**Supplementary Fig S1.a.** Alignment of tryptic and semi-tryptic peptide sequences derived from in-gel digestion of SDS-PAGE bands of *Naja naja* crude venom with snake venom protein families reported in the Elapidae database. The protein alignment was done using Clustal Omega programme (<https://www.ebi.ac.uk/Tools/msa/clustalo/>). The distinct peptides obtained for each of the following proteins has been highlighted in green or blue (two colours have been used in case of adjacent distinct/unique peptides). The amino acid substitutions within the unique/distinct peptides obtained from MS/MS are highlighted in red colour.

Phospholipase A2

P25498.1 ---------------------------NLYQFKNMIKCTVPS-RSWLDFANYGCYCGRGGSGTPVDDLDRCCQIHDNCYNEAGKISGCWPYFKTYSYECSQGTLTCKGDNNSCAASVCDC

AAR08048.1 --------------------SNRPMPLNLYQFKNMIQCTVPS-RSWQDFADYGCYCGKGGSGTPVDDLDRCCQVHDNCYNEAENISGCRPYFKTYSYECTQGTLTCKGDNNACAASVCDC

PSNJ2K ---------------------------NLYQFKNMIQCTVPN-RSWWDFADYGCYCGRGGSGTPVDDLDRCCQVHDNCYDEAEKISRCWPYFKTYSYECSQGTLTCKNGNNACAAAVCDC

AAA66027.1 MNPAHLLILAAVCVSPLGASSNRPMPLNLYQFKNMIQCTVPN-RSWWHFADYGCYCGRGGSGTPVDDLDRCCQIHDNCYNEAEKISRCWPYFKTYSYECSQGTLTCKGGNNACAAAVCDC

BAA36403.1 MNPAHLLILAAVCVSPLGAFSNRPMPLNLYQFKNMIQCTVPN-RSWWDFADYGCYCGRGGSGTPVDDLDRCCQVHDNCYNEAEKISRCWPYFKTYSYECSQGTLTCKGDNDACAAAVCDC

AED89576.1 MNPAHLLVLAAVCISLLGASSIAPQPLNLYQFGNMINCTMPGGSPLLDYADYGCYCGSGGGGTPVDDLDRCCQAHDNCYGEAETVHKCNPFWTFYSYECSEGQLTCRDNDTNCKEFVCNC

JAS04993.1 MNPAHLLFLASVCVSLLGASSIPPEPLNLYQFKNMIKCTNT--RHWLSFTNYGCYCGYGGSGTPVDELDRCCQVHDKCYDTAKRVHKCFPSVRTYSYDCSEGKLTCKDNNTKCKDFVCNC

P25498.1 DRLAAICFAGAPYNNDNYNINLKARCQ

AAR08048.1 DRLAAICFAGAPYNDANYNIDLKARCN

PSNJ2K DRLAAICFAGAPYNNNNYNIDLKARCQ

AAA66027.1 DRLAAICFAGAPYNDNNYNIDLKARCQ

BAA36403.1 DRLAAICFAGAPYNNNNYNIDLKARCQ

AED89576.1 DLEAANCFAKAPYIEENYNINLNR-CT

JAS04993.1 DRTAALCFAKAPYNDKNYNIDLKR-CQ

Snake Venom Metalloprotease

AAM51550.1 MIQALLVAICLAVFPYQGSSIILESGNVNDYEVVYPQKVPALSKGGVQNPQPETKYEDTMQYEFHVNGEPVVLHLERNKGLFSEDYTETHYAPDGREITTSSPVQDHCYYHGYIQNEADS

ACN50006.1 MIQALLVIICLAVFPHQGSSIILESGNVNDYEVVYPQKVPALLKGGVQNPQPETKYEDTMRYEFQVNGEPVVLHLERNKGLFSEDYTETHYAPDGREITTSPPVQDHCYYHGYIQNEADS

AAF00693.1 ------------MIQLSWSSIILESGNVNDYEVVYPQKVPALLKGGVQNPQPETKYEDTMQYEFQVNGEPVVLHLERNKGLFSEDYTETHYAPDGREITTSPPVQDHCYYHGYFQNEADS

JAS05092.1 MIQALLVTICLAVFPYQGSSIILESGNVNDYEVVYPQKVPALPKGRIQNPQPETKYEDTMQYEFQVNGEPVVLHLERNKGLFSEDYTETHYSSDDTEITTSPPVQDHCYYHGYIQNDADS

F8RKW1.1 MIEVLLVTICFTVFPYQGSSIILESGNVNDYEVVYPQKVPALPKGGVQNPQPETKYEDTMQYEFHVNGEPVVLHLERNKGLFSEDYTETHYAPDGREITTSPPVQDHCYYHGYIQNEADS

ADF43026.1 MIQALLVIICLAVFPHQGSSIILESGNVNDYEVVYPQKVPALLKGGVQNPQPETKYEDTMRYEFQVNGEPVVLHLERNKGLFSEDYTETHYAPDGREITTSPPVQDHCYYHGYIQNEADS

ADG02948.1 MIQALLVIICLAVFPHQGSSIILESGNVNDYEVVYPQKVPALLKGGVQNPQPETKYEDTMRYEFQVNGEPVVLHLERNKGLFSEDYTETHYAPDGREITTSPPVQDHCYYHGYIQNEADS

P82942.1 ------------------------------------------------------------------------------------------------------------------------

AAM51550.1 SAVISACDGLKGHFKHQGETYFIEPLELSDSEAHAIYKDENVEEEEEIPKICGVTQTTWESDEPIEKSSQLTNTPEQDRYLQAKKYIEFYVVVDNVMYRKYTGKLHVITRRVYEMVNALN

ACN50006.1 SAVISACDGLKGHFEHQGETYFIEPLKISNSEAHAIYKDENVENEDETPEICGVTETTWESDESIEKTSQLTNTPEQDRYLQAKKYIEFYVVVDNIMYRHYKRDQPVIKRKVYEMINTMN

AAF00693.1 SAVISACDGLKGHFKLQGEIYFIEPLKISDSEAHAIYKDENVEEEDETPKICGVTDTTWESDEPIKKTSLLTNTPEQDRYLQAEKYIEFYMVVDNIMYRHYKRNQLVIKRKVYEMINTMN

JAS05092.1 SAVISACDGLKGHFKHQGETYFIEPLKLSESGSHAIYKDENVEKEDETLKICVVTQTTWESDESIEKISQLTNTPEQDRYLQVKKYIEFYVVVDNRMYRHYKCKKRAIKRRVYEMVNLLN

F8RKW1.1 SAAISACDGLKGHFKHRGETYFIEPLKLSNSESHAIYKDEHVEKEDEIPKICGVTQTTSESDEPIEKISQLTNTPEQDRYLQVKKYIELYVVVDNRMYRNYNSNRDAINERVYEMVNTLN

ADF43026.1 SAVISACNGLKGHFKHQGETYFIEPLELSESEAHAIYKDENVEKEDETPKICAVTQTTWESDESIEKTSQLTNTPEQDRYLQVKKYIEFYLVVDNKMYKNHTS-NQELRTRVYEMVNYLN

ADG02948.1 SAVISACDGLKGHFEHQGETYFIEPLKISNSEAHAIYKDENVENEDETPEICGVTETTWESDESIEKTSQLTNTPEQDRYLQDKKYIEFYVIVDNRMYRYYNNDKPAIKIRVYEMINAVN

P82942.1 -----------------------------------------------------------------------TNTPEQDRYLQAEKYIEFYVIVDNRMYRYYNYDKPAIKIRVYEMINAVN

AAM51550.1 TMYRRLNFHIALIGLEIWSNGNEINVQSDVQATLDLFGEWRENKLLPRKRNDNAQLLTSTEFNGTTTGLGYIGSLCSPKKSVAVVQDHSKSTSMVAITMAHQMGHNLGMNDDRASCTCGS

ACN50006.1 MIYRRLNFHIALIGLEIWSNINEINVQSDVRATLNLFGEWREKKLLPRKRNDNAQLLTGIDFNGTPVGLAYIGSICNPKTSAAVVQDYSSRTRMVAITMAHEMGHNLGMNHDRGFCTCGF

AAF00693.1 MIYRRLNFHIALIGLEIWSNINEINVQSDVKATLDLFGEWREKKLLPRKRNDNAQLLTGIDFNGTPVGLAYIGSICNPKTSAAVVQDYSKSTRMVAITMAHEMGHNLGMNHDKGFCTCGF

JAS05092.1 TIYRPLNFYIALIGLEIWSHRDKINIETDAGITLNSFGEWRENVLLPRKRNDNAQLLTRIQFNGTVIGLGYVGTICSLQKSVAVIQDYSRKSNLVASAMAHEMGHNLGINHDRASCSCTA

F8RKW1.1 VMYRPLNFFIALIGLEIWSNQDEINIEPEVAVTLRSFGEWRNTTLLPRKRNDNAQLLTGIDFNGATVGLAYVGTLCSPTQSVAVIQDHSKRTSMVASTMAHELGHNLGINHDSASCNCNA

ADF43026.1 TKYRRLNFHIALIGLEIWSNQDKVDMDPGANVTLKSFAEWRAK-LPPHKRNDNAQLLTGIDFNGTTVGLAYTGTLCTW-GSVAVVQDYSRRTILMASTMAHELGHNMGIHHDKANCRCSH

ADG02948.1 TKFRPLKIHIALIGLEIWSNKDKFEVKPAASVTLKSFGEWRETVLLPRKRNDNAQLLTGIDFNGNTVGRAYIGSLCKTNESVAIVQDYNRRISLVASTMTHELGHNLGIHHDKASCICIP

P82942.1 TKFRPLKIHIALIGLEIWSNEDKFEVKPAASVTLKSFREWRQTVLLPRKRNDNAQLLTGINLNGTAVGIAYPGSLCTQ-RSVFVVQDYNRRMSLVASTMTHELGHNLGIHHDEASCICIP

AAM51550.1 NKCIMSTK-YYESLSEFSSCSVQEHREYLLRDRPQCILNKPSRKAIVTPPVCGNYFVERGEECDCGSPEDCQNTCCDAATCKLQHEAQCDSGECCEKCKFKGAGAECRAAKNDCDFPELC

ACN50006.1 NKCVMSTR-RTKPAYQFSSCSVREHQRYLLRDRPQCILNKPLSTDIVSPPICGNYFVEVGEECDCGSPADCQSACCNATTCKLQHEAQCDSEECCEKCKFKGARAECRAAKDDCDLPELC

AAF00693.1 NKCVMSTR-RTKPAYQFSSCSVREHQRYLLRDRPQCILNKPLSTDIVSPPICGNYFVEVGEECDCGSPADCQSACCNATTCKLQHEAQCDSEECCEKCKFKGAGAECRAAKDDCDLPELC

JAS05092.1 GPCIMFPTISFKPFYEFSSCSVQEHQRYLLRDRPQCILNKPLSTDIITPSVCGNHLVDVGEECDCGSPQDCQSACCNATTCKLQHEAQCDSEECCEKCKFKK-GAECRAAKDDCDLPEFC

F8RKW1.1 GPCIMSATISNQPFSKFSSCSVQEHQRYLLRVRPQCILNKPLSTDIVTPPVCGNYFVERGEECDCGSPQDCQSACCNATTCKPQHEAQCDSGECCEKCKFKKAGAECRAAKDDCDLPESC

ADF43026.1 SPCIMSDTISDEPFYEFSSCSVREHQEYLLRERPQCILNKPSRKAIVSRPVCGNNFVEVGEQCDCGSLQDCQSTCCNATTCKLQPHAQCDSEECCEKCKFKGAETECRAAKDDCDLPEFC

ADG02948.1 GPCIMLKKR-TAPAFQFSSCSIREYREYLLRDRPQCILNKPLSTDIVSPPICGNYFVEVGEECDCGSPQACQSACCNAAT-----------------CQFKGAETECRVAKDDCDLPELC

P82942.1 GPCIMLKKR-TAPAFQFSSCSIRDYQEYLLRDRPQCILNKPLSTDIVSPAICGNYFVEEGEECDCGSPAACQSACCDAAT-----------------CKFNGAGAECRAAKHDCDLPELC

AAM51550.1 TGRSAKCPKDSFQRNGHPCQNNQGYCYNGTCPTLTNQCATLWGPGAKMSPGLCFMLNWNARSCGLCRKENGRKILCAAKDVKCGRLFCKKKNSMICHCPPPSKDPNYGMVAPGTKCGVKK

ACN50006.1 TGQSAECPTDVFQRNGLPCQNNQGYCYNGKCPIMTNQCIALRGPGVKVSRDSCFTLNQRTRGCGLCRMEYGRKIPCAAKDVKCGRLFCKRRNSMICNCSISPRDPNYGMVEPGTKCGDGM

AAF00693.1 TGQSAECPTDVFQRNGLPCQN-NGYCYNGKCPIMTNQCIALRGPGVKVSRDSCFTLNQRTRGCGLCRMEYGRKIPCAAKDVKCGRLFCKKRNSMICNCSISPRDPSYGMVEPGTKCGDGM

JAS05092.1 TGRSAECPTDSFQRNGHPCQNNQGYCYNGKCPIMKNQCIALMGSGVKVSRDMCFTLNQRGKGCGFCRKENGANIPCAAKDVKCGRLFCKKGNSMTCRCSVSPRDPDYGMVEPGTKCGDGM

F8RKW1.1 TGQSAKCPTDSFQRNGHPCQNNEGYCYNGKCPIMTNQCIALGGPGVNVSPDECFTLKQNVPECGFCRIENGRKIPCAEKDKMCGKLLCEKGNA-TCICFPTTHDPDYGMVEPGTKCGDGK

ADF43026.1 TGQSAECPTDSLQRNGHPCQNNQGYCYNGKCPTMENQCITLLGPNYTVGPAGCFKNNRKGDDVSHCRKENGAKIPCAAKDEKCGTLYCTEIKKTGCIVPVSPRDPDSRMVEPGTKCEDKK

ADG02948.1 TGQSAECPTDSLQRNGHPCQNNQGYCYNRTCPTLTNQCITLLGPHFTVSPKGCFDLNMRGDDGSFCGMEDGTKIPCAAKDVKCGRLYCTEKNTMSCLIPP---NPDGIMAEPGTKCGDGM

P82942.1 TGQSAECPTDSLQRNGHPCQNNQGYCYNGKCPTLTNQCIALLGPHFTVSPKGCFDLNMRGDDGSFCRMEDGTKIPCAAKDVKCGRLYCTEKNTMSCLIPP---NPDGIMAEPGTKCGDGM

AAM51550.1 VCRNRQCVKV----

ACN50006.1 VCSNRQCVDVKTAY

AAF00693.1 VCSNRQCVDVKTAY

JAS05092.1 VCSNRQCVKVQTAY

F8RKW1.1 VCINRQCVDVQTAY

ADF43026.1 VCSKSQCVKV----

ADG02948.1 VCSKGQCVDVQTAY

P82942.1 VCSKGQCVDVQTAY

5’-Nuclueotidase

JAS05036.1 MPTSRRRSGAHGCPRSAPSAMWRLVGAVCFCAALSVAAAGSFKLTILHTNDVHARVEQTSRDSGKCTREDCYGGVARRATKIREIRASHRNVLLLDAGDQYQGTVWFNYFKGREVVHFMN

JAS05036.1 SLRYDAMALGNHEFDNGLNGLLDPLLKNVKFPILSANIRPKGPIASNISGYILPYKIINVGSEKVGIIGYTTKETPVLSNPGPYLEFRDEVEELQKQADKLTTLGVNKIIALGHSGFKED

JAS05036.1 CRIAQKVKGVDVVVGGHTNTFLYTGSPPSNEVPAGNYPFMQLSDDGRQVPVVQAYAFGKYLGYLNVIFDDKGKVIKASGNPILLNKSIQEDPAVKAEVSRMKVQLQKYSKQEIGKTIVYL

JAS05036.1 NGTTHACRFHECNLGNLICDAVVYNNLRHPDDNEWNHVSMCIVNGGGIRSPIDEKANNGIITLEELTAVLPFGGTFDLLQIKGSALRQAFEHSVHRHGQGTGELLQVSGIKVLYDLSQKP

JAS05036.1 GKRVVSLNVLCTECRVPAYVPLQMEKTYKVLLPSFLAAGGDGYYMLKGDSSNHSSGDLDISIVSDYIKRMGKVFPAMEGRVMFSAGTLFQAHHS

Phosphodiesterase

JAI09046.1 MQVLFISLVAVALGLGLGLGLKQSKQPQESCRNRCNETFRGELSYCSCDNKCTEREACCWDYQDICVLPTQSWSCNKLRCGERRMANVLCSCSEDCLTKKDCCTDYKSICKRETSWLKDQCASSSAAQCPEGFDQSPLIL

JAI09046.1 FSMDGFRAEYLETWDTLMPNINKLKTCGTHAKYMRAVYPTKTFVNHYTIVTGLYAETHGIIDNNIYDVNLNQNFSLSGRNMRNPAWWGGQPIWNTATYQGLKAATYFWPGSEVKINGSYPAIYKAYNKSTPFEARVMEVL

JAI09046.1 QWLDLPRAKRPDFSTLYIEEPDTTGHKYGPVSGQVIKSLQMADRTLGMLMEGLKQRNLHNCVNLILLADHGMEAISCNRLEYMADYFNTVDFFMYEGAAPRIRSKNVPKDFYTFDSEAIVKNLTCRKPKQHFKAYLAKDL

JAI09046.1 PKRLHFANNVRIDKVNLMVDRQWLAVRNKKYKYCSGGTHGYDNEFKSMEAIFLAHGPDFKEKNEVTSFENIEVYNLMCDLLKLKPAPNNGTHGSLNHLLKNPFYNPSPAKEQSSPLLCDFGPVPSPDLSGCKCSSITDLE

JAI09046.1 AVNQRLNLNDQAKTQCEADNLPYGRPHVLQHSKYCLLHQTKYISAYSQDILMPLWNSYTISKSLVKPTSVPPSASDCLRLDVRIPTAQSQTCSNYQPDLTITPGFLYPPDFSSSGPEQYDALITSNIVPMYKEFTRLWNY

