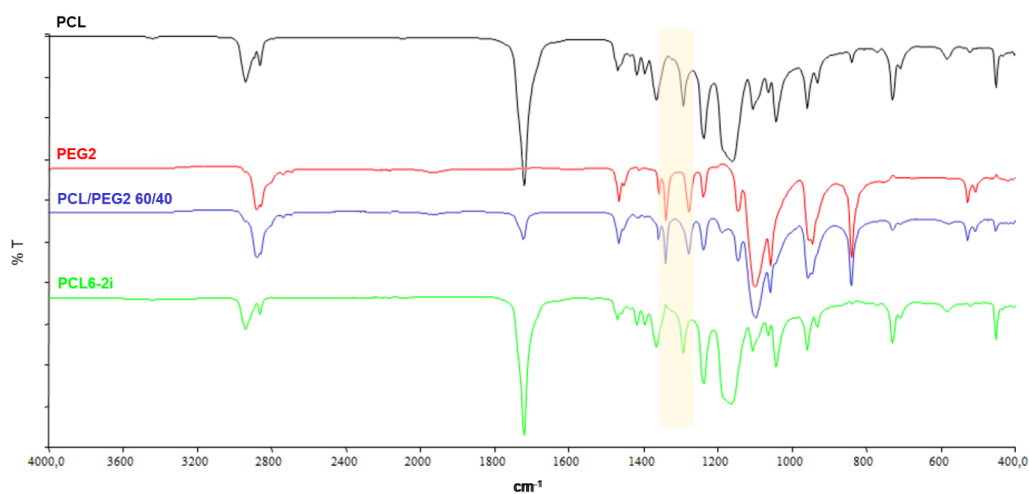


## SUPPLEMENTARY MATERIALS

### FIGURE S1

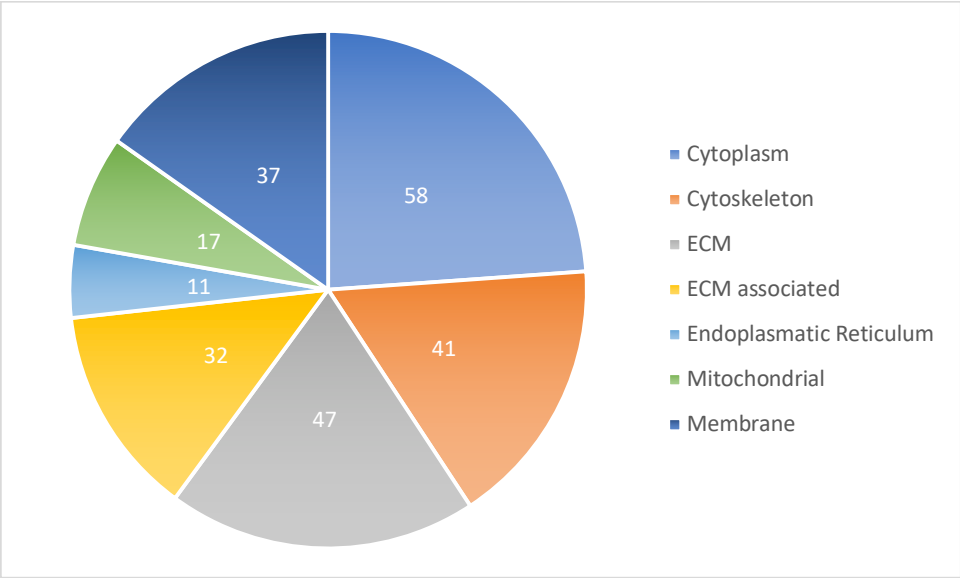
Figure S1 shows a comparison between FTIR-ATR spectra of PCL, PEG2 and PCL/PEG2 60/40 films before and after PEG2 removal. The same results have been observed for samples containing 30 % (wt) of PEG2 or PEG1 as porogen.



*Figure S1: FTIR-ATR spectra of PCL, PEG2 and blend films before and after PEG2 removal.*

**FIGURE S2**

Figure S2 shows the classification of proteins extracted from CMC and PCL7-2i membranes respect to their cellular localization.



*Figure S2. ECM protein classification according to their localization.*

**TABLE S1**

Table S1 shows the 243 proteins extracted from CMC and PCL7-2i membranes and identified by the Mass Spectrometry analysis.

N	Score	%Cov(95)	Uniprot Code	Gene name	Name	Peptides(95%)	Compartment	Biological Processes	Molecular Function	PANTHER ID
197	5,16	5,432999879	Q08211	DHX9_HUMAN	ATP-dependent RNA helicase A OS=Homo sapiens GN=DHX9 PE=1 SV=4	4	cito	ATP-dependent RNA helicase A (RHA) (EC 3.6.4.13) (DEAH box protein 9) (Leukophysin) (LKP) (Nuclear DNA helicase II) (NDH II)		
477	0,98	5,32400012	P23526	SAHH_HUMAN	Adenosylhomocysteinase OS=Homo sapiens GN=AHCY PE=1 SV=4	2	cyto			
73	16,73	28,79999876	P06733	ENOA_HUMAN	Alpha-enolase OS=Homo sapiens GN=ENO1 PE=1 SV=2	8	cyto	Alpha-enolase (EC 4.2.1.11) (2-phospho-D-glycerate hydro-lyase) (C-myc promoter-binding protein) (Enolase 1) (MBP-1) (MPB-1) (Non-neural enolase) (NNE) (Phosphopyruvate hydratase) (Plasminogen-binding protein)	DNA binding; M band; carbohydrate metabolic process; cytoplasm; cytosol; extracellular space; extracellular vesicular exosome; gluconeogenesis; glucose metabolic process; glycolytic process; magnesium ion binding; negative regulation of cell growth; negative regulation of transcription from RNA polymerase II promoter; negative regulation of transcription, DNA-templated; nucleus; phosphopyruvate hydratase activity; phosphopyruvate hydratase complex; plasma membrane; poly(A) RNA binding; protein binding; response to virus; sequence-specific DNA binding transcription factor activity; small molecule metabolic process; transcription corepressor activity; transcription, DNA-templated	Cytoplasm. Cell membrane. Cytoplasmic myofibril sarcomere line. Nucleus.
414	4,07	4,157999903	P50995	ANX11_HUMAN	Annexin A11 OS=Homo sapiens GN=ANXA11 PE=1 SV=1	2	cyto	Required for midbody formation and completion of the terminal phase of cytokinesis		
30	46,65	43,38999987	P08133	ANXA6_HUMAN	Annexin A6 OS=Homo sapiens GN=ANXA6 PE=1 SV=3	24	cyto	May regulate the release of Ca <sup>2+</sup> from intracellular stores.		

421	1,72	4,926000163	Q93088	BHMT1_HUMAN	Betaine--homocysteine S-methyltransferase 1 OS=Homo sapiens GN=BHMT PE=1 SV=2	2	cyto	Involved in the regulation of homocysteine metabolism.		
270	3,2	9,459000081	P27824	CALX_HUMAN	Calnexin OS=Homo sapiens GN=CANX PE=1 SV=2	3	cyto	Calnexin (cDNA FLJ55574, highly similar to Calnexin)		
220	4,35	9,091000259	P31944	CASPE_HUMAN	Caspase-14 OS=Homo sapiens GN=CASP14 PE=1 SV=2	3	cyto	Non-apoptotic caspase involved in epidermal differentiation.		
129	8,83	6,148999929	Q00610	CLH1_HUMAN	Clathrin heavy chain 1 OS=Homo sapiens GN=CLTC PE=1 SV=5	8	cyto			
256	3,7	10,80000028	O75131	CPNE3_HUMAN	Copine-3 OS=Homo sapiens GN=CPNE3 PE=1 SV=1	3	cyto	calcium-dependent phospholipid binding; cytoplasm; cytosol; extracellular vesicular exosome; lipid metabolic process; poly(A) RNA binding; protein phosphorylation; protein serine/threonine kinase activity; transporter activity; vesicle-mediated transport		
219	4,41	0,961900037	Q5D862	FILA2_HUMAN	Filaggrin-2 OS=Homo sapiens GN=FLG2 PE=1 SV=1	2	cyto			
221	4,34	8,049999923	Q13642	FHL1_HUMAN	Four and a half LIM domains protein 1 OS=Homo sapiens GN=FHL1 PE=1 SV=4	2	cyto			
44	24,66	64,17999864	P04406	G3P_HUMAN	Glyceraldehyde-3-phosphate dehydrogenase OS=Homo sapiens GN=GAPDH PE=1 SV=3	27	cyto	Glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12)		
160	6,73	18,06000024	P62826	RAN_HUMAN	GTP-binding nuclear protein Ran OS=Homo sapiens GN=RAN PE=1 SV=3	4	cyto	GTP-binding nuclear protein Ran (Fragment)	GTP binding; GTPase activity; intracellular protein transport; nucleocytoplasmic transport; small GTPase mediated signal transduction	
138	8,13	25,54999888	P63244	GBLP_HUMAN	Guanine nucleotide-binding protein subunit beta-2-like 1 OS=Homo sapiens GN=GNB2L1 PE=1 SV=3	5	cyto	Guanine nucleotide-binding protein subunit beta-2-like 1		
72	17,24	17,96000004	P11142	HSP7C_HUMAN	Heat shock cognate 71 kDa protein OS=Homo sapiens GN=HSPA8 PE=1 SV=1	10	cyto	Heat shock cognate 71 kDa protein		

131	8,6	36,10000014	P04792	HSPB1_HUMAN	Heat shock protein beta-1 OS=Homo sapiens GN=HSPB1 PE=1 SV=2	4	cyto	Heat shock protein beta-1 (HspB1) (28 kDa heat shock protein) (Estrogen-regulated 24 kDa protein) (Heat shock 27 kDa protein) (HSP 27) (Stress-responsive protein 27) (SRP27)		
524	3,82	3,962000087	P07900	HS90A_HUMAN	Heat shock protein HSP 90-alpha OS=Homo sapiens GN=HSP90AA1 PE=1 SV=5	2	cyto	Molecular chaperone that promotes the maturation, structural maintenance and proper regulation of specific target proteins involved for instance in cell cycle control and signal transduction		
120	9,38	10,63999981	P08238	HS90B_HUMAN	Heat shock protein HSP 90-beta OS=Homo sapiens GN=HSP90AB1 PE=1 SV=4	5	cyto			
317	2,26	1,963	P19367	HXK1_HUMAN	Hexokinase-1 OS=Homo sapiens GN=HK1 PE=1 SV=3	2	cyto	Hexokinase-1	ATP binding; glycolytic process; hexokinase activity	
64	17,94	17,50999987	Q86YZ3	HORN_HUMAN	Hornerin OS=Homo sapiens GN=HRNR PE=1 SV=2	14	cyto	Component of the epidermal cornified cell envelopes		
241	4	6,23300001	P50502	F10A1_HUMAN	Hsc70-interacting protein OS=Homo sapiens GN=ST13 PE=1 SV=2	2	cyto			
95	12,46	19,68999952	Q5T749	KPRP_HUMAN	Keratinocyte proline-rich protein OS=Homo sapiens GN=KPRP PE=1 SV=1	7	cyto			
228	4,11	6,627000123	P00338	LDHA_HUMAN	L-lactate dehydrogenase A chain OS=Homo sapiens GN=LDHA PE=1 SV=2	2	cyto	L-lactate dehydrogenase A chain (LDH-A) (EC 1.1.1.27) (Cell proliferation-inducing gene 19 protein) (LDH muscle subunit) (LDH-M) (Renal carcinoma antigen NY-REN-59)	L-lactate dehydrogenase activity; cellular metabolic process; cellular response to extracellular stimulus; cilium; cytosol; extracellular vesicular exosome; glycolytic process; mitochondrion; nucleus; protein binding; pyruvate metabolic process; small molecule metabolic process; substantia nigra development	

