Supplements

Table S1: Proteins of the Co identified by peptide mass fingerprinting in spots from Coomassie-stained gels arranged by their function. Accession: Accession number from UniProtKB/Swiss-Prot; Entry name: Entry name from UniProtKB/Swiss-Prot; Gene name: from UniProtKB/Swiss-Prot; Regulation (P7)/Regulation (P637): Differential expression in comparison to P90; Control/PD: Spot volume quotient; H: Number of differential expressed spots per biological replicate; Score: Mascot MOWSE-score; Qm: Number of mass values (tryptic peptides) assigned to the identified protein; MW: Theoretical molecular mass (Da); pI: Theoretical pI value taken from the Mascot report.(*) Spots marked with [+] contain multiple proteins within one spot or show no distinct regulation within one fraction. The full description for the cellular location is given in the list of abbreviations.

SpotID	Accession	Entry name	Gene name	Funct. Group/Protein Name	Regulation [P7]	Regulation [P637]	cell. Localisation	H	Control/ PD	Score	MW	pI	Qm	(*)
				Proteins Carbohydrate Metabolism	(SVQ ≤ 0.6)	(SVQ ≥ 1.67)			(P90/P7,P637)		(calc.)			
923	**P51635**	AK1A1_RAT	**Akr1a1**	Alcohol dehydrogenase [NADP(+)]	up	-	Cts, M	6	0.57	207	36711	6.84	17	
492	**P07943**	ALDR_RAT	**Akr1b1**	Aldose reductase	down	-	Cp	6	1.90	159	36230	6.26	14	
274	**P09117**	ALDOC_RAT	**Aldoc**	Fructose-bisphosphate aldolase C	-	up	Cp, Mito, A	6	0.59	252	39658	6.67	24	
359	**P08461**	ODP2_RAT	**Dlat**	Dihydrolipoyllysine-residue acetyltransferase component of pyruvate dehydrogenase complex, mitochondrial	down	-	Mmt	6	2.72	209	67637	8.76	23	
341/5	**Q01205**	ODO2_RAT	**Dlst**	Dihydrolipoyllysine-residue succinyltransferase component of 2-oxoglutarate dehydrogenase complex, mitochondrial	down	down	Mito	6	1.80	96	49236	8.89	15	
539/294	**P04764**	ENOA_RAT	**Eno1**	Alpha-enolase	down	up	Cp, M	6	1.69	349	47440	6.16	37	
15	**P07323**	ENOG_RAT	**Eno2**	Gamma-enolase	down	-	Cp, M	5	4.01	342	47510	5.03	35	
763	**P04797**	G3P_RAT	**Gapdh**	Glyceraldehyde-3-phosphate dehydrogenase	down	-	Cp, Nc	6	2.22	250	36090	8.14	36	
312	**P42123**	LDHB_RAT	**Ldhb**	L-lactate dehydrogenase B chain	down	-	Cp	6	2.66	307	36874	5.7	32	
319	**O88989**	MDHC_RAT	**Mdh1**	Malate dehydrogenase, cytoplasmic	down	-	Cp	6	4.08	153	36631	6.16	21	
527/633	**B1WC26**	B1WC26_RAT	**Nans**	N-acetylneuraminic acid synthase	down	down	Cp, Cts	5	2.81	67	40482	6.39	8	
520	**P26284**	ODPA_RAT	**Pdha1**	Pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial	down	-	Mmt	6	2.30	255	43883	8.49	30	
41	**P49432**	ODPB_RAT	**Pdhb**	Pyruvate dehydrogenase E1 component subunit beta, mitochondrial	down	-	Mmt	5	2.39	149	39299	6.2	21	
754	**P25113**	PGAM1_RAT	**Pgam1**	Phosphoglycerate mutase 1	down	-	Nc, Cts	6	4.91	227	28928	6.67	23	
519/422	**P16617**	PGK1_RAT	**Pgk1**	Phosphoglycerate kinase 1	down	down	Cp	6	4.26	129	47398	8.72	24	
652	**P11980**	KPYM_RAT	**Pkm2**	Pyruvate kinase isozymes M1/M2	down	-	Cp, Nc	6	12.97	385	58294	6.63	45	
586,702	**Q920L2**	DHSA_RAT	**Sdha**	Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial	down	-	Mim	6	2.49	338	72596	6.75	30	+
326	**B2RZ24**	B2RZ24_RAT	**Sucla2**	Succinyl-CoA synthetase beta-A chain	down	-	Mito, Mmt	6	5.35	249	47700	6.06	30	
751	**P48500**	TPIS_RAT	**Tpi1**	Triosephosphate isomerase	down	-	Nc, Cts	6	4.51	196	27345	6.89	20	