JAI09046.1 FHSTLLPKYATERNGLNVISGPIFDYNYDGHFDSYDTIKQYVNNTKIPIPTHYFVVLTSCENSTNTPLNCPPGSLKVLSFILPHRPDNSESCADKSPNNLWVEERMQTHTARVRDVELLTGLDFYSVLKQPLSETLRLKT

JAI09046.1 FLPIFVNSVN

L-Amino acid oxidase

ABN72546.1 MNVLFIFSLLFLAALESCADDRRSPLEECFQQNDYEEILEIARNGLKKTSNPKHVVVVGAGMAGLSAAYVLAGAGHKVTLLEASERVGGRVITYHNDREGWYVNMGPMRLPERHRIVREY

ABN72546.1 IRKFGLKLNEFFQENENAWYYINNIRKRVWEVKKDPSLLKYPVKPSEEGKSASQLYQEPLRKVIEELKRTNCSYILNKYDSYSTKEYLIKEGNLSRGAVDMIGDLLNEDSSYHLSFMESL

ABN72546.1 KSDALFSYEKRFDEIVGGFDQLPISMYQAIAEMVHLNARVIKIQYDAEKVRVTYQTPAKTFVTADYVIVCSTSRAARRIYFEPPLPPKKAHALRSIHYRSATKIFLTCSKKFWEADGI

ABN72546.1 HGGKSTTDLPSRFIHYPNHNFTSGIGVIMAYVLADDSDFFQALDTKTCADIVINDLSLIHDLPKREIQALCYPSIKKWNLDKYTMGSITSF

Three Finger Toxins

AAD40974.1 MKTLLLTLVVVTIVCLDLGYTRTCFITPDVK---SKPCPPGQEVCYTKTWCDGFCGIRGKRVDLGCAATCPTPKKTGIDIICCSTDDCNTFPLRPRGRLSSIKDHP

P34074.2 ---------------------IRCFITPRVS---SQACPDG-HVCYTKTWCDNFCGINGKRVDLGCAATCPTV-KPGVDIKCCSTDNCNPFPTRKRP---------

P25668.1 ---------------------IRCFITPDIT---SKDCPNG-HVCYTKTWCDGFCSIRGKRVDLGCAATCPTV-RTGVDIQCCSTDDCDPFPTRKRP---------

AAD08812.1 MKTLLLTLLVVTIVCLDLGYTLECHNQQSSETPTTTGCSGGETNCYKKSW-RD---HRGYRIERGC--GCPSV-KKGIEINCCTTDRCNN----------------

AAD08814.1 MKTLLLTLLVVTIVCLDLGYTLECHNQQSSQAPTTTGCSGGETNCYKKGW-RD---HRGYRIERGC--GCPSV-KKGIEINCCTTDRCNN----------------

AAF21774.1 METLLLTLLVVTIVCLDLGYTLECHNQQSSQTPTTTGCSGGETNCYKKRW-RD---HRGYRTERGC--GCPSV-KNGIEINCCTTDRCNN----------------

P82935.2 MKTLLLTLVVVTIVCLDLGYTLTCLNCPEMFCGKFQICRNGEKICFKKLHQRR---PLSWRYIRGCADTCPVG-KPYEMIECCSTDKCNR----------------

P29181.1 ---------------------LTCLNCPEVYCRRFQICRDGEKICFKKFDQRN---LLGKRYRRGCAATCPEA-KPREIVQCCSTDKCNR----------------

P14541.1 ------------LKCHNTQLPFIYKTCPEGKNLCFKATLKKFPLKIPIKRGCADNCPKNSALLKYVCCSTDKCN

P01464.1 ------------LKCH-KLVPPFWKTCPEGKNLCYKMYMVA-TPMIPVKRGCIDVCPKNSALVKYMCCNTNKCN

BAU24666.1 VVTIVCLDLGYTLQCN-KLVPIASKTCPPGKNLCYKMFMVS-DLTIPVKRGCIDVCPKNSLLVKYVCCNTDRCN

P01446.1 ------------LKCN-KLIPLAYKTCPAGKNLCYKMFMVS-NKTVPVKRGCIDACPKNSLLVKYVCCNTDRCN

BAU24665.1 VVTIVCLDLGYTLKCN-KLVPLFYKTCPAGKNLCYKMYMVA-TPKVPVKRGCIDVCPKSSLLVKYVCCNTDRCN

P82464.1 TICYNHLTRTSETTEICPDSWYFCYKIS-LADGNDVRIKRGCTFTCPELRPTGIYVYCCRRDKCNQ

P82463.1 LTCVKEKSIFGVTTEDCPDGQNLCFKRWHMIVPGRYKKTRGCAATCPIAENRD-VIECCSTDKCNL

P82462.1 LICVKEKFLFSETTETCPDGQNVCFNQAHLIYPGKYKRTRGCAATCPKLQNRD-VIFCCSTDKCNL

CAA90964.1 MKTLLLTMVVVTIVCLDLGYTLKCHNTQLPFIYKTCPEGKNLCFKATLKKFPLKFPVKRGCADNCPKNSALLKYVCCSTDKCN

AAB18383.1 MKTLLLTLVVVTIVCLDLGYTLKCNK-LVPLFYKTCPAGKNLCYKMFMVAT-PKVPVKRGCIDVCPKNSLLVKYVCCNTDRCN

P59275.1 LECHNQQSSQTPTTKTCS-GETNCYKKWWSDHRG----TIIERGC--GCPKVKPGVNLNCCRRDRCNN-------

P59276.1 LECHNQQSSQAPTTKTCS-GETNCYKKWWSDHRG----TIIERGC--GCPKVKPGVNLNCCRTDRCNN-------

2CTX IRCFITPD---ITSKDCPNGHV-CYTKTWCDAFCSIRGKRVDLGCAATCPTVKTGVDIQCCSTDNCNPFPTRKRP

P85092.1 LTCVTSKSIFGITTEDCPDGQNLCFKRRH---YVVPKIYDSTRGCAATCPIPENYDSIHCCKTDKCNE-------

P01400.1 LTCLICPEKYCNKVHTCRNGENICFKRFY---EGNLLGKRYPRGCAATCPEAKPREIVECCSTDKCNH-------

Cobra Venom Factor

AAA68989.1 MERMALYLVAALLIGFPGSSHGALYTLITPAVLRTDTEEQILVEAHGDSTPKQLDIFVHDFPRKQKTLFQTRVDMNPAGGMLVTPTIEIPAKEVSTDSRQNQYVVVQVTGPQVRLEKVVL

AAA68989.1 LSYQSSFLFIQTDKGIYTPGSPVLYRVFSMDHNTSKMNKTVIVEFQTPEGILVSSNSVDL--NFFWPYNLPDLVSLGTWRIVAKYEHSPE-NYTAYFDVRKYVLPSFEVRLQPSEKFFYI

AAA68989.1 DGNENFHVSITARYLYGEEVEGVAFVLFGVKIDDAKKSIPDSLTRIPIIDGDGKATLKRDTFRSRFPNLNELVGHTLYASVTVMTESGSDMVVTEQSGIHIVASPYQIHFTKTPKYFKPG

AAA68989.1 MPYELTVYVTNPDGSPAAHVPVVSEAFHSMGTTLSDGTAKLILNIPLNAQSLPITVRTNHGDLPRERQATKSMTAIAYQTQGGSGNYLHVAITSTEIKPGDNLPVNFNVKGNANSLKQIK

AAA68989.1 YFTYLILNKGKIFKVGRQPRRDGQNLVTMNLHITPDLIPSFRFVAYYQVGNNEIVADSVWVDVKDTCMGTLVVKGD----NLIQMPGAAMKIKLEGDPGARVGLVAVDKAVYVLNDKYKI

AAA68989.1 SQAKIWDTIEKSDFGCTAGSGQNNLGVFEDAGLALTTSTNLNTKQRSAAKCPQPANRRRRSSVLLLDSNASKAAEFQDQDLRKCCEDVMHENPMGYTCEKRAKYIQEGDACKAAFLECCR

AAA68989.1 YIKGVRDENQRESELFLARDDNEDGFIADSDIISRSDFPKSWLWLTKDLTEEPNSQGISSKTMSFYLRDSITTWVVLAVSFTPTKGICVAEPYEIRVMKVFFIDLQMPYSVVKNEQVEIR

AAA68989.1 AILHNYVNEDIYVRVELLYNPAFCSASTKGQRYRQQFPIKALSSRAVPFVIVPLEQGLHDVEIKASVQEA-LWSDGVRKKLKVVPEGVQKSIVTIVKLDPRAKGVGGTQLEVIKARKLDD

AAA68989.1 RVPDTEIETKIIIQGDPVAQIIENSIDGSKLNHLIITPSGCGEQNMIRMAAPVIATYYLDTTEQWETLGINRRTEAVNQIVTGYAQQMVYKKADHSYAAFTNRASSSWLTAYVVKVFAMA

AAA68989.1 AKMVAGISHEIICGGVRWLILNRQQPDGAFKENAPVLSGTMQGGIQGAEEEVYLTAFILVALLESKTICNDYVNSLDSSIKKATNYLLKKYEKLQRPYTTALTAYALAAADQLNDDRVLM

AAA68989.1 AASTGRDHWEEYNAHTHNIEGTSYALLALLKMKKFDQTGPIVRWLTDQNFYGETYGQTQATVMAFQALAEYEIQMPTHKDLNLDITIELPDREVPIRYRINYENALLARTVETKLNQDIT

AAA68989.1 VTASGDGKATMTILTFYNAQLQEKANVCNKFHLNVSVENIHLN---AMGAKGALMLKICTRYLGEVDSTMTIIDISMLTGFLPDAEDLTRLSKGVDRYISRYEVDNNMAQKVAVIIYLNK

AAA68989.1 VSHSEDECLHFKILKHFEVGFIQPGSVKVYSYYNLDEKCTKFYHPDKGTGLLNKICIGNVCRCAGETCSSLNHQERIDVPLQIEKACETNVDYVYKTKLLRIEEQDGNDIYVMDVLEVIK

AAA68989.1 QGTDENPRAKTHQYISQRKCQEALNLKVNDDYLIWGSRSDLLPTKDKISYIITKNTWIERWPHEDECQEEEFQKLCDDFAQFSYTLTEFGCPT

Cysteine-rich seceretory protein

AAP85301.1 MIAF-SLLCFAAVLQQSFGNVDFNSESTRRKKKQKEIVDLHNSLRRRVSPTASNMLKMEWYPEAASNAERWANTCSLNHSPDNLRVLEGIQCGESIYMSSNARTWTEIIHLWHDEYKNFV

ACE73578.1 MIAFVVLLSLAAVLQQSSGTVDFASESSNKRENQKQIVDKHNALRRSVRPTARNMLQMEWNSNAAQNAKRWADRCTFAHSPPHLRTVGIFSCGENLFMSSQPYAWSKVIQSWYDENKKFV

ACH73168.1 MIAFIVLLSLAAVLQQSSGTVDFASESSNKRENQKQIVDKHNALRRSVRPTARNMLQMEWNSNAAQNAKRWADRCSFAHSPPHLRTVGKIGCGENLFMSSQPYAWSRVIQSWYDENKKFV

AAP85301.1 YGVGANPPGSVTGHYTQIVWYQTYRAGCAVSYCPSSAWSYFYVCQYCPSGNFQGKTATPYKLGPPCGDCPSACDNGLCTNPCTIYNKLTNCDSLLKQSSCQDDWIKSNCPASCFCRNKII

ACE73578.1 YGVGANPPGSVIGHYTQIVWYKSHLLGCAVTRCSSS--KYIYVCQYCPAGNIIGSTATPYKSGPPCGDCPSACVNGLCTNPCKYNDDYTNCKSLAKQDRCQTEWIKSKCGASCFCRTEII

ACH73168.1 YGVGANPPGSVIGHYTQIVWYNSHLLGCGAAKCSSS--KYLYVCQYCPAGNIIGSIATPYKSGPPCGDCPSACVNGLCTNPCKHHNVFSNCQSLAKQNACQTEWMKSKCAASCFCRTEII

Nerve Growth Factor

AAS94269.1 -----MSMLCYTLITAFLIGIWAAPKSEDNVPLGSPATSDLSDTSCAQTHEGLKTSRNTDQRHPAPQKAEDQELRTAANIIVDPKLFQKRQFQSPRVLFSTQPPLLSRDEESVEFLDNED

A59218 MVHSVMSMLCYTLIIAFLIGIWAAPKSEDNVPLGSPATSDLSDTSCAQTHEGLKTSRNTDQHHPAPQKAEDQELRTAANIIVDPKLFQKRQFQSPRVLFSTQPPLLSRDEESVEFLDNED

AAS94269.1 SLNRNIRAKREDHPVHNLGEHSVCDSVSAWVTKTTATDIKGNTVTVMENVNLDNKVYKQYFFETKCKNPNPVPSGCRGIDSSHWNSYCTETDTFIKALTMEGNQASWRFIRIDTACVCVITKKTGN

A59218 SLNRNIRAKREDHPVHNLGEHSVCDSVSAWVTKTTATDIKGNTVTVMENVNLDNKVYKQYFFETKCKNPNPEPSGCRGIDSSHWNSYCTETDTFIKALTMEGNQASWRFIRIETACVCVITKKKGN

Acetylcholinesterase

JAS05178.1 MLRFFWSRLSIFFFLSLVCKCASNNDTPVVTSSGPMKGKIVLTRSGSVAAYLGIPYAEPPVKKLRFQNPVPRQPWSEVLEATSFGNSCPQTNITGLPDKDVWVPNTPLSEDCLFLNIWAPHPRPSRPVPVLVWIQGMGFI

JAS05178.1 TGTASLDVYNGAILSATENVIVASMNYRLGGLGFLYLPPYAPGNMGLRDQHLALTWLKENIALFGGDPAQLTLVGQSAGAVLVGCHLLSPLSQPLFARAVLQSGVPNAIWPWKSPREAHRDAIMLSKQVGCAKDSDSAVV

JAS05178.1 SCLQEIDFGHENFTQLTLINSLTTDGNFLPGNVPNLLDAAILQGKPILTGVTDDEGSAFVLLMYSSTKTNGGILTWEQLLQGVTITMRRGTKKEVAHTVAKKFSEANHGQYRLAFSQYMRDYFMVCPLVELAAKIRKARK

JAS05178.1 PVYVYAFSHHPSGSGWPEWVGTPHGAEIPYVFGTMASATNRSITEAEEALSRRTMRYWAQFARGGTPTGAKADEVQWPLYNATEQNFFHIRRGSPQLKRLSPAPLCDFLATLPESNIQS

Cholinesterase

ETE70564.1 MPCLLCPSLLCCLLLLLLPFPLASSSTSNGGTVVITSSGPIKGKQVLSGLGSVTAYLGIPYAEPPLGKLRFQKPLPHQPWNQTLEATNFGNSCPQFLFLDELEAEIWSPKTPLSEDCLSLNIWVSNPQPSSPVPVLVWIH

ETE70564.1 GGGYLGGTASVDVFNGASLAATENVIVVTINYRLGALGFLYLPPAAPGNLGLWDQQLALKWIKENAAAFGGDPSRVTIFGQSVGGASVNFHLFAPKSQDLFAQAVMQSGTANAFWAWRPPEEAKRISLEFVHLLGCSKDN

ETE70564.1 NTSIGHCLQTKNVSEFIQHEISLFRKLGFFLNFPFKPTVDGDFLLGNPENLMEKGQIQLKPVLIGKNSDEGDSTVHYIFSDINDNLINQEQLLKGIQLLVPTEGATEDFVQTVALRHSEGNHGPAKYRSALSHFFADRII

ETE70564.1 ACPLIEAAGNIRKTGSPVYAYLFAHRPSGSVWPEWTGASHGAEIPYIFGTLESILPINQTHTEAEARLSRKMMHYWAEFARTGNPTGLVATKDEWPLYNATEQNFFVLNSESSQEMEKEPVHHCGFLKNHFSMAEDPLAS

ETE70564.1 TSASNGDTVVITSSGPIKGKQFLAGLGSVTAYLVIPYAEPPLGKLRFQNPLPHQPRNQTLETTSFGNSCSQSIYYEDTAAMVWNPRTPLSEDCLSHNIWVPHPQPSSPVPVFVWIHGDGYGGCSEDSNTSIGHCLQTKNV

ETE70564.1 SELIQQQGSLFLNEDCLLNFPFRPTIDGDFLLGDPEKLVEEEQIQVKPVLIGKVSDEGSTFIHDLFSDIKESLINEEQLLKGIQLLVPNATEDVVQSIALRNPAGLVATKDEWLLYNATEQNFFVLNSEPSQKTEKEPTH

ETE70564.1 HCGFLKKHLSKSEDPYIAIMLRFFWSRLSFFFFLSLVCKCASNNDTPVVTSSGPIKGKIVLTRSGSVTAYLGIPYAEPPVKKLRFQKPVPHQPWSEVLEATRFGNSCPQTNITGLPDKDIWVPNTPLSEDCLFLNIWAPH

ETE70564.1 PRPSRPVPVLVWIQGMGFITGTASSDVYNGAILSATENVIVASMNYRLGGLGFLYLPPYAPGNMGLWDQHLALKWLKDNIALFGGDPAQLTLVGQSAGAVLVGCHLLSPLSQPLFARAVLQSGVPNAIWPWKSPQEAHRD

ETE70564.1 AIMLSKQVGCAKDSDSAVVSCLQEIDFGHENFTQLTLINSLTTDGNFLPGNVPNLLDTAILEGKPILTGVTDDEGSAFVLLMYSSTKTNGGILTWEQLLQGVTITMRRGTKKEVAHTVAQKFSEANHGQYRLAFSQYMRD

ETE70564.1 YFMVCPLVELAAKIRKARKPVYVYSFSHHPSGSGWPEWIGTPHGAEIPYVFGTMASATNQSITEAEEALSRQTMRYWAQFARGGTPTGTKADGVQWPLYDATEQNFFHISTDPPQLKRLSPAPLCDFLATLPENDIQS

Thaicobrin

P82885.1 SPPGNWQKADVTFDSNTAFESLVVSPDKKTVENVGVSQVAPDNPERFDGSPCVLGSPGFRSGKHFFEVKYGTQREWAVGLAGKSVKRKGYLRLVPEERIWQKGLWWLG

Phospholipase B

ETE59578.1 DLHYATVYWLEAEKSFQVKDLLDKNGDAYGYYNDTVQSTGWGILEIKAGYGNQLVSNEILMYAAGFLEGYLTASRMRDHVANLYHQLIKNVTIEQKVKDFMQKQDEWTRQQIKNNKDDPFWRHAGYIIAQLDGLYMGNLE

ETE59578.1 WAKRQKRTPLTEFEVSFLNAIGDLLDLISALSPESRNNDSNMYQWDMGHCSALIKVLPGYENIYFAHSSWFTYAATLRIYKHWDFRITDPQTKTGRASFSSYPGFLISLDDFYILGSGLIMLQTTNSVFNLSLLKQVVPE

ETE59578.1 SLFAWERVRIANMMADSGKTWAQTFEKQNSGTYNNQYMILDTKKIKLRRSIEDGSLYIIEQVPNLVEYSDQTTILRKGYWPSYNIPFHKVIYNMSGYREYVQKYGLDFSYELAPRAKIFRRDQGKVTDMESMKHIMRYNN

ETE59578.1 YKNDPYAKHNPCNTICCRQDLNYKTPVADINMAAKFTAYAINGPPVEKGLPIFSWVHFNKTTHQGLPESYNFDFVTMKPVL

Cystatin

ACR83850.1 MVHFQLPVAAPLCLLCALLLLPSATMIPGGLSPRSVSDPDVQKAAAFAVQEYNARSANAHYYKELRVVEAQSQVVAGEKYYLMMELVKTKCAKTAGKPKVYKEIQNCELPPKAQQEKLTCHFQVWSRPWLDKTELTKMSCN

**Supplementary Fig S1.b.** Alignment of tryptic and semi-tryptic peptide sequences derived from in-gel digestion of SDS-PAGE bands of *Naja kaouthia* crude venom with snake venom protein families reported in the Elapidae database. The protein alignment was done using Clustal Omega programme (<https://www.ebi.ac.uk/Tools/msa/clustalo/>). The distinct peptides obtained for each of the following proteins has been highlighted in green or blue (two colours have been used in case of adjacent distinct/unique peptides). The amino acid substitutions within the unique/distinct peptides obtained from MS/MS are highlighted in red colour.

