

Supplemental Table 1: MS/MS peptide identification for alpha tubulin and voltage-dependent anion-selective channel 2. Raw data were searched with the Sequest node of Proteome Discover 1.4, using the uniprot_ref_mouse database. Variable modifications of methionine oxidation (M^{OX}), proline oxidation (P^{OX}), cysteine pyridylethylation (C^{PE}) and cysteine succination (C^{2SC}) were considered.

Swiss-Prot Accession #	Protein Identity	% Coverage	Peptides Identified	PSMs	M+ (Da)	Charge
P68368	Tubulin alpha-4A chain	64.06	RAFVHWYVGEGM ^{OX} EEGEFSEAR	4	2502.13694	3
			AVC ^{PE} MLSNTTAIAEAWAR	4	1912.94756	2
			AVC ^{PE} M ^{OX} LSNTTAIAEAWAR	6	1928.93364	2
			AYHEQLSVAEITNAC ^{PE} FEPANQMVK	9	2798.34463	4
			AYHEQLSVAEITNAC ^{PE} FEP ^{OX} ANQMVK	18	2814.34062	2
			QLFHPEQLITGKEDAANNYAR	15	2415.22353	4
			AFVHWYVGEGMEEGEFSEAREDMAALEK	20	3217.45107	4
			AFVHWYVGEGM ^{OX} EEGEFSEAREDMAALEK	22	3233.44863	4
			AFVHWYVGEGM ^{OX} EEGEFSEAREDM ^{OX} AALEK	7	3249.43813	4
			LISQIVSSITASLR	54	1487.88874	3
			AVFVDLEPTVIDEIR	7	1715.93387	3
			FDGALNVDLTFQTNLVPYPR	55	2409.22647	3
			TIGGGDDSF ^{PE} ETGAGK	5	2115.94512	2
			RNLDIRPTYTNLNR	15	1874.99306	4
			DVNAAIAAIK	3	985.57237	2
			IHFPLATYAPVISA EK	16	1756.97991	2
			SIQFVDWC ^{PE} PTGFK	2	1632.79997	2
			LDHKFDLMYAK	10	1380.70647	2
			LDHKFDLM ^{OX} YAK	12	1396.70098	2
			LSVDYGKK	9	909.50780	2
			EIIDPVLDR	3	1069.59599	2
			VGINYQPPTVVPGGDLAK	29	1824.99455	2
			GHYTIGK	13	775.41216	2
			YMAC ^{PE} C ^{PE} LLYR	8	1345.63249	2
			YM ^{OX} AC ^{PE} C ^{PE} LLYR	7	1361.62883	2
			GDVVPK	6	614.35112	2
			HVPR	3	508.30171	2

G3UX26	Voltage-dependent anion-selective channel protein 2 (VDAC 2)	50.88	YQLDPTASISAK	3	1293.66265	2
			LTFDFFFSPNTGKK	6	1556.78325	2
			VNNSSLIGVGYTQTLRPGVK	10	2103.14580	2
			TGDFQLHTNVNNGTEFGGSLYQK	1	2527.16764	3
			WNTDNTLGTEIAIEDQICPEQGLK	1	2567.24631	3
			VSGTLETK	2	834.45195	2
			SNFAVGYR	2	913.44621	3
			SFNAGGHK	5	817.39092	3
			FGIAAK	3	606.35832	3
			DIFNK	1	636.33269	2
			LTLSALVDGK	2	1016.59844	2
			GFGFGLVK	3	824.46269	2

Supplemental Table 2: MS/MS peptide identification for voltage-dependent anion-selective channels 1 and 2 spots. Raw data were searched with the Sequest HT node of Proteome Discover 1.4 (SP1), using the uniprot_ref_mouse database.

Swiss-Prot Accession #	Protein Identity	% Coverage	Peptides Identified	PSMs	M+ (Da)	Charge
Q60932	Voltage-dependent anion-selective channel protein 1 (VDAC 1)	55.74	LTFDSSFSPNTGKK	75	1528.77349	2
			TKSENGLEFTSSGSANTETTK	75	2189.02787	3
			VNSSLIGLGYTQTLKPGIK	418	2103.18559	2
			SRVTQSNFAVGKY	194	1456.75847	2
			WNTDNTLGTEITVEDQLAR	4	2176.06182	2
			WTEYGLTFTEK	48	1374.66203	2
			GYGFGLIK	39	854.47923	2
			KLETAVNLAWTAGNSNTR	4	1946.01889	3
			LTLSALLDGKNVNAGGHK	143	1808.00882	3
			TDEFQLHTNVNDGTEFGGSIYQK	9	2600.19815	3
Q60930	Voltage-dependent anion-selective channel protein 2 (VDAC 2)	21.69	GFGFGLVK	19	824.46825	2
			LTFDSSFSPNTGKK	86	1556.80364	2
			LTLSALVDGK	89	1016.60130	2
			VNSSLIGVGYTQTLRPGVK	89	2103.16167	2
			YQLDPTASISAK	75	1293.67204	2