66	17,67	20,37999928	Q14764	MVP_HUMAN	Major vault protein OS=Homo sapiens GN=MVP PE=1 SV=4	12	cyto	Major vault protein (MVP) (Lung resistance-related protein)	ERBB signaling pathway; cell proliferation; cytoplasm; cytoskeleton; extracellular vesicular exosome; mRNA transport; negative regulation of protein autophosphorylation; negative regulation of protein tyrosine kinase activity; negative regulation of signaling; nuclear pore; nucleus; perinuclear region of cytoplasm; protein activation cascade; protein binding; protein kinase binding; protein phosphatase binding; protein transport; ribonucleoprotein complex	
292	2,72	16,77999943	P21741	MK_HUMAN	Midkine OS=Homo sapiens GN=MDK PE=1 SV=1	2	cyto	Midkine (Fragment)	adrenal gland development; behavioral fear response; cell migration; cerebellar granular layer development; cerebral cortex development; defecation; dentate gyrus development; negative regulation of neuron apoptotic process; positive regulation of transcription, DNA-templated; regulation of behavior; response to drug; response to glucocorticoid; response to wounding; short-term memory	
301	2,52	25,58000088	P00387	NB5R3_HUMAN	NADH-cytochrome b5 reductase 3 OS=Homo sapiens GN=CYB5R3 PE=1 SV=3	4	cyto	NADH-cytochrome b5 reductase 3 (B5R) (Cytochrome b5 reductase) (EC 1.6.2.2) (Diaphorase-1) [Cleaved into: NADH-cytochrome b5 reductase 3 membrane-bound form; NADH-cytochrome b5 reductase 3 soluble form]		
243	4	13,01999986	Q13765	NACA_HUMAN	Nascent polypeptide-associated complex subunit alpha OS=Homo sapiens GN=NACA PE=1 SV=1	2	cyto	Prevents inappropriate targeting of non-secretory polypeptides to the endoplasmic reticulum (ER). Binds to nascent polypeptide chains as they emerge from the ribosome and blocks their interaction with the signal recognition particle		

289	2,85	17,11000055	P15531	NDKA_HUMAN	Nucleoside diphosphate kinase A OS=Homo sapiens GN=NME1 PE=1 SV=1	2	cyto	Major role in the synthesis of nucleoside triphosphates other than ATP.		
289	2,53	17,11000055	P22392	NDKB_HUMAN	Nucleoside diphosphate kinase B OS=Homo sapiens GN=NME2 PE=1 SV=1	2	cyto	Major role in the synthesis of nucleoside triphosphates other than ATP.		
174	6,14	48,48000109	P62937	PPIA_HUMAN	Peptidyl-prolyl cis-trans isomerase A OS=Homo sapiens GN=PPIA PE=1 SV=2	6	cyto	PPIases accelerate the folding of proteins		
185	5,85	22,22000062	P23284	PIIB_HUMAN	Peptidyl-prolyl cis-trans isomerase B OS=Homo sapiens GN=PIIB PE=1 SV=2	5	cyto			
314	2,32	13,57000023	Q06830	PRDX1_HUMAN	Peroxiredoxin-1 OS=Homo sapiens GN=PRDX1 PE=1 SV=1	3	cyto	cell proliferation; cytoplasm; cytosol; erythrocyte homeostasis; extracellular space; extracellular vesicular exosome; heme binding; hydrogen peroxide catabolic process; melanosome; mitochondrial matrix; natural killer cell mediated cytotoxicity; nuclear euchromatin; nucleolus; nucleus; peroxidase activity; peroxisomal matrix; poly(A) RNA binding; protein binding; regulation of NF-kappaB import into nucleus; regulation of stress-activated MAPK cascade; removal of superoxide radicals; retina homeostasis; skeletal system development; thioredoxin peroxidase activity		
299	2,6	4,447999969	P36871	PGM1_HUMAN	Phosphoglucomutase-1 OS=Homo sapiens GN=PGM1 PE=1 SV=3	2	cyto	This enzyme participates in both the breakdown and synthesis of glucose.		
126	9,04	22,05999941	P00558	PGK1_HUMAN	Phosphoglycerate kinase 1 OS=Homo sapiens GN=PGK1 PE=1 SV=3	7	cyto	its role as a glycolytic enzyme,		

125	8,37	64,1900003	P0CG47	UBB_HUMAN	Polyubiquitin-B OS=Homo sapiens GN=UBB PE=1 SV=1	5	cyto			
125	8,37	64,38000202	P0CG48	UBC_HUMAN	Polyubiquitin-C OS=Homo sapiens GN=UBC PE=1 SV=3	5	cyto			
232	4,05	38,10000122	P31949	S10AB_HUMAN	Protein S100-A11 OS=Homo sapiens GN=S100A11 PE=1 SV=2	3	cyto	S100 protein binding; calcium ion binding; calcium-dependent protein binding; cytoplasm; extracellular space; extracellular vesicular exosome; negative regulation of DNA replication; negative regulation of cell proliferation; nucleus; protein binding; protein homodimerization activity; ruffle; signal transduction		
205	4,91	33,66999924	Q99584	S10AD_HUMAN	Protein S100-A13 OS=Homo sapiens GN=S100A13 PE=1 SV=1	3	cyto	Plays a role in the export of proteins that lack a signal peptide and are secreted by an alternative pathway		



45	23,89	34,63999927	P21980	TGM2_HUMAN	Protein-glutamine gamma-glutamyltransferase 2 OS=Homo sapiens GN=TGM2 PE=1 SV=2	17	cyto	GTP binding; apoptotic cell clearance; blood vessel remodeling; branching involved in salivary gland morphogenesis; extracellular vesicular exosome; isopeptide cross-linking via N6-(L-isoglutamyl)-L-lysine; metal ion binding; mitochondrion; plasma membrane; positive regulation of I-kappaB kinase/NF-kappaB signaling; positive regulation of apoptotic process; positive regulation of cell adhesion; positive regulation of cytosolic calcium ion concentration involved in phospholipase C-activating G-protein coupled signaling pathway; positive regulation of inflammatory response; positive regulation of smooth muscle cell proliferation; protein binding; protein homooligomerization; protein-glutamine gamma-glutamyltransferase activity; salivary gland cavitation		
241	4	9,583000094	Q8IZP2	ST134_HUMAN	Putative protein FAM10A4 OS=Homo sapiens GN=ST13P4 PE=5 SV=1	2	cyto			
241	4	9,75600034	Q8NFI4	F10A5_HUMAN	Putative protein FAM10A5 OS=Homo sapiens GN=ST13P5 PE=5 SV=1	3	cyto			
31	43,6	54,24000025	P14618	KPYM_HUMAN	Pyruvate kinase isozymes M1/M2 OS=Homo sapiens GN=PKM PE=1 SV=4	29	cyto	Glycolytic enzyme that catalyzes the transfer of a phosphoryl group from phosphoenolpyruvate (PEP) to ADP, generating ATP		
440	2,64	2,914999984	Q59EK9	RUN3A_HUMAN	RUN domain-containing protein 3A OS=Homo sapiens GN=RUNDC3A PE=2 SV=2	2	cyto			

533	0,54	7,833000273	O95084	PRS23_HUMAN	Serine protease 23 OS=Homo sapiens GN=PRSS23 PE=1 SV=1	2	cyto	serine-type endopeptidase activity		
115	9,73	27,27000117	P60174	TPIS_HUMAN	Triosephosphate isomerase OS=Homo sapiens GN=TP11 PE=1 SV=3	5	cyto			
125	9,06	43,59000027	P62979	RS27A_HUMAN	Ubiquitin-40S ribosomal protein S27a OS=Homo sapiens GN=RPS27A PE=1 SV=2	6	cyto			
125	8,37	38,28000128	P62987	RL40_HUMAN	Ubiquitin-60S ribosomal protein L40 OS=Homo sapiens GN=UBA52 PE=1 SV=2	5	cyto			
439	1,42	23,65999967	P05109	S10A8_HUMAN	Protein S100-A8 OS=Homo sapiens GN=S100A8 PE=1 SV=1	2	cyto	S100A8 is a calcium- and zinc-binding protein which plays a prominent role in the regulation of inflammatory processes and immune response.		
183	5,86	37,72000074	P06702	S10A9_HUMAN	Protein S100-A9 OS=Homo sapiens GN=S100A9 PE=1 SV=1	4	cyto	S100A9 is a calcium- and zinc-binding protein which plays a prominent role in the regulation of inflammatory processes and immune response.		
271	3,17	13,42999935	Q9H0U4	RAB1B_HUMAN	Ras-related protein Rab-1B OS=Homo sapiens GN=RAB1B PE=1 SV=1	2	cyto			

151	7,3	33,14999938	P84077	ARF1_HUMAN	ADP-ribosylation factor 1 OS=Homo sapiens GN=ARF1 PE=1 SV=2	5	cyto	ADP-ribosylation factor 1	COP1 coating of Golgi vesicle; GTP binding; GTP catabolic process; GTPase activity; Golgi membrane; antigen processing and presentation of exogenous peptide antigen via MHC class II; cell junction; cellular copper ion homeostasis; cytosol; dendritic spine organization; extracellular vesicular exosome; long term synaptic depression; membrane organization; neuron projection; perinuclear region of cytoplasm; phosphatidylinositol biosynthetic process; phospholipid metabolic process; plasma membrane; poly(A) RNA binding; post-Golgi vesicle-mediated transport; postsynaptic density; postsynaptic membrane; protein binding; protein transport; receptor signaling protein activity; regulation of Arp2/3 complex- mediated actin nucleation; regulation of defense response to virus by virus; regulation of receptor internalization; retrograde vesicle-mediated transport, Golgi to ER; sarcomere; small GTPase mediated signal transduction; small molecule metabolic process; viral process	Golgi apparatus. Cytoplasm ° perinuclear region. Cell junction ° synapse ° synaptosome. Cell junction ° synapse ° postsynaptic cell membrane ° postsynaptic density.
151	7,3	33,14999938	P61204	ARF3_HUMAN	ADP-ribosylation factor 3 OS=Homo sapiens GN=ARF3 PE=1 SV=2	5	cyto			

367	4	17,21999943	P18085	ARF4_HUMAN	ADP-ribosylation factor 4 OS=Homo sapiens GN=ARF4 PE=1 SV=3	2	cyto	ADP-ribosylation factor 4	GTP binding; Golgi apparatus; activation of phospholipase D activity; brain development; cell migration; cytosol; epidermal growth factor receptor binding; epidermal growth factor receptor signaling pathway; extracellular vesicular exosome; negative regulation of apoptotic process; positive regulation of transcription from RNA polymerase II promoter; protein ADP-ribosylation; protein binding; protein transport; regulation of reactive oxygen species metabolic process; response to axon injury; ruffle membrane; small GTPase mediated signal transduction; vesicle-mediated transport	
171	6,18	6,291999668	O00391	QSOX1_HUMAN	Sulfhydryl oxidase 1 OS=Homo sapiens GN=QSOX1 PE=1 SV=3	5	cyto	cell redox homeostasis; extracellular space; flavin-linked sulfhydryl oxidase activity; integral component of Golgi membrane; protein disulfide isomerase activity; protein folding		
271	3,17	13,42999935	Q92928	RAB1C_HUMAN	Putative Ras-related protein Rab-1C OS=Homo sapiens GN=RAB1C PE=5 SV=2	2	cyto	Protein transport. Probably involved in vesicular traffic		
271	3,17	13,16999942	P62820	RAB1A_HUMAN	Ras-related protein Rab-1A OS=Homo sapiens GN=RAB1A PE=1 SV=3	2	cyto	The small GTPases Rab are key regulators of intracellular membrane trafficking, from the formation of transport vesicles to their fusion with membranes.		
33	39,22	11,6899997	Q9Y490	TLN1_HUMAN	Talin-1 OS=Homo sapiens GN=TLN1 PE=1 SV=3	20	cyto	Probably involved in connections of major cytoskeletal structures to the plasma membrane.		
295	2,68	9,578999877	Q14847	LASP1_HUMAN	LIM and SH3 domain protein 1 OS=Homo sapiens GN=LASP1 PE=1 SV=2	2	cytosk	Plays an important role in the regulation of dynamic actin-based, cytoskeletal activities.		
465	1,12	5,033000186	Q9NR12	PDL17_HUMAN	PDZ and LIM domain protein 7 OS=Homo sapiens GN=PDLIM7 PE=1 SV=1	2	cytosk	May function as a scaffold on which the coordinated assembly of proteins can occur.		

