

APPENDIX P

Supplemental Table 4 Orthologous proteins of peptide sequences generated from ion-exchange chromatography-purified *N. kaouthia* venom protein components (P3) by 2D-LC/MS-MS and database search

Reference					P(pro)	Score	Coverage	MW	Accession	Peptide(Hits)	
Scan(s), File (salt concentration)	Peptides	MH+	ΔM	z	P(pep)	X_{corr}	ΔCn	Sp	RSp	Ions	Count
1. CO3_NAJKA Cobra venom factor precursor (CVF) (Complement C3 homolog)					0	228.26	16.38	184516.00	54035743.0	34 (29 2 3 0 0)	
2946, P3_20mM	K.YIQEGDACK.A	1084.18	-0.917	2	1	2.45	0.09	726.86	15.0	13/16	4
3399, P3_60mM	K.FYHPDK.E	806.89	-0.574	2	0	2.09	0.11	684.79	11.0	39335	10
3759 - 3762, P3_20mM	K.NEQVEIR.A	887.96	-0.588	2	0	2.45	0.01	816.51	9.0	39398	36
3810 - 3813, P3_20mM	R.VPDTEIETK.I	1032.13	-0.693	2	0	3.05	0.24	689.45	1.0	14/16	
4029 - 4032, P3_60mM	K.IKLEGDPGAR.V	1056.20	-0.687	2	0	2.91	0.09	602.16	45.0	14/18	6
4149, P3_20mM	K.DLTEEPNSQGISSK.T	1505.57	-0.934	2	0	3.98	0.24	1245.93	1.0	21/26	
4311, P3_20mM	K.LNQDITVTASGDGK.A	1419.52	-0.886	2	0	4.94	0.39	1555.90	1.0	20/26	
4317, P3_20mM	K.LNQDITVTASGDGK.A	1419.52	-0.844	2	0	4.91	0.38	1570.14	1.0	20/26	
4635 - 4638, P3_20mM	R.VGLVAVDK.A	800.97	-0.511	2	0	2.79	0.12	1180.86	1.0	13/14	29
4695, P3_20mM	K.AVYVLNDK.Y	922.06	-0.630	2	0	2.79	0.05	564.04	9.0	39430	6
5205 - 5208, P3_60mM	R.QNQYVVVQVTGPQVR.L	1715.93	-1.083	2	0	5.18	0.39	2068.48	1.0	22/28	
5253 - 5256, P3_20mM	K.GVGGTQLEVIK.A	1101.28	-0.763	2	0	3.25	0.15	824.59	1.0	16/20	
5367, P3_60mM	R.AILHNYVNEDIYVR.V	1719.92	-1.165	2	0	5.18	0.36	2026.96	1.0	20/26	
5376, P3_60mM	R.AILHNYVNEDIYVR.V	1719.92	-1.091	2	0	5.13	0.36	2304.47	1.0	22/26	
5415 - 5418, P3_80mM	K.HFEVGFQPGSVK.V	1445.65	-1.033	2	0	3.69	0.33	1215.64	1.0	18/24	4
5445, P3_60mM	K.GIYTPGSPVLYR.V	1323.52	-0.929	2	0	2.63	0.34	575.07	1.0	15/22	
5448, P3_80mM	K.HFEVGFQPGSVK.V	1445.65	-1.055	2	0	3.25	0.10	1257.85	1.0	16/24	4
5454, P3_60mM	K.GIYTPGSPVLYR.V	1323.52	-0.925	2	0	2.45	0.29	767.54	1.0	17/22	
5526, P3_60mM	R.IDVPLQIEK.A	1055.25	-0.819	2	1	2.11	0.14	322.48	40.0	39371	
5700 - 5703, P3_20mM	R.IDVPLQIEK.A	1055.25	-0.795	2	0	2.55	0.18	516.42	2.0	13/16	
5727 - 5730, P3_20mM	R.INYENALLAR.T	1177.33	-0.783	2	0	3.62	0.11	1243.75	1.0	17/18	
5937, P3_20mM	R.DDNEDGFIADSDIISR.S	1782.80	-1.290	2	0	4.93	0.38	1563.59	1.0	23/30	
5943, P3_20mM	R.DDNEDGFIADSDIISR.S	1782.80	-1.206	2	0	5.22	0.40	1697.46	1.0	23/30	
5958 - 5961, P3_20mM	K.ASVQEALWSDGVR.K	1418.54	-0.923	2	0	4.18	0.30	1645.99	1.0	19/24	
5964 - 5967, P3_60mM	R.VELLYNPAFCSASTK.G	1700.94	-1.224	2	0	4.34	0.33	1526.77	1.0	22/28	
6252 - 6255, P3_20mM	K.VNDDYLIWGSR.S	1338.45	-0.919	2	0	4.13	0.31	1441.83	1.0	18/20	
6351 - 6354, P3_60mM	K.YFTYLILNK.G	1175.40	-0.929	2	0	2.64	0.18	652.59	9.0	13/16	1
6477, P3_80mM	K.DLNLDITIELPDR.E	1527.70	-1.271	2	0	4.05	0.21	1608.15	1.0	19/24	
6486, P3_80mM	K.DLNLDITIELPDR.E	1527.70	-1.225	2	0	3.97	0.20	1074.48	2.0	17/24	

Supplemental Table 4 Orthologous proteins of peptide sequences generated from ion-exchange chromatography-purified *N. kaouthia* venom protein components (P3) by 2D-LC/MS-MS and database search

Reference					P(pro)	Score	Coverage	MW	Accession	Peptide(Hits)	
Scan(s), File (salt concentration)	Peptides	MH+	ΔM	z	P(pep)	X_{corr}	ΔCn	Sp	RSp	Ions	Count
6510, P3_80mM	K.ATMTILTFYNAQLQEK.A	1873.16	-1.528	2	0	5.06	0.31	2363.94	1.0	22/30	
6519, P3_80mM	K.ATMTILTFYNAQLQEK.A	1873.16	-0.530	2	0	5.22	0.29	2103.86	1.0	22/30	
6591, P3_100mM	K.DLNLDITIELPDR.E	1527.70	-0.224	2	0	3.97	0.23	1084.17	7.0	17/24	
6711 - 6714, P3_60mM	K.DLNLDITIELPDR.E	1527.70	-1.288	2	0	3.66	0.18	1524.99	1.0	19/24	
6759, P3_60mM	K.SWLWLTK.D	934.12	-0.755	1	0	2.29	0.11	621.57	26.0	39337	
2. PSNJ2K phospholipase A2 (EC 3.1.1.4) II - monocled cobra					0	84.29		13454.95	67172.0	74 (59 10 4 0 1)	
3177 - 3180, P3_20mM	R.CCQVHDNCYDEAEK.I	1828.94	-1.850	2	0	5.17	0.02	1491.45	2.0	21/26	1
3198 - 3201, P3_20mM	R.CCQVHDNCYDEAEK.I	1828.94	-2.252	2	0	5.53	0.18	1275.37	1.0	20/26	1
3354, P3_60mM	R.CCQVHDNCYDEAEK.I	1828.94	-1.390	2	0	4.27	0.27	1051.18	1.0	19/26	1
3657 - 3660, P3_20mM	K.NGNNACAAAVCDCLR.L	1668.78	-0.283	2	0	4.20	0.45	1376.25	2.0	20/28	
3672, P3_80mM	K.NGNNACAAAVCDCLR.L	1668.78	0.498	2	0	2.99	0.49	529.63	2.0	13/28	
3681, P3_80mM	K.NGNNACAAAVCDCLR.L	1668.78	0.694	2	0	2.55	0.42	334.36	14.0	39414	
3711, P3_200mM	K.NGNNACAAAVCDCLR.L	1668.78	1.533	2	0	2.28	0.46	348.50	27.0	39414	
3714, P3_20mM	K.NGNNACAAAVCDCLR.L	1668.78	2.539	2	0	3.20	0.48	546.28	12.0	13/28	
3723, P3_20mM	K.NGNNACAAAVCDCLR.L	1668.78	0.820	2	0	2.96	0.48	476.39	9.0	39444	
3777 - 3780, P3_20mM	K.NM*IQCTVPCR.S	1249.45	-0.954	2	0	3.50	0.28	1019.71	1.0	16/18	6
3801, P3_20mM	K.NM*IQCTVPCR.S	1249.45	-0.931	2	0	3.17	0.10	929.31	2.0	15/18	6
3807, P3_20mM	K.NM*IQCTVPCR.S	1249.45	-0.930	2	0	3.26	0.11	1041.87	2.0	16/18	6
3843 - 3846, P3_20mM	R.GGSGTPVDDLDR.C	1189.21	-0.800	2	0	3.42	0.37	510.43	1.0	16/22	35
3876, P3_60mM	K.NGNNACAAAVCDCLR.L	1668.78	0.615	2	0	2.42	0.52	429.37	11.0	39444	
3882, P3_60mM	K.NGNNACAAAVCDCLR.L	1668.78	0.693	2	0	3.01	0.43	473.25	13.0	39444	
4147 - 4150, P3_0mM	K.NGNNACAAAVCDCLR.L	1668.78	0.679	2	0	3.16	0.45	644.36	2.0	14/28	
4168, P3_0mM	K.NGNNACAAAVCDCLR.L	1668.78	1.696	2	0	2.47	0.41	490.20	11.0	39444	
4182, P3_20mM	R.GGSGTPVDDLDR.C	1189.21	-0.826	2	0	2.69	0.45	473.48	9.0	16/22	35
4191, P3_20mM	R.GGSGTPVDDLDR.C	1189.21	-0.698	2	0	2.97	0.32	415.80	57.0	14/22	35
4248 - 4251, P3_80mM	K.TYSYEQSQTLTCK.G	1698.86	-1.343	2	0	4.48	0.41	2495.25	1.0	22/26	15
4293, P3_200mM	K.TYSYEQSQTLTCK.G	1698.86	-1.386	2	0	4.19	0.43	1583.23	1.0	20/26	15
4350, P3_20mM	K.NMIQCTVPCR.S	1233.45	-0.971	2	0	2.74	0.26	1191.50	1.0	16/18	6
4356, P3_20mM	K.NMIQCTVPCR.S	1233.45	-0.852	2	0	3.42	0.12	1071.29	2.0	15/18	6
4383, P3_100mM	K.TYSYEQSQTLTCK.G	1698.86	-1.342	2	0	4.84	0.41	2018.58	1.0	21/26	15

Supplemental Table 4 Orthologous proteins of peptide sequences generated from ion-exchange chromatography-purified *N. kaouthia* venom protein components (P3) by 2D-LC/MS-MS and database search

Reference					P(pro)	Score	Coverage	MW	Accession	Peptide(Hits)	
Scan(s), File (salt concentration)	Peptides	MH+	ΔM	z	P(pep)	X_{corr}	ΔCn	Sp	RSp	Ions	Count
4392, P3_20mM	K.TYSYECSQGTLTCK.G	1698.86	-0.353	3	0	3.57	0.34	463.39	11.0	24/52	15
4392 - 4395, P3_60mM	K.TYSYECSQGTLTCK.G	1698.86	-1.304	2	0	5.09	0.44	2766.74	1.0	23/26	15
4395, P3_100mM	K.TYSYECSQGTLTCK.G	1698.86	-1.381	2	0	3.79	0.45	610.50	1.0	18/26	15
4419, P3_20mM	K.TYSYECSQGTLTCK.G	1698.86	-1.103	2	0	4.45	0.37	2237.39	1.0	21/26	15
4428, P3_20mM	K.TYSYECSQGTLTCK.G	1698.86	-1.184	2	0	4.27	0.29	2165.64	1.0	21/26	15
4431 - 4434, P3_20mM	R.GGSGTPVDDLDR.C	1189.21	-0.654	1	0	2.42	0.27	249.67	4.0	39438	35
4443, P3_100mM	K.NMIQCTVPNR.S	1233.45	-0.970	2	0	2.30	0.03	626.36	19.0	39404	6
4449, P3_60mM	R.GGSGTPVDDLDR.C	1189.21	-0.826	2	0	2.33	0.39	414.34	2.0	15/22	35
4458, P3_60mM	R.GGSGTPVDDLDR.C	1189.21	-0.784	2	0	3.17	0.31	534.10	4.0	17/22	35
4458, P3_100mM	R.GGSGTPVDDLDR.C	1189.21	-0.823	2	1	2.31	0.05	319.08	180.0	14/22	35
4461 - 4464, P3_60mM	K.NMIQCTVPNR.S	1233.45	-0.933	2	0	3.53	0.27	1188.89	1.0	16/18	6
4467, P3_20mM	R.GGSGTPVDDLDR.C	1189.21	-0.672	1	0	2.61	0.17	275.53	15.0	39438	35
4473, P3_20mM	R.GGSGTPVDDLDR.C	1189.21	-0.654	1	0	2.28	0.12	285.17	38.0	39438	35
4476, P3_20mM	K.NMIQCTVPNR.S	1233.45	-0.846	1	0	2.06	0.20	138.07	3.0	39404	6
4482, P3_20mM	K.NMIQCTVPNR.S	1233.45	-0.826	1	0	2.26	0.21	169.69	1.0	13/18	6
4536 - 4539, P3_20mM	R.GGSGTPVDDLDR.C	1189.21	-0.782	2	0	3.43	0.28	595.75	1.0	18/22	35
4557, P3_20mM	K.TYSYECSQGTLTCK.G	1698.86	-1.143	2	0	4.96	0.41	2324.06	1.0	22/26	15
4572, P3_20mM	K.TYSYECSQGTLTCK.G	1698.86	-1.187	2	0	5.12	0.41	2052.21	1.0	21/26	15
4579 - 4582, P3_0mM	K.NGNNACAAVCDCLR.L	1668.78	-1.380	2	0	2.50	0.13	404.00	61.0	15/28	
4719 - 4722, P3_20mM	K.NMIQCTVPNR.S	1233.45	0.088	2	0	2.90	0.02	1037.50	2.0	16/18	6
4875, P3_20mM	R.GGSGTPVDDLDR.C	1189.21	-0.779	2	0	2.70	0.24	382.52	45.0	15/22	35
4899, P3_20mM	R.GGSGTPVDDLDR.C	1189.21	-0.783	2	1	2.94	0.36	553.82	1.0	17/22	35
5271 - 5274, P3_20mM	R.GGSGTPVDDLDR.C	1189.21	-0.825	2	0	2.31	0.16	427.57	9.0	15/22	35
5619 - 5622, P3_200mM	-.NLYQFKNMIQCTVPNR.S	2027.36	-0.806	3	0	3.58	0.17	1261.16	1.0	28/60	3
5637 - 5640, P3_20mM	R.GGSGTPVDDLDR.C	1189.21	-0.858	2	0	2.65	0.30	389.21	3.0	15/22	35
5673, P3_80mM	-.NLYQFKNMIQCTVPNR.S	2027.36	-0.769	3	0	4.08	0.12	1325.15	4.0	28/60	3
5682, P3_80mM	-.NLYQFKNMIQCTVPNR.S	2027.36	-1.737	3	0	4.18	0.25	1155.70	1.0	27/60	3
5784, P3_20mM	K.TYSYECSQGTLTCK.G	1698.86	-1.266	2	1	2.38	0.04	479.60	54.0	16/26	15
5832 - 5835, P3_60mM	R.CWPYFK.T	901.07	-0.726	1	0	1.64	0.06	260.46	5.0	39304	5
5994 - 5997, P3_20mM	R.GGSGTPVDDLDR.C	1189.21	-0.826	2	0	2.71	0.32	346.50	31.0	14/22	35

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Reference					P(pro)	Score	Coverage	MW	Accession	Peptide(Hits)	
Scan(s), File (salt concentration)	Peptides	MH+	ΔM	z	P(pep)	X_{corr}	ΔCn	Sp	RSp	Ions	Count
6015 - 6018, P3_400mM	R.LAAICFAGAPYNNNNYNIDLK.A	2357.63	-0.781	2	0	5.67	0.08	1606.35	1.0	28/40	5
6033, P3_400mM	R.LAAICFAGAPYNNNNYNIDLK.A	2357.63	-1.312	3	0	5.78	0.04	2615.71	1.0	39/80	5
6111, P3_20mM	K.NMIQCTVPNR.S	1233.45	-1.056	2	0	2.48	0.12	826.40	5.0	13/18	6
6219, P3_20mM	K.NMIQCTVPNR.S	1233.45	-1.055	2	0	2.84	0.14	976.37	2.0	14/18	6
6288, P3_20mM	K.NMIQCTVPNR.S	1233.45	-1.471	2	0	2.25	0.07	862.24	2.0	14/18	6
6390 - 6393, P3_20mM	R.GSGGTPVDDLDR.C	1189.21	-0.821	2	0	2.57	0.22	546.58	9.0	17/22	35
6735 - 6738, P3_20mM	R.GSGGTPVDDLDR.C	1189.21	-0.799	2	0	2.90	0.26	539.20	1.0	17/22	35
6762, P3_20mM	K.NMIQCTVPNR.S	1233.45	-1.015	2	0	2.93	0.21	1114.59	1.0	15/18	6
7107 - 7110, P3_20mM	R.GSGGTPVDDLDR.C	1189.21	-0.864	2	0	3.49	0.39	465.65	16.0	16/22	35
7320, P3_20mM	K.TYSYECSQGLTCK.G	1698.86	0.741	2	0	3.29	0.33	529.92	1.0	18/26	15
7347, P3_20mM	K.TYSYECSQGLTCK.G	1698.86	-1.341	2	0	3.32	0.34	355.04	2.0	15/26	15
7722, P3_20mM	K.NMIQCTVPNR.S	1233.45	1.870	2	0	2.49	0.05	766.72	25.0	13/18	6
7848 - 7851, P3_20mM	R.GSGGTPVDDLDR.C	1189.21	-0.899	2	0	3.14	0.32	448.97	8.0	16/22	35
8154, P3_20mM	K.NMIQCTVPNR.S	1233.45	-1.092	2	0	2.36	0.13	904.11	2.0	14/18	6
8262, P3_20mM	R.GSGGTPVDDLDR.C	1189.21	-0.862	2	0	2.85	0.26	398.73	6.0	14/22	35
8727 - 8730, P3_20mM	R.GSGGTPVDDLDR.C	1189.21	-0.864	2	0	2.79	0.24	308.66	30.0	14/22	35
9177 - 9183, P3_20mM	R.GSGGTPVDDLDR.C	1189.21	-0.887	2	0	2.44	0.34	386.63	56.0	15/22	35
9969 - 9972, P3_20mM	R.GSGGTPVDDLDR.C	1189.21	-0.905	2	0	2.07	0.26	265.95	67.0	13/22	35
10707 - 10710, P3_20mM	R.GSGGTPVDDLDR.C	1189.21	-0.883	2	0	2.70	0.23	312.03	127.0	14/22	35
12189, P3_20mM	R.GSGGTPVDDLDR.C	1189.21	-0.937	2	0	2.01	0.23	291.63	133.0	39438	35
3. PA21_NAJAT Phospholipase A2 1 precursor (Phosphatidylcholine 2-acylhydrolase)					0	84.29		16013.10	464331.0	53 (46 6 0 1 0)	
3177 - 3180, P3_20mM	R.CCQVHDNICYNEAEK.I	1827.96	-0.866	2	0	5.08	0.25	1705.37	1.0	22/26	9
3198 - 3201, P3_20mM	R.CCQVHDNICYNEAEK.I	1827.96	-1.268	2	0	4.52	0.33	1104.23	2.0	19/26	9
3354, P3_60mM	R.CCQVHDNICYNEAEK.I	1827.96	-0.405	2	0	4.35	0.02	936.07	2.0	18/26	9
3552 - 3555, P3_20mM	K.GGNNACAAAVCDCDR.L	1611.72	-1.130	2	0	4.54	0.04	1677.42	1.0	21/28	9
3648, P3_20mM	K.GGNNACAAAVCDCDR.L	1611.72	-0.127	2	0	3.33	0.44	1565.02	2.0	20/28	9
3654, P3_20mM	K.GGNNACAAAVCDCDR.L	1611.72	-0.171	2	0	3.42	0.41	1385.66	2.0	19/28	9
3843 - 3846, P3_20mM	R.GSGGTPVDDLDR.C	1189.21	-0.800	2	0	3.42	0.37	510.43	1.0	16/22	35
3849, P3_20mM	K.NM*IQCTVPSR.S	1222.42	-0.950	2	0	2.29	0.00	1188.38	1.0	16/18	12
3867, P3_20mM	K.NM*IQCTVPSR.S	1222.42	-0.904	2	0	2.91	0.00	1227.91	1.0	16/18	12

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4077, P3_20mM	K.GGNNACAAVDCDR.L	1611.72	-1.136	2	0	2.82	0.22	367.70	36.0	15/28	9
4182, P3_20mM	R.GGSGTPVDDLDR.C	1189.21	-0.826	2	0	2.69	0.45	473.48	9.0	16/22	35
4191, P3_20mM	R.GGSGTPVDDLDR.C	1189.21	-0.698	2	0	2.97	0.32	415.80	57.0	14/22	35
4248 - 4251, P3_80mM	K.TYSYEQSGTLTCK.G	1698.86	-1.343	2	0	4.48	0.41	2495.25	1.0	22/26	15
4293, P3_200mM	K.TYSYEQSGTLTCK.G	1698.86	-1.386	2	0	4.19	0.43	1583.23	1.0	20/26	15
4383, P3_100mM	K.TYSYEQSGTLTCK.G	1698.86	-1.342	2	0	4.84	0.41	2018.58	1.0	21/26	15
4392, P3_20mM	K.TYSYEQSGTLTCK.G	1698.86	-0.353	3	0	3.57	0.34	463.39	11.0	24/52	15
4392 - 4395, P3_60mM	K.TYSYEQSGTLTCK.G	1698.86	-1.304	2	0	5.09	0.44	2766.74	1.0	23/26	15
4395, P3_100mM	K.TYSYEQSGTLTCK.G	1698.86	-1.381	2	0	3.79	0.45	610.50	1.0	18/26	15
4419, P3_20mM	K.TYSYEQSGTLTCK.G	1698.86	-1.103	2	0	4.45	0.37	2237.39	1.0	21/26	15
4428, P3_20mM	K.TYSYEQSGTLTCK.G	1698.86	-1.184	2	0	4.27	0.29	2165.64	1.0	21/26	15
4431 - 4434, P3_20mM	R.GGSGTPVDDLDR.C	1189.21	-0.654	1	0	2.42	0.27	249.67	4.0	39438	35
4449, P3_60mM	R.GGSGTPVDDLDR.C	1189.21	-0.826	2	0	2.33	0.39	414.34	2.0	15/22	35
4458, P3_60mM	R.GGSGTPVDDLDR.C	1189.21	-0.784	2	0	3.17	0.31	534.10	4.0	17/22	35
4458, P3_100mM	R.GGSGTPVDDLDR.C	1189.21	-0.823	2	1	2.31	0.05	319.08	180.0	14/22	35
4467, P3_20mM	R.GGSGTPVDDLDR.C	1189.21	-0.672	1	0	2.61	0.17	275.53	15.0	39438	35
4473, P3_20mM	R.GGSGTPVDDLDR.C	1189.21	-0.654	1	0	2.28	0.12	285.17	38.0	39438	35
4524 - 4527, P3_20mM	K.NMIQCTVPSR.S	1206.42	-0.906	2	0	2.92	0.00	1290.81	1.0	17/18	12
4536 - 4539, P3_20mM	R.GGSGTPVDDLDR.C	1189.21	-0.782	2	0	3.43	0.28	595.75	1.0	18/22	35
4557, P3_20mM	K.TYSYEQSGTLTCK.G	1698.86	-1.143	2	0	4.96	0.41	2324.06	1.0	22/26	15
4572, P3_20mM	K.TYSYEQSGTLTCK.G	1698.86	-1.187	2	0	5.12	0.41	2052.21	1.0	21/26	15
4617 - 4620, P3_400mM	K.TYSYEQSGTLTCKGGN NACAAAVDCDR.L	3291.56	-0.977	3	0	4.34	0.49	1192.79	2.0	29/112	9
4875, P3_20mM	R.GGSGTPVDDLDR.C	1189.21	-0.779	2	0	2.70	0.24	382.52	45.0	15/22	35
4899, P3_20mM	R.GGSGTPVDDLDR.C	1189.21	-0.783	2	1	2.94	0.36	553.82	1.0	17/22	35
5271 - 5274, P3_20mM	R.GGSGTPVDDLDR.C	1189.21	-0.825	2	0	2.31	0.16	427.57	9.0	15/22	35
5637 - 5640, P3_20mM	R.GGSGTPVDDLDR.C	1189.21	-0.858	2	0	2.65	0.30	389.21	3.0	15/22	35
5784, P3_20mM	K.TYSYEQSGTLTCK.G	1698.86	-1.266	2	1	2.38	0.04	479.60	54.0	16/26	15
5994 - 5997, P3_20mM	R.GGSGTPVDDLDR.C	1189.21	-0.826	2	0	2.71	0.32	346.50	31.0	14/22	35
6015 - 6018, P3_400mM	R.LAAICFAGAPYN NNNYNIDLK.A	2357.63	-0.781	2	0	5.67	0.08	1606.35	1.0	28/40	5

Supplemental Table 4 Orthologous proteins of peptide sequences generated from ion-exchange chromatography-purified *N. kaouthia* venom protein components (P3) by 2D-LC/MS-MS and database search

Reference					P(pro)	Score	Coverage	MW	Accession	Peptide(Hits)	
Scan(s), File (salt concentration)	Peptides	MH+	ΔM	z	P(pep)	X_{corr}	ΔCn	Sp	RSp	Ions	Count
6033, P3_400mM	R.LAAICFAGAPYN NNNYNIDLK.A	2357.63	-1.312	3	0	5.78	0.04	2615.71	1.0	39/80	5
6039 - 6042, P3_60mM	K.ISGCWPYFK.T	1158.35	-0.838	2	0	3.47	0.27	907.36	1.0	14/16	8
6075, P3_60mM	K.ISGCWPYFK.T	1158.35	-0.842	2	0	2.99	0.11	939.65	1.0	14/16	8
6390 - 6393, P3_20mM	R.GGSGTPVDDLDR.C	1189.21	-0.821	2	0	2.57	0.22	546.58	9.0	17/22	35
6735 - 6738, P3_20mM	R.GGSGTPVDDLDR.C	1189.21	-0.799	2	0	2.90	0.26	539.20	1.0	17/22	35
7107 - 7110, P3_20mM	R.GGSGTPVDDLDR.C	1189.21	-0.864	2	0	3.49	0.39	465.65	16.0	16/22	35
7320, P3_20mM	K.TYSYECSQGLTCK.G	1698.86	0.741	2	0	3.29	0.33	529.92	1.0	18/26	15
7347, P3_20mM	K.TYSYECSQGLTCK.G	1698.86	-1.341	2	0	3.32	0.34	355.04	2.0	15/26	15
7848 - 7851, P3_20mM	R.GGSGTPVDDLDR.C	1189.21	-0.899	2	0	3.14	0.32	448.97	8.0	16/22	35
8262, P3_20mM	R.GGSGTPVDDLDR.C	1189.21	-0.862	2	0	2.85	0.26	398.73	6.0	14/22	35
8727 - 8730, P3_20mM	R.GGSGTPVDDLDR.C	1189.21	-0.864	2	0	2.79	0.24	308.66	30.0	14/22	35
9177 - 9183, P3_20mM	R.GGSGTPVDDLDR.C	1189.21	-0.887	2	0	2.44	0.34	386.63	56.0	15/22	35
9969 - 9972, P3_20mM	R.GGSGTPVDDLDR.C	1189.21	-0.905	2	0	2.07	0.26	265.95	67.0	13/22	35
10707 - 10710, P3_20mM	R.GGSGTPVDDLDR.C	1189.21	-0.883	2	0	2.70	0.23	312.03	127.0	14/22	35
12189, P3_20mM	R.GGSGTPVDDLDR.C	1189.21	-0.937	2	0	2.01	0.23	291.63	133.0	39438	35
4. Phospholipase A2 (E.C.3.1.1.4)					0	78.28	80.51	13143.61	443186.0	53 (45 5 0 3 0)	
3177 - 3180, P3_20mM	R.CCQVHDNCYNEAEK.I	1827.96	-0.866	2	0	5.08	0.25	1705.37	1.0	22/26	9
3198 - 3201, P3_20mM	R.CCQVHDNCYNEAEK.I	1827.96	-1.268	2	0	4.52	0.33	1104.23	2.0	19/26	9
3354, P3_60mM	R.CCQVHDNCYNEAEK.I	1827.96	-0.405	2	0	4.35	0.02	936.07	2.0	18/26	9
3552 - 3555, P3_20mM	K.GGNNACAAAVCDCDR.L	1611.72	-1.130	2	0	4.54	0.04	1677.42	1.0	21/28	9
3648, P3_20mM	K.GGNNACAAAVCDCDR.L	1611.72	-0.127	2	0	3.33	0.44	1565.02	2.0	20/28	9
3654, P3_20mM	K.GGNNACAAAVCDCDR.L	1611.72	-0.171	2	0	3.42	0.41	1385.66	2.0	19/28	9
3843 - 3846, P3_20mM	R.GGSGTPVDDLDR.C	1189.21	-0.800	2	0	3.42	0.37	510.43	1.0	16/22	35
3849, P3_20mM	K.NM*IQCTVPSR.S	1222.42	-0.950	2	0	2.29	0.00	1188.38	1.0	16/18	12
3867, P3_20mM	K.NM*IQCTVPSR.S	1222.42	-0.904	2	0	2.91	0.00	1227.91	1.0	16/18	12
4077, P3_20mM	K.GGNNACAAAVCDCDR.L	1611.72	-1.136	2	0	2.82	0.22	367.70	36.0	15/28	9
4182, P3_20mM	R.GGSGTPVDDLDR.C	1189.21	-0.826	2	0	2.69	0.45	473.48	9.0	16/22	35
4191, P3_20mM	R.GGSGTPVDDLDR.C	1189.21	-0.698	2	0	2.97	0.32	415.80	57.0	14/22	35
4248 - 4251, P3_80mM	K.TYSYECSQGLTCK.G	1698.86	-1.343	2	0	4.48	0.41	2495.25	1.0	22/26	15

Supplemental Table 4 Orthologous proteins of peptide sequences generated from ion-exchange chromatography-purified *N. kaouthia* venom protein components (P3) by 2D-LC/MS-MS and database search

Reference					P(pro)	Score	Coverage	MW	Accession	Peptide(Hits)	
Scan(s), File (salt concentration)	Peptides	MH+	ΔM	z	P(pep)	X_{corr}	ΔCn	Sp	RSp	Ions	Count
4293, P3_200mM	K.TYSYECSQGTLTCK.G	1698.86	-1.386	2	0	4.19	0.43	1583.23	1.0	20/26	15
4383, P3_100mM	K.TYSYECSQGTLTCK.G	1698.86	-1.342	2	0	4.84	0.41	2018.58	1.0	21/26	15
4392, P3_20mM	K.TYSYECSQGTLTCK.G	1698.86	-0.353	3	0	3.57	0.34	463.39	11.0	24/52	15
4392 - 4395, P3_60mM	K.TYSYECSQGTLTCK.G	1698.86	-1.304	2	0	5.09	0.44	2766.74	1.0	23/26	15
4395, P3_100mM	K.TYSYECSQGTLTCK.G	1698.86	-1.381	2	0	3.79	0.45	610.50	1.0	18/26	15
4419, P3_20mM	K.TYSYECSQGTLTCK.G	1698.86	-1.103	2	0	4.45	0.37	2237.39	1.0	21/26	15
4428, P3_20mM	K.TYSYECSQGTLTCK.G	1698.86	-1.184	2	0	4.27	0.29	2165.64	1.0	21/26	15
4431 - 4434, P3_20mM	R.GGSGTPVDDLDR.C	1189.21	-0.654	1	0	2.42	0.27	249.67	4.0	39438	35
4449, P3_60mM	R.GGSGTPVDDLDR.C	1189.21	-0.826	2	0	2.33	0.39	414.34	2.0	15/22	35
4458, P3_60mM	R.GGSGTPVDDLDR.C	1189.21	-0.784	2	0	3.17	0.31	534.10	4.0	17/22	35
4458, P3_100mM	R.GGSGTPVDDLDR.C	1189.21	-0.823	2	1	2.31	0.05	319.08	180.0	14/22	35
4467, P3_20mM	R.GGSGTPVDDLDR.C	1189.21	-0.672	1	0	2.61	0.17	275.53	15.0	39438	35
4473, P3_20mM	R.GGSGTPVDDLDR.C	1189.21	-0.654	1	0	2.28	0.12	285.17	38.0	39438	35
4524 - 4527, P3_20mM	K.NMIQCTVPSR.S	1206.42	-0.906	2	0	2.92	0.00	1290.81	1.0	17/18	12
4536 - 4539, P3_20mM	R.GGSGTPVDDLDR.C	1189.21	-0.782	2	0	3.43	0.28	595.75	1.0	18/22	35
4557, P3_20mM	K.TYSYECSQGTLTCK.G	1698.86	-1.143	2	0	4.96	0.41	2324.06	1.0	22/26	15
4572, P3_20mM	K.TYSYECSQGTLTCK.G	1698.86	-1.187	2	0	5.12	0.41	2052.21	1.0	21/26	15
4617 - 4620, P3_400mM	K.TYSYECSQGTLTCKGGN NACAAAVCDCDR.L	3291.56	-0.977	3	0	4.34	0.49	1192.79	2.0	29/112	9
4875, P3_20mM	R.GGSGTPVDDLDR.C	1189.21	-0.779	2	0	2.70	0.24	382.52	45.0	15/22	35
4899, P3_20mM	R.GGSGTPVDDLDR.C	1189.21	-0.783	2	1	2.94	0.36	553.82	1.0	17/22	35
5271 - 5274, P3_20mM	R.GGSGTPVDDLDR.C	1189.21	-0.825	2	0	2.31	0.16	427.57	9.0	15/22	35
5637 - 5640, P3_20mM	R.GGSGTPVDDLDR.C	1189.21	-0.858	2	0	2.65	0.30	389.21	3.0	15/22	35
5784, P3_20mM	K.TYSYECSQGTLTCK.G	1698.86	-1.266	2	1	2.38	0.04	479.60	54.0	16/26	15
5994 - 5997, P3_20mM	R.GGSGTPVDDLDR.C	1189.21	-0.826	2	0	2.71	0.32	346.50	31.0	14/22	35
6015 - 6018, P3_400mM	R.LAAICFAGAPYNDNDYNINLK.A	2358.61	-1.766	2	0	5.54	0.18	1489.38	2.0	27/40	
6033, P3_400mM	R.LAAICFAGAPYNDNDYNINLK.A	2358.61	-2.297	3	0	5.10	0.36	1645.12	4.0	34/80	
6039 - 6042, P3_60mM	K.ISGCWPYFK.T	1158.35	-0.838	2	0	3.47	0.27	907.36	1.0	14/16	8
6075, P3_60mM	K.ISGCWPYFK.T	1158.35	-0.842	2	0	2.99	0.11	939.65	1.0	14/16	8
6390 - 6393, P3_20mM	R.GGSGTPVDDLDR.C	1189.21	-0.821	2	0	2.57	0.22	546.58	9.0	17/22	35
6735 - 6738, P3_20mM	R.GGSGTPVDDLDR.C	1189.21	-0.799	2	0	2.90	0.26	539.20	1.0	17/22	35