Phospholipase A2

Q7LZI1.1 HSCEICHNVGKSCEGSVEPCT--SPEDQCGTVVLEFSPAPVSFRSIHKN------CFSSS----LCKLGSFDVNVGQNTYVRGRIQCCDEERCEEPQFSGHCAS-HPNGYYCPGIFGLFS

AED89576.1 ----------------MNPAHLLVLAAVCISLLGASSIAPQPLNLYQFGNMINCTMPGGSPLLDYADYGCYCGSGGGGTPVDDLDRCCQAHD--------NCYGEAETVHKCNPFWTFYS

P60044.1 ------------------------------------SNRPMPLNRWQFKNMISCTVPSRS-WWDFADYGCYCGRGGSGTPVDDLDRCCQVHD--------NCYNEAEKISGCNPRFRTYS

1MH2 -------------------------------------------NTWQFKNMISCTVPSRS-WWDFADYGCYCGRGGSGTPSDDLDRCCQTHD--------NCYNEAEKISGCNPRFRTYS

P25498.1 -------------------------------------------NLYQFKNMIKCTVPSRS-WLDFANYGCYCGRGGSGTPVDDLDRCCQIHD--------NCYNEAGKISGCWPYFKTYS

P60045.1 ------------------------------------SNRPMPLNLYQFKNMIQCTVPSRS-WQDFADYGCYCGKGGSGTPVDDLDRCCQVHD--------NCYNEAENISGCRPYFKTYS

PSNJ2K -------------------------------------------NLYQFKNMIQCTVPNRS-WWDFADYGCYCGRGGSGTPVDDLDRCCQVHD--------NCYDEAEKISRCWPYFKTYS

BAA36403.1 ----------------MNPAHLLILAAVCVSPLGAFSNRPMPLNLYQFKNMIQCTVPNRS-WWDFADYGCYCGRGGSGTPVDDLDRCCQVHD--------NCYNEAEKISRCWPYFKTYS

AAF82186.1 ----------------MNPAHLLILAAVCVSPLGASSNRPMPLNLYQFKNMIQCTVPNRS-WWDFADYGCYCGRGGSGTPVDDLDRCCQVHD--------NCYGEAEKISRCWPYFKTYS

AAA66027.1 ----------------MNPAHLLILAAVCVSPLGASSNRPMPLNLYQFKNMIQCTVPNRS-WWHFADYGCYCGRGGSGTPVDDLDRCCQIHD--------NCYNEAEKISRCWPYFKTYS

Q7LZI1.1 LDSSANEAVCKGTETKCINI--------------AGYRKEMYPGDIAYNIKGCISSCPELSLSNRTHEVDRNELIKVECTDAVKIPPSECQSSGI

AED89576.1 YECSEGQLTCRDNDTNCKEFVCNCDLEAANCFAKAPYIEENYNINLN----RCT-----------------------------------------

P60044.1 YECTAGTLTCTGRNNACAASVCDCDRLAAICFAGAPYNDNNYNIDLQ----ARCN----------------------------------------

1MH2 YACTAGTLTCTGRNNACAASVCDCDRNAAICFAGAPYNDSNYNIDLQ----ARCN----------------------------------------

P25498.1 YECSQGTLTCKGDNNSCAASVCDCDRLAAICFAGAPYNNDNYNINLK----ARCQ----------------------------------------

P60045.1 YECTQGTLTCKGDNNACAASVCDCDRLAAICFAGAPYNDANYNIDLK----ARCN----------------------------------------

PSNJ2K YECSQGTLTCKNGNNACAAAVCDCDRLAAICFAGAPYNNNNYNIDLK----ARCQ----------------------------------------

BAA36403.1 YECSQGTLTCKGDNDACAAAVCDCDRLAAICFAGAPYNNNNYNIDLK----ARCQ----------------------------------------

AAF82186.1 YECSQGTLTCKGGNDACAAAVCDCDRLAAICFAGAPYNDNNYNIDLK----ARCQ----------------------------------------

AAA66027.1 YECSQGTLTCKGGNNACAAAVCDCDRLAAICFAGAPYNDNNYNIDLK----ARCQ----------------------------------------

Cobra venom factor

I51018 MERMALYLVAALLIGFPGSSHGALYTLITPAVLRTDTEEQILVEAHGDSTPKQLDIFVHDFPRKQKTLFQTRVDMNPAGGMLVTPTIEIPAKEVSTDSRQNQYVVVQVTGPQVRLEKVVL

I51018 LSYQSSFLFIQTDKGIYTPGSPVLYRVFSMDHNTSKMNKTVIVEFQTPEGILVSSNSVDL--NFFWPYNLPDLVSLGTWRIVAKYEHSPE-NYTAYFDVRKYVLPSFEVRLQPSEKFFYI

I51018 DGNENFHVSITARYLYGEEVEGVAFVLFGVKIDDAKKSIPDSLTRIPIIDGDGKATLKRDTFRSRFPNLNELVGHTLYASVTVMTESGSDMVVTEQSGIHIVASPYQIHFTKTPKYFKPG

I51018 MPYELTVYVTNPDGSPAAHVPVVSEAFHSMGTTLSDGTAKLILNIPLNAQSLPITVRTNHGDLPRERQATKSMTAIAYQTQGGSGNYLHVAITSTEIKPGDNLPVNFNVKGNANSLKQIK

I51018 YFTYLILNKGKIFKVGRQPRRDGQNLVTMNLHITPDLIPSFRFVAYYQVGNNEIVADSVWVDVKDTCMGTLVVKGD----NLIQMPGAAMKIKLEGDPGARVGLVAVDKAVYVLNDKYKI

I51018 SQAKIWDTIEKSDFGCTAGSGQNNLGVFEDAGLALTTSTNLNTKQRSAAKCPQPANRRRRSSVLLLDSNASKAAEFQDQDLRKCCEDVMHENPMGYTCEKRAKYIQEGDACKAAFLECCR

I51018 YIKGVRDENQRESELFLARDDNEDGFIADSDIISRSDFPKSWLWLTKDLTEEPNSQGISSKTMSFYLRDSITTWVVLAVSFTPTKGICVAEPYEIRVMKVFFIDLQMPYSVVKNEQVEIR

I51018 AILHNYVNEDIYVRVELLYNPAFCSASTKGQRYRQQFPIKALSSRAVPFVIVPLEQGLHDVEIKASVQEA-LWSDGVRKKLKVVPEGVQKSIVTIVKLDPRAKGVGGTQLEVIKARKLDD

I51018 RVPDTEIETKIIIQGDPVAQIIENSIDGSKLNHLIITPSGCGEQNMIRMAAPVIATYYLDTTEQWETLGINRRTEAVNQIVTGYAQQMVYKKADHSYAAFTNRASSSWLTAYVVKVFAMA

I51018 AKMVAGISHEIICGGVRWLILNRQQPDGAFKENAPVLSGTMQGGIQGAEEEVYLTAFILVALLESKTICNDYVNSLDSSIKKATNYLLKKYEKLQRPYTTALTAYALAAADQLNDDRVLM

I51018 AASTGRDHWEEYNAHTHNIEGTSYALLALLKMKKFDQTGPIVRWLTDQNFYGETYGQTQATVMAFQALAEYEIQMPTHKDLNLDITIELPDREVPIRYRINYENALLARTVETKLNQDIT

I51018 VTASGDGKATMTILTFYNAQLQEKANVCNKFHLNVSVENIHLN---AMGAKGALMLKICTRYLGEVDSTMTIIDISMLTGFLPDAEDLTRLSKGVDRYISRYEVDNNMAQKVAVIIYLNK

I51018 VSHSEDECLHFKILKHFEVGFIQPGSVKVYSYYNLDEKCTKFYHPDKGTGLLNKICIGNVCRCAGETCSSLNHQERIDVPLQIEKACETNVDYVYKTKLLRIEEQDGNDIYVMDVLEVIK

I51018 QGTDENPRAKTHQYISQRKCQEALNLKVNDDYLIWGSRSDLLPTKDKISYIITKNTWIERWPHEDECQEEEFQKLCDDFAQFSYTLTEFGCPT

Cysteine-rich seceretory protein

ACH73168.1 MIAFIVLLSLAAVLQQSSGTVDFASESSNKRENQKQIVDKHNALRRSVRPTARNMLQMEWNSNAAQNAKRWADRCSFAHSPPHLRTVGKIGCGENLFMSSQPYAWSRVIQSWYDENKKFV

Q8JI38.1 MIAFIVLLSLAAVLQQSSGTVDFASESSNKRENQKEIVDKHNALRRSVRPTARNMLQMEWNSDAAQNAQRWADRCSFAHSPSHLRTVGKFSCGENLFMSSQPYAWSRVIQSWYDENKNFI

P84807.1 -------------------DVDFNSESTRRKNKQKEIVDLHNSLKKTV------------------------------------------------------------------------

AAP81292.1 MIAF-TLLSLAAVLQQSFGNVDFNSESTRRQKKQKEIVDLHNSLRRSVSPTASNMLKMQWYPEAASNAERWASNCNLGHSPDYSRVLEGIQCGENIYMSSNPRAWTEIIQLWHDEYKNFV

AAP85301.1 MIAF-SLLCFAAVLQQSFGNVDFNSESTRRKKKQKEIVDLHNSLRRRVSPTASNMLKMEWYPEAASNAERWANTCSLNHSPDNLRVLEGIQCGESIYMSSNARTWTEIIHLWHDEYKNFV

ACH73168.1 YGVGANPPGSVIGHYTQIVWYNSHLLGCGAAKCSSSK--YLYVCQYCPAGNIIGSIATPYKSGPPCGDCPSACVNGLCTNPCKHHNVFSNCQSLAKQNACQTEWMKSKCAASCFCRTEII

Q8JI38.1 YDVGANPPGSVIGHYTQIVWYKSHLLGCAAARCSSSK--YLYVCQYCPAGNIIGSIATPYKSGPPCGDCPSACVNGLCTNPCKHENEFTNCQSLVKQTGCQNTWIQSKCPASCFCRTEII

P84807.1 ------------------------------------------------------------------------------------------------------------------------

AAP81292.1 YGVGANPPGSVTGHYTQIVWYKTYRIGCAVNYCPSSEYNYFYVCQYCPSGNMRGSTATPYKSGPTCGDCPSACDNGLCTNPCTLYNEYTNCDSLVKQSSCQDEWIKSKCPASCFCHNKII

AAP85301.1 YGVGANPPGSVTGHYTQIVWYQTYRAGCAVSYCPSSAWSYFYVCQYCPSGNFQGKTATPYKLGPPCGDCPSACDNGLCTNPCTIYNKLTNCDSLLKQSSCQDDWIKSNCPASCFCRNKII

Ohanin like protein

P82885.1 SPPGNWQKADVTFDSNTAFESLVVSPDKKTVENVGVSQVAPDNPERFDGSPCVLGSPGFRSGKHFFEVKYGTQREWAVGLAGKSVKRKGYLRLVPEERIWQKGLWWLG

5’-Nuclueotidase

JAI09047.1 MPTSRRRSGAHGCPRSAPSAMWRLVGAVCFCAALSVAAAGSFKLTILHTNDVHARVEQTSRDSGKCTREDCYGGVARRATKIREIRASHRNVLLLDAGDQYQGTVWFNYFKGREVVHFMN

JAI09047.1 SLRYDAMALGNHEFDNGLNGLLDPLLKNVKFPILSANIRPKGPIASNISGYILPYKIINVGSEKVGIIGYTTKETPVLSNPGPYLEFRDEVEELQKQADKLTTLGVNKIIALGHSGFKED

JAI09047.1 CRIAQKVKGVDVVVGGHTNTFLYTGSPPSNEVPAGNYPFMQLSDDGRQVPVVQAYAFGKYLGYLNVIFDDKGKVIKASGNPILLNKSIQEDPAVKAEVSRMKVQLQKYSKQEIGKTIVYL

JAI09047.1 NGTTHACRFHECNLGNLICDAVVYNNLRHPDDNEWNHVSMCIVNGGGIRSPIDEKANNGIITLEELTAVLPFGGTFDLLQIKGSALRQAFEHSVHRHGQGTGELLQVSGIKVLYDLSQKP

JAI09047.1 GKRVVSLNVLCTECRVPAYVPLQMEKTYKVLLPSFLAAGGDGYYMLKGDSSNHSSGDLDISIVSDYIKRMGKVFPAMEGRVMFSAGTLFQAHHS

**L-amino acid oxidase**

ABN72546.1 MNVLFIFSLLFLAALESCADDRRSPLEECFQQNDYEEILEIARNGLKKTSNPKHVVVVGAGMAGLSAAYVLAGAGHKVTLLEASERVGGRVITYHNDREGWYVNMGPMRLPERHRIVREY

ABN72546.1 IRKFGLKLNEFFQENENAWYYINNIRKRVWEVKKDPSLLKYPVKPSEEGKSASQLYQEPLRKVIEELKRTNCSYILNKYDSYSTKEYLIKEGNLSRGAVDMIGDLLNEDSSYHLSFMESL

ABN72546.1 KSDALFSYEKRFDEIVGGFDQLPISMYQAIAEMVHLNARVIKIQYDAEKVRVTYQTPAKT--FVTADYVIVCSTSRAARRIYFEPPLPPKKAHALRSIHYRSATKIFLTCSKKFWEADGI

ABN72546.1 HGGKSTTDLPSRFIHYPNHNFTSGIGVIMAYVLADDSDFFQALDTKTCADIVINDLSLIHDLPKREIQALCYPS-IKKWNLDKYTMGSITSF

Acetylecholinesterase

JAA74736.1 --------MPAPWPWWLQLVLCILSSVAVLPGRASELKVSTQMGLVRGLSLPVLDGHVSAFLGIPFAEPPVGRMRFLRPEPVKPWQHILDATSYQRACYQAVDNSYPGFQGTEMWNPNRG

JAA74736.1 MSEDCLYLNIWVPSPRPRDVPVLVWIYGGGFYSGAASLDVYDGRFLTYTQNVIVVSLSYRVGAFGFLGLPGSPEAPGNMGLLDQRLALQWIQNNIHHFGGNPSAVTIFGESAGAASVGMH

JAA74736.1 LLSTQSRALFQRAILQSGGPNAPWATVTPAESRRRAALLGKQLGCQFNNDSELVSCLRSKTPQELIDEEWSVLPYKSIFRFPFVPVIDGDFFPDTPEAMLSSGNFKETQVLLGVVKDEGS

JAA74736.1 YFLIYGLPGFSKDNESLINQADFLEGVRMSVPHANDIATEAVVMQYTDWQDQDNGEKNREALDDIVGDHNVICPVVQFANDYAKRNNKVYAYLFDHRASNLLWPPWIGGPPRLRDRVCLW

JAA74736.1 IAPQRQPELHTPREGAEPQ-DDXLLGQLXPDREPHRPCREGR------------------GLAHLHRLPAAVCPAQHPAA----GHPTQPAGPDLR------

Hylauronidase

JAS05169.1 MCHLWIKCLATWILLKRFNGVHVMQTRAPMYPNEPFLVFWNAPTTQCQLRYKVALDLKTFHIVTNANESLSGSAVTIFYPTQLGIYPHIDDHGNFVNGIIPQNESITKHLNKTKSNINHM

JAS05169.1 IPLKTFHGLGVIDWENWRPQWDRNWGSKNVYRNRSIQFAKELHPDLSEHAIKRLAKEEFEKAGKSFMRDTLLLAENMRPDGYWGYYLYPDCYNYNYKKKPEQYTGKCPDIEMSRNDQLIW

JAS05169.1 LWRDSTALFPSIYLETILKSSANALKFVHHRLKESMRIASMARKDYALPVFVYARPFYAYTFEPLTEEDWVTTIGETAAMGAAGIVFWGSMQYASTIESCQKVKDYI----------N--

JAS05169.1 ------GPFGHYIINVTSA--AKI---CSHFLCKGKGRCVRKH------------SDSNAFLHLFPESFRIMVQANATHKKAIVKGKLELENLKY--LRKNFICQ---CYQGWKGLYCEE