458	1,17	61,36000156	P62328	TYB4_HUMAN	Thymosin beta-4 OS=Homo sapiens GN=TMSB4X PE=1 SV=2	2	cytosk	Plays an important role in the organization of the cytoskeleton		
17	88,09	72,32000232	P08670	VIME_HUMAN	Vimentin OS=Homo sapiens GN=VIM PE=1 SV=4	91	cytosk			
122	9,34	9,961999953	Q05682	CALD1_HUMAN	Caldesmon OS=Homo sapiens GN=CALD1 PE=1 SV=3	6	cytosk	Actin- and myosin-binding protein implicated in the regulation of actomyosin interactions in smooth muscle and nonmuscle cells (could act as a bridge between myosin and actin filaments).		
287	2,88	8,50699991	P27816	MAP4_HUMAN	Microtubule-associated protein 4 OS=Homo sapiens GN=MAP4 PE=1 SV=3	4	cytosk			
32	39,44	7,19500035	Q15149	PLEC_HUMAN	Plectin OS=Homo sapiens GN=PLEC PE=1 SV=3	19	cytosk	ankyrin binding; apoptotic process; cell junction assembly; cellular component disassembly involved in execution phase of apoptosis; costamere; cytoskeleton; cytosol; extracellular matrix organization; extracellular vesicular exosome; hemidesmosome; hemidesmosome assembly; plasma membrane; poly(A) RNA binding; protein binding; sarcolemma; sarcoplasm; structural constituent of muscle		
50	22,24	15,57999998	Q8WUJ3	K1199_HUMAN	Protein KIAA1199 OS=Homo sapiens GN=KIAA1199 PE=2 SV=2	15	cytosk	apoptotic process; calcium-dependent protein binding; cell cycle; cell division; cytosol; extracellular vesicular exosome; immunological synapse; melanosome; microtubule organizing center; protein binding; protein transport; viral life cycle; viral process		

210	4,74	6,177999824	Q16181	SEPT7_HUMAN	Septin-7 OS=Homo sapiens GN=SEPT7 PE=1 SV=2	3	cytosk	GTP binding; axon terminus; axoneme; cilium morphogenesis; cleavage furrow; condensed chromosome kinetochore; cytokinesis; extracellular vesicular exosome; identical protein binding; midbody; mitosis; nucleus; protein binding; protein heterooligomerization; regulation of embryonic cell shape; septin complex; spindle; stress fiber; structural molecule activity; synapse		
113	10,01	38,11999857	P05452	TETN_HUMAN	Tetranectin OS=Homo sapiens GN=CLEC3B PE=1 SV=3	6	cytosk	carbohydrate binding; ossification; skeletal system development		
454	1,21	9,273999929	P67936	TPM4_HUMAN	Tropomyosin alpha-4 chain OS=Homo sapiens GN=TPM4 PE=1 SV=3	2	cytosk	Binds to actin filaments in muscle and non-muscle cells.		
454	1,14	8,099000156	P07951	TPM2_HUMAN	Tropomyosin beta chain OS=Homo sapiens GN=TPM2 PE=1 SV=1	2	cytosk			
39	31,68	47,45000005	Q71U36	TBA1A_HUMAN	Tubulin alpha-1A chain OS=Homo sapiens GN=TUBA1A PE=1 SV=1	22	cytosk			
39	33,69	50,33000112	P68363	TBA1B_HUMAN	Tubulin alpha-1B chain OS=Homo sapiens GN=TUBA1B PE=1 SV=1	23	cytosk			
365	29,68	43,88000071	Q9BQE3	TBA1C_HUMAN	Tubulin alpha-1C chain OS=Homo sapiens GN=TUBA1C PE=1 SV=1	20	cytosk			
522	24,37	41,96000099	P68366	TBA4A_HUMAN	Tubulin alpha-4A chain OS=Homo sapiens GN=TUBA4A PE=1 SV=1	18	cytosk			
43	25,08	43,47000122	P07437	TBB5_HUMAN	Tubulin beta chain OS=Homo sapiens GN=TUBB PE=1 SV=2	17	cytosk			
196	21,13	37,38999963	P04350	TBB4A_HUMAN	Tubulin beta-4A chain OS=Homo sapiens GN=TUBB4A PE=1 SV=2	13	cytosk			
196	23,29	40,0000006	P68371	TBB4B_HUMAN	Tubulin beta-4B chain OS=Homo sapiens GN=TUBB4B PE=1 SV=1	15	cytosk			

425	1,67	3,085999936	P18206	VINC_HUMAN	Vinculin OS=Homo sapiens GN=VCL PE=1 SV=4	2	cytosk			
143	8,02	31,929999959	P23528	COF1_HUMAN	Cofilin-1 OS=Homo sapiens GN=CFL1 PE=1 SV=3	4	cytosk	Binds to F-actin and exhibits pH-sensitive F-actin depolymerizing activity. Regulates actin cytoskeleton dynamics. Important for normal progress through mitosis and normal cytokinesis.	actin filament depolymerization; cell projection organization; cortical actin cytoskeleton; establishment of cell polarity; lamellipodium; negative regulation of cell size; neural crest cell migration; neural fold formation; positive regulation of actin filament depolymerization; protein import into nucleus; protein phosphorylation; response to amino acid	
36	36,33	42,579999957	P06396	GELS_HUMAN	Gelsolin OS=Homo sapiens GN=GSN PE=1 SV=1	31	cytosk	Calcium-regulated, actin-modulating protein that binds to the plus (or barbed) ends of actin monomers or filaments, preventing monomer exchange (end-blocking or capping)		
276	3,12	2,559999935	Q15746	MYLK_HUMAN	Myosin light chain kinase, smooth muscle OS=Homo sapiens GN=MYLK PE=1 SV=4	2	cytosk	Myosin light chain kinase, smooth muscle (MLCK) (smMLCK) (EC 2.7.11.18) (Kinase-related protein) (KRP) (Telokin) [Cleaved into: Myosin light chain kinase, smooth muscle, deglutamylation form]	ATP binding; actin filament organization; aorta smooth muscle tissue morphogenesis; bleb assembly; calmodulin-dependent protein kinase activity; cellular hypotonic response; cleavage furrow; cytoplasm; cytosol; lamellipodium; metal ion binding; muscle contraction; myosin light chain kinase activity; positive regulation of calcium ion transport; positive regulation of cell migration; positive regulation of wound healing; protein binding; protein phosphorylation; smooth muscle contraction; stress fiber; tonic smooth muscle contraction	
97	11,51	59,60000157	P60660	MYL6_HUMAN	Myosin light polypeptide 6 OS=Homo sapiens GN=MYL6 PE=1 SV=2	7	cytosk			
199	5,11	23,980000062	P19105	ML12A_HUMAN	Myosin regulatory light chain 12A OS=Homo sapiens GN=MYL12A PE=1 SV=2	3	cytosk			

199	5,11	23,83999974	O14950	ML12B_HUMAN	Myosin regulatory light chain 12B OS=Homo sapiens GN=MYL12B PE=1 SV=2	3	cytosk			
187	20,74	8,299999684	P35580	MYH10_HUMAN	Myosin-10 OS=Homo sapiens GN=MYH10 PE=1 SV=3	11	cytosk	ATP binding; motor activity; myosin complex		
10	114,21	34,02999938	P35579	MYH9_HUMAN	Myosin-9 OS=Homo sapiens GN=MYH9 PE=1 SV=4	70	cytosk	ADP binding; ATP binding; ATP catabolic process; ATPase activity; actin binding; actin cytoskeleton; actin cytoskeleton reorganization; actin filament binding; actin filament-based movement; actin-dependent ATPase activity; actomyosin; actomyosin contractile ring; actomyosin structure organization; angiogenesis; axon guidance; blood vessel endothelial cell migration; cell leading edge; cell-cell adherens junction; cleavage furrow; cortical cytoskeleton; cytokinesis; cytoplasm; cytosol; establishment of T cell polarity; establishment of meiotic spindle localization; extracellular vesicular exosome; immunological synapse; in utero embryonic development; integrin-mediated signaling pathway; leukocyte migration; meiotic spindle organization; membrane protein ectodomain proteolysis; microfilament motor activity; monocyte differentiation; motor activity; myoblast fusion; myosin II complex; myosin II filament; neuromuscular junction; nucleus; plasma membrane; platelet formation; poly(A) RNA binding; protein anchor;		



								protein binding; protein complex; protein homodimerization activity; protein transport; regulation of cell shape; ruffle; single organismal cell-cell adhesion; spindle; stress fiber; termination of G-protein coupled receptor signaling pathway; uropod; uropod organization		
144	8	21,0800007	P29966	MARCS_HUMAN	Myristoylated alanine-rich C-kinase substrate OS=Homo sapiens GN=MARCKS PE=1 SV=4	5	cytosk	actin cytoskeleton; actin filament binding; calmodulin binding; cell cortex; centrosome; energy reserve metabolic process; extracellular vesicular exosome; germinal vesicle; plasma membrane; regulation of insulin secretion; small molecule metabolic process		
234	31,26	36,59999967	P68032	ACTC_HUMAN	Actin, alpha cardiac muscle 1 OS=Homo sapiens GN=ACTC1 PE=1 SV=1	28	cytosk	ATP binding; ATP catabolic process; ATPase activity; I band; actin filament; actin filament-based movement; actin-myosin filament sliding; actomyosin structure organization; actomyosin, actin portion; apoptotic process; blood microparticle; cardiac muscle contraction; cardiac muscle tissue morphogenesis; cardiac myofibril assembly; cytoplasm; cytosol; extracellular space; extracellular vesicular exosome; heart contraction; muscle filament sliding; myosin binding; negative regulation of apoptotic process; response to drug; response to ethanol;		

