE TKYGLKNKGENSELMNCDCEVAFAACLDEVPSKTYWLLSKATEKVSIPVIKKFYFDWYGNSCYNLTCSGRSLRNN ECAKPVAEYNGPTGFLNPYING *	Phospholipase A2 (218546750)
sdc14190_g1_i2	RLKEGDLKIKGRPSYFYFRYNNRVSLKTRVDTVLSWLDLPHDSRPSFITFYINEPDHTSHRHGPFSSQQVEAALRKIE NLFQQLMAGLQTRGLINCNVNIIIVGDHGMDSVECDKVILLKDYVNSSDVYFMAGPVGRIKPKHYAESSIQNIVNEF RCHRPEVLVYRKSELPKHYHFSANRKIEPVIIDLPSKWITIAQSVDPNYCGGGAHGYDNLNPDMMNTIFVAYGPSFKR NLVVKPFLNVELYEMMSELIQVTEPNNGTYGSLHNILRNPQLLPNTPTPKAFTTCVISGLQRRNGNLSCNCKEN FSTGGTYLPNERRRNEEALIPWGAIPILKGTDSLAVCHLVNSDYVTA FHKELKLPLWTSFTISKKNSLFSGTSKFTSSK CWLADGRIPAENLANCTHYRELAKEYPGLQQRPLFPIAFASSETSELSVQLMTNAVPMYQHFRSEMWLQFLILLSK WSHKFSSLNVVMGPAFDINGNGVRPHIKDLMKDDKIPVPTHYFAVVTYCHSTDPIETCRSADIEVLSFLIPHRNYP DNCQNVNEYFLKHS AKVKDVEIITGLNFFTQLSPYTAISLRTHLVEELWNV *	Venom phosphodiesterase 2 (387014162)
HYALURONIDASES		
sdc14512_g1_i1	<u>MSSIFFVCVILNWVFSTSDAN</u> FEVFWNVPSLCSIKFGVNMTQTVLKHNILVNNGETFTGDKITLIYESGIGKYPHID PKKGDVNGGLPRLDSLDEHLKLAEKDIQIIPNPNFNGLGIIDWEAWRPIWEYHWGSLGVYKNKTLDLVKKHEHPS WSKQIIESTAKNLWESTAKQWMLKTLELAKNLRPHGMWCYYLFPDCYNYFGKDQPSQFFCNMIKSNNDRLSW MWDASAALCPSIYFIEFQKYNESQRIWYLYGKLSEAVRVSRPHTQIYPYINYMVHVSRIPVKPDQFWKMLSMTAS LGLDGAVIWGSSGYLQSKKTCEDELAYVENIIGPAVTTISSNVKRCSSQTVCNGRGKCTWPKEPFTSWKYLIDSKGH DFDAQNIICRCQNHNGRYCS *	Hyaluronidase 1 (597439573)
sdc14647_g1_i1	<u>MLLILISMFSLSALG</u> VDFNVYWHVPSSPCSERFNINVTHKLLKCNVLVNSGEKFRGDKIVWFYETFGFRFPYMDDV NSYMDGGIPQLGNLTSHLEWAERHVEEIPNPNFDGIAVIDWREWRIYDYNWEVYQNVTKELVRKNNPSIREEEI ESTARIQWEEAAKKWLLETCLKVRMRPKAKWCYYSFPDCYNHQRGDVPDFTCRKEIQRHNDRLSWLWKEST ALCPSIKLGSREEKYDDSERQWYLYGRLSEARRV ASPNTLIYFPVSSFRNPNWESLDSFLDMIGAPASMGFDGAVIS	Hyaluronidase 1 (597439573)

	GSSKYIRDKNDC EELDWYVTAVICPAVTKVYTQFHKCSRTVCTNDGRCTWPYEIFNSMDYMLYDSCRNFNSKAVF CRCEENEGRYCDKYYYNDYY *	
sdc14647_g1_i5	<u>MLLILIISMFSLSALGV</u> DFNVYWHVPSSPCSERFNINVTHKLLKCNVLVNSGEKFRGDKIVWIFYGLKFGYMKTDNG VDYYVNGGIPQFANLTYQLKWVETNIAELIPNPNFDGIAVIDWREWRPIYDYNWEVYQNVTKELVRKNNPSIREE EIESTARIQWEEAAKKWLLETCLKVKRMRPKAKWCYYSFPDCYNHQRGDVPHDFTCRKEIQRHNDRLSWLWKES TALCPSIKLSREEKYDDSERQWYLYGRLSEARRVASPNTLIYPFVSSFRNPNWESLDSFLDMIGAPASMGFDGAVIS GFSKYIRYKNDC	Hyaluronidase 1 (597439573)
sdc14647_g1_i2	<u>MLLILIISMFSLSALGV</u> DFNVYWHVPSSPCSERFNINVTHKLLKCNVLVNSGEKFRGDKIVWIFYEYTFGRFPYMDDV NSYMDGGIPQLGNLTSHLEWAERHVEEIPNPNFDGIAVIDWREWRPIYDYNWEVYQNVTKELVRKNNPSIREEEI ESTARIQWEEAAKKWLLETCLKVKRMRPKAKWCYYSFPDCYNHQRGDVPHDFTCRKEIQRHNDRIPSWI *	Hyaluronidase 2 (573016564)
sdc14647_g1_i3	PCSEMFNINVTTHKLLKCNVLVNNGEFEWGDKFVWFYELKFGMFPIHTVNGEHIYNDGGIPQFDNLTFHLAWAE TEIEQLTDPNFDGIGVIDWRQWNPIYDYNLGSKSIIYKLTKELVKENNPSIREEEIESTARIQWEEAAKKWLLETCLK VKRMRPKAKWCYYSFPDCYNHQRGDVPHDFACRKEIQQHNDRIPSWI *	Hyaluronidase 2 (573016564)
sdc14647_g1_i4	PCSEMFNINVTTHKLLKCNVLVNNGEFEWGDKFVWFYELKFGMFPIHTVNGEHIYNDGGIPQFDNLTFHLAWAE TEIEQLTDPNFDGIGVIDWRQWNPIYDYNLGSKSIIYKLTKELVKENNPSIREEEIESTARIQWEEAAKKWLLETCLK VKRMRPKAKWCYYSFPDCYNHQRGDVPHDFACRKEIQQHNDRLSWLWKESTALCPSIKLSREEKYDDSERQW YLYGRLSEARRVA	Hyaluronidase 2 (573016564)
La 1 LIKE PEPTIDES		
sdc12897_g1_i1	<u>MRSVIMEPPYTAVLLGLLLAFSVFNFSMG</u> FGESCKGGPYSIIPVGQEMDPTTCTSYKCINYNRKYVLQTSTCATVK PPCKGMGSFQGNRFPNCCPIVTCTGG *	La1 like protein 13 (430802824)
sdc14036_g1_i1	<u>MKYLYFAVFFGCLCSLISVSMGGGE</u> VCVLGGMTIPVGQEKKDPKSCVLYKCVGVNNRVLIEKSVCQPQVKGRGCK SVDGPPSAPFPDCCPTSLCRGKQWDR *	La1 like protein 15 (430802826)
sdc10164_g1_i1	<u>MLFSDRTLRCILISCLFFTISDA</u> YMYYPQEDGSCIDGSGKERQLNDVWYDDSKCEENACLKGRGTPYIQTGCG VVEPG	Putative secreted protein (240247657)
sdc13004_g1_i1	<u>MTLLNLVLICMYFIVTNA</u> YMYYPQELGSVDCTDRRNGVHHPVGEQWYIDELCESNTCKQFKDLSLAITSGCGV VEPGPGCKLVRGTGSYPDCCLDEV *	Putative secreted protein (240247657)
sdc7328_g1_i1	DIPYEEKQDPAKCTLYKCEKDAGRIVLNTVTCAPQEPKTGCRNVDSFVELFPDPCCPLVVCNAPVYGG *	SV_SVC-Cer 1 (522802545)
sdc14589_g1_i1	<u>MKKLIFSLVLICIFIAIEA</u> YTYIAPQEPGSVDCTDELGVHHPLGEVWYNEERCERLVCQGYGNLSITSGCGIVSA PGCKLVKSGSYPKCCPKPVCRR *	Toxin like protein 14 (430802832)
sdc5116_g1_i1	<u>MDRNIIFFVLFPFVVLGNDD</u> LRFITYKNDVVFPLTEGKCNAGSGRLINQGDTWYSDEYCEKFKCLRTGILGHVEVR GCAPVYPIRPNCTVVHHKGVYPDCCDGDIVCNEQQEPKSDVEMAEILIRALLEESNKK *	Venom protein 7 (149134066)
VENOM COMPONENTS		
VENOM PROTEINS		

