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The best proteomics: combination of good gels, addressing quality control, and mining the data

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Our principal goal: to understand the molecular basis of human chronic conditions/diseases, to develop prevention or therapies.

Strategy: <u>a proteomics approach</u>

Hypothesis: Actions of "beneficial" agents such as dietary anti-oxidants in normal and disease tissue will reveal subproteomes of proteins "at risk" for disease-relevant changes.

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Database of protein differences in GSE vs CT brains

	#matched	Accession	MOWSE	Obs	Pred	Obs	Pred	Nature of
	рер	#		m.w.	m.w.	pl	pl	change in GSE brains
Mitochondrial matrix proteinprecursorP60	10	P19227	*1.26E+04	64900	60956	5.6	5.9	+1.5
Creatine Kinase BB chain	12	P07335	*1.66E+05	45600	42712	5.45	5.3	+1.52 Translocation to Acidic pH
Actin	8	P10365	*2.18E+05	42000	41636	5.3	5.4	Less complex
GFAP	20	P47819	*9.67E+09	49000	49943	5.4	5.3	- 1.6
14-3-3 epsilon	10	P42655	*1.41E+09	31900	29174	4.49	4.6	- 2.1
Alpha Enolase	9	P04764	*6.64E+05	46000	46985	6.0	6.2	Less complex
Gamma Enolase	10	P07323	95	47000	47111	5.12	5.03	Less complex
RIKEN cDNA (NM 025994)	9	NP080270	169 95	26000 26000	25084 25084	5.0 5.1	5.0	-1.56
HSC-70	12	gi4103877	110	70321	42455	5.9	6.64	+1.63
HSC-71	16	gi123644	105	70386	71195	5.43	5.49	+1.91
Neurof ilament L Tripl et protein	14	gi13929098	120	61025	61298	4.61	4.63	+1.63
Neurofilament M	19	gi8393823	153	95086	95591	4.75	4.76	+1.73
triplet protein							=	





Validation of protein identifications and quantitations

Protein	LC-MS/MS	Western blot
CK-BB	+	+
Hsp60	+	+
GFAP		
Actin		+
NFL-M	+	
α-enolase	+	
γ-enolase	+	
Hsc70		
Hsc71		
14-3-3e		+
NFL-L		+

(Kim et al., 2005, in Luo and Packer, Oxidative Stress & Neurodegeneration)

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