25	**Q68FY0**	QCR1_RAT	**Uqcrc1**	Cytochrome b-c1 complex subunit 1, mitochondrial	down	-	Mim	6	6.72	215	53500	5.57	24	
				Proteins Amino Acid Metabolism										
556/324	**P10860**	DHE3_RAT	**Glud1**	Glutamate dehydrogenase 1, mitochondrial	down	up	Mmt	6	2.27	279	61719	8.05	39	
521/280	**P09606**	GLNA_RAT	**Glul**	Glutamine synthetase	down	up	Cp, Mito	6	2.22	278	42982	6.64	33	
198	**F1M9V7**	F1M9V7_RAT	**Npepps**	Aminopeptidase puromycin sensitive	-	up	Nc, Cp	6	0.57	117	103963	5.53	27	
127	**O09175**	AMPB_RAT	**Rnpep**	Aminopeptidase B	-	down	Sc, Cp	5	2.26	178	73372	5.47	23	
28	**Q5RJQ4**	SIR2_RAT	**Sirt2**	NAD-dependent protein deacetylase sirtuin-2	p7: abs	-	Cp, Csk	4	-	269	39921	6.67	23	+
				Proteins Fat Metabolism										
518/329	**Q5XI22**	THIC_RAT	**Acat2**	Acetyl-CoA acetyltransferase, cytosolic	down	down	Cp	6	2.22	74	41538	6.86	8	
328	**Q6P6R2**	DLDH_RAT	**Dld**	Dihydrolipoyl dehydrogenase, mitochondrial	-	up	Mmt	5	0.49	105	54574	7.96	16	
154	**P17425**	HMCS1_RAT	**Hmgcs1**	Hydroxymethylglutaryl-CoA synthase, cytoplasmic	up	-	Cp	5	0.35	191	58025	5.58	26	
88	**O35760**	IDI1_RAT	**Idi1**	Isopentenyl-diphosphate Delta-isomerase 1	p90: abs	-	Per	5	-	115	26722	5.57	8	
372	**P30349**	LKHA4_RAT	**Lta4h**	Leukotriene A-4 hydrolase	down	-	Cp	6	3.05	127	69759	5.69	18	
442	**O35264**	PA1B2_RAT	**Pafah1b2**	Platelet-activating factor acetylhydrolase IB subunit beta	-	up	Cp	6	0.51	89	25736	5.57	9	
				Proteins Energy Metabolism										
657/748	**P15999**	ATPA_RAT	**Atp5a1**	ATP synthase subunit alpha, mitochondrial	down	down	Mim, M	5	4.20	364	59831	9.22	41	
741/521	**P31399**	ATP5H_RAT	**Atp5h**	ATP synthase subunit d, mitochondrial	down	down	Mito, Mim	6	4.07	165	18809	6.17	14	
28,49	**P07335**	KCRB_RAT	**Ckb**	Creatine kinase B-type	down	-	Cp	6	2.70	175	42983	5.39	26	+
558/110	**P25809**	KCRU_RAT	**Ckmt1**	Creatine kinase U-type, mitochondrial	down	down	Mito, Mim	6	4.26	129	47398	8.72	24	
153/141	**Q66HF1**	NDUS1_RAT	**Ndufs1**	NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial	down	up	Mim	6	1.98	362	80331	5.65	44	
330	**Q641Y2**	NDUS2_RAT	**Ndufs2**	NADH dehydrogenase [ubiquinone] iron-sulfur protein 2, mitochondrial	down	-	Mim	6	3.76	233	52927	6.52	31	
729	**D3ZG43**	D3ZG43_RAT	**Ndufs3**	NADH dehydrogenase (Ubiquinone) Fe-S protein 3 (Predicted), isoform CRA_c	down	-	Mito, Mm	5	1.99	187	30379	7.07	17	
128	**P19234**	NDUV2_RAT	**Ndufv2**	NADH dehydrogenase [ubiquinone] flavoprotein 2, mitochondrial	-	p637: abs	Mim	5	-	129	27703	6.23	12	
750	**P20788**	UCRI_RAT	**Uqcrfs1**	Cytochrome b-c1 complex subunit Rieske, mitochondrial	down	-	Mim	6	4.51	63	29712	9.04	13	
				Degratory Proteins										

