APPENDIX K

Supplemental Table 1: Orthologous proteins in database matched with the tryptic peptide sequences generated from proteins in circles no. 1-24 of **Figure 53**. MH+, protonated molecular mass; X_{corr}, cross correlation; ΔC_n, delta correlation; Sp, primary score; RSp, ranking of primary score.

Circle no.	Matched peptides	% coverage	Orthologous protein (s)/peptides	MH+	Charge	X_{corr}	Score ΔC_n	Sp	RSp
1	10	6.8	Cobra venom factor precursor				230.3		
			K.LNGDITVTASGDGK.A	1418.71	2	4.983	0.804	1952.4	1
			K.ACETNVDYVYK.T	1361.64	2	3.980	0.79	938.7	1
			R.WPHEDECQEEEFQK.L	1890.79	3	4.802	0.626	2707.6	1
			K.VYSYYNLDEK.C	1293.6	2	3.205	0.751	908.8	1
			K.DKISYIITK.N	1080.63	2	2.423	0.499	1075	1
			K.ISYIITK.N	837.51	1	1.766	0.452	554.2	1
			K.DKISYIITK.N	1080.63	2	2.349	0.492	1057.7	1
			K.ISYIITK.N	837.51	1	1.683	0.489	612.4	1
			K.LNQDITVTASGDGK.A	1418.71	2	5.004	0.785	1722.8	1
			K.LNQDITVTASGDGK.A	1418.71	2	4.831	0.685	1785.1	1
			R.IDVPLQIEK.A	1054.61	2	2.460	0.625	530.5	1
			R.IDVPLQIEK.A	1054.61	1	1.828	0.437	455	1
			K.ACETNVDYVYK.T	1361.64	2	3.897	0.744	1092.7	1
			K.ACETNVDYVYK.T	1361.64	2	3.784	0.790	891.7	1
			R.INYENALLAR.T	1176.64	1	1.966	0.521	256.6	1
			K.VYSYYNLDEKK.C	1293.6	2	3.020	0.774	882.2	1
			K.VNDDYLIWGSR.S	1337.65	2	3.900	0.835	1347.8	1
			K.VNDDYLIWGSR.S	1337.65	1	2.235	0.699	373.1	1
			K.ATM*TILTFYNAQLQEK.A	1887.95	2	5.692	0.708	2449	1

* indicates predicted oxidation

Supplemental Table 1−continued

Circle no.	Matched Peptides	% coverage	Orthologous protein (s)/peptides	MH+	Charge	X_{corr}	Score ΔC_n	Sp	RSp
1			R.IDVPLQIEK.A	1054.61	2	2.180	0.566	464.5	1
			R.INYENALLAR.T	1176.64	2	4.170	0.572	1377.6	1
			K.ACETNVDYVYK.T	1361.64	2	2.993	0.762	992.6	1
			K.ACETNVDYVYK.T	1361.64	2	2.344	0.650	915.1	1
	4	2.5	Complement C3 precursor				50.2		
			R.KCQEALNLK.L	1103.62	2	3.027	0.572	848.5	1
			K.VSHSEDECLHFK.I	1487.69	2	4.031	0.730	1448.1	1
			K.CQEALNLK.L	975.52	2	2.453	0.496	418.1	1
			K.HFEVGFIQPGSVK.V	1444.76	2	4.192	0.771	1657.8	1
			K.HFEVGFIQPGSVK.V	1444.76	2	4.193	0.729	1148.2	1
2	1	5.7	Nerve growth factor beta-chain precursor, monocled cobra				20.1		
			R.FIRIET#ACVCVITK.K	1789.94	2	2.127	0.165	220.4	1
			R.FIRIET#ACVCVITK.K	1789.94	2	2.487	0.236	234.2	1
3	4	3.3	Cobra vevom factor precursor-monocled cobra				78.4		
			K.GDNLIQM*PGAAM*K.I	1377.65	2	3.793	0.767	1126.9	1
			K.GDNLIQMPGAAM*K.I	1361.66	2	2.353	0.714	576.4	2
			K.GDNLIQM*PGAAMK.I	1361.66	2	3.889	0.395	1066.7	1
			K.GDNLIQMPGAAMK.I	1345.66	2	4.142	0.801	1102.1	1
			R.KYVLPSFEVR.L	1237.69	2	3.484	0.059	990.4	2
			R.VDMNPAGGMLVTPTIEIPAK.E	2054.07	2	5.834	0.704	1706.8	1
			K.QLDIFVHDFPR.K	1386.72	2	2.687	0.801	347.6	1

