

De novo venom gland transcriptomics of the Malayan Pit Viper, *Calloselasma rhodostoma* (Kuhl, 1824) from Malaysia: Unravelling diversity of toxin genes in a medically important basal crotaline

Supplementary File 2. Low abundance transcripts

Accession	Amino acid sequence	
V8NV17 CRiSP	1	MAKNPSIPWLIPTLFLFLTHGIHCFFLPNATHLENILNQYQDGQPHSRAKRSISRSDQD 60
LCCL domain_Oh	61	EILMLHNKLRGEVYPSASNMEYM-----NSTHFPAGQRLF 120
	121	HPLHRSPSFHVQSWYDEVKDYTPYPHECNPCPDRCCTGPMCTHYTQMVMWATTNKIGCAI 180
	181	NVCKRIDVWGEVWENAVYLVCNYSKGNWIGEAPYKNGRSCSECPSPSYGGGCRANLCYKE 240
	241	KVVEKPETDRANEVELQKVPVRIQPKSVKPTKEKKPTEVNYMTQVIKCDTKMRDTCRGST 300
	301	CNRYLCPAGCLNSKAKVGFPPKYESASSICRAAIHSGVLDNRGGLVDITRKGRSDDFFVMS 360
	361	VRNGVQTFISKYKPSNGFAVSKVTVTLDCTTVEELCPFKKPTTHCPRRLKSSSRKAKRE 420
	421	SHNPSMPAMEQMCKNSSICKAAVHAGVIGDSSGGYVDVMPVDKKKVYNGSLRNGIRSESL 480
	481	KTPREGKAFRIFAVRQ 496
Cr-CRP01	1	MAKNPTVPWL VAPSLFLFLTHGIQCFFLP SATHLERILNQYQDGQPHSRGKRSISRDDR 60
	61	EILTLHNKLRGEVYPSASNMEYMRWDEELERSAESWAQQCIWDHGPA SLLLSIGQNLAVH 120
	121	WGRHRSPGYHVQSWYDEVKDYTPYPHECNPRCPDRCRGVPCTHYTQMVMWATTKNMGCAI 180
	181	NVCKRMVWGEVWENAVYLVCNYSKGNWIGEAPYKNGRPCSECPSPSYGGGCQANLCYKE 240
	241	KAVEKSETDRANEVEIQKVPDRIQPKSVKPAKEKKPVEVTYMTQAICKDTKMRDTCRGST 300
	301	CNRYLCPAGCLNSKAKVGFPPNYESASSICRAAIHSGVLDNRGGLVDITRKGRSDDFFVMS 360
	361	VRNGIRTLSKHKPSNGFAVLKVIQVTLDCYTTVEELCPFKKPTTHCPRSYCPAYCKNE-P 420
	421	NHWATVYGTNIYADNSSICKAAVHAGVIGDSSGGYVDVMPVDKKKVYNGSLRNGIRSESL 480
	481	KTPREGKAFRIFAVRQ 496

Sequence alignment of Cr-CPR01 (Putative cysteine-rich secretory protein (CRiSP)) identified in *Calloselasma rhodostoma* venom gland transcriptome in comparison to selected CRiSP retrieved from UniProtKB database, Cysteine-rich secretory protein LCCL domain-containing 2, UniProtID: V8NV17. Abbreviation: Oh – *Ophiophagus hannah*

