

Protein Report

Project Info

Name: Venom protein identification 26082013 Date: August 26, 2013

Sample Info & Protocols

Name: **Southern Copperhead + Tryptase** Date: August 26, 2013

Search Result Info

Search Result	Location	Search Engine	Database	Ident. Compounds
Amazon vertebrates_swissprot july_Mascot_2013-08-28 18:47:18	/Venom protein identification 26082013/Acc + T 3rd batch 5 ul_RC5_01_2660.d/ProteinAnalysisResults.mgf	Mascot, 2.3.02	SwissProt_July2013, uniprotswissprotJuly2013.fasta	3/501 (FDR:0.00%)

Protein 1: L-amino-acid oxidase (Fragment) OS=Bothrops jararacussu PE=1 SV=1

Accession: OXLA_BOTJR	Score: 70.21
Database: SwissProt_July2013	MW [kDa]: 56.30
Seq. Coverage [%]: 2.40 %	pI: 5.73
	No. of Peptides: 2

10	20	30	40	50	60	70	80	90	100	110	120
MNVFFMFSKP	GKLADDRNPL	EECFRETQYE	EFLEIAKNGL	STTSNPKRVV	IVGAGMSGLS	AAYVLANAGH	QVTVLEASER	AGGQVKTYRN	EKEGWYANLG	PMRLPEKHRI	VREYIRKFGI
130	140	150	160	170	180	190	200	210	220	230	240
QLNEFSQENE	NAWYFIKNI	KRVGEVKNKP	GVLDPVKPS	EVGKSAGQLY	EESLQKAVEE	LRRTNCSYML	NKYDTYSTKE	YLLKEGNLSP	GAVDMIGDLL	NEDSGYYVSF	IESLKHDDIF
250	260	270	280	290	300	310	320	330	340	350	360
AYEKRFDEIV	GGMDKLPTSM	YQAIQEKVHL	NARVIKIQQD	VKEVTVTYQT	SEKETLSVTA	DYVIVCTTSR	AARRIKFEPP	LPPKKAHALR	SVHYRSGTKI	FLTCTKKFWE	DDGIHGGKST
370	380	390	400	410	420	430	440	450	460	470	480
TDLPSRFIYY	PNHNFPNGVG	VIIAYGIGDD	ANYFEALDFE	DCGDIVINDL	SLIHQLPKEE	IQAICRPSMI	QRWSLDKYAM	GGITFTTPYQ	FQHFSEALTA	PVDRIYFAGE	YTAQAHGWIA
490	500										
STIKSGPEGL	DVNRASE										

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
148	1	441.3400	155.90	3	29.0	27.7	2	314-324	R.RIKFEPPLPPK.K	
137	2	432.0000	148.58	3	27.8	26.9	2	315-325	R.IKFEPPLPPK.A	

Protein Report

Project Info

Name: Venom protein identification 26082013 Date: August 26, 2013
 Sample Info & Protocols Date: August 26, 2013

Name: **Common lancehead + Trypsase**

Search Result Info

Search Result	Location	Search Engine	Database	Ident. Compounds
Amazon vertebrates_swissprot july_Mascot_2013-08-28 18:47:18	/Venom protein identification 26082013/Ba + T 2nd batch 7 ul_BA5_01_2683.d/ProteinAnalysisResults.mgf	Mascot, 2.3.02	SwissProt_July2013, uniprotswissprotJuly2013.fasta	4/501 (FDR:0.00%)

Protein 1: **L-amino-acid oxidase (Fragment) OS=Bothrops jararacussu PE=1 SV=1**

Accession: OXLA_BOTJR Score: 146.69
 Database: SwissProt_July2013 MW [kDa]: 56.30
 Seq. Coverage [%]: 6.20 % pI: 5.73
 No. of Peptides: 4