[#] indicates predicted phosphorylation; * indicates predicted oxidation

Supplemental Table 1−continued

Circle no.	Matched peptides	% coverage	Orthologous protein (s)/peptides	MH+	Charge	X_{corr}	Score ΔC_n	Sp	RSp
3			K.QLDIFVHDFPR.K	1386.72	2	3.017	0.779	758.8	1
	3	2.2	Complement C3 precursor				68.3		
			R.TDTEEQILVEAHGDSTPK.S	1969.94	2	5.218	0.768	2020.4	1
			R.TDTEEQILVEAHGDSTPK.S	1969.94	2	5.209	0.731	1839.1	1
			R.TDTEEQILVEAHGDSTPK.S	1969.94	3	3.200	0.727	1137.6	1
			R.TDTEEQILVEAHGDSTPK.S	1969.94	3	3.767	0.582	1287.9	1
			R.EYVLPSFEVR.L	1238.64	2	3.278	0.506	1157.1	1
			R.EYVLPSFEVR.L	1238.64	2	2.882	0.432	1064.5	1
			K.YFTYLILNK.G	1174.65	2	2.941	0.474	1009.5	1
4	5	4.1	Cobra venom factor precursor, monocled cobra				116.3		
			R.VFSMDHNTSK.M	1165.53	2	2.578	0.659	647.9	1
			K.GDNLIQM*PGAAM*K.I	1377.65	2	3.733	0.725	933.8	1
			K.GDNLIQMPGAAM*K.I	1361.66	2	2.199	0.746	545.3	2
			K.GDNLIQM*PGAAMK.I	1361.66	2	3.758	0.415	1161.4	1
			K.GDNLIQM*PGAAMK.I	1361.66	2	3.583	0.431	908.2	1
			K.GDNLIQMPGAAM*K.I	1361.66	2	2.037	0.748	553.1	2
			R.QNQYVVVQVTGPQVR.L	1714.92	2	4.535	0.654	1697.0	1
			K.GDNLIQMPGAAMK.I	1345.66	2	3.354	0.772	1073	1
			R.VDM*NPAGGM*LVTPTIEIPAK.E	2086.06	2	5.688	0.867	1624	1
			R.VDM*NPAGGM*LVTPTIEIPAK.E	2086.06	2	5.715	0.879	1890	1
			R.KLVLPSFEVR.L	1237.69	2	3.040	0.086	1083.6	1
			K.YVLPSFEVR.L	1109.6	2	2.067	0.778	515.4	1

