Supplementary Table 1A.

Proteins identified after nanoLC tandem MS and database searches of archival formalin-fixed human-brain-tissue scrapings (~16 mm^2) after treatment at pH 9, 65 °C for 60 min. Scores >35 indicate identity or extensive homology ($p<0.05$).

Protein name	Accession number	Theoretical molecular weight/pI	Distinct Peptide Matches	Sequence coverage (%)	Mowse score
Glial fibrillary acidic protein	gi|15488941	49880.21/5.42	9	21.1	312
ATP synthase alpha subunit	gi|34468	59750.63/9.16	2	4.7	95
Peroxiredoxin 1	gi|55959887	18975.76/6.42	2	11.7	86
Contactin	gi|414791	113334.44/5.62	4	4	85
Dihydropyrimidinase-like 2	gi|45501286	62293.63/5.95	3	4	83
ATP synthase beta subunit	gi|179279	56896.26/5.38	3	6	70
2-phosphopyruvate-hydratase alpha-enolase; carbonate dehydratase	gi|693933	47108.86/7.01	2	4	59
Microtubule-associated protein 1B isoform 1	gi|5174525	270620.40/4.73	1	0.4	58
Ferritin heavy chain	gi|182777	6328.01/4.88	1	18	54
Glutamate transporter	gi|825504	59572.31/8.52	1	2.2	53
Cathepsin D (lysosomal aspartyl protease)	gi|54697170	44552.22/6.10	2	3.2	52
NFASC protein	gi|34782959	33173.75/8.11	1	3.4	50
Alpha-globin	gi|183801	3285.77/8.51	1	32	48
Prohibitin	gi|46360168	29820.15/5.57	1	4	45
Myelin basic protein	gi|187403	6464.28/11.56	1	17	38
ATP synthase, H^+ transporting, mitochondrial F1 complex, O subunit (oligomycin sensitivity conferring protein)	gi|54696534	23305.33/10.0	1	5.6	38

Serine protease inhibitor Kazal-type 5 precursor (Lympho-epithelial Kazal-type-related inhibitor) (LEKTI)	gi|13959398	120758.62/8.50	2	1.2	36
CNP protein	gi|20380838	47578.63/9.17	1	2.1	36
Pyruvate kinase	gi|35505	57877.82/7.58	1	1.5	35
Guanine nucleotide-binding protein	gi|386750	40046.62/5.35	1	7.1	35

Supplementary Table 1B:

Proteins identified after nanoLC tandem MS and database searches of archival formalin-fixed human-brain-tissue scrapings (~16 mm^2) after treatment at pH 4, 95 °C for 60 min. Scores >35 indicate identity or extensive homology ($p<0.05$). Asterisk (∗) indicates that amongst other common peptides, at least one distinct peptide differentiated between various protein isotypes.

Protein name	Accession number	Theoretical molecular weight/pI	Distinct Peptide Matches	Sequence coverage	Mowse score
Glial fibrillary acidic protein	gi|15488941	49880.21/5.42	16	39	492
Guanine nucleotide-binding protein	gi|386750	80075.23/5.35	5	14.4	182
Tubulin, beta 2 ∗	gi|4507729	49906.97/4.78	3	7.6	114
Alpha-enolase	gi|1167843	47168.96/7.01	3	8.5	112
Dihydropyrimidinase-like 2	gi|45501286	62293.63/5.95	3	5.6	108
Alpha II spectrin	gi|1805280	285065.99/5.22	3	1.7	104
Neurofilament-66; NF-66	gi|994844	54908.18/5.48	3	6.1	101
Mutant beta-actin (beta'-actin)	gi|28336	41812.80/5.22	3	9.6	94
Annexin VI isoform 1	gi|71773329	75873.27/5.42	1	2.4	92
Alpha-tubulin ∗	gi|37492	50157.68/5.02	2	5.3	90
Ferritin light subunit	gi|182516	16394.65/5.65	1	10.5	78
ATP synthase alpha subunit	gi|34468	59750.63/9.16	2	4	77
Glutamate transporter	gi|825504	52705.16/5.72	2	3.5	71
Hypothetical protein	gi|12052826	22468.87/8.80	1	5.5	71
Aquaporin 4 isoform a	gi|4502181	28069.65/6.17	1	2.2	59
Elongation factor 1 alpha	gi|181965	24196.26/9.61	1	5.5	50
Creatine kinase-B	gi|180555	42487.11/5.34	1	3	50
Migration-inducing gene 10 protein	gi|41350401	44614.69/8.30	2	6.2	47