								sarcomere; skeletal muscle thin filament assembly		
234	31,28	42,44000018	P68133	ACTS_HUMAN	Actin, alpha skeletal muscle OS=Homo sapiens GN=ACTA1 PE=1 SV=1	29	cytosk			
234	29,26	33,68999958	P62736	ACTA_HUMAN	Actin, aortic smooth muscle OS=Homo sapiens GN=ACTA2 PE=1 SV=1	27	cytosk			
19	70,06	68,00000072	P60709	ACTB_HUMAN	Actin, cytoplasmic 1 OS=Homo sapiens GN=ACTB PE=1 SV=1	77	cytosk			
364	69,88	67,72999763	P63261	ACTG_HUMAN	Actin, cytoplasmic 2 OS=Homo sapiens GN=ACTG1 PE=1 SV=1	76	cytosk			
234	29,26	33,77999961	P63267	ACTH_HUMAN	Actin, gamma-enteric smooth muscle OS=Homo sapiens GN=ACTG2 PE=1 SV=1	27	cytosk			
40	28,09	23,88000041	P12814	ACTN1_HUMAN	Alpha-actinin-1 OS=Homo sapiens GN=ACTN1 PE=1 SV=2	15	cytosk	Alpha-actinin-1 (Alpha-actinin cytoskeletal isoform) (F-actin cross-linking protein) (Non-muscle alpha-actinin-1)	Z disc; actin filament bundle assembly; blood coagulation; calcium ion binding; cell junction assembly; cell projection; cytoplasm; cytoskeleton; cytosol; dendritic spine; double-stranded RNA binding; extracellular matrix organization; extracellular region; extracellular vesicular exosome; fascia adherens; focal adhesion; focal adhesion assembly; integrin binding; ion channel binding; negative regulation of cellular component movement; nucleus; plasma membrane; platelet activation; platelet alpha granule lumen; platelet degranulation; protein binding; pseudopodium; regulation of apoptotic process; ruffle; vinculin binding	Cytoplasm ° cytoskeleton. Cytoplasm ° myofibril ° Z line. Cell membrane. Cell junction. Cell projection ° ruffle.

135	21,15	16,35999978	O43707	ACTN4_HUMAN	Alpha-actinin-4 OS=Homo sapiens GN=ACTN4 PE=1 SV=2	11	cytosk	Alpha-actinin-4 (F-actin cross-linking protein) (Non-muscle alpha-actinin 4)	Z disc; actin binding; actin filament binding; actin filament bundle assembly; blood coagulation; calcium ion binding; cell-cell junction; cortical cytoskeleton; cytoplasm; extracellular region; extracellular vesicular exosome; integrin binding; negative regulation of cellular component movement; neuron projection; nucleoside binding; nucleus; perinuclear region of cytoplasm; platelet activation; platelet alpha granule lumen; platelet degranulation; poly(A) RNA binding; positive regulation of cellular component movement; positive regulation of pinocytosis; positive regulation of sodium:proton antiporter activity; protein binding; protein complex; protein homodimerization activity; protein transport; pseudopodium; regulation of apoptotic process; response to hypoxia; ribonucleoprotein complex; stress fiber; tight junction assembly	Nucleus. Cytoplasm. Cell junction.
60	18,72	25,42000115	Q07065	CKAP4_HUMAN	Cytoskeleton-associated protein 4 OS=Homo sapiens GN=CKAP4 PE=1 SV=2	12	cytosk	Cytoskeleton-associated protein 4 (63-kDa cytoskeleton-linking membrane protein) (Climp-63) (p63)	cytoskeleton; endoplasmic reticulum membrane; extracellular vesicular exosome; integral component of membrane; lipid particle; membrane; perinuclear region of cytoplasm; plasma membrane; poly(A) RNA binding	

9	114,36	37,85000145	P21333	FLNA_HUMAN	Filamin-A OS=Homo sapiens GN=FLNA PE=1 SV=4	64	cytosk	Filamin-A (FLN-A) (Actin-binding protein 280) (ABP-280) (Alpha-filamin) (Endothelial actin-binding protein) (Filamin-1) (Non-muscle filamin)	Fc-gamma receptor I complex binding; Myb complex; Rac GTPase binding; Ral GTPase binding; Rho GTPase binding; actin crosslink formation; actin cytoskeleton; actin cytoskeleton reorganization; actin filament; actin filament binding; adenylate cyclase-inhibiting dopamine receptor signaling pathway; apical dendrite; blood coagulation; cell junction assembly; cilium assembly; cortical cytoskeleton; cytoplasm; cytoplasmic sequestering of protein; cytosol; dendritic shaft; early endosome to late endosome transport; epithelial to mesenchymal transition; establishment of protein localization; extracellular region; extracellular vesicular exosome; glycoprotein binding; mRNA transcription from RNA polymerase II promoter; negative regulation of protein catabolic process; negative regulation of sequence-specific DNA binding transcription factor activity; neuronal cell body; nucleus; perinuclear region of cytoplasm; plasma membrane; platelet activation; platelet degranulation; poly(A) RNA binding; positive regulation of I-kappaB kinase/NF-kappaB signaling; positive regulation of transcription factor import into nucleus; protein binding; protein homodimerization activity; protein localization to cell surface; protein stabilization; receptor clustering; signal transducer activity; small GTPase binding; spindle assembly involved in mitosis; trans-Golgi network; transcription factor binding	
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38	36,61	12,65999973	Q14315	FLNC_HUMAN	Filamin-C OS=Homo sapiens GN=FLNC PE=1 SV=3	22	cytosk	Filamin-C (FLN-C) (FLNc) (ABP-280-like protein) (ABP-L) (Actin-binding-like protein) (Filamin-2) (Gamma-filamin)	Z disc; ankyrin binding; cell junction assembly; costamere; cytoplasm; cytoskeletal protein binding; cytoskeleton; cytosol; muscle fiber development; protein binding; sarcolemma; sarcoplasm	
94	12,71	44,78000104	P04075	ALDOA_HUMAN	Fructose-bisphosphate aldolase A OS=Homo sapiens GN=ALDOA PE=1 SV=2	12	cytosk	Fructose-bisphosphate aldolase A (EC 4.1.2.13) (Lung cancer antigen NY-LU-1) (Muscle-type aldolase)	ATP biosynthetic process; I band; actin binding; actin cytoskeleton; actin filament organization; blood coagulation; carbohydrate metabolic process; cytoskeletal protein binding; cytosol; extracellular region; extracellular space; extracellular vesicular exosome; fructose 1,6-bisphosphate metabolic process; fructose binding; fructose metabolic process; fructose-bisphosphate aldolase activity; gluconeogenesis; glucose metabolic process; glycolytic process; identical protein binding; muscle cell cellular homeostasis; nucleus; platelet activation; platelet alpha granule lumen; platelet degranulation; poly(A) RNA binding; protein binding; protein homotetramerization; regulation of cell shape; small molecule metabolic process; striated muscle contraction; tubulin binding	
426	1,66	3,308999911	Q9UHI8	ATSI_HUMAN	A disintegrin and metalloproteinase with thrombospondin motifs 1 OS=Homo sapiens GN=ADAMTS1 PE=1 SV=4	2	ECM	Cleaves aggrecan, a cartilage proteoglycan, Active metalloprotease, which may be associated with various inflammatory processes		
265	3,34	4,306000099	P01009	A1AT_HUMAN	Alpha-1-antitrypsin OS=Homo sapiens GN=SERPINA1 PE=1 SV=3	2	ECM	Its primary target is elastase		
3	241,16	48,1400013	P98160	PGBM_HUMAN	Basement membrane-specific heparan sulfate proteoglycan core protein OS=Homo sapiens GN=HSPG2 PE=1 SV=4	153	ECM	Basement membrane-specific heparan sulfate proteoglycan core protein (HSPG) (Perlecan) (PLC) [Cleaved into: Endorepellin; LG3 peptide]		

128	8,87	16,25999957	Q66K79	CBPZ_HUMAN	Carboxypeptidase Z OS=Homo sapiens GN=CPZ PE=1 SV=2	6	ECM	Carboxypeptidase Z (CPZ) (EC 3.4.17.-)		
252	3,89	6,316000223	Q76M96	CCD80_HUMAN	Coiled-coil domain- containing protein 80 OS=Homo sapiens GN=CCDC80 PE=1 SV=1	4	ECM	Promotes cell adhesion and matrix assembly.		
18	73,79	57,51000047	P02452	CO1A1_HUMAN	Collagen alpha-1(I) chain OS=Homo sapiens GN=COL1A1 PE=1 SV=5	131	ECM			
261	3,5	6,187000126	P02458	CO2A1_HUMAN	Collagen alpha-1(II) chain OS=Homo sapiens GN=COL2A1 PE=1 SV=3	6	ECM			
116	9,72	10,36999971	P02461	CO3A1_HUMAN	Collagen alpha-1(III) chain OS=Homo sapiens GN=COL3A1 PE=1 SV=4	12	ECM			
146	7,85	3,055999987	P02462	CO4A1_HUMAN	Collagen alpha-1(IV) chain OS=Homo sapiens GN=COL4A1 PE=1 SV=3	4	ECM			
168	6,23	7,126999646	P20908	CO5A1_HUMAN	Collagen alpha-1(V) chain OS=Homo sapiens GN=COL5A1 PE=1 SV=3	11	ECM			
25	55,46	40,07999897	P12109	CO6A1_HUMAN	Collagen alpha-1(VI) chain OS=Homo sapiens GN=COL6A1 PE=1 SV=3	49	ECM			
20	65,59	20,60000002	Q99715	COCA1_HUMAN	Collagen alpha-1(XII) chain OS=Homo sapiens GN=COL12A1 PE=1 SV=2	40	ECM			
412	1,8	2,521999925	P39059	COFA1_HUMAN	Collagen alpha-1(XV) chain OS=Homo sapiens GN=COL15A1 PE=1 SV=2	2	ECM			
222	4,33	1,807999983	Q07092	COGA1_HUMAN	Collagen alpha-1(XVI) chain OS=Homo sapiens GN=COL16A1 PE=1 SV=2	2	ECM			
23	57,24	51,16999745	P08123	CO1A2_HUMAN	Collagen alpha-2(I) chain OS=Homo sapiens GN=COL1A2 PE=1 SV=7	58	ECM			
264	3,35	1,576999947	P08572	CO4A2_HUMAN	Collagen alpha-2(IV) chain OS=Homo sapiens GN=COL4A2 PE=1 SV=4	2	ECM			
83	14,64	12,21000031	P05997	CO5A2_HUMAN	Collagen alpha-2(V) chain OS=Homo sapiens GN=COL5A2 PE=1 SV=3	10	ECM			