JAS05169.1 HHNK----EGN-------------------------------------------------------------------------------------------------------------

JAS05169.1 ------------------------------------------------------------------------------------------------------------------------

JAS05169.1 ----------------------------------------------------------------------------------------

**Three finger toxins**

AAD40974.1 MKTLLLTLVVVTIVCLDLGYTRTCFITP-----DVKSKPCPPGQEVCYTKTWCDGFCGIRGKRVDLGCAATCPTPKKTGIDIICCSTDDCNTFPLRPRGRLSSIKDHP

P59275.1 ---------------------LECHNQQSSQT--PTTKTCS-GETNCYKKWWSD----HRGTIIERGCG--CPKV-KPGVNLNCCRRDRCNN----------------

P59276.1 ---------------------LECHNQQSSQA--PTTKTCS-GETNCYKKWWSD----HRGTIIERGCG--CPKV-KPGVNLNCCRTDRCNN----------------

AAY63884.1 MKTLLLTLLVVTIVCLDLGYTLECHNQQSSQT--PTTTGCSGGETNCYKKRWRD----HRGYRTERGCG--CPSV-KNGIEINCCTTDRCNN----------------

Q9YGJ5.1 MKTLLLTLLVVTIVCLDLGYTLECHNQQSSQA--PTTTGCSGGETNCYKKSWRD----HRGYRIERGCG--CPSV-KKGIEINCCTTDRCNN----------------

P14541.1 ---------------------LKCHNTQ--LP--FIYKTCPEGKNLCFKATLKKF---PLKIPIKRGCADNCPKN-SALLKYVCCSTDKCN-----------------

P01451.1 ---------------------LKC-NKL--VP--IAYKTCPEGKNLCYKMFMMS----DLTIPVKRGCIDVCPKN-SLLVKYVCCNTDRCN-----------------

P01446.1 ---------------------LKC-NKL--IP--LAYKTCPAGKNLCYKMFMVS----NKTVPVKRGCIDACPKN-SLLVKYVCCNTDRCN-----------------

JK0222 ---------------------LKC-NKL--VP--LFYKTCPAGKNLCYKMFMVA----TPKVPVKRGCIDVCPKS-SLLVKYVCCNTDRCN-----------------

AAC27685.1 MKTLLLTLVVVTIVCLDLGYTLKC-NKL--VP--LFYKTCPAGKNLCYKMYMVA----TPKVPVKRGCIDVCPKS-SLLVKYVCCNTDRCN-----------------

P29181.1 ---------------------LTCLNCPEVYC--RRFQICRDGEKICFKKFDQRN---LLGKRYRRGCAATCPEA-KPREIVQCCSTDKCNR----------------

P01400.1 ---------------------LTCLICPEKYC--NKVHTCRNGENICFKRFYEGN---LLGKRYPRGCAATCPEA-KPREIVECCSTDKCNH----------------

P29180.1 ---------------------LTCLICPEKYC--NKVHTCLNGEKICFKRYSERK---LLGKRYIRGCADTCPVR-KPREIVQCCSTDKCNH----------------

P82463.1 ---------------------LTCVKEKSIFG--VTTEDCPDGQNLCFKRWHMIV---PGRYKKTRGCAATCPIA-ENRDVIECCSTDKCNL----------------

sp|P82464.1 ---------------------TICYNHLTRTSE--TTEICPDSWYFCYKISLAD----GNDVRIKRGCTFTCPELRPTGIYVYCCRRDKCNQ----------------

prf||765048A ---------------------LEC-NKLVPI----AHKTCPEGKNLCYKMFMVS----TSTVPVKRGCIDVCPKD-SALVKYVCCNTDRCN-----------------

BAU24666.1 ---------VVTIVCLDLGYTLQC-NKLVPI----ASKTCPPGKNLCYKMFMVS----DLTIPVKRGCIDVCPKN-SLLVKYVCCNTDRCN-----------------

sp|P34074.2 ---------------------IRCFIT-----PRVSSQACPDG-HVCYTKTWCDNFCGINGKRVDLGCAATCPTV-KPGVDIKCCSTDNCNPFPTRKRP---------

sp|O42257.1 MKTLLLTLVLVTIMCLDLGYTIRCFIT-----PDVTSTDCPNG-HVCYTKTWCDGFCSSRGRRVELGCAATCPTV-KPGVDIQCCSTDNCNPFPTRP-----------

sp|P25668.1 ---------------------IRCFIT-----PDITSKDCPNG-HVCYTKTWCDGFCSIRGKRVDLGCAATCPTV-RTGVDIQCCSTDDCDPFPTRKRP---------

sp|P01391.1 ---------------------IRCFIT-----PDITSKDCPNG-HVCYTKTWCDAFCSIRGKRVDLGCAATCPTV-KTGVDIQCCSTDNCNPFPTRKRP---------

sp|P58370.1 MKTLLLTLVVVTIMCLDLGYTLECKICNFKTCPTDELRHCASGETICYKTFWNT----HRGLRIDRGCAATCPTV-KPGVNIICCKTDNCN-----------------

sp|P01427.1 ---------------------LECHNQQSSQPP--TTKTCS-GETNCYKKWWSD----HRGTIIERGCG--CPKV-KPGVNLNCCRTDRCNN----------------

sp|P82935.2 MKTLLLTLVVVTIVCLDLGYTLTCLNCPEMFCG--KFQICRNGEKICFKKLHQRR---PLSWRYIRGCADTCPVG-KPYEMIECCSTDKCNR----------------

JAB52868.1 MKTLLLTLVVVTIVCLDLGYTKTCYKYDTLFGK--TTETCADGQNICFKRWHMLV---PGRYHVSRGCAATCPKA-QNHDSVECCAKENCNA----------------

|P82462.1 ---------------------LICVKEKFLFSE--TTETCPDGQNVCFNQAHLIY---PGKYKRTRGCAATCPKL-QNRDVIFCCSTDKCNL----------------

Phospholipase B

ETE59578.1 ------------------------------------DLHYATVYWLEAEKSFQVKDLLDKNGDAYGYYNDTVQSTGWGILEIKAGYGNQLVSNEILMYAAGFLEGYLTASRMRDHVANLY

ETE59578.1 HQLIKNVTIEQKVKDFMQKQDEWTRQQIKNNKDDPFWRHAGYIIAQLDGLYMGNLEWAKRQKRTPLTEFEVSFLNAIGDLLDLISALSPESRNND-------SNMYQWDMGHCSALIKVL

ETE59578.1 PGYENIYFAHSSWFTYAATLRIYKHWDFRITDPQTKTGRASFSSYPGFLISLDDFYILGSGLIMLQTTNSVFNLSLLKQVVPESLFAWERVRIANMMADSGKTWAQTFEKQNSGTYNNQY

ETE59578.1 MILDTKKIKLRRSIEDGSLYIIEQVPNLVEYSDQTTILRKGYWPSYNIPFHKVIYNMSGYREYVQKYGLDFSYELAPRAKIFRRDQGKVTDMESMKHIMRYNNYKNDPYAKHNPCNTICC

ETE59578.1 RQDLNYKTP---------VADINMAAKFTAYAINGPPVEKGLPIFSWVHFNKTTHQGLPESYNFDFVTMKPVL

Snake venom metalloproteases

AAF00693.1 ------------MIQLSWSSIILESGNVNDYEVVYPQKVPALLKGGVQNPQPETKYEDTMQYEFQVNGEPVVLHLERNKGLFSEDYTETHYAPDGREITTSPPVQDHCYYHGYFQNEADS

JAS05092.1 MIQALLVTICLAVFPYQGSSIILESGNVNDYEVVYPQKVPALPKGRIQNPQPETKYEDTMQYEFQVNGEPVVLHLERNKGLFSEDYTETHYSSDDTEITTSPPVQDHCYYHGYIQNDADS

JAB52758.1 MIQALLVTICLAVFPYKGSSIVLESGNVNDYEVVYPQKVPLLPKRGVQNPQPETKYEDTMQYEFQMKGEPVVLHLERNKGLFSEDYTETHYAPDGRIITTSPPVQDHCYYHGYIQNDADS

ABQ01137.1 MIQASLVTICFMVFPYQGSSIILESGNVNDYEVVYPQKVPALPKGGVQNPQPETKYEDTMQYEFQVNGEPVVLHLERNKELFSEDYTEIHYSSDDTEIITSPPVQNHCYYHGYIQNEANS

ADF43026.1 MIQALLVIICLAVFPHQGSSIILESGNVNDYEVVYPQKVPALLKGGVQNPQPETKYEDTMRYEFQVNGEPVVLHLERNKGLFSEDYTETHYAPDGREITTSPPVQDHCYYHGYIQNEADS

P82942.1 ------------------------------------------------------------------------------------------------------------------------

AAF00693.1 SAVISACDGLKGHFKLQGEIYFIEPLKISDSEAHAIYKDENVEEEDETPKICGVTDTTWESDEPIKKTSLLTNTPEQDRYLQAEKYIEFYMVVDNIMYRHYKRNQLVIKRKVYEMINTMN

JAS05092.1 SAVISACDGLKGHFKHQGETYFIEPLKLSESGSHAIYKDENVEKEDETLKICVVTQTTWESDESIEKISQLTNTPEQDRYLQVKKYIEFYVVVDNRMYRHYKCKKRAIKRRVYEMVNLLN

JAB52758.1 SAVISACDGLKGHFKHQGETYFIEPLKLSDSEAHAIYKDENVEKEDVTLKICGVTQTTLESDEPIEKISQLTNTPEQDRYLQVKKYIEFYVVVDNRMYRYYKRKKHVIKRRVYEMVNLLN

ABQ01137.1 SAVISACDGLKGHFKYQGETYFIEPLKLSDSKSHAIYKDENVEEEEETP-NCGITQTTSESDEPIEKISRLTNTPEQERYLQVKKYIELYVVVDNKMYRNYDSNRHAIKRKVYETINLLN

ADF43026.1 SAVISACNGLKGHFKHQGETYFIEPLELSESEAHAIYKDENVEKEDETPKICAVTQTTWESDESIEKTSQLTNTPEQDRYLQVKKYIEFYLVVDNKMYKNHTS-NQELRTRVYEMVNYLN

P82942.1 -----------------------------------------------------------------------TNTPEQDRYLQAEKYIEFYVIVDNRMYRYYNYDKPAIKIRVYEMINAVN

AAF00693.1 MIYRRLNFHIALIGLEIWSNINEINVQSDVKATLDLFGEWREK-KLLPRKRNDNAQLLTGIDFNGTPVGLA-YIGSICNPKTSAAVVQDYSKSTRMVAITMAHEMGHNLGMNHDKGFCTC

JAS05092.1 TIYRPLNFYIALIGLEIWSHRDKINIETDAGITLNSFGEWREN-VLLPRKRNDNAQLLTRIQFNGTVIGLG-YVGTICSLQKSVAVIQDYSRKSNLVASAMAHEMGHNLGINHDRASCSC

JAB52758.1 KMYRHLNFHIALTGLEIWTKRDEINVRSNVAVTLDLFGKWREK-KLLPRKRNDNAQLLTRIDFNGNTLGLA-HIGSLCSPKTSVAVVQDYGKGTSMVAVTMAHEMGHNLGINHDKGSCTC

ABQ01137.1 MMYRPLNFLIALIGLEIWSNRDRINIEPEVAVTLKSFGKWRET-DLLPPKRNDNAQLLTQMEFNGTTVGLA-YVGSICSPEESVAVMEVYSRRTNIMASGMAHELGHNLGITHDNPSCNC

ADF43026.1 TKYRRLNFHIALIGLEIWSNQDKVDMDPGANVTLKSFAEWRAK--LPPHKRNDNAQLLTGIDFNGTTVGLA-YTGTLCTW-GSVAVVQDYSRRTILMASTMAHELGHNMGIHHDKANCRC

P82942.1 TKFRPLKIHIALIGLEIWSNEDKFEVKPAASVTLKSFREWRQT-VLLPRKRNDNAQLLTGINLNGTAVGIA-YPGSLCTQ-RSVFVVQDYNRRMSLVASTMTHELGHNLGIHHDEASCIC

AAF00693.1 GFNKCVMST-RRTKPAYQFSSCSVREHQRYLLRDRPQCILNKPLSTDIVSPPICGNYFVEVGEECDCGSPADCQSACCNATTCKLQHEAQCDSEECCEKCKFKGAGAECRAAKDDCDLPE

JAS05092.1 TAGPCIMFPTISFKPFYEFSSCSVQEHQRYLLRDRPQCILNKPLSTDIITPSVCGNHLVDVGEECDCGSPQDCQSACCNATTCKLQHEAQCDSEECCEKCKFKK-GAECRAAKDDCDLPE

JAB52758.1 GSNKCIMST-RRTKPAYQFSSCSVQEHQRYLLRDRPQCILNKPLSTDIVSPPVCGNYFVEVGEECDCGSPQDCQSACCDARTCKLKHKAQCDSEECCEKCKFKKAGAKCRAAKDDCDLPE

ABQ01137.1 NARLCIMSAIISFEPLSEFSSCSIQEHQRYLLRDRPQCILNRPLSTDIVTPPVCGNYLVEVGEECDCGFPVDCQSACCNATTCKLQHEAQCDSEECCEKCKLKKAGAECRAAKDDCDLPE

ADF43026.1 SHSPCIMSDTISDEPFYEFSSCSVREHQEYLLRERPQCILNKPSRKAIVSRPVCGNNFVEVGEQCDCGSLQDCQSTCCNATTCKLQPHAQCDSEECCEKCKFKGAETECRAAKDDCDLPE

P82942.1 IPGPCIMLKKR-TAPAFQFSSCSIRDYQEYLLRDRPQCILNKPLSTDIVSPAICGNYFVEEGEECDCGSPAACQSACCDAAT-----------------CKFNGAGAECRAAKHDCDLPE

AAF00693.1 LCTGQSAECPTDVFQRNGLPCQN-NGYCYNGKCPIMTNQCIALRGPGVKVSRDSCFTLNQRTRGCGLCRMEYGRKIPCAAKDVKCGRLFCKKRNSMICNCSISPRDPSYGMVEPGTKCGD

JAS05092.1 FCTGRSAECPTDSFQRNGHPCQNNQGYCYNGKCPIMKNQCIALMGSGVKVSRDMCFTLNQRGKGCGFCRKENGANIPCAAKDVKCGRLFCKKGNSMTCRCSVSPRDPDYGMVEPGTKCGD

JAB52758.1 LCTGRSAKCPTDSFQRNGHPCQNNQGYCYNGKCPIMKNQCIALMGSGVKVSRDMCFTLNQRGKGCGFCRKENGANIPCAAKDVKCGRLFCKKGNSMTCRCSVSPRDPDYGMVEPGTKCGD

ABQ01137.1 ICTGQSAECPMDSFQRNGHPCQNNQGYCYNGKCPIMTNQCIDLWGPGVNVSPDICFTLNQYSQGCGFCRMENGTKIPCAAKDKMCGKLVCEKGNS-TCTCFPTTDDPDYGMVEPGTKCGD

ADF43026.1 FCTGQSAECPTDSLQRNGHPCQNNQGYCYNGKCPTMENQCITLLGPNYTVGPAGCFKNNRKGDDVSHCRKENGAKIPCAAKDEKCGTLYCTEIKKTGCIVPVSPRDPDSRMVEPGTKCED

P82942.1 LCTGQSAECPTDSLQRNGHPCQNNQGYCYNGKCPTLTNQCIALLGPHFTVSPKGCFDLNMRGDDGSFCRMEDGTKIPCAAKDVKCGRLYCTEKNTMSCLIPP---NPDGIMAEPGTKCGD

AAF00693.1 GMVCSNRQCVDVKTAY

JAS05092.1 GMVCSNRQCVKVQTAY

JAB52758.1 GMVCSNRQCVKVQTAY

ABQ01137.1 GMVCSNRQCVDVKTAY

ADF43026.1 KKVCSKSQCVKV----

P82942.1 GMVCSKGQCVDVQTAY

Phosphodiesterase

JAI09691.1 MIMQKVLFISLVAVALGLGLGLGLKQSKQPQESCRNRCNETFRGELSYCSCDNKCTEREACCWDYQDICVLPTQSWSCNKLRCGERRMANVLCSCSEDCLTKKDCCTDYKSICKRETSWLKDQCASSSAAQCPEGFDQSP

JAI09691.1 LILFSMDGFRAEYLETWDTLMPNINKLKTCGTHAKYMRAVYPTKTFVNHYTIVTGLYAETHGIIDNNIYDVNLNQNFSLSGRNMRNPAWWGGQPIWNTATYQGLKAATYFWPGSEVKINGSYPAIYKAYNKSTPFEARVM

JAI09691.1 EVLQWLDLPRAKRPDFSTLYIEEPDTTGHKYGPVSGQVIKSLQMADRTLGMLMEGLKQRNLHNCVNLILLADHGMEAISCNRLEYMADYFNTVDFFMYEGAAPRIRSKNVPKDFYTFDSEAIVKNLTCRKPKQHFKAYLA

JAI09691.1 KDLPKRLHFANNVRIDKVNLMVDRQWLAVRNKKYKYCSGGTHGYDNEFKSMEAIFLAHGPDFKEKNEVTSFENIEVYNLMCDLLKLKPAPNNGTHGSLNHLLKNPFYNPSPAKEQSSPLLCDFGPVPSPDLSGCKCSSIT

JAI09691.1 DLEAVNQRLNLNDQAKTQCEADNLPYGRPHVLQHSKYCLLHQTKYISAYSQDILMPLWNSYTISKSLVKPTSVPPSASDCLRLDVRIPTAQSQTCSNYQPDLTITPGFLYPPDFSSSGPEQYDALITSNIVPMYKEFTRL

JAI09691.1 WNYFHSTLLPKYATERNGLNVISGPIFDYNYDGHFDSYDTIKQYVNNTKIPIPTHYFVVLTSCENSTNTPLNCPPGSLKVLSFILPHRPDNSESCADKSPNNLWVEERMQTHTARVRDVELLTGLDFYSVLKQPLSETLR