Accession	Amino acid sequence	
V5NTD 5'NUC Ca	1	MQTPKRRRGAQGCPRSSPS--PPLLLLVRVAVWFCAALSVAAGSFELTILHTNDVHARVEQ 60
	61	TSRDSGKCTGQDCYGGVARRATKIRELRAKHRHVLLLDAGDQYQGTWVFNFFKGREVVVF 120
	121	MNSLRDAMALGNHEFDNGLAGLLDPLLKHANFPILSANIRPKGSIASNISGYILPYKII 180
	181	NVGSEKVGIIIGYTTKETPVLSNPGPYLEFRDEVEELQNHANKLTTLGVNKIIALGHSGLF 240
	241	EDQRIARKVKGVDDVVVGHTNTFLYTGSPPSTEVAAGNYPFMVQSDDGQVPPVQAYAFG 300
	301	KYLGYLNVIFDDKGNVIKSSGNPILLNKDISEDQDIKAEVNKMKIQLHNYSSQEIGKTIV 360
	361	YLNGTQACRFHECNLGNLICDAVIYNNVRHPDDNEWNHVMCIVNGGGIRSPIDERTNN 420
	421	GTITLEELTAVLPFGGTFDQLQIKGSALKQAFEHSVHRHGEHGMGELLQVSGIKVVYDLR 480
	481	KPGSRVLSLNLCTECRVPTYVPLEKEKTYKLLPSFLAAGGDGYHMLKGDSSNHSSGNL 540
	541	DISIVGDYIKRMGKVFPAVEGRMIFSAAGTLFQAQLFTWGLCVSLLYFIL 590
Cr-NUC01	1	MQTPKR--GTPGCPPSPSPPPPPPLLVGAVWFCALLSLAASFELTLLHTNDVHARVEQ 60
	61	TSRDSGKCTGQECYGGVARRATKIRELRAKHRHVLLLDAGDQYQGTIWFNFFFKGREVVTF 120
	121	MNRLRYDAMALGNHEFDNGLAGVLDPLLKYASFPILSANIIPKGPIASNISGYILPYKII 180
	181	NVGSEKVGIIIGYTTKETPVLSNPGPYLEFRDEVEELQKHVNKLTTLGVNKKIALLGHSGLF 240
	241	EDQRIAQKVKGVDDVVIGHTNTFLYTGTTPSTEVAAGNYPFMVQSDDGQVPPVQAYAFG 300
	301	KYLGYLNVIFDDKGNVIKASGNPILLNKDIPEDQDVKTEVNKMKIQLHNYSSQEIGKTIV 360
	361	YLNGTTHACRFHECNLGNLICDAVIYDNVRHPDDNEWNHVMCIINGGGIRSPIDERANN 420
	421	GTITLEELTAVLPFGGTFDQLQVKGDAKQAFEHSVHRHGGQGTGELLQTSIGIKVVYDLR 480
	481	RPGMRVSLKVLCTECRVPTYVPLETGKTYKLLPSFLASGGDGYHMLKGDASNHSSGNL 540
	541	DISIVGDYIKRMGKVFPAVEGRMIFSAAGTLFQAQLFTWALCISLLYFIL 590

Sequence alignment of Cr-NUC01 (Putative 5'nucleotidase (5'NUC)) identified in *Calloselasma rhodostoma* venom gland transcriptome in comparison to selected 5'NUC

retrieved from UniProtKB database, Snake venom 5'-nucleotidase, UniProtID: F8S0Z7.
Abbreviation: Ca – *Crotalus adamanteus*