48,56	**P22062**	PIMT_RAT	**Pcmt1**	Protein-L-isoaspartate(D-aspartate) O-methyltransferase	p7: abs	-	Cp	5	-	60	24683	7.14	8	+
918/460	**P60901**	PSA6_RAT	**Psma6**	Proteasome subunit alpha type-6	up	up	Cp, Nc	6	0.43	178	27838	6.34	19	
536	**Q63347**	PRS7_RAT	**Psmc2**	26S protease regulatory subunit 7	up	-	Cp, Nc	6	0.32	367	48943	5.59	38	
105	**Q63570**	PRS6B_RAT	**Psmc4**	26S protease regulatory subunit 6B	-	p637: abs	Cp, Nc	4	-	80	47493	5.09	10	
				Proteins Antioxidants										
778	**Q9Z339**	GSTO1_RAT	**Gsto1**	Glutathione S-transferase omega-1	down	-	Cp, Cts	6	1.74	78	27936	6.25	8	
66	**P08009**	GSTM4_RAT	**Gstm3**	Glutathione S-transferase Yb-3	p7: abs	-	Cp	5	-	267	25835	6.84	27	
716	**P35704**	PRDX2_RAT	**Prdx2**	Peroxiredoxin-2	down	-	Cp	6	2.05	108	21941	5.34	8	
713	**O35244**	PRDX6_RAT	**Prdx6**	Peroxiredoxin-6	down	-	Cp, Lyso	5	4.82	233	24860	5.64	18	
743/457	**Q9Z0V6**	PRDX3_RAT	**Prdx3**	Thioredoxin-dependent peroxide reductase, mitochondrial	down	up	Mito	5	2.56	88	28563	7.14	8	
				Proteins Biosynthesis										
400	**O35567**	PUR9_RAT	**Atic**	Bifunctional purine biosynthesis protein PURH	-	up	Mito, Cts	4	0.46	102	64681	6.69	13	
24,54	**Q9Z1N4**	BPNT1_RAT	**Bpnt1**	3'(2'),5'-bisphosphate nucleotidase 1	-	up	Cts	6	0.48	62	33495	5.58	10	+
719	**Q68FR6**	EF1G_RAT	**Eef1g**	Elongation factor 1-gamma	up	-	Rs, Cts	5	0.50	176	50371	6.31	20	
658	**Q5I0G4**	SYG_RAT	**Gars**	Glycine--tRNA ligase	up	-	Cp, Mito	6	0.52	259	72669	5.76	31	
595	**Q9WTT6**	GUAD_RAT	**Gda**	Guanine deaminase	up	-	Cts	6	0.29	245	51554	5.56	33	
624,566	**Q9JMJ4**	PRP19_RAT	**Prpf19**	Pre-mRNA-processing factor 19	-	down	Nc, Cp	4	2.14	91	55661	6.14	11	+
600	**Q6P799**	SYSC_RAT	**Sars**	Serine--tRNA ligase, cytoplasmic	up	-	Cp	6	0.15	120	59064	5.86	20	
535	**P85834**	EFTU_RAT	**Tufm**	Elongation factor Tu, mitochondrial	down	-	Mito	6	2.02	295	49890	7.23	27	
				Proteins Signal Transduction										
29	**P59215**	GNAO_RAT	**Gnao1**	Guanine nucleotide-binding protein G(o) subunit alpha	down	-	M, hGc	4	-	167	40613	5.34	23	
45	**P54313**	GBB2_RAT	**Gnb2**	Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-2	down	-	M, Cp	6	4.36	161	38048	5.6	19	
480	**P62994**	GRB2_RAT	**Grb2**	Growth factor receptor-bound protein 2	-	up	Nc, Cp	6	0.56	89	25736	5.57	9	
525	**P63086**	MK01_RAT	**Mapk1**	Mitogen-activated protein kinase 1	down	-	Nc, Cp	6	2.17	292	41648	6.5	26	
108	**F1M7Y3**	F1M7Y3_RAT	**Rap1gds1**	RAP1, GTP-GDP dissociation stimulator 1	up	-	Cp	5	0.48	82	57128	5.48	18	
836	**P35213**	1433B_RAT	**Ywhab**	14-3-3 protein beta/alpha	up	-	Cp, Mel	6	0.45	158	28365	4.81	23	+

836	**P68511**	1433F_RAT	**Ywhah**	14-3-3 protein eta	up	-	Cp	6	0.45	158	28365	4.81	23	+
836	**P63102**	1433Z_RAT	**Ywhaz**	14-3-3 protein zeta/delta	up	-	Cp, Mel	6	0.45	158	28365	4.81	23	+
				Proteins Regulation										
123	**P48037**	ANXA6_RAT	**Anxa6**	Annexin A6	down	-	Cp, Mel	6	1.89	152	76106	5.39	33	
755	**P27139**	CAH2_RAT	**Ca2**	Carbonic anhydrase 2	down	-	Cp	6	12.94	122	29267	6.89	13	
746	**P45592**	COF1_RAT	**Cfl1**	Cofilin-1	down	-	Nm, Cp	5	1.75	175	18749	8.22	15	
327	**Q07266**	DREB_RAT	**Dbn1**	Drebrin	up	-	Cp	6	0.55	222	78223	4.46	36	
575	**P50399**	GDIB_RAT	**Gdi2**	Rab GDP dissociation inhibitor beta	up	-	Cp, M	6	0.60	340	51018	5.93	38	
322	**Q68FS4**	AMPL_RAT	**Lap3**	Cytosol aminopeptidase	-	up	Cp	6	0.54	192	56514	6.77	27	
494/518	**Q99MZ8**	LASP1_RAT	**Lasp1**	LIM and SH3 domain protein 1	down	down	Cp, Csk	6	1.71	216	30350	6.61	19	
728	**Q64361**	LXN_RAT	**Lxn**	Latexin	down	-	Cp	6	1.99	71	25735	5.77	8	
742	**O88767**	PARK7_RAT	**Park7**	Protein DJ-1	down	-	Cp, Nc, Mito	6	2.24	214	20190	6.32	18	
406	**P62138**	PP1A_RAT	**Ppp1ca**	Serine/threonine-protein phosphatase PP1-alpha catalytic subunit	-	up	Cp, Nc	5	0.56	268	38229	5.94	21	
572/628	**Q6AXV4**	SAM50_RAT	**Samm50**	Sorting and assembly machinery component 50 homolog	down	down	Mom, Cp	6	2.22	246	52384	6.34	26	
31/34	**P70566**	TMOD2_RAT	**Tmod2**	Tropomodulin-2	down	down	Cp, Csk	6	3.83	135	39468	5.34	13	
581	**Q5RKI0**	WDR1_RAT	**Wdr1**	WD repeat-containing protein 1	down	-	Cp, Csk	6	2.03	305	66824	6.15	33	
				Chaperones										
104/210	**P18418**	CALR_RAT	**Calr**	Calreticulin	down	down	ER	5	2.01	192	48137	4.33	17	
55	**P63036**	DNJA1_RAT	**Dnaja1**	DnaJ homolog subfamily A member 1	p7: abs	-	M, La	5	-	99	45581	6.65	9	
130	**P82995**	HS90A_RAT	**Hsp90aa1**	Heat shock protein HSP 90-alpha	-	up	Cp, Mel	5	0.34	215	83571	4.97	39	+
130	**P34058**	HS90B_RAT	**Hsp90ab1**	Heat shock protein HSP 90-beta	-	up	Cp, Mel	5	0.34	319	83571	4.97	49	+
68/568	**P63018**	HSP7C_RAT	**Hspa8**	Heat shock cognate 71 kDa protein	up	up	Cp, Mel	6	0.12	279	71055	5.37	42	
101	**P63039**	CH60_RAT	**Hspd1**	60 kDa heat shock protein, mitochondrial	down	-	Mmt	6	1.81	139	61088	5.91	14	
420/332	**Q5XHZ0**	TRAP1_RAT	**Trap1**	Heat shock protein 75 kDa, mitochondrial	down	down	Mito	5	1.92	115	80639	6.56	18	
				Structural Proteins										
27	**P60711**	ACTB_RAT	**Actb**	Actin, cytoplasmic 1	down	-	Cp, Csk	6	2.70	62	42052	5.29	11	