JAI09691.1 LKTFLPIFVNSVN

Nerve growth factor

A59218 MVHSVMSMLCYTLIIAFLIGIWAAPKSEDNVPLGSPATSDLSDTSCAQTHEGLKTSRNTDQHHPAPQKAEDQELRTAANIIVDPKLFQKRQFQSPRVLFSTQPPLLSRDEESVEFLDNEDSLNRNIRAKREDHPVHNLGE

A59218 HSVCDSVSAWVTKTTATDIKGNTVTVMENVNLDNKVYKQYFFETKCKNPNPEPSGCRGIDSSHWNSYCTETDTFIKALTMEGNQASWRFIRIETACVCVITKKKGN

**Supplementary table S1a:** List of orthologous proteins of *Naja naja* venom toxins identified by tandem mass spectroscopy analysis of SDS-PAGE bands against Elapidae database. The table shows the identified peptide ions, their mass, charge (z), score for the ID, ΔM (ppm), modified residues. Posttranslational modifications carbamidomethylation of cysteine and oxidation of methionine residues are represented in lower cases viz. ‘c’ and ‘m’ respectively.

|  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Protein Family** | **Accession** | **Description** | **-10lgP** | **Coverage (%)** | **Avg. Mass (Da)** | **Peptide** | **-10lgP** | **ppm** | **m/z** | **z** | **#Spec** |
| Phospholipase A2 | PSNJ2K | phospholipase A2 | 178.22 | 78 | 13455 | ccQVHDNcYDEAEKISR | 33.59 | -0.9 | 546.7275 | 4 | 1 |
|  |  |  |  |  | TYSYEcSQGTLTCKN | 32.29 | 1 | 877.8725 | 2 | 1 |
| BAA36403.1 | phospholipase A2 | 206.26 | 73 | 16271 | ccQVHDNcYNEAEKISR | 57.62 | -0.4 | 728.3066 | 3 | 2 |
|  |  |  |  |  | GGSGTPVDDLDRccQVHDNcYNEAEK | 41.36 | 0.6 | 999.4123 | 3 | 3 |
|  |  |  |  |  | LAAIcFAGAPYNNNNYNIDLKAR | 39.75 | 0.3 | 861.7642 | 3 | 1 |
|  |  |  |  |  | KGDNDACAAAVCDcDRLAAIcFAGAPYNNNNYNIDLK | 36.6 | -5.4 | 1340.922 | 3 | 1 |
|  |  |  |  |  | KTYSYECSQGTLTCKGDNDAcAAAVcDcDR | 23.95 | -9.3 | 1121.444 | 3 | 1 |
| P25498.1 | Acidic phospholipase A2 E | 113.43 | 52 | 13229 | LAAIcFAGAPYNNDNYNINLK | 33.78 | -1.1 | 786.0504 | 3 | 1 |
| AED89576.1 | phospholipase A2 precursor | 36.9 | 9 | 15957 | SGGGGTPVDDLDR | 36.9 | 0 | 623.2889 | 2 | 2 |
| JAS04993.1 | Phospholipase A2 5b | 65.46 | 13 | 16300 | GGSGTPVDELDR | 37.44 | 0.1 | 601.7861 | 2 | 1 |
| AAR08048.1 | phospholipase A2 | 154.76 | 47 | 13969 | NLYQFKNmIQcTVPSR | 62.72 | 1.9 | 1007.997 | 2 | 2 |
|  |  |  |  |  | TYSYEcTQGTLTcKGD | 24.56 | 2.6 | 942.3954 | 2 | 1 |
| AAA66027.1 | phospholipase A2 | 184.52 | 69 | 16189 | ccQIHDNcYNEAEK | 54.04 | 0.4 | 920.8564 | 2 | 3 |
|  |  |  |  |  | GGNNAcAAAVcDcDR | 50.04 | 0.2 | 805.809 | 2 | 1 |
|  |  |  |  |  |  |  |  |  |  |  |
| Snake venom metalloprotease |  |  |  |  |  |  |  |  |  |  |  |
| ADF43026.1 | metalloproteinase atrase A | 128.94 | 10 | 68254 | VYEMVNYLNTK | 60.96 | -0.8 | 687.3416 | 2 | 1 |
|  |  |  |  |  | GSVAVVQDYSR | 50.32 | 0.6 | 590.8018 | 2 | 2 |
|  |  |  |  |  | ERPQcILNKPSR | 45.32 | -0.2 | 499.9365 | 3 | 1 |
|  |  |  |  |  | EHQEYLLR | 41.73 | 0.7 | 544.2805 | 2 | 1 |
|  |  |  |  |  | LQPHAQcDSEEccEK | 40.27 | -0.3 | 630.9185 | 3 | 1 |
|  |  |  |  |  | SFAEWR | 30.5 | 0.1 | 398.1929 | 2 | 1 |
| ADG02948.1 | metalloproteinase atrase B | 105.03 | 11 | 66246 | VYEmINAVNTK | 50.43 | -0.5 | 649.3262 | 2 | 1 |
|  |  |  |  |  | YYNNDKPAIK | 39.21 | -0.5 | 613.3139 | 2 | 2 |
|  |  |  |  |  | NTmScLIPPNPDGImAEPGTK | 25.17 | 1.3 | 1138.025 | 2 | 1 |
| JAS05092.1 | Metalloproteinase type III 2 | 106.23 | 8 | 68997 | cPTDSFQR | 39.57 | -0.4 | 505.7214 | 2 | 1 |
|  |  |  |  |  | AAKDDcDLPEFcTGR | 35.41 | -1.2 | 877.8762 | 2 | 1 |
| AAM51550.1 | mocarhagin 1 | 126.47 | 7 | 68176 | VYEmVNALNTmYR | 66.34 | 0.5 | 818.3793 | 2 | 1 |
|  |  |  |  |  | DRPQcILNKPSR | 34.92 | -0.1 | 495.2647 | 3 | 1 |
| P82942.1 | Hemorrhagic metalloproteinase-disintegrin-like kaouthiagin | 175.86 | 30 | 44493 | YYNYDKPAIK | 62.98 | 0.1 | 637.8245 | 2 | 2 |
|  |  |  |  |  | cPTLTNQcIALLGPHFTVSPK | 56.47 | 0.4 | 785.405 | 3 | 1 |
|  |  |  |  |  | DYQEYLLR | 54.14 | -0.8 | 550.2741 | 2 | 1 |
|  |  |  |  |  | GcFDLNMR | 45.7 | -0.6 | 506.7203 | 2 | 1 |
|  |  |  |  |  | RTAPAFQFSScSIR | 42.78 | 0 | 543.2718 | 3 | 1 |
|  |  |  |  |  | mEDGTKIPcAAK | 39.34 | 0 | 668.8154 | 2 | 2 |
|  |  |  |  |  | QTVLLPR | 30.29 | 0.3 | 413.761 | 2 | 1 |
| ACN50006.1 | atragin precursor | 257.34 | 31 | 69181 | NGLPcQNNQGYcYNGK | 69.79 | 1.7 | 943.9006 | 2 | 1 |
|  |  |  |  |  | DPNYGmVEPGTK | 62.93 | -0.7 | 662.2975 | 2 | 11 |
| AAF00693.1 | cobrin precursor | 271.75 | 41 | 67662 | YIEFYmVVDNImYR | 72.29 | 0.4 | 944.4368 | 2 | 6 |
|  |  |  |  |  | AAKDDcDLPELcTGQSAEcPTDVFQR | 70.01 | -0.6 | 995.0998 | 3 | 1 |
|  |  |  |  |  | TSAAVVQDYSKSTR | 59.83 | 0.2 | 756.8864 | 2 | 2 |
|  |  |  |  |  | DPSYGmVEPGTK | 56.75 | -0.2 | 648.7923 | 2 | 1 |
|  |  |  |  |  | LQHEAQcDSEEccEK | 56.45 | 0.4 | 961.8696 | 2 | 3 |
|  |  |  |  |  | cPIMTNQcIALR | 54.92 | 0.1 | 738.8597 | 2 | 1 |
|  |  |  |  |  | RTKPAYQFSScSVR | 49.46 | 0.1 | 562.9509 | 3 | 2 |
|  |  |  |  |  | ATLDLFGEWREK | 48.72 | -1.2 | 732.8768 | 2 | 1 |
|  |  |  |  |  | VSRDScFTLNQR | 46.51 | -0.9 | 494.9083 | 3 | 1 |
|  |  |  |  |  | TNTPEQDRYLQAEK | 43.09 | 0.3 | 846.9133 | 2 | 1 |
|  |  |  |  |  | SNINEINVQSDVK | 41.65 | 0.7 | 730.3735 | 2 | 1 |
|  |  |  |  |  | KVYEmINTmNmIYR | 41.04 | 0 | 618.6247 | 3 | 1 |
|  |  |  |  |  | RNSmIcNcSISPR | 40.49 | -0.9 | 537.5776 | 3 | 1 |
|  |  |  |  |  | NSMIcNcSISPRD | 39.52 | -0.2 | 777.3287 | 2 | 1 |
|  |  |  |  |  | KRNDNAQLLTGIDFNGTPVGLAYIGSIcNPK | 37.38 | 0.2 | 837.4359 | 4 | 1 |
|  |  |  |  |  | GFcTcGFNK | 36.24 | 0.2 | 545.726 | 2 | 2 |
|  |  |  |  |  | DRPQcILNKPLSTD | 30.16 | -1.3 | 552.9499 | 3 | 1 |
|  |  |  |  |  | NQLVIK | 28.41 | 0.4 | 357.7292 | 2 | 1 |
| F8RKW1.1 | Zinc metalloproteinase-disintegrin-like MTP4 | 64.91 | 4 | 68240 | NGHPcQNNEGYcYNGK | 45.58 | 3.8 | 956.3821 | 2 | 1 |
| 5'-Nucleotidase | JAS05036.1 | Ecto-5'-nucleotidase 1c | 275.46 | 45 | 62983 | FHEcNLGNLIcDAVVYNNLR | 79.88 | 0.6 | 1211.076 | 2 | 2 |
|  |  |  |  |  | HGQGTGELLQVSGIK | 79.09 | 0.2 | 762.4126 | 2 | 4 |
|  |  |  |  |  | LTILHTNDVHAR | 73.5 | 0 | 695.3835 | 2 | 5 |
|  |  |  |  |  | YDAmALGNHEFDNGLNGLLDPLLK | 71.04 | 0.9 | 1323.648 | 2 | 2 |
|  |  |  |  |  | ASGNPILLNK | 59.41 | -0.5 | 513.8005 | 2 | 6 |
|  |  |  |  |  | VLLPSFLAAGGDGYYmLKGD | 55.39 | -0.5 | 1052.026 | 2 | 1 |
|  |  |  |  |  | NVKFPILSANIRPK | 51.4 | -0.6 | 532.9907 | 3 | 6 |
|  |  |  |  |  | VVSLNVLcTEcR | 49.73 | 0.2 | 725.3632 | 2 | 1 |
|  |  |  |  |  | VGIIGYTTK | 49.4 | -0.2 | 476.279 | 2 | 5 |
|  |  |  |  |  | YLGYLNVIFDDKGK | 48.05 | 0.1 | 822.9353 | 2 | 1 |
|  |  |  |  |  | ISGYILPYK | 43.35 | -0.1 | 527.3025 | 2 | 4 |
|  |  |  |  |  | ETPVLSNPGPYLEFRDEVEELQK | 41.18 | 2.3 | 1345.174 | 2 | 1 |
|  |  |  |  |  | QVPVVQAYAFGK | 41.12 | 0.5 | 653.8617 | 2 | 3 |
|  |  |  |  |  | SIQEDPAVK | 38.91 | -0.4 | 493.7611 | 2 | 2 |
|  |  |  |  |  | QAFEHSVHR | 36.44 | 0.2 | 555.7757 | 2 | 1 |
|  |  |  |  |  | GREVVHFmNSLR | 35.7 | -0.2 | 487.5856 | 3 | 1 |
|  |  |  |  |  | VFPAmEGR | 35 | 0 | 461.7262 | 2 | 2 |
|  |  |  |  |  | IINVGSEK | 31.2 | -0.2 | 430.2477 | 2 | 2 |
|  |  |  |  |  | YDLSQKPGKR | 30.12 | 1 | 596.3282 | 2 | 1 |
| Phosphodiesterase | JAI09046.1 | Phosphodiesterase | 264.9 | 34 | 96652 | AEYLETWDTLMPNINK | 74.43 | 0.7 | 969.47 | 2 | 1 |
|  |  |  |  |  | LWNYFHSTLLPK | 72.98 | 0 | 759.9088 | 2 | 4 |
|  |  |  |  |  | AATYFWPGSEVK | 71.03 | -0.4 | 678.3349 | 2 | 5 |
|  |  |  |  |  | cSSITDLEAVNQR | 67.89 | 0.3 | 746.8569 | 2 | 6 |
|  |  |  |  |  | NPFYNPSPAK | 66.23 | -0.5 | 567.7823 | 2 | 9 |
|  |  |  |  |  | YcSGGTHGYDNEFK | 66.21 | -0.2 | 817.8305 | 2 | 2 |
|  |  |  |  |  | AKRPDFSTLYIEEPDTTGHK | 61.79 | -0.3 | 1153.076 | 2 | 3 |
|  |  |  |  |  | YISAYSQDILMPLWNSYTISK | 61.53 | 0.2 | 1247.122 | 2 | 1 |
|  |  |  |  |  | TLGmLmEGLK | 58.9 | -0.3 | 562.788 | 2 | 4 |
|  |  |  |  |  | TPLNcPPGSLK | 54.41 | -0.1 | 592.3105 | 2 | 1 |
|  |  |  |  |  | IDKVNLMVDR | 53.93 | -0.4 | 601.8315 | 2 | 2 |
|  |  |  |  |  | YcLLHQTK | 52.93 | 0.1 | 531.7737 | 2 | 4 |
|  |  |  |  |  | NGLNVISGPIFDYNYDGHFD | 52.83 | 2 | 1129.016 | 2 | 1 |
|  |  |  |  |  | SKNVPKDFYTFDSEAIVK | 48.99 | -0.5 | 696.6927 | 3 | 1 |
|  |  |  |  |  | MANVLcScSEDcLTKK | 47.38 | 1.1 | 958.4238 | 2 | 2 |
|  |  |  |  |  | FSSSGPEQYDALITSNIVPmYK | 42.96 | 1.9 | 1232.093 | 2 | 1 |
|  |  |  |  |  | QPLSETLR | 39.12 | -0.2 | 472.2639 | 2 | 2 |
|  |  |  |  |  | VLSFILPHRPD | 34.34 | 0 | 647.3693 | 2 | 1 |
|  |  |  |  |  | QWLAVR | 33.92 | 0.2 | 386.7269 | 2 | 1 |
|  |  |  |  |  | GPVSGQVIK | 32.95 | -0.4 | 442.7635 | 2 | 1 |
|  |  |  |  |  | NLHNcVNLILLADHGmEAIScNR | 31.02 | 0.2 | 894.0968 | 3 | 1 |
| L-amino acid oxidase | ABN72546.1 | L-amino acid oxidase | 221.77 | 48 | 51439 | LNEFFQENENAWYYINNIR | 72.66 | 1.6 | 1239.082 | 2 | 1 |
|  |  |  |  |  | VLADDSDFFQALDTK | 72.27 | 2 | 842.9085 | 2 | 1 |
|  |  |  |  |  | HVVVVGAGmAGLSAAYVLAGAGHK | 70.3 | 0.1 | 751.0721 | 3 | 1 |
|  |  |  |  |  | TFVTADYVIVcSTSR | 63.87 | 1.6 | 859.9259 | 2 | 1 |
|  |  |  |  |  | TcADIVINDLSLIHDLPKR | 57.82 | 0.5 | 731.7284 | 3 | 2 |
|  |  |  |  |  | SDALFSYEKR | 49.64 | -0.9 | 608.3033 | 2 | 1 |
|  |  |  |  |  | EIQALcYPSIKK | 45.02 | 0 | 725.3921 | 2 | 1 |
|  |  |  |  |  | VTLLEASER | 42.47 | 2.2 | 509.2835 | 2 | 1 |
|  |  |  |  |  | RIYFEPPLPPKK | 37.91 | -0.2 | 495.6255 | 3 | 1 |
|  |  |  |  |  | STTDLPSR | 37.6 | -0.2 | 438.7246 | 2 | 1 |
|  |  |  |  |  | VTYQTPAK | 31.34 | -0.2 | 454.2477 | 2 | 1 |
|  |  |  |  |  | KVIEELKR | 29.37 | 0.1 | 338.8817 | 3 | 2 |
|  |  |  |  |  | REIQALcYPSIK | 28.93 | -0.3 | 493.2657 | 3 | 1 |
|  |  |  |  |  | IFLTcSK | 28.47 | 0.7 | 434.7338 | 2 | 1 |
|  |  |  |  |  | PSLLKYPVKPSEEGK | 27.6 | 0.2 | 557.9821 | 3 | 1 |
|  |  |  |  |  | FDEIVGGFDQLPISmYQAIAEmVHLNAR | 25.93 | 2.5 | 1066.189 | 3 | 1 |
|  |  |  |  |  | VWEVKKDPSLLK | 22.75 | -0.1 | 361.2157 | 4 | 1 |