Calmodulin	gi|825635	17162.95/4.06	1	4.6	46
P25 protein	gi|26251744	24948.04/9.55	1	4	45
CaMK-II, beta	gi|1245392	15140.95/5.17	1	8	44
Beta-fodrin	gi|425553	146243.24/5.18	1	0.7	42
Histone H2B	gi|31977	13950.19/10.31	2	13.5	39
ATP synthase, H^+ transporting, mitochondrial F1 complex, beta poly-peptide	gi|16741373	56559.90/5.26	1	3.6	36

Supplementary Table 1C:

Proteins identified after nanoLC tandem MS and database searches of archival formalin-fixed human-brain-tissue scrapings (~16 mm^2) after treatment at pH 6, 95 °C for 60 min. Scores >35 indicate identity or extensive homology ($p<0.05$). Asterisk (∗) indicates that amongst other common peptides, at least one distinct peptide differentiated between various protein isotypes.

Protein name	Accession number	Theoretical molecular weight/pI	Distinct Peptide Matches	Sequence coverage	Mowse score
Glial fibrillary acidic protein	gi|15488941	49880.21/5.42	14	32	558
Dihydropyrimidinase-like 2	gi|45501286	62293.63/5.95	5	9.3	160
Pyruvate kinase	gi|35505	57877.82/7.58	4	7.2	123
Tubulin, beta 2 ∗	gi|4507729	49906.97/4.78	4	10.8	123
Neurofilament-66; NF-66	gi|994844	54908.18/5.48	3	5.1	116
ATP synthase alpha subunit	gi|34468	59750.63/9.16	2	4.7	111
Annexin VI isoform 1	gi|71773329	75873.27/5.42	1	2.4	107
Alpha-tubulin ∗	gi|37492	50157.68/5.02	2	5.3	100
Guanine nucleotide-binding protein	gi|386750	40046.62/5.35	2	5.4	94
Mutant beta-actin (beta-actin)	gi|28336	41812.80/5.22	2	6	86
Contactin	gi|414791	113334.44/5.62	2	2	82
Tenascin R	gi|1589549	149619.99/4.71	2	1.2	76
Ferritin light subunit	gi|182516	16394.65/5.65	1	10.5	71
Hexokinase 1	gi|184021	102502.95/6.44	3	3.2	71
Ubiquitin	gi|229532	8450.74/6.56	1	12.2	70
Glutamate transporter	gi|825504	52705.16/5.72	1	2.2	62
Unnamed protein product	gi|32097	11267.61/10.86	2	18.8	59
Cytosolic malate dehydro-genase	gi|5174539	36426.12/6.91	1	4	56
Spectrin, beta, non-erythrocytic 1 isoform 1	gi|4507195	274631.28/5.41	1	0.4	56

Hypothetical protein	gi|12052826	22468.87/8.80	1	5.5	54
Chain C, Annexin V	gi|809190	35805.58/4.94	1	5	49
Microtubule-associated protein 1B isoform 1	gi|5174525	35805.58/4.94	1	0.4	46
Ezrin (p81) (Cytovillin) (Villin-2)	gi|119717	69398.78/5.94	1	1.5	44
Myelin basic protein	gi|187403	6464.28/11.56	1	17	44
Transketolase	gi|37267	67793.56/7.89	1	1.9	39
PREDICTED: similar to KIAA0445 protein	gi|51461034	67793.56/7.89	2	0.9	36
T-complex protein 1, Beta subunit (TCP-1-BETA)	gi|1871210	22938.29/5.88	1	6.9	35

Supplementary Table 1D:

Proteins identified after nanoLC tandem MS and database searches of archival formalin-fixed human-brain-tissue scrapings (~16 mm^2) after treatment at pH 9, 95 °C for 60 min. Scores >35 indicate identity or extensive homology ($p<0.05$). Asterisk (∗) indicates that amongst other common peptides, at least one distinct peptide differentiated between various protein isotypes.

Protein name	Accession number	Theoretical molecular weight/pI	Distinct Peptide Matches	Sequence coverage	Mowse score
Glial fibrillary acidic protein	gi|15488941	49880.21/5.42	14	33	617
Beta-tubulin ∗	gi|338695	49758.90/4.75	12	22.3	265
Tubulin, beta 2 ∗	gi|4507729	49906.97/4.78	7	20	239
Alpha-tubulin ∗	gi|37492	50157.68/5.02	4	11.1	221
Tubulin, beta 4 ∗	gi|15489150	49585.77/4.78	9	24.3	219
Mutant beta-actin (beta-actin)	gi|28336	41812.80/5.22	6	15	196
Neurofilament, light polypeptide 68 kDa	gi|5453762	61776.85/4.66	5	8.8	166
Alpha-enolase	gi|1167843	47168.96/7.01	2	7.8	141
ATP synthase beta subunit	gi|179279	56896.26/5.38	3	8.3	128
Creatine kinase-B	gi|180555	42487.11/5.34	3	9.2	124
Internexin neuronal inter-mediate filament protein, alpha	gi|14249342	55390.65/5.34	3	6.4	124
Thiol-specific antioxidant protein	gi|438069	21857.00/6.83	3	19.2	104
Alpha-tubulin ∗	gi|32015	49793.21/4.95	2	5.4	102
ATP synthase alpha subunit	gi|34468	59750.63/9.16	3	7.2	98
Peroxiredoxin 1	gi|55959887	18975.76/6.42	2	13.5	98
Glutamate transporter	gi|825504	52705.16/5.72	1	2.2	95
Spectrin, beta, non-	gi|4507195	274631.28/5.41	1	0.4	91