Accession	Amino acid sequence	
A0A2H4N395 PLB-like Bm	1	MIRFGNPSSS-----DKRRQRCRSWCWGG-LLLLWAVAETRA DIHYATVYWLEAEKSFQIK 60
	61	DVLDKNGDAYGYNDTIQSTGWGILEIKAGYGNQPI SNEILMYAAGFLEGYLTASHMSDH 120
	121	FANLFPLMIKNVIEQKVDFIQKQDEWTRQQIKNNKDDPFWRNAGYVIAQLDGLYMGNV 180
	181	EWAKRQKRTPLTDFEISFLNAIGDLLDIPALQSTLRKSDFRSMPDVPRIYQWDMGHCSA 240
	241	LIKVLPGYENIYFAHSSWFTYAATLRIYKHLDFKITDPQTKTGRASFSSYPGFLSSLDDF 300
	301	YILGSGLTMLQTTNSVLNLSLLKKVVPESLFAWERVRIANMMADSGKTWAETFEKQNSGT 360
	361	YNNQYMILDTKKIKLQRSLEDGTLYIEQVPKLVKYS DQTKVLRNGYWPSYNIPFDKEIY 420
	421	NMSGYGEYVQRHGLEFSYEMAPRAKIFRRDQGKITDMESMKSIMRYNNYKEDPYAKRNPC 480
	481	NTICCRQDLDRRTPVPAGCYDSKVADISMAAKFTAYAISGPTVEKGLPVFSWVNFNKT KH 540
	541	QGLPESYNFDFVTM KPVL 558
Cr-PLB01	1	MIRLGHPSSSSSSWEKRRQRCRSWSWG LLLLLWAVAETRA DIHYATVYWLEAEKSFQIK 60
	61	DVLDKNGNAYGYNDTIQSTGWGILEIKAGYGNQPI SNEILMYAAGFLEGYLTASHMSDH 120
	121	FANLYPLMIKNVIEQKVDFIQKQDKWTRQQIKNNKDDPFWRNAGYVIAQLDGLYMGNV 180
	181	EWAKRQKKTPLTIFKISFLNAVGDLLDIPALYSNLRKSDVRSMPDVPRIYQWDMGHCSA 240
	241	LIKVLPGYENIYFAHSSWFTYAATLRIYKHLDFKITDPQTKTGRASFSSYPGFLVSLDDF 300
	301	YILGNGMVLQTTNSVFNLSLLKKVVPESLFAWERVRIANMMADSGKTWAETFEKQNSGT 360
	361	YNNQYMIIDTKIKLRRSLEDGTLYIVEQVPKLVKYS DQTKVLRNGYWSSYNIPFDKVIY 420
	421	NISGYGEYVQRFGLFSYEMAPRAKIFRRDQGKVTDMESMKSIMRYNNYKEDPYAKHNPC 480
	481	NTICCRQDLDRRSPVPAGCYDSKVTDISMAAKFTAYAINGPPVEKGLPVFSWIDFNKTKH 540
	541	QGLPESYNFDFVIM KPVL 558

Sequence alignment of Cr-PLB01 (Putative phospholipase B (PLB)) identified in *Calloselasma rhodostoma* venom gland transcriptome in comparison to selected PLB retrieved from UniProtKB database, Phospholipase B-like, UniProtID: A0A2H4N395. Abbreviation: Bm – *Bothrops moojeni*

Accession	Amino acid sequence	
V8P8E3 NLB Oh	1	----- 60
	61	----MCWKPMGISGKNYKQMPMPTSSKELDFVGH SVRTKLDLKRQEVSRLRMLLKAKMD 120
	121	ATMEQDVQVDHLALLKQFEHLDSQNQHTFEARDLELLIKTATKDLENYDAAHHEEFKRYE 180
	181	MMKEHERREY LKSLDEEKREEEAHFEELKKKHKEHPKVNVP-TPTVMGCWMSRNRHFS 240
	241	LRSGGVEFREM QFEHSRGAPAKEV---FFLQLEKVYDPRNEEDDMLEMEEEERLRMREHVM 300
	301	KNVDLNKDRLVTLDEFVKSTQRKEFNEADGWETVEETQIYSEAE LQRFEAE LKAQEEELS 360
	361	RRAEQLHQEHKELQQRQVELDAQKEYQQVVLQMEQRKSQQLEQAPQVGP GGELKFQAQP 420
	421	PHAAPADHASPPESQPGAPGAPEHDSQKDQTEALQNQAHEVAVQ 480
Cr-NLB01	1	QIRWRTTLLQQCVLLTTYIVII LEAVPIDVDKTKVKEEEKDSATVENPDTGLYYDAYLRQ 60
	61	VIEVLETDKHFREKLQTADIEQIKSGKLSKELDLVG HKVRTKLDLKRQEVARLRMLIKA 120
	121	KIDAYQDSGVDHQALLKQFGHLNHNPNHTFEVKDL DMLIKTATHDLENYDNERHEEFKKY 180
	181	EMMKEHERREY LKTLDEEKRHQEEAKYEDMKKKHNDHPKVNHPGSKDQLKEVWEEADGLD 240
	241	PNDFDPKTF FFKLHDVNADGFLDEQELEALFTRELEKVYDPRNEEDDMVEMEEERLRMREH 300
	301	VMNEVDINKDRLVTL EEFMRATEKREFLEPENWETLDQQQVFTEDDLKEFESHIVQKEDE 360
	361	LQKQALELQKKREELQQQQDFLQAQKQELEMAVKQMEQKKLQQGH-PPSGPGGELKFQ-- 420
	421	-PSVSQLD-GNVQNHVPVAPGNI PVQEAARS DHVQSH----- 480