* indicates predicted oxidation

Supplemental Table 1−continued

Circle no.	Matched peptides	% coverage	Orthologous protein (s)/peptides	MH+	Charge	X_{corr}	Score ΔC_n	Sp	RSp
4	4	2.8	Complement C3 precursor				68.3		
			K.DTCM*GTLVVK.G	1139.57	2	2.880	0.692	627.1	1
			R.TDTEEQILVEAHGDSTPK.S	1969.94	2	5.248	0.763	1796.7	1
			R.TDTEEQILVEAHGDSTPK.S	1969.94	3	3.758	0.661	1008.3	1
			K.DTCMGTLVVK.G	1123.58	2	2.422	0.621	618.5	1
			K.DTCMGTLVVK.G	1123.58	2	2.466	0.616	749.4	1
			R.EYVLPSFEVR.L	1238.64	2	2.777	0.54	1083.6	1
			K.YFTYLILNK.G	1174.65	2	2.767	0.536	982.8	1
5	4	3.5	Cobra venom factor precursor, monocled cobra				76.3		
			K.GDNLIQMPGAAM*K.I	1361.66	2	2.006	0.789	635.4	2
			K.GDNLIQM*PGAAMK.I	1361.66	2	3.547	0.435	1027.7	1
			K.GDNLIQMPGAAM*K.I	1361.66	2	2.523	0.762	553.8	2
			K.GDNLIQM*PGAAMK.I	1361.66	2	3.984	0.367	1058.4	1
			R.QNQYVVVQVTGPQVR.L	1714.92	2	5.056	0.786	2007.5	1
			K.GDNLIQMPGAAMK.I	1375.66	2	4.127	0.824	1179	1
			R.VDM*NPAGGM*LVTPTIEIPAK.E	2086.06	2	5.821	0.873	1561.6	1
			R.KYVLPSFEVR.L	1237.69	2	3.283	0.047	974.5	1
	3	2.3	Complement C3 precursor				48.3		
			K.IKLEGDPGAR.V	1055.58	2	2.273	0.657	432.9	1
			R.TDTEEQILVEAHGDSTPK.S	1969.94	3	4.157	0.586	1266.6	1
			R.TDTEEQILVEAHGDSTPK.S	1969.94	3	3.863	0.711	1152.2	1

* indicates predicted oxidation

Supplemental Table 1−continued

Circle no.	Matched peptides	% coverage	Orthologous protein (s)/peptides	MH+	Charge	X_{corr}	Score ΔC_n	Sp	RSp
			R.EYVLPSFEVR.L	1238.64	2	2.964	0.471	849.6	1
			R.EYVLPSFEVR.L	1238.64	2	3.130	0.495	974.5	1
6	4	3.5	Cobra venom factor precursor, monocled cobra				106.4		
			K.GDNLIQM*PGAAM*K.I	1377.65	2	3.906	0.807	1134.1	1
			K.GDNLIQMPGAAM*K.I	1361.66	2	2.079	0.742	690.7	2
			K.GDNLIQM*PGAAMK.I	1361.66	2	3.655	0.431	987.1	1
			K.GDNLIQM*PGAAMK.I	1361.66	2	3.564	0.422	1028.1	1
			K.GDNLIQMPGAAM*K.I	1361.66	2	2.059	0.753	617.8	2
			R.QNQYVVVQVTGPQVR.L	1714.92	2	4.799	0.694	1911.9	1
			R.QNQYVVVQVTGPQVR.L	1714.92	2	4.935	0.747	1963.4	1
			K.GDNLIQMPGAAMK.I	1345.66	2	3.694	0.761	1124.9	1
			K.GDNLIQMPGAAMK.I	1345.66	2	4.028	0.805	1614.4	1
			R.KYVLPSFEVR.L	1237.69	2	3.047	0.054	1269.5	1
			R.VDMNPAGGMLVTPTIEIPAK.E	2054.07	2	6.010	0.702	1789.6	1
6	3	2.2	Complement C3 precursor				38.2		
			R.TDTEEQILVEAHGDSTPK.S	1969.94	3	3.669	0.646	1064.8	1
			R.TDTEEQILVEAHGDSTPK.S	1969.94	3	3.629	0.654	1133.8	1
			R.EYVLPSFEVR.L	1238.64	2	2.882	0.503	1092.8	2
			K.YFTYLILNK.G	1174.65	2	2.848	0.486	957.6	1
7	1	8.4	Chain A structure of an acidic phospholipase A2 of *Ophiophagus hannah*				24.1		
			K.ENINDTTT#R.C	1256.55	2	2.149	0.033	524.3	2
			K.ENINDTT#TR.C	1256.55	2	2.096	0.085	386.8	4

