

Supplementary Table 4: List of total proteins identified in macroalbuminuria group by LC-MS/MS using orbitrap

Accession	Accession ID	Gene symbol	Description	% coverage	% number of proteins	% number of unique peptides	% number of peptides of PSMs	Maximum score	Number of AAs	MW (kDa)	Isoelectric point	Localization	Biological Process	Molecular Function	Signal TM
IP100001593	P42785	MTOR	Lysosomal Pro-X carboxypeptidase	10.89	2	3	3	6	496	55.8	7.21	Lysosome	Proteolysis	Carboxypeptidase activity	Yes 1
IP100002147	P36222	CHI3L1	Chitinase-3-like protein 1	13.05	2	3	4	7.26	383	42.6	8.46	Extracellular region	Polysaccharide catabolic process	Chitinase activity	Yes
IP100003351	Q16610	GSTP1	Isoform 1 of extracellular matrix protein 1	19.07	4	6	14	27.31	540	60.6	6.71	Extracellular region	Positive regulation of signal transduction	Laminin binding	Yes
IP100004500	O15049	N4BP3	NEDD4-binding protein 3	3.49	1	1	1	2.98	544	60.4	8.10	Extrinsic to membrane			No
IP100004573	P01833	PIGR	Polymeric immunoglobulin receptor	18.72	1	11	50	85.90	764	83.2	5.74	Extracellular region			Yes 1
IP100004656	P61769	LYZ	Beta-2-microglobulin	40.34	4	5	47	88.15	119	13.7	6.52	Golgi membrane	Regulation of leukocyte mediated cytotoxicity		Yes
IP100005126	P52799	EFNB2	Ephrin-B2	4.80	1	1	1	3.61	333	36.9	8.85	Plasma membrane	Vasculature development	Ephrin receptor binding	Yes 1
IP100005721	P59665	DEFA1	Neutrophil defensin 1	32.98	2	1	5	12.60	94	10.2	6.99	Extracellular region	Cell killing		Yes
IP100006114	P36955	CD14	Pigment epithelium-derived factor	41.39	3	13	143	218.37	418	46.3	6.38	Extracellular region	Cell proliferation	Enzyme inhibitor activity	Yes
IP100006705	P11684	CETP	Uteroglobin	41.76	1	3	5	8.38	91	10.0	5.06	Extracellular region	Negative regulation of transcription from RNA polymerase II promoter	Enzyme inhibitor activity	Yes
IP100007047	P05109	S100A8	Protein S100-A8	60.22	1	5	14	15.54	93	10.8	7.03	Nucleolus	Defense response	Calcium ion binding	No
IP100007199	Q9UJK5	SERPINA10	Protein Z-dependent protease inhibitor	7.23	1	2	4	11.31	484	55.1	7.64	Extracellular region	Response to wounding	Enzyme inhibitor activity	Yes
IP100007221	P05154		Plasma serine protease inhibitor	32.27	2	10	62	40.10	406	45.7	9.26	Extracellular region	Membrane fusion	Pattern binding	Yes
IP100007240	P05160	SERPING1	Coagulation factor XIII B chain	2.27	1	1	1	3.18	661	75.5	6.39	Extracellular region	Blood coagulation		Yes
IP100007664			Plasma glutamate carboxypeptidase	21.40	4	7	16	23.46	472	51.9	6.18	Cell fraction	Proteolysis	Carboxypeptidase activity	
IP100007778	Q8TC97		Di-N-acetylchitinase	16.10	2	4	11	16.47	385	43.7	6.64	Lysosome	Polysaccharide catabolic process	Chitinase activity	Yes
IP100008753	P80297	MT1X	Metallothionein-1X	19.67	6	1	1	3.20	61	6.1	7.96	Nucleus	Response to inorganic substance	Copper ion binding	No
IP100009027	Q4ZG28	REG1A	Lithostathine-1-alpha	33.73	3	4	19	19.59	166	18.7	5.94	Extracellular region	Positive regulation of cell proliferation	Sugar binding	Yes

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IP100009028	P05452	CLEC3B	Tetranectin	23.27	2	3	3	9	8.62	22.6	5.67	Extracellular region	Skeletal system development	Sugar binding	Yes
IP100009030	P13473	CDH1	Isoform LAMP-2A of Lysosome-associated membrane glycoprotein 2	2.93	3	1	1	2	4.96	44.9	5.63	Cell membrane	Platelet activation		Yes 1
IP100009653	Q9H756	REG1A	Leucine-rich repeat-containing protein 19	3.51	1	1	3	5.38	42.3	370	5.12	Integral to membrane			Yes 1
IP100009823	P15085	CPA1	Carboxypeptidase A1	12.65	5	4	4	9	13.78	47.1	5.76	Extracellular region	Proteolysis	Carboxypeptidase activity	Yes
IP100009865	P13645	KRT10	Keratin, type I cytoskeletal 10	41.78	7	23	24	1492	871.02	58.8	5.21	Cytoskeleton	Ectoderm development	Structural molecule activity	No
IP100010471	Q59GX5		Plastin-2	8.45	2	3	7	13.83	70.2	627	5.43	Cell fraction	Cell activation	Actin binding	No
IP100010675	Q03403	TFF2	Trefoil factor 2	21.71	1	2	4	7.97	14.3	129	5.81	Extracellular region	Digestion	Protein binding	Yes
IP100011229	P07339	CTSD	Cathepsin D	23.54	6	6	6	24	24.61	412	6.54	Lysosome.	Autophagic vacuole formation	Endopeptidase activity	Yes
IP100011252	P07357	C8A	Complement component C8 alpha chain	14.21	1	5	5	9	17.85	584	6.47	Melanosome Extracellular region	Adaptive immune response		Yes
IP100011261	P07360	C8B	Complement component C8 gamma chain	34.16	2	4	4	15	50.01	202	8.31	Extracellular region	Adaptive immune response	Retinoid binding	Yes
IP100011302	P13987	C6	CD59 glycoprotein	25.00	1	4	4	30	25.78	128	6.48	Cell fraction	Cell surface receptor linked signal transduction	Protein binding	Yes
IP100012587	P60484	TPP1	Phosphatidylinositol-3,4,5-trisphosphate 3-phosphatase and dual-specificity protein phosphatase PTEN	9.43	1	1	1	2	3.36	403	6.37	Mitochondrion	Regulation of cyclin-dependent protein kinase activity	Magnesium ion binding	No
IP100012760	Q6NT58	LEP	Leptin	7.78	1	1	1	1	3.80	167	6.37	Extracellular region	Ovulation from ovarian follicle	Hormone activity	Yes
IP100013179	P41222	LEP	Prostaglandin-H2 D-isomerase	42.63	4	4	4	623	837.21	190	7.80	Rough ER	Prostaglandin biosynthetic process	Prostaglandin-D synthase activity	Yes
IP100013682	Q5J1K8	ART3	Isoform 3 of Ecto-ADP-ribosyltransferase 3	6.94	6	2	2	3	6.38	389	6.06	Plasma membrane	Protein amino acid ADP-ribosylation	NAD+ ADP-ribosyltransferase activity	Yes
IP100013885	P31944	OBSCN	Caspase-14	25.62	1	5	5	9	9.40	242	5.58	Lysosome	Proteolysis	Endopeptidase activity	No
IP100013933	P15924		Isoform DPI of desmoplakin	7.18	3	13	13	43	27.91	2871	6.81	Cell junction desmosome	Ectoderm development	Structural molecule activity	No

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IP 00014048	P07998	THBS1	Ribonuclease pancreatic	50.64	1	4	4	134	90.90	17.6	8.79	Extracellular region		Nuclease activity	Yes 1
IP 00014375	Q07075	ENPEP	Glutamyl aminopeptidase	2.61	1	2	2	5	2.37	109.2	5.47	Plasma membrane	Angiogenesis	Aminopeptidase activity	No 1
IP 00015309	Q99456	SECISBP2	Keratin, type I cytoskeletal 12	1.82	1	1	1	1	3.10	53.5	4.78	Cytoskeleton	Sensory perception	Structural molecule activity	No
IP 00016915	Q16270		Insulin-like growth factor-binding protein 7	29.08	1	5	5	9	7.64	29.1	7.90	Extracellular region	Regulation of cell growth	Insulin-like growth factor binding	Yes
IP 00017601	Q1L857	CP	Ceruloplasmin	35.68	8	30	30	335	435.83	122.1	5.72	Extracellular region	Transition metal ion transport	Ferroxidase activity	Yes
IP 00017704	Q14019	CEA	Coactosin-like protein	11.27	1	1	1	1	4.77	15.9	5.67	Cytoskeleton	Defense response	Actin binding	No
IP 00018236	Q6LBL5	GM2A	Ganglioside GM2 activator	15.54	1	2	2	18	29.08	20.8	5.31	Lysosome	Defense response	Beta-N-acetylhexosaminidase activity	Yes
IP 00018953	P27487	DPP4	Dipeptidyl peptidase 4	10.70	2	6	6	27	34.35	88.2	6.04	Cell membrane	Response to hypoxia	Endopeptidase activity	Yes 1
IP 00019359	P35527	THBS4	Keratin, type I cytoskeletal 9	54.09	1	23	23	561	318.70	62.0	5.24	Cytoskeleton	Cytoskeleton organization	Structural molecule activity	No
IP 00019399	P35542		Serum amyloid A-4 protein	8.46	1	1	1	4	9.23	14.7	9.07	Extracellular region	Acute inflammatory response		Yes
IP 00019449	P10153	RNASE2	Non-secretory ribonuclease	19.88	2	3	3	76	36.18	18.3	8.73	Lysosome	RNA catabolic process	Nuclease activity	Yes
IP 00019568	Q69EZ8		Prothrombin (fragment)	32.48	2	13	13	53	104.29	70.0	5.90	Extracellular region	Protein import into nucleus, translocation	Endopeptidase activity	No
IP 00019576	P00742	CP	Coagulation factor X	6.15	1	2	2	3	7.09	54.7	5.94	Cell fraction	Proteolysis	Endopeptidase activity	Yes 1
IP 00019580	Q9JUM2		Plasminogen	9.14	5	5	5	18	20.79	90.5	7.24	Cell fraction	Proteolysis	Endopeptidase activity	Yes
IP 00019581	Q96EF3		Coagulation factor XII	2.93	1	1	1	5	8.73	67.8	7.74	Extracellular region	Kinin cascade	Endopeptidase activity	Yes
IP 00019591	Q53F89	CFB	cDNA FLJ55673, highly similar to complement factor B	24.25	18	14	23	191	181.91	140.9	7.18	Extracellular region	Complement activation	Serine-type endopeptidase activity	Yes
IP 00019943	P43652	MCAM	Afamin	25.71	1	13	13	61	55.38	69.0	5.90	Extracellular region	Vitamin transport	Vitamin E binding	Yes
IP 00019954	Q6BD2	CST6	Cystatin-M	48.32	1	4	4	14	51.72	16.5	8.09	Cornified envelope	Ectoderm development	Enzyme inhibitor activity	Yes
IP 00020091	P19652	ORM2	Alpha-1-acid glycoprotein 2	55.72	1	6	11	179	241.26	23.6	5.11	Extracellular region	Acute-phase response	Binding	Yes
IP 00020986	P51884	PSMD7	Lumican	35.21	3	9	9	78	73.39	38.4	6.61	Extracellular	Sensory perception	Structural molecule activity	Yes

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IP 00020996	P35858	IGFALS	Insulin-like growth factor-binding protein complex acid labile subunit	7.60	2	3	3	11	605	66.0	6.79	Cell fraction	Cell adhesion	Insulin-like growth factor binding	Yes
IP 00021085	O75594	CALB1	Peptidoglycan recognition protein 1	37.24	1	4	4	24	196	21.7	8.59	Extracellular region	Peptidoglycan metabolic process	Pattern binding	Yes
IP 00021304	P35908	KRT2	Keratin, type II cytoskeletal 2	69.61	3	28	34	530	645	65.8	8.00	Cytoskeleton	Cell activation	Structural molecule activity	No
IP 00021794	P10619		epidermal Lysosomal protective protein	7.50	3	2	2	5	480	54.4	6.61	Lysosome	Proteolysis	Carboxypeptidase activity	Yes
IP 00021828	P04080	VTN	Cystatin-B	45.92	1	3	3	5	98	11.1	7.56	Nucleolus	Behavior	Protease binding	No
IP 00021841	P02647	APOA1	Apolipoprotein A-I	43.82	2	13	13	134	267	30.8	5.76	Extracellular region	Regulation of cytokine production	Beta-amyloid binding	Yes
IP 00021854	P02652	APOA2	Apolipoprotein A-II	43.00	1	3	3	16	100	11.2	6.62	Extracellular region	Regulation of cytokine production	Enzyme inhibitor activity	Yes
IP 00021856	P02655	APOC1	Apolipoprotein C-II	20.79	1	1	1	6	101	11.3	4.72	Extracellular region	Cholesterol efflux production	Lipase inhibitor activity	Yes
IP 00021857	P02656	APOC3	Apolipoprotein C-III	16.16	2	1	1	5	99	10.8	5.41	Extracellular region	Neutral lipid metabolic process	Enzyme inhibitor activity	Yes
IP 00021885	P02671	FGA	Isoform 1 of fibrinogen alpha chain	28.52	4	15	15	148	866	94.9	6.01	Cell fraction	Cell activation	Protein binding	Yes
IP 00022331	P04180	ANXA1	Phosphatidylcholine-sterol acyltransferase	13.86	1	3	3	5	440	49.5	6.11	Extracellular region	Cellular amino acid derivative metabolic process	Carboxylesterase activity	Yes 2
IP 00022371	Q68DR3	HRG	Histidine-rich glycoprotein	28.19	1	11	11	99	525	59.5	7.50	Extracellular region	Regulation of blood coagulation	Pattern binding	Yes
IP 00022389	P02741	FGG	Isoform 1 of C-reactive protein	5.36	1	2	2	5	224	25.0	5.63	Extracellular region	Adaptive immune response	Calcium ion binding	Yes
IP 00022391	P02743	APCS	Serum amyloid P-component	11.21	1	2	2	4	223	25.4	6.54	Extracellular region	Acute inflammatory response	Calcium ion binding	Yes
IP 00022394	P02747	C1QC	Complement C1q subcomponent subunit	7.35	1	1	1	2	245	25.8	8.41	Extracellular region	Adaptive immune response		Yes
IP 00022395	P02748	C9	Complement C9 component C9	27.73	1	11	11	44	559	63.1	5.59	Extracellular region	Cytolysis by symbiont of host cells		Yes
IP 00022417	P02750	LRG1	Leucine-rich alpha-2-glycoprotein	36.02	1	7	7	68	347	38.2	6.95	Extracellular region	Fat cell differentiation		Yes

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IP100022426	P02760	AMBIP	Protein AMBP	54.55	2	17	17	2239	1665.87	352	39.0	6.25	Cell fraction	Negative regulation of immune system process	Enzyme inhibitor activity	Yes
IP100022432	P02766		Transferrin	65.31	4	8	8	428	1055.42	147	15.9	5.76	Extracellular region	Transport	Hormone activity	Yes
IP100022488	P02790	PPBP	Hemopexin	44.37	1	12	12	596	812.66	462	51.6	7.02	Extracellular region	Regulation of protein amino acid phosphorylation	Iron ion binding	Yes
IP100022810	P53634		Isoform 1 of dipeptidyl peptidase 1	12.53	1	3	3	36	34.72	463	51.8	6.99	Lysosome	Proteolysis	Endopeptidase activity	No
IP100022895	Q7Z3U3		Alpha-1B-glycoprotein	42.42	4	11	11	181	329.07	495	54.2	5.87	Extracellular region			No
IP100022974	P12273	PIP	Prolactin-inducible protein	32.19	1	3	3	57	142.89	146	16.6	8.05	Extracellular region		Actin binding	Yes
IP100023019	P04278	SHBG	Isoform 1 of sex hormone-binding globulin	22.14	8	5	5	18	34.90	402	43.8	6.71	Lysosome	Reproductive developmental process	Steroid binding	Yes
IP100023728	Q92820	GGH	Gamma-glutamyl hydrolase	32.39	1	7	7	27	23.51	318	35.9	7.11	Lysosome	Glutamine metabolic process	Peptidase activity	Yes
IP100025318	O75368		SH3 domain-binding glutamic acid-rich-like protein	37.72	1	3	3	5	10.79	114	12.8	5.25	Cytoplasm		SH3 domain binding	No
IP100025753	Q02413		Desmoglein-1	6.48	1	4	4	26	23.58	1049	113.7	5.03	Cytosol	Cell-cell junction assembly	Calcium ion binding	Yes
IP100025861	P12830	CDH1	Cadherin-1	17.35	4	8	8	86	56.05	882	97.4	4.73	Plasma membrane	<i>In utero</i> embryonic development	Calcium ion binding	Yes 1
IP100026199	P22352	COL5A1	Glutathione peroxidase 3	19.47	1	3	3	4	12.79	226	25.5	8.05	Cell fraction	Response to reactive oxygen species	Peroxidase activity	Yes
IP100026256	P14384	CPM	Filaggrin	2.51	6	3	3	4	6.38	4061	434.9	9.25	Plasma membrane	Proteolysis	Carboxypeptidase activity	Yes
IP100026926	Q02747	SEMG2	Guanylin	9.57	1	1	1	3	10.30	115	12.4	4.59	Extracellular region	Signal transduction	Hormone activity	Yes 1
IP100027444	P30740	SERPINB1	Leukocyte elastase inhibitor	18.47	1	5	5	20	28.47	379	42.7	6.28	Cytoplasm	Regulation of proteolysis	Enzyme inhibitor activity	No
IP100027462	P06702	S100A9	Protein S100-A9	74.56	2	6	6	58	73.70	114	13.2	6.13	Cytoplasm	Cell motion	Calcium ion binding	No
IP100027482	P08185		Corticosteroid-binding globulin	13.58	1	4	4	14	27.69	405	45.1	6.04	Extracellular region	Steroid metabolic process	Enzyme inhibitor activity	Yes
IP100027547	P81605	DLK1	Dermcidin	32.73	2	3	3	7	9.65	110	11.3	6.54	Extracellular region	Cell killing	Manganese ion binding	Yes

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IP 00028911	Q14118	DAG1	Dystroglycan	3.02	4	2	9	14.32	895	97.4	8.56	Plasma membrane	Morphogenesis of an epithelium	Calcium ion binding	Yes 1
IP 00029039	Q53S56	REG3A	Regenerating islet-derived protein 3-alpha	13.14	1	1	4	16.13	175	19.4	7.64	Cell fraction	Acute inflammatory response	Sugar binding	Yes
IP 00029193	Q04756	KRT17	Hepatocyte growth factor activator	1.83	2	1	1	3.10	655	70.6	7.24	Extracellular region	Proteolysis	Endopeptidase activity	Yes 1
IP 00029235	P24592	PTPRD	Insulin-like growth factor-binding protein 6	6.25	1	1	8	8.57	240	25.3	7.81	Extracellular region	Regulation of cell growth	Insulin-like growth factor binding	Yes
IP 00029260	P08571		Monocyte differentiation antigen CD14	27.20	2	7	111	98.17	375	40.1	6.23	Cell membrane	Regulation of cytokine production	Lipopolysaccharide binding	Yes
IP 00029739	Q14006	CFH	Isoform 1 of complement factor H	13.24	4	10	11	51.54	1231	139.0	6.61	Cell fraction	Immune effector process		Yes
IP 00032179	P01008	SERPINC1	Antithrombin-III	51.94	2	18	292	395.11	464	52.6	6.71	Extracellular region	Response to nutrient	Pattern binding	Yes
IP 00032195	Q16082	HSPB2	Heat shock protein beta-2	6.19	1	1	1	3.20	307	33.1	6.64	Cell fraction	Response to unfolded protein	Enzyme activator activity	No
IP 00032220	Q86U78	AGT	Angiotensinogen	33.40	2	11	187	258.02	485	53.1	6.32	Extracellular region	Ovulation from ovarian follicle	Enzyme inhibitor activity	Yes
IP 00032288	Q9H8J5	MANSC1	MANSC domain-containing protein 1	3.48	1	1	1	3.44	431	46.8	6.54	Integral to membrane			Yes 1
IP 00032291	P01031	C5	Complement C5	7.34	2	7	15	16.92	1676	188.2	6.52	Extracellular region	MAPKK cascade	Enzyme inhibitor activity	Yes
IP 00032293	P01034	CFL1	Cystatin-C	41.10	1	4	202	429.30	146	15.8	8.75	Extracellular region	Defense response	Beta-amylloid binding	Yes 1
IP 00032311	P18428	LBP	Lipopolysaccharide-binding protein	14.97	1	6	34	49.55	481	53.3	6.70	Cell activation	Cell activation	Lipopolysaccharide binding	Yes
IP 00032325	P01040	CSTA	Cystatin-A	53.06	2	3	22	31.18	98	11.0	5.50	Cytoplasm	Ectoderm development	Protease binding	No
IP 00032328	P01042		Isoform HMW of kininogen-1	21.89	4	1	12	54.73	644	71.9	6.81	Extracellular region	Muscle system process	Pattern binding	Yes
IP 00033583	Q96P63	FGB	Serpin B12	4.20	2	1	2	3.48	405	46.2	5.53	Cytoplasm	Regulation of catabolic process	Enzyme inhibitor activity	No
IP 00069985	Q9Y5B2		Junction adhesion molecule	4.25	4	1	1	3.06	259	28.1	8.29	Plasma membrane	Defense response		Yes 1
IP 00103636	Q14508		Isoform 2 of WAP four-disulfide core domain protein 2	43.84	3	2	12	17.88	73	8.1	7.50	Extracellular region	Proteolysis	Enzyme inhibitor activity	Yes 1
IP 00150200	P07307	ASGR2	Isoform 3 of asialoglycoprotein receptor 2	3.83	7	1	1	3.53	287	32.5	5.80	Integral to membrane	Endocytosis	Asialoglycoprotein receptor activity	No 1

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IP100163207	Q96PD5	PGLYRP	Isoform 1 of N-acetylmuramoyl-L-alanine amidase	32.81	2	9	9	42	75.26	62.2	7.55	Extracellular region	Peptidoglycan metabolic process	Pattern binding	Yes
IP100163563	Q96S96	PEBP4	Phosphatidylethanol amine-binding protein 4	31.28	1	3	6	16.30	227	25.7	6.54	Lysosome			Yes
IP100165972	Q6FWH3		Complement factor D preproprotein	43.46	1	7	45	93.02	260	27.8	7.25	Extracellular region	Immune effector process	Endopeptidase activity	Yes
IP100166729	P25311	AZGP1	Zinc-alpha-2-glycoprotein	41.61	6	11	173	106.95	298	34.2	6.05	Extracellular region	Immune response	Nuclease activity	Yes
IP100170635	Q8WVN6	SECTM1	Secreted and transmembrane protein 1	20.97	1	3	114	178.65	248	27.0	7.43	Extracellular region	Immune response	Cytokine activity	Yes 1
IP100176710	Q5VSP4	LCN1P1	Putative lipocalin 1-like protein 1	6.79	2	1	2	3.17	162	17.9	5.00	Extracellular region	Proteolysis	Enzyme inhibitor activity	Yes
IP100186736	Q969P0	IGSF8	Isoform 3 of immunoglobulin superfamily member 8	3.61	2	1	1	3.03	526	55.8	8.78	Integral to membrane	Cell motion		Yes 1
IP100215746	P15090	FABP4	Fatty acid-binding protein, adipocyte	25.00	3	3	16	42.50	132	14.7	7.14	Cell fraction	Cytokine production	Fatty acid binding	No
IP100215894	P01042		Isoform LMW of kininogen-1	32.55	5	2	13	54.73	427	47.9	6.65	Extracellular region , extracellular space	Muscle system process	Pattern binding	Yes
IP100215983	P00915	PLAU	Carbonic anhydrase 1	41.00	4	6	6	18	26.26	28.9	7.12	Golgi apparatus	One-carbon metabolic process	Carbonate dehydratase activity	No
IP100216691	P07737	PFN1	Profilin-1	31.43	1	3	3	9	20.28	15.0	8.27	Cytoskeleton	Embryonic epithelial tube formation	Actin-binding	No
IP100217963	P08779	KRT16	Keratin, type I cytoskeletal 16	43.13	22	13	18	159	88.62	51.2	5.05	Cytoskeleton	Cytoskeleton organization	Structural molecule activity	No
IP100218413	P43251		Biotinidase	15.10	5	6	6	22	40.32	61.1	6.25	Golgi apparatus	Ectoderm development	Biotin carboxylase activity	Yes
IP100218732	Q96P91		Serum paraoxonase/arylesterase 1	14.65	2	4	4	6	12.30	39.7	5.22	Cell fraction	Cellular amino acid derivative metabolic process	Aryldialkyl phosphatase activity	No
IP100218733	P00441	SOD1	Superoxide dismutase (Cu-Zn)	53.90	2	5	5	14	25.57	15.9	6.13	Cytoplasm	MAPKKK cascade	Superoxide dismutase activity	No
IP100218875	Q567T5	FIX	Isoform C of osteopontin	25.44	7	5	5	9	29.23	32.3	4.55	Extracellular region	Skeletal system development	Cytokine activity	Yes
IP100219025	P35754	SAA4	Glutaredoxin-1	47.17	1	2	2	6	15.55	11.8	8.09	Cytosol	Generation of precursor metabolites and energy	Electron carrier activity	No

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Supplementary Table 4: Contd...

Accession	Accession ID	Gene symbol	Description	% coverage	% number of proteins	% number of unique peptides	% number of PSMs	Maximum score	Number of AAs	MW (kDa)	Isoelectric point	Localization	Biological Process	Molecular function	Signal TM
IP100219619	Q9H6X2	FLJ22002	Isoform 3 of anthrax toxin receptor 1	14.48	8	2	2	14	20.38	33.3	6.68	Cell membrane	Actin cytoskeleton reorganization	Actin filament binding	Yes 1
IP100219648	O75379	VAMP4	Isoform 2 of vesicle-associated membrane protein 4	15.00	2	1	1	3.00	140	16.2	6.60	Golgi membrane	Vesicle-mediated transport		No 1
IP100219684	P05413	FABP3	Fatty acid-binding protein, heart	10.53	1	2	2	3	10.39	14.8	6.80	Cytosol	Cellular amino acid derivative metabolic process	Lipid transporter activity	No
IP100219713	P02679	FGB	Isoform gamma-A of fibrinogen gamma chain	32.72	6	10	10	73	54.69	49.5	6.09	Extracellular region	Cell activation	Calcium ion binding	Yes 1
IP100219806	P31151	S100A7	Protein S100-A7	42.57	2	5	5	26	36.50	11.5	6.77	Extracellular region	Response to reactive oxygen species	Calcium ion binding	No
IP100220327	P04264	KRT1	Keratin, type II cytoskeletal 1	60.87	12	32	36	575	340.04	66.0	8.12	Cytoskeleton	Complement activation, lectin pathway	Structural molecule activity	No
IP100221224	Q8IVL7		Aminopeptidase N	26.06	1	18	18	156	268.89	109.5	5.48	Cell fraction	Angiogenesis	Aminopeptidase activity	No
IP100221362	Q9JUL3	PYCARD	Isoform 3 of apoptosis-associated speck-like protein containing a CARD	11.85	3	1	1	3	5.02	15.0	7.44	Cytosol	Regulation of cytokine production	Endopeptidase activity	No
IP100232492	Q14134	TRIM29	Isoform beta of tripartite motif-containing protein 29	3.51	2	1	1	1	3.05	63.8	6.98	Cytoplasm	Transcription	DNA binding	No
IP100289933	Q13477	LSAMP	Isoform 2 of mucosal addressin cell adhesion molecule 1	5.54	3	1	1	9	14.17	28.7	5.80	Membrane	Cell adhesion, immune response		Yes
IP100290085	P19022	KRT4	Cadherin-2	5.41	7	5	5	7	22.56	99.7	4.81	Membrane	Blood vessel development	Calcium ion binding	Yes 1
IP100290315	P10645	C7	Chromogranin-A	22.54	2	5	5	11	15.81	45.7	4.60	Extracellular region	Circulatory system process	Calcium ion binding	Yes
IP100291136	P12109	COL6A1	Collagen alpha-1 (VI) chain	15.66	2	10	10	50	51.32	108.5	5.43	Extracellular region	Cell adhesion	Growth factor binding	Yes
IP100291175	P18206	VCL	Isoform 1 of vinculin	4.41	3	3	3	6	9.74	116.6	6.09	Extracellular region	Cell motion	Actin binding	No
IP100291866	P05155	GAPDH	Plasma protease C1 inhibitor	26.20	3	12	12	125	183.04	55.1	6.55	Extracellular region	Regulation of complement activation	Complement binding	Yes
IP100292530	P19827		Inter-alpha-trypsin inhibitor heavy chain H1	18.44	6	11	11	40	53.82	101.3	6.79	Extracellular region	Cell activation	Enzyme inhibitor activity	Yes 1

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Supplementary Table 4: Contd...

Accession	Accession	Gene symbol	Description	% coverage	% number of proteins	% number of unique peptides	% number of PSMs	Maximum score	Number of AAs	MW (kDa)	Isoelectric point	Localization	Biological process	Molecular function	Signal
IPi00292946	P05543	REG1A	Thyroxine-binding globulin	40.00	1	11	54	78.48	415	46.3	6.30	Extracellular region	Aging	Enzyme inhibitor activity	Yes
IPi00293088	P10253		Lysosomal alpha-glucosidase	20.90	2	11	57	38.34	952	105.3	5.99	Lysosome	Maltose metabolic process	Alpha-glucosidase activity	Yes
IPi00293275	Q8NHS7	PTPRS	Protein tyrosine phosphatase, receptor type, sigma isoform 3 precursor	2.40	7	2	3	4.69	1501	168.3	6.54	Plasma membrane	Protein amino acid dephosphorylation	Phosphoprotein phosphatase activity	Yes 1
IPi00293350	Q99598	TSNAX	Translin-associated protein X	14.14	1	1	1	3.33	290	33.1	6.55	Perinuclear region of cytoplasm	Gamete generation	DNA binding	No
IPi00294004	P07225	PROS1	Vitamin K-dependent protein S	3.55	5	2	5	10.79	676	75.1	5.67	Golgi lumen	Blood coagulation	Enzyme inhibitor activity	Yes
IPi00294395	Q05CV3	C8B	Complement component C8 beta chain	14.38	1	5	16	31.63	591	67.0	8.13	Extracellular region	Adaptive immune response	Protein complex binding	Yes 1
IPi00295414	P39059	TGFBR2	Collagen alpha-1 (XV) chain	2.31	1	2	4	16.88	1388	141.6	5.00	Extracellular region	Angiogenesis	Structural molecule activity	Yes
IPi00296537	P23142	FBLN1	Isoform C of fibulin-1	7.76	8	3	8	14.54	683	74.4	5.24	Extracellular region	Interspecies interaction between organisms	Structural molecule activity	Yes
IPi00296608	P10643		Complement component C7	11.98	1	4	7	36.70	843	93.5	6.48	Extracellular region	Adaptive immune response	Structural molecule activity	Yes
IPi00296777	Q8N4S1		SPARC-like protein 1	16.87	4	2	6	9.68	664	75.2	4.81	Extracellular region	Signal transduction	Calcium ion binding	Yes
IPi00297284	P18065	GM2A	Insulin-like growth factor-binding protein 2 precursor	8.54	3	2	4	10.67	328	35.1	7.50	Extracellular region	Regulation of cell growth	Insulin-like growth factor binding	Yes
IPi00298497	P02675	FGB	Fibrinogen beta chain	42.97	3	14	112	102.53	491	55.9	8.27	Extracellular region	Cell activation	Protein binding	Yes
IPi00298547	Q99497	PARK7	Protein DJ-1	7.94	1	1	1	3.00	189	19.9	6.79	Mitochondrion	Response to reactive oxygen species	Peroxioredoxin activity	No
IPi00298690			43 kDa protein	13.73	6	2	3	5.56	386	43.3	7.02		Cell adhesion	Antigen binding	
IPi00298971	P04004		Vitronectin	21.13	2	8	53	33.25	478	54.3	5.80	Extracellular region	Immune response	Pattern binding	Yes
IPi00299435	Q13790	APOF	Apolipoprotein F precursor	3.99	1	1	1	2.99	326	35.4	5.64	Extracellular region	Lipid transport	Lipid transporter activity	Yes
IPi00299503	P80108	GPLD1	Isoform 1 of phosphatidylinositol-glycan-specific phospholipase D	1.79	1	1	1	3.14	840	92.3	6.37	Extracellular region	GPI anchor metabolic process	Phospholipase activity	Yes

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Supplementary Table 4: Contd...

Accession	Accession	Gene symbol	Description	% coverage	% number of proteins	% number of unique peptides	% number of peptides	Maximum score	Number of AAs	MW (kDa)	Isoelectric point	Localization	Biological process	Molecular function	Signal TM
IP100299547	P80188	LCN2	Isoform 1 of neutrophil gelatinase-associated lipocalin	40.91	2	5	13	42.01	198	22.6	8.91	Extracellular region	Response to virus		Yes
IP100304273	P06727	GSN	Apolipoprotein A-IV	49.24	2	15	171	196.77	396	45.4	5.38	Extracellular region	Response to reactive oxygen species	Lipid transporter activity	Yes
IP100305380	P22692	IGFBP4	Insulin-like growth factor-binding protein 4	12.02	1	3	7	15.42	258	27.9	7.15	Extracellular region	Skeletal system development	Insulin-like growth factor binding	Yes
IP100305469			Adapter molecule crk isoform b	8.33	3	1	1	3.75	204	22.9	5.48	Endosome	Regulation of transcription	SH3/SH2 adaptor activity	
IP100306378	O00187	MASP2	Isoform 2 of mannan-binding lectin serine protease 2	35.68	3	4	22	23.39	185	20.6	5.96	Extracellular region	Complement activation, lectin pathway	Endopeptidase activity	Yes
IP100306483	Q5T0F9	CC2D1B	Isoform 3 of coiled-coil and C2 domain-containing protein 1B	3.38	4	1	1	3.03	532	59.3	9.07				No
IP100328550	P35443		Thrombospondin-4	5.31	5	3	3	6.79	961	105.8	4.68	Extracellular region	Cell motion	Pattern binding	Yes
IP100328609	P29622	SERPINA4	Kallistatin	24.59	1	7	15	28.37	427	48.5	7.75	Extracellular region		Enzyme inhibitor activity	Yes
IP100329775	Q961Y4		Isoform 1 of carboxypeptidase B2	10.17	3	3	3	10.66	423	48.4	7.71	Extracellular region	Proteolysis	Carboxypeptidase activity	Yes
IP100334282	Q92520	FAM3C	Protein FAM3C	28.63	3	4	21	75.86	227	24.7	8.29	Extracellular region	Regulation of transcription, DNA-dependent	Cytokine activity	Yes 1
IP100374563	Q5XG79	MANBA	Agtrin	4.11	2	6	16	22.37	2045	214.7	6.40	Extracellular region		Structural molecule activity	Yes
IP100375426	Q6LAF8	HBA2	Cathepsin H	8.05	2	2	4	10.32	323	36.2	8.10	Lysosome	Proteolysis	Endopeptidase activity	Yes
IP100376379	Q7Z794	DLK1	Keratin, type II cytoskeletal 1b	12.28	1	5	6	35.07	578	61.9	5.99	Cytoskeleton		Structural molecule activity	No
IP100384444	P02533	KRT14	Keratin, type I cytoskeletal 14	41.95	23	8	116	100.61	472	51.5	5.16	Cytoskeleton	Cytoskeleton organization	Structural molecule activity	No
IP100384697	P02768	TTR	Isoform 2 of serum albumin	10.55	10	4	40	26.02	417	47.3	6.35	Extracellular region	Cytolysis by symbiont of host cells	DNA binding	Yes
IP100386975	Q9HB00	DSC1	Isoform 1B of desmocollin-1	8.93	2	5	5	8.25	840	93.8	5.53	Cell fraction	Cell adhesion	Calcium ion binding	Yes 1
IP100395488	Q6EMK4	VASN	Vasorin	20.21	1	7	75	127.25	673	71.7	7.39	Extracellular region			Yes 1
IP100397801	Q5D862	FLG2	Filaggrin-2	6.32	1	6	6	14.63	2391	247.9	8.31	Extracellular region	Ecotoderm development	Structural molecule activity	No
IP100398625	Q86Y23	HRNR	Homerin	17.93	1	15	82	32.61	2850	282.2	10.04	Cornified envelope		Calcium ion binding	No

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Supplementary Table 4: Contd...

Accession	Accession ID	Gene symbol	Description	% coverage	% number of proteins	% number of unique peptides	% number of peptides	% number of PSMs	Maximum score	Number of AAs	MW (kDa)	Isoelectric point	Localization	Biological Process	Molecular Function	Signal TM
IP100410714	Q9BX83	HBA2	Hemoglobin subunit alpha	10.56	1	1	1	3	10.87	142	15.2	8.68	Extracellular region	Gas transport	Oxygen transporter activity	No
IP100413587	P55957	BID	Isoform 1 of BH3-interacting domain death agonist	14.36	3	2	2	2	3.28	195	22.0	5.44	h_death Pathway: Induction of apoptosis through DR and DR/death receptors	Release of cytochrome c from mitochondria	Death receptor binding	No
IP100413958	Q14315	CDH1	Isoform 2 Vasorinof filamin-C	3.23	2	5	5	8	16.56	2692	287.1	5.97	Cytoskeleton	Actin binding	Actin binding	No
IP100414467	Q5KU26	COL1C2	Isoform 1 of collectin-12	1.35	1	1	1	1	2.98	742	81.5	5.69	Integral to membrane	Protein complex assembly	Scavenger receptor activity	No
IP100418163	Q6U2E9	ACTB	Complement component 4B preproprotein	35.26	6	1	37	279	281.76	1744	192.6	7.27	Extracellular space	Complement activation	Endopeptidase inhibitor activity	Yes
IP100418676	Q0P6H9	TMEM62	Transmembrane protein 62	5.75	1	1	1	2	3.25	643	73.1	9.26	Integral to membrane	Cell activation		Yes
IP100441094	Q5ZPR3		Isoform 3 of CD276 antigen	3.65	4	1	1	6	12.09	493	52.7	5.52	Plasma membrane			Yes
IP100450768	Q14666		Keratin, type I cytoskeletal 17	21.06	18	4	11	54	29.95	432	48.1	5.02	Cytoplasm	Epidermis development	Protein binding	No
IP100465016	O00391	QSOX1	Isoform 2 of sulfhydryl oxidase 1	7.62	4	3	3	10	18.63	604	66.8	8.56	Golgi membrane	Protein folding	Oxidoreductase activity	Yes
IP100465431	Q9Y2P4		Galectin-3	4.40	1	1	1	1	3.09	250	26.1	8.56	Plasma membrane	Very-long-chain fatty acid metabolic process	Nucleotide binding	Yes
IP100465436	Q8TAK2		Catalase	2.85	1	1	1	2	3.31	527	59.7	7.39	Lysosome	Response to reactive oxygen species	Nucleotide binding	No
IP100465439	P04075		Fructose-bisphosphate aldolase A	7.42	2	2	2	2	2.30	364	39.4	8.09	Extracellular region	Muscle system process	Actin binding	No
IP100477227	Q8N1N4	KRT78	Isoform 1 of keratin, type II cytoskeletal 78	13.27	2	4	6	16	17.10	520	56.8	6.02	Cytoskeleton		Structural molecule activity	No
IP100478003	P01023	AGT	Alpha-2-macroglobulin	40.71	7	38	38	232	361.38	1474	163.2	6.46	Extracellular region	Regulation of complement activation, lectin pathway	Enzyme inhibitor activity	Yes
IP100479116	P22792	CPN2	Carboxypeptidase N subunit 2	7.89	1	2	2	10	10.00	545	60.6	5.99	Extracellular region	Posttranscriptional regulation of gene expression		Yes
IP100479723	P02751	FN1	Isoform 10 of fibronectin	9.42	18	11	11	35	26.04	2176	239.5	5.88	ER-Golgi intermediate compartment	Cell morphogenesis	Pattern binding	No

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Supplementary Table 4: Contd...

Accession	Accession ID	Gene symbol	Description	% coverage	% number of proteins	% number of unique peptides	% number of peptides of PSMs	Maximum score	Number of AAs	MW (kDa)	Isoelectric point	Localization	Biological Process	Molecular function	Signal TM	
IP100480192	Q5VY30	CTBS	Retinol binding protein 4, plasma	62.81	3	8	8	1015	1970.87	22.9	6.09	Extracellular region	Skeletal system development	Retinoid binding	No	
IP100514229	Q5T093	RER1	RER1 retention in ER1 homolog	19.66	2	1	1	3.27	117	13.4	10.40	Retrograde vesicle-mediated transport	Retrograde vesicle-mediated transport, Golgi to ER		No	
IP100514669	Q5T123	PPT1	SH3 domain binding glutamic acid-rich protein like 3	32.95	4	3	3	21	36.27	9.4	9.36	Extracellular region	Cellular homeostasis	Electron carrier activity	No	
IP100515092	Q5TBF5	OGN	Osteoglycin	12.69	2	2	2	9	15.48	30.4	8.34	Extracellular region		Growth factor activity	No	
IP100549413	Q5T3N1	ANXA1	Annexin A1	14.22	3	2	2	4	9.17	22.7	5.53	Cornified envelope	Lipid transport	Enzyme inhibitor activity	No	
IP100550731	Q8TCD0		Putative uncharacterized protein	41.00	19	1	6	255	233.21	239	26.2	8.06				Yes
IP100552123	Q5J876	CP	Isoform 2 of V-set and immunoglobulin domain-containing protein 4	19.31	7	4	4	6	11.33	321	35.5	8.15	Extracellular region		Enzyme inhibitor activity	Yes
IP100552768	O60744	TXN	Thioredoxin, isoform CRA_b	15.29	2	1	1	10	7.30	9.4	6.04	Mitochondrion	Generation of precursor metabolites and energy		No	
IP100554711	P14923	JUP	Junction plakoglobin	12.48	4	6	6	24	10.90	81.7	6.14	Cell junction	Protein complex assembly	Structural molecule activity	No	
IP100555577	Q59GA0		Thy-1 cell surface antigen variant (fragment)	20.00	2	2	2	4	5.11	15.9	9.00	Membrane	T cell receptor signaling pathway	GPI anchor binding	Yes	
IP100555812	P02774	GC	Vitamin D-binding protein precursor	57.38	5	19	19	321	352.35	474	52.9	5.45	Extracellular region	Vitamin metabolic process	Actin binding	Yes
IP100556324	Q59F63		Transforming growth factor, beta-induced, 68kDa variant (fragment)	5.79	5	1	1	2	6.60	242	25.8	5.55			No	
IP100556415	Q59FA5	DCHS2	Transgelin variant (fragment)	15.34	2	2	2	3	9.88	18.3	6.58	Plasma membrane	Muscle organ development	Actin binding	No	
IP100639831	Q9H948		Isoform 2 of selenocysteine insertion sequence-binding protein 2	2.56	2	1	1	4	6.67	781	87.3	Nucleus	Translation	RNA binding	No	
IP100643490	Q68DC4	MDH2	Putative uncharacterized protein DKFP779G2333	10.74	4	4	4	20	21.11	540	59.2	5.63	Membrane	Cell activation	Integrin binding	Yes

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Supplementary Table 4: Contd...

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IP100643525	Q5JNX2		Uncharacterized protein	35.26	5	1	37	281.76	1744	192.6	7.08	Extracellular region	Adaptive immune response	Enzyme inhibitor activity	Yes
IP100643888	Q8N1K5	THEMIS	Isoform 3 of protein THEMIS	3.49	4	1	4	6.27	544	62.5	6.27	Cytoplasm, nucleus	Cell activation	Developmental protein	No
IP100644184	Q8IWX7		Isoform 2 of protein unc-45 homolog B	2.12	3	1	1	3.21	850	94.8	7.85	Muscle organ development	Muscle organ development	No	
IP100644697	Q9Y5Z4	C7	HEBP2 protein (fragment)	13.08	3	2	3	7.31	214	24.0	5.38	Cytosol			No
IP100644989	Q53RC7	DAF	Isoform 1 of protein disulfide-isomerase A6	3.18	2	1	2	3.19	440	48.1	5.08	Protein folding	Protein folding	Protein disulfide isomerase activity	Yes
IP100645038	Q5T985	ACTA1	Inter-alpha (globulin) inhibitor H2	24.81	4	13	13	96.58	935	105.2	7.03		Polysaccharide metabolic process	Enzyme inhibitor activity	Yes
IP100645213	Q5SRP4	APOM	Apolipoprotein M, isoform CRA_a	11.21	3	1	2	6.94	116	13.0	7.75	Extracellular region	Lipid transport	Lipid transporter activity	No
IP100645500	E9PFN7		cDNA FLJ55526, highly similar to complement C2	17.57	13	1	10	67.82	723	80.1	7.46	Extracellular region	Adaptive immune response	Endopeptidase activity	Yes
IP100646773	P06396	GSN	Isoform 2 of gelsolin	35.16	7	15	15	147.00	731	80.6	5.85	Cytoplasm, cytoskeleton	Response to acid	Actin binding	Yes
IP100657767	Q2VP91	EFNB2	FLNA protein (fragment)	9.12	6	2	2	6.58	307	33.0	6.38				No
IP100746033			47 kDa protein	5.49	3	1	1	3.53	419	47.1	7.46	Lysosome		Alpha-N-acetylgucosaminidase activity	Yes
IP100749381	Q9NS71		Gastrokine-1	7.04	1	1	2	6.83	199	22.0	6.32	Extracellular region	Digestion	Growth factor activity	Yes
IP100783665	O75079	LAMA5	Laminin subunit alpha-5	0.51	1	1	1	2.35	3695	399.5	6.99	Extracellular region	Cell morphogenesis	Integrin binding	Yes
IP100783862	P30043	SERPINA4	Flavin reductase	6.80	2	1	1	3.02	206	22.1	7.65	Extracellular region	Oxidation reduction	Blivverdin reductase activity	Yes
IP100783987	P01024	C3	Complement C3 (fragment)	49.55	3	56	56	655.99	1663	187.0	6.40	Extracellular region	Regulation of type III hypersensitivity	Enzyme inhibitor activity	Yes
IP100788781			Uncharacterized protein	15.84	2	1	1	3.79	101	11.2	6.07		Ectoderm development	Fatty acid binding	
IP100789173	C9J7H8	LDHB	Uncharacterized protein	10.95	3	1	1	3.21	137	14.8	5.54	Cell fraction	Monosaccharide metabolic process	Nucleotide binding	No
IP100789477	B7Z4X2		cDNA FLJ58679, highly similar to lactoferrin	18.77	8	9	9	110.13	666	73.1	7.85	Extracellular region	Transition metal ion transport	Endopeptidase activity	
IP100790784	Q310J7		Isoform 2 of Alpha-1-antitrypsin	13.37	4	3	3	10.46	359	40.2	5.47	Extracellular region	Response to hypoxia	Protease binding	No

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Supplementary Table 4: Contd...

Accession	Accession ID	Gene symbol	Description	% coverage	% number of proteins	% number of unique peptides	% number of peptides	% number of PSMs	Maximum score	Number of AAs	MW (kDa)	Isoelectric point	Localization	Biological Process	Molecular Function	Signal TM
IP100792087			Uncharacterized protein	5.13	3	1	1	1	3.14	234	26.3	4.54	Protein complex assembly			
IP100792115	Q68DS3	SERPINA5	Putative uncharacterized protein DKFZp686H17246	29.38	2	1	3	3	12.31	160	17.8	5.05	Extracellular region	Skeletal system development	Sugar binding	No
IP100792354			10 kDa protein	11.76	1	1	1	1	3.28	85	9.6	7.90	Extracellular region		Enzyme inhibitor activity	Yes
IP100795257	Q6YHK3		32 kDa protein	9.90	7	2	2	4	3.29	293	31.5	7.61	Nucleoplasm	Mitotic cell cycle	Structural constituent of ribosome	
IP100795527			21 kDa protein	76.22	26	5	5	22	27.79	185	20.8	7.40				
IP100795633			CLU	17.86	5	8	8	34	51.99	448	52.3	6.38	Extracellular region	Cell morphogenesis		
IP100796012	Q15020		Squamous cell carcinoma antigen 1	8.23	3	1	1	1	3.15	158	18.2	7.55	Cytoplasm	Immune response	Enzyme inhibitor activity	
IP100796636	Q9UIP81		Hemoglobin (fragment)	45.71	9	3	3	4	16.42	105	11.5	6.37	Hemoglobin complex	Oxygen transport	Heme binding	No
IP100796776	E7EU87		cDNA FLJ54081, highly similar to keratin, type II cytoskeletal 5	26.63	8	8	14	135	55.47	567	60.1	6.19	Cytoskeleton	Ectoderm development	Structural molecule activity	No
IP100797471			42 kDa protein	13.66	11	3	4	77	50.05	366	41.6	5.53	Cytoskeleton			
IP100797778			91 kDa protein	4.97	3	1	1	1	3.38	825	90.7	9.09	MAPKK cascade	Spliceosome assembly	Structural molecule activity	
IP100807475	P16383	C2orf3	Isoform 2 of GC-rich sequence DNA-binding factor	2.56	2	1	1	3	9.13	743	84.8	6.20	Nucleus	Transcription	DNA binding	No
IP100815665	Q6PK75		Trypsin-2	14.17	8	2	2	4	11.33	247	26.5	4.92	Extracellular region	Proteolysis	Endopeptidase activity	Yes
IP100828004	Q8NG19		Multi-functional protein MFP	26.82	6	4	4	11	15.23	261	26.7	9.32	Extracellular matrix	Cell adhesion	Binding	No
IP100828108	P16070	DSP	Isoform 15 of CD44 antigen	15.65	19	3	3	19	14.65	294	32.1	5.21	Cell fraction	Syncytium formation by plasma membrane fusion	Pattern binding	Yes 1
IP100844090	Q9UJML4	COL5A1	Collagen alpha-1 (V) chain	2.94	1	3	3	3	7.38	1838	183.4	5.06	Extracellular region	Blood vessel development	Pattern binding	Yes
IP100847442	Q1JUQ5		FK506 binding protein12	15.22	3	1	1	1	3.83	92	10.1	5.90	Cell fraction	Cell activation	Peptidyl-prolyl cis-trans isomerase activity	
IP100847557	Q92835	PVRL2	Isoform 3 of phosphatidylinositol-3,4,5-trisphosphate 5-phosphatase 1	1.95	3	1	1	3	6.25	976	109.2	8.68	Cytosol	Regulation of cytokine production	Inositol or phosphatidylinositol phosphatase activity	No

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Supplementary Table 4: Contd...

Accession	Accession ID	Gene symbol	Description	% coverage	N ₁ number of proteins	N ₂ number of unique peptides	N ₃ number of peptides	N ₄ number of PSMs	Maximum score	Number of AAs	MW (kDa)	Isoelectric point	Localization	Biological process	Molecular function	Signal TM	
IP100847635	P01011	SERPINA3	Isoform 1 of alpha-1-antitrypsin	57.68	3	17	17	2197	2756.94	423	47.6	5.52	Extracellular region	Tissue homeostasis	DNA binding	Yes	
IP100852577	Q6DHW4	LTBP2	HCG2040025	65.09	4	1	4	79	58.66	106	11.4	7.87				Yes	
IP100855846	Q9P1F3	C6orf115	UPF0727 protein C6orf115	16.05	1	1	1	5	11.72	81	9.1	6.29				No	
IP100871427	A8MSY9	EFCAB5	Uncharacterized protein	2.59	5	1	1	2	6.20	926	106.8	5.38	Extracellular region		Calcium ion binding	No	
IP100873598			Uncharacterized protein	9.23	14	1	6	35	23.45	455	49.1	4.79	Cytoskeleton	Ectoderm development	Structural molecule activity		
IP100878623	B0QYF8	COL7A1	Myoglobin	54.55	6	6	6	27	55.81	143	16.0	7.69	Stress fiber	Response to reactive oxygen species	Oxygen transporter activity	No	
IP100878987	Q86Y46	F2	Isoform 2 of keratin, type II cytoskeletal 73	9.45	9	3	4	50	38.59	381	42.0	8.25	Cytoskeleton		Structural molecule activity	Yes	
IP100879231	P08697	CD14	Alpha-2-antiplasmin	23.63	5	7	7	48	66.87	491	54.5	6.29	Extracellular space	Acute inflammatory response	Protease binding	Yes	
IP100879357	A8W476	CDH13	Cadherin 13 soluble isoform 2	15.43	3	2	2	10	36.02	175	19.6	8.47	Extracellular region	Angiogenesis	Calcium ion binding	Yes	
IP100879368	Q8TCZ8	APOE	Apolipoprotein E	13.89	4	2	2	2	3.87	216	24.6	5.85	Extracellular region	Response to reactive oxygen species	Beta-amyloid binding	No	
IP100879573	P05546	SERPIND1	Heparin cofactor 2	14.03	2	5	5	14	29.25	499	57.0	6.90	Extracellular region	Chemotaxis	Pattern binding	Yes	
IP100879709	P13671		Complement component 6 precursor	11.35	1	9	9	36	57.13	943	105.7	6.79	Extracellular region	<i>In utero</i> embryonic development		Yes	
IP100879984	C9JCT1		cDNA FLJ51250, highly similar to plasma kallikrein	2.53	4	1	1	1	3.79	514	57.6	8.34	Extracellular region	Kinin cascade	Endopeptidase activity	No	
IP100883722	Q6LBM9	CFHR1	Complement factor H-related 1	17.71	6	3	4	19	20.14	271	30.8	7.81				Yes	
IP100884926	P02763		Alpha-1-acid glycoprotein 1 precursor	67.66	2	10	15	565	889.87	201	23.5	5.11	Extracellular region				
IP100888683	Q13835		Similar to plakophilin 1, partial	2.40	3	1	1	2	3.56	625	69.2	8.81	Cytoskeleton	Cell adhesion	Structural molecule activity	Yes	
IP100890724	Q6E0U4	DMKN	Isoform 7 of dermokin	4.61	8	1	1	1	4.22	369	35.3	6.43	Extracellular region				
IP100892952	C9JIE7	LRRIQ1	Uncharacterized protein	11.49	3	1	1	9	8.75	148	15.4	9.22	Extracellular region	Cell adhesion		Yes 1	
IP100893223	C9JMK5	PIK3IP1	Uncharacterized protein	17.93	5	2	2	7	10.52	145	16.0	7.90	Integral to membrane			Yes	

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Supplementary Table 4: Contd...

Accession	Accession ID	Gene symbol	Description	% coverage	% number of proteins	% number of unique peptides	% number of peptides	% number of PSMs	Maximum score	Number of AAs	MW (kDa)	Isoelectric point	Localization	Biological Process	Molecular Function	Signal
IP100893243	E7ENY2	GBP1	22 kDa protein	8.95	6	1	1	1	3.43	190	21.9	7.27	Intracellular	Intracellular signaling cascade	Zinc ion binding	No
IP100893264			30 kDa protein	7.64	3	1	1	1	3.39	275	29.9	6.10	Integral to membrane			
IP100893729	B1Q3B4	FTL	Ferritin (fragment)	14.85	2	1	1	2	6.63	101	11.2	8.78		Cellular iron ion homeostasis	Ferric iron binding	No
IP100893884			Uncharacterized protein	14.94	10	1	1	1	3.00	87	9.8	4.61		Sensory perception	Calcium ion binding	
IP100895858	E9PE45	C2	72 kDa type IV collagenase isoform b	3.11	2	1	1	1	3.73	610	68.8	5.34	Extracellular region	Skeletal system development	Endopeptidase activity	No
IP100895943			Serum amyloid A2 isoform b	16.87	3	1	1	13	28.02	83	9.2	7.18	Extracellular region	Cell activation		
IP100896413	E9PGN5	HEXA	Inter-alpha (globulin) inhibitor H4 isoform 2 precursor	39.33	8	22	22	216	207.36	900	99.8	6.47		Acute inflammatory response	Enzyme inhibitor activity	Yes
IP100902623	B3KQX7		Major prion protein	7.36	5	1	1	7	11.37	163	18.2	5.76	ER	Protein complex assembly	Copper ion binding	Yes 2
IP100902680			cDNA FLJ39696 fis, clone SMINT2011033, highly similar to sorting and assembly machinery component 50 homolog	10.95	3	1	1	1	3.13	274	30.2	8.62	Protein complex assembly	Protein complex assembly		
IP100903238	E7EU55		cDNA FLJ11717 fis, clone HEMBA1005241	14.96	2	1	1	2	3.15	127	14.5	6.54	Cytosol	Release of cytochrome c from mitochondria	Gamma-glutamyl cyclotransferase activity	No
IP100908746	B4DRT4	PEBP1	cDNA FLJ51535, highly similar to phosphatidylethanol amine-binding protein 1	60.65	4	5	5	16	21.33	155	17.3	6.00		Regulation of neurotransmitter levels	Nucleotide binding	No
IP100909059	B4DRR0		cDNA FLJ53910, highly similar to keratin, type II cytoskeletal 6A	31.59	10	2	16	151	78.27	535	57.8	8.00	Cytoskeleton	Ectoderm development	Structural molecule activity	No
IP100909207	B4DF70		cDNA FLJ60461, highly similar to peroxiredoxin-2	15.85	6	3	3	4	6.68	183	20.1	8.78	Cell fraction	MAPKKK cascade	Peroxidase activity	No
IP100909308	B4DTK3		cDNA FLJ57891, highly similar to tropomyosin beta chain	8.23	16	1	1	1	3.28	158	17.8	4.81				No
IP100909509	B4DNH8		cDNA FLJ59138, highly similar to annexin A2	19.07	6	3	3	13	7.19	194	21.7	6.35			Calcium ion binding	No
IP100909594	Q8TCS7		cDNA FLJ58413, highly similar to complement component C7	13.17	1	1	4	7	11.07	486	53.7	5.40	Extracellular region	Adaptive immune response		Yes

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Supplementary Table 4: Contd...

Accession	ID	Gene symbol	Description	% coverage	% number of proteins	% number of unique peptides	% number of peptides	% number of PSMs	Maximum score	Number of AAs	MW (kDa)	Isoelectric point	Localization	Biological process	Molecular function	Signal TM
IP 00910358	B4DVT0		cDNA FLJ53460, highly similar to Y + L amino acid transporter 1	6.20	2	1	1	1	3.29	484	53.3	5.30	Plasma membrane	Protein complex assembly	Amine transporter activity	No
IP 00910380	D6RA29		cDNA FLJ54278, highly similar to SPARC-like protein 1	16.38	3	1	5	12	10.28	519	58.5	4.94	Extracellular space	Calcium ion binding	Calcium ion binding	Yes
IP 00910625	P02749		cDNA FLJ51265, moderately similar to beta-2-glycoprotein 1	42.70	2	10	10	86	86.72	274	30.3	7.85	Extracellular region	Negative regulation of angiogenesis	Eukaryotic cell surface binding	Yes
IP 00910738	B4DKV4		cDNA FLJ60647, highly similar to keratin, type II cytoskeletal 6B	31.94	3	1	14	105	44.87	526	55.7	8.43	Keratin filament		Structural molecule activity	No
IP 00910755	E7EUG1		cDNA FLJ51707, highly similar to heat-shock protein 105 kDa	4.54	1	1	1	14	22.09	639	71.2	8.46		Response to unfolded protein	Nucleotide binding	No
IP 00911004	E7EPA8		cDNA FLJ59939, highly similar to protein disulfide-isomerase	7.17	3	1	1	2	8.57	223	24.5	9.57	Cell fraction	Cellular amino acid derivative metabolic process	Protein disulfide isomerase activity	Yes
IP 00915302	Q8TDA8	GSS	Glutathione synthetase	5.51	2	1	1	4	3.39	363	40.3	5.11	Cell fraction	Peptide metabolic process	Nucleotide binding	No
IP 00916240			16 kDa protein	19.46	2	1	2	3	10.14	149	16.4	6.30	Extracellular region	Cell proliferation	Sugar binding	
IP 00917285	B4DFW2	TIMP2	cDNA FLJ57920, highly similar to metalloproteinase inhibitor 2	7.91	3	1	1	2	6.40	177	20.0	7.17	Extracellular region	Regulation of nucleotide metabolic process	Enzyme inhibitor activity	No
IP 00922213	Q9H382		cDNA FLJ53292, highly similar to homo sapiens FN1, transcript variant 5, mRNA	8.19	2	1	5	24	20.83	1014	111.2	6.21	Extracellular region	Cell morphogenesis	Pattern binding	No
IP 00922577	B7Z3P3		cDNA FLJ53768, highly similar to hepatocyte growth factor-like protein	6.10	6	1	1	1	3.25	164	17.8	9.11				Yes
IP 00922737	B7ZAK5		ADAM DEC1 isoform 2	3.84	2	1	1	1	3.94	391	43.5	7.01	Extracellular region	Proteolysis	Endopeptidase activity	No
IP 00923515	B9EJG1	AMY2A	Amylase, alpha 2A	4.15	3	1	1	2	3.61	265	30.3	7.05		Carbohydrate metabolic process	Catalytic activity	Yes
IP 00924537	C9JXX4	IGFBP5	Uncharacterized protein	6.01	2	1	1	2	3.49	233	25.5	7.31	Extracellular region	Skeletal system development	Insulin-like growth factor binding	Yes
IP 00925214	D6RJG1	CASP12	Uncharacterized protein	7.58	1	1	1	23	12.71	277	31.0	5.74	Intracellular	Apoptosis	Cysteine-type endopeptidase activity	No

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Supplementary Table 4: Contd...

Accession	Accession ID	Gene symbol	Description	% coverage	% number of proteins	% number of unique peptides	% number of peptides of PSMs	Maximum score	Number of AAs	MW (kDa)	Isoelectric point	Localization	Biological process	Molecular function	Signal TM
IP100939169	O75882	CREG1	Isoform 3 of attractin	1.67	5	2	2	3.16	1198	133.6	6.98	Extracellular region	Defense response	Sugar binding	Yes 1
IP100939926	Q95460		MHC class I antigen (fragment)	15.73	100	1	1	3.38	89	10.4	8.50				
IP100940046	E7ERV9	ASAH1	cDNA FLJ40980 fis, clone UTERU2014464, highly similar to acid ceramidase	9.51	4	2	2	21.74	305	34.6	7.77		Membrane lipid metabolic process	Hydrolase activity	No
IP100940960	P61916	NPC2	Epididymal secretory protein E1	25.83	2	2	3	4.30	151	16.6	7.65	Lysosome	Lipid transport	Steroid binding	Yes
IP100943326	P98160		Basement membrane-specific heparan sulfate proteoglycan core protein variant	5.17	3	16	155	163.25	4374	466.8	6.49	Lysosome	Skeletal system development		
IP100945490	C9J8S2	RARRES2	Uncharacterized protein	17.61	2	1	1	3.54	159	17.8	10.21		Retinoid metabolic process		Yes
IP100946055	CPB1	CPB1	Uncharacterized protein	22.03	6	1	2	3.88	59	6.6	5.22	Extracellular region	Proteolysis	Carboxypeptidase activity	Yes
IP100946286	COL6A3	COL6A3	Collagen alpha-3(VI) chain isoform 4 precursor	4.20	9	7	8	13.33	2570	278.0	8.15	Extracellular region	Cell adhesion	Enzyme inhibitor activity	Yes
IP100947285	E9PBV3	SBSN	Suprabasin isoform 1 precursor	26.27	3	6	36	26.48	590	60.5	7.01				Yes
IP100953573	C9JX84	ITIH3	Uncharacterized protein	15.71	5	8	36	47.08	885	99.2	5.80				
IP100953689	P02765	AHSG	Alpha-2-HS-glycoprotein	44.14	4	8	128	184.29	367	39.3	5.72	Extracellular region	Skeletal system development	Enzyme inhibitor activity	Yes
IP100956045	D3DU30		Intercellular adhesion molecule 2, isoform CRA_b	12.16	2	2	19	27.60	255	27.8	6.89				
IP100956313			58 kDa protein	37.27	14	4	19	51.17	542	58.3	8.00				
IP100964180			Protein	8.11	6	1	1	3.88	185	21.9	5.77				
IP100965211	E7EM93		50 kDa protein	4.05	2	1	3	3.47	444	50.0	6.79				
IP100965297	D6RJF7	NEK11	Uncharacterized protein	11.79	6	1	1	3.13	212	24.2	9.22				
IP100966295			Light chain of factor I	19.97	5	8	45	63.11	576	65.0	7.50				
IP100967014	D6RBV2	LMAN2	Uncharacterized protein	32.31	5	6	44	59.81	325	36.5	6.65	Membrane			Yes
IP100967340	Q6P1X2	LRBA	LRBA protein	1.83	3	1	1	3.35	2575	286.8	5.52			Binding	No
IP100967366	D6REX5	FGF	Uncharacterized protein	11.29	4	2	2	11.14	310	35.1	7.66			Selenium binding	Yes
IP100969595	D6W5J8	hCG_1639753	HCG1639753, isoform CRA_a	29.87	1	1	9	26.45	77	8.3	6.24			Binding	No

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Accession	Accession ID	Gene symbol	Description	% coverage	% number of proteins	% number of unique peptides	% number of peptides	Maximum score	Number of AAs	MW (kDa)	Isoelectric point	Localization	Biological process	Molecular function	Signal TM
IP100972938	P00740		Coagulation factor IX	6.62	2	2	2	9.62	423	47.6	6.11	Golgi lumen			
IP100973279	O95613	PCNT	Isoform 2 of pericentrin	1.05	2	1	1	3.10	3139	355.7	5.47	Cytoplasm	G2/M transition of mitotic cell cycle	Calmodulin binding	No
IP100973362	B7Z6J1		cDNA FLJ55035, highly similar to dihydrolipoyllysine-residue succinyltransferase component of 2-oxoglutarate dehydrogenase complex, mitochondrial	8.43	3	1	1	7.92	166	17.9	8.06				

MW: Molecular weight, FN1: Fibronectin 1, ER: Endoplasmic reticulum, LC-MS/MS: Liquid chromatography-tandem mass spectrometry, HMW: High-molecular-weight, LMW: Low molecular weight, PSM: Peptide spectrum match, AA: Amino acids