

Supplementary File

Table S1. LC-MS/MS results of purified CP-LAAO.

Accession	-10lgP	Coverage (%)	#Peptides	#Unique	Avg. Mass	Description
A0A024BTN9 OXLA_BOTSC	252.91	24	11	2	56376	L-amino acid oxidase Bs29 (Fragment) <i>Bothriechis schlegelii</i>
P81382 OXLA_CALRH	221.31	35	11	4	58221	L-amino-acid oxidase <i>Calloselasma rhodostoma</i>
P0DI84 OXLA_VIPAA	215.1	21	10	3	54748	L-amino-acid oxidase <i>Vipera ammodytes ammodytes</i>
Q6WP39 OXLA_TRIST	200.14	25	10	2	58601	L-amino-acid oxidase <i>Trimeresurus stejnegeri</i>
X2JCV5 OXLA_CERCE	141.97	16	9	2	58557	L-amino acid oxidase <i>Cerastes cerastes</i>

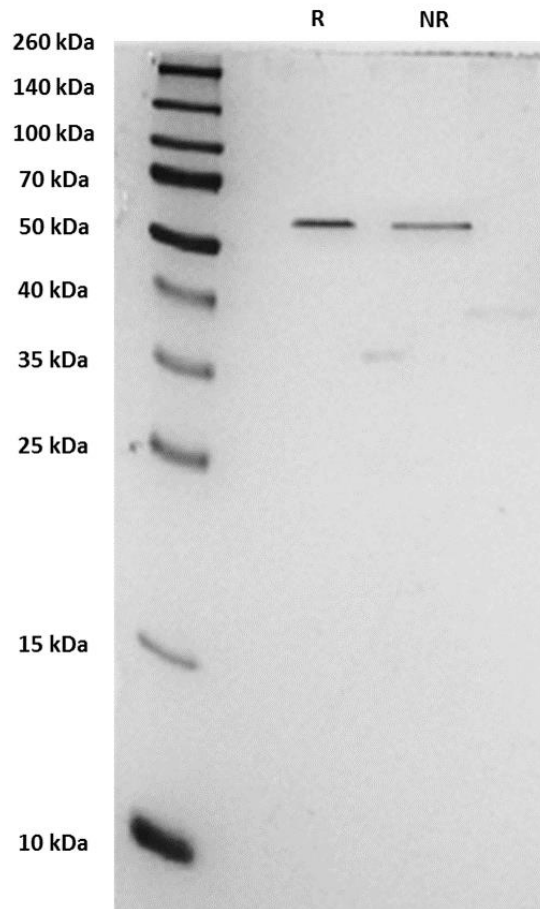


Figure S1. SDS-PAGE of purified L-amino acid oxidase (reduced (R) and non-reduced (NR)) aligned with Pierce Broad Range Spectra Multicolour protein ladder (E)

Table S2 Partial peptide sequences of CP-LAAO identified from LC-MS/MS and *de novo* sequencing