sdcl837_g1_i1	<u>MKLVLVLACLI</u> <u>AFH</u> <u>AVAG</u> <u>QES</u> <u>CS</u> <u>SS</u> <u>DC</u> <u>ED</u> <u>GE</u> <u>CC</u> <u>LE</u> <u>D</u> <u>F</u> <u>Y</u> <u>Q</u> <u>D</u> <u>T</u> <u>A</u> <u>K</u> <u>C</u> <u>E</u> <u>K</u> <u>S</u> <u>E</u> <u>R</u> <u>K</u> <u>F</u> <u>C</u> <u>S</u> <u>E</u> <u>E</u> <u>S</u> <u>A</u> <u>Q</u> <u>S</u> <u>A</u> <u>D</u> <u>D</u> <u>R</u> <u>Y</u> <u>L</u> <u>F</u> <u>Y</u> <u>C</u> <u>P</u> <u>C</u> <u>K</u> <u>D</u> <u>G</u> LSCIVTEN	BLTX651 (671759197)
sdcl1506_g1_i1	<u>LLI</u> <u>LS</u> <u>V</u> <u>V</u> <u>L</u> <u>V</u> <u>V</u> <u>V</u> <u>Y</u> <u>A</u> <u>R</u> <u>D</u> <u>K</u> <u>S</u> <u>E</u> <u>C</u> <u>E</u> <u>L</u> <u>H</u> <u>R</u> <u>E</u> <u>R</u> <u>E</u> <u>Q</u> <u>K</u> <u>R</u> <u>I</u> <u>G</u> <u>V</u> <u>G</u> <u>K</u> <u>L</u> <u>V</u> <u>P</u> <u>E</u> <u>C</u> <u>E</u> <u>E</u> <u>N</u> <u>G</u> <u>D</u> <u>Y</u> <u>K</u> <u>L</u> <u>Q</u> <u>C</u> <u>H</u> <u>G</u> <u>G</u> <u>T</u> <u>R</u> <u>F</u> <u>C</u> <u>Q</u> <u>C</u> <u>W</u> <u>D</u> <u>I</u> <u>K</u> <u>G</u> <u>H</u> <u>P</u> <u>I</u> <u>T</u> <u>P</u> <u>P</u> <u>S</u> <u>M</u> <u>F</u> <u>L</u> <u>K</u> <u>S</u> CECHREKKIAEEGDIIAGFIPRCKKNGKYEEKQCWASTGTCWCVDEDGKKTSDPTRDDIDC *	Ctenitoxinlike-lyc-1 (522802644)
sdcl3673_g1_i1	<u>M</u> <u>K</u> <u>T</u> <u>F</u> <u>I</u> <u>S</u> <u>I</u> <u>V</u> <u>V</u> <u>L</u> <u>S</u> <u>I</u> <u>A</u> <u>G</u> <u>T</u> <u>L</u> <u>A</u> <u>Q</u> <u>K</u> <u>K</u> <u>T</u> <u>E</u> <u>C</u> <u>Q</u> <u>E</u> <u>S</u> <u>R</u> <u>E</u> <u>K</u> <u>A</u> <u>L</u> <u>K</u> <u>S</u> <u>N</u> <u>A</u> <u>R</u> <u>I</u> <u>K</u> <u>A</u> <u>I</u> <u>I</u> <u>P</u> <u>V</u> <u>C</u> <u>D</u> <u>T</u> <u>N</u> <u>G</u> <u>D</u> <u>Y</u> <u>A</u> <u>G</u> <u>L</u> <u>Q</u> <u>C</u> <u>H</u> <u>E</u> <u>G</u> <u>S</u> <u>K</u> <u>F</u> <u>C</u> <u>S</u> <u>C</u> <u>W</u> <u>R</u> <u>K</u> <u>D</u> <u>G</u> <u>T</u> <u>P</u> <u>I</u> <u>T</u> <u>Q</u> <u>P</u> <u>S</u> <u>G</u> KIKACECHRQKDESSKKGLIGAFIPQCAEDGKFHKKQCWGSTGHCWCADPETGKNTTQVRVGKLS *	Ctenitoxinlike-lyc-1 (522802644)
sdcl1734_g1_i2	<u>M</u> <u>K</u> <u>T</u> <u>V</u> <u>I</u> <u>A</u> <u>I</u> <u>V</u> <u>L</u> <u>A</u> <u>C</u> <u>F</u> <u>V</u> <u>A</u> <u>V</u> <u>V</u> <u>V</u> <u>S</u> <u>E</u> <u>E</u> <u>T</u> <u>A</u> <u>C</u> <u>Q</u> <u>R</u> <u>A</u> <u>R</u> <u>E</u> <u>R</u> <u>Q</u> <u>L</u> <u>Q</u> <u>N</u> <u>R</u> <u>N</u> <u>S</u> <u>V</u> <u>I</u> <u>V</u> <u>N</u> <u>R</u> <u>C</u> <u>D</u> <u>E</u> <u>N</u> <u>G</u> <u>N</u> <u>Y</u> <u>E</u> <u>A</u> <u>L</u> <u>Q</u> <u>V</u> <u>S</u> <u>D</u> <u>G</u> <u>S</u> <u>W</u> <u>K</u> <u>I</u> <u>C</u> <u>F</u> <u>T</u> <u>P</u> <u>D</u> <u>G</u> <u>D</u> <u>V</u> <u>I</u> <u>Q</u> <u>G</u> <u>P</u> <u>S</u> <u>R</u> TIEYCECFKTRYELSKQNLPSSEKLPDCKATGEFVALQSDGVSHWCVDKVTGEKTTEPRPLSRISITCD *	Thyropin 2 (629510299)
sdcl4254_g1_i1	<u>A</u> <u>F</u> <u>E</u> <u>M</u> <u>W</u> <u>Y</u> <u>G</u> <u>V</u> <u>W</u> <u>L</u> <u>V</u> <u>G</u> <u>L</u> <u>V</u> <u>G</u> <u>L</u> <u>A</u> <u>A</u> <u>G</u> <u>A</u> <u>K</u> <u>P</u> <u>D</u> <u>C</u> <u>P</u> <u>P</u> <u>C</u> <u>K</u> <u>K</u> <u>E</u> <u>S</u> <u>C</u> <u>A</u> <u>P</u> <u>L</u> <u>N</u> <u>C</u> <u>L</u> <u>A</u> <u>G</u> <u>L</u> <u>V</u> <u>K</u> <u>D</u> <u>I</u> <u>C</u> <u>D</u> <u>C</u> <u>F</u> <u>V</u> <u>C</u> <u>G</u> <u>R</u> <u>T</u> <u>E</u> <u>G</u> <u>E</u> <u>R</u> <u>C</u> <u>D</u> <u>N</u> <u>L</u> <u>A</u> <u>L</u> <u>P</u> <u>L</u> <u>P</u> <u>Y</u> <u>R</u> <u>R</u> <u>K</u> YGYCGENLECLRLTDLAPEDPDEGICVCLKQEAIACANDGNTYENECKLTEARYKLRLDNLRAVSRGPCRSAPKII SPPETTKNRTGGSAAALSCEVTGWPIPVIEWKVDHGDGIMSPMPSDRPRISVQTRGGPGNYEVTSWLQMQLNELRD HATYWCIAARNDGESTASAQIRIVNFRPFNEI *	Insulin like growth factor binding related protein 1 (351720390)
sdcl2109_g1_i1	<u>S</u> <u>V</u> <u>T</u> <u>K</u> <u>M</u> <u>V</u> <u>I</u> <u>V</u> <u>L</u> <u>I</u> <u>L</u> <u>M</u> <u>T</u> <u>T</u> <u>A</u> <u>G</u> <u>L</u> <u>C</u> <u>R</u> <u>G</u> <u>A</u> <u>A</u> <u>I</u> <u>V</u> <u>D</u> <u>G</u> <u>E</u> <u>L</u> <u>I</u> <u>C</u> <u>S</u> <u>C</u> <u>D</u> <u>D</u> <u>V</u> <u>L</u> <u>C</u> <u>Q</u> <u>I</u> <u>G</u> <u>N</u> <u>C</u> <u>P</u> <u>L</u> <u>G</u> <u>E</u> <u>V</u> <u>K</u> <u>G</u> <u>I</u> <u>C</u> <u>G</u> <u>C</u> <u>C</u> <u>N</u> <u>E</u> <u>A</u> <u>H</u> <u>D</u> <u>V</u> <u>G</u> <u>E</u> <u>P</u> <u>C</u> <u>G</u> <u>S</u> <u>L</u> <u>N</u> <u>Y</u> <u>G</u> <u>G</u> ICGVGLKCEPNEFKQLPG	Orphan peptide AbOp5 (723219378)
sdcl4152_g1_i1	<u>D</u> <u>I</u> <u>C</u> <u>R</u> <u>R</u> <u>S</u> <u>O</u> <u>K</u> <u>T</u> <u>O</u> <u>I</u> <u>H</u> <u>I</u> <u>F</u> <u>A</u> <u>L</u> <u>S</u> <u>S</u> <u>Y</u> <u>R</u> <u>V</u> <u>N</u> <u>R</u> <u>I</u> <u>A</u> <u>N</u> <u>R</u> <u>C</u> <u>T</u> <u>M</u> <u>I</u> <u>R</u> <u>L</u> <u>V</u> <u>I</u> <u>F</u> <u>S</u> <u>V</u> <u>L</u> <u>V</u> <u>S</u> <u>I</u> <u>Y</u> <u>S</u> <u>L</u> <u>S</u> <u>C</u> <u>P</u> <u>W</u> <u>R</u> <u>E</u> <u>E</u> <u>D</u> <u>P</u> <u>T</u> <u>K</u> <u>Y</u> <u>C</u> <u>G</u> <u>P</u> <u>P</u> <u>P</u> <u>E</u> <u>N</u> <u>C</u> <u>A</u> <u>K</u> <u>G</u> <u>V</u> <u>T</u> <u>T</u> <u>D</u> <u>V</u> <u>C</u> <u>G</u> <u>C</u> CPVCYKVEGEVCGGPWGVYGDCEGLVCDKGASLEEGEFDQREGVCKPE *	Tbah01400 (757181026)