199,211	**Q9QXQ0**	ACTN4_RAT	**Actn4**	Alpha-actinin-4	-	up	Nc, Cp	6	0.57	162	105306	5.27	33	+
138	**Q62950**	DPYL1_RAT	**Crmp1**	Dihydropyrimidinase-related protein 1	up	-	Cp, Csk	6	0.49	274	62499	6.64	29	
50,348/119,372,394,578,590	**P47942**	DPYL2_RAT	**Dpysl2**	Dihydropyrimidinase-related protein 2	-	up	Cp	6	0.44	226	62638	5.95	27	+
567,599	**Q62952**	DPYL3_RAT	**Dpysl3**	Dihydropyrimidinase-related protein 3	up	-	Cp, Gc	6	0.09	293	62327	6.04	46	+
399,418	**Q9JHU0**	DPYL5_RAT	**Dpysl5**	Dihydropyrimidinase-related protein 5	up	-	Cp	6	0.11	364	62071	6.6	44	+
321/577	**P85845**	FSCN1_RAT	**Fscn1**	Fascin	up	up	Cp, Csk	6	0.31	263	55198	6.29	29	
40,52	**P47819**	GFAP_RAT	**Gfap**	Glial fibrillary acidic protein	down	up	Cp	5	5.13	398	49984	5.35	44	
237	**D4A6B2**	D4A6B2_RAT	**Immt**	Mitochondrial inner membrane protein	down	-	Mito, Mim	5	2.17	378	83104	5.34	49	
18	**P23565**	AINX_RAT	**Ina**	Alpha-internexin	down	-	Nf	6	2.72	440	56253	5.2	45	
103	**P19527**	NFL_RAT	**Nefl**	Neurofilament light polypeptide	down	-	Nf, A	6	5.77	433	61355	4.63	52	
266	**P12839**	NFM_RAT	**Nefm**	Neurofilament medium polypeptide	down	-	Nf, Csk, A	6	2.73	326	95848	4.77	46	
537	**B5DFG5**	B5DFG5_RAT	**Sept6**	Septin-6	down	-	Cr, Cp	6	2.01	281	49147	6.23	28	
325/117	**B0BNF1**	SEPT8_RAT	**Sept8**	Septin-8	down	down	Cp, Csk	6	1.80	93	51562	5.74	13	
102,103	**P68370**	TBA1A_RAT	**Tuba1a**	Tubulin alpha-1A chain	-	up	Cp, Csk	6	0.56	204	50788	4.94	21	+
85	**Q6P9V9**	TBA1B_RAT	**Tuba1b**	Tubulin alpha-1B chain	-	up	Cp, Csk	6	0.21	200	50804	4.94	35	+
51	**Q6AYZ1**	TBA1C_RAT	**Tuba1c**	Tubulin alpha-1C chain	down	-	Cp, Csk	6	3.28	113	50590	4.96	9	
85	**Q4QRB4**	TBB3_RAT	**Tubb3**	Tubulin beta-3 chain	-	up	Cp, Csk	6	0.21	236	50842	4.82	38	+
85	**B4F7C2**	RCG45085	**Tubb4**	Tubulin, beta 4A class IVa	-	up	Cp, MT	6	0.21	231	50010	4.78	39	+
				Transport Proteins										
695	**P85515**	ACTZ_RAT	**Actr1a**	Alpha-centractin	up	-	Cp, Cts	6	0.52	231	42701	6.19	23	
662	**P02770**	ALBU_RAT	**Alb**	Serum albumin	up	-	Sc	6	0.16	422	70682	6.09	52	
13/28	**Q5M7T6**	Q5M7T6_RAT	**Atp6v0d1**	ATPase, H+ transporting, lysosomal 38kDa, V0 subunit d1	down	down	M	6	2.97	186	40731	4.89	17	
118,119	**D4A133**	D4A133_RAT	**Atp6v1a**	ATPase, H+ transporting, lysosomal 70kDa, V1 subunit A	down	-	Mito, Cts	6	1.83	360	68564	5.42	54	+
60	**P62815**	VATB2_RAT	**Atp6v1b2**	V-type proton ATPase subunit B, brain isoform	down	-	M, Mel	5	4.93	334	56857	5.57	41	
43/89	**P85969**	SNAB_RAT	**Napb**	Beta-soluble NSF attachment protein	down	down	M	4	6.07	330	33791	5.32	32	
700	**Q9QUL6**	NSF_RAT	**Nsf**	Vesicle-fusing ATPase	down	-	Cp	6	2.15	77	83170	6.55	16	
431	**Q9Z2L0**	VDAC1_RAT	**Vdac1**	Voltage-dependent anion-selective channel protein 1	down	down	Mom, M	5	2.81	215	30851	8.62	19	
767	**P81155**	VDAC2_RAT	**Vdac2**	Voltage-dependent anion-selective channel protein 2	down	-	Mom	5	3.22	126	32353	7.44	10	