26	51,98	33,950001	P12110	CO6A2_HUMAN	Collagen alpha-2(VI) chain OS=Homo sapiens GN=COL6A2 PE=1 SV=4	44	ECM			
2	259,93	51,59000158	P12111	CO6A3_HUMAN	Collagen alpha-3(VI) chain OS=Homo sapiens GN=COL6A3 PE=1 SV=5	193	ECM			
65	17,91	56,36000037	P81605	DCD_HUMAN	Dermcidin OS=Homo sapiens GN=DCD PE=1 SV=2	17	ECM	DCD-1 displays antimicrobial activity thereby limiting skin infection by potential pathogens in the first few hours after bacterial colonization		
92	13,5	37,02000082	P15502	ELN_HUMAN	Elastin OS=Homo sapiens GN=ELN PE=1 SV=3	9	ECM	Elastin (Elastin (Supravalvular aortic stenosis, Williams-Beuren syndrome), isoform CRA_e)	extracellular matrix structural constituent; proteinaceous extracellular matrix	
15	92,47	56,40000105	Q9Y6C2	EMIL1_HUMAN	EMILIN-1 OS=Homo sapiens GN=EMILIN1 PE=1 SV=2	72	ECM	May be responsible for anchoring smooth muscle cells to elastic fibers, and may be involved not only in the formation of the elastic fiber, but also in the processes that regulate vessel assembly. Has cell adhesive capacity.		
405	1,9	2,563999966	Q9BXX0	EMIL2_HUMAN	EMILIN-2 OS=Homo sapiens GN=EMILIN2 PE=1 SV=3	2	ECM	May be responsible for anchoring smooth muscle cells to elastic fibers, and may be involved not only in the formation of the elastic fiber, but also in the processes that regulate vessel assembly		

6	151,39	38,73000145	P35555	FBN1_HUMAN	Fibrillin-1 OS=Homo sapiens GN=FBN1 PE=1 SV=3	100	ECM	basement membrane; calcium ion binding; extracellular matrix disassembly; extracellular matrix organization; extracellular matrix structural constituent; extracellular region; extracellular space; heart development; kidney development; microfibril; protein binding; proteinaceous extracellular matrix; sequestering of BMP in extracellular matrix; sequestering of TGFbeta in extracellular matrix; skeletal system development		
27	55,12	15,08000046	P35556	FBN2_HUMAN	Fibrillin-2 OS=Homo sapiens GN=FBN2 PE=1 SV=3	30	ECM	anatomical structure morphogenesis; bone trabecula formation; calcium ion binding; embryonic limb morphogenesis; extracellular matrix disassembly; extracellular matrix organization; extracellular matrix structural constituent; extracellular region; microfibril; positive regulation of bone mineralization; positive regulation of osteoblast differentiation; proteinaceous extracellular matrix; sequestering of TGFbeta in extracellular matrix		
1	442,67	80,22000194	P02751	FN1_HUMAN	Fibronectin OS=Homo sapiens GN=FN1 PE=1 SV=4	527	ECM	Fibronectins bind cell surfaces and various compounds including collagen, fibrin, heparin, DNA, and actin.		



55	19,11	20,34000009	P23142	FBLN1_HUMAN	Fibulin-1 OS=Homo sapiens GN=FBLN1 PE=1 SV=4	11	ECM	Fibulin-1 (FIBL-1)	basement membrane; calcium ion binding; embryo implantation; extracellular matrix organization; extracellular matrix structural constituent; extracellular region; extracellular space; peptidase activator activity; proteinaceous extracellular matrix; viral process	
21	61,94	44,42999959	P98095	FBLN2_HUMAN	Fibulin-2 OS=Homo sapiens GN=FBLN2 PE=1 SV=2	59	ECM	Its binding to fibronectin and some other ligands is calcium dependent. May act as an adapter that mediates the interaction between FBN1 and ELN	calcium ion binding; extracellular region	
89	13,97	70,3700006	P09382	LEG1_HUMAN	Galectin-1 OS=Homo sapiens GN=LGALS1 PE=1 SV=2	9	ECM	Galectin-1 (Gal-1) (14 kDa laminin-binding protein) (HLBP14) (14 kDa lectin) (Beta-galactoside-binding lectin L-14-I) (Galaptin) (HBL) (HPL) (Lactose-binding lectin 1) (Lectin galactoside-binding soluble 1) (Putative MAPK-activating protein PM12) (S-Lac lectin 1)	T cell costimulation; apoptotic process; cell surface; cellular response to glucose stimulus; cellular response to organic cyclic compound; cytoplasm; extracellular space; galactoside binding; intracellular; lactose binding; multicellular organismal response to stress; myoblast differentiation; negative regulation of cell-substrate adhesion; negative regulation of neuron projection development; nucleus; plasma cell differentiation; poly(A) RNA binding; positive regulation of I-kappaB kinase/NF-kappaB signaling; positive regulation of erythrocyte aggregation; protein binding; proteinaceous extracellular matrix; regulation of apoptotic process; response to axon injury; response to drug; signal transducer activity; signal transduction	Secreted &° extracellular space &° extracellular matrix.

159	6,75	3,790999949	P11047	LAMC1_HUMAN	Laminin subunit gamma-1 OS=Homo sapiens GN=LAMC1 PE=1 SV=3	4	ECM	Laminin subunit gamma-1 (Laminin B2 chain) (Laminin-1 subunit gamma) (Laminin-10 subunit gamma) (Laminin-11 subunit gamma) (Laminin-2 subunit gamma) (Laminin-3 subunit gamma) (Laminin-4 subunit gamma) (Laminin-6 subunit gamma) (Laminin-7 subunit gamma) (Laminin-8 subunit gamma) (Laminin-9 subunit gamma) (S-laminin subunit gamma) (S-LAM gamma)	axon guidance; basement membrane; cell adhesion; cell migration; endoderm development; extracellular matrix disassembly; extracellular matrix organization; extracellular matrix structural constituent; extracellular region; extracellular space; extracellular vesicular exosome; glycosphingolipid binding; hemidesmosome assembly; laminin-1 complex; laminin-10 complex; laminin-11 complex; positive regulation of epithelial cell proliferation; protein complex assembly; substrate adhesion-dependent cell spreading	
229	4,1	0,985199958	Q8N2S1	LTBP4_HUMAN	Latent-transforming growth factor beta-binding protein 4 OS=Homo sapiens GN=LTBP4 PE=1 SV=2	2	ECM	Latent-transforming growth factor beta-binding protein 4		
226	4,18	3,48800011	Q9Y4K0	LOXL2_HUMAN	Lysyl oxidase homolog 2 OS=Homo sapiens GN=LOXL2 PE=1 SV=1	2	ECM			
356	2,02	12,62000054	P08493	MGP_HUMAN	Matrix Gla protein OS=Homo sapiens GN=MGP PE=1 SV=2	5	ECM			
54	20,24	8,133000135	Q9NR99	MXRA5_HUMAN	Matrix-remodeling-associated protein 5 OS=Homo sapiens GN=MXRA5 PE=2 SV=3	15	ECM			
85	14,38	39,80999887	P35625	TIMP3_HUMAN	Metalloproteinase inhibitor 3 OS=Homo sapiens GN=TIMP3 PE=1 SV=2	10	ECM	Metalloproteinase inhibitor 3 (Protein MIG-5) (Tissue inhibitor of metalloproteinases 3) (TIMP-3)	basement membrane; cellular response to organic substance; metal ion binding; metalloendopeptidase inhibitor activity; negative regulation of endopeptidase activity; negative regulation of membrane protein ectodomain proteolysis; nucleus; protein binding; visual perception	Secreted K149 extracellular space â€œ extracellular matrix.
47	23,06	19,13000047	Q14112	NID2_HUMAN	Nidogen-2 OS=Homo sapiens GN=NID2 PE=1 SV=3	14	ECM	Nidogen-2 (NID-2) (Osteonidogen)	basement membrane; basement membrane organization; calcium ion binding; cell adhesion; cell surface; cell-matrix adhesion; collagen binding; extracellular matrix organization; extracellular region; protein binding	Secreted â€œ extracellular space â€œ extracellular matrix â€œ basement membrane.

111	10,15	8,612000197	Q15063	POSTN_HUMAN	Periostin OS=Homo sapiens GN=POSTN PE=1 SV=2	5	ECM	Induces cell attachment and spreading and plays a role in cell adhesion		
74	16,37	11,69999987	Q92626	PXDN_HUMAN	Peroxidasin homolog OS=Homo sapiens GN=PXDN PE=1 SV=2	10	ECM	Plays a role in extracellular matrix formation		
57	18,84	41,47000015	O00622	CYR61_HUMAN	Protein CYR61 OS=Homo sapiens GN=CYR61 PE=1 SV=1	15	ECM	Promotes cell proliferation, chemotaxis, angiogenesis and cell adhesion. Appears to play a role in wound healing by up-regulating, in skin fibroblasts, the expression of a number of genes involved in angiogenesis, inflammation and matrix remodeling including VEGA-A, VEGA-C, MMP1, MMP3, TIMP1, uPA, PAI-1 and integrins alpha-3 and alpha-5		
98	11,4	24,21000004	P41221	WNT5A_HUMAN	Protein Wnt-5a OS=Homo sapiens GN=WNT5A PE=1 SV=2	6	ECM	Golgi lumen; Wnt signaling pathway; Wnt signaling pathway; calcium modulating pathway; activation of JUN kinase activity; activation of MAPK activity; activation of protein kinase B activity; ameboidal cell migration; anterior/posterior axis specification, embryo; axon guidance; canonical Wnt signaling pathway; cartilage development; cell fate commitment; cell surface; cellular protein localization; cellular response to calcium ion; cellular response to interferon-gamma; cellular response to lipopolysaccharide; cellular response to retinoic acid; cellular response to transforming growth factor beta stimulus; cervix development; clathrin-coated endocytic vesicle		

								membrane; cochlea morphogenesis; convergent extension involved in organogenesis; dopaminergic neuron differentiation; embryonic digit morphogenesis; embryonic skeletal system development; endoplasmic reticulum lumen; epithelial cell proliferation involved in mammary gland duct elongation; epithelial to mesenchymal transition; establishment of planar polarity; extracellular region; extracellular space; extracellular vesicular exosome; face development; frizzled binding; genitalia development; heart looping; hematopoietic stem cell proliferation; hindgut morphogenesis; hypophysis morphogenesis; keratinocyte differentiation; lateral sprouting involved in mammary gland duct morphogenesis; lens development in camera-type eye; lung development; male gonad development; mammary gland branching involved in thelarche; mesenchymal-epithelial cell signaling; midgut development; negative chemotaxis; negative regulation of BMP signaling pathway; negative regulation of apoptotic process; negative regulation of axon extension involved in axon guidance; negative regulation of canonical Wnt signaling pathway; negative regulation of epithelial cell proliferation;		
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								<p>negative regulation of fat cell differentiation; negative regulation of fibroblast growth factor receptor signaling pathway; negative regulation of mesenchymal cell proliferation; negative regulation of prostatic bud formation; negative regulation of synapse assembly; negative regulation of transcription, DNA-templated; neural tube closure; neuron differentiation; non-canonical Wnt signaling pathway via JNK cascade; olfactory bulb interneuron development; optic cup formation involved in camera-type eye development; palate development; planar cell polarity pathway involved in cardiac muscle tissue morphogenesis; planar cell polarity pathway involved in cardiac right atrium morphogenesis; planar cell polarity pathway involved in neural tube closure; planar cell polarity pathway involved in outflow tract morphogenesis; planar cell polarity pathway involved in pericardium morphogenesis; planar cell polarity pathway involved in ventricular septum morphogenesis; plasma membrane; positive regulation of JNK cascade; positive regulation of NF-kappaB transcription factor activity; positive regulation of T cell chemotaxis; positive regulation of angiogenesis; positive regulation of cGMP metabolic process; positive</p>		
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								<p> regulation of cartilage development; positive regulation of cell-cell adhesion mediated by cadherin; positive regulation of chemokine biosynthetic process; positive regulation of cytokine secretion involved in immune response; positive regulation of endothelial cell migration; positive regulation of endothelial cell proliferation; positive regulation of fibroblast proliferation; positive regulation of inflammatory response; positive regulation of interferon-gamma production; positive regulation of interleukin-1 beta secretion; positive regulation of interleukin-6 production; positive regulation of interleukin-8 secretion; positive regulation of macrophage activation; positive regulation of macrophage cytokine production; positive regulation of meiosis; positive regulation of mesenchymal cell proliferation; positive regulation of neuron projection development; positive regulation of ossification; positive regulation of peptidyl-serine phosphorylation; positive regulation of peptidyl-threonine phosphorylation; positive regulation of protein catabolic process; positive regulation of protein kinase C signaling; positive regulation of response to cytokine stimulus; positive regulation of thymocyte </p>		
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								apoptotic process; positive regulation of transcription from RNA polymerase II promoter; positive regulation of transcription, DNA-templated; positive regulation of type I interferon-mediated signaling pathway; post-anal tail morphogenesis; primitive streak formation; protein phosphorylation; proteinaceous extracellular matrix; receptor agonist activity; receptor tyrosine kinase-like orphan receptor binding; regulation of branching involved in mammary gland duct morphogenesis; response to organic substance; sequence-specific DNA binding transcription factor activity; somitogenesis; transcription regulatory region DNA binding; type B pancreatic cell development; urinary bladder development; uterus development; vagina development; wound healing		
303	2,49	2,850000001	Q9HCB6	SPON1_HUMAN	Spondin-1 OS=Homo sapiens GN=SPON1 PE=1 SV=2	2	ECM			
154	7,07	23,04999977	Q6UWP8	SBSN_HUMAN	Suprabasin OS=Homo sapiens GN=SBSN PE=2 SV=2	6	ECM			
14	98,19	38,20999861	P24821	TENA_HUMAN	Tenascin OS=Homo sapiens GN=TNC PE=1 SV=3	63	ECM			
35	36,37	28,09000015	Q6ZMP0	THSD4_HUMAN	Thrombospondin type-1 domain-containing protein 4 OS=Homo sapiens GN=THSD4 PE=2 SV=2	21	ECM	elastic fiber assembly; extracellular vesicular exosome; metalloendopeptidase activity; microfibril		
207	4,85	26,37999952	P48307	TFPI2_HUMAN	Tissue factor pathway inhibitor 2 OS=Homo sapiens GN=TFPI2 PE=1 SV=1	4	ECM	May play a role in the regulation of plasmin-mediated matrix remodeling.		