sdcl4453_g2_i1	<u>M</u> <u>L</u> <u>F</u> <u>R</u> <u>I</u> <u>A</u> <u>V</u> <u>S</u> <u>L</u> <u>L</u> <u>L</u> <u>V</u> <u>V</u> <u>C</u> <u>V</u> <u>Y</u> <u>S</u> <u>L</u> <u>S</u> <u>C</u> <u>P</u> <u>L</u> <u>C</u> <u>W</u> <u>E</u> <u>N</u> <u>P</u> <u>S</u> <u>V</u> <u>C</u> <u>G</u> <u>T</u> <u>T</u> <u>P</u> <u>T</u> <u>D</u> <u>C</u> <u>K</u> <u>L</u> <u>G</u> <u>L</u> <u>T</u> <u>K</u> <u>D</u> <u>A</u> <u>C</u> <u>G</u> <u>C</u> <u>D</u> <u>V</u> <u>C</u> <u>K</u> <u>I</u> <u>E</u> <u>G</u> <u>E</u> <u>K</u> <u>C</u> <u>A</u> <u>G</u> <u>P</u> <u>F</u> <u>R</u> <u>T</u> <u>S</u> <u>G</u> <u>E</u> <u>C</u> <u>G</u> <u>K</u> <u>G</u> <u>L</u> <u>K</u> CVISDDEPQHNRFAQEGTCMPEN *	Tbah01400 (757181026)
sdcl4453_g2_i2	<u>M</u> <u>L</u> <u>F</u> <u>R</u> <u>I</u> <u>A</u> <u>V</u> <u>S</u> <u>L</u> <u>L</u> <u>L</u> <u>V</u> <u>V</u> <u>C</u> <u>V</u> <u>Y</u> <u>S</u> <u>L</u> <u>S</u> <u>C</u> <u>P</u> <u>L</u> <u>C</u> <u>W</u> <u>E</u> <u>N</u> <u>P</u> <u>S</u> <u>V</u> <u>C</u> <u>G</u> <u>T</u> <u>T</u> <u>P</u> <u>T</u> <u>D</u> <u>C</u> <u>K</u> <u>L</u> <u>G</u> <u>L</u> <u>T</u> <u>K</u> <u>D</u> <u>A</u> <u>C</u> <u>G</u> <u>C</u> <u>D</u> <u>V</u> <u>C</u> <u>K</u> <u>I</u> <u>E</u> <u>G</u> <u>E</u> <u>K</u> <u>C</u> <u>G</u> <u>G</u> <u>P</u> <u>W</u> <u>R</u> <u>T</u> <u>S</u> <u>G</u> <u>N</u> <u>C</u> <u>G</u> <u>K</u> <u>G</u> <u>L</u> KCEIPKDLPKHIQRQAVGTCKPE *	Tbah01400 (757181026)
sdcl4388_g1_i1	<u>M</u> <u>N</u> <u>R</u> <u>Y</u> <u>W</u> <u>L</u> <u>I</u> <u>S</u> <u>F</u> <u>I</u> <u>L</u> <u>L</u> <u>G</u> <u>I</u> <u>L</u> <u>M</u> <u>G</u> <u>G</u> <u>M</u> <u>A</u> <u>Q</u> <u>D</u> <u>C</u> <u>M</u> <u>Q</u> <u>C</u> <u>G</u> <u>T</u> <u>Y</u> <u>Q</u> <u>C</u> <u>Y</u> <u>T</u> <u>T</u> <u>P</u> <u>A</u> <u>E</u> <u>C</u> <u>P</u> <u>A</u> <u>G</u> <u>T</u> <u>V</u> <u>T</u> <u>D</u> <u>M</u> <u>C</u> <u>D</u> <u>C</u> <u>L</u> <u>V</u> <u>C</u> <u>A</u> <u>K</u> <u>D</u> <u>E</u> <u>D</u> <u>E</u> <u>E</u> <u>C</u> <u>G</u> <u>L</u> <u>W</u> <u>D</u> <u>M</u> <u>R</u> <u>G</u> <u>K</u> <u>C</u> <u>G</u> EGLTCVKENGDDENSVGVCKKE *	Tbah02469 (757181036)
sdcl11340_g1_i1	<u>S</u> <u>R</u> <u>E</u> <u>S</u> <u>K</u> <u>V</u> <u>T</u> <u>N</u> <u>K</u> <u>M</u> <u>D</u> <u>L</u> <u>R</u> <u>L</u> <u>F</u> <u>V</u> <u>L</u> <u>T</u> <u>V</u> <u>L</u> <u>I</u> <u>V</u> <u>S</u> <u>C</u> <u>H</u> <u>C</u> <u>L</u> <u>P</u> <u>S</u> <u>K</u> <u>R</u> <u>N</u> <u>D</u> <u>A</u> <u>C</u> <u>G</u> <u>P</u> <u>F</u> <u>P</u> <u>S</u> <u>N</u> <u>C</u> <u>R</u> <u>V</u> <u>G</u> <u>V</u> <u>T</u> <u>K</u> <u>D</u> <u>I</u> <u>D</u> <u>G</u> <u>C</u> <u>P</u> <u>V</u> <u>C</u> <u>T</u> <u>K</u> <u>D</u> <u>V</u> <u>G</u> <u>E</u> <u>E</u> <u>C</u> <u>G</u> <u>S</u> <u>W</u> <u>N</u> <u>A</u> <u>Y</u> <u>G</u> <u>I</u> <u>C</u> <u>N</u> VDLICQTNGQSDNDYELPIGICVPARRFSSRNILKRMIGGRH *	Venom insulin like growth factor binding protein 1 (149134032)
sdcl4478_g1_i1	<u>M</u> <u>N</u> <u>K</u> <u>F</u> <u>W</u> <u>M</u> <u>I</u> <u>S</u> <u>F</u> <u>I</u> <u>L</u> <u>L</u> <u>G</u> <u>I</u> <u>F</u> <u>T</u> <u>S</u> <u>S</u> <u>M</u> <u>A</u> <u>L</u> <u>S</u> <u>C</u> <u>M</u> <u>P</u> <u>C</u> <u>G</u> <u>E</u> <u>Y</u> <u>E</u> <u>C</u> <u>E</u> <u>P</u> <u>L</u> <u>P</u> <u>A</u> <u>H</u> <u>C</u> <u>P</u> <u>A</u> <u>G</u> <u>I</u> <u>G</u> <u>R</u> <u>D</u> <u>I</u> <u>C</u> <u>G</u> <u>C</u> <u>C</u> <u>P</u> <u>V</u> <u>C</u> <u>A</u> <u>Q</u> <u>A</u> <u>E</u> <u>N</u> <u>E</u> <u>I</u> <u>C</u> <u>G</u> <u>G</u> <u>P</u> <u>W</u> <u>D</u> <u>M</u> <u>N</u> <u>G</u> <u>R</u> <u>C</u> <u>G</u> <u>D</u> <u>G</u> <u>L</u> TCVKEKHDDDYEFNQSGVCKKV *	Venom insulin like growth factor binding protein 1 (149134032)
sdcl4478_g2_i1	<u>V</u> <u>S</u> <u>L</u> <u>E</u> <u>T</u> <u>K</u> <u>H</u> <u>L</u> <u>K</u> <u>N</u> <u>I</u> <u>N</u> <u>M</u> <u>N</u> <u>K</u> <u>F</u> <u>W</u> <u>T</u> <u>I</u> <u>S</u> <u>F</u> <u>V</u> <u>L</u> <u>L</u> <u>G</u> <u>I</u> <u>F</u> <u>T</u> <u>S</u> <u>S</u> <u>M</u> <u>A</u> <u>L</u> <u>S</u> <u>C</u> <u>L</u> <u>P</u> <u>C</u> <u>Y</u> <u>E</u> <u>R</u> <u>E</u> <u>C</u> <u>E</u> <u>P</u> <u>L</u> <u>P</u> <u>A</u> <u>H</u> <u>C</u> <u>P</u> <u>A</u> <u>G</u> <u>I</u> <u>G</u> <u>K</u> <u>D</u> <u>I</u> <u>C</u> <u>Y</u> <u>C</u> <u>C</u> <u>P</u> <u>V</u> <u>C</u> <u>A</u> <u>Q</u> <u>A</u> <u>E</u> <u>N</u> <u>E</u> <u>E</u> <u>C</u> <u>G</u> <u>G</u> <u>P</u> WDMLGRCGDGLTCVKEEDDYIDFNRRGGICKKV *	Venom insulin like growth factor binding protein 1 (149134032)
sdcl4478_g1_i2	<u>M</u> <u>N</u> <u>K</u> <u>F</u> <u>W</u> <u>M</u> <u>I</u> <u>S</u> <u>F</u> <u>I</u> <u>L</u> <u>L</u> <u>G</u> <u>I</u> <u>F</u> <u>T</u> <u>S</u> <u>S</u> <u>M</u> <u>A</u> <u>L</u> <u>S</u> <u>C</u> <u>T</u> <u>S</u> <u>C</u> <u>G</u> <u>E</u> <u>Y</u> <u>E</u> <u>C</u> <u>L</u> <u>P</u> <u>L</u> <u>P</u> <u>A</u> <u>H</u> <u>C</u> <u>P</u> <u>A</u> <u>G</u> <u>I</u> <u>G</u> <u>R</u> <u>D</u> <u>I</u> <u>C</u> <u>G</u> <u>C</u> <u>C</u> <u>P</u> <u>V</u> <u>C</u> <u>A</u> <u>Q</u> <u>A</u> <u>E</u> <u>N</u> <u>E</u> <u>I</u> <u>C</u> <u>G</u> <u>G</u> <u>P</u> <u>W</u> <u>D</u> <u>M</u> <u>D</u> <u>G</u> <u>R</u> <u>C</u> <u>G</u> <u>D</u> <u>G</u> <u>L</u> TCVHEKNDDDDYIEVCKKV *	Venom insulin like growth factor binding protein 1 (149134032)