Sequence alignment of Cr-NLB01 (Nucleobindin (NLB)) identified in *Calloselasma rhodostoma* venom gland transcriptome in comparison to selected NLB retrieved from UniProtKB database, Nucleobindin-1, UniProtID: V8P8E3. Abbreviation: Oh – *Ophiophagus hannah*

Accession	Amino acid sequence	
B1Q3K2 NGF Pf	1	MSMLCYTLIIAFLIGIWAAPKSEDNVPLGSPATSDLSDTSCAKTHEALKTSRNTDQHYP
	61	PKKAEDQEFGSAANIIVDPKLFQKRRFQSPRVLFSTQPPPLSRDEQSVDNANSLNRNIRS
	121	KREDHPVHNRGEYSVCDSSVSVWVANKTTATDIRGNLVTVMVDVNLNNNVYKQYFFETKCR
	181	NPNPVPTGCRGIDSRHWNSYCTTTHTFVRALTMEGNQASWRFIRIDTACVCVISRKNENF
	241	G
Cr-NGF01	1	MSMLCYTLIIAFLIGIWAAPKSEDNVPLGSPATSDLSDNCAKTHEALKTSRNTDQHYP
	61	PKKAEDQEFGSAANIIVDPKLFQRRRFQSPRVLFSTQPPPLSRDEQSVDNANSLNRNIRA
	121	KREDHPVHNRGEYSVCDSSVSVWVANKTTATDIRGNVVTVMVDINLNNNAYKQYFFETKCR
	181	NPNPVPTGCRGIDARHWNSYCTTTHTFVRALTMEGNQASWRFIRIDTACVCVISRKN---
	241	-

Sequence alignment of Cr-NGF01 (Putative nerve growth factor (NGF)) identified in *Calloselasma rhodostoma* venom gland transcriptome in comparison to selected NGF retrieved from UniProtKB database, Nerve growth factor, UniProtID: B1Q3K2. Abbreviation: Pf – *Protobothrops flavoviridis*

Accession	Amino acid sequence	
P67862 VEGF Pf	1	MAAYLLAVAILFCIQGWPSGTVQGQVMPFMEVYSRSACQTRETLVPILKEYPDEVSHLFK
	61	PSCVPVLRGCGCCSDESLTCTATGKHSVGREIMRVDPHKGTSKMEVMQFKEHTACECRPR
	121	SPGDVNNGKDKRNPEEGGPRARFPFV
Cr-NLB01	1	MAAYLLAVAILFCIQGWPSGTVQGQVMPFMEVYSRSACQTRETLVPILKEYPDEVSHLFK
	61	PSCVPVLRGCGCCSDESLTCTATGKHSVGREIMRVDPHKGTSKMEVMQFKEHTACECRPR
	121	SPGDVNNGKDKRNPEEGGPRARFPFV

Sequence alignment of Cr-VGF01 (Snake venom vascular endothelial growth factor (VEGF)) identified in *Calloselasma rhodostoma* venom gland transcriptome in comparison to selected VGF retrieved from UniProtKB database, Snake venom vascular endothelial growth factor toxin, UniProtID: P67862. Abbreviation: Pf – *Protobothrops flavoviridis*