42	25,22	34,2599988	Q15582	BGH3_HUMAN	Transforming growth factor-beta-induced protein ig-h3 OS=Homo sapiens GN=TGFB1 PE=1 SV=1	15	ECM	May play a role in cell-collagen interactions		
77	15,25	14,84999955	P04004	VTNC_HUMAN	Vitronectin OS=Homo sapiens GN=VTN PE=1 SV=1	21	ECM	Vitronectin is a cell adhesion and spreading factor found in serum and tissues. Vitronectin interact with glycosaminoglycans and proteoglycans.		
195	5,27	4,058999941	Q8IUX7	AEBP1_HUMAN	Adipocyte enhancer-binding protein 1 OS=Homo sapiens GN=AEBP1 PE=1 SV=1	3	ECM associated	Adipocyte enhancer-binding protein 1 (AE-binding protein 1) (Aortic carboxypeptidase-like protein)	DNA binding; carboxypeptidase activity; cell adhesion; cytoplasm; extracellular space; extracellular vesicular exosome; metalloproteinase activity; muscle organ development; nucleus; sequence-specific DNA binding transcription factor activity; skeletal system development; transcription corepressor activity; transcription, DNA-templated; zinc ion binding	



29	48,72	46,30999863	P07355	ANXA2_HUMAN	Annexin A2 OS=Homo sapiens GN=ANXA2 PE=1 SV=2	39	ECM associated	Annexin A2 (Annexin II) (Annexin-2) (Calpactin I heavy chain) (Calpactin-1 heavy chain) (Chromobindin-8) (Lipocortin II) (Placental anticoagulant protein IV) (PAP-IV) (Protein I) (p36)	S100 protein binding; Schmidt-Lanterman incisure; angiogenesis; basement membrane; body fluid secretion; calcium ion binding; calcium-dependent phospholipid binding; cell cortex; cell surface; cellular response to acid; collagen fibril organization; early endosome; extracellular space; extracellular vesicular exosome; extrinsic component of plasma membrane; fibrinolysis; lipid particle; macropinosome; melanosome; membrane budding; membrane raft assembly; midbody; myelin sheath adaxonal region; negative regulation of catalytic activity; nucleus; osteoclast development; perinuclear region of cytoplasm; phosphatidylinositol-4,5-bisphosphate binding; phospholipase A2 inhibitor activity; poly(A) RNA binding; positive regulation of binding; positive regulation of fibroblast proliferation; positive regulation of protein phosphorylation; positive regulation of vesicle fusion; protein binding; protein complex; protein heterotetramerization; protein targeting to plasma membrane; ruffle; sarcolemma	Secreted &° extracellular space &° extracellular matrix &° basement membrane. Melanosome.
278	3,1	8,078999817	P15169	CBPN_HUMAN	Carboxypeptidase N catalytic chain OS=Homo sapiens GN=CPN1 PE=1 SV=1	2	ECM associated			
181	6	24,43999946	O94907	DKK1_HUMAN	Dickkopf-related protein 1 OS=Homo sapiens GN=DKK1 PE=1 SV=1	4	ECM associated			
82	14,71	31,15000129	O95967	FBLN4_HUMAN	EGF-containing fibulin-like extracellular matrix protein 2 OS=Homo sapiens GN=EFEMP2 PE=1 SV=3	8	ECM associated	EGF-containing fibulin-like extracellular matrix protein 2 (Fibulin-4) (FIBL-4) (Protein UPH1)	basement membrane; blood coagulation; calcium ion binding; extracellular matrix organization; extracellular matrix structural constituent; extracellular region; extracellular vesicular exosome; membrane; protein binding; transmembrane signaling receptor activity	Secreted.

279	3,05	6,59700036	P09038	FGF2_HUMAN	Fibroblast growth factor 2 OS=Homo sapiens GN=FGF2 PE=1 SV=3	2	ECM associated	Fibroblast growth factor 2 (FGF-2) (Basic fibroblast growth factor) (bFGF) (Heparin-binding growth factor 2) (HBGF-2)	C21-steroid hormone biosynthetic process; Fc-epsilon receptor signaling pathway; MAPK import into nucleus; Ras protein signal transduction; activation of MAPK activity; activation of MAPKK activity; branching involved in ureteric bud morphogenesis; cell migration involved in sprouting angiogenesis; chemoattractant activity; chemotaxis; chondroblast differentiation; corticotropin hormone secreting cell differentiation; cytokine activity; cytosol; embryonic morphogenesis; epidermal growth factor receptor signaling pathway; extracellular matrix organization; extracellular region; extracellular space; fibroblast growth factor receptor binding; fibroblast growth factor receptor signaling pathway; glial cell differentiation; growth factor activity; heparin binding; hyaluronan catabolic process; innate immune response; inositol phosphate biosynthetic process; insulin receptor signaling pathway; ligand-dependent nuclear receptor transcription coactivator activity; lung development; mammary gland epithelial cell differentiation; negative regulation of blood vessel endothelial cell migration; negative regulation of cell death; negative regulation of cell growth; negative regulation of cell proliferation; negative regulation of fibroblast migration; negative regulation of transcription, DNA-templated; negative regulation of wound healing; nervous system development; neurotrophin TRK receptor signaling pathway; nucleus; organ induction; organ morphogenesis; phosphatidylinositol biosynthetic process; phosphatidylinositol-mediated signaling; positive
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									<p>chemotaxis; positive regulation of ERK1 and ERK2 cascade; positive regulation of angiogenesis; positive regulation of blood vessel endothelial cell migration; positive regulation of cardiac muscle cell proliferation; positive regulation of cell division; positive regulation of cell fate specification; positive regulation of cell proliferation; positive regulation of cerebellar granule cell precursor proliferation; positive regulation of endothelial cell proliferation; positive regulation of osteoblast differentiation; positive regulation of phosphatidylinositol 3-kinase activity; positive regulation of phospholipase C activity; positive regulation of transcription from RNA polymerase II promoter; positive regulation of transcription, DNA-templated; protein binding; regulation of angiogenesis; regulation of cell cycle; regulation of retinal cell programmed cell death; release of sequestered calcium ion into cytosol; response to axon injury; signal transduction; stem cell development; substantia nigra development; thyroid-stimulating hormone-secreting cell differentiation; wound healing</p>	
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288	2,87	4,890000075	P28799	GRN_HUMAN	Granulins OS=Homo sapiens GN=GRN PE=1 SV=2	2	ECM associated	Granulins (Proepithelin) (PEPI) [Cleaved into: Acrogranin (Glycoprotein of 88 Kda) (Progranulin); Paragranulin; Granulin-1 (Granulin G); Granulin-2 (Granulin F); Granulin-3 (Granulin B); Granulin-4 (Granulin A); Granulin-5 (Granulin C); Granulin-6 (Granulin D); Granulin-7 (Granulin E)]		
69	17,35	61,9599998	O60565	GREM1_HUMAN	Gremlin-1 OS=Homo sapiens GN=GREM1 PE=1 SV=1	13	ECM associated	Gremlin-1 (Cell proliferation-inducing gene 2 protein) (Cysteine knot superfamily 1, BMP antagonist 1) (DAN domain family member 2) (Down-regulated in Mos-transformed cells protein) (Increased in high glucose protein 2) (IHG-2)	BMP binding; activation of transmembrane receptor protein tyrosine kinase activity; apoptotic process; branching involved in ureteric bud morphogenesis; cell migration involved in sprouting angiogenesis; cell morphogenesis; cell surface; cell-cell signaling; collagen fibril organization; determination of dorsal identity; embryonic limb morphogenesis; extracellular space; mesenchymal to epithelial transition involved in metanephros morphogenesis; morphogen activity; negative regulation of BMP signaling pathway; negative regulation of bone mineralization; negative regulation of bone mineralization involved in bone maturation; negative regulation of bone remodeling; negative regulation of bone trabecula formation; negative regulation of branching involved in ureteric bud morphogenesis; negative regulation of canonical Wnt signaling pathway; negative regulation of cell growth; negative regulation of monocyte chemotaxis; negative regulation of osteoblast proliferation; negative regulation of osteoclast proliferation; negative regulation of pathway-restricted SMAD protein phosphorylation; negative regulation of transcription, DNA-templated; positive regulation of NF-kappaB import into nucleus;	