Table S2: Results of the Western Blot validation by using ProXima AQ-4, Ref. 1.28/CLIQS, version 1.1. For each analyzed protein (Drebrin, Alpha-Internexin, Neurofilament low, Neurofilament mid/high, Park 7) its specific band volume per lane (developmental stage: P7, P90, P637), the additional backround volume and its predicted molecular weight is listed.

Drebrin						
Lane 1 (P7)						
Band No		**Volume**	**Vol+BkGnd**	**BkGnd**	**Peak+BkGnd**	**MW**
	1	26586526,38	39255187,00	12668660,62	10682,81	295.192
	2	66365375,00	108516055,00	42150680,00	21090,40	122.458
	3	36364510,48	65804616,00	29440105,52	15337,34	96.475
	4	24252947,00	41973472,00	17720525,00	9924,63	47.907
	5	7741313,29	19863832,00	12122518,71	4516,18	40.282
	6	31895019,35	44672344,00	12777324,65	12184,46	31.562
Lane 2 (P90)						
Band No		**Volume**	**Vol+BkGnd**	**BkGnd**	**Peak+BkGnd**	**MW**
	1	18680385,52	47991494,00	29311108,48	9220,90	130.191
	2	14787758,01	48544888,00	33757129,99	7606,25	103.219
	3	1238598,02	13993818,00	12755219,98	2927,68	75.000
	4	1326326,99	11601799,00	10275472,01	2428,38	48.590
	5	15196532,46	34369206,00	19172673,54	7107,52	40.953
	6	23137010,42	38935668,00	15798657,58	8025,62	31.663
Lane 3 (P637)						
Band No		**Volume**	**Vol+BkGnd**	**BkGnd**	**Peak+BkGnd**	**MW**
	1	20758714,19	46901789,00	26143074,81	9873,04	125.125
	2	28503182,54	51747419,00	23244236,46	11688,61	98.030
	3	5449481,17	17070722,00	11621240,83	3978,19	72.904
	4	2089178,81	12348332,00	10259153,19	2873,21	48.590
	5	19552669,93	37008187,00	17455517,07	9097,19	40.953
	6	31359036,05	45213073,00	13854036,95	11862,00	32.074
Alpha-Internexin						
Lane 1 (P7)						
Band No		**Volume**	**Vol+BkGnd**	**BkGnd**	**Peak+BkGnd**	**MW**
	1	75548663,00	75548663,00	0,00	15452,16	66.071
Lane 2 (P90)						
Band No		**Volume**	**Vol+BkGnd**	**BkGnd**	**Peak+BkGnd**	**MW**
	1	17414285,00	17414285,00	0,00	2915,23	129.659
	2	104216855,00	104216855,00	0,00	15465,63	66.329
Lane 3 (P637)						
Band No		**Volume**	**Vol+BkGnd**	**BkGnd**	**Peak+BkGnd**	**MW**
	1	39632653,00	39632653,00	0,00	6408,47	121.671
	2	167260154,00	167260154,00	0,00	26740,49	64.299

Neurofilament_68

Lane 1 (P7)

Band No		Volume	Vol+BkGnd	BkGnd	Peak+BkGnd	MW
	1	1995467,81	3751657,00	1756189,19	1045,51	63.783

Lane 2 (P90)

Band No		Volume	Vol+BkGnd	BkGnd	Peak+BkGnd	MW
	1	12569827,00	17889872,00	5320045,00	2921,32	65.987

Lane 3 (P637)

Band No		Volume	Vol+BkGnd	BkGnd	Peak+BkGnd	MW
	1	15242036,73	21158599,00	5916562,27	3502,83	66.239

Neurofilament_160_200

Lane 1 (P7)