Supplemental Table 4 Orthologous proteins of peptide sequences generated from ion-exchange chromatography-purified *N. kaouthia* venom protein components (P3) by 2D-LC/MS-MS and database search

Reference					P(pro)	Score	Coverage	MW	Accession	Peptide(Hits)	
Scan(s), File (salt concentration)	Peptides	MH+	ΔM	z	P(pep)	X_{corr}	ΔCn	Sp	RSp	Ions	Count
7107 - 7110, P3_20mM	R.GGSGTPVDDLDR.C	1189.21	-0.864	2	0	3.49	0.39	465.65	16.0	16/22	35
7320, P3_20mM	K.TYSYEC SQGLTCK.G	1698.86	0.741	2	0	3.29	0.33	529.92	1.0	18/26	15
7347, P3_20mM	K.TYSYEC SQGLTCK.G	1698.86	-1.341	2	0	3.32	0.34	355.04	2.0	15/26	15
7848 - 7851, P3_20mM	R.GGSGTPVDDLDR.C	1189.21	-0.899	2	0	3.14	0.32	448.97	8.0	16/22	35
8262, P3_20mM	R.GGSGTPVDDLDR.C	1189.21	-0.862	2	0	2.85	0.26	398.73	6.0	14/22	35
8727 - 8730, P3_20mM	R.GGSGTPVDDLDR.C	1189.21	-0.864	2	0	2.79	0.24	308.66	30.0	14/22	35
9177 - 9183, P3_20mM	R.GGSGTPVDDLDR.C	1189.21	-0.887	2	0	2.44	0.34	386.63	56.0	15/22	35
9969 - 9972, P3_20mM	R.GGSGTPVDDLDR.C	1189.21	-0.905	2	0	2.07	0.26	265.95	67.0	13/22	35
10707 - 10710, P3_20mM	R.GGSGTPVDDLDR.C	1189.21	-0.883	2	0	2.70	0.23	312.03	127.0	14/22	35
12189, P3_20mM	R.GGSGTPVDDLDR.C	1189.21	-0.937	2	0	2.01	0.23	291.63	133.0	39438	35
5. PA22_NAJAT Phospholipase A2 2 precursor					0	76.29	58.90	15949.01	24638099	49 (44 4 0 1)	
(Phosphatidylcholine 2-acylhydrolase)											
3204, P3_20mM	R.CCQVHDHCYNEAEK.I	1850.99	-2.399	2	0	4.16	0.32	548.55	2.0	17/26	
3552 - 3555, P3_20mM	K.GGNNACAAVDCDCR.L	1611.72	-1.130	2	0	4.54	0.04	1677.42	1.0	21/28	9
3648, P3_20mM	K.GGNNACAAVDCDCR.L	1611.72	-0.127	2	0	3.33	0.44	1565.02	2.0	20/28	9
3654, P3_20mM	K.GGNNACAAVDCDCR.L	1611.72	-0.171	2	0	3.42	0.41	1385.66	2.0	19/28	9
3843 - 3846, P3_20mM	R.GGSGTPVDDLDR.C	1189.21	-0.800	2	0	3.42	0.37	510.43	1.0	16/22	35
3849, P3_20mM	K.NM*IQCTVPSR.S	1222.42	-0.950	2	0	2.29	0.00	1188.38	1.0	16/18	12
3867, P3_20mM	K.NM*IQCTVPSR.S	1222.42	-0.904	2	0	2.91	0.00	1227.91	1.0	16/18	12
4077, P3_20mM	K.GGNNACAAVDCDCR.L	1611.72	-1.136	2	0	2.82	0.22	367.70	36.0	15/28	9
4182, P3_20mM	R.GGSGTPVDDLDR.C	1189.21	-0.826	2	0	2.69	0.45	473.48	9.0	16/22	35
4191, P3_20mM	R.GGSGTPVDDLDR.C	1189.21	-0.698	2	0	2.97	0.32	415.80	57.0	14/22	35
4248 - 4251, P3_80mM	K.TYSYEC SQGLTCK.G	1698.86	-1.343	2	0	4.48	0.41	2495.25	1.0	22/26	15
4293, P3_200mM	K.TYSYEC SQGLTCK.G	1698.86	-1.386	2	0	4.19	0.43	1583.23	1.0	20/26	15
4383, P3_100mM	K.TYSYEC SQGLTCK.G	1698.86	-1.342	2	0	4.84	0.41	2018.58	1.0	21/26	15
4392, P3_20mM	K.TYSYEC SQGLTCK.G	1698.86	-0.353	3	0	3.57	0.34	463.39	11.0	24/52	15
4392 - 4395, P3_60mM	K.TYSYEC SQGLTCK.G	1698.86	-1.304	2	0	5.09	0.44	2766.74	1.0	23/26	15
4395, P3_100mM	K.TYSYEC SQGLTCK.G	1698.86	-1.381	2	0	3.79	0.45	610.50	1.0	18/26	15
4419, P3_20mM	K.TYSYEC SQGLTCK.G	1698.86	-1.103	2	0	4.45	0.37	2237.39	1.0	21/26	15
4428, P3_20mM	K.TYSYEC SQGLTCK.G	1698.86	-1.184	2	0	4.27	0.29	2165.64	1.0	21/26	15

Supplemental Table 4 Orthologous proteins of peptide sequences generated from ion-exchange chromatography-purified *N. kaouthia* venom protein components (P3) by 2D-LC/MS-MS and database search

Reference					P(pro)	Score	Coverage	MW	Accession	Peptide(Hits)	
Scan(s), File (salt concentration)	Peptides	MH+	ΔM	z	P(pep)	X_{corr}	ΔCn	Sp	RSp	Ions	Count
4431 - 4434, P3_20mM	R.GGSGTPVDDLDR.C	1189.21	-0.654	1	0	2.42	0.27	249.67	4.0	39438	35
4449, P3_60mM	R.GGSGTPVDDLDR.C	1189.21	-0.826	2	0	2.33	0.39	414.34	2.0	15/22	35
4458, P3_60mM	R.GGSGTPVDDLDR.C	1189.21	-0.784	2	0	3.17	0.31	534.10	4.0	17/22	35
4458, P3_100mM	R.GGSGTPVDDLDR.C	1189.21	-0.823	2	1	2.31	0.05	319.08	180.0	14/22	35
4467, P3_20mM	R.GGSGTPVDDLDR.C	1189.21	-0.672	1	0	2.61	0.17	275.53	15.0	39438	35
4473, P3_20mM	R.GGSGTPVDDLDR.C	1189.21	-0.654	1	0	2.28	0.12	285.17	38.0	39438	35
4524 - 4527, P3_20mM	K.NMIQCTVPSR.S	1206.42	-0.906	2	0	2.92	0.00	1290.81	1.0	17/18	12
4536 - 4539, P3_20mM	R.GGSGTPVDDLDR.C	1189.21	-0.782	2	0	3.43	0.28	595.75	1.0	18/22	35
4557, P3_20mM	K.TYSYECSQGLTCK.G	1698.86	-1.143	2	0	4.96	0.41	2324.06	1.0	22/26	15
4572, P3_20mM	K.TYSYECSQGLTCK.G	1698.86	-1.187	2	0	5.12	0.41	2052.21	1.0	21/26	15
4617 - 4620, P3_400mM	K.TYSYECSQGLTCKGGN NACAAAVCDCDR.L	3291.56	-0.977	3	0	4.34	0.49	1192.79	2.0	29/112	9
4875, P3_20mM	R.GGSGTPVDDLDR.C	1189.21	-0.779	2	0	2.70	0.24	382.52	45.0	15/22	35
4899, P3_20mM	R.GGSGTPVDDLDR.C	1189.21	-0.783	2	1	2.94	0.36	553.82	1.0	17/22	35
5271 - 5274, P3_20mM	R.GGSGTPVDDLDR.C	1189.21	-0.825	2	0	2.31	0.16	427.57	9.0	15/22	35
5637 - 5640, P3_20mM	R.GGSGTPVDDLDR.C	1189.21	-0.858	2	0	2.65	0.30	389.21	3.0	15/22	35
5784, P3_20mM	K.TYSYECSQGLTCK.G	1698.86	-1.266	2	1	2.38	0.04	479.60	54.0	16/26	15
5994 - 5997, P3_20mM	R.GGSGTPVDDLDR.C	1189.21	-0.826	2	0	2.71	0.32	346.50	31.0	14/22	35
6015 - 6018, P3_400mM	R.LAAICFAGAPYNNNNYNIDLK.A	2357.63	-0.781	2	0	5.67	0.08	1606.35	1.0	28/40	5
6033, P3_400mM	R.LAAICFAGAPYNNNNYNIDLK.A	2357.63	-1.312	3	0	5.78	0.04	2615.71	1.0	39/80	5
6390 - 6393, P3_20mM	R.GGSGTPVDDLDR.C	1189.21	-0.821	2	0	2.57	0.22	546.58	9.0	17/22	35
6735 - 6738, P3_20mM	R.GGSGTPVDDLDR.C	1189.21	-0.799	2	0	2.90	0.26	539.20	1.0	17/22	35
7107 - 7110, P3_20mM	R.GGSGTPVDDLDR.C	1189.21	-0.864	2	0	3.49	0.39	465.65	16.0	16/22	35
7320, P3_20mM	K.TYSYECSQGLTCK.G	1698.86	0.741	2	0	3.29	0.33	529.92	1.0	18/26	15
7347, P3_20mM	K.TYSYECSQGLTCK.G	1698.86	-1.341	2	0	3.32	0.34	355.04	2.0	15/26	15
7848 - 7851, P3_20mM	R.GGSGTPVDDLDR.C	1189.21	-0.899	2	0	3.14	0.32	448.97	8.0	16/22	35
8262, P3_20mM	R.GGSGTPVDDLDR.C	1189.21	-0.862	2	0	2.85	0.26	398.73	6.0	14/22	35
8727 - 8730, P3_20mM	R.GGSGTPVDDLDR.C	1189.21	-0.864	2	0	2.79	0.24	308.66	30.0	14/22	35
9177 - 9183, P3_20mM	R.GGSGTPVDDLDR.C	1189.21	-0.887	2	0	2.44	0.34	386.63	56.0	15/22	35
9969 - 9972, P3_20mM	R.GGSGTPVDDLDR.C	1189.21	-0.905	2	0	2.07	0.26	265.95	67.0	13/22	35
10707 - 10710, P3_20mM	R.GGSGTPVDDLDR.C	1189.21	-0.883	2	0	2.70	0.23	312.03	127.0	14/22	35

Supplemental Table 4 Orthologous proteins of peptide sequences generated from ion-exchange chromatography-purified *N. kaouthia* venom protein components (P3) by 2D-LC/MS-MS and database search

Reference					P(pro)	Score	Coverage	MW	Accession	Peptide(Hits)	
Scan(s), File (salt concentration)	Peptides	MH+	ΔM	z	P(pep)	X_{corr}	ΔCn	Sp	RSp	Ions	Count
12189, P3_20mM	R.GGSGTPVDDLDR.C	1189.21	-0.937	2	0	2.01	0.23	291.63	133.0	39438	35
6. PSNJ3K phospholipase A2 (EC 3.1.1.4) III - monocled cobra					0	76.29		13270.76	2144440.0	28 (22 5 0 1 0)	
3177 - 3180, P3_20mM	R.CCQVHDNICYDEAEK.I	1828.94	-1.850	2	0	5.17	0.02	1491.45	2.0	21/26	1
3198 - 3201, P3_20mM	R.CCQVHDNICYDEAEK.I	1828.94	-2.252	2	0	5.53	0.18	1275.37	1.0	20/26	1
3354, P3_60mM	R.CCQVHDNICYDEAEK.I	1828.94	-1.390	2	0	4.27	0.27	1051.18	1.0	19/26	1
3552 - 3555, P3_20mM	K.GGNNACAAAVCDCDR.L	1611.72	-1.130	2	0	4.54	0.04	1677.42	1.0	21/28	9
3648, P3_20mM	K.GGNNACAAAVCDCDR.L	1611.72	-0.127	2	0	3.33	0.44	1565.02	2.0	20/28	9
3654, P3_20mM	K.GGNNACAAAVCDCDR.L	1611.72	-0.171	2	0	3.42	0.41	1385.66	2.0	19/28	9
3849, P3_20mM	K.NM*IQCTVPSR.S	1222.42	-0.950	2	0	2.29	0.00	1188.38	1.0	16/18	12
3867, P3_20mM	K.NM*IQCTVPSR.S	1222.42	-0.904	2	0	2.91	0.00	1227.91	1.0	16/18	12
4077, P3_20mM	K.GGNNACAAAVCDCDR.L	1611.72	-1.136	2	0	2.82	0.22	367.70	36.0	15/28	9
4248 - 4251, P3_80mM	K.TYSYEC SQGLTCK.G	1698.86	-1.343	2	0	4.48	0.41	2495.25	1.0	22/26	15
4293, P3_200mM	K.TYSYEC SQGLTCK.G	1698.86	-1.386	2	0	4.19	0.43	1583.23	1.0	20/26	15
4383, P3_100mM	K.TYSYEC SQGLTCK.G	1698.86	-1.342	2	0	4.84	0.41	2018.58	1.0	21/26	15
4392, P3_20mM	K.TYSYEC SQGLTCK.G	1698.86	-0.353	3	0	3.57	0.34	463.39	11.0	24/52	15
4392 - 4395, P3_60mM	K.TYSYEC SQGLTCK.G	1698.86	-1.304	2	0	5.09	0.44	2766.74	1.0	23/26	15
4395, P3_100mM	K.TYSYEC SQGLTCK.G	1698.86	-1.381	2	0	3.79	0.45	610.50	1.0	18/26	15
4419, P3_20mM	K.TYSYEC SQGLTCK.G	1698.86	-1.103	2	0	4.45	0.37	2237.39	1.0	21/26	15
4428, P3_20mM	K.TYSYEC SQGLTCK.G	1698.86	-1.184	2	0	4.27	0.29	2165.64	1.0	21/26	15
4524 - 4527, P3_20mM	K.NMIQCTVPSR.S	1206.42	-0.906	2	0	2.92	0.00	1290.81	1.0	17/18	12
4557, P3_20mM	K.TYSYEC SQGLTCK.G	1698.86	-1.143	2	0	4.96	0.41	2324.06	1.0	22/26	15
4572, P3_20mM	K.TYSYEC SQGLTCK.G	1698.86	-1.187	2	0	5.12	0.41	2052.21	1.0	21/26	15
4617 - 4620, P3_400mM	K.TYSYEC SQGLTCKGGN NACAAAVCDCDR.L	3291.56	-0.977	3	0	4.34	0.49	1192.79	2.0	29/112	9
5784, P3_20mM	K.TYSYEC SQGLTCK.G	1698.86	-1.266	2	1	2.38	0.04	479.60	54.0	16/26	15
6015 - 6018, P3_400mM	R.LAAICFAGAPYNNNNYNIDLK.A	2357.63	-0.781	2	0	5.67	0.08	1606.35	1.0	28/40	5
6033, P3_400mM	R.LAAICFAGAPYNNNNYNIDLK.A	2357.63	-1.312	3	0	5.78	0.04	2615.71	1.0	39/80	5
6039 - 6042, P3_60mM	K.ISGCWPYFK.T	1158.35	-0.838	2	0	3.47	0.27	907.36	1.0	14/16	8
6075, P3_60mM	K.ISGCWPYFK.T	1158.35	-0.842	2	0	2.99	0.11	939.65	1.0	14/16	8
7320, P3_20mM	K.TYSYEC SQGLTCK.G	1698.86	0.741	2	0	3.29	0.33	529.92	1.0	18/26	15
7347, P3_20mM	K.TYSYEC SQGLTCK.G	1698.86	-1.341	2	0	3.32	0.34	355.04	2.0	15/26	15

Supplemental Table 4 Orthologous proteins of peptide sequences generated from ion-exchange chromatography-purified *N. kaouthia* venom protein components (P3) by 2D-LC/MS-MS and database search

Reference					P(pro)	Score	Coverage	MW	Accession	Peptide(Hits)	
Scan(s), File (salt concentration)	Peptides	MH+	ΔM	z	P(pep)	X_{corr}	ΔCn	Sp	RSp	Ions	Count
7. PA21_NAJKA Phospholipase A2 isozyme 1 precursor (Phosphatidylcholine 2-acylhydrolase) (NnkPLA-I) (CM-II)				0	74.29			16271.38	24638468.0	70 (65 4 1 0 0)	
3177 - 3180, P3_20mM	R.CCQVHDNICYNEAEK.I	1827.96	-0.866	2	0	5.08	0.25	1705.37	1.0	22/26	9
3198 - 3201, P3_20mM	R.CCQVHDNICYNEAEK.I	1827.96	-1.268	2	0	4.52	0.33	1104.23	2.0	19/26	9
3354, P3_60mM	R.CCQVHDNICYNEAEK.I	1827.96	-0.405	2	0	4.35	0.02	936.07	2.0	18/26	9
3657 - 3660, P3_20mM	K.GDNDACAAAVCDCDR.L	1670.74	-2.252	2	0	4.51	0.07	1551.50	1.0	21/28	
3672, P3_80mM	K.GDNDACAAAVCDCDR.L	1670.74	-1.472	2	0	4.69	0.36	1207.24	1.0	18/28	
3681, P3_80mM	K.GDNDACAAAVCDCDR.L	1670.74	-1.276	2	0	4.18	0.39	1169.13	1.0	20/28	
3711, P3_200mM	K.GDNDACAAAVCDCDR.L	1670.74	-0.437	2	0	3.90	0.42	1064.15	1.0	18/28	
3714, P3_20mM	K.GDNDACAAAVCDCDR.L	1670.74	0.570	2	0	5.28	0.39	1702.98	1.0	21/28	
3723, P3_20mM	K.GDNDACAAAVCDCDR.L	1670.74	-1.149	2	0	5.15	0.41	1816.97	1.0	22/28	
3777 - 3780, P3_20mM	K.NM*IQCTVTPNR.S	1249.45	-0.954	2	0	3.50	0.28	1019.71	1.0	16/18	6
3801, P3_20mM	K.NM*IQCTVTPNR.S	1249.45	-0.931	2	0	3.17	0.10	929.31	2.0	15/18	6
3807, P3_20mM	K.NM*IQCTVTPNR.S	1249.45	-0.930	2	0	3.26	0.11	1041.87	2.0	16/18	6
3843 - 3846, P3_20mM	R.GGSGTPVDDLDR.C	1189.21	-0.800	2	0	3.42	0.37	510.43	1.0	16/22	35
3876, P3_60mM	K.GDNDACAAAVCDCDR.L	1670.74	-1.355	2	0	4.73	0.47	1333.70	1.0	19/28	
3882, P3_60mM	K.GDNDACAAAVCDCDR.L	1670.74	-1.277	2	0	4.52	0.33	1584.98	1.0	21/28	
4147 - 4150, P3_0mM	K.GDNDACAAAVCDCDR.L	1670.74	-1.290	2	0	5.04	0.37	1589.18	1.0	21/28	
4168, P3_0mM	K.GDNDACAAAVCDCDR.L	1670.74	-0.274	2	0	4.03	0.38	1310.22	1.0	19/28	
4182, P3_20mM	R.GGSGTPVDDLDR.C	1189.21	-0.826	2	0	2.69	0.45	473.48	9.0	16/22	35
4191, P3_20mM	R.GGSGTPVDDLDR.C	1189.21	-0.698	2	0	2.97	0.32	415.80	57.0	14/22	35
4248 - 4251, P3_80mM	K.TYSYEC SQGLTCK.G	1698.86	-1.343	2	0	4.48	0.41	2495.25	1.0	22/26	15
4293, P3_200mM	K.TYSYEC SQGLTCK.G	1698.86	-1.386	2	0	4.19	0.43	1583.23	1.0	20/26	15
4350, P3_20mM	K.NMIQCTVTPNR.S	1233.45	-0.971	2	0	2.74	0.26	1191.50	1.0	16/18	6
4356, P3_20mM	K.NMIQCTVTPNR.S	1233.45	-0.852	2	0	3.42	0.12	1071.29	2.0	15/18	6
4383, P3_100mM	K.TYSYEC SQGLTCK.G	1698.86	-1.342	2	0	4.84	0.41	2018.58	1.0	21/26	15
4392, P3_20mM	K.TYSYEC SQGLTCK.G	1698.86	-0.353	3	0	3.57	0.34	463.39	11.0	24/52	15
4392 - 4395, P3_60mM	K.TYSYEC SQGLTCK.G	1698.86	-1.304	2	0	5.09	0.44	2766.74	1.0	23/26	15
4395, P3_100mM	K.TYSYEC SQGLTCK.G	1698.86	-1.381	2	0	3.79	0.45	610.50	1.0	18/26	15
4419, P3_20mM	K.TYSYEC SQGLTCK.G	1698.86	-1.103	2	0	4.45	0.37	2237.39	1.0	21/26	15
4428, P3_20mM	K.TYSYEC SQGLTCK.G	1698.86	-1.184	2	0	4.27	0.29	2165.64	1.0	21/26	15

Supplemental Table 4 Orthologous proteins of peptide sequences generated from ion-exchange chromatography-purified *N. kaouthia* venom protein components (P3) by 2D-LC/MS-MS and database search

Reference					P(pro)	Score	Coverage	MW	Accession	Peptide(Hits)	
Scan(s), File (salt concentration)	Peptides	MH+	ΔM	z	P(pep)	X_{corr}	ΔCn	Sp	RSp	Ions	Count
4431 - 4434, P3_20mM	R.GGSGTPVDDLDR.C	1189.21	-0.654	1	0	2.42	0.27	249.67	4.0	39438	35
4443, P3_100mM	K.NMIQCTVPNR.S	1233.45	-0.970	2	0	2.30	0.03	626.36	19.0	39404	6
4449, P3_60mM	R.GGSGTPVDDLDR.C	1189.21	-0.826	2	0	2.33	0.39	414.34	2.0	15/22	35
4458, P3_60mM	R.GGSGTPVDDLDR.C	1189.21	-0.784	2	0	3.17	0.31	534.10	4.0	17/22	35
4458, P3_100mM	R.GGSGTPVDDLDR.C	1189.21	-0.823	2	1	2.31	0.05	319.08	180.0	14/22	35
4461 - 4464, P3_60mM	K.NMIQCTVPNR.S	1233.45	-0.933	2	0	3.53	0.27	1188.89	1.0	16/18	6
4467, P3_20mM	R.GGSGTPVDDLDR.C	1189.21	-0.672	1	0	2.61	0.17	275.53	15.0	39438	35
4473, P3_20mM	R.GGSGTPVDDLDR.C	1189.21	-0.654	1	0	2.28	0.12	285.17	38.0	39438	35
4476, P3_20mM	K.NMIQCTVPNR.S	1233.45	-0.846	1	0	2.06	0.20	138.07	3.0	39404	6
4482, P3_20mM	K.NMIQCTVPNR.S	1233.45	-0.826	1	0	2.26	0.21	169.69	1.0	13/18	6
4536 - 4539, P3_20mM	R.GGSGTPVDDLDR.C	1189.21	-0.782	2	0	3.43	0.28	595.75	1.0	18/22	35
4557, P3_20mM	K.TYSYEC SQGLTCK.G	1698.86	-1.143	2	0	4.96	0.41	2324.06	1.0	22/26	15
4572, P3_20mM	K.TYSYEC SQGLTCK.G	1698.86	-1.187	2	0	5.12	0.41	2052.21	1.0	21/26	15
4719 - 4722, P3_20mM	K.NMIQCTVPNR.S	1233.45	0.088	2	0	2.90	0.02	1037.50	2.0	16/18	6
4875, P3_20mM	R.GGSGTPVDDLDR.C	1189.21	-0.779	2	0	2.70	0.24	382.52	45.0	15/22	35
4899, P3_20mM	R.GGSGTPVDDLDR.C	1189.21	-0.783	2	1	2.94	0.36	553.82	1.0	17/22	35
5271 - 5274, P3_20mM	R.GGSGTPVDDLDR.C	1189.21	-0.825	2	0	2.31	0.16	427.57	9.0	15/22	35
5637 - 5640, P3_20mM	R.GGSGTPVDDLDR.C	1189.21	-0.858	2	0	2.65	0.30	389.21	3.0	15/22	35
5784, P3_20mM	K.TYSYEC SQGLTCK.G	1698.86	-1.266	2	1	2.38	0.04	479.60	54.0	16/26	15
5832 - 5835, P3_60mM	R.CWPYFK.T	901.07	-0.726	1	0	1.64	0.06	260.46	5.0	39304	5
5994 - 5997, P3_20mM	R.GGSGTPVDDLDR.C	1189.21	-0.826	2	0	2.71	0.32	346.50	31.0	14/22	35
6015 - 6018, P3_400mM	R.LAAICFAGAPYNNNNYNIDLK.A	2357.63	-0.781	2	0	5.67	0.08	1606.35	1.0	28/40	5
6033, P3_400mM	R.LAAICFAGAPYNNNNYNIDLK.A	2357.63	-1.312	3	0	5.78	0.04	2615.71	1.0	39/80	5
6111, P3_20mM	K.NMIQCTVPNR.S	1233.45	-1.056	2	0	2.48	0.12	826.40	5.0	13/18	6
6219, P3_20mM	K.NMIQCTVPNR.S	1233.45	-1.055	2	0	2.84	0.14	976.37	2.0	14/18	6
6288, P3_20mM	K.NMIQCTVPNR.S	1233.45	-1.471	2	0	2.25	0.07	862.24	2.0	14/18	6
6390 - 6393, P3_20mM	R.GGSGTPVDDLDR.C	1189.21	-0.821	2	0	2.57	0.22	546.58	9.0	17/22	35
6735 - 6738, P3_20mM	R.GGSGTPVDDLDR.C	1189.21	-0.799	2	0	2.90	0.26	539.20	1.0	17/22	35
6762, P3_20mM	K.NMIQCTVPNR.S	1233.45	-1.015	2	0	2.93	0.21	1114.59	1.0	15/18	6
7107 - 7110, P3_20mM	R.GGSGTPVDDLDR.C	1189.21	-0.864	2	0	3.49	0.39	465.65	16.0	16/22	35

Supplemental Table 4 Orthologous proteins of peptide sequences generated from ion-exchange chromatography-purified *N. kaouthia* venom protein components (P3) by 2D-LC/MS-MS and database search

Reference					P(pro)	Score	Coverage	MW	Accession	Peptide(Hits)	
Scan(s), File (salt concentration)	Peptides	MH+	ΔM	z	P(pep)	X_{corr}	ΔCn	Sp	RSp	Ions	Count
7320, P3_20mM	K.TYSYECSQGLTCK.G	1698.86	0.741	2	0	3.29	0.33	529.92	1.0	18/26	15
7347, P3_20mM	K.TYSYECSQGLTCK.G	1698.86	-1.341	2	0	3.32	0.34	355.04	2.0	15/26	15
7722, P3_20mM	K.NMIQCTVPNR.S	1233.45	1.870	2	0	2.49	0.05	766.72	25.0	13/18	6
7848 - 7851, P3_20mM	R.GGSGTPVDDLDR.C	1189.21	-0.899	2	0	3.14	0.32	448.97	8.0	16/22	35
8154, P3_20mM	K.NMIQCTVPNR.S	1233.45	-1.092	2	0	2.36	0.13	904.11	2.0	14/18	6
8262, P3_20mM	R.GGSGTPVDDLDR.C	1189.21	-0.862	2	0	2.85	0.26	398.73	6.0	14/22	35
8727 - 8730, P3_20mM	R.GGSGTPVDDLDR.C	1189.21	-0.864	2	0	2.79	0.24	308.66	30.0	14/22	35
9177 - 9183, P3_20mM	R.GGSGTPVDDLDR.C	1189.21	-0.887	2	0	2.44	0.34	386.63	56.0	15/22	35
9969 - 9972, P3_20mM	R.GGSGTPVDDLDR.C	1189.21	-0.905	2	0	2.07	0.26	265.95	67.0	13/22	35
10707 - 10710, P3_20mM	R.GGSGTPVDDLDR.C	1189.21	-0.883	2	0	2.70	0.23	312.03	127.0	14/22	35
12189, P3_20mM	R.GGSGTPVDDLDR.C	1189.21	-0.937	2	0	2.01	0.23	291.63	133.0	39438	35
8. CO3_NAJNA Complement					0	68.18		184925.00	399269.0	9 (5 2 2 0 0)	
2946, P3_20mM	K.YIQEGDACK.A	1084.18	-0.917	2	1	2.45	0.09	726.86	15.0	13/16	4
3399, P3_60mM	K.FYHPDK.E	806.89	-0.574	2	0	2.09	0.11	684.79	11.0	39335	10
3759 - 3762, P3_20mM	K.NEQVEIR.A	887.96	-0.588	2	0	2.45	0.01	816.51	9.0	39398	36
4029 - 4032, P3_60mM	K.IKLEGDPGAR.V	1056.20	-0.687	2	0	2.91	0.09	602.16	45.0	14/18	6
4635 - 4638, P3_20mM	R.VGLVAVDK.A	800.97	-0.511	2	0	2.79	0.12	1180.86	1.0	13/14	29
4695, P3_20mM	K.AVYVLNDK.Y	922.06	-0.630	2	0	2.79	0.05	564.04	9.0	39430	6
5415 - 5418, P3_80mM	K.HFEVGFQPGSVK.V	1445.65	-1.033	2	0	3.69	0.33	1215.64	1.0	18/24	4
5448, P3_80mM	K.HFEVGFQPGSVK.V	1445.65	-1.055	2	0	3.25	0.10	1257.85	1.0	16/24	4
6351 - 6354, P3_60mM	K.YFTYLILNK.G	1175.40	-0.929	2	0	2.64	0.18	652.59	9.0	13/16	1
9. PA2_NAJNA Phospholipase A2, acidic (Phosphatidylcholine 2-acylhydrolase)					0	66.30		13345.82	129514.0	49 (42 6 0 0 1)	
3177 - 3180, P3_20mM	R.CCQVHDNICYNEAEK.I	1827.96	-0.866	2	0	5.08	0.25	1705.37	1.0	22/26	9
3198 - 3201, P3_20mM	R.CCQVHDNICYNEAEK.I	1827.96	-1.268	2	0	4.52	0.33	1104.23	2.0	19/26	9
3354, P3_60mM	R.CCQVHDNICYNEAEK.I	1827.96	-0.405	2	0	4.35	0.02	936.07	2.0	18/26	9
3843 - 3846, P3_20mM	R.GGSGTPVDDLDR.C	1189.21	-0.800	2	0	3.42	0.37	510.43	1.0	16/22	35
3849, P3_20mM	K.NM*IKCTVPSR.S	1222.46	-0.993	2	0	2.29	0.17	1188.38	1.0	16/18	3
3867, P3_20mM	K.NM*IKCTVPSR.S	1222.46	-0.947	2	0	2.91	0.10	1227.91	1.0	16/18	3
4182, P3_20mM	R.GGSGTPVDDLDR.C	1189.21	-0.826	2	0	2.69	0.45	473.48	9.0	16/22	35
4191, P3_20mM	R.GGSGTPVDDLDR.C	1189.21	-0.698	2	0	2.97	0.32	415.80	57.0	14/22	35

