

# Polymer “ruthenium-cyclopentadienyl” conjugates - new emerging anti-cancer drugs

Tiago Moreira<sup>a,b</sup>, Rita Francisco<sup>a,b</sup>, Elisabeta Comsa<sup>c</sup>, Sophie Duban-Deweer<sup>d</sup>, Valérie Labas<sup>e</sup>, Ana-Paula Teixeira-Gomes<sup>e</sup>, Lucie Combes-Soia<sup>e</sup>, Fernanda Marques<sup>f</sup>, António Matos<sup>g</sup>, Audrey Favrelle<sup>h</sup>, Cyril Rousseau<sup>i</sup>, Philippe Zinck<sup>h</sup>, Pierre Falson<sup>c</sup>, M. Helena Garcia<sup>a</sup>, Ana Preto<sup>b</sup>, Andreia Valente<sup>a,\*</sup>

<sup>a</sup>Centro de Química Estrutural, Faculdade de Ciências da Universidade de Lisboa, Campo Grande, 1749-016 Lisboa, Portugal.

<sup>b</sup>Centre of Molecular and Environmental Biology (CBMA), Department of Biology, University of Minho, Portugal. Campus de Gualtar, Braga 4710-057, Portugal

<sup>c</sup>Drug Resistance & Membrane Proteins team, Molecular Microbiology and Structural Biochemistry Laboratory, CNRS-UCBL1 UMR 5086, IBCP, 69367 Lyon France

<sup>d</sup>Laboratoire de la barrière hémato-encéphalique (LBHE), Plateau Spectrométrie de Masse de l'ARTois (SMART), Université d'Artois, EA 2465, Lens F-62300, France.

<sup>e</sup>Plate-forme de Chirurgie et d'Imagerie pour la Recherche et l'Enseignement (CIRE), Pôle d'Analyse et d'Imagerie des Biomolécules (PAIB), PRC, INRA, CNRS, Université de Tours, IFCE, 37380 Nouzilly, France.

<sup>f</sup>Centro de Ciências e Tecnologias Nucleares, Instituto Superior Técnico, Universidade de Lisboa, E.N.10, 2695-066 Bobadela LRS, Portugal

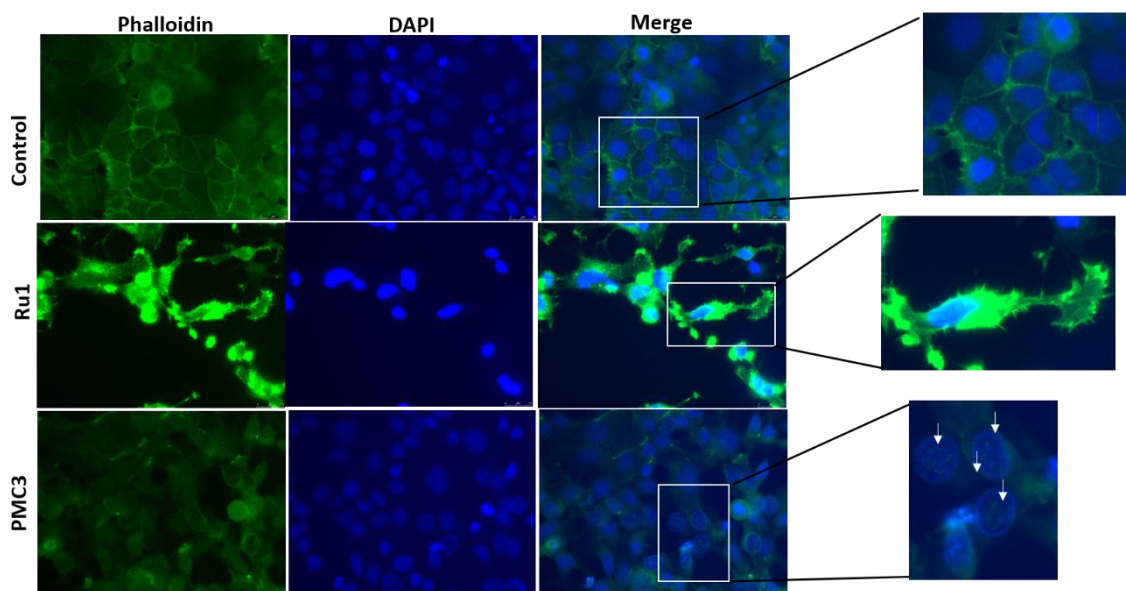
<sup>g</sup>Centro de Investigação Interdisciplinar Egas Moniz, Egas Moniz-Cooperativa de Ensino Superior CRL, Campus Universitário, Quinta da Granja, Monte de Caparica, 2829-511 Caparica, Portugal.

<sup>h</sup>Univ. Lille, CNRS, Centrale Lille, ENSCL, Univ. Artois, UMR 8181 - UCCS - Unité de Catalyse et Chimie du Solide, F-59000 Lille (France)...

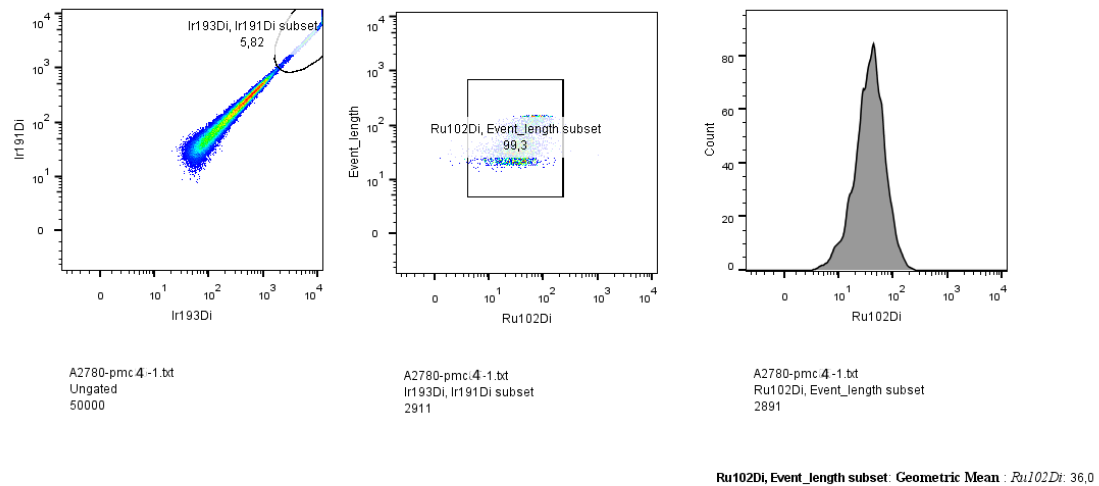
<sup>i</sup>Unity of Catalysis and Solid State Chemistry, UMR CNRS 8181, University of Artois, 62000 Lens, France.

**Table S1.** *In vitro* cytotoxic activity of complexes **PMC1–PMC3** and **Ru1** against MCF7 and breast adenocarcinoma at 24 h measured as the half-inhibitory concentration ( $IC_{50}$ ).

Compound	MCF7, 24 h ( $\mu$ M)
<b>PMC1</b>	$23.1 \pm 5.4$
<b>PMC2</b>	$2.22 \pm 0.90$
<b>PMC3</b>	$4.25 \pm 1.15$
<b>Ru1</b>	$17.4 \pm 7.2$



**Figure S1.** Ruthenium-based compounds interfere with actin filaments (cytoskeleton). MCF7 cells were incubated for 24 h with the  $IC_{50}$  doses of ruthenium-based compounds **Ru1** and **PMC3**[41]. Control cells were incubated with 0.1% of DMSO, since the compounds were solubilized in the referred organic solvent. Shown micographies are representative of each condition.



**Figure S2.** Example analysis of ruthenium uptake in ovarian cancer cells – analysis of A2780 cell populations after treatment with 20  $\mu$ M PMC4 using the FlowJo v.10 software for mass cytometry: at first the cells of interest were selected (live single cells are identified using iridium-labeled DNA), then in the gated population and ruthenium accumulation was quantified using GeoMean as a measure of the isotope abundance.

Protein description				Exclusive Unique Peptide Count																							
				PMC3 Pool 1				PMC3 Pool 2				Ru1 Pool 1				Ru1 Pool 2				Control Pool 1				Control Pool 2			
#	Identified Proteins (354)	UniprotKB Accession Number	Theoretical Molecular Weight	R1	R2	R3	R4	R1	R2	R3	R4	R1	R2	R3	R4	R1	R2	R3	R4	R1	R2	R3	R4	R1	R2	R3	R4
1	Cluster of Vimentin	VIME_HUMAN	54 kDa	34	31	31	28	32	28	28	19	30	28	23	26	15	10	9	8	39	41	37	33	31	31	26	18
1.1	Vimentin	VIME_HUMAN	54 kDa	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	0	0	1	0	0	0
1.2	Vimentin	VIME_PANTR	54 kDa	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0	0
1.3	Vimentin	VIME_BOVIN	54 kDa	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2	Cluster of Actin-2	ACT2_SUIBO	42 kDa	26	31	21	22	23	23	22	8	12	25	22	17	10	0	3	6	8	6	6	7	25	30	24	12
2.1	Actin-2	ACT2_SUIBO	42 kDa	1	1	1	1	1	1	1	0	1	1	0	1	0	0	0	0	1	1	1	1	1	1	1	0
2.2	Beta-actin-like protein 2	ACTBL_HUMAN	42 kDa	1	1	0	0	1	1	1	0	1	0	1	0	0	0	0	0	1	0	0	0	0	1	0	0
2.3	Actin-18 O	ACT18_DICDI	43 kDa	0	1	1	1	1	1	1	0	0	1	1	1	0	0	0	0	0	0	0	0	0	1	1	0
2.4	Actin-3	ACT3_SOYBN	42 kDa	0	1	1	0	0	0	1	0	0	0	1	0	1	0	0	0	0	0	0	0	0	1	0	0
2.5	Actin	ACT_CRYPV	42 kDa	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	1	0	0
2.6	Actin, cytoplasmic 1	ACTB_CRIGR	42 kDa	1	1	1	1	0	1	1	0	0	1	0	1	1	0	0	0	0	0	0	0	1	1	1	1
2.7	Actin	ACT_KOMPG	42 kDa	1	1	0	1	0	0	1	1	0	1	1	0	0	0	0	0	1	1	1	1	0	0	1	1
2.8	Actin, cytoplasmic	ACTC_BRABE	42 kDa	0	0	0	0	0	0	1	1	0	1	1	1	0	0	0	0	0	0	0	0	0	1	1	1
2.9	Actin, cytoplasmic	ACTC_STYPL	42 kDa	0	1	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
2.1	Actin-53 (Fragment)	ACT2_TOBAC	37 kDa	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	1	0
2.11	Actin	ACT_ASPOR	42 kDa	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0
2.12	Actin	ACT_ACHBI	42 kDa	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2.13	Actin, muscle	ACTM_PISOC	42 kDa	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2.14	Actin-1	ACT1_SCHMA	42 kDa	0	0	0	0	0	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0	1	1	0	0
2.15	Actin, cytoplasmic type 8	ACT8_XENLA	42 kDa	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2.16	Actin-A3b, cytoplasmic	ACT3B_HELAM	42 kDa	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0
2.17	Actin-17	ACT17_DICDI	42 kDa	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0
2.18	Actin-1	ACT1_AEDAE	42 kDa	0	0	0	0	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0



7.8	Heat shock 70 kDa protein 1-like	HS71L_BOVIN	70 kDa	0	0	0	0	0	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
7.9	Heat shock protein SSA1	HSP71_CANAL	70 kDa	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
8	Cluster of Histone H2A type 1-C	H2A1C_HUMAN	14 kDa	11	9	8	4	9	9	6	2	4	3	4	3	2	0	0	2	7	7	7	4	9	9	6	4
8.1	Histone H2A type 1-C	H2A1C_HUMAN	14 kDa	1	1	1	0	1	1	1	0	0	0	1	0	0	0	0	0	1	1	1	1	1	1	2	1
8.2	Histone H2A type 2-A	H2A2A_HUMAN	14 kDa	4	3	4	1	4	3	2	0	1	1	1	1	0	0	0	0	3	3	3	1	4	4	2	1
8.3	Histone H2A.V	H2AV_BOVIN	14 kDa	1	1	0	0	0	0	0	0	0	1	0	0	0	0	0	0	1	1	1	0	1	1	0	0
8.4	Histone H2A, embryonic	H2AE_PSAMI	13 kDa	1	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0
8.5	Histone H2A-III	H2A3_VOLCA	14 kDa	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
8.6	Probable histone H2A.4	H2A4_ORYSI	17 kDa	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
8.7	Histone H2A.Z-like	H2AZL_XENLA	13 kDa	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0
9	Cluster of Annexin A2	ANXA2_HUMAN	39 kDa	18	15	12	11	15	13	13	8	17	16	8	12	10	9	8	7	2	2	2	2	14	16	9	5
9.1	Annexin A2	ANXA2_HUMAN	39 kDa	2	1	1	1	2	2	1	1	2	2	1	2	1	1	1	1	0	0	0	0	2	3	1	0
10	Cluster of Histone H1.4	H14_MOUSE	22 kDa	3	6	0	4	7	5	6	4	0	0	0	4	0	0	0	4	12	12	13	12	13	12	11	12
10.1	Histone H1.4	H14_MOUSE	22 kDa	0	2	0	1	2	2	1	1	0	0	0	1	0	0	0	1	3	2	3	2	3	2	2	2
10.2	Histone H1.2	H12_HUMAN	21 kDa	1	1	0	1	2	1	1	1	0	0	0	1	0	0	0	1	2	2	2	2	2	2	2	2
10.3	Histone H1.2	H12_BOVIN	21 kDa	1	2	0	1	2	1	1	0	0	0	0	1	0	0	0	1	2	2	2	2	2	2	2	2
11	Cluster of Elongation factor 1-alpha 1	EF1A1_FELCA	50 kDa	10	8	6	6	9	6	6	5	7	7	6	6	3	4	4	3	4	5	4	4	7	9	6	5
11.1	Elongation factor 1-alpha 1	EF1A1_FELCA	50 kDa	6	5	3	3	6	3	2	0	4	4	3	2	1	2	1	1	2	3	2	1	4	5	2	2
11.2	Elongation factor 1-alpha 2	EF1A2_DROME	51 kDa	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
12	Cluster of Keratin, type II cytoskeletal 1	K2C1_HUMAN	66 kDa	16	11	11	10	25	20	17	7	4	2	2	3	8	10	5	7	11	16	9	9	14	14	6	5
12.1	Keratin, type II cytoskeletal 1	K2C1_HUMAN	66 kDa	9	7	7	6	13	10	9	4	2	1	0	1	4	5	3	5	7	8	5	5	6	7	2	2
12.2	Keratin, type II cytoskeletal 8	K2C8_HUMAN	54 kDa	0	0	0	0	2	1	0	0	0	0	0	0	0	2	0	0	0	0	0	0	2	2	0	0
12.3	Keratin, type II cytoskeletal 2 epidermal	K22E_HUMAN	65 kDa	2	0	0	0	3	2	1	0	0	0	0	0	1	0	0	0	1	2	0	0	0	0	0	0
12.4	Keratin, type II cytoskeletal 8	K2C8_RAT	54 kDa	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0

13	Cluster of Nuclease-sensitive element-binding protein 1	YBOX1_BOVIN	36 kDa	8	6	3	2	7	6	2	0	3	2	2	0	2	2	0	0	12	12	13	8	6	5	3	2	
13.1	Nuclease-sensitive element-binding protein 1	YBOX1_BOVIN	36 kDa	5	5	3	2	5	4	2	0	3	2	2	0	2	2	0	0	7	6	7	5	6	4	3	2	
13.2	Y-box-binding protein 3	YBOX3_HUMAN	40 kDa	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	2	2	0	0	0	0	0	
14	Cluster of Nucleolin	NUCL_HUMAN	77 kDa	6	6	3	7	6	8	5	0	7	5	2	3	0	0	0	0	21	18	19	14	6	7	5	2	
14.1	Nucleolin	NUCL_HUMAN	77 kDa	6	6	3	7	6	8	5	0	7	5	2	3	0	0	0	0	21	18	19	14	6	7	5	2	
15	Cluster of Calreticulin	CALR_HUMAN	48 kDa	8	7	6	6	10	10	9	4	6	7	5	3	3	0	0	0	7	7	9	4	5	7	3	0	
15.1	Calreticulin	CALR_HUMAN	48 kDa	4	4	4	4	5	6	5	3	3	5	4	3	3	0	0	0	2	3	4	2	2	4	2	0	
16	Cluster of Tropomyosin alpha-3 chain	TPM3_RAT	29 kDa	3	2	3	3	7	6	3	0	0	0	0	0	0	0	0	0	9	13	8	9	12	14	9	3	
16.1	Tropomyosin alpha-3 chain	TPM3_RAT	29 kDa	2	1	1	2	4	4	2	0	0	0	0	0	0	0	0	0	5	7	5	5	8	7	6	3	
16.2	Tropomyosin alpha-4 chain	TPM4_HUMAN	29 kDa	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0	0	
16.3	Tropomyosin alpha-4 chain	TPM4_HORSE	29 kDa	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
17	Far upstream element-binding protein 2	FUBP2_HUMAN	73 kDa	13	13	13	8	12	10	6	3	5	5	2	3	4	3	2	0	17	16	19	15	11	12	10	5	
18	Cluster of Histone H4	H4_ACRAS	11 kDa	8	7	6	5	7	7	6	3	4	3	2	4	3	3	2	3	0	2	2	2	7	7	4	4	
18.1	Histone H4	H4_ACRAS	11 kDa	4	3	2	1	3	3	2	1	2	0	0	1	0	0	0	0	0	1	1	0	3	3	0	1	
19	Cluster of Glyceraldehyde-3-phosphate dehydrogenase	G3P_HUMAN	36 kDa	9	9	6	6	8	6	5	3	13	10	9	6	3	3	2	3	6	4	4	4	6	6	5	3	
19.1	Glyceraldehyde-3-phosphate dehydrogenase	G3P_HUMAN	36 kDa	7	7	4	4	6	4	3	1	11	8	7	4	1	1	1	1	4	2	2	2	4	4	3	1	
20	Cluster of Histone H2B type 1-B	H2B1B_HUMAN	14 kDa	3	1	2	3	3	3	2	2	1	3	3	2	2	2	2	2	2	2	3	2	2	2	3	3	
20.1	Histone H2B type 1-B	H2B1B_HUMAN	14 kDa	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	
20.2	Histone H2B type 1-N	H2B1N_BOVIN	14 kDa	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
21	Cluster of Tubulin beta-5 chain	TBB5_RAT	50 kDa	19	17	16	13	17	14	11	6	14	12	7	8	8	6	4	4	4	7	5	3	23	18	15	6	
21.1	Tubulin beta-5 chain	TBB5_RAT	50 kDa	2	2	2	2	2	2	2	1	3	2	2	2	1	1	1	1	1	1	1	1	1	3	2	2	2
21.2	Tubulin beta chain	TBB_CERBT	50 kDa	1	1	0	0	1	0	0	0	0	1	0	0	1	0	0	0	0	1	0	0	1	1	1	0	
21.3	Tubulin beta chain	TBB_PENDI	50 kDa	0	0	0	1	0	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0	1	1	1	0	





30	Cluster of Integrin beta-1	ITB1_HUMAN	88 kDa	8	6	6	5	9	8	7	3	2	0	0	0	6	4	3	2	6	8	6	7	8	8	5	4
30.1	Integrin beta-1	ITB1_HUMAN	88 kDa	4	3	3	3	4	4	3	1	1	0	0	0	3	2	1	0	2	3	3	3	3	3	2	1
31	Cluster of 14-3-3 protein epsilon	1433E_SHEEP	29 kDa	9	6	5	2	8	5	4	2	11	9	3	10	2	0	0	0	0	0	0	0	6	6	5	0
31.1	14-3-3 protein epsilon	1433E_SHEEP	29 kDa	4	3	3	2	2	2	1	2	5	4	3	4	0	0	0	0	0	0	0	0	2	2	1	0
31.2	14-3-3 protein zeta/delta	1433Z_HUMAN	28 kDa	2	1	1	0	3	1	1	0	3	2	0	2	2	0	0	0	0	0	0	0	2	2	2	0
31.3	14-3-3 protein theta	1433T_BOVIN	28 kDa	1	0	0	0	1	1	1	0	0	0	0	1	0	0	0	0	0	0	0	0	1	1	1	0
31.4	14-3-3 protein sigma	1433S_HUMAN	28 kDa	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0
31.5	14-3-3 protein beta/alpha	1433B_CHICK	28 kDa	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0
31.6	14-3-3 protein gamma	1433G_BOVIN	28 kDa	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0
32	Cluster of Pyruvate kinase PKM	KPYM_HUMAN	58 kDa	7	9	6	4	5	4	5	2	7	4	6	5	3	2	0	3	0	0	0	0	12	11	8	3
32.1	Pyruvate kinase PKM	KPYM_HUMAN	58 kDa	1	1	1	1	1	1	1	0	1	1	1	1	1	0	0	0	0	0	0	0	1	1	1	0
33	Cluster of Keratin, type I cytoskeletal 10	K1C10_HUMAN	59 kDa	5	5	5	5	9	8	8	5	0	4	0	1	5	6	4	4	5	4	3	2	4	6	2	2
33.1	Keratin, type I cytoskeletal 10	K1C10_HUMAN	59 kDa	5	5	5	5	6	6	5	3	0	3	0	0	3	3	3	2	5	4	3	2	2	2	0	0
33.2	Keratin, type I cytoskeletal 18	K1C18_HUMAN	48 kDa	0	0	0	0	1	1	1	1	0	1	0	1	1	1	0	0	0	0	0	1	2	1	1	1
33.3	Keratin, type I cytoskeletal 19	K1C19_HUMAN	44 kDa	0	0	0	0	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	1	2	1	1	1
33.4	Keratin, type I cytoskeletal 14	K1C14_HUMAN	52 kDa	0	0	0	0	0	0	0	0	0	0	0	0	1	0	1	0	0	0	0	0	0	0	0	0
34	Cluster of Alpha-actinin-4	ACTN4_HUMAN	105 kDa	8	10	5	6	4	5	3	0	15	14	14	11	3	3	0	0	0	0	0	0	4	4	4	2
34.1	Alpha-actinin-4 O	ACTN4_HUMAN	105 kDa	4	5	3	3	2	3	1	0	7	6	5	6	0	0	0	0	0	0	0	0	2	2	1	0
34.2	Alpha-actinin, sarcomeric	ACTN_ANOGA	107 kDa	0	1	0	0	0	0	0	0	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0
34.3	Alpha-actinin-1	ACTN1_BOVIN	103 kDa	1	1	0	0	0	0	0	0	3	2	2	2	0	0	0	0	0	0	0	0	0	0	0	0
35	Cofilin-1	COF1_HUMAN	19 kDa	5	4	2	3	6	5	4	3	5	5	4	2	0	0	0	0	6	7	6	5	5	6	5	2
36	Cluster of Glucosidase 2 subunit beta	GLU2B_HUMAN	59 kDa	5	7	6	6	10	8	6	4	2	2	3	2	0	0	0	0	8	10	10	6	7	9	6	4
36.1	Glucosidase 2 subunit beta	GLU2B_HUMAN	59 kDa	4	6	5	5	9	7	5	3	1	1	2	1	0	0	0	0	7	9	9	5	6	8	5	3
37	Cluster of Ubiquitin-60S ribosomal protein L40	RL40_DROME	15 kDa	3	4	3	2	3	4	3	4	3	4	3	2	5	5	3	2	3	3	3	3	4	3	4	4





64	LIM and SH3 domain protein 1 O	LASP1_HUMAN	30 kDa	0	3	2	2	2	2	2	0	0	0	0	2	0	0	0	0	4	4	3	2	2	2	2	2
65	Far upstream element-binding protein 1	FUBP1_HUMAN	68 kDa	2	3	2	0	2	2	0	2	0	0	0	0	0	0	0	6	7	7	5	0	0	0	0	
66	Alpha-1-antiproteinase	A1AT_BOVIN	46 kDa	0	0	0	0	5	3	4	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
67	Serine/arginine-rich splicing factor 7	SRSF7_BOVIN	27 kDa	2	3	3	2	0	2	1	0	1	2	0	2	0	0	0	4	4	3	3	0	1	0	0	
68	Cluster of Malate dehydrogenase, mitochondrial	MDHM_HUMAN	36 kDa	3	3	2	4	3	3	5	3	6	6	7	4	0	0	0	0	0	0	0	0	3	3	0	
68.1	Malate dehydrogenase, mitochondrial	MDHM_HUMAN	36 kDa	1	1	0	1	1	1	2	1	2	2	2	1	0	0	0	0	0	0	0	0	1	1	0	
68.2	Malate dehydrogenase, mitochondrial	MDHM_MOUSE	36 kDa	0	0	0	1	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
69	Cluster of Nascent polypeptide-associated complex subunit alpha, muscle-specific form	NACAM_HUMAN	205 kDa	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	6	5	6	0	0	0	0	0	
69.1	Nascent polypeptide-associated complex subunit alpha, muscle-specific form	NACAM_HUMAN	205 kDa	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
69.2	Nascent polypeptide-associated complex subunit alpha, muscle-specific form	NACAM_MOUSE	220 kDa	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
70	Heterogeneous nuclear ribonucleoprotein D0	HNRPD_HUMAN	38 kDa	2	2	2	2	1	1	1	0	0	0	0	1	0	0	0	4	7	6	3	2	2	1	0	
71	RNA-binding protein FUS	FUS_BOVIN	52 kDa	0	0	0	0	2	1	0	0	0	0	1	0	0	0	0	6	6	5	3	2	2	1	1	
72	Cluster of Peroxiredoxin-1	PRDX1_HUMAN	22 kDa	2	3	2	2	4	2	2	0	2	2	2	2	2	1	0	0	1	0	0	1	2	0	0	
72.1	Peroxiredoxin-1	PRDX1_HUMAN	22 kDa	1	2	1	1	2	1	1	0	1	1	1	1	1	1	0	0	0	1	0	0	0	0	0	
72.2	Peroxiredoxin-2	PRDX2_PONAB	19 kDa	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	
73	Cluster of Heterogeneous nuclear ribonucleoprotein A/B	ROAA_MOUSE	31 kDa	2	2	2	2	2	2	2	0	2	0	0	1	0	0	0	6	6	6	4	3	3	1	0	
73.1	Heterogeneous nuclear ribonucleoprotein A/B	ROAA_MOUSE	31 kDa	1	1	1	1	1	1	1	0	1	0	0	1	0	0	0	1	1	1	1	1	1	1	0	
73.2	Heterogeneous nuclear ribonucleoprotein A/B	ROAA_HUMAN	36 kDa	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	2	2	1	1	1	0	0	

74	Eukaryotic translation initiation factor 4B	IF4B_HUMAN	69 kDa	0	0	0	0	0	0	0	0	0	0	0	0	0	0	4	4	3	2	2	2	0	0		
75	Elongation factor 2	EF2_PONAB	95 kDa	5	5	0	0	4	3	3	0	10	6	4	3	0	0	0	0	0	0	4	3	2	0		
76	Superoxide dismutase [Mn], mitochondrial	SODM_PONPY	25 kDa	0	0	0	2	3	4	3	2	0	0	0	0	2	0	0	0	4	2	2	0	6	6	5	3
77	Cluster of Protein disulfide-isomerase A3	PDIA3_HUMAN	57 kDa	4	2	4	5	6	4	4	2	2	2	4	5	2	4	0	0	0	0	0	4	3	2	0	
77.1	Protein disulfide-isomerase A3	PDIA3_HUMAN	57 kDa	2	1	2	2	3	1	2	1	1	2	1	2	2	2	0	0	0	0	0	1	1	1	0	
78	4F2 cell-surface antigen heavy chain	4F2_HUMAN	68 kDa	6	5	4	3	6	4	3	2	3	3	0	4	0	0	0	0	2	2	2	0	0	0	0	
79	Cluster of Caveolin-1	CAV1_HORSE	21 kDa	3	0	0	0	4	3	0	0	0	0	0	0	0	0	0	0	2	3	0	2	3	0	0	
79.1	Caveolin-1	CAV1_HORSE	21 kDa	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
79.2	Caveolin-1	CAV1_MOUSE	21 kDa	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
80	Annexin A1	ANXA1_HUMAN	39 kDa	7	4	4	2	3	3	0	0	3	2	3	0	3	2	0	0	0	0	0	3	2	0	0	
81	Cluster of Hemoglobin fetal subunit beta	HBBF_BOVIN	16 kDa	0	0	0	0	10	8	7	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
81.1	Hemoglobin fetal subunit beta	HBBF_BOVIN	16 kDa	0	0	0	0	6	6	4	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
81.2	Hemoglobin subunit beta	HBB_EULFU	16 kDa	0	0	0	0	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
81.3	Hemoglobin subunit delta	HBD_ATEGE	16 kDa	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
82	Cluster of Protein disulfide-isomerase A6	PDIA6_HUMAN	48 kDa	4	3	5	2	3	4	2	0	5	5	4	3	0	0	0	0	0	0	0	2	2	0	0	
82.1	Protein disulfide-isomerase A6	PDIA6_HUMAN	48 kDa	2	1	3	1	2	2	0	0	3	3	2	1	0	0	0	0	0	0	0	1	1	0	0	
83	10 kDa heat shock protein, mitochondrial	CH10_HUMAN	11 kDa	0	0	0	0	0	2	2	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	
84	Elongation factor 1-delta	EF1D_HUMAN	31 kDa	3	0	0	2	4	4	2	0	4	0	2	0	0	0	0	0	5	4	5	4	3	2	2	0
85	Cluster of CD166 antigen	CD166_HUMAN	65 kDa	4	4	0	0	4	0	0	0	0	0	0	0	0	0	0	8	9	9	5	3	3	0	0	
85.1	CD166 antigen	CD166_HUMAN	65 kDa	2	1	0	0	2	0	0	0	0	0	0	0	0	0	0	3	3	3	0	1	2	0	0	
86	Cluster of Perilipin-3	PLIN3_PIG	48 kDa	0	0	2	0	4	2	0	0	0	0	0	0	2	0	0	0	3	3	2	0	5	3	0	0
86.1	Perilipin-3	PLIN3_PIG	48 kDa	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	
86.2	Perilipin-3	PLIN3_PONAB	47 kDa	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
87	Endoplasmic reticulum resident protein 29	ERP29_HUMAN	29 kDa	4	2	2	2	5	4	3	2	2	2	0	0	0	0	0	3	4	3	3	4	2	2	0	

88	Cluster of Heterogeneous nuclear ribonucleoproteins A2/B1	ROA2_HUMAN	37 kDa	3	0	0	0	2	0	2	0	2	2	2	2	0	0	0	0	3	2	2	2	0	0	0	0
88.1	Heterogeneous nuclear ribonucleoproteins A2/B1	ROA2_HUMAN	37 kDa	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	1	1	1	1	0	0	0	0
89	Myosin light polypeptide 6	MYL6_BOVIN	17 kDa	0	0	0	0	3	2	2	2	0	0	0	0	0	0	0	3	4	3	2	2	2	2	3	
90	Complement component 1 Q subcomponent-binding protein, mitochondrial	C1QBP_HUMAN	31 kDa	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	4	3	3	2	2	0	0	0	
91	Cluster of Filamin-A	FLNA_HUMAN	281 kDa	4	3	0	2	0	2	0	0	8	7	5	3	3	3	0	0	0	0	0	2	3	2	0	
91.1	Filamin-A	FLNA_HUMAN	281 kDa	1	1	0	1	0	1	0	0	2	2	1	2	1	1	0	0	0	0	0	1	1	1	0	
91.2	Filamin-A	FLNA_MOUSE	281 kDa	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
92	Fructose-bisphosphate aldolase A	ALDOA_HUMAN	39 kDa	2	2	2	0	0	0	0	0	6	6	6	4	0	0	0	0	0	0	0	0	0	0	0	
93	60S acidic ribosomal protein P2	RLA2_BOVIN	12 kDa	0	0	0	0	2	0	2	0	0	0	0	0	0	0	0	3	3	2	2	0	2	0	0	
94	Heterogeneous nuclear ribonucleoproteins C1/C2	HNRPC_MOUSE	34 kDa	3	3	4	4	3	3	2	0	3	4	4	5	2	3	0	0	0	0	0	2	3	3	0	
95	Caprin-1	CAPR1_HUMAN	78 kDa	0	0	0	0	2	2	0	0	0	0	0	0	0	0	0	4	6	5	5	0	2	0	0	
96	Protein S100-A6	S10A6_MOUSE	10 kDa	0	0	0	0	2	2	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
97	Serine/arginine-rich splicing factor 1	SRSF1_CHICK	28 kDa	0	0	0	0	2	2	2	0	0	0	0	0	2	0	0	0	2	2	2	0	0	0	0	
98	Phosphoglycerate mutase 1	PGAM1_BOVIN	29 kDa	2	3	2	0	3	3	0	0	3	3	3	3	0	0	0	0	0	0	0	0	0	0	0	
99	Cluster of Transferrin receptor protein 1	TFR1_HUMAN	85 kDa	3	3	2	2	2	3	3	2	3	2	0	2	3	2	0	0	3	3	2	3	0	2	0	0
99.1	Transferrin receptor protein 1	TFR1_HUMAN	85 kDa	1	1	0	0	0	1	1	1	1	0	0	0	2	1	0	0	1	1	0	1	0	0	0	0
100	Transgelin-2	TAGL2_HUMAN	22 kDa	0	0	0	0	2	0	2	0	0	0	0	0	0	0	0	4	6	4	2	5	4	2	0	
101	Heterogeneous nuclear ribonucleoprotein A1	ROA1_HUMAN	39 kDa	0	0	2	2	0	0	0	0	2	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
102	Importin subunit beta-1	IMB1_HUMAN	97 kDa	3	2	2	2	2	2	0	0	3	3	0	0	0	0	0	0	0	0	2	0	2	3	0	0
103	High mobility group protein B2	HMGB2_BOVIN	24 kDa	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	2	2	2	2	0	2	3	0	
104	Serpin H1	SERPH_HUMAN	46 kDa	3	2	2	0	2	2	0	0	2	0	0	0	0	0	0	0	0	0	0	2	0	0	0	
105	Profilin-1	PROF1_HUMAN	15 kDa	0	0	0	0	2	3	0	0	3	5	4	0	0	0	0	0	0	0	0	0	0	0	0	0
106	Serine/arginine-rich splicing factor 3	SRSF3_MOUSE	19 kDa	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	2	2	2	1	0	1	0	0	





124.	Nucleoside diphosphate kinase B	NDKB_BOVIN	17 kDa	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0			
125	Membrane-associated progesterone receptor component 2	PGRC2_HUMAN	24 kDa	2	3	2	2	3	3	2	0	2	2	0	2	2	0	0	0	2	2	0	2	2	2	2	0
126	Hepatoma-derived growth factor O	HDGF_HUMAN	27 kDa	0	0	0	0	2	0	2	0	0	0	0	0	0	0	0	4	3	2	4	0	0	2	0	
127	Keratin, type I cytoskeletal 9	K1C9_HUMAN	62 kDa	4	3	3	0	7	5	3	0	0	0	0	0	2	0	0	0	0	2	2	0	0	0	0	
128	Protein SET	SET_HUMAN	33 kDa	2	0	0	0	0	0	0	0	2	0	0	0	0	0	0	2	3	2	0	0	0	0	0	
129	Protein CutA	CUTA_HUMAN	19 kDa	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	3	3	0	0	
130	Heterogeneous nuclear ribonucleoprotein D-like	HNRDL_RAT	35 kDa	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	5	5	4	4	1	1	0	0	
131	Cluster of Hemoglobin subunit alpha	HBA_BOVIN	15 kDa	0	0	0	0	5	4	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
131.	Hemoglobin subunit alpha O	HBA_BOVIN	15 kDa	0	0	0	0	3	2	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
131.	Hemoglobin subunit alpha	HBA_SPECI	15 kDa	0	0	0	0	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
132	Variant surface antigen C	VLPC_MYCHR	16 kDa	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	2	3	0	
133	Nuclear autoantigenic sperm protein	NASP_HUMAN	85 kDa	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	5	6	3	3	0	0	0	0	
134	Proteasome subunit alpha type-6	PSA6_HUMAN	27 kDa	3	5	3	2	2	2	2	0	2	0	0	0	0	0	2	0	0	0	0	0	0	0	0	
135	Small ubiquitin-related modifier 2	SUMO2_DANRE	11 kDa	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	2	0	0	0	
136	Heterogeneous nuclear ribonucleoprotein K	HNRPK_BOVIN	51 kDa	3	3	4	3	2	2	0	0	4	4	2	2	0	0	0	0	0	0	0	2	2	0	0	
137	Cluster of Transitional endoplasmic reticulum ATPase	TERA_HUMAN	89 kDa	0	0	0	0	3	2	0	0	6	5	3	3	0	0	0	0	0	0	0	0	3	0	0	
137.	Transitional endoplasmic reticulum ATPase	TERA_HUMAN	89 kDa	0	0	0	0	1	0	0	0	3	2	2	1	0	0	0	0	0	0	0	0	1	0	0	
138	Stathmin	STMN1_GEKJA	17 kDa	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0	2	2	2	4	4	0	
139	Uncharacterized protein C19orf43	CS043_HUMAN	18 kDa	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	2	0	0	0	
140	T-complex protein 1 subunit eta	TCPH_BOVIN	59 kDa	3	2	0	0	2	0	0	0	2	2	0	0	0	0	0	0	0	0	0	2	0	0	0	
141	Thioredoxin	THIO_HUMAN	12 kDa	0	0	0	0	2	2	0	0	0	0	0	0	0	0	0	3	2	0	0	0	0	0	0	