$^{\#}$ indicates predicted phosphorylation; * indicates predicted oxidation

Supplemental Table 1−continued

Circle no.	Matched peptides	% coverage	Orthologous protein (s)/peptides	MH+	Charge	X_{corr}	Score ΔC_n	Sp	RSp
7			K.ENINDT#TTR.C	1256.55	2	2.167	0.008	395.0	3
8,9, 10			No matched protein						
11	1	4.4	Venom protein 2				20.5		
			K.YGSEVESDIAAILEVFSKLR.Y	2226.17	2	2.208	0.544	198.9	1
			K.YGSEVESDIAAILEVFSKLR.Y	2226.17	2	2.404	0.451	233.2	1
12, 13 14, 15			No matched protein						
16	4	42	PA2_NAJNA phospholipase A2, acidic phosphatidylcholine				98.3		
			R.GGSGTPVDDLDR.C	1188.55	2	2.721	0.622	587.9	1
			K.TYSYECSQGTLTCK.G	1697.78	2	4.931	0.712	2221.6	1
			R.GGSGTPVDDLDR.C	1188.55	2	3.254	0.720	642.8	1
			R.GGSGTPVDDLDR.C	1188.55	1	1.912	0.609	285.8	1
			K.NMKCTVPSR.S	1205.64	2	3.062	0.000	1214.0	1
			K.NMKCTVPSR.S	1205.64	2	3.309	0.000	1209.6	1
			R.CCGVHDNCYNEAEK.I	1826.78	2	5.327	0.032	786.4	1
			R.CCGVHDNCYNEAEK.I	1826.78	2	4.237	0.246	847.9	1
			K.TYSYECSQGTLTCK.G	1697.78	2	5.082	0.714	3015.3	1
			R.GGSGTPVDDLDR.C	1188.55	2	3.109	0.677	556.9	1

# indicates predicted phosphorylation

Supplemental Table 1−continued

Circle no.	Matched peptides	% coverage	Orthologous protein (s)/peptides	MH+	Charge	X_{corr}	Score ΔC_n	Sp	RSp
16	3	33.6	Phospholipase A2 (EC 3.1.1.4.) II, monocled cobra				74.3		
			R.CCQVHDNCYDEAEK.I	1827.77	3	3.603	0.780	1220.1	1
			K.NMIQCTVPNR.S	1232.62	1	2.004	0.632	122	1
			R.CCQVHDNCYDEAEK.I	1827.77	3	3.660	0.754	1862.9	1
			R.CCQVHDNCYDEAEK.I	1827.77	2	5.158	0.267	671.7	3
			K.NM*IQCTVPNR.S	1248.61	2	3.398	0.507	835.8	1
			R.CCQVHDNCYDEAEK.I	1827.77	2	4.262	0.006	679.4	2
			-.NLYQFKNM*IQCTVPNR.S	2042.03	3	4.500	0.8	908.1	1
			K.NMIQCTVPNR.S	1232.62	2	3.597	0.487	1272.8	1
	3	33	Chain A, crystal structure of a C49 phospholipase A2 of Indian Cobra (*Naja naja sagittifera)*				64.5		
			K.GNNNACAASSCDCDR.L	1671.68	2	2.284	0.487	730.7	1
			R.NM*IECTVPSR.S	1222.59	2	3.101	0.635	1123.5	1
			R.NMIECTVPSR.S	1206.59	2	2.593	0.723	1214	1
			R.NMIECTVPSR.S	1206.59	2	2.977	0.737	1209.6	1
			K.TYTYQCS#GGTLTCK	1719.74	2	2.565	0.193	405.3	1
			K.TYTYQCSGGTL#TCK	1719.74	2	2.248	0.200	244.9	4
			K.T#YTYQCSGGTLTCK	1719.74	2	2.230	0.531	336.7	3
			K.TYT#YQCSGGTLTCK	1719.74	2	2.786	0.080	377.7	2
17	5	64.7	Phospholipase A2 (EC 3.1.1.4.) II, monocled cobra				182.3		
			R.CCQVHDNCYDEAEK.I	1827.77	3	3.613	0.742	1179.2	1
			K.NM*IQCTVPNR.S	1248.61	2	3.163	0.679	857.9	1
			K.NMIQCTVPNR.S	1232.62	1	2.522	0.502	182.9	1