sdc30596_g1_i1	<u>CPNTSSFDKMKSLITAFFALACTTVHTFSNRELEELFCSLPNHLAARWIDCILEDAAESISKSANVVHTCVDEFWD</u> VKGLGDSLISMQCNDIRDDNVGECIMEKAKSLDFDQPPTEEEFLAVKNRIEPCFLTAK *	Venom protein 29 (317412178)
sdc25935_g1_i1	<u>QIFSENMGKLLFICLILLGISISAMALSCPRCEPDKCSPPPADCPAGIVKDVCHCCFRCAQAENEKCGGPWGIAGKC</u> GDGLTCVKETREGESPLGSIHRIGVCQKE *	Venom protein 302 (317412179)
CAP SUPERFAMILY		
sdc13900_g1_i1	<u>MAPTIVPVFIIWAVTINCIDSVDLCDERYTNITKEHTMCKPVNEDCNFLRVGKIFSKQLLRTHNDIRNSIRKFVVGKEY</u> KLATNMELMEWDEELYAMARMHTLQCVDKPCDNLCHQIDDFPVEQNFAVKTFKRSEVKHNGPVKRFQTVIKG WAAELQSYDPDVVNNLTITDKLPHTWNILRATTVFVGCASMNFYEDEPSVFKEVYVCNYGPANLTEGEQIYKTG NKSCSDCEDNGVCDEEFKNLCVPSELEEGSTENFPEGETTNLEEANTQETTYIEEGSTENFPSEETTYIEIMESSPSKE NISREVPETYTSIVQENETYFVTEVYTETSMEEYTTTELVPSEKK *	CAP-Iso-1 (522802633)
sdc13157_g2_i1	<u>INIFYKQTTKLKVMILGIIHFIIIGPLPTSNFTSTEKLFIKSGSVICEIGKNCNSLLTSLNGNIIHDVNVERQRLTIGFYE</u> GLPIATNMLKMIRDCDLEAKAQQAETCALQKSSHCRPPNDAEGEMNISVRKYNMNNQKGDVYDRLRDQVLR WKPPMGKEYKGPLTQLVKSYLEIDINNREWANYVRANVWVKVCGGIADVEMP NATFMEVFVCYFGSPKIRDGDE LYLAAGCVQCSQCPNGTRCRNGLCELEEFFGWKNILKCQEKYPNFAPSTNYERSPENGP CYEVATTTAEITPRPTT PALLTMEEIITEDILKFSIEDSAQACVDNTCSPGWSYNSGRVWSSFQIAR *	CAP-Lyc-1 (522802698)
sdc13157_g2_i2	<u>INIFYKQTTKLKVMILGIIHFIIIGPLPTSNFTSTEKLFIKSGSVICEIGKNCNSLLTSLNGNIIHDVNVERQRLTIGFYE</u> GLPIATNMLKMIRDCDLEAKAQQAETCALQKSSHCRPPNDAEGEMNISVRKYNMNNQKGDVYDRLRDQVLRWKP PMGKEYKGPLTQLVKSYLEIDINNREWANYVRANVWVKVCGGIADVEMP NATFMEVFVCYFGSPKIRDGDELYLA AGCVQCSQCPNGTRCRNGLCELEEFFGWKNILKCQEKYPNFAPSTNYERSPENGP CYEVATTTAEITPRPTTPALLT MEEIITEDILKFSIEDSAQACVDNTCSPGWSYNSGKAEIKGEGICMATVAFREKINLSGYSLKIQYSLTSGDEMASE VVAFAFEVNNKMGTIQKRIKYENGNNHMF LDIPWPVGVEFRVGFARSKLHDEQFEVIVDEVII LRGNCPQI *	CAP-Lyc-1 (522802698)
sdc13879_g1_i1	<u>MKQNHSMFFAMKAMVLIVIRFLIFDVFSKGVIAGSARLIFKDSNYKDCHIGTSECNFADIHKWFLKNHNSIRSTG</u> TAGQSATNMLMMEWDQKLTDAAQSYAEELPVSC LPERANFSGEVNTDIREHPYQSAASLSERIRKVLKYWKEE VDDYDSMLTNQIRSYKIVSRDMQRWANVVRATTWKVGC GVIDYSGKENPFNEIIVCFYKNAKLKEGEELYKIG KPCTECPQGTSCSEYLKTLCEVNPGKCPITSNERTIEESCSTKGNTVWRCSVEQGTEDCLAERACSSFWEIDVIGKFK KISVSGMCSSVNIFHKEIQIDEPACFIFEYIKEPTLSQAVKSEVTGFILQSNQYSEKVTASDDAKEWTPIKVDIPWTGI AVQVGVGVRSPPTAGKQDIKVRNFSVVTGKCT *	CAP-Lyc-1 (522802698)
sdc3852_g1_i1	<u>VTKQAAIMIPVLLTSLTLTCHVVLSSQSCPEIYLRFSKDHTYCRRTCKVMKSGVTEEDKKIILDMHNKYRNKIALGQ</u> ETEPQQPPAANMMQMEWDDELAKVAQAHA SLCKFDHDTGPRQVENFNVGQNL YITMMSKINWKKASV WYTSEVKLFYPQYREPYVFGAWGHFSQMIWAKTWKVCGGMAMYEEENMDKILYTCNYGPAGNMQGGTTYIKG NPCSQCPKNTQCSNEYRGLCKSLTPDGPQEDNSKSSNDLILYCDFSTNDPAECKNVQITGSKQFQTRKIYSGEYKTV VLNGGDSITIKLGKAQSEKGICPFIYGYFGPNRDGDAKQSAVSIGFSAPGINFGQPTKIEYGGSSFWTIGMQMQFNQ EMESTIKLEAYPGAAPQYFNVKAFGIGRGKCPKF *	CAP-Uro-1 (522802590)
sdc11413_g1_i1	<u>NMMQMEWDDELARVAQAHANLCVFKHDKGKERAVENFPVGQNLLKFSPAIRKWEAINSWYKQEVCFFLPEYI</u> KPFHSGDYGHFSQFTWATTWKIGCGFTAYSEGGKNFSLYTCNYGPTGNILQGTQYIVGEPSCQCPENTEC SKPYPG	CAP-Uro-1 (522802590)