Accession		Amino acid sequence	
P60615 Alpha bungarotoxin Bm	1 61	MKTLTLLTLVVVTIVCLDLGYTIVCHTTATSPISAVTCCPPGENLCYRKMWCDAFCSRRGKV VELGCAATCPSKKPYEEVTCSTDKCNPHPKQRPG	60 120
Cr-FTX01	1 61	MKTLTLLTLVVVTIVCLDLGYTIVCHTTATSPISAVTCCPPGENLCYRKMWCDAFCSRRGKV VELGCAATCPSKKPYEEVTCSTDKCNPHPKQRPG	60 120
Q7ZT13 NTX-like Bm	1 61	MKTLTLLTLVVLTIACLDLGYTKTCFNDDLTNPKTTELCRHSMYFCFKNSWIAGGVERIER GCSLTCPDIKYNKYIYCCTRDNCNA	60 120
Cr-FTX02	1 61	MKTLTLLTLVVLTIACLDLGYTKTCFNDDLTNPKTTELCRHSMYFCFKNSWIAGGVERIER GCSLTCPDIKYNKYIYCCTRDNCNA	60 120
Q8JFX7 MTX Bm	1 61	MKTLTLLTLVVVTIICLDLGYTEMCMCVRPYPFMSSCCPEGQDRCYKSYWVNENGGKQKKYHG KYPVILERGCVTACTGPGSGSIYNLYTCCPTNRCGSSSTSG	60 120
Cr-FTX03	1 61	-----TLVVVTIICLDLGYTEMCMCVRPYPFMSSCCPEGQDRCYKSYWVNENGGKQKKYHG KYPVILERGCVTACTGPGSGSIYNLYTCCPTNRCGSSSTSG	60 120
P15817 Kappa bungarotoxin Bm	1 61	MKTLTLLSLVVVTIVCLDLGYTRTCLISPSSTPQTCPNGQDICFRKAQCDNFCNHRGPVIEQG CVATCPQFRSNYRSLCCRTDNCNH	60 120
Cr-FTX04	1 61	-----CLDLGYTRTCLISPSSTPQTCPNGQDICFRKAQCDNFCNHRGPVIEQG CVATCPQFRSNYISLLCCRTDNCN-	60 120
Q9YGI0 Gamma bungarotoxin Bm	1 61	MKTLTLLTLVVVTIVCLDLGYTMQCKTCSFYTCNPSETCPDGKNICVKRSWTAVRGDGPKREI RRECAATCPPSKLGLTVFCCTTDNCNH	60 120
Cr-FTX05	1 61	-----VCLDLGYTLKCKTCPFYNCNPSETCPGGKNICVKRSWTAVRGDGPKHEI RRECAATCPPKPGGLTVFCCTTDNCNH	60 120
A5X2W6 3FTX Sce	1 61	MKTLVLVILGVVAFVYLDGYSLECYSCNMFTFSILPLKLCRSVMCEGLDQCYINKTLFPV LKIEKGCTTNCQTWTDKCCETNKNII	60 120
Cr-FTX06	1 61	-----VAMFYFNHLGYSIQCYQCNNPCSRRLV-----MTCPESLRQCYTNKTDTS GRPAGKGCTMNCIENEQIKCCNTSRCN--	60 120
Q9YGI8 SNTX Bm	1 61	MKTLTLLTLVVVTIICLDLGYTRKCLIKYSQANESSKTCPSGQLLCLKKWEIGNPSGKEVK RGCVATCPKPKKNEIIQCCAKDKCNK	60 120
Cr-FTX07	1 61	-----TLVVLTIIVCLDLGYTRKCLIKYSQANESSKTCPSGQLLCLKKWEIGNPSGKEVK RGCVATC-----	60 120
A5X2W7 3FTX Sce	1 61	MKTLVTGVVAFVYLEPGYSLICEACNLPNCDFLPPPCPKGFNQCYKKWNILGLSVMNIE RGCTANCTPNAQTKCCNTNLCNA	60 120
Cr-FTX08	1 61	-----GYSIQCYQCNNP-CSRRVLMTCPESLRQCYT--NKTDTSGRPAG KGCTMNCIENEQIKCCNTSRCN-	60 120
F5CPD4 3FTX Ma	1 61	MKALLFALFLVAFLEKDPVKSMQCYKCGVSGCHLKITCSEDEKFCYKRYNKISFIRTYGCAK TCTEENNWTASVYCCTTNLCNT	60 120
Cr-FTX09	1 61	-KALLSALLLVAFLEKDPVKSMCEYRCGVSGCHLKITCSAEETFCYKWLNKIS----- -----	60 120