Band No		Volume	Vol+BkGnd	BkGnd	Peak+BkGnd	MW
	1	20879447,00	34849577,00	13970130,00	4697,49	213.101

Lane 2 (P90)

Band No		Volume	Vol+BkGnd	BkGnd	Peak+BkGnd	MW
	1	50165595,62	118501367,00	68335771,38	11974,21	217.933

Lane 3 (P637)

Band No		Volume	Vol+BkGnd	BkGnd	Peak+BkGnd	MW
	1	44778696,86	118535844,00	73757147,14	11528,21	226.475

PARK7-DJ1

Lane 1 (P7)

Band No		Volume	Vol+BkGnd	BkGnd	Peak+BkGnd	MW
	1	20564806,00	20564806,00	0,00	4714,64	-

Lane 2 (P90)

Band No		Volume	Vol+BkGnd	BkGnd	Peak+BkGnd	MW
	1	20907825,00	27239353,00	6331528,00	4743,45	-

Lane 3 (P637)

Band No		Volume	Vol+BkGnd	BkGnd	Peak+BkGnd	MW
	1	21993026,00	21993026,00	0,00	3641,44	-

Figure S1: Spot editing and segmentation. To perform an accurate segmentation of spots, the manual editing of spots was supported by 3D-projection. The manual editing of spots has been applied to all reference and to all template gels. An example of the latter is shown.

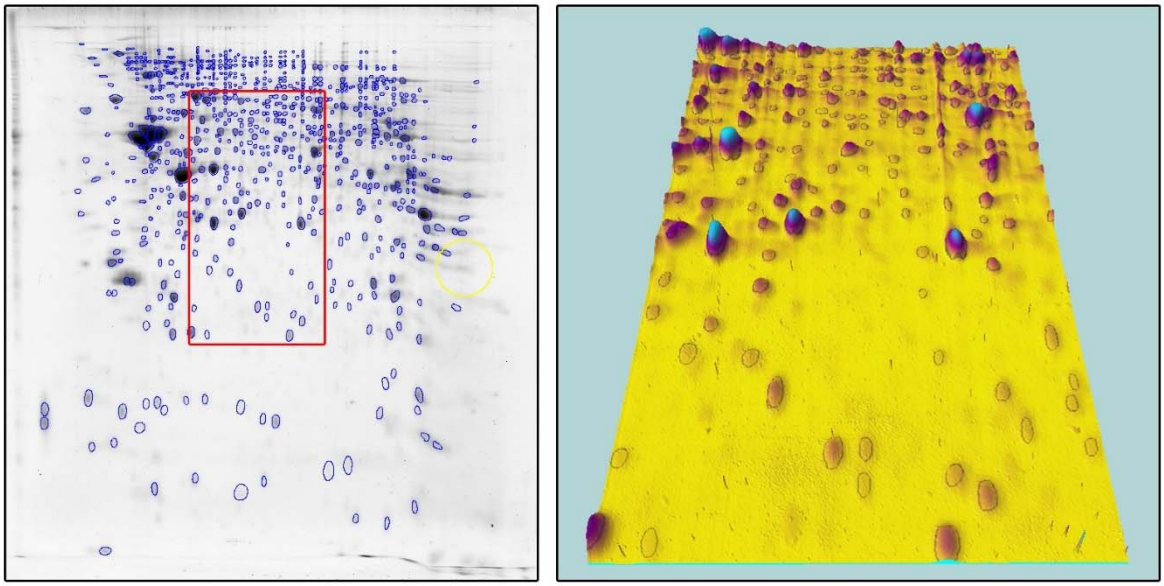

Figure S2: Differential expession of proteins of P90 in comparison to P7 (green: up-regulated proteins).