Protein Accession	Peptide	Unique	-10lgP	Mass	Length	ppm	m/z	z	RT
P81382 OXLA_CALRH	MNVFFMFSLFLAALGSC(+57.02)ADDR.N	N	27.62	2524.195	22	-42	632.0296	4	4.62
Q6WP39 OXLA_TRIST	MNVFFMFSLFLAALGSC(+57.02)ADDR.N	N	27.62	2524.195	22	-42	632.0296	4	4.62
Q6WP39 OXLA_TRIST	A.DDRNPLEEC(+57.02)FR.E	N	64.97	1449.631	11	1.9	484.2184	3	8.02
Q6WP39 OXLA_TRIST	A.DDRNPLEEC(+57.02)FRET DYEEFLEIAR.N	N	83.83	2945.314	23	-0.5	737.3353	4	12.89
P0DI84 OXLA_VIPAA	K.TS(+79.97)NPKHVVVVGAGMS(+79.97).G	Y	19.82	1641.699	15	46.6	411.4511	4	5.11
A0A024BTN9 OXLA_BOTSC	K.HVVIVGAGMSGLSAAAYVLGAGHQVTVLEASER.A	Y	125.43	3248.698	33	-5.3	813.1774	4	13.32
A0A024BTN9 OXLA_BOTSC	G.LSAAAYVLGAGHQVTVLEASER.A	N	51.43	2241.175	22	-1.8	748.0644	3	11.36
A0A024BTN9 OXLA_BOTSC	K.HVVVR(sub I)YGAGMSGLSAAAYVLGAGHQVTVLEASER.A	Y	34.74	3291.715	33	-9.1	823.9285	4	12.65
P81382 OXLA_CALRH	K.HVVIVGAGMAGLSAAAYVLGAGHQVTVLEASERPGGR.V	Y	38.6	3599.899	37	-3.2	720.9849	5	13.49
A0A024BTN9 OXLA_BOTSC	K.EGWY(-18.01)ANLGPMR(+14.02).L	N	16.65	1288.602	11	33.1	645.3298	2	12.18
P0DI84 OXLA_VIPAA	K.EGWY(-18.01)ANLGPMR(+14.02).I	N	16.65	1288.602	11	33.1	645.3298	2	12.18
P0DI84 OXLA_VIPAA	R.KFGLNLFNEFSQENDNAWYFIK.N	Y	16.84	2576.233	21	-2.7	645.0639	4	24.93
P81382 OXLA_CALRH	K.DPGLLKYPVKPSEAGKSAGQLYEESLGK.V	Y	18.84	2960.549	28	58.3	741.1877	4	21.45
Q6WP39 OXLA_TRIST	R.FDEIVDGMMDK(+27.99)LPTSMYR.A	Y	16.01	2043.928	17	5	682.3201	3	8.6
A0A024BTN9 OXLA_BOTSC	K.LPTSMYQAI.E	N	16.34	1022.511	9	6.1	512.2657	2	9.61
X2JCV5 OXLA_CERCE	K.LPTSMYQAI.Q	N	16.34	1022.511	9	6.1	512.2657	2	9.61
X2JCV5 OXLA_CERCE	E.VTVTYQTPAK.N	Y	50.75	1106.597	10	-0.7	554.3055	2	5.87
X2JCV5 OXLA_CERCE	K.K(sub E)VTVTYQTPAK.N	Y	22.86	1234.692	11	-3.1	618.3514	2	5.42
A0A024BTN9 OXLA_BOTSC	K.IFLTC(+57.02)TK.K	N	53.04	881.4681	7	0.5	441.7415	2	7.18
Q6WP39 OXLA_TRIST	K.IFLTC(+57.02)TK.K	N	53.04	881.4681	7	0.5	441.7415	2	7.18
X2JCV5 OXLA_CERCE	K.IFLTC(+57.02)TK.K	N	53.04	881.4681	7	0.5	441.7415	2	7.18
A0A024BTN9 OXLA_BOTSC	K.FWEDDGIHGK.S	N	64.75	1259.557	11	1.5	420.8603	3	6.71
P81382 OXLA_CALRH	K.FWEDDGIHGK.S	N	64.75	1259.557	11	1.5	420.8603	3	6.71
P0DI84 OXLA_VIPAA	K.FWEDDGIHGK.S	N	64.75	1259.557	11	1.5	420.8603	3	6.71
X2JCV5 OXLA_CERCE	K.FWEDDGIHGK.S	N	64.75	1259.557	11	1.5	420.8603	3	6.71
Q6WP39 OXLA_TRIST	R.EDEGIHGKSTTDLPSR.F	N	17.69	1797.849	17	-0.3	450.4695	4	4.36

P81382 OXLA_CALRH	G.VIIAYGIGDDANFFQALDFKDC(+57.02)ADIVFNDLSLIHQPK.K	Y	34.59	4295.161	38	-8.9	1074.788	4	17.15
P0DI84 OXLA_VIPAA	K.EEIP(sub Q)SFC(+57.02)YPSMIQK.W	Y	34.52	1727.79	14	25.3	576.9518	3	8.9
A0A024BTN9 OXLA_BOTSC	G.ITTFIPYQFQHFSEA.L	N	23.41	1815.847	15	-3.1	908.9279	2	10.85
Q6WP39 OXLA_TRIST	G.ITTFIPYQFQHFSEA.L	N	23.41	1815.847	15	-3.1	908.9279	2	10.85
X2JCV5 OXLA_CERCE	G.ITTFIPYQFQHFSEA.L	N	23.41	1815.847	15	-3.1	908.9279	2	10.85
P81382 OXLA_CALRH	R.IYFAGEYTAQAHGWIDSTIK.S	N	19.99	2270.101	20	-5.9	757.7031	3	27.83
X2JCV5 OXLA_CERCE	R.IYFAGEYTAQAHGWIDSTIK.S	N	19.99	2270.101	20	-5.9	757.7031	3	27.83