Sequence alignment of Cr-FTX01, Cr-FTX02, Cr-FTX03, Cr-FTX04, Cr-FTX05, Cr-FTX06, Cr-FTX07, Cr-FTX08, Cr-FTX09 (Three-finger toxin (3FTX)) identified in *Calloselasma rhodostoma* venom gland transcriptome in comparison to selected 3FTX retrieved from UniProtKB database, Alpha bungarotoxin, UniProtID: P60615; Neurotoxin-like protein, UniProtID: Q7ZT13; Muscarinic toxin, UniProtID: Q8JFX7; Kappa bungarotoxin, UniProtID: P15817; Gamma bungarotoxin, UniProtID: Q9YGI0; 3FTX, UniProtID: A5X2W6, A5X2W7 and F5CPD4; Short neurotoxin, UniProtID: Q9YGI8. Abbreviation: NTX – Neurotoxin; MTX – Muscarinic toxin; 3FTX – Three-finger toxin; SNTX – Short neurotoxin; Bm – *Bungarus multicinctus*; Sce – *Sistrurus catenatus edwardsii*; Ma – *Micrurus altirostris*

Accession	Amino acid sequence	
T2HQN1 APP Oo	1	MQGMDIEDKSSKMHCMKGKHVAIICGVVIAVGLILGLGLGLKPEACNPDPEDNGQVSTK 60
	61	PPTSSTPDVTNPSSSVFCSAKNDENGAWTNFRLPNYVHPVHYDLDLTPEMEADEVYTG MV 120
	121	NISIRLEEQTTRHLWLHLRETKITEMPQLRISSGQVIEIKRCFGYEPQEYVVVEAEEDLR 180
	181	PGNYFLSMKFKGYLNGSLVGFYSTTYGENGKTKYIAATDHEPTDARKSFPCFDEPNKKAT 240
	241	YTISITHEQDYEAISNMPVEKTISLDNKWTKTIFKKSVPMSSTYLVAVAVHQFKYEERISA 300
	301	RGIPLRVYAQPQQINTAIYAANVTKVVFDFYFENYFNMNYSPLKLDKIAIPDFGTGAMENW 360
	361	GLITYRETNLLYDSRESAASNKQRVAAVVAHELHVQWFGNIVTMDWDDLLWLNFGFASFF 420
	421	EFMGVNATEEKWQMLDQILIDLLPVLKDDSLVSSHPIITVNVSSPDEITSVFDGISYSKG 480
	481	ASILRMLEDWISPDHFRAGCQKYLKDHYFKNAKTDDFWKAMQEVSGKPVREVMDTWTRQM 540
	541	GYPVLKVALNSTVTQQRFLDPKADPSKPFSSQFSYKWNIPVKWKEGNTSSITFYNKSEVA 600
