

Fig. S1: Agarose gel electrophoresis of genomic DNA (VRU) isolated from shed skin of *Daboia russelii*.

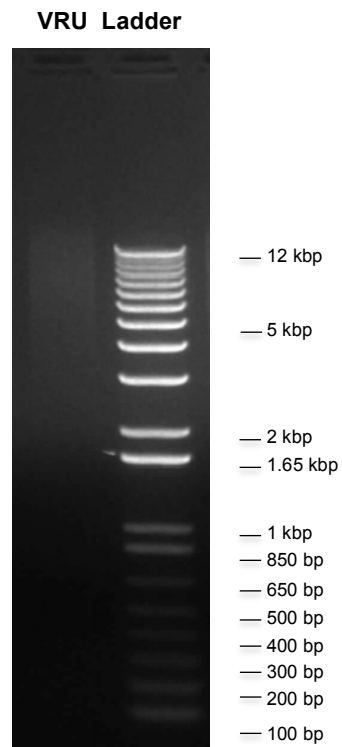


Fig. S2: Exon-intron structures for all the putative toxin gene homologs in Russell's viper.

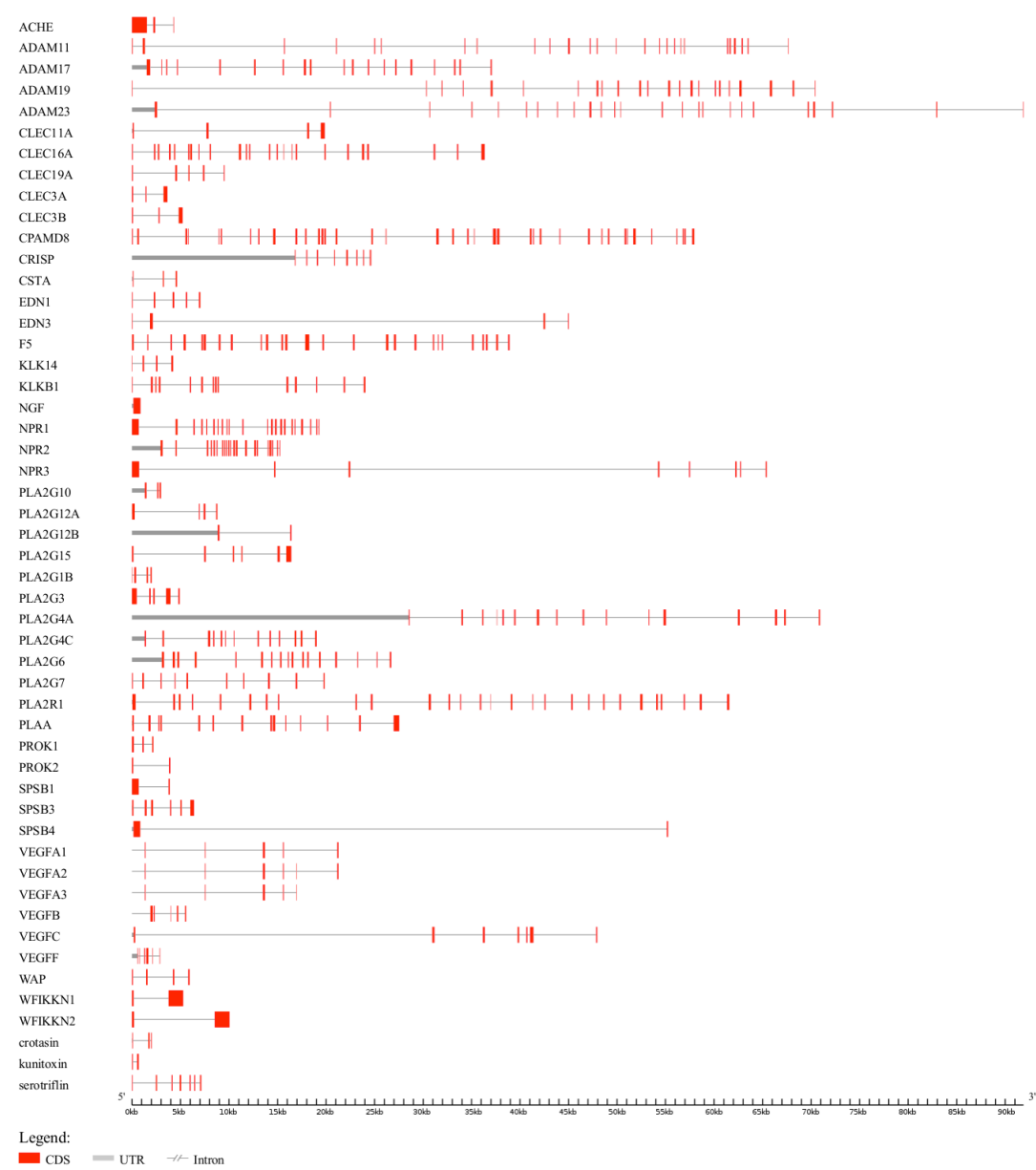


Fig. S3: Comparison of 10 toxin family protein sequences from venom-associated proteins from venom/venom gland of Russell's viper, *Daboia russelii* (Sharma *et al.*, 2016) with the putative venom homologs from genome sequencing, assembly and annotation of *Daboia russelii*'s (this manuscript). Comparative analyses were performed using blastp, with the venom/venom gland associated protein sequence as the query (accession IDs from Supplementary Figure S1 of Sharma et al. 2016), against the putative venom homologs from skin. In the multiple sequence alignments, red indicates an identical match in comparison in at least one of the compared venom protein sequences. Light gray indicates non-identical amino acid.**Fig. S6:** Graphical summary of comparative domain analysis across 18 completely sequenced snake species.

I. PLA2 Family

Accession	Description
lcl Query_172485	PLA2G10
P86169.1	RecName: Full=Basic phospholipase A2 A; Short=svPLA2; AltName: Full=Crotoxin basic chain 1; AltName: Full=Phosphatidylcholine 2-acylhydrolase phospholipase A2 [Echis coloratus]
AAK49822.1	RecName: Full=Basic phospholipase A2 Tpu-G6D49; Short=svPLA2; AltName: Full=Phosphatidylcholine 2-acylhydrolase; Flags: Precursor
Q2YHJ7.1	ammodytin 11(C) variant [Vipera berus berus]
CAE47155.1	RecName: Full=Acidic phospholipase A2 Tgc-E6; Short=svPLA2; AltName: Full=Phosphatidylcholine 2-acylhydrolase; Flags: Precursor
A8E2V8.1	RecName: Full=Acidic phospholipase A2; Short=svPLA2; AltName: Full=Phosphatidylcholine 2-acylhydrolase
P21789.1	phospholipase A2 acidic subunit, PLA2-I subunit A [Vipera aspis, zinnikeri, venom, Peptide, 122 aa]
AAB36471.1	Chain G, Crystal Structure Of Rv4RV7 COMPLEX
1OQS_G	RecName: Full=Acidic phospholipase A2 RV-7; Short=svPLA2; AltName: Full=F7; AltName: Full=Phosphatidylcholine 2-acylhydrolase; AltName: Full=Phospholipase A2 inhibitor; AltName: Full=S4; AltName: Full=Viperotoxin F; AltName: Full=Viperotoxin non-toxic acidic component; Flags: Precursor
P31100.1	Chain A, X-ray Structure Of Acidic Phospholipase A2 From Indian Saw- Scaled Viper (echis Carinatus) With A Potent Platelet Aggregation Inhibitory Activity
1O26_A	RecName: Full=Basic phospholipase A2 RVV-VD; Short=svPLA2; AltName: Full=Phosphatidylcholine 2-acylhydrolase; AltName: Full=R1
P81458.1	RecName: Full=Basic phospholipase A2 VRV-PL-Villa; Short=svPLA2; AltName: Full=DPLA2; AltName: Full=P1; AltName: Full=Phosphatidylcholine 2-acylhydrolase; AltName: Full=Phospholipase A2 4; Short=PLA24
P59071.1	RecName: Full=Basic phospholipase A2 DsM-S1; Short=svPLA2; AltName: Full=Phosphatidylcholine 2-acylhydrolase; Flags: Precursor
A8CG84.1	RecName: Full=Acidic phospholipase A2 2; Short=svPLA2; AltName: Full=Phosphatidylcholine 2-acylhydrolase; AltName: Full=Phospholipase A2 isozyme II; Short=PLA2-II
P81478.1	RecName: Full=Basic phospholipase A2 3; Short=PLA23; Short=svPLA2; AltName: Full=Phosphatidylcholine 2-acylhydrolase
P86368.1	
Query_172485	1 [36] [Q] [LQ] [A] [MI] [G] [TGR] [PL] [YI] [Y] [G] [C] [G] [G] [G] [R] [G] [P] [K] [D] [X] [X] [C] [F] [H] [D] [C] [Y] [G] [R] [A] [S] [S] [C] [P] [K] [T] [Y] [P] [Q] [G] [G] [C] [D] [D] [C] [R] [K] [C] [E] [C] [D] [R] [A] [A] [C] [L] [A] [S] [S] [Y] [N] [Y] [F] [P] [D] [Q] [C] [G] [R] [K] [T] [C] [4] 162 618
P86169	1 [16] [L] [L] [Q] [F] [R] [K] [I] [K] [P] [E] [T] [K] [M] [A] [I] [P] [F] [A] [Y] [S] [H] [Y] [G] [C] [Y] [G] [G] [G] [R] [G] [P] [K] [D] [R] [C] [F] [H] [D] [C] [Y] [G] [R] [A] [S] [S] [C] [P] [K] [T] [Y] [P] [Q] [G] [G] [C] [D] [D] [C] [R] [K] [C] [E] [C] [D] [R] [A] [A] [C] [L] [A] [S] [S] [Y] [N] [Y] [F] [P] [D] [Q] [C] [G] [R] [K] [T] [C] [4] 122
AAK49822	1 [16] [L] [L] [Q] [F] [R] [M] [I] [K] [E] [T] [K] [G] [F] [A] [I] [A] [Y] [S] [H] [Y] [G] [C] [Y] [G] [G] [G] [R] [G] [P] [K] [D] [R] [C] [F] [H] [D] [C] [Y] [G] [R] [A] [S] [S] [C] [P] [K] [T] [Y] [P] [Q] [G] [G] [C] [D] [D] [C] [R] [K] [C] [E] [C] [D] [R] [A] [A] [C] [L] [A] [S] [S] [Y] [N] [Y] [F] [P] [D] [Q] [C] [G] [R] [K] [T] [C] [4] 138
Q2YHJ7	1 [16] [L] [L] [E] [F] [G] [R] [M] [I] [K] [E] [T] [K] [G] [F] [A] [I] [A] [Y] [S] [H] [Y] [G] [C] [Y] [G] [G] [G] [R] [G] [P] [K] [D] [R] [C] [F] [H] [D] [C] [Y] [G] [R] [A] [S] [S] [C] [P] [K] [T] [Y] [P] [Q] [G] [G] [C] [D] [D] [C] [R] [K] [C] [E] [C] [D] [R] [A] [A] [C] [L] [A] [S] [S] [Y] [N] [Y] [F] [P] [D] [Q] [C] [G] [R] [K] [T] [C] [4] 138
CAE47155	1 [16] [L] [L] [S] [Q] [G] [D] [M] [I] [K] [E] [T] [K] [G] [F] [A] [I] [A] [Y] [S] [H] [Y] [G] [C] [Y] [G] [G] [G] [R] [G] [P] [K] [D] [R] [C] [F] [H] [D] [C] [Y] [G] [R] [A] [S] [S] [C] [P] [K] [T] [Y] [P] [Q] [G] [G] [C] [D] [D] [C] [R] [K] [C] [E] [C] [D] [R] [A] [A] [C] [L] [A] [S] [S] [Y] [N] [Y] [F] [P] [D] [Q] [C] [G] [R] [K] [T] [C] [4] 138
A8E2V8	1 [16] [L] [L] [S] [Q] [G] [D] [M] [I] [K] [E] [T] [K] [G] [F] [A] [I] [A] [Y] [S] [H] [Y] [G] [C] [Y] [G] [G] [G] [R] [G] [P] [K] [D] [R] [C] [F] [H] [D] [C] [Y] [G] [R] [A] [S] [S] [C] [P] [K] [T] [Y] [P] [Q] [G] [G] [C] [D] [D] [C] [R] [K] [C] [E] [C] [D] [R] [A] [A] [C] [L] [A] [S] [S] [Y] [N] [Y] [F] [P] [D] [Q] [C] [G] [R] [K] [T] [C] [4] 139
P21789	1 [16] [L] [L] [Q] [F] [R] [M] [I] [K] [E] [T] [K] [G] [F] [A] [I] [A] [Y] [S] [H] [Y] [G] [C] [Y] [G] [G] [G] [R] [G] [P] [K] [D] [R] [C] [F] [H] [D] [C] [Y] [G] [R] [A] [S] [S] [C] [P] [K] [T] [Y] [P] [Q] [G] [G] [C] [D] [D] [C] [R] [K] [C] [E] [C] [D] [R] [A] [A] [C] [L] [A] [S] [S] [Y] [N] [Y] [F] [P] [D] [Q] [C] [G] [R] [K] [T] [C] [4] 120
AAB36471	1 [16] [L] [L] [Q] [F] [R] [M] [I] [K] [E] [T] [K] [G] [F] [A] [I] [A] [Y] [S] [H] [Y] [G] [C] [Y] [G] [G] [G] [R] [G] [P] [K] [D] [R] [C] [F] [H] [D] [C] [Y] [G] [R] [A] [S] [S] [C] [P] [K] [T] [Y] [P] [Q] [G] [G] [C] [D] [D] [C] [R] [K] [C] [E] [C] [D] [R] [A] [A] [C] [L] [A] [S] [S] [Y] [N] [Y] [F] [P] [D] [Q] [C] [G] [R] [K] [T] [C] [4] 122
1OQS_G	1 [16] [L] [L] [Q] [F] [R] [M] [I] [K] [E] [T] [K] [G] [F] [A] [I] [A] [Y] [S] [H] [Y] [G] [C] [Y] [G] [G] [G] [R] [G] [P] [K] [D] [R] [C] [F] [H] [D] [C] [Y] [G] [R] [A] [S] [S] [C] [P] [K] [T] [Y] [P] [Q] [G] [G] [C] [D] [D] [C] [R] [K] [C] [E] [C] [D] [R] [A] [A] [C] [L] [A] [S] [S] [Y] [N] [Y] [F] [P] [D] [Q] [C] [G] [R] [K] [T] [C] [4] 122
P31100	1 [16] [L] [L] [Q] [F] [R] [M] [I] [K] [E] [T] [K] [G] [F] [A] [I] [A] [Y] [S] [H] [Y] [G] [C] [Y] [G] [G] [G] [R] [G] [P] [K] [D] [R] [C] [F] [H] [D] [C] [Y] [G] [R] [A] [S] [S] [C] [P] [K] [T] [Y] [P] [Q] [G] [G] [C] [D] [D] [C] [R] [K] [C] [E] [C] [D] [R] [A] [A] [C] [L] [A] [S] [S] [Y] [N] [Y] [F] [P] [D] [Q] [C] [G] [R] [K] [T] [C] [4] 138
1O26_A	1 [16] [L] [L] [Q] [F] [R] [M] [I] [K] [E] [T] [K] [G] [F] [A] [I] [A] [Y] [S] [H] [Y] [G] [C] [Y] [G] [G] [G] [R] [G] [P] [K] [D] [R] [C] [F] [H] [D] [C] [Y] [G] [R] [A] [S] [S] [C] [P] [K] [T] [Y] [P] [Q] [G] [G] [C] [D] [D] [C] [R] [K] [C] [E] [C] [D] [R] [A] [A] [C] [L] [A] [S] [S] [Y] [N] [Y] [F] [P] [D] [Q] [C] [G] [R] [K] [T] [C] [4] 120
P81458	1 [16] [L] [L] [Q] [F] [R] [M] [I] [K] [E] [T] [K] [G] [F] [A] [I] [A] [Y] [S] [H] [Y] [G] [C] [Y] [G] [G] [G] [R] [G] [P] [K] [D] [R] [C] [F] [H] [D] [C] [Y] [G] [R] [A] [S] [S] [C] [P] [K] [T] [Y] [P] [Q] [G] [G] [C] [D] [D] [C] [R] [K] [C] [E] [C] [D] [R] [A] [A] [C] [L] [A] [S] [S] [Y] [N] [Y] [F] [P] [D] [Q] [C] [G] [R] [K] [T] [C] [4] 121
P59071	1 [16] [L] [L] [E] [F] [G] [R] [M] [I] [K] [E] [T] [K] [G] [F] [A] [I] [A] [Y] [S] [H] [Y] [G] [C] [Y] [G] [G] [G] [R] [G] [P] [K] [D] [R] [C] [F] [H] [D] [C] [Y] [G] [R] [A] [S] [S] [C] [P] [K] [T] [Y] [P] [Q] [G] [G] [C] [D] [D] [C] [R] [K] [C] [E] [C] [D] [R] [A] [A] [C] [L] [A] [S] [S] [Y] [N] [Y] [F] [P] [D] [Q] [C] [G] [R] [K] [T] [C] [4] 121
A8CG84	1 [16] [L] [L] [E] [F] [G] [R] [M] [I] [K] [E] [T] [K] [G] [F] [A] [I] [A] [Y] [S] [H] [Y] [G] [C] [Y] [G] [G] [G] [R] [G] [P] [K] [D] [R] [C] [F] [H] [D] [C] [Y] [G] [R] [A] [S] [S] [C] [P] [K] [T] [Y] [P] [Q] [G] [G] [C] [D] [D] [C] [R] [K] [C] [E] [C] [D] [R] [A] [A] [C] [L] [A] [S] [S] [Y] [N] [Y] [F] [P] [D] [Q] [C] [G] [R] [K] [T] [C] [4] 137
P81478	1 [16] [L] [L] [Q] [F] [R] [M] [I] [K] [E] [T] [K] [G] [F] [A] [I] [A] [Y] [S] [H] [Y] [G] [C] [Y] [G] [G] [G] [R] [G] [P] [K] [D] [R] [C] [F] [H] [D] [C] [Y] [G] [R] [A] [S] [S] [C] [P] [K] [T] [Y] [P] [Q] [G] [G] [C] [D] [D] [C] [R] [K] [C] [E] [C] [D] [R] [A] [A] [C] [L] [A] [S] [S] [Y] [N] [Y] [F] [P] [D] [Q] [C] [G] [R] [K] [T] [C] [4] 122
P86368	1 [16] [L] [L] [E] [F] [G] [R] [M] [I] [K] [E] [T] [K] [G] [F] [A] [I] [A] [Y] [S] [H] [Y] [G] [C] [Y] [G] [G] [G] [R] [G] [P] [K] [D] [R] [C] [F] [H] [D] [C] [Y] [G] [R] [A] [S] [S] [C] [P] [K] [T] [Y] [P] [Q] [G] [G] [C] [D] [D] [C] [R] [K] [C] [E] [C] [D] [R] [A] [A] [C] [L] [A] [S] [S] [Y] [N] [Y] [F] [P] [D] [Q] [C] [G] [R] [K] [T] [C] [4] 121