[#] indicates predicted phosphorylation; * indicates predicted oxidation

Supplemental Table 1−continued

Circle no.	Matched peptides	% coverage	Orthologous protein (s)/peptides	MH+	charge	X_{corr}	Score ΔC_n	Sp	RSp
17			K.NMIQCTVPNR.S	1232.62	1	2.837	0.513	202.4	1
			R.GGSGTPVDDLDRCCQVHDNCYDEAEKI	2997.3	3	5.197	0.789	696	1
			R.CCQVHDNCYDEAEK.I	1827.77	3	3.360	0.731	1143.7	1
			K.NM*IQCTVPNR.S	1248.61	2	3.313	0.499	881.7	1
			K.NM*IQCTVPNR.S	1248.61	2	3.328	0.542	940.0	1
			K.NMIQCTVPNR.S	1232.62	2	3.187	0.650	1139.4	1
			R.LAAICFAGAPYNNNNYNIDLK.A	2356.17	2	5.103	0.809	1374.5	1
			R.CWPYFK.T	900.44	1	1.923	0.430	270.4	1
			K.NMIQCTVPNR.S	1232.62	2	3.204	0.675	1240.6	1
			K.NM*IQCTVPNR.S	1248.61	2	2.182	0.766	526.3	1
			R.LAAICFAGAPYNNNNYNIDLK.A	2356.17	2	5.189	0.270	1636.5	1
			R.CWPYFK.T	900.44	1	1.979	0.488	267.1	1
			R.CWPYFK.T	900.44	1	2.234	0.533	301.8	1
			K.NMIQCTVPNR.S	1232.62	2	2.825	0.623	957.3	1
			R.LAAICFAGAPYNNNNYNIDLK.A	2356.17	2	5.180	0.048	1508.1	1
			R.CWPYFK.T	900.44	1	1.965	0.455	190.7	1
	2	20.3	Chain A, crystal structure of a C49 phospholipase A2 of Indian Cobra				146.4		
			R.NM*IECTVPSR.S	1222.59	2	2.714	0.583	1125.2	1
			R.NM*IECTVPSR.S	1222.59	2	2.793	0.487	1105.4	1
			R.NMIECTVPSR.S	1206.59	2	3.152	0.549	1198.8	1
			K.TYT#YQCSGGTLTCK.G	1719.74	2	3.177	0.149	474.3	1
			K.T#YTYQCSGGTLTCK.G	1719.74	2	2.609	0.300	421.7	2
			K.TYTYQCS#GGTLTCK.G	1719.74	2	2.703	0.179	379.5	3
			K.TYTYQCSGGT#LTCK.G	1719.74	2	2.225	0.577	203.2	5

[#] indicates predicted phosphorylation; * indicates predicted oxidation

Supplemental Table 1−continued

Circle no.	Matched peptides	% coverage	Orthologous protein (s)/peptides	MH+	charge	X_{corr}	Score ΔC_n	Sp	RSp
17			K.T#YTYQCSGGTLTCK.G	1719.74	2	2.624	0.292	603.4	1
			K.TYT#YQCSGGTLTCK.G	1719.74	2	3.055	0.141	603.4	1
			K.TYTYQCS#GGTLTCK.G	1719.74	2	2.163	0.43	430	2
	4	41.2	PA2_NAJNA phopholipase A2, acidic phosphatidylcholine				110.2		
			K.TYSYECSQGTKTCK.G	1697.78	2	4.569	0.691	2548.7	1
			R.GGSGTPVDDLDR.C	1188.55	2	3.090	0.714	481.4	1
			R.GGSGTPVDDLDR.C	1188.55	1	2.136	0.607	320.0	1
			R.GGSGTPVDDLDR.C	1188.55	1	2.027	0.665	167.4	1
			R.GGSGTPVDDLDR.C	1188.55	2	2.762	0.693	408.2	1
			K.ISGCWPYFK.T	1157.58	2	3.048	0.701	895.4	1
			R.GGSGTPVDDLDR.C	1188.55	2	2.916	0.699	531.8	1
			R.GGSGTPVDDLDR.C	1188.55	2	3.129	0.746	440.5	1
			R.SWWDFADYGCYCGR.G	1842.76	2	4.975	0.801	2062.4	1
			R.GGSGTPVDDLDR.C	1188.55	2	2.811	0.668	497.0	1
			K.ISGCWPYFK.T	1157.58	2	2.932	0.682	618.0	1
	2	29.4	PA21_NAJOX phospholipase A2 isozyme E (phosphatidylcholine)				42.3		
			R.LAAICFAGAPYNNDNYNINLK.A	2356.17	2	5.119	0.058	1374.5	1
			R.S#WLDFANYGCYGR.G	1848.75	2	2.185	0.363	1201.4	1
			R.LAAICFAGAPYNNDNYNINLK.A	2356.17	2	5.051	0.038	1515.2	3
			R.S#WLDFANYGCYGR.G	1848.75	2	2.007	0.446	1046.7	1
			R.LAAICFAGAPYNNDNYNINLK.A	2356.17	2	4.695	0.746	1284.8	3