	601	GITITRPSNLPDPSFLKVNKDHVGFYRVNYPEQVWRTLADIMMKDQNFNLADRAGFIDD 660
	661	AFALARAGLLKYADALNLTRYLQNETEYIPWQRAVVAVSYIGQMVEDDKALYPKFQRYFG 720
	721	SLVKPIASELKWENEDHIKSLRLTTVLEFACNMDDPEALGNASLLFKNWTSGISLDVNL 780
	781	RLLVYRFGMQHSGDEEAWNYMFEKYRTATLAQEKEKLLYGLASVKNITLLNRFLNCKNT 840
	841	TLIRSQDVFTVLRYISFNSYGKTMAWDWRLNWEYLVKRYTLNDRNLGRLISRISGTFNT 900
	901	ELQLWQMFNFERYPDAGAGEASRKQALETTKSNIEWLQYRDDVATWLENSE----- 960
Cr-APP01	1	MQGMDIEDKSSKMPCKMGKHVAIICGVVIAVGLILGLGLGLKPEACSPDPEDNGQVSTQ 60
	61	PPTSSTPDVTSASGSSVFCSAQNDEIGAWSNFRLPVSVLPVHYDLDLTPEMEADEVYTG MV 120
	121	NISIRLEKLTTKHLWLHLRETKITEMPQLRTSSGQVIEIKRCFGYEPQEYVVVEAEELR 180
	181	PGNYFLSMKFKGYLNGSLVGFYSTTYGENGKTKYIAATDHEPTDARKSFPCFDEPNKKAT 240
	241	YTISITHERDYEAISNMPVEKTISLDNKWTKTIFKKSVPMSSTYLVAVAVHQFKYEERISS 300
	301	RGIPLRVYAQPQQINTAIYAANVTKVVFDFYFENYFNMNYSPLKLDKIAIPDFGTGAMENW 360
	361	GLITYRETNLLYDSQESAASNKQRVAAVVAHEVVHQQWFGNIVTMDWDDLLWLNFGFASFF 420
	421	EFMGVNATEEKWQMLDQILIDLLPVLKDDSLVSSHAITVNVSSPDEITSVFDGISYSKG 480
	481	ASILRMLEDWISPDQFKAGCQKYLTDHYFKNAKTDDFWKAMQVVSQKPVKEVMDTWTRQM 540
	541	GYPVLKVALNSTITQQRFLDPKADPSQPFSSQFSYKWNIPVKWKEGNTSSITFYNKSELA 600
	601	GITITRPSDAPPDSFLKVNKDHVGFYRVNYPEVWHALANIMMKDQNFNLADRAGFIDD 660
	661	AFALARAGLLKYADALNLTRYLQNETEYIPWQRAVVAVSYIGQMVEDDKALYPKFQRYFG 720
	721	SLVKPIASELKWENEDHIKSLRLTTVLEFACNMDDPEALGNASLLFKNWTSGISLDVNL 780
	781	RLLVYRFGMQNSGDEQAWNYMFEKYRTATLAQEKEKLLYGLASVKNITLLNRFLSCIKNT 840
	841	TLIRSQDVFTVLRYISFNSYGKTMAWDWRLNWEYLVKRYTLNDRNLGRLISRISGTFNT 900
	901	ELQLWQMFNFERYPDAGAGEASRKQALETTKSNIEWLQYRDDVATWLENSEQTNFI 960