II. SVSPs Family

Accession	Description	Links
Q9PT51.1	RecName: Full=Beta-fibrinogenase brevinase; AltName: Full=Snake venom serine protease; Short=SVSP; Contains: RecName: Full=Beta-fibrinogenase brevinase chain A; Contains: RecName: Full=Beta-fibrinogenase brevinase chain B	Related Information
BAM44992.1	hypothetical protein [Gloydius blomhoffii]	
E0Y418.1	RecName: Full=Serine protease VLSP-1; AltName: Full=Snake venom serine protease; Short=SVSP; Flags: Precursor	Related Information
E0Y420.1	RecName: Full=Serine protease VLSP-3; AltName: Full=Snake venom serine protease; Short=SVSP; Flags: Precursor	Related Information
Q9PT40.1	RecName: Full=Venom serine proteinase-like protein 2; Short=VLP2; Flags: Precursor	Related Information
E0Y419.1	RecName: Full=Beta-fibrinogenase; Short=VLBF; AltName: Full=Snake venom serine protease; Short=SVSP; Flags: Precursor	
P84788.1	RecName: Full=Thrombin-like enzyme elegaxobin-1; Short=SVTLE; AltName: Full=Elegaxobin I; AltName: Full=Fibrinogen-clotting enzyme; AltName: Full=Snake venom serine protease; Short=SVSP	
ADP88560.1	serine beta-fibrinogenase-like protein precursor [Dabolia siamensis]	Related Information
O13059.1	RecName: Full=Snake venom serine protease 1; Short=SVSP 1; Flags: Precursor	
P18964.1	RecName: Full=Factor V activator RVV-V alpha; AltName: Full=Russel's viper venom FV activator alpha; Short=RVV-V alpha; AltName: Full=Snake venom serine protease; Short=SVSP	Related Information
AD147565.1	serine protease [Echis carinatus sochureki]	
lcl Query_10001	lcl Query_227806 KLK14	
lcl Query_10002	KLKB1	
Query_10001	1-----XXXXXXXXX[5]XXXKV[LGKHNLK]VEF[EQ]V[D/A-QA]PHPEYN[R]K[NKD]MLIRL-----RP[RLP]AKNG-----CAN[V]V[SKQC]KAY[G-KITS]H[LCAGV/QXXXXXXGDSGGPL]CHG[V]G[VSWG]P[CAQ]G[HPGVYXXXXXXWI]N[I]K[NWIRSLYDGF]ex167748	
Query_10002	1[369]J[L]CQTSRSPVCV[Q]P[RE]Q[R]-----VVGGSNRSAG[E]P[V]V[LHT]VLPV[S]QCGG[I]I[Q]QW[LTA]AHC[R]5[E]HWDIY[SI]IL[QS]H[N]ETAFF[V]V[K]I[I]HPRYE[TE]D[DI]L[L]KLRP[N]SA[Q]Q[P]CLPSREELNAYT[C]V[GNG]-T[SRG]SIT[D]LQKV[I]L[P]ABC[P]Y[PE]RTIT[DN]LCAGY[XXXXXX]GDSGGPL[C]4[J]N[V]V[GI]SWG[S]CA[PG]PGVYTNV[RF]DWI[EQ]TLE[X]-----629	
Q9PT51	1GMHYIYLGVHNVSQYDDEQRRYPKKYFCLSSRNYPQNDNDIMLIRLNPVRNSAHIAPLSLPSSPP--SVGSVCRVMGNGTITSFNHETYPDVPHCANINILDYEVCRAYAGLPATSRTLCAGILEGGKDSKRGDSGGPLICHGEIQGIVSWGGNICAQPREPGLYTKVFYDIDWIQSIAGNTTVNCPP---233	
BAM44992.1	1MVLIRVLANLILQLSYAQSSSELVIGGDECHINERSLVVLFN--S-SFLCGGTLINERWVLTAAHCDMKNFQMLFGVHKKILNEDEQTRDPKEKFCPNKKKKDDENDKDIMLIRLDSPVNSSEHIAPLSLPSSPP--TVDSVCRIMGNGTISKTEETYPDVPHCANINILDHVTCRAAYPVLAAESTLCAGILEGGKDTCVGDSGGPLICHGQIQGIVSWGGHPCGQSGSPGVYTKVFDHLDWIKSIAGNTAATCP---258	
E0Y418	1MVLIRVLANLIVLHLSYAQSSSELVIGGDECHINEHPFLALMYN+TS-MKFRBCGOTLLINERWVLTAAHCDMENMQIYLGVDKRNPNKQDQTRVPKEMFFCLSNKSYTPWDKDIMLIRLNSPVYTSHTIAPLSLPSSPP--TVGSVCRIMGNGAITSPHETYPDVPHCANIEIYDVSCKRAYGGLPEKSRTLCAGVLQGGIDTCLADSGGPLICHGQFQGIIVAMGRHPCAPQLPAPYTKVFYDSYDWIQSIAGNTAATCP---260	
E0Y420	1MVLIRVLANLIVQLSYAQSSSELVIGGDECHINERSLVLYLNSN--PQCGOTLINERWVLSAAHCDMENMEIYLGVBHLSLPHKQKRRQPKKFFCLSSKSYTTEWOKDIMLIRLNPVTSHTIAPLSLPSSPP--SVGSVCRIMGNGTITSFNHETLDPHCANINILNVTVCRAASPRLPQSRTLCAGILQGGIDACKGDSGGPLICHGQIQGIVSWGHRHPCAPLAPGHYTNVFYDIDWIQSIAGNTATCP---259	
Q9PT40	1MVLIRVLANLIVQLSYAQSSSELVIGGDECHINEHPPFVALHT+RS-KRYFCAGTLINERWVLTAAHCDRKNIRIILGVHNSVPHEDQDIRVPEKFFCLSSKSYTTEWOKDIMLIRLKKPVNDSTHIVPLSLPSSPP--SVGSVCRIMGNGTITTKVYTPDVPHCANINMFDSVCRKRVKRLPEKSRTLCAGILQGGIDSKVDSGGPLICHGQIQGIVSWGHRHPCAPLPHKPALYTNVFYDIDWIQSIAGNTATCP---260	
E0Y419	1MVLIRVLANLILQLSYAQSSSELVVGDECHINERSLVFLYN--SS--FGCGOTLINERWVLSAAHCDMENMRIYLGWHNFSLPMNQKRRVAKKFFCLSSKSYTTEWOKDIMLIRLKNRPVYTSHTIVAPLSLPSSPP--SVGSVCRIMGNGAITSPHETYPDVPHCANINILNVTVCRAAHWLPQAQSRTLCAGILQGGIDTCRGDSGGPLICHGQIQGIVSWGDNPCAPLKPGHYTNVFYDIDWIQSIAGNTTATCP---257	
P84788	1-----VIGGDECHINEHPFLVLVY--Y-DYQCGOTLINERWVLTAAHCHNGKMEIYLGVBHKKVPNKDVORRVPEKFFCDSSKSYTKWNKDIMLIRLDRPVRSSEHIAPLSLPSSPP--SVGSVCRVMGNGTITSFQETYPDVPHCAKINILDYSECRAYPGLPPKSRTLCAGVLEGKDTCCGDSGGPLICHGQFQGIIVSWGDDPCAQPHPEPGSYTNVFDHLDWIKGIAGNTATATCP---233	
ADP88560	1MVLIRVLANLIVQLSYAQSSSELVVGDECHINERSLVAIFR--S-TGFCSGTLINERWVLTAAHCDMENRVIYLGVBHNLFLNNAS--RLPKEKFFCLSSKSYTTEWOKDIMLIRLDRPVTSHTIAPLSLPSSPP--SVGSVCRIMGNGAITSPHETYPDVPHCANINILPVSVCRAYKGLPAQSRTLCAGILEGGIDGSCMGDSGGPLICHGMRHGIIVAMGDDPCAQPHRPHVYTNVFYDIDWIQSIAGNTAATCP---256	
O13059	1MVLIRVLANLILQLSYAQSSSELVVGDECHINERSLVAIFR--S-TGFCSGTLINERWVLTAAHCDRNNFMKFGANSQKVLNEDEQIRNKEKFCPNKKKNNEVLKDIMLIRLDSVNSSEHIAPLSLPSSPP--SVGSVCRIMGNGSITTKVYTPDVFPYCANILDLDAECKPGYPELLPEYRTLCAGIVQGGKDTCCGDSGGPLICHGQFHHIVSYGHPGCPQLKPGIYTTVFEDYNWIKSIAGNTAATCP---238	
P18964	1-----VVGDECHINEHPFLVALYT+TS-STINCGGALINERWVLTAAHCDRNIRIRLGMHSHKIRNEDEQIRVPAGKYFCLMTPFNGLDKDIMLIRLRPVYTSHTIAVSLPSSRP--GVGSRCRIMGNGSITTEDTYPDVPHCTNIFIVKHKCEPLYPWPAQSRTLCAGILEGGKDTCCGDSGGPLICHGQIQGIVAGGSEPCQHLKPAVYTKVFEDYNWIKSIAGNRTVTCPP---236	
AD147565	1MVLIRVLANLIVQLSYAQSSSELVVGDECHINEHPFVALHT+RS-KRFRCTGTLINERWVLTAAHCDRNIRIRLGVHNKVRNEENRVPAREKVPYCSSTKYTTEWOKDIMLIRLKNRPVNNSHTIAPLSLPSPA--SVGSVCRIMGNGTITTKVYTPDVPHCANIKIFDYSVCRGAYKRLPEKSRTLCAGVLEGGIDCKADTGGPLICHGQFQGIASWGGQPCAQLKPALYT-----237	

III. RVV X light chain (Alpha subunit)

Accession		Description	Links
Q696W1.1		RecName: Full=Snaclec coagulation factor X-activating enzyme light chain 2; AltName: Full=VL factor X activator light chain 2; Short=VLFXA light chain 2; Flags: Precursor	Related Information
ADK22819.1		factor X activator light chain 2 [Daboia siamensis]	
ADJ67473.1		factor X activator light chain 2 [Daboia russellii russellii]	
lcl Query_10001		lcl Query_119202 CLEC19A	
lcl Query_10002		PLA2R1	

Query_10001	1	[14]XXXXXXXXXXXXQALPESILSYCPPLFWTEYEGCYRFPPIHKTWAADLYCAEF81g1KSARLXXXXSEENFVYLLVNSRVPGIITDIWGL--DLRQBENFEW/DGSPHYNYWDN[10]ESRLCVQIWIYSSXXXXXXXXXCAREFPFVCKIPSLA[3]	188	44%
Query_10002	1	[145]PWCATTSSTHEQDERWGLCPMSGSGDFFWEINTDTQCYIIRLLVSWFAAVVACDGG---APLSITFMDEQKIGLLXXXWK-EAMTWGL--WDEFTAGWWSDGAPLALNLLAD[8]--ACCAAPHLA--EQHWNFGSYSCESGLPFWCKIYN[1107]	1411	29%
Q696W1	1	MGRSISVSGLLAVFLSLSGTGAGLDCPPDSSLYRYFCYRVFKLQ-KWADAERFCMEHP---NNGHLVSIESMEEAEPVQALLSKITGKFITHFWIGLITEDKKQQCSSEWSGDSSVSDNLDKR	158	
ADK22819	1	MGRFISVSGLLVFLSLSGTGAGLDCPPDSSLYRYFCYRVFKH-KTWEAAERFCMEHP---NNGHLVSIESMEEAEPVAKLLSNITEKFITHFWIGLMIKDKQECCSSEWSGDSSVSDNLDKR	158	
ADJ67473	1	MGRFISVSGLLAVFLSLSGTGAGLDCPPDSSPYRYFCYRVFKLR-KWEAAERFCMEHP---NNGHLVSIESMEEAEPVAKLLSNTTGKFITHFWIGLRIKDKQECCSSEWSGDSSVSDNLDKE	158	

IV. RVV X light chain (Beta subunit)

Accession	Description	Links
Q4PRC8.1	RecName: Full=Snaclec 5; AltName: Full=C-type lectin-like 5; Flags: Precursor	Related Information
Q4PRC9.1	RecName: Full=Snaclec 4; AltName: Full=C-type lectin-like 4; Flags: Precursor	Related Information
AAB22478.1	coagulation factor X activating enzyme light chain, RVV-X-light chain, LC1=metalloproteinase with disintegrin (platelet aggregation inhibitor)-like and C-type lectin-like domains [Vipera russelli=Russell's viper, Siamensis, venom, Peptide, 123 aa]	
lcl Query_10001	lcl Query_125072 CLEC19A	
lcl Query_10002	PLA2R1	
Query_10001 1	[14]XXXXXXXXXXXXX[LPSRLSYSCP--WTF--YBGICY--FFD--KTWA-ADLC-C-EFSLG-KAKLXXXXSE--FV--LVNRSY--P--PTIWMGLN--DLRQE-N-EWTDG--DY--W][12]EE--C-QDHYYS[4]XXXXXXXXCS--FFVCK--P[5]188 48%	
Query_10002 1	[606]-----[E--FNRSC--GW-S-Y-L-NCYKVF--S-K-TW--AE--C-RPF--[HL-S--GVVEEDF--KL--M--XD--RQ-WIG-N--NPLSG--EWSDG--VSS--L--S]--ENC--AKTK--WEP--FFD--CNS-H--LCK--P[662]1411 47%	
Q4PRC8 1	MGRFISISFGLLVMLFSLSGTGAKQDCLSDWSF--YBGICYKVFNEKTIWEDAEKFTBQK---KGSHLLSLNIAEADFVLKKTLMAL-KD--GVIMMGLN--DVWNECHNGWGTGAKLDYKAWN	EGTNCFVFKIAKNHNSHMDCSSTHNFVCKFRV148
Q4PRC9 1	MGRFISISFGLLVVFLSLSGTEAAFCPSGWSA--YDQNCYKVFTEENNWADA EKFTBQK---KGSHLVSLHSREEEFVVMILISENL-EY--PATWIGLG--NNWKDCRMWSDRGNVKYKALA	EESYCLIMITHEKVNKSMTCNFIAPVVCKF--146
AAB22478 1	-----VLD-----CPSGWS--YBQRCYKGFNDLKNWTDAEKFTBQK---KGSHLVSLHSREEEFVVMILISENL-EY--PATWIGLG--NNWKDCRMWSDRGNVKYKALA	EESYCLIMITHEKEWKSRTCNFIAPVVCKF--123

V. RVV X heavy chain

[illegible]

VI. CRISPs (Helveprins) Family

Accession		Description	Links
ACE73567.1		cysteine-rich secretory protein Dr-CRPK [Daboia russelii]	
ACE73571.1		cysteine-rich secretory protein Pg-CRP [Ceropheidon godmani]	
ACE73568.1		cysteine-rich secretory protein Dr-CRPB [Daboia russelii]	
ACE73566.1		cysteine-rich secretory protein Cv-CRP [Crotalus viridis]	
ACE73560.1		cysteine-rich secretory protein Ch-CRPKa [Crotalus horridus]	
ACE73575.1		cysteine-rich secretory protein Da-CRPa [Deinagkistrodon acutus]	
AAB48565.1		prepro-cysteine-rich venom protein [Protobothrops mucrosquamatus]	
Ic Query_10001		Ic Query_208126 CRISP	
Ic Query_10002		serotriflin	
Query_10001	1	[40]SVDFDSESPPKPEIQNEIVDLHNSLRSSVPTASNNMLKMEWYPEAANAERWAFRCILNHSFYNSRVIXXKCGENMSSPWTWITWETKFNFTYGVGANPPNAVIGHYTTQVVVYKSYVGCAAA CPSS YNYFTVC XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXNPCRHENVFSNCNDLVKGCQNNNMKSNCPSFCRNEIXX	262 92%
Query_10002	1	[19]VDFDSESPPKPEIQNEIVDLHNSLRSSVPTASNNMLKMEWAAARWAACRISPGRGKCGENMSSPWTWITWETKFNFTYGVGANPPNAVIGHYTTQVVVYKSYVGCAAA CPSS YNYFTVC XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXNPCRHENVFSNCNDLVKGCQNNNMKSNCPSFCRNEIXX	241 84%
ACE73567	1	[19]SVDFDSESPPKPEIQNEIVDLHNSLRSSVPTASNNMLKMEWYPEAANAERWAFRCILNHSFYNSRVIGGKCGENIYMSPPMKWTAIHAWHGEYKDFYGVGANPPNAVIGHYTTQVVVYKSYRIGCAAAAYCPSSSEYNYFTVCQVCPAGNIIGKIATPTTSGPPCGDCPSACDNGLCTNPNCTREDKYTNCSLVQKSGCQDTWMQSNCPAICFCQNKII	239
ACE73571	1	[19]SVDFDSESPPKPEIQNEIVDLHNSLRSSVPTASNNMLKMEWYPEAANAERWAFRCIESHSRNSRVIGGKCGENIYMSPIPITWNEIIGHWGEYKDFYGVGANPPNAVIGHYTTQVVVYKSYRIGCAAAAYCPSSSEYNYFTVCQVCPAGNIRGKTATPTKSGPPCGDCPSACDNGLCTNPNCTREDKYTNCSLVQKSGCQDTWMQSNCPAICFCQNKII	240
ACE73568	1	SVDFDSESPPKPEIQNEIVFHNLSLRSSVPTASNNMLKMEWYPEAANAERWAFRCILNHSFYNSRVIGGKCGENIYMSNPWKTEIRKWHDEKKNFTYGVGANPPNAVIGHYTTQVVVYKSYRIGCAAAAYCPSSSEYNYFTVCQVCPAGNIRGKTATPTKSGPPCGDCPSACDNGLCTNPNCTREDKYTNCSLVQKSGCQDTWMQSNCPAICFCQNKII	221
ACE73566	1	SVDFDSESPPKPEIQNEIVDLHNSLRSSVPTASNNMLKMEWYPEAANAERWAFRCIESHSRDSRVLEGKCGENIYMSPPMKWTEIIGHWGEYKDFYGVGANPPNAVIGHYTTQVVVYKSYRIGCAAAAYCPSSSEYNYFTVCQVCPAGNIIGKIATPTTSGPPCGDCPSACDNGLCTNPNCTREDKYTNCSLVQKSGCQDTWMQSNCPAICFCQNKII	221
ACE73560	1	SVDFDSESPPKPEIQNEIVDLHNSLRSSVPTASNNMLKMEWYPEAANAERWAFRCIESHSRDSRVLEGKCGENIYMSPPWKTEIIGHWGEYKDFYGVGANPPNAVIGHYTTQVVVYKSYRIGCAAAAYCPSSSEYNYFTVCQVCPAGNIRGKTATPTKSGPPCGDCPSACDNGLCTNPNCTREDKYTNCSLVQKSGCQDTWMQSNCPAICFCQNKII	221
ACE73575	1	SVDFDSESPPKPEIQNEIVDLHNSLRSSVPTASNNMLKMEWYPEAANAERWAFRCIESHSRDSRVLEGKCGENIYMSPPMKWTEIIGHWGEYKDFYGVGANPPNAVIGHYTTQVVVYKSHHLVC-CCLPLSKYSYFTVCQVCPAGNIIGKIATPTTSGPPCGDCPSACDNGLCTNPNCTQEDKYTNCSLLQQDSQCQDAGHSEKCSASFCQNKII	220
AAB48565	1	-----MEWYPEAANAERWAFRCIESHSRDSRVIGGKCGENIYMSPPAKWTDIIGHWGEYKDFYGVGANPPNAVIGHYTTQVVVYKSYRIGCAAAAYCPSSSEYNYFTVCQVCPAGNIIGKIATPTTSGPPCGDCPSACDNGLCTNPNCTQEDKYTNCSLVQKSGCQDAGHSEKCSASFCQNKII	183

VII. Snaclec Family

Accession	Description	Links
Q38L02.1	RecName: Full=Snaclec dabocetin subunit alpha; AltName: Full=C-type lectin-like 8; Flags: Precursor	Related Information
ADK22822.1	dabocetin beta subunit [Dabolia russelli russelli]	
ADK22832.1	P31 beta subunit [Dabolia siamensis]	
Q719L9.1	RecName: Full=Snaclec crotoctetin-1; Short=CRC1; Flags: Precursor	Related Information
B4XSY9.1	RecName: Full=Snaclec A14; AltName: Full=C-type lectin A14; Flags: Precursor	Related Information
P81113.1	RecName: Full=Snaclec alboaggregin-A subunit beta; AltName: Full=Alboaggregin-A subunit 3; Short=AL-A subunit 3	
Ic Query_10001	Ic Query_48204 PLA2R1	
Ic Query_10002	CLEC19A	

Query_100011

Query_100021

[Q38L02](#)

[ADK22822](#)

[Q719L9](#)

[B4XSY9](#)

[P81113](#)

1

1

1

1

1

1

[165]

[14]

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[14]

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[14]

-----SG-G- --CQIFWLNITVQ CYDINLISVLSWNAWACQDQ-----A/L SITDMHQKYIGLIXX/TKAWG- W'GLN--GOLDTAW W WSDGA/LANWLNHP[7]-ACCA/NLK--GN--W'S SCE:G P/VCKVYLA[1107]

XXXXXXXXXXXXXXXXXLPBILBYCP:W--TEYEGCYRFFP-19KTWFAA/C:EP:1gIK A/LXXXXBEEVFP/LVSRVP/PFD- WNGLN--D RQE: N EWTGDS DY:W GHQ[10]E/CQDWHRY:XXXXXXXXXCSR PPVCK P/LA[9]

NGRPIFVSFGLLVVFVLSLGGAD--CPSEW--SEBDSHCYVFP-LKTWDAEKFCTQQA---NGHLASISVEEAMFVAGLASFLTKRYB-AMTGLRdgsEKGQCSHRWDGSAVSFVTK--YTKFGLRKE-TKH-EWTLPCDERPPICKSWVLH

NGRPIFVSFGLLVVFVLSLGGADQCLSDW--SFYEGCYKVFH-EKKTWEDAERKFCNEQV---NGGYLVSPRSSEEMDFVIMTFFPIRFD--F-FWIGLR--DFWRDCYWRSDGVNLDYKAN--SR

NGRPIFVSFGLLVVFVLSLGGTEAGSFCPSGNW--SFYEGQHCYKVE-PLKNWTDAEKFCREQH---KGSHLASIHSEEEAFVSKVASKVLKFGS---VWIGLN--DPWHNCNWEWSDNARFDYKAMTRRP