[#] indicates predicted phosphorylation

Supplemental Table 1−continued

Circle no.	Matched peptides	% coverage	Orthologous protein (s)/peptides	MH+	charge	X_{corr}	Score ΔC_n	Sp	RSp
17	1	11.8	Chain B, crystal structure of a zinc containing dimer of phospholipase A2 of Indian Cobra				30.2		
			R.CCQTHDNCYNEAEK.I	1828.76	3	3.740	0.034	1083.5	2
			R.CCQTHDNCYNEAEK.I	1828.76	3	3.567	0.058	1071.7	2
			R.CCQTHDNCYNEAEK.I	1828.76	2	3.136	0.527	487.0	1
18	4	42	PA2_NAJNA phospholipase A2, acidic phosphatidylcholine				60.2		
			R.CCQVHDNCYNEAEK.I	1826.78	2	4.959	0.018	1351.0	1
			K.TYSYECSQGTLTCK.G	1697.78	2	4.886	0.712	2918.1	1
			K.NMIKCTVPSR.S	1205.64	2	3.257	0.126	1200.7	1
			R.GGSGTPVDDLDR.C	1188.55	1	2.345	0.629	345.8	1
			K.NMIKCTVPSR.S	1205.64	1	2.039	0.160	236.5	1
			K.TYSYECSQGTLTCK.G	1697.78	2	4.028	0.712	2010.7	1
	3	42	Phospholipase A2 (EC 3.1.1.4.) II, monocled cobra				56.3		3
			R.CCQVHDNCYDEAEK.I	1827.77	2	4.871	0.365	1177.6	2
			R.CCQVHDNCYDEAEK.I	1827.77	2	5.149	0.252	1281.0	1
			R.CCQVHDNCYDEAEK.I	1827.77	3	3.820	0.803	1207.8	2
			R.GGSGTPCDDLDRCCQVHDNCYDEAEK.I	2997.30	3	5.282	0.752	692.9	1
			R.CCQVHDNCYDEAEK.I	1827.77	3	3.612	0.057	813.1	1
			K.NMIQCTVPNR.S	1232.62	2	2.937	0.600	1125.4	1