Sequence alignment of Cr-APP01 (Aminopeptidase A (APP)) identified in *Calloselasma rhodostoma* venom gland transcriptome in comparison to selected APP retrieved from UniProtKB database, Aminopeptidase, UniProtID: T2HQN1. Abbreviation: Oo – *Ovophis okinavensis*

Accession	Amino acid sequence	
J3SEZ3 PDE Ca	1	MIQQKVLFI SLVAVTLGLGLGLKESVQPQVSCRYRCNETFSKMASGCSCDDKTERQA 60
	61	CCSDYEDTCVLPTQSWSCSKLRCEKRIANVLCSCSDDCLEKKDCCTDYKSICKGETSWL 120
	121	KDKCASSGATQCPAGFEQSPLILFSMDGFRAGYLENWDLSMPNINKLKTCGTHAKYMRV 180
	181	YPTKTFVNHYTIATGLYPESHGIIIDNNIYDVNLNLFSLSSSTARNPAWWGGQPIWHTAT 240
	241	YQGLKAATYFWPGSEVKINGSYPTIFKNYNKSI PFARVTEVLKWLDPKAKRPDFTLY 300
	301	IEEPDTTGHKYGPVSGEIIKALQMA DRTLGMLEGLKQRNLHNCVNLI LADHGMEEISC 360
	361	DRLEYMANYFNNVDFMYEGPAPRIRSKNVPKDFYTFDSEGI VKNLTCRKPKQYFKAYLS 420
	421	KDLPKRLHYANNIRIDKVNLMVDQQWMAVRDKKFTRCKGGTHGYDNEFKSMQAI FLAHGP 480
	481	GFNEKNEVTSFENIEVYNLMCDLLKLPAPNNGTHGSLNHLLKNPFYTPSPA KEQSSPLS 540
	541	CPFGPVPSPDVSGCKCSSITELEKVNQRLN LNNAKTESEAHNLPYGRPQVLQNH SKYCL 600
	601	LHQAKYISAYSQDILMPLWSSYTIYRSTSTSVPPSASDCLRLDVRI PAAQSQTCSNYQPD 660
	661	LTITPGFLYPNPNFSSNFEQYDALITSNIVPMFKGFTRLWNYFHTTLIPKYARERNGLNV 720
	721	ISGPIFDYNDGHFDSYDTIKQHVNTKIPIPTHYFVVLTSCE NQINTPLNCLGPKVLVS 780
	781	FILPHRPDNSESCADTSPENLWVEERI QIHTARVRDVLLTGLNFYSGLKQPLPETLQLK 840
	841	TFLPIFVNPVN 900
Cr-PDE01	1	----- 60
	61	----- 120
	121	-----FEQSPLILFSMDGFRAGYLEAWESLMPNINKLKICGTHAKYMR A 180
	181	YPTKTFVNHYTIVTGLYPESHGIIIDNNMYDVNLNLFSLSSSVAKNPAWWGGQPIWNTVT 240
	241	YQGLKAATYFWPGSEVKINGSYPTIYKNYNKSM PFARVTEVL SWLDLPKAERP DFTLY 300
	301	IEEPDTTGHQYGPVSGQVIKALQMA DQTLGMLEGLKQRNLHNCVNLI LADHGMEEISC 360
	361	NRLEYMDSYFNKVDFMYEGPAPRIRSKNVPKDFYTFDSEGI VKNLTCRNPKQYFKAYLS 420
	421	KDLPKRLHYVNNVRIDKVNLMVDEKWM AVRDKKFSRCKGGTHGYDNEFKSMQAI FLAHGP 480
	481	GFKGKNEVTSFENIEVYNLLCDLLKLPAPNNGTHGSLNHLLKNPFYTPSPA KEQSSPLS 540
	541	CPFGPTSPDVSGCKCSITNLEKVNQRLN LNDAQIVSEVNNLPYGRPQVL RNDNKYCL 600
	601	LHQTKYISAYSQDILMPLWSSYTIYRSQRTSVPPSALDCLRLDVRI PAVQSQICSNYQTD 660
	661	LTITPGFLYPNPNFSSNFEQYDALITSNIVPMFKGFTRLWNYFHTI LLPKYAKERNGVN 720
	721	ITGPIFDYNDGHFDSYGTIKEHVINTKIPIPTHYFVVLTSCE NQINTPLNCLGPKVLVS 780
	781	FILPHRPDNSESCADTSPENLWVEERI QIHTARVRDVLLTGLNFYSGLKQPLPETLQLK 840
	841	TFLPIFESP-- 900

Sequence alignment of Cr-PDE01 (Phosphodiesterase (PDE)) identified in *Calloselasma rhodostoma* venom gland transcriptome in comparison to selected PDE retrieved from UniProtKB database, Phosphodiesterase, UniProtID: J3SEZ3. Abbreviation: Ca – *Crotalus adamanteus*

Accession	Amino acid sequence	
Q8AY45 KSPI Bc	1	MSSGGLLLLLLGLLTLWAELTPVSSRKRHPDCDKPPDTKICQTVVRAFYKPSAKRCVQFR 60
	61	YGGCNGNGNHFKSDHLRCCECLEYP 120
Cr-KUN01	1	-SSGGLLLLLLGLLTLWAELTPVSSRKRHPDCDKPPDTKICQTVVRAFYKPSAKRCVQFR 60
	61	YGGCNGNGNHFKSDHLRCCECLEYP 120

Sequence alignment of Cr-KUN01 (Kunitz-type Serine Proteinase Inhibitor (KSPI)) identified in *Calloselasma rhodostoma* venom gland transcriptome in comparison to selected KSPI retrieved from UniProtKB database, Kunitz-type serine protease inhibitor, UniProtID: Q8AY45. Abbreviation: Bc – *Bungarus candidus*