| Three finger toxins | P85092.1 | Rho-elapitoxin-Da1a | 41.9 | 29 | 7291 | SIFGITTEDcPDGQNLcFK | 33.7 | 0.9 | 1101.497 | 2 | 1 |
| P14541.1 | Cytotoxin | 65.15 | 35 | 6994 | FPLKIPIKR | 29.9 | -0.3 | 371.2497 | 3 | 1 |
| P82464.1 | Muscarinic toxin-like protein 3 | 74.82 | 29 | 7624 | ISLADGNDVR | 60.37 | -1.3 | 530.2744 | 2 | 1 |
|  |  |  |  |  | TIcYNHLTR | 28.88 | -1.7 | 393.1969 | 3 | 1 |
| P82935.2 | Tryptophan-containing weak neurotoxin | 90.7 | 28 | 9915 | LTcLNcPEMFcGK | 67.89 | 0.4 | 815.3485 | 2 | 10 |
|  |  |  |  |  | RPLSWR | 29.59 | 0.2 | 407.7378 | 2 | 1 |
| AAB87417.1 | long neurotoxin | 100.36 | 43 | 9841 | VELGcAATcPTVK | 43.63 | -1.4 | 703.3433 | 2 | 2 |
| P34074.2 | Long neurotoxin 1 | 127.21 | 51 | 7768 | PDGHVcYTK | 28.77 | -1.7 | 538.7442 | 2 | 1 |
| P25668.1 | Long neurotoxin 1 | 135.44 | 46 | 7847 | TWcDGFcSIR | 39.91 | 0.4 | 651.2739 | 2 | 3 |
| 2CTX | Alpha-Cobratoxin | 208.42 | 97 | 7831 | TGVDIQccSTDNcNPFPTRK | 68.66 | 0.5 | 1185.518 | 2 | 2 |
|  |  |  |  |  | GKRVDLGcAATcPTVK | 54.86 | -0.8 | 866.9446 | 2 | 3 |
|  |  |  |  |  | TWcDAFcSIR | 47.28 | -0.6 | 658.2812 | 2 | 14 |
|  |  |  |  |  | cFITPDITSKDcPNGHVcYTK | 38.3 | -2.9 | 838.3776 | 3 | 3 |
|  |  |  |  |  | KTGVDIQCCSTDNcNPFPTR | 32.22 | 0.2 | 752.6664 | 3 | 1 |
| AAB18383.1 | cardiotoxin 3a | 94.18 | 28 | 9065 | mFmVATPK | 46.72 | -0.4 | 478.7324 | 2 | 1 |
| AAD08812.1 | post synaptic alpha neurotoxin | 65.45 | 45 | 9220 | LEcHNQQSSETPTTTGcSGGETNcYK | 29.38 | 2.3 | 982.7383 | 3 | 1 |
| AAD08814.1 | post synaptic alpha neurotoxin | 70.71 | 46 | 9159 | TLECHNQQSSQAPTTTGcSGGETNcYK | 28.41 | 1 | 1480.118 | 2 | 3 |
| P59275.1 | Cobrotoxin-b | 100.31 | 48 | 6944 | TcSGETNcYKK | 30.91 | -1 | 674.2863 | 2 | 1 |
|  |  |  |  |  | GTIIER | 28.82 | 0.1 | 344.7031 | 2 | 1 |
|  |  |  |  |  | VKPGVNLNCcRR | 26.14 | -6.3 | 708.3671 | 2 | 1 |
| CAA90964.1 | cardiotoxin V | 102.44 | 27 | 9323 | LKcHNTQLPFIYK | 47.64 | -0.4 | 554.6323 | 3 | 1 |
|  |  |  |  |  | KFPLKFPVK | 39.76 | -0.6 | 552.3521 | 2 | 1 |
| AAF21774.1 | neurotoxin preprotein | 163.04 | 51 | 9262 | NGIEINccTTDRcNN | 40.74 | 2 | 920.8741 | 2 | 1 |
|  |  |  |  |  | LEcHNQQSSQTPTTTGcSGGETNcYKK | 30.39 | -1.1 | 769.0807 | 4 | 1 |
| AAD40974.1 | long neurotoxin | 57.88 | 10 | 11269 | TWcDGFcGIR | 48.53 | -0.7 | 636.268 | 2 | 13 |
|  |  |  |  |  |  |  |  |  |  |  |
| P29181.1 | Weak neurotoxin 7 | 65.95 | 32 | 7637 | FQIcRDGEK | 26.26 | -0.2 | 576.7768 | 2 | 1 |
| P01464.1 | Cytotoxin 5 | 70.07 | 35 | 6856 | MYMVATPMIPVKR | 25.69 | -0.6 | 512.9412 | 3 | 1 |
| P82463.1 | Muscarinic toxin-like protein 2 | 98.98 | 34 | 7298 | WHmIVPGR | 43.76 | -1.2 | 506.2627 | 2 | 2 |
|  |  |  |  |  | TRGcAATcPIAENR | 35.23 | -0.6 | 526.2485 | 3 | 1 |
| P82462.1 | Muscarinic toxin-like protein 1 | 101.45 | 63 | 7366 | FLFSETTETcPDGQNVcFNQAHLIYPGK | 55.83 | 2.7 | 1091.841 | 3 | 2 |
|  |  |  |  |  | DVIFccSTDKcNL | 41.83 | -0.1 | 816.3467 | 2 | 1 |
| P01400.1 | Weak toxin S4C11 | 111.31 | 48 | 7430 | FYEGNLLGKR | 58.83 | 0.3 | 598.8249 | 2 | 1 |
|  |  |  |  |  | LTcLIcPEK | 46.97 | 0.4 | 567.2885 | 2 | 1 |
|  |  |  |  |  | GcAATcPEAKPR | 45.87 | -4.1 | 659.3029 | 2 | 1 |
| P59276.1 | Cobrotoxin-c | 134.13 | 52 | 6859 | LEcHNQQSSQAPTTK | 75.32 | 0.6 | 864.9026 | 2 | 5 |
|  |  |  |  |  | WWSDHR | 36.34 | -0.2 | 443.7013 | 2 | 1 |
| P01446.1 | Cytotoxin 3 | 141.78 | 80 | 6717 | LIPLAYKTcPAGK | 56.59 | 1.1 | 716.4058 | 2 | 1 |
|  |  |  |  |  | RGCIDACPKNSLLVK | 35.14 | -6.1 | 808.9293 | 2 | 2 |
|  |  |  |  |  | LKcNKLIPLAYK | 31.78 | -1.1 | 487.6262 | 3 | 1 |
| BAU24665.1 | cytotoxin 9 | 154.41 | 83 | 8041 | SSLLVKYVccNTDRcN | 52.75 | 1.8 | 994.9547 | 2 | 2 |
|  |  |  |  |  | TcPAGKNLcYK | 50.49 | -1.3 | 656.312 | 2 | 1 |
|  |  |  |  |  | LKcNKLVPLFYK | 44.11 | 0.5 | 761.9448 | 2 | 2 |
|  |  |  |  |  | mYmVATPKVPVKR | 26.42 | -0.6 | 517.9507 | 3 | 1 |
| BAU24666.1 | cytotoxin 11 | 188.41 | 83 | 7959 | LVPIASKTcPPGK | 53.42 | 0 | 684.3893 | 2 | 1 |
|  |  |  |  |  | LQcNKLVPIASK | 50.87 | -1.4 | 685.8939 | 2 | 3 |
|  |  |  |  |  | NSLLVKYVccNTDRcN | 49.31 | 0.6 | 1008.459 | 2 | 2 |
|  |  |  |  |  | TcPPGKNLcYK | 43.53 | 0.1 | 669.3207 | 2 | 2 |
|  |  |  |  |  | RGcIDVcPK | 27.16 | 0.6 | 552.7684 | 2 | 1 |
|  |  |  |  |  | mFmVSDLTIPVKRG | 25.99 | 1.3 | 813.4241 | 2 | 1 |
| Cobra venom factor | AAA68989.1 | cobra venom factor | 327.24 | 30 | 184517 | DDNEDGFIADSDIISR | 85.16 | 0.3 | 891.3951 | 2 | 4 |
|  |  |  |  |  | IIIQGDPVAQIIENSIDGSK | 83.05 | -0.3 | 1055.573 | 2 | 1 |
|  |  |  |  |  | DLTEEPNSQGISSK | 81.77 | 0.6 | 752.8604 | 2 | 8 |
|  |  |  |  |  | AVPFVIVPLEQGLHDVEIK | 74.22 | 0.7 | 1052.097 | 2 | 8 |
|  |  |  |  |  | VELLYNPAFcSASTK | 70.99 | 0.1 | 850.4217 | 2 | 2 |
|  |  |  |  |  | IEEQDGNDIYVmDVLEVIK | 66.14 | 1.9 | 1119.548 | 2 | 1 |
|  |  |  |  |  | KLDDRVPDTEIETK | 65.69 | 0.8 | 829.934 | 2 | 5 |
|  |  |  |  |  | HFEVGFIQPGSVK | 61.84 | 0.9 | 722.8834 | 2 | 1 |
|  |  |  |  |  | AKGVGGTQLEVIK | 61.7 | -0.3 | 650.3849 | 2 | 2 |
|  |  |  |  |  | VNDDYLIWGSR | 61.04 | 0.1 | 669.3279 | 2 | 1 |
|  |  |  |  |  | GDNLIQmPGAAmK | 60.58 | -0.3 | 689.3285 | 2 | 1 |
|  |  |  |  |  | ASVQEALWSDGVRK | 58.88 | 0.6 | 773.4051 | 2 | 2 |
|  |  |  |  |  | GIcVAEPYEIR | 55.33 | 0.1 | 653.8267 | 2 | 1 |
|  |  |  |  |  | AcETNVDYVYK | 54.73 | 1 | 681.3064 | 2 | 1 |
|  |  |  |  |  | LNQDITVTASGDGK | 51.62 | 0.9 | 709.8604 | 2 | 1 |
|  |  |  |  |  | ALYTLITPAVLR | 48.66 | 0.3 | 665.9084 | 2 | 1 |
|  |  |  |  |  | VAVIIYLNK | 47.68 | 0.1 | 516.8263 | 2 | 1 |
|  |  |  |  |  | VDmNPAGGmLVTPTIEIPAKEVSTDSR | 46.86 | 0.8 | 954.1412 | 3 | 1 |
|  |  |  |  |  | cAGETcSSLNHQER | 46.39 | 1.1 | 824.8447 | 2 | 2 |
|  |  |  |  |  | VYSYYNLDEK | 46.1 | 0.4 | 647.3037 | 2 | 1 |
|  |  |  |  |  | LKVVPEGVQK | 45.55 | 0.3 | 366.2291 | 3 | 3 |
|  |  |  |  |  | FYHPDKGTGLLNK | 42.06 | 0.6 | 745.394 | 2 | 1 |
|  |  |  |  |  | VFFIDLQmPYSVVKNEQVEIR | 41.84 | 3.5 | 857.4519 | 3 | 1 |
|  |  |  |  |  | IDVPLQIEK | 41.41 | -0.5 | 527.8105 | 2 | 1 |
|  |  |  |  |  | KYVLPSFEVR | 40.76 | -0.2 | 619.3505 | 2 | 1 |
|  |  |  |  |  | TmSFYLR | 38.22 | -0.5 | 467.2283 | 2 | 5 |
|  |  |  |  |  | YRQQFPIK | 34.4 | -0.6 | 540.3031 | 2 | 4 |
|  |  |  |  |  | SIVTIVKLD | 34.34 | -0.1 | 494.3078 | 2 | 2 |
|  |  |  |  |  | SDLLPTKDK | 32.79 | 0.3 | 508.7849 | 2 | 2 |
|  |  |  |  |  | YLGEVDSTmTIIDISmLTGFLPDAEDLTR | 32.11 | 0.9 | 1083.525 | 3 | 1 |
|  |  |  |  |  | IcIGNVcR | 30.67 | -0.9 | 496.2437 | 2 | 1 |
|  |  |  |  |  | YRINYENALLAR | 25.97 | 4.6 | 748.4078 | 2 | 1 |
|  |  |  |  |  | SWLWLTK | 24.91 | 0.2 | 467.2633 | 2 | 1 |
| Cysteine-rich seceretory protein | ACE73578.1 | cysteine-rich seceretory protein Bc-CRPa | 167.71 | 23 | 26443 | cTFAHSPPHLR | 49.69 | -0.1 | 441.5522 | 3 | 1 |
|  |  |  |  |  |  |  |  |  |  |  |
| ACH73168.1 | kaouthin-2 precursor | 222.45 | 47 | 26216 | NmLQmEWNSNAAQNAK | 99.66 | 0.6 | 941.4152 | 2 | 4 |
|  |  |  |  |  | YLYVcQYcPAGNIIGSIATPYK | 94.23 | 0.5 | 1276.122 | 2 | 1 |
|  |  |  |  |  | IGcGENLFmSSQPYAWSR | 73.79 | 1.5 | 1059.974 | 2 | 1 |
|  |  |  |  |  | VIQSWYDENKK | 58.56 | -1.1 | 705.3558 | 2 | 2 |
|  |  |  |  |  | HHNVFSNcQSLAK | 53.82 | 0.5 | 514.581 | 3 | 4 |
|  |  |  |  |  | QNAcQTEWmK | 45.42 | 1.8 | 656.2776 | 2 | 1 |
|  |  |  |  |  | QIVDKHNALR | 43.27 | 0.2 | 597.3412 | 2 | 3 |
|  |  |  |  |  | cSFAHSPPHLR | 41.27 | -0.7 | 654.8165 | 2 | 4 |
|  |  |  |  |  |  |  |  |  |  |  |
| AAP85301.1 | natrin | 300.93 | 63 | 26882 | VLEGIQcGESIYmSSNAR | 108.51 | 0.7 | 1015.47 | 2 | 9 |
|  |  |  |  |  | SYFYVcQYcPSGNFQGK | 70.39 | 2.3 | 1052.951 | 2 | 2 |
|  |  |  |  |  | WANTcSLNHSPDNLR | 63.39 | 0.7 | 892.9109 | 2 | 6 |
|  |  |  |  |  | QSScQDDWIK | 60.02 | -0.2 | 633.7745 | 2 | 5 |
|  |  |  |  |  | LTNcDSLLK | 58.16 | 0.1 | 532.2763 | 2 | 10 |
|  |  |  |  |  | SNcPAScFcR | 55.96 | 0 | 629.7417 | 2 | 5 |
|  |  |  |  |  | GNVDFNSESTR | 50.03 | -0.5 | 613.2755 | 2 | 1 |
|  |  |  |  |  | NFVYGVGANPPGSVTGH | 45.54 | 0 | 836.9075 | 2 | 1 |
|  |  |  |  |  | RVSPTASNmLKmEWYPEAASNAER | 41.51 | 0.1 | 924.1023 | 3 | 2 |
|  |  |  |  |  | NVDFNSESTRR | 38.03 | 0.4 | 662.8159 | 2 | 4 |
|  |  |  |  |  | KQKEIVDLHNSLR | 32.18 | -0.8 | 527.3016 | 3 | 2 |
|  |  |  |  |  | TATPYK | 26.9 | 0.2 | 340.6844 | 2 | 1 |
| Nerve growth factor | AAS94269.1 | nerve growth factor II | 179.99 | 37 | 27030 | IDTAcVcVITK | 39.75 | 0.6 | 640.3232 | 2 | 1 |
|  |  |  |  |  |  |  |  |  |  |  |
| A59218 | nerve growth factor beta chain | 182.93 | 37 | 27648 | GIDSSHWNSYcTETDTFIK | 75.1 | 4.3 | 1130.999 | 2 | 1 |
|  |  |  |  |  | IETAcVcVITK | 59.63 | 0.6 | 647.3311 | 2 | 1 |
|  |  |  |  |  | ALTmEGNQASWR | 58.97 | -1.3 | 690.3214 | 2 | 1 |
|  |  |  |  |  | TTATDIKGNTVTVmENVNLDNKVYK | 56.24 | 0.6 | 928.8082 | 3 | 1 |
|  |  |  |  |  | EDHPVHNLGEHSVcDSVSAWVTK | 47.32 | 0.3 | 868.4032 | 3 | 2 |
| Acetylcholinesterase | JAS05178.1 | Acetylcholinesterase | 47.76 | 2 | 59175 | SITEAEEALSR | 47.76 | 0.6 | 603.3044 | 2 | 1 |
| Cholinesterase | ETE70564.1 | Cholinesterase | 47.76 | 1 | 153465 | SITEAEEALSR | 47.76 | 0.6 | 603.3044 | 2 | 1 |
| Ohanin like protein | P82885.1 | Thaicobrin | 162.24 | 68 | 12038 | ADVTFDSNTAFESLVVSPDKK | 74.36 | 0.3 | 1135.563 | 2 | 8 |
|  |  |  |  |  |  | TVENVGVSQVAPDNPERFDGSPCVLGSPGFRS | 34.21 | -8.1 | 1106.524 | 3 | 1 |
|  |  |  |  |  |  | HFFEVK | 32.97 | 0.3 | 403.7135 | 2 | 3 |
|  |  |  |  |  |  | YGTQREWAVGLAGK | 32.69 | 1.7 | 512.6046 | 3 | 1 |
| Phospholipase B | ETE59578.1 | Phospholipase B-like 1 | 45.03 | 3 | 58279 | QNSGTYNNQYmILDTK | 45.03 | 3.1 | 953.439 | 2 | 1 |
| Cystatin | ACR83850.1 | cystatin precursor | 45.39 | 9 | 15772 | AAAFAVQEYNAR | 45.39 | -0.3 | 655.8278 | 2 | 1 |