10	20	30	40	50	60	70	80	90	100	110	120
MNVFFMFSKP	GKLADDRNPL	EECFRETDYE	EFLEIAKNGL	STTSNPKRVV	IVGAGMSGLS	AAYVLANAGH	QVTVLEASER	AGGQVKTYRN	EKEGWYANLG	PMRLPEKHRI	VREYIRKFGI
130	140	150	160	170	180	190	200	210	220	230	240
QLNEFSQENE	NAWYFIKIR	KRVGEVKNKP	GVLDPVKPVS	EVGKSAGQLY	EESLQKAVEE	LRRTNCSYML	NKYDITYSTKE	YLLKEGNLSP	GAVDMIGDLL	NEDSGYVVSF	IESLKHDDIF
250	260	270	280	290	300	310	320	330	340	350	360
AYEKRFDEIV	GGMDKLPTSM	YQAIQEKVHL	NARVIKIQQD	VKEVTVTYQT	SEKETLSVTA	DYVIVCTTSR	AARRIKFEP	LPPKKAHALR	SVHYRSGTKI	FLTCTKFW	DDGIHGGKST
370	380	390	400	410	420	430	440	450	460	470	480
TDLPSRFIYY	PNHNFNGVG	VIIAYGIGDD	ANYFEALDFE	DCGDIVINDL	SLIHQLPKEE	IQAICRPSMI	QRWSLDKYAM	GGITTFPTYQ	FQHFSEALTA	PVDRIYFAGE	YTAQAHGWIA
490	500										
STIKSGPEGL	DVNRASE										

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
165	2	441.3500	178.56	3	28.2	34.7	2	314-324	R.RIKFEPPLPPK.K	
114	1	463.6000	90.68	3	22.5	47.9	1	347-358	K.KFWEDDGIHGGK.S	
125	1	420.9300	167.17	3	23.6	37.1	0	348-358	K.FWEDDGIHGGK.S	
57	1	438.7800	126.03	2	15.9	27.0	0	359-366	K.STTDLPSR.F	

Protein Report

Project Info

Name: venom protein identification 27082013

Date: August 27, 2013

Sample Info & Protocols

Name: **Western diamondback rattlesnake + Tryptase**

Date: August 27, 2013

Search Result Info

Search Result	Location	Search Engine	Database	Ident. Compounds
Amazon vertebrates_swissprot july_Mascot_2013-08-28 18:47:40	/venom protein identification 27082013 /Ca + Tryptase_II_BE2_01_2132.d/Ca + Tryptase_II_BE2_01_2132.mgf	Mascot, 2.3.02	SwissProt_July2013, uniprotswissprotJuly2013.fasta	6/484 (FDR:0.00%)

Protein 1: Snake venom metalloproteinase atrolysin-C OS=Crotalus atrox PE=1 SV=1

Accession:	VM1AC_CROAT	Score:	90.91
Database:	SwissProt_July2013	MW [kDa]:	46.70
Seq. Coverage [%]:	3.90 %	pI:	4.85
		No. of Peptides:	2

10	20	30	40	50	60	70	80	90	100	110	120
MIEVVLVTIC	LAVFPYQGSS	IILESGNVND	YEVVYPRKVT	ALPKGAVQPK	YEDAMQYELK	VNGEPVVLHL	EKNKELFSKD	YSETHYSPDG	RKITTNPSVE	DHCYRGRIE	NDADSTASIS
130	140	150	160	170	180	190	200	210	220	230	240
ACNGLKGHFK	LQGELYLIEP	LELSDSEAHA	VFKLENVEKE	DEAPKMGVVT	QNWESYEPIK	KASDLNLPD	QQNLPQRYIE	LVVVADHRVF	MKYNSDLNTI	RTRVHEIVNF	INGFYRSLNI
250	260	270	280	290	300	310	320	330	340	350	360
HVSLTDLEIW	SNEDQINIQS	ASSDTLNAFA	EWRETDLLNR	KSHDNAQLLT	AIELDEETLG	LAPLGTMCDP	KL SIGIVQDH	SPINLLMGVT	MAHELGHNLG	MEHDGKDCLR	GASLCIMRPG
370	380	390	400	410	420						
LTKGRSYEFS	ADSMHYERF	LKQYKQCIL	NKPLRIDPVS	TPVSGNELLE	AGEE						

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
98	1	548.2400	-64.01	2	22.2	64.5	0	213-221	K.YNSDLNTIR.T	
80	1	430.6700	-132.91	2	21.3	26.4	0	274-280	R.ETDLLNR.K	

Protein Report

L-amino-acid oxidase OS=Crotalus adamanteus PE=1 SV=1

Protein 2:

Accession:

OXLA_CROAD

Score:

65.46

Database:

SwissProt_July2013

MW [kDa]:

58.60

Seq. Coverage [%]:

3.30 %

pl:

6.32

No. of Peptides:

2

10	20	30	40	50	60	70	80	90	100	110	120
MNVFFMFSLL	FLAALGSCAH	DRNPLEECFR	ETDYEEFLEI	AKNGLTATSN	PKRVVIVGAG	MAGLSAAYVL	AGAGHQVTVL	EASERVGGRV	RTYRKKDWYA	NLGPMLPTK	HRIVREYIKK
130	140	150	160	170	180	190	200	210	220	230	240
FDLKLNFSQ	ENENAWYFIK	NIRKRVREVK	NNPGLLEYPV	KPSEEGKSAA	QLYVESLRKV	VEELRSTNCK	YILDKYDTYS	TKEYLLKEGN	LSPGAVDMIG	DLLNEDSGYY	VSFIESLKHD
250	260	270	280	290	300	310	320	330	340	350	360
DIFGYEKRFD	EIVGGMDQLP	TSMYEAIKEK	VQVHFNARVI	EQQNDREAT	VTYQTSANEM	SSVTADYVIV	CTTSRAARRI	KFEPPLPPKK	AHALRSVHYR	SGTKIFLTCT	KKFWEDDGIH
370	380	390	400	410	420	430	440	450	460	470	480
GGKSTTDLPS	RFIYYPNHNF	TSGVGVI IAY	GIGDDANFFQ	ALDFKDCADI	VINDLSLIHE	LPKEDIQTFC	HPSMIQRWSL	DKYAMGGITT	FTPYQFQHFS	EALTAPFKRI	YFAGEYTAQF
490	500	510	520								
HGWIDSTIKS	GLTAARDVNR	ASENPSGIHL	SNDNEF								

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
71	2	557.7900	-11.11	2	20.0	35.7	0	279-287	R.VIEIQQNDR.E	
21	3	438.6800	-101.90	2	16.1	29.8	0	364-371	K.STTDLPSR.F	

Protein Report

Protein 3: Snake venom metalloproteinase adamalysin-2 OS=Crotalus adamanteus PE=1 SV=2
Accession: VM1A2_CROAD **Score:** 62.52
Database: SwissProt_July2013 **MW [kDa]:** 23.10
Seq. Coverage [%]: 4.40 % **pI:** 9.58
No. of Peptides: 1

10	20	30	40	50	60	70	80	90	100	110	120
QQNLPQRYIE	LVVVADRRVF	MK YNSDLNII	RTRVHEIVNI	INGFYRSLNI	DVSLVNLEIW	SGQDPLTIQS	SSSNTLNSEG	LWREKVLLNK	KKKDNAQLLT	AIEFKCETLG	KAYLNSMCNP
130	140	150	160	170	180	190	200	210			
RSSVGIVKDH	SPINLLVAVT	MAHELGHNLG	MEHDGKDCLR	GASLCIMRPG	LTPGRSYEFS	DDSMGYQKF	LNQYKQCIL	NKP			

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
204	2	554.2800	-23.97	2	29.7	62.5	0	23-31	K.YNSDLNIIR.T	

Protein Report

Project Info

Name: venom protein identification 27082013

Date: August 27, 2013

Sample Info & Protocols

Date: August 27, 2013

Name: **Russell's viper + Trypsase**

Search Result Info

Search Result	Location	Search Engine	Database	Ident. Compounds
Amazon vertebrates_swissprot july_Mascot_2013-08-28 18:47:40	/venom protein identification 27082013 /Dr + Trypsase_II_BE4_01_2134.d/Dr + Trypsase_II_BE4_01_2134.mgf	Mascot, 2.3.02	SwissProt_July2013, uniprotswissprotJuly2013.fasta	4/501 (FDR:0.00%)

Protein 1: L-amino-acid oxidase OS=Daboia russelii PE=1 SV=1

Accession: OXLA_DABRR

Score: 96.50

Database: SwissProt_July2013

MW [kDa]: 56.90

Seq. Coverage [%]: 5.00 %

pl: 8.55


No. of Peptides: 2

10	20	30	40	50	60	70	80	90	100	110	120
MNVFFMFSLL	FLATLGSCAD	DKNFLEECFR	EDDYEEFLEI	AKNGLKRTSN	PKHIVIVGAG	MSGLSAAYVL	AGAGHKVTVL	EASERPGGRV	RTHRNKVEGW	YANLGPMPRV	EKHRIIREYI
130	140	150	160	170	180	190	200	210	220	230	240
RKFGKLNLF	VQETENGWYF	IKNIRKRVGE	VKIDPGLLKY	PVKPSEAGKS	AGQLYQESLG	KAVELKRTN	CSYILNKYDT	YSTKEYLIKE	GNLSPGAVDM	IGDLLNEDSG	YVVSFIESLK
250	260	270	280	290	300	310	320	330	340	350	360
HDDIFAYEKR	FDEIVGGMDQ	LPTSMYRAIE	ESVHFVKARVI	KIQQNAEKVT	VTVYQTTQK.NL	LLETADYVIV	CTTSRAARRI	TFKPLPPPK	AHALRSVHYR	SGTKIFLTCT	KKFWEDDGIQ
370	380	390	400	410	420	430	440	450	460	470	480
GKSTTDLPS	RFIYYPNHNE	TGVGVIILAY	GIGDDANFFQ	ALNLNECADI	VFNDLSSIHQ	LPKKDLQTFC	YPSIIQKWSL	DKYAMGAIIT	FTFYQFHFS	EALTAPVGRV	FFAGEYTANA
490	500	510									
HGWIDSTIKS	GLTAARDVNR	ASEL									