NGRPIFVSFGLLVVFVLSLGGADPDCPSGNW--SAYDQCYRVIR-QLKTWEDAERFCTKGA---KGAILVSVESAGEADFVAQVAENIKQKRYT-VWIGLRIGHKQCCSTKWSGSSVRYENLLKSY

NGRPIFVSFGLLVVFVLSLGGADPDCPPDW--SAYDQCYKAPD-EPKESGDAERFCTQQA---NGHLVSVESVEAEFVAQLISEBIFTSADY-VWIGLRdgsKAPVCYKRWDSGSRVYKVIIRF

-----GFDCPFQW--SSYEGCYKYVN-KKMNWEDAESFCREQH---KRSHLVSPHSSGEVDFV---VSKTTPILRYDFVWNGLS--DIWKECTKEWSDGARLDYKANSG--

KSYCLVSK---TTNN-EWLSMDCSRTRYPVCKFXG--

1411

188

154

150

150

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516

536

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150

125

VIII. KSPI Family

Accession		Description		Links
Ic Query_140082		kunitoxin		
Q2ES47.1		RecName: Full=Kunitz-type serine protease inhibitor 4; AltName: Full=Kunitz protease inhibitor 4; AltName: Full=Kunitz protease inhibitor IV; Flags: Precursor		Related Information
CAL69605.1		trypsin inhibitor-4 precursor [Dabolia siamensis]		Related Information
CAL69613.1		trypsin inhibitor-5 precursor [Dabolia siamensis]		Related Information
Query_140082	1	MSSG LLLLLGFTLMA L PXXXXXXXXXXXXXXXXXG C A R FYYNPASKKC EF YGGC GNANNF T D C TC XXXXXXXX	91 79%	
Q2ES47	1	MSSGLLLLLGLLTLMAELTPISGQDRPKFCHLPVDSGICRAHIPRFYYPASKQCQCFIYGGCGGNANFPETRDQCRHTCGGK-----	84	
CAL69605	1	MSSGLLLLLGLLTLMAELTPISGHDRPKFCYLPADPGECHAYIRSFIYDSESKKCKEFIYGGCGGNANFPTRDKCRQTCRAPRKGRT-	90	
CAL69613	1	MSSGLLLLLGLLTLMAELTPISGHDRPKFCYLPADPGECLAHMRSFIYDSESKKCKEFIYGGCGGNANFPFRDKCRQTCGASAKGRPT-	90	

IX. VNGF

Accession		Description	Links
Ic Query_80281		NGF	
AEH59580.1		venom nerve growth factor 2 [Dabola russelii]	
Query_80281	1	MSMLCYTLIIAFLIGIRAAPKSEDNVSLRSPATPDLSDTSCAKTHEALKTSRNTDQHYPAPNKAEDQEFGSAANIIVDPKLFQKRRFQSPRVLFSTQPPPLSRDEQSVFELDNADSLNRRIRAKRATHPVHNQGEFSVCDSSVSVVANKTTATDMRGHVVTVHVDVNLNNVYFQYFFETKCKNPNVPFSGCRGIDAKHWN SYCTTTDTTFVRALTMERNQASWRFIRINTACVCVISRKNDNFQXALK 248 100%	
AEH59580	1	MSMLCYTLIIAFLIGIRAAPKSEDNVSLRSPATPDLSDTSCAKTHEALKTSRNTDQHYPAPNKAEDQEFGSAANIIVDPKLFQKRRFQSPRVLFSTQPPPLSRDEQSVFELDNADSLNRRIRAKRATHPVHNQGEFSVCDSSVSVVANKTTATDMRGHVVTVHVDVNLNNVYKQYFFE TKCKNPNVPFSGCRGIDAKHWN SYCTTTDTTFVRALTMERNQASWRFIRINTACVCVISRKNDNF----- 243	

X. VEGF

[illegible]

Fig. S4: Sequence similarity between proteins belonging to eight major venom families and their blood homologs in king cobra, *Ophiophagus hannah*. The homolog with the highest identity was considered, in case of more than one homolog for a venom family.

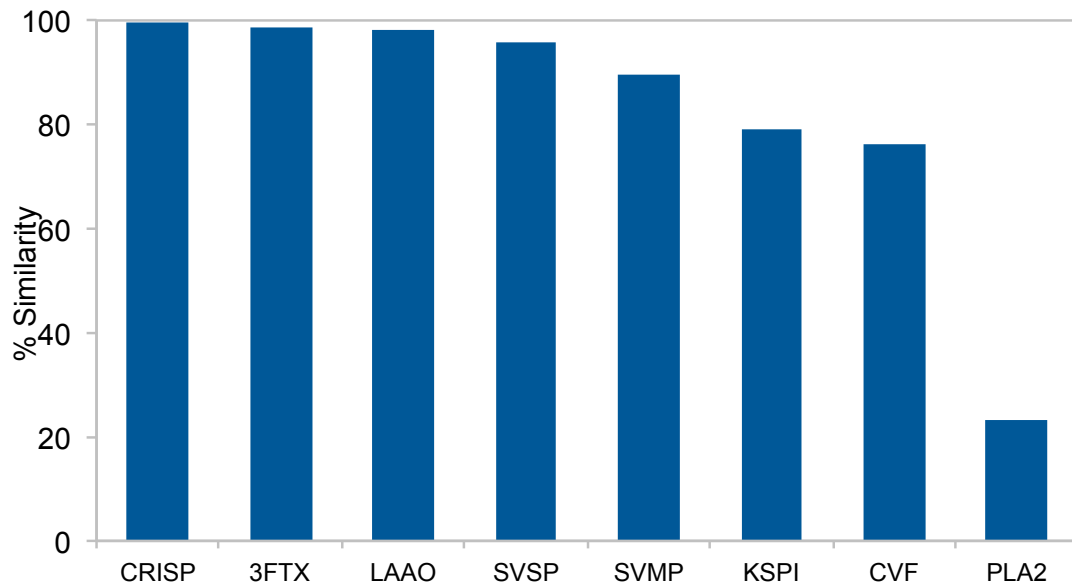


Fig. S5: Comparison of eight toxin family protein sequences from venom-associated proteins from venom gland of king cobra *Ophiophagus hannah* with the putative venom protein homologs from the predicted genome sequencing, assembly and annotation of *Ophiophagus hannah* blood (PRJNA201683; Vonk *et al.* 2013). Additional file 4 from Tan *et al.* 2015 was used as a reference for procuring the accession ID of the venom/venom gland associated protein from *Ophiophagus hannah*. Comparative analyses were performed using blastp, with the venom/venom gland associated protein sequence as the query, against PRJNA201683. In the multiple sequence alignments, the topmost sequence is from the venom/venom gland, and the remaining sequences are from blood. Red indicates an identical match in comparison in at least one of the predicted protein sequence. Blue indicates that amino acid is variable in all the sequences used for comparison. Light gray indicates non-identical amino acid.

I. 3FTX (three finger toxin family)

Accession	Description	Links
Q53B59.1	RecName: Full=Long neurotoxin OH-37; Flags: Precursor	Related Information
ETE56610.1	hypothetical protein L345_17679 [Ophiophagus hannah]	
ETE57194.1	hypothetical protein L345_17093 [Ophiophagus hannah]	
ETE56824.1	hypothetical protein L345_17464 [Ophiophagus hannah]	
ETE58964.1	hypothetical protein L345_15308 [Ophiophagus hannah]	
Q53B59	1 MKTLLLTLLVVVTIVCLDLGYSLICFTS----PHSSVTCAPGENCFLKSWCDAwcgSRGKLSFGCAATCPKVPGIDIECCSTDNCNPhpklrp	91
ETE56610	1 -----YTRICHKS----SFISETCPDGGQNLCLYKSWCDIfcgSRGERLEFGCAATCPVKPGVNIIECCSTDNCNPhpklrp	72
ETE57194	1 MKNLLLTFLVVTIVCLDLGYTLICHRV-----HGLQTCPEDEKFCFRKTTMFF---PNHPVLLMGCTYSCPTAK---YSVCCSTDCKNK-----	78
ETE56824	1 MKTVLLTLVVVTIVCLDLGHTLICVKQyTifGVTPEICADGQNLCKYKTHMVY---PGGYDHTRGCAATCPKMKNHDTVHCCTTDCKNL-----	86
ETE58964	1 MKTLLLTLLVVVTIVCLDLGHTRICLTdyskvSETIEICPDGQNFCKFKPKGI---PFLPWVNRGCAATCPKPEPKVYVDCCARDCKNR-----	86
Accession	Description	Links
Q2VBP8.1	RecName: Full=Long neurotoxin LNTX1; Flags: Precursor	Related Information
ETE56610.1	hypothetical protein L345_17679 [Ophiophagus hannah]	
ETE57194.1	hypothetical protein L345_17093 [Ophiophagus hannah]	
ETE56824.1	hypothetical protein L345_17464 [Ophiophagus hannah]	
ETE58964.1	hypothetical protein L345_15308 [Ophiophagus hannah]	
Q2VBP8	1 MKILLLTLLVVVTIVCLDLGYTTCCKYKTERI--ISETCPPGQQLCYMKTWCDVfcgSRGRVIEIGCTATCPTVKPHEQITCCSTDNCNPhpkmkqr	94
ETE56610	1 -----YTRICHKS--F--ISETCPDGGQNLCLYKSWCDIfcgSRGERLEFGCAATCPVKPGVNIIECCSTDNCNPhpklrp	72
ETE57194	1 MKNLLLTFLVVTIVCLDLGYTLICHRVHGL-----QTCEPDEKFCFRKTTMFF---PNHPVLLMGCTYSCPTAK---YSVCCSTDCKNK-----	78
ETE56824	1 MKTVLLTLVVVTIVCLDLGHTLICVKQYTI FgVTPEICADGQNLCKYKTHMVY---PGGYDHTRGCAATCPKMKNHDTVHCCTTDCKNL-----	86
ETE58964	1 MKTLLLTLLVVVTIVCLDLGHTRICLTdYSKvseTIEICPDGQNFCKFKPKGI---PFLPWVNRGCAATCPKPEPKVYVDCCARDCKNR-----	86
Accession	Description	Links
P84716.1	RecName: Full=Neurotoxin-like protein 1	
ETE58964.1	hypothetical protein L345_15308 [Ophiophagus hannah]	
ETE56824.1	hypothetical protein L345_17464 [Ophiophagus hannah]	
ETE56610.1	hypothetical protein L345_17679 [Ophiophagus hannah]	
P84716	1 -----MKCLTKYSRVSETSQCCHVQNLCKFKWQKGK---KVSRGCTATCPKPKKDEVIQCCAADKCNK-----	61
ETE58964	1 MKTLLLTLLVVVTIVCLDLGHTRICLTdYSKvseTIEICPDGQNFCKFKPKGI---PFLPWVNRGCAATCPKPEPKVYVDCCARDCKNR-----	86
ETE56824	1 MKTVLLTLVVVTIVCLDLGHTLICVKQYTI FgVTPEICADGQNLCKYKTHMVY---PGGYDHTRGCAATCPKMKNHDTVHCCTTDCKNL-----	86
ETE56610	1 -----YTRICHKS--F--SFISETCPDGGQNLCLYKSWCDIfcgSRGERLEFGCAATCPVKPGVNIIECCSTDNCNPhpklrp	72
Accession	Description	Links
Q2VBP1.1	RecName: Full=Short neurotoxin SNTX11; Flags: Precursor	Related Information
ETE57194.1	hypothetical protein L345_17093 [Ophiophagus hannah]	
ETE58964.1	hypothetical protein L345_15308 [Ophiophagus hannah]	
ETE56824.1	hypothetical protein L345_17464 [Ophiophagus hannah]	

Q2VBP1	1	MKTL LL TLV VT IVCLDLGYTLICHRVHGL-----QTCEPDQKFCFRKTTMFFPNH-PVLLMGCTYSCPT E K---YSVCCSTD K CNK	78
ETE57194	1	MKNLLLTFLVVTIVCLDLGYTLICHRVHGL-----QTCEPDEKFCFRKTTMFFPNH-PVLLMGCTYSCPT A K---YSVCCSTD K CNK	78
ETE58964	1	MKTL LL TLV VT IVCLDLGHTRICLT D YSKVSETIEICPDGQNF C FKFKGI-PFLPWVNRGCAATCPK P EPKVYV D CCARD K CNR	86
ETE56824	1	MKT V LLTLV VT IVCLDLGHTLICV K QYTFGV T PEICADGQNL C YK T WHMVY-PGGYDHTRGCAATCPK M KNHD T VHCC T TDKCNL	86

Accession	Description		Links
A8N286.1	RecName: Full=Haditoxin; AltName: Full=Muscarinic toxin-like protein 3 homolog; Short=MTLP-3 homolog; Flags: Precursor		Related Information
ETE56205.1	hypothetical protein L345_18084 [Ophiophagus hannah]		
ETE58964.1	hypothetical protein L345_15308 [Ophiophagus hannah]		
ETE57194.1	hypothetical protein L345_17093 [Ophiophagus hannah]		
ETE56824.1	hypothetical protein L345_17464 [Ophiophagus hannah]		
ETE56610.1	hypothetical protein L345_17679 [Ophiophagus hannah]		
A8N286	1	MKTL LL TLVV VT IV V LDLGY T TKCYNHQ ST TPPETE I ICPDSGYFCYKSSWIDGR-----EGR I ERGCT I TCPE L TP G KYV C CR R DKCNQ-----	86
ETE56205	1	-----YTTKCYNHQ ST TPPETE I ICPDSGYFCYKSSWIDGRvffleptlelpnaPENWRSRR T CCL--CPAW V PlrSHPVARQSKQCKErgswtvvprlsqqqrlegetffrgrgremlgel	115
ETE58964	1	MKTL LL TLVV VT IVCLDLGHTRICLT D YSKVSETIEICPDGQNF C FKFKGI-----PFLPWVNRGCAATCPK P EP-KVYV D CCARD K CNR-----	86
ETE57194	1	MKNLLLTFLVV VT IVCLDLGYTLICHRVHGL-----QTCEPDEKFCFRKTTM-----ff-----PNHPVLLMGCTYSCPT A KY-----SVCCSTD K CNK-----	78
ETE56824	1	MKT V LLTLVV VT IVCLDLGHTLICV K QYTFGV T PEICADGQNL C Y K TWHMVY-----PGGYDHTRGCAATCPK M KN-HDTVHCC T TDKCNL-----	86
ETE56610	1	-----YTRICHKSSFI---SETCPDGQNL C YLKSWCDIF-----cgSRGERLEFGCAATCPE V KVP-GVNI E CCSTD N CNPhpklrp-----	72

Accession	Description	Links	
Q2VBN1.1	RecName: Full=Muscarinic toxin MTX6; Flags: Precursor	Related Information	
ETE56824.1	hypothetical protein L345_17464 [Ophiophagus hannah]		
ETE58964.1	hypothetical protein L345_15308 [Ophiophagus hannah]		
ETE57194.1	hypothetical protein L345_17093 [Ophiophagus hannah]		
ETE56610.1	hypothetical protein L345_17679 [Ophiophagus hannah]		
ETE56656.1	hypothetical protein L345_17632 [Ophiophagus hannah]		
Q2VBN1	1	MKTL LL TLV VT IV I CLDLGYTL C LT HE SLF F ETTETC S DGQNL C Y A -----KWF A VF--PGA R R D GCAATCP I KVPLE I VNCCTTDKCNL-----	86
ETE56824	1	MKT V LLTLV VT IVCLDLGHTLICV K QYTFGV T PEICADGQNL C Y K -----TW H MVY--PGGYD H TRGCAATCPKMK N HDTV H CC T TDKCNL-----	86
ETE58964	1	MKTL LL TLV VT IVCLDLGHTRICLT D YSKVSETIEICPDGQNF C FK-----KF P KGI--PFLPWVNRGCAATCPKPE P KVYV D CCARD K CNR-----	86
ETE57194	1	MKNLLLTFLVVTIVCLDLGYTLICHRVHGL-----QTCEPDEKFCFRK-----TM F F--F--PNHPVL L MGCTYSCPTAK - --YSVCCSTD K CNK-----	78
ETE56610	1	-----YTRICHKSSFI---SETCPDGQNL C YLK-----Sw C DI F cgSRGERLEFGCAATCEV K PGVNI E CCSTD N CNPhpklrp	72
ETE56656	1	-----MTCYTQYSLSPPTTKTCPDGQNL C YKRLelpnapenwrsrrtclchawvplrsrsiAG Q SKQc-KERNK F FRGCAACPKAEH N E-----	84

Accession	Description	Links
Q53B61.1	RecName: Full=Weak neurotoxin OH-72; Flags: Precursor	Related Information
ETE58964.1	hypothetical protein L345_15308 [Ophiophagus hannah]	
ETE56824.1	hypothetical protein L345_17464 [Ophiophagus hannah]	
ETE57194.1	hypothetical protein L345_17093 [Ophiophagus hannah]	
ETE56610.1	hypothetical protein L345_17679 [Ophiophagus hannah]	

Q53B61	1	-----LTLV VT IVCLDLGYTL C CL C PEYCKR I HTC S DGEN C FK G FY G K---QL G K Q RRGCAATCPEGK P NE I VQCCSTD D CNH-----	81
ETE58964	1	MKTL LL TLV VT IVCLDLGHTRICLT D YSKVSETIEICPDGQNF C FKFK P KGI---PFLPWVNRGCAATCPKPE P KVYV D CCARD K CNR-----	86
ETE56824	1	MKT V LLTLV VT IVCLDLGHTLICV K QYTFGV T PEICADGQNL C YK T WHMVY---PGGYD H TRGCAATCPKMK N HDTV H CC T TDKCNL-----	86
ETE57194	1	MKNLLLTFLVVTIVCLDLGYTLICHRVHGL-----LQTCEPDEKFCFRKTTM F F---PNHPV L LMGCTYSCPT A K - --YSVCCSTD K CNK-----	78
ETE56610	1	-----YTRICHK S SF---ISETCPDGQNL C YLKSWCDIFcgSRGERLEFGCAATCEV K PGVNI E CCSTD N CNPhpklrp	72

Accession	Description	Links
Q2VBN2.1	RecName: Full=Weak neurotoxin WNTX34; Flags: Precursor	Related Information
ETE58964.1	hypothetical protein L345_15308 [Ophiophagus hannah]	
ETE56824.1	hypothetical protein L345_17464 [Ophiophagus hannah]	
ETE57194.1	hypothetical protein L345_17093 [Ophiophagus hannah]	
ETE56610.1	hypothetical protein L345_17679 [Ophiophagus hannah]	

Q2VBN2 1 MKTLLLTIVVVTIVCLDLGYSLCLCPQYCKRIITCRRNGENCFKRIFYGK---LLCKQPRRGCAATCPPEAKSRIVQCCSTDICNH----- 86
ETE58964 1 MKTLLLTIVVVTIVCLDLGHTRICLTDSKVSETIEICPDGQNFCKKFPKGI---PFLPWVNRGCAATCPKPEPKVYVCCARDKCN----- 86
ETE56824 1 MKTVLLTIVVVTIVCLDLGHGLICVKQYTFIGVTPEICADGQNLCKYKTHMVY---PGGYDHTRGCAATCPKMKNHDTVHCCTTDKCNL----- 86
ETE57194 1 MKNLLTFLVVTIVCLDLGYTLICHRVHG-----LQTCPEDEKFCFRKTTMFF---PNHPVLLMGCTYSCPTAK---YSVCCSTDKCNK----- 78
ETE56610 1 -----YTRICHKSSF---ISETCPDGQNLCKYLSWCDIfcgSRGERLEFGCAATCPEVKPGVNIQCCSTDNCPHPklrp 72