Supplemental Table 1−continued

Circle no.	Matched peptides	% coverage	Orthologous protein (s)/peptides	MH+	charge	X_{corr}	Score ΔC_n	Sp	RSp
	2	17.1	PA21_NAJAT phopholipase A2 precursor (phosphatidylcholine)				40.2		
			K.GGNNACAAAVCDCDR.L	1610.70	2	4.105	0.759	1878.1	1
			K.NMIQCTVPSR.S	1205.61	2	3.257	0.000	1200.7	1
			K.NMIQCTVPSR.S	1205.61	1	2.039	0.000	236.5	1
19	2	29.7	Chain A, crystal structure of a C49 phospholipase A2 of Indian cobra				94.3		
			K.TYT#YQCSGGTLTCK.G	1719.74	2	2.437	0.026	236.6	2
			K.TYTYQCSGGT#LTCK.G	1719.74	2	2.056	0.16	205.5	4
			K.TYTYQCS#GGTLTCK.G	1719.74	2	2.373	0.156	292.3	1
			K.T#YTYQCSGGTLTCK.G	1719.74	2	2.046	0.519	206.0	3
			K.TYT#YQCSGGTLTCK.G	1719.74	2	2.218	0.115	487.8	1
			K.TYT#YQCSGGTLTCK.G	1719.74	2	2.468	0.103	754.6	1
			K.T#YTYQCSGGTLTCK.G	1719.74	2	2.215	0.362	680.7	2
			R.LAAICFAGAPYNDNNYNIDLK.A	2357.15	2	5.624	0.782	1246.9	1
			R.LAAICFAGAPYNDNNYNIDLK.A	2357.15	3	6.173	0.812	2550.8	1
			R.LAAICFAGAPYNDNNYNIDLK.A	2357.15	2	5.388	0.058	1607.1	2
			R.LAAICFAGAPYNDNNYNIDLK.A	2357.15	3	5.416	0.759	2787.6	1
	4	41.2	PA2_NAJNA phopholipase A2, acidic phosphatidylcholine				80.3		
			R.GGSGTPVDDLDR.C	1188.55	2	2.638	0.691	461.4	1
			R.GGSGTPVDDLDR.C	1188.55	2	2.696	0.665	535.2	1

# indicates predicted phosphorylation

Supplemental Table 1−continued

Circle no.	Matched peptides	% coverage	Orthologous protein (s)/peptides	MH+	charge	X_{corr}	Score ΔC_n	Sp	RSp
			K.TYSYECSQGTLTCK.G	1697.78	2	3.765	0.751	2358.1	1
			K.ISGCWPYFK.T	1157.58	2	3.422	0.790	968.7	1
			R.SWWDFADYGCYCGR.G	1842.76	2	4.986	0.855	2250.5	1
			K.TYSYECSQGTLTCK.G	1697.78	2	4.381	0.743	1961.2	1
			R.SWWDFADYGCYCGR.G	1842.76	3	5.466	0.754	3000.5	1
			R.GGSGTPVDDLDR.C	1188.55	2	2.562	0.668	567.2	1
	3	37.8	Phospholipase A2 (EC 3.1.1.4.) II, monocled cobra				60.6		
			R.CCQVHDNCYDEAEK.I	1827.77	3	2.776	0.070	236.3	1
			K.NMIQCTVPNR.S	1232.62	2	3.498	0.642	1261.5	1
			K.NM*IQCTVPNR.S	1248.61	2	3.043	0.541	970.8	1
			K.NM*IQCTVPNR.S	1248.61	2	2.709	0.506	949.5	1
			K.NMIQCTVPNR.S	1232.62	2	3.446	0.663	1052.4	1
			R.LAAICFAGAPYNNNNYNIDLK.A	2356.17	2	5.654	0.047	1612.0	1
20	2	29.4	PA21_NAJOX phospholipase A2 isozyme E (phosphatidylcholine)				36.3		
			R.LAAICFAGAPYNNDNYNINLK.A	2356.17	2	4.885	0.719	1364.7	2
			R.S#WLDFANYGCYCGR.G	1848.75	2	2.159	0.277	1452.4	1
			R.S#WLDFANYGCYCGR.G	1848.75	3	3.056	0.597	2343.0	1
			R.S#WLDFANYGCYCGR.G	1848.75	3	2.799	0.650	2281.9	1