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**Supplementary table S1b:** List of orthologous proteins of *Naja kaouthia* venom toxins identified by tandem mass spectroscopy analysis of SDS-PAGE bands against Elapidae database. The table shows the identified peptide ions, their mass, charge (z), score for the ID, ΔM (ppm), modified residues. Posttranslational modifications carbamidomethylation of cysteine and oxidation of methionine residues are represented in lower cases viz. ‘c’ and ‘m’ respectively.

|  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Protein family** | **Accession** | **Description** | **-10lgP** | **Coverage (%)** | **Avg. Mass (Da)** | **Peptide** | **-10lgP** | **ppm** | **m/z** | **z** | **#Spec** |
| Phospholipase A2 | P25498.1 | Acidic phospholipase A2 | 108.86 | 39 | 13229 | LAAIcFAGAPYNNDNYNINLK | 53.81 | 0.4 | 1178.574 | 2 | 1 |
| AED89576.1 | Putative phospholipase A2 precursor | 43.33 | 9 | 15957 | SGGGGTPVDDLDR | 43.33 | -0.7 | 623.2885 | 2 | 1 |
| Q7LZI1.1 | Phospholipase A2 inhibitor | 100.26 | 19 | 20452 | LGSFDVNVGQNTYVR | 63.41 | 0.9 | 834.9214 | 2 | 1 |
|  |  |  |  |  | EmYPGDIAYNIK | 50.6 | 0.7 | 715.3375 | 2 | 1 |
|  |  |  |  |  | cINIAGYRK | 34.63 | 1.9 | 547.7934 | 2 | 1 |
| AAF82186.1 | Acidic phospholipase A2 | 172.11 | 62 | 16097 | KGGNDACAAAVcDCDRLAAIcFAGAPYNDNNYNIDLK | 24.63 | -9.3 | 1321.91 | 3 | 1 |
| AAA66027.1 | Phospholipase A2 | 167.72 | 53 | 16189 | ccQIHDNcYNEAEKISR | 54.14 | 0 | 732.9788 | 3 | 1 |
| BAA36403.1 | Phospholipase A2 | 199.68 | 73 | 16271 | ccQVHDNcYNEAEKISR | 70.17 | -0.1 | 728.3068 | 3 | 2 |
|  |  |  |  |  | GGSGTPVDDLDRccQVHDNcYNEAEK | 54.22 | -1.9 | 1498.611 | 2 | 3 |
|  |  |  |  |  | TYSYEcSQGTLTcKGDND | 49.46 | 1 | 1049.921 | 2 | 1 |
|  |  |  |  |  | SWWDFADYGcYcGR | 49.32 | 2.2 | 921.8557 | 2 | 6 |
|  |  |  |  |  | GDNDACAAAVcDcDRLAAIcFAGAPYNNNNYNIDLK | 33.02 | 1.8 | 1317.241 | 3 | 1 |
|  |  |  |  |  | LAAIcFAGAPYNNNNYNIDLKAR | 24.54 | 0.7 | 861.7646 | 3 | 1 |
| PSNJ2K | Phospholipase A2 | 160.81 | 77 | 13455 | ccQVHDNcYDEAEKISR | 54.46 | 1.7 | 728.6362 | 3 | 2 |
| P60044.1 | Acidic phospholipase A2 | 144.34 | 60 | 14073 | GRNNAcAASVCDcDRLAAIcFAGAPYNDNNYNIDLQ | 25.51 | 1.4 | 1336.251 | 3 | 1 |
| 1MH2 | Chain B, Crystal Structure Of A Zinc Containing Dimer Of Phospholipase A2 | 65.54 | 25 | 13127 | TYSYAcTAGTLTcTGR | 20.21 | -7.1 | 891.8865 | 2 | 1 |
| Snake venom metalloprotease | ADF43026.1 | Metalloproteinase atrase A | 172.3 | 24 | 68254 | AAKDDcDLPEFcTGQSAEcPTDSLQR | 59.16 | 0.3 | 991.0886 | 3 | 1 |
|  |  |  |  |  | cGTLYcTEIKK | 49.92 | 0.3 | 686.8338 | 2 | 2 |
|  |  |  |  |  | TRVYEmVNYLNTK | 43.49 | -0.5 | 823.9136 | 2 | 2 |
|  |  |  |  |  | EHQEYLLR | 41.58 | -0.2 | 544.28 | 2 | 3 |
|  |  |  |  |  | GSVAVVQDYSRR | 38.34 | 0.2 | 668.8521 | 2 | 1 |
|  |  |  |  |  | LQPHAQcDSEEccEK | 36.17 | 0.4 | 945.8748 | 2 | 1 |
|  |  |  |  |  | TNTPEQDRYLQVK | 34.35 | -0.4 | 796.407 | 2 | 1 |
|  |  |  |  |  | TGcIVPVSPRD | 29.68 | 0.2 | 600.8058 | 2 | 1 |
|  |  |  |  |  | SFAEWR | 27.58 | 0.4 | 398.193 | 2 | 1 |
|  |  |  |  |  | ERPQcILNKPSRK | 27.24 | 0.4 | 542.6352 | 3 | 1 |
| JAS05092.1 | Metalloproteinase type III 2 | 114.42 | 10 | 68997 | AAKDDcDLPEFcTGR | 41.68 | 0.2 | 877.8774 | 2 | 1 |
| P82942.1 | Hemorrhagic metalloproteinase-disintegrin-like kaouthiagin; | 188.86 | 42 | 44493 | YYNYDKPAIK | 62.44 | -0.2 | 637.8243 | 2 | 2 |
|  |  |  |  |  | VYEmINAVNTK | 59.18 | 0.2 | 649.3266 | 2 | 1 |
|  |  |  |  |  | HDcDLPELcTGQSAEcPTDSLQR | 56.44 | 2.3 | 897.0497 | 3 | 1 |
|  |  |  |  |  | DYQEYLLR | 48.72 | -0.2 | 550.2744 | 2 | 1 |
|  |  |  |  |  | NGHPcQNNQGYcYNGK | 41.2 | 0.4 | 637.5937 | 3 | 1 |
|  |  |  |  |  | NTmScLIPPNPDGImAEPGTK | 36.07 | -1.2 | 1138.022 | 2 | 2 |
|  |  |  |  |  | GcFDLNmRGDDGSFcR | 35.4 | -0.1 | 641.5907 | 3 | 1 |
|  |  |  |  |  | QTVLLPR | 28.74 | 1 | 413.7613 | 2 | 1 |
| AAF00693.1 | Cobrin precursor | 281.77 | 42 | 67662 | AAKDDcDLPELcTGQSAEcPTDVFQR | 81.72 | 0.7 | 995.1011 | 3 | 2 |
|  |  |  |  |  | YIEFYmVVDNImYR | 80.39 | 1.3 | 944.4377 | 2 | 2 |
|  |  |  |  |  | NDNAQLLTGIDFNGTPVGLAYIGSIcNPK | 77.37 | 0.2 | 1021.513 | 3 | 2 |
|  |  |  |  |  | TSAAVVQDYSKSTR | 65.27 | 0.4 | 756.8865 | 2 | 2 |
|  |  |  |  |  | SNINEINVQSDVK | 58.94 | 0.3 | 730.3732 | 2 | 1 |
|  |  |  |  |  | DPSYGmVEPGTK | 57.84 | 0.4 | 648.7927 | 2 | 1 |
|  |  |  |  |  | cPImTNQcIALR | 57.15 | 0.3 | 746.8573 | 2 | 6 |
|  |  |  |  |  | TNTPEQDRYLQAEK | 56.11 | -0.1 | 846.9129 | 2 | 2 |
|  |  |  |  |  | KVYEmINTmNmIYR | 50.19 | -0.1 | 618.6246 | 3 | 2 |
|  |  |  |  |  | GFcTcGFNK | 46.91 | 0 | 545.7258 | 2 | 2 |
|  |  |  |  |  | ATLDLFGEWREK | 40.29 | 0.3 | 732.8779 | 2 | 1 |
|  |  |  |  |  | RNSmIcNcSISPR | 40.16 | -0.6 | 537.5777 | 3 | 2 |
|  |  |  |  |  | NQLVIKR | 18.54 | -0.1 | 435.7796 | 2 | 1 |
| ABQ01137.1 | Microlepidotease-1 | 97.4 | 8 | 68710 | AAKDDcDLPEIcTGQSAE | 33.56 | 1 | 990.4207 | 2 | 1 |
| JAB52758.1 | Snake venom metalloproteinase 1 | 93.15 | 11 | 69037 | AAKDDcDLPELcTGR | 38.82 | 0.2 | 574.2593 | 3 | 1 |
| Three finger toxins | JAB52868.1 | Three-finger toxin 12 | 39.6 | 9 | 9596 | WHmLVPGR | 39.6 | 0 | 506.2633 | 2 | 1 |
| P59275.1 | Cobrotoxin-b | 70.39 | 43 | 6944 | LEcHNQQSSQTPTTK | 39.78 | 2.1 | 879.9092 | 2 | 1 |
| JK0222 | Cytotoxin 10 | 80.61 | 27 | 6747 | mFmVATPK | 39.14 | -0.9 | 478.7322 | 2 | 1 |
| AAD40974.1 | Long neurotoxin precursor | 53.87 | 14 | 11269 | RVDLGCAATCPTPK | 28.34 | 0.6 | 716.3582 | 2 | 1 |
| AAC27685.1 | Cardiotoxin-2a | 138.74 | 67 | 9054 | LKcNKLVPLFYK | 42.73 | -0.3 | 508.2985 | 3 | 3 |
|  |  |  |  |  | SSLLVK | 31.71 | -0.1 | 323.7103 | 2 | 1 |
|  |  |  |  |  | VPVKRGcIDVcPK | 30.6 | 0.1 | 509.9427 | 3 | 1 |
|  |  |  |  |  | NLcYKmYmVATPK | 28.51 | 0.6 | 825.8885 | 2 | 1 |
| P01446.1 | Cytotoxin 3; | 132.38 | 100 | 6717 | LIPLAYKTcPAGK | 55.99 | 1.2 | 716.4059 | 2 | 1 |
|  |  |  |  |  | mFmVSNK | 35.21 | -0.2 | 444.7012 | 2 | 1 |
|  |  |  |  |  | LKcNKLIPLAYK | 33.15 | -0.1 | 487.6267 | 3 | 1 |
|  |  |  |  |  | RGCIDACPKNSLLVK | 26.11 | -6.7 | 808.9288 | 2 | 1 |
|  |  |  |  |  | TVPVKR | 20.45 | 0.5 | 350.2294 | 2 | 1 |
| P01451.1 | Cytotoxin 1 | 104.22 | 80 | 6821 | mFMMSDLTIPVKR | 25.43 | 9 | 528.9412 | 3 | 1 |
| AAY63884.1 | Neurotoxin | 163.54 | 57 | 9262 | NGIEINccTTDRcNN | 62.38 | 1.1 | 920.8732 | 2 | 1 |
|  |  |  |  |  | LEcHNQQSSQTPTTTGCSGGETNCYKK | 23.21 | 1.6 | 740.572 | 4 | 1 |
| P59276.1 | Cobrotoxin-c | 118.48 | 70 | 6859 | LEcHNQQSSQAPTTK | 63.93 | 0.3 | 864.9023 | 2 | 4 |
|  |  |  |  |  | TcSGETNcYKK | 32.37 | 0 | 674.287 | 2 | 1 |
|  |  |  |  |  | GTIIER | 27.36 | 0 | 344.703 | 2 | 1 |
| P01400.1 | Weak toxin S4C11 | 109 | 48 | 7430 | FYEGNLLGKR | 57.36 | -0.4 | 598.8245 | 2 | 3 |
| P82463.1 | Muscarinic toxin-like protein 2 | 92.45 | 62 | 7298 | GcAATcPIAENR | 48.52 | 1.6 | 660.2962 | 2 | 1 |
|  |  |  |  |  | WHmIVPGR | 48.06 | -0.3 | 506.2631 | 2 | 1 |
|  |  |  |  |  | SIFGVTTEDcPDGQNLcFKR | 22.74 | 2.1 | 1172.541 | 2 | 1 |
| Q9YGJ5.1 | Alpha-neurotoxin NTX-2 | 40.86 | 39 | 9189 | WRDHR | 24.28 | 1.1 | 385.1967 | 2 | 1 |
|  |  |  |  |  | TLECHNQQSSQAPTTTGcSGGETNcYK | 22.14 | 1.1 | 987.081 | 3 | 1 |
| P14541.1 | Cytotoxin homolog; | 89.54 | 21 | 6994 | LKcHNTQLPFIYK | 48.05 | -0.3 | 554.6324 | 3 | 1 |
| P29181.1 | Weak neurotoxin 7 | 80.75 | 38 | 7637 | GcAATcPEAKPR | 49.31 | -3.2 | 659.3035 | 2 | 1 |
|  |  |  |  |  | FQIcRDGEKIcFK | 23.86 | 1.3 | 567.6138 | 3 | 1 |
| P29180.1 | Weak neurotoxin 6 | 60.37 | 34 | 7568 |  |  |  |  |  |  |
|  |  |  |  |  | LTcLIcPEK | 45.67 | 0.5 | 567.2886 | 2 | 1 |
|  |  |  |  |  | EIVQccSTDKcNH | 29.39 | 0.4 | 825.8375 | 2 | 1 |
| P25668.1 | Long neurotoxin 1 | 147.43 | 46 | 7847 | cFITPDITSKDcPNGHVcYTK | 63.79 | 1.1 | 1257.068 | 2 | 6 |
|  |  |  |  |  | TWcDGFcSIR | 46.07 | -0.6 | 651.2733 | 2 | 4 |
| BAU24666.1 | cytotoxin 11, partial | 192.89 | 83 | 7959 | LQcNKLVPIASK | 49.79 | 1.4 | 685.8958 | 2 | 2 |
|  |  |  |  |  | NLcYKmFmVSDLTIPVKR | 43.1 | -0.3 | 749.7158 | 3 | 1 |
|  |  |  |  |  | PIASKTcPPGK | 36.33 | -1.3 | 578.3124 | 2 | 1 |
| P01391.1 | Alpha-cobratoxin | 232.86 | 97 | 7831 | TGVDIQccSTDNcNPFPTR | 79.84 | 1.2 | 1121.471 | 2 | 16 |
|  |  |  |  |  | TWcDAFcSIR | 46.81 | 0.4 | 658.2818 | 2 | 14 |
| P34074.2 | Long neurotoxin 1 | 151.75 | 51 | 7768 | GKRVDLGcAATcPTVK | 67.13 | 0.9 | 866.946 | 2 | 2 |
|  |  |  |  |  | PDGHVcYTK | 34.88 | -2.6 | 538.7437 | 2 | 1 |
| 765048A | Toxin CM2e | 105.1 | 50 | 6669 | GcIDVcPKD | 26.75 | 0.2 | 532.2311 | 2 | 1 |
| O42257.1 | Long neurotoxin 7 | 134.4 | 44 | 9841 | RVELGcAATcPTVK | 41.33 | -0.4 | 781.3946 | 2 | 1 |
| P82462.1 | Muscarinic toxin-like protein 1 | 116.05 | 69 | 7366 | FLFSETTETcPDGQNVcFNQAHLIYPGK | 64.29 | 1.1 | 1091.839 | 3 | 1 |
|  |  |  |  |  | LQNRDVIFccSTDKcNL | 42.37 | 5.9 | 1071.996 | 2 | 1 |
| P82464.1 | Muscarinic toxin-like protein 3; | 117.01 | 55 | 7624 | ISLADGNDVR | 68.11 | -0.4 | 530.2749 | 2 | 1 |
|  |  |  |  |  | TSETTEIcPDSWYFcYK | 61.83 | 3.6 | 1093.96 | 2 | 1 |
|  |  |  |  |  | TIcYNHLTR | 53.93 | -0.7 | 589.2923 | 2 | 2 |
| P01427.1 | Short neurotoxin 1 | 52.28 | 18 | 6885 | VKPGVNLNccR | 52.28 | -0.9 | 658.8311 | 2 | 4 |
| P82935.2 | Tryptophan-containing weak neurotoxin | 101.2 | 28 | 9915 | LTcLNcPEMFcGK | 75.13 | 0.4 | 815.3485 | 2 | 1 |
| P58370.1 | Alpha-neurotoxin homolog 8 | 37.24 | 15 | 9591 | IDRGcAATcPTVK | 37.24 | -9 | 724.8463 | 2 | 1 |
| Cobra venom factor | I51018 | Cobra venom factor | 352.59 | 33 | 184517 | DLTEEPNSQGISSK | 88.35 | 0.8 | 752.8605 | 2 | 7 |
|  |  |  |  |  | AVPFVIVPLEQGLHDVEIK | 86.29 | 1.3 | 1052.097 | 2 | 8 |
|  |  |  |  |  | ATmTILTFYNAQLQEK | 82.3 | 2.4 | 944.4819 | 2 | 2 |
|  |  |  |  |  | IEEQDGNDIYVmDVLEVIK | 79.93 | 0.7 | 1119.547 | 2 | 1 |
|  |  |  |  |  | VELLYNPAFcSASTK | 76.89 | 0.5 | 850.422 | 2 | 2 |
|  |  |  |  |  | AILHNYVNEDIYVR | 76.5 | 0.6 | 859.9472 | 2 | 4 |
|  |  |  |  |  | KLDDRVPDTEIETK | 76.44 | 0.1 | 829.9335 | 2 | 8 |
|  |  |  |  |  | IIIQGDPVAQIIENSIDGSK | 74.94 | -1.9 | 1055.571 | 2 | 1 |
|  |  |  |  |  | LNQDITVTASGDGK | 73.75 | 1.2 | 709.8605 | 2 | 1 |
|  |  |  |  |  | AcETNVDYVYK | 68.38 | 0.8 | 681.3063 | 2 | 1 |
|  |  |  |  |  | TDTEEQILVEAHGDSTPK | 67.78 | 1.8 | 985.4729 | 2 | 1 |
|  |  |  |  |  | YRINYENALLAR | 67.72 | 1 | 748.4052 | 2 | 2 |
|  |  |  |  |  | AKGVGGTQLEVIK | 60.59 | 0.1 | 650.3852 | 2 | 3 |
|  |  |  |  |  | VYSYYNLDEK | 59.69 | -0.1 | 647.3034 | 2 | 1 |
|  |  |  |  |  | KYVLPSFEVR | 56.47 | -0.3 | 619.3504 | 2 | 2 |
|  |  |  |  |  | cAGETcSSLNHQER | 55.68 | 0.8 | 824.8444 | 2 | 2 |
|  |  |  |  |  | GIcVAEPYEIR | 49.4 | 0.4 | 653.8269 | 2 | 3 |
|  |  |  |  |  | YRQQFPIK | 43.18 | 0 | 540.3034 | 2 | 9 |
|  |  |  |  |  | IDVPLQIEK | 41.11 | -0.4 | 527.8105 | 2 | 1 |
|  |  |  |  |  | LKVVPEGVQK | 39.82 | -0.1 | 548.8398 | 2 | 4 |
|  |  |  |  |  | VmKVFFIDLQmPYSVVK | 39.42 | 0.2 | 692.7019 | 3 | 1 |
|  |  |  |  |  | SIVTIVKLD | 39.28 | -1.1 | 494.3073 | 2 | 2 |
|  |  |  |  |  | FYHPDKGTGLLNK | 38.69 | 1.2 | 745.3944 | 2 | 2 |
|  |  |  |  |  | TmSFYLR | 38.68 | -0.7 | 467.2282 | 2 | 2 |
|  |  |  |  |  | ARDDNEDGFIADSDIISR | 35.54 | -1.2 | 670.3109 | 3 | 1 |
|  |  |  |  |  | SDLLPTKDKISYIITK | 34.93 | -0.2 | 612.3555 | 3 | 1 |
|  |  |  |  |  | VVPEGVQKSIVTIVK | 29.99 | -0.3 | 798.4899 | 2 | 1 |
|  |  |  |  |  | SWLWLTK | 27.3 | 0.4 | 467.2634 | 2 | 1 |
| Nerve growth factor | A59218 | Nerve growth factor beta chain precursor | 167.99 | 27648 | 30 | TTATDIKGNTVTVMENVNLDNKVYK | 66.78 | 0.3 | 923.4763 | 3 | 1 |
|  |  |  |  |  | ALTMEGNQASWR | 64.39 | -0.3 | 682.3246 | 2 | 1 |
|  |  |  |  |  | GIDSSHWNSYcTETDTFIK | 64.34 | 1.8 | 1130.997 | 2 | 1 |
|  |  |  |  |  | IETAcVcVITK | 63.05 | 0.1 | 647.3307 | 2 | 1 |
|  |  |  |  |  | QYFFETK | 36.96 | 0.3 | 481.7346 | 2 | 2 |
| Cysteine-rich seceretory protein | AAP85301.1 | natrin | 283.18 | 60 | 26882 | QSScQDDWIK | 57.99 | 0.1 | 633.7747 | 2 | 6 |
|  |  |  |  |  | RVSPTASNmLKmEWYPEAASNAER | 57 | 0 | 924.1022 | 3 | 2 |
|  |  |  |  |  | KQKEIVDLHNSLR | 52.98 | -0.4 | 790.449 | 2 | 3 |
|  |  |  |  |  | NGLcTNPcTIYNK | 52.35 | 1.6 | 777.8569 | 2 | 1 |
|  |  |  |  |  | NVDFNSESTRR | 38.64 | 0.2 | 662.8157 | 2 | 6 |
|  |  |  |  |  | SNcPAScFcRNK | 37.21 | 0.7 | 750.8112 | 2 | 1 |
| AAP81292.1 | Opharin precursor | 188.02 | 24 | 26895 | QSScQDEWIK | 32.92 | -0.5 | 640.7821 | 2 | 1 |
|  |  |  |  |  | VSPTASNmLKmQ | 25.53 | -0.4 | 669.823 | 2 | 1 |
| ACH73168.1 | Kaouthin-2 precursor | 205.55 | 51 | 26216 | HHNVFSNcQSLAK | 55.53 | -0.5 | 514.5805 | 3 | 3 |
|  |  |  |  |  | VDFASESSNKR | 39.84 | 0 | 620.3018 | 2 | 2 |
| P84807.1 | Cysteine-rich venom protein 25-A | 89.79 | 38 | 3430 | DVDFNSESTRR | 44.62 | -1.1 | 663.3069 | 2 | 1 |
| Q8JI38.1 | Cysteine-rich venom protein latisemin | 109.33 | 15 | 26416 | ENQKEIVDKHNALR | 23.51 | 0.1 | 565.3042 | 3 | 1 |
| Phosphodiesterase | JAI09691.1 | Ectonucleotide pyrophosphatase/phosphodiesterase family member 3 | 249.93 | 31 | 97025 | cSSITDLEAVNQR | 77.9 | 0.1 | 746.8568 | 2 | 3 |
|  |  |  |  |  | AEYLETWDTLmPNINK | 68.53 | 1.2 | 977.468 | 2 | 1 |
|  |  |  |  |  | YISAYSQDILmPLWNSYTISK | 66.93 | 0.4 | 1255.12 | 2 | 2 |
|  |  |  |  |  | NGLNVISGPIFDYNYDGHFD | 64.28 | 0.9 | 1129.014 | 2 | 1 |
|  |  |  |  |  | LWNYFHSTLLPK | 62.21 | 0.4 | 759.9091 | 2 | 3 |
|  |  |  |  |  | NPFYNPSPAK | 62.02 | -0.1 | 567.7825 | 2 | 4 |
|  |  |  |  |  | AATYFWPGSEVK | 61.08 | 1.2 | 678.3359 | 2 | 2 |
|  |  |  |  |  | TLGmLmEGLK | 60.58 | -0.5 | 562.7879 | 2 | 3 |
|  |  |  |  |  | YcLLHQTK | 54.42 | -0.4 | 531.7735 | 2 | 3 |
|  |  |  |  |  | AKRPDFSTLYIEEPDTTGHK | 49.69 | 1 | 1153.078 | 2 | 3 |
|  |  |  |  |  | NLHNcVNLILLADHGmEAIScNR | 48.67 | 0.5 | 894.097 | 3 | 1 |
|  |  |  |  |  | IDKVNLmVDR | 46.61 | -0.1 | 609.8291 | 2 | 2 |
|  |  |  |  |  | FSSSGPEQYDALITSNIVPmYK | 42.49 | 1.1 | 1232.092 | 2 | 1 |
|  |  |  |  |  | TPLNcPPGSLK | 40.22 | -0.2 | 592.3105 | 2 | 1 |
|  |  |  |  |  | SKNVPKDFYTFDSEAIVK | 31.73 | -1.9 | 696.6917 | 3 | 1 |
|  |  |  |  |  | QWLAVR | 31.4 | -0.1 | 386.7268 | 2 | 1 |
|  |  |  |  |  | YKYcSGGTHGYDNEFK | 31.35 | -0.2 | 642.6088 | 3 | 1 |
|  |  |  |  |  | QPLSETLR | 29.38 | -1 | 472.2635 | 2 | 1 |
|  |  |  |  |  | VLSFILPHRPD | 28.3 |  | 647.3696 | 1 | 1 |
| Ohanin like protein | P82885.1 | Thaicobrin | 148.88 | 61 | 12038 | TVENVGVSQVAPDNPERFDGSPcVLGSPGFR | 62.16 | 1.4 | 1096.531 | 3 | 3 |
|  |  |  |  |  | YGTQREWAVGLAGK | 42.38 | -0.9 | 512.6032 | 3 | 1 |
| 5'-Neucleotidase | JAI09047.1 | Ecto-5'-nucleotidase 1c | 235.23 | 43 | 62983 | FHEcNLGNLIcDAVVYNNLR | 63.54 | -0.1 | 807.7194 | 3 | 1 |
|  |  |  |  |  | VLLPSFLAAGGDGYYmLKGD | 62.94 | 1.1 | 1052.028 | 2 | 1 |
|  |  |  |  |  | YDAmALGNHEFDNGLNGLLDPLLK | 62.66 | 0.9 | 882.7679 | 3 | 1 |
|  |  |  |  |  | LTILHTNDVHAR | 55.98 | -0.6 | 463.9245 | 3 | 2 |
|  |  |  |  |  | QAFEHSVHR | 47.04 | -0.7 | 555.7752 | 2 | 2 |
|  |  |  |  |  | SIQEDPAVK | 41.14 | -0.2 | 493.7612 | 2 | 1 |
|  |  |  |  |  | IINVGSEK | 35.69 | 0.7 | 430.2481 | 2 | 1 |
|  |  |  |  |  | VFPAmEGR | 32.21 | -0.4 | 461.726 | 2 | 1 |
|  |  |  |  |  | GREVVHFmNSLR | 28.4 | 0 | 487.5857 | 3 | 1 |
|  |  |  |  |  | ETPVLSNPGPYLEFRDEVEELQK | 23.46 | 1.1 | 897.1176 | 3 | 1 |
| L-amino acid oxidase | ABN72546.1 | L-amino acid oxidase, partial | 285.44 | 65 | 51439 | VTLLEASER | 58.49 | -0.6 | 509.282 | 2 | 4 |
|  |  |  |  |  | KFWEADGIHGGK | 56.16 | -0.2 | 672.8383 | 2 | 1 |
|  |  |  |  |  | STTDLPSR | 36.61 | -0.2 | 438.7246 | 2 | 1 |
|  |  |  |  |  | KVIEELKR | 35.95 | -0.3 | 507.8188 | 2 | 3 |
|  |  |  |  |  | GAVDmIGDLLNED | 30.24 | -1.1 | 689.313 | 2 | 1 |
|  |  |  |  |  | SASQLYRESLQK | 28.08 | 0 | 705.3727 | 2 | 2 |
|  |  |  |  |  | RFDEIVGGFD | 26.59 | -0.7 | 577.777 | 2 | 1 |
|  |  |  |  |  | EYLIK | 20.76 | 0.9 | 333.1973 | 2 | 1 |
| Acetylcholinesterase | JAA74736.1 | ACN-Den-1, partial | 119.68 | 7 | 60425 | AVTIFGESAGAASVGmHLLSTQSR | 67.54 | 0.9 | 1203.609 | 2 | 2 |
|  |  |  |  |  | NNKVYAYLFDHR | 41.74 | -0.5 | 513.928 | 3 | 1 |
| Hyaluronidase | JAS05169.1 | Hyaluronidase | 113.14 | 11 | 52018 | APmYPNEPFLVFWNAPTTQcQLR | 62.16 | 0.6 | 932.7811 | 3 | 1 |
|  |  |  |  |  | HSDSNAFLHLFPESFR | 54.21 | -0.3 | 635.3075 | 3 | 1 |
|  |  |  |  |  | KDYALPVFVYAR | 38.13 | 0 | 481.2661 | 3 | 1 |
| Phospholipase B | ETE59578.1 | Phospholipase B-like 1 | 84.05 | 11 | 58279 | IANmmADSGKTWAQTFEK | 27.14 | 1.2 | 687.6529 | 3 | 1 |