II. SVMP (snake venom metalloproteases)

Accession	Description	Links
A3R0T9.1	RecName: Full=Zinc metalloproteinase-disintegrin-like ohanin; AltName: Full=Snake venom metalloproteinase; Short=SVMP; Flags: Precursor	Related Information
ETE62121.1	hypothetical protein L345_12124 [Ophiophagus hannah]	
ETE62122.1	hypothetical protein L345_12125 [Ophiophagus hannah]	
A3R0T9 1	MIQVLLVTICLVVFPYQGSSIIILESGKVNDYEVVYPQKIPVLPKSKIQRREQKMYEDTMKYEFKVNGEPVVLHLEKNKELFSKDYTTETHYSPDGREITTSPPVEDHCYYHGYIQSDIDSTAILNACNGLKgyfrHHGEAYHIEPLKFSDEAHAVYKYEN	160
ETE62121 1	MIQVLLVTICLVVFPYQGSSIIILESGKVNDYEVVYPQKIPVLPKSKIQRREQKMYEDTMKYEFKVNGEPVVLHLEKNKELFSKDYTTETHYSPDGREITTSPPVEDHCYYHGYIQSDIDSTAILNACNGLK---HHGEAYHIEPLKFSDEAHAVYKYEN	156
ETE62122 1	-----MQYEFKVNGEPVVLHLEKNKELFSKDYSETHYSPDGREITTSPPLENR-----GEGYLIEPLKLSNDEAHALFKYES	72
A3R0T9 161	IEKEDETPKICGVKHSWTESDEPIEKISQKDFLEEK-----KYLELYIVADYVMFRKYGRNVTIRMRVFDMVNYITVVYKALNIRVALIGFEIWSLKDKFVINASTKNNLLHFSIWRSTVL--RKRNDNAQLLTGVDLNGYTLGSAYLKAMCDVLQS	312
ETE62121 157	IEKEDETPKICGVKHSWTESDEPIEKISQVSISSIEE-----FRKYSRNVTAIRMRVFDMVNYITVVYKALNIRVALIGFEIWSLKDKFVINASTKNNLLHFSIWRSTVL--RKRNDNAQLLTGVDLNGYTLGSAYLKAMCDVLQS	294
ETE62122 73	LEKEDKTLKTCGVTNTTWKSDEPLKKTSTMSIEKKeylqarKYVEFYIVADNRMFRKYSRSIAAIRMRAFDIVNFINMVYKPLKVHIALIGLEIWSNKKIEISKTAGATLSHFSSWRKTVLkHKRNDNAQLLTDIDFTGSTVGLAYVGTMCNSLSS	232
A3R0T9 313	VGIVQDYSKSPYLVGAAMAHEIGHNLGMEHDTKTCSCMRGNCIMSPEEEGSDFFPMFSSCSLYDFQNYMLTTPQCLINKPSNTSIIKNAVCGNYVEEAGEECDCGSPEQCENNCCAAATCKLKPGAKCAKAGACCKKCQFKKAGAECAARNECDLPEFC	472
ETE62121 295	VGIVQDYSKSPYLVGAAMAHEIGHNLGMEHDTKTCSCMRGNCIMSPEEEGSDFFPMFSSCSLYDFQNYMLTETPQCLINKPSNTSIIKNAVCGNYVEEAGEECDCGSPEQCENNCCAAATCKLKPGAKCAKAGACCKKCQFKKAGAECAARNECDLPEFC	454
ETE62122 233	TAVIQDHSTDPIAMGATMAHEMGHNFGMNHDTDLCTCKTGPCIMA-DKQGYITPQEFSSCSLQFYQNYTMNETPQCIINRP---LIKDVI-----SP-----	320
A3R0T9 473	IGQSAECPMDRFHKNHSGCQNDQGYCFRGYCPTLAKQCITLWGSDAKVAPDECQFNNTNGNEYDYCKKTNNNVIPCKPTDvkcgrrlycTGGTENPSEGEKISS----DPCKASYSEIEDIGMVDHRTKCGEKMVCS---DGKCIPL-----	611
ETE62121 455	IGQSAECPMDRFHKNHSGCQNNQGYCFRGYCPTLAKQCITLWGSDAKVAPDECQFNNTNGNEYDYCKKTNNNVIPCKPTK-----RFPVPKPNPASKMTQallvTICLVVFPYQGRLLQRHEEKTKEYEDTMKYEFklnGEPPVVLnleknkrifskdyt	606
ETE62122	-----	

III. PLA2 (phospholipases)

Accession	Description	Links
Q9DF33.1	RecName: Full=Acidic phospholipase A2 2; Short=svPLA2; AltName: Full=APLA2-2; AltName: Full=Phosphatidylcholine 2-acylhydrolase; Flags: Precursor	Related Information
ETE72123.1	Group 10 secretory phospholipase A2 [Ophiophagus hannah]	
ETE60513.1	hypothetical protein L345_13748 [Ophiophagus hannah]	
ETE72712.1	hypothetical protein L345_01439 [Ophiophagus hannah]	
ETE56084.1	hypothetical protein L345_18206 [Ophiophagus hannah]	
ETE59137.1	Otoconin-90 [Ophiophagus hannah]	
Q9DF33	1	-----mNPANLLVLSAVCVSLL-----GASSIPQPIhLVQFNGMIRCTIPgSIPWWDYSDYGCYCGSGGSGTPVDELDRCCQVHDNCYTQAQQLTECS--PYSKRYSYDCSEg
ETE72123	1	-----aaeaqlagrgeadapaeapgrdgrfpglqlMAPTLLLALLLALPGLLrtghplGKAPSRPRR--gILQLAGMIQCTTG--RTPLAYIRYGCYCGWGGFGWPKDQVDWCCFKHDCCYGKAE--EENCA--PKTRRYPWECKDS
ETE60513		-----MIQLSTV--TYGLANFTNYGCHCGPGTQGLPVDAlDRCCSHDCCYNKVE--MYGCN--PKVLNYQFYAQRD
ETE72712		-----MVSTLLCYGDRlQIPLLALNLYGCHCGTGGFGKPLDAVDRCCFLHDCCYRHTRlSLKCHNRVKWQRYKILCKTS
ETE56084		-----MMETpYLKIYSYKCSER
ETE59137	641	rggavtqkdatvafdnslrghlfkiageepvtfsttvpesp-----SPPEESFREVCDFRSFLgW---GDNGKlKQE--FPQLGEMLYCLTN--RCPEEFELYGCFQGEGRGHPTDELDRCCFSHQCCLEQIK--RLGCQP--EKKSRSSEVVCFDH
Q9DF33	103	TLTCK-----ADNDEC*AFVC*CDRVAAICFA*--PYNKENINID-TTR-----C-----
ETE72123	136	KAKCD-----DIEDKCQKMACECDRDAAKCLAKA--PYNVTLLFWP-DTRCAEKGPTCpdd-----
ETE60513	67	KVKCV-----KSRDRCEKMVCECDQKAASCFQKHlvTYNPQFRNLP-VANCRAQRPF-----
ETE72712	75	ETECR-----S-KSICGRTACECDQLAECLTAA--KPQRKHSFYK-RDLCQGAKGSCpamhqnwtktlh-----
ETE56084	18	TVTCRgkyhkpqptrlsktgipfqdrangephlnasstpfrlgaqlhngvklrglaashnsaafvlvmpIprftisffpDDNDECGAFICNCDRVAAHCFAAS--PYNNNNYNIDLKARCQ-----
ETE59137	783	TPTCVgW-----TLCENLLCSCDKAAAECEMAA--PFNESWRLSG-RQACQEDKLAC-----rwagrvrppsspprgartsseeeesss

Accession	Description	Links
P80966.2	RecName: Full=Acidic phospholipase A2 1; Short=svPLA2; AltName: Full=APLA2-1; AltName: Full=OHV A-PLA2; Short=OHV-APLA2; AltName: Full=Phosphatidylcholine 2-acylhydrolase; Flags: Precursor	Related Information
ETE72123.1	Group 10 secretory phospholipase A2 [Ophiophagus hannah]	
ETE56084.1	hypothetical protein L345_18206 [Ophiophagus hannah]	
ETE60513.1	hypothetical protein L345_13748 [Ophiophagus hannah]	
ETE72712.1	hypothetical protein L345_01439 [Ophiophagus hannah]	
ETE59137.1	Otoconin-90 [Ophiophagus hannah]	
P80966	1	-----mNPANLLVLSAVC---VSLLGASSIPQPLH-LQFGNMIQCTVPGFlSWIKYADYGCYCGAGGSGTPVDKLDRCQVHDNCYTQAQQLPACSS---ImdsP*VKIYS
ETE72123	1	-----aaeaqlagrgeadapaeapgrdgrfpglqlMAPTLLLALLLALPGLLRTGHPLGKaPSRPRRGILQLAGMIQCTTGRT--PLAYIRYGCYCGWGGFGWPKDQVDWCCFKHDCCYGKAE--EENCA-----PKTRRYP
ETE56084	1	-----mMETPYLKIYSYKCSERTVTCCKGYH-KQPTR--LSKTG-----IPFQDRAMQEP*LNHASSTPFRLG--AQLHNGVlKRLGAASHNSAAfvlvmpIprftisf
ETE60513		-----MIQLSTVTY-gLANFTNYGCHCGPGTQGLPVDAlDRCCSHDCCYNKVE--MYGCN-----PKVLNYQ
ETE72712		-----MVSTLLCYGDRlQI---P--LLALNLYGCHCGTGGFGKPLDAVDRCCFLHDCCYRHTRLSLKCHNR-----VKWQRYK
ETE59137	641	rggavtqkdatvafdnslrghlfkiageepvtfsttvpes-----SPPEESFREVCDFRSFLQWDNG---KLQEFFPQLGEMLYCLTNRC--PEEFELYGCFQGEGRGHPTDELDRCCFSHQCCLEQIK--RLGCQPE-----KKSRSSE
P80966	102	YDCSER*TVTC*ADNDEC*AFICNCDRVAAHCFAAS--PYNNNNYNIDT*TRC-----
ETE72123	130	WECKDSKAKCDDIEDKCQKMACECDRDAAKCLAKA--PYNVTLLFWPD-TRCAEKGPTCpdd-----
ETE56084	95	FPFD-----DNDECGAFICNCDRVAAHCFAAS--PYNNNNYNIDLKARCQ-----
ETE60513	61	FYAQRDKVKCVKSRDRCEKMVCECDQKAASCFQKHlvTYNPQFRNLPV-ANCRARPF-----
ETE72712	69	LLCTSETECR-SKSICGRTACECDQLAECLTAA--KPQRKHSFYKR-DLCQGAKGSCpamhqnwtktlh-----
ETE59137	777	VVCFDHTPTCV-GWTLLENLLCSCDKAAAECEMAA--PFNESWRLSGR-QACQEDKLAC-----rwagrvrppsspprga

IV. CRISP (cysteine rich secretory proteins)

Accession		Description	Links
ACN93671.1		opharin precursor [Ophiophagus hannah]	
ETE62137.1		hypothetical protein L345_12110 [Ophiophagus hannah]	
ETE58161.1		hypothetical protein L345_16118 [Ophiophagus hannah]	
ACN93671	1	-----MIAF ^T -LLSLAAVLQQSSGTVDFASESSNKRENQKQIVDKHNALRRSVKPTARNMLQMEWNSNAAQNAKRWADRC ^S FAHSPPHLR ^A VGKFCGENLFMSSQPYAWSRVIQSWYDENKKFVYGVGANPPGSGVIGHYTQIVWYKSHLLGCAAARCS	153
ETE62137	1	myypveMIAFI ^f LLSLAAVLQQSSGTVDFASESSNKRENQKQIVDKHNALRRSVKPTARNMLQMEWNSNAAQNAKRWADRC ^S FAHSPPHLR ^T VGKFCGENLFMSSQPYAWSRVIQSWYDENKKFVYGVGANPPGSGVIGHYTQIVWYKSHLLGCAAARCS	160
ETE58161	1	-----MLILI-----PSQPGDKKK-QKEIVDLHNSLRRSVSP ^T ASNMLKM ^Q WYPEAASNAERWASNCILGHSPDYSRV ^L EGIQCGENLYKSSHPHAGSRVIQSLYDEYKYFNYGVGANLPASLIGHYTQIVWYKTYRIGCAVNYCP	135
ACN93671	154	SSKY--LYVCQYCPAGNIRGSIATPYKSGPPCGDCPSACDNLCTNPCKYKDDFSNCQSLAKQTKCQTEWIKSKCPASCFC ^H HNKII	237
ETE62137	161	SSKY--LYVCQYCPAGNIRGSIATPYKSGPPCGDCPSACVNLCTNPCKYKDDFSNCQSLAKQTKCQTEWIKSKCPASCFC ^R TEII	244
ETE58161	136	SSEYnyFYVCQYCPSGNMRGSTATPYKSGPTCGDCPSACDNLCTNPCTLYNEYTNCDSL ^V KQSSCQDEWIKSKCPASCFC ^H HNKII	221
Accession		Description	Links
ACN93671.1		opharin precursor [Ophiophagus hannah]	
ETE62137.1		hypothetical protein L345_12110 [Ophiophagus hannah]	
ETE58161.1		hypothetical protein L345_16118 [Ophiophagus hannah]	
ACN93671	1	-----MIAF ^T -LLSLAAVLQQSSGTVDFASESSNKRENQKQIVDKHNALRRSVKPTARNMLQMEWNSNAAQNAKRWADRC ^S FAHSPPHLR ^A VGKFCGENLFMSSQPYAWSRVIQSWYDENKKFVYGVGANPPGSGVIGHYTQIVWYKSHLLGCAAARCS	153
ETE62137	1	myypveMIAFI ^f LLSLAAVLQQSSGTVDFASESSNKRENQKQIVDKHNALRRSVKPTARNMLQMEWNSNAAQNAKRWADRC ^S FAHSPPHLR ^T VGKFCGENLFMSSQPYAWSRVIQSWYDENKKFVYGVGANPPGSGVIGHYTQIVWYKSHLLGCAAARCS	160
ETE58161	1	-----MLILI-----PSQPGDKKK-QKEIVDLHNSLRRSVSP ^T ASNMLKM ^Q WYPEAASNAERWASNCILGHSPDYSRV ^L EGIQCGENLYKSSHPHAGSRVIQSLYDEYKYFNYGVGANLPASLIGHYTQIVWYKTYRIGCAVNYCP	135
ACN93671	154	SSKY--LYVCQYCPAGNIRGSIATPYKSGPPCGDCPSACDNLCTNPCKYKDDFSNCQSLAKQTKCQTEWIKSKCPASCFC ^H HNKII	237
ETE62137	161	SSKY--LYVCQYCPAGNIRGSIATPYKSGPPCGDCPSACVNLCTNPCKYKDDFSNCQSLAKQTKCQTEWIKSKCPASCFC ^R TEII	244
ETE58161	136	SSEYnyFYVCQYCPSGNMRGSTATPYKSGPTCGDCPSACDNLCTNPCTLYNEYTNCDSL ^V KQSSCQDEWIKSKCPASCFC ^H HNKII	221

V. KUN (kunitoxin)

Accession		Description	Links
B6RLX2.1		RecName: Full=Kunitz-type serine protease inhibitor TCI; AltName: Full=Trypsin and chymotrypsin bi-functional serine protease inhibitor; Short=OH-TCI; Flags: Precursor	Related Information
ETE57835.1		hypothetical protein L345_16446 [Ophiophagus hannah]	
ETE56995.1		hypothetical protein L345_17293 [Ophiophagus hannah]	
B6RLX2	1	MSSGRLLLLLGLLTLWAELTPVSGLGRPKFCELPVSGFCKAYIPSFYYPNDASACQKFIYGGCGGNANKFKTIEECHRTCVG	83
ETE57835	1	MASGGLLLLLGLLTLWAELTPVSGQDCPKFCYLPAAETGPCKAKMPRFYYPNASKQCEKFTYGGCKGNDNNFKTLDQCRYTCTV-	82
ETE56995	1	MSSGGLLLLLGLLTLWAELTPVSSQDRPGFCLLRPDRGPCEGNIRAFYYSPSSNSCQEFYIYGGCQGNANRFKTNNECHHTCIVE	83

VI. LAAO (L amino acid oxidases)

Accession		Description	Links
P81383.3		RecName: Full=L-amino-acid oxidase; Short=LAO; Short=LAO; Short=Oh-LAAO; Flags: Precursor	Related Information
ETE56914.1		hypothetical protein L345_17374 [Ophiophagus hannah]	
ETE59524.1		hypothetical protein L345_14746 [Ophiophagus hannah]	
P81383	1	MND F - L LLLLLVFLGVPRSENHVINLEE---CFQEP EYENWLATASHGLTKTLNPKKIVIVGAGISGLTAAKLFREAGHEVVILEASDRVGGRICKTHREDGWYVDVGPMPRVQTHRIVREYIKKFNISLNPFRQTDENAWYLIKHVQRKMSA--NNPENF	154
ETE56914	1	L--F L LLLLLVFLGVPRSENHVINLEE---CFQEP EYENWLATASHGLTKTLNPKKIVIVGAGISGLTAAKLFREAGHEVVILEASDRVGGRICKTHREDGWYVDVGPMPRVKTHRIVREYIKKFNISLNPFRQTDENAWYLIKHVQRKMSA--NNPENF	153
ETE59524	1	MTIW-----VSENHANEQEDwmkCFEDPNYEELLNIA RNGLKTSPEKKIVIVGAGISGLTAAKLLKDAGHQVHILEASNRI GGRINTHREKDWYVELGAMRLPKAHRICREYIKKFNLSLNPFFVLSNKNAWYLFRRRRERSAvnENPNVF	147
P81383	155	GYQLNPNERGKSASQLFDETLDKVTDDCT Q KEKYDS F STKEYLIKEGKLSTGAVEMIGDFLNEEAGFHNSFLISVMDHFLFL-----NNSFDEITGGFDQLPE R FFKDMDSIVHLNSTVEKIVHINNKVTVFY--EGLSTNMRLVADYVLITATA	303
ETE56914	154	GYQLNPNERGKSASQLFDETLDKVV L R-SR R DVQAD K SNALEYLIKEGKLSTGAVEMIGDFLNEEAGFHNSFLISVMDHFLFL-----NNSFDEITGGFDQLPESFFKDMDSIVHLNSTVEKIVHINNKVTVFY--EGLSTNMRLVADYVLITATA	301
ETE59524	148	GYPMRNTELGKSAEELYKSTLDR T T K NC T RL K MKYDS Y STKEYLIKEGNLSSGAV-----AMIGDLFNKGVEYYVSFFTSvlnyitfsdENGFEETGGFDQLPNSFYQEMSRIIHLNSRVEKIIRSGKKVKVFFhkEDEDDSSLLIVDYVLVTATA	299
P81383	304	RATRLIKFVPPPLSIPKTRALRSLIYASATKIILVCTDKFWEKDGIGHGRSITDLP SRVIYYPNHDF T NGIGVLLASYTWYSDSEFY T TLSDCKVDVVMDDLVEIHNVSKDYLKSVCGKHVVQKWALDQYSMGAFSTYTPYQ I THYSQMLAQNEGRIYFA	463
ETE56914	302	RATRLIKFVPPPLSIPKTRALRSLIYASATKIILVCTDKFWEKDGIGHGRSITDLP SRVIYYPNHDF T NGIGVLLASYTWYSDSEFY T TLSDCKVDVVMDDLVEIHNVSKDYLKSVCGKHVVQKWALDQYSMGAFSTYTPYQ I THYSQMLAQNEGRIYFA	461
ETE59524	300	KATRLIKFQPPPLSHLKAYALYSLHYTSATKVVLVCTDKFWEREGIRGGVSMTDNPTRLVSYPSHDFPGGLGVLLVSYTVDDDAFFVPLSDDECLDVVMNDLSKIHNISKIYLESV CNRHVIQKWALDKFSMGAFSFPTPYQYSFFIKALFQNEGRVYFA	459
P81383	464	GEYTAHPHGW I ETSMKSAIREAINIH-NA-----	491
ETE56914	462	GEYTAHPHGW I ETSMKSAIREAINIH-NA-----	489
ETE59524	460	GEHTTYPFAWIDSAMKSAIRAASNIHlNAhksisqelkesaw	501