Supplemental Table 4 Orthologous proteins of peptide sequences generated from ion-exchange chromatography-purified *N. kaouthia* venom protein components (P3) by 2D-LC/MS-MS and database search

Reference					P(pro)	Score	Coverage	MW	Accession	Peptide(Hits)	
Scan(s), File (salt concentration)	Peptides	MH+	ΔM	z	P(pep)	X_{corr}	ΔCn	Sp	RSp	Ions	Count
4248 - 4251, P3_80mM	K.TYSYEC SQGLTCK.G	1698.86	-1.343	2	0	4.48	0.41	2495.25	1.0	22/26	15
4293, P3_200mM	K.TYSYEC SQGLTCK.G	1698.86	-1.386	2	0	4.19	0.43	1583.23	1.0	20/26	15
4383, P3_100mM	K.TYSYEC SQGLTCK.G	1698.86	-1.342	2	0	4.84	0.41	2018.58	1.0	21/26	15
4392, P3_20mM	K.TYSYEC SQGLTCK.G	1698.86	-0.353	3	0	3.57	0.34	463.39	11.0	24/52	15
4392 - 4395, P3_60mM	K.TYSYEC SQGLTCK.G	1698.86	-1.304	2	0	5.09	0.44	2766.74	1.0	23/26	15
4395, P3_100mM	K.TYSYEC SQGLTCK.G	1698.86	-1.381	2	0	3.79	0.45	610.50	1.0	18/26	15
4419, P3_20mM	K.TYSYEC SQGLTCK.G	1698.86	-1.103	2	0	4.45	0.37	2237.39	1.0	21/26	15
4428, P3_20mM	K.TYSYEC SQGLTCK.G	1698.86	-1.184	2	0	4.27	0.29	2165.64	1.0	21/26	15
4431 - 4434, P3_20mM	R.GGSGTPVDDLDR.C	1189.21	-0.654	1	0	2.42	0.27	249.67	4.0	39438	35
4449, P3_60mM	R.GGSGTPVDDLDR.C	1189.21	-0.826	2	0	2.33	0.39	414.34	2.0	15/22	35
4458, P3_60mM	R.GGSGTPVDDLDR.C	1189.21	-0.784	2	0	3.17	0.31	534.10	4.0	17/22	35
4458, P3_100mM	R.GGSGTPVDDLDR.C	1189.21	-0.823	2	1	2.31	0.05	319.08	180.0	14/22	35
4467, P3_20mM	R.GGSGTPVDDLDR.C	1189.21	-0.672	1	0	2.61	0.17	275.53	15.0	39438	35
4473, P3_20mM	R.GGSGTPVDDLDR.C	1189.21	-0.654	1	0	2.28	0.12	285.17	38.0	39438	35
4524 - 4527, P3_20mM	K.NMIKCTVPSR.S	1206.46	-0.949	2	0	2.92	0.10	1290.81	1.0	17/18	3
4536 - 4539, P3_20mM	R.GGSGTPVDDLDR.C	1189.21	-0.782	2	0	3.43	0.28	595.75	1.0	18/22	35
4557, P3_20mM	K.TYSYEC SQGLTCK.G	1698.86	-1.143	2	0	4.96	0.41	2324.06	1.0	22/26	15
4572, P3_20mM	K.TYSYEC SQGLTCK.G	1698.86	-1.187	2	0	5.12	0.41	2052.21	1.0	21/26	15
4875, P3_20mM	R.GGSGTPVDDLDR.C	1189.21	-0.779	2	0	2.70	0.24	382.52	45.0	15/22	35
4899, P3_20mM	R.GGSGTPVDDLDR.C	1189.21	-0.783	2	1	2.94	0.36	553.82	1.0	17/22	35
5271 - 5274, P3_20mM	R.GGSGTPVDDLDR.C	1189.21	-0.825	2	0	2.31	0.16	427.57	9.0	15/22	35
5352 - 5355, P3_20mM	-.NLYQFK.N	812.94	-0.581	2	0	2.11	-	377.60	2.0	39335	29
5637 - 5640, P3_20mM	R.GGSGTPVDDLDR.C	1189.21	-0.858	2	0	2.65	0.30	389.21	3.0	15/22	35
5784, P3_20mM	K.TYSYEC SQGLTCK.G	1698.86	-1.266	2	1	2.38	0.04	479.60	54.0	16/26	15
5994 - 5997, P3_20mM	R.GGSGTPVDDLDR.C	1189.21	-0.826	2	0	2.71	0.32	346.50	31.0	14/22	35
6015 - 6018, P3_400mM	R.LAAICFAGAPYNDNNY NIDLK.A	2358.61	-1.766	2	0	6.01	0.06	1606.35	1.0	28/40	14
6033, P3_400mM	R.LAAICFAGAPYNDNNY NIDLK.A	2358.61	-2.297	3	0	5.56	0.08	2173.72	2.0	37/80	14
6039 - 6042, P3_60mM	K.ISGCWPYFK.T	1158.35	-0.838	2	0	3.47	0.27	907.36	1.0	14/16	8
6075, P3_60mM	K.ISGCWPYFK.T	1158.35	-0.842	2	0	2.99	0.11	939.65	1.0	14/16	8

Supplemental Table 4 Orthologous proteins of peptide sequences generated from ion-exchange chromatography-purified *N. kaouthia* venom protein components (P3) by 2D-LC/MS-MS and database search

Reference					P(pro)	Score	Coverage	MW	Accession	Peptide(Hits)	
Scan(s), File (salt concentration)	Peptides	MH+	ΔM	z	P(pep)	X_{corr}	ΔCn	Sp	RSp	Ions	Count
6390 - 6393, P3_20mM	R.GGSGTPVDDLDR.C	1189.21	-0.821	2	0	2.57	0.22	546.58	9.0	17/22	35
6735 - 6738, P3_20mM	R.GGSGTPVDDLDR.C	1189.21	-0.799	2	0	2.90	0.26	539.20	1.0	17/22	35
7107 - 7110, P3_20mM	R.GGSGTPVDDLDR.C	1189.21	-0.864	2	0	3.49	0.39	465.65	16.0	16/22	35
7320, P3_20mM	K.TYSYEQSQTLTCK.G	1698.86	0.741	2	0	3.29	0.33	529.92	1.0	18/26	15
7347, P3_20mM	K.TYSYEQSQTLTCK.G	1698.86	-1.341	2	0	3.32	0.34	355.04	2.0	15/26	15
7848 - 7851, P3_20mM	R.GGSGTPVDDLDR.C	1189.21	-0.899	2	0	3.14	0.32	448.97	8.0	16/22	35
8262, P3_20mM	R.GGSGTPVDDLDR.C	1189.21	-0.862	2	0	2.85	0.26	398.73	6.0	14/22	35
8727 - 8730, P3_20mM	R.GGSGTPVDDLDR.C	1189.21	-0.864	2	0	2.79	0.24	308.66	30.0	14/22	35
9177 - 9183, P3_20mM	R.GGSGTPVDDLDR.C	1189.21	-0.887	2	0	2.44	0.34	386.63	56.0	15/22	35
9969 - 9972, P3_20mM	R.GGSGTPVDDLDR.C	1189.21	-0.905	2	0	2.07	0.26	265.95	67.0	13/22	35
10707 - 10710, P3_20mM	R.GGSGTPVDDLDR.C	1189.21	-0.883	2	0	2.70	0.23	312.03	127.0	14/22	35
12189, P3_20mM	R.GGSGTPVDDLDR.C	1189.21	-0.937	2	0	2.01	0.23	291.63	133.0	39438	35
10. PA2D_NAJSP Phospholipase A2, acidic D precursor (Phosphatidylcholine 2-acylhydrolase) (APLA)					0	64.30		16097.18	25453171.0	38 (34 3 1 0 0)	
3552 - 3555, P3_20mM	K.GGNDACAAAVCDCDR.L	1612.71	-2.115	2	0	4.35	0.46	1677.42	1.0	21/28	
3648, P3_20mM	K.GGNDACAAAVCDCDR.L	1612.71	-1.112	2	0	5.14	0.35	1799.20	1.0	21/28	
3654, P3_20mM	K.GGNDACAAAVCDCDR.L	1612.71	-1.156	2	0	4.85	0.29	1754.06	1.0	21/28	
3777 - 3780, P3_20mM	K.NM*IQCTV PNR.S	1249.45	-0.954	2	0	3.50	0.28	1019.71	1.0	16/18	6
3801, P3_20mM	K.NM*IQCTV PNR.S	1249.45	-0.931	2	0	3.17	0.10	929.31	2.0	15/18	6
3807, P3_20mM	K.NM*IQCTV PNR.S	1249.45	-0.930	2	0	3.26	0.11	1041.87	2.0	16/18	6
4077, P3_20mM	K.GGNDACAAAVCDCDR.L	1612.71	-2.121	2	1	3.45	0.15	562.64	3.0	17/28	
4086, P3_20mM	K.GGNDACAAAVCDCDR.L	1612.71	-2.113	2	0	3.13	0.14	346.50	36.0	14/28	
4248 - 4251, P3_80mM	K.TYSYEQSQTLTCK.G	1698.86	-1.343	2	0	4.48	0.41	2495.25	1.0	22/26	15
4293, P3_200mM	K.TYSYEQSQTLTCK.G	1698.86	-1.386	2	0	4.19	0.43	1583.23	1.0	20/26	15
4350, P3_20mM	K.NMIQCTV PNR.S	1233.45	-0.971	2	0	2.74	0.26	1191.50	1.0	16/18	6
4356, P3_20mM	K.NMIQCTV PNR.S	1233.45	-0.852	2	0	3.42	0.12	1071.29	2.0	15/18	6
4383, P3_100mM	K.TYSYEQSQTLTCK.G	1698.86	-1.342	2	0	4.84	0.41	2018.58	1.0	21/26	15
4392, P3_20mM	K.TYSYEQSQTLTCK.G	1698.86	-0.353	3	0	3.57	0.34	463.39	11.0	24/52	15
4392 - 4395, P3_60mM	K.TYSYEQSQTLTCK.G	1698.86	-1.304	2	0	5.09	0.44	2766.74	1.0	23/26	15
4395, P3_100mM	K.TYSYEQSQTLTCK.G	1698.86	-1.381	2	0	3.79	0.45	610.50	1.0	18/26	15
4419, P3_20mM	K.TYSYEQSQTLTCK.G	1698.86	-1.103	2	0	4.45	0.37	2237.39	1.0	21/26	15

Supplemental Table 4 Orthologous proteins of peptide sequences generated from ion-exchange chromatography-purified *N. kaouthia* venom protein components (P3) by 2D-LC/MS-MS and database search

Reference					P(pro)	Score	Coverage	MW	Accession	Peptide(Hits)	
Scan(s), File (salt concentration)	Peptides	MH+	ΔM	z	P(pep)	X_{corr}	ΔCn	Sp	RSp	Ions	Count
4428, P3_20mM	K.TYSYECSQGTLTCK.G	1698.86	-1.184	2	0	4.27	0.29	2165.64	1.0	21/26	15
4443, P3_100mM	K.NMIQCTVPNR.S	1233.45	-0.970	2	0	2.30	0.03	626.36	19.0	39404	6
4461 - 4464, P3_60mM	K.NMIQCTVPNR.S	1233.45	-0.933	2	0	3.53	0.27	1188.89	1.0	16/18	6
4476, P3_20mM	K.NMIQCTVPNR.S	1233.45	-0.846	1	0	2.06	0.20	138.07	3.0	39404	6
4482, P3_20mM	K.NMIQCTVPNR.S	1233.45	-0.826	1	0	2.26	0.21	169.69	1.0	13/18	6
4557, P3_20mM	K.TYSYECSQGTLTCK.G	1698.86	-1.143	2	0	4.96	0.41	2324.06	1.0	22/26	15
4572, P3_20mM	K.TYSYECSQGTLTCK.G	1698.86	-1.187	2	0	5.12	0.41	2052.21	1.0	21/26	15
4617 - 4620, P3_400mM	K.TYSYECSQGTLTCKGGN DACAAAVCDCLR.L	3292.54	-1.962	3	0	4.70	0.08	1466.71	1.0	31/112	
4719 - 4722, P3_20mM	K.NMIQCTVPNR.S	1233.45	0.088	2	0	2.90	0.02	1037.50	2.0	16/18	6
5784, P3_20mM	K.TYSYECSQGTLTCK.G	1698.86	-1.266	2	1	2.38	0.04	479.60	54.0	16/26	15
5832 - 5835, P3_60mM	R.CWPYFK.T	901.07	-0.726	1	0	1.64	0.06	260.46	5.0	39304	5
6015 - 6018, P3_400mM	R.LAAICFAGAPYNDNNYNIDLK.A	2358.61	-1.766	2	0	6.01	0.06	1606.35	1.0	28/40	14
6033, P3_400mM	R.LAAICFAGAPYNDNNYNIDLK.A	2358.61	-2.297	3	0	5.56	0.08	2173.72	2.0	37/80	14
6111, P3_20mM	K.NMIQCTVPNR.S	1233.45	-1.056	2	0	2.48	0.12	826.40	5.0	13/18	6
6219, P3_20mM	K.NMIQCTVPNR.S	1233.45	-1.055	2	0	2.84	0.14	976.37	2.0	14/18	6
6288, P3_20mM	K.NMIQCTVPNR.S	1233.45	-1.471	2	0	2.25	0.07	862.24	2.0	14/18	6
6762, P3_20mM	K.NMIQCTVPNR.S	1233.45	-1.015	2	0	2.93	0.21	1114.59	1.0	15/18	6
7320, P3_20mM	K.TYSYECSQGTLTCK.G	1698.86	0.741	2	0	3.29	0.33	529.92	1.0	18/26	15
7347, P3_20mM	K.TYSYECSQGTLTCK.G	1698.86	-1.341	2	0	3.32	0.34	355.04	2.0	15/26	15
7722, P3_20mM	K.NMIQCTVPNR.S	1233.45	1.870	2	0	2.49	0.05	766.72	25.0	13/18	6
8154, P3_20mM	K.NMIQCTVPNR.S	1233.45	-1.092	2	0	2.36	0.13	904.11	2.0	14/18	6

Supplemental Table 5 Orthologous proteins of peptide sequences generated from ion-exchange chromatography-purified *N. kaouthia* venom protein components (P4) by 2D-LC/MS-MS and database search

Reference				P(pro)	Score	Coverage	MW	Accession	Peptide(Hits)		
Scan(s), File (salt concentration)	Peptides	MH+	ΔM	z	P(pep)	X_{corr}	ΔCn	Sp	RSp	Ions	Count
1. CO3_NAJKA Cobra venom factor precursor (CVF)				0		182.31		184516.00	54035743.0	47 (37 9 1 0 0)	
4575 - 4578, P4_20mM	K.LNQDITVTASGDGK.A	1419.52	-0.889	2	0	4.51	0.35	1347.37	1.0	20/26	
4719 - 4722, P4_20mM_02	K.LNQDITVTASGDGK.A	1419.52	-0.948	2	0	4.28	0.39	1700.05	1.0	21/26	
4887, P4_20mM	R.VGLVAVDK.A	800.97	-0.494	2	0	2.72	0.09	1209.94	1.0	13/14	29
5451 - 5454, P4_20mM	K.GVGGTQLEVIK.A	1101.28	-0.727	2	0	3.75	0.25	1094.04	1.0	17/20	
5643, P4_20mM	R.QNQYVVVQVTGPQVR.L	1715.93	-1.141	2	0	4.24	0.46	1115.97	1.0	19/28	
5649, P4_20mM	R.QNQYVVVQVTGPQVR.L	1715.93	-1.065	2	0	4.51	0.42	1098.43	1.0	19/28	
5655 - 5658, P4_20mM_02	K.IWDTIEK.S	905.03	-0.514	2	0	2.25	0.00	520.60	9.0	39398	8
5706 - 5709, P4_20mM_02	K.GVGGTQLEVIK.A	1101.28	-0.745	2	0	3.79	0.26	887.46	2.0	17/20	
6207 - 6210, P4_20mM	K.ASVQEALWSDGVR.K	1418.54	-0.965	2	0	3.38	0.29	1351.40	1.0	18/24	
6246, P4_80mM	R.VDMNPAGGMLVTPTIEIPAK.E	2055.45	-1.612	2	0	5.56	0.32	1666.41	1.0	26/38	
6255, P4_80mM	R.VDMNPAGGMLVTPTIEIPAK.E	2055.45	-0.732	2	0	5.70	0.30	1864.28	1.0	25/38	
6540, P4_20mM	K.VNDDYLIWGSR.S	1338.45	-0.862	2	0	3.50	0.28	1050.73	1.0	16/20	
6549, P4_20mM_02	R.DDNEDGFIADSDIISR.S	1782.80	-1.128	2	0	4.47	0.37	1768.64	1.0	23/30	
6567, P4_20mM	K.VNDDYLIWGSR.S	1338.45	0.059	2	0	4.07	0.23	1411.04	1.0	17/20	
6666, P4_80mM	K.DLNLDITIELPDR.E	1527.70	-1.150	2	0	4.04	0.17	1637.97	1.0	20/24	
6669, P4_200mM	K.DLNLDITIELPDR.E	1527.70	-1.232	2	0	3.47	0.27	1327.65	1.0	17/24	
6672, P4_80mM	K.DLNLDITIELPDR.E	1527.70	-1.231	2	0	3.66	0.19	1650.24	1.0	20/24	
6678, P4_200mM	K.DLNLDITIELPDR.E	1527.70	-1.187	2	0	3.69	0.22	1654.39	1.0	19/24	
6828, P4_60mM	R.AILHNYVNEDIYVR.V	1719.92	-1.132	2	0	4.61	0.34	1900.62	1.0	20/26	
6924, P4_20mM_02	K.VNDDYLIWGSR.S	1338.45	-1.327	2	0	3.04	0.30	945.62	1.0	15/20	
6945, P4_20mM_02	K.VNDDYLIWGSR.S	1338.45	0.896	2	0	3.43	0.17	1418.36	2.0	17/20	
6972, P4_80mM	K.LILNIPLNAQSLPITVR.T	1876.28	-1.440	2	0	4.95	0.44	1232.40	1.0	24/32	
6981, P4_80mM	K.LILNIPLNAQSLPITVR.T	1876.28	-1.439	2	0	4.90	0.46	1059.07	1.0	22/32	
7023, P4_200mM	K.LILNIPLNAQSLPITVR.T	1876.28	-1.443	2	0	3.72	0.32	914.42	1.0	22/32	
7115, P4_0mM	K.DLTEEPNSQGISSK.T	1505.57	-0.977	2	0	3.69	0.19	977.49	1.0	19/26	
7160, P4_0mM	K.DLTEEPNSQGISSK.T	1505.57	-1.015	2	0	4.25	0.21	1178.33	1.0	21/26	
7242, P4_80mM	R.SDFPKSWLWLT.K.D	1508.74	-0.236	2	0	2.17	0.03	731.85	1.0	15/22	
7395, P4_80mM	K.IIIQGPVAQIIENSIDGSK.L	2111.38	-1.513	2	0	5.51	0.46	1881.59	1.0	26/38	

Supplemental Table 5 Orthologous proteins of peptide sequences generated from ion-exchange chromatography-purified *N. kaouthia* venom protein components (P4) by 2D-LC/MS-MS and database search

Reference				P(pro)	Score	Coverage	MW	Accession	Peptide(Hits)		
Scan(s), File (salt concentration)	Peptides	MH+	ΔM	z	P(pep)	X_{corr}	ΔCn	Sp	RSp	Ions	Count
7401, P4_80mM	K.IIIQGDPVAQIIENSIDGSK.L	2111.38	-1.590	2	0	5.72	0.51	1445.32	1.0	25/38	
7403, P4_0mM	K.LNQDITVTASGDGK.A	1419.52	-0.926	2	0	4.03	0.19	1118.00	1.0	18/26	
7416, P4_80mM	K.IIIQGDPVAQIIENSIDGSK.L	2111.38	-0.982	3	0	5.20	0.33	1092.81	6.0	29/76	
7552, P4_100mM	K.DLNLDITIELPDR.E	1527.70	-1.225	2	0	3.67	0.17	1397.79	1.0	18/24	
7608, P4_200mM	R.IEEQDGNDIYVMDVLEVIK.Q	2223.49	-0.099	3	0	4.00	0.00	1275.82	2.0	27/72	
7749, P4_20mM_02	K.SWLWLT.K.D	934.12	-0.844	2	0	2.30	0.13	568.14	49.0	39398	
7782 - 7785, P4_60mM	R.VDMNPAGGMLVTPTIEIPAK.E	2055.45	-1.617	2	0	5.91	0.28	1760.16	1.0	26/38	
7840, P4_400mM	K.DLNLDITIELPDREVPIR.Y	2122.41	1.195	3	0	2.87	0.15	723.45	14.0	24/68	
7927, P4_100mM	R.IEEQDGNDIYVM*DVLEVIK.Q	2239.49	-0.423	2	0	2.15	0.06	277.12	11.0	13/36	
8226, P4_60mM	K.DLNLDITIELPDR.E	1527.70	-1.148	2	0	3.36	0.03	1409.22	1.0	19/24	
8316, P4_20mM	R.IEEQDGNDIYVMDVLEVIK.Q	2223.49	-1.728	2	0	4.51	0.37	1384.25	1.0	22/36	
8325, P4_20mM	R.IEEQDGNDIYVMDVLEVIK.Q	2223.49	-1.651	2	0	4.69	0.47	1018.87	1.0	20/36	
8343, P4_60mM	K.SWLWLT.K.D	934.12	-0.698	1	0	2.40	0.04	564.05	25.0	39337	
8413, P4_100mM	R.IEEQDGNDIYVMDVLEVIK.Q	2223.49	-1.611	2	0	5.04	0.43	1424.72	1.0	22/36	
8434, P4_100mM	R.IEEQDGNDIYVMDVLEVIK.Q	2223.49	-1.614	2	0	4.91	0.41	1544.76	1.0	22/36	
8860, P4_400mM	R.IEEQDGNDIYVMDVLEVIK.Q	2223.49	-1.655	2	0	5.47	0.45	1628.06	1.0	24/36	
8866, P4_400mM	R.IEEQDGNDIYVMDVLEVIK.Q	2223.49	-1.691	2	0	6.19	0.40	1937.40	1.0	25/36	
10514, P4_0mM	K.LILNIPLNAQSLPITVR.T	1876.28	-1.242	2	0	3.74	0.37	602.76	1.0	18/32	
10613, P4_0mM	K.LILNIPLNAQSLPITVR.T	1876.28	-1.198	2	0	4.82	0.45	1055.16	1.0	23/32	
2. albumin [Bos taurus]					0	78.19	16.14	69323.13	30794280.0	15 (13 1 0 1 0)	
5067, P4_20mM_02	K.AEFVEVTK.L	923.04	-0.650	2	0	2.38	0.05	586.56	3.0	39430	5
5076, P4_20mM_02	K.AEFVEVTK.L	923.04	-0.696	2	0	2.57	0.03	683.38	5.0	13/14	5
6180, P4_20mM	K.LVNELTEFAK.T	1164.33	-0.782	2	0	3.15	0.10	737.52	1.0	15/18	4
6363, P4_S001_0mM01	K.LVVSTQTALA.-	1003.17	-0.825	2	0	3.03	0.33	334.76	42.0	39434	5
6369, P4_S001_0mM01	K.LVVSTQTALA.-	1003.17	-0.821	2	0	2.91	0.32	374.00	5.0	13/18	5
6432, P4_60mM	K.HLVDEPQNLIK.Q	1306.49	-0.860	2	0	3.30	0.18	875.64	1.0	16/20	6
6444, P4_60mM	K.HLVDEPQNLIK.Q	1306.49	-0.819	2	0	2.98	0.15	882.97	1.0	16/20	6
6507 - 6510, P4_20mM_02	K.LVNELTEFAK.T	1164.33	-0.860	2	0	3.33	0.15	900.80	1.0	16/18	4
6681, P4_60mM	K.KVPQVSTPTLVEVSR.N	1640.91	-1.110	2	0	2.55	0.10	564.68	2.0	15/28	43
6702, P4_20mM_02	K.HLVDEPQNLIK.Q	1306.49	1.898	2	0	2.71	0.10	658.87	2.0	13/20	6

Supplemental Table 5 Orthologous proteins of peptide sequences generated from ion-exchange chromatography-purified *N. kaouthia* venom protein components (P4) by 2D-LC/MS-MS and database search

Reference					P(pro)	Score	Coverage	MW	Accession	Peptide(Hits)	
Scan(s), File (salt concentration)	Peptides	MH+	ΔM	z	P(pep)	X_{corr}	ΔCn	Sp	RSp	Ions	Count
6762, P4_20mM_02	K.HLVDEPQNLIK.Q	1306.49	1.195	2	0	2.74	0.18	646.54	1.0	14/20	6
6813, P4_60mM	R.RPCFSALTPDETYVVK.A	1882.13	-1.520	3	0	3.76	0.16	929.28	28.0	26/60	5
6825, P4_60mM	R.RPCFSALTPDETYVVK.A	1882.13	-0.559	3	0	3.08	0.09	745.17	79.0	23/60	5
7230, P4_60mM	K.KQTALVELLK.H	1143.40	-0.728	2	0	2.93	0.10	1115.26	2.0	16/18	13
7839 - 7842, P4_60mM	K.DAIPENLPPLTADFAEDK.D	1957.13	-1.014	2	0	3.34	0.03	533.18	1.0	20/34	4
3. ALBU_BOVIN Serum albumin precursor (Allergen Bos d 6) (BSA)					0	78.19		69293.09	1351907.0	15 (13 1 0 1 0)	
5067, P4_20mM_02	K.AEFVEVTK.L	923.04	-0.650	2	0	2.38	0.05	586.56	3.0	39430	5
5076, P4_20mM_02	K.AEFVEVTK.L	923.04	-0.696	2	0	2.57	0.03	683.38	5.0	13/14	5
6180, P4_20mM	K.LVNELTEFAK.T	1164.33	-0.782	2	0	3.15	0.10	737.52	1.0	15/18	4
6363, P4_S001_0mM01	K.LVVSTQTALA.-	1003.17	-0.825	2	0	3.03	0.33	334.76	42.0	39434	5
6369, P4_S001_0mM01	K.LVVSTQTALA.-	1003.17	-0.821	2	0	2.91	0.32	374.00	5.0	13/18	5
6432, P4_60mM	K.HLVDEPQNLIK.Q	1306.49	-0.860	2	0	3.30	0.18	875.64	1.0	16/20	6
6444, P4_60mM	K.HLVDEPQNLIK.Q	1306.49	-0.819	2	0	2.98	0.15	882.97	1.0	16/20	6
6507 - 6510, P4_20mM_02	K.LVNELTEFAK.T	1164.33	-0.860	2	0	3.33	0.15	900.80	1.0	16/18	4
6681, P4_60mM	K.KVPQVSTPTLVEVSR.N	1640.91	-1.110	2	0	2.55	0.10	564.68	2.0	15/28	43
6702, P4_20mM_02	K.HLVDEPQNLIK.Q	1306.49	1.898	2	0	2.71	0.10	658.87	2.0	13/20	6
6762, P4_20mM_02	K.HLVDEPQNLIK.Q	1306.49	1.195	2	0	2.74	0.18	646.54	1.0	14/20	6
6813, P4_60mM	R.RPCFSALTPDETYVVK.A	1882.13	-1.520	3	0	3.76	0.16	929.28	28.0	26/60	5
6825, P4_60mM	R.RPCFSALTPDETYVVK.A	1882.13	-0.559	3	0	3.08	0.09	745.17	79.0	23/60	5
7230, P4_60mM	K.KQTALVELLK.H	1143.40	-0.728	2	0	2.93	0.10	1115.26	2.0	16/18	13
7839 - 7842, P4_60mM	K.DAIPENLPPLTADFAEDK.D	1957.13	-1.014	2	0	3.34	0.03	533.18	1.0	20/34	4
4. 754920A albumin					0	76.19		66136.48	229552.0	15 (12 2 0 1 0)	
5067, P4_20mM_02	K.AEFVEVTK.L	923.04	-0.650	2	0	2.38	0.05	586.56	3.0	39430	5
5076, P4_20mM_02	K.AEFVEVTK.L	923.04	-0.696	2	0	2.57	0.03	683.38	5.0	13/14	5
6180, P4_20mM	K.LVNELTEFAK.T	1164.33	-0.782	2	0	3.15	0.10	737.52	1.0	15/18	4
6363, P4_S001_0mM01	K.LVVSTQTALA.-	1003.17	-0.825	2	0	3.03	0.33	334.76	42.0	39434	5
6369, P4_S001_0mM01	K.LVVSTQTALA.-	1003.17	-0.821	2	0	2.91	0.32	374.00	5.0	13/18	5
6432, P4_60mM	K.HLVDEPQNLIK.Q	1306.49	-0.860	2	0	3.30	0.18	875.64	1.0	16/20	6
6444, P4_60mM	K.HLVDEPQNLIK.Q	1306.49	-0.819	2	0	2.98	0.15	882.97	1.0	16/20	6
6507 - 6510, P4_20mM_02	K.LVNELTEFAK.T	1164.33	-0.860	2	0	3.33	0.15	900.80	1.0	16/18	4

Supplemental Table 5 Orthologous proteins of peptide sequences generated from ion-exchange chromatography-purified *N. kaouthia* venom protein components (P4) by 2D-LC/MS-MS and database search

Reference				P(pro)	Score	Coverage	MW	Accession	Peptide(Hits)		
Scan(s), File (salt concentration)	Peptides	MH+	ΔM	z	P(pep)	X_{corr}	ΔCn	Sp	RSp	Ions	Count
6681, P4_60mM	K.KVPQVSTPTLVEVSR.N	1640.91	-1.110	2	0	2.55	0.10	564.68	2.0	15/28	43
6702, P4_20mM_02	K.HLVDEPQNLIK.Q	1306.49	1.898	2	0	2.71	0.10	658.87	2.0	13/20	6
6762, P4_20mM_02	K.HLVDEPQNLIK.Q	1306.49	1.195	2	0	2.74	0.18	646.54	1.0	14/20	6
6813, P4_60mM	R.RPCFSALTPDETYVVK.A	1882.13	-1.520	3	0	3.76	0.16	929.28	28.0	26/60	5
6825, P4_60mM	R.RPCFSALTPDETYVVK.A	1882.13	-0.559	3	0	3.08	0.09	745.17	79.0	23/60	5
7230, P4_60mM	K.KQTALVELLK.H	1143.40	-0.728	2	0	2.93	0.10	1115.26	2.0	16/18	13
7839 - 7842, P4_60mM	K.DAIPEDLPPLTADFAEDK.D	1958.11	-1.999	2	0	3.24	0.30	478.80	2.0	19/34	
5. A Chain A, Crystal Structure Of Natrin From Naja Atra Snake Venom					0	68.21		24953.96	71041970.0	16 (12 2 1 1 0)	
4272 - 4275, P4_20mM	-.NVDNFSESTR.R	1169.18	-0.732	2	0	2.53	0.14	436.62	3.0	13/18	3
4407, P4_20mM_02	-.NVDNFSESTR.R	1169.18	-0.752	2	0	3.07	0.11	653.11	2.0	15/18	3
4416, P4_20mM_02	-.NVDNFSESTR.R	1169.18	-0.749	2	0	3.12	0.11	606.84	1.0	15/18	3
4791 - 4794, P4_20mM	R.VSPTASNMLK.M	1048.24	-0.765	2	0	2.06	0.30	329.35	4.0	15/18	2
4989 - 4992, P4_20mM_02	R.VSPTASNMLK.M	1048.24	-0.806	2	0	2.43	0.38	263.82	11.0	13/18	2
5310, P4_20mM	K.M*EWYPEAASNAER.W	1570.67	1.623	2	0	3.37	0.18	807.90	1.0	17/24	3
5352, P4_20mM_02	K.LTNCDSLK.Q	1064.24	-0.770	2	0	2.14	0.08	479.42	43.0	39432	2
5361, P4_20mM_02	K.LTNCDSLK.Q	1064.24	-0.681	2	0	2.27	0.12	534.25	8.0	13/16	2
5535 - 5538, P4_20mM_02	K.EIVDLHNSLR.R	1196.34	-0.765	2	0	2.80	0.20	364.52	4.0	15/18	4
5739, P4_S001_0mM01	-.NVDNFSESTR.R	1169.18	-0.715	2	0	2.21	0.10	379.71	20.0	39434	3
5745, P4_S001_0mM01	-.NVDNFSESTR.R	1169.18	-0.708	2	0	2.68	0.06	490.27	7.0	13/18	3
5805 - 5808, P4_20mM	K.MEWYPEAASNAER.W	1554.67	-1.131	2	0	4.25	0.34	1296.16	1.0	22/24	3
6075 - 6078, P4_20mM_02	K.MEWYPEAASNAER.W	1554.67	-1.071	2	0	3.86	0.34	1000.01	1.0	20/24	3
6120 - 6123, P4_60mM	K.QKEIVDLHNSLR.R	1452.64	-0.828	2	0	3.12	0.30	582.09	2.0	17/22	4
8852, P4_0mM	K.MEWYPEAASNAER.W	1554.67	-1.229	2	0	2.01	0.11	461.86	65.0	14/24	3
8861, P4_0mM	K.MEWYPEAASNAER.W	1554.67	-1.150	2	0	2.89	0.23	869.57	5.0	17/24	3
6. A Chain A, Crystal Structure Of Natrin, A Snake Venom Crisp From Taiwan Cobra (Naja Atra)					0	68.21		24926.93	85543948.0	16 (12 2 1 1 0)	
4272 - 4275, P4_20mM	-.NVDNFSESTR.R	1169.18	-0.732	2	0	2.53	0.14	436.62	3.0	13/18	3
4407, P4_20mM_02	-.NVDNFSESTR.R	1169.18	-0.752	2	0	3.07	0.11	653.11	2.0	15/18	3
4416, P4_20mM_02	-.NVDNFSESTR.R	1169.18	-0.749	2	0	3.12	0.11	606.84	1.0	15/18	3
4791 - 4794, P4_20mM	R.VSPTASNMLK.M	1048.24	-0.765	2	0	2.06	0.30	329.35	4.0	15/18	2
4989 - 4992, P4_20mM_02	R.VSPTASNMLK.M	1048.24	-0.806	2	0	2.43	0.38	263.82	11.0	13/18	2