[#] indicates predicted phosphorylation; * indicates predicted oxidation

Supplemental Table 1−continued

Circle no.	Matched peptides	% coverage	Orthologous protein (s)/peptides	MH+	charge	X_{corr}	Score ΔC_n	Sp	RSp
	1	11.8	Chain A, crystal structure of A C49 phospholipase A2 of Indian Cobra				30.3		
			R.LAAICFAGAPYNNDNYNINLK.A	2357.15	2	5.089	0.008	1442.6	1
			R.LAAICFAGAPYNNDNYNINLK.A	2357.15	3	5.565	0.778	1911.3	1
			R.LAAICFAGAPYNNDNYNINLK.A	2357.15	3	5.925	0.758	2571.2	1
21	2	29.4	PA21_NAJOX phospholipase A2 isozyme E (phosphatidylcholine)				34.6		
			R.LAAICFAGAPYNNDNYNINLK.A	2356.17	2	5.104	0.050	1455.5	3
			R.S#WLDFANYGCYCGR.G	1848.75	2	2.159	0.232	1204.1	1
			R.S#WLDFANYGCYCGR.G	1848.75	3	3.143	0.625	2035.0	1
			R.LAAICFAGAPYNNDNYNINLK.A	2356.17	2	4.279	0.693	1122.1	2
	1	17.8	Chain A, crystal structure of A C49 phospholipase A2 of Indian Cobra				34.3		
			R.LAAICFAGAPYNDNNYNIDLK.A	2357.15	2	5.742	0.797	1226.4	1
			R.LAAICFAGAPYNDNNYNIDLK.A	2357.15	2	5.045	0.764	1578.1	2
			R.LAAICFAGAPYNDNNYNIDLK.A	2357.15	3	5.523	0.769	2612.3	1
			R.LAAICFAGAPYNDNNYNIDLK.A	2357.15	2	4.297	0.061	1187.3	1
	2	19.3	PA2_NAJNA phospholipase A2, acidic (phosphatidylcholine)				30.3		
			K.ISGCWPYFK.T	1157.58	2	3.474	0.706	771.6	1

[#] indicates predicted phosphorylation

Supplemental Table 1−continued

Circle no.	Matched Peptides	% coverage	Orthologous protein (s)/peptides	MH+	charge	X_{corr}	Score ΔC_n	Sp	RSp
			R.SWWDFADYGCYCGR.G	1842.76	2	5.202	0.798	2228.6	1
			R.SWWDFADYGCYCGR.G	1842.76	2	5.075	0.236	2325.5	2
22	1	20	Cytotoxin 1 of monocled cobra				22.2		
			K.M*FMM*SDLTIPVK.R	1444.69	2	2.907	0.183	522.8	1
			K.M*FM*MSDLTIPVK.R	1444.69	2	2.537	0.474	362.4	3
			K.MFM*M*SDLTIPVK.R	1444.69	2	3.117	0.067	504.3	2
23	-	-	No matched protein						
24	3	54.9	NXL1_NAJKA long neurotoxin 1 (neurotoxin 3 or a-Cobra toxin)				80.3		
			K.TGVDIQCCSTDNCNPFPTR.K	2242.02	2	5.808	0.212	2149.9	1
			K.TGVDIQCCSTDNCNPFPTR.K	2242.02	2	5.251	0.158	2286.5	1
			R.CFITPDITSK.D	1181.62	2	2.511	0.75	715.7	1
			R.CFITPDITSK.D	1181.62	1	2.482	0.487	248.0	1
			K.TWCDAFCSIR.G	1315.62	2	3.068	0.486	1130.1	1
			R.CFITPDITSK.D	1181.62	2	2.684	0.659	664.6	1
			R.CFITPDITSK.D	1181.62	2	3.017	0.688	961.5	1
			K.TWCDAFCSIR.G	1315.62	2	3.169	0.555	1124.4	1

* indicates predicted oxidation

Supplemental Table 1−continued

Circle no.	Matched Peptides	% coverage	Orthologous protein (s)/peptides	MH+	charge	X_{corr}	Score ΔC_n	Sp	RSp
24	1	28.2	NXL2_NAJNA long neurotoxin 2 (toxin B)				56.4		
			R.TGVDIQCCSTDDCDPFPTRK.R	2372.09	3	4.688	0.795	947.7	1
			R.TGVDIQCCSTDDCDPFPTRK.R	2372.09	3	4.281	0.706	888.3	1
			R.TGVDIQCCSTDDCDPFPTR.K	2243.99	2	4.574	0.774	2149.9	1
			R.TGVDIQCCSTDDCDPFPTR.K	2243.99	2	4.423	0.808	2286.5	1
			R.TGVDIQCCSTDDCDPFPTR.K	2243.99	3	5.595	0.717	3258.5	1
			R.TGVDIQCCSTDDCDPFPTR.K	2243.99	3	5.292	0.728	3282.0	1