	LCKSKTRDGPQMTKPPSEDYALYCDFSSDDPDKCRDVKISGSRNFTTRHIYSGNYKTVILEGGEYVTIDLGMAKNE DGICPFVYIRCGPNNATETIGLVMEISFSVPGNTPQSPMKIYPNAGTSFSPIGVHMRSNFEFKSTITLRAKDDGAPQF VDVRIWGIKSDCKNPPL *	
sdc14327_g1_i1	<u>GIFLFHLCSEMERVLCTVLFLOILWWMSAGCKYERVGRHHTMCIYSAHACPNSQLIRSGGITTRDKNLIVKIHNQVR</u> SKVALGKVHGLPPAADMRVMTWDNELAKIAQRWADQCTEGHDKLRDTERESVGQNVALRWSYDHKDLLKDK PDWPFIDLSWKEYDEFGFSSSHISPFVFKYSVGHYTMQMIWAETHKIGCGFTYYKHPQKGYTKIYVCNYSPPGGNIIQGT MYKTSPRGATCSDSSLQLSREYKGLCEKSRRSRIRRRNSNRRKRVISQTRHERSRTFQFSKQQKSRNARRKGSTN *	Putative scp tpx 1 ag5 pr1 (757180984)
sdc11413_g2_i1	<u>MKVLPIVSCLLLTQCSSILCLSCSETDYGKYDEDTRDIKIPISLWRTPTSGRNKVETLESKECPLLYQRYSSNHTYCKTS</u> TCDIIFKGVNSGEKKMILHIHNSLRRKLANGQETRYRQLPSAANMMQMEW	Putative cysteine rich secretory peptide (757180946)
sdc11413_g2_i2	<u>YMVFEINKSDFSSYSTRMKVLPIVSCLLLTQCSSILCLSCSETDYGKYDEDTRDIKIPISLWRTPTSGRNKVETLESKEC</u> PLLYQRYSSNHTYCKTSTCDIIFKGVNSGEKKMILHIHNSLRRKLANGQETRYRQLPSAANMMQMEW	Putative cysteine rich secretory peptide (757180946)
sdc14601_g1_i1	<u>MNTKGCIIGYVPOTLMFVLIATVVSSLGKNICDTRYRNIHPEHSMCKTRNYTCKFRSGIEENVQPLDLHNNHIRNSI</u> QKVVGNNYFEGRNMMNMQWDRELYLIAQRHVLQCTDLPDCSQCHQIDRFHVEQNFAVNTFSSVNHSFNCSVE RFKRVIRDWASELRKYNPCVVERFQFLGLPTNWTNIFRATTLKVGCAVSYDSQTKGRFTEIYVCNYPALLTEGV EIYKPNYQNCNECSNNIKCNTSTPLQSRDLRQQLDYQQRARKSQRQLIARAPVIGKSKRQIITPTTTTTEQFQNH PTEIDLLVDSGHIYPSTPETEAHTTETTKITITATPVPISEIITTEKKIPTKDTATPTVKSSTETEIDLLIASETIFPSISTTESST IGTAKPIPTTTPVSTSRSANPEYNIYTQITNTETIIPSPDTEVDLIEASEIISTSTTEEASMTGVTKPDIGLVEVSEIISTST TESSISEATILD	Tbah00853 (324497915)
sdc14601_g1_i2	<u>MNTKGCIIGYVPOTLMFVLIATVVSSLGKNICDTRYRNIHPEHSMCKTRNYTCKFRSGIEENVQPLDLHNNHIRNSI</u> QKVVGNNYFEGRNMMNMQWDRELYLIAQRHVLQCTDLPDCSQCHQIDRFHVEQNFAVNTFSSVNHSFNCSVE RFKRVIRDWASELRKYNPCVVERFQFLGLPTNWTNIFRATTLKVGCAVSYDSQTKGRFTEIYVCNYPALLTEGV EIYKPNYQNCNECSNNIKCNTSTPLQSRDLRQQLDYQQRARKSQRQLIARAPVIEEYMEVDIPEQTRSGLLFLNTI YIEEPSCFISYKKNAPWISPLTSSVYGIAVRTESNDYVMVQRDQTDVYDWMHVFLDIPWIKVFIQVGVGIRTDYGA GEQHIQIKDLVLRRTCSAL *	Tbah00853 (556052306)
sdc11381_g1_i3	<u>MESMIIIVTTCLIFDIFVSNGVTDDSAYLIFKHNTYKDCIIGENGCNLKEVQMMFLERHNFMRSGIAGSDSTTEPDAA</u> NMLMMEWDQSLANDAQNAYQNCLEGRGCQPEEAGFNGEVNIYTNSYDKADAHVESLPTRISNTIWSWVYDSVH GHSSEDIKSLLSYKSDSPTMHQWANVIRATTWKMGCGIADILISPGANQFSEIIVCFYKNSKLNDELYKIGQPC TNCPPGTICSYKESLSNLCEIPGYCPITSNELTVEDSCYRSELQRTSIWNCSAEDDTENCRPERPCASVWKIDPYGKF KKITVSGMCTSANMYQKEIEINEPACFIFEYIKEPSVNQAISTVTGFLVQSNGKYSEKVTVSEDVDKWTPVKLDIY WTGIPLQIGISVRSRSTPTTGEQEIKNFLIVTGSCA *	Venom allergen 5 (675383069)
sdc11381_g1_i2	<u>MESMIIIVTTCLIFDIFVSNGVTDDSAYLIFKHNTYKDCIIGENGCNLKEVQMMFLERHNFMRSGIAGSDSTTEPDAA</u> NMLMMVIRATTWKMGCGIADILISPGANQFSEIIVCFYKNSKLNDELYKIGQPCNTNCPPGTICSYKESLSNLCEI PGYCPITSNELTVEDSCYRSELQRTSIWNCSAEDDTENCRPERPCASVWKIDPYGKFKKITVSGMCTSANMYQKEIE INEPACFIFEYIKEPSVNQAISTVTGFLVQSNGKYSEKVTVSEDVDKWTPVKLDIYWTGIPLQIGISVRSRSTPTTGE QEIKNFLIVTGSCA *	Venom allergen 5 (675383069)