1 MNVFFMFSLL FLAALGSCAD DRNPLEECFR ETDYEEFLEI ARxxxxxTSNP KHVVRVVGAGM SGLSAAYVLA GAGHQVTVLE
 81 ASERPGGRxx xxxxxxEGWY ANLGPMRxxx xxxxxxxxxxxx KFGNLNLEFS QENDNAWYFI Kxxxxxxxxx xDPGLLKYPV
 161 KPSEAGKSAG QLYEESLGKx xxxxxxxxxxxx xxxxxxxxxxxx xxxxxxxxxxxx xxxxxxxxxxxx xxxxxxxxxxxx xxxxxxxxxxxx
 241 xxxxxxxxFD EIVDGMKLP TSMYQAixxx xxxxxxxxxxxx xxxxxKVTV TYQTPAKxxx xxxxxxxxxxxx xxxxxxxxxxxx
 321 xxxxxxxxxxxx xxxxxxxxxxxx xxxifLTCTK KFWEDDGIHG GKSTTDLPSR xxxxxxxxxxxx xxxvIIAYG IGD DANFFQA
 401 LDFKDCADIV FNDLSLIHQL PKEEIPSFY PSMIQKxxxx xxxxxxITTF FTPYQFQHFS EAxxxxxxxxI YFAGEYTAQA
 481 HGWIDSTIKx xxxxxxxxxxxx xxxxxxxxxxxx xxxxxxxxxxxx

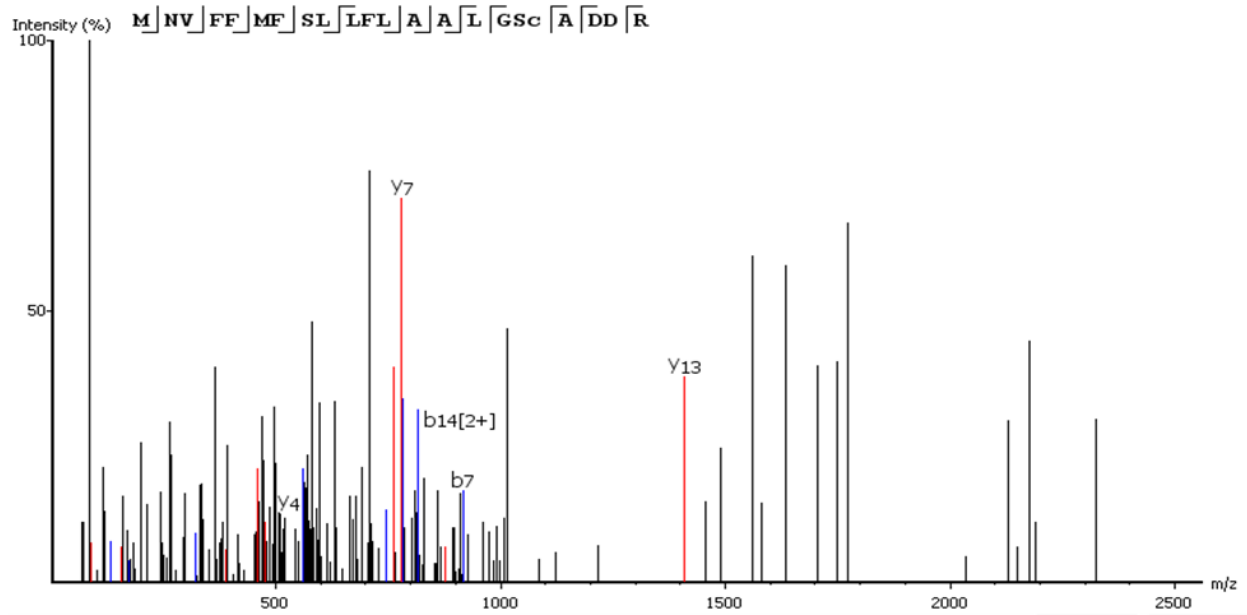


Figure S2. Partial amino acid sequence of *C. purpureomaculatus* LAAO identified from LC-MS/MS (Top panel). Highlighted amino acid (red) represents mutation in the peptide sequence compared to similar proteins from other snake species. Mass to charge ratio (M/Z) of high confidence peptide match obtained from LC-MS/MS for *C. purpureomaculatus* LAAO (bottom panel).