Supplemental Table 5 Orthologous proteins of peptide sequences generated from ion-exchange chromatography-purified *N. kaouthia* venom protein components (P4) by 2D-LC/MS-MS and database search

Reference				P(pro)	Score	Coverage	MW	Accession	Peptide(Hits)		
Scan(s), File (salt concentration)	Peptides	MH+	ΔM	z	P(pep)	X_{corr}	ΔCn	Sp	RSp	Ions	Count
5310, P4_20mM	K.M*EWYPEAASNAER.W	1570.67	1.623	2	0	3.37	0.18	807.90	1.0	17/24	3
5352, P4_20mM_02	K.LTNCDSLK.Q	1064.24	-0.770	2	0	2.14	0.08	479.42	43.0	39432	2
5361, P4_20mM_02	K.LTNCDSLK.Q	1064.24	-0.681	2	0	2.27	0.12	534.25	8.0	13/16	2
5535 - 5538, P4_20mM_02	K.EIVDLHNSLR.R	1196.34	-0.765	2	0	2.80	0.20	364.52	4.0	15/18	4
5739, P4_S001_0mM01	-.NVDFNSESTR.R	1169.18	-0.715	2	0	2.21	0.10	379.71	20.0	39434	3
5745, P4_S001_0mM01	-.NVDFNSESTR.R	1169.18	-0.708	2	0	2.68	0.06	490.27	7.0	13/18	3
5805 - 5808, P4_20mM	K.MEWYPEAASNAER.W	1554.67	-1.131	2	0	4.25	0.34	1296.16	1.0	22/24	3
6075 - 6078, P4_20mM_02	K.MEWYPEAASNAER.W	1554.67	-1.071	2	0	3.86	0.34	1000.01	1.0	20/24	3
6120 - 6123, P4_60mM	K.QKEIVDLHNSLR.R	1452.64	-0.828	2	0	3.12	0.30	582.09	2.0	17/22	4
8852, P4_0mM	K.MEWYPEAASNAER.W	1554.67	-1.229	2	0	2.01	0.11	461.86	65.0	14/24	3
8861, P4_0mM	K.MEWYPEAASNAER.W	1554.67	-1.150	2	0	2.89	0.23	869.57	5.0	17/24	3
7. ALB protein [Bos taurus]					0	68.19		69235.06	74267962.0	14 (12 1 0 1 0)	
5067, P4_20mM_02	K.AEFVEVTK.L	923.04	-0.650	2	0	2.38	0.05	586.56	3.0	39430	5
5076, P4_20mM_02	K.AEFVEVTK.L	923.04	-0.696	2	0	2.57	0.03	683.38	5.0	13/14	5
6180, P4_20mM	K.LVNELTEFAK.T	1164.33	-0.782	2	0	3.15	0.10	737.52	1.0	15/18	4
6363, P4_S001_0mM01	K.LVVSTQTALA.-	1003.17	-0.825	2	0	3.03	0.33	334.76	42.0	39434	5
6369, P4_S001_0mM01	K.LVVSTQTALA.-	1003.17	-0.821	2	0	2.91	0.32	374.00	5.0	13/18	5
6432, P4_60mM	K.HLVDEPQNLIK.Q	1306.49	-0.860	2	0	3.30	0.18	875.64	1.0	16/20	6
6444, P4_60mM	K.HLVDEPQNLIK.Q	1306.49	-0.819	2	0	2.98	0.15	882.97	1.0	16/20	6
6507 - 6510, P4_20mM_02	K.LVNELTEFAK.T	1164.33	-0.860	2	0	3.33	0.15	900.80	1.0	16/18	4
6702, P4_20mM_02	K.HLVDEPQNLIK.Q	1306.49	1.898	2	0	2.71	0.10	658.87	2.0	13/20	6
6762, P4_20mM_02	K.HLVDEPQNLIK.Q	1306.49	1.195	2	0	2.74	0.18	646.54	1.0	14/20	6
6813, P4_60mM	R.RPCFSALTPDETYVPK.A	1882.13	-1.520	3	0	3.76	0.16	929.28	28.0	26/60	5
6825, P4_60mM	R.RPCFSALTPDETYVPK.A	1882.13	-0.559	3	0	3.08	0.09	745.17	79.0	23/60	5
7230, P4_60mM	K.KQTALVELLK.H	1143.40	-0.728	2	0	2.93	0.10	1115.26	2.0	16/18	13
7839 - 7842, P4_60mM	K.DAIPENLPPLTADFAEDK.D	1957.13	-1.014	2	0	3.34	0.03	533.18	1.0	20/34	4
8. THAI_NAJKA Thaibobrin					0	60.34		12037.50	32363235.0	32 (31 0 0 0 1)	
4785 - 4788, P4_20mM	K.TVENVGVSQVAPDNPER.F	1811.93	-0.719	2	0	4.10	0.33	1339.43	1.0	23/32	
4818 - 4821, P4_20mM	K.TVENVGVSQVAPDNPER.F	1811.93	0.305	3	0	3.89	0.06	1273.02	2.0	34/64	
4833, P4_20mM	K.TVENVGVSQVAPDNPER.F	1811.93	-1.101	2	0	4.32	0.10	950.62	1.0	20/32	

Supplemental Table 5 Orthologous proteins of peptide sequences generated from ion-exchange chromatography-purified *N. kaouthia* venom protein components (P4) by 2D-LC/MS-MS and database search

Reference				P(pro)	Score	Coverage	MW	Accession	Peptide(Hits)		
Scan(s), File (salt concentration)	Peptides	MH+	ΔM	z	P(pep)	X_{corr}	ΔCn	Sp	RSp	Ions	Count
4995 - 4998, P4_20mM_02	K.TVENVGVSQVAPDNPER.F	1811.93	-1.100	2	0	4.32	0.36	1334.11	1.0	23/32	
5061, P4_20mM_02	K.TVENVGVSQVAPDNPER.F	1811.93	-1.142	2	0	4.16	0.15	995.84	1.0	20/32	
5109, P4_20mM_02	K.TVENVGVSQVAPDNPER.F	1811.93	-0.445	3	0	3.79	0.09	1098.22	1.0	30/64	
5283, P4_20mM_02	K.HFFEVK.Y	806.93	-0.500	2	0	2.57	0.00	638.40	16.0	39365	2
5289, P4_20mM_02	K.HFFEVK.Y	806.93	-0.498	2	0	2.55	0.02	493.62	46.0	39335	2
5499, P4_200mM	R.FDGSPCVLGSPGFR.S	1496.67	2.335	2	0	2.44	0.19	240.24	121.0	39412	
5523, P4_200mM	R.FDGSPCVLGSPGFR.S	1496.67	-1.199	2	0	2.49	0.15	569.01	1.0	14/26	
5535, P4_80mM	R.FDGSPCVLGSPGFR.S	1496.67	2.327	2	0	2.95	0.08	442.66	63.0	39442	
5739 - 5742, P4_20mM	R.EWAVGLAGK.S	931.07	-0.680	2	0	2.14	0.13	529.52	6.0	13/16	2
5754 - 5757, P4_20mM	R.EWAVGLAGK.S	931.07	-0.630	1	0	2.76	0.17	355.72	4.0	39402	2
5772, P4_20mM	R.EWAVGLAGK.S	931.07	-0.677	2	0	2.33	0.02	349.86	75.0	39402	2
5778, P4_20mM	R.EWAVGLAGK.S	931.07	-0.633	1	0	2.81	0.02	384.65	5.0	39432	2
5856, P4_S001_0mM01	K.TVENVGVSQVAPDNPER.F	1811.93	-1.018	2	0	4.32	0.38	1262.90	1.0	22/32	
5994 - 5997, P4_20mM_02	R.EWAVGLAGK.S	931.07	-0.657	2	0	2.06	0.12	723.55	1.0	15/16	2
6000 - 6003, P4_20mM	R.FDGSPCVLGSPGFR.S	1496.67	-1.058	2	0	4.27	0.38	1109.32	1.0	19/26	
6003 - 6006, P4_20mM_02	R.EWAVGLAGK.S	931.07	-0.611	1	0	2.69	0.17	358.45	2.0	39432	2
6015, P4_20mM_02	R.EWAVGLAGK.S	931.07	-0.612	1	0	2.74	0.13	392.29	2.0	39432	2
6024, P4_20mM_02	R.EWAVGLAGK.S	931.07	-0.611	1	0	2.68	0.10	328.11	7.0	39402	2
6264 - 6267, P4_20mM_02	R.FDGSPCVLGSPGFR.S	1496.67	-1.040	2	0	3.80	0.37	1097.07	1.0	19/26	
6351 - 6354, P4_20mM_02	R.FDGSPCVLGSPGFR.S	1496.67	-0.996	2	0	3.80	0.29	1248.84	1.0	20/26	
6372 - 6375, P4_80mM	K.ADVTFDSNTAFESLVVSPDK.K	2143.29	-1.499	2	0	6.82	0.53	1863.50	1.0	28/38	1
7068 - 7071, P4_60mM	R.FDGSPCVLGSPGFR.S	1496.67	-0.121	2	0	4.44	0.35	1559.08	1.0	22/26	
7430 - 7433, P4_0mM	K.TVENVGVSQVAPDNPER.F	1811.93	-1.116	2	0	4.34	0.34	1246.87	1.0	22/32	
7439, P4_0mM	K.TVENVGVSQVAPDNPER.F	1811.93	-0.508	3	0	3.49	0.13	1030.78	12.0	29/64	
7611 - 7614, P4_60mM	K.ADVTFDSNTAFESLVVSPDKK.T	2271.47	-1.489	2	0	4.92	0.52	1890.92	1.0	25/40	1
7658, P4_0mM	K.TVENVGVSQVAPDNPER.F	1811.93	-1.057	2	0	4.26	0.18	1263.82	1.0	22/32	
7793 - 7796, P4_0mM	K.TVENVGVSQVAPDNPER.F	1811.93	-1.100	2	0	4.58	0.33	1209.29	1.0	22/32	
7905, P4_60mM	K.ADVTFDSNTAFESLVVSPDK.K	2143.29	-1.385	2	0	6.06	0.53	1888.79	1.0	27/38	1
7917, P4_60mM	K.ADVTFDSNTAFESLVVSPDK.K	2143.29	-1.382	2	0	6.44	0.56	2040.43	1.0	28/38	1

Supplemental Table 5 Orthologous proteins of peptide sequences generated from ion-exchange chromatography-purified *N. kaouthia* venom protein components (P4) by 2D-LC/MS-MS and database search

Reference					P(pro)	Score	Coverage	MW	Accession	Peptide(Hits)	
Scan(s), File (salt concentration)	Peptides	MH+	ΔM	z	P(pep)	X_{corr}	ΔCn	Sp	RSp	Ions	Count
9. CRVP1_NAJAT Natrin-1 precursor (Cysteine-rich venom protein 1) (NA-CRVP1) (Protein G2a)					0	58.21		26882.29	48428837.0	11 (8 2 0 1 0)	
4791 - 4794, P4_20mM	R.VSPTASNMLK.M	1048.24	-0.765	2	0	2.06	0.30	329.35	4.0	15/18	2
4989 - 4992, P4_20mM_02	R.VSPTASNMLK.M	1048.24	-0.806	2	0	2.43	0.38	263.82	11.0	13/18	2
5310, P4_20mM	K.M*EWYPEAASNAER.W	1570.67	1.623	2	0	3.37	0.18	807.90	1.0	17/24	3
5352, P4_20mM_02	K.LTNCDSSLK.Q	1064.24	-0.770	2	0	2.14	0.08	479.42	43.0	39432	2
5361, P4_20mM_02	K.LTNCDSSLK.Q	1064.24	-0.681	2	0	2.27	0.12	534.25	8.0	13/16	2
5535 - 5538, P4_20mM_02	K.EIVDLHNSLR.R	1196.34	-0.765	2	0	2.80	0.20	364.52	4.0	15/18	4
5805 - 5808, P4_20mM	K.MEWYPEAASNAER.W	1554.67	-1.131	2	0	4.25	0.34	1296.16	1.0	22/24	3
6075 - 6078, P4_20mM_02	K.MEWYPEAASNAER.W	1554.67	-1.071	2	0	3.86	0.34	1000.01	1.0	20/24	3
6120 - 6123, P4_60mM	K.QKEIVDLHNSLR.R	1452.64	-0.828	2	0	3.12	0.30	582.09	2.0	17/22	4
8852, P4_0mM	K.MEWYPEAASNAER.W	1554.67	-1.229	2	0	2.01	0.11	461.86	65.0	14/24	3
8861, P4_0mM	K.MEWYPEAASNAER.W	1554.67	-1.150	2	0	2.89	0.23	869.57	5.0	17/24	3
10. serum albumin [<i>Bos indicus</i>]					0	58.19		53924.78	76445989.0	11 (10 1 0 0 0)	
5076, P4_20mM_02	K.AEFVEVTK.L	923.04	-0.696	2	0	2.57	0.03	683.38	5.0	13/14	5
6363, P4_S001_0mM01	K.LVVSTQTALA.-	1003.17	-0.825	2	0	3.03	0.33	334.76	42.0	39434	5
6369, P4_S001_0mM01	K.LVVSTQTALA.-	1003.17	-0.821	2	0	2.91	0.32	374.00	5.0	13/18	5
6432, P4_60mM	K.HLVDEPQNLIK.Q	1306.49	-0.860	2	0	3.30	0.18	875.64	1.0	16/20	6
6444, P4_60mM	K.HLVDEPQNLIK.Q	1306.49	-0.819	2	0	2.98	0.15	882.97	1.0	16/20	6
6702, P4_20mM_02	K.HLVDEPQNLIK.Q	1306.49	1.898	2	0	2.71	0.10	658.87	2.0	13/20	6
6762, P4_20mM_02	K.HLVDEPQNLIK.Q	1306.49	1.195	2	0	2.74	0.18	646.54	1.0	14/20	6
6813, P4_60mM	R.RPCFSALTPDETYVPK.A	1882.13	-1.520	3	0	3.76	0.16	929.28	28.0	26/60	5
6825, P4_60mM	R.RPCFSALTPDETYVPK.A	1882.13	-0.559	3	0	3.08	0.09	745.17	79.0	23/60	5
7230, P4_60mM	K.KQTALVELLK.H	1143.40	-0.728	2	0	2.93	0.10	1115.26	2.0	16/18	13
7839 - 7842, P4_60mM	K.DAIPENLPPLTADFAEDK.D	1957.13	-1.014	2	0	3.34	0.03	533.18	1.0	20/34	4

Supplemental Table 6: Orthologous proteins of peptide sequences generated from ion-exchange chromatography-purified *N. kaouthia* venom protein components (P5) by 2D-LC/MS-MS and database search

Reference		MH+	ΔM	z	P(pro)	Score	Coverage	MW	Accession	Peptide(Hits)	Count
Scan(s), File (salt concentration)	Peptides				P(pep)	X_{corr}	ΔCn	Sp	RSp	Ions	
1. CO3_NAJKA Cobra venom factor precursor (CVF)					0	274.27	20.89	184516.00	54035743.0	55 (53 1 1 0 0)	
(Complement C3 homolog)											
4446 - 4449, P5_20mM	R.VPDTEIETK.I	1032.13	-0.674	2	0	3.07	0.12	707.95	1.0	14/16	
4572 - 4575, P5_60mM	K.IKLEGDPGAR.V	1056.20	-0.704	2	0	2.81	0.12	505.99	77.0	13/18	6
4650, P5_60mM	R.KCQEALNLK.L	1104.31	-0.833	2	0	2.47	0.17	668.28	58.0	39432	5
4656, P5_60mM	R.KCQEALNLK.L	1104.31	-0.835	2	0	2.93	0.14	781.74	10.0	13/16	5
4746, P5_20mM	K.DLTEEPNSQGISSK.T	1505.57	-1.011	2	0	3.93	0.22	891.46	1.0	19/26	
4752, P5_20mM	K.DLTEEPNSQGISSK.T	1505.57	-0.977	2	0	3.81	0.22	736.61	1.0	18/26	
4803, P5_60mM	K.VSHSEDECLHFK.I	1488.61	-1.058	3	0	3.05	0.31	519.04	85.0	18/44	1
4809, P5_60mM	K.VSHSEDECLHFK.I	1488.61	-1.186	3	0	2.54	0.02	879.57	11.0	21/44	1
4911, P5_20mM	K.LNQDITVTASGDGK.A	1419.52	2.996	2	0	4.88	0.38	1970.89	1.0	22/26	
4926, P5_20mM	K.LNQDITVTASGDGK.A	1419.52	-0.882	2	0	4.74	0.37	1594.65	1.0	20/26	
4950 - 4953, P5_0mM	K.DLTEEPNSQGISSK.T	1505.57	-1.014	2	0	3.78	0.18	1090.95	1.0	21/26	
5064, P5_0mM	K.LNQDITVTASGDGK.A	1419.52	-1.005	2	0	4.70	0.42	1733.67	1.0	21/26	
5070, P5_0mM	K.LNQDITVTASGDGK.A	1419.52	-1.050	2	0	5.00	0.36	1191.66	1.0	19/26	
5196 - 5199, P5_20mM	K.ACETNVDYVYK.T	1362.49	-0.982	2	0	3.49	0.35	884.82	1.0	15/20	
5292 - 5295, P5_20mM	R.VGLVAVDK.A	800.97	-0.474	2	0	2.89	0.10	1166.81	1.0	13/14	29
5331, P5_20mM	K.AVYVLNDK.Y	922.06	-0.664	2	0	2.81	0.07	670.84	4.0	13/14	6
5613, P5_20mM	R.IPIIDGDGK.A	928.06	-0.672	2	0	2.60	0.20	592.34	3.0	39432	
5625, P5_20mM	R.IPIIDGDGK.A	928.06	-1.146	2	0	2.39	0.17	392.76	14.0	39432	
5646 - 5649, P5_80mM	R.TDTEEQILVEAHGDSTPK.S	1971.07	-1.417	3	0	3.03	0.01	611.49	22.0	25/68	1
5811, P5_20mM	K.IWDTIEK.S	905.03	2.327	2	0	2.14	0.00	542.07	8.0	39398	8
5814 - 5817, P5_20mM	K.GVGGTQLEVIK.A	1101.28	-0.744	2	0	3.68	0.23	851.51	1.0	16/20	
5820, P5_20mM	K.IWDTIEK.S	905.03	2.283	2	0	2.22	0.00	565.63	9.0	39398	8
5874, P5_20mM	R.TDTEEQILVEAHGDSTPK.S	1971.07	-1.187	3	0	3.30	0.28	669.52	3.0	26/68	1
5880, P5_20mM	R.TDTEEQILVEAHGDSTPK.S	1971.07	-1.239	3	0	2.75	0.09	957.97	1.0	29/68	1
5922 - 5925, P5_20mM	R.QNQYVVVQVTGPQVR.L	1715.93	-1.198	2	0	3.90	0.35	1323.68	1.0	21/28	
5937, P5_20mM	R.QNQYVVVQVTGPQVR.L	1715.93	2.107	3	0	3.86	0.01	679.88	47.0	22/56	
5958, P5_20mM	R.QNQYVVVQVTGPQVR.L	1715.93	-1.223	3	0	4.38	0.07	941.59	90.0	24/56	

Supplemental Table 6: Orthologous proteins of peptide sequences generated from ion-exchange chromatography-purified *N. kaouthia* venom protein components (P5) by 2D-LC/MS-MS and database search

Reference					P(pro)	Score	Coverage	MW	Accession	Peptide(Hits)	
Scan(s), File (salt concentration)	Peptides	MH+	ΔM	z	P(pep)	X_{corr}	ΔCn	Sp	RSp	Ions	Count
5961 - 5964, P5_60mM	K.GIYTPGSPVLYR.V	1323.52	-1.091	2	0	2.81	0.30	436.36	6.0	14/22	
6135, P5_80mM	K.GIYTPGSPVLYR.V	1323.52	-1.130	2	0	2.18	0.31	357.94	3.0	39438	
6141 - 6144, P5_20mM	K.GICVAEPEYR.V	1307.50	-1.006	2	0	3.10	0.20	1119.82	1.0	15/20	
6147, P5_80mM	K.GIYTPGSPVLYR.V	1323.52	-1.087	2	0	2.63	0.28	500.37	2.0	14/22	
6255 - 6258, P5_20mM	R.IDVPLQIEK.A	1055.25	-0.695	2	0	2.28	0.07	401.13	45.0	39402	
6267, P5_0mM	R.DDNEDGFIADSDIISR.S	1782.80	-1.331	2	0	4.63	0.43	2050.65	1.0	25/30	
6273, P5_0mM	R.DDNEDGFIADSDIISR.S	1782.80	-1.244	2	0	5.13	0.41	1640.59	1.0	23/30	
6276, P5_80mM	K.HFEVGFIQPGSVK.V	1445.65	-1.243	3	0	2.93	0.03	873.86	50.0	24/48	4
6291 - 6294, P5_20mM	R.INYENALLAR.T	1177.33	-0.741	2	0	3.75	0.20	1109.58	2.0	16/18	
6429, P5_20mM	K.ASVQEALWSDGVR.K	1418.54	-1.423	2	0	3.19	0.14	514.07	60.0	15/24	
6483, P5_20mM	K.ASVQEALWSDGVR.K	1418.54	-0.942	2	0	3.92	0.28	1422.27	1.0	17/24	
6513, P5_20mM	K.ASVQEALWSDGVR.K	1418.54	-0.868	2	0	3.71	0.18	1407.53	1.0	17/24	
6537 - 6540, P5_20mM	R.DDNEDGFIADSDIISR.S	1782.80	-1.168	2	0	5.46	0.41	1532.59	1.0	23/30	
6708 - 6711, P5_20mM	R.VELLYNPAFCSASTK.G	1700.94	-1.305	2	0	4.61	0.40	1458.18	1.0	22/28	
6741 - 6744, P5_80mM	K.VNDDYLIWGSR.S	1338.45	-0.969	2	0	3.91	0.33	1670.85	1.0	18/20	
6813 - 6816, P5_20mM	K.VNDDYLIWGSR.S	1338.45	-0.898	2	0	3.71	0.30	1450.08	1.0	18/20	
6954 - 6957, P5_60mM	K.YFTYLILNK.G	1175.40	-0.946	2	0	2.70	0.26	773.51	2.0	13/16	1
7257 - 7260, P5_60mM	K.DLNLDITIELPDR.E	1527.70	-1.168	2	0	4.07	0.24	1453.73	1.0	20/24	
7374 - 7377, P5_100mM	K.DLNLDITIELPDR.E	1527.70	-1.331	2	0	4.28	0.24	1638.86	1.0	20/24	
7422 - 7425, P5_80mM	K.DLNLDITIELPDR.E	1527.70	-0.753	2	0	4.05	0.26	1542.54	1.0	20/24	
7518 - 7521, P5_20mM	K.DLNLDITIELPDR.E	1527.70	-1.229	2	0	4.31	0.23	1589.97	1.0	21/24	
8208, P5_80mM	K.IIIQGDPAQIENSIDGSK.L	2111.38	-0.588	2	0	4.94	0.48	1676.66	1.0	25/38	
8217, P5_80mM	K.IIIQGDPAQIENSIDGSK.L	2111.38	-1.545	2	0	4.92	0.44	1520.28	1.0	25/38	
8259, P5_200mM	K.DLNLDITIELPDR.E	1527.70	-1.224	2	0	4.29	0.25	1637.60	1.0	20/24	
8265, P5_200mM	K.DLNLDITIELPDR.E	1527.70	-1.227	2	0	3.97	0.22	1517.53	1.0	19/24	
8559, P5_200mM	K.LILNIPLNAQSLPITVR.T	1876.28	-1.528	2	0	4.99	0.45	977.25	1.0	22/32	
8571, P5_200mM	K.LILNIPLNAQSLPITVR.T	1876.28	-1.446	2	0	5.03	0.40	873.07	1.0	21/32	
9378, P5_400mM	R.IEEQDGNDIYVMDVLEVIK.Q	2223.49	-0.689	2	0	5.49	0.39	1438.29	1.0	22/36	

Supplemental Table 6: Orthologous proteins of peptide sequences generated from ion-exchange chromatography-purified *N. kaouthia* venom protein components (P5) by 2D-LC/MS-MS and database search

Reference					P(pro)	Score	Coverage	MW	Accession	Peptide(Hits)	
Scan(s), File (salt concentration)	Peptides	MH+	ΔM	z	P(pep)	X_{corr}	ΔCn	Sp	RSp	Ions	Count
2. PA21_NAJKA Phospholipase A2 isozyme 1 precursor (Phosphatidylcholine 2-acylhydrolase) (NnkPLA-I) (CM-II)					0	90.32		16271.38	24638468.0	58 (37 12 2 3 4)	
3792 - 3795, P5_20mM	R.CCQVHDNICYNEAEK.I	1827.96	-1.387	2	0	5.36	0.02	1353.83	1.0	21/26	9
3909 - 3912, P5_20mM	R.CCQVHDNICYNEAEK.I	1827.96	-0.210	3	0	3.88	0.38	1268.66	4.0	26/52	9
4395 - 4398, P5_20mM	K.NM*IQCTVPNR.S	1249.45	-0.934	2	0	3.17	0.33	1024.74	1.0	16/18	6
4425, P5_60mM	K.NM*IQCTVPNR.S	1249.45	-1.129	2	0	2.47	0.18	795.10	1.0	14/18	6
4431, P5_60mM	K.NM*IQCTVPNR.S	1249.45	-1.136	2	0	2.90	0.25	870.16	1.0	15/18	6
4686, P5_0mM	K.GDNDACAAAVCDCDR.L	1670.74	-2.314	2	0	4.19	0.01	1283.71	2.0	19/28	
4761 - 4764, P5_20mM	R.GGSGTPVDDLDR.C	1189.21	-0.841	2	0	2.74	0.21	523.22	24.0	16/22	35
4854, P5_0mM	R.GGSGTPVDDLDR.C	1189.21	-0.899	2	0	2.63	0.23	326.85	50.0	13/22	35
4929 - 4932, P5_60mM	K.TYSYEC SQGLTCK.G	1698.86	-1.299	2	0	4.57	0.45	2413.46	1.0	22/26	15
4971 - 4974, P5_20mM	K.TYSYEC SQGLTCK.G	1698.86	-1.163	2	0	5.00	0.44	2552.72	1.0	22/26	15
4986 - 4989, P5_20mM	K.TYSYEC SQGLTCK.G	1698.86	-1.162	2	0	4.22	0.29	2238.66	1.0	21/26	15
4995 - 5001, P5_60mM	K.NMIQCTVPNR.S	1233.45	-0.961	2	0	2.99	0.12	1159.69	1.0	16/18	6
5028, P5_60mM	K.NMIQCTVPNR.S	1233.45	-0.979	2	0	2.78	0.03	823.22	12.0	13/18	6
5034 - 5037, P5_80mM	K.TYSYEC SQGLTCK.G	1698.86	-1.363	2	0	4.83	0.42	2220.20	1.0	21/26	15
5058 - 5061, P5_20mM	K.NMIQCTVPNR.S	1233.45	-0.915	2	0	3.70	0.14	1245.61	2.0	16/18	6
5076 - 5079, P5_100mM	K.NMIQCTVPNR.S	1233.45	-0.973	2	0	3.34	0.21	800.17	4.0	13/18	6
5085 - 5088, P5_20mM	R.GGSGTPVDDLDR.C	1189.21	-0.725	1	0	2.41	0.27	246.51	3.0	39438	35
5097, P5_0mM	K.TYSYEC SQGLTCK.G	1698.86	-0.300	2	0	5.06	0.47	2221.61	1.0	21/26	15
5103, P5_80mM	K.NMIQCTVPNR.S	1233.45	-1.053	2	0	3.13	0.17	1053.84	2.0	15/18	6
5103 - 5106, P5_20mM	R.GGSGTPVDDLDR.C	1189.21	-0.781	2	0	3.55	0.28	587.43	1.0	18/22	35
5109, P5_0mM	K.TYSYEC SQGLTCK.G	1698.86	-0.307	2	0	5.05	0.43	2419.65	1.0	21/26	15
5109, P5_80mM	K.NMIQCTVPNR.S	1233.45	-1.011	2	0	3.47	0.28	1292.52	2.0	16/18	6
5148, P5_80mM	R.GGSGTPVDDLDR.C	1189.21	-0.820	2	0	2.70	0.16	326.14	60.0	15/22	35
5208 - 5211, P5_0mM	R.GGSGTPVDDLDR.C	1189.21	-0.720	2	0	3.31	0.34	602.88	1.0	18/22	35
5235, P5_0mM	R.GGSGTPVDDLDR.C	1189.21	-0.736	1	0	2.62	0.28	330.73	1.0	13/22	35
5244, P5_0mM	R.GGSGTPVDDLDR.C	1189.21	-0.733	1	0	1.97	0.26	262.91	5.0	39438	35
5256, P5_0mM	K.NMIQCTVPNR.S	1233.45	-0.977	2	0	2.26	0.03	315.35	46.0	14/18	6
5757 - 5760, P5_400mM	R.GGSGTPVDDLDR.C	1189.21	-0.844	2	0	2.82	0.32	438.41	3.0	16/22	35

Supplemental Table 6: Orthologous proteins of peptide sequences generated from ion-exchange chromatography-purified *N. kaouthia* venom protein components (P5) by 2D-LC/MS-MS and database search