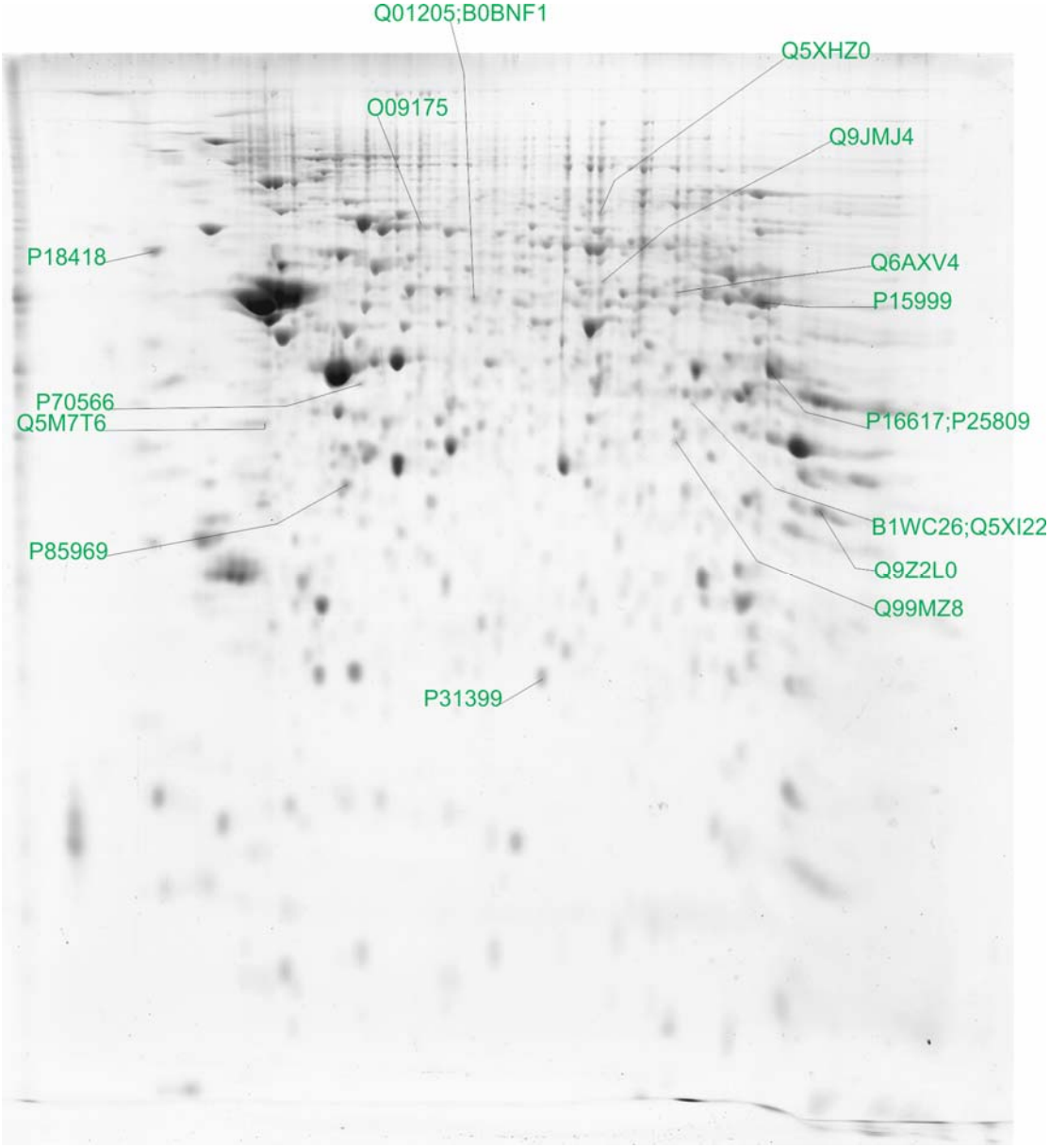

Figure S3: Differential expession of proteins of P637 in comparison to P90 (pink: up-regulated proteins).

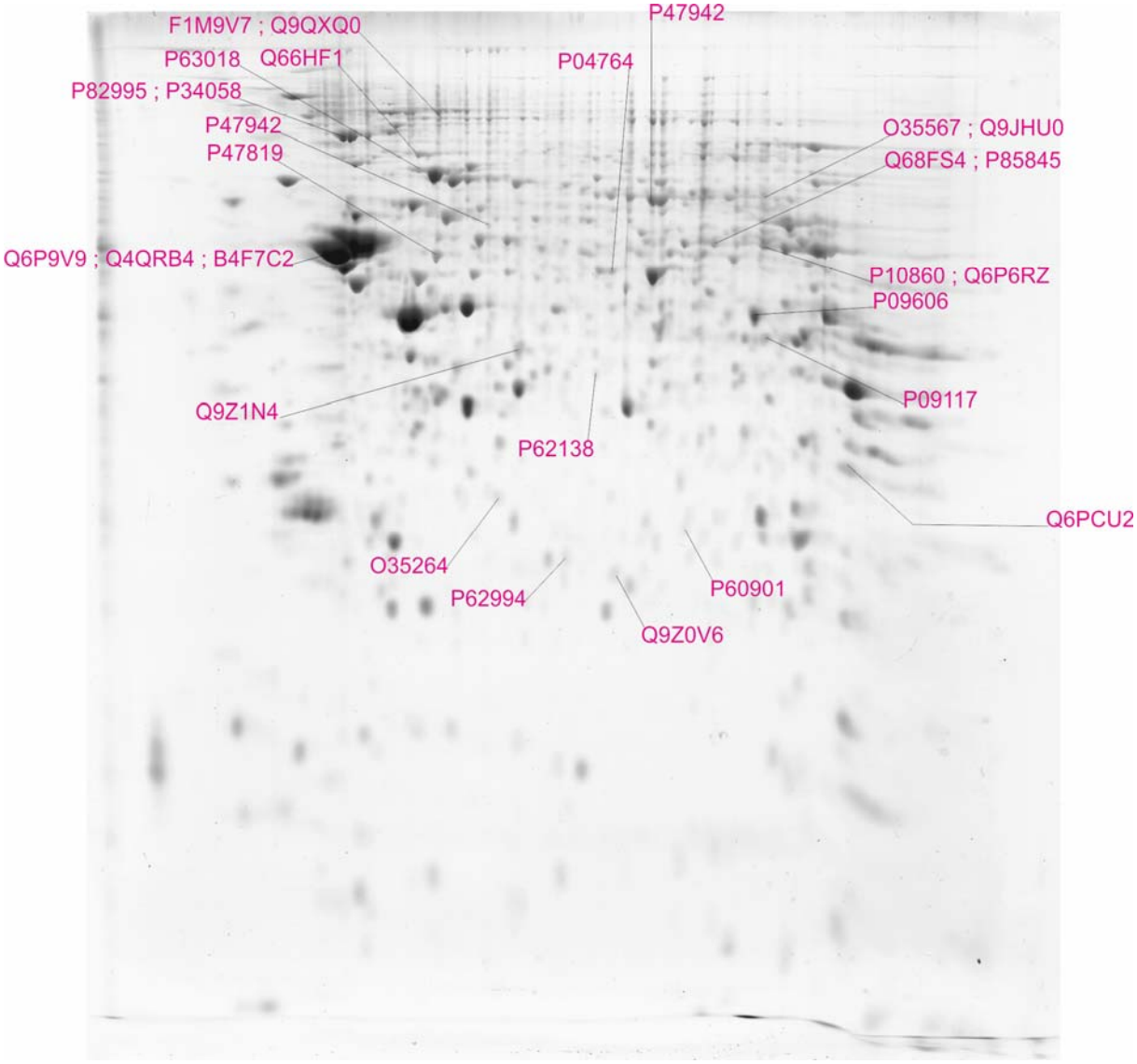
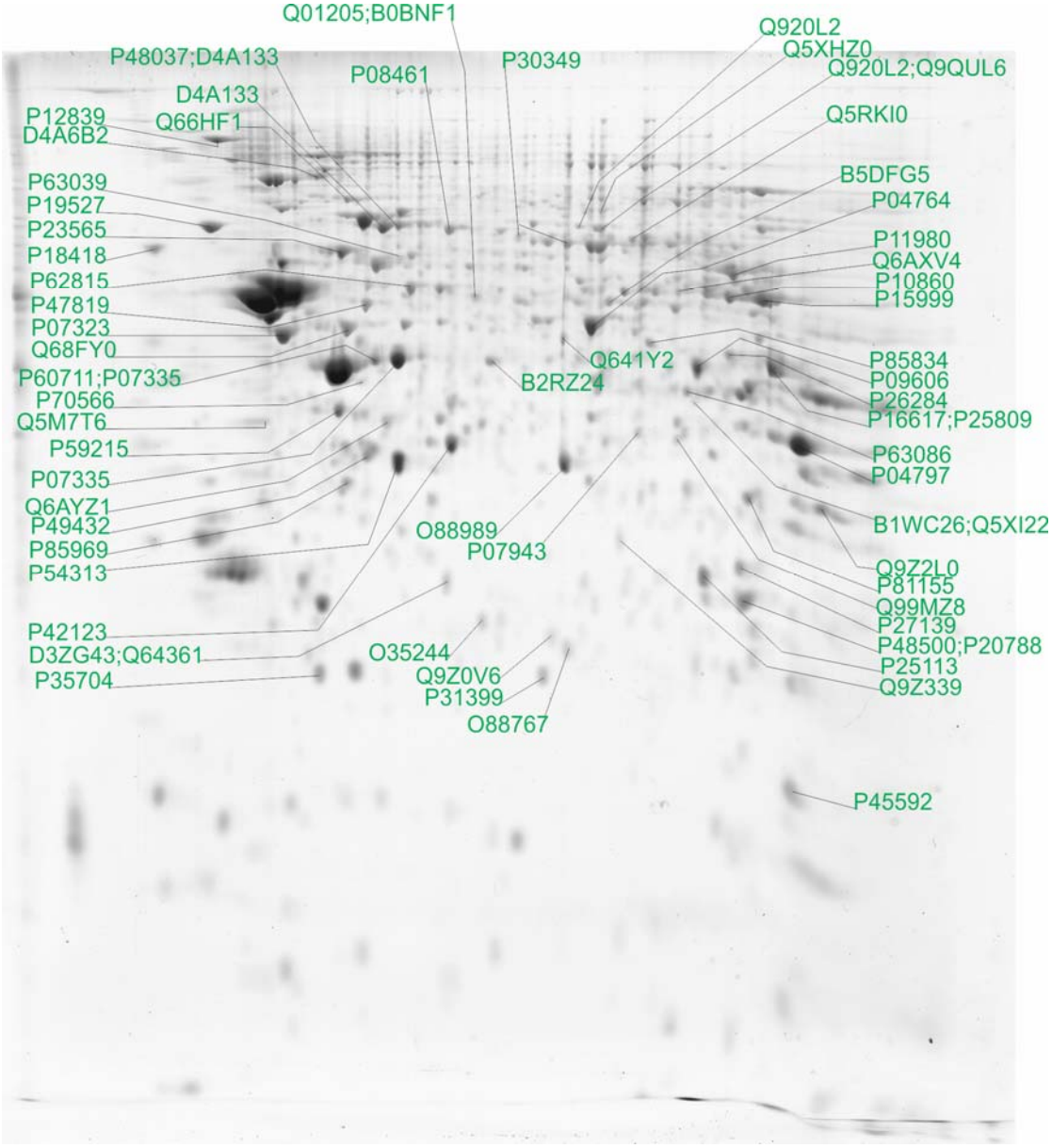
Figure S4: Differential expession of proteins of P90 in comparison to P637 (green: up-regulated proteins).