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
50	2	584.7800	-58.23	2	18.7	49.9	0	289-298	K.VTVTYQTTQK.N	
147	1	520.5800	-56.45	3	24.9	30.8	2	490-504	K.SGLTAARDVNRASEL.-	

Protein Report

Protein 2: Protease inhibitor 2 OS=Daboia russelii PE=2 SV=1
Accession: IVBI2_DABRR **Score:** 63.36
Database: SwissProt_July2013 **MW [kDa]:** 9.70
Seq. Coverage [%]: 13.10 % **pI:** 9.84
No. of Peptides: 2

10 20 30 40 50 60 70 80 90
 MSSGGLLLLL GLLTLWAEPT PISGQDRPKF CFLRPDFGRY GHPRPRFYYN PATNQCQGL AQRSE**ENTNN** **FDTRDKCRQT** CGRK


Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
19	4	555.7300	-25.48	2	15.0	41.5	0	66-74	R.ENTNNFDTR.D	
12	1	677.2500	-81.37	2	13.5	23.1	1	66-76	R.ENTNNFDTRDK.C	

Protein Report

Project Info

Name: venom protein identification 27082013

Date: August 27, 2013

Sample Info & Protocols

Name: **Saw-scaled viper + Tryptase**

Date: August 27, 2013

Search Result Info

Search Result	Location	Search Engine	Database	Ident. Compounds
Amazon vertebrates_swissprot july_Mascot_2013-08-28 18:47:40	/venom protein identification /Ec + Tryptase_II_BE6_01_2137.d/Ec + Tryptase_II_BE6_01_2137.mgf	Mascot, 2.3.02	SwissProt_July2013, uniprotswissprotJuly2013.fasta	1/445 (FDR:0.00%)

Protein 1: L-amino-acid oxidase OS=Vipera ammodytes ammodytes PE=1 SV=1

Accession: OXLA_VIPAA	Score: 48.50
Database: SwissProt_July2013	MW [kDa]: 54.70
Seq. Coverage [%]: 1.90 %	pl: 7.71
	No. of Peptides: 1

10	20	30	40	50	60	70	80	90	100	110	120
DRNPLEECFR	ETDYEEFLEI	ARNGLKKTSN	PKHVVVVGAG	MSGLSAAYVL	AGAGHKVTVL	EASERAGGRV	RTHRNSKEGW	YANLGPMRIP	EKHRIVREYI	RKFGNLNNEF	SQENDNAWYF
130	140	150	160	170	180	190	200	210	220	230	240
IKNIRKRVGE	VNKDPGLLKY	PVKPSEEGKS	AGQLYEESLG	SAVKDLKRTN	CSYILNKYDT	YSTKEYLIKE	GNLSPGAVDM	IGDLLNEDSG	YYVSFIESLK	HDDIFAYEKR	FDEIVGGMDQ
250	260	270	280	290	300	310	320	330	340	350	360
LPTSMYRAIE	EKVKFNARVI	KIQQNANQVT	VTYQTPEKDT	SSNTADYVIV	CTTSRAARRI	QFEPPLPPKK	QHALRSVHYR	SGTKIFLTCS	SKFWEDDGIH	GGKSTDLPS	RFIYYPNHNF
370	380	390	400	410	420	430	440	450	460	470	480
STGVGVIIAY	GIGDDANFFQ	ALKFKDCADI	VFNDLSLIHQ	LPKEEIQSFC	YPSMIQKWSL	DKYAMGAIIT	FTPYQFQRF	EALTAPQGR	FFAGEYTAEA	HGWIDSTIKS	GLTAARDVNR
490											

ASEQ

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	P	Range	Sequence	Modification
62	3	502.2200	-108.63	2	22.1	48.5	0	57-65	K.VTVLEASER.A	