erythrocytic 1 isoform 1					
Alpha II spectrin	gi|1805280	285065.99/5.22	2	0.8	81
Unnamed protein product	gi|32097	11267.61/10.86	3	38	81
Hexokinase 1	gi|184021	102502.95/6.44	1	1.3	77
B-cell receptor associated protein	gi|1673514	23635.11/9.57	1	3.8	58
Dihydropyrimidinase-like 2	gi|30582727	67017.42/5.62	2	3.1	56
Glucose phosphate iso-merase	gi|1336765	63189.21/8.42	3	4.1	55
Human gamma enolase	gi|31165	47268.58/4.91	1	2.3	52
Heat shock 70kDa protein 8 isoform 1	gi|5729877	70898.09/5.37	2	3.1	51
Elongation factor 1 alpha	gi|181965	24196.26/9.61	1	5	49
Beta-globin	gi|183817	18930.80/6.28	2	18	49
Ferritin light subunit	gi|182516	16394.65/5.65	1	10.5	49
Myelin associated glycol-protein isoform b precursor	gi|18104957	63965.78/4.91	1	2.1	43
Alpha-globin	gi|28549	13582.53/7.97	1	9.4	42
Synapsin IIb	gi|1594277	52284.79/7.61	1	2.1	40
3-hydroxyacyl-CoA dehydrogenase	gi|2078327	33571.63/8.69	1	4	40
Epithelial cell marker protein 1	gi|187302	27776.08/4.72	1	2.8	35

Supplementary Table 2A.

Proteins identified in human brain tissue treated at pH 9, 95 °C for 2 h. Scores >35 indicate identity or extensive homology ($p<0.05$). Asterisk (∗) indicates that amongst other common peptides, at least one distinct peptide differentiated between various protein isotypes.

Protein name	Accession number	pI/Theoretical molecular weight	Distinct Peptide Matches	Sequence coverage (%)	Mowse score
Glial fibrillary acidic protein	gi|4503979	5.42/49850	17	38	971
Beta actin	gi|4501885	5.29/41710	6	17	262
Tubulin, beta polypeptide ∗	gi|18088719	4.75/49640	5	12	248
Tubulin 5-beta ∗	gi|35959	4.18/49599	5	12	232
Tubulin, beta 2 ∗	gi|4507729	4.78/49875	4	9	195
Alpha-tubulin ∗	gi|37492	5.02/50126	3	8	181
Tubulin alpha 6 ∗	gi|14389309	4.96/49863	3	8	151
ATP synthase, H^+ transporting, mitochondrial F1 complex, alpha subunit precursor	gi|4757810	9.16/59714	3	7	139
ATP synthase, H^+ transporting, mitochondrial F1 complex, beta polypeptide	gi|16741373	5.26/56525	1	2	90
Creatine kinase	gi|180570	5.342591	2	4	83
Chain C, Human Platelet Profilin Complexed With An L-Pro10- Iodotyrosine Peptide	gi|5542167	3.5/905	2	100	78
Dihydropyrimidinase-like 2	gi|30582727	5.62/66975	2	6	70
14-3-3 protein epsilon isoform transcript variant 1	gi|62131678	4.76/26487	1	5	63
Glucocorticoid receptor AF-1 specific elongation	gi|7108915	9.08/46240	1	2	55

factor					
HIST1H4I protein	gi|45767731	11.36/11332	1	7	53
Na^+/K^+ -ATPase alpha 2 subunit proprotein	gi|4502271	5.47/112193	1	1	48
Ferritin light subunit	gi|182516	5.65/16384	1	10	48
Heat shock protein 90kD	gi|225608	4.79/83242	1	1	46
Thiol-specific antioxidant protein	gi|438069	6.84/21843	1	5	45
Glyceraldehyde-3-phosphate dehydrogenase	gi|31645	8.26/36031	1	4	44

Supplementary Table 2B.