**Supplementary Table S2a:** Immuno-affinity chromatography study showing partial / least immuno-recognized proteins of EI *Naja naja* by commercial PAVs. The LC-MS/MS data was searched against Elapidae family of proteins. \*The SDS-PAGE is shown in Fig. 4a.

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| **Accession no** | **Description** | **Source organism** | **Protein family** | **-10lgP** | **Coverage (%)** | **Avg. Mass (Da)** | **SDS-PAGE band(s)\*** |
| **Nn vs BSVL** | | | | | | | |
| 2CTX | Alpha-cobratoxin | *Naja kaouthia* | 3FTx | 37.3 | 47.9 | 7.8 | NnB1 |
| BAU24666.1 | cytotoxin 11 | *Naja naja* | 3FTx | 30.3 | 35.0 | 8.0 | NnB1-B2 |
| AAR08048.1 | phospholipase A2 isoform 3 precursor | *Naja sagittifera* | PLA2 | 18.6 | 20.6 | 14.0 | NnB1 |
| P01400.1 | Weak toxin S4C11 | *Naja melanoleuca* | 3FTx | 17.7 | 27.7 | 7.4 | NnB1 |
| P82463.1 | Muscarinic toxin-like protein 2 | *Naja kaouthia* | 3FTx | 12.2 | 29.2 | 7.3 | NnB1 |
| P59275.1 | Cobrotoxin-b | *Naja kaouthia* | 3FTx | 11.3 | 18.0 | 6.9 | NnB1 |
| P82464.1 | Muscarinic toxin-like protein 3 | *Naja kaouthia* | 3FTx | 9.3 | 15.4 | 7.6 | NnB1 |
| P82935.2 | Tryptophan-containing weak neurotoxin | *Naja kaouthia* | 3FTx | 9.2 | 25.6 | 9.9 | NnB1 |
| P01446.1 | Cytotoxin 3 | *Naja naja* | 3FTx | 18.0 | 33.3 | 6.7 | NnB3 |
| **Nn vs PSVPL** | | | | | | | |
| P82463.1 | Muscarinic toxin-like protein 2 | *Naja kaouthia* | 3FTx | 15.2 | 29.2 | 7.3 | NnP1 |
| 2CTX | Alpha-cobratoxin | *Naja kaouthia* | 3FTx | 37.3 | 47.9 | 7.8 | NnP1 |
| P82885.1 | Thaicobrin | *Naja kaouthia* | OLP | 14.2 | 15.7 | 12.0 | NnP1 |
| BAU24666.1 | cytotoxin 11 | *Naja naja* | 3FTx | 40.2 | 35.0 | 8.0 | NnP2-P3 |
| P01464.1 | Cytotoxin 5 | *Naja annulifera* | 3FTx | 31.0 | 43.3 | 6.9 | NnP2 |
| P34074.2 | Long neurotoxin 1 | *Naja annulata annulata* | 3FTx | 23.6 | 19.7 | 7.8 | NnP2 |
| P82464.1 | Muscarinic toxin-like protein 3 | *Naja kaouthia* | 3FTx | 19.5 | 41.5 | 7.6 | NnP2 |
| P82462.1 | Muscarinic toxin-like protein 1 | *Naja kaouthia* | 3FTx | 18.3 | 43.1 | 7.4 | NnP2 |
| P01400.1 | Weak toxin S4C11 | *Naja melanoleuca* | 3FTx | 10.4 | 13.8 | 7.4 | NnP2 |
| BAA36403.1 | phospholipase A2 | *Naja kaouthia* | PLA2 | 9.2 | 11.8 | 16.3 | NnP2 |
| P82935.2 | Tryptophan-containing weak neurotoxin | *Naja kaouthia* | 3FTx | 9.2 | 25.6 | 9.9 | NnP2 |
| P01446.1 | Cytotoxin 3 | *Naja naja* | 3FTx | 31.9 | 37.0 | 6.7 | NnP3 |
| BAU24665.1 | cytotoxin 9 | *Naja naja* | 3FTx | 31.1 | 41.7 | 8.0 | NnP3 |

**Supplementary Table S2a:** Immuno-affinity chromatography study showing partial / least immuno-recognized proteins of EI *Naja kaouthia* by commercial PAVs. The LC-MS/MS data was searched against Elapidae family of proteins. \*The SDS-PAGE is shown in Fig. 4a.

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| **Accession no** | **Description** | **Source organism** | **Protein family** | **-10lgP** | **Coverage (%)** | **Avg. Mass (kDa)** | **SDS-PAGE band(s)\*** |
| **Nk vs BSVL** | | | | | | | |
| P01391.1 | Alpha-cobratoxin | *Naja kaouthia* | 3FTx | 68.9 | 77.5 | 7.8 | NkB1-B3 |
| BAA36403.1 | phospholipase A2 | *Naja kaouthia* | PLA2 | 63.8 | 52.1 | 16.3 | NkB1 |
| P25668.1 | Long neurotoxin 1 | *Naja naja* | 3FTx | 62.0 | 77.5 | 7.8 | NkB1 |
| P60044.1 | Acidic phospholipase A2 | *Naja sagittifera* | PLA2 | 36.1 | 28.6 | 14.1 | NkB1 |
| AAF82186.1 | Acidic phospholipase A2 | *Naja sputatrix* | PLA2 | 59.4 | 41.8 | 16.1 | NkB1 |
| BAU24666.1 | cytotoxin 11 | *Naja naja* | 3FTx | 31.3 | 35.0 | 8.0 | NkB1-B3 |
| P58370.1 | Alpha-neurotoxin homolog 8 | *Micrurus corallinus* | 3FTx | 15.2 | 15.1 | 9.6 | NkB1 |
| P82885.1 | Thaicobrin | *Naja kaouthia* | OLP | 14.2 | 15.7 | 12.0 | NkB1 |
| O42257.1 | Long neurotoxin 7 | *Naja sputatrix* | 3FTx | 14.2 | 14.4 | 9.8 | NkB1-B2 |
| P82463.1 | Muscarinic toxin-like protein 2 | *Naja kaouthia* | 3FTx | 11.5 | 18.5 | 7.3 | NkB1 |
| Q9YGJ5.1 | Alpha-neurotoxin NTX-2 | *Naja sputatrix* | 3FTx | 11.2 | 19.4 | 9.2 | NkB1 |
| P82464.1 | Muscarinic toxin-like protein 3 | *Naja kaouthia* | 3FTx | 9.2 | 15.4 | 7.6 | NkB1 |
| P01427.1 | Short neurotoxin 1 | *Naja oxiana* | 3FTx | 9.2 | 18.0 | 6.9 | NkB1 |
| **Nk vs PSVPL** | | | | | | | |
| P01391.1 | Alpha-cobratoxin | *Naja kaouthia* | 3FTx | 64.2 | 60.6 | 7.8 | NkP1-P2 |
| P60044.1 | Acidic phospholipase A2 | *Naja sagittifera* | PLA2 | 53.1 | 41.2 | 14.1 | NkP1 |
| BAA36403.1 | phospholipase A2 | *Naja kaouthia* | PLA2 | 52.1 | 33.6 | 16.3 | NkP1 |
| P82885.1 | Thaicobrin | *Naja kaouthia* | OLP | 34.9 | 48.1 | 12.0 | NkP1 |
| A59218 | Nerve growth factor beta chain precursor | *Naja kaouthia* | NGF | 22.6 | 25.9 | 27.6 | NkP1 |
| BAU24666.1 | cytotoxin 11 | *Naja naja* | 3FTx | 35.2 | 35.0 | 8.0 | NkP1-P3 |
| P29180.1 | Weak neurotoxin 6 | *Naja naja* | 3FTx | 11.4 | 13.8 | 7.6 | NkP1-P2 |
| O42257.1 | Long neurotoxin 7 | *Naja sputatrix* | 3FTx | 12.2 | 14.4 | 9.8 | NkP2 |
| P29180.1 | Weak neurotoxin 6 | *Naja naja* | 3FTx | 11.4 | 14.5 | 7.6 | NkP2 |
| P34074.2 | Long neurotoxin 1 | *Naja annulata annulata* | 3FTx | 9.1 | 18.3 | 7.8 | NkP2 |
| P82464.1 | Muscarinic toxin-like protein 3 | *Naja kaouthia* | 3FTx | 8.3 | 15.4 | 7.62 | NkP2-P3 |
| P82935.2 | Tryptophan-containing weak neurotoxin | *Naja kaouthia* | 3FTx | 11.2 | 25.6 | 9.92 | NkP1 |
| Q9YGJ5.1 | Alpha-neurotoxin NTX-2 | *Naja sputatrix* | 3FTx | 11.2 | 19.4 | 9.2 | NkP1 |
| P58370.1 | Alpha-neurotoxin homolog 8 | *Micrurus corallinus* | 3FTx | 15.2 | 15.1 | 9.6 | NkP1 |