Reference					P(pro)	Score	Coverage	MW	Accession	Peptide(Hits)	
Scan(s), File (salt concentration)	Peptides	MH+	ΔM	z	P(pep)	X_{corr}	ΔCn	Sp	RSp	Ions	Count
5772 - 5775, P5_200mM	K.TYSYEC SQGTLTCK.G	1698.86	-1.386	2	0	4.40	0.46	2345.55	1.0	22/26	15
5865 - 5868, P5_200mM	K.NMIQCTV PNR.S	1233.45	-1.058	2	0	3.34	0.15	1184.11	2.0	15/18	6
5913, P5_200mM	R.GGSGTPV DDLDR.C	1189.21	-0.777	2	0	2.24	0.10	587.62	1.0	18/22	35
6249 - 6252, P5_20mM	R.GGSGTPV DDLDR.C	1189.21	-0.760	2	0	2.14	0.13	374.20	65.0	14/22	35
6411 - 6414, P5_60mM	R.CWPYFK.T	901.07	-0.756	1	0	1.66	0.01	312.88	18.0	39304	5
6648 - 6651, P5_60mM	R.LAAICFAGAPYNNNNYNIDLK.A	2357.63	-1.197	2	0	5.38	0.11	1207.11	1.0	25/40	5
6654, P5_60mM	R.LAAICFAGAPYNNNNYNIDLK.A	2357.63	-0.925	3	0	6.33	0.11	2800.82	1.0	40/80	5
6663, P5_0mM	R.LAAICFAGAPYNNNNYNIDLK.A	2357.63	-1.049	3	0	4.20	0.03	1188.74	1.0	29/80	5
6663, P5_60mM	R.LAAICFAGAPYNNNNYNIDLK.A	2357.63	-0.862	3	0	6.28	0.08	2805.06	3.0	40/80	5
6690, P5_20mM	R.CWPYFK.T	901.07	-0.724	1	0	1.56	-	258.73	19.0	39304	5
6705, P5_100mM	R.LAAICFAGAPYNNNNYNIDLK.A	2357.63	-0.981	3	0	5.60	0.01	2104.04	1.0	36/80	5
6708 - 6711, P5_100mM	R.LAAICFAGAPYNNNNYNIDLK.A	2357.63	-1.273	2	0	5.93	0.08	1560.95	1.0	28/40	5
6714, P5_100mM	R.LAAICFAGAPYNNNNYNIDLK.A	2357.63	-1.886	3	0	5.49	0.01	2708.04	1.0	40/80	5
6753, P5_20mM	K.NMIQCTV PNR.S	1233.45	-0.018	2	0	2.59	0.14	809.67	1.0	14/18	6
6798, P5_80mM	R.LAAICFAGAPYNNNNYNIDLK.A	2357.63	-1.719	2	0	4.94	0.12	1303.05	1.0	25/40	5
6801, P5_80mM	R.LAAICFAGAPYNNNNYNIDLK.A	2357.63	-0.919	3	0	5.28	0.05	2516.87	1.0	39/80	5
6804, P5_80mM	R.LAAICFAGAPYNNNNYNIDLK.A	2357.63	-1.674	2	0	5.59	0.09	1389.76	1.0	26/40	5
6807, P5_80mM	R.LAAICFAGAPYNNNNYNIDLK.A	2357.63	-0.871	3	0	6.38	0.09	2365.52	2.0	41/80	5
6939 - 6942, P5_20mM	R.LAAICFAGAPYNNNNYNIDLK.A	2357.63	-0.837	3	0	4.53	0.14	2099.96	1.0	38/80	5
6990, P5_20mM	R.LAAICFAGAPYNNNNYNIDLK.A	2357.63	0.247	2	0	4.61	-	1154.92	2.0	24/40	5
7383 - 7386, P5_20mM	R.GGSGTPV DDLDR.C	1189.21	-0.862	2	1	2.17	0.09	358.11	72.0	14/22	35
7545, P5_400mM	R.LAAICFAGAPYNNNNYNIDLK.A	2357.63	-1.825	3	0	5.96	0.09	2604.56	1.0	39/80	5
7548 - 7551, P5_400mM	R.LAAICFAGAPYNNNNYNIDLK.A	2357.63	-1.132	2	0	5.44	0.06	1270.85	4.0	26/40	5
7560, P5_200mM	R.LAAICFAGAPYNNNNYNIDLK.A	2357.63	-0.793	2	0	5.57	0.06	1453.59	1.0	26/40	5
7563, P5_200mM	R.LAAICFAGAPYNNNNYNIDLK.A	2357.63	-0.981	3	0	5.70	0.06	2260.52	1.0	39/80	5
7566, P5_200mM	R.LAAICFAGAPYNNNNYNIDLK.A	2357.63	-1.679	2	0	5.48	0.05	1438.17	1.0	26/40	5
7590, P5_200mM	R.LAAICFAGAPYNNNNYNIDLK.A	2357.63	1.202	2	0	4.87	-	1117.29	5.0	25/40	5
7596, P5_200mM	R.LAAICFAGAPYNNNNYNIDLK.A	2357.63	1.246	2	0	4.72	-	1252.99	2.0	24/40	5
7752, P5_20mM	R.GGSGTPV DDLDR.C	1189.21	-0.903	2	0	2.95	0.35	374.32	41.0	15/22	35
8634, P5_400mM	R.SWDFADYGCYCGR.G	1843.98	-1.544	2	0	4.12	0.25	1773.88	1.0	20/26	15

Supplemental Table 6: Orthologous proteins of peptide sequences generated from ion-exchange chromatography-purified *N. kaouthia* venom protein components (P5) by 2D-LC/MS-MS and database search

Reference					P(pro)	Score	Coverage	MW	Accession	Peptide(Hits)	
Scan(s), File (salt concentration)	Peptides	MH+	ΔM	z	P(pep)	X_{corr}	ΔCn	Sp	RSp	Ions	Count
3. PSNJ2K phospholipase A2 (EC 3.1.1.4) II - monocled cobra					0	86.32		13454.95	67172.0	59 (37 14 2 2 4)	
3792 - 3795, P5_20mM	R.CCQVHDNICYDEAEK.I	1828.94	-2.372	2	0	5.28	0.39	1188.48	2.0	20/26	1
3909 - 3912, P5_20mM	R.CCQVHDNICYDEAEK.I	1828.94	-1.195	3	0	4.47	0.05	1678.98	1.0	28/52	1
4395 - 4398, P5_20mM	K.NM*IQCTVPNR.S	1249.45	-0.934	2	0	3.17	0.33	1024.74	1.0	16/18	6
4425, P5_60mM	K.NM*IQCTVPNR.S	1249.45	-1.129	2	0	2.47	0.18	795.10	1.0	14/18	6
4431, P5_60mM	K.NM*IQCTVPNR.S	1249.45	-1.136	2	0	2.90	0.25	870.16	1.0	15/18	6
4659, P5_0mM	K.NGNNACAAAVCDCDR.L	1668.78	-1.338	2	0	3.80	0.35	852.53	1.0	16/28	
4686, P5_0mM	K.NGNNACAAAVCDCDR.L	1668.78	-0.345	2	0	4.15	0.38	1334.52	1.0	19/28	
4761 - 4764, P5_20mM	R.GGSGTPVDDLDR.C	1189.21	-0.841	2	0	2.74	0.21	523.22	24.0	16/22	35
4854, P5_0mM	R.GGSGTPVDDLDR.C	1189.21	-0.899	2	0	2.63	0.23	326.85	50.0	13/22	35
4929 - 4932, P5_60mM	K.TYSYEC SQGLTCK.G	1698.86	-1.299	2	0	4.57	0.45	2413.46	1.0	22/26	15
4971 - 4974, P5_20mM	K.TYSYEC SQGLTCK.G	1698.86	-1.163	2	0	5.00	0.44	2552.72	1.0	22/26	15
4986 - 4989, P5_20mM	K.TYSYEC SQGLTCK.G	1698.86	-1.162	2	0	4.22	0.29	2238.66	1.0	21/26	15
4995 - 5001, P5_60mM	K.NMIQCTVPNR.S	1233.45	-0.961	2	0	2.99	0.12	1159.69	1.0	16/18	6
5028, P5_60mM	K.NMIQCTVPNR.S	1233.45	-0.979	2	0	2.78	0.03	823.22	12.0	13/18	6
5034 - 5037, P5_80mM	K.TYSYEC SQGLTCK.G	1698.86	-1.363	2	0	4.83	0.42	2220.20	1.0	21/26	15
5058 - 5061, P5_20mM	K.NMIQCTVPNR.S	1233.45	-0.915	2	0	3.70	0.14	1245.61	2.0	16/18	6
5076 - 5079, P5_100mM	K.NMIQCTVPNR.S	1233.45	-0.973	2	0	3.34	0.21	800.17	4.0	13/18	6
5085 - 5088, P5_20mM	R.GGSGTPVDDLDR.C	1189.21	-0.725	1	0	2.41	0.27	246.51	3.0	39438	35
5097, P5_0mM	K.TYSYEC SQGLTCK.G	1698.86	-0.300	2	0	5.06	0.47	2221.61	1.0	21/26	15
5103, P5_80mM	K.NMIQCTVPNR.S	1233.45	-1.053	2	0	3.13	0.17	1053.84	2.0	15/18	6
5103 - 5106, P5_20mM	R.GGSGTPVDDLDR.C	1189.21	-0.781	2	0	3.55	0.28	587.43	1.0	18/22	35
5109, P5_0mM	K.TYSYEC SQGLTCK.G	1698.86	-0.307	2	0	5.05	0.43	2419.65	1.0	21/26	15
5109, P5_80mM	K.NMIQCTVPNR.S	1233.45	-1.011	2	0	3.47	0.28	1292.52	2.0	16/18	6
5148, P5_80mM	R.GGSGTPVDDLDR.C	1189.21	-0.820	2	0	2.70	0.16	326.14	60.0	15/22	35
5208 - 5211, P5_0mM	R.GGSGTPVDDLDR.C	1189.21	-0.720	2	0	3.31	0.34	602.88	1.0	18/22	35
5235, P5_0mM	R.GGSGTPVDDLDR.C	1189.21	-0.736	1	0	2.62	0.28	330.73	1.0	13/22	35
5244, P5_0mM	R.GGSGTPVDDLDR.C	1189.21	-0.733	1	0	1.97	0.26	262.91	5.0	39438	35
5256, P5_0mM	K.NMIQCTVPNR.S	1233.45	-0.977	2	0	2.26	0.03	315.35	46.0	14/18	6
5757 - 5760, P5_400mM	R.GGSGTPVDDLDR.C	1189.21	-0.844	2	0	2.82	0.32	438.41	3.0	16/22	35

Supplemental Table 6: Orthologous proteins of peptide sequences generated from ion-exchange chromatography-purified *N. kaouthia* venom protein components (P5) by 2D-LC/MS-MS and database search

Reference					P(pro)	Score	Coverage	MW	Accession	Peptide(Hits)	
Scan(s), File (salt concentration)	Peptides	MH+	ΔM	z	P(pep)	X_{corr}	ΔCn	Sp	RSp	Ions	Count
5772 - 5775, P5_200mM	K.TYSYECSQGLTCK.G	1698.86	-1.386	2	0	4.40	0.46	2345.55	1.0	22/26	15
5865 - 5868, P5_200mM	K.NMIQCTVPNR.S	1233.45	-1.058	2	0	3.34	0.15	1184.11	2.0	15/18	6
5913, P5_200mM	R.GGSGTPVDDLDR.C	1189.21	-0.777	2	0	2.24	0.10	587.62	1.0	18/22	35
6249 - 6252, P5_20mM	R.GGSGTPVDDLDR.C	1189.21	-0.760	2	0	2.14	0.13	374.20	65.0	14/22	35
6411 - 6414, P5_60mM	R.CWPYFK.T	901.07	-0.756	1	0	1.66	0.01	312.88	18.0	39304	5
6648 - 6651, P5_60mM	R.LAAICFAGAPYNNNNYNIDLK.A	2357.63	-1.197	2	0	5.38	0.11	1207.11	1.0	25/40	5
6654, P5_60mM	R.LAAICFAGAPYNNNNYNIDLK.A	2357.63	-0.925	3	0	6.33	0.11	2800.82	1.0	40/80	5
6663, P5_0mM	R.LAAICFAGAPYNNNNYNIDLK.A	2357.63	-1.049	3	0	4.20	0.03	1188.74	1.0	29/80	5
6663, P5_60mM	R.LAAICFAGAPYNNNNYNIDLK.A	2357.63	-0.862	3	0	6.28	0.08	2805.06	3.0	40/80	5
6690, P5_20mM	R.CWPYFK.T	901.07	-0.724	1	0	1.56	-	258.73	19.0	39304	5
6705, P5_100mM	R.LAAICFAGAPYNNNNYNIDLK.A	2357.63	-0.981	3	0	5.60	0.01	2104.04	1.0	36/80	5
6708 - 6711, P5_100mM	R.LAAICFAGAPYNNNNYNIDLK.A	2357.63	-1.273	2	0	5.93	0.08	1560.95	1.0	28/40	5
6714, P5_100mM	R.LAAICFAGAPYNNNNYNIDLK.A	2357.63	-1.886	3	0	5.49	0.01	2708.04	1.0	40/80	5
6753, P5_20mM	K.NMIQCTVPNR.S	1233.45	-0.018	2	0	2.59	0.14	809.67	1.0	14/18	6
6798, P5_80mM	R.LAAICFAGAPYNNNNYNIDLK.A	2357.63	-1.719	2	0	4.94	0.12	1303.05	1.0	25/40	5
6801, P5_80mM	R.LAAICFAGAPYNNNNYNIDLK.A	2357.63	-0.919	3	0	5.28	0.05	2516.87	1.0	39/80	5
6804, P5_80mM	R.LAAICFAGAPYNNNNYNIDLK.A	2357.63	-1.674	2	0	5.59	0.09	1389.76	1.0	26/40	5
6807, P5_80mM	R.LAAICFAGAPYNNNNYNIDLK.A	2357.63	-0.871	3	0	6.38	0.09	2365.52	2.0	41/80	5
6939 - 6942, P5_20mM	R.LAAICFAGAPYNNNNYNIDLK.A	2357.63	-0.837	3	0	4.53	0.14	2099.96	1.0	38/80	5
6990, P5_20mM	R.LAAICFAGAPYNNNNYNIDLK.A	2357.63	0.247	2	0	4.61	-	1154.92	2.0	24/40	5
7383 - 7386, P5_20mM	R.GGSGTPVDDLDR.C	1189.21	-0.862	2	1	2.17	0.09	358.11	72.0	14/22	35
7545, P5_400mM	R.LAAICFAGAPYNNNNYNIDLK.A	2357.63	-1.825	3	0	5.96	0.09	2604.56	1.0	39/80	5
7548 - 7551, P5_400mM	R.LAAICFAGAPYNNNNYNIDLK.A	2357.63	-1.132	2	0	5.44	0.06	1270.85	4.0	26/40	5
7560, P5_200mM	R.LAAICFAGAPYNNNNYNIDLK.A	2357.63	-0.793	2	0	5.57	0.06	1453.59	1.0	26/40	5
7563, P5_200mM	R.LAAICFAGAPYNNNNYNIDLK.A	2357.63	-0.981	3	0	5.70	0.06	2260.52	1.0	39/80	5
7566, P5_200mM	R.LAAICFAGAPYNNNNYNIDLK.A	2357.63	-1.679	2	0	5.48	0.05	1438.17	1.0	26/40	5
7590, P5_200mM	R.LAAICFAGAPYNNNNYNIDLK.A	2357.63	1.202	2	0	4.87	-	1117.29	5.0	25/40	5
7596, P5_200mM	R.LAAICFAGAPYNNNNYNIDLK.A	2357.63	1.246	2	0	4.72	-	1252.99	2.0	24/40	5
7752, P5_20mM	R.GGSGTPVDDLDR.C	1189.21	-0.903	2	0	2.95	0.35	374.32	41.0	15/22	35
8634, P5_400mM	R.SWDFADYGCYCGR.G	1843.98	-1.544	2	0	4.12	0.25	1773.88	1.0	20/26	15

Supplemental Table 6: Orthologous proteins of peptide sequences generated from ion-exchange chromatography-purified *N. kaouthia* venom protein components (P5) by 2D-LC/MS-MS and database search

Reference					P(pro)	Score	Coverage	MW	Accession	Peptide(Hits)	
Scan(s), File (salt concentration)	Peptides	MH+	ΔM	z	P(pep)	X_{corr}	ΔCn	Sp	RSp	Ions	Count
4. PA21_NAJAT Phospholipase A2 1 precursor (Phosphatidylcholine 2-acylhydrolase)					0	86.32		16013.10	464331.0	64 (37 17 3 4 3)	
3792 - 3795, P5_20mM	R.CCQVHDNICYNEAEK.I	1827.96	-1.387	2	0	5.36	0.02	1353.83	1.0	21/26	9
3909 - 3912, P5_20mM	R.CCQVHDNICYNEAEK.I	1827.96	-0.210	3	0	3.88	0.38	1268.66	4.0	26/52	9
4149 - 4152, P5_20mM	K.GGNNACAAAVCDCDR.L	1611.72	-1.095	2	0	4.62	0.06	1858.79	1.0	22/28	9
4263 - 4266, P5_20mM	K.GGNNACAAAVCDCDR.L	1611.72	-0.150	2	0	3.20	0.43	1699.10	2.0	21/28	9
4461 - 4464, P5_20mM	K.NM*IQCTVPSR.S	1222.42	0.091	2	0	3.52	0.03	1222.83	1.0	16/18	12
4635, P5_0mM	K.GGNNACAAAVCDCDR.L	1611.72	-1.367	2	0	4.72	0.08	1610.32	1.0	20/28	9
4641, P5_0mM	K.GGNNACAAAVCDCDR.L	1611.72	-1.291	2	0	4.29	0.05	1656.74	1.0	20/28	9
4677, P5_0mM	K.GGNNACAAAVCDCDR.L	1611.72	-0.289	2	0	4.04	0.43	2056.21	1.0	22/28	9
4683, P5_0mM	K.GGNNACAAAVCDCDR.L	1611.72	1.668	2	0	3.33	0.45	1609.92	2.0	20/28	9
4761 - 4764, P5_20mM	R.GGSGTPVDDLDR.C	1189.21	-0.841	2	0	2.74	0.21	523.22	24.0	16/22	35
4854, P5_0mM	R.GGSGTPVDDLDR.C	1189.21	-0.899	2	0	2.63	0.23	326.85	50.0	13/22	35
4929 - 4932, P5_60mM	K.TYSYEC SQGLTCK.G	1698.86	-1.299	2	0	4.57	0.45	2413.46	1.0	22/26	15
4971 - 4974, P5_20mM	K.TYSYEC SQGLTCK.G	1698.86	-1.163	2	0	5.00	0.44	2552.72	1.0	22/26	15
4986 - 4989, P5_20mM	K.TYSYEC SQGLTCK.G	1698.86	-1.162	2	0	4.22	0.29	2238.66	1.0	21/26	15
5034 - 5037, P5_80mM	K.TYSYEC SQGLTCK.G	1698.86	-1.363	2	0	4.83	0.42	2220.20	1.0	21/26	15
5058, P5_60mM	K.NMIQCTVPSR.S	1206.42	-1.027	2	0	2.98	0.01	1167.82	2.0	16/18	12
5085 - 5088, P5_20mM	R.GGSGTPVDDLDR.C	1189.21	-0.725	1	0	2.41	0.27	246.51	3.0	39438	35
5097, P5_0mM	K.TYSYEC SQGLTCK.G	1698.86	-0.300	2	0	5.06	0.47	2221.61	1.0	21/26	15
5103 - 5106, P5_20mM	R.GGSGTPVDDLDR.C	1189.21	-0.781	2	0	3.55	0.28	587.43	1.0	18/22	35
5109, P5_0mM	K.TYSYEC SQGLTCK.G	1698.86	-0.307	2	0	5.05	0.43	2419.65	1.0	21/26	15
5124, P5_100mM	K.NMIQCTVPSR.S	1206.42	-1.070	2	0	2.18	0.14	576.51	33.0	39434	12
5124 - 5127, P5_20mM	K.NMIQCTVPSR.S	1206.42	-0.948	2	0	2.86	0.00	1221.15	3.0	16/18	12
5148, P5_80mM	R.GGSGTPVDDLDR.C	1189.21	-0.820	2	0	2.70	0.16	326.14	60.0	15/22	35
5169, P5_80mM	K.NMIQCTVPSR.S	1206.42	-1.032	2	0	2.68	0.07	1037.93	3.0	15/18	12
5208 - 5211, P5_0mM	R.GGSGTPVDDLDR.C	1189.21	-0.720	2	0	3.31	0.34	602.88	1.0	18/22	35
5235, P5_0mM	R.GGSGTPVDDLDR.C	1189.21	-0.736	1	0	2.62	0.28	330.73	1.0	13/22	35
5244, P5_0mM	R.GGSGTPVDDLDR.C	1189.21	-0.733	1	0	1.97	0.26	262.91	5.0	39438	35
5757 - 5760, P5_400mM	R.GGSGTPVDDLDR.C	1189.21	-0.844	2	0	2.82	0.32	438.41	3.0	16/22	35
5772 - 5775, P5_200mM	K.TYSYEC SQGLTCK.G	1698.86	-1.386	2	0	4.40	0.46	2345.55	1.0	22/26	15

Supplemental Table 6: Orthologous proteins of peptide sequences generated from ion-exchange chromatography-purified *N. kaouthia* venom protein components (P5) by 2D-LC/MS-MS and database search

Reference					P(pro)	Score	Coverage	MW	Accession	Peptide(Hits)	
Scan(s), File (salt concentration)	Peptides	MH+	ΔM	z	P(pep)	X_{corr}	ΔCn	Sp	RSp	Ions	Count
5913, P5_200mM	R.GGSGTPVDDLDR.C	1189.21	-0.777	2	0	2.24	0.10	587.62	1.0	18/22	35
5919 - 5922, P5_200mM	K.NMIQCTVPSR.S	1206.42	-1.052	2	0	2.18	0.07	769.71	28.0	13/18	12
6051, P5_20mM	K.NMIQCTVPSR.S	1206.42	1.676	2	0	2.21	0.04	606.31	62.0	39434	12
6249 - 6252, P5_20mM	R.GGSGTPVDDLDR.C	1189.21	-0.760	2	0	2.14	0.13	374.20	65.0	14/22	35
6552 - 6555, P5_60mM	K.ISGCWPYFK.T	1158.35	-1.004	2	0	3.41	0.36	924.26	1.0	14/16	8
6648 - 6651, P5_60mM	R.LAAICFAGAPYNNNNYNIDLK.A	2357.63	-1.197	2	0	5.38	0.11	1207.11	1.0	25/40	5
6654, P5_60mM	R.LAAICFAGAPYNNNNYNIDLK.A	2357.63	-0.925	3	0	6.33	0.11	2800.82	1.0	40/80	5
6663, P5_0mM	R.LAAICFAGAPYNNNNYNIDLK.A	2357.63	-1.049	3	0	4.20	0.03	1188.74	1.0	29/80	5
6663, P5_60mM	R.LAAICFAGAPYNNNNYNIDLK.A	2357.63	-0.862	3	0	6.28	0.08	2805.06	3.0	40/80	5
6705, P5_100mM	R.LAAICFAGAPYNNNNYNIDLK.A	2357.63	-0.981	3	0	5.60	0.01	2104.04	1.0	36/80	5
6708 - 6711, P5_100mM	R.LAAICFAGAPYNNNNYNIDLK.A	2357.63	-1.273	2	0	5.93	0.08	1560.95	1.0	28/40	5
6714, P5_100mM	R.LAAICFAGAPYNNNNYNIDLK.A	2357.63	-1.886	3	0	5.49	0.01	2708.04	1.0	40/80	5
6723 - 6726, P5_80mM	K.ISGCWPYFK.T	1158.35	-0.961	2	0	3.62	0.29	826.82	1.0	13/16	8
6795, P5_20mM	K.ISGCWPYFK.T	1158.35	-0.924	2	0	3.22	0.12	968.86	1.0	14/16	8
6798, P5_80mM	R.LAAICFAGAPYNNNNYNIDLK.A	2357.63	-1.719	2	0	4.94	0.12	1303.05	1.0	25/40	5
6801, P5_20mM	K.ISGCWPYFK.T	1158.35	-0.884	2	0	3.18	0.11	712.92	1.0	39432	8
6801, P5_80mM	R.LAAICFAGAPYNNNNYNIDLK.A	2357.63	-0.919	3	0	5.28	0.05	2516.87	1.0	39/80	5
6804, P5_80mM	R.LAAICFAGAPYNNNNYNIDLK.A	2357.63	-1.674	2	0	5.59	0.09	1389.76	1.0	26/40	5
6807, P5_80mM	R.LAAICFAGAPYNNNNYNIDLK.A	2357.63	-0.871	3	0	6.38	0.09	2365.52	2.0	41/80	5
6864, P5_20mM	K.ISGCWPYFK.T	1158.35	-0.802	2	0	3.00	0.08	950.52	1.0	14/16	8
6927, P5_20mM	K.ISGCWPYFK.T	1158.35	-0.878	2	0	3.30	0.16	916.44	1.0	14/16	8
6939 - 6942, P5_20mM	R.LAAICFAGAPYNNNNYNIDLK.A	2357.63	-0.837	3	0	4.53	0.14	2099.96	1.0	38/80	5
6990, P5_20mM	R.LAAICFAGAPYNNNNYNIDLK.A	2357.63	0.247	2	0	4.61	-	1154.92	2.0	24/40	5
7161, P5_20mM	K.ISGCWPYFK.T	1158.35	-0.960	2	0	2.72	0.22	725.65	2.0	39432	8
7176, P5_20mM	K.ISGCWPYFK.T	1158.35	-1.041	2	0	2.89	0.12	887.36	1.0	13/16	8
7383 - 7386, P5_20mM	R.GGSGTPVDDLDR.C	1189.21	-0.862	2	1	2.17	0.09	358.11	72.0	14/22	35
7545, P5_400mM	R.LAAICFAGAPYNNNNYNIDLK.A	2357.63	-1.825	3	0	5.96	0.09	2604.56	1.0	39/80	5
7548 - 7551, P5_400mM	R.LAAICFAGAPYNNNNYNIDLK.A	2357.63	-1.132	2	0	5.44	0.06	1270.85	4.0	26/40	5
7560, P5_200mM	R.LAAICFAGAPYNNNNYNIDLK.A	2357.63	-0.793	2	0	5.57	0.06	1453.59	1.0	26/40	5
7563, P5_200mM	R.LAAICFAGAPYNNNNYNIDLK.A	2357.63	-0.981	3	0	5.70	0.06	2260.52	1.0	39/80	5

Supplemental Table 6: Orthologous proteins of peptide sequences generated from ion-exchange chromatography-purified *N. kaouthia* venom protein components (P5) by 2D-LC/MS-MS and database search

Reference					P(pro)	Score	Coverage	MW	Accession	Peptide(Hits)	
Scan(s), File (salt concentration)	Peptides	MH+	ΔM	z	P(pep)	X_{corr}	ΔCn	Sp	RSp	Ions	Count
7566, P5_200mM	R.LAAICFAGAPYNNNNYNIDLK.A	2357.63	-1.679	2	0	5.48	0.05	1438.17	1.0	26/40	5
7590, P5_200mM	R.LAAICFAGAPYNNNNYNIDLK.A	2357.63	1.202	2	0	4.87	-	1117.29	5.0	25/40	5
7596, P5_200mM	R.LAAICFAGAPYNNNNYNIDLK.A	2357.63	1.246	2	0	4.72	-	1252.99	2.0	24/40	5
7752, P5_20mM	R.GSGTTPVDDLDR.C	1189.21	-0.903	2	0	2.95	0.35	374.32	41.0	15/22	35
8634, P5_400mM	R.SWWDFADYGCYCGR.G	1843.98	-1.544	2	0	4.12	0.25	1773.88	1.0	20/26	15
5. CO3_NAJNA Complement C3 precursor					0	86.17		184925.00	399269.0	14 (13 0 1 0 0)	
4572 - 4575, P5_60mM	K.IKLEGDPGAR.V	1056.20	-0.704	2	0	2.81	0.12	505.99	77.0	13/18	6
4650, P5_60mM	R.KCQEALNLK.L	1104.31	-0.833	2	0	2.47	0.17	668.28	58.0	39432	5
4656, P5_60mM	R.KCQEALNLK.L	1104.31	-0.835	2	0	2.93	0.14	781.74	10.0	13/16	5
4803, P5_60mM	K.VSHSEDECLHFK.I	1488.61	-1.058	3	0	3.05	0.31	519.04	85.0	18/44	1
4809, P5_60mM	K.VSHSEDECLHFK.I	1488.61	-1.186	3	0	2.54	0.02	879.57	11.0	21/44	1
5292 - 5295, P5_20mM	R.VGLVAVDK.A	800.97	-0.474	2	0	2.89	0.10	1166.81	1.0	13/14	29
5331, P5_20mM	K.AVYVLNDK.Y	922.06	-0.664	2	0	2.81	0.07	670.84	4.0	13/14	6
5646 - 5649, P5_80mM	R.TDTEEQILVEAHGDSTPK.S	1971.07	-1.417	3	0	3.03	0.01	611.49	22.0	25/68	1
5811, P5_20mM	K.IWDTIEK.S	905.03	2.327	2	0	2.14	0.00	542.07	8.0	39398	8
5820, P5_20mM	K.IWDTIEK.S	905.03	2.283	2	0	2.22	0.00	565.63	9.0	39398	8
5874, P5_20mM	R.TDTEEQILVEAHGDSTPK.S	1971.07	-1.187	3	0	3.30	0.28	669.52	3.0	26/68	1
5880, P5_20mM	R.TDTEEQILVEAHGDSTPK.S	1971.07	-1.239	3	0	2.75	0.09	957.97	1.0	29/68	1
6276, P5_80mM	K.HFEVGFIQGSVK.V	1445.65	-1.243	3	0	2.93	0.03	873.86	50.0	24/48	4
6954 - 6957, P5_60mM	K.YFTYLILNK.G	1175.40	-0.946	2	0	2.70	0.26	773.51	2.0	13/16	1
6. Phospholipase A2 (E.C.3.1.1.4)					0	82.32		13143.61	443186.0	70 (34 12 14 10 0)	
3792 - 3795, P5_20mM	R.CCQVHDNICYNEAEK.I	1827.96	-1.387	2	0	5.36	0.02	1353.83	1.0	21/26	9
3909 - 3912, P5_20mM	R.CCQVHDNICYNEAEK.I	1827.96	-0.210	3	0	3.88	0.38	1268.66	4.0	26/52	9
4149 - 4152, P5_20mM	K.GGNNACAAAVCDCLR.L	1611.72	-1.095	2	0	4.62	0.06	1858.79	1.0	22/28	9
4263 - 4266, P5_20mM	K.GGNNACAAAVCDCLR.L	1611.72	-0.150	2	0	3.20	0.43	1699.10	2.0	21/28	9
4461 - 4464, P5_20mM	K.NM*IQCTVPSR.S	1222.42	0.091	2	0	3.52	0.03	1222.83	1.0	16/18	12
4635, P5_0mM	K.GGNNACAAAVCDCLR.L	1611.72	-1.367	2	0	4.72	0.08	1610.32	1.0	20/28	9
4641, P5_0mM	K.GGNNACAAAVCDCLR.L	1611.72	-1.291	2	0	4.29	0.05	1656.74	1.0	20/28	9
4677, P5_0mM	K.GGNNACAAAVCDCLR.L	1611.72	-0.289	2	0	4.04	0.43	2056.21	1.0	22/28	9
4683, P5_0mM	K.GGNNACAAAVCDCLR.L	1611.72	1.668	2	0	3.33	0.45	1609.92	2.0	20/28	9

Supplemental Table 6: Orthologous proteins of peptide sequences generated from ion-exchange chromatography-purified *N. kaouthia* venom protein components (P5) by 2D-LC/MS-MS and database search