191	Clathrin heavy chain 1	CLH1_BOVIN	192 kDa	3	3	2	0	0	0	0	0	0	2	0	2	0	0	0	0	0	0	2	0	0
192	Polypyrimidine tract-binding protein 1	PTBP1_HUMAN	57 kDa	4	4	0	0	0	0	0	0	4	2	0	0	0	0	0	0	0	0	0	0	0
193	Coiled-coil domain-containing protein 86	CCD86_HUMAN	40 kDa	0	0	0	0	0	0	0	0	0	0	0	0	0	2	3	3	2	0	0	0	0
194	T-complex protein 1 subunit beta	TCPB_HUMAN	57 kDa	2	0	0	0	0	0	0	0	4	0	2	0	0	0	0	0	0	0	0	0	0
195	T-complex protein 1 subunit delta	TCPD_BOVIN	58 kDa	3	3	3	0	0	0	0	0	3	3	2	3	0	0	0	0	0	0	0	0	0
196	Cluster of T-complex protein 1 subunit epsilon	TCPE_HUMAN	60 kDa	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
196.1	T-complex protein 1 subunit epsilon	TCPE_HUMAN	60 kDa	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
197	Single-stranded DNA-binding protein, mitochondrial	SSBP_HUMAN	17 kDa	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0
198	Acidic leucine-rich nuclear phosphoprotein 32 family member E	AN32E_HUMAN	31 kDa	0	0	0	0	0	0	0	0	0	0	0	0	0	2	3	3	2	0	0	0	0
199	Cluster of Neutral alpha-glucosidase AB	GANAB_HUMAN	107 kDa	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
199.1	Neutral alpha-glucosidase AB	GANAB_HUMAN	107 kDa	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
200	X-ray repair cross-complementing protein 5	XRCC5_HUMAN	83 kDa	2	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
201	Cluster of Plectin	PLEC_HUMAN	532 kDa	0	0	0	0	0	0	0	0	2	3	3	0	0	0	0	0	0	2	0	0	0
201.1	Plectin	PLEC_HUMAN	532 kDa	0	0	0	0	0	0	0	0	1	3	1	0	0	0	0	0	0	0	0	0	0
202	Peroxiredoxin-4	PRDX4_HUMAN	31 kDa	1	1	1	1	1	1	1	0	1	1	0	0	1	0	0	0	0	0	0	0	0
203	Cluster of Scaffold attachment factor B1	SAFB1_HUMAN	103 kDa	0	0	0	0	0	0	0	0	0	0	0	0	0	4	2	2	0	0	0	0	0
203.1	Scaffold attachment factor B1	SAFB1_HUMAN	103 kDa	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	1	0	0	0	0	0
203.2	Scaffold attachment factor B2	SAFB2_HUMAN	107 kDa	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0	0
204	Tissue factor	TF_HUMAN	33 kDa	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	2	2	0	0
205	60S ribosomal protein L7a	RL7A_MACFA	30 kDa	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0
206	A-kinase anchor protein 2	AKAP2_HUMAN	95 kDa	2	0	0	0	0	0	0	0	0	0	0	0	0	4	3	2	0	0	0	0	0
207	Cellular nucleic acid-binding protein	CNBP_BOVIN	19 kDa	0	0	0	0	0	0	0	0	0	0	0	0	0	2	2	3	0	0	0	0	0

208	Cluster of Hypoxia up-regulated protein 1 O	HYOU1_HUMAN	111 kDa	3	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
208.1	Hypoxia up-regulated protein 1	HYOU1_HUMAN	111 kDa	1	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
209	PEST proteolytic signal-containing nuclear protein	PCNP_HUMAN	19 kDa	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0
210	Ubiquitin-associated protein 2-like	UBP2L_HUMAN	115 kDa	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0
211	Heterogeneous nuclear ribonucleoprotein L	HNRPL_HUMAN	64 kDa	0	2	2	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0
212	UV excision repair protein RAD23 homolog B	RD23B_HUMAN	43 kDa	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0
213	Protein disulfide-isomerase A4	PDIA4_HUMAN	73 kDa	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
214	Myoferlin	MYOF_HUMAN	235 kDa	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0
215	T-complex protein 1 subunit gamma	TCPG_RAT	61 kDa	0	0	0	2	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0
216	40S ribosomal protein S21	RS21_BOVIN	9 kDa	0	0	0	0	0	0	0	0	0	0	0	0	0	3	3	3	3	0	0	0	0
217	Cluster of Small nuclear ribonucleoprotein-associated protein B	RSMB_MOUSE	24 kDa	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
217.1	Small nuclear ribonucleoprotein-associated protein B	RSMB_MOUSE	24 kDa	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
218	Lumican	LUM_BOVIN	39 kDa	0	0	0	0	3	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
219	Cluster of Spliceosome RNA helicase DDX39B	DX39B_BOVIN	49 kDa	0	0	0	0	0	0	0	2	0	2	2	0	0	0	0	0	0	0	0	0	0
219.1	Spliceosome RNA helicase DDX39B	DX39B_BOVIN	49 kDa	0	0	0	0	0	0	1	0	1	1	0	0	0	0	0	0	0	0	0	0	0
220	Cluster of Cytochrome c	CYC_ATESP	12 kDa	2	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
220.1	Cytochrome c	CYC_ATESP	12 kDa	2	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
221	Eukaryotic initiation factor 4A-III	IF4A3_DANRE	46 kDa	1	1	1	1	0	1	0	0	1	1	1	1	0	0	0	0	0	0	0	0	0
222	Glycine--tRNA ligase	SYG_HUMAN	83 kDa	0	0	0	0	0	0	0	2	2	0	0	0	0	0	0	0	0	0	0	0	0
223	Proteasome subunit beta type-2	PSB2_HUMAN	23 kDa	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
224	Heat shock protein beta-1	HSPB1_HUMAN	23 kDa	0	0	0	0	3	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
225	Prothymosin alpha	PTMA_BOVIN	12 kDa	0	0	0	0	0	0	0	0	0	0	0	0	0	2	2	2	2	0	0	0	0

226	39S ribosomal protein L12, mitochondrial	RM12_HUMAN	21 kDa	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0
227	Eukaryotic translation initiation factor 3 subunit F	EIF3F_HUMAN	38 kDa	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
228	Cluster of Proteasome subunit beta type-4 (Fragment)	PSB4_PIG	17 kDa	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
228.1	Proteasome subunit beta type-4 O	PSB4_HUMAN	29 kDa	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
229	Cluster of T-complex protein 1 subunit alpha	TCPA_MONDO	61 kDa	0	0	0	0	0	0	0	3	0	2	2	0	0	0	0	0	0	0	0	0	0	0
229.1	T-complex protein 1 subunit alpha	TCPA_CRIGR	60 kDa	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
230	Proteasome subunit alpha type-2	PSA2_HUMAN	26 kDa	3	2	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
231	Cleavage stimulation factor subunit 2	CSTF2_HUMAN	61 kDa	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0
232	Proteasome activator complex subunit 1	PSME1_HUMAN	29 kDa	0	0	2	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
233	Cluster of Membrane-associated progesterone receptor component 1	PGRC1_HUMAN	22 kDa	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	2	2	0	0	0	0	0
233.1	Membrane-associated progesterone receptor component 1	PGRC1_HUMAN	22 kDa	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	0	0	0	0	0
234	Proteasome subunit alpha type-4	PSA4_BOVIN	29 kDa	3	3	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
235	40S ribosomal protein S28	RS28_BOVIN	8 kDa	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	2	2	2	0	0	0	0
236	Cluster of Transcription intermediary factor 1-beta	TIF1B_HUMAN	89 kDa	0	2	0	0	0	0	0	2	2	0	0	0	0	0	0	0	0	0	0	0	0	0
236.1	Transcription intermediary factor 1-beta	TIF1B_HUMAN	89 kDa	0	1	0	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0
237	Src substrate cortactin	SRC8_HUMAN	62 kDa	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	2	2	0	0	0	0
238	Glucose-6-phosphate isomerase	G6PI_HUMAN	63 kDa	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
239	Cluster of T-complex protein 1 subunit zeta	TCPZ_HUMAN	58 kDa	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
239.1	T-complex protein 1 subunit zeta	TCPZ_HUMAN	58 kDa	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
240	Deoxyuridine 5'-triphosphate	DUT_HUMAN	27 kDa	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0	0

241	nucleotidohydrolase, mitochondrial Thyroid hormone receptor- associated protein 3	TR150_HUMAN	109 kDa	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	2	0	0	0	0
242	Glyceraldehyde-3- phosphate dehydrogenase	G3P_DANRE	36 kDa	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0
243	Cluster of Ras-related protein Rab-10	RAB10_CHICK	23 kDa	1	1	1	1	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0
243.	Ras-related protein Rab- 10	RAB10_CHICK	23 kDa	1	1	1	1	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0
244	60S ribosomal protein L12	RL12_CHILA	18 kDa	0	0	0	0	0	0	0	0	0	0	2	2	0	0	0	0	0	0	0	0	0
245	Lupus La protein homolog	LA_BOVIN	47 kDa	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
246	Filamin-C	FLNC_HUMAN	291 kDa	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0
247	60S ribosomal protein L18	RL18_HUMAN	22 kDa	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	2	0
248	Filamin-B	FLNB_HUMAN	278 kDa	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0
249	26S proteasome non- ATPase regulatory subunit 2	PSMD2_HUMAN	100 kDa	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
250	Cluster of Adenylyl cyclase- associated protein 1	CAP1_HUMAN	52 kDa	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0
250.	Adenylyl cyclase- associated protein 1	CAP1_HUMAN	52 kDa	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0
251	Heterogeneous nuclear ribonucleoprotein Q	HNRPQ_HUMAN	70 kDa	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0
252	U4/U6.U5 tri-snRNP- associated protein 1	SNUT1_HUMAN	90 kDa	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	4	2	0	0	0	0
253	Cluster of Pre-mRNA 3'- end-processing factor FIP1	FIP1_HUMAN	67 kDa	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0
253.	Pre-mRNA 3'-end- processing factor FIP1	FIP1_HUMAN	67 kDa	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0
254	Drebrin-like protein	DBNL_HUMAN	48 kDa	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
255	Cell surface glycoprotein MUC18	MUC18_HUMAN	72 kDa	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	2	2	0	0	0	0
256	Matrin-3	MATR3_HUMAN	95 kDa	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
257	Fatty acid synthase	FAS_HUMAN	273 kDa	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
258	Annexin A6	ANXA6_HUMAN	76 kDa	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
259	40S ribosomal protein S25	RS25_MOUSE	14 kDa	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	2	0	0	0



260	116 kDa U5 small nuclear ribonucleoprotein component	USS1_BOVIN	109 kDa	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0
261	60S acidic ribosomal protein P0-like	RLA0L_HUMAN	34 kDa	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
262	Exportin-2	XPO2_BOVIN	110 kDa	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
263	Phosphatidylethanolamine-binding protein 1	PEBP1_HUMAN	21 kDa	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0
264	Serine/threonine-protein phosphatase PP1-alpha catalytic subunit	PP1A_BOVIN	38 kDa	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

**Table S1.1.** List of proteins identified by nanoLC-MS/MS in **PMC3, Ru1** and control conditions – **Exclusive Unique Peptide Count**. Identification by Mascot search engine v 2.3. Validation: within Scaffold software using Peptide and Protein Prophet (criteria at 95%)

				Exclusive Unique Spectrum Count																							
Protein description				PMC3 Pool 1				PMC3 Pool 2				Ru1 Pool 1				Ru1 Pool 2				Control Pool 1				Control Pool 2			
#	Identified Proteins (354)	UniprotKB Accession Number	Theoretical Molecular Weight	R1	R2	R3	R4	R1	R2	R3	R4	R1	R2	R3	R4	R1	R2	R3	R4	R1	R2	R3	R4	R1	R2	R3	R4
1	Cluster of Vimentin	VIME_HUMAN	54 kDa	52	46	43	35	46	39	35	21	47	44	33	34	18	11	9	8	64	65	57	49	45	46	35	18
1.1	Vimentin	VIME_HUMAN	54 kDa	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	0	0	1	0	0	0
1.2	Vimentin	VIME_PANTR	54 kDa	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0	0
1.3	Vimentin	VIME_BOVIN	54 kDa	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2	Cluster of Actin-2	ACT2_SUIBO	42 kDa	44	48	35	31	39	37	31	9	21	37	29	21	12	0	3	6	11	9	9	8	38	46	31	14
2.1	Actin-2	ACT2_SUIBO	42 kDa	4	4	2	2	4	3	1	0	3	1	0	1	0	0	0	0	2	2	2	1	4	3	1	0
2.2	Beta-actin-like protein 2	ACTBL_HUMAN	42 kDa	1	1	0	0	1	1	1	0	1	0	1	0	0	0	0	0	1	0	0	0	0	1	0	0
2.3	Actin-18 O	ACT18_DICDI	43 kDa	0	1	1	1	1	1	1	0	0	1	1	1	0	0	0	0	0	0	0	0	0	1	1	0

2.4	Actin-3	ACT3_SOYBN	42 kDa	0	1	1	0	0	0	1	0	0	0	1	0	1	0	0	0	0	0	1	0	0			
2.5	Actin	ACT_CRYPV	42 kDa	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	1	0	0		
2.6	Actin, cytoplasmic 1	ACTB_CRIGR	42 kDa	1	1	1	1	0	1	2	0	0	1	0	1	1	0	0	0	0	0	0	1	1	2	1	
2.7	Actin	ACT_KOMPG	42 kDa	1	1	0	1	0	0	1	1	0	1	1	0	0	0	0	0	1	1	1	1	0	0	1	1
2.8	Actin, cytoplasmic	ACTC_BRABE	42 kDa	0	0	0	0	0	0	2	1	0	2	1	1	0	0	0	0	0	0	0	1	1	1	1	
2.9	Actin, cytoplasmic	ACTC_STYPL	42 kDa	0	1	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	1	
2.1	Actin-53 (Fragment)	ACT2_TOBAC	37 kDa	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	1	0	0	
2.11	Actin	ACT_ASPOR	42 kDa	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	
2.12	Actin	ACT_ACHBI	42 kDa	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2.13	Actin, muscle	ACTM_PISOC	42 kDa	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2.14	Actin-1	ACT1_SCHMA	42 kDa	0	0	0	0	0	1	0	0	0	1	0	0	0	0	0	0	0	0	0	1	1	0	0	0
2.15	Actin, cytoplasmic type 8	ACT8_XENLA	42 kDa	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2.16	Actin-A3b, cytoplasmic	ACT3B_HELAM	42 kDa	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0
2.17	Actin-17	ACT17_DICDI	42 kDa	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0
2.18	Actin-1	ACT1_AEDAE	42 kDa	0	0	0	0	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0
2.19	Actin-3	ACT3_DICDI	42 kDa	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0
2.2	Actin, cytoskeletal 3 (Fragment)	ACT3_LYTPI	19 kDa	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0
2.21	Actin	ACT_ENTHI	42 kDa	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2.22	Putative actin-23	ACT23_DICDI	40 kDa	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2.23	Actin, clone 302 (Fragment)	ACT3_ARTSX	37 kDa	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0
3	Cationic trypsin	TRY1_BOVIN	26 kDa	11	9	8	7	10	10	9	4	8	10	7	8	7	5	4	4	12	14	10	10	10	10	10	6
4	Neuroblast differentiation-associated protein AHNAK	AHNK_HUMAN	629 kDa	47	56	31	25	58	49	29	12	5	6	0	2	0	2	0	0	62	63	63	32	78	88	55	25

5	Cluster of Heat shock protein HSP 90-beta	HS90B_PONAB	83 kDa	60	54	41	38	43	33	35	15	46	45	35	33	11	9	7	6	5	4	4	2	18	17	13	6
5.1	Heat shock protein HSP 90-beta	HS90B_PONAB	83 kDa	17	19	13	12	12	7	7	0	15	11	11	9	2	1	2	1	1	0	0	1	6	4	3	1
5.2	Endoplasmic	ENPL_HUMAN	92 kDa	4	4	3	2	4	3	3	2	2	3	1	3	2	1	1	0	0	0	0	0	1	1	0	0
5.3	Heat shock protein HSP 90-alpha	HS90A_BOVIN	85 kDa	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5.4	Heat shock protein HSP 90-alpha	HS90A_CHICK	84 kDa	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6	Cluster of Nucleophosmin	NPM_HUMAN	33 kDa	13	14	11	5	13	11	8	3	10	7	4	4	0	0	0	0	23	21	21	11	12	11	5	3
6.1	Nucleophosmin	NPM_HUMAN	33 kDa	6	8	6	1	7	5	0	0	3	2	1	0	0	0	0	0	11	8	9	2	5	4	1	0
6.2	Nucleophosmin	NPM_BOVIN	33 kDa	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	2	0	0	0	0	0	0
7	Cluster of Heat shock cognate 71 kDa protein	HSP7C_BOVIN	71 kDa	39	34	33	29	56	49	43	21	36	35	24	23	16	10	9	7	4	4	5	0	11	16	13	6
7.1	Heat shock cognate 71 kDa protein	HSP7C_BOVIN	71 kDa	11	8	7	8	7	5	4	2	9	8	5	5	1	1	0	0	0	0	1	0	2	1	2	1
7.2	78 kDa glucose-regulated protein	GRP78_HUMAN	72 kDa	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	0	0	0	0	1	1	1	0
7.3	Heat shock 70 kDa protein cognate 1	HSP7A_DROME	71 kDa	0	1	1	1	0	1	1	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0
7.4	Heat shock 70 kDa protein	HSP70_NEUCR	71 kDa	0	1	0	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7.5	Heat shock 70 kDa protein 1	HSP71_PONAB	70 kDa	0	0	0	0	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7.6	Heat shock 70 kDa protein	HSP70_PYRSA	72 kDa	0	0	1	1	0	1	0	0	1	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0
7.7	78 kDa glucose-regulated protein	GRP78_ICTTR	72 kDa	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7.8	Heat shock 70 kDa protein 1-like	HS71L_BOVIN	70 kDa	0	0	0	0	0	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7.9	Heat shock protein SSA1	HSP71_CANAL	70 kDa	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
8	Cluster of Histone H2A type 1-C	H2A1C_HUMAN	14 kDa	15	13	11	4	12	11	7	2	5	4	5	3	2	0	0	2	12	12	10	7	12	12	9	4
8.1	Histone H2A type 1-C	H2A1C_HUMAN	14 kDa	3	3	3	0	3	2	1	0	0	0	1	0	0	0	0	0	3	3	3	3	3	3	4	1
8.2	Histone H2A type 2-A	H2A2A_HUMAN	14 kDa	5	3	5	1	4	3	2	0	1	1	1	1	0	0	0	0	5	5	3	1	4	4	2	1
8.3	Histone H2A.V	H2AV_BOVIN	14 kDa	1	1	0	0	0	0	0	0	1	0	0	0	0	0	0	0	1	1	1	0	1	1	0	0



14	Cluster of Nucleolin	NUCL_HUMAN	77 kDa	8	7	4	7	9	8	5	0	8	5	2	3	0	0	0	0	31	25	25	16	8	8	5	2
14.1	Nucleolin	NUCL_HUMAN	77 kDa	8	7	4	7	9	8	5	0	8	5	2	3	0	0	0	0	31	25	25	16	8	8	5	2
15	Cluster of Calreticulin	CALR_HUMAN	48 kDa	13	11	8	7	16	16	10	5	9	9	6	4	4	0	0	0	9	10	11	4	7	7	3	0
15.1	Calreticulin	CALR_HUMAN	48 kDa	7	7	6	5	9	11	6	4	6	7	5	4	4	0	0	0	3	5	5	2	3	4	2	0
16	Cluster of Tropomyosin alpha-3 chain	TPM3_RAT	29 kDa	4	2	3	3	9	8	3	0	0	0	0	0	0	0	0	0	12	19	12	12	18	22	12	3
16.1	Tropomyosin alpha-3 chain	TPM3_RAT	29 kDa	3	1	1	2	6	6	2	0	0	0	0	0	0	0	0	0	7	11	8	7	11	11	8	3
16.2	Tropomyosin alpha-4 chain	TPM4_HUMAN	29 kDa	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0	0
16.3	Tropomyosin alpha-4 chain	TPM4_HORSE	29 kDa	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
17	Far upstream element-binding protein 2	FUBP2_HUMAN	73 kDa	15	14	13	8	12	10	6	3	5	5	2	3	4	3	2	0	21	20	23	17	12	13	10	5
18	Cluster of Histone H4	H4_ACRAS	11 kDa	10	8	7	6	8	8	7	4	5	4	3	5	4	3	2	3	0	2	3	2	9	8	5	4
18.1	Histone H4	H4_ACRAS	11 kDa	5	3	2	1	3	3	2	1	2	0	0	1	0	0	0	0	0	1	1	0	4	3	0	1
19	Cluster of Glyceraldehyde-3-phosphate dehydrogenase	G3P_HUMAN	36 kDa	13	12	6	7	10	6	5	3	18	14	11	7	3	3	2	3	7	4	4	4	8	6	5	3
19.1	Glyceraldehyde-3-phosphate dehydrogenase	G3P_HUMAN	36 kDa	11	10	4	5	8	4	3	1	16	12	9	5	1	1	1	1	5	2	2	2	6	4	3	1
20	Cluster of Histone H2B type 1-B	H2B1B_HUMAN	14 kDa	4	2	3	4	4	4	3	3	2	4	4	2	3	3	2	2	3	3	4	3	3	3	4	4
20.1	Histone H2B type 1-B	H2B1B_HUMAN	14 kDa	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0
20.2	Histone H2B type 1-N	H2B1N_BOVIN	14 kDa	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
21	Cluster of Tubulin beta-5 chain	TBB5_RAT	50 kDa	22	18	16	13	17	14	11	6	17	13	7	8	8	6	4	4	4	7	5	3	28	21	16	7
21.1	Tubulin beta-5 chain	TBB5_RAT	50 kDa	2	2	2	2	2	2	2	1	3	2	2	2	1	1	1	1	1	1	1	1	3	2	2	2
21.2	Tubulin beta chain	TBB_CERBT	50 kDa	2	1	0	0	1	0	0	0	0	1	0	0	1	0	0	0	0	1	0	0	2	1	1	0
21.3	Tubulin beta chain	TBB_PENDI	50 kDa	0	0	0	1	0	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0	1	1	1	0
21.4	Tubulin beta-4B chain	TBB4B_HUMAN	50 kDa	0	1	0	0	1	1	1	0	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0
21.5	Tubulin beta-1 chain (Fragment)	TBB1_DAUCA	36 kDa	1	0	1	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	1	0

21.6	Tubulin beta-1 chain	TBB1_DROME	50 kDa	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0		
21.7	Tubulin beta-2 chain	TBB2_DROER	50 kDa	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0		
21.8	Tubulin beta-4A chain	TBB4A_BOVIN	50 kDa	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
22	Cluster of CD44 antigen	CD44_HUMAN	82 kDa	6	6	6	5	8	9	5	3	4	5	4	3	5	4	3	2	8	9	9	7	7	8	6	3
22.1	CD44 antigen	CD44_HUMAN	82 kDa	2	2	2	1	2	3	1	1	2	1	1	1	2	1	1	1	3	3	4	2	2	2	1	1
23	Cluster of Tubulin alpha chain	TBA_XENLA	50 kDa	13	15	11	8	10	10	9	0	15	8	9	6	8	5	2	4	3	0	0	0	19	14	12	5
23.1	Tubulin alpha chain	TBA_XENLA	50 kDa	2	2	1	1	1	1	1	0	1	1	1	1	1	1	1	1	1	0	0	0	2	1	1	1
23.2	Tubulin alpha-5 chain	TBA5_ARATH	50 kDa	0	1	1	0	1	1	1	0	1	0	1	0	0	0	0	0	0	0	0	1	1	1	0	
23.3	Tubulin alpha-3 chain	TBA3_CAEEL	50 kDa	0	1	0	1	0	1	0	0	1	1	0	1	0	0	0	0	0	0	0	1	1	1	0	
23.4	Tubulin alpha chain	TBA_ENTDO	50 kDa	1	0	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	1	0	0	0	
24	Cluster of 60 kDa heat shock protein, mitochondrial	CH60_HUMAN	61 kDa	20	18	17	12	22	16	10	2	17	17	10	11	3	4	2	3	4	4	2	0	7	6	5	0
24.1	60 kDa heat shock protein, mitochondrial	CH60_HUMAN	61 kDa	16	15	15	9	18	13	8	2	13	13	7	9	2	2	1	2	4	4	2	0	5	5	3	0
25	Cluster of Alpha-enolase	ENOA_HUMAN	47 kDa	12	12	7	7	14	9	4	0	12	10	6	7	11	6	4	4	0	0	0	0	20	19	12	3
25.1	Alpha-enolase	ENOA_HUMAN	47 kDa	6	6	3	2	4	4	1	0	5	4	1	3	3	3	1	1	0	0	0	0	10	7	5	0
26	Cluster of ADP/ATP translocase 2	ADT2_BOVIN	33 kDa	5	7	0	0	6	0	5	2	6	0	0	0	6	3	0	0	0	0	0	0	6	7	6	2
26.1	ADP/ATP translocase 2	ADT2_BOVIN	33 kDa	2	2	0	0	2	0	2	0	2	0	0	0	2	0	0	0	0	0	0	0	2	2	2	1
26.2	ADP/ATP translocase 3	ADT3_BOVIN	33 kDa	2	2	0	0	2	0	0	0	2	0	0	0	2	0	0	0	0	0	0	0	2	2	2	0
27	High mobility group protein B1	HMGB1_BOVIN	25 kDa	4	7	5	5	3	3	0	0	5	3	0	0	0	0	0	0	15	14	16	14	7	6	4	0
28	Cluster of Protein disulfide-isomerase	PDIA1_HUMAN	57 kDa	11	10	8	4	17	11	10	6	4	4	2	2	6	3	2	0	7	3	2	2	6	5	3	0
28.1	Protein disulfide-isomerase O	PDIA1_HUMAN	57 kDa	1	0	0	0	3	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
29	Cluster of Galectin-1	LEG1_HUMAN	15 kDa	8	5	5	5	6	7	4	3	4	5	3	4	0	0	0	0	8	7	7	6	0	6	0	0
29.1	Galectin-1	LEG1_HUMAN	15 kDa	2	1	1	1	1	2	1	0	1	1	1	1	0	0	0	0	3	2	2	2	0	2	0	0

29.2	Galectin-1	LEG1_MOUSE	15 kDa	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
30	Cluster of Integrin beta-1	ITB1_HUMAN	88 kDa	8	6	6	5	12	10	8	3	2	0	0	0	7	5	3	2	7	9	6	7	9	10	5	4
30.1	Integrin beta-1	ITB1_HUMAN	88 kDa	4	3	3	3	7	6	4	1	1	0	0	0	4	3	1	0	2	3	3	3	3	3	2	1
31	Cluster of 14-3-3 protein epsilon	1433E_SHEEP	29 kDa	10	6	5	2	9	5	4	2	12	10	4	10	2	0	0	0	0	0	0	0	7	6	5	0
31.1	14-3-3 protein epsilon	1433E_SHEEP	29 kDa	4	3	3	2	2	2	1	2	6	5	4	4	0	0	0	0	0	0	0	0	2	2	1	0
31.2	14-3-3 protein zeta/delta	1433Z_HUMAN	28 kDa	2	1	1	0	4	1	1	0	3	2	0	2	2	0	0	0	0	0	0	0	3	2	2	0
31.3	14-3-3 protein theta	1433T_BOVIN	28 kDa	1	0	0	0	1	1	1	0	0	0	0	1	0	0	0	0	0	0	0	0	1	1	1	0
31.4	14-3-3 protein sigma	1433S_HUMAN	28 kDa	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
31.5	14-3-3 protein beta/alpha	1433B_CHICK	28 kDa	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0
31.6	14-3-3 protein gamma	1433G_BOVIN	28 kDa	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0
32	Cluster of Pyruvate kinase PKM	KPYM_HUMAN	58 kDa	8	9	7	4	6	5	5	2	7	4	6	5	3	2	0	3	0	0	0	0	14	11	8	3
32.1	Pyruvate kinase PKM	KPYM_HUMAN	58 kDa	1	1	1	1	1	1	1	0	1	1	1	1	1	0	0	0	0	0	0	0	1	1	1	0
33	Cluster of Keratin, type I cytoskeletal 10	K1C10_HUMAN	59 kDa	6	6	6	6	10	9	8	5	0	4	0	1	5	6	4	4	5	4	3	2	4	6	2	2
33.1	Keratin, type I cytoskeletal 10	K1C10_HUMAN	59 kDa	6	6	6	6	7	7	5	3	0	3	0	0	3	3	3	2	5	4	3	2	2	2	0	0
33.2	Keratin, type I cytoskeletal 18	K1C18_HUMAN	48 kDa	0	0	0	0	1	1	1	1	0	1	0	1	1	1	0	0	0	0	0	0	1	2	1	1
33.3	Keratin, type I cytoskeletal 19	K1C19_HUMAN	44 kDa	0	0	0	0	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	2	1	1
33.4	Keratin, type I cytoskeletal 14	K1C14_HUMAN	52 kDa	0	0	0	0	0	0	0	0	0	0	0	0	1	0	1	0	0	0	0	0	0	0	0	0
34	Cluster of Alpha-actinin-4	ACTN4_HUMAN	105 kDa	8	10	5	6	4	5	3	0	15	16	16	11	3	3	0	0	0	0	0	0	4	4	4	2
34.1	Alpha-actinin-4 O	ACTN4_HUMAN	105 kDa	4	5	3	3	2	3	1	0	7	8	7	6	0	0	0	0	0	0	0	0	2	2	1	0
34.2	Alpha-actinin, sarcomeric	ACTN_ANOGA	107 kDa	0	1	0	0	0	0	0	0	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0
34.3	Alpha-actinin-1	ACTN1_BOVIN	103 kDa	1	1	0	0	0	0	0	0	3	2	2	2	0	0	0	0	0	0	0	0	0	0	0	0
35	Cofilin-1	COF1_HUMAN	19 kDa	5	4	2	3	6	5	4	3	5	5	4	2	0	0	0	0	7	9	7	5	5	6	5	2

36	Cluster of Glucosidase 2 subunit beta	GLU2B_HUMAN	59 kDa	5	7	6	7	11	10	8	5	2	2	3	2	0	0	0	0	9	11	11	7	8	11	7	5	
36.1	Glucosidase 2 subunit beta	GLU2B_HUMAN	59 kDa	4	6	5	6	10	9	7	4	1	1	2	1	0	0	0	0	8	10	10	6	7	10	6	4	
37	Cluster of Ubiquitin-60S ribosomal protein L40	RL40_DROME	15 kDa	3	4	3	2	4	4	3	4	3	4	3	2	5	5	3	2	4	3	4	3	5	3	4	4	
37.1	Ubiquitin-60S ribosomal protein L40	RL40_DROME	15 kDa	2	2	2	1	3	2	2	2	2	2	2	1	2	2	1	0	3	2	3	2	3	2	2	2	
38	Calnexin	CALX_HUMAN	68 kDa	10	6	5	2	8	4	6	0	2	2	0	0	0	0	0	3	3	0	0	0	0	0	0	0	
39	Stress-induced-phosphoprotein 1	STIP1_HUMAN	63 kDa	5	6	5	3	5	4	0	0	3	2	0	0	0	0	0	12	12	10	7	2	5	3	0	0	
40	Nucleolar and coiled-body phosphoprotein 1	NOLC1_HUMAN	74 kDa	4	2	0	0	3	2	0	0	0	0	0	0	0	0	0	9	9	9	3	3	2	0	0	0	
41	Cluster of Elongation factor 1-beta	EF1B_HUMAN	25 kDa	3	3	3	3	4	3	2	2	0	2	0	0	0	0	0	5	5	4	5	3	3	3	3	2	
41.1	Elongation factor 1-beta O	EF1B_HUMAN	25 kDa	3	3	3	3	4	3	2	2	0	2	0	0	0	0	0	5	5	4	5	3	3	3	3	2	
42	High mobility group protein HMG-I/HMG-Y	HMGA1_CRIGR	12 kDa	4	4	2	0	4	3	0	0	0	0	0	0	2	0	0	0	3	4	3	3	4	5	2	0	
43	Cluster of Histone H3.1	H31_MUSPA	15 kDa	5	2	0	0	5	2	0	0	2	2	0	0	0	0	0	2	0	0	0	5	3	0	0	0	
43.1	Histone H3.1	H31_MUSPA	15 kDa	3	1	0	0	3	1	0	0	1	1	0	0	0	0	0	1	0	0	0	3	1	0	0	0	
43.2	Histone H3.3 type 1	H331_CAEEL	15 kDa	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0	
44	Nucleoprotein TPR	TPR_HUMAN	267 kDa	5	4	4	2	6	2	2	0	2	0	0	0	0	0	0	9	10	10	10	3	2	0	0	0	
45	Tumor protein D54	TPD54_HUMAN	22 kDa	5	2	0	0	4	2	0	0	0	0	0	0	0	0	0	4	4	6	2	5	3	2	0	0	
46	Cluster of Elongation factor 1-gamma	EF1G_HUMAN	50 kDa	7	7	5	5	4	5	2	2	8	7	5	6	4	3	0	0	2	0	0	0	4	3	4	0	
46.1	Elongation factor 1-gamma	EF1G_HUMAN	50 kDa	1	1	1	1	1	1	1	0	2	2	1	1	1	1	0	0	1	0	0	0	1	1	1	0	0
47	Cluster of Serum albumin	ALBU_BOVIN	69 kDa	3	2	0	0	15	15	15	9	0	0	0	0	2	2	0	2	0	0	0	0	0	0	0	0	0
47.1	Serum albumin	ALBU_BOVIN	69 kDa	1	1	0	0	10	10	10	6	0	0	0	0	1	1	0	1	0	0	0	0	0	0	0	0	0
48	Cluster of Reticulon-4	RTN4_HUMAN	130 kDa	7	6	4	2	7	6	3	5	3	4	2	3	3	0	0	0	3	3	3	0	0	0	0	0	0
48.1	Reticulon-4	RTN4_HUMAN	130 kDa	4	4	2	1	4	3	1	3	2	2	1	2	1	0	0	0	2	2	1	0	0	0	0	0	0
49	Cluster of Prelamin-A/C	LMNA_HUMAN	74 kDa	6	6	6	5	8	5	6	4	8	8	6	9	5	4	4	5	0	0	0	0	3	4	4	0	0



49.1	Prelamin-A/C	LMNA_HUMAN	74 kDa	6	6	6	4	8	5	6	4	7	7	5	8	4	3	3	4	0	0	0	0	3	4	4	0
50	60S acidic ribosomal protein P1	RLA1_BOVIN	12 kDa	2	0	0	0	2	2	0	0	2	0	0	0	0	0	0	2	2	2	0	2	2	0	0	
51	Cluster of L-lactate dehydrogenase A chain	LDHA_HUMAN	37 kDa	5	4	3	1	1	1	2	0	7	5	5	4	2	2	2	1	0	0	0	0	5	3	3	0
51.1	L-lactate dehydrogenase A chain	LDHA_HUMAN	37 kDa	1	1	1	1	1	1	1	0	2	1	1	0	1	1	0	0	0	0	0	2	2	1	0	
51.2	L-lactate dehydrogenase B chain	LDHB_MACFA	37 kDa	3	2	1	0	0	0	0	0	3	2	2	3	0	0	0	0	0	0	0	0	0	0	0	0
52	Cluster of Peptidyl-prolyl cis-trans isomerase A	PPIA_SYMSY	18 kDa	5	4	4	3	3	5	4	0	5	4	2	3	2	0	0	0	6	5	5	3	6	5	5	2
52.1	Peptidyl-prolyl cis-trans isomerase A	PPIA_SYMSY	18 kDa	2	1	2	1	1	3	2	0	2	2	2	1	0	0	0	0	3	2	2	1	3	2	2	1
53	Cluster of Myosin-9	MYH9_HUMAN	227 kDa	3	5	0	0	13	11	6	5	2	0	0	0	5	0	0	0	10	11	9	5	5	3	2	0
53.1	Myosin-9	MYH9_HUMAN	227 kDa	0	1	0	0	2	2	1	1	0	0	0	0	1	0	0	0	2	2	2	1	1	1	1	0
54	Plasminogen activator inhibitor 1 RNA-binding protein	PAIRB_HUMAN	45 kDa	3	3	2	0	3	3	2	0	0	0	0	0	0	0	0	9	9	8	4	4	3	3	0	
55	Transketolase	TKT_HUMAN	68 kDa	8	7	3	2	6	3	3	0	5	4	0	4	2	0	0	0	0	0	0	2	0	0	0	
56	Stress-70 protein, mitochondrial	GRP75_PONAB	74 kDa	7	7	6	5	9	7	3	0	7	4	4	5	2	0	0	0	2	2	2	0	3	2	0	0
57	Cluster of THO complex subunit 4	THOC4_HUMAN	27 kDa	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	9	10	8	4	2	2	0	0	
57.1	THO complex subunit 4	THOC4_HUMAN	27 kDa	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	5	6	5	2	0	0	0	0	
58	Cluster of Alpha-2-HS-glycoprotein	FETUA_BOVIN	38 kDa	0	0	0	0	10	10	8	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
58.1	Alpha-2-HS-glycoprotein	FETUA_BOVIN	38 kDa	0	0	0	0	6	5	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
59	Serine/arginine-rich splicing factor 2	SRSF2_CHICK	26 kDa	2	3	3	2	3	2	2	0	2	0	0	0	0	0	0	5	5	6	4	3	3	2	0	
60	Cluster of Voltage-dependent anion-selective channel protein 1	VDAC1_BOVIN	31 kDa	5	5	5	4	4	5	4	0	5	5	4	4	5	5	3	3	0	0	0	0	2	3	2	0
60.1	Voltage-dependent anion-selective channel protein 1	VDAC1_BOVIN	31 kDa	0	0	0	1	0	1	1	0	0	1	0	1	0	1	0	1	0	0	0	0	0	0	0	0
61	Heterogeneous nuclear ribonucleoprotein U	HNRPU_HUMAN	91 kDa	4	5	4	3	3	3	2	0	6	5	4	3	2	0	0	0	0	0	0	0	3	2	0	0