Proteins identified in ~64 mm^2 human brain tissue treated at pH 9, 95 °C for 3 h. Scores >35 indicate identity or extensive homology ($p<0.05$). Asterisk (∗) indicates that amongst other common peptides, at least one distinct peptide differentiated between various protein isotypes.

Protein name	Accession number	pI/Theoretical molecular weight	Distinct Peptide Matches	Sequence coverage	Mowse score
Glial fibrillary acidic protein	gi|4503979	5.42/49880.21	17	40%	994
Mutant beta-actin (beta'-actin)	gi|28336	5.22/41786	5	12%	219
Tubulin alpha 6 ∗	gi|14389309	4.96/49863	3	9%	207
Tubulin 5-beta ∗	gi|35959	4.81/49599	4	10%	205
Beta-tubulin ∗	gi|338695	4.75/49727	4	10%	200
Alpha-tubulin ∗	gi|37492	5.02/50126	3	9%	159
Chain C, Human Platelet Profilin Complexed With An L-Pro10- Iodotyrosine Peptide	gi|5542167	3.5/905	2	100%	88
Beta-subunit (AA 1-312)	gi|28931	4.9/34026	1	4%	87
Beta globin	gi|687685	4.7/4604	1	30%	71
14-3-3 protein epsilon isoform transcript variant 1	gi|62131678	4.76/26487	1	5%	65
Thiol-specific antioxidant protein	gi|438069	6.84/21843	1	5%	59
Chain A, Solution Structure Of Calcium-Calmodulin N-Terminal Domain	gi|16974825	3.9/8483	1	17%	53
ATP synthase, H^+ transporting, mitochondrial F1 complex, alpha subunit precursor	gi|4757810	9.16/59714	1	2%	53
NF-L	gi|1279504	4.66/61739	1	2%	50
Pyruvate kinase	gi|35505	7.58/57841	1	1%	39

Creatine kinase-B	gi|180555	5.34/42460	1	2%	38

Supplementary Table 3.

Table showing proteins identified in ~16 mm^2 mouse brain tissue after 60-min treatment at pH 9 and 95 °C. Individual ions scores >41 indicate identity or extensive homology ($p<0.05$). Asterisk (∗) indicates that amongst other common peptides, at least one unique peptide differentiated between various protein isotypes.

Protein name	Accession number	pI/Theoretical molecular weight	Distinct Peptide Matches	Sequence coverage	Mowse score
Unnamed protein product [Mus musculus]	gi|74223170	4.84/49889	10	27%	546
Tubulin, beta 2 [Mus musculus] ∗	gi|13542680	4.79/49783	10	28%	522
ATP synthase beta-subunit [Mus musculus]	gi|2623222	5.14/56344	5	12%	278
ATP synthase, H^+ transporting, mitochondrial F1 complex, alpha subunit, isoform 1 [Mus musculus]	gi|6680748	9.22/59716	3	7%	244
Gamma-actin [Mus musculus]	gi|809561	5.56/40992	3	9%	216
Tubulin, alpha 6 [Mus musculus] ∗	gi|13435777	4.96/49877	3	8%	179
Ulip2 protein [Mus musculus]	gi|1915913	5.95/62132	2	5%	158
Tubulin, alpha 1 [Mus musculus] ∗	gi|53733821	4.94/50120	3	8%	151
Creatine kinase, brain [Mus musculus]	gi|10946574	5.40/42686	2	7%	140
Calcium/calmodulin-dependent protein kinase type II alpha chain (CaM-kinase II alpha chain)	gi|125284	6.88/54291	2	4%	131
Beta-globin	gi|193767	4.65/5687	2	44%	100
Ubiquitin A-52 residue ribosomal protein fusion product 1	gi|56541098	9.87/14719	2	22%	88

Atp1a1 protein [Mus musculus]	gi|16307541	5.15/108338	1	1%	87
Enolase 2, gamma neuronal [Mus musculus]	gi|7305027	4.99/47267	1	2%	80
Malate dehydrogenase [Mus musculus]	gi|1200100	8.83/35574	1	3%	74
Aspartate aminotransferase precursor [Mus musculus]	gi|2690302	9.05/47382	1	3%	73
Aldolase 1, A isoform [Mus musculus]	gi|6671539	8.31/39331	1	2%	64
14-3-3 zeta [Mus musculus]	gi|1526539	4.7/27737	1	4%	59
Lactate dehydrogenase 1, A chain [Mus musculus]	gi|6754524	7.62/36475	1	3%	53
Heat shock 70 protein [Mus musculus]	gi|1661134	5.37/70793	1	1%	50
Brain abundant, membrane attached signal protein 1 [Mus musculus]	gi|45598372	4.50/22074	1	6%	45
Cytochrome C oxidase subunit 2 [Mus musculus]	gi|62461713	4.6/25959	1	3%	43