Reference					P(pro)	Score	Coverage	MW	Accession	Peptide(Hits)	
Scan(s), File (salt concentration)	Peptides	MH+	ΔM	z	P(pep)	X_{corr}	ΔCn	Sp	RSp	Ions	Count
4761 - 4764, P5_20mM	R.GGSGTPVDDLDR.C	1189.21	-0.841	2	0	2.74	0.21	523.22	24.0	16/22	35
4854, P5_0mM	R.GGSGTPVDDLDR.C	1189.21	-0.899	2	0	2.63	0.23	326.85	50.0	13/22	35
4929 - 4932, P5_60mM	K.TYSYECSQGTLTCK.G	1698.86	-1.299	2	0	4.57	0.45	2413.46	1.0	22/26	15
4971 - 4974, P5_20mM	K.TYSYECSQGTLTCK.G	1698.86	-1.163	2	0	5.00	0.44	2552.72	1.0	22/26	15
4986 - 4989, P5_20mM	K.TYSYECSQGTLTCK.G	1698.86	-1.162	2	0	4.22	0.29	2238.66	1.0	21/26	15
5034 - 5037, P5_80mM	K.TYSYECSQGTLTCK.G	1698.86	-1.363	2	0	4.83	0.42	2220.20	1.0	21/26	15
5058, P5_60mM	K.NMIQCTVPSR.S	1206.42	-1.027	2	0	2.98	0.01	1167.82	2.0	16/18	12
5085 - 5088, P5_20mM	R.GGSGTPVDDLDR.C	1189.21	-0.725	1	0	2.41	0.27	246.51	3.0	39438	35
5097, P5_0mM	K.TYSYECSQGTLTCK.G	1698.86	-0.300	2	0	5.06	0.47	2221.61	1.0	21/26	15
5103 - 5106, P5_20mM	R.GGSGTPVDDLDR.C	1189.21	-0.781	2	0	3.55	0.28	587.43	1.0	18/22	35
5109, P5_0mM	K.TYSYECSQGTLTCK.G	1698.86	-0.307	2	0	5.05	0.43	2419.65	1.0	21/26	15
5124, P5_100mM	K.NMIQCTVPSR.S	1206.42	-1.070	2	0	2.18	0.14	576.51	33.0	39434	12
5124 - 5127, P5_20mM	K.NMIQCTVPSR.S	1206.42	-0.948	2	0	2.86	0.00	1221.15	3.0	16/18	12
5148, P5_80mM	R.GGSGTPVDDLDR.C	1189.21	-0.820	2	0	2.70	0.16	326.14	60.0	15/22	35
5169, P5_80mM	K.NMIQCTVPSR.S	1206.42	-1.032	2	0	2.68	0.07	1037.93	3.0	15/18	12
5208 - 5211, P5_0mM	R.GGSGTPVDDLDR.C	1189.21	-0.720	2	0	3.31	0.34	602.88	1.0	18/22	35
5235, P5_0mM	R.GGSGTPVDDLDR.C	1189.21	-0.736	1	0	2.62	0.28	330.73	1.0	13/22	35
5244, P5_0mM	R.GGSGTPVDDLDR.C	1189.21	-0.733	1	0	1.97	0.26	262.91	5.0	39438	35
5757 - 5760, P5_400mM	R.GGSGTPVDDLDR.C	1189.21	-0.844	2	0	2.82	0.32	438.41	3.0	16/22	35
5772 - 5775, P5_200mM	K.TYSYECSQGTLTCK.G	1698.86	-1.386	2	0	4.40	0.46	2345.55	1.0	22/26	15
5913, P5_200mM	R.GGSGTPVDDLDR.C	1189.21	-0.777	2	0	2.24	0.10	587.62	1.0	18/22	35
5919 - 5922, P5_200mM	K.NMIQCTVPSR.S	1206.42	-1.052	2	0	2.18	0.07	769.71	28.0	13/18	12
6051, P5_20mM	K.NMIQCTVPSR.S	1206.42	1.676	2	0	2.21	0.04	606.31	62.0	39434	12
6249 - 6252, P5_20mM	R.GGSGTPVDDLDR.C	1189.21	-0.760	2	0	2.14	0.13	374.20	65.0	14/22	35
6552 - 6555, P5_60mM	K.ISGCWPYFK.T	1158.35	-1.004	2	0	3.41	0.36	924.26	1.0	14/16	8
6648 - 6651, P5_60mM	R.LAAICFAGAPYNDNDYNINLK.A	2358.61	-2.182	2	0	5.22	0.11	1140.46	2.0	24/40	
6654, P5_60mM	R.LAAICFAGAPYNDNDYNINLK.A	2358.61	-1.910	3	0	6.33	0.08	2800.82	1.0	40/80	
6663, P5_0mM	R.LAAICFAGAPYNDNDYNINLK.A	2358.61	-2.034	3	0	4.13	0.07	1040.46	4.0	27/80	
6663, P5_60mM	R.LAAICFAGAPYNDNDYNINLK.A	2358.61	-1.847	3	0	5.91	0.10	2807.38	2.0	40/80	
6705, P5_100mM	R.LAAICFAGAPYNDNDYNINLK.A	2358.61	-1.966	3	0	5.15	0.09	1919.70	2.0	35/80	

Supplemental Table 6: Orthologous proteins of peptide sequences generated from ion-exchange chromatography-purified *N. kaouthia* venom protein components (P5) by 2D-LC/MS-MS and database search

Reference					P(pro)	Score	Coverage	MW	Accession	Peptide(Hits)	
Scan(s), File (salt concentration)	Peptides	MH+	ΔM	z	P(pep)	X_{corr}	ΔCn	Sp	RSp	Ions	Count
6708 - 6711, P5_100mM	R.LAAICFAGAPYNDNDYNINLK.A	2358.61	-2.258	2	0	5.63	0.38	1448.82	2.0	27/40	
6714, P5_100mM	R.LAAICFAGAPYNDNDYNINLK.A	2358.61	-2.871	3	1	4.99	0.43	2282.13	3.0	38/80	
6723 - 6726, P5_80mM	K.ISGCWPYFK.T	1158.35	-0.961	2	0	3.62	0.29	826.82	1.0	13/16	8
6729, P5_100mM	R.LAAICFAGAPYNDNDYNINLK.A	2358.61	2.472	3	0	6.22	0.08	2590.66	1.0	40/80	
6735, P5_100mM	R.LAAICFAGAPYNDNDYNINLK.A	2358.61	2.159	2	0	6.04	0.32	1293.38	2.0	24/40	
6741, P5_100mM	R.LAAICFAGAPYNDNDYNINLK.A	2358.61	2.429	2	0	5.69	0.28	1279.75	2.0	24/40	
6753, P5_100mM	R.LAAICFAGAPYNDNDYNINLK.A	2358.61	2.564	3	0	5.85	0.30	2055.37	2.0	37/80	
6795, P5_20mM	K.ISGCWPYFK.T	1158.35	-0.924	2	0	3.22	0.12	968.86	1.0	14/16	8
6798, P5_80mM	R.LAAICFAGAPYNDNDYNINLK.A	2358.61	-2.704	2	0	5.09	0.10	1164.74	2.0	24/40	
6801, P5_20mM	K.ISGCWPYFK.T	1158.35	-0.884	2	0	3.18	0.11	712.92	1.0	39432	8
6801, P5_80mM	R.LAAICFAGAPYNDNDYNINLK.A	2358.61	-1.904	3	0	5.08	0.07	2308.18	2.0	38/80	
6804, P5_80mM	R.LAAICFAGAPYNDNDYNINLK.A	2358.61	-2.659	2	0	5.48	0.35	1177.18	2.0	24/40	
6807, P5_80mM	R.LAAICFAGAPYNDNDYNINLK.A	2358.61	-1.856	3	0	6.09	0.11	2331.07	3.0	41/80	
6864, P5_20mM	K.ISGCWPYFK.T	1158.35	-0.802	2	0	3.00	0.08	950.52	1.0	14/16	8
6867, P5_80mM	R.LAAICFAGAPYNDNDYNINLK.A	2358.61	2.130	2	0	5.90	0.13	1001.68	2.0	23/40	
6927, P5_20mM	K.ISGCWPYFK.T	1158.35	-0.878	2	0	3.30	0.16	916.44	1.0	14/16	8
6939 - 6942, P5_20mM	R.LAAICFAGAPYNDNDYNINLK.A	2358.61	-1.822	3	0	4.60	0.08	2099.96	1.0	38/80	
6990, P5_20mM	R.LAAICFAGAPYNDNDYNINLK.A	2358.61	-0.738	2	0	5.65	0.02	1154.92	2.0	24/40	
7161, P5_20mM	K.ISGCWPYFK.T	1158.35	-0.960	2	0	2.72	0.22	725.65	2.0	39432	8
7176, P5_20mM	K.ISGCWPYFK.T	1158.35	-1.041	2	0	2.89	0.12	887.36	1.0	13/16	8
7383 - 7386, P5_20mM	R.GSGTPVDDLDR.C	1189.21	-0.862	2	1	2.17	0.09	358.11	72.0	14/22	35
7545, P5_400mM	R.LAAICFAGAPYNDNDYNINLK.A	2358.61	-2.810	3	0	5.69	0.11	2392.98	2.0	38/80	
7548 - 7551, P5_400mM	R.LAAICFAGAPYNDNDYNINLK.A	2358.61	-2.117	2	0	5.29	0.36	1500.10	2.0	26/40	
7560, P5_200mM	R.LAAICFAGAPYNDNDYNINLK.A	2358.61	-1.777	2	0	5.00	0.24	1073.79	4.0	23/40	
7563, P5_200mM	R.LAAICFAGAPYNDNDYNINLK.A	2358.61	-1.966	3	0	5.13	0.15	1794.88	4.0	36/80	
7566, P5_200mM	R.LAAICFAGAPYNDNDYNINLK.A	2358.61	-2.664	2	0	4.94	0.41	1324.12	2.0	25/40	
7590, P5_200mM	R.LAAICFAGAPYNDNDYNINLK.A	2358.61	0.217	2	0	5.88	0.19	1183.86	4.0	24/40	
7596, P5_200mM	R.LAAICFAGAPYNDNDYNINLK.A	2358.61	0.261	2	0	5.63	0.16	1400.56	1.0	25/40	
7626 - 7629, P5_400mM	R.LAAICFAGAPYNDNDYNINLK.A	2358.61	2.353	2	0	5.48	0.12	1063.01	3.0	24/40	
7752, P5_20mM	R.GSGTPVDDLDR.C	1189.21	-0.903	2	0	2.95	0.35	374.32	41.0	15/22	35

Supplemental Table 6: Orthologous proteins of peptide sequences generated from ion-exchange chromatography-purified *N. kaouthia* venom protein components (P5) by 2D-LC/MS-MS and database search

Reference					P(pro)	Score	Coverage	MW	Accession	Peptide(Hits)	
Scan(s), File (salt concentration)	Peptides	MH+	ΔM	z	P(pep)	X_{corr}	ΔCn	Sp	RSp	Ions	Count
8634, P5_400mM	R.SWWDFADYGCYCGR.G	1843.98	-1.544	2	0	4.12	0.25	1773.88	1.0	20/26	15
7. A Chain A, Crystal Structure Of Natrin From Naja Atra Snake Venom					0	80.20		24953.96	71041970.0	13 (13 0 0 0 0)	
4677 - 4680, P5_20mM	-.NVDFNSESTR.R	1169.18	-0.771	2	0	3.09	0.08	559.15	3.0	15/18	3
4824 - 4827, P5_60mM	R.RVSPTASNMLK.M	1204.43	-0.873	2	0	3.13	0.12	1004.13	1.0	16/20	2
5121, P5_60mM	R.WANTCSLNHSPDNL.R.V	1785.92	-0.360	3	0	2.67	0.04	612.20	7.0	25/56	2
5181, P5_20mM	R.VSPTASNMLK.M	1048.24	-0.844	2	0	2.08	0.05	253.30	44.0	39434	2
5187, P5_20mM	R.VSPTASNMLK.M	1048.24	-0.803	2	0	2.06	0.26	257.31	98.0	13/18	2
5202, P5_60mM	K.QKEIVDLHNSLR.R	1452.64	-1.007	2	0	3.22	0.21	433.56	2.0	14/22	4
5211, P5_60mM	K.QKEIVDLHNSLR.R	1452.64	-0.925	2	0	3.23	0.29	522.04	1.0	15/22	4
5454 - 5457, P5_60mM	K.EIVDLHNSLR.R	1196.34	-0.806	2	0	3.28	0.15	545.87	1.0	16/18	4
5532, P5_20mM	K.LTNCDSLK.Q	1064.24	-0.728	2	0	2.48	0.13	441.93	22.0	39432	2
5622, P5_80mM	K.EIVDLHNSLR.R	1196.34	-0.946	2	0	2.30	0.10	300.02	24.0	13/18	4
5928 - 5931, P5_60mM	K.MEWYPEAASNAER.W	1554.67	-1.253	2	0	3.55	0.30	1000.26	1.0	20/24	3
5931, P5_20mM	K.EIVDLHNSLR.R	1196.34	-0.821	2	0	2.49	0.13	236.25	177.0	39434	4
6147 - 6150, P5_20mM	K.MEWYPEAASNAER.W	1554.67	-1.073	2	0	4.03	0.32	1182.43	1.0	21/24	3
8. PA2_NAJNA Phospholipase A2, acidic (Phosphatidylcholine 2-acylhydrolase)					0	76.35		13345.82	129514.0	66 (48 7 5 3 3)	
3792 - 3795, P5_20mM	R.CCQVHDNICYNEAEK.I	1827.96	-1.387	2	0	5.36	0.02	1353.83	1.0	21/26	9
3909 - 3912, P5_20mM	R.CCQVHDNICYNEAEK.I	1827.96	-0.210	3	0	3.88	0.38	1268.66	4.0	26/52	9
4461 - 4464, P5_20mM	K.NM*IKCTVPSR.S	1222.46	0.048	2	0	3.52	0.05	1222.83	1.0	16/18	3
4761 - 4764, P5_20mM	R.GSGTPVDDLDR.C	1189.21	-0.841	2	0	2.74	0.21	523.22	24.0	16/22	35
4854, P5_0mM	R.GSGTPVDDLDR.C	1189.21	-0.899	2	0	2.63	0.23	326.85	50.0	13/22	35
4929 - 4932, P5_60mM	K.TYSYECQGLTCK.G	1698.86	-1.299	2	0	4.57	0.45	2413.46	1.0	22/26	15
4971 - 4974, P5_20mM	K.TYSYECQGLTCK.G	1698.86	-1.163	2	0	5.00	0.44	2552.72	1.0	22/26	15
4986 - 4989, P5_20mM	K.TYSYECQGLTCK.G	1698.86	-1.162	2	0	4.22	0.29	2238.66	1.0	21/26	15
5034 - 5037, P5_80mM	K.TYSYECQGLTCK.G	1698.86	-1.363	2	0	4.83	0.42	2220.20	1.0	21/26	15
5058, P5_60mM	K.NMIKCTVPSR.S	1206.46	-1.071	2	0	2.98	0.10	1167.82	2.0	16/18	3
5085 - 5088, P5_20mM	R.GSGTPVDDLDR.C	1189.21	-0.725	1	0	2.41	0.27	246.51	3.0	39438	35
5097, P5_0mM	K.TYSYECQGLTCK.G	1698.86	-0.300	2	0	5.06	0.47	2221.61	1.0	21/26	15
5103 - 5106, P5_20mM	R.GSGTPVDDLDR.C	1189.21	-0.781	2	0	3.55	0.28	587.43	1.0	18/22	35
5109, P5_0mM	K.TYSYECQGLTCK.G	1698.86	-0.307	2	0	5.05	0.43	2419.65	1.0	21/26	15

Supplemental Table 6: Orthologous proteins of peptide sequences generated from ion-exchange chromatography-purified *N. kaouthia* venom protein components (P5) by 2D-LC/MS-MS and database search

Reference					P(pro)	Score	Coverage	MW	Accession	Peptide(Hits)	
Scan(s), File (salt concentration)	Peptides	MH+	ΔM	z	P(pep)	X_{corr}	ΔCn	Sp	RSp	Ions	Count
5124, P5_100mM	K.NMIKCTVPSR.S	1206.46	-1.113	2	0	2.18	0.15	576.51	33.0	39434	3
5124 - 5127, P5_20mM	K.NMIKCTVPSR.S	1206.46	-0.992	2	0	2.86	0.11	1221.15	3.0	16/18	3
5148, P5_80mM	R.GGSGTPVDDLDR.C	1189.21	-0.820	2	0	2.70	0.16	326.14	60.0	15/22	35
5169, P5_80mM	K.NMIKCTVPSR.S	1206.46	-1.075	2	0	2.68	0.16	1037.93	3.0	15/18	3
5208 - 5211, P5_0mM	R.GGSGTPVDDLDR.C	1189.21	-0.720	2	0	3.31	0.34	602.88	1.0	18/22	35
5235, P5_0mM	R.GGSGTPVDDLDR.C	1189.21	-0.736	1	0	2.62	0.28	330.73	1.0	13/22	35
5244, P5_0mM	R.GGSGTPVDDLDR.C	1189.21	-0.733	1	0	1.97	0.26	262.91	5.0	39438	35
5757 - 5760, P5_400mM	R.GGSGTPVDDLDR.C	1189.21	-0.844	2	0	2.82	0.32	438.41	3.0	16/22	35
5772 - 5775, P5_200mM	K.TYSYECSQGTLTCK.G	1698.86	-1.386	2	0	4.40	0.46	2345.55	1.0	22/26	15
5913, P5_200mM	R.GGSGTPVDDLDR.C	1189.21	-0.777	2	0	2.24	0.10	587.62	1.0	18/22	35
5919 - 5922, P5_200mM	K.NMIKCTVPSR.S	1206.46	-1.095	2	0	2.18	0.10	769.71	28.0	13/18	3
5994 - 5997, P5_20mM	-.NLYQFK.N	812.94	-0.623	2	0	2.01	-	367.04	2.0	39335	29
6051, P5_20mM	K.NMIKCTVPSR.S	1206.46	1.633	2	0	2.21	0.05	606.31	62.0	39434	3
6249 - 6252, P5_20mM	R.GGSGTPVDDLDR.C	1189.21	-0.760	2	0	2.14	0.13	374.20	65.0	14/22	35
6411, P5_20mM	-.NLYQFK.N	812.94	-0.575	1	0	2.02	-	326.31	8.0	39304	29
6552 - 6555, P5_60mM	K.ISGCWPYFK.T	1158.35	-1.004	2	0	3.41	0.36	924.26	1.0	14/16	8
6648 - 6651, P5_60mM	R.LAAICFAGAPYNDNNYNIDLK.A	2358.61	-2.182	2	0	5.87	0.08	1207.11	1.0	25/40	14
6654, P5_60mM	R.LAAICFAGAPYNDNNYNIDLK.A	2358.61	-1.910	3	0	6.90	0.08	2800.82	1.0	40/80	14
6663, P5_0mM	R.LAAICFAGAPYNDNNYNIDLK.A	2358.61	-2.034	3	0	4.26	0.01	1134.83	2.0	28/80	14
6663, P5_60mM	R.LAAICFAGAPYNDNNYNIDLK.A	2358.61	-1.847	3	0	6.40	0.02	2807.38	2.0	40/80	14
6705, P5_100mM	R.LAAICFAGAPYNDNNYNIDLK.A	2358.61	-1.966	3	0	5.57	0.07	1919.70	2.0	35/80	14
6708 - 6711, P5_100mM	R.LAAICFAGAPYNDNNYNIDLK.A	2358.61	-2.258	2	0	6.20	0.04	1560.95	1.0	28/40	14
6714, P5_100mM	R.LAAICFAGAPYNDNNYNIDLK.A	2358.61	-2.871	3	0	5.45	0.05	2282.13	3.0	38/80	14
6723 - 6726, P5_80mM	K.ISGCWPYFK.T	1158.35	-0.961	2	0	3.62	0.29	826.82	1.0	13/16	8
6729, P5_100mM	R.LAAICFAGAPYNDNNYNIDLK.A	2358.61	2.472	3	0	6.64	0.06	2590.66	1.0	40/80	14
6735, P5_100mM	R.LAAICFAGAPYNDNNYNIDLK.A	2358.61	2.159	2	0	6.08	0.07	1524.66	1.0	26/40	14
6741, P5_100mM	R.LAAICFAGAPYNDNNYNIDLK.A	2358.61	2.429	2	0	5.78	0.10	1508.78	1.0	26/40	14
6753, P5_100mM	R.LAAICFAGAPYNDNNYNIDLK.A	2358.61	2.564	3	0	6.04	0.08	2055.37	2.0	37/80	14
6795, P5_20mM	K.ISGCWPYFK.T	1158.35	-0.924	2	0	3.22	0.12	968.86	1.0	14/16	8
6798, P5_80mM	R.LAAICFAGAPYNDNNYNIDLK.A	2358.61	-2.704	2	0	5.51	0.08	1164.74	2.0	24/40	14

Supplemental Table 6: Orthologous proteins of peptide sequences generated from ion-exchange chromatography-purified *N. kaouthia* venom protein components (P5) by 2D-LC/MS-MS and database search

Reference					P(pro)	Score	Coverage	MW	Accession	Peptide(Hits)	
Scan(s), File (salt concentration)	Peptides	MH+	ΔM	z	P(pep)	X_{corr}	ΔCn	Sp	RSp	Ions	Count
6801, P5_20mM	K.ISGCWPYFK.T	1158.35	-0.884	2	0	3.18	0.11	712.92	1.0	39432	8
6801, P5_80mM	R.LAAICFAGAPYNDNNYNIDLK.A	2358.61	-1.904	3	0	5.37	0.02	2308.18	2.0	38/80	14
6804, P5_80mM	R.LAAICFAGAPYNDNNYNIDLK.A	2358.61	-2.659	2	0	6.04	0.07	1389.76	1.0	26/40	14
6807, P5_80mM	R.LAAICFAGAPYNDNNYNIDLK.A	2358.61	-1.856	3	0	6.67	0.04	2564.32	1.0	42/80	14
6864, P5_20mM	K.ISGCWPYFK.T	1158.35	-0.802	2	0	3.00	0.08	950.52	1.0	14/16	8
6867, P5_80mM	R.LAAICFAGAPYNDNNYNIDLK.A	2358.61	2.130	2	0	5.60	0.37	1001.68	2.0	23/40	14
6927, P5_20mM	K.ISGCWPYFK.T	1158.35	-0.878	2	0	3.30	0.16	916.44	1.0	14/16	8
6939 - 6942, P5_20mM	R.LAAICFAGAPYNDNNYNIDLK.A	2358.61	-1.822	3	0	4.94	0.07	2099.96	1.0	38/80	14
6990, P5_20mM	R.LAAICFAGAPYNDNNYNIDLK.A	2358.61	-0.738	2	0	5.74	0.02	1154.92	2.0	24/40	14
7161, P5_20mM	K.ISGCWPYFK.T	1158.35	-0.960	2	0	2.72	0.22	725.65	2.0	39432	8
7176, P5_20mM	K.ISGCWPYFK.T	1158.35	-1.041	2	0	2.89	0.12	887.36	1.0	13/16	8
7383 - 7386, P5_20mM	R.GSGTPVDDLDR.C	1189.21	-0.862	2	1	2.17	0.09	358.11	72.0	14/22	35
7545, P5_400mM	R.LAAICFAGAPYNDNNYNIDLK.A	2358.61	-2.810	3	0	6.25	0.05	2604.56	1.0	39/80	14
7548 - 7551, P5_400mM	R.LAAICFAGAPYNDNNYNIDLK.A	2358.61	-2.117	2	0	5.76	0.05	1746.94	1.0	28/40	14
7560, P5_200mM	R.LAAICFAGAPYNDNNYNIDLK.A	2358.61	-1.777	2	0	5.67	0.02	1453.59	1.0	26/40	14
7563, P5_200mM	R.LAAICFAGAPYNDNNYNIDLK.A	2358.61	-1.966	3	0	5.35	0.08	2012.83	2.0	37/80	14
7566, P5_200mM	R.LAAICFAGAPYNDNNYNIDLK.A	2358.61	-2.664	2	0	5.57	0.02	1438.17	1.0	26/40	14
7590, P5_200mM	R.LAAICFAGAPYNDNNYNIDLK.A	2358.61	0.217	2	0	6.23	0.04	1401.24	1.0	26/40	14
7596, P5_200mM	R.LAAICFAGAPYNDNNYNIDLK.A	2358.61	0.261	2	0	5.81	0.01	1400.56	1.0	25/40	14
7626 - 7629, P5_400mM	R.LAAICFAGAPYNDNNYNIDLK.A	2358.61	2.353	2	0	5.40	0.33	1121.50	2.0	25/40	14
7752, P5_20mM	R.GSGTPVDDLDR.C	1189.21	-0.903	2	0	2.95	0.35	374.32	41.0	15/22	35
8634, P5_400mM	R.SWDFADYGCYCGR.G	1843.98	-1.544	2	0	4.12	0.25	1773.88	1.0	20/26	15
9. PSNJ3K phospholipase A2 (EC 3.1.1.4) III - monocled cobra					0	72.32		13270.76	2144440.0	51 (23 19 3 3 3)	
3792 - 3795, P5_20mM	R.CCQVHDNICYDEAEK.I	1828.94	-2.372	2	0	5.28	0.39	1188.48	2.0	20/26	1
3909 - 3912, P5_20mM	R.CCQVHDNICYDEAEK.I	1828.94	-1.195	3	0	4.47	0.05	1678.98	1.0	28/52	1
4149 - 4152, P5_20mM	K.GGNNACAAAVCDCDR.L	1611.72	-1.095	2	0	4.62	0.06	1858.79	1.0	22/28	9
4263 - 4266, P5_20mM	K.GGNNACAAAVCDCDR.L	1611.72	-0.150	2	0	3.20	0.43	1699.10	2.0	21/28	9
4461 - 4464, P5_20mM	K.NM*IQCTVPSR.S	1222.42	0.091	2	0	3.52	0.03	1222.83	1.0	16/18	12
4635, P5_0mM	K.GGNNACAAAVCDCDR.L	1611.72	-1.367	2	0	4.72	0.08	1610.32	1.0	20/28	9
4641, P5_0mM	K.GGNNACAAAVCDCDR.L	1611.72	-1.291	2	0	4.29	0.05	1656.74	1.0	20/28	9

Supplemental Table 6: Orthologous proteins of peptide sequences generated from ion-exchange chromatography-purified *N. kaouthia* venom protein components (P5) by 2D-LC/MS-MS and database search

Reference					P(pro)	Score	Coverage	MW	Accession	Peptide(Hits)	
Scan(s), File (salt concentration)	Peptides	MH+	ΔM	z	P(pep)	X_{corr}	ΔCn	Sp	RSp	Ions	Count
4677, P5_0mM	K.GGNNACAAVCDCLR.L	1611.72	-0.289	2	0	4.04	0.43	2056.21	1.0	22/28	9
4683, P5_0mM	K.GGNNACAAVCDCLR.L	1611.72	1.668	2	0	3.33	0.45	1609.92	2.0	20/28	9
4929 - 4932, P5_60mM	K.TYSYEC SQGLTCK.G	1698.86	-1.299	2	0	4.57	0.45	2413.46	1.0	22/26	15
4971 - 4974, P5_20mM	K.TYSYEC SQGLTCK.G	1698.86	-1.163	2	0	5.00	0.44	2552.72	1.0	22/26	15
4986 - 4989, P5_20mM	K.TYSYEC SQGLTCK.G	1698.86	-1.162	2	0	4.22	0.29	2238.66	1.0	21/26	15
5034 - 5037, P5_80mM	K.TYSYEC SQGLTCK.G	1698.86	-1.363	2	0	4.83	0.42	2220.20	1.0	21/26	15
5058, P5_60mM	K.NMIQCTVPSR.S	1206.42	-1.027	2	0	2.98	0.01	1167.82	2.0	16/18	12
5097, P5_0mM	K.TYSYEC SQGLTCK.G	1698.86	-0.300	2	0	5.06	0.47	2221.61	1.0	21/26	15
5109, P5_0mM	K.TYSYEC SQGLTCK.G	1698.86	-0.307	2	0	5.05	0.43	2419.65	1.0	21/26	15
5124, P5_100mM	K.NMIQCTVPSR.S	1206.42	-1.070	2	0	2.18	0.14	576.51	33.0	39434	12
5124 - 5127, P5_20mM	K.NMIQCTVPSR.S	1206.42	-0.948	2	0	2.86	0.00	1221.15	3.0	16/18	12
5169, P5_80mM	K.NMIQCTVPSR.S	1206.42	-1.032	2	0	2.68	0.07	1037.93	3.0	15/18	12
5772 - 5775, P5_200mM	K.TYSYEC SQGLTCK.G	1698.86	-1.386	2	0	4.40	0.46	2345.55	1.0	22/26	15
5919 - 5922, P5_200mM	K.NMIQCTVPSR.S	1206.42	-1.052	2	0	2.18	0.07	769.71	28.0	13/18	12
6051, P5_20mM	K.NMIQCTVPSR.S	1206.42	1.676	2	0	2.21	0.04	606.31	62.0	39434	12
6552 - 6555, P5_60mM	K.ISGCWPYFK.T	1158.35	-1.004	2	0	3.41	0.36	924.26	1.0	14/16	8
6648 - 6651, P5_60mM	R.LAAICFAGAPYNNNNYNIDLK.A	2357.63	-1.197	2	0	5.38	0.11	1207.11	1.0	25/40	5
6654, P5_60mM	R.LAAICFAGAPYNNNNYNIDLK.A	2357.63	-0.925	3	0	6.33	0.11	2800.82	1.0	40/80	5
6663, P5_0mM	R.LAAICFAGAPYNNNNYNIDLK.A	2357.63	-1.049	3	0	4.20	0.03	1188.74	1.0	29/80	5
6663, P5_60mM	R.LAAICFAGAPYNNNNYNIDLK.A	2357.63	-0.862	3	0	6.28	0.08	2805.06	3.0	40/80	5
6705, P5_100mM	R.LAAICFAGAPYNNNNYNIDLK.A	2357.63	-0.981	3	0	5.60	0.01	2104.04	1.0	36/80	5
6708 - 6711, P5_100mM	R.LAAICFAGAPYNNNNYNIDLK.A	2357.63	-1.273	2	0	5.93	0.08	1560.95	1.0	28/40	5
6714, P5_100mM	R.LAAICFAGAPYNNNNYNIDLK.A	2357.63	-1.886	3	0	5.49	0.01	2708.04	1.0	40/80	5
6723 - 6726, P5_80mM	K.ISGCWPYFK.T	1158.35	-0.961	2	0	3.62	0.29	826.82	1.0	13/16	8
6795, P5_20mM	K.ISGCWPYFK.T	1158.35	-0.924	2	0	3.22	0.12	968.86	1.0	14/16	8
6798, P5_80mM	R.LAAICFAGAPYNNNNYNIDLK.A	2357.63	-1.719	2	0	4.94	0.12	1303.05	1.0	25/40	5
6801, P5_20mM	K.ISGCWPYFK.T	1158.35	-0.884	2	0	3.18	0.11	712.92	1.0	39432	8
6801, P5_80mM	R.LAAICFAGAPYNNNNYNIDLK.A	2357.63	-0.919	3	0	5.28	0.05	2516.87	1.0	39/80	5
6804, P5_80mM	R.LAAICFAGAPYNNNNYNIDLK.A	2357.63	-1.674	2	0	5.59	0.09	1389.76	1.0	26/40	5
6807, P5_80mM	R.LAAICFAGAPYNNNNYNIDLK.A	2357.63	-0.871	3	0	6.38	0.09	2365.52	2.0	41/80	5

Supplemental Table 6: Orthologous proteins of peptide sequences generated from ion-exchange chromatography-purified *N. kaouthia* venom protein components (P5) by 2D-LC/MS-MS and database search

Reference					P(pro)	Score	Coverage	MW	Accession	Peptide(Hits)	
Scan(s), File (salt concentration)	Peptides	MH+	ΔM	z	P(pep)	X_{corr}	ΔCn	Sp	RSp	Ions	Count
6864, P5_20mM	K.ISGCWPYFK.T	1158.35	-0.802	2	0	3.00	0.08	950.52	1.0	14/16	8
6927, P5_20mM	K.ISGCWPYFK.T	1158.35	-0.878	2	0	3.30	0.16	916.44	1.0	14/16	8
6939 - 6942, P5_20mM	R.LAAICFAGAPYNNNNYNIDLK.A	2357.63	-0.837	3	0	4.53	0.14	2099.96	1.0	38/80	5
6990, P5_20mM	R.LAAICFAGAPYNNNNYNIDLK.A	2357.63	0.247	2	0	4.61	-	1154.92	2.0	24/40	5
7161, P5_20mM	K.ISGCWPYFK.T	1158.35	-0.960	2	0	2.72	0.22	725.65	2.0	39432	8
7176, P5_20mM	K.ISGCWPYFK.T	1158.35	-1.041	2	0	2.89	0.12	887.36	1.0	13/16	8
7545, P5_400mM	R.LAAICFAGAPYNNNNYNIDLK.A	2357.63	-1.825	3	0	5.96	0.09	2604.56	1.0	39/80	5
7548 - 7551, P5_400mM	R.LAAICFAGAPYNNNNYNIDLK.A	2357.63	-1.132	2	0	5.44	0.06	1270.85	4.0	26/40	5
7560, P5_200mM	R.LAAICFAGAPYNNNNYNIDLK.A	2357.63	-0.793	2	0	5.57	0.06	1453.59	1.0	26/40	5
7563, P5_200mM	R.LAAICFAGAPYNNNNYNIDLK.A	2357.63	-0.981	3	0	5.70	0.06	2260.52	1.0	39/80	5
7566, P5_200mM	R.LAAICFAGAPYNNNNYNIDLK.A	2357.63	-1.679	2	0	5.48	0.05	1438.17	1.0	26/40	5
7590, P5_200mM	R.LAAICFAGAPYNNNNYNIDLK.A	2357.63	1.202	2	0	4.87	-	1117.29	5.0	25/40	5
7596, P5_200mM	R.LAAICFAGAPYNNNNYNIDLK.A	2357.63	1.246	2	0	4.72	-	1252.99	2.0	24/40	5
8634, P5_400mM	R.SWWNFADYGCYCGR.G	1842.99	-0.559	2	0	3.10	0.46	1372.20	2.0	18/26	
10. PA2D_NAJSP Phospholipase A2, acidic D precursor (Phosphatidylcholine 2-acylhydrolase) (APLA)					0	70.35		16097.18	25453171.0	54 (40 10 3 0 1)	
4149 - 4152, P5_20mM	K.GGNDACAAAVCDCDR.L	1612.71	-2.080	2	0	4.35	0.50	1858.79	1.0	22/28	
4263 - 4266, P5_20mM	K.GGNDACAAAVCDCDR.L	1612.71	-1.135	2	0	5.07	0.37	1863.92	1.0	22/28	
4395 - 4398, P5_20mM	K.NM*IQCTVPNR.S	1249.45	-0.934	2	0	3.17	0.33	1024.74	1.0	16/18	6
4425, P5_60mM	K.NM*IQCTVPNR.S	1249.45	-1.129	2	0	2.47	0.18	795.10	1.0	14/18	6
4431, P5_60mM	K.NM*IQCTVPNR.S	1249.45	-1.136	2	0	2.90	0.25	870.16	1.0	15/18	6
4635, P5_0mM	K.GGNDACAAAVCDCDR.L	1612.71	-2.352	2	0	4.35	0.41	1458.50	2.0	19/28	
4641, P5_0mM	K.GGNDACAAAVCDCDR.L	1612.71	-2.276	2	0	4.07	0.44	1506.78	2.0	19/28	
4677, P5_0mM	K.GGNDACAAAVCDCDR.L	1612.71	-1.274	2	0	5.18	0.22	2056.21	1.0	22/28	
4683, P5_0mM	K.GGNDACAAAVCDCDR.L	1612.71	0.684	2	0	4.68	0.29	1882.84	1.0	21/28	
4929 - 4932, P5_60mM	K.TYSYEQSQTLTCK.G	1698.86	-1.299	2	0	4.57	0.45	2413.46	1.0	22/26	15
4971 - 4974, P5_20mM	K.TYSYEQSQTLTCK.G	1698.86	-1.163	2	0	5.00	0.44	2552.72	1.0	22/26	15
4986 - 4989, P5_20mM	K.TYSYEQSQTLTCK.G	1698.86	-1.162	2	0	4.22	0.29	2238.66	1.0	21/26	15
4995 - 5001, P5_60mM	K.NMIQCTVPNR.S	1233.45	-0.961	2	0	2.99	0.12	1159.69	1.0	16/18	6
5028, P5_60mM	K.NMIQCTVPNR.S	1233.45	-0.979	2	0	2.78	0.03	823.22	12.0	13/18	6
5034 - 5037, P5_80mM	K.TYSYEQSQTLTCK.G	1698.86	-1.363	2	0	4.83	0.42	2220.20	1.0	21/26	15