VII. CVF (cobra venom factor)

Accession		Description		Links
AFJ59923.1		OVF precursor protein [Ophiophagus hannah]		Related Information
ETE59418.1		Complement C3 [Ophiophagus hannah]		
ETE58564.1		Cobra venom factor [Ophiophagus hannah]		
AFJ59923	1	[908] LKV-VPEGVQKCIVTIIKLDPRAGKVDGTQREVVVKARKLDDKVPDTEIETKITIQADPVAQIIENSIDGSKLNHLIITPSGCGEQNMIRMTAPVIATYYLDTTEQWETLGRNHRNEAVKQIMTGYAQQMVYKKA[10]ASSTWLTAYVVKVFAMA	1068	
ETE59418	1	MDIqKPEGEQKNIVTIIELDPsvKGIgGTQEQTvTANKLDDKVPETEIETKISVLGDPVAQVIEDSIDGSKLKHLIITPSGCGEQNMITMTPSVIATYYLDDATGQWENLGVDRrTEAVKQIMKGIQDSKLQLLL	151	LLLLRLTAYVVKVFAMA
ETE58564		-----LTAYVVKIFALA	12	
AFJ59923	1069	TKMVAGISHEIICGGVRWLILNRQQPDGAFKENAPVLSGTMQGGIQGDESEVTATAFTLVALLESKITICNDSVNSLDSSIKATDYLLKKYEKLQRPYTTALTAYALAAADRLNDDR[9]NRWEEYNAHTHNVEGTSYALLALLKMKKFDQTGPVVRWLT	1234	
ETE59418	152	AKMVKDISHEIICGGVKWLILNRQQPDGVFKENAPVIHGEMLGGTGGAEPESLTAFVMAALLESRSVCNEHINILDDSSINKATDYLLKKYEKLQRPYTTALTAYALAAADRLNDDR	268	
ETE58564	13	AKTVKDISHEIICGGVRWLILSRQQPDGVFKENAPVLSGTMQGGIQGAEPVCLTGFTLVALLESRSICNEYINVRD-----VVMGSVKSHHQR	142	NCWEEYNAHTHNIEGTSYALLALLKMKKFEAGPvVKWLI
AFJ59923	1235	DQNFYGGTYGQTQATVMFQALAEYKIQMPTHKDLNLDIIIKLPERELPLHYRLDATNAILARTAETKLNQDFTVSASGDGTATMTILTIVYNAQLQEKANVCNKPHLDVSVENIHLNFKAKGAKGALMLKICRYLGEVDSTMTIIDVSMLTGFL	1390	
ETE59418	269	-----ATVMVFQALAEYEIQMPTHKDLNLDIAIKLPERELPVRYRINYENALLARTTETKLNEDFTVSASGDGKATMTILTIVYNAQLREDANVCNKPHLDVSVENVQLNLKQAKGAKGALKLKICTRYLGEVDSTMTIIDVSMLTGFF	411	
ETE58564	143	DQKYGGTYGQT[27]QATVMVFQALAEYEIQMPTHKDLNLDIVIKLPERNLPLRYRLDATNAILARTAENVQYFSKY-----LQKQAKGAKGALKLKICTRYLGEVDSTMTIIDVSLLTGfV	281	
AFJ59923	1391	PDAEDLTRLSEGVDRYISRYEDNNMAQKVAVIIYLDK[41]FYHPDKGTGLLNKICVGNICRCAAEETCSLLSQEKIDLPLRIQKACASNVDYVYKTKLLRIEEKDGYDIYVMDVLEVIKPGTDENPQANARQYISQRKCQEALNLNVNDDYLIWGLRS	1587	
ETE59418	412	PDAEDLTRLKSGVDRIYSKFEIDNNMAQKGTVIIYLDKFYHPDKGTGLLNKICHGNICRCAEETCSLLNQKKIDLQLRIQKACAPNVDYVYKTKLLRIEEKDGNDIYVMDVLEVIKPGTDRNPQAKARQYVSQRKCQEALNLKLDNDYLIWGLSS	567	
ETE58564	282	PDAEDLMKLSKGVDRYISKFEINNMAQKGTVIIYLD-----		
AFJ59923	1588	DLWPMKDKFSYLITKNTWIERWPHDEECQDEEFQNLCLDFAHLSNLTIFGCPT	1641	
ETE59418	568	DLWPKKDDISYLITKNTWIERWPSDEECQDEEFQNLCDFAQLSNTLTIFGCPT	621	
ETE58564		-----		

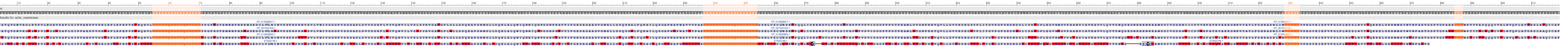
VIII. SVSP (snake venom serine proteases)

Accession		Description	Links
A8QL56.1		RecName: Full=Alpha- and beta-fibrinogenase OhS1; AltName: Full=Snake venom serine protease; Short=SVSP; Flags: Precursor	Related Information
ETE72364.1		hypothetical protein L345_01814 [Ophiophagus hannah]	
ETE66745.1		hypothetical protein L345_07470 [Ophiophagus hannah]	
A8QL56	1	-----MALIRVLASLLILQLSYA-----TPF-DRIIGGFECNEYEHRSLVHLYNSSGFFCSGTLNHEWVLTAAHCNRDDIQIKLGVHNVSVNYEDEQIRVPKEKLCCHSTNNCTQ	106
ETE72364	1	-----MAMIRVLASLLILQLSYSKSLdngakeTPiDLIMGGSECYKSEHPFLVYLYNSAGFFCSGTLNHEWVLTAAHCNRKDIQIKLGIHNVHVHYEDEQIRVPKEKLCCLSTKNCTQ	115
ETE66745	1	ivykpedsarlcivghldlqnkkdptfcppthpntfdddddnddddTSSNPMFSQSPISCCYGKAI-----IPF-DRIIGGFECNKNEHRSLVYLYNSAGXQGFSA-----	100
A8QL56	107	LGQDIMLIRLNSSVNYSEHIAPLSLPSNRPSMGSVCRVMGWGLLTSPEVTFPKVPHCV DINILHIQVCQAAYPSMSENYLLCAGVLEGGKDSCKGDSGGPLICNR IQGIVSWG GFPCAQLLEPGVYTKVFDYIDWIEGIIAGNTSVTCPSDNF	260
ETE72364	116	WSQDIMLIRLNSSVKNSEHIGPLSLPSSPPNMSSVC SVMGWGITTSPEVTYPVPYCVNIQILHNLVCQAAYPTMSGKNILCAGALEGGKDSCKGDSGGPLICNEIQGIVSWG RFPCAQLLEPGVYTKVFDYIDWIEGIIAGNTSVICP----	265
ETE66745	101	-----QGPCSTTNGCSPLHTATVTTPFKVPHCV DINILHIQVCQAAYPSMSENYLLCAGVLEGGKDSCKGDSGGPLICNR IQGVVSWG GFPCAQLLEPGVYTKVFDYIDWIEGIIAGNTSVTCPSDNF	223

Fig. S6: Graphical summary of comparative domain analysis performed for all toxin-associated genes across 18 completely sequenced snake species.

A ACHE

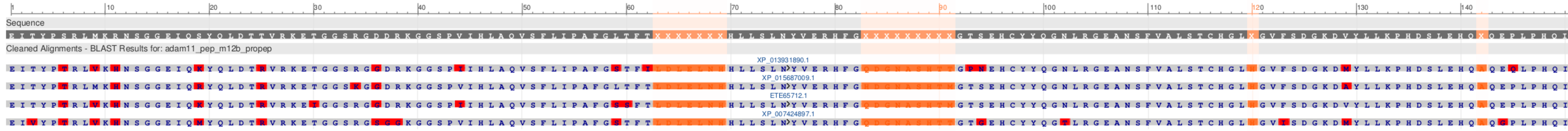
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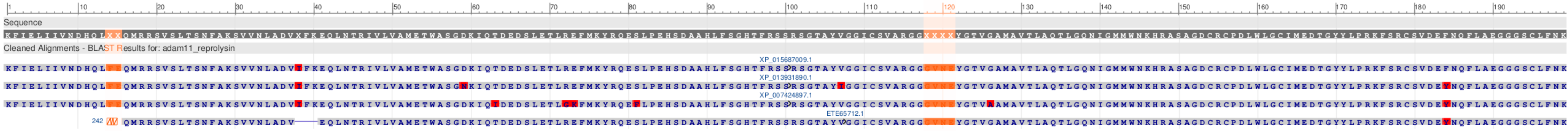
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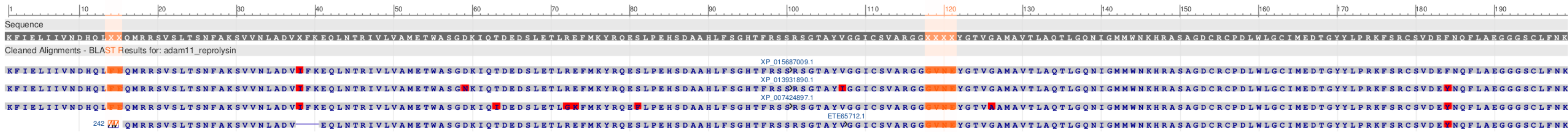
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Reprolysin



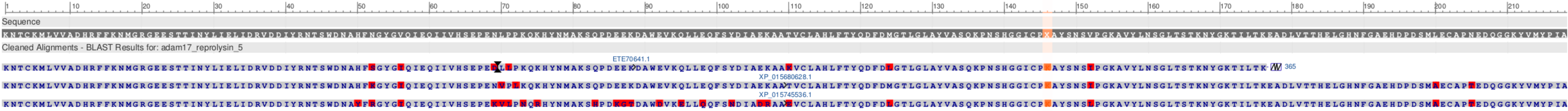
ADAM_CR



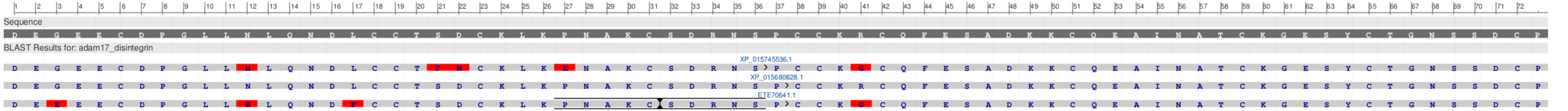
C ADAM17



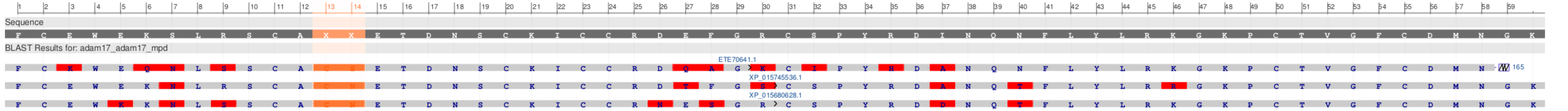
Reprolysin_5



Disintegrin

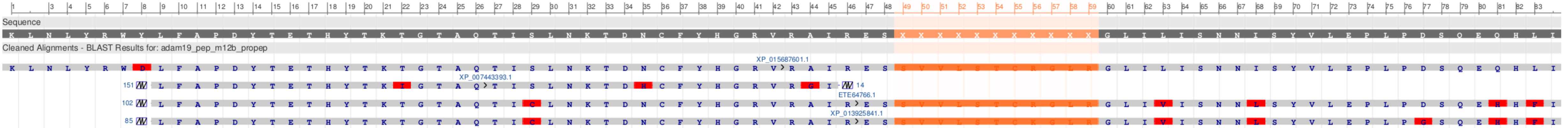


ADAM17_MPD

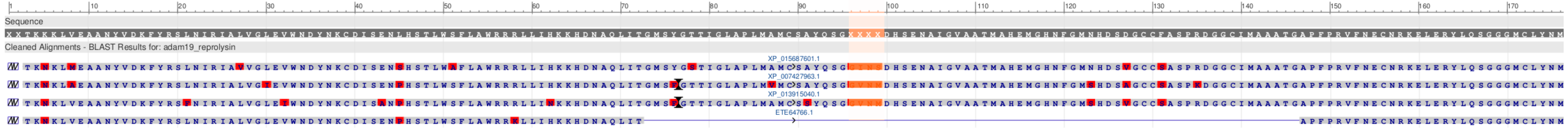




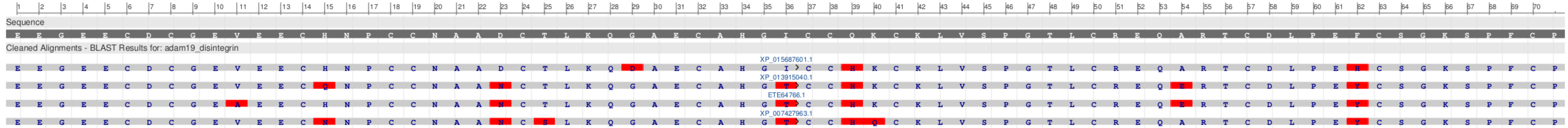
Pep M12B Propep



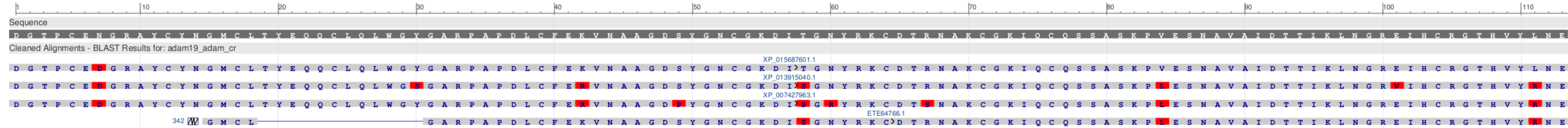
Reprolysin



Disintegrin



ADAM_CR



ADAM23



Sequence alignment visualization showing the alignment of a query sequence (adam23_pep_m12B_propep) with a reference sequence (XP_007436516.1). The alignment is displayed as a sequence of amino acids with a scale from 1 to 100. The query sequence is highlighted in blue, and the reference sequence is highlighted in red. The alignment shows a high degree of similarity between the two sequences.

Sequence: A V H L A Q A S F Q I E A F G S T F I L D L S L N N D L L S A D Y V E I H Y E D D D K P Q Y S K G G E H C Y Y H G S I R G I P K S K A A I S T C N G L H G M F E D N T Y V Y L I E P L E L T H S X S S T G R L H V

Cleaned Alignments - BLAST Results for: adam23_pep_m12B_propep

XP_007436516.1

A V H L A Q A S F **K** I E A F G S **K** F I L D L S > L N N D L L S **S** D Y V E I H Y E D D D K P Q Y S K

XP_015673507.1

A V H L A Q A S F Q I E A F G S T F I L D L S L N N D L L S A D Y V E I H Y E D D D K P Q Y S K G G E H C > Y Y H G S I R G I P K S K A A I S T C N G L H G M F E D N T Y V Y L I E P L E **I** T H S **M** S S T G R L H V

ETE72756.1

A V H L A Q A S F Q I E A F G S **A** F I L D L S L N N D L L S A D Y V E I H Y E D D D K P Q Y S K G G E H C > Y Y H G S I R G I P K S K A A I S T C N G L H G M F E D N T Y V Y L I E P L E L T H S **M** S **N** A G R **P** H V

Sequence alignment of adam23_reprolysin with XP_015673507.1, XP_007442177.1, and ETE72756.1. The alignment shows high similarity between the sequences, with some gaps and mismatches highlighted. The alignment is displayed in a table format with columns for the sequences and a 'Score' column.

Sequence	Score
KYLELMIVNDHKMFQKHRSSHSNTNNFAKSVVNLVDIAIYKEQLNTRVVLVAVETWSDRDRIRVHSDPRQMLHDFSRYRQNFQIKQHADAVHLLSNVFFHYKRRSSLSYFGGICSVARGVGVNEYGLSWAIAQELSQSLAQNLGIQWEPASRKPXXXXXXXXXXXXXXXXXXVYHSRKFSKCSIAEYRDFLLRGGGFCLFNRR	100
Cleaned Alignments - BLAST Results for: adam23_reprolysin	
KYLELMIVNDHKMFQKHRSSHSNTNNFAKSVVNLVDIAIYKEQLNTRVVLVAVETWSDRDRIRVHSDPRQMLHDFSRYRQNFQIKQHADAVHLLSNVFFHYKRRSSLSYFGGICSVARGVGVNEYGLSWAIAQELSQSLAQNLGIQWEPASRKPXXXXXXXXXXXXXXXXXXVYHSRKFSKCSIAEYRDFLLRGGGFCLFNRR	XP_015673507.1
KYLELMIVNDYKMFQKHRSSHSNTNNFAKSVVNLVDIAIYKEQLNTRVVLVAVETWSDRDRIRVHSDPRQMLHDFSRYRQNFQIKQHADAVHLLSNVFFHYKRRSSLSYFGGICSVARGVGVNEYGLSWAIAQELSQSLAQNLGIQWEPASRKPXXXXXXXXXXXXXXXXXXVYHSRKFSKCSIAEYRDFLLRGGGFCLFNRR	XP_007442177.1
KYLELMIVNDYKMFQKHRSSHSNTNNFAKSVVNLVDIAIYKEQLNTRVVLVAVETWSDRDRIRVHSDPRQMLHDFSRYRQNFQIKQHADAVHLLSNVFFHYKRRSSLSYFGGICSVARGVGVNEYGLSWAIAQELSQSLAQNLGIQWEPASRKPXXXXXXXXXXXXXXXXXXVYHSRKFSKCSIAEYRDFLLRGGGFCLFNRR	ETE72756.1
KYLELMIVNDYKMFQKHRSSHSNTNNFAKSVVNLVDIAIYKEQLNTRVVLVAVETWSDRDRIRVHSDPRQMLHDFSRYRQNFQIKQHADAVHLLSNVFFHYKRRSSLSYFGGICSVARGVGVNEYGLSWAIAQELSQSLAQNLGIQWEPASRKPXXXXXXXXXXXXXXXXXXVYHSRKFSKCSIAEYRDFLLRGGGFCLFNRR	XP_013914319.1

1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69				
Sequence																																																																								
E	P	G	E	D	C	D	C	G	I	O	T	X	X	X	X	X	X	X	K	K	C	S	L	S	N	G	A	H	C	S	D	G	P	C	C	N	E	T	C	L	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	N	E	C	D	I	T	E	I	C	T	G	D	S	G	O	C	P
Cleaned Alignments - BLAST Results for: adam23_disintegrin																																																																								
E	P	G	E	D	C	D	C	G	V	Q	T	D	C	H	A	E	C	C	K	K	C	S	L	S	N	G	A	H	C	S	D	G	P	C	C	N	E	T	C	L	F	F	P	R	G	F	E	C	R	Y	A	V	N	E	C	D	I	T	E	I	C	T	G	D	S	G	Q	C	P			
E	P	G	E	D	C	D	C	G	I	Q	T	D	C	H	A	E	C	C	K	K	C	S	L	S	N	G	A	H	C	S	D	G	P	C	C	N	E	T	C	L	F	F	P	R	G	F	E	C	R	Y	A	V	N	E	C	D	I	T	E	I	C	T	G	D	S	G	Q	C	P			
E	P	G	E	D	C	D	C	G	I	Q	T	D	C	H	A	D	C	C	K	K	C	S	L	S	N	G	A	H	C	S	D	G	P	C	C	N	E	T	C	L	F	F	P	R	G	F	E	C	R	Y	A	V	N	E	C	D	I	T	E	I	C	T	G	D	S	G	Q	C	P			
E	P	G	E	D	C	D	C	G	I	Q	T	F	F	P	R	G	F	E											C																																											
																						XP_007442177.1																																																		
																						XP_013914319.1																																																		
																						XP_015673507.1																																																		
																						ETE72756.1																																																		

Sequence alignment of adam23_adam_cr with ETE72756.1, XP_007442177.1, XP_015673507.1, and XP_013914319.1. The alignment shows high similarity with some mismatches highlighted in red.

Sequence	ETE72756.1	XP_007442177.1	XP_015673507.1	XP_013914319.1
D G F A C D S N Q G R C Y N G E C K T R D N Q C K F I W G N K A S G S H K H C Y E K L N T E G T Q K G N C G K D G D K W I P C H K H D V F C G L L L C A N L D G V P R I G H L Q G E I I P T S F F H Q X X X X X C S C A H V L L D D E T	D G F A C D S N Q G R C Y N G E C K T R D N Q C K Y I W G N K A S G S H K H C Y E K L N T E G T Q K G N C G K D G D K W I P C H K H D V F C G L L L C A N L D G V P R I G H L Q G E I I P T S F F H Q G V V V V C S C A H V L L D D E T	D G F A C D S N Q G R C Y N G E C K T R D N Q C R Y I W G N K A S G S H K H C Y E K L N T E G T Q K G N C G K D G D K W I S C H K H D V F C G L L L C A N L D G V P R I G H L Q G E I I P T S F F H Q G V V V V C S C A H V L L D D E T	D G F A C D S N Q G R C Y N G E C K T R D N Q C K Y I W G N K A S V S H K H C Y E K L N T E G T Q K G N C G K D G D K W I P C H K H D V F C G L L L C A N L D G V P R I G H L Q G E I I P T S F F H Q G V V V V C S C T H V L L D D E T	D G F A C D S N Q G R C Y S G E C K T R D N Q C K Y I W G N K A S G S H K H C Y E K L N T E G T Q K G N C G K D G D K W I P C H K H D V F C G L L L C A N L D G A P R I G Y L Q G E I I P T S F F H Q G V V V V C S C A H V L L D D E T

A horizontal grey bar representing a protein structure. A green oval with a wavy left edge is attached to the right end of the bar. The text "Lectin-C" is written in black inside the green oval.