									positive regulation of NF-kappaB transcription factor activity; positive regulation of angiogenesis; positive regulation of branching involved in ureteric bud morphogenesis; positive regulation of cardiac muscle cell differentiation; positive regulation of cell proliferation; positive regulation of peptidyl-tyrosine autophosphorylation; positive regulation of receptor activity; positive regulation of receptor internalization; positive regulation of telomerase activity; positive regulation of transcription from RNA polymerase II promoter; positive regulation of transcription from RNA polymerase II promoter involved in myocardial precursor cell differentiation; protein binding; proximal/distal pattern formation; receptor agonist activity; regulation of epithelial to mesenchymal transition; regulation of focal adhesion assembly; signal transduction; transmembrane receptor protein tyrosine kinase activator activity; ureteric bud formation; vascular endothelial growth factor receptor 2 binding	
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268	5,34	5,178999901	Q14520	HABP2_HUMAN	Hyaluronan-binding protein 2 OS=Homo sapiens GN=HABP2 PE=1 SV=1	3	ECM associated	Hyaluronan-binding protein 2 (EC 3.4.21.-) (Factor VII-activating protease) (Factor seven-activating protease) (FSAP) (Hepatocyte growth factor activator-like protein) (Plasma hyaluronan-binding protein) [Cleaved into: Hyaluronan-binding protein 2 50 kDa heavy chain; Hyaluronan-binding protein 2 50 kDa heavy chain alternate form; Hyaluronan-binding protein 2 27 kDa light chain; Hyaluronan-binding protein 2 27 kDa light chain alternate form]	cell adhesion; extracellular region; extracellular space; glycosaminoglycan binding; serine-type endopeptidase activity	Secreted.
202	4,99	28,33000124	P01344	IGF2_HUMAN	Insulin-like growth factor II OS=Homo sapiens GN=IGF2 PE=1 SV=1	5	ECM associated	Insulin-like growth factor II (IGF-II) (Somatomedin-A) [Cleaved into: Insulin-like growth factor II; Insulin-like growth factor II Ala-25 Del; Preptin]		
106	10,52	19,07999963	P18065	IBP2_HUMAN	Insulin-like growth factor-binding protein 2 OS=Homo sapiens GN=IGFBP2 PE=1 SV=2	5	ECM associated			
76	15,68	39,86000121	P17936	IBP3_HUMAN	Insulin-like growth factor-binding protein 3 OS=Homo sapiens GN=IGFBP3 PE=1 SV=2	11	ECM associated			
124	9,15	26,73999965	P22692	IBP4_HUMAN	Insulin-like growth factor-binding protein 4 OS=Homo sapiens GN=IGFBP4 PE=1 SV=2	5	ECM associated			
53	20,48	50,37000179	P24593	IBP5_HUMAN	Insulin-like growth factor-binding protein 5 OS=Homo sapiens GN=IGFBP5 PE=1 SV=1	14	ECM associated			
231	4,05	13,83000016	Q16270	IBP7_HUMAN	Insulin-like growth factor-binding protein 7 OS=Homo sapiens GN=IGFBP7 PE=1 SV=1	2	ECM associated			

213	4,63	2,964000031	P19827	ITIH1_HUMAN	Inter-alpha-trypsin inhibitor heavy chain H1 OS=Homo sapiens GN=ITIH1 PE=1 SV=3	3	ECM associated	May act as a carrier of hyaluronan in serum or as a binding protein between hyaluronan and other matrix protein, including those on cell surfaces in tissues to regulate the localization, synthesis and degradation of hyaluronan which are essential to cells undergoing biological processes.		
71	17,26	9,831000119	P19823	ITIH2_HUMAN	Inter-alpha-trypsin inhibitor heavy chain H2 OS=Homo sapiens GN=ITIH2 PE=1 SV=2	10	ECM associated			
112	10,12	9,212999791	Q06033	ITIH3_HUMAN	Inter-alpha-trypsin inhibitor heavy chain H3 OS=Homo sapiens GN=ITIH3 PE=1 SV=2	7	ECM associated			
172	6,17	3,548000008	Q14624	ITIH4_HUMAN	Inter-alpha-trypsin inhibitor heavy chain H4 OS=Homo sapiens GN=ITIH4 PE=1 SV=4	3	ECM associated			
179	6,01	2,639999986	P01042	KNG1_HUMAN	Kininogen-1 OS=Homo sapiens GN=KNG1 PE=1 SV=2	4	ECM associated	Kininogens are inhibitors of thiol proteases		
48	22,63	11,7399998	Q14766	LTBP1_HUMAN	Latent-transforming growth factor beta-binding protein 1 OS=Homo sapiens GN=LTBP1 PE=1 SV=4	12	ECM associated	Latent-transforming growth factor beta-binding protein 1 (LTBP-1) (Transforming growth factor beta-1-binding protein 1) (TGF-beta1-BP-1)	calcium ion binding; extracellular matrix; extracellular matrix organization; extracellular region; protein binding; proteinaceous extracellular matrix; sequestering of TGFbeta in extracellular matrix; transforming growth factor beta binding; transforming growth factor beta-activated receptor activity; transmembrane receptor protein serine/threonine kinase signaling pathway	
180	6,01	9,329999983	P36955	PEDF_HUMAN	Pigment epithelium-derived factor OS=Homo sapiens GN=SERPINF1 PE=1 SV=4	3	ECM associated	Neurotrophic protein; induces extensive neuronal differentiation in retinoblastoma cells		
249	3,98	12,55999953	P37802	TAGL2_HUMAN	Transgelin-2 OS=Homo sapiens GN=TAGLN2 PE=1 SV=3	2	ECM associated			

208	4,84	20,70000023	O00300	TR11B_HUMAN	Tumor necrosis factor receptor superfamily member 11B OS=Homo sapiens GN=TNFRSF11B PE=1 SV=3	4	ECM associated			
176	6,08	13,1099999	P02647	APOA1_HUMAN	Apolipoprotein A-I OS=Homo sapiens GN=APOA1 PE=1 SV=1	9	ECM associated	Participates in the reverse transport of cholesterol from tissues to the liver for excretion by promoting cholesterol efflux from tissues		
250	3,92	0,372599997	P04114	APOB_HUMAN	Apolipoprotein B-100 OS=Homo sapiens GN=APOB PE=1 SV=2	2	ECM associated	Apolipoprotein B is a major protein constituent of chylomicrons (apo B-48), LDL (apo B-100) and VLDL (apo B-100). Apo B-100 functions as a recognition signal for the cellular binding and internalization of LDL particles by the apoB/E receptor.		
247	4	19,19	P02656	APOC3_HUMAN	Apolipoprotein C-III OS=Homo sapiens GN=APOC3 PE=1 SV=1	2	ECM associated	Component of triglyceride-rich very low density lipoproteins (VLDL) and high density lipoproteins (HDL) in plasma	extracellular region; lipid binding; lipid transport; lipoprotein metabolic process	



91	13,82	17,98000038	P02649	APOE_HUMAN	Apolipoprotein E OS=Homo sapiens GN=APOE PE=1 SV=1	18	ECM associated	Apolipoprotein E (Apo-E)	G-protein coupled receptor signaling pathway; Golgi apparatus; N-methyl-D-aspartate receptor clustering; aging; alpha-amino-3-hydroxy-5-methyl-4-isoxazole propionate selective glutamate receptor clustering; antioxidant activity; artery morphogenesis; beta-amyloid binding; blood microparticle; cGMP-mediated signaling; cell death; cellular calcium ion homeostasis; cellular response to cholesterol; cellular response to growth factor stimulus; cellular response to interleukin-1; cholesterol catabolic process; cholesterol efflux; cholesterol homeostasis; cholesterol metabolic process; cholesterol transporter activity; chylomicron; chylomicron remnant clearance; cytoplasm; cytoskeleton organization; dendrite; dendritic spine maintenance; early endosome; endocytic vesicle lumen; extracellular region; extracellular space; extracellular vesicular exosome; extrinsic component of external side of plasma membrane; fatty acid homeostasis; fibril organization; heparin binding; high-density lipoprotein particle; high-density lipoprotein particle assembly; high-density lipoprotein particle clearance; high-density lipoprotein particle remodeling; hydroxyapatite binding; identical protein binding; intermediate-density lipoprotein particle; intracellular transport; late endosome; lipid binding; lipid transporter activity; lipoprotein biosynthetic process; lipoprotein catabolic process; lipoprotein metabolic process; lipoprotein particle binding; long-chain fatty acid transport; long-chain fatty acid transporter activity; low-density lipoprotein particle; low-density lipoprotein particle	Secreted.
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									receptor binding; low-density lipoprotein particle remodeling; maintenance of location in cell; metal chelating activity; negative regulation of MAP kinase activity; negative regulation of beta-amyloid formation; negative regulation of blood coagulation; negative regulation of blood vessel endothelial cell migration; negative regulation of cholesterol biosynthetic process; negative regulation of dendritic spine development; negative regulation of endothelial cell proliferation; negative regulation of inflammatory response; negative regulation of neuron apoptotic process; negative regulation of platelet activation; negative regulation of postsynaptic membrane organization; negative regulation of presynaptic membrane organization; neuronal cell body; nitric oxide mediated signal transduction; nucleus; oligodendrocyte differentiation; peripheral nervous system axon regeneration; phosphatidylcholine-sterol O-acyltransferase activator activity; phospholipid binding; phospholipid efflux; phototransduction, visible light; plasma membrane; positive regulation of axon extension; positive regulation of beta-amyloid formation; positive regulation of cGMP biosynthetic process; positive regulation of cholesterol efflux; positive regulation of cholesterol esterification; positive regulation of dendritic spine development; positive regulation of lipid biosynthetic process; positive regulation of low-density lipoprotein particle receptor catabolic process; positive regulation of membrane protein ectodomain proteolysis; positive regulation of neuron death;	
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									positive regulation of nitric-oxide synthase activity; protein binding; protein homodimerization activity; protein import; receptor-mediated endocytosis; regulation of Cdc42 protein signal transduction; regulation of axon extension; regulation of beta-amyloid clearance; regulation of neuron death; regulation of neuronal synaptic plasticity; regulation of protein kinase activity; response to dietary excess; response to ethanol; response to insulin; response to reactive oxygen species; response to retinoic acid; retinoid metabolic process; reverse cholesterol transport; small molecule metabolic process; synaptic transmission, cholinergic; tau protein binding; triglyceride metabolic process; vasodilation; very-low-density lipoprotein particle; very-low-density lipoprotein particle clearance; very-low-density lipoprotein particle receptor binding; very-low-density lipoprotein particle remodeling	
267	3,3	10,63999981	O95445	APOM_HUMAN	Apolipoprotein M OS=Homo sapiens GN=APOM PE=1 SV=2	3	ECM associated			
499	0,75	8,259999752	P07858	CATB_HUMAN	Cathepsin B OS=Homo sapiens GN=CTSB PE=1 SV=3	2	ECM associated	Thiol protease which is believed to participate in intracellular degradation and turnover of proteins.		
258	3,65	16,43999964	Q9NZT1	CALL5_HUMAN	Calmodulin-like protein 5 OS=Homo sapiens GN=CALML5 PE=1 SV=2	2	ECM associated			

109	10,33	9,283000231	P02774	VTDB_HUMAN	Vitamin D-binding protein OS=Homo sapiens GN=GC PE=1 SV=1	8	ECM associated	actin binding; blood microparticle; calcidiol binding; cytosol; extracellular region; lysosomal lumen; small molecule metabolic process; steroid metabolic process; vitamin D binding; vitamin D metabolic process; vitamin transport; vitamin transporter activity		
90	16,13	19,72000003	P11021	GRP78_HUMAN	78 kDa glucose-regulated protein OS=Homo sapiens GN=HSPA5 PE=1 SV=2	9	er			
236	4,02	7,124000043	Q12797	ASPH_HUMAN	Aspartyl/asparaginyl beta-hydroxylase OS=Homo sapiens GN=ASPH PE=1 SV=3	2	er	Aspartyl/asparaginyl beta-hydroxylase (EC 1.14.11.16) (Aspartate beta-hydroxylase) (ASP beta-hydroxylase) (Peptide-aspartate beta-dioxygenase)	activation of cysteine-type endopeptidase activity; activation of store-operated calcium channel activity; calcium channel complex; calcium ion binding; calcium ion transmembrane transport; cellular response to calcium ion; cortical endoplasmic reticulum; detection of calcium ion; electron carrier activity; endoplasmic reticulum; endoplasmic reticulum membrane; face morphogenesis; integral component of endoplasmic reticulum membrane; integral component of membrane; ion channel binding; junctional sarcoplasmic reticulum membrane; limb morphogenesis; muscle contraction; negative regulation of cell proliferation; palate development; pattern specification process; peptide-aspartate beta-dioxygenase activity; peptidyl-aspartic acid hydroxylation; plasma membrane; positive regulation of calcium ion transport into cytosol; positive regulation of intracellular protein transport; positive regulation of proteolysis; positive regulation of ryanodine-sensitive calcium-release channel activity; positive regulation of transcription, DNA-templated; protein binding; regulation of	Endoplasmic reticulum membrane; Single-pass type II membrane protein.