Table S2. Amino acid sequences of peptides.

	Transcript	Sequence (MS/MS)
Enzymes	sdc14619_g1_i3	GYDWTDALAYAK
		EFADAFFEFR
		SLGGWPLLGETIK
		IGEIIEGSYLENTITIAK
		TETIANIYGWTIVNGYGR
		ANYYFGLPLGNLFNNR
	sdc14619_g1_i1	LHLELNTEQIDILLLNK
		KLnGFYEKIGEIIEGSYLEnTITIAK
		TcKLLEQnTTKTETIANIYGWTIVnGYGR
	sdc14393_g1_i1	LGEIIEGSHLENVINIVK
		HFYFVTIK
CAP	sdc14212_g1_i1	NDEHITLLHcDcEEAFDK
		FSLTFIK
		ELYVNFEPLPGQK
	sdc3852_g1_i1	AFDScLQNAANK
		YGLTNDGEYTLLNcncDK
		FAYFTVYAPK
	sdc13900_g1_i1	LEAYPGAAPQYFNVK
		QSAVSIGFSAPGINFGQPTK
		EPYVFGAWGHFSQmIWAK
	sdc13900_g1_i1	mHTLQcVDKPDcNLcHQIDDFPVEQNFAVK
		LATNmELmEWDEELYAmAR
La1-like	sdc13004_g1_i1	YmYYDPQELGSVDcTDR
		RnGVHHPVGEQWYIDELcESNTcK
		DLSLAITSGcGVVEPGPGcK
		NGVHHPVGEqWYIDELcESnTcK
	sdc14036_g1_i1	GTGSYPDccLDEVc
		SVDGPPSAPFPDccPTSLcR
	sdc12897_g1_i1	GGEVcVLGGMTIPVGQEK
		GGPYSIIPVGQEMTDPTTcTSYKcINYNRK
	sdc14589_g1_i1	KYVLQTSTcATVKPPcK
		YTYIAPQEPGSVDcTDELGVHHPLGEVWYNEER
NaTx	sdc14462_g1_i1	HGAHGGScYSIPSR
		KQEAGYGYcYDR
		YcWcEGK
		KGGSTIPcLK
	sdc14462_g1_i2	HGGDSYcVDVcAK
		GDYVWcGLPGGENKEcEDVcR
	sdc14462_g2_i2	GGSTIPcLK
		IcAEHGAHGGScHGLPSR
	sdc15193_g1_i1	DKnGDWIWcGLPGGK
		YcWcEAP
KTx	sdc14273_g1_i2	TcYcEGLTITK
	sdc14273_g1_i2	SGEPPiWPcR
	sdc13949_g1_i1	FGKGGKcDGPK
		mRAPTGGcPFSDALcANYcKK
Sc	sdc14222_g4_i2	GcQETVQQIGYcHGTK
		LDSScILGHDR
		AIDEFVPmIPVPPSVSGALQK
	sdc14222_g4_i1	LDTPcIFGIDKK
		AIDVLTPmIPVPVVGIVNK
	sdc14222_g4_i1	cKcGKPLnYK

NDBP	sdc12606_g1_i1	IGTNPPQAAT
		IWNNSDFVK
	sdc4010_g1_i1	NIWNNSDIVK
	sdc14358_g12_i1	GFWGDVWSGIK
	sdc14358_g5_i1	IFGAIWNGIK
	sdc6540_g1_i1	GFWGNVWEGIK
		VLPSSLSSGK
	sdc28695_g1_i1	FWGFLAK
	sdc13544_g1_i1	YFWTYTFPK
	sdc14106_g1_i1	FPFFLASLIPSAINLVK

Table S3. Twenty two sequences of Calcins and putative Calcins isolated from the venom or deduced from cDNA or transcriptome analysis of 14 scorpion species in 12 genera and 8 families. Code = UniProt accession numbers; except for those with the names given in the original publications (listed in the references). * Possible not true Scorpion calcins.

Code	Species	Family	Reference
Q8I6X9	<i>Mesobuthus martensii</i>	Buthidae	UniProt
B8QG00	<i>Hoffmannihadrurus gertschi</i>	Caraboctonidae	UniProt
Ctyc5	<i>Chaerilus tryznai</i>	Chaerilidae	1
Ctric74	<i>Chaerilus triscostatus</i>	Chaerilidae	1
Ctric58	<i>Chaerilus triscostatus</i>	Chaerilidae	1
Ctryc59 *	<i>Chaerilus tryznai</i>	Chaerilidae	1
Ctric33 *	<i>Chaerilus triscostatus</i>	Chaerilidae	1
Ctryc40 *	<i>Chaerilus tryznai</i>	Chaerilidae	1
Ctric36 *	<i>Chaerilus triscostatus</i>	Chaerilidae	1
P60252	<i>Opisthophthalmus carinatus</i>	Scorpionidae	UniProt
P60253	<i>Opisthophthalmus carinatus</i>	Scorpionidae	UniProt
FD664155	<i>Heterometrus petersii</i>	Scorpionidae	UniProt
P59868	<i>Pandinus imperator</i>	Scorpionidae	UniProt
P60254	<i>Scorpio palmatus</i>	Scorpionidae	UniProt
Smp33	<i>Scorpio palmatus</i>	Scorpionidae	2
FD664670	<i>Scorpiops magerisonae</i>	Scorpiopidae	UniProt
GH547959	<i>Scorpiops jendeki</i>	Scorpiopidae	UniProt
sd9999	<i>Superstitionia donensis</i>	Superstitioniidae	This study
sd13987	<i>Superstitionia donensis</i>	Superstitioniidae	This study
L0GBR1	<i>Urodacus yaschenkoi</i>	Urodacidae	3
ViCaTx1	<i>Thorellius intrepidus</i>	Vaejovidae	3
VpCaTx1	<i>Mesomexovis punctatus</i>	Vaejovidae	3

Table S4. Ninety six sequences of Scorpines and putative Scorpines isolated from the venom or deduced from cDNA or transcriptome analysis of 34 scorpion species in 22 genera and 10 families; one sequence of the Pfam domain “Toxin 38” from a mite (Ixodae); and one sequence of a Potassium channel α toxin from one scorpion species. Code = UniProt accession numbers, except for those with the names given in the original publications (listed in the references).