62	Cluster of HLA class I histocompatibility antigen, A-2 alpha chain	1A02_HUMAN	41 kDa	0	0	0	0	5	5	5	0	0	0	0	0	7	3	3	2	0	0	0	0	5	4	4	0
62.1	HLA class I histocompatibility antigen, A-2 alpha chain	1A02_HUMAN	41 kDa	0	0	0	0	2	2	1	0	0	0	0	0	3	2	2	1	0	0	0	0	2	2	1	0
62.2	HLA class I histocompatibility antigen, Cw-12 alpha chain	1C12_HUMAN	41 kDa	0	0	0	0	1	1	1	0	0	0	0	0	1	0	0	0	0	0	0	0	1	0	1	0
63	Small nuclear ribonucleoprotein Sm D1	SMD1_MACFA	13 kDa	4	3	3	0	3	3	0	0	4	4	0	4	0	0	0	0	0	0	0	0	0	0	0	0
64	LIM and SH3 domain protein 1 O	LASP1_HUMAN	30 kDa	0	3	2	2	2	3	3	0	0	0	0	2	0	0	0	0	6	5	5	3	3	3	3	3
65	Far upstream element-binding protein 1	FUBP1_HUMAN	68 kDa	3	4	2	0	2	3	0	2	0	0	0	0	0	0	0	6	7	9	5	0	0	0	0	0
66	Alpha-1-antiproteinase	A1AT_BOVIN	46 kDa	0	0	0	0	6	4	5	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
67	Serine/arginine-rich splicing factor 7	SRSF7_BOVIN	27 kDa	3	4	3	2	0	2	1	0	2	2	0	3	0	0	0	0	5	5	4	3	0	1	0	0
68	Cluster of Malate dehydrogenase, mitochondrial	MDHM_HUMAN	36 kDa	3	3	2	4	3	3	5	3	8	7	8	5	0	0	0	0	0	0	0	0	0	3	3	0
68.1	Malate dehydrogenase, mitochondrial	MDHM_HUMAN	36 kDa	1	1	0	1	1	1	2	1	2	2	2	1	0	0	0	0	0	0	0	0	0	1	1	0
68.2	Malate dehydrogenase, mitochondrial	MDHM_MOUSE	36 kDa	0	0	0	1	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
69	Cluster of Nascent polypeptide-associated complex subunit alpha, muscle-specific form	NACAM_HUMAN	205 kDa	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	7	6	8	0	0	0	0	0	0
69.1	Nascent polypeptide-associated complex subunit alpha, muscle-specific form	NACAM_HUMAN	205 kDa	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
69.2	Nascent polypeptide-associated complex subunit alpha, muscle-specific form	NACAM_MOUSE	220 kDa	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
70	Heterogeneous nuclear ribonucleoprotein D0	HNRPD_HUMAN	38 kDa	3	3	2	2	1	1	1	0	0	0	0	1	0	0	0	0	5	9	8	3	2	3	1	0
71	RNA-binding protein FUS	FUS_BOVIN	52 kDa	0	0	0	0	4	1	0	0	0	0	1	0	0	0	0	8	11	10	5	4	4	1	1	1

72	Cluster of Peroxiredoxin-1	PRDX1_HUMAN	22 kDa	2	4	2	2	5	2	2	0	3	3	2	2	2	2	1	0	0	1	0	0	1	2	0	0
72.1	Peroxiredoxin-1	PRDX1_HUMAN	22 kDa	1	3	1	1	3	1	1	0	2	2	1	1	1	1	0	0	0	1	0	0	0	0	0	0
72.2	Peroxiredoxin-2	PRDX2_PONAB	19 kDa	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	
73	Cluster of Heterogeneous nuclear ribonucleoprotein A/B	ROAA_MOUSE	31 kDa	2	2	2	2	2	2	2	0	2	0	0	1	0	0	0	0	7	7	7	4	3	3	1	0
73.1	Heterogeneous nuclear ribonucleoprotein A/B	ROAA_MOUSE	31 kDa	1	1	1	1	1	1	1	0	1	0	0	1	0	0	0	0	1	1	1	1	1	1	1	0
73.2	Heterogeneous nuclear ribonucleoprotein A/B	ROAA_HUMAN	36 kDa	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	3	3	1	1	1	0	0
74	Eukaryotic translation initiation factor 4B	IF4B_HUMAN	69 kDa	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	5	5	4	2	2	2	0	0
75	Elongation factor 2	EF2_PONAB	95 kDa	5	5	0	0	4	3	3	0	10	6	4	3	0	0	0	0	0	0	0	0	4	3	2	0
76	Superoxide dismutase [Mn], mitochondrial	SODM_PONPY	25 kDa	0	0	0	2	3	4	3	2	0	0	0	0	2	0	0	0	4	2	2	0	6	6	5	3
77	Cluster of Protein disulfide-isomerase A3	PDIA3_HUMAN	57 kDa	5	3	5	5	6	4	4	2	3	3	5	5	3	4	0	0	0	0	0	0	4	3	2	0
77.1	Protein disulfide-isomerase A3	PDIA3_HUMAN	57 kDa	3	2	3	2	3	1	2	1	2	3	2	2	3	2	0	0	0	0	0	0	1	1	1	0
78	4F2 cell-surface antigen heavy chain	4F2_HUMAN	68 kDa	7	7	5	4	8	5	4	2	4	3	0	5	0	0	0	0	2	2	2	0	0	0	0	0
79	Cluster of Caveolin-1	CAV1_HORSE	21 kDa	4	0	0	0	5	3	0	0	0	0	0	0	0	0	0	0	3	3	0	3	4	0	0	
79.1	Caveolin-1	CAV1_HORSE	21 kDa	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
79.2	Caveolin-1	CAV1_MOUSE	21 kDa	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
80	Annexin A1	ANXA1_HUMAN	39 kDa	7	5	4	2	3	3	0	0	3	2	3	0	3	2	0	0	0	0	0	0	3	2	0	0
81	Cluster of Hemoglobin fetal subunit beta	HBBF_BOVIN	16 kDa	0	0	0	0	12	9	8	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
81.1	Hemoglobin fetal subunit beta	HBBF_BOVIN	16 kDa	0	0	0	0	8	7	5	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
81.2	Hemoglobin subunit beta	HBB_EULFU	16 kDa	0	0	0	0	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
81.3	Hemoglobin subunit delta	HBD_ATEGE	16 kDa	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
82	Cluster of Protein disulfide-isomerase A6	PDIA6_HUMAN	48 kDa	4	3	5	2	3	4	2	0	6	5	4	3	0	0	0	0	0	0	0	0	2	2	0	0







131. 2	Hemoglobin subunit alpha	HBA_SPECI	15 kDa	0	0	0	0	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
132	Variant surface antigen C	VLPC_MYCHR	16 kDa	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	2	3	0
133	Nuclear autoantigenic sperm protein	NASP_HUMAN	85 kDa	0	0	0	0	0	0	0	0	0	0	0	0	0	7	8	3	3	0	0	0	0
134	Proteasome subunit alpha type-6	PSA6_HUMAN	27 kDa	4	5	3	2	2	2	2	0	2	0	0	0	0	2	0	0	0	0	0	0	0
135	Small ubiquitin-related modifier 2	SUMO2_DANRE	11 kDa	0	2	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	2	0	0	0
136	Heterogeneous nuclear ribonucleoprotein K	HNRPK_BOVIN	51 kDa	3	3	4	3	2	2	0	0	4	4	2	2	0	0	0	0	2	2	0	0	
137	Cluster of Transitional endoplasmic reticulum ATPase	TERA_HUMAN	89 kDa	0	0	0	0	3	2	0	0	6	5	3	3	0	0	0	0	0	0	3	0	0
137. 1	Transitional endoplasmic reticulum ATPase	TERA_HUMAN	89 kDa	0	0	0	0	1	0	0	0	3	2	2	1	0	0	0	0	0	0	1	0	0
138	Stathmin	STMN1_GEKJA	17 kDa	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0	2	2	2	4	4	0
139	Uncharacterized protein C19orf43	CS043_HUMAN	18 kDa	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	2	0	0	0
140	T-complex protein 1 subunit eta	TCPH_BOVIN	59 kDa	3	2	0	0	2	0	0	0	2	2	0	0	0	0	0	0	0	2	0	0	0
141	Thioredoxin	THIO_HUMAN	12 kDa	0	0	0	0	2	2	0	0	0	0	0	0	0	3	2	0	0	0	0	0	0
142	Cluster of Phosphoglycerate kinase 1	PGK1_HUMAN	45 kDa	4	3	0	0	2	0	0	0	3	0	0	0	0	0	0	0	0	4	5	2	0
142. 1	Phosphoglycerate kinase 1	PGK1_HUMAN	45 kDa	4	3	0	0	2	0	0	0	3	0	0	0	0	0	0	0	0	4	4	1	0
143	Cluster of CD9 antigen	CD9_HUMAN	25 kDa	2	2	3	0	3	3	0	2	0	0	0	0	0	3	0	2	0	2	2	0	0
143. 1	CD9 antigen	CD9_HUMAN	25 kDa	1	1	2	0	2	2	0	1	0	0	0	0	0	2	0	2	0	1	1	0	0
144	Cluster of Acidic leucine-rich nuclear phosphoprotein 32 family member A O	AN32A_HUMAN	29 kDa	0	0	0	0	0	0	0	0	0	0	0	0	0	5	3	0	0	2	2	0	0
144. 1	Acidic leucine-rich nuclear phosphoprotein 32 family member A	AN32A_HUMAN	29 kDa	0	0	0	0	0	0	0	0	0	0	0	0	0	4	3	0	0	2	2	0	0
145	TATA-binding protein-associated factor 2N	RBP56_HUMAN	62 kDa	0	0	0	0	0	0	0	0	0	0	0	0	0	7	8	4	2	0	0	0	0
146	Splicing factor 1	SF01_HUMAN	68 kDa	0	0	0	0	0	0	0	0	0	0	0	0	0	2	2	3	2	0	0	0	0

147	Chloride intracellular channel protein 1	CLIC1_BOVIN	27 kDa	0	0	0	0	0	0	2	2	0	0	0	0	0	0	0	0	0	0	0	0	0			
148	Eukaryotic translation initiation factor 4H	IF4H_HUMAN	27 kDa	0	0	0	0	0	0	0	0	0	0	0	0	0	0	4	3	2	3	0	2	0	0		
149	Histone H3, embryonic O	H3_PYCHE	15 kDa	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
150	PDZ and LIM domain protein 1	PDLI1_HUMAN	36 kDa	0	0	0	0	0	0	0	0	0	0	0	0	0	0	5	6	6	4	0	0	0	0		
151	Cluster of Integrin alpha-3	ITA3_HUMAN	117 kDa	0	0	0	0	4	3	3	2	0	0	0	0	4	0	0	0	0	0	0	2	3	0		
151.1	Integrin alpha-3	ITA3_HUMAN	117 kDa	0	0	0	0	1	0	2	1	0	0	0	0	2	0	0	0	0	0	0	0	2	0		
151.2	Integrin alpha-3	ITA3_MOUSE	117 kDa	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0		
152	40S ribosomal protein S12	RS12_MOUSE	15 kDa	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	2	0	0	0		
153	Cluster of ATP synthase subunit beta, mitochondrial	ATPB_MOUSE	56 kDa	3	3	0	0	3	2	2	0	0	0	0	0	0	0	0	0	0	0	3	2	0	0		
153.1	ATP synthase subunit beta, mitochondrial	ATPB_MOUSE	56 kDa	2	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0		
154	Heterogeneous nuclear ribonucleoprotein H	HNRH1_HUMAN	49 kDa	3	3	2	3	2	2	2	0	2	2	2	2	0	0	0	0	0	0	2	2	0	0		
155	Reticulocalbin-1	RCN1_HUMAN	39 kDa	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	4	2	2	0		
156	Cluster of Proteasome subunit alpha type-7	PSA7_HUMAN	28 kDa	3	3	3	2	0	0	2	0	0	2	0	2	0	0	0	0	0	0	0	0	0	0		
156.1	Proteasome subunit alpha type-7	PSA7_HUMAN	28 kDa	2	2	2	1	0	0	1	0	0	1	0	1	0	0	0	0	0	0	0	0	0	0		
157	Cytoskeleton-associated protein 4	CKAP4_HUMAN	66 kDa	0	2	0	0	4	7	4	2	0	0	0	0	0	0	2	0	0	0	0	0	0	0		
158	60S ribosomal protein L6	RL6_HUMAN	33 kDa	2	3	2	0	0	0	0	0	3	2	0	0	0	0	0	0	0	0	0	0	0	0		
159	Cluster of Eukaryotic initiation factor 4A-I	IF4A1_MACFA	46 kDa	3	2	3	3	0	0	0	0	2	3	2	3	2	1	0	0	0	0	0	0	1	2	2	2
159.1	Eukaryotic initiation factor 4A-I O	IF4A1_MACFA	46 kDa	2	2	2	2	0	0	0	0	1	2	1	2	1	1	0	0	0	0	0	1	1	1	1	
160	Cluster of Kinectin	KTN1_HUMAN	156 kDa	0	2	0	2	0	2	0	0	0	0	0	0	0	0	3	4	3	2	2	2	3	0		
160.1	Kinectin	KTN1_HUMAN	156 kDa	0	1	0	1	0	1	0	0	0	0	0	0	0	0	2	2	2	1	1	1	2	0		
161	Mesencephalic astrocyte-derived neurotrophic factor O	MANF_HUMAN	21 kDa	0	3	0	0	2	2	0	0	0	0	0	0	0	0	2	0	2	0	0	0	0	0		



162	Cluster of Proteasome subunit beta type-1	PSB1_BOVIN	26 kDa	6	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
162.1	Proteasome subunit beta type-1	PSB1_BOVIN	26 kDa	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
162.2	Proteasome subunit beta type-1	PSB1_MOUSE	26 kDa	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
163	Microtubule-associated protein 4	MAP4_HUMAN	121 kDa	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	2	3	
164	60S ribosomal protein L7	RL7_BOVIN	29 kDa	0	0	0	0	0	0	2	2	0	0	0	0	0	0	0	0	0	0	0	0	0
165	Splicing factor, proline- and glutamine-rich	SFPQ_HUMAN	76 kDa	0	0	0	0	0	0	3	0	2	0	0	0	0	0	0	0	0	0	0	0	0
166	Ran-specific GTPase-activating protein	RANG_HUMAN	23 kDa	0	0	0	0	0	0	0	0	0	0	0	0	0	3	3	3	0	0	0	0	0
167	Serine/arginine repetitive matrix protein 2	SRRM2_HUMAN	300 kDa	0	0	0	0	0	0	0	0	0	0	0	0	0	3	3	7	3	0	0	0	0
168	Cluster of T-complex protein 1 subunit theta	TCPQ_HUMAN	60 kDa	0	0	0	2	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0
168.1	T-complex protein 1 subunit theta	TCPQ_HUMAN	60 kDa	0	0	0	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0
169	Proteasome subunit beta type-6	PSB6_HUMAN	25 kDa	2	2	2	2	0	0	2	2	0	0	2	0	0	0	0	0	0	0	0	0	0
170	Splicing factor 3B subunit 2	SF3B2_HUMAN	100 kDa	0	0	0	0	0	0	0	0	0	0	0	0	0	3	4	3	2	0	0	0	0
171	5'-nucleotidase	5NTD_HUMAN	63 kDa	3	3	0	3	5	4	3	2	0	0	0	0	0	0	0	0	0	0	0	0	0
172	Cluster of Dihydrolipoyl dehydrogenase, mitochondrial	DLDH_HUMAN	54 kDa	2	0	2	0	4	2	0	0	0	0	0	0	0	0	0	0	0	2	3	0	0
172.1	Dihydrolipoyl dehydrogenase, mitochondrial	DLDH_HUMAN	54 kDa	1	0	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0
173	Peptidyl-prolyl cis-trans isomerase FKBP1A	FKB1A_BOVIN	12 kDa	0	0	0	0	0	0	0	0	0	0	0	0	0	2	2	2	2	0	0	0	0
174	CD59 glycoprotein	CD59_HUMAN	14 kDa	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
175	Prohibitin-2	PHB2_HUMAN	33 kDa	5	3	3	2	0	0	0	3	2	3	2	0	0	0	0	0	0	0	0	0	0
176	Cluster of GTP-binding nuclear protein Ran	RAN_CHICK	24 kDa	2	0	3	0	0	0	0	3	4	3	3	0	0	0	0	0	0	0	0	0	0
176.1	GTP-binding nuclear protein Ran	RAN_CHICK	24 kDa	1	0	1	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0
177	Proliferation marker protein Ki-67	KI67_HUMAN	359 kDa	0	0	0	0	0	0	0	0	0	0	0	0	0	7	6	4	3	0	0	0	0



197	Single-stranded DNA-binding protein, mitochondrial	SSBP_HUMAN	17 kDa	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0
198	Acidic leucine-rich nuclear phosphoprotein 32 family member E	AN32E_HUMAN	31 kDa	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	3	3	2	0	0	0	0
199	Cluster of Neutral alpha-glucosidase AB	GANAB_HUMAN	107 kDa	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
199.1	Neutral alpha-glucosidase AB	GANAB_HUMAN	107 kDa	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
200	X-ray repair cross-complementing protein 5	XRCC5_HUMAN	83 kDa	2	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
201	Cluster of Plectin	PLEC_HUMAN	532 kDa	0	0	0	0	0	0	0	2	3	3	0	0	0	0	0	2	0	0	0	0	0	0
201.1	Plectin	PLEC_HUMAN	532 kDa	0	0	0	0	0	0	0	1	3	1	0	0	0	0	0	0	0	0	0	0	0	0
202	Peroxiredoxin-4	PRDX4_HUMAN	31 kDa	1	1	1	1	1	1	1	0	1	1	0	0	1	0	0	0	0	0	0	0	0	0
203	Cluster of Scaffold attachment factor B1	SAFB1_HUMAN	103 kDa	0	0	0	0	0	0	0	0	0	0	0	0	0	0	4	2	2	0	0	0	0	0
203.1	Scaffold attachment factor B1	SAFB1_HUMAN	103 kDa	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	1	0	0	0	0	0
203.2	Scaffold attachment factor B2	SAFB2_HUMAN	107 kDa	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0	0
204	Tissue factor	TF_HUMAN	33 kDa	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	2	2	0	0
205	60S ribosomal protein L7a	RL7A_MACFA	30 kDa	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0
206	A-kinase anchor protein 2	AKAP2_HUMAN	95 kDa	2	0	0	0	0	0	0	0	0	0	0	0	0	0	4	3	2	0	0	0	0	0
207	Cellular nucleic acid-binding protein	CNBP_BOVIN	19 kDa	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	2	3	0	0	0	0	0
208	Cluster of Hypoxia up-regulated protein 1 O	HYOU1_HUMAN	111 kDa	3	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
208.1	Hypoxia up-regulated protein 1	HYOU1_HUMAN	111 kDa	1	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
209	PEST proteolytic signal-containing nuclear protein	PCNP_HUMAN	19 kDa	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0
210	Ubiquitin-associated protein 2-like	UBP2L_HUMAN	115 kDa	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0
211	Heterogeneous nuclear ribonucleoprotein L	HNRPL_HUMAN	64 kDa	0	2	2	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0
212	UV excision repair protein RAD23 homolog B	RD23B_HUMAN	43 kDa	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0









2.2	Beta-actin-like protein 2	ACTBL_HUMAN	42 kDa	18.9 0%	21.3 0%	7.98 %	14.1 0%	12.8 0%	18.6 0%	17.3 0%	0	22.6 0%	14.1 0%	18.9 0%	14.1 0%	0	0	0	0	9.04 %	0	0	0	0	17.3 0%	7.98 %	0
2.3	Actin-18 O	ACT18_DICDI	43 kDa	0	8.68 %	6.32 %	6.32 %	6.32 %	6.32 %	6.32 %	0	0	6.32 %	6.32 %	6.32 %	0	0	0	0	0	0	0	0	0	6.32 %	6.32 %	0
2.4	Actin-3	ACT3_SOYBN	42 kDa	0	11.7 0%	12.0 0%	0	0	5.85 %	12.0 0%	0	0	0	9.04 %	5.85 %	12.0 0%	0	0	0	0	0	0	0	0	11.7 0%	0	0
2.5	Actin	ACT_CRYPV	42 kDa	0	0	0	0	0	0	0	0	0	9.31 %	0	0	0	0	0	0	0	0	0	0	0	9.31 %	0	0
2.6	Actin, cytoplasmic 1	ACTB_CRIGR	42 kDa	69.3 0%	71.2 0%	58.4 0%	58.4 0%	62.7 0%	59.7 0%	56.5 0%	27.5 0%	0	59.7 0%	50.7 0%	46.4 0%	37.6 0%	0	0	21.1 0%	0	0	0	0	65.9 0%	65.6 0%	58.4 0%	37.3 0%
2.7	Actin	ACT_KOMPG	42 kDa	17.0 0%	17.0 0%	0	17.0 0%	0	0	15.4 0%	10.4 0%	0	17.0 0%	14.1 0%	0	0	0	0	0	10.4 0%	10.4 0%	10.4 0%	10.4 0%	0	0	17.0 0%	10.4 0%
2.8	Actin, cytoplasmic	ACTC_BRA BE	42 kDa	0	0	0	0	0	0	42.9 0%	32.0 0%	0	45.9 0%	41.6 0%	38.4 0%	0	0	0	21.1 0%	0	0	0	0	0	44.3 0%	44.5 0%	31.7 0%
2.9	Actin, cytoplasmic	ACTC_STYPL	42 kDa	0	39.2 0%	0	0	0	0	33.3 0%	0	0	0	0	0	0	0	0	0	0	0	0	0	0	33.6 0%	35.2 0%	28.3 0%
2.1	Actin-53 (Fragment)	ACT2_TOBAC	37 kDa	0	0	0	0	0	0	0	0	0	0	14.3 0%	0	0	0	0	0	0	0	0	0	0	0	17.6 0%	0
2.1	Actin	ACT_ASPO R	42 kDa	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	6.40 %	0	0
2.1	Actin	ACT_ACHBI	42 kDa	0	19.4 0%	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2.1	Actin, muscle	ACTM_PISOC	42 kDa	0	0	38.8 0%	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2.1	Actin-1	ACT1_SCHMA	42 kDa	0	0	0	0	0	28.5 0%	0	0	0	28.5 0%	0	0	0	0	0	0	0	0	0	0	28.5 0%	28.5 0%	0	0
2.1	Actin, cytoplasmic type 8	ACT8_XENLA	42 kDa	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	53.7 0%	0	0	0









11	Cluster of Elongation factor 1-alpha 1	EF1A1_FELCA	50 kDa	33.1 0%	33.1 0%	20.8 0%	20.8 0%	40.3 0%	23.8 0%	18.0 0%	11.3 0%	27.1 0%	27.1 0%	20.8 0%	19.7 0%	9.96 %	11.0 0%	12.6 0%	7.58 %	13.4 0%	19.5 0%	14.3 0%	10.2 0%	26.8 0%	35.1 0%	19.7 0%	17.1 0%
11.1	Elongation factor 1-alpha 1	EF1A1_FELCA	50 kDa	33.1 0%	33.1 0%	20.8 0%	20.8 0%	40.3 0%	23.8 0%	18.0 0%	11.3 0%	27.1 0%	27.1 0%	20.8 0%	19.7 0%	9.96 %	11.0 0%	12.6 0%	7.58 %	13.4 0%	19.5 0%	14.3 0%	10.2 0%	26.8 0%	35.1 0%	19.7 0%	17.1 0%
11.2	Elongation factor 1-alpha 2	EF1A2_DROME	51 kDa	14.1 0%	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
12	Cluster of Keratin, type II cytoskeletal 1	K2C1_HUMAN	66 kDa	36.2 0%	28.9 0%	32.3 0%	26.2 0%	42.9 0%	37.9 0%	35.4 0%	18.0 0%	8.85 %	4.04 %	3.73 %	5.90 %	19.3 0%	24.1 0%	14.0 0%	18.8 0%	25.3 0%	31.4 0%	21.0 0%	24.1 0%	22.2 0%	25.3 0%	12.0 0%	10.1 0%
12.1	Keratin, type II cytoskeletal 1	K2C1_HUMAN	66 kDa	36.2 0%	28.9 0%	32.3 0%	26.2 0%	42.9 0%	37.9 0%	35.4 0%	18.0 0%	8.85 %	4.04 %	3.73 %	5.90 %	19.3 0%	24.1 0%	14.0 0%	18.8 0%	25.3 0%	31.4 0%	21.0 0%	24.1 0%	22.2 0%	25.3 0%	12.0 0%	10.1 0%
12.2	Keratin, type II cytoskeletal 8	K2C8_HUMAN	54 kDa	0	0	0	0	8.70 %	4.35 %	0	0	0	0	0	0	4.55 %	0	0	0	0	0	0	0	8.70 %	8.70 %	0	0
12.3	Keratin, type II cytoskeletal 2 epidermal	K22E_HUMAN	65 kDa	9.55 %	0	0	0	14.2 0%	8.92 %	5.95 %	0	0	0	0	5.32 %	0	0	0	5.16 %	8.92 %	0	0	0	0	0	0	0
12.4	Keratin, type II cytoskeletal 8	K2C8_RAT	54 kDa	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	4.35 %	0	0	0
13	Cluster of Nuclease-sensitive element-binding protein 1	YBOX1_BOVIN	36 kDa	56.2 0%	56.2 0%	24.4 0%	18.2 0%	56.5 0%	40.4 0%	18.2 0%	0	24.4 0%	18.2 0%	18.2 0%	0	18.2 0%	18.2 0%	0	0	57.7 0%	59.0 0%	60.5 0%	42.6 0%	51.5 0%	40.4 0%	24.4 0%	18.2 0%
13.1	Nuclease-sensitive element-binding protein 1	YBOX1_BOVIN	36 kDa	56.2 0%	56.2 0%	24.4 0%	18.2 0%	56.5 0%	40.4 0%	18.2 0%	0	24.4 0%	18.2 0%	18.2 0%	0	18.2 0%	18.2 0%	0	0	57.7 0%	59.0 0%	60.5 0%	42.6 0%	51.5 0%	40.4 0%	24.4 0%	18.2 0%
13.2	Y-box-binding protein 3	YBOX3_HUMAN	40 kDa	18.3 0%	0	0	0	0	0	0	0	0	0	0	0	0	0	0	28.0 0%	25.3 0%	20.2 0%	10.8 0%	0	0	0	0	
14	Cluster of Nucleolin	NUCL_HUMAN	77 kDa	16.9 0%	16.9 0%	8.31 %	17.9 0%	16.9 0%	20.3 0%	13.2 0%	0	18.3 0%	12.3 0%	5.21 %	6.90 %	0	0	0	0	31.3 0%	30.8 0%	33.0 0%	25.8 0%	16.9 0%	18.3 0%	12.8 0%	5.92 %
14.1	Nucleolin	NUCL_HUMAN	77 kDa	16.9 0%	16.9 0%	8.31 %	17.9 0%	16.9 0%	20.3 0%	13.2 0%	0	18.3 0%	12.3 0%	5.21 %	6.90 %	0	0	0	0	31.3 0%	30.8 0%	33.0 0%	25.8 0%	16.9 0%	18.3 0%	12.8 0%	5.92 %



20.2	Histone H2B type 1-N	H2B1N_BOVIN	14 kDa	27.0	0	15.1	15.1	15.1	15.1	15.1	15.1	0	15.1	15.1	0	15.1	15.1	15.1	15.1	15.1	15.1	15.1	15.1	15.1	15.1		
	Cluster of Tubulin beta-5 chain	TBB5_RAT	50 kDa	56.8	51.8	47.3	30.0	48.6	37.6	26.6	14.6	35.4	29.3	18.2	24.8	23.6	13.5	9.01	9.01	11.9	20.0	14.2	8.78	66.9	46.8	39.6	16.0
21.1	Tubulin beta-5 chain	TBB5_RAT	50 kDa	56.8	51.8	47.3	30.0	48.6	37.6	26.6	14.6	35.4	29.3	18.2	24.8	23.6	13.5	9.01	9.01	11.9	20.0	14.2	8.78	66.9	46.8	39.6	16.0
21.2	Tubulin beta chain	TBB_CERBT	50 kDa	8.05	8.05	0	0	8.05	0	0	0	0	8.05	0	0	8.05	0	0	0	0	8.05	0	0	8.05	8.05	8.05	0
21.3	Tubulin beta chain	TBB_PENDI	50 kDa	0	0	0	8.05	0	8.05	0	0	0	8.05	0	0	0	0	0	0	0	0	0	0	8.05	8.05	8.05	0
21.4	Tubulin beta-4B chain	TBB4B_HUMAN	50 kDa	47.2	44.9	37.8	20.4	41.8	30.8	19.8	0	27.9	23.1	14.8	0	0	10.8	6.29	0	0	0	0	0	53.3	0	0	0
21.5	Tubulin beta-1 chain (Fragment)	TBB1_DAUCA	36 kDa	8.25	0	8.25	0	8.25	8.25	0	0	0	0	0	0	0	0	0	0	0	0	0	0	8.25	0	8.25	0
21.6	Tubulin beta-1 chain	TBB1_DROME	50 kDa	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	48.3	0	0	0
21.7	Tubulin beta-2 chain	TBB2_DROER	50 kDa	23.5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	36.8	0	0	0
21.8	Tubulin beta-4A chain	TBB4A_BOVIN	50 kDa	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	33.8	0	0
22	Cluster of CD44 antigen	CD44_HUMAN	82 kDa	9.43	7.68	7.68	6.47	11.2	11.2	6.47	5.12	4.58	4.58	4.58	3.37	6.33	5.12	5.12	3.37	7.68	11.2	8.09	7.68	9.84	9.84	6.47	5.12
22.1	CD44 antigen	CD44_HUMAN	82 kDa	9.43	7.68	7.68	6.47	11.2	11.2	6.47	5.12	4.58	4.58	4.58	3.37	6.33	5.12	5.12	3.37	7.68	11.2	8.09	7.68	9.84	9.84	6.47	5.12
23	Cluster of Tubulin alpha chain	TBA_XENL A	50 kDa	38.1	41.6	30.7	26.5	27.4	27.4	27.4	0	36.7	19.6	26.1	19.6	21.2	17.1	6.68	14.3	13.1	0	0	0	47.0	33.0	33.0	17.1
23.1	Tubulin alpha chain	TBA_XENL A	50 kDa	38.1	41.6	30.7	26.5	27.4	27.4	27.4	0	36.7	19.6	26.1	19.6	21.2	17.1	6.68	14.3	13.1	0	0	0	47.0	33.0	33.0	17.1



29.1	Galectin-1	LEG1_HUMAN	15 kDa	52.6 0%	46.7 0%	40.7 0%	40.7 0%	40.7 0%	52.6 0%	45.2 0%	33.3 0%	46.7 0%	46.7 0%	31.9 0%	31.9 0%	0	0	0	0	58.5 0%	58.5 0%	58.5 0%	52.6 0%	0	52.6 0%	0	0	
29.2	Galectin-1	LEG1_MOUSE	15 kDa	20.0 0%	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
30	Cluster of Integrin beta-1	ITB1_HUMAN	88 kDa	13.4 0%	11.4 0%	10.0 0%	8.77 %	14.7 0%	12.9 0%	12.7 0%	4.51 %	3.76 %	0	0	0	11.4 0%	7.27 %	5.01 %	2.88 %	10.3 0%	13.5 0%	11.4 0%	12.0 0%	14.4 0%	15.3 0%	8.52 %	6.27 %	
30.1	Integrin beta-1	ITB1_HUMAN	88 kDa	13.4 0%	11.4 0%	10.0 0%	8.77 %	14.7 0%	12.9 0%	12.7 0%	4.51 %	3.76 %	0	0	0	11.4 0%	7.27 %	5.01 %	2.88 %	10.3 0%	13.5 0%	11.4 0%	12.0 0%	14.4 0%	15.3 0%	8.52 %	6.27 %	
31	Cluster of 14-3-3 protein epsilon	1433E_SHEEP	29 kDa	29.8 0%	25.1 0%	16.9 0%	9.02 %	25.3 0%	12.9 0%	9.80 %	9.02 %	38.0 0%	30.2 0%	13.7 0%	21.6 0%	13.5 0%	0	0	0	0	0	0	0	20.8 0%	13.9 0%	12.7 0%	0	
31.1	14-3-3 protein epsilon	1433E_SHEEP	29 kDa	29.8 0%	25.1 0%	16.9 0%	9.02 %	20.4 0%	12.9 0%	8.24 %	9.02 %	38.0 0%	30.2 0%	13.7 0%	21.6 0%	0	0	0	0	0	0	0	0	12.2 0%	12.2 0%	7.45 %	0	
31.2	14-3-3 protein zeta/delta	1433Z_HUMAN	28 kDa	17.6 0%	9.80 %	8.98 %	0	25.3 0%	9.80 %	9.80 %	0	28.6 0%	20.8 0%	0	12.7 0%	13.5 0%	0	0	0	0	0	0	0	20.8 0%	13.9 0%	12.7 0%	0	
31.3	14-3-3 protein theta	1433T_BOVINE	28 kDa	13.9 0%	0	0	0	9.80 %	9.80 %	9.80 %	0	0	0	0	8.98 %	0	0	0	0	0	0	0	0	8.98 %	8.98 %	8.98 %	0	
31.4	14-3-3 protein sigma	1433S_HUMAN	28 kDa	0	0	0	0	0	0	0	0	12.1 0%	16.1 0%	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
31.5	14-3-3 protein beta/alpha	1433B_CHICK	28 kDa	0	0	0	0	0	0	0	0	0	0	0	6.97 %	0	0	0	0	0	0	0	0	0	0	0	0	0
31.6	14-3-3 protein gamma	1433G_BOVINE	28 kDa	0	0	0	0	0	0	0	0	0	0	0	8.91 %	0	0	0	0	0	0	0	0	0	0	0	0	0
32	Cluster of Pyruvate kinase PKM	KPYM_HUMAN	58 kDa	26.9 0%	28.4 0%	19.4 0%	11.1 0%	21.3 0%	14.3 0%	15.8 0%	3.95 %	26.9 0%	12.1 0%	18.5 0%	13.9 0%	9.60 %	4.90 %	0	6.03 %	0	0	0	0	40.7 0%	35.6 0%	26.2 0%	6.40 %	
32.1	Pyruvate kinase PKM	KPYM_HUMAN	58 kDa	26.9 0%	28.4 0%	19.4 0%	11.1 0%	21.3 0%	14.3 0%	15.8 0%	3.95 %	26.9 0%	12.1 0%	18.5 0%	13.9 0%	9.60 %	4.90 %	0	6.03 %	0	0	0	0	40.7 0%	35.6 0%	26.2 0%	6.40 %	
33	Cluster of Keratin, type I cytoskeletal 10	K1C10_HUMAN	59 kDa	13.5 0%	13.5 0%	13.5 0%	13.5 0%	19.7 0%	18.2 0%	15.1 0%	9.93 %	0	9.59 %	0	4.88 %	8.56 %	8.56 %	8.56 %	6.85 %	16.3 0%	11.6 0%	9.59 %	4.97 %	7.88 %	12.1 0%	6.50 %	6.50 %	



33.1	Keratin, type I cytoskeletal 10	K1C10_HUMAN	59 kDa	13.5 0%	13.5 0%	13.5 0%	13.5 0%	19.7 0%	18.2 0%	15.1 0%	9.93 %	0	9.59 %	0	0	8.56 %	8.56 %	8.56 %	6.85 %	16.3 0%	11.6 0%	9.59 %	4.97 %	7.88 %	7.88 %	0	0
33.2	Keratin, type I cytoskeletal 18	K1C18_HUMAN	48 kDa	0	0	0	0	4.88 %	4.88 %	4.88 %	4.88 %	0	4.88 %	0	4.88 %	4.88 %	4.88 %	0	0	0	0	0	0	4.88 %	12.1 0%	4.88 %	4.88 %
33.3	Keratin, type I cytoskeletal 19	K1C19_HUMAN	44 kDa	0	0	0	0	7.75 %	5.50 %	7.75 %	0	0	0	0	0	0	0	0	0	0	0	0	5.50 %	9.75 %	6.50 %	6.50 %	
33.4	Keratin, type I cytoskeletal 14	K1C14_HUMAN	52 kDa	0	0	0	0	0	0	0	0	0	0	0	0	5.08 %	0	5.08 %	0	0	0	0	0	0	0	0	0
34	Cluster of Alpha-actinin-4	ACTN4_HUMAN	105 kDa	9.77 %	11.5 0%	7.35 %	8.67 %	5.82 %	6.59 %	4.61 %	0	14.9 0%	15.8 0%	15.5 0%	13.4 0%	4.17 %	4.17 %	0	0	0	0	0	5.38 %	5.38 %	4.72 %	2.63 %	
34.1	Alpha-actinin-4 O	ACTN4_HUMAN	105 kDa	9.77 %	11.5 0%	7.35 %	8.67 %	5.82 %	6.59 %	4.61 %	0	14.9 0%	15.8 0%	15.5 0%	13.4 0%	4.17 %	4.17 %	0	0	0	0	0	5.38 %	5.38 %	4.72 %	2.63 %	
34.2	Alpha-actinin, sarcomeric	ACTN_ANOGA	107 kDa	0	2.39 %	0	0	0	0	0	0	2.39 %	3.58 %	3.69 %	0	0	0	0	0	0	0	0	0	0	0	0	0
34.3	Alpha-actinin-1	ACTN1_BOVIN	103 kDa	5.61 %	5.16 %	2.69 %	0	0	0	0	0	9.53 %	9.42 %	11.0 0%	7.17 %	0	0	0	0	0	0	0	0	0	0	0	0
35	Cofilin-1	COF1_HUMAN	19 kDa	41.0 0%	32.5 0%	17.5 0%	25.9 0%	54.2 0%	32.5 0%	32.5 0%	24.1 0%	32.5 0%	33.1 0%	25.9 0%	17.5 0%	0	0	0	0	54.2 0%	61.4 0%	54.2 0%	32.5 0%	42.8 0%	49.4 0%	32.5 0%	13.3 0%
36	Cluster of Glucosidase 2 subunit beta	GLU2B_HUMAN	59 kDa	11.7 0%	11.6 0%	10.6 0%	10.6 0%	23.5 0%	13.8 0%	10.6 0%	8.33 %	4.36 %	4.36 %	6.44 %	4.55 %	0	0	0	0	20.8 0%	23.5 0%	23.5 0%	10.4 0%	12.3 0%	22.5 0%	10.6 0%	8.33 %
36.1	Glucosidase 2 subunit beta	GLU2B_HUMAN	59 kDa	11.7 0%	11.6 0%	10.6 0%	10.6 0%	23.5 0%	13.8 0%	10.6 0%	8.33 %	4.36 %	4.36 %	6.44 %	4.55 %	0	0	0	0	20.8 0%	23.5 0%	23.5 0%	10.4 0%	12.3 0%	22.5 0%	10.6 0%	8.33 %
37	Cluster of Ubiquitin-60S ribosomal protein L40	RL40_DROME	15 kDa	21.1 0%	28.1 0%	21.1 0%	19.5 0%	21.1 0%	30.5 0%	21.1 0%	28.1 0%	21.1 0%	30.5 0%	21.1 0%	19.5 0%	37.5 0%	37.5 0%	28.9 0%	16.4 0%	21.1 0%	21.1 0%	21.1 0%	21.1 0%	30.5 0%	21.1 0%	30.5 0%	30.5 0%
37.1	Ubiquitin-60S ribosomal protein L40	RL40_DROME	15 kDa	21.1 0%	28.1 0%	21.1 0%	19.5 0%	21.1 0%	30.5 0%	21.1 0%	28.1 0%	21.1 0%	30.5 0%	21.1 0%	19.5 0%	37.5 0%	37.5 0%	28.9 0%	16.4 0%	21.1 0%	21.1 0%	21.1 0%	21.1 0%	30.5 0%	21.1 0%	30.5 0%	30.5 0%
38	Calnexin	CALX_HUMAN	68 kDa	30.1 0%	10.5 0%	9.97 %	4.90 %	20.9 0%	7.26 %	8.11 %	0	4.56 %	4.56 %	0	0	0	0	0	0	6.93 %	12.0 0%	0	0	0	0	0	0

39	Stress-induced-phosphoprotein 1	STIP1_HUMAN	63 kDa	12.0 0%	7.92 %	10.3 0%	7.37 %	9.76 %	9.02 %	0	0	6.08 %	4.97 %	0	0	0	0	0	26.0 0%	28.4 0%	20.8 0%	11.6 0%	5.52 %	6.81 %	7.37 %	0	
40	Nucleolar and coiled-body phosphoprotein 1	NOLC1_HUMAN	74 kDa	5.58 %	5.44 %	0	0	5.44 %	5.44 %	0	0	0	0	0	0	0	0	0	7.44 %	9.73 %	11.4 0%	7.30 %	5.58 %	5.44 %	0	0	
41	Cluster of Elongation factor 1-beta	EF1B_HUMAN	25 kDa	23.1 0%	23.1 0%	23.1 0%	23.1 0%	23.1 0%	23.1 0%	12.4 0%	12.4 0%	0	16.4 0%	0	0	0	0	0	23.1 0%	40.4 0%	23.1 0%	23.1 0%	23.1 0%	23.1 0%	23.1 0%	23.1 0%	12.4 0%
41.1	Elongation factor 1-beta O	EF1B_HUMAN	25 kDa	23.1 0%	23.1 0%	23.1 0%	23.1 0%	23.1 0%	23.1 0%	12.4 0%	12.4 0%	0	16.4 0%	0	0	0	0	0	23.1 0%	40.4 0%	23.1 0%	23.1 0%	23.1 0%	23.1 0%	23.1 0%	23.1 0%	12.4 0%
42	High mobility group protein HMG-I/HMG-Y	HMGAI_C RIGR	12 kDa	41.1 0%	41.1 0%	41.1 0%	0	41.1 0%	41.1 0%	0	0	0	0	0	0	0	0	0	23.4 0%	23.4 0%	23.4 0%	23.4 0%	23.4 0%	23.4 0%	23.4 0%	0	
43	Cluster of Histone H3.1	H31_MUSPA	15 kDa	32.4 0%	31.6 0%	0	0	31.6 0%	31.6 0%	0	0	31.6 0%	31.6 0%	0	0	0	0	0	31.6 0%	0	0	0	32.4 0%	31.6 0%	0	0	
43.1	Histone H3.1	H31_MUSPA	15 kDa	32.4 0%	31.6 0%	0	0	31.6 0%	31.6 0%	0	0	31.6 0%	31.6 0%	0	0	0	0	0	31.6 0%	0	0	0	32.4 0%	31.6 0%	0	0	
43.2	Histone H3.3 type 1	H331_CAEL	15 kDa	31.6 0%	0	0	0	31.6 0%	0	0	0	0	0	0	0	0	0	0	0	0	0	0	31.6 0%	31.6 0%	0	0	
44	Nucleoprotein TPR	TPR_HUMAN	267 kDa	4.06 %	3.34 %	2.79 %	1.06 %	4.78 %	1.61 %	1.61 %	0	0.76 %	0	0	0	0	0	0	7.41 %	7.87 %	6.69 %	6.69 %	1.95 %	0.76 %	0	0	
45	Tumor protein D54	TPD54_HUMAN	22 kDa	41.7 0%	21.4 0%	0	0	27.7 0%	21.4 0%	0	0	0	0	0	0	0	0	0	35.0 0%	35.0 0%	49.0 0%	28.6 0%	41.7 0%	21.4 0%	21.4 0%	0	
46	Cluster of Elongation factor 1-gamma	EF1G_HUMAN	50 kDa	19.2 0%	16.5 0%	11.2 0%	13.5 0%	8.47 %	10.8 0%	5.49 %	6.18 %	16.7 0%	13.7 0%	11.2 0%	13.5 0%	11.2 0%	8.47 %	0	5.26 %	0	0	0	11.2 0%	8.47 %	8.47 %	0	
46.1	Elongation factor 1-gamma	EF1G_HUMAN	50 kDa	19.2 0%	16.5 0%	11.2 0%	13.5 0%	8.47 %	10.8 0%	5.49 %	6.18 %	16.7 0%	13.7 0%	11.2 0%	13.5 0%	11.2 0%	8.47 %	0	5.26 %	0	0	0	11.2 0%	8.47 %	8.47 %	0	
47	Cluster of Serum albumin	ALBU_BOVIN	69 kDa	6.59 %	4.45 %	0	0	26.7 0%	18.5 0%	19.4 0%	17.8 0%	0	0	0	0	0	0	0	4.45 %	0	0	0	0	0	0	0	
47.1	Serum albumin	ALBU_BOVIN	69 kDa	6.59 %	4.45 %	0	0	26.7 0%	18.5 0%	19.4 0%	17.8 0%	0	0	0	0	0	0	0	4.45 %	0	0	0	0	0	0	0	

48	Cluster of Reticulon-4	RTN4_HUMAN	130 kDa	9.65%	8.31%	3.44%	2.35%	9.65%	6.80%	3.69%	5.45%	3.44%	3.44%	2.35%	5.20%	2.27%	0	0	0	5.12%	5.12%	2.27%	0	0	0	0	0	
48.1	Reticulon-4	RTN4_HUMAN	130 kDa	9.65%	8.31%	3.44%	2.35%	9.65%	6.80%	3.69%	5.45%	3.44%	3.44%	2.35%	5.20%	2.27%	0	0	0	5.12%	5.12%	2.27%	0	0	0	0	0	
49	Cluster of Prelamin-A/C	LMNA_HUMAN	74 kDa	10.7%	10.2%	10.2%	9.94%	13.6%	9.94%	11.9%	7.98%	10.8%	12.5%	12.5%	16.1%	8.73%	8.73%	7.53%	9.64%	0	0	0	0	7.08%	7.08%	8.89%	0	
49.1	Prelamin-A/C	LMNA_HUMAN	74 kDa	10.7%	10.2%	10.2%	9.94%	13.6%	9.94%	11.9%	7.98%	10.8%	12.5%	12.5%	16.1%	8.73%	8.73%	7.53%	9.64%	0	0	0	0	7.08%	7.08%	8.89%	0	
50	60S acidic ribosomal protein P1	RLA1_BOVIN	12 kDa	42.1%	0	0	0	42.1%	42.1%	0	0	42.1%	0	0	0	0	0	0	42.1%	42.1%	42.1%	0	42.1%	42.1%	0	0	0	
51	Cluster of L-lactate dehydrogenase A chain	LDHA_HUMAN	37 kDa	18.0%	12.0%	11.4%	11.4%	11.4%	11.4%	15.1%	0	14.1%	14.1%	14.5%	14.7%	14.2%	9.04%	11.1%	7.53%	0	0	0	0	26.2%	13.9%	17.2%	0	
51.1	L-lactate dehydrogenase A chain	LDHA_HUMAN	37 kDa	11.4%	11.4%	11.4%	11.4%	11.4%	11.4%	15.1%	0	11.4%	11.4%	14.5%	0	14.2%	9.04%	11.1%	7.53%	0	0	0	0	26.2%	13.9%	17.2%	0	
51.2	L-lactate dehydrogenase B chain	LDHB_MARCFA	37 kDa	18.0%	12.0%	7.49%	0	0	0	0	0	14.1%	14.1%	12.0%	14.7%	0	0	0	0	0	0	0	0	0	0	0	0	0
52	Cluster of Peptidyl-prolyl cis-trans isomerase A	PPIA_SYMSY	18 kDa	33.9%	27.3%	33.9%	23.0%	27.3%	34.5%	33.9%	0	33.9%	33.9%	17.6%	23.0%	16.4%	0	0	0	33.9%	33.9%	33.9%	13.9%	27.9%	33.9%	33.9%	13.9%	
52.1	Peptidyl-prolyl cis-trans isomerase A	PPIA_SYMSY	18 kDa	33.9%	27.3%	33.9%	23.0%	27.3%	34.5%	33.9%	0	33.9%	33.9%	17.6%	23.0%	16.4%	0	0	0	33.9%	33.9%	33.9%	13.9%	27.9%	33.9%	33.9%	13.9%	0
53	Cluster of Myosin-9	MYH9_HUMAN	227 kDa	3.06%	5.36%	0	0	10.7%	7.19%	4.64%	3.93%	2.24%	0	0	0	3.52%	0	0	0	8.01%	8.47%	6.63%	4.13%	4.44%	2.76%	1.33%	0	
53.1	Myosin-9	MYH9_HUMAN	227 kDa	3.06%	5.36%	0	0	10.7%	7.19%	4.64%	3.93%	2.24%	0	0	0	3.52%	0	0	0	8.01%	8.47%	6.63%	4.13%	4.44%	2.76%	1.33%	0	
54	Plasminogen activator inhibitor 1 RNA-binding protein	PAIRB_HUMAN	45 kDa	7.84%	13.0%	7.84%	0	7.84%	7.84%	8.58%	0	0	0	0	0	0	0	0	0	25.5%	25.5%	13.0%	13.0%	13.0%	7.84%	13.0%	0	



62.1	HLA class I histocompatibility antigen, A-2 alpha chain	1A02_HUMAN	41 kDa	0	0	0	0	18.4	18.4	14.8	0	0	0	0	0	18.4	11.8	11.8	8.22	0	0	0	0	18.4	18.4	14.8	0
								0%	0%	0%						0%	0%	0%	%					0%	0%	0%	
62.2	HLA class I histocompatibility antigen, Cw-12 alpha chain	1C12_HUMAN	41 kDa	0	0	0	0	10.4	10.4	13.9	0	0	0	0	0	10.4	0	0	0	0	0	0	0	10.4	0	10.4	0
								0%	0%	0%						0%								0%		0%	
63	Small nuclear ribonucleoprotein Sm D1	SMD1_MAF	13 kDa	27.7	27.7	27.7	0	27.7	27.7	0	0	27.7	27.7	0	27.7	0	0	0	0	0	0	0	0	0	0	0	
				0%	0%	0%		0%	0%			0%	0%		0%												
64	LIM and SH3 domain protein 1 O	LASP1_HUMAN	30 kDa	0	27.2	10.3	10.3	22.2	10.3	10.3	0	0	0	0	10.3	0	0	0	0	33.0	34.1	27.2	10.3	10.3	10.3	10.3	10.3
					0%	0%	0%	0%	0%	0%				0%	0%				0%	0%	0%	0%	0%	0%	0%	0%	
65	Far upstream element-binding protein 1	FUBP1_HUMAN	68 kDa	4.04	6.06	4.04	0	4.04	4.04	0	4.04	0	0	0	0	0	0	0	0	13.8	17.2	18.6	11.3	0	0	0	0
				%	%	%		%	%		%									0%	0%	0%	0%				
66	Alpha-1-antitrypsin	A1AT_BOVIN	46 kDa	0	0	0	0	18.3	10.3	10.6	6.49	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
								0%	0%	0%	%																
67	Serine/arginine-rich splicing factor 7	SRSF7_BOVIN	27 kDa	11.1	20.0	15.7	11.1	0	17.0	13.2	0	13.2	11.1	0	11.1	0	0	0	0	24.7	24.7	20.0	21.7	0	13.2	0	0
				0%	0%	0%	0%		0%	0%		0%	0%		0%					0%	0%	0%	0%		0%		
68	Cluster of Malate dehydrogenase, mitochondrial	MDHM_HUMAN	36 kDa	14.5	14.5	10.4	14.5	17.8	17.8	21.0	9.76	31.4	31.4	34.9	21.3	0	0	0	0	0	0	0	0	0	16.9	14.5	0
				0%	0%	0%	0%	0%	0%	0%	%	0%	0%	0%	0%										0%	0%	
68.1	Malate dehydrogenase, mitochondrial	MDHM_HUMAN	36 kDa	14.5	14.5	10.4	14.5	17.8	17.8	21.0	9.76	31.4	31.4	34.9	21.3	0	0	0	0	0	0	0	0	0	16.9	14.5	0
				0%	0%	0%	0%	0%	0%	0%	%	0%	0%	0%	0%										0%	0%	
68.2	Malate dehydrogenase, mitochondrial	MDHM_MOUSE	36 kDa	0	0	0	14.5	0	0	14.5	9.76	0	0	0	17.2	0	0	0	0	0	0	0	0	0	0	0	0
							0%			0%	%				0%												
	Cluster of Nascent polypeptide-associated complex subunit alpha, muscle-specific form	NACAM_HUMAN	205 kDa	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2.89	2.89	2.89	0	0	0	0	0
																				%	%	%					
69.1	Nascent polypeptide-associated complex subunit	NACAM_HUMAN	205 kDa	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2.89	2.89	2.89	0	0	0	0	0
																				%	%	%					

	alpha, muscle-specific form Nascent polypeptide-associated complex subunit			0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2.74	0	2.74	0	0	0	0	0
69.2	alpha, muscle-specific form Heterogeneous nuclear ribonucleoprotein D0	NACAM_MOUSE	220 kDa	11.0	11.0	11.0	8.73	9.01	9.01	6.76	0	0	0	0	6.76	0	0	0	18.9	25.6	19.4	15.2	11.0	11.0	9.01	0
70	RNA-binding protein FUS	HNRPD_HUMAN	38 kDa	0	0	0	0	11.9	7.41	0	0	0	0	7.41	0	0	0	0	19.5	19.5	20.9	11.9	11.9	11.9	7.41	7.41
71	Cluster of Peroxiredoxin-1	FUS_BOVIN	52 kDa	20.6	36.7	16.6	20.6	32.7	20.6	20.6	0	20.6	20.6	20.6	14.6	20.6	20.6	11.6	0	15.1	0	0	11.6	14.1	0	0
72	Peroxiredoxin-1	PRDX1_HUMAN	22 kDa	0%	0%	0%	0%	0%	0%	0%		0%	0%	0%	0%	0%	0%		0%	0%	0%	0%	0%	0%	0%	0%
72.1	Peroxiredoxin-2	PRDX1_HUMAN	22 kDa	0	0	0	0	14.1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	14.1	0	0
72.2	Cluster of Heterogeneous nuclear ribonucleoprotein A/B	PRDX2_PONAB	19 kDa	11.2	11.2	11.2	11.2	11.2	11.2	11.2	0	7.72	0	0	8.42	0	0	0	19.6	19.6	19.6	15.8	11.2	11.2	8.42	0
73	Heterogeneous nuclear ribonucleoprotein A/B	ROAA_MOUSE	31 kDa	11.2	11.2	11.2	11.2	11.2	11.2	11.2	0	7.72	0	0	8.42	0	0	0	18.6	18.6	18.6	15.8	11.2	11.2	8.42	0
73.1	Heterogeneous nuclear ribonucleoprotein A/B	ROAA_MOUSE	31 kDa	0	5.42	0	0	0	0	0	0	0	0	0	0	0	0	0	19.6	19.6	19.6	11.4	7.53	7.53	0	0
73.2	Eukaryotic translation initiation factor 4B	ROAA_HUMAN	36 kDa	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	13.9	13.9	9.00	6.71	6.71	6.71	0	0
74		IF4B_HUMAN	69 kDa																0%	0%	%	%	%	%		

75	Elongation factor 2	EF2_PONAB	95 kDa	10.5 0%	9.44 %	0	0	7.81 %	5.71 %	5.83 %	0	22.1 0%	11.0 0%	7.34 %	5.71 %	0	0	0	0	0	0	0	7.81 %	5.71 %	4.20 %	0							
76	Superoxide dismutase [Mn], mitochondrial	SODM_PONPY	25 kDa	0	0	0	10.4 0%	19.4 0%	25.7 0%	16.7 0%	10.4 0%	0	0	0	0	10.4 0%	0	0	0	0	0	38.7 0%	23.4 0%	15.3 0%	0	43.7 0%	47.7 0%	30.6 0%	16.7 0%				
77	Cluster of Protein disulfide-isomerase A3	PDIA3_HUMAN	57 kDa	13.3 0%	5.94 %	10.5 0%	12.7 0%	14.9 0%	10.3 0%	9.31 %	4.55 %	5.94 %	5.35 %	10.3 0%	13.1 0%	5.35 %	9.70 %	0	0	0	0	0	0	0	0	10.3 0%	7.33 %	5.15 %	0				
77.1	Protein disulfide-isomerase A3	PDIA3_HUMAN	57 kDa	13.3 0%	5.94 %	10.5 0%	12.7 0%	14.9 0%	10.3 0%	9.31 %	4.55 %	5.94 %	5.35 %	10.3 0%	13.1 0%	5.35 %	9.70 %	0	0	0	0	0	0	0	0	10.3 0%	7.33 %	5.15 %	0				
78	4F2 cell-surface antigen heavy chain	4F2_HUMAN	68 kDa	14.1 0%	11.1 0%	7.30 %	7.62 %	14.1 0%	8.10 %	6.51 %	4.29 %	6.51 %	6.51 %	0	9.52 %	0	0	0	0	0	0	4.13 %	4.13 %	4.13 %	0	0	0	0	0	0			
79	Cluster of Caveolin-1	CAV1_HORSE	21 kDa	30.3 0%	0	0	0	30.3 0%	25.8 0%	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	25.8 0%	30.3 0%	0	16.3 0%	30.3 0%	0	0	
79.1	Caveolin-1	CAV1_HORSE	21 kDa	30.3 0%	0	0	0	30.3 0%	25.8 0%	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	25.8 0%	30.3 0%	0	16.3 0%	30.3 0%	0	0	
79.2	Caveolin-1	CAV1_MOUSE	21 kDa	0	0	0	0	30.3 0%	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
80	Annexin A1	ANXA1_HUMAN	39 kDa	27.5 0%	19.1 0%	15.9 0%	7.80 %	14.7 0%	14.7 0%	0	0	15.9 0%	11.6 0%	15.6 0%	0	13.9 0%	7.51 %	0	0	0	0	0	0	0	0	0	15.3 0%	11.6 0%	0	0	0		
81	Cluster of Hemoglobin fetal subunit beta	HBBF_BOVIN	16 kDa	0	0	0	0	64.1 0%	64.1 0%	48.3 0%	38.6 0%	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
81.1	Hemoglobin fetal subunit beta	HBBF_BOVIN	16 kDa	0	0	0	0	64.1 0%	64.1 0%	48.3 0%	38.6 0%	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
81.2	Hemoglobin subunit beta	HBB_EULFU	16 kDa	0	0	0	0	15.6 0%	0	15.6 0%	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
81.3	Hemoglobin subunit delta	HBD_ATEGE	16 kDa	0	0	0	0	19.7 0%	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
82	Cluster of Protein disulfide-isomerase A6	PDIA6_HUMAN	48 kDa	15.2 0%	11.8 0%	18.6 0%	6.59 %	12.3 0%	15.2 0%	6.14 %	0	18.6 0%	18.6 0%	15.2 0%	9.55 %	0	0	0	0	0	0	0	0	0	0	0	8.86 %	8.86 %	0	0	0	0	

82.1	Protein disulfide-isomerase A6	PDIA6_HUMAN	48 kDa	15.2 0%	11.8 0%	18.6 0%	6.59 %	12.3 0%	15.2 0%	6.14 %	0	18.6 0%	18.6 0%	15.2 0%	9.55 %	0	0	0	0	0	0	0	8.86 %	8.86 %	0	0	
83	10 kDa heat shock protein, mitochondrial	CH10_HUMAN	11 kDa	0	0	0	0	0	21.6 0%	21.6 0%	0	0	0	0	0	0	0	0	0	0	0	21.6 0%	0	0	0	0	
84	Elongation factor 1-delta	EF1D_HUMAN	31 kDa	18.9 0%	0	0	12.8 0%	23.1 0%	20.6 0%	8.90 %	0	23.1 0%	0	8.90 %	0	0	0	0	0	29.2 0%	20.6 0%	26.3 0%	20.6 0%	18.5 0%	9.96 %	8.90 %	0
85	Cluster of CD166 antigen	CD166_HUMAN	65 kDa	14.1 0%	14.4 0%	0	0	14.1 0%	0	0	0	0	0	0	0	0	0	0	0	25.2 0%	28.5 0%	25.2 0%	15.8 0%	10.6 0%	8.58 %	0	0
85.1	CD166 antigen	CD166_HUMAN	65 kDa	14.1 0%	14.4 0%	0	0	14.1 0%	0	0	0	0	0	0	0	0	0	0	0	25.2 0%	28.5 0%	25.2 0%	15.8 0%	10.6 0%	8.58 %	0	0
86	Cluster of Perilipin-3	PLIN3_PIG	48 kDa	0	0	7.37 %	0	18.2 0%	7.37 %	0	0	0	0	0	0	0	0	0	0	11.3 0%	11.3 0%	7.37 %	0	18.7 0%	14.3 0%	0	0
86.1	Perilipin-3	PLIN3_PIG	48 kDa	0	0	7.37 %	0	18.2 0%	7.37 %	0	0	0	0	0	0	0	0	0	0	11.3 0%	11.3 0%	7.37 %	0	18.7 0%	14.3 0%	0	0
86.2	Perilipin-3	PLIN3_PONAB	47 kDa	0	0	7.37 %	0	18.2 0%	7.37 %	0	0	0	0	0	0	0	0	0	0	11.3 0%	11.3 0%	7.37 %	0	18.7 0%	14.3 0%	0	0
87	Endoplasmic reticulum resident protein 29	ERP29_HUMAN	29 kDa	23.4 0%	9.58 %	9.58 %	9.58 %	29.1 0%	19.9 0%	14.2 0%	11.5 0%	9.58 %	9.58 %	0	0	0	0	0	0	14.2 0%	24.5 0%	14.2 0%	14.2 0%	24.5 0%	9.58 %	10.3 0%	0
88	Cluster of Heterogeneous nuclear ribonucleoproteins A2/B1	ROA2_HUMAN	37 kDa	16.4 0%	0	0	0	9.09 %	0	7.33 %	0	7.33 %	7.33 %	7.33 %	7.33 %	0	0	0	0	16.4 0%	9.09 %	9.09 %	9.09 %	0	0	0	0
88.1	Heterogeneous nuclear ribonucleoproteins A2/B1	ROA2_HUMAN	37 kDa	16.4 0%	0	0	0	9.09 %	0	7.33 %	0	7.33 %	7.33 %	7.33 %	7.33 %	0	0	0	0	16.4 0%	9.09 %	9.09 %	9.09 %	0	0	0	0
89	Myosin light polypeptide 6	MYL6_BOVIN	17 kDa	0	0	0	0	26.5 0%	19.2 0%	19.2 0%	15.9 0%	0	0	0	0	0	0	0	0	35.8 0%	43.0 0%	26.5 0%	15.9 0%	19.2 0%	19.2 0%	15.9 0%	25.8 0%



	Complement component 1 Q subcomponent-binding protein, mitochondrial	C1QBP_HUMAN	31 kDa	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	30.1	25.5	19.5	14.9	20.2	0	0	0			
																												0%	0%	0%	0%	0%						
90				2.38	1.85	0	1.28	0	1.44	0	0	4.38	4.50	3.17	1.78	1.93	1.93	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1.10	1.78	1.10	0		
				%	%		%		%			%	%	%	%	%	%															%	%	%				
91	Cluster of Filamin-A	FLNA_HUMAN	281 kDa	2.38	1.85	0	1.28	0	1.44	0	0	4.38	4.50	3.17	1.78	1.93	1.93	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1.10	1.78	1.10	0			
				%	%		%		%			%	%	%	%	%	%														%	%	%					
91.1	Filamin-A	FLNA_HUMAN	281 kDa	0	0	0	0	0	0	0	0	3.78	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
												%																										
91.2	Filamin-A	FLNA_MOUSE	281 kDa	8.24	10.2	8.24	0	0	0	0	0	23.4	23.4	23.4	14.3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
				%	0%	%						0%	0%	0%	0%																							
92	Fructose-bisphosphate aldolase A	ALDOA_HUMAN	39 kDa	0	0	0	0	27.0	0	27.0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
								0%		0%																												
93	60S acidic ribosomal protein P2	RLA2_BOVIN	12 kDa	12.5	12.5	15.7	15.7	12.5	12.5	7.35	0	12.5	15.7	15.7	18.5	7.35	10.5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	7.35	12.5	12.5	0			
				0%	0%	0%	0%	0%	0%	%		0%	0%	0%	0%	%	0%															%	0%	0%				
94	Heterogeneous nuclear ribonucleoproteins C1/C2	HNRPC_MOUSE	34 kDa	0	0	0	0	9.17	9.17	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	11.3	13.8	11.3	12.0	0	7.19	0	0
								%	%																						0%	0%	0%	0%		%		
95	Caprin-1	CAPR1_HUMAN	78 kDa	0	0	0	0	36.0	36.0	36.0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
								0%	0%	0%																												
96	Protein S100-A6	S10A6_MOUSE	10 kDa	0	0	0	0	10.5	10.5	10.5	0	0	0	0	0	0	10.5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	10.5	10.5	10.5	0	0	0	0
								0%	0%	0%						0%																0%	0%	0%				
97	Serine/arginine-rich splicing factor 1	SRSF1_CHICK	28 kDa	11.8	20.1	11.8	0	20.1	20.1	0	0	20.1	20.1	20.1	20.1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
				0%	0%	0%		0%	0%			0%	0%	0%	0%																							
98	Phosphoglycerate mutase 1	PGAM1_BOVIN	29 kDa	5.00	5.00	3.29	3.29	3.29	5.00	5.00	3.42	5.00	3.29	0	3.29	5.26	2.50	0	0	0	0	0	0	0	0	0	0	0	0	0	5.00	5.00	3.29	5.00	0	3.29	0	0
				%	%	%	%	%	%	%	%	%	%		%	%	%														%	%	%	%		%		
99	Cluster of Transferrin receptor protein 1	TFR1_HUMAN	85 kDa	5.00	5.00	3.29	3.29	3.29	5.00	5.00	3.42	5.00	3.29	0	3.29	5.26	2.50	0	0	0	0	0	0	0	0	0	0	0	0	5.00	5.00	3.29	5.00	0	3.29	0	0	
				%	%	%	%	%	%	%	%	%	%		%	%	%														%	%	%	%		%		
99.1	Transferrin receptor protein 1	TFR1_HUMAN	85 kDa	5.00	5.00	3.29	3.29	3.29	5.00	5.00	3.42	5.00	3.29	0	3.29	5.26	2.50	0	0	0	0	0	0	0	0	0	0	0	0	5.00	5.00	3.29	5.00	0	3.29	0	0	
				%	%	%	%	%	%	%	%	%	%		%	%	%														%	%	%	%		%		

10				0	0	0	0	20.1	0	16.1	0	0	0	0	0	0	0	0	34.2	45.7	29.1	16.1	38.7	38.7	14.6	0
0	Transgelin-2	TAGL2_HU	22 kDa					0%		0%									0%	0%	0%	0%	0%	0%	0%	
	Heterogeneous nuclear ribonucleoprotein A1	ROA1_HUMAN	39 kDa	0	0	8.60	8.60	0	0	0	0	8.60	8.60	0	0	0	0	0	0	0	0	0	0	0	0	0
10				4.57	2.74	2.74	2.74	2.74	2.74	0	0	4.68	4.68	0	0	0	0	0	0	0	2.74	0	2.74	4.45	0	0
10	Importin subunit beta-1	IMB1_HUMAN	97 kDa	%	%	%	%	%	%			%	%								%		%	%		
	High mobility group protein B2	HMGB2_BOVIN	24 kDa	0	14.4	0	0	0	0	0	0	0	0	0	0	0	0	0	20.1	20.6	20.6	20.1	0	14.4	22.0	0
10				12.9	9.81	9.81	0	9.81	9.81	0	0	9.81	0	0	0	0	0	0	0	0	0	0	9.81	0	0	0
10	Serpin H1	SERPH_HUMAN	46 kDa	0%	%	%		%	%			%														
	Profilin-1	PROF1_HUMAN	15 kDa	0	0	0	0	22.9	22.9	0	0	22.1	35.0	35.0	0	0	0	0	0	0	0	0	0	0	0	0
10	Serine/arginine-rich splicing factor 3	SRSF3_MOUSE	19 kDa	0	0	0	0	0	12.8	0	0	0	0	0	0	0	0	0	18.3	18.3	18.3	14.0	0	12.8	0	0
	Cluster of Moesin	MOES_HUMAN	68 kDa	3.29	3.29	3.29	3.29	3.29	3.29	0	3.29	5.55	5.55	5.55	3.99	5.55	0	0	0	0	0	0	3.29	3.29	3.29	0
10				%	%	%	%	%	%		%	%	%	%	%	%							%	%	%	
10	Moesin	MOES_HUMAN	68 kDa	3.29	3.29	3.29	3.29	3.29	3.29	0	3.29	5.55	5.55	5.55	3.99	5.55	0	0	0	0	0	0	3.29	3.29	3.29	0
7.1	Cluster of Lamina-associated polypeptide 2, isoforms beta/gamma	LAP2B_HUMAN	51 kDa	11.9	0	6.39	6.39	6.39	6.39	6.39	0	0	0	0	0	0	0	0	29.3	17.8	17.6	6.39	6.39	12.1	6.39	6.39
	Lamina-associated polypeptide 2, isoforms beta/gamma	LAP2B_HUMAN	51 kDa	0%		%	%	%	%	%									0%	0%	0%	%	%	0%	%	%
10				11.9	0	6.39	6.39	6.39	6.39	6.39	0	0	0	0	0	0	0	0	29.3	17.8	17.6	6.39	6.39	12.1	6.39	6.39
8.1	Brain acid soluble protein 1	BASP1_HUMAN	23 kDa	0%	0%	0%	0	23.3	0	0	0	0	0	0	0	0	0	0	51.1	51.1	51.1	0	51.1	23.3	0	0





13 1.2	Hemoglobin subunit alpha	HBA_SPEC I	15 kDa	0	0	0	0	17.0 0%	17.0 0%	17.0 0%	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
13 2	Variant surface antigen C	VLPC_MYC HR	16 kDa	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	22.5 0%	22.5 0%	22.5 0%	0
13 3	Nuclear autoantigenic sperm protein	NASP_HU MAN	85 kDa	0	0	0	0	0	0	0	0	0	0	0	0	0	0	10.9 0%	14.6 0%	5.84 %	5.33 %	0	0	0	0	0	
13 4	Proteasome subunit alpha type-6	PSA6_HU MAN	27 kDa	15.9 0%	30.1 0%	15.9 0%	12.2 0%	12.2 0%	12.2 0%	8.94 %	0	0	0	0	0	0	0	8.94 %	0	0	0	0	0	0	0	0	
13 5	Small ubiquitin-related modifier 2	SUMO2_D ANRE	11 kDa	0	33.3 0%	0	0	0	0	0	0	0	0	0	0	0	0	33.3 0%	0	0	0	33.3 0%	0	0	0	0	
13 6	Heterogeneous nuclear ribonucleoprotein K	HNRPK_BOVIN	51 kDa	9.91 %	10.3 0%	13.6 0%	9.48 %	6.68 %	6.68 %	0	0	11.0 0%	11.0 0%	6.25 %	4.31 %	0	0	0	0	0	0	6.25 %	6.25 %	0	0	0	
13 7	Cluster of Transitional endoplasmic reticulum ATPase	TERA_HU MAN	89 kDa	0	0	0	0	5.71 %	3.60 %	0	0	10.0 0%	7.57 %	3.85 %	5.33 %	0	0	0	0	0	0	0	5.71 %	0	0	0	
13 7.1	Transitional endoplasmic reticulum ATPase	TERA_HU MAN	89 kDa	0	0	0	0	5.71 %	3.60 %	0	0	10.0 0%	7.57 %	3.85 %	5.33 %	0	0	0	0	0	0	0	5.71 %	0	0	0	
13 8	Stathmin	STMN1_G EKJA	17 kDa	0	0	0	0	0	0	0	0	0	0	0	0	0	0	28.2 0%	0	20.1 0%	16.8 0%	17.4 0%	36.9 0%	26.8 0%	0		
13 9	Uncharacterized protein C19orf43	CS043_HU MAN	18 kDa	0	0	0	0	0	0	0	0	0	0	0	0	0	0	15.3 0%	0	0	0	15.3 0%	0	0	0		
14 0	T-complex protein 1 subunit eta	TCPH_BOVIN	59 kDa	10.5 0%	8.66 %	0	0	8.66 %	0	0	0	8.66 %	8.66 %	0	0	0	0	0	0	0	0	8.66 %	0	0	0		
14 1	Thioredoxin	THIO_HU MAN	12 kDa	0	0	0	0	31.4 0%	31.4 0%	0	0	0	0	0	0	0	0	45.7 0%	45.7 0%	0	0	0	0	0	0	0	
14 2	Cluster of Phosphoglycerate kinase 1	PGK1_HU MAN	45 kDa	11.0 0%	8.39 %	0	0	6.71 %	0	0	0	11.5 0%	0	0	0	0	0	0	0	0	0	16.8 0%	16.1 0%	7.67 %	0		

14 2.1	Phosphoglycerate kinase 1	PGK1_HUMAN	45 kDa	11.0 0%	8.39 %	0	0	6.71 %	0	0	0	11.5 0%	0	0	0	0	0	0	0	0	0	16.8 0%	16.1 0%	7.67 %	0
14 3	Cluster of CD9 antigen	CD9_HUMAN	25 kDa	16.2 0%	9.65 %	20.6 0%	0	20.6 0%	20.6 0%	0	9.65 %	0	0	0	0	0	0	20.6 0%	0	15.4 0%	0	16.2 0%	9.65 %	0	0
14 3.1	CD9 antigen	CD9_HUMAN	25 kDa	16.2 0%	9.65 %	20.6 0%	0	20.6 0%	20.6 0%	0	9.65 %	0	0	0	0	0	0	20.6 0%	0	15.4 0%	0	16.2 0%	9.65 %	0	0
14 4	Cluster of Acidic leucine-rich nuclear phosphoprotein 32 family member A O	AN32A_HUMAN	29 kDa	0	0	0	0	0	0	0	0	0	0	0	0	0	0	22.1 0%	31.7 0%	0	0	22.1 0%	22.1 0%	0	0
14 4.1	Acidic leucine-rich nuclear phosphoprotein 32 family member A	AN32A_HUMAN	29 kDa	0	0	0	0	0	0	0	0	0	0	0	0	0	0	22.1 0%	31.7 0%	0	0	22.1 0%	22.1 0%	0	0
14 5	TATA-binding protein-associated factor 2N	RBP56_HUMAN	62 kDa	0	0	0	0	0	0	0	0	0	0	0	0	0	0	18.1 0%	18.1 0%	11.3 0%	8.45 %	0	0	0	0
14 6	Splicing factor 1	SF01_HUMAN	68 kDa	0	0	0	0	0	0	0	0	0	0	0	0	0	0	5.95 %	5.95 %	7.67 %	5.95 %	0	0	0	0
14 7	Chloride intracellular channel protein 1	CLIC1_BOVIN	27 kDa	0	0	0	0	0	0	12.4 0%	12.4 0%	0	0	0	0	0	0	0	0	0	0	0	0	0	0
14 8	Eukaryotic translation initiation factor 4H	IF4H_HUMAN	27 kDa	0	0	0	0	0	0	0	0	0	0	0	0	0	0	35.1 0%	25.0 0%	20.2 0%	11.3 0%	0	11.3 0%	0	0
14 9	Histone H3, embryonic O	H3_PYPHE	15 kDa	24.3 0%	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
15 0	PDZ and LIM domain protein 1	PDL1_HUMAN	36 kDa	0	0	0	0	0	0	0	0	0	0	0	0	0	0	27.4 0%	28.9 0%	27.1 0%	17.6 0%	0	0	0	0

15 1	Cluster of Integrin alpha-3	ITA3_HUMAN	117 kDa	0	0	0	0	3.71 %	3.04 %	3.52 %	2.85 %	0	0	0	0	5.04 %	0	0	0	0	0	0	0	2.18 %	3.90 %	0
15 1.1	Integrin alpha-3	ITA3_HUMAN	117 kDa	0	0	0	0	3.71 %	2.09 %	3.52 %	2.85 %	0	0	0	0	5.04 %	0	0	0	0	0	0	0	0	3.90 %	0
15 1.2	Integrin alpha-3	ITA3_MOUSE	117 kDa	0	0	0	0	3.04 %	3.04 %	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2.18 %	0	0
15 2	40S ribosomal protein S12	RS12_MOUSE	15 kDa	24.2 0%	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	24.2 0%	0	0
15 3	Cluster of ATP synthase subunit beta, mitochondrial	ATPB_MOUSE	56 kDa	10.0 0%	9.64 %	0	0	9.64 %	6.05 %	5.10 %	0	0	0	0	0	0	0	0	0	0	0	0	0	9.64 %	6.05 %	0
15 3.1	ATP synthase subunit beta, mitochondrial	ATPB_MOUSE	56 kDa	10.0 0%	9.64 %	0	0	9.64 %	6.05 %	5.10 %	0	0	0	0	0	0	0	0	0	0	0	0	0	9.64 %	6.05 %	0
15 4	Heterogeneous nuclear ribonucleoprotein H	HNRH1_HUMAN	49 kDa	11.1 0%	10.5 0%	7.35 %	7.35 %	7.35 %	7.35 %	7.35 %	0	7.57 %	7.57 %	7.35 %	7.35 %	0	0	0	0	0	0	0	0	7.35 %	7.35 %	0
15 5	Reticulocalbin-1	RCN1_HUMAN	39 kDa	0	0	0	0	0	10.6 0%	0	0	0	0	0	0	0	0	0	0	0	0	0	0	11.8 0%	10.6 0%	10.6 0%
15 6	Cluster of Proteasome subunit alpha type-7	PSA7_HUMAN	28 kDa	15.7 0%	15.7 0%	15.7 0%	10.1 0%	0	0	10.5 0%	0	0	10.1 0%	0	10.1 0%	0	0	0	0	0	0	0	0	0	0	0
15 6.1	Proteasome subunit alpha type-7	PSA7_HUMAN	28 kDa	15.7 0%	15.7 0%	15.7 0%	10.1 0%	0	0	10.5 0%	0	0	10.1 0%	0	10.1 0%	0	0	0	0	0	0	0	0	0	0	0
15 7	Cytoskeleton-associated protein 4	CKAP4_HUMAN	66 kDa	0	5.48 %	0	0	12.5 0%	16.4 0%	9.14 %	4.82 %	0	0	0	0	0	0	0	0	6.98 %	0	0	0	0	0	0
15 8	60S ribosomal protein L6	RL6_HUMAN	33 kDa	12.2 0%	12.2 0%	12.2 0%	0	0	0	0	0	12.2 0%	8.33 %	0	0	0	0	0	0	0	0	0	0	0	0	0
15 9	Cluster of Eukaryotic initiation factor 4A-I	IF4A1_MANNA	46 kDa	13.3 0%	10.8 0%	13.3 0%	13.3 0%	0	0	0	0	9.85 %	13.3 0%	9.85 %	13.3 0%	9.85 %	7.39 %	0	0	0	0	0	0	7.39 %	9.85 %	9.85 %
				5.91 %																						





16 8.1	T-complex protein 1 subunit theta	TCPO_HU MAN	60 kDa	0	0	0	4.56 %	0	0	0	0	0	0	0	5.11 %	0	0	0	0	0	0	0	0	0	0	
16 9	Proteasome subunit beta type-6	PSB6_HU MAN	25 kDa	8.79 %	8.79 %	8.79 %	8.79 %	0	0	8.79 %	8.79 %	0	0	8.79 %	8.79 %	0	0	0	0	0	0	0	0	0		
17 0	Splicing factor 3B subunit 2	SF3B2_HU MAN	100 kDa	0	0	0	0	0	0	0	0	0	0	0	0	0	0	7.15 %	9.61 %	7.15 %	5.47 %	0	0	0		
17 1	5'-nucleotidase Cluster of Dihydropyridyl dehydrogenase, mitochondrial	5NTD_HU MAN	63 kDa	7.84 %	7.84 %	0	7.84 %	14.5 0%	9.41 %	7.84 %	4.88 %	0	0	0	0	0	0	0	0	0	0	0	0	0		
17 2	Dihydropyridyl dehydrogenase, mitochondrial	DLDH_HU MAN	54 kDa	6.29 %	0	6.29 %	0	11.0 0%	4.91 %	0	0	0	0	0	0	0	0	0	0	0	0	4.91 %	8.45 %	0	0	
17 2.1	Dihydropyridyl dehydrogenase, mitochondrial	DLDH_HU MAN	54 kDa	6.29 %	0	6.29 %	0	11.0 0%	4.91 %	0	0	0	0	0	0	0	0	0	0	0	0	4.91 %	8.45 %	0	0	
17 3	Peptidyl-prolyl cis-trans isomerase FKBP1A	FKB1A_BO VIN	12 kDa	0	0	0	0	0	0	19.5 0%	0	0	0	0	0	0	0	0	25.0 0%	25.0 0%	25.0 0%	25.0 0%	0	0	0	0
17 4	CD59 glycoprotein	CD59_HU MAN	14 kDa	0	0	0	0	0	0	19.5 0%	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
17 5	Prohibitin-2 Cluster of GTP- binding nuclear protein Ran	PHB2_HU MAN	33 kDa	24.1 0%	14.0 0%	14.0 0%	7.69 %	0	0	0	0	14.0 0%	7.69 %	11.4 0%	7.69 %	0	0	0	0	0	0	0	0	0	0	
17 6	GTP-binding nuclear protein Ran	RAN_CHIC K	24 kDa	11.6 0%	0	16.7 0%	0	0	0	0	0	11.6 0%	16.2 0%	11.6 0%	16.2 0%	0	0	0	0	0	0	0	0	0	0	
17 6.1	GTP-binding nuclear protein Ran	RAN_CHIC K	24 kDa	11.6 0%	0	16.7 0%	0	0	0	0	0	11.6 0%	16.2 0%	11.6 0%	16.2 0%	0	0	0	0	0	0	0	0	0	0	
17 7	Proliferation marker protein Ki-67	KI67_HUM AN	359 kDa	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3.16 %	2.73 %	1.63 %	1.26 %	0	0	0	0
17 8	Thioredoxin domain- containing protein 5	TXND5_H UMAN	48 kDa	6.48 %	6.48 %	0	0	6.48 %	6.48 %	0	0	6.48 %	6.71 %	6.71 %	0	0	0	0	0	0	4.17 %	0	0	0	0	

17	RNA-binding protein EWS	EWS_HUMAN	68 kDa	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	7.62	7.62	5.03	5.18	0	0	0	5.03
18	60S ribosomal protein L4	RL4_HUMAN	48 kDa	0	8.20	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
18	Cluster of Glutathione S-transferase omega-1	GSTO1_HUMAN	28 kDa	0	10.8	4.98	4.98	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
18	Glutathione S-transferase omega-1	GSTO1_HUMAN	28 kDa	0	10.8	4.98	4.98	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
18	Eukaryotic translation initiation factor 6	IF6_HUMAN	27 kDa	17.1	0	0	0	0	0	0	22.9	13.1	22.9	13.1	0	0	0	0	0	0	0	0	0	0	0	0	
18	Proteasome subunit beta type-3	PSB3_BOVIN	23 kDa	23.4	23.4	14.6	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
18	Proteasome subunit alpha type-5	PSA5_MOUSE	26 kDa	0	12.9	0	12.9	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
18	CD97 antigen	CD97_HUMAN	92 kDa	0	0	0	0	5.87	3.95	0	0	0	0	0	0	0	0	0	0	0	0	0	5.87	3.47	5.03	0	
18	Protein deglycase DJ-1	PARK7_HUMAN	20 kDa	0	0	0	0	22.2	0	0	0	0	0	0	0	0	0	0	22.2	0	0	0	0	0	0	0	
18	Beta-2-glycoprotein 1	APOH_BOVIN	38 kDa	0	0	0	0	10.7	10.7	15.1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
18	Small nuclear ribonucleoprotein Sm D3	SMD3_MOUSE	14 kDa	0	15.1	0	0	0	15.1	0	0	15.1	15.1	0	0	0	0	0	0	0	0	0	0	0	0	0	
18	Prohibitin	PHB_HUMAN	30 kDa	13.2	23.2	8.09	8.82	0	0	0	13.2	9.56	0	13.2	0	0	0	0	0	0	0	0	0	0	0	0	
19	Aspartate aminotransferase, mitochondrial	AATM_HUMAN	48 kDa	8.60	0	0	0	0	0	0	5.12	5.12	5.12	5.12	0	0	0	0	0	0	0	0	0	0	0	0	
19	Clathrin heavy chain 1	CLH1_BOVIN	192 kDa	2.03	2.03	1.31	0	0	0	0	0	1.43	0	1.31	0	0	0	0	0	0	0	0	0	1.19	0	0	



20 1.1	Plectin	PLEC_HUMAN	532 kDa	0	0	0	0	0	0	0	0	0.98%	0.96%	0.71%	0	0	0	0	0	0.43%	0	0	0	0	0	0	0
20 2	Peroxiredoxin-4 Cluster of Scaffold attachment factor B1	PRDX4_HUMAN	31 kDa	16.2	16.2	16.2	16.2	16.2	16.2	12.9	0	12.2	16.2	0	0	16.2	0	0	0	0	0	0	0	0	0	0	0
20 3	Scaffold attachment factor B1	SAFB1_HUMAN	103 kDa	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	7.43%	2.83%	3.93%	0	0	0	0	0
20 3.1	Scaffold attachment factor B1	SAFB1_HUMAN	103 kDa	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	7.43%	0	3.93%	0	0	0	0	0
20 3.2	Scaffold attachment factor B2	SAFB2_HUMAN	107 kDa	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	7.24%	2.83%	0	0	0	0	0	0
20 4	Tissue factor	TF_HUMAN	33 kDa	0	0	0	0	12.2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	12.2	12.2	0	0	0
20 5	60S ribosomal protein L7a	RL7A_MCA	30 kDa	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	10.9	0	0	
20 6	A-kinase anchor protein 2	AKAP2_HUMAN	95 kDa	5.01%	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	8.38%	6.05%	3.84%	0	0	0	0	0
20 7	Cellular nucleic acid-binding protein	CNBP_BOVIN	19 kDa	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	22.4	22.4	31.8	0	0	0	0	0
20 8	Cluster of Hypoxia up-regulated protein 1 O	HYOU1_HUMAN	111 kDa	6.81%	0	0	0	0	3.20%	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
20 8.1	Hypoxia up-regulated protein 1	HYOU1_HUMAN	111 kDa	6.81%	0	0	0	0	3.20%	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
20 9	PEST proteolytic signal-containing nuclear protein	PCNP_HUMAN	19 kDa	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	10.1	0	0	0	0	0	0	0
21 0	Ubiquitin-associated protein 2-like	UBP2L_HUMAN	115 kDa	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2.67	0	0	0	0	0















2	Cluster of Actin-2	ACT2_SUIBO	42 kDa	100 %	100 %	100 %	100 %	100 %	100 %	100 %	100 %	100 %	100 %	100 %	100 %	100 %	100 %	100 %	100 %	100 %	100 %	100 %	100 %	100 %	100 %		
2.1	Actin-2	ACT2_SUIBO	42 kDa	100 %	100 %	99 %	100 %	100 %	97 %	0 %	100 %	96 %	0 %	98 %	0 %	0 %	0 %	0 %	100 %	100 %	100 %	97 %	100 %	100 %	98 %	0 %	
2.2	Beta-actin-like protein 2	ACTBL_HUMAN	42 kDa	99 %	99 %	95 %	95 %	100 %	100 %	100 %	0 %	99 %	97 %	99 %	96 %	0 %	0 %	0 %	0 %	99 %	0 %	0 %	0 %	99 %	96 %	0 %	
2.3	Actin-18 O	ACT18_DICDI	43 kDa	0 %	100 %	98 %	98 %	99 %	98 %	100 %	0 %	0 %	100 %	97 %	96 %	0 %	0 %	0 %	0 %	0 %	0 %	0 %	0 %	97 %	98 %	0 %	
2.4	Actin-3	ACT3_SOYBN	42 kDa	0 %	99 %	100 %	0 %	0 %	98 %	99 %	0 %	0 %	0 %	100 %	95 %	100 %	0 %	0 %	0 %	0 %	0 %	0 %	0 %	99 %	0 %	0 %	
2.5	Actin	ACT_CRYPV	42 kDa	0 %	0 %	0 %	0 %	0 %	0 %	0 %	0 %	0 %	0 %	0 %	0 %	0 %	0 %	0 %	0 %	0 %	0 %	0 %	0 %	98 %	0 %	0 %	
2.6	Actin, cytoplasmic 1	ACTB_CRIGR	42 kDa	100 %	100 %	100 %	100 %	100 %	100 %	97 %	99 %	0 %	100 %	99 %	100 %	99 %	0 %	0 %	97 %	0 %	0 %	0 %	0 %	100 %	100 %	100 %	100 %
2.7	Actin	ACT_KOMPG	42 kDa	100 %	100 %	0 %	100 %	0 %	0 %	99 %	96 %	0 %	100 %	100 %	0 %	0 %	0 %	0 %	0 %	100 %	97 %	100 %	98 %	0 %	0 %	98 %	99 %
2.8	Actin, cytoplasmic	ACTC_BRABE	42 kDa	0 %	0 %	0 %	0 %	0 %	0 %	100 %	99 %	0 %	100 %	100 %	100 %	0 %	0 %	0 %	95 %	0 %	0 %	0 %	0 %	99 %	100 %	100 %	
2.9	Actin, cytoplasmic	ACTC_STYPL	42 kDa	0 %	100 %	0 %	0 %	0 %	0 %	100 %	0 %	0 %	0 %	0 %	0 %	0 %	0 %	0 %	0 %	0 %	0 %	0 %	0 %	98 %	100 %	100 %	
2.1	Actin-53 (Fragment)	ACT2_TOBAC	37 kDa	0 %	0 %	0 %	0 %	0 %	0 %	0 %	0 %	0 %	0 %	95 %	0 %	0 %	0 %	0 %	0 %	0 %	0 %	0 %	0 %	0 %	96 %	0 %	
2.11	Actin	ACT_ASPOR	42 kDa	0 %	0 %	0 %	0 %	0 %	0 %	0 %	0 %	0 %	0 %	0 %	0 %	0 %	0 %	0 %	0 %	0 %	0 %	0 %	0 %	99 %	0 %	0 %	
2.12	Actin	ACT_ACHBI	42 kDa	0 %	99 %	0 %	0 %	0 %	0 %	0 %	0 %	0 %	0 %	0 %	0 %	0 %	0 %	0 %	0 %	0 %	0 %	0 %	0 %	0 %	0 %	0 %	
2.13	Actin, muscle	ACTM_PISOC	42 kDa	0 %	0 %	98 %	0 %	0 %	0 %	0 %	0 %	0 %	0 %	0 %	0 %	0 %	0 %	0 %	0 %	0 %	0 %	0 %	0 %	0 %	0 %	0 %	
2.14	Actin-1	ACT1_SCHMA	42 kDa	0 %	0 %	0 %	0 %	0 %	96 %	0 %	0 %	0 %	97 %	0 %	0 %	0 %	0 %	0 %	0 %	0 %	0 %	0 %	100 %	99 %	0 %	0 %	
2.15	Actin, cytoplasmic type 8	ACT8_XENLA	42 kDa	0 %	0 %	0 %	0 %	0 %	0 %	0 %	0 %	0 %	0 %	0 %	0 %	0 %	0 %	0 %	0 %	0 %	0 %	0 %	98 %	0 %	0 %	0 %	









16.2	Tropomyosin alpha-4 chain	TPM4_HUMAN	29 kDa	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	100	100	0	0	0	98%	0	0
16.3	Tropomyosin alpha-4 chain	TPM4_HORSE	29 kDa	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	98%	0	0	0	0	0	0
17	Far upstream element-binding protein 2	FUBP2_HUMAN	73 kDa	100	100	100	100	100	100	100	100	100	100	100	100	100	100	0	100	100	100	100	100	100	100	
18	Cluster of Histone H4	H4_ACRAS	11 kDa	100	100	100	100	100	100	100	100	100	100	100	100	100	100	0	100	100	100	100	100	100	100	
18.1	Histone H4	H4_ACRAS	11 kDa	100	100	100	100	100	100	100	100	100	100	100	100	100	100	0	100	100	100	100	100	100	100	
19	Cluster of Glyceraldehyde-3-phosphate dehydrogenase	G3P_HUMAN	36 kDa	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	
19.1	Glyceraldehyde-3-phosphate dehydrogenase	G3P_HUMAN	36 kDa	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	
20	Cluster of Histone H2B type 1-B	H2B1B_HUMAN	14 kDa	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	
20.1	Histone H2B type 1-B	H2B1B_HUMAN	14 kDa	98%	97%	96%	96%	97%	96%	96%	96%	99%	96%	96%	100	96%	96%	96%	96%	96%	96%	96%	96%	96%	96%	
20.2	Histone H2B type 1-N	H2B1N_BOVINE	14 kDa	100	0	99%	100	100	100	99%	99%	0	100	100	0	99%	99%	99%	99%	99%	99%	100	99%	99%	99%	
21	Cluster of Tubulin beta-5 chain	TBB5_RAT	50 kDa	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	
21.1	Tubulin beta-5 chain	TBB5_RAT	50 kDa	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	99%	100	100	100	
21.2	Tubulin beta chain	TBB_CERBT	50 kDa	100	100	0	0	100	0	0	0	0	100	0	0	99%	0	0	0	0	98%	0	0	100	100	
21.3	Tubulin beta chain	TBB_PENDI	50 kDa	0	0	0	95%	0	100	0	0	0	96%	0	0	0	0	0	0	0	0	0	100	97%	99%	



21.4	Tubulin beta-4B chain	TBB4B_HUMAN	50 kDa	100 %	100 %	95 %	97 %	100 %	99 %	99 %	0	99 %	98 %	100 %	0	0	97 %	97 %	0	0	0	0	0	95 %	0	0	0
21.5	Tubulin beta-1 chain (Fragment)	TBB1_DAUCA	36 kDa	98 %	0	98 %	0	99 %	100 %	0	0	0	0	0	0	0	0	0	0	0	0	0	100 %	0	97 %	0	
21.6	Tubulin beta-1 chain	TBB1_DROME	50 kDa	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	100 %	0	0	0	
21.7	Tubulin beta-2 chain	TBB2_DROER	50 kDa	96 %	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	100 %	0	0	0	
21.8	Tubulin beta-4A chain	TBB4A_BOVIN	50 kDa	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	98 %	0	0	
22	Cluster of CD44 antigen	CD44_HUMAN	82 kDa	100 %	100 %	100 %	100 %	100 %	100 %	100 %	100 %	100 %	100 %	100 %	100 %	100 %	100 %	100 %	100 %	100 %	100 %	100 %	100 %	100 %	100 %	100 %	100 %
22.1	CD44 antigen	CD44_HUMAN	82 kDa	100 %	100 %	100 %	100 %	100 %	100 %	100 %	100 %	100 %	100 %	100 %	100 %	100 %	100 %	100 %	100 %	100 %	100 %	100 %	100 %	100 %	100 %	100 %	100 %
23	Cluster of Tubulin alpha chain	TBA_XENLA	50 kDa	100 %	100 %	100 %	100 %	100 %	100 %	0	100 %	100 %	100 %	100 %	100 %	100 %	100 %	100 %	100 %	100 %	0	0	0	100 %	100 %	100 %	100 %
23.1	Tubulin alpha chain	TBA_XENLA	50 kDa	100 %	100 %	100 %	100 %	100 %	100 %	0	100 %	100 %	100 %	100 %	100 %	100 %	100 %	100 %	100 %	100 %	0	0	0	100 %	100 %	100 %	100 %
23.2	Tubulin alpha-5 chain	TBA5_ARATH	50 kDa	0	100 %	99 %	0	100 %	100 %	100 %	0	100 %	100 %	0	0	0	0	0	0	0	0	0	100 %	98 %	100 %	0	
23.3	Tubulin alpha-3 chain	TBA3_CAEEL	50 kDa	0	99 %	0	99 %	100 %	97 %	0	100 %	100 %	0	98 %	0	0	0	0	0	0	0	0	100 %	100 %	99 %	0	
23.4	Tubulin alpha chain	TBA_ENTDO	50 kDa	100 %	0	100 %	0	0	0	0	0	100 %	0	0	0	0	0	0	0	0	0	0	100 %	0	0	0	
24	Cluster of 60 kDa heat shock protein, mitochondrial	CH60_HUMAN	61 kDa	100 %	100 %	100 %	100 %	100 %	100 %	100 %	100 %	100 %	100 %	100 %	100 %	100 %	100 %	100 %	100 %	100 %	0	100 %	100 %	100 %	0		
24.1	60 kDa heat shock protein, mitochondrial	CH60_HUMAN	61 kDa	100 %	100 %	100 %	100 %	100 %	100 %	100 %	100 %	100 %	100 %	100 %	100 %	100 %	100 %	100 %	100 %	100 %	0	100 %	100 %	100 %	0		



















81.2	Hemoglobin subunit beta	HBB_EULFU	16 kDa	0	0	0	0	99%	0	96%	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
81.3	Hemoglobin subunit delta	HBD_ATEGE	16 kDa	0	0	0	0	99%	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
82	Cluster of Protein disulfide-isomerase A6	PDIA6_HUMAN	48 kDa	100	100	100	100	100	100	100	100	100	100	100	0	0	0	0	0	0	0	0	100	100	0	0
82.1	Protein disulfide-isomerase A6	PDIA6_HUMAN	48 kDa	100	100	100	100	100	100	100	100	100	100	100	0	0	0	0	0	0	0	0	100	100	0	0
83	10 kDa heat shock protein, mitochondrial	CH10_HUMAN	11 kDa	0	0	0	0	0	100	100	0	0	0	0	0	0	0	0	0	0	0	100	0	0	0	0
84	Elongation factor 1-delta	EF1D_HUMAN	31 kDa	100	0	0	0	100	100	100	100	100	100	0	0	0	0	0	0	0	0	100	100	100	100	100
85	Cluster of CD166 antigen	CD166_HUMAN	65 kDa	100	100	0	0	100	0	0	0	0	0	0	0	0	0	0	0	0	0	100	100	100	100	100
85.1	CD166 antigen	CD166_HUMAN	65 kDa	100	100	0	0	100	0	0	0	0	0	0	0	0	0	0	0	0	0	100	100	100	100	100
86	Cluster of Perilipin-3	PLIN3_PIG	48 kDa	0	0	100	0	100	100	0	0	0	0	0	0	0	0	0	0	0	0	100	100	100	100	100
86.1	Perilipin-3	PLIN3_PIG	48 kDa	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	100	0	0	0	0
86.2	Perilipin-3	PLIN3_PONAB	47 kDa	0	0	95%	0	100	95%	0	0	0	0	0	0	95%	0	0	0	0	99%	99%	96%	0	100	100
87	Endoplasmic reticulum resident protein 29	ERP29_HUMAN	29 kDa	100	100	100	100	100	100	100	100	100	100	0	0	0	0	0	0	0	0	100	100	100	100	100
88	Cluster of Heterogeneous nuclear ribonucleoproteins A2/B1	ROA2_HUMAN	37 kDa	100	0	0	0	100	0	100	0	100	100	100	100	0	0	0	0	0	0	100	100	100	100	0
88.1	Heterogeneous nuclear ribonucleoproteins A2/B1	ROA2_HUMAN	37 kDa	100	0	0	0	100	0	96%	0	97%	96%	97%	99%	0	0	0	0	0	0	100	100	100	100	0

89	Myosin light polypeptide 6	MYL6_BOVIN	17 kDa	0	0	0	0	100	100	100	100	0	0	0	0	0	0	0	100	100	100	100	100	100	100	100	100
90	Complement component 1 Q subcomponent-binding protein, mitochondrial	C1QBP_HUMAN	31 kDa	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	100	100	100	100	100	0	0	0	
91	Cluster of Filamin-A	FLNA_HUMAN	281 kDa	100	100	0	100	100	0	0	100	100	100	100	100	100	0	0	0	0	0	0	100	100	100	0	
91.1	Filamin-A	FLNA_HUMAN	281 kDa	100	100	0	100	100	0	0	100	100	100	100	100	100	0	0	0	0	0	0	100	100	100	0	
91.2	Filamin-A	FLNA_MOUSE	281 kDa	0	0	0	0	0	0	0	98%	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
92	Fructose-bisphosphate aldolase A	ALDOA_HUMAN	39 kDa	100	100	100	0	0	0	0	0	100	100	100	100	0	0	0	0	0	0	0	0	0	0	0	
93	60S acidic ribosomal protein P2	RLA2_BOVIN	12 kDa	0	0	0	0	100	0	100	0	0	0	0	0	0	0	0	100	100	100	100	0	100	0	0	
94	Heterogeneous nuclear ribonucleoproteins C1/C2	HNRPC_MOUSE	34 kDa	100	100	100	100	100	100	100	0	100	100	100	100	100	0	0	0	0	0	0	100	100	100	0	
95	Caprin-1	CAPR1_HUMAN	78 kDa	0	0	0	0	100	100	0	0	0	0	0	0	0	0	0	100	100	100	100	0	100	0	0	
96	Protein S100-A6	S10A6_MOUSE	10 kDa	0	0	0	0	100	100	100	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
97	Serine/arginine-rich splicing factor 1	SRSF1_CHICK	28 kDa	0	0	0	0	100	100	100	0	0	0	0	0	0	0	0	0	0	0	100	100	100	0	0	
98	Phosphoglycerate mutase 1	PGAM1_BOVIN	29 kDa	100	100	100	0	100	100	0	0	100	100	100	100	0	0	0	0	0	0	0	0	0	0	0	
99	Cluster of Transferrin receptor protein 1	TFR1_HUMAN	85 kDa	100	100	100	100	100	100	100	100	100	100	100	100	0	0	0	100	100	100	100	0	100	0	0	



110	Cluster of Triosephosphate isomerase	TPIS_HUMAN	31 kDa	100 %	100 %	100 %	100 %	100 %	100 %	100 %	0	100 %	100 %	100 %	100 %	100 %	0	0	0	100 %	100 %	100 %	0	0	0	0	0
110.1	Triosephosphate isomerase	TPIS_HUMAN	31 kDa	100 %	100 %	100 %	100 %	100 %	100 %	100 %	0	100 %	100 %	100 %	100 %	100 %	0	0	0	99%	100 %	100 %	0	0	0	0	0
111	Proteolipid protein 2	PLP2_HUMAN	17 kDa	0	0	0	0	0	100 %	100 %	100 %	0	0	0	0	0	0	0	0	0	0	0	100 %	100 %	100 %	0	0
112	SAP domain-containing ribonucleoprotein	SARNP_HUMAN	24 kDa	0	100 %	100 %	100 %	0	0	100 %	100 %	0	0	0	0	0	0	0	0	100 %	100 %	100 %	100 %	100 %	100 %	100 %	100 %
113	Multifunctional protein ADE2	PUR6_HUMAN	47 kDa	100 %	100 %	100 %	100 %	100 %	100 %	100 %	0	100 %	0	0	0	100 %	0	0	0	0	0	0	0	0	0	0	0
114	Proteasome subunit alpha type-1	PSA1_HUMAN	30 kDa	100 %	100 %	100 %	100 %	100 %	0	0	0	100 %	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
115	Transcription factor BTF3	BTF3_HUMAN	22 kDa	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	100 %	100 %	100 %	0	0	0	0	0
116	Ribosome-binding protein 1	RRBP1_HUMAN	152 kDa	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	100 %	100 %	0	100 %	100 %	100 %	100 %
117	40S ribosomal protein SA	RSSA_BOVIN	33 kDa	100 %	100 %	100 %	100 %	100 %	0	0	100 %	100 %	100 %	100 %	0	0	0	0	0	0	0	0	100 %	100 %	0	100 %	0
118	Cluster of Neutral amino acid transporter B(0)	AAAT_HUMAN	57 kDa	100 %	100 %	100 %	100 %	100 %	0	0	100 %	100 %	0	0	0	0	0	0	0	100 %	100 %	100 %	0	0	0	0	0
118.1	Neutral amino acid transporter B(0)	AAAT_HUMAN	57 kDa	100 %	100 %	100 %	96%	100 %	100 %	0	0	100 %	100 %	0	0	0	0	0	0	100 %	100 %	100 %	0	0	0	0	0
119	Superoxide dismutase [Cu-Zn]	SODC_HUMAN	16 kDa	0	0	0	0	100 %	0	0	0	0	0	0	0	0	0	0	0	100 %	100 %	100 %	100 %	100 %	100 %	100 %	0
120	Voltage-dependent anion-selective channel protein 2	VDAC2_RAT	32 kDa	0	100 %	100 %	100 %	0	0	0	0	100 %	0	100 %	100 %	100 %	0	0	0	0	0	0	0	0	0	0	0
121	Annexin A5	ANXA5_PANT R	36 kDa	100 %	100 %	100 %	100 %	100 %	100 %	100 %	0	100 %	100 %	100 %	100 %	0	0	0	0	0	0	0	0	100 %	100 %	0	0



132	Variant surface antigen C	VLPC_MYCHR	16 kDa	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	100	100	100	0			
133	Nuclear autoantigenic sperm protein	NASP_HUMAN	85 kDa	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	100	100	100	100	0	0	0	0
134	Proteasome subunit alpha type-6	PSA6_HUMAN	27 kDa	100	100	100	100	100	100	100	100	0	0	0	0	0	0	0	0	0	0	100	0	0	0	0	0	0	0
135	Small ubiquitin-related modifier 2	SUMO2_DANRE	11 kDa	0	100	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	100	0	0	0	100	0	0	0
136	Heterogeneous nuclear ribonucleoprotein K	HNRPK_BOVIN	51 kDa	100	100	100	100	100	100	0	0	100	100	100	100	0	0	0	0	0	0	0	0	0	0	100	100	0	0
137	Cluster of Transitional endoplasmic reticulum ATPase	TERA_HUMAN	89 kDa	0	0	0	0	100	100	0	0	100	100	100	100	0	0	0	0	0	0	0	0	0	0	0	100	0	0
137.1	Transitional endoplasmic reticulum ATPase	TERA_HUMAN	89 kDa	0	0	0	0	100	97%	0	0	100	100	100	100	0	0	0	0	0	0	0	0	0	0	0	100	0	0
138	Stathmin	STMN1_GEKJA	17 kDa	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	100	0	100	100	100	100	100	0
139	Uncharacterized protein C19orf43	CS043_HUMAN	18 kDa	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	100	0	0	0	100	0	0	0
140	T-complex protein 1 subunit eta	TCPH_BOVIN	59 kDa	100	100	0	0	100	0	0	0	100	100	0	0	0	0	0	0	0	0	0	0	0	0	100	0	0	0
141	Thioredoxin	THIO_HUMAN	12 kDa	0	0	0	0	100	100	0	0	0	0	0	0	0	0	0	0	0	0	100	100	0	0	0	0	0	0
142	Cluster of Phosphoglycerate kinase 1	PGK1_HUMAN	45 kDa	100	100	0	0	100	0	0	0	100	0	0	0	0	0	0	0	0	0	0	0	0	0	100	100	100	0
142.1	Phosphoglycerate kinase 1	PGK1_HUMAN	45 kDa	100	100	0	0	100	0	0	0	100	0	0	0	0	0	0	0	0	0	0	0	0	0	100	100	100	0
143	Cluster of CD9 antigen	CD9_HUMAN	25 kDa	100	100	100	0	100	100	0	100	0	0	0	0	0	0	0	0	0	0	100	0	100	0	100	100	0	0

143.	1	CD9 antigen	CD9_HUMAN	25 kDa	100	100	100	0	100	100	0	99%	0	0	0	0	0	0	100	100	100	100	0	0
		Cluster of Acidic leucine-rich nuclear phosphoprotein 32 family member A O	AN32A_HUMAN	29 kDa	0	0	0	0	0	0	0	0	0	0	0	0	0	0	100	100	100	100	0	0
		Acidic leucine-rich nuclear phosphoprotein 32 family member A	AN32A_HUMAN	29 kDa	0	0	0	0	0	0	0	0	0	0	0	0	0	0	100	100	100	100	0	0
		TATA-binding protein-associated factor 2N	RBP56_HUMAN	62 kDa	0	0	0	0	0	0	0	0	0	0	0	0	0	0	100	100	100	100	0	0
		Splicing factor 1	SF01_HUMAN	68 kDa	0	0	0	0	0	0	0	0	0	0	0	0	0	0	100	100	100	100	0	0
		Chloride intracellular channel protein 1	CLIC1_BOVIN	27 kDa	0	0	0	0	0	100	100	0	0	0	0	0	0	0	0	0	0	0	0	0
		Eukaryotic translation initiation factor 4H	IF4H_HUMAN	27 kDa	0	0	0	0	0	0	0	0	0	0	0	0	0	0	100	100	100	100	100	0
		Histone H3, embryonic O	H3_PYCHE	15 kDa	100	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
		PDZ and LIM domain protein 1	PDLI1_HUMAN	36 kDa	0	0	0	0	0	0	0	0	0	0	0	0	0	0	100	100	100	100	0	0
		Cluster of Integrin alpha-3	ITA3_HUMAN	117 kDa	0	0	0	0	100	100	100	100	0	0	0	0	100	0	0	0	0	0	0	100
		Integrin alpha-3	ITA3_HUMAN	117 kDa	0	0	0	0	100	100	100	99%	0	0	0	0	100	0	0	0	0	0	0	100
		Integrin alpha-3	ITA3_MOUSE	117 kDa	0	0	0	0	100	100	0	0	0	0	0	0	0	0	0	0	0	0	100	0
		40S ribosomal protein S12	RS12_MOUSE	15 kDa	100	0	0	0	0	0	0	0	0	0	0	0	0	0	0	100	100	0	0	0





162.1	Proteasome subunit beta type-1	PSB1_BOVIN	26 kDa	98%	100%	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
162.2	Proteasome subunit beta type-1	PSB1_MOUSE	26 kDa	95%	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
163	Microtubule-associated protein 4	MAP4_HUMAN	121 kDa	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	100%	0	0	100%	100%				
164	60S ribosomal protein L7	RL7_BOVIN	29 kDa	0	0	0	0	0	0	0	0	100%	100%	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
165	Splicing factor, proline- and glutamine-rich	SFPO_HUMAN	76 kDa	0	0	0	0	0	0	0	0	100%	100%	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
166	Ran-specific GTPase-activating protein	RANG_HUMAN	23 kDa	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	100%	100%	100%	0	0	0	0		
167	Serine/arginine repetitive matrix protein 2	SRRM2_HUMAN	300 kDa	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	100%	100%	100%	100%	0	0	0	0	
168	Cluster of T-complex protein 1 subunit theta	TCPO_HUMAN	60 kDa	0	0	0	100%	0	0	0	0	0	0	0	100%	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
168.1	T-complex protein 1 subunit theta	TCPO_HUMAN	60 kDa	0	0	0	100%	0	0	0	0	0	0	0	100%	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
169	Proteasome subunit beta type-6	PSB6_HUMAN	25 kDa	100%	100%	100%	100%	0	0	100%	100%	0	0	100%	100%	0	0	100%	0	0	0	0	0	0	0	0	0	0	0	0	
170	Splicing factor 3B subunit 2	SF3B2_HUMAN	100 kDa	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	100%	100%	100%	100%	0	0	0	0
171	5'-nucleotidase Cluster of	5NTD_HUMAN	63 kDa	100%	100%	0	100%	100%	100%	100%	100%	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
172	Dihydropyridyl dehydrogenase, mitochondrial	DLDH_HUMAN	54 kDa	100%	0	100%	0	100%	100%	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	100%	100%	0	0	
172.1	Dihydropyridyl dehydrogenase, mitochondrial	DLDH_HUMAN	54 kDa	99%	0	100%	0	100%	99%	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	97%	100%	0	0



185	CD97 antigen	CD97_HUMAN	92 kDa	0	0	0	0	100	100	0	0	0	0	0	0	0	0	0	0	0	0	0	100	100	100	0
186	Protein deglycase DJ-1	PARK7_HUMAN	20 kDa	0	0	0	0	100		0	0	0	0	0	0	0	0	0	0	100	0	0	0	0	0	0
187	Beta-2-glycoprotein 1	APOH_BOVIN	38 kDa	0	0	0	0	100	100	100	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
188	Small nuclear ribonucleoprotein Sm D3	SMD3_MOUSE	14 kDa	0	100	0	0	100		0	0	100	100	0	0	0	0	0	0	0	0	0	0	0	0	0
189	Prohibitin	PHB_HUMAN	30 kDa	100	100	100	100			100	100		100		0	0	0	0	0	0	0	0	0	0	0	0
190	Aspartate aminotransferase, mitochondrial	AATM_HUMAN	48 kDa	100	%	0	0	0	0	0	0	100	100	100	100	0	0	0	0	0	0	0	0	0	0	0
191	Clathrin heavy chain 1	CLH1_BOVIN	192 kDa	100	100	100	0	0	0	0	0	100		100		0	0	0	0	0	0	0	0	100	0	0
192	Polypyrimidine tract-binding protein 1	PTBP1_HUMAN	57 kDa	100	100	0	0	0	0	0	0	100	100	0	0	0	0	0	0	0	0	0	0	0	0	0
193	Coiled-coil domain-containing protein 86	CCD86_HUMAN	40 kDa	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	100	100	100	100	0	0	0
194	T-complex protein 1 subunit beta	TCPB_HUMAN	57 kDa	100	%	0	0	0	0	0	0	100		100		0	0	0	0	0	0	0	0	0	0	0
195	T-complex protein 1 subunit delta	TCPD_BOVIN	58 kDa	100	%	100	%	0	0	0	0	100	100	100	100	0	0	0	0	0	0	0	0	0	0	0
196	Cluster of T-complex protein 1 subunit epsilon	TCPE_HUMAN	60 kDa	100	%	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
196.1	T-complex protein 1 subunit epsilon	TCPE_HUMAN	60 kDa	99%	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
197	Single-stranded DNA-binding protein, mitochondrial	SSBP_HUMAN	17 kDa	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	100	%	0	0	0	0

198	Acidic leucine-rich nuclear phosphoprotein 32 family member E	AN32E_HUMAN	31 kDa	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	100	100	100	100	0	0	0	0
199	Cluster of Neutral alpha-glucosidase AB	GANAB_HUMAN	107 kDa	100	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
199.1	Neutral alpha-glucosidase AB	GANAB_HUMAN	107 kDa	100	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
200	X-ray repair cross-complementing protein 5	XRCC5_HUMAN	83 kDa	100	100	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
201	Cluster of Plectin	PLEC_HUMAN	532 kDa	0	0	0	0	0	0	0	100	100	100	0	0	0	0	0	0	100	0	0	0	0	0	0	
201.1	Plectin	PLEC_HUMAN	532 kDa	0	0	0	0	0	0	0	100	100	100	0	0	0	0	0	0	0	97%	0	0	0	0	0	
202	Peroxiredoxin-4	PRDX4_HUMAN	31 kDa	100	100	100	100	100	100	100	100	100	0	100	100	0	0	0	0	0	0	0	0	0	0	0	
203	Cluster of Scaffold attachment factor B1	SAFB1_HUMAN	103 kDa	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	100	100	100	0	0	0	0	
203.1	Scaffold attachment factor B1	SAFB1_HUMAN	103 kDa	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	100	0	100	0	0	0	0	
203.2	Scaffold attachment factor B2	SAFB2_HUMAN	107 kDa	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	100	99%	0	0	0	0	0	
204	Tissue factor	TF_HUMAN	33 kDa	0	0	0	0	100	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	100	100	0	
205	60S ribosomal protein L7a	RL7A_MACFA	30 kDa	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	100	0	
206	A-kinase anchor protein 2	AKAP2_HUMAN	95 kDa	100	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	100	100	100	0	0	0	0	
207	Cellular nucleic acid-binding protein	CNBP_BOVIN	19 kDa	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	100	100	100	0	0	0	0	















Proteins Informations					Quantitative Value (Normalized Weighted Spectra)							Quantitative Value (Normalized Average Precursor Intensity)						
					PCM3 vs ctrl		Ru1 vs ctrl		Average			PCM3 vs ctrl		Ru1 vs ctrl		Average		
#	Protein description	Accession Number	Gene Name	Mol. Weight	T-Test : p-value	Fold Change Ref ctrl	T-Test : p-value	Fold Change Ref ctrl	PCM 3	Ru1	ctrl	T-Test : p-value	Fold Change Ref control	T-Test : p-value	Fold Change Ref control	PCM3	Ru1	ctrl
2.1	Actin-2	ACT2_SUIBO	ACT2	42 kDa	0.27	1.6	0.4	0.6	10.49	4.00	6.77	0.039	2	0.35	0.6	1.66E+08	5.02E+07	8.47E+07
2.2	Beta-actin-like protein 2	ACTBL_HUMAN	ACTBL2	42 kDa	0.015	3.7	0.15	3.2	2.06	1.80	0.56	0.04	3	0.36	1.9	1.24E+08	8.05E+07	4.15E+07
2.6	Actin, cytoplasmic 1	ACTB_CRIGR	ACTB	42 kDa	0.065	1.9	0.91	1.1	15.13	8.63	8.15	0.0061	2.4	0.42	1.5	1.02E+08	6.50E+07	4.22E+07
4	Neuroblast differentiation-associated protein AHNAK	AHNAK_HUMAN	AHNAK	629 kDa	0.012	0.6	< 0.00010	0.02	69.19	2.81	117.38	0.89	1	0.00035	0.3	3.66E+07	9.42E+06	3.74E+07
5.1	Heat shock protein HSP 90-beta	HS90B_PONAB	HSP90AB1	83 kDa	< 0.00010	5	0.0016	4.9	73.94	72.49	14.66	< 0.00010	2.1	0.045	1.6	5.71E+07	4.18E+07	2.66E+07
5.2	Endoplasmic	ENPL_HUMAN	HSP90B1	92 kDa	< 0.00010	6.2	< 0.00010	9.9	21.76	34.84	3.53	< 0.00010	4.4	< 0.00010	3.8	4.95E+07	4.22E+07	1.12E+07
5.3	Heat shock protein HSP 90-alpha	HS90A_BOVIN	HSP90AA1	85 kDa	< 0.00010	INF	0.019	INF	15.91	11.28	0.00	< 0.00010	INF	0.02	INF	5.85E+07	2.83E+07	0.00E+00
5.4	Heat shock protein HSP 90-alpha	HS90A_CHICK	HSP90AA1	84 kDa	< 0.00010	26	0.022	18	20.84	14.21	0.79	< 0.00010	6.8	0.081	3.5	5.55E+07	2.84E+07	8.17E+06
6.1	Nucleophosmin	NPM_HUMAN	NPM1	33 kDa	0.071	0.5	0.0052	0.1	45.69	13.26	90.67	0.72	0.9	0.0089	0.2	8.00E+07	2.09E+07	8.88E+07
7	Cluster of Heat shock cognate 71 kDa protein	HSP7C_BOVIN	HSPA8	71 kDa	< 0.00010	7.9	< 0.00010	8.9	119.26	133.96	15.02	< 0.00010	2.6	0.00018	2.2	5.57E+07	4.65E+07	2.15E+07
7.1	Heat shock cognate 71 kDa protein	HSP7C_BOVIN	HSPA8	71 kDa	0.0024	5.8	0.0038	6.2	44.45	48.20	7.71	0.0061	1.9	0.21	1.4	5.48E+07	3.93E+07	2.83E+07
7.2	78 kDa glucose-regulated protein	GRP78_HUMAN	HSPA5	72 kDa	0.00021	6.4	0.0018	10	46.83	75.88	7.31	0.00015	3.1	< 0.00010	2.6	5.72E+07	4.74E+07	1.84E+07
7.3	Heat shock 70 kDa protein cognate 1	HSP7A_DROME	Hsc70-1	71 kDa	0.014	INF	0.15	INF	1.55	0.62	0.00	0.0067	INF	0.15	INF	5.11E+07	2.31E+07	0.00E+00
7.5	Heat shock 70 kDa protein 1	HSP71_PONAB	HSPA1	70 kDa	0.026	INF	1	INF	12.95	0.00	0.00	0.027	INF	1	INF	2.73E+07	0.00E+00	0.00E+00
7.7	78 kDa glucose-regulated protein	GRP78_ICTTR	HSPA5	72 kDa	0.0011	INF	0.059	INF	10.10	8.26	0.00	0.00015	INF	0.027	INF	4.60E+07	2.49E+07	0.00E+00
8.1	Histone H2A type 1-C O	H2A1C_HUMAN	HIST1H2AC	14 kDa	0.11	0.7	< 0.00010	0.2	17.55	4.79	26.10	0.46	1.3	0.74	1.1	2.49E+08	2.10E+08	1.89E+08
8.2	Histone H2A type 2-A	H2A2A_HUMAN	HIST2H2AA3	14 kDa	0.85	1	0.00053	0.2	16.22	3.65	16.85	0.28	2.2	0.58	0.8	1.77E+08	6.24E+07	8.04E+07
9.1	Annexin A2	ANXA2_HUMAN	ANXA2	39 kDa	0.015	2	0.0016	3.9	60.88	117.15	30.36	0.00097	2.3	0.00059	2.4	6.08E+07	6.26E+07	2.61E+07
10.1	Histone H1.4	H14_MOUSE	Hist1h1e	22 kDa	0.0065	0.1	0.0044	0.09	7.24	4.33	48.34	0.00015	0.1	< 0.00010	0.01	2.95E+07	4.04E+06	2.94E+08
10.2	Histone H1.2	H12_HUMAN	HIST1H1C	21 kDa	0.00083	0.08	0.00063	0.04	5.57	2.81	70.50	< 0.00010	0.1	< 0.00010	0.008	3.94E+07	2.81E+06	3.41E+08

10.3	Histone H1.2	H12_BOVIN	HIST1H1C	21 kDa	0.0011	0.08	0.0012	0.06	3.73	3.04	49.55	< 0.00010	0.1	< 0.00010	0.01	4.04E+07	4.04E+06	3.74E+08
11.1	Elongation factor 1-alpha 1	EF1A1_FELCA	EEF1A1	50 kDa	0.0098	2	0.00031	4.4	39.57	89.36	20.12	0.0042	1.7	0.012	2.1	1.17E+08	1.45E+08	6.86E+07
12.1	Keratin, type II cytoskeletal 1	K2C1_HUMAN	KRT1	66 kDa	< 0.00010	2.2	0.14	2.4	54.80	60.70	25.25	0.0001	1.7	0.63	0.9	4.35E+07	2.32E+07	2.56E+07
13.1	Nuclease-sensitive element-binding protein 1	YBOX1_BOVIN	YBX1	36 kDa	0.011	0.5	0.00097	0.3	27.03	15.88	56.79	0.067	0.7	< 0.00010	0.2	4.86E+07	1.34E+07	7.19E+07
13.2	Y-box-binding protein 3	YBOX3_HUMAN	YBX3	40 kDa	0.034	0.06	0.024	0	0.16	0.00	2.52	0.068	0.2	0.025	0	2.20E+06	0.00E+00	1.42E+07
14.1	Nucleolin	NUCL_HUMAN	NCL	77 kDa	0.021	0.3	0.0095	0.2	16.41	9.61	54.76	0.23	0.7	0.035	0.4	2.80E+07	1.62E+07	4.10E+07
15.1	Calreticulin	CALR_HUMAN	CALR	48 kDa	0.0012	2.5	0.56	0.8	29.24	9.38	11.90	0.043	1.7	0.58	0.8	4.33E+07	2.01E+07	2.55E+07
16.1	Tropomyosin alpha-3 chain	TPM3_RAT	Tpm3	29 kDa	0.00016	0.3	< 0.00010	0	6.70	0.00	24.35	0.0088	0.5	< 0.00010	0	3.07E+07	0.00E+00	5.59E+07
17	Far upstream element-binding protein 2	FUBP2_HUMAN	KHSRP	73 kDa	0.016	0.6	0.00066	0.4	32.93	19.28	53.33	0.51	0.9	0.021	0.6	3.97E+07	2.76E+07	4.30E+07
18.1	Histone H4	H4_ACRAS	His4	11 kDa	0.0016	2.6	0.033	2.8	50.74	55.36	19.51	< 0.00010	3.8	0.00063	3.2	1.76E+08	1.51E+08	4.65E+07
19.1	Glyceraldehyde-3-phosphate dehydrogenase	G3P_HUMAN	GAPDH	36 kDa	0.016	1.7	< 0.00010	4	46.51	106.48	26.73	0.017	1.7	< 0.00010	2.5	7.55E+07	1.08E+08	4.37E+07
21.4	Tubulin beta-4B chain	TBB4B_HUMAN	TUBB4B	50 kDa	0.028	3.9	0.11	3.7	3.32	3.13	0.85	0.017	4.6	0.14	3.3	3.38E+07	2.39E+07	7.32E+06
22.1	CD44 antigen	CD44_HUMAN	CD44	82 kDa	0.054	0.7	0.65	0.9	25.12	32.96	37.52	0.27	0.8	0.0006	0.3	9.80E+07	3.50E+07	1.26E+08
23.1	Tubulin alpha chain	TBA_XENLA	tuba	50 kDa	0.59	1.2	0.066	1.9	16.88	25.55	13.66	0.42	1.3	0.021	2	3.87E+07	5.79E+07	2.91E+07
24.1	60 kDa heat shock protein, mitochondrial	CH60_HUMAN	HSPD1	61 kDa	< 0.00010	4.5	0.00047	3.8	34.72	29.02	7.73	< 0.00010	3.3	< 0.00010	3.2	3.79E+07	3.70E+07	1.15E+07
25.1	Alpha-enolase	ENOA_HUMAN	ENO1	47 kDa	0.74	0.9	0.041	2.1	17.21	41.60	19.98	0.56	1.3	0.055	1.9	2.77E+07	4.14E+07	2.20E+07
27	High mobility group protein B1	HMGB1_BOVIN	HMGB1	25 kDa	0.028	0.4	0.0023	0.1	9.69	3.29	23.90	0.42	0.8	0.00052	0.1	4.19E+07	7.88E+06	5.41E+07
28.1	Protein disulfide-isomerase	PDIA1_HUMAN	P4HB	57 kDa	0.00074	4.6	0.066	4.2	19.89	18.13	4.30	0.004	2.4	0.42	1.4	3.41E+07	2.01E+07	1.42E+07
29.1	Galectin-1	LEG1_HUMAN	LGALS1	15 kDa	0.21	1.5	0.86	0.9	16.92	10.59	11.60	0.018	2	0.69	0.8	5.09E+07	2.05E+07	2.54E+07
31	Cluster of 14-3-3 protein epsilon	1433E_SHEEP	YWHAE	29 kDa	0.0087	3.1	0.034	4.9	12.71	20.39	4.16	0.004	3.2	0.12	2.5	2.33E+07	1.83E+07	7.26E+06
32.1	Pyruvate kinase PKM	KPYM_HUMAN	PKM	58 kDa	0.69	0.8	0.18	1.8	11.29	24.12	13.43	0.022	2.2	0.072	2.3	4.09E+07	4.30E+07	1.90E+07
33.1	Keratin, type I cytoskeletal 10	K1C10_HUMAN	KRT10	59 kDa	< 0.00010	3.4	0.12	3.4	23.09	22.90	6.74	0.0026	2.2	0.91	1.1	3.43E+07	1.65E+07	1.57E+07
33.3	Keratin, type I cytoskeletal 19	K1C19_HUMAN	KRT19	44 kDa	0.51	0.6	0.089	0	0.82	0.00	1.43	0.66	1.3	0.022	0	1.48E+07	0.00E+00	1.10E+07
34.1	Alpha-actinin-4	ACTN4_HUMAN	ACTN4	105 kDa	0.098	1.9	0.023	3.9	11.70	24.09	6.19	0.1	1.8	0.12	2	2.40E+07	2.56E+07	1.30E+07

34.3	Alpha-actinin-1	ACTN1_BOVIN	ACTN1	103 kDa	0.068	INF	0.025	INF	1.46	5.74	0.00	0.079	INF	0.024	INF	1.23E+07	1.84E+07	0.00E+00
35	Cofilin-1	COF1_HUMAN	CFL1	19 kDa	0.006	0.5	0.0035	0.3	10.80	6.93	20.42	0.21	0.8	0.0089	0.4	4.81E+07	2.26E+07	6.23E+07
36.1	Glucosidase 2 subunit beta	GLU2B_HUMAN	PRKCSH	59 kDa	0.82	0.9	< 0.00010	0.1	24.15	2.47	25.88	0.37	0.9	< 0.00010	0.2	3.55E+07	8.14E+06	4.03E+07
38	Calnexin	CALX_HUMAN	CANX	68 kDa	0.00016	20	0.55	1.9	10.51	1.00	0.52	0.0083	4.2	0.72	0.7	2.88E+07	4.82E+06	6.88E+06
39	Stress-induced-phosphoprotein 1	STIP1_HUMAN	STIP1	63 kDa	0.14	0.4	0.017	0.09	5.17	1.01	11.60	0.24	0.7	0.0031	0.2	1.54E+07	3.79E+06	2.29E+07
40	Nucleolar and coiled-body phosphoprotein 1	NOLC1_HUMAN	NOLC1	74 kDa	0.045	0.2	0.014	0	2.69	0.00	13.62	0.076	0.3	0.0099	0	3.98E+06	0.00E+00	1.27E+07
41.1	Elongation factor 1-beta	EF1B_HUMAN	EEF1B2	25 kDa	0.0018	0.4	< 0.00010	0.01	8.99	0.27	23.75	0.045	0.5	0.0021	0.06	4.34E+07	5.94E+06	9.40E+07
42	High mobility group protein HMG-I/HMG-Y	HMG1_CRIGR	HMG1	12 kDa	0.37	0.7	0.0013	0.1	4.62	0.67	6.37	0.039	0.4	0.0019	0.06	3.82E+07	5.71E+06	9.88E+07
44	Nucleoprotein TPR	TPR_HUMAN	TPR	267 kDa	0.11	0.4	0.011	0.02	5.65	0.32	13.73	0.66	1.2	0.011	0.09	1.52E+07	1.21E+06	1.31E+07
45	Tumor protein D54	TPD54_HUMAN	TPD52L2	22 kDa	0.034	0.3	0.0011	0	3.41	0.00	10.59	0.029	0.4	0.00057	0	1.52E+07	0.00E+00	4.33E+07
46.1	Elongation factor 1-gamma	EF1G_HUMAN	EEF1G	50 kDa	0.0017	5	0.0027	6.9	14.56	20.00	2.90	< 0.00010	4.4	0.029	3.2	4.32E+07	3.19E+07	9.83E+06
47.1	Serum albumin	ALBU_BOVIN	ALB	69 kDa	0.035	INF	0.066	INF	33.69	10.15	0.00	0.0069	INF	0.082	INF	4.96E+07	1.83E+07	0.00E+00
48.1	Reticulon-4	RTN4_HUMAN	RTN4	130 kDa	0.00034	30	0.014	13	17.28	7.36	0.57	< 0.00010	4.7	0.34	1.8	5.30E+07	2.05E+07	1.13E+07
49.1	Prelamin-A/C	LMNA_HUMAN	LMNA	74 kDa	0.0025	4	< 0.00010	14	13.69	46.05	3.38	0.0055	2.9	0.0047	3.6	2.33E+07	2.89E+07	8.11E+06
50	60S acidic ribosomal protein P1	RLA1_BOVIN	RPLP1	12 kDa	0.14	0.3	0.031	0.04	2.80	0.32	8.54	0.17	0.4	0.024	0.08	1.01E+07	2.01E+06	2.59E+07
51.2	L-lactate dehydrogenase B chain	LDHB_MACFA	LDHB	37 kDa	0.064	INF	0.035	INF	1.23	5.86	0.00	0.061	INF	0.024	INF	1.53E+07	1.94E+07	0.00E+00
53.1	Myosin-9	MYH9_HUMAN	MYH9	227 kDa	0.65	1.2	0.026	0.3	11.29	2.49	9.24	0.39	0.8	0.016	0.3	1.10E+07	4.06E+06	1.45E+07
54	Plasminogen activator inhibitor 1 RNA-binding protein	PAIRB_HUMAN	SERBP1	45 kDa	0.016	0.3	0.0014	0	4.42	0.00	15.45	0.098	0.4	0.0097	0	9.88E+06	0.00E+00	2.57E+07
55	Transketolase	TKT_HUMAN	TKT	68 kDa	0.0017	22	0.043	12	8.69	4.70	0.39	0.00024	24	0.047	12	3.51E+07	1.75E+07	1.48E+06
56	Stress-70 protein, mitochondrial	GRP75_PONAB	HSPA9	74 kDa	< 0.00010	9.3	0.018	6.8	11.28	8.21	1.22	0.052	1.9	0.6	1.3	2.12E+07	1.43E+07	1.10E+07
57.1	THO complex subunit 4	THOC4_HUMAN	ALYREF	27 kDa	0.0072	0	0.0072	0	0.00	0.00	13.62	0.0032	0	0.0032	0	0.00E+00	0.00E+00	2.54E+07
58.1	Alpha-2-HS-glycoprotein	FETUA_BOVIN	AHSG	38 kDa	0.048	INF	1	INF	11.86	0.00	0.00	0.023	INF	1	INF	2.70E+07	0.00E+00	0.00E+00
59	Serine/arginine-rich splicing factor 2	SRSF2_CHICK	SRSF2	26 kDa	0.13	0.5	0.0026	0.03	7.72	0.42	14.20	0.39	1.2	0.00022	0.09	5.60E+07	4.06E+06	4.53E+07
60.1	Voltage-dependent anion-selective channel protein 1	VDAC1_BOVIN	VDAC1	31 kDa	0.00047	7.4	0.00055	23	6.34	19.84	0.86	0.0026	4	0.00093	3.8	3.32E+07	3.15E+07	8.21E+06

61	Heterogeneous nuclear ribonucleoprotein U HLA class I	HNRPU_HUMAN	HNRNPU	91 kDa	0.014	7.2	0.017	11	6.43	9.60	0.89	0.0074	5.1	0.064	5	2.89E+07	2.83E+07	5.64E+06
62.1	histocompatibility antigen, A-2 alpha chain	1A02_HUMAN	HLA-A	41 kDa	0.52	1.6	0.035	10	2.90	18.63	1.80	0.76	1.2	0.32	2.1	1.48E+07	2.53E+07	1.19E+07
63	Small nuclear ribonucleoprotein Sm D1	SMD1_MACFA	SNRPD1	13 kDa	0.022	INF	0.063	INF	3.99	4.86	0.00	0.011	INF	0.066	INF	2.08E+07	2.49E+07	0.00E+00
64	LIM and SH3 domain protein 1	LASP1_HUMAN	LASP1	30 kDa	0.0012	0.3	< 0.00010	0.03	3.88	0.48	14.45	0.0041	0.4	< 0.00010	0.04	2.39E+07	2.65E+06	6.06E+07
65	Far upstream element-binding protein 1	FUBP1_HUMAN	FUBP1	68 kDa	0.3	0.5	0.033	0	3.80	0.00	7.19	0.29	1.7	0.037	0	2.86E+07	0.00E+00	1.64E+07
66	Alpha-1-antipeptinase	A1AT_BOVIN	SERPINA1	46 kDa	0.02	INF	1	INF	11.65	0.00	0.00	0.051	INF	1	INF	2.49E+07	0.00E+00	0.00E+00
68.1	Malate dehydrogenase, mitochondrial	MDHM_HUMAN	MDH2	36 kDa	0.0086	3.7	0.077	4.9	7.70	10.35	2.11	0.00011	5.8	0.092	4.5	2.05E+07	1.58E+07	3.53E+06
70	Heterogeneous nuclear ribonucleoprotein D0	HNRPD_HUMAN	HNRNPD	38 kDa	0.071	0.5	0.0027	0.07	5.19	0.83	11.11	0.5	0.9	< 0.00010	0.07	2.92E+07	2.44E+06	3.44E+07
71	RNA-binding protein FUS	FUS_BOVIN	FUS	52 kDa	0.00052	0.08	0.00048	0.06	1.62	1.28	20.09	0.00012	0.2	< 0.00010	0.05	3.65E+06	1.10E+06	2.32E+07
72.1	Peroxiredoxin-1	PRDX1_HUMAN	PRDX1	22 kDa	< 0.00010	24	0.0024	52	8.70	18.89	0.36	0.0014	8.4	0.0036	6.6	9.66E+07	7.56E+07	1.15E+07
73.1	Heterogeneous nuclear ribonucleoprotein A/B	ROAA_MOUSE	Hnrnpab	31 kDa	0.059	0.5	0.0019	0.07	2.43	0.38	5.18	0.17	0.7	0.00017	0.09	2.23E+07	2.85E+06	3.24E+07
73.2	Heterogeneous nuclear ribonucleoprotein A/B	ROAA_HUMAN	HNRNPAB	36 kDa	0.0079	0.06	0.0049	0	0.39	0.00	6.86	0.022	0.2	0.0016	0	3.63E+06	0.00E+00	1.95E+07
74	Eukaryotic translation initiation factor 4B	IF4B_HUMAN	EIF4B	69 kDa	0.0044	0	0.0044	0	0.00	0.00	11.18	0.0012	0	0.0012	0	0.00E+00	0.00E+00	2.05E+07
76	Superoxide dismutase [Mn], mitochondrial	SODM_PONPY	SOD2	25 kDa	0.091	0.4	0.0055	0.08	5.26	1.00	12.15	0.19	0.6	0.0017	0.09	1.57E+07	2.51E+06	2.75E+07
77.1	Protein disulfide-isomerase A3	PDIA3_HUMAN	PDIA3	57 kDa	0.00085	6.4	0.021	8.5	9.41	12.38	1.46	0.00016	4.3	0.017	3.8	2.63E+07	2.28E+07	6.07E+06
78	4F2 cell-surface antigen heavy chain	4F2_HUMAN	SLC3A2	68 kDa	< 0.00010	16	0.19	4.3	11.99	3.31	0.77	< 0.00010	6.9	0.38	2	2.62E+07	7.70E+06	3.78E+06
79.1	Caveolin-1	CAV1_HORSE	CAV1	21 kDa	0.33	0.5	0.021	0	1.21	0.00	2.38	0.58	0.7	0.029	0	1.11E+07	0.00E+00	1.59E+07
80	Annexin A1	ANXA1_HUMAN	ANXA1	39 kDa	0.048	3.4	0.065	3.6	5.25	5.59	1.56	0.13	2.6	0.49	1.7	1.14E+07	7.33E+06	4.33E+06
81.1	Hemoglobin fetal subunit beta	HBBF_BOVIN		16 kDa	0.025	INF	1	INF	16.66	0.00	0.00	0.021	INF	1	INF	3.38E+07	0.00E+00	0.00E+00
82.1	Protein disulfide-isomerase A6	PDIA6_HUMAN	PDIA6	48 kDa	0.0046	4.9	0.091	4.2	8.35	7.12	1.69	0.0066	7.1	0.065	5.6	1.45E+07	1.14E+07	2.03E+06
85.1	CD166 antigen	CD166_HUMAN	ALCAM	65 kDa	0.028	0.2	0.0064	0	1.24	0.00	6.23	0.029	0.3	0.0022	0	3.13E+06	0.00E+00	1.16E+07
89	Myosin light polypeptide 6	MYL6_BOVIN	MYL6	17 kDa	0.23	0.5	0.011	0	4.10	0.00	8.34	0.27	0.7	< 0.00010	0	2.32E+07	0.00E+00	3.48E+07
90	Complement component 1 Q subcomponent-	C1QBP_HUMAN	C1QBP	31 kDa	0.022	0	0.022	0	0.00	0.00	9.25	0.0098	0	0.0098	0	0.00E+00	0.00E+00	1.77E+07

	binding protein, mitochondrial																	
91.1	Filamin-A	FLNA_HUMAN	FLNA	281 kDa	0.45	1.8	0.0036	11	2.24	14.06	1.26	0.9	0.9	0.082	2.5	6.86E+06	1.88E+07	7.47E+06
92	Fructose-bisphosphate aldolase A	ALDOA_HUMAN	ALDOA	39 kDa	0.082	INF	0.022	INF	0.75	13.83	0.00	0.06	INF	0.027	INF	8.59E+06	1.98E+07	0.00E+00
93	60S acidic ribosomal protein P2	RLA2_BOVIN	RPLP2	12 kDa	0.037	0.2	0.012	0	1.24	0.00	7.95	0.059	0.2	0.0094	0	9.68E+06	0.00E+00	4.00E+07
94	Heterogeneous nuclear ribonucleoproteins C1/C2	HNRPC_MOUSE	Hnrnpc	34 kDa	0.02	5.4	0.012	9.7	6.29	11.33	1.16	0.0036	4.2	0.012	4.5	2.91E+07	3.07E+07	6.89E+06
95	Caprin-1	CAPR1_HUMAN	CAPRIN1	78 kDa	0.025	0.04	0.019	0	0.47	0.00	10.66	0.034	0.1	0.016	0	3.49E+06	0.00E+00	2.88E+07
98	Phosphoglycerate mutase 1	PGAM1_BOVIN	PGAM1	29 kDa	0.0077	INF	0.024	INF	1.72	7.57	0.00	0.0048	INF	0.026	INF	2.12E+07	3.71E+07	0.00E+00
99.1	Transferrin receptor protein 1	TFR1_HUMAN	TFRC	85 kDa	0.018	2.3	0.21	2	5.10	4.45	2.20	0.043	2	0.33	1.6	1.53E+07	1.23E+07	7.73E+06
100	Transgelin-2	TAGL2_HUMAN	TAGLN2	22 kDa	0.002	0.2	< 0.00010	0	1.14	0.00	6.73	0.0099	0.2	0.00085	0	2.28E+06	0.00E+00	1.16E+07
102	Importin subunit beta-1	IMB1_HUMAN	KPNB1	97 kDa	0.24	1.9	0.77	1.3	3.85	2.68	2.04	0.044	3	0.98	1	6.36E+06	2.15E+06	2.11E+06
103	High mobility group protein B2	HMGB2_BOVIN	HMGB2	24 kDa	0.013	0.05	0.0093	0	0.17	0.00	3.66	0.0082	0.07	0.0044	0	3.03E+06	0.00E+00	4.39E+07
104	Serpin H1	SERPH_HUMAN	SERPINH1	46 kDa	0.015	9.3	0.84	1.3	3.66	0.53	0.39	0.024	9.5	0.85	1.3	1.07E+07	1.48E+06	1.13E+06
106	Serine/arginine-rich splicing factor 3	SRSF3_MOUSE	Srsf3	19 kDa	0.017	0.03	0.014	0	0.14	0.00	4.19	0.015	0.06	0.01	0	3.11E+06	0.00E+00	5.56E+07
108.1	Lamina-associated polypeptide 2, isoforms beta/gamma	LAP2B_HUMAN	TMPO	51 kDa	0.019	0.3	0.0011	0	2.45	0.00	8.22	0.01	0.5	< 0.00010	0	2.67E+07	0.00E+00	4.92E+07
109	Brain acid soluble protein 1 O	BASP1_HUMAN	BASP1	23 kDa	0.31	0.5	0.016	0	2.41	0.00	4.47	0.55	0.7	0.0078	0	5.82E+06	0.00E+00	7.93E+06
110.1	Triosephosphate isomerase	TPIS_HUMAN	TPI1	31 kDa	0.0049	4.6	0.023	11	5.32	12.78	1.17	0.15	2	0.2	2.2	2.25E+07	2.53E+07	1.15E+07
112	SAP domain-containing ribonucleoprotein	SARNP_HUMAN	SARNP	24 kDa	0.24	0.6	< 0.00010	0	6.01	0.00	9.96	0.0086	0.5	< 0.00010	0	1.82E+07	0.00E+00	3.66E+07
113	Multifunctional protein ADE2	PUR6_HUMAN	PAICS	47 kDa	< 0.00010	INF	0.21	INF	6.13	1.76	0.00	0.0031	INF	0.25	INF	2.48E+07	5.87E+06	0.00E+00
114	Proteasome subunit alpha type-1	PSA1_HUMAN	PSMA1	30 kDa	0.0084	INF	0.33	INF	5.16	0.27	0.00	0.0035	INF	0.33	INF	1.51E+07	1.66E+06	0.00E+00
116	Ribosome-binding protein 1	RRBP1_HUMAN	RRBP1	152 kDa	0.019	0	0.019	0	0.00	0.00	10.03	0.0097	0	0.0097	0	0.00E+00	0.00E+00	8.74E+06
117	40S ribosomal protein SA	RSSA_BOVIN	RPSA	33 kDa	0.026	5.4	0.054	7.7	4.87	6.95	0.90	0.047	3.3	0.26	2.3	2.23E+07	1.54E+07	6.70E+06
119	Superoxide dismutase [Cu-Zn]	SODC_HUMAN	SOD1	16 kDa	0.0025	0.04	0.0017	0	0.28	0.00	7.05	0.0074	0.1	0.0022	0	4.69E+06	0.00E+00	4.50E+07
120	Voltage-dependent anion-selective channel protein 2	VDAC2_RAT	Vdac2	32 kDa	0.061	INF	0.029	INF	2.63	6.12	0.00	0.1	INF	0.026	INF	2.66E+07	2.02E+07	0.00E+00



121	Annexin A5	ANXA5_PANTR	ANXA5	36 kDa	0.0013	6	0.079	5.4	4.88	4.40	0.81	0.008	5	0.16	3.7	1.47E+07	1.08E+07	2.96E+06
123	Chaperone protein dnaK2	DNAK2_PROMA	dnaK2	68 kDa	0.033	INF	1	INF	3.85	0.00	0.00	0.1	INF	1	INF	6.20E+07	0.00E+00	0.00E+00
124.1	Nucleoside diphosphate kinase B	NDKB_BOVIN	NME2	17 kDa	1	INF	0.024	INF	0.00	4.21	0.00	1	INF	0.032	INF	0.00E+00	2.25E+07	0.00E+00
126	Hepatoma-derived growth factor	HDGF_HUMAN	HDGF	27 kDa	0.11	0.3	0.0069	0	1.32	0.00	4.15	0.028	0.2	0.0045	0	3.54E+06	0.00E+00	1.75E+07
127	Keratin, type I cytoskeletal 9	K1C9_HUMAN	KRT9	62 kDa	0.0045	15	0.52	3.1	6.23	1.34	0.43	0.025	6.3	0.94	1.1	1.52E+07	2.64E+06	2.41E+06
130	Heterogeneous nuclear ribonucleoprotein D-like	HNRDL_RAT	Hnrnpdl	35 kDa	0.012	0.05	0.0084	0	0.35	0.00	7.30	0.0069	0.1	0.0013	0	3.56E+06	0.00E+00	2.94E+07
133	Nuclear autoantigenic sperm protein	NASP_HUMAN	NASP	85 kDa	0.047	0	0.047	0	0.00	0.00	4.02	0.025	0	0.025	0	0.00E+00	0.00E+00	1.26E+07
134	Proteasome subunit alpha type-6	PSA6_HUMAN	PSMA6	27 kDa	0.00097	INF	0.26	INF	5.46	3.59	0.00	0.00017	INF	0.15	INF	4.60E+07	7.43E+06	0.00E+00
136	Heterogeneous nuclear ribonucleoprotein K	HNRPK_BOVIN	HNRNPK	51 kDa	0.022	7.3	0.075	6.7	3.64	3.33	0.50	0.012	5	0.18	2.8	1.73E+07	9.88E+06	3.49E+06
138	Stathmin O	STMN1_GEKJA	STMN1	17 kDa	0.0059	0	0.0059	0	0.00	0.00	3.53	0.00061	0	0.00061	0	0.00E+00	0.00E+00	2.98E+07
143.1	CD9 antigen	CD9_HUMAN	CD9	25 kDa	0.064	3.1	0.023	0	2.53	0.00	0.81	0.36	1.7	0.046	0	2.04E+07	0.00E+00	1.23E+07
145	TATA-binding protein-associated factor 2N	RBP56_HUMAN	TAF15	62 kDa	0.022	0	0.022	0	0.00	0.00	5.40	0.035	0	0.035	0	0.00E+00	0.00E+00	2.10E+07
146	Splicing factor 1	SF01_HUMAN	SF1	68 kDa	0.029	0	0.029	0	0.00	0.00	2.98	0.026	0	0.026	0	0.00E+00	0.00E+00	9.49E+06
148	Eukaryotic translation initiation factor 4H O	IF4H_HUMAN	EIF4H	27 kDa	0.023	0	0.023	0	0.00	0.00	2.67	0.0082	0	0.0082	0	0.00E+00	0.00E+00	1.60E+07
150	PDZ and LIM domain protein 1 O	PDL1_HUMAN	PDLIM1	36 kDa	0.021	0	0.021	0	0.00	0.00	2.57	0.033	0	0.033	0	0.00E+00	0.00E+00	9.48E+06
154	Heterogeneous nuclear ribonucleoprotein H	HNRH1_HUMAN	HNRNPH1	49 kDa	0.024	5.3	0.094	4.6	4.30	3.75	0.82	0.046	2.8	0.77	1.3	1.29E+07	5.82E+06	4.65E+06
156.1	Proteasome subunit alpha type-7	PSA7_HUMAN	PSMA7	28 kDa	0.014	INF	0.15	INF	3.53	0.92	0.00	0.0092	INF	0.15	INF	2.89E+07	6.33E+06	0.00E+00
157	Cytoskeleton-associated protein 4	CKAP4_HUMAN	CKAP4	66 kDa	0.021	14	0.33	0	3.28	0.00	0.23	0.028	8.2	0.33	0	1.40E+07	0.00E+00	1.70E+06
159.1	Eukaryotic initiation factor 4A-l	IF4A1_MACFA	EIF4A1	46 kDa	0.45	1.8	0.011	5	3.18	9.09	1.81	0.9	1.1	0.28	1.6	1.31E+07	1.98E+07	1.22E+07
160.1	Kinectin	KTN1_HUMAN	KTN1	156 kDa	0.015	0.2	0.0012	0	0.99	0.00	4.30	0.024	0.3	< 0.00010	0	5.50E+06	0.00E+00	1.57E+07
167	Serine/arginine repetitive matrix protein 2	SRRM2_HUMAN	SRRM2	300 kDa	0.067	0	0.067	0	0.00	0.00	2.78	0.02	0	0.02	0	0.00E+00	0.00E+00	1.66E+07
169	Proteasome subunit beta type-6	PSB6_HUMAN	PSMB6	25 kDa	0.0092	INF	0.15	INF	5.57	4.29	0.00	0.0012	INF	0.062	INF	4.26E+07	1.13E+07	0.00E+00
170	Splicing factor 3B subunit 2	SF3B2_HUMAN	SF3B2	100 kDa	0.02	0	0.02	0	0.00	0.00	2.11	0.024	0	0.024	0	0.00E+00	0.00E+00	1.82E+07
171	5'-nucleotidase	5NTD_HUMAN	NT5E	63 kDa	0.00034	INF	1	INF	4.04	0.00	0.00	< 0.00010	INF	1	INF	1.73E+07	0.00E+00	0.00E+00

173	Peptidyl-prolyl cis-trans isomerase FKBP1A	FKB1A_BOVIN	FKBP1A	12 kDa	0.032	0	0.032	0	0.00	0.00	1.53	0.023	0	0.023	0	0.00E+00	0.00E+00	1.56E+07
175	Prohibitin-2	PHB2_HUMAN	PHB2	33 kDa	0.026	INF	0.028	INF	3.25	2.74	0.00	0.025	INF	0.031	INF	1.25E+07	1.27E+07	0.00E+00
176.1	GTP-binding nuclear protein Ran	RAN_CHICK	RAN	24 kDa	0.2	INF	0.02	INF	0.47	2.75	0.00	0.16	INF	0.021	INF	6.40E+06	2.62E+07	0.00E+00
177	Proliferation marker protein Ki-67 O	KI67_HUMAN	MKI67	359 kDa	0.021	0	0.021	0	0.00	0.00	1.99	0.03	0	0.03	0	0.00E+00	0.00E+00	7.03E+06
179	RNA-binding protein EWS	EWS_HUMAN	EWSR1	68 kDa	0.04	0	0.04	0	0.00	0.00	3.02	0.013	0	0.013	0	0.00E+00	0.00E+00	1.42E+07
182	Eukaryotic translation initiation factor 6	IF6_HUMAN	EIF6	27 kDa	0.33	INF	0.022	INF	0.21	5.44	0.00	0.33	INF	0.027	INF	1.57E+06	1.67E+07	0.00E+00
189	Prohibitin	PHB_HUMAN	PHB	30 kDa	0.021	INF	0.06	INF	1.70	2.03	0.00	0.025	INF	0.065	INF	1.31E+07	1.18E+07	0.00E+00
190	Aspartate aminotransferase, mitochondrial	AATM_HUMAN	GOT2	48 kDa	0.33	INF	0.031	INF	0.34	3.81	0.00	0.33	INF	0.046	INF	4.77E+06	1.91E+07	0.00E+00
193	Coiled-coil domain-containing protein 86	CCD86_HUMAN	CCDC86	40 kDa	0.02	0	0.02	0	0.00	0.00	2.46	0.03	0	0.03	0	0.00E+00	0.00E+00	1.40E+07
195	T-complex protein 1 subunit delta	TCPD_BOVIN	CCT4	58 kDa	0.068	INF	0.027	INF	1.22	3.25	0.00	0.082	INF	0.038	INF	6.10E+06	1.03E+07	0.00E+00
198	Acidic leucine-rich nuclear phosphoprotein 32 family member E	AN32E_HUMAN	ANP32E	31 kDa	0.021	0	0.021	0	0.00	0.00	2.80	0.037	0	0.037	0	0.00E+00	0.00E+00	1.15E+07
202	Peroxiredoxin-4	PRDX4_HUMAN	PRDX4	31 kDa	< 0.00010	INF	0.15	INF	5.25	2.23	0.00	< 0.00010	INF	0.065	INF	4.28E+07	2.04E+07	0.00E+00
216	40S ribosomal protein S21	RS21_BOVIN	RPS21	9 kDa	0.025	0	0.025	0	0.00	0.00	1.95	0.023	0	0.023	0	0.00E+00	0.00E+00	9.21E+06
221	Eukaryotic initiation factor 4A-III	IF4A3_DANRE	eif4a3	46 kDa	0.014	INF	0.049	INF	1.17	2.14	0.00	0.0061	INF	0.021	INF	1.18E+07	1.03E+07	0.00E+00
225	Prothymosin alpha	PTMA_BOVIN	PTMA	12 kDa	0.059	0	0.059	0	0.00	0.00	2.21	0.029	0	0.029	0	0.00E+00	0.00E+00	2.58E+07
235	40S ribosomal protein S28	RS28_BOVIN	RPS28	8 kDa	0.023	0	0.023	0	0.00	0.00	1.58	0.024	0	0.024	0	0.00E+00	0.00E+00	8.94E+06

**Table S2.1.** Differential proteins

Proteins Informations				Quantitative Value (Normalized Weighted Spectra)		Quantitative Value (Normalized Average Precursor Intensity)	
#	Identified Proteins	Accession Number	Gene name	Ru1 vs control			
				T-Test: p-value	Fold Change Ref control	T-Test: p-value	Fold Change Ref control
34.3	Alpha-actinin-1	ACTN1_BOVIN	ACTN1	0.025	INF	0.024	INF
4	Neuroblast differentiation-associated protein AHNAK	AHNK_HUMAN	AHNAK	< 0.00010	0.02	0.00035	0.3
85	CD166 antigen	CD166_HUMAN	ALCAM	0.0064	0	0.0022	0
92	Fructose-bisphosphate aldolase A	ALDOA_HUMAN	ALDOA	0.022	INF	0.027	INF
57	THO complex subunit 4	THOC4_HUMAN	ALYREF	0.0072	0	0.0032	0
9	Annexin A2	ANXA2_HUMAN	ANXA2	0.0016	3.9	0.00059	2.4
90	Complement component 1 Q subcomponent-binding protein, mitochondrial	C1QBP_HUMAN	C1QBP	0.022	0	0.0098	0
95	Caprin-1	CAPR1_HUMAN	CAPRIN1	0.019	0	0.016	0
35	Cofilin-1	COF1_HUMAN	CFL1	0.0035	0.3	0.0089	0.4
11	Elongation factor 1-alpha 1	EF1A1_FELCA	EEF1A1	0.00031	4.4	0.012	2.1
41	Elongation factor 1-beta	EF1B_HUMAN	EEF1B2	< 0.00010	0.01	0.002	0.06
46	Elongation factor 1-gamma	EF1G_HUMAN	EEF1G	0.0027	6.9	0.029	3.2
74	Eukaryotic translation initiation factor 4B	IF4B_HUMAN	EIF4B	0.0044	0	0.0012	0
182	Eukaryotic translation initiation factor 6	IF6_HUMAN	EIF6	0.022	INF	0.027	INF
65	Far upstream element-binding protein 1	FUBP1_HUMAN	FUBP1	0.033	0	0.037	0
71	RNA-binding protein FUS	FUS_BOVIN	FUS	0.00048	0.06	< 0.00010	0.05
19	Glyceraldehyde-3-phosphate dehydrogenase	G3P_HUMAN	GAPDH	< 0.00010	4	< 0.00010	2.5
10	Histone H1.4	H14_MOUSE	H1F4	0.044	0.09	< 0.00010	0.01
18	Histone H4	H4_ACRAS	H4	0.033	2.8	0.00063	3.2
10.2	Histone H1.2	H12_HUMAN	HIST1H1C	0.00063	0.04	< 0.00010	0.008
42	High mobility group protein HMG-I/HMG-Y	HMGA1_CRIGR	HMGA1	0.0013	0.1	0.0019	0.06
27	High mobility group protein B1	HMGB1_BOVIN	HMGB1	0.0023	0.1	0.00052	0.1
73	Heterogeneous nuclear ribonucleoprotein A/B	ROAA_MOUSE	HNRNPAB	0.002	0.03	0.00031	0.1

94	Heterogeneous nuclear ribonucleoproteins C1/C2	HNRPC_MOUSE	HNRNPC	0.012	9.7	0.012	4.5
70	Heterogeneous nuclear ribonucleoprotein D0	HNRPD_HUMAN	HNRNPD	0.0027	0.07	< 0.00010	0.07
130	Heterogeneous nuclear ribonucleoprotein D-like	HNRDL_RAT	HNRNPDL	0.0084	0	0.0013	0
24	60 kDa heat shock protein, mitochondrial	CH60_HUMAN	HSP60	0.00047	3.8	< 0.00010	3.2
5.3	Heat shock protein HSP 90-alpha	HS90A_BOVIN	HSP90AA1	0.019	INF	0.02	INF
5.2	Endoplasmic	ENPL_HUMAN	HSP90B1	< 0.00010	9.9	< 0.00010	3.8
7.2	78 kDa glucose-regulated protein	GRP78_HUMAN	HSPA5	0.0018	10	< 0.00010	2.6
7	Heat shock cognate 71 kDa protein	HSP7C_BOVIN	HSPA8	< 0.00010	8.9	0.00018	2.2
64	LIM and SH3 domain protein 1	LASP1_HUMAN	LASP1	< 0.00010	0.03	< 0.00010	0.04
51.2	L-lactate dehydrogenase B chain	LDHB_MACFA	LDHB	0.035	INF	0.024	INF
49	Prelamin-A/C	LMNA_HUMAN	LMNA	< 0.00010	14	0.0047	3.6
53	Myosin-9 O	MYH9_HUMAN	MYH9	0.026	0.3	0.016	0.3
89	Myosin light polypeptide 6	MYL6_BOVIN	MYL6	0.011	0	< 0.00010	0
14	Nucleolin	NUCL_HUMAN	NCL	0.0095	0.2	0.035	0.4
40	Nucleolar and coiled-body phosphoprotein 1	NOLC1_HUMAN	NOLC1	0.014	0	0.0099	0
6	Nucleophosmin	NPM_HUMAN	NPM1	0.0052	0.1	0.0089	0.2
77	Protein disulfide-isomerase A3	PDIA3_HUMAN	PDIA3	0.021	8.5	0.017	3.8
98	Phosphoglycerate mutase 1 O	PGAM1_BOVIN	PGAM1	0.024	INF	0.026	INF
72	Peroxiredoxin-1 O	PRDX1_HUMAN	PRDX1	0.0027	33	0.0047	5.4
36	Glucosidase 2 subunit beta	GLU2B_HUMAN	PRKCSH	< 0.00010	0.1	< 0.00010	0.2
50	60S acidic ribosomal protein P1	RLA1_BOVIN	RPLP1	0.031	0.04	0.024	0.08
93	60S acidic ribosomal protein P2	RLA2_BOVIN	RPLP2	0.012	0	0.0094	0
116	Ribosome-binding protein 1	RRBP1_HUMAN	RRBP1	0.019	0	0.0097	0
112	SAP domain-containing ribonucleoprotein	SARNP_HUMAN	SARNP	< 0.00010	0	< 0.00010	0
54	Plasminogen activator inhibitor 1 RNA-binding protein	PAIRB_HUMAN	SERBP1	0.0014	0	0.0097	0
119	Superoxide dismutase [Cu-Zn]	SODC_HUMAN	SOD1	0.0017	0	0.0022	0
76	Superoxide dismutase [Mn], mitochondrial	SODM_PONPY	SOD2	0.0055	0.08	0.0017	0.09
59	Serine/arginine-rich splicing factor 2	SRSF2_CHICK	SRSF2	0.0026	0.03	0.00022	0.09

39	Stress-induced-phosphoprotein 1	STIP1_HUMAN	STIP1	0.017	0.09	0.0031	0.2
145	TATA-binding protein-associated factor 2N	RBP56_HUMAN	TAF15	0.022	0	0.035	0
100	Transgelin-2	TAGL2_HUMAN	TAGLN2	< 0.00010	0	0.00085	0
108	Lamina-associated polypeptide 2, isoforms beta/gamma	LAP2B_HUMAN	TMPO	0.0011	0	< 0.00010	0
45	Tumor protein D54	TPD54_HUMAN	TPD52L2	0.0011	0	0.00057	0
16	Tropomyosin alpha-3 chain	TPM3_RAT	TPM3	< 0.00010	0	< 0.00010	0
44	Nucleoprotein TPR O	TPR_HUMAN	TPR	0.011	0.02	0.011	0.09
60	Voltage-dependent anion-selective channel protein 1	VDAC1_BOVIN	VDAC1	0.00055	23	0.00093	3.8
120	Voltage-dependent anion-selective channel protein 2	VDAC2_RAT	VDAC2	0.029	INF	0.026	INF
13	Nuclease-sensitive element-binding protein 1	YBOX1_BOVIN	YBX1	0.00097	0.3	< 0.00010	0.2

**Table S2.2.** List of quantified proteins for Ru1 vs control comparison using two label-free quantitative methods (Normalized weighted spectra and normalized Average Precursor Intensity)

Proteins Informations				Quantitative Value (Normalized Weighted Spectra)		Quantitative Value (Normalized Average Precursor Intensity)	
				PMC3 vs control			
#	Identified Proteins	Accession Number	Gene name	T-Test : p-value	Fold Change Ref control	T-Test : p-value	Fold Change Ref control
58	Alpha-2-HS-glycoprotein	FETUA_BOVIN	AHSG	0.048	INF	0.023	INF
47	Serum albumin	ALBU_BOVIN	ALB	0.035	INF	0.0069	INF
9	Annexin A2	ANXA2_HUMAN	ANXA2	0.015	2	0.00097	2.3
38	Calnexin	CALX_HUMAN	CANX	0.00016	20	0.0083	4.2
46	Elongation factor 1-gamma	EF1G_HUMAN	EEF1G	0.0017	5	< 0.00010	4.4
18	Histone H4	H4_ACRAS	H4	0.0016	2.6	< 0.00010	3.8
94	Heterogeneous nuclear ribonucleoproteins C1/C2	HNRPC_MOUSE	HNRNPC	0.02	5.4	0.0036	4.2
61	Heterogeneous nuclear ribonucleoprotein U	HNRPU_HUMAN	HNRNPU	0.014	7.2	0.0074	5.1
5.3	Heat shock protein HSP 90-alpha	HS90A_BOVIN	HSP90AA1	< 0.00010	INF	< 0.00010	INF

5	Heat shock protein HSP 90-beta	HS90B_PONAB	HSP90AB1	< 0.00010	7	< 0.00010	2.2
5.2	Endoplasmic	ENPL_HUMAN	HSP90B1	< 0.00010	6.2	< 0.00010	4.4
7.5	Heat shock 70 kDa protein 1	HSP71_PONAB	HSPA1	0.026	INF	0.027	INF
7.2	78 kDa glucose-regulated protein	GRP78_HUMAN	HSPA5	0.00021	6.4	0.00015	3.1
7	Heat shock cognate 71 kDa protein	HSP7C_BOVIN	HSPA8	< 0.00010	7.9	< 0.00010	2.6
24	60 kDa heat shock protein, mitochondrial	CH60_HUMAN	HSP60	< 0.00010	4.5	< 0.00010	3.3
127	Keratin, type I cytoskeletal 9	K1C9_HUMAN	KRT9	0.0045	15	0.025	6.3
49	Prelamin-A/C	LMNA_HUMAN	LMNA	0.0025	4	0.0055	2.9
68	Malate dehydrogenase, mitochondrial	MDHM_HUMAN	MDH2	0.0086	3.7	0.00011	5.8
28	Protein disulfide-isomerase	PDIA1_HUMAN	P4HB	0.00074	4.6	0.004	2.4
113	Multifunctional protein ADE2	PUR6_HUMAN	PAICS	< 0.00010	INF	0.0031	INF
77	Protein disulfide-isomerase A3	PDIA3_HUMAN	PDIA3	0.00085	6.4	0.00016	4.3
82	Protein disulfide-isomerase A6	PDIA6_HUMAN	PDIA6	0.0046	4.9	0.0066	7.1
72	Peroxiredoxin-1	PRDX1_HUMAN	PRDX1	< 0.00010	16	0.0014	8.4
202	Peroxiredoxin-4	PRDX4_HUMAN	PRDX4	< 0.00010	INF	< 0.00010	INF
114	Proteasome subunit alpha type-1	PSA1_HUMAN	PSMA1	0.0084	INF	0.0035	INF
134	Proteasome subunit alpha type-6	PSA6_HUMAN	PSMA6	0.00097	INF	0.00017	INF
169	Proteasome subunit beta type-6	PSB6_HUMAN	PSMB6	0.0092	INF	0.0012	INF
48	Reticulon-4	RTN4_HUMAN	RTN4	0.00034	30	< 0.00010	4.7
78	4F2 cell-surface antigen heavy chain	4F2_HUMAN	SLC3A2	< 0.00010	16	< 0.00010	6.9
99	Transferrin receptor protein 1	TFR1_HUMAN	TFRC	0.018	2.3	0.043	2
55	Transketolase	TKT_HUMAN	TKT	0.0017	22	0.00024	24
60	Voltage-dependent anion-selective channel protein 1	VDAC1_BOVIN	VDAC1	0.00047	7.4	0.0026	4
31	14-3-3 protein epsilon	1433E_SHEEP	YWHAE	0.0087	3.1	0.004	3.2
81	Hemoglobin fetal subunit beta	HBBF_BOVIN	HBB	0.026	INF	0.02	INF
85	CD166 antigen	CD166_HUMAN	ALCAM	0.028	0.2	0.029	0.3
57	THO complex subunit 4	THOC4_HUMAN	ALYREF	0.0072	0	0.0032	0

90	Complement component 1 Q subcomponent-binding protein, mitochondrial	C1QBP_HUMAN	C1QBP	0.022	0	0.0098	0
95	Caprin-1	CAPR1_HUMAN	CAPRIN1	0.025	0.04	0.034	0.1
41	Elongation factor 1-beta	EF1B_HUMAN	EEF1B2	0.0018	0.4	0.045	0.5
74	Eukaryotic translation initiation factor 4B	IF4B_HUMAN	EIF4B	0.0044	0	0.0012	0
71	RNA-binding protein FUS	FUS_BOVIN	FUS	0.00052	0.08	0.00012	0.2
10.2	Histone H1.2	H12_HUMAN	HIST1H1C	0.00083	0.08	< 0.00010	0.1
10	Histone H1.4	H14_MOUSE	H1F4	0.0065	0.1	0.00015	0.1
130	Heterogeneous nuclear ribonucleoprotein D-like	HNRDL_RAT	HNRNPDL	0.012	0.05	0.0069	0.1
116	Ribosome-binding protein 1	RRBP1_HUMAN	RRBP1	0.019	0	0.0097	0
119	Superoxide dismutase [Cu-Zn]	SODC_HUMAN	SOD1	0.0025	0.04	0.0074	0.1
145	TATA-binding protein-associated factor 2N	RBP56_HUMAN	TAF15	0.022	0	0.035	0
100	Transgelin-2	TAGL2_HUMAN	TAGLN2	0.002	0.2	0.0099	0.2
108	Lamina-associated polypeptide 2, isoforms beta/gamma	LAP2B_HUMAN	TMPO	0.019	0.3	0.01	0.5
45	Tumor protein D54	TPD54_HUMAN	TPD52L2	0.034	0.3	0.029	0.4
16	Tropomyosin alpha-3 chain	TPM3_RAT	TPM3	0.00011	0.3	0.0081	0.5

**Table S2.3.** List of quantified proteins for PMC3 vs control comparison using two label-free quantitative methods (Normalized weighted spectra and normalized Average Precursor Intensity)

#	Accession Number	Coefficient of Variation on Normalized Weighted Spectra									Coefficient of Variation on Normalized Average Precursor Intensity								
		ctrl	ctrl pool 1	ctrl pool 2	PMC 3	PMC3 pool 1	PMC3 pool 2	Ru1	Ru1 pool 1	Ru1 pool 2	ctrl	ctrl pool 1	ctrl pool 2	PMC 3	PMC3 pool 1	PMC3 pool 2	Ru1	Ru1 pool 1	Ru1 pool 2
1	VIME_HUMAN	18%	6%	5%	19%	5%	25%	23%	6%	6%	30%	17%	32%	33%	25%	26%	56%	19%	21%
2	ACT2_SUIBO	94%	27%	20%	25%	19%	29%	78%	43%	84%	38%	27%	5%	7%	9%	5%	69%	25%	74%
3	TRY1_BOVIN	24%	25%	18%	22%	8%	23%	47%	8%	7%	25%	23%	30%	55%	23%	32%	32%	24%	21%
4	AHNK_HUMAN	39%	15%	7%	14%	18%	5%	120%	74%	200%	36%	15%	47%	24%	13%	30%	110%	71%	200%
5	HS90B_PONAB	80%	12%	24%	32%	21%	18%	44%	15%	18%	28%	22%	25%	14%	12%	13%	28%	11%	26%
6	NPM_HUMAN	75%	41%	52%	30%	40%	19%	140%	68%	NaN%	60%	42%	72%	48%	37%	61%	140%	71%	NaN%

7	HSP7C_BOVIN	100%	79%	46%	30%	36%	19%	21%	13%	21%	45%	69%	17%	18%	12%	25%	22%	11%	31%
8	H2A1C_HUMAN	42%	45%	46%	47%	47%	50%	83%	40%	120%	45%	51%	38%	160%	55%	150%	120%	31%	120%
9	ANXA2_HUMAN	100%	37%	13%	11%	6%	14%	47%	12%	27%	79%	47%	22%	19%	10%	23%	18%	27%	3%
10	H14_MOUSE	65%	42%	72%	85%	89%	54%	220%	200%	200%	35%	18%	47%	50%	71%	18%	190%	200%	200%
11	EF1A1_FELCA	73%	19%	23%	28%	5%	25%	43%	26%	36%	39%	30%	15%	21%	11%	18%	48%	42%	58%
12	K2C1_HUMAN	20%	13%	21%	26%	14%	10%	100%	38%	30%	24%	15%	22%	17%	21%	14%	43%	28%	45%
13	YBOX1_BOVIN	43%	12%	47%	61%	32%	90%	95%	68%	120%	24%	21%	24%	50%	15%	81%	100%	87%	120%
14	NUCL_HUMAN	75%	7%	47%	45%	9%	74%	110%	28%	NaN%	58%	13%	29%	60%	44%	69%	110%	26%	NaN%
15	CALR_HUMAN	66%	44%	90%	31%	15%	13%	94%	37%	200%	49%	29%	71%	44%	48%	46%	120%	68%	200%
16	TPM3_RAT	34%	21%	33%	88%	12%	100%	NaN%	NaN%	NaN%	34%	34%	38%	53%	25%	72%	NaN%	NaN%	NaN%
17	FUBP2_HUMAN	35%	20%	8%	30%	25%	9%	63%	34%	69%	22%	18%	4%	26%	15%	26%	50%	21%	78%
18	H4_ACRAS	110%	88%	30%	19%	9%	27%	68%	13%	35%	97%	110%	18%	21%	8%	28%	33%	28%	40%
19	G3P_HUMAN	67%	30%	26%	21%	3%	15%	13%	14%	14%	51%	20%	21%	33%	34%	23%	15%	9%	18%
20	H2B1B_HUMAN	41%	20%	26%	15%	10%	20%	35%	37%	18%	48%	36%	34%	42%	25%	59%	45%	47%	39%
21	TBB5_RAT	110%	43%	48%	17%	10%	19%	33%	21%	24%	38%	30%	26%	41%	41%	32%	26%	23%	30%
22	CD44_HUMAN	42%	17%	29%	23%	20%	20%	71%	13%	10%	44%	11%	53%	43%	18%	47%	48%	55%	43%
23	TBA_XENLA	110%	200%	10%	47%	13%	68%	31%	20%	44%	93%	200%	12%	49%	26%	69%	22%	24%	13%
24	CH60_HUMAN	84%	100%	81%	36%	22%	47%	40%	12%	44%	67%	76%	67%	20%	14%	28%	26%	29%	25%
25	ENOA_HUMAN	110%	NaN%	20%	43%	11%	69%	38%	6%	17%	110%	NaN%	14%	46%	27%	67%	27%	26%	30%
26	ADT2_BOVIN	140%	NaN%	64%	110%	120%	110%	160%	200%	120%	110%	NaN%	32%	89%	120%	76%	160%	200%	120%
27	HMGB1_BOVIN	60%	19%	69%	80%	21%	120%	190%	120%	NaN%	46%	20%	69%	78%	46%	120%	190%	120%	NaN%
28	PDIA1_HUMAN	85%	94%	74%	48%	22%	36%	110%	25%	69%	75%	61%	74%	37%	53%	9%	85%	110%	79%
29	LEG1_HUMAN	94%	30%	200%	22%	23%	22%	120%	34%	NaN%	90%	16%	200%	31%	34%	27%	120%	45%	NaN%
30	ITB1_HUMAN	37%	28%	22%	50%	23%	23%	120%	200%	45%	32%	17%	6%	43%	26%	14%	120%	200%	53%
31	1433E_SHEEP	160%	NaN%	90%	34%	35%	23%	90%	25%	200%	140%	NaN%	74%	34%	45%	17%	87%	23%	200%
32	KPYM_HUMAN	110%	NaN%	18%	25%	12%	34%	64%	32%	77%	110%	NaN%	28%	27%	30%	28%	64%	40%	73%
33	K1C10_HUMAN	33%	20%	46%	38%	33%	16%	100%	150%	35%	21%	27%	14%	22%	23%	17%	86%	120%	51%
34	ACTN4_HUMAN	110%	NaN%	21%	53%	15%	70%	83%	25%	130%	110%	NaN%	13%	42%	17%	67%	64%	7%	120%



35	COF1_HUMAN	35%	16%	43%	40%	30%	20%	120%	37%	NaN%	43%	39%	43%	32%	32%	29%	110%	27%	NaN%
36	GLU2B_HUMAN	46%	27%	51%	75%	45%	70%	130%	63%	NaN%	26%	25%	27%	28%	41%	10%	110%	17%	NaN%
37	RL40_DROME	60%	44%	61%	59%	26%	62%	76%	40%	48%	53%	55%	55%	35%	23%	31%	61%	14%	80%
38	CALX_HUMAN	190%	120%	NaN%	52%	27%	81%	200%	130%	NaN%	190%	120%	NaN%	53%	31%	76%	190%	120%	NaN%
39	STIP1_HUMAN	94%	28%	86%	82%	38%	120%	210%	140%	NaN%	56%	5%	72%	73%	38%	120%	210%	140%	NaN%
40	NOLC1_HUMAN	100%	47%	130%	120%	120%	120%	NaN%	NaN%	NaN%	95%	31%	120%	120%	130%	120%	NaN%	NaN%	NaN%
41	EF1B_HUMAN	45%	17%	7%	21%	18%	25%	280%	200%	NaN%	67%	18%	47%	27%	14%	31%	280%	200%	NaN%
42	HMG1A1_CRIGR	56%	19%	80%	87%	75%	120%	280%	NaN%	200%	68%	55%	84%	89%	71%	120%	280%	NaN%	200%
43	H31_MUSPA	200%	200%	140%	140%	170%	130%	200%	130%	NaN%	140%	200%	120%	120%	120%	120%	230%	160%	NaN%
44	TPR_HUMAN	94%	11%	120%	58%	47%	78%	280%	200%	NaN%	84%	14%	120%	49%	27%	68%	280%	200%	NaN%
45	TPD54_HUMAN	69%	68%	76%	140%	150%	120%	NaN%	NaN%	NaN%	64%	33%	71%	120%	130%	120%	NaN%	NaN%	NaN%
46	EF1G_HUMAN	130%	200%	73%	52%	19%	21%	64%	8%	120%	110%	200%	71%	31%	16%	31%	73%	29%	120%
47	ALBU_BOVIN	NaN%	NaN%	NaN%	120%	120%	50%	140%	NaN%	71%	NaN%	NaN%	NaN%	89%	120%	32%	150%	NaN%	81%
48	RTN4_HUMAN	140%	69%	NaN%	58%	4%	76%	92%	37%	200%	140%	69%	NaN%	27%	24%	35%	100%	42%	200%
49	LMNA_HUMAN	150%	NaN%	80%	45%	34%	53%	43%	35%	40%	150%	NaN%	84%	18%	17%	19%	43%	53%	31%
50	RLA1_BOVIN	110%	85%	120%	150%	200%	120%	280%	200%	NaN%	100%	72%	130%	160%	200%	150%	280%	200%	NaN%
51	LDHA_HUMAN	150%	NaN%	81%	59%	44%	69%	52%	35%	20%	140%	NaN%	73%	56%	33%	74%	65%	18%	70%
52	PPIA_SYMSY	50%	18%	24%	57%	33%	75%	98%	25%	200%	43%	50%	42%	51%	27%	79%	100%	37%	200%
53	MYH9_HUMAN	52%	10%	67%	100%	120%	44%	240%	200%	200%	51%	39%	70%	75%	120%	34%	190%	200%	200%
54	PAIRB_HUMAN	71%	10%	71%	68%	68%	77%	NaN%	NaN%	NaN%	95%	67%	79%	71%	80%	73%	NaN%	NaN%	NaN%
55	TKT_HUMAN	280%	NaN%	200%	68%	44%	87%	110%	78%	200%	280%	NaN%	200%	54%	24%	70%	120%	69%	200%
56	GRP75_PONAB	88%	69%	120%	43%	14%	69%	89%	15%	200%	89%	71%	120%	44%	22%	67%	100%	52%	200%
57	THOC4_HUMAN	90%	30%	130%	NaN%	NaN%	NaN%	NaN%	NaN%	NaN%	80%	32%	120%	NaN%	NaN%	NaN%	NaN%	NaN%	NaN%
58	FETUA_BOVIN	NaN%	NaN%	NaN%	130%	NaN%	57%	NaN%	NaN%	NaN%	NaN%	NaN%	NaN%	110%	NaN%	22%	NaN%	NaN%	NaN%
59	SRSF2_CHICK	75%	35%	69%	49%	32%	68%	280%	200%	NaN%	46%	13%	72%	49%	28%	74%	280%	200%	NaN%
60	VDAC1_BOVIN	150%	NaN%	77%	50%	31%	74%	60%	11%	12%	140%	NaN%	74%	46%	26%	68%	33%	39%	32%
61	HNRPU_HUMAN	210%	NaN%	130%	82%	37%	69%	93%	33%	200%	190%	NaN%	120%	63%	38%	68%	110%	48%	200%

62	1A02_HUMAN	140%	NaN%	72%	140%	NaN%	69%	110%	NaN%	18%	140%	NaN%	69%	140%	NaN%	73%	120%	NaN%	48%
63	SMD1_MACFA	NaN%	NaN%	NaN%	110%	110%	120%	140%	69%	NaN%	NaN%	NaN%	NaN%	96%	85%	120%	140%	71%	NaN%
64	LASP1_HUMAN	46%	45%	54%	80%	80%	91%	280%	200%	NaN%	43%	39%	26%	65%	67%	67%	280%	200%	NaN%
65	FUBP1_HUMAN	120%	41%	NaN%	68%	67%	75%	NaN%	NaN%	NaN%	120%	46%	NaN%	85%	68%	120%	NaN%	NaN%	NaN%
66	A1AT_BOVIN	NaN%	NaN%	NaN%	110%	NaN%	11%	NaN%	NaN%	NaN%	NaN%	NaN%	NaN%	130%	NaN%	60%	NaN%	NaN%	NaN%
67	SRSF7_BOVIN	120%	55%	200%	79%	38%	120%	160%	88%	NaN%	100%	35%	200%	89%	48%	120%	140%	74%	NaN%
68	MDHM_HUMAN	200%	NaN%	130%	55%	51%	54%	110%	22%	NaN%	190%	NaN%	120%	25%	26%	29%	110%	30%	NaN%
69	NACAM_HUMAN	140%	72%	NaN%	NaN%	NaN%	NaN%	NaN%	NaN%	NaN%	140%	74%	NaN%	NaN%	NaN%	NaN%	NaN%	NaN%	NaN%
70	HNRPD_HUMAN	69%	33%	77%	76%	35%	89%	280%	200%	NaN%	44%	11%	68%	50%	38%	69%	280%	200%	NaN%
71	FUS_BOVIN	56%	37%	37%	200%	NaN%	130%	280%	200%	NaN%	31%	14%	46%	210%	NaN%	140%	280%	200%	NaN%
72	PRDX1_HUMAN	150%	200%	120%	44%	19%	68%	75%	38%	70%	160%	200%	140%	58%	12%	75%	61%	63%	67%
73	ROAA_MOUSE	72%	30%	70%	76%	56%	76%	200%	130%	NaN%	50%	13%	82%	54%	27%	69%	190%	120%	NaN%
74	IF4B_HUMAN	83%	48%	120%	NaN%	NaN%	NaN%	NaN%	NaN%	NaN%	70%	35%	120%	NaN%	NaN%	NaN%	NaN%	NaN%	NaN%
75	EF2_PONAB	140%	NaN%	69%	90%	120%	71%	110%	20%	NaN%	140%	NaN%	69%	88%	120%	71%	110%	32%	NaN%
76	SODM_PONPY	76%	67%	9%	100%	200%	39%	280%	NaN%	200%	61%	100%	21%	110%	200%	50%	280%	NaN%	200%
77	PDIA3_HUMAN	160%	NaN%	92%	51%	70%	17%	94%	84%	120%	140%	NaN%	68%	28%	35%	24%	67%	27%	120%
78	4F2_HUMAN	140%	69%	NaN%	25%	27%	25%	150%	84%	NaN%	140%	74%	NaN%	22%	25%	13%	140%	70%	NaN%
79	CAV1_HORSE	110%	120%	120%	200%	200%	170%	NaN%	NaN%	NaN%	120%	130%	120%	140%	200%	120%	NaN%	NaN%	NaN%
80	ANXA1_HUMAN	190%	NaN%	120%	73%	28%	120%	87%	74%	120%	190%	NaN%	120%	81%	59%	120%	120%	120%	130%
81	HBBF_BOVIN	NaN%	NaN%	NaN%	110%	NaN%	29%	NaN%	NaN%	NaN%	NaN%	NaN%	NaN%	110%	NaN%	9%	NaN%	NaN%	NaN%
82	PDIA6_HUMAN	190%	NaN%	120%	55%	45%	72%	110%	21%	NaN%	190%	NaN%	120%	71%	61%	72%	110%	23%	NaN%
83	CH10_HUMAN	280%	200%	NaN%	190%	NaN%	120%	NaN%	NaN%	NaN%	280%	200%	NaN%	190%	NaN%	120%	NaN%	NaN%	NaN%
84	EF1D_HUMAN	74%	40%	70%	95%	130%	79%	190%	120%	NaN%	57%	14%	82%	89%	120%	78%	190%	120%	NaN%
85	CD166_HUMAN	88%	17%	120%	140%	120%	200%	NaN%	NaN%	NaN%	76%	34%	140%	140%	120%	200%	NaN%	NaN%	NaN%
86	PLIN3_PIG	110%	71%	130%	140%	200%	120%	280%	NaN%	200%	93%	71%	130%	170%	200%	120%	280%	NaN%	200%
87	ERP29_HUMAN	52%	27%	67%	63%	43%	54%	190%	120%	NaN%	56%	25%	82%	32%	27%	39%	190%	120%	NaN%

88	ROA2_HUMAN	120%	32%	NaN%	150%	200%	120%	120%	40%	NaN%	110%	32%	NaN%	150%	200%	120%	110%	16%	NaN%
89	MYL6_BOVIN	96%	62%	84%	130%	NaN%	56%	NaN%	NaN%	NaN%	36%	27%	28%	110%	NaN%	15%	NaN%	NaN%	NaN%
90	C1QBP_HUMAN	110%	35%	200%	NaN%	NaN%	NaN%	NaN%	NaN%	NaN%	95%	23%	200%	NaN%	NaN%	NaN%	NaN%	NaN%	NaN%
91	FLNA_HUMAN	150%	NaN%	85%	130%	87%	200%	71%	10%	120%	140%	NaN%	69%	130%	80%	200%	73%	16%	120%
92	ALDOA_HUMAN	NaN%	NaN%	NaN%	150%	81%	NaN%	110%	19%	NaN%	NaN%	NaN%	NaN%	140%	67%	NaN%	110%	31%	NaN%
93	RLA2_BOVIN	98%	23%	200%	210%	NaN%	140%	NaN%	NaN%	NaN%	94%	28%	200%	190%	NaN%	120%	NaN%	NaN%	NaN%
94	HNRPC_MOUSE	150%	NaN%	77%	83%	42%	83%	87%	52%	140%	150%	NaN%	79%	51%	13%	68%	69%	28%	120%
95	CAPR1_HUMAN	110%	26%	200%	190%	NaN%	120%	NaN%	NaN%	NaN%	100%	36%	200%	220%	NaN%	150%	NaN%	NaN%	NaN%
96	S10A6_MOUSE	NaN%	NaN%	NaN%	160%	NaN%	95%	NaN%	NaN%	NaN%	NaN%	NaN%	NaN%	140%	NaN%	71%	NaN%	NaN%	NaN%
97	SRSF1_CHICK	150%	80%	NaN%	140%	NaN%	71%	280%	NaN%	200%	140%	69%	NaN%	140%	NaN%	72%	280%	NaN%	200%
98	PGAM1_BOVIN	NaN%	NaN%	NaN%	91%	75%	120%	110%	25%	NaN%	NaN%	NaN%	NaN%	85%	67%	120%	110%	29%	NaN%
99	TFR1_HUMAN	90%	30%	200%	46%	30%	48%	100%	67%	120%	92%	38%	200%	42%	16%	67%	86%	69%	120%
100	TAGL2_HUMAN	51%	26%	73%	210%	NaN%	140%	NaN%	NaN%	NaN%	67%	61%	75%	190%	NaN%	120%	NaN%	NaN%	NaN%
101	ROA1_HUMAN	NaN%	NaN%	NaN%	190%	120%	NaN%	190%	120%	NaN%	NaN%	NaN%	NaN%	200%	130%	NaN%	210%	140%	NaN%
102	IMB1_HUMAN	160%	200%	120%	68%	31%	120%	190%	120%	NaN%	170%	200%	120%	65%	9%	120%	190%	120%	NaN%
103	HMGB2_BOVIN	94%	60%	160%	280%	200%	NaN%	NaN%	NaN%	NaN%	83%	40%	120%	280%	200%	NaN%	NaN%	NaN%	NaN%
104	SERPH_HUMAN	280%	NaN%	200%	86%	71%	120%	280%	200%	NaN%	280%	NaN%	200%	95%	83%	120%	280%	200%	NaN%
105	PROF1_HUMAN	NaN%	NaN%	NaN%	220%	NaN%	150%	150%	83%	NaN%	NaN%	NaN%	NaN%	190%	NaN%	120%	140%	73%	NaN%
106	SRSF3_MOUSE	100%	30%	200%	280%	NaN%	200%	NaN%	NaN%	NaN%	96%	28%	200%	280%	NaN%	200%	NaN%	NaN%	NaN%
107	MOES_HUMAN	140%	NaN%	71%	46%	20%	71%	85%	19%	200%	140%	NaN%	67%	47%	16%	68%	87%	24%	200%
108	LAP2B_HUMAN	69%	34%	73%	96%	97%	98%	NaN%	NaN%	NaN%	25%	29%	11%	65%	71%	67%	NaN%	NaN%	NaN%
109	BASP1_HUMAN	100%	69%	130%	130%	72%	200%	NaN%	NaN%	NaN%	91%	69%	120%	110%	75%	200%	NaN%	NaN%	NaN%
110	TPIS_HUMAN	140%	70%	NaN%	58%	33%	86%	100%	19%	200%	140%	67%	NaN%	56%	40%	78%	95%	20%	200%
111	PLP2_HUMAN	170%	NaN%	100%	170%	NaN%	100%	NaN%	NaN%	NaN%	150%	NaN%	83%	140%	NaN%	67%	NaN%	NaN%	NaN%

11 2	SARNP_HUMAN	50%	51%	53%	130%	86%	140%	NaN%	NaN%	NaN%	20%	22%	20%	85%	70%	120%	NaN%	NaN%	NaN%
11 3	PUR6_HUMAN	NaN%	NaN%	NaN%	46%	19%	68%	220%	200%	200%	NaN%	NaN%	NaN%	79%	67%	73%	240%	200%	200%
11 4	PSA1_HUMAN	NaN%	NaN%	NaN%	92%	25%	120%	280%	200%	NaN%	NaN%	NaN%	NaN%	81%	28%	160%	280%	200%	NaN%
11 5	BTF3_HUMAN	140%	73%	NaN%	NaN%	NaN%	NaN%	NaN%	NaN%	NaN%	150%	75%	NaN%	NaN%	NaN%	NaN%	NaN%	NaN%	NaN%
11 6	RRBP1_HUMAN	110%	120%	30%	NaN%	NaN%	NaN%	NaN%	NaN%	NaN%	94%	120%	49%	NaN%	NaN%	NaN%	NaN%	NaN%	NaN%
11 7	RSSA_BOVIN	190%	NaN%	120%	86%	41%	120%	110%	78%	200%	190%	NaN%	120%	71%	33%	120%	110%	68%	200%
11 8	AAAT_HUMAN	150%	75%	NaN%	92%	69%	120%	230%	160%	NaN%	150%	79%	NaN%	78%	48%	120%	190%	120%	NaN%
11 9	SODC_HUMAN	73%	38%	68%	280%	NaN%	200%	NaN%	NaN%	NaN%	75%	56%	110%	280%	NaN%	200%	NaN%	NaN%	NaN%
12 0	VDAC2_RAT	NaN%	NaN%	NaN%	140%	67%	NaN%	120%	120%	120%	NaN%	NaN%	NaN%	160%	92%	NaN%	110%	130%	120%
12 1	ANXA5_PANTR	190%	NaN%	120%	49%	22%	73%	120%	35%	NaN%	210%	NaN%	130%	60%	33%	95%	130%	50%	NaN%
12 2	ICAL_HUMAN	200%	200%	200%	NaN%	NaN%	NaN%	NaN%	NaN%	NaN%	240%	200%	200%	NaN%	NaN%	NaN%	NaN%	NaN%	NaN%
12 3	DNAK2_PROMA	NaN%	NaN%	NaN%	120%	NaN%	40%	NaN%	NaN%	NaN%	NaN%	NaN%	NaN%	160%	NaN%	93%	NaN%	NaN%	NaN%
12 4	NDKA_HUMAN	NaN%	NaN%	NaN%	NaN%	NaN%	NaN%	110%	25%	NaN%	NaN%	NaN%	NaN%	NaN%	NaN%	NaN%	120%	40%	NaN%
12 5	PGRC2_HUMAN	68%	74%	72%	69%	14%	72%	140%	82%	200%	77%	73%	94%	49%	17%	76%	130%	94%	200%
12 6	HDFG_HUMAN	89%	31%	200%	220%	NaN%	150%	NaN%	NaN%	NaN%	84%	12%	200%	190%	NaN%	120%	NaN%	NaN%	NaN%
12 7	K1C9_HUMAN	210%	140%	NaN%	77%	71%	83%	280%	NaN%	200%	190%	120%	NaN%	90%	120%	75%	280%	NaN%	200%
12 8	SET_HUMAN	150%	80%	NaN%	280%	200%	NaN%	280%	200%	NaN%	140%	72%	NaN%	280%	200%	NaN%	280%	200%	NaN%
12 9	CUTA_HUMAN	140%	200%	120%	280%	200%	NaN%	NaN%	NaN%	NaN%	150%	200%	120%	280%	200%	NaN%	NaN%	NaN%	NaN%
13 0	HNRDL_RAT	92%	18%	140%	280%	200%	NaN%	NaN%	NaN%	NaN%	71%	17%	120%	280%	200%	NaN%	NaN%	NaN%	NaN%
13 1	HBA_BOVIN	NaN%	NaN%	NaN%	140%	NaN%	71%	NaN%	NaN%	NaN%	NaN%	NaN%	NaN%	140%	NaN%	72%	NaN%	NaN%	NaN%
13 2	VLPC_MYCHR	140%	NaN%	70%	NaN%	NaN%	NaN%	NaN%	NaN%	NaN%	170%	NaN%	100%	NaN%	NaN%	NaN%	NaN%	NaN%	NaN%
13 3	NASP_HUMAN	130%	57%	NaN%	NaN%	NaN%	NaN%	NaN%	NaN%	NaN%	110%	27%	NaN%	NaN%	NaN%	NaN%	NaN%	NaN%	NaN%
13 4	PSA6_HUMAN	NaN%	NaN%	NaN%	68%	20%	92%	240%	200%	200%	NaN%	NaN%	NaN%	56%	43%	70%	190%	200%	200%

13 5	SUMO2_DANRE	190%	200%	200%	280%	200%	NaN%	NaN%	NaN%	NaN%	190%	200%	200%	280%	200%	NaN%	NaN%	NaN%	NaN%
13 6	HNRPK_BOVIN	190%	NaN%	120%	91%	38%	120%	120%	45%	NaN%	190%	NaN%	120%	69%	23%	120%	110%	21%	NaN%
13 7	TERA_HUMAN	280%	NaN%	200%	200%	NaN%	130%	110%	21%	NaN%	280%	NaN%	200%	190%	NaN%	120%	110%	23%	NaN%
13 8	STMN1_GEKJA	87%	69%	81%	NaN%	NaN%	NaN%	NaN%	NaN%	NaN%	64%	70%	68%	NaN%	NaN%	NaN%	NaN%	NaN%	NaN%
13 9	CS043_HUMAN	190%	200%	200%	NaN%	NaN%	NaN%	NaN%	NaN%	NaN%	230%	200%	200%	NaN%	NaN%	NaN%	NaN%	NaN%	NaN%
14 0	TCPH_BOVIN	280%	NaN%	200%	180%	130%	200%	220%	150%	NaN%	280%	NaN%	200%	180%	120%	200%	190%	120%	NaN%
14 1	THIO_HUMAN	210%	140%	NaN%	220%	NaN%	150%	NaN%	NaN%	NaN%	190%	120%	NaN%	190%	NaN%	120%	NaN%	NaN%	NaN%
14 2	PGK1_HUMAN	140%	NaN%	75%	160%	120%	200%	280%	200%	NaN%	140%	NaN%	72%	150%	130%	200%	280%	200%	NaN%
14 3	CD9_HUMAN	110%	120%	120%	89%	100%	83%	NaN%	NaN%	NaN%	110%	120%	120%	88%	110%	67%	NaN%	NaN%	NaN%
14 4	AN32A_HUMAN	140%	120%	150%	NaN%	NaN%	NaN%	NaN%	NaN%	NaN%	130%	120%	130%	NaN%	NaN%	NaN%	NaN%	NaN%	NaN%
14 5	RBP56_HUMAN	110%	20%	NaN%	NaN%	NaN%	NaN%	NaN%	NaN%	NaN%	120%	44%	NaN%	NaN%	NaN%	NaN%	NaN%	NaN%	NaN%
14 6	SF01_HUMAN	120%	35%	NaN%	NaN%	NaN%	NaN%	NaN%	NaN%	NaN%	110%	30%	NaN%	NaN%	NaN%	NaN%	NaN%	NaN%	NaN%
14 7	CLIC1_BOVIN	NaN%	NaN%	NaN%	200%	NaN%	130%	NaN%	NaN%	NaN%	NaN%	NaN%	NaN%	230%	NaN%	150%	NaN%	NaN%	NaN%
14 8	IF4H_HUMAN	110%	47%	200%	NaN%	NaN%	NaN%	NaN%	NaN%	NaN%	92%	36%	200%	NaN%	NaN%	NaN%	NaN%	NaN%	NaN%
14 9	H3_PYCHE	NaN%	NaN%	NaN%	280%	200%	NaN%	NaN%	NaN%	NaN%	NaN%	NaN%	NaN%	280%	200%	NaN%	NaN%	NaN%	NaN%
15 0	PDL1_HUMAN	110%	14%	NaN%	NaN%	NaN%	NaN%	NaN%	NaN%	NaN%	120%	41%	NaN%	NaN%	NaN%	NaN%	NaN%	NaN%	NaN%
15 1	ITA3_HUMAN	230%	NaN%	150%	120%	NaN%	36%	280%	NaN%	200%	190%	NaN%	120%	120%	NaN%	36%	280%	NaN%	200%
15 2	RS12_MOUSE	210%	200%	200%	280%	200%	NaN%	NaN%	NaN%	NaN%	190%	200%	200%	280%	200%	NaN%	NaN%	NaN%	NaN%
15 3	ATPB_MOUSE	190%	NaN%	120%	96%	120%	81%	NaN%	NaN%	NaN%	220%	NaN%	140%	91%	120%	77%	NaN%	NaN%	NaN%
15 4	HNRH1_HUMAN	190%	NaN%	120%	83%	64%	71%	120%	34%	NaN%	190%	NaN%	120%	48%	22%	70%	110%	31%	NaN%
15 5	RCN1_HUMAN	150%	NaN%	81%	280%	NaN%	200%	NaN%	NaN%	NaN%	140%	NaN%	72%	280%	NaN%	200%	NaN%	NaN%	NaN%
15 6	PSA7_HUMAN	NaN%	NaN%	NaN%	100%	42%	200%	190%	120%	NaN%	NaN%	NaN%	NaN%	94%	23%	200%	190%	120%	NaN%
15 7	CKAP4_HUMAN	280%	200%	NaN%	100%	200%	20%	NaN%	NaN%	NaN%	280%	200%	NaN%	95%	200%	26%	NaN%	NaN%	NaN%

15	8	RL6_HUMAN	NaN%	NaN%	NaN%	150%	78%	NaN%	190%	120%	NaN%	NaN%	NaN%	NaN%	140%	73%	NaN%	200%	130%	NaN%
15	9	IF4A1_MACFA	130%	NaN%	58%	140%	67%	NaN%	73%	34%	120%	110%	NaN%	14%	110%	5%	NaN%	69%	36%	120%
16	0	KTN1_HUMAN	70%	43%	110%	160%	130%	200%	NaN%	NaN%	NaN%	53%	36%	74%	140%	120%	200%	NaN%	NaN%	NaN%
16	1	MANF_HUMAN	190%	120%	NaN%	140%	200%	120%	NaN%	NaN%	NaN%	190%	120%	NaN%	150%	200%	120%	NaN%	NaN%	NaN%
16	2	PSB1_BOVIN	NaN%	NaN%	NaN%	220%	140%	NaN%	NaN%	NaN%	NaN%	NaN%	NaN%	NaN%	190%	120%	NaN%	NaN%	NaN%	NaN%
16	3	MAP4_HUMAN	140%	200%	120%	NaN%	NaN%	NaN%	NaN%	NaN%	NaN%	140%	200%	120%	NaN%	NaN%	NaN%	NaN%	NaN%	NaN%
16	4	RL7_BOVIN	NaN%	NaN%	NaN%	NaN%	NaN%	NaN%	190%	120%	NaN%	NaN%	NaN%	NaN%	NaN%	NaN%	NaN%	190%	120%	NaN%
16	5	SFPQ_HUMAN	NaN%	NaN%	NaN%	NaN%	NaN%	NaN%	220%	150%	NaN%	NaN%	NaN%	NaN%	NaN%	NaN%	NaN%	210%	140%	NaN%
16	6	RANG_HUMAN	140%	68%	NaN%	NaN%	NaN%	NaN%	NaN%	NaN%	NaN%	160%	88%	NaN%	NaN%	NaN%	NaN%	NaN%	NaN%	NaN%
16	7	SRRM2_HUMAN	140%	72%	NaN%	NaN%	NaN%	NaN%	NaN%	NaN%	NaN%	110%	11%	NaN%	NaN%	NaN%	NaN%	NaN%	NaN%	NaN%
16	8	TCPQ_HUMAN	NaN%	NaN%	NaN%	280%	200%	NaN%	280%	200%	NaN%	NaN%	NaN%	NaN%	280%	200%	NaN%	280%	200%	NaN%
16	9	PSB6_HUMAN	NaN%	NaN%	NaN%	94%	41%	170%	180%	130%	200%	NaN%	NaN%	NaN%	70%	7%	120%	140%	120%	200%
17	0	SF3B2_HUMAN	110%	10%	NaN%	NaN%	NaN%	NaN%	NaN%	NaN%	NaN%	110%	24%	NaN%	NaN%	NaN%	NaN%	NaN%	NaN%	NaN%
17	1	5NTD_HUMAN	NaN%	NaN%	NaN%	60%	89%	33%	NaN%	NaN%	NaN%	NaN%	NaN%	NaN%	51%	71%	30%	NaN%	NaN%	NaN%
17	2	DLDH_HUMAN	190%	NaN%	120%	120%	130%	120%	NaN%	NaN%	NaN%	190%	NaN%	120%	120%	120%	120%	NaN%	NaN%	NaN%
17	3	FKB1A_BOVIN	120%	39%	NaN%	NaN%	NaN%	NaN%	NaN%	NaN%	NaN%	110%	22%	NaN%	NaN%	NaN%	NaN%	NaN%	NaN%	NaN%
17	4	CD59_HUMAN	NaN%	NaN%	NaN%	280%	NaN%	200%	NaN%	NaN%	NaN%	NaN%	NaN%	NaN%	280%	NaN%	200%	NaN%	NaN%	NaN%
17	5	PHB2_HUMAN	NaN%	NaN%	NaN%	110%	30%	NaN%	120%	33%	NaN%	NaN%	NaN%	NaN%	110%	27%	NaN%	120%	38%	NaN%
17	6	RAN_CHICK	NaN%	NaN%	NaN%	210%	140%	NaN%	110%	10%	NaN%	NaN%	NaN%	NaN%	190%	120%	NaN%	110%	17%	NaN%
17	7	KI67_HUMAN	110%	15%	NaN%	NaN%	NaN%	NaN%	NaN%	NaN%	NaN%	120%	37%	NaN%	NaN%	NaN%	NaN%	NaN%	NaN%	NaN%
17	8	TXND5_HUMAN	280%	200%	NaN%	110%	120%	120%	140%	68%	NaN%	280%	200%	NaN%	110%	120%	120%	160%	91%	NaN%
17	9	EWS_HUMAN	120%	27%	200%	NaN%	NaN%	NaN%	NaN%	NaN%	NaN%	99%	37%	200%	NaN%	NaN%	NaN%	NaN%	NaN%	NaN%
18	0	RL4_HUMAN	NaN%	NaN%	NaN%	280%	200%	NaN%	NaN%	NaN%	NaN%	NaN%	NaN%	NaN%	280%	200%	NaN%	NaN%	NaN%	NaN%

18																			
1	GSTO1_HUMAN	NaN%	NaN%	NaN%	140%	70%	NaN%	NaN%	NaN%	NaN%	NaN%	NaN%	NaN%	150%	79%	NaN%	NaN%	NaN%	NaN%
18																			
2	IF6_HUMAN	NaN%	NaN%	NaN%	280%	200%	NaN%	110%	20%	NaN%	NaN%	NaN%	NaN%	280%	200%	NaN%	110%	31%	NaN%
18																			
3	PSB3_BOVIN	NaN%	NaN%	NaN%	160%	86%	NaN%	NaN%	NaN%	NaN%	NaN%	NaN%	NaN%	140%	69%	NaN%	NaN%	NaN%	NaN%
18																			
4	PSA5_MOUSE	NaN%	NaN%	NaN%	200%	130%	NaN%	NaN%	NaN%	NaN%	NaN%	NaN%	NaN%	190%	120%	NaN%	NaN%	NaN%	NaN%
18																			
5	CD97_HUMAN	150%	NaN%	79%	190%	NaN%	120%	NaN%	NaN%	NaN%	NaN%	NaN%	140%	NaN%	71%	190%	NaN%	120%	NaN%
18																			
6	PARK7_HUMAN	280%	200%	NaN%	280%	NaN%	200%	NaN%	NaN%	NaN%	NaN%	NaN%	280%	200%	NaN%	280%	NaN%	200%	NaN%
18																			
7	APOH_BOVIN	NaN%	NaN%	NaN%	150%	NaN%	77%	NaN%	NaN%	NaN%	NaN%	NaN%	NaN%	NaN%	140%	NaN%	73%	NaN%	NaN%
18																			
8	SMD3_MOUSE	NaN%	NaN%	NaN%	190%	200%	200%	190%	120%	NaN%	NaN%	NaN%	NaN%	190%	200%	200%	190%	120%	NaN%
18																			
9	PHB_HUMAN	NaN%	NaN%	NaN%	110%	16%	NaN%	140%	67%	NaN%	NaN%	NaN%	NaN%	NaN%	110%	28%	NaN%	140%	71%
19																			
0	AATM_HUMAN	NaN%	NaN%	NaN%	280%	200%	NaN%	120%	39%	NaN%	NaN%	NaN%	NaN%	NaN%	280%	200%	NaN%	130%	55%
19																			
1	CLH1_BOVIN	280%	NaN%	200%	140%	67%	NaN%	190%	120%	NaN%	NaN%	NaN%	280%	NaN%	200%	150%	80%	NaN%	200%
19																			
2	PTBP1_HUMAN	NaN%	NaN%	NaN%	190%	120%	NaN%	190%	120%	NaN%	NaN%	NaN%	NaN%	NaN%	190%	120%	NaN%	190%	120%
19																			
3	CCD86_HUMAN	110%	12%	NaN%	NaN%	NaN%	NaN%	NaN%	NaN%	NaN%	NaN%	NaN%	120%	36%	NaN%	NaN%	NaN%	NaN%	NaN%
19																			
4	TCPB_HUMAN	NaN%	NaN%	NaN%	280%	200%	NaN%	190%	120%	NaN%	NaN%	NaN%	NaN%	NaN%	NaN%	280%	200%	NaN%	210%
19																			
5	TCPD_BOVIN	NaN%	NaN%	NaN%	140%	73%	NaN%	110%	32%	NaN%	NaN%	NaN%	NaN%	NaN%	150%	81%	NaN%	120%	48%
19																			
6	TCPE_HUMAN	NaN%	NaN%	NaN%	280%	200%	NaN%	NaN%	NaN%	NaN%	NaN%	NaN%	NaN%	NaN%	NaN%	280%	200%	NaN%	NaN%
19																			
7	SSBP_HUMAN	280%	200%	NaN%	NaN%	NaN%	NaN%	NaN%	NaN%	NaN%	NaN%	NaN%	280%	200%	NaN%	NaN%	NaN%	NaN%	NaN%
19																			
8	AN32E_HUMAN	110%	15%	NaN%	NaN%	NaN%	NaN%	NaN%	NaN%	NaN%	NaN%	NaN%	120%	47%	NaN%	NaN%	NaN%	NaN%	NaN%
19																			
9	GANAB_HUMAN	NaN%	NaN%	NaN%	280%	200%	NaN%	NaN%	NaN%	NaN%	NaN%	NaN%	NaN%	NaN%	NaN%	280%	200%	NaN%	NaN%
20																			
0	XRCC5_HUMAN	NaN%	NaN%	NaN%	210%	140%	NaN%	NaN%	NaN%	NaN%	NaN%	NaN%	NaN%	NaN%	NaN%	190%	120%	NaN%	NaN%
20																			
1	PLEC_HUMAN	280%	200%	NaN%	NaN%	NaN%	NaN%	160%	90%	NaN%	NaN%	NaN%	280%	200%	NaN%	NaN%	NaN%	190%	120%
20																			
2	PRDX4_HUMAN	NaN%	NaN%	NaN%	47%	5%	71%	180%	120%	200%	NaN%	NaN%	NaN%	NaN%	51%	37%	71%	140%	120%
20																			
3	SAFB1_HUMAN	150%	82%	NaN%	NaN%	NaN%	NaN%	NaN%	NaN%	NaN%	NaN%	NaN%	140%	71%	NaN%	NaN%	NaN%	NaN%	NaN%

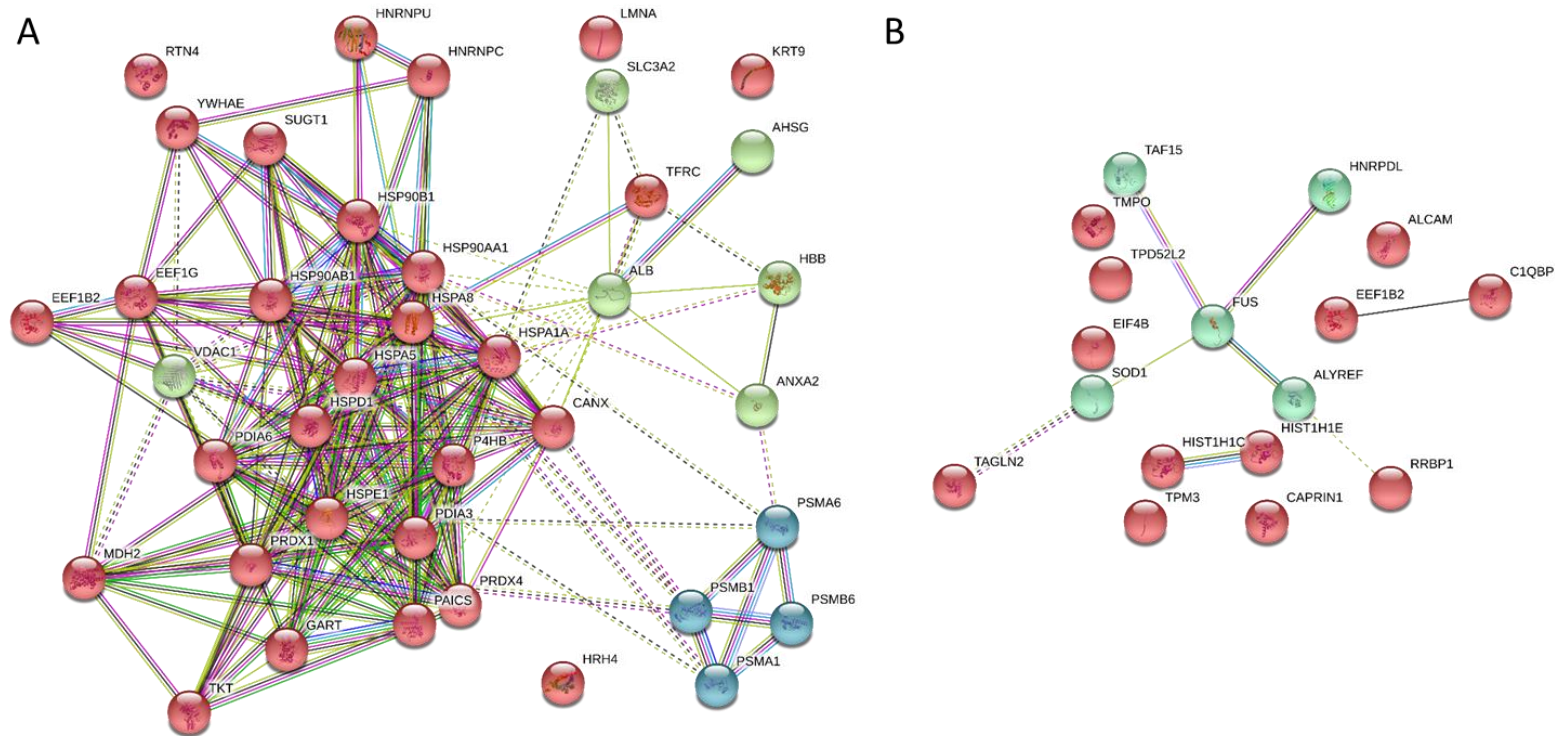




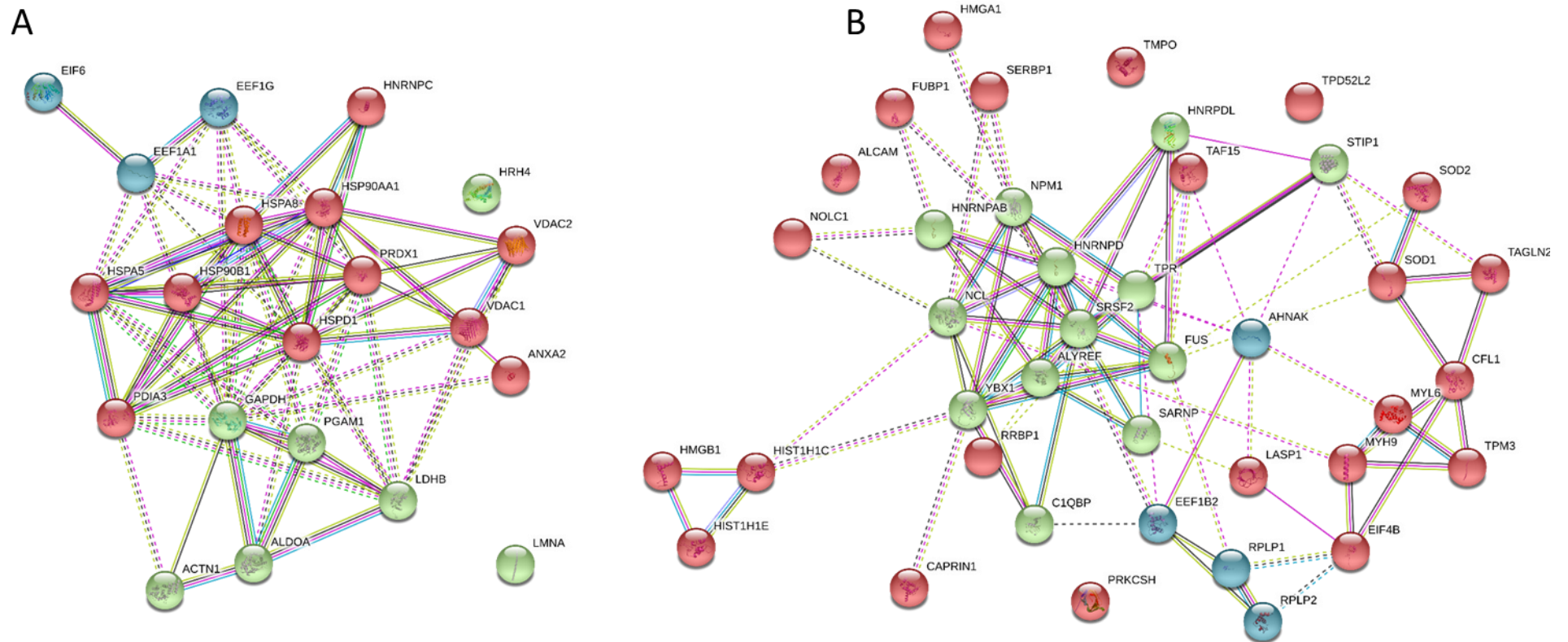


250	CAP1_HUMAN	NaN%	NaN%	NaN%	NaN%	NaN%	NaN%	280%	200%	NaN%	NaN%	NaN%	NaN%	NaN%	NaN%	NaN%	280%	200%	NaN%
251	HNRPQ_HUMAN	NaN%	NaN%	NaN%	NaN%	NaN%	NaN%	280%	200%	NaN%	NaN%	NaN%	NaN%	NaN%	NaN%	NaN%	280%	200%	NaN%
252	SNUT1_HUMAN	150%	75%	NaN%	NaN%	NaN%	NaN%	NaN%	NaN%	NaN%	150%	81%	NaN%	NaN%	NaN%	NaN%	NaN%	NaN%	NaN%
253	FIP1_HUMAN	280%	200%	NaN%	NaN%	NaN%	NaN%	NaN%	NaN%	NaN%	280%	200%	NaN%	NaN%	NaN%	NaN%	NaN%	NaN%	NaN%
254	DBNL_HUMAN	280%	200%	NaN%	NaN%	NaN%	NaN%	NaN%	NaN%	NaN%	280%	200%	NaN%	NaN%	NaN%	NaN%	NaN%	NaN%	NaN%
255	MUC18_HUMAN	150%	81%	NaN%	NaN%	NaN%	NaN%	NaN%	NaN%	NaN%	160%	96%	NaN%	NaN%	NaN%	NaN%	NaN%	NaN%	NaN%
256	MATR3_HUMAN	NaN%	NaN%	NaN%	280%	200%	NaN%	NaN%	NaN%	NaN%	NaN%	NaN%	NaN%	280%	200%	NaN%	NaN%	NaN%	NaN%
257	FAS_HUMAN	NaN%	NaN%	NaN%	280%	200%	NaN%	NaN%	NaN%	NaN%	NaN%	NaN%	NaN%	280%	200%	NaN%	NaN%	NaN%	NaN%
258	ANXA6_HUMAN	NaN%	NaN%	NaN%	280%	200%	NaN%	NaN%	NaN%	NaN%	NaN%	NaN%	NaN%	280%	200%	NaN%	NaN%	NaN%	NaN%
259	RS25_MOUSE	220%	150%	NaN%	NaN%	NaN%	NaN%	NaN%	NaN%	NaN%	190%	120%	NaN%	NaN%	NaN%	NaN%	NaN%	NaN%	NaN%
260	U5S1_BOVIN	NaN%	NaN%	NaN%	NaN%	NaN%	NaN%	280%	200%	NaN%	NaN%	NaN%	NaN%	NaN%	NaN%	NaN%	280%	200%	NaN%
261	RLA0L_HUMAN	NaN%	NaN%	NaN%	280%	200%	NaN%	NaN%	NaN%	NaN%	NaN%	NaN%	NaN%	280%	200%	NaN%	NaN%	NaN%	NaN%
262	XPO2_BOVIN	NaN%	NaN%	NaN%	280%	200%	NaN%	NaN%	NaN%	NaN%	NaN%	NaN%	NaN%	280%	200%	NaN%	NaN%	NaN%	NaN%
263	PEBP1_HUMAN	NaN%	NaN%	NaN%	NaN%	NaN%	NaN%	280%	200%	NaN%	NaN%	NaN%	NaN%	NaN%	NaN%	NaN%	280%	200%	NaN%
264	PP1A_BOVIN	NaN%	NaN%	NaN%	280%	200%	NaN%	NaN%	NaN%	NaN%	NaN%	NaN%	NaN%	280%	200%	NaN%	NaN%	NaN%	NaN%

**Table S2.4.** Coefficients of variation (CV) for all proteomic experiments and for each identified protein.



**Figure S4. STRING network views for PMC3 condition.** A protein-protein interactions (PPI) analysis was carried out using STRING database involving : A) 34 differential proteins more abundant in PMC3 linked via 206 interactions with a PPI enrichment p-value  $<1.0e-16$ , B) 17 differential proteins less abundant in PMC3 linked via 8 interactions with a PPI enrichment p-value at 0.001. Colored lines between the proteins indicate the various types of interaction evidence (light blue and pink : knows interactions from curated databases and experiments respectively; green, red and blue : predicted interactions; light green, black and purple : text mining, co-expression and protein homology analyses).



**Figure S5. STRING network views for Ru1 condition.** A protein-protein interactions (PPI) analysis was carried out using STRING database involving : A) 21 differential proteins more abundant in Ru1 linked via 72 interactions with a PPI enrichment p-value  $<2.22e-16$ , B) 40 differential proteins less abundant in Ru1 linked via 8 interactions with a PPI enrichment p-value  $<1.0e-16$ . Colored lines between the proteins indicate the various types of interaction evidence (light blue and pink : knows interactions from curated databases and experiments respectively; green, red and blue : predicted interactions; light green, black and purple : text mining, co-expression and protein homology analyses).