Supplemental Table 6: Orthologous proteins of peptide sequences generated from ion-exchange chromatography-purified *N. kaouthia* venom protein components (P5) by 2D-LC/MS-MS and database search

Reference					P(pro)	Score	Coverage	MW	Accession	Peptide(Hits)	
Scan(s), File (salt concentration)	Peptides	MH+	ΔM	z	P(pep)	X_{corr}	ΔCn	Sp	RSp	Ions	Count
5058 - 5061, P5_20mM	K.NMIQCTVPNR.S	1233.45	-0.915	2	0	3.70	0.14	1245.61	2.0	16/18	6
5076 - 5079, P5_100mM	K.NMIQCTVPNR.S	1233.45	-0.973	2	0	3.34	0.21	800.17	4.0	13/18	6
5097, P5_0mM	K.TYSYECSQGLTCK.G	1698.86	-0.300	2	0	5.06	0.47	2221.61	1.0	21/26	15
5103, P5_80mM	K.NMIQCTVPNR.S	1233.45	-1.053	2	0	3.13	0.17	1053.84	2.0	15/18	6
5109, P5_0mM	K.TYSYECSQGLTCK.G	1698.86	-0.307	2	0	5.05	0.43	2419.65	1.0	21/26	15
5109, P5_80mM	K.NMIQCTVPNR.S	1233.45	-1.011	2	0	3.47	0.28	1292.52	2.0	16/18	6
5256, P5_0mM	K.NMIQCTVPNR.S	1233.45	-0.977	2	0	2.26	0.03	315.35	46.0	14/18	6
5772 - 5775, P5_200mM	K.TYSYECSQGLTCK.G	1698.86	-1.386	2	0	4.40	0.46	2345.55	1.0	22/26	15
5865 - 5868, P5_200mM	K.NMIQCTVPNR.S	1233.45	-1.058	2	0	3.34	0.15	1184.11	2.0	15/18	6
6411 - 6414, P5_60mM	R.CWPYFK.T	901.07	-0.756	1	0	1.66	0.01	312.88	18.0	39304	5
6648 - 6651, P5_60mM	R.LAAICFAGAPYNDNNYNIDLK.A	2358.61	-2.182	2	0	5.87	0.08	1207.11	1.0	25/40	14
6654, P5_60mM	R.LAAICFAGAPYNDNNYNIDLK.A	2358.61	-1.910	3	0	6.90	0.08	2800.82	1.0	40/80	14
6663, P5_0mM	R.LAAICFAGAPYNDNNYNIDLK.A	2358.61	-2.034	3	0	4.26	0.01	1134.83	2.0	28/80	14
6663, P5_60mM	R.LAAICFAGAPYNDNNYNIDLK.A	2358.61	-1.847	3	0	6.40	0.02	2807.38	2.0	40/80	14
6690, P5_20mM	R.CWPYFK.T	901.07	-0.724	1	0	1.56	-	258.73	19.0	39304	5
6705, P5_100mM	R.LAAICFAGAPYNDNNYNIDLK.A	2358.61	-1.966	3	0	5.57	0.07	1919.70	2.0	35/80	14
6708 - 6711, P5_100mM	R.LAAICFAGAPYNDNNYNIDLK.A	2358.61	-2.258	2	0	6.20	0.04	1560.95	1.0	28/40	14
6714, P5_100mM	R.LAAICFAGAPYNDNNYNIDLK.A	2358.61	-2.871	3	0	5.45	0.05	2282.13	3.0	38/80	14
6729, P5_100mM	R.LAAICFAGAPYNDNNYNIDLK.A	2358.61	2.472	3	0	6.64	0.06	2590.66	1.0	40/80	14
6735, P5_100mM	R.LAAICFAGAPYNDNNYNIDLK.A	2358.61	2.159	2	0	6.08	0.07	1524.66	1.0	26/40	14
6741, P5_100mM	R.LAAICFAGAPYNDNNYNIDLK.A	2358.61	2.429	2	0	5.78	0.10	1508.78	1.0	26/40	14
6753, P5_20mM	K.NMIQCTVPNR.S	1233.45	-0.018	2	0	2.59	0.14	809.67	1.0	14/18	6
6753, P5_100mM	R.LAAICFAGAPYNDNNYNIDLK.A	2358.61	2.564	3	0	6.04	0.08	2055.37	2.0	37/80	14
6798, P5_80mM	R.LAAICFAGAPYNDNNYNIDLK.A	2358.61	-2.704	2	0	5.51	0.08	1164.74	2.0	24/40	14
6801, P5_80mM	R.LAAICFAGAPYNDNNYNIDLK.A	2358.61	-1.904	3	0	5.37	0.02	2308.18	2.0	38/80	14
6804, P5_80mM	R.LAAICFAGAPYNDNNYNIDLK.A	2358.61	-2.659	2	0	6.04	0.07	1389.76	1.0	26/40	14
6807, P5_80mM	R.LAAICFAGAPYNDNNYNIDLK.A	2358.61	-1.856	3	0	6.67	0.04	2564.32	1.0	42/80	14
6867, P5_80mM	R.LAAICFAGAPYNDNNYNIDLK.A	2358.61	2.130	2	0	5.60	0.37	1001.68	2.0	23/40	14
6939 - 6942, P5_20mM	R.LAAICFAGAPYNDNNYNIDLK.A	2358.61	-1.822	3	0	4.94	0.07	2099.96	1.0	38/80	14
6990, P5_20mM	R.LAAICFAGAPYNDNNYNIDLK.A	2358.61	-0.738	2	0	5.74	0.02	1154.92	2.0	24/40	14

Supplemental Table 6: Orthologous proteins of peptide sequences generated from ion-exchange chromatography-purified *N. kaouthia* venom protein components (P5) by 2D-LC/MS-MS and database search

Reference		MH+	ΔM	z	P(pro)	Score	Coverage	MW	Accession	Peptide(Hits)	Count
Scan(s), File (salt concentration)	Peptides				P(pep)	X_{corr}	ΔCn	Sp	RSp	Ions	
7545, P5_400mM	R.LAAICFAGAPYNDNNYNIDLK.A	2358.61	-2.810	3	0	6.25	0.05	2604.56	1.0	39/80	14
7548 - 7551, P5_400mM	R.LAAICFAGAPYNDNNYNIDLK.A	2358.61	-2.117	2	0	5.76	0.05	1746.94	1.0	28/40	14
7560, P5_200mM	R.LAAICFAGAPYNDNNYNIDLK.A	2358.61	-1.777	2	0	5.67	0.02	1453.59	1.0	26/40	14
7563, P5_200mM	R.LAAICFAGAPYNDNNYNIDLK.A	2358.61	-1.966	3	0	5.35	0.08	2012.83	2.0	37/80	14
7566, P5_200mM	R.LAAICFAGAPYNDNNYNIDLK.A	2358.61	-2.664	2	0	5.57	0.02	1438.17	1.0	26/40	14
7590, P5_200mM	R.LAAICFAGAPYNDNNYNIDLK.A	2358.61	0.217	2	0	6.23	0.04	1401.24	1.0	26/40	14
7596, P5_200mM	R.LAAICFAGAPYNDNNYNIDLK.A	2358.61	0.261	2	0	5.81	0.01	1400.56	1.0	25/40	14
7626 - 7629, P5_400mM	R.LAAICFAGAPYNDNNYNIDLK.A	2358.61	2.353	2	0	5.40	0.33	1121.50	2.0	25/40	14
8634, P5_400mM	R.SWWDFADYGCYCGR.G	1843.98	-1.544	2	0	4.12	0.25	1773.88	1.0	20/26	15

Supplemental Table 7: Orthologous proteins of peptide sequences generated from ion-exchange chromatography-purified *N. kaouthia* venom protein components (P8) by 2D-LC/MS-MS and database search

Reference					P(pro)	Score	Coverage	MW	Accession	Peptide(Hits)	
Scan(s), File (salt concentration)	Peptides	MH+	ΔM	z	P(pep)	X_{corr}	ΔCn	Sp	RSp	Ions	Count
1. NXLI_NAJKA Long neurotoxin 1 (Neurotoxin 3) (\square-cobratoxin) (Cbtx)					0	90.33	95.77	7831.05	128930.0	57 (51 2 2 0 2)	
5235 - 5238, P8_20mM	K.DCPNGHVCTYK.T	1351.49	-1.041	2	0	2.91	0.34	332.25	159.0	13/20	6
5274, P8_20mM	K.DCPNGHVCTYK.T	1351.49	-1.018	2	0	3.22	0.32	423.61	6.0	15/20	6
5679, P8_60mM	R.GKRVDLGCAATCPTVK.T	1734.04	-0.439	3	0	2.84	0.08	650.61	9.0	22/60	4
5685, P8_60mM	R.GKRVDLGCAATCPTVK.T	1734.04	-0.376	3	0	2.54	0.07	822.04	6.0	21/60	4
5964 - 5967, P8_0mM	R.VDLGCAATCPTVK.T	1392.63	-1.097	2	0	4.57	0.49	1875.90	1.0	20/24	7
6063 - 6066, P8_60mM	K.RVDLGCAATCPTVK.T	1548.81	-1.042	2	0	4.01	0.38	1141.23	1.0	19/26	5
6117 - 6120, P8_60mM	K.RVDLGCAATCPTVK.T	1548.81	-1.210	3	0	3.25	0.11	1308.55	3.0	24/52	5
6831 - 6834, P8_20mM	K.RVDLGCAATCPTVK.T	1548.81	-1.001	2	0	3.40	0.13	796.49	1.0	16/26	5
7065, P8_60mM	R.CFITPDITSKDCPNGHVCTYK.T	2514.84	-2.749	4	0	3.95	0.23	1165.38	14.0	36/120	6
7221 - 7224, P8_20mM	R.VDLGCAATCPTVK.T	1392.63	-1.014	2	0	4.44	0.49	1531.36	1.0	18/24	7
7245 - 7248, P8_20mM	R.VDLGCAATCPTVK.T	1392.63	-0.953	2	0	4.61	0.38	1418.14	1.0	18/24	7
7260, P8_20mM	R.VDLGCAATCPTVK.T	1392.63	-0.969	1	0	3.05	0.36	386.73	1.0	14/24	7
7269, P8_20mM	R.VDLGCAATCPTVK.T	1392.63	-0.969	1	0	2.55	0.39	307.46	1.0	13/24	7
7293, P8_20mM	R.VDLGCAATCPTVK.T	1392.63	-0.969	1	0	2.72	0.21	241.54	4.0	39440	7
7299, P8_20mM	R.VDLGCAATCPTVK.T	1392.63	-0.985	1	0	3.00	0.28	347.79	2.0	14/24	7
7497 - 7500, P8_60mM	-.IRCFITPDITSK.D	1451.72	-0.945	2	0	3.64	0.29	1125.92	1.0	18/22	6
7587 - 7590, P8_20mM	R.VDLGCAATCPTVK.T	1392.63	-1.017	2	0	4.22	0.41	1574.71	1.0	18/24	7
7743, P8_60mM	R.CFITPDITSK.D	1182.37	-0.738	2	0	2.42	0.17	776.77	3.0	14/18	6
7749, P8_60mM	R.CFITPDITSK.D	1182.37	-0.742	2	1	2.51	0.09	712.31	6.0	13/18	6
8109 - 8112, P8_20mM	K.TGVDIQCCSTDNCNPFPTTR.K	2243.44	-1.449	2	0	5.37	0.44	2234.44	1.0	24/36	
8115 - 8118, P8_20mM	K.TGVDIQCCSTDNCNPFPTTR.K	2243.44	-1.101	3	0	6.63	0.36	3918.00	1.0	41/72	
8127, P8_20mM	K.TGVDIQCCSTDNCNPFPTTR.K	2243.44	-1.452	2	0	4.72	0.31	1633.80	1.0	21/36	
8133, P8_20mM	K.TGVDIQCCSTDNCNPFPTTR.K	2243.44	-1.575	2	0	4.89	0.34	2100.50	1.0	23/36	
8640, P8_20mM	R.CFITPDITSK.D	1182.37	-0.783	2	0	2.96	0.33	899.65	2.0	15/18	6
8646, P8_20mM	R.CFITPDITSK.D	1182.37	-0.776	2	0	2.42	0.16	585.28	15.0	39434	6
8670, P8_20mM	R.CFITPDITSK.D	1182.37	-0.834	1	0	3.09	0.31	272.52	1.0	13/18	6
8676, P8_20mM	R.CFITPDITSK.D	1182.37	-0.830	1	0	2.96	0.38	274.19	1.0	13/18	6
8682, P8_20mM	R.CFITPDITSK.D	1182.37	-0.830	1	0	3.11	0.31	275.52	1.0	13/18	6

Supplemental Table 7: Orthologous proteins of peptide sequences generated from ion-exchange chromatography-purified *N. kaouthia* venom protein components (P8) by 2D-LC/MS-MS and database search

Reference					P(pro)	Score	Coverage	MW	Accession	Peptide(Hits)	
Scan(s), File (salt concentration)	Peptides	MH+	ΔM	z	P(pep)	X_{corr}	ΔCn	Sp	RSp	Ions	Count
8700, P8_20mM	R.CFITPDITSK.D	1182.37	-0.830	1	0	3.20	0.24	295.56	1.0	13/18	6
8712, P8_20mM	R.CFITPDITSK.D	1182.37	-0.818	2	0	2.56	-	956.16	2.0	15/18	6
8958, P8_20mM	R.CFITPDITSK.D	1182.37	-0.782	2	0	3.10	0.29	830.84	2.0	15/18	6
8970, P8_20mM	R.CFITPDITSK.D	1182.37	-0.816	2	0	2.80	0.27	834.71	2.0	15/18	6
9312 - 9315, P8_20mM	R.CFITPDITSK.D	1182.37	-0.723	2	0	2.73	0.02	706.21	5.0	14/18	6
9633 - 9636, P8_20mM	K.TWCDAFCSIR.G	1316.49	-0.960	2	0	3.47	0.24	1071.18	1.0	16/18	1
9675 - 9678, P8_20mM	K.TWCDAFCSIR.G	1316.49	-0.891	1	1	2.70	0.23	309.39	1.0	13/18	1
9714, P8_20mM	K.TWCDAFCSIR.G	1316.49	-0.891	1	0	2.18	0.12	243.13	4.0	39404	1
9960, P8_20mM	K.TWCDAFCSIR.G	1316.49	-2.941	2	0	2.77	0.07	865.36	1.0	15/18	1
9975, P8_20mM	K.TWCDAFCSIR.G	1316.49	-2.899	2	0	3.47	0.15	981.67	1.0	16/18	1
10521, P8_20mM	K.TWCDAFCSIR.G	1316.49	-1.138	2	0	2.04	0.05	995.18	1.0	15/18	1
10806, P8_20mM	R.VDLGCAATCPTVK.T	1392.63	2.680	2	0	2.95	0.19	596.78	14.0	13/24	7
10812, P8_20mM	R.VDLGCAATCPTVK.T	1392.63	2.794	2	0	2.69	0.16	551.68	2.0	13/24	7
10869 - 10872, P8_20mM	K.TWCDAFCSIR.G	1316.49	-1.075	2	0	2.84	0.14	970.62	1.0	15/18	1
11244, P8_20mM	R.VDLGCAATCPTVK.T	1392.63	-1.113	2	0	3.14	0.24	753.86	18.0	15/24	7
11247, P8_20mM	K.TWCDAFCSIR.G	1316.49	-1.103	2	0	2.89	0.12	957.08	1.0	15/18	1
11268, P8_20mM	K.TWCDAFCSIR.G	1316.49	-1.100	2	0	3.03	0.06	967.65	1.0	15/18	1
11490, P8_20mM	R.VDLGCAATCPTVK.T	1392.63	-1.156	2	0	3.94	0.34	1255.45	1.0	16/24	7
11520, P8_20mM	R.VDLGCAATCPTVK.T	1392.63	-1.110	2	0	3.93	0.30	1087.09	1.0	15/24	7
11640, P8_20mM	K.TWCDAFCSIR.G	1316.49	-1.139	2	0	3.03	0.13	1027.44	1.0	15/18	1
11691, P8_20mM	K.TWCDAFCSIR.G	1316.49	-1.097	2	0	2.92	0.05	957.47	1.0	15/18	1
12015 - 12018, P8_20mM	K.TWCDAFCSIR.G	1316.49	-1.096	2	0	2.88	0.12	927.85	1.0	15/18	1
12360, P8_20mM	K.TWCDAFCSIR.G	1316.49	-1.060	2	0	2.95	0.23	840.20	1.0	14/18	1
12405, P8_20mM	K.TWCDAFCSIR.G	1316.49	-1.059	2	0	2.85	0.08	970.46	1.0	15/18	1
12438 - 12441, P8_20mM	R.CFITPDITSK.D	1182.37	-0.816	2	1	2.28	-	685.01	35.0	13/18	6
12753, P8_20mM	K.TWCDAFCSIR.G	1316.49	-1.099	2	0	2.45	0.18	905.61	1.0	15/18	1
12801, P8_20mM	K.TWCDAFCSIR.G	1316.49	-1.098	2	0	2.64	0.18	949.78	1.0	15/18	1
13035, P8_20mM	R.VDLGCAATCPTVK.T	1392.63	-1.119	2	0	3.76	0.39	1054.58	1.0	16/24	7
13539, P8_20mM	K.TWCDAFCSIR.G	1316.49	-1.140	2	0	2.30	0.09	973.30	1.0	14/18	1

Supplemental Table 7: Orthologous proteins of peptide sequences generated from ion-exchange chromatography-purified *N. kaouthia* venom protein components (P8) by 2D-LC/MS-MS and database search

Reference					P(pro)	Score	Coverage	MW	Accession	Peptide(Hits)	
Scan(s), File (salt concentration)	Peptides	MH+	ΔM	z	P(pep)	X_{corr}	ΔCn	Sp	RSp	Ions	Count
2. NXL3_NAJNA Long neurotoxin 3 (Toxin C)					0	80.23		7833.02	128947.0	53 (47 2 2 0 2)	
5235 - 5238, P8_20mM	K.DCPNGHVCYTK.T	1351.49	-1.041	2	0	2.91	0.34	332.25	159.0	13/20	6
5274, P8_20mM	K.DCPNGHVCYTK.T	1351.49	-1.018	2	0	3.22	0.32	423.61	6.0	15/20	6
5679, P8_60mM	R.GKRVDLGCAATCPTVK.T	1734.04	-0.439	3	0	2.84	0.08	650.61	9.0	22/60	4
5685, P8_60mM	R.GKRVDLGCAATCPTVK.T	1734.04	-0.376	3	0	2.54	0.07	822.04	6.0	21/60	4
5964 - 5967, P8_0mM	R.VDLGCAATCPTVK.T	1392.63	-1.097	2	0	4.57	0.49	1875.90	1.0	20/24	7
6063 - 6066, P8_60mM	K.RVDLGCAATCPTVK.T	1548.81	-1.042	2	0	4.01	0.38	1141.23	1.0	19/26	5
6117 - 6120, P8_60mM	K.RVDLGCAATCPTVK.T	1548.81	-1.210	3	0	3.25	0.11	1308.55	3.0	24/52	5
6831 - 6834, P8_20mM	K.RVDLGCAATCPTVK.T	1548.81	-1.001	2	0	3.40	0.13	796.49	1.0	16/26	5
7065, P8_60mM	R.CFITPDITSKDCPNGHVCYTK.T	2514.84	-2.749	4	0	3.95	0.23	1165.38	14.0	36/120	6
7221 - 7224, P8_20mM	R.VDLGCAATCPTVK.T	1392.63	-1.014	2	0	4.44	0.49	1531.36	1.0	18/24	7
7245 - 7248, P8_20mM	R.VDLGCAATCPTVK.T	1392.63	-0.953	2	0	4.61	0.38	1418.14	1.0	18/24	7
7260, P8_20mM	R.VDLGCAATCPTVK.T	1392.63	-0.969	1	0	3.05	0.36	386.73	1.0	14/24	7
7269, P8_20mM	R.VDLGCAATCPTVK.T	1392.63	-0.969	1	0	2.55	0.39	307.46	1.0	13/24	7
7293, P8_20mM	R.VDLGCAATCPTVK.T	1392.63	-0.969	1	0	2.72	0.21	241.54	4.0	39440	7
7299, P8_20mM	R.VDLGCAATCPTVK.T	1392.63	-0.985	1	0	3.00	0.28	347.79	2.0	14/24	7
7497 - 7500, P8_60mM	-.IRCFITPDITSK.D	1451.72	-0.945	2	0	3.64	0.29	1125.92	1.0	18/22	6
7587 - 7590, P8_20mM	R.VDLGCAATCPTVK.T	1392.63	-1.017	2	0	4.22	0.41	1574.71	1.0	18/24	7
7743, P8_60mM	R.CFITPDITSK.D	1182.37	-0.738	2	0	2.42	0.17	776.77	3.0	14/18	6
7749, P8_60mM	R.CFITPDITSK.D	1182.37	-0.742	2	1	2.51	0.09	712.31	6.0	13/18	6
8640, P8_20mM	R.CFITPDITSK.D	1182.37	-0.783	2	0	2.96	0.33	899.65	2.0	15/18	6
8646, P8_20mM	R.CFITPDITSK.D	1182.37	-0.776	2	0	2.42	0.16	585.28	15.0	39434	6
8670, P8_20mM	R.CFITPDITSK.D	1182.37	-0.834	1	0	3.09	0.31	272.52	1.0	13/18	6
8676, P8_20mM	R.CFITPDITSK.D	1182.37	-0.830	1	0	2.96	0.38	274.19	1.0	13/18	6
8682, P8_20mM	R.CFITPDITSK.D	1182.37	-0.830	1	0	3.11	0.31	275.52	1.0	13/18	6
8700, P8_20mM	R.CFITPDITSK.D	1182.37	-0.830	1	0	3.20	0.24	295.56	1.0	13/18	6
8712, P8_20mM	R.CFITPDITSK.D	1182.37	-0.818	2	0	2.56	0.22	956.16	2.0	15/18	6
8958, P8_20mM	R.CFITPDITSK.D	1182.37	-0.782	2	0	3.10	0.29	830.84	2.0	15/18	6
8970, P8_20mM	R.CFITPDITSK.D	1182.37	-0.816	2	0	2.80	0.27	834.71	2.0	15/18	6
9312 - 9315, P8_20mM	R.CFITPDITSK.D	1182.37	-0.723	2	0	2.73	0.02	706.21	5.0	14/18	6

Supplemental Table 7: Orthologous proteins of peptide sequences generated from ion-exchange chromatography-purified *N. kaouthia* venom protein components (P8) by 2D-LC/MS-MS and database search

Reference					P(pro)	Score	Coverage	MW	Accession	Peptide(Hits)	
Scan(s), File (salt concentration)	Peptides	MH+	ΔM	z	P(pep)	X_{corr}	ΔCn	Sp	RSp	Ions	Count
9633 - 9636, P8_20mM	K.TWCDAFCSIR.G	1316.49	-0.960	2	0	3.47	0.24	1071.18	1.0	16/18	1
9675 - 9678, P8_20mM	K.TWCDAFCSIR.G	1316.49	-0.891	1	1	2.70	0.23	309.39	1.0	13/18	1
9714, P8_20mM	K.TWCDAFCSIR.G	1316.49	-0.891	1	0	2.18	0.12	243.13	4.0	39404	1
9960, P8_20mM	K.TWCDAFCSIR.G	1316.49	-2.941	2	0	2.77	0.07	865.36	1.0	15/18	1
9975, P8_20mM	K.TWCDAFCSIR.G	1316.49	-2.899	2	0	3.47	0.15	981.67	1.0	16/18	1
10521, P8_20mM	K.TWCDAFCSIR.G	1316.49	-1.138	2	0	2.04	0.05	995.18	1.0	15/18	1
10806, P8_20mM	R.VDLGCAATCPTVK.T	1392.63	2.680	2	0	2.95	0.19	596.78	14.0	13/24	7
10812, P8_20mM	R.VDLGCAATCPTVK.T	1392.63	2.794	2	0	2.69	0.16	551.68	2.0	13/24	7
10869 - 10872, P8_20mM	K.TWCDAFCSIR.G	1316.49	-1.075	2	0	2.84	0.14	970.62	1.0	15/18	1
11244, P8_20mM	R.VDLGCAATCPTVK.T	1392.63	-1.113	2	0	3.14	0.24	753.86	18.0	15/24	7
11247, P8_20mM	K.TWCDAFCSIR.G	1316.49	-1.103	2	0	2.89	0.12	957.08	1.0	15/18	1
11268, P8_20mM	K.TWCDAFCSIR.G	1316.49	-1.100	2	0	3.03	0.06	967.65	1.0	15/18	1
11490, P8_20mM	R.VDLGCAATCPTVK.T	1392.63	-1.156	2	0	3.94	0.34	1255.45	1.0	16/24	7
11520, P8_20mM	R.VDLGCAATCPTVK.T	1392.63	-1.110	2	0	3.93	0.30	1087.09	1.0	15/24	7
11640, P8_20mM	K.TWCDAFCSIR.G	1316.49	-1.139	2	0	3.03	0.13	1027.44	1.0	15/18	1
11691, P8_20mM	K.TWCDAFCSIR.G	1316.49	-1.097	2	0	2.92	0.05	957.47	1.0	15/18	1
12015 - 12018, P8_20mM	K.TWCDAFCSIR.G	1316.49	-1.096	2	0	2.88	0.12	927.85	1.0	15/18	1
12360, P8_20mM	K.TWCDAFCSIR.G	1316.49	-1.060	2	0	2.95	0.23	840.20	1.0	14/18	1
12405, P8_20mM	K.TWCDAFCSIR.G	1316.49	-1.059	2	0	2.85	0.08	970.46	1.0	15/18	1
12438 - 12441, P8_20mM	R.CFITPDITSK.D	1182.37	-0.816	2	1	2.28	0.22	685.01	35.0	13/18	6
12753, P8_20mM	K.TWCDAFCSIR.G	1316.49	-1.099	2	0	2.45	0.18	905.61	1.0	15/18	1
12801, P8_20mM	K.TWCDAFCSIR.G	1316.49	-1.098	2	0	2.64	0.18	949.78	1.0	15/18	1
13035, P8_20mM	R.VDLGCAATCPTVK.T	1392.63	-1.119	2	0	3.76	0.39	1054.58	1.0	16/24	7
13539, P8_20mM	K.TWCDAFCSIR.G	1316.49	-1.140	2	0	2.30	0.09	973.30	1.0	14/18	1
3. A Chain A, Crystal Structure Of Natrin From Naja Atra Snake Venom					0	66.22		24953.96	71041970.0	21 (16 5 0 00)	
5586, P8_0mM	-.NVDFNSESTR.R	1169.18	-0.835	2	0	2.04	0.21	226.83	70.0	39373	3
5613, P8_0mM	-.NVDFNSESTR.R	1169.18	-0.709	2	0	3.07	0.12	621.69	1.0	15/18	3
5751, P8_20mM	R.VSPTASNM*LK.M	1064.24	-0.727	2	0	2.16	0.05	248.90	28.0	13/18	2
5757, P8_20mM	R.VSPTASNM*LK.M	1064.24	-0.688	2	0	2.51	0.24	236.90	27.0	39434	2
5853, P8_60mM	-.NVDFNSESTR.R	1169.18	-0.787	2	0	2.35	0.16	387.60	5.0	39434	3

Supplemental Table 7: Orthologous proteins of peptide sequences generated from ion-exchange chromatography-purified *N. kaouthia* venom protein components (P8) by 2D-LC/MS-MS and database search

Reference					P(pro)	Score	Coverage	MW	Accession	Peptide(Hits)	
Scan(s), File (salt concentration)	Peptides	MH+	ΔM	z	P(pep)	X_{corr}	ΔCn	Sp	RSp	Ions	Count
5892, P8_60mM	-.NVDFNSESTR.R	1169.18	-1.952	2	0	2.09	0.21	433.87	14.0	39434	3
5925, P8_60mM	R.RVSPTASNMLK.M	1204.43	-0.829	2	0	2.92	0.10	1066.69	1.0	16/20	2
5934, P8_60mM	R.RVSPTASNMLK.M	1204.43	-0.868	2	0	2.82	0.06	1173.26	1.0	17/20	2
6144, P8_20mM	-.NVDFNSESTRR.K	1325.37	-0.695	2	0	2.06	0.16	237.38	88.0	13/20	3
6528 - 6531, P8_20mM	-.NVDFNSESTR.R	1169.18	-0.753	2	0	2.48	0.05	387.71	4.0	14/18	3
6570, P8_20mM	-.NVDFNSESTR.R	1169.18	-0.709	2	0	3.00	0.12	665.88	1.0	16/18	3
6582, P8_20mM	-.NVDFNSESTR.R	1169.18	-0.708	2	0	3.35	0.17	670.97	1.0	16/18	3
6612, P8_20mM	-.NVDFNSESTR.R	1169.18	-0.703	1	0	2.25	0.17	160.09	16.0	39404	3
6681, P8_20mM	R.RVSPTASNMLK.M	1204.43	-0.828	2	0	2.76	0.06	880.09	2.0	15/20	2
6687, P8_20mM	R.RVSPTASNMLK.M	1204.43	-0.751	2	0	2.64	0.12	872.88	1.0	15/20	2
7314, P8_20mM	R.VSPTASNMLK.M	1048.24	-0.720	1	0	2.05	0.10	237.12	80.0	39373	2
7326, P8_20mM	R.VSPTASNMLK.M	1048.24	-0.757	1	0	1.90	0.08	230.22	110.0	39373	2
7893 - 7896, P8_20mM	K.EIVDLHNSLR.R	1196.34	-0.747	2	0	3.00	0.20	406.20	1.0	15/18	4
8805, P8_20mM	K.MEWYPEAASNAER.W	1554.67	-1.076	2	0	4.19	0.32	1346.83	2.0	22/24	3
8811, P8_20mM	K.MEWYPEAASNAER.W	1554.67	-1.072	2	0	4.35	0.29	1206.44	1.0	21/24	3
12465, P8_20mM	K.MEWYPEAASNAER.W	1554.67	0.611	2	1	2.75	0.05	649.30	3.0	16/24	3
4. A Chain A, Crystal Structure Of Natrin, A Snake Venom Crisp From Taiwan Cobra (Naja Atra)					0	66.22		24926.93	85543948.0	21 (16 5 0 0 0)	
5586, P8_0mM	-.NVDFNSESTR.R	1169.18	-0.835	2	0	2.04	0.21	226.83	70.0	39373	3
5613, P8_0mM	-.NVDFNSESTR.R	1169.18	-0.709	2	0	3.07	0.12	621.69	1.0	15/18	3
5751, P8_20mM	R.VSPTASNMLK.M	1064.24	-0.727	2	0	2.16	0.05	248.90	28.0	13/18	2
5757, P8_20mM	R.VSPTASNMLK.M	1064.24	-0.688	2	0	2.51	0.24	236.90	27.0	39434	2
5853, P8_60mM	-.NVDFNSESTR.R	1169.18	-0.787	2	0	2.35	0.16	387.60	5.0	39434	3
5892, P8_60mM	-.NVDFNSESTR.R	1169.18	-1.952	2	0	2.09	0.21	433.87	14.0	39434	3
5925, P8_60mM	R.RVSPTASNMLK.M	1204.43	-0.829	2	0	2.92	0.10	1066.69	1.0	16/20	2
5934, P8_60mM	R.RVSPTASNMLK.M	1204.43	-0.868	2	0	2.82	0.06	1173.26	1.0	17/20	2
6144, P8_20mM	-.NVDFNSESTRR.K	1325.37	-0.695	2	0	2.06	0.16	237.38	88.0	13/20	3
6528 - 6531, P8_20mM	-.NVDFNSESTR.R	1169.18	-0.753	2	0	2.48	0.05	387.71	4.0	14/18	3
6570, P8_20mM	-.NVDFNSESTR.R	1169.18	-0.709	2	0	3.00	0.12	665.88	1.0	16/18	3
6582, P8_20mM	-.NVDFNSESTR.R	1169.18	-0.708	2	0	3.35	0.17	670.97	1.0	16/18	3
6612, P8_20mM	-.NVDFNSESTR.R	1169.18	-0.703	1	0	2.25	0.17	160.09	16.0	39404	3