									cardiac muscle contraction by regulation of the release of sequestered calcium ion; regulation of cell communication by electrical coupling; regulation of inositol 1,4,5-trisphosphate-sensitive calcium-release channel activity; regulation of protein depolymerization; regulation of protein stability; regulation of release of sequestered calcium ion into cytosol by sarcoplasmic reticulum; regulation of ryanodine-sensitive calcium-release channel activity; response to ATP; sarcoplasmic reticulum lumen; sarcoplasmic reticulum membrane; structural constituent of muscle; structural molecule activity	
493	0,81	12,47000024	P27797	CALR_HUMAN	Calreticulin OS=Homo sapiens GN=CALR PE=1 SV=1	3	cr	Calreticulin (CRP55) (Calregulin) (Endoplasmic reticulum resident protein 60) (ERp60) (HACBP) (grp60)		
194	5,35	13,95000007	P04844	RPN2_HUMAN	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2 OS=Homo sapiens GN=RPN2 PE=1 SV=3	4	cr	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2 (EC 2.4.99.18) (Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 63 kDa subunit) (RIBIIR) (Ribophorin II) (RPN-II) (Ribophorin-2)	SRP-dependent cotranslational protein targeting to membrane; aging; autophagic vacuole membrane; cellular protein metabolic process; cellular protein modification process; endoplasmic reticulum membrane; gene expression; integral component of membrane; oligosaccharyltransferase complex; post-translational protein modification; protein N-linked glycosylation via asparagine; response to drug; ribosome binding; rough endoplasmic reticulum; transferase activity, transferring glycosyl groups; translation	

198	7,35	6,475999951	P14625	ENPL_HUMAN	Endoplasmin OS=Homo sapiens GN=HSP90B1 PE=1 SV=1	5	er	Endoplasmin (94 kDa glucose-regulated protein) (GRP-94) (Heat shock protein 90 kDa beta member 1) (Tumor rejection antigen 1) (gp96 homolog)	ATP binding; ER-associated ubiquitin-dependent protein catabolic process; RNA binding; actin rod assembly; activation of signaling protein activity involved in unfolded protein response; calcium ion binding; cellular protein metabolic process; cellular response to ATP; cytosol; endocytic vesicle lumen; endoplasmic reticulum; endoplasmic reticulum lumen; endoplasmic reticulum membrane; endoplasmic reticulum unfolded protein response; extracellular region; extracellular vesicular exosome; innate immune response; low-density lipoprotein particle receptor binding; melanosome; midbody; negative regulation of apoptotic process; nucleus; perinuclear region of cytoplasm; plasma membrane; protein binding; protein folding; protein phosphatase binding; protein transport; regulation of phosphoprotein phosphatase activity; response to hypoxia; sequestering of calcium ion; toll-like receptor signaling pathway; virion binding	Endoplasmic reticulum lumen. Melanosome.
266	3,31	2,985000052	Q8IWU6	SULF1_HUMAN	Extracellular sulfatase Sulf-1 OS=Homo sapiens GN=SULF1 PE=1 SV=1	2	er	Diminishes HSPG (heparan sulfate proteoglycans) sulfation,		
80	14,77	7,588999718	Q9P2E9	RRBP1_HUMAN	Ribosome-binding protein 1 OS=Homo sapiens GN=RRBP1 PE=1 SV=4	9	er	Acts as a ribosome receptor and mediates interaction between the ribosome and the endoplasmic reticulum membrane.		
240	4	3,454999998	P16615	AT2A2_HUMAN	Sarcoplasmic/endoplasmic reticulum calcium ATPase 2 OS=Homo sapiens GN=ATP2A2 PE=1 SV=1	2	er			
12	104,81	60,68000197	P07996	TSP1_HUMAN	Thrombospondin-1 OS=Homo sapiens GN=THBS1 PE=1 SV=2	96	er	Adhesive glycoprotein that mediates cell-to-cell and cell-to-matrix interaction		

327	2,14	11,15999967	Q9Y3B3	TMED7_HUMAN	Transmembrane emp24 domain-containing protein 7 OS=Homo sapiens GN=TMED7 PE=1 SV=2	2	er	Potential role in vesicular protein trafficking, mainly in the early secretory pathway.		
192	5,35	7,874000072	P07237	PDIA1_HUMAN	Protein disulfide-isomerase OS=Homo sapiens GN=P4HB PE=1 SV=3	3	er			
170	6,32	13,7500003	P08758	ANXA5_HUMAN	Annexin A5 OS=Homo sapiens GN=ANXA5 PE=1 SV=2	4	membr	This protein is an anticoagulant protein that acts as an indirect inhibitor of the thromboplastin-specific complex, which is involved in the blood coagulation cascade		
123	9,24	18,28999966	P21589	5NTD_HUMAN	5'-nucleotidase OS=Homo sapiens GN=NT5E PE=1 SV=1	6	membr	5'-nucleotidase (5'-NT) (EC 3.1.3.5) (Ecto-5'-nucleotidase) (CD antigen CD73)	5'-nucleotidase activity; AMP catabolic process; DNA metabolic process; adenosine biosynthetic process; anchored component of membrane; dephosphorylation; extracellular vesicular exosome; membrane; metal ion binding; negative regulation of inflammatory response; nucleobase-containing small molecule metabolic process; nucleotide binding; plasma membrane; purine nucleobase metabolic process; purine nucleotide catabolic process; pyrimidine nucleobase metabolic process; pyrimidine nucleoside catabolic process; small molecule metabolic process	
46	23,52	19,13000047	P15144	AMPN_HUMAN	Aminopeptidase N OS=Homo sapiens GN=ANPEP PE=1 SV=4	17	membr	Aminopeptidase N (AP-N) (hAPN) (EC 3.4.11.2) (Alanyl aminopeptidase) (Aminopeptidase M) (AP-M) (Microsomal aminopeptidase) (Myeloid plasma membrane glycoprotein CD13) (gp150) (CD antigen CD13)	aminopeptidase activity; angiogenesis; angiotensin maturation; cell differentiation; cellular protein metabolic process; cytosol; endoplasmic reticulum-Golgi intermediate compartment; external side of plasma membrane; extracellular vesicular exosome; integral component of plasma membrane; lysosomal membrane; metalloproteinase activity; receptor activity; viral process; virus receptor activity; zinc ion binding	Cell membrane; Single-pass type II membrane protein. Cytoplasmic domain.

93	13,22	29,76999879	P04083	ANXA1_HUMAN	Annexin A1 OS=Homo sapiens GN=ANXA1 PE=1 SV=2	8	membr	Annexin A1 (Annexin I) (Annexin-1) (Calpactin II) (Calpactin-2) (Chromobindin-9) (Lipocortin I) (Phospholipase A2 inhibitory protein) (p35)	alpha-beta T cell differentiation; arachidonic acid secretion; basolateral plasma membrane; calcium ion binding; calcium-dependent phospholipid binding; cell surface receptor signaling pathway; cellular component movement; cellular response to glucocorticoid stimulus; cellular response to hydrogen peroxide; cilium; cornified envelope; cytoplasm; endocrine pancreas development; estrous cycle phase; extracellular region; extracellular space; extracellular vesicular exosome; gliogenesis; hepatocyte differentiation; inflammatory response; insulin secretion; keratinocyte differentiation; mitochondrial membrane; negative regulation of acute inflammatory response; negative regulation of apoptotic process; negative regulation of catalytic activity; negative regulation of protein secretion; neutrophil clearance; neutrophil homeostasis; nucleus; peptide cross-linking; phospholipase A2 inhibitor activity; phospholipid binding; positive regulation of G1/S transition of mitotic cell cycle; positive regulation of neutrophil apoptotic process; positive regulation of prostaglandin biosynthetic process; positive regulation of vesicle fusion; protein binding; protein binding, bridging; protein complex; receptor binding; regulation of cell proliferation; response to X-ray; response to drug; response to estradiol; response to interleukin-1; response to peptide hormone; sarcolemma; signal transduction; structural molecule activity	Nucleus. Cytoplasm. Cell projection & cilium. Basolateral cell membrane.
259	3,57	17,41999984	Q03135	CAV1_HUMAN	Caveolin-1 OS=Homo sapiens GN=CAV1 PE=1 SV=4	2	membr	Caveolin-1	Golgi membrane; MAPK cascade; T cell costimulation; acrosomal membrane; angiogenesis; apical plasma membrane; apoptotic signaling	



									<p> pathway; basolateral plasma membrane; blood coagulation; calcium ion homeostasis; calcium ion transport; caveola; caveola assembly; caveolin-mediated endocytosis; cell cortex; cellular calcium ion homeostasis; cellular response to hyperoxia; cellular response to starvation; cholesterol binding; cholesterol homeostasis; cholesterol transport; cilium; cytoplasmic vesicle; cytosolic calcium ion homeostasis; endocytic vesicle membrane; endoplasmic reticulum; endosome; enzyme binding; inactivation of MAPK activity; integral component of plasma membrane; intracellular; lactation; leukocyte migration; lipid particle; lipid storage; maintenance of protein location in cell; mammary gland development; mammary gland involution; membrane depolarization; membrane raft; negative regulation of BMP signaling pathway; negative regulation of JAK-STAT cascade; negative regulation of MAPK cascade; negative regulation of anoikis; negative regulation of canonical Wnt signaling pathway; negative regulation of cytokine-mediated signaling pathway; negative regulation of endothelial cell proliferation; negative regulation of epithelial cell differentiation; negative regulation of nitric oxide biosynthetic process; negative regulation of nitric-oxide synthase activity; negative regulation of peptidyl-serine phosphorylation; negative regulation of pinocytosis; negative regulation of protein binding; negative regulation of protein ubiquitination; negative regulation of transcription from RNA polymerase II promoter; negative regulation of tyrosine </p>	
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									<p>phosphorylation of Stat5 protein; nitric oxide homeostasis; nitric oxide metabolic process; nitric-oxide synthase binding; patched binding; peptidase activator activity; perinuclear region of cytoplasm; plasma membrane; positive regulation of calcium ion transport into cytosol; positive regulation of canonical Wnt signaling pathway; positive regulation of extrinsic apoptotic signaling pathway; positive regulation of intrinsic apoptotic signaling pathway; positive regulation of metalloenzyme activity; positive regulation of peptidyl-serine phosphorylation; positive regulation of vasoconstriction; protein binding; protein complex; protein complex scaffold; protein homooligomerization; protein localization; receptor binding; receptor internalization involved in canonical Wnt signaling pