

Supplementary Table 8: Unique proteome of proteinuric group (MIA and MA) group when compared to NA group

Accession	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	Biologic process	Molecular function
IP100555812	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
IP100878623	Myoglobin	54.55	6	6	6	27	55.81	143	16.0	7.69	Stress fiber	Response to reactive oxygen species	Oxygen transporter activity
IP100218733	Superoxide dismutase (Cu-Zn)	53.90	2	5	5	14	25.57	154	15.9	6.13	Cytoplasm	MAPKKK cascade	Superoxide dismutase activity
IP100022429	Alpha-1-acid glycoprotein 1	53.23	2	7	10	298	292.31	201	23.5	5.02	Extracellular region	Acute-phase response	Protein binding
IP100796636	Hemoglobin (fragment)	45.71	9	3	3	4	16.42	105	11.5	6.37	Hemoglobin complex	Oxygen transport	Heme binding
IP100968044	Uncharacterized protein	44.87	6	1	1	1	2.73	78	8.8	8.18			
IP100021854	Apolipoprotein A-II	43.00	1	3	3	16	43.06	100	11.2	6.62	Extracellular region	Regulation of cytokine production	Enzyme inhibitor activity
IP100298497	Fibrinogen beta chain	42.97	3	14	14	112	102.53	491	55.9	8.27	Extracellular region	Cell activation	Protein binding
IP100010290	FABP1 protein (fragment)	42.54	3	3	3	10	16.81	134	15.1	9.51	Cytoplasm	Lipid transport	Chromatin binding
IP100550731	Putative uncharacterized protein	41.00	19	1	6	255	233.21	239	26.2	8.06			
IP100025318	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

Contd...

Supplementary Table 8: Contd...

Accession	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	Biologic Process	Molecular Function
IP100790892	6 kDa protein	35.29	8	1	1	1	3.85	51	5.6	4.89	Phosphopyruvate hydratase complex	Monosaccharide metabolic process	Magnesium ion binding
IP100643525	Uncharacterized protein	35.26	5	1	37	277	281.76	1744	192.6	7.08	Extracellular region	Adaptive immune response	Enzyme inhibitor activity
IP100646773	Isoform 2 of gelsolin	35.16	7	15	15	155	147.00	731	80.6	5.85	Cytoplasm, cytoskeleton	Response to acid	Actin binding
IP100793930	TUBA1B protein	34.63	24	1	7	19	30.21	335	37.2	4.98	Microtubule	Microtubule-based movement	GTP binding
IP100011261	Complement component C8 gamma chain	34.16	2	4	4	15	50.01	202	22.3	8.31	Extracellular region	Adaptive immune response	Retinoid binding
IP100647896	Tubulin, beta	33.33	12	2	8	15	24.24	372	41.7	4.91	Cytosol	M phase of mitotic cell cycle	Nucleotide binding
IP100878470	8 kDa protein	33.33	1	1	1	2	2.81	78	8.3	7.34		Cell killing	Calcium ion binding
IP100005721	Neutrophil defensin 1	32.98	2	1	1	5	12.60	94	10.2	6.99	Extracellular region	Cell killing	Endopeptidase activity
IP100219713	Isoform gamma-A of fibrinogen gamma chain	32.72	6	10	10	73	54.69	437	49.5	6.09	Extracellular region	Cell activation	Calcium ion binding
IP100926178	Uncharacterized protein	32.69	3	1	1	1	3.41	52	5.7	4.78	Axon	Regulation of translation	
IP100019568	Prothrombin (fragment)	32.48	2	13	13	53	104.29	622	70.0	5.90	Extracellular region	Protein import into nucleus, translocation	Endopeptidase activity
IP100909059	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
IP100163563	Phosphatidylethanolamine-binding protein 4	31.28	1	3	3	6	16.30	227	25.7	6.54	Lysosome		
IP100013895	Protein S100-A11	29.52	1	1	1	3	6.13	105	11.7	7.12	Nucleus	Regulation of DNA replication	Calcium ion binding
IP100022371	Histidine-rich glycoprotein	28.19	1	11	11	99	88.18	525	59.5	7.50	Extracellular region	Regulation of blood coagulation	Pattern binding
IP100828004	MFP	26.82	6	4	4	11	15.23	261	26.7	9.32	Extracellular matrix	Cell adhesion	Binding
IP100180675	Tubulin alpha-1A chain	25.72	16	1	7	25	38.17	451	50.1	5.06	Cytosol	Protein complex assembly	Nucleotide binding
IP100218875	Isoform C of osteopontin	25.44	7	5	5	9	29.23	287	32.3	4.55	Extracellular region	Skeletal system development	Cytokine activity
IP100215746	Fatty acid-binding protein, adipocyte	25.00	3	3	3	16	42.50	132	14.7	7.14	Cell fraction	Cytokine production	Fatty acid binding
IP100645038	Inter-alpha (globulin) inhibitor H2	24.81	4	13	13	61	96.58	935	105.2	7.03		Polysaccharide metabolic process	Enzyme inhibitor activity
IP100328609	Kallistatin	24.59	1	7	7	15	28.37	427	48.5	7.75	Extracellular region	Cell killing	Enzyme inhibitor activity
IP100007752	Tubulin beta-2C chain	24.49	9	1	7	16	27.70	445	49.8	4.89	Cytosol	Cell killing	Nucleotide binding
IP100019591	cDNA FLJ55673, highly similar to complement factor B	24.25	18	14	23	191	181.91	1266	140.9	7.18	Extracellular region	Complement activation	Serine-type endopeptidase activity
IP100879231	Alpha-2-antiplasmin	23.63	5	7	7	48	66.87	491	54.5	6.29	Extracellular space	Acute inflammatory response	Protease binding
IP100011229	Cathepsin D	23.54	6	6	6	24	24.61	412	44.5	6.54	Lysosome, Melanosome	Autophagic vacuole formation	Endopeptidase activity

Contd...

Supplementary Table 8: Contd...

Accession	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	Biologic Process	Molecular Function
IP100290315	Chromogranin-A	22.54	2	5	5	11	15.81	457	50.7	4.60	Extracellular region	Circulatory system process	Calcium ion binding
IP100910975	CMRF35-like molecule 9 isoform 3 precursor	22.34	5	3	3	4	6.67	273	29.9	6.54		Immune response	
IP100023019	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
IP100946055	Uncharacterized protein	22.03	6	1	1	2	3.88	59	6.6	5.22	Extracellular region	Proteolysis	Carboxypeptidase activity
IP100032328	Isoform HMW of kininogen-1	21.89	4	1	12	61	54.73	644	71.9	6.81	Extracellular region	Muscle system process	Pattern binding
IP100298971	Vitronectin	21.13	2	8	8	53	33.25	478	54.3	5.80	Extracellular region	Immune response	Pattern binding
IP100021856	Apolipoprotein C-II	20.79	1	1	1	6	19.30	101	11.3	4.72	Extracellular region	Cholesterol efflux	Lipase inhibitor activity
IP100555789	Glia maturation factor, beta variant (fragment)	20.54	3	1	1	1	2.65	112	12.9	5.17	Intracellular		Actin binding
IP100877925	Uncharacterized protein	20.45	5	3	3	4	8.81	264	29.5	6.93	Extracellular region	Acute inflammatory response	Protease binding
IP100966681	Uncharacterized protein	20.20	1	1	1	1	2.67	99	11.0	5.17			
IP100021439	Actin, cytoplasmic 1	20.00	23	2	4	20	11.77	375	41.7	5.48	Histone acetyltransferase complex	Cell morphogenesis	Nucleotide binding
IP100966295	Light chain of factor I	19.97	5	8	8	45	63.11	576	65.0	7.50			
IP100008753	Metallothionein-1X	19.67	6	1	1	1	3.20	61	6.1	7.96	Nucleus	Response to inorganic substance	Copper ion binding
IP100514229	RER1 homolog	19.66	2	1	1	1	3.27	117	13.4	10.40	Retrograde vesicle-mediated transport	Retrograde vesicle-mediated transport, Golgi to ER	
IP100916240	16 kDa protein	19.46	2	1	2	3	10.14	149	16.4	6.30	Extracellular region	Cell proliferation	Sugar binding
IP100552123	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
IP100443913	cDNA FLJ46325 fis, clone TEST14043371	19.25	1	1	1	1	2.52	161	18.7	9.11			
IP100909509	cDNA FLJ59138, highly similar to Annexin A2	19.07	6	3	3	13	7.19	194	21.7	6.35			
IP100003351	Isoform 1 of extracellular matrix protein 1	19.07	4	6	6	14	27.31	540	60.6	6.71	Extracellular region	Positive regulation of signal transduction	Laminin binding
IP100386621	CALM3 protein	18.92	7	2	2	3	5.37	148	16.6	4.44		Cell cycle	Calcium ion binding
IP100966568	Protein	18.55	8	1	1	1	2.48	124	13.2	9.67			
IP100017951	cDNA: FLJ23429 fis, clone HRC10578	18.46	1	1	1	1	2.92	195	21.1	9.47			
IP100292530	Inter-alpha-trypsin inhibitor heavy chain H1	18.44	6	11	11	40	53.82	911	101.3	6.79	Extracellular region	Cell activation	Enzyme inhibitor activity
IP100010182	Isoform 1 of acyl-CoA-binding protein	18.39	7	1	1	1	2.55	87	10.0	6.57	Cell fraction	Transport	Acyl-CoA binding

Contd...

Supplementary Table 8: Contd...

Accession	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	Biologic Process	Molecular function
IP100643462	27 kDa protein	18.14	1	1	1	1	2.67	226	26.6	6.54			
IP100401212	GPM6A protein	17.95	4	1	1	1	2.55	78	8.9	6.51	Cell surface		Ion channel activity
IP100883722	Complement factor H-related 1	17.71	6	3	4	19	20.14	271	30.8	7.81			
IP100945490	Uncharacterized protein	17.61	2	1	1	1	3.54	159	17.8	10.21		Retinoid metabolic process	
IP100645500	cDNA FLJ5526, highly similar to complement C2	17.57	13	1	10	34	67.82	723	80.1	7.46	Extracellular region	Adaptive immune response	Endopeptidase activity
IP100098827	Heat shock protein beta-11	17.36	1	1	1	1	2.53	144	16.3	5.03		Cell adhesion	
IP100554556	Isoform C of protein CutA	17.31	3	1	1	2	4.18	156	16.8	5.21	Cornified envelope	Protein complex assembly	Retinoic acid receptor activity
IP100640115	cDNA FLJ77784	17.20	4	1	4	10	18.44	378	42.4	4.96	Cytoskeleton	M phase of mitotic cell cycle	Nucleotide binding
IP100908954	cDNA FLJ52511, highly similar to abhydrolase domain-containing protein 14B	16.92	5	1	1	1	3.13	130	13.9	6.11	Lysosome		
IP100921523	Isoform 1 of complement factor B (fragment)	16.88	11	8	8	28	15.26	764	85.5	7.06	Extracellular region	Complement activation, alternative pathway	Complement binding
IP100925319	Uncharacterized protein	16.67	4	1	1	1	2.99	96	10.3	5.29		Morphogenesis of an epithelium	Calcium ion binding
IP100855846	UPF0727 protein C6orf115	16.05	1	1	1	5	11.72	81	9.1	6.29			
IP100909207	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
IP100939926	MHC class I antigen (fragment)	15.73	100	1	1	1	3.38	89	10.4	8.50		Polysaccharide metabolic process	Enzyme inhibitor activity
IP100953573	Uncharacterized protein	15.71	5	8	8	36	47.08	885	99.2	5.80		Angiogenesis	Calcium ion binding
IP100879357	Cadherin 13 soluble isoform 2	15.43	3	2	2	10	36.02	175	19.6	8.47	Extracellular region	Muscle organ development	Actin binding
IP100556415	Transgelin variant	15.34	2	2	2	3	9.88	163	18.3	6.58	Plasma membrane	Cell activation	Peptidyl-prolyl cis-trans isomerase activity
IP100847442	FK506 binding protein12	15.22	3	1	1	1	3.83	92	10.1	5.90	Cell fraction	Tissue homeostasis	Endopeptidase activity
IP100554538	Uncharacterized protein	15.14	7	4	4	19	23.10	555	60.3	6.39	Cytosol	Vesicle-mediated transport	
IP100219648	Isoform 2 of vesicle-associated membrane protein 4	15.00	2	1	1	1	3.00	140	16.2	6.60	Golgi membrane	Cell activation	Lipopolysaccharide binding
IP100032311	Lipopolysaccharide-binding protein	14.97	1	6	6	34	49.55	481	53.3	6.70	Cell activation		
IP100903238	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
IP100893884	Uncharacterized protein	14.94	10	1	1	1	3.00	87	9.8	4.61		Sensory perception	Calcium ion binding
IP100514530	Uncharacterized protein	14.88	23	1	3	17	12.02	289	32.3	5.31	Stress fiber	Muscle system process	Nucleotide binding
IP100966346	23 kDa protein	14.85	9	2	2	2	2.45	202	23.2	7.53		Protein ADP-ribosylation	NAD(P) ⁺ -protein-arginine ADP-ribosyltransferase activity

Contd...

Supplementary Table 8: Contd...

Accession	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	Biologic Process	Molecular Function
IP100893729	Ferritin (fragment)	14.85	2	1	1	2	6.63	101	11.2	8.78		Cellular iron ion homeostasis	Ferric iron binding
IP100218732	Serum paraoxonase/arylesterase 1	14.65	2	4	4	6	12.30	355	39.7	5.22	Cell fraction	Cellular amino acid derivative metabolic process	Aryldialkylphosphatase activity
IP100853068	Hemoglobin alpha-2	14.55	2	1	1	1	2.78	110	11.9	8.76	Cytosol	Gas transport	Oxygen transporter activity
IP100294395	Complement component C8 beta chain	14.38	1	5	5	16	31.63	591	67.0	8.13	Extracellular region	Adaptive immune response	Protein complex binding
IP100413587	Isoform 1 of BH3-interacting domain death agonist	14.36	3	2	2	2	3.28	195	22.0	5.44	h_deathPathway:induction of apoptosis through DR and DR/death receptors	Release of cytochrome c	Death receptor binding
IP100549413	Annexin A1	14.22	3	2	2	4	9.17	204	22.7	5.53	Cornified envelope	Lipid transport	Enzyme inhibitor activity
IP100011252	Complement component C8 alpha chain	14.21	1	5	5	9	17.85	584	65.1	6.47	Extracellular region	Adaptive immune response	
IP100815665	Trypsin-2	14.17	8	2	2	4	11.33	247	26.5	4.92	Extracellular region	Proteolysis	Endopeptidase activity
IP100293350	Translin-associated protein X	14.14	1	1	1	1	3.33	290	33.1	6.55	Perinuclear region of cytoplasm	Gamete generation	DNA binding
IP100163119	Isoform 1 of gastrotropin	14.06	2	1	1	2	3.09	128	14.4	6.80	Cytosol	Steroid metabolic process	Fatty acid binding
IP100879573	Heparin cofactor 2	14.03	2	5	5	14	29.25	499	57.0	6.90	Extracellular region	Chemotaxis	Pattern binding
IP100909283	cDNA FLJ58514, highly similar to cadherin-11	13.74	3	6	6	10	13.96	779	85.5	4.83	Plasma membrane	Skeletal system development	Calcium ion binding
IP100797471	42 kDa protein	13.66	11	3	4	77	50.05	366	41.6	5.53	Cytoskeleton	Cell activation	Structural molecule activity
IP100021263	14-3-3 protein zeta/delta	13.47	4	2	2	5	11.93	245	27.7	4.79	Cell fraction	Cell activation	Transcription factor binding
IP100790784	Isoform 2 of alpha-1-antitrypsin	13.37	4	3	3	8	10.46	359	40.2	5.47	Extracellular region	Response to hypoxia	Protease binding
IP100477227	Isoform 1 of keratin, type II cytoskeletal 78	13.27	2	4	6	16	17.10	520	56.8	6.02	Cytoskeleton	Immune effector process	Structural molecule activity
IP100029739	Isoform 1 of complement factor H	13.24	4	10	11	31	51.54	1231	139.0	6.61	Cell fraction	Adaptive immune response	
IP100909594	cDNA FLJ58413, highly similar to complement component C7	13.17	1	1	4	7	11.07	486	53.7	5.40	Extracellular region	Acute inflammatory response	Sugar binding
IP100029039	Regenerating islet-derived protein 3-alpha	13.14	1	1	1	4	16.13	175	19.4	7.64	Cell fraction	Mature ribosome assembly	Protein binding
IP100644697	HEBP2 protein (fragment)	13.08	3	2	2	3	7.31	214	24.0	5.38	Cytosol		
IP100010105	Eukaryotic translation initiation factor 6	13.06	3	2	2	3	6.10	245	26.6	4.68	Cytoplasm. Nucleus		
IP100002147	Chitinase-3-like protein 1	13.05	2	3	3	4	7.26	383	42.6	8.46	Extracellular region	Polysaccharide catabolic process	Chitinase activity

Contd...

Supplementary Table 8: Contd...

Accession	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	Biologic Process	Molecular Function
IP100515092	Osteoglycin	12.69	2	2	2	9	15.48	268	30.4	8.34	Extracellular region		Growth factor activity
IP100892879	27 kDa protein	12.65	3	2	2	11	12.21	245	26.7	8.56	Plasma membrane	Cell adhesion	
IP100877884	17 kDa protein	12.42	2	1	1	1	2.31	153	17.0	4.92	Extracellular region	Single fertilization	
IP100376379	Keratin, type II cytoskeletal 1b	12.28	1	5	6	37	35.07	578	61.9	5.99	Cytoskeleton		Structural molecule activity
IP100305380	Insulin-like growth factor-binding protein 4	12.02	1	3	3	7	15.42	258	27.9	7.15	Extracellular region	Skeletal system development	Insulin-like growth factor binding
IP100296608	Complement component C7	11.98	1	4	7	21	36.70	843	93.5	6.48	Extracellular region	Adaptive immune response	
IP100221362	Isoform 3 of apoptosis-associated speck-like protein containing a CARD	11.85	3	1	1	3	5.02	135	15.0	7.44	Cytosol	Regulation of cytokine production	Endopeptidase activity
IP100926622	Putative uncharacterized protein PLGL	11.83	5	1	1	3	4.67	93	10.6	5.21	Extracellular region		
IP100965297	Uncharacterized protein	11.79	6	1	1	1	3.13	212	24.2	9.22			ATP binding
IP100792354	10 kDa protein	11.76	1	1	1	1	3.28	85	9.6	7.90			Enzyme activator activity
IP100003437	Guanylate cyclase activator 2B	11.61	1	1	1	1	2.46	112	12.1	6.48	Extracellular region	Circulatory system process	Aminomethyltransferase activity
IP100011604	Glycine cleavage system H protein, mitochondrial	11.56	2	1	1	1	3.85	173	18.9	4.88	Mitochondrion		
IP100789150	Uncharacterized protein	11.48	3	1	1	1	2.50	122	13.7	5.25	Plasma membrane	Immune response	
IP100023673	Galectin-3-binding protein	11.45	5	5	5	13	7.91	585	65.3	5.27	Extracellular region	Defense response	Scavenger receptor activity
IP100879709	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	
IP100794822	23 kDa protein	11.34	1	1	1	1	2.58	194	22.7	9.52	Nuclear envelope	RNA localization	Peptidase activity
IP100643158	43 kDa protein	11.29	10	2	3	7	12.13	381	42.5	4.83	Cytoskeleton	Protein complex assembly	Nucleotide binding
IP100967366	Uncharacterized protein	11.29	4	2	2	5	11.14	310	35.1	7.66			Selenium binding
IP100017704	Coactosin-like protein	11.27	1	1	1	1	4.77	142	15.9	5.67	Cytoskeleton	Defense response	Actin binding
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	
IP100917449	Protein	10.92	3	1	1	2	5.35	119	13.2	6.54	Extracellular region	Release of cytochrome c from mitochondria	Gamma-glutamyl cyclotransferase activity
IP100383486	22 kDa protein	10.88	3	1	1	1	2.77	193	22.0	5.69	ER	RNA processing	RNA binding
IP100910734	cDNA FLJ53641, highly similar to Intercellular adhesion molecule 1	10.59	4	3	3	3	7.72	444	48.1	8.16	Membrane	Cell activation	Integrin binding
IP100410714	Hemoglobin subunit alpha	10.56	1	1	1	3	10.87	142	15.2	8.68	Extracellular region	Gas transport	Oxygen transporter activity
IP100384697	Isoform 2 of serum albumin	10.55	10	4	4	40	26.02	417	47.3	6.35	Extracellular region	Cytolysis by symbiont of host cells	DNA binding

Contd..

Supplementary Table 8: Contd...

Accession	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	Biologic process	Molecular function
IP00219684	Fatty acid-binding protein, heart	10.53	1	2	2	3	10.39	133	14.8	6.80	Cytosol	Cellular amino acid derivative metabolic process	Lipid transporter activity
IP00329775	Isoform 1 of carboxypeptidase B2	10.17	3	3	3	3	10.66	423	48.4	7.71	Extracellular region	Proteolysis	Carboxypeptidase activity
IP00795257	32 kDa protein	9.90	7	2	2	4	3.29	293	31.5	7.61	Extracellular region	Skeletal system development	Enzyme inhibitor activity
IP00027851	cDNA FLJ53927, highly similar to beta-hexosaminidase alpha chain	9.81	4	4	4	5	7.89	540	62.0	5.26	Membrane		Beta-N-acetylhexosaminidase activity
IP00015881	Isoform 1 of macrophage colony-stimulating factor 1	9.75	4	4	4	20	22.29	554	60.1	5.29	Extracellular region	Cell activation	Cytokine activity
IP00873419	38 kDa protein	9.68	3	1	1	1	2.90	341	37.7	5.20	Integral to membrane		
IP00016334	Isoform 1 of cell surface glycoprotein MUC18	9.60	2	3	3	4	5.33	646	71.6	5.76	Plasma membrane	Cell adhesion	
IP00026926	Guanlylin	9.57	1	1	1	3	10.30	115	12.4	4.59	Extracellular region	Signal transduction	Hormone activity
IP00332887	Signal-regulatory protein alpha precursor	9.52	5	3	3	4	5.95	504	54.9	6.98	Plasma membrane	Cell adhesion	SH3 domain binding
IP00940046	cDNA FLJ40980 fis, clone UTERU2014464, highly similar to ACID CERAMIDASE	9.51	4	2	2	11	21.74	305	34.6	7.77		Membrane lipid metabolic process	Hydrolase activity
IP00893517	Putative uncharacterized protein EFEMP1	9.49	12	3	3	4	2.94	411	46.4	4.92	Ubiquitin ligase complex	Proteolysis	Ubiquitin-protein ligase activity
IP00878987	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
IP00012587	Phosphatidylinositol-3,4,5-trisphosphate 3-phosphatase and dual-specificity protein phosphatase PTEN	9.43	1	1	1	2	3.36	403	47.1	6.37	Mitochondrion	Regulation of cyclin-dependent protein kinase activity	Magnesium ion binding
IP00219131	Isoform 1 of ICOS ligand	9.27	4	2	2	2	5.86	302	33.3	5.31	Membrane	Cell activation	Receptor binding
IP00873598	Uncharacterized protein	9.23	14	1	6	35	23.45	455	49.1	4.79	Cytoskeleton	Ectoderm development	Structural molecule activity
IP00019580	Plasminogen	9.14	5	5	5	18	20.79	810	90.5	7.24	Cell fraction	Proteolysis	Endopeptidase activity
IP00657767	FLNA protein (fragment)	9.12	6	2	2	2	6.58	307	33.0	6.38			
IP00410360	Isoform 2 of neuroguidin	9.00	3	1	1	1	2.50	311	35.2	9.33	Filopodium	Regulation of translation	
IP00386975	Isoform 1B of desmocollin-1	8.93	2	5	5	11	8.25	840	93.8	5.53	Cell fraction	Cell adhesion	Calcium ion binding
IP00056357	UPF0556 protein C19orf10	8.67	1	1	1	1	2.38	173	18.8	6.68	Extracellular region	Positive regulation of cell proliferation	Growth factor activity
IP00297284	Insulin-like growth factor-binding protein 2 precursor	8.54	3	2	2	4	10.67	328	35.1	7.50	Extracellular region	Regulation of cell growth	Insulin-like growth factor binding
IP00298793	Beta-mannosidase	8.53	2	5	5	8	11.00	879	100.8	5.52	Cell fraction	Glycoprotein catabolic process	Beta-mannosidase activity
IP00798210	Isoform 4 of mesothelin	8.53	6	3	3	5	10.80	621	67.9	6.20	Extracellular region	Cell adhesion	Antigen binding
IP00292130	Dermatopontin	8.46	1	1	1	4	6.37	201	24.0	4.82	Extracellular region	Cell adhesion	

Contd..

Supplementary Table 8: Contd...

Accession	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	Biologic Process	Molecular Function
IP100019399	Serum amyloid A-4 protein	8.46	1	1	1	4	9.23	130	14.7	9.07	Extracellular region	Acute inflammatory response	
IP100305469	Adapter molecule crk isoform b	8.33	3	1	1	1	3.75	204	22.9	5.48	Endosome	Regulation of transcription	SH3/SH2 adaptor activity
IP100909308	cDNA FLJ57891, highly similar to tropomyosin beta chain	8.23	16	1	1	1	3.28	158	17.8	4.81		Immune response	Enzyme inhibitor activity
IP100796012	Squamous cell carcinoma antigen 1	8.23	3	1	1	1	3.15	158	18.2	7.55	Cytoplasm	Purine nucleotide metabolic process	Nucleotide binding
IP100945626	Uncharacterized protein	8.21	2	1	1	1	2.28	134	14.7	7.14	Nuclear envelope	Cell morphogenesis	Pattern binding
IP100922213	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		
IP100216773	ALB protein	8.08	10	3	3	46	21.14	396	45.1	6.10	Extracellular space	Cytolysis by symbiont of host cells	DNA binding
IP100298547	Protein DJ-1	7.94	1	1	1	1	3.00	189	19.9	6.79	Mitochondrion	Response to reactive oxygen species	Peroxiredoxin activity
IP100220281	Isoform alpha-1 of guanine nucleotide-binding protein G(o) subunit alpha	7.91	2	2	2	3	5.26	354	40.0	5.53	Cell fraction	Response to reactive oxygen species	Nucleotide binding
IP100012760	Leptin	7.78	1	1	1	1	3.80	167	18.6	6.37	Extracellular region	Ovulation from ovarian follicle	Hormone activity
IP100296537	Isoform C of fibulin-1	7.76	8	3	3	8	14.54	683	74.4	5.24	Extracellular region	Interspecies interaction between organisms	Structural molecule activity
IP100893264	30 kDa protein	7.64	3	1	1	1	3.39	275	29.9	6.10	Integral to membrane	Cell adhesion	Insulin-like growth factor binding
IP100020996	Insulin-like growth factor-binding protein complex acid labile subunit	7.60	2	3	3	11	20.47	605	66.0	6.79	Cell fraction	Apoptosis	Cysteine-type endopeptidase activity
IP100925214	Uncharacterized protein	7.58	1	1	1	23	12.71	277	31.0	5.74	Intracellular	Protein complex assembly	Copper ion binding
IP100902623	Major prion protein	7.36	5	1	1	7	11.37	163	18.2	5.76	ER	Mitotic cell cycle	
IP100301364	Isoform 1 of S-phase kinase-associated protein 1	7.36	1	1	1	1	2.51	163	18.6	4.54	Mitotic cell cycle	Adaptive immune response	
IP100022394	Component C1q subcomponent subunit C	7.35	1	1	1	2	7.75	245	25.8	8.41	Extracellular region	MAPKKK cascade	Enzyme inhibitor activity
IP100032291	Component C5	7.34	2	7	7	15	16.92	1676	188.2	6.52	Extracellular region		
IP100902750	cDNA FLJ38893 fis, clone NOVARI000091, highly similar to colorectal mutant cancer protein	7.30	3	1	1	1	2.85	411	46.1	5.05			
IP100007199	Protein Z-dependent protease inhibitor	7.23	1	2	2	4	11.31	484	55.1	7.64	Extracellular region	Response to wounding	Enzyme inhibitor activity
IP100013933	Isoform DPI of desmoplakin	7.18	3	13	13	43	27.91	2871	331.6	6.81	Cell junction , desmosome	Ectoderm development	Structural molecule activity

Contd...

Supplementary Table 8: Contd...

Accession	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	Biologic Process	Molecular Function
IP100911004	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
IP100384282	Cytovillin 2 (fragment)	7.09	7	1	1	1	2.54	141	16.2	9.31	Cytoplasm		Cytoskeletal protein binding
IP100749381	Gastrokine-1	7.04	1	1	1	2	6.83	199	22.0	6.32	Extracellular region	Digestion	Growth factor activity
IP100013682	isoform 3 of Ecto-ADP-ribosyltransferase 3	6.94	6	2	2	3	6.38	389	43.9	6.06	Plasma membrane	Protein amino acid ADP-ribosylation	NAD+ ADP-ribosyltransferase activity
IP100176710	Putative lipocalin 1-like protein 1	6.79	2	1	1	2	3.17	162	17.9	5.00	Extracellular region	Proteolysis	Enzyme inhibitor activity
IP100479027	Blood coagulation inhibitor, disintegrin domain containing protein	6.74	1	1	1	1	2.78	356	39.2	6.89			
IP100892906	18 kDa protein	6.67	7	1	1	1	2.25	165	18.0	8.12	Cytosol	Protein localization	Selenium binding
IP100972938	Coagulation factor IX	6.62	2	2	2	7	9.62	423	47.6	6.11	Golgi lumen		
IP100020599	Calreticulin	6.47	1	2	2	2	4.72	417	48.1	4.44	Cell fraction	Negative regulation of transcription from RNA polymerase II promoter	Opsonin binding
IP100946958	23 kDa protein	6.47	7	1	1	1	2.31	201	22.7	6.14			
IP100644990	cDNA FLJ25604 fis, clone JTH14207	6.39	2	1	1	1	2.73	548	61.3	8.94	Plasma membrane	Intracellular signaling cascade	Guanyl-nucleotide exchange factor activity
IP100025204	CD5 antigen-like	6.34	1	1	1	1	2.52	347	38.1	5.47	Extracellular region	Apoptosis	Scavenger receptor activity
IP100929685	Sex hormone-binding globulin isoform 2 precursor	6.25	2	1	1	1	2.37	384	41.7	6.71	Extracellular region	Reproductive development	Steroid binding
IP100029235	Insulin-like growth factor-binding protein 6	6.25	1	1	1	8	8.57	240	25.3	7.81	Extracellular region	Regulation of cell growth	Insulin-like growth factor binding
IP100910358	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
IP100032195	Heat shock protein beta-2	6.19	1	1	1	1	3.20	307	33.1	6.64	Cell fraction	Response to unfolded protein	Enzyme activator activity
IP100019576	Coagulation factor X	6.15	1	2	2	3	7.09	488	54.7	5.94	Cell fraction	Proteolysis	Endopeptidase activity
IP100922577	cDNA FLJ53768, highly similar to hepatocyte growth factor-like protein	6.10	6	1	1	1	3.25	164	17.8	9.11			
IP100924537	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
IP100166205	Isoform 2 of keratin, type II cytoskeletal 78	5.85	2	2	2	4	2.46	410	45.0	5.20	Cytoskeleton		Structural molecule activity
IP100644497	Conserved hypothetical protein	5.80	16	1	1	3	5.54	293	31.8	5.62		Immune response	Antigen binding
IP100556324	Transforming growth factor, beta-induced, 68kDa variant (fragment)	5.79	5	1	1	2	6.60	242	25.8	5.55			
IP100416676	Transmembrane protein 62	5.75	1	1	1	2	3.25	643	73.1	9.26	Integral to membrane		
IP100428511	Neurexin-1-beta	5.66	1	1	1	1	2.30	442	46.6	7.80	Plasma membrane	Cell morphogenesis	Calcium channel regulator activity

Contd...

Supplementary Table 8: Contd...

Accession	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	Biologic Process	Molecular Function
IP 00292069	Isoform 2 of complement decay-accelerating factor	5.51	9	2	2	3	4.68	381	41.4	7.59	Cell membrane	Adaptive immune response	Blood group antigen
IP 00915302	Glutathione synthetase	5.51	2	1	1	4	3.39	363	40.3	5.11	Cell fraction	Peptide metabolic process	Nucleotide binding
IP 00746033	47 kDa protein	5.49	3	1	1	1	3.53	419	47.1	7.46	Lysosome	Alpha-N-acetylglucosaminidase activity	Structural molecule activity
IP 00414684	Isoform 2 of semenogelin-1	5.47	2	1	1	1	3.65	402	45.3	9.38	Extracellular region	Insemination	Calcium ion binding
IP 00022389	Isoform 1 of C-reactive protein	5.36	1	2	2	5	17.55	224	25.0	5.63	Extracellular region	Adaptive immune response	Pattern binding
IP 00328550	Thrombospondin-4	5.31	5	3	3	3	6.79	961	105.8	4.68	Extracellular region	Cell motion	Protein binding
IP 00639961	Uncharacterized protein	5.23	1	1	1	2	4.48	325	34.7	9.39	Cytosol	Protein folding	Platelet activation
IP 00965713	Uncharacterized protein	5.15	2	1	1	1	2.54	272	31.2	7.25	Fibrinogen complex	Mitochondrion organization	Protein binding, bridging
IP 00103423	Isoform 4 of coxsackievirus and adenovirus receptor	5.00	6	1	1	1	2.39	200	22.4	8.43	Extracellular region	Vitamin metabolic process	Glutathione transferase activity
IP 00642936	Glutathione S-transferase omega 1 family member 9	5.00	2	1	1	1	2.36	200	23.3	7.21	Cytoplasm	Spliceosome assembly	RNA binding
IP 00797778	91 kDa protein	4.97	3	1	1	1	3.38	825	90.7	9.09	MAPKK cascade	Vasculature development	Ephrin receptor binding
IP 00413773	Isoform 6 of astrotactin-2	4.81	1	1	1	1	2.39	395	44.5	5.86	Integral to membrane	Retinoid metabolic process	Alcohol dehydrogenase (NAD) activity
IP 00005126	Ephrin-B2	4.80	1	1	1	1	3.61	333	36.9	8.85	Plasma membrane	Cell adhesion	Protein binding
IP 00106494	cDNA FLJ55219, highly similar to dehydrogenase/reductase SDR family member 9	4.75	1	1	1	1	2.88	379	41.9	8.90	Cell fraction	Cell adhesion	Protein binding
IP 00013303	Limbic system-associated membrane protein	4.73	2	1	1	2	3.99	338	37.4	6.98	Plasma membrane	Inositol metabolic process	Nucleotide binding
IP 00296589	ITPK1 protein (fragment)	4.73	1	1	1	1	2.61	444	48.6	5.19	Intracellular	Skeletal system development	Calcium ion binding
IP 00011685	Collagen alpha-1 (X) chain	4.71	1	1	1	1	2.60	680	66.1	9.67	Extracellular region	Response to unfolded protein	Nucleotide binding
IP 00890724	Isoform 7 of dermokine	4.61	8	1	1	1	4.22	369	35.3	6.43	Extracellular region	Cell motion	Actin binding
IP 00910755	cDNA FLJ51707, highly similar to heat-shock protein 105 kDa	4.54	1	1	1	14	22.09	639	71.2	8.46		Antigen processing and presentation of exogenous peptide antigen	
IP 00964934	cDNA FLJ51424, highly similar to tumor necrosis factor receptor superfamily member 16	4.50	2	1	1	1	2.46	333	35.7	4.70		Very-long-chain fatty acid metabolic process	Nucleotide binding
IP 00291175	Isoform 1 of Vinculin	4.41	3	3	3	6	9.74	1066	116.6	6.09	Extracellular region	Cell motion	Actin binding
IP 00871537	Gamma-interferon-inducible lysosomal thiol reductase preproprotein	4.40	2	1	1	1	2.52	250	27.9	4.88	Lysosome	Antigen processing and presentation of exogenous peptide antigen	
IP 00465431	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

Contd...

Supplementary Table 8: Contd...

Accession	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	Biologic Process	Molecular function
IP 00642882	31 kDa protein	4.32	3	1	1	1	2.56	278	30.7	9.09	Plasma membrane	Cell adhesion	Sugar binding
IP 00178015	Meprin A subunit beta	4.28	1	1	1	1	2.66	701	79.5	5.74	Cell fraction	Proteolysis	Endopeptidase activity
IP 00069985	Junction adhesion molecule	4.25	4	1	1	1	3.06	259	28.1	8.29	Plasma membrane	Defense response	
IP 00033583	Serpine B12	4.20	2	1	1	2	3.48	405	46.2	5.53	Cytoplasm	Regulation of catabolic process	Enzyme inhibitor activity
IP 00749485	Isoform 3 of matrilin-4	4.17	5	1	1	1	2.70	432	47.5	5.92	Extracellular region	Skeletal system development	Nucleotide binding
IP 00909967	Soluble PDGFRb variant 1	4.17	2	1	1	1	2.87	336	37.4	4.87	Skeletal system development	Skeletal system development	
IP 00923515	Amylase, alpha 2A	4.15	3	1	1	2	3.61	265	30.3	7.05		Carbohydrate metabolic process	Catalytic activity
IP 00247167	Nonspecific cytotoxic cell receptor protein 1 homolog	4.00	1	1	1	2	2.48	275	30.8	6.62		Macromolecule catabolic process	
IP 00299435	Apolipoprotein F precursor	3.99	1	1	1	1	2.99	326	35.4	5.64	Extracellular region	Lipid transport	Lipid transporter activity
IP 00607744	Isoform 2 of DNAJ homolog subfamily C member 11	3.84	1	1	1	1	2.50	521	58.9	7.61		Protein folding	Heat shock protein binding
IP 00922737	ADAM DEC1 isoform 2	3.84	2	1	1	1	3.94	391	43.5	7.01	Extracellular region	Proteolysis	Endopeptidase activity
IP 00150200	Isoform 3 of asiologlycoprotein receptor 2	3.83	7	1	1	1	3.53	287	32.5	5.80	Integral to membrane	Endocytosis	Asialoglycoprotein receptor activity
IP 00908698	Soluble EPHA1 variant 1	3.80	3	1	1	2	3.31	474	51.0	7.61	Plasma membrane	Protein amino acid phosphorylation	Nucleotide binding
IP 00186736	Isoform 3 of immunoglobulin superfamily member 8	3.61	2	1	1	1	3.03	526	55.8	8.78	Integral to membrane	Cell motion	
IP 00815674	LPHN1 protein (fragment)	3.61	3	1	1	1	2.50	388	43.9	8.28	Plasma membrane	Cell surface receptor linked signal transduction	Sugar binding
IP 00294004	Vitamin K-dependent protein S	3.55	5	2	2	5	10.79	676	75.1	5.67	Golgi lumen	Blood coagulation	Enzyme inhibitor activity
IP 00232492	Isoform beta of tripartite motif-containing protein 29	3.51	2	1	1	1	3.05	570	63.8	6.98	Cytoplasm	Transcription	DNA binding
IP 00643888	Isoform 3 of protein THEMIS	3.49	4	1	1	4	6.27	544	62.5	6.27	Cytoplasm, nucleus	Cell activation	Developmental protein
IP 00004500	NEDD4-binding protein 3	3.49	1	1	1	1	2.98	544	60.4	8.10	Extrinsic to membrane		
IP 00032288	MANSC domain-containing protein 1	3.48	1	1	1	1	3.44	431	46.8	6.54	Integral to membrane		Chitinase activity
IP 00099883	Isoform 1 of G-protein coupled receptor family C group 5 member C	3.40	4	1	1	1	2.57	441	48.2	8.43	Mitochondrion	Cell surface receptor linked signal transduction	
IP 00306483	Isoform 3 of coiled-coil and C2 domain-containing protein 1B	3.38	4	1	1	1	3.03	532	59.3	9.07			
IP 00909555	cDNA FLJ51602, highly similar to interferon-induced guanylate-binding protein 1	3.36	2	1	1	26	9.82	357	41.2	6.73	Plasma membrane	Immune response	Nucleotide binding
IP 00247063	Nephrilysin	3.33	1	2	2	2	2.94	750	85.5	5.73	Cell fraction	Proteolysis	Endopeptidase activity
IP 00154366	Isoform XLas-3 of guanine nucleotide-binding protein G(s) subunit alpha isoforms XLas	3.19	3	1	1	1	2.63	752	77.6	5.03	Golgi membrane	Skeletal system development	Nucleotide binding
IP 00397579	Isoform 2 of liprin-alpha-4	3.18	5	1	1	1	2.65	692	77.0	7.77	Cell surface		

Contd...

Supplementary Table 8: Contd...

Accession	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	Biologic Process	Molecular Function
IP 00644989	Isoform 1 of protein disulfide-isomerase A6	3.18	2	1	1	2	3.19	440	48.1	5.08	Protein folding	Protein folding	Protein disulfide isomerase activity
IP 00895858	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
IP 00022213	Gastricsin	3.09	1	1	1	1	2.35	388	42.4	4.46	Extracellular region	Proteolysis	Endopeptidase activity
IP 00337399	Isoform 4 of sodium/calcium exchanger 3	3.06	5	1	1	1	2.49	620	68.9	5.14	Integral to membrane	Ion transport	Calcium:sodium antiporter activity
IP 00028911	Dystroglycan	3.02	4	2	2	9	14.32	895	97.4	8.56	Plasma membrane	Morphogenesis of an epithelium	Calcium ion binding
IP 00016645	Isoform 1 of ephrin type-A receptor 7	3.01	6	2	2	7	8.17	998	112.0	5.80	Plasma membrane	Cell morphogenesis	Nucleotide binding
IP 00917696	Candidate tumor suppressor protein 1	3.01	2	1	1	2	2.38	798	89.1	6.27	Cell fraction	Endocytosis	Low-density lipoprotein receptor activity
IP 00412771	CD2-associated protein	2.97	1	1	1	1	2.50	639	71.4	6.40	Ruffle	M phase of mitotic cell cycle	Structural molecule activity
IP 00844090	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
IP 00019581	Coagulation factor XII	2.93	1	1	1	5	8.73	615	67.8	7.74	Extracellular region	Kinin cascade	Endopeptidase activity
IP 00910395	cDNA FLJ56819, highly similar to protocadherin-8	2.85	4	1	1	1	2.30	596	63.1	7.09	Plasma membrane	Somitogenesis	Calcium ion binding
IP 00872788	Dihydropyrimidinase-related protein 3	2.81	7	1	1	1	2.54	570	61.9	6.49	Cytoskeleton		Dihydropyrimidinase activity
IP 00289275	Cartilage intermediate layer protein 1	2.79	2	2	2	4	5.73	1184	132.5	8.38	Extracellular region	Negative regulation of signal transduction	Alkaline phosphatase activity
IP 00878551	cDNA FLJ59430, highly similar to protein disulfide-isomerase	2.65	2	1	1	1	2.64	452	51.2	4.88	Extracellular region	Cellular amino acid derivative metabolic process	Protein disulfide isomerase activity
IP 00871427	Uncharacterized protein	2.59	5	1	1	2	6.20	926	106.8	5.38	Extracellular region		Calcium ion binding
IP 00807475	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
IP 00639831	Isoform 2 of selenocysteine insertion sequence-binding protein 2	2.56	2	1	1	4	6.67	781	87.3	8.76	Nucleus	Translation	RNA binding
IP 00879984	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
IP 00026256	Flilaggrin	2.51	6	3	3	4	6.38	4061	434.9	9.25	Plasma membrane	Proteolysis	Carboxypeptidase activity
IP 00793420	Bone morphogenetic protein type II receptor	2.45	2	1	1	1	2.65	530	59.9	5.66	Plasma membrane	Formation of primary germ layer	Nucleotide binding
IP 00910597	cDNA FLJ56823, highly similar to protein-glutamine gamma-glutamyltransferase E	2.44	2	1	1	1	2.38	533	58.8	7.15		Hair follicle development	Nucleotide binding
IP 00007240	Coagulation factor XIII B chain	2.27	1	1	1	1	3.18	661	75.5	6.39	Extracellular region	Blood coagulation	Enzyme inhibitor activity
IP 00072918	322 kDa protein	2.25	9	5	5	9	7.61	2976	322.0	6.90		Cell adhesion	

Contd...

Supplementary Table 8: Contd...

Accession	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	Biologic Process	Molecular function	
IP 00376436	Isoform 4 of vacuolar protein sorting-associated protein 13B	2.20	5	1	1	1	2.80	863	97.3	5.16	Nuclear chromosome	Double-strand break repair via homologous recombination	Nuclease activity	
IP 00644184	Isoform 2 of protein unc-45 homolog B	2.12	3	1	1	1	3.21	850	94.8	7.85	Muscle organ development	Muscle organ development		
IP 00328243	Phospholipase D3	2.04	1	1	1	2	2.58	490	54.7	6.47	ER	Lipid catabolic process	Phospholipase activity	
IP 00741107	Isoform 3 of melanoma inhibitory activity protein 3	2.00	3	1	1	1	2.46	500	56.5	4.45	ER	Positive regulation of immune system process		
IP 00847557	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	
IP 00329771	Isoform 2 of a disintegrin and metalloproteinase with thrombospondin motifs 9	1.84	3	1	1	1	2.80	1629	182.6	7.68	Extracellular region	Proteolysis	Endopeptidase activity	
IP 00029193	Hepatocyte growth factor activator	1.83	2	1	1	1	3.10	655	70.6	7.24	Extracellular region	Proteolysis	Endopeptidase activity	
IP 00967340	LRBA protein	1.83	3	1	1	1	3.35	2575	286.8	5.52			Binding	
IP 00015309	Keratin, type I cytoskeletal 12	1.82	1	1	1	1	3.10	494	53.5	4.78	Cytoskeleton	Sensory perception	Structural molecule activity	
IP 00299503	Isoform 1 of phosphatidylinositol-glycan-specific phospholipase D	1.79	1	1	1	1	3.14	840	92.3	6.37	Extracellular region	GPI anchor metabolic process	Phospholipase activity	
IP 00738216	Uncharacterized protein KIAA0947	1.72	1	1	1	1	3.08	2266	247.7	5.48				Endopeptidase activity
IP 00788877	Isoform 6 of MAP kinase-activating death domain protein	1.56	10	1	1	1	2.59	1479	163.9	6.32	Plasma membrane	MAPKK cascade	Small GTPase regulator activity	
IP 00967837	111 kDa protein	1.55	2	1	1	1	2.28	970	110.7	7.02				Nucleotide binding
IP 00386324	Seven transmembrane helix receptor	1.50	1	1	1	1	2.55	1465	156.5	10.83	Cytoskeleton	Microtubule-based process		
IP 00893273	latent-transforming growth factor beta-binding protein 1 isoform 5 precursor	1.46	9	1	1	1	3.18	1300	142.6	4.93	Extracellular region		Protein kinase activity	
IP 00414467	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	
IP 00868965	Isoform 2 of NACHT and WD repeat domain-containing protein 1	1.33	3	1	1	1	2.54	1358	150.7	7.05			Nucleotide binding	
IP 00646555	SCAN domain-containing protein 3	1.28	1	1	1	1	2.39	1325	151.6	6.73	Nucleus	DNA integration	DNA binding	
IP 00028931	Desmoglein-2	1.25	1	1	1	2	3.31	1118	122.2	5.24	Plasma membrane	Cell adhesion	Calcium ion binding	
IP 00402215	Isoform 3 of collagen alpha-1 (XIV) chain	1.18	3	1	1	3	5.08	1701	183.0	5.29	Extracellular region	Cell adhesion	Structural molecule activity	
IP 00924656	228 kDa protein	1.18	1	1	1	1	2.60	2115	227.8	7.93			G2/M transition of mitotic cell cycle	Calmodulin binding
IP 00973279	Isoform 2 of pericentrin	1.05	2	1	1	1	3.10	3139	355.7	5.47	Cytoplasm			
IP 00292150	Latent-transforming growth factor beta-binding protein 2	1.04	1	1	1	2	3.20	1821	194.9	5.19	Extracellular region	Protein targeting	Calcium ion binding	

Contd...

Supplementary Table 8: Contd...

Accession	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	Biologic process	Molecular function
IP100296099	Thrombospondin-1	1.03	1	1	1	1	2.56	1170	129.3	4.94	Extracellular region	MAPKKK cascade	Pattern binding
IP100180408	Myosin-15	0.92	1	1	1	1	2.52	1946	224.5	5.85	Cytoskeleton		Nucleotide binding
IP100022449	Isoform 1 of dedicator of cytokinesis protein 2	0.87	1	1	1	1	2.42	1830	211.8	6.87	Cytosol	Cell morphogenesis	Small GTPase regulator activity
IP100644296	456 kDa protein	0.78	17	2	2	2	2.46	4222	455.9	5.20	Plasma membrane	Protein amino acid phosphorylation	Nucleotide binding
IP100385005	Putative uncharacterized protein DKFZp686M1993	0.75	5	1	1	1	2.27	1607	183.2	5.53	Centrosome	Regulation of neuron differentiation	Microtubule binding
IP100936444	cDNA FLJ59081, highly similar to Mucin-5B	0.74	3	1	1	1	3.32	5706	590.4	6.67	Extracellular region	Cell adhesion	Enzyme inhibitor activity
IP100328113	Fibrillin-1	0.45	1	1	1	2	5.12	2871	312.0	4.93	Microfibril	Skeletal system development	Structural molecule activity

MW: Molecular-weight, MFP: Multi-functional protein, HMW: High-molecular-weight, RER1: Retention in endoplasmic reticulum 1, HEBP2: Heme binding protein 2, FN1: Fibronectin 1, MAP: Mitogen-activated protein kinase, MA: Macroalbuminuria, MiA: Microalbuminuria, NA: Normoalbuminuria, ER: Endoplasmic reticulum, GPI: Glycosylphosphatidylinositol, PSM: Peptide spectrum match, AA: Amino acids

Contd...