Code	Species	Family	Pfam	Reference
Q6XLL8_KTx6	<i>Opisthacanthus cayaporum</i>	Hormuridae	Toxin 2	UniProt
A0A023FQN5_acari	<i>Amblyomma cajennense</i>	Ixodae	Toxin 38	UniProt
P69939	<i>Androctonus australis</i>	Buthidae	Toxin 38	UniProt
A0A0K0LBZ4	<i>Androctonus bicolor</i>	Buthidae	Toxin 38	UniProt
A0A0K0LC02	<i>Androctonus bicolor</i>	Buthidae	Toxin 38	UniProt
A0A0K0LC05	<i>Androctonus bicolor</i>	Buthidae	Toxin 38	UniProt
A0A0K0LC06	<i>Androctonus bicolor</i>	Buthidae	Toxin 38	UniProt
A0A0K0LC08	<i>Androctonus bicolor</i>	Buthidae	Toxin 38	UniProt
A0A0K0LC09	<i>Androctonus bicolor</i>	Buthidae	Toxin 38	UniProt
A0A0K0LC11	<i>Androctonus bicolor</i>	Buthidae	Toxin 38	UniProt
A0A0K0LC14	<i>Androctonus bicolor</i>	Buthidae	Toxin 38	UniProt
A0A0K0LC17	<i>Androctonus bicolor</i>	Buthidae	Toxin 38	UniProt
A0A0K0LCI9	<i>Androctonus bicolor</i>	Buthidae	Toxin 38	UniProt
A0A0K0LCJ0	<i>Androctonus bicolor</i>	Buthidae	Toxin 38	UniProt
T1E6W5	<i>Australobuthus xerolimniorum</i>	Buthidae	Toxin 38	UniProt
B8XH40	<i>Buthus occitanus</i>	Buthidae	Toxin 38	UniProt
B8XH36	<i>Buthus occitanus</i>	Buthidae	Toxin 38	UniProt
T1DEK6	<i>Isometroides vescus</i>	Buthidae	Toxin 38	UniProt
T1E6Y1	<i>Isometroides vescus</i>	Buthidae	Toxin 38	UniProt
T1E6Z4	<i>Lychas buchari</i>	Buthidae	Toxin 38	UniProt
C6ZH27	<i>Lychas mucronatus</i>	Buthidae	Toxin 38	UniProt
D9U2A7	<i>Lychas mucronatus</i>	Buthidae	Toxin 38	UniProt
D9U2B1	<i>Lychas mucronatus</i>	Buthidae	Toxin 38	UniProt
P0CI42	<i>Lychas mucronatus</i>	Buthidae	Toxin 38	UniProt
P0CI49	<i>Lychas mucronatus</i>	Buthidae	Toxin 38	UniProt
P0CJ45	<i>Lychas mucronatus</i>	Buthidae	Toxin 38	UniProt
A9XE59	<i>Mesobuthus eupeus</i>	Buthidae	Toxin 38	UniProt
A9XE60	<i>Mesobuthus eupeus</i>	Buthidae	Toxin 38	UniProt
P0CH57	<i>Mesobuthus eupeus</i>	Buthidae	Toxin 38	UniProt
A0A088D9S1	<i>Mesobuthus eupeus</i>	Buthidae	Toxin 38	UniProt
A0A088D9U2	<i>Mesobuthus eupeus</i>	Buthidae	Toxin 38	UniProt
A0A088DAE8	<i>Mesobuthus eupeus</i>	Buthidae	Toxin 38	UniProt
A0A088DB26	<i>Mesobuthus eupeus</i>	Buthidae	Toxin 38	UniProt
A0A088DB53	<i>Mesobuthus eupeus</i>	Buthidae	Toxin 38	UniProt
E4VNZ9	<i>Mesobuthus eupeus</i>	Buthidae	Toxin 38	UniProt
E4VP14	<i>Mesobuthus eupeus</i>	Buthidae	Toxin 38	UniProt
E4VP34	<i>Mesobuthus eupeus</i>	Buthidae	Toxin 38	UniProt
Code	Species	Family	Pfam	Reference
E4VP56	<i>Mesobuthus eupeus</i>	Buthidae	Toxin 38	UniProt
E4VP57	<i>Mesobuthus eupeus</i>	Buthidae	Toxin 38	UniProt
A0A059UI30	<i>Mesobuthus gibbosus</i>	Buthidae	Toxin 38	UniProt
Q9N661	<i>Mesobuthus martensii</i>	Buthidae	Toxin 38	UniProt
Q9NJC6	<i>Mesobuthus martensii</i>	Buthidae	Toxin 38	UniProt
A0A0C9RFQ9	<i>Tityus bahiensis</i>	Buthidae	Toxin 38	UniProt
A0A0C9S3A8	<i>Tityus bahiensis</i>	Buthidae	Toxin 38	UniProt
Q0GY42	<i>Tityus costatus</i>	Buthidae	Toxin 38	UniProt
Q5G8A6	<i>Tityus costatus</i>	Buthidae	Toxin 38	UniProt
Q0GY43	<i>Tityus discrepans</i>	Buthidae	Toxin 38	UniProt
Q0GY44	<i>Tityus discrepans</i>	Buthidae	Toxin 38	UniProt
P69940	<i>Tityus serrulatus</i>	Buthidae	Toxin 38	UniProt
P86822	<i>Tityus serrulatus</i>	Buthidae	Toxin 38	UniProt
P0C2F3	<i>Tityus stigmurus</i>	Buthidae	Toxin 38	UniProt
P0C8W4	<i>Tityus stigmurus</i>	Buthidae	Toxin 38	UniProt
K9LZ65	<i>Tityus stigmurus</i>	Buthidae	Toxin 38	UniProt
Q0GY45	<i>Tityus trivittatus</i>	Buthidae	Toxin 38	UniProt
Q0GY46	<i>Tityus trivittatus</i>	Buthidae	Toxin 38	UniProt
T1DMR0	<i>Cercophonium squama</i>	Botrhiuridae	Toxin 38	UniProt
T1DP99	<i>Cercophonium squama</i>	Botrhiuridae	Toxin 38	UniProt

T1E6W8	<i>Cercophonius squama</i>	Bothriuridae	Toxin 38	UniProt
P0C8W5	<i>Hoffmannihadrurus gertschi</i>	Caraboctonidae	Toxin 38	UniProt
Q0GY40	<i>Hoffmannihadrurus gertschi</i>	Caraboctonidae	Toxin 38	UniProt
Q0GY41	<i>Hoffmannihadrurus gertschi</i>	Caraboctonidae	Toxin 38	UniProt
Ctri27	<i>Chaerilus tricoatus</i>	Chaerilidae	Toxin 38	1
Ctri13	<i>Chaerilus tricoatus</i>	Chaerilidae	Toxin 38	1
Ctri9164	<i>Chaerilus tricoatus</i>	Chaerilidae	Toxin 38	1
Ctry44	<i>Chaerilus tryznai</i>	Chaerilidae	Toxin 38	1
Ctry51	<i>Chaerilus tryznai</i>	Chaerilidae	Toxin 38	1
Ctry22350	<i>Chaerilus tryznai</i>	Chaerilidae	Toxin 38	1
C7G3K3	<i>Liocheles australasiae</i>	Hormuridae	Toxin 38	UniProt
C5J891	<i>Opisthacanthus cayaporum</i>	Hormuridae	Toxin 38	UniProt
P0C2F4	<i>Heterometrus laoticus</i>	Scorpionidae	Toxin 38	UniProt
Q5WQZ7	<i>Opisthophthalmus carinatus</i>	Scorpionidae	Toxin 38	UniProt
Q5WQZ9	<i>Opisthophthalmus carinatus</i>	Scorpionidae	Toxin 38	UniProt
Q5WR01	<i>Opisthophthalmus carinatus</i>	Scorpionidae	Toxin 38	UniProt
Q5WR03	<i>Opisthophthalmus carinatus</i>	Scorpionidae	Toxin 38	UniProt
H2CYP8	<i>Pandinoides cavimanus</i>	Scorpionidae	Toxin 38	UniProt
H2CYQ1	<i>Pandinoides cavimanus</i>	Scorpionidae	Toxin 38	UniProt
P56972	<i>Pandinus imperator</i>	Scorpionidae	Toxin 38	UniProt
P0DL47	<i>Euscorplops validus</i>	Scorpiopidae	Toxin 38	UniProt
sdc34997_g1_i1	<i>Superstitionia donensis</i>	Superstitioniidae	Toxin 38	This study
Code	Species	Family	Pfam	Reference
sdc1422_g4_i1	<i>Superstitionia donensis</i>	Superstitioniidae	Toxin 38	This study
sdc1422_g4_i2	<i>Superstitionia donensis</i>	Superstitioniidae	Toxin 38	This study
sdc20456_g1_i1	<i>Superstitionia donensis</i>	Superstitioniidae	Toxin 38	This study
sdc4553_g1_i1	<i>Superstitionia donensis</i>	Superstitioniidae	Toxin 38	This study
sdc23468_g1_i1	<i>Superstitionia donensis</i>	Superstitioniidae	Toxin 38	This study
T1DEJ8	<i>Urodacus manicatus</i>	Urodacidae	Toxin 38	UniProt
T1DMR6	<i>Urodacus manicatus</i>	Urodacidae	Toxin 38	UniProt
T1E6X2	<i>Urodacus manicatus</i>	Urodacidae	Toxin 38	UniProt
L0G8Z0	<i>Urodacus yaschenkoi</i>	Urodacidae	Toxin 38	UniProt
L0GCW2	<i>Urodacus yaschenkoi</i>	Urodacidae	Toxin 38	UniProt
VpScp1p1	<i>Mesomexovis punctatus</i>	Vaejovidae	Toxin 38	3
VsScp1p1	<i>Mesomexovis subcristatus</i>	Vaejovidae	Toxin 38	3
VsScp1p2	<i>Mesomexovis subcristatus</i>	Vaejovidae	Toxin 38	3
ViScp1p1	<i>Thorellius intrepidus</i>	Vaejovidae	Toxin 38	3
ViScp1p2	<i>Thorellius intrepidus</i>	Vaejovidae	Toxin 38	3
ViScp1p3	<i>Thorellius intrepidus</i>	Vaejovidae	Toxin 38	3
VmScp1p1	<i>Vaejovis mexicanus</i>	Vaejovidae	Toxin 38	3
VmScp1p2	<i>Vaejovis mexicanus</i>	Vaejovidae	Toxin 38	3
VmScp1p3	<i>Vaejovis mexicanus</i>	Vaejovidae	Toxin 38	3

Table S5. Thirty six sequences of La1-like and putative La1-like peptides isolated from the venom or deduced from cDNA or transcriptome analysis of 23 scorpion species in 18 genera and 9 families. Code = UniProt accession numbers, except for those with the names given in the original publications (listed in the references).

Code	Species name	Family	Reference
T1DMQ9	<i>Cercophonius squama</i>	Botrhiuridae	UniProt
T1DP97	<i>Cercophonius squama</i>	Botrhiuridae	UniProt
D2CF17	<i>Mesobuthus martensii</i>	Buthidae	UniProt
A0A0K0LCC5	<i>Androctonus bicolor</i>	Buthidae	UniProt
E4VP44	<i>Mesobuthus eupeus</i>	Buthidae	UniProt
F1CJ59	<i>Hottentotta judaicus</i>	Buthidae	UniProt
F1CJA0	<i>Hottentotta judaicus</i>	Buthidae	UniProt
FE193686	<i>Lychas mucronatus</i>	Buthidae	UniProt
FD660409	<i>Isometrus maculatus</i>	Buthidae	UniProt
Ctry	<i>Chaerilus tryznai</i>	Chaerilidae	1
Ctri	<i>Chaerilus triscostatus</i>	Chaerilidae	1
C5J895	<i>Opisthacanthus cayaporum</i>	Hormuridae	UniProt
P0C5F3	<i>Liocheles australasiae</i>	Hormuridae	UniProt
C5J8B8	<i>Opisthacanthus cayaporum</i>	Hormuridae	UniProt
H2CYP1	<i>Pandinoides cavimanus</i>	Scorpionidae	UniProt
K7WMX6	<i>Heterometrus spinifer</i>	Scorpionidae	UniProt
JN315721	<i>Pandinoides cavimanus</i>	Scorpionidae	UniProt
KC140563	<i>Heterometrus spinifer</i>	Scorpionidae	UniProt
Smp73	<i>Scorpio palmatus</i>	Scorpionidae	2
FD664111	<i>Heterometrus petersii</i>	Scorpionidae	UniProt
FD664431	<i>Scorpiops margerisonae</i>	Scorpiopidae	UniProt
GH548227	<i>Scorpiops jedenki</i>	Scorpiopidae	UniProt
GH547861	<i>Scorpiops jedenki</i>	Scorpiopidae	UniProt
GH547772	<i>Scorpiops jedenki</i>	Scorpiopidae	UniProt
GH547797	<i>Scorpiops jedenki</i>	Scorpiopidae	UniProt
sdc5116	<i>Superstitionia donensis</i>	Superstitioniidae	This study
sdc7328	<i>Superstitionia donensis</i>	Superstitioniidae	This study
sdc12897	<i>Superstitionia donensis</i>	Superstitioniidae	This study
sdc14036	<i>Superstitionia donensis</i>	Superstitioniidae	This study
L0GB04	<i>Urodacus yaschenkoi</i>	Urodacidae	UniProt
L0GCJ1	<i>Urodacus yaschenkoi</i>	Urodacidae	UniProt
L0GCW8	<i>Urodacus yaschenkoi</i>	Urodacidae	UniProt
ViLa1lp1	<i>Thorellius intrepidus</i>	Vaejovidae	3
VmLa1lp1	<i>Vaejovis mexicanus</i>	Vaejovidae	3
VpLa1lp1	<i>Mesomexovis punctatus</i>	Vaejovidae	3
VsLa1lp1	<i>Mesomexovis subcristatus</i>	Vaejovidae	3

Table S6. Twenty sequences of Potassium channel κ toxins from 8 scorpion species in 4 genera and 3 families, plus 12 sequences of Potassium channel α toxins and Chlorotoxins from nine scorpion species as outgroups; isolated from the venom or deduced from cDNA or transcriptome analysis of a total of 17 scorpion species. Code = UniProt accession numbers, except for those with the names given in the original publications (listed in the references). Type = Name of the corresponding type of toxin.

Code	Species	Family	Type	Reference
P86436	<i>Androctonus australis</i>	Buthidae	Chlorotoxin	UniProt
P59887	<i>Hottentotta indicus</i>	Buthidae	Chlorotoxin	UniProt
P83400	<i>Hottentotta tamulus</i>	Buthidae	Chlorotoxin	UniProt
P45639	<i>Leiurus quinquestriatus</i>	Buthidae	Chlorotoxin	UniProt
P0CI86	<i>Lychas mucronatus</i>	Buthidae	unknown	UniProt
A9QLM3	<i>Lychas mucronatus</i>	Buthidae	Unknown	UniProt
Q6WGI9	<i>Parabuthus granulatus</i>	Buthidae	Scorpion acidic α KTx toxin	UniProt
P86271	<i>Tityus serrulatus</i>	Buthidae	Unknown	UniProt
P0C183	<i>Tityus trivittatus</i>	Buthidae	unknown	UniProt
B3A0L5	<i>Tityus trivittatus</i>	Buthidae	κ KTx	UniProt
P86110	<i>Opisthacanthus cayaporum</i>	Hormuridae	κ KTx	UniProt
C5J893	<i>Opisthacanthus cayaporum</i>	Hormuridae	κ KTx	UniProt
P0C1Z3	<i>Opisthacanthus madagascariensis</i>	Hormuridae	κ KTx	UniProt
P0C1Z4	<i>Opisthacanthus madagascariensis</i>	Hormuridae	κ KTx	UniProt
P82851	<i>Heterometrus fulvipes</i>	Scorpionidae	κ KTx	UniProt
P82850	<i>Heterometrus fulvipes</i>	Scorpionidae	κ KTx	UniProt
P0DJ41	<i>Heterometrus laoticus</i>	Scorpionidae	κ KTx	UniProt
P0DJ36	<i>Heterometrus petersii</i>	Scorpionidae	κ KTx	UniProt
P0DJ38	<i>Heterometrus petersii</i>	Scorpionidae	κ KTx	UniProt
P0DJ35	<i>Heterometrus petersii</i>	Scorpionidae	κ KTx	UniProt
P0DJ39	<i>Heterometrus petersii</i>	Scorpionidae	κ KTx	UniProt
P0DJ34	<i>Heterometrus petersii</i>	Scorpionidae	κ KTx	UniProt
P0DJ37	<i>Heterometrus petersii</i>	Scorpionidae	κ KTx	UniProt
P0DJ40	<i>Heterometrus petersii</i>	Scorpionidae	κ KTx	UniProt
P0DJ33	<i>Heterometrus petersii</i>	Scorpionidae	κ KTx	UniProt
P0DJ33	<i>Heterometrus petersii</i>	Scorpionidae	κ KTx	UniProt
P83655	<i>Heterometrus spinifer</i>	Scorpionidae	κ KTx	UniProt
P0DL35	<i>Scorpiops jendeki</i>	Scorpiopidae	unknown	UniProt
sdc14251_g2_i1	<i>Superstitionia donensis</i>	Superstitioniidae	κ KTx	This study
sdc13949_g1_i1	<i>Superstitionia donensis</i>	Superstitioniidae	α KTx	This study
sdc26193_g1_i1	<i>Superstitionia donensis</i>	Superstitioniidae	Alpha	This study
VmKTx2	<i>Vaejovis mexicanus</i>	Vaejovidae	κ KTx	3

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