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Sequence	X	X	W	L	G	I	T	D	M	V	N	E	G	K	F	V	D	V	N	G	M	V	L	N	Y	F	N	W	D	R	L	O	P	N	G	G	K	R	E	N	C	V	L	F	S	O	P	G	O	G	K	W	G	D	E	V	C	R	T	V	K	R	Y	V	C	E	
BLAST Results for: clec3a_lectin_c																																																																			
128	W	L	G	I	T	D	M	V	N	E	G	K	F	V	D	V	N	G	M	V	L	N	Y	F	N	W	D	R	S	Q	P	N	>	G	G	K	R	E	N	C	V	L	F	S	Q	S	G	H	G	K	W	V	D	E	V	C	R	T	V	K	R	Y	V	C	E		
128	W	L	G	V	T	D	M	V	N	E	G	K	F	V	D	V	N	G	M	V	L	N	Y	V	N	W	D	R	S	Q	P	N	>	G	G	K	R	E	N	C	V	L	F	S	Q	P	G	Q	G	K	W	A	D	E	V	C	R	T	V	K	R	Y	V	C	E		
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G *CLEC3B*



1	10	20	30	40	50	60	70	80	90	100	110
Sequence											
A K T Y H E A S E D C I S Q G G T L S T P Q T G D E N D A L Y D Y V R K T L G N E A E I W L G I N D L A A E G K W V D M T S N S I S Y K N W E T E I T T Q P D G G K Q E N C A A L S A V A V G K W F D K R C R D Q L L Y V C Q											
BLAST Results for: clec3b_lectin_c											
XP_015678397.1											
A K T Y H E A S E D C I S Q G G T L S T P Q T G D E N D A L Y D Y V R K T L G N E A E I W L G I N D L A V E G K W V D M T S N S I S Y K N W E T E I T T Q P D G G K Q E N C A A L S A V A V G K W F D K R C R D Q L L Y V C Q											
ETE62426.1											
A K S Y H E A N E D C I S Q G G T L S T P Q T G D E N D A L Y D Y V R K T L G N E V E I W L G I N D L A V E G K W V D M T S S S I S Y K N W E T E I T T Q P D G G K Q E N C A A L S A V A V G K W F D K R C R D Q L L Y V C Q											
XP_013921676.1											
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XP_007425059.1											
M K T Y H E A S E D C I S Q G G T L S T P Q T G D E N D A L Y D Y V R K T L G T E V E V W L G I N D L A V E G K W V D M T S N G I G Y K N W E T E I T T Q P D G G K Q E N C A A L S A V A V G K W F D K R C R D Q L L Y V C Q											

FPL

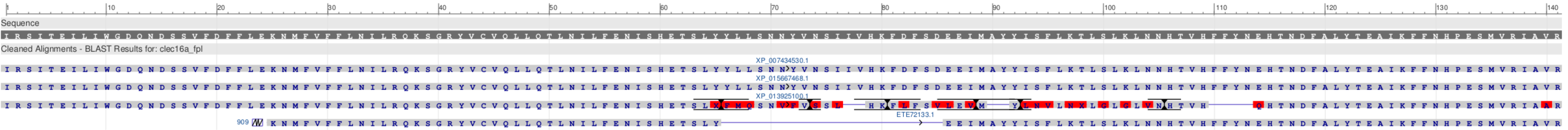
XP_007423150.1

XP 013913781.1

FTF68897.1

CLEC16A

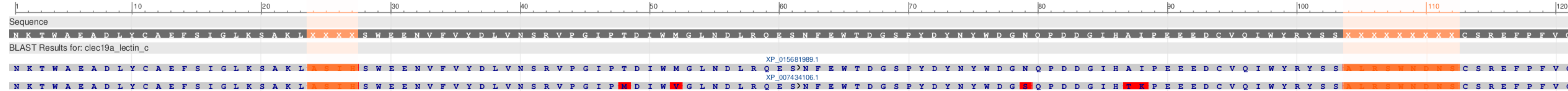
FPL



J

CLEC19A

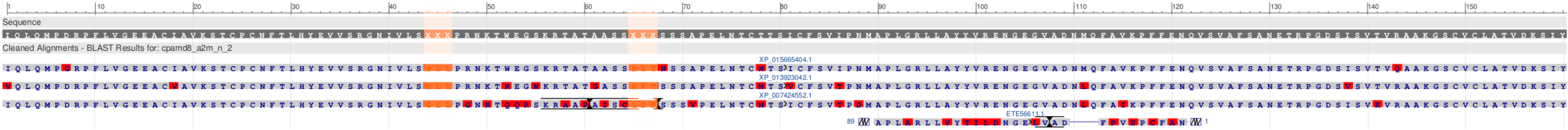
Lectin C



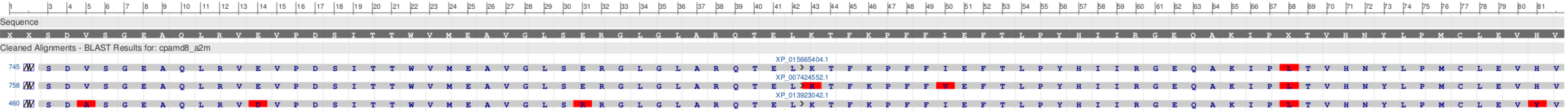
K CPAMD8



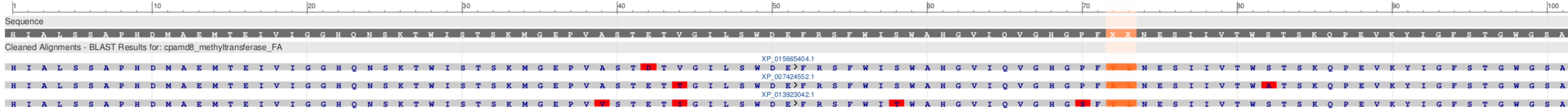
A2M_N_2



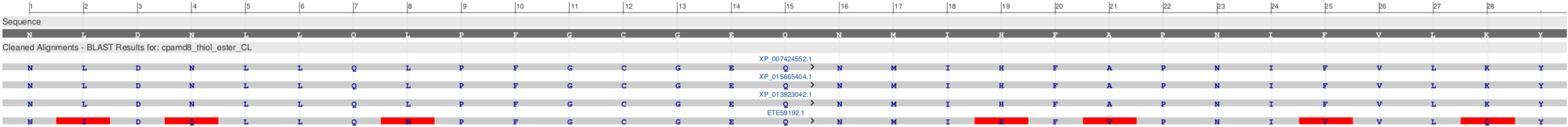
A2M



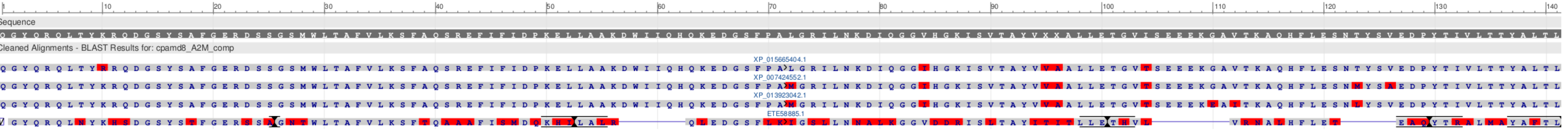
methyltransferase FA



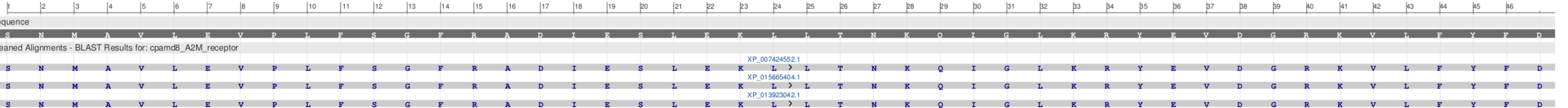
thiol_ester_CL



A2M_comp



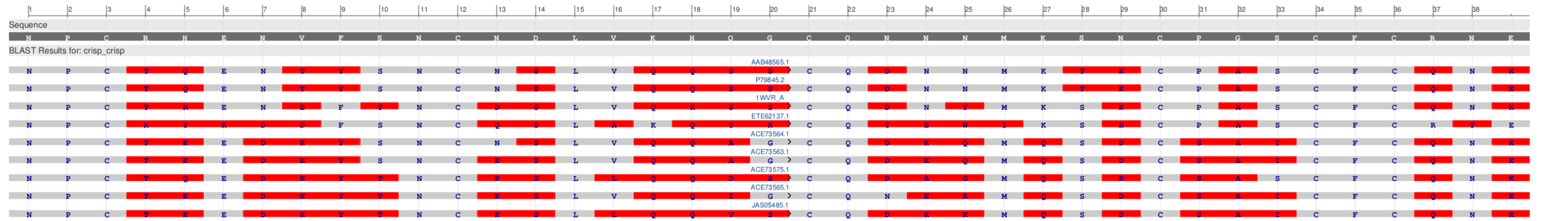
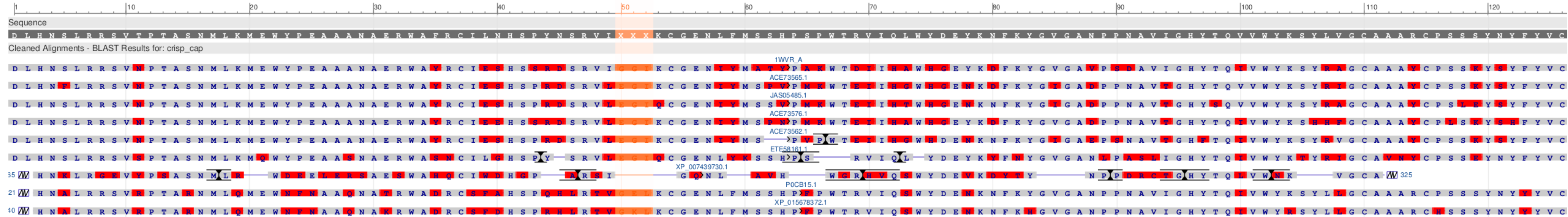
A2M_receptor



L CRISP



CAP



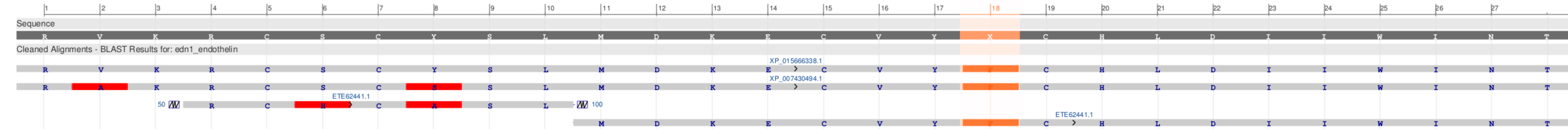
cystatin

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Sequence	X	I	K	S	Q	L	E	E	K	E	S	R	N	F	T	T	F	N	A	I	S	Y	K	T	O	V	V	A	G	I	N	Y	F	I
BLAST Results for: csta_cystatin																																		
22 	I	K	S	Q	L	E	E	K	E	S	R	N	F	T	I	F	N	A	V	S	Y	K	T	Q	V	V	A	G	V	N	Y	F	I	
22 	I	K	S	Q	L	E	E	K	E	S	R	N	F	N	I	F	D	A	V	L	Y	K	A	Q	M	V	A	G	V	N	Y	F	I	

N

EDN1

endothelin



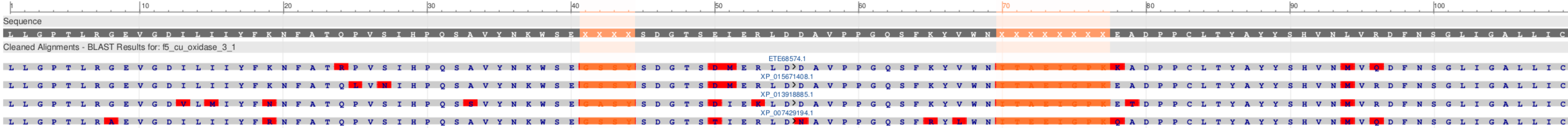
O

EDN3

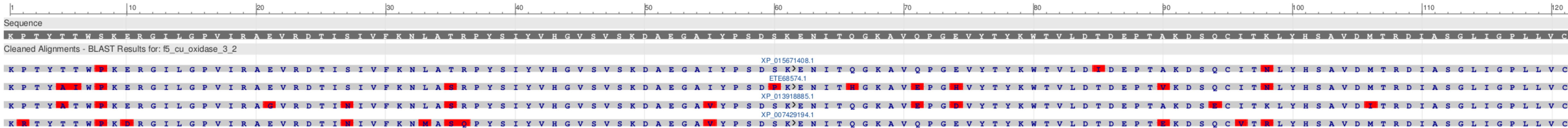
endothelin

1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23		
Sequence																								
R	A	K	R	C	T	C	Y	T	Y	K	D	K	E	C	V	Y	Y	C	H	L	D	I	I	
Cleaned Alignments - BLAST Results for: edn3_endothelin																								
R	A	K	R	C	T	C	Y	T	Y	K	D	XP_015679653.1	K	E	C	V	Y	Y	C	H	L	D	I	I
R	A	K	R	C	T	C	Y	T	Y	K	D	XP_013919048.1	K	E	C	V	Y	Y	C	H	L	D	I	I
R	A	K	R	C	T	C	Y	T	Y	K	D	ETE61352.1	K	E	C	V	Y	Y	C	H	L	D	I	I
R	A	K	R	C	T	C	Y	T	Y	K	D	XP_007432959.1	K	E	C	V	Y	Y	C	H	L	D	I	I
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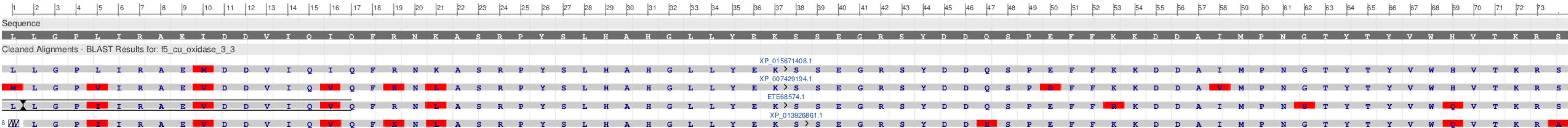
Cu_oxidase_3



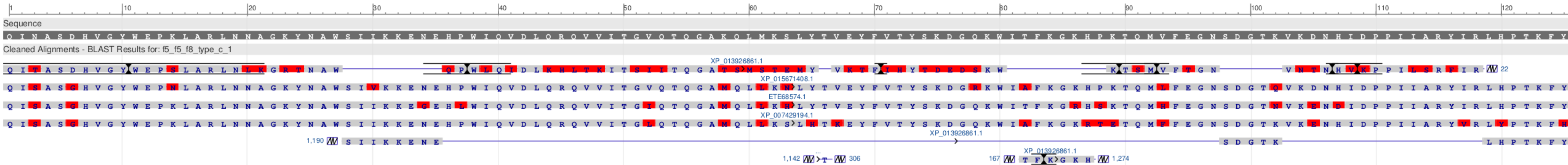
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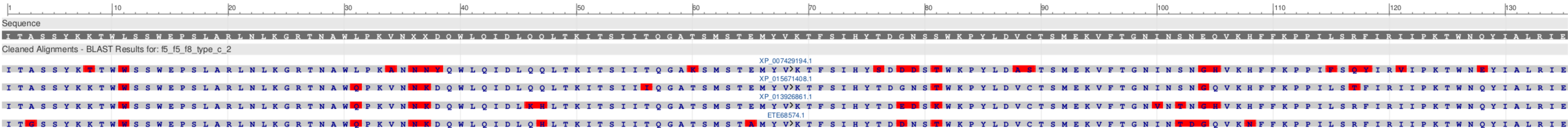
Cu_oxidase_3



F5_F8_Type_C



F5_F8_Type_C

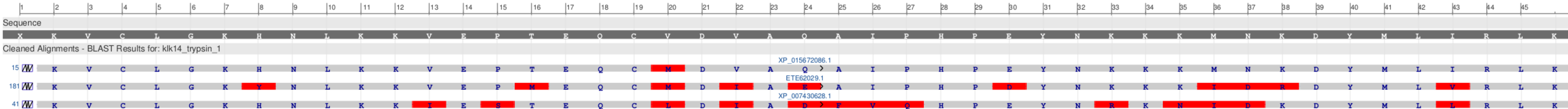


Q

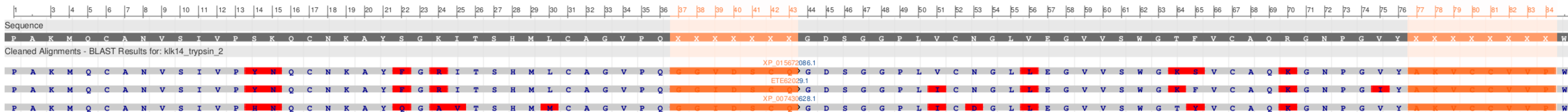
KLK14



Trypsin



Trypsin



R

PAN

PAN

PAN

Trypsin

KLKB1



Sequence

C M T E I Y R N T Y I E G G D I S R V Y T P T A D Y C Q L V C T Y H P R C L L F S Y V P G S W V K T T A R F S C F L K E I D A O E L P K I H R E G V I S G H S Q K Q

Cleaned Alignments - BLAST Results for: klkb1_pan_1_1

XP_015687301.1
XP_013913095.1
XP_015745547.1

C M S E M Y R N T Y I Q G G D I S R V Y T P T A D Y C Q L V C T Y H P R C L L F S Y V P G S W V K T T A R F S C F L K E I D A Q E L P K I H R E G I S G H S Q K Q

C M S E I Y R N T Y I E G G D I S R Y Y T P T A D Y C Q M V C T Y H P R C L L F S Y V P G S W V K T T A R F S C F L K E I D T Q E L P K I H R E G I S G H S K K Q

M S K I Y R N T Y I Q G G D I S K V Y T P T A D Y C Q M V C T Y H P R C L L F S Y V P G S W V K T T A R F S C F L K E I D T Q E L P K V P Q E G I S G H S L K Q

Sequence

K V Y E G L D M Q G E N Y N I T T A D N Y H H C Q Q R C T N D K H C Y F F T Y T L E S F H S V P L R N K C Y L K Y S S T G T P N Q I R Q L R D V I S G

Cleaned Alignments - BLAST Results for: klkb1_pan_1_2

XP_015687301.1
XP_015745547.1
XP_013913095.1

K V Y E G L D M Q G E N Y N I T T A D N Y H H C Q Q R C T N D K H C Y F F T Y T L E S F H S V P L R N K C Y L K Y S S T G T P N Q I R Q L R D V V S G

K V Y E G L D M Q G E N Y N I T T A D N Y H H C Q Q R C T N D K H C Y F F T Y T L E S F H S V P L R N K C Y L K Y S S T G T P T Q I R Q L R D V V S G

K V Y E G L D M Q G E N Y N I T T A D N Y H H C Q Q R C T N D K H C Y F F T Y T L E S F H S V P L R N K C Y L K Y S S T G T P T N I K Q R D V V S G

Sequence

C Q M D L F Q H F A F S G I T V A K I L T P D K F V C R T V C T Y R P N C L F F T F L S S E W E V K S E R Y T C L M M T S R S E K P E K I T E R A N V I S G F S L L N

Cleaned Alignments - BLAST Results for: klkb1_pan_1_3

XP_015687301.1
XP_013913095.1
XP_015745547.1
ETE61973.1

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C Q M D F F Q H F A F S G I T V A K V L T P D K F F C R T V C T Y R P N C L F F T F L S S E W E V K S Q R Y T C L M M T S R S E K P E K I T E R A N V I S G F S L L N

C Q M D F F Q H F A F S G I T V A K V L T P D K F V C R T V C T Y R P N C L F F T F L S S E W E V K S Q R Y T C L M M T S R S E K P E K I T E R A N V I S G F S L L N

68 C Q F > F T 287

ETE61973.1

M T S R S E K P E K I T K R E N V I S G F S L L N

Sequence

V V G G S N S S A G E W P W Q V S L H T V L P V Q S H Q C G G S I I S D Q W I L T A A H C F K N F O L T E H W H I Y S S I L K Q S E M T N E T A F F K V Q K L I I H P R Y E F T E T G Y D I A L L K L D R P M N F S A L Q O P I C L P S E E E I N M A Y T E C W V T G W G Y T E E R G S I T D M L Q K V K I P L I P N A E C Q F O Y P E H T I T D K M L C A G Y S X X X X X X X O G D S G G P L S C K F E N S W Y V V G I T S W G E G C A R P G Q P G V Y T N V A K F V D W

BLAST Results for: klkb1_trypsin

XP_015687301.1
XP_015745547.1
XP_013913095.1
ETE61973.1

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V V G G S N S S A G E W P W Q V S L H T V L P V Q S H Q C G G S I I S D Q W I L T A A H C F K N F O L T E H W H I Y S S I L K Q S E M T N E T A F F K V Q K L I I H P R Y E F T E T G Y D I A L L K L D R P M N F S A L Q O P I C L P S E E E I N M A Y T E C W V T G W G Y T E E R G S I T D M L Q K V K I P L I P N A E C Q F O Y P E H T I T D K M L C A G Y S X X X X X X X O G D S G G P L S C K F E N S W Y V V G I T S W G E G C A R P G Q P G V Y T N V A K F V D W

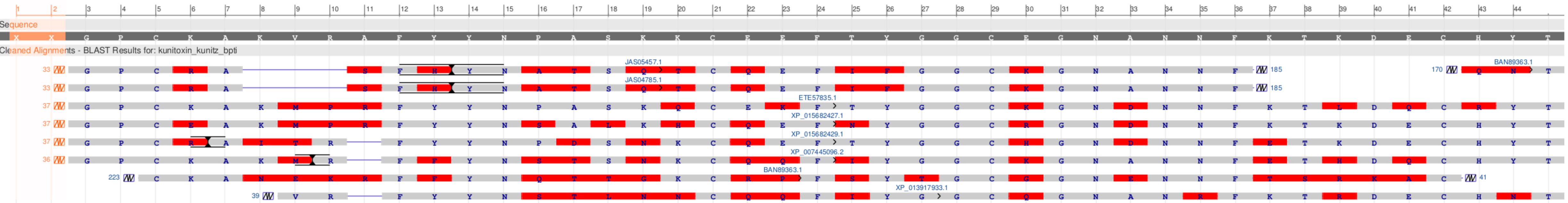
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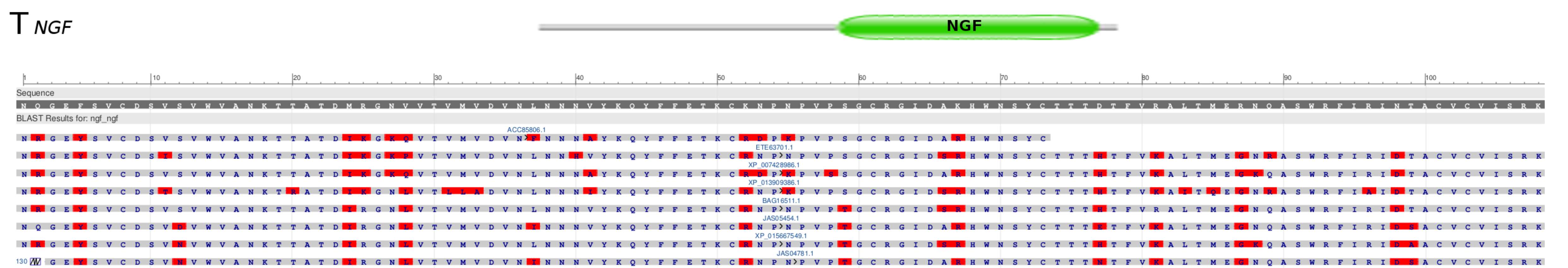
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S

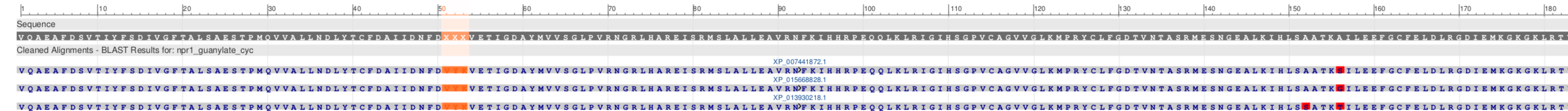
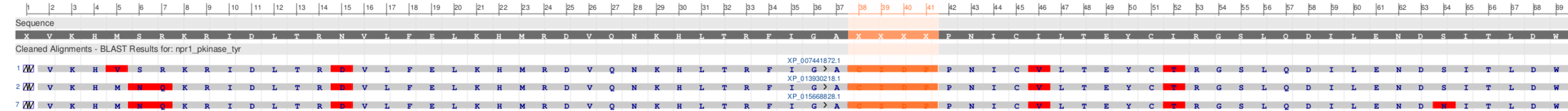
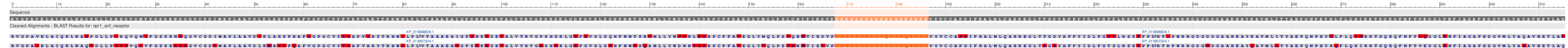
kunitoxin

kunitz BPTI

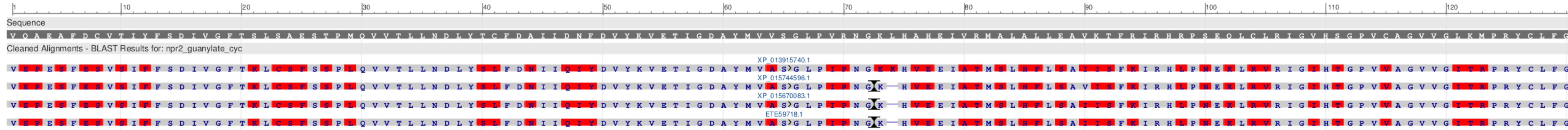
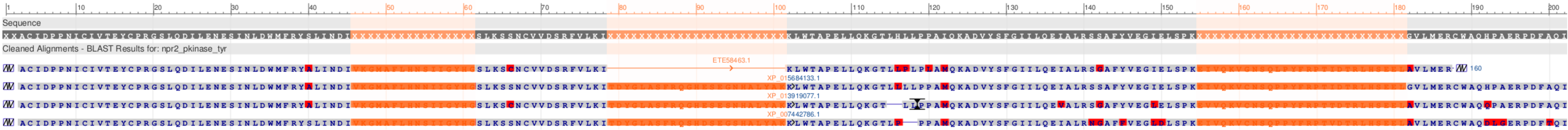




U *NPR1*

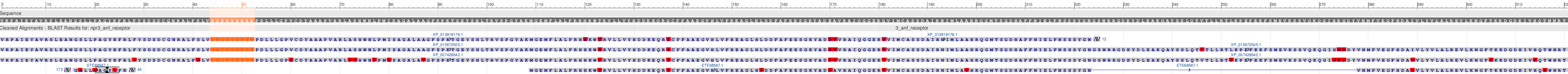


V NPR2

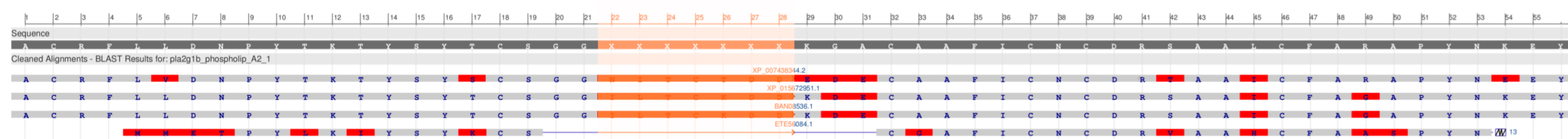


W

NPR3



phospholip A2

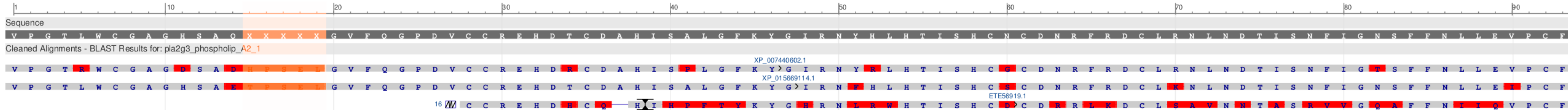


Y PLA2G3

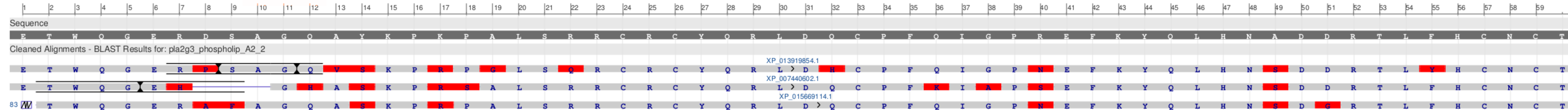
phospholip_A2

phospholip_A2

phospholip_A2



phospholip_A2

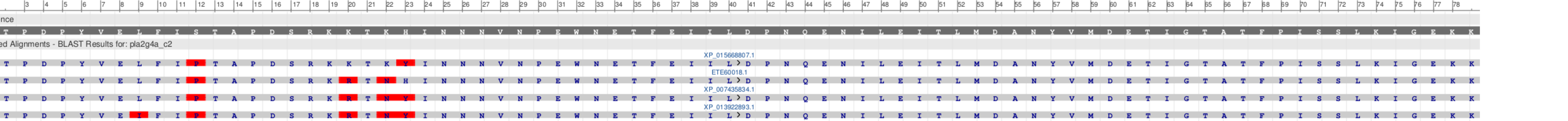


Z

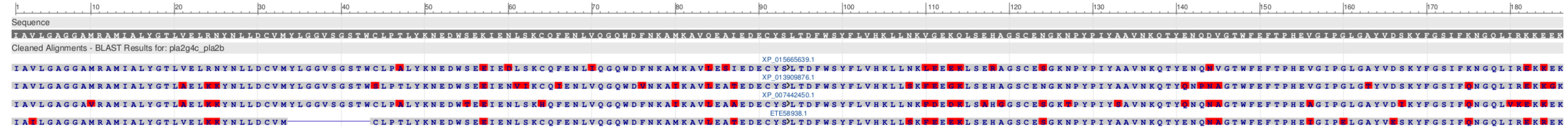
PLA2G4A

C2

PLA2_B



AA *PLA2G4C*



AB

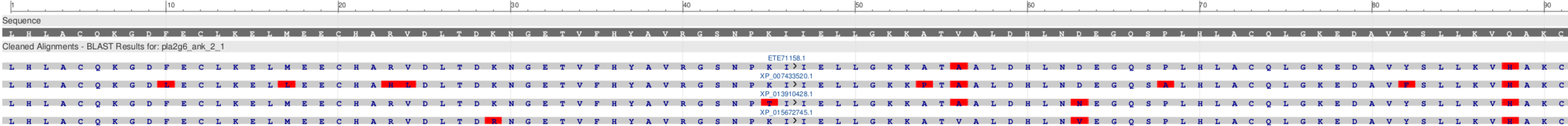
PLA2G6

Ank_2

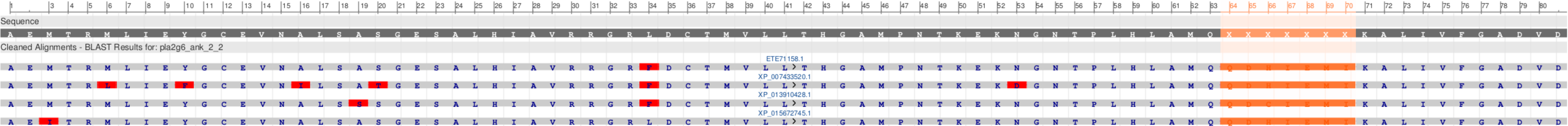
Ank_2

Patatin

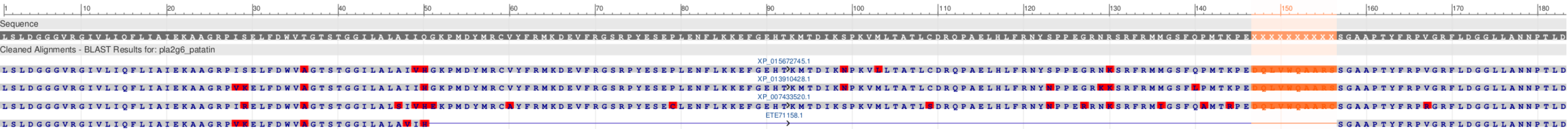
Ank_2



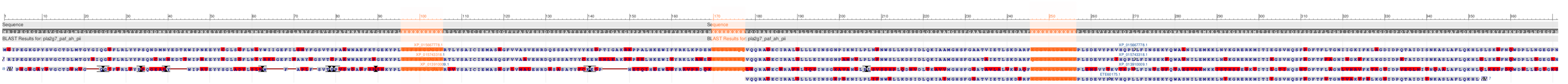
Ank_2



Patatin

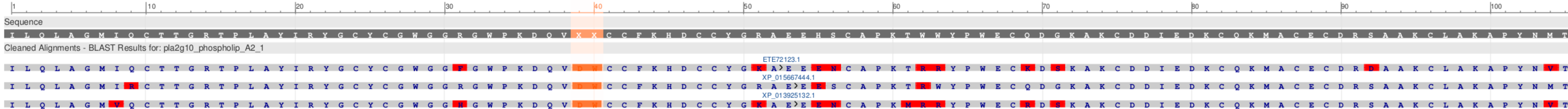


AC PLA2G7



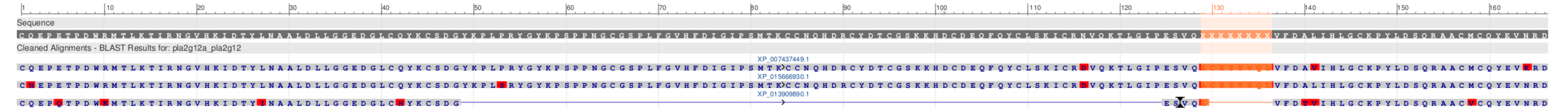
AD *PLA2G10*

phospholip_A2

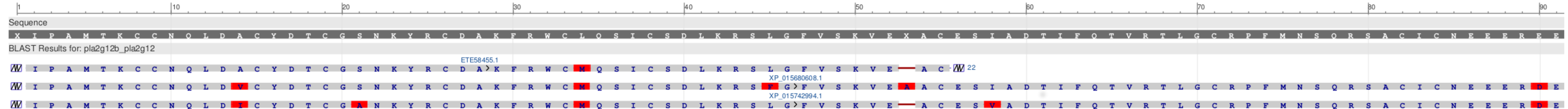


AE

PLA2G12A



AF *PLA2G12B*

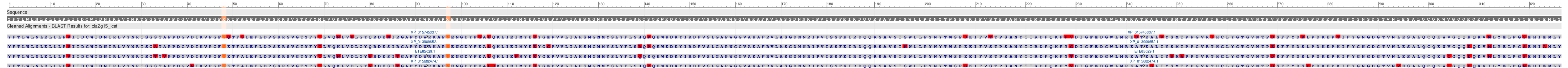


AG

PLA2G15

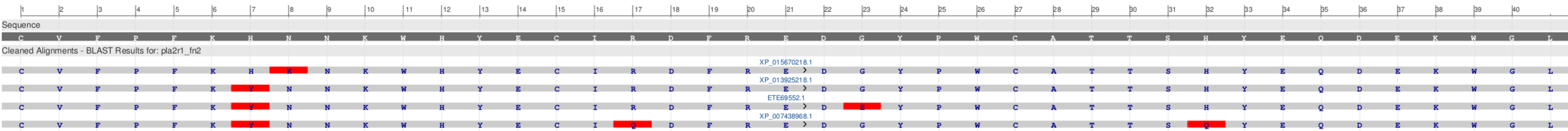


LCAT

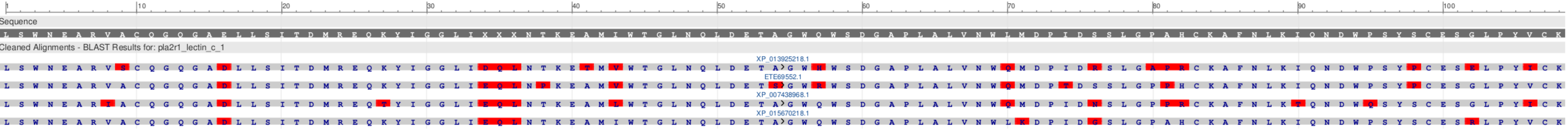




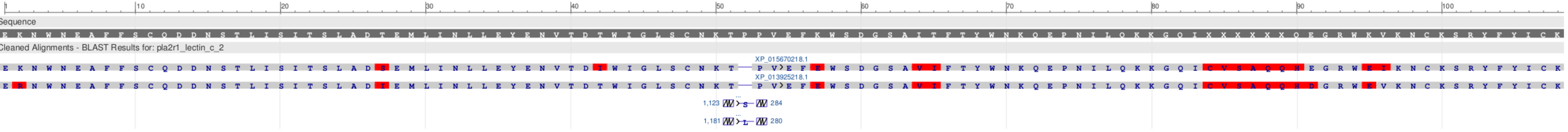
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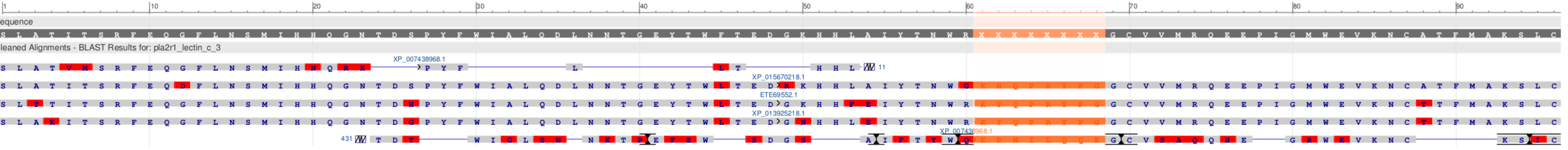
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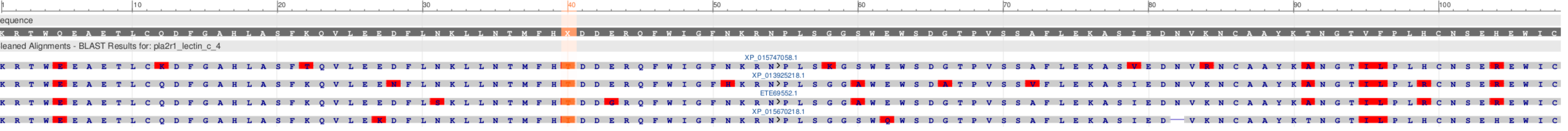
Lectin C



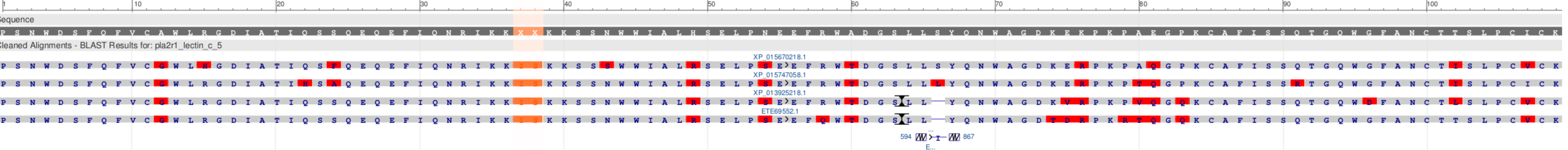
Lectin C



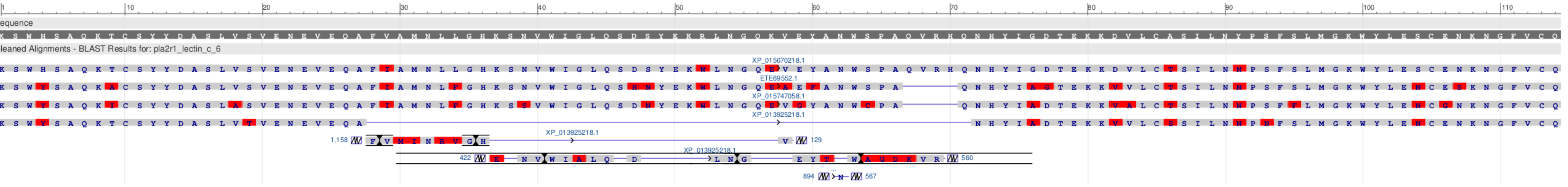
Lectin C



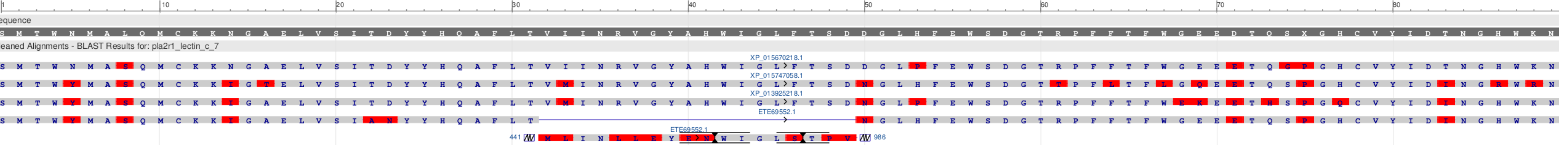
Lectin C



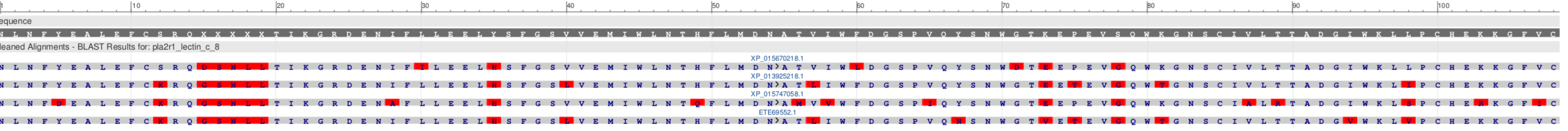
Lectin C



Lectin C



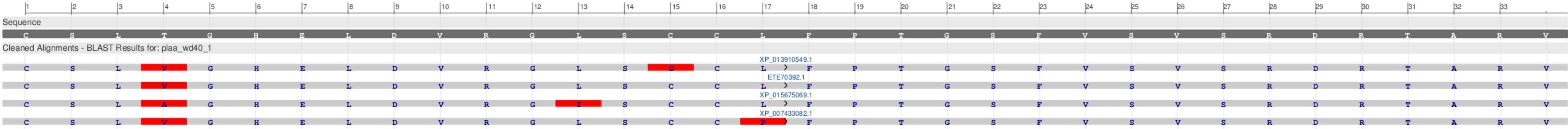
Lectin C



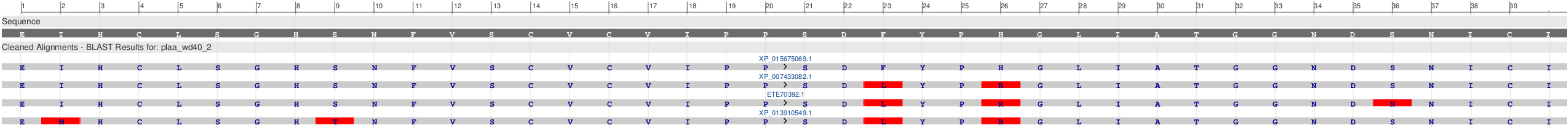
AI PLAA



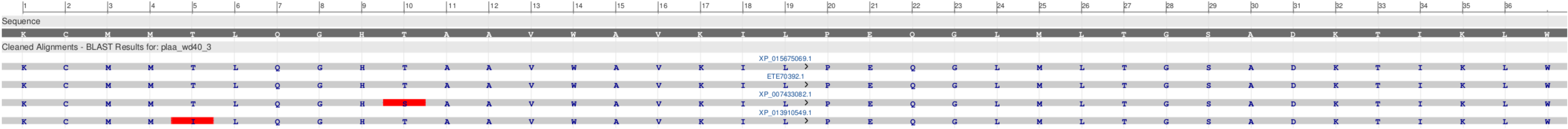
WD40



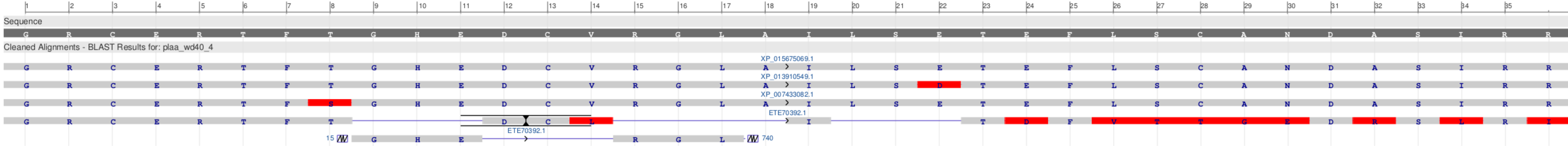
WD40



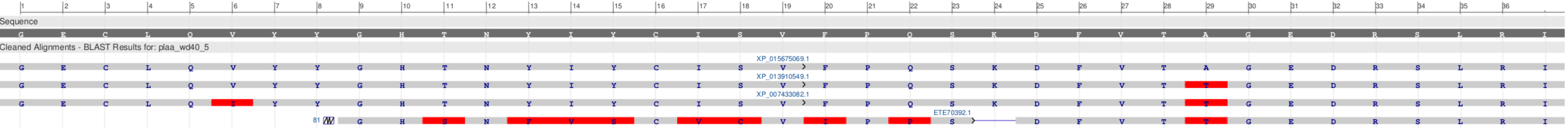
WD40



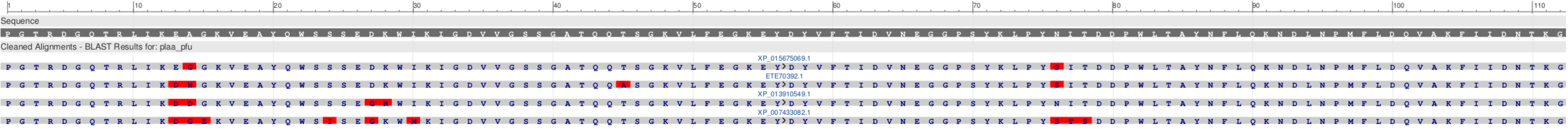
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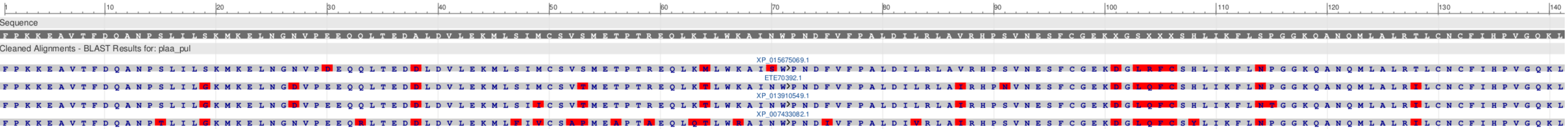
WD40



PFU



PUL



prokinectin

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Sequence	X	D	L	Q	C	G	S	G	T	C	C	A	I	S	L	W	L	R	G	L	R	M	C	T	P	L	G	R	E	G	D	E	C	H	P	I	S	H	K	V	P	F	F	G	K	R	Q	H	H	T	C	P	C	L	P	N	L	I	C	S	K	F	T	D	G	R	Y	R	C		
BLAST Results for: prok1_prokinectin																																																																							
6 	D	L	Q	C	G	S	G	T	C	C	A	I	S	L	W	L	R	G	L	R	M	C	T	P	L	G	R	E	G	D	E	C	H	P	>	I	S	H	K	V	P	F	F	G	K	R	Q	H	H	T	C	P	C	L	P	N	F	I	C	S	K	F	T	D	G	R	Y	R	C		
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																							M	C	T	P	L	G	R	E	G	D	E	C	H	P	I	S	H	K	V	P	F	F	G	K	>	R	Q	H	H	T	C	P	C	L	P	N	L	I	C	S	K	F	T	D	G	R	Y	R	C

prokinectin

1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71		
Sequence																																																																								
A	C	D	R	D	L	Q	C	G	G	G	M	C	C	A	V	S	L	W	I	Q	S	L	R	I	C	T	P	M	G	I	F	G	E	D	C	H	P	L	S	H	K	V	P	F	W	G	R	R	M	H	H	S	C	P	C	E	P	N	L	A	C	V	R	I	S	P	S	K	Y	K	C	
BLAST Results for: prok2_prokinectin																																																																								
																																			XP_015678356.1																																					
A	C	D	R	D	L	Q	C	G	G	G	M	C	C	A	V	S	L	W	I	Q	S	L	R	I	C	T	P	M	G	I	F	G	E	D	C	>	H	P	L	S	H	K	I	P	F	W	G	R	R	L	H	H	S	C	P	C	E	P	N	L	A	C	V	R	I	S	P	S	K	Y	K	C
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											ETE69821.1																																																													
											M C C A V S L W I Q S L R I C T P M G I F G E D C H P L S H K > I P F W G R R M H H S C P C E P N L A C V R I S P S K Y K C																																																													

AL serotriflin



Sequence

1 10 20 30 40 50 60 70 80 90 100 110 120

D L H N S L R R S V T P T A S N M L K M E W S S N A A Q N A K R W A D R C S F A H S P O H L R T M G K L K C G E N L F M S S H P S P W T R V I O L W Y D E Y K N F K Y G V G A N P P N A V I G H Y T O V V W Y K S Y L V G C A A A R C P S S S Y N Y F Y V C H

BLAST Results for: serotriflin_cap

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ACE73565.1
JAS05485.1
POCB15.1
XP_015678372.1
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XP_013911769.1

D H H N N L R R T V S P T A S N M L R M E W H P D A A K N A K R W A D K C S F A H S P V N Q R T V G E L Q C G E N L F M S S T H P Y S W T A V T Q S W Y D E R K D F K Y G V G P I Q P N A V T G H Y T Q V V W Y K S R L L G C A A A K C P A S K F K Y Y Y V C H

D L H N S L R R S V N P T A S N M L K M E W Y P E A A A N A E R W A Y R C S H S P R D S R V L E G I K C G E N I Y M S P V P W T E I I H G W H D E N K N F K Y G I G A E P S N A V T G H F T Q I V W Y K S Y R V G C A A A Y C P S S K Y S Y F Y V C Q

D L H N F L R R S V N P T A S N M L K M E W Y P E A A A N A E R W A Y R C S H S P R D S R V L E G I K C G E N I Y M S S P V P M K W T E I I H G W H G E N K D F K Y G I G A D P P N A V T G H Y T Q V V W Y K S Y R I G C A A A Y C P S S K Y S Y F Y V C Q

D L H N S L R R S V N P T A S N M L K M E W Y P E A A A N A E R W A Y R C S H S P R D S R V L E G I Q C G E N I Y M S S S V P M K W T E I I H T W H G E N K N F K Y G I G A D P P N A V T G H Y S Q V V W Y K S Y R A G C A A A Y C P S L E Y S Y F Y V C Q

21 H N A L R R S V R P T A R N M L Q M E W N F N A A Q N A T R W A D R C S F A H S P Q H L R T V G E L K C G E N L F M S S H P F P W T R V I Q S W Y D E N K N F K Y G V G A N P P N A V I G H Y T Q I V W Y K S Y L L G C A A A R C P S S S S Y N Y Y Y V C H

40 H N A L R R S V R P T A R N M L Q M E W N F N A A Q N A K R W A D R C S F D H S P R H L R T V G K L K C G E N L F M S S H P F P W T R V I Q S W Y D E N K N F K H G V G A N P P N A V I G H Y T Q I V W Y R S Y L L G C A A A R C H S S S S Y N Y Y Y V C H

46 H N A L R R S V K P T A R N M L Q M E W N S N A A Q N A K R W A D R C S F A H S P P H L R T V G K F S C G E N L F M S S Q P Y A W S R V I Q S W Y D E N K K F V Y G V G A N P P G S V I G H Y T Q I V W Y K S H L L G C A A A R C S S S K Y L Y V C Q

E W N S N A A Q N A K R W A D R C T F A H S P G H L R T V G R L G C G E N L F M S S H P Y S W T R V I Q S W Y D E Y K N F R Y G V G A N P P G S V I G H F T Q I V W Y N S Y L V G C A A A R C S S S R F K Y F Y V C Q

Sequence

1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38

N P C R H E N V F S N C N D L V K H Q G C Q N N N M K S N C P G S C F C R N E

BLAST Results for: serotriflin_crisp

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XP_007436999.1
ETE62137.1
ACE73564.1
ACE73575.1
XP_013911763.1
ACE73565.1
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N P C K H I D R Y T N C D S L V Q Q I G C Q N N N M K S D C P A S C F C H N E

N P C T Q E N T Y S N C N S L V Q Q S S C Q D N N M K T K C P A S C F C Q N K

N P C T H E D T Y S N C N A L V K E H K C Q I K S C P A S C F C T T E

N P C K Y K D D F S N C Q S L A K Q T K C Q T E W I K S K C P A S C F C R T E

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N P C T Q E D K Y T N C K S L L Q Q D S C Q D A G M Q S K C S A S C F C Q N K

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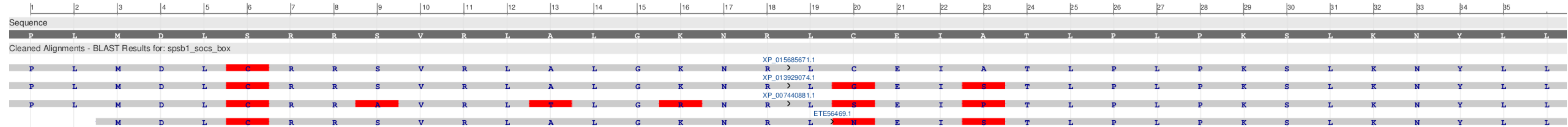
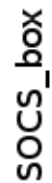
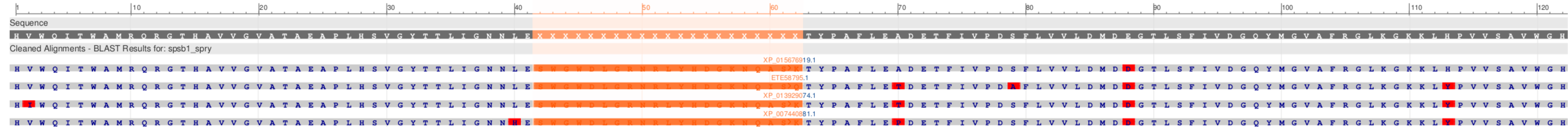
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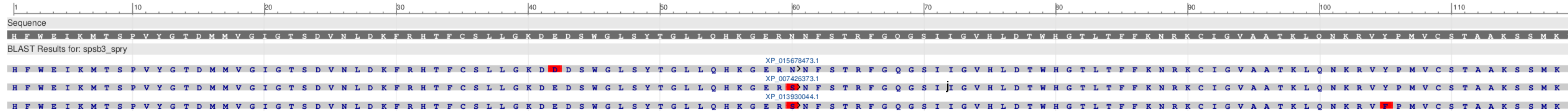
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187 D C P S S C 47

AM *SPSB1*



AN *SPSB3*



AO *SPSB4*

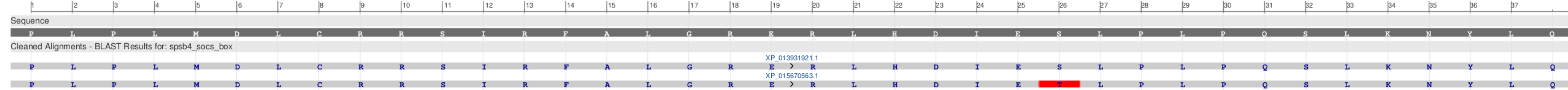
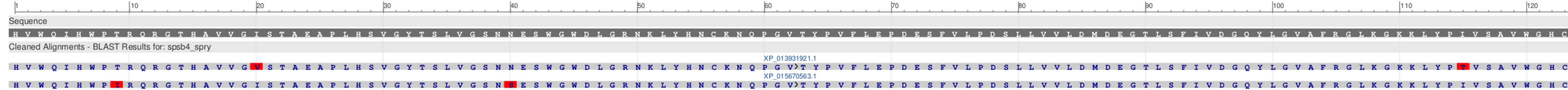


Diagram illustrating the structure of a protein, showing two domains: PDGF (green oval) and VEGF-C (red rectangle).

PDF

VEGF-C

1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43													
Sequence																																																							
X	H	C	E	P	C	S	E	R	R	K	H	L	Y	K	Q	D	P	L	T	C	K	C	S	C	K	F	T	D	S	R	C	K	S	K	Q	L	E	L	N	E	R	T	C												
BLAST Results for: vegfa1_vegfc																																																							
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A diagram of a protein structure consisting of two domains. The first domain is a green oval labeled "PDGF". The second domain is a red rectangle labeled "VEGF-C". The two domains are connected by a thin grey line.

1	3	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77			
Sequence																																																																													
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BLAST Results for: vegfa2_pdgf																																																																													
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PDGF

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PDGF

Sequence

Cleaned Alignments - BLAST Results for: vegfb_pdgf

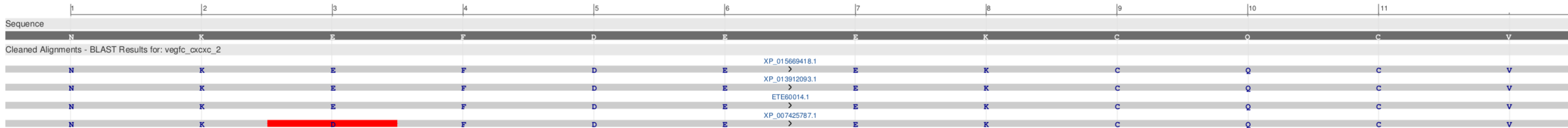
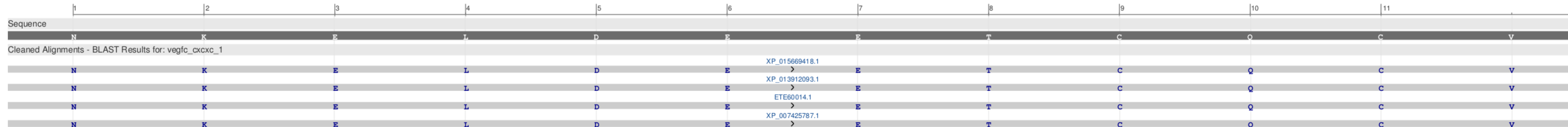
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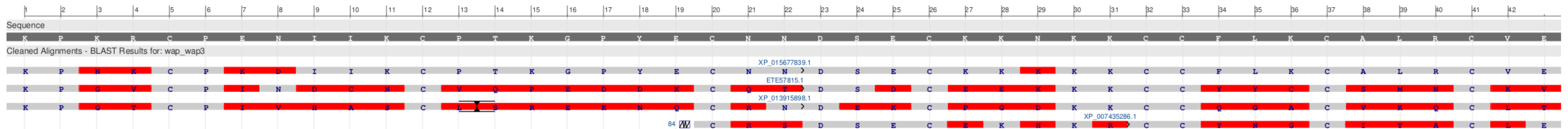
A horizontal grey bar represents a protein structure. A green oval labeled "PDGF" is positioned on the left side of the bar. To the right of the oval, there are two red squares, each labeled "CXCXC".



AU *VEGFF*

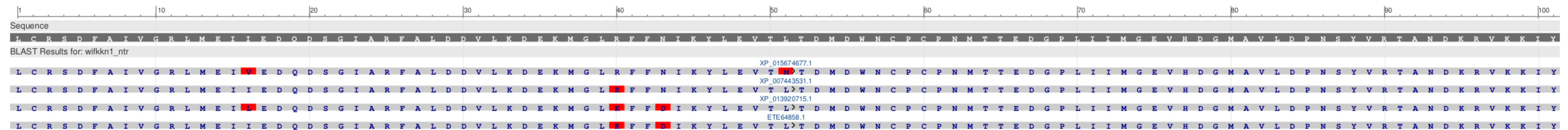
PDGF

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Sequence		X	X	S	H	I	F	K	P	S	C	V	I	L	W	X	C	A	S	C	C	N	D	D	S	L	K	C	X	X
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NTR

NTR

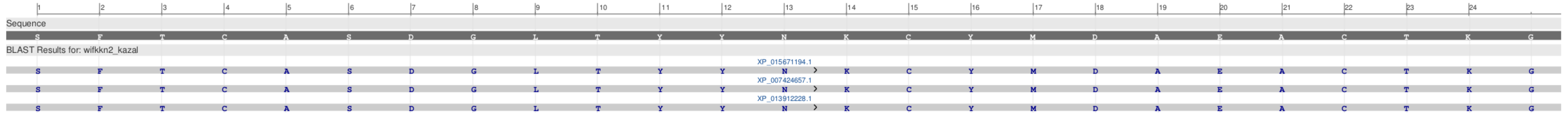


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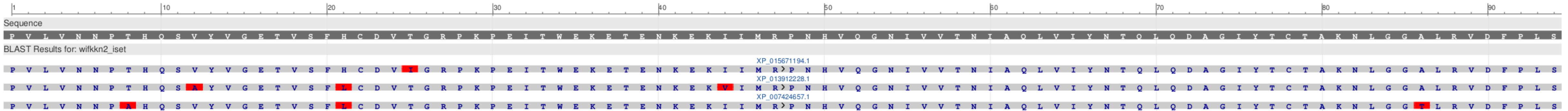
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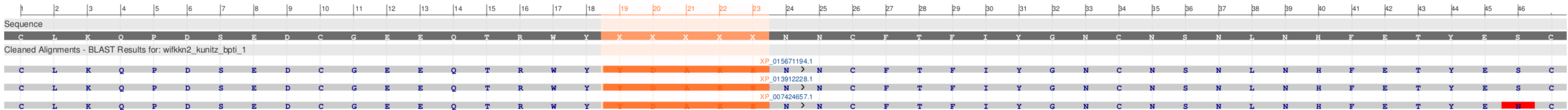
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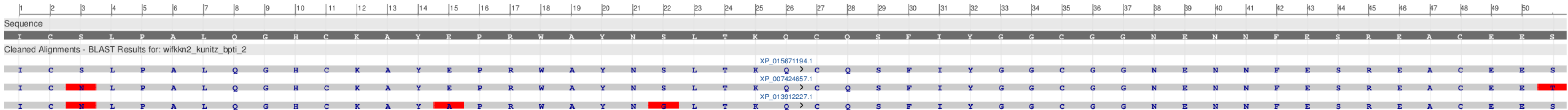
1-set



Kunitz BPTI



Kunitz BPTI



NTR