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Scan(s), File (salt concentration)	Peptides	MH+	ΔM	z	P(pep)	X_{corr}	ΔCn	Sp	RSp	Ions	Count
6681, P8_20mM	R.RVSPTASNMLK.M	1204.43	-0.828	2	0	2.76	0.06	880.09	2.0	15/20	2
6687, P8_20mM	R.RVSPTASNMLK.M	1204.43	-0.751	2	0	2.64	0.12	872.88	1.0	15/20	2
7314, P8_20mM	R.VSPTASNMLK.M	1048.24	-0.720	1	0	2.05	0.10	237.12	80.0	39373	2
7326, P8_20mM	R.VSPTASNMLK.M	1048.24	-0.757	1	0	1.90	0.08	230.22	110.0	39373	2
7893 - 7896, P8_20mM	K.EIVDLHNSLR.R	1196.34	-0.747	2	0	3.00	0.20	406.20	1.0	15/18	4
8805, P8_20mM	K.MEWYPEAASNAER.W	1554.67	-1.076	2	0	4.19	0.32	1346.83	2.0	22/24	3
8811, P8_20mM	K.MEWYPEAASNAER.W	1554.67	-1.072	2	0	4.35	0.29	1206.44	1.0	21/24	3
12465, P8_20mM	K.MEWYPEAASNAER.W	1554.67	0.611	2	1	2.75	0.05	649.30	3.0	16/24	3
5. toxin B					0	60.20		7705.84	229595.0	28 (20 5 1 0 2)	
5235 - 5238, P8_20mM	K.DCPNGHV CYTK.T	1351.49	-1.041	2	0	2.91	0.34	332.25	159.0	13/20	6
5274, P8_20mM	K.DCPNGHV CYTK.T	1351.49	-1.018	2	0	3.22	0.32	423.61	6.0	15/20	6
7065, P8_60mM	R.CFITPDITSKDCPNGHV CYTK.T	2514.84	-2.749	4	0	3.95	0.23	1165.38	14.0	36/120	6
7497 - 7500, P8_60mM	-.IRCFITPDITSK.D	1451.72	-0.945	2	0	3.64	0.29	1125.92	1.0	18/22	6
7668, P8_60mM	R.TGVDIQCCSTDDCPFPTR.K	2130.33	-1.032	2	0	3.41	0.04	1158.84	1.0	19/34	
7743, P8_60mM	R.CFITPDITSK.D	1182.37	-0.738	2	0	2.42	0.17	776.77	3.0	14/18	6
7749, P8_60mM	R.CFITPDITSK.D	1182.37	-0.742	2	1	2.51	0.09	712.31	6.0	13/18	6
8043, P8_20mM	R.TGVDIQCCSTDDCPFPTR.K	2258.50	2.544	3	0	3.56	0.16	445.68	139.0	24/72	
8580 - 8583, P8_20mM	R.TGVDIQCCSTDDCPFPTR.K	2130.33	2.540	2	0	4.09	0.07	1043.48	2.0	18/34	
8640, P8_20mM	R.CFITPDITSK.D	1182.37	-0.783	2	0	2.96	0.33	899.65	2.0	15/18	6
8646, P8_20mM	R.CFITPDITSK.D	1182.37	-0.776	2	0	2.42	0.16	585.28	15.0	39434	6
8670, P8_20mM	R.CFITPDITSK.D	1182.37	-0.834	1	0	3.09	0.31	272.52	1.0	13/18	6
8676, P8_20mM	R.CFITPDITSK.D	1182.37	-0.830	1	0	2.96	0.38	274.19	1.0	13/18	6
8682, P8_20mM	R.CFITPDITSK.D	1182.37	-0.830	1	0	3.11	0.31	275.52	1.0	13/18	6
8700, P8_20mM	R.CFITPDITSK.D	1182.37	-0.830	1	0	3.20	0.24	295.56	1.0	13/18	6
8712, P8_20mM	R.CFITPDITSK.D	1182.37	-0.818	2	0	2.56	-	956.16	2.0	15/18	6
8844, P8_20mM	R.TGVDIQCCSTDDCPFPTR.K	2130.33	-2.528	2	0	3.39	0.09	1327.37	1.0	21/34	
8850, P8_20mM	R.TGVDIQCCSTDDCPFPTR.K	2130.33	-1.029	2	0	3.77	0.11	1198.26	1.0	20/34	
8958, P8_20mM	R.CFITPDITSK.D	1182.37	-0.782	2	0	3.10	0.29	830.84	2.0	15/18	6
8970, P8_20mM	R.CFITPDITSK.D	1182.37	-0.816	2	0	2.80	0.27	834.71	2.0	15/18	6
9312 - 9315, P8_20mM	R.CFITPDITSK.D	1182.37	-0.723	2	0	2.73	0.02	706.21	5.0	14/18	6

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Scan(s), File (salt concentration)	Peptides	MH+	ΔM	z	P(pep)	X_{corr}	ΔCn	Sp	RSp	Ions	Count
9900 - 9903, P8_20mM	R.TGVDIQCCSTDDCPFPTR.K	2130.33	-0.945	2	0	3.52	0.18	839.41	4.0	17/34	
10620, P8_20mM	R.TGVDIQCCSTDDCPFPTR.K	2130.33	-0.925	2	0	3.29	0.14	972.05	4.0	18/34	
11226, P8_20mM	R.TGVDIQCCSTDDCPFPTR.K	2130.33	-0.246	2	0	3.69	0.00	1389.18	1.0	21/34	
11613, P8_20mM	R.TGVDIQCCSTDDCPFPTR.K	2130.33	-0.366	2	0	3.55	0.09	1038.13	4.0	18/34	
11646, P8_20mM	R.TGVDIQCCSTDDCPFPTR.K	2130.33	-1.656	2	0	3.59	0.02	1155.26	1.0	20/34	
12414 - 12417, P8_20mM	R.TGVDIQCCSTDDCPFPTR.K	2130.33	-0.928	2	0	3.68	0.01	1241.35	1.0	20/34	
12438 - 12441, P8_20mM	R.CFITPDITSK.D	1182.37	-0.816	2	1	2.28	-	685.01	35.0	13/18	6
6. NXL4_NAJNA Long neurotoxin 4 (Toxin D)					0	58.23		7889.04	128950.0	32 (28 2 0 0 2)	
5235 - 5238, P8_20mM	K.DCPNGHVCYTK.T	1351.49	-1.041	2	0	2.91	0.34	332.25	159.0	13/20	6
5274, P8_20mM	K.DCPNGHVCYTK.T	1351.49	-1.018	2	0	3.22	0.32	423.61	6.0	15/20	6
5679, P8_60mM	R.GERVDLGCAATCPTVK.T	1734.98	-1.380	3	0	2.62	0.13	757.00	2.0	24/60	1
5964 - 5967, P8_0mM	R.VDLGCAATCPTVK.T	1392.63	-1.097	2	0	4.57	0.49	1875.90	1.0	20/24	7
7065, P8_60mM	R.CFITPDITSKDCPNGHVCYTK.T	2514.84	-2.749	4	0	3.95	0.23	1165.38	14.0	36/120	6
7221 - 7224, P8_20mM	R.VDLGCAATCPTVK.T	1392.63	-1.014	2	0	4.44	0.49	1531.36	1.0	18/24	7
7245 - 7248, P8_20mM	R.VDLGCAATCPTVK.T	1392.63	-0.953	2	0	4.61	0.38	1418.14	1.0	18/24	7
7260, P8_20mM	R.VDLGCAATCPTVK.T	1392.63	-0.969	1	0	3.05	0.36	386.73	1.0	14/24	7
7269, P8_20mM	R.VDLGCAATCPTVK.T	1392.63	-0.969	1	0	2.55	0.39	307.46	1.0	13/24	7
7293, P8_20mM	R.VDLGCAATCPTVK.T	1392.63	-0.969	1	0	2.72	0.21	241.54	4.0	39440	7
7299, P8_20mM	R.VDLGCAATCPTVK.T	1392.63	-0.985	1	0	3.00	0.28	347.79	2.0	14/24	7
7497 - 7500, P8_60mM	-.IRCFITPDITSK.D	1451.72	-0.945	2	0	3.64	0.29	1125.92	1.0	18/22	6
7587 - 7590, P8_20mM	R.VDLGCAATCPTVK.T	1392.63	-1.017	2	0	4.22	0.41	1574.71	1.0	18/24	7
7743, P8_60mM	R.CFITPDITSK.D	1182.37	-0.738	2	0	2.42	0.17	776.77	3.0	14/18	6
7749, P8_60mM	R.CFITPDITSK.D	1182.37	-0.742	2	1	2.51	0.09	712.31	6.0	13/18	6
8640, P8_20mM	R.CFITPDITSK.D	1182.37	-0.783	2	0	2.96	0.33	899.65	2.0	15/18	6
8646, P8_20mM	R.CFITPDITSK.D	1182.37	-0.776	2	0	2.42	0.16	585.28	15.0	39434	6
8670, P8_20mM	R.CFITPDITSK.D	1182.37	-0.834	1	0	3.09	0.31	272.52	1.0	13/18	6
8676, P8_20mM	R.CFITPDITSK.D	1182.37	-0.830	1	0	2.96	0.38	274.19	1.0	13/18	6
8682, P8_20mM	R.CFITPDITSK.D	1182.37	-0.830	1	0	3.11	0.31	275.52	1.0	13/18	6
8700, P8_20mM	R.CFITPDITSK.D	1182.37	-0.830	1	0	3.20	0.24	295.56	1.0	13/18	6
8712, P8_20mM	R.CFITPDITSK.D	1182.37	-0.818	2	0	2.56	-	956.16	2.0	15/18	6

Supplemental Table 7: Orthologous proteins of peptide sequences generated from ion-exchange chromatography-purified *N. kaouthia* venom protein components (P8) by 2D-LC/MS-MS and database search

Reference					P(pro)	Score	Coverage	MW	Accession	Peptide(Hits)	
Scan(s), File (salt concentration)	Peptides	MH+	ΔM	z	P(pep)	X_{corr}	ΔCn	Sp	RSp	Ions	Count
8958, P8_20mM	R.CFITPDITSK.D	1182.37	-0.782	2	0	3.10	0.29	830.84	2.0	15/18	6
8970, P8_20mM	R.CFITPDITSK.D	1182.37	-0.816	2	0	2.80	0.27	834.71	2.0	15/18	6
9312 - 9315, P8_20mM	R.CFITPDITSK.D	1182.37	-0.723	2	0	2.73	0.02	706.21	5.0	14/18	6
10806, P8_20mM	R.VDLGCAATCPTVK.T	1392.63	2.680	2	0	2.95	0.19	596.78	14.0	13/24	7
10812, P8_20mM	R.VDLGCAATCPTVK.T	1392.63	2.794	2	0	2.69	0.16	551.68	2.0	13/24	7
11244, P8_20mM	R.VDLGCAATCPTVK.T	1392.63	-1.113	2	0	3.14	0.24	753.86	18.0	15/24	7
11490, P8_20mM	R.VDLGCAATCPTVK.T	1392.63	-1.156	2	0	3.94	0.34	1255.45	1.0	16/24	7
11520, P8_20mM	R.VDLGCAATCPTVK.T	1392.63	-1.110	2	0	3.93	0.30	1087.09	1.0	15/24	7
12438 - 12441, P8_20mM	R.CFITPDITSK.D	1182.37	-0.816	2	1	2.28	-	685.01	35.0	13/18	6
13035, P8_20mM	R.VDLGCAATCPTVK.T	1392.63	-1.119	2	0	3.76	0.39	1054.58	1.0	16/24	7
7. NXL5_NAJNA Long neurotoxin 5 (Toxin E)					0	58.23		7862.96	128952.0	32 (28 2 0 0 2)	
5235 - 5238, P8_20mM	K.DCPNGHV CYTK.T	1351.49	-1.041	2	0	2.91	0.34	332.25	159.0	13/20	6
5274, P8_20mM	K.DCPNGHV CYTK.T	1351.49	-1.018	2	0	3.22	0.32	423.61	6.0	15/20	6
5679, P8_60mM	R.GERVDLGCAATCPTVK.T	1734.98	-1.380	3	0	2.62	0.13	757.00	2.0	24/60	1
5964 - 5967, P8_0mM	R.VDLGCAATCPTVK.T	1392.63	-1.097	2	0	4.57	0.49	1875.90	1.0	20/24	7
7065, P8_60mM	R.CFITPDITSKDCPNGHV CYTK.T	2514.84	-2.749	4	0	3.95	0.23	1165.38	14.0	36/120	6
7221 - 7224, P8_20mM	R.VDLGCAATCPTVK.T	1392.63	-1.014	2	0	4.44	0.49	1531.36	1.0	18/24	7
7245 - 7248, P8_20mM	R.VDLGCAATCPTVK.T	1392.63	-0.953	2	0	4.61	0.38	1418.14	1.0	18/24	7
7260, P8_20mM	R.VDLGCAATCPTVK.T	1392.63	-0.969	1	0	3.05	0.36	386.73	1.0	14/24	7
7269, P8_20mM	R.VDLGCAATCPTVK.T	1392.63	-0.969	1	0	2.55	0.39	307.46	1.0	13/24	7
7293, P8_20mM	R.VDLGCAATCPTVK.T	1392.63	-0.969	1	0	2.72	0.21	241.54	4.0	39440	7
7299, P8_20mM	R.VDLGCAATCPTVK.T	1392.63	-0.985	1	0	3.00	0.28	347.79	2.0	14/24	7
7497 - 7500, P8_60mM	-.IRCFITPDITSK.D	1451.72	-0.945	2	0	3.64	0.29	1125.92	1.0	18/22	6
7587 - 7590, P8_20mM	R.VDLGCAATCPTVK.T	1392.63	-1.017	2	0	4.22	0.41	1574.71	1.0	18/24	7
7743, P8_60mM	R.CFITPDITSK.D	1182.37	-0.738	2	0	2.42	0.17	776.77	3.0	14/18	6
7749, P8_60mM	R.CFITPDITSK.D	1182.37	-0.742	2	1	2.51	0.09	712.31	6.0	13/18	6
8640, P8_20mM	R.CFITPDITSK.D	1182.37	-0.783	2	0	2.96	0.33	899.65	2.0	15/18	6
8646, P8_20mM	R.CFITPDITSK.D	1182.37	-0.776	2	0	2.42	0.16	585.28	15.0	39434	6
8670, P8_20mM	R.CFITPDITSK.D	1182.37	-0.834	1	0	3.09	0.31	272.52	1.0	13/18	6
8676, P8_20mM	R.CFITPDITSK.D	1182.37	-0.830	1	0	2.96	0.38	274.19	1.0	13/18	6

Supplemental Table 7: Orthologous proteins of peptide sequences generated from ion-exchange chromatography-purified *N. kaouthia* venom protein components (P8) by 2D-LC/MS-MS and database search

Reference					P(pro)	Score	Coverage	MW	Accession	Peptide(Hits)	
Scan(s), File (salt concentration)	Peptides	MH+	ΔM	z	P(pep)	X_{corr}	ΔCn	Sp	RSp	Ions	Count
8682, P8_20mM	R.CFITPDITSK.D	1182.37	-0.830	1	0	3.11	0.31	275.52	1.0	13/18	6
8700, P8_20mM	R.CFITPDITSK.D	1182.37	-0.830	1	0	3.20	0.24	295.56	1.0	13/18	6
8712, P8_20mM	R.CFITPDITSK.D	1182.37	-0.818	2	0	2.56	-	956.16	2.0	15/18	6
8958, P8_20mM	R.CFITPDITSK.D	1182.37	-0.782	2	0	3.10	0.29	830.84	2.0	15/18	6
8970, P8_20mM	R.CFITPDITSK.D	1182.37	-0.816	2	0	2.80	0.27	834.71	2.0	15/18	6
9312 - 9315, P8_20mM	R.CFITPDITSK.D	1182.37	-0.723	2	0	2.73	0.02	706.21	5.0	14/18	6
10806, P8_20mM	R.VDLGCAATCPTVK.T	1392.63	2.680	2	0	2.95	0.19	596.78	14.0	13/24	7
10812, P8_20mM	R.VDLGCAATCPTVK.T	1392.63	2.794	2	0	2.69	0.16	551.68	2.0	13/24	7
11244, P8_20mM	R.VDLGCAATCPTVK.T	1392.63	-1.113	2	0	3.14	0.24	753.86	18.0	15/24	7
11490, P8_20mM	R.VDLGCAATCPTVK.T	1392.63	-1.156	2	0	3.94	0.34	1255.45	1.0	16/24	7
11520, P8_20mM	R.VDLGCAATCPTVK.T	1392.63	-1.110	2	0	3.93	0.30	1087.09	1.0	15/24	7
12438 - 12441, P8_20mM	R.CFITPDITSK.D	1182.37	-0.816	2	1	2.28	-	685.01	35.0	13/18	6
13035, P8_20mM	R.VDLGCAATCPTVK.T	1392.63	-1.119	2	0	3.76	0.39	1054.58	1.0	16/24	7
8. CRVP1_NAJAT Natrin-1 precursor (Cysteine-rich venom protein 1) (NA-CRVP1) (Protein G2a)					0	48.22		26882.29	48428837.0	12 (11 1 0 0 0)	
5751, P8_20mM	R.VSPTASNM*LK.M	1064.24	-0.727	2	0	2.16	0.05	248.90	28.0	13/18	2
5757, P8_20mM	R.VSPTASNM*LK.M	1064.24	-0.688	2	0	2.51	0.24	236.90	27.0	39434	2
5925, P8_60mM	R.RVSPTASNMLK.M	1204.43	-0.829	2	0	2.92	0.10	1066.69	1.0	16/20	2
5934, P8_60mM	R.RVSPTASNMLK.M	1204.43	-0.868	2	0	2.82	0.06	1173.26	1.0	17/20	2
6681, P8_20mM	R.RVSPTASNMLK.M	1204.43	-0.828	2	0	2.76	0.06	880.09	2.0	15/20	2
6687, P8_20mM	R.RVSPTASNMLK.M	1204.43	-0.751	2	0	2.64	0.12	872.88	1.0	15/20	2
7314, P8_20mM	R.VSPTASNMLK.M	1048.24	-0.720	1	0	2.05	0.10	237.12	80.0	39373	2
7326, P8_20mM	R.VSPTASNMLK.M	1048.24	-0.757	1	0	1.90	0.08	230.22	110.0	39373	2
7893 - 7896, P8_20mM	K.EIVDLHNSLR.R	1196.34	-0.747	2	0	3.00	0.20	406.20	1.0	15/18	4
8805, P8_20mM	K.MEWYPEAASNAER.W	1554.67	-1.076	2	0	4.19	0.32	1346.83	2.0	22/24	3
8811, P8_20mM	K.MEWYPEAASNAER.W	1554.67	-1.072	2	0	4.35	0.29	1206.44	1.0	21/24	3
12465, P8_20mM	K.MEWYPEAASNAER.W	1554.67	0.611	2	1	2.75	0.05	649.30	3.0	16/24	3
9. NXL1_NAJNA Long neurotoxin 1 (Toxin A)					0	40.20		7847.00	128932.0	17 (14 1 0 0 2)	
5235 - 5238, P8_20mM	K.DCPNGHV CYTK.T	1351.49	-1.041	2	0	2.91	0.34	332.25	159.0	13/20	6
5274, P8_20mM	K.DCPNGHV CYTK.T	1351.49	-1.018	2	0	3.22	0.32	423.61	6.0	15/20	6
7065, P8_60mM	R.CFITPDITSKDCPNGHV CYTK.T	2514.84	-2.749	4	0	3.95	0.23	1165.38	14.0	36/120	6

Supplemental Table 7: Orthologous proteins of peptide sequences generated from ion-exchange chromatography-purified *N. kaouthia* venom protein components (P8) by 2D-LC/MS-MS and database search

Reference					P(pro)	Score	Coverage	MW	Accession	Peptide(Hits)	
Scan(s), File (salt concentration)	Peptides	MH+	Δ M	z	P(pep)	X_{corr}	Δ Cn	Sp	RSp	Ions	Count
7497 - 7500, P8_60mM	-.IRCFITPDITSK.D	1451.72	-0.945	2	0	3.64	0.29	1125.92	1.0	18/22	6
7743, P8_60mM	R.CFITPDITSK.D	1182.37	-0.738	2	0	2.42	0.17	776.77	3.0	14/18	6
7749, P8_60mM	R.CFITPDITSK.D	1182.37	-0.742	2	1	2.51	0.09	712.31	6.0	13/18	6
8640, P8_20mM	R.CFITPDITSK.D	1182.37	-0.783	2	0	2.96	0.33	899.65	2.0	15/18	6
8646, P8_20mM	R.CFITPDITSK.D	1182.37	-0.776	2	0	2.42	0.16	585.28	15.0	39434	6
8670, P8_20mM	R.CFITPDITSK.D	1182.37	-0.834	1	0	3.09	0.31	272.52	1.0	13/18	6
8676, P8_20mM	R.CFITPDITSK.D	1182.37	-0.830	1	0	2.96	0.38	274.19	1.0	13/18	6
8682, P8_20mM	R.CFITPDITSK.D	1182.37	-0.830	1	0	3.11	0.31	275.52	1.0	13/18	6
8700, P8_20mM	R.CFITPDITSK.D	1182.37	-0.830	1	0	3.20	0.24	295.56	1.0	13/18	6
8712, P8_20mM	R.CFITPDITSK.D	1182.37	-0.818	2	0	2.56	-	956.16	2.0	15/18	6
8958, P8_20mM	R.CFITPDITSK.D	1182.37	-0.782	2	0	3.10	0.29	830.84	2.0	15/18	6
8970, P8_20mM	R.CFITPDITSK.D	1182.37	-0.816	2	0	2.80	0.27	834.71	2.0	15/18	6
9312 - 9315, P8_20mM	R.CFITPDITSK.D	1182.37	-0.723	2	0	2.73	0.02	706.21	5.0	14/18	6
12438 - 12441, P8_20mM	R.CFITPDITSK.D	1182.37	-0.816	2	1	2.28	-	685.01	35.0	13/18	6
10. NXL1_NAJNA Long neurotoxin 1 (Toxin A)					0	40.20		7847.00	128932.0	17 (14 1 0 0 2)	
5235 - 5238, P8_20mM	K.DCPNGHV CYTK.T	1351.49	-1.041	2	0	2.91	0.34	332.25	159.0	13/20	6
5274, P8_20mM	K.DCPNGHV CYTK.T	1351.49	-1.018	2	0	3.22	0.32	423.61	6.0	15/20	6
7065, P8_60mM	R.CFITPDITSKDCPNGHV CYTK.T	2514.84	-2.749	4	0	3.95	0.23	1165.38	14.0	36/120	6
7497 - 7500, P8_60mM	-.IRCFITPDITSK.D	1451.72	-0.945	2	0	3.64	0.29	1125.92	1.0	18/22	6
7743, P8_60mM	R.CFITPDITSK.D	1182.37	-0.738	2	0	2.42	0.17	776.77	3.0	14/18	6
7749, P8_60mM	R.CFITPDITSK.D	1182.37	-0.742	2	1	2.51	0.09	712.31	6.0	13/18	6
8640, P8_20mM	R.CFITPDITSK.D	1182.37	-0.783	2	0	2.96	0.33	899.65	2.0	15/18	6
8646, P8_20mM	R.CFITPDITSK.D	1182.37	-0.776	2	0	2.42	0.16	585.28	15.0	39434	6
8670, P8_20mM	R.CFITPDITSK.D	1182.37	-0.834	1	0	3.09	0.31	272.52	1.0	13/18	6
8676, P8_20mM	R.CFITPDITSK.D	1182.37	-0.830	1	0	2.96	0.38	274.19	1.0	13/18	6
8682, P8_20mM	R.CFITPDITSK.D	1182.37	-0.830	1	0	3.11	0.31	275.52	1.0	13/18	6
8700, P8_20mM	R.CFITPDITSK.D	1182.37	-0.830	1	0	3.20	0.24	295.56	1.0	13/18	6
8712, P8_20mM	R.CFITPDITSK.D	1182.37	-0.818	2	0	2.56	-	956.16	2.0	15/18	6
8958, P8_20mM	R.CFITPDITSK.D	1182.37	-0.782	2	0	3.10	0.29	830.84	2.0	15/18	6
8970, P8_20mM	R.CFITPDITSK.D	1182.37	-0.816	2	0	2.80	0.27	834.71	2.0	15/18	6

Supplemental Table 7: Orthologous proteins of peptide sequences generated from ion-exchange chromatography-purified *N. kaouthia* venom protein components (P8) by 2D-LC/MS-MS and database search

Reference					P(pro)	Score	Coverage	MW	Accession	Peptide(Hits)	
Scan(s), File (salt concentration)	Peptides	MH+	ΔM	z	P(pep)	X_{corr}	ΔCn	Sp	RSp	Ions	Count
9312 - 9315, P8_20mM	R.CFITPDITSK.D	1182.37	-0.723	2	0	2.73	0.02	706.21	5.0	14/18	6
12438 - 12441, P8_20mM	R.CFITPDITSK.D	1182.37	-0.816	2	1	2.28	-	685.01	35.0	13/18	6
11. NXL2_NAJNA Long neurotoxin 2 (Toxin B)					0	40.20		7820.92	128943.0	17 (14 1 0 0 2)	
5235 - 5238, P8_20mM	K.DCPNGHV CYTK.T	1351.49	-1.041	2	0	2.91	0.34	332.25	159.0	13/20	6
5274, P8_20mM	K.DCPNGHV CYTK.T	1351.49	-1.018	2	0	3.22	0.32	423.61	6.0	15/20	6
7065, P8_60mM	R.CFITPDITSKDCPNGHV CYTK.T	2514.84	-2.749	4	0	3.95	0.23	1165.38	14.0	36/120	6
7497 - 7500, P8_60mM	-.IRCFITPDITSK.D	1451.72	-0.945	2	0	3.64	0.29	1125.92	1.0	18/22	6
7743, P8_60mM	R.CFITPDITSK.D	1182.37	-0.738	2	0	2.42	0.17	776.77	3.0	14/18	6
7749, P8_60mM	R.CFITPDITSK.D	1182.37	-0.742	2	1	2.51	0.09	712.31	6.0	13/18	6
8640, P8_20mM	R.CFITPDITSK.D	1182.37	-0.783	2	0	2.96	0.33	899.65	2.0	15/18	6
8646, P8_20mM	R.CFITPDITSK.D	1182.37	-0.776	2	0	2.42	0.16	585.28	15.0	39434	6
8670, P8_20mM	R.CFITPDITSK.D	1182.37	-0.834	1	0	3.09	0.31	272.52	1.0	13/18	6
8676, P8_20mM	R.CFITPDITSK.D	1182.37	-0.830	1	0	2.96	0.38	274.19	1.0	13/18	6
8682, P8_20mM	R.CFITPDITSK.D	1182.37	-0.830	1	0	3.11	0.31	275.52	1.0	13/18	6
8700, P8_20mM	R.CFITPDITSK.D	1182.37	-0.830	1	0	3.20	0.24	295.56	1.0	13/18	6
8712, P8_20mM	R.CFITPDITSK.D	1182.37	-0.818	2	0	2.56	-	956.16	2.0	15/18	6
8958, P8_20mM	R.CFITPDITSK.D	1182.37	-0.782	2	0	3.10	0.29	830.84	2.0	15/18	6
8970, P8_20mM	R.CFITPDITSK.D	1182.37	-0.816	2	0	2.80	0.27	834.71	2.0	15/18	6
9312 - 9315, P8_20mM	R.CFITPDITSK.D	1182.37	-0.723	2	0	2.73	0.02	706.21	5.0	14/18	6
12438 - 12441, P8_20mM	R.CFITPDITSK.D	1182.37	-0.816	2	1	2.28	-	685.01	35.0	13/18	6
12. NXL1_NAJHH Long neurotoxin 1 (Toxin CM-5)					0	36.23		7821.10	128929.0	20 (19 0 1 0 0)	
5679, P8_60mM	R.GKRVDLGCAATCPTVK.T	1734.04	-0.439	3	0	2.84	0.08	650.61	9.0	22/60	4
5685, P8_60mM	R.GKRVDLGCAATCPTVK.T	1734.04	-0.376	3	0	2.54	0.07	822.04	6.0	21/60	4
5964 - 5967, P8_0mM	R.VDLGCAATCPTVK.T	1392.63	-1.097	2	0	4.57	0.49	1875.90	1.0	20/24	7
6063 - 6066, P8_60mM	K.RVDLGCAATCPTVK.T	1548.81	-1.042	2	0	4.01	0.38	1141.23	1.0	19/26	5
6117 - 6120, P8_60mM	K.RVDLGCAATCPTVK.T	1548.81	-1.210	3	0	3.25	0.11	1308.55	3.0	24/52	5
6831 - 6834, P8_20mM	K.RVDLGCAATCPTVK.T	1548.81	-1.001	2	0	3.40	0.13	796.49	1.0	16/26	5
7221 - 7224, P8_20mM	R.VDLGCAATCPTVK.T	1392.63	-1.014	2	0	4.44	0.49	1531.36	1.0	18/24	7
7245 - 7248, P8_20mM	R.VDLGCAATCPTVK.T	1392.63	-0.953	2	0	4.61	0.38	1418.14	1.0	18/24	7
7260, P8_20mM	R.VDLGCAATCPTVK.T	1392.63	-0.969	1	0	3.05	0.36	386.73	1.0	14/24	7

Supplemental Table 7: Orthologous proteins of peptide sequences generated from ion-exchange chromatography-purified *N. kaouthia* venom protein components (P8) by 2D-LC/MS-MS and database search

Reference					P(pro)	Score	Coverage	MW	Accession	Peptide(Hits)	
Scan(s), File (salt concentration)	Peptides	MH+	ΔM	z	P(pep)	X_{corr}	ΔCn	Sp	RSp	Ions	Count
7269, P8_20mM	R.VDLGCAATCPTVK.T	1392.63	-0.969	1	0	2.55	0.39	307.46	1.0	13/24	7
7293, P8_20mM	R.VDLGCAATCPTVK.T	1392.63	-0.969	1	0	2.72	0.21	241.54	4.0	39440	7
7299, P8_20mM	R.VDLGCAATCPTVK.T	1392.63	-0.985	1	0	3.00	0.28	347.79	2.0	14/24	7
7587 - 7590, P8_20mM	R.VDLGCAATCPTVK.T	1392.63	-1.017	2	0	4.22	0.41	1574.71	1.0	18/24	7
8109 - 8112, P8_20mM	K.PGVDIKCCSTDNCNPFPTK.K	2239.50	2.496	2	0	3.03	0.46	433.23	157.0	13485	2
10806, P8_20mM	R.VDLGCAATCPTVK.T	1392.63	2.680	2	0	2.95	0.19	596.78	14.0	13/24	7
10812, P8_20mM	R.VDLGCAATCPTVK.T	1392.63	2.794	2	0	2.69	0.16	551.68	2.0	13/24	7
11244, P8_20mM	R.VDLGCAATCPTVK.T	1392.63	-1.113	2	0	3.14	0.24	753.86	18.0	15/24	7
11490, P8_20mM	R.VDLGCAATCPTVK.T	1392.63	-1.156	2	0	3.94	0.34	1255.45	1.0	16/24	7
11520, P8_20mM	R.VDLGCAATCPTVK.T	1392.63	-1.110	2	0	3.93	0.30	1087.09	1.0	15/24	7
13035, P8_20mM	R.VDLGCAATCPTVK.T	1392.63	-1.119	2	0	3.76	0.39	1054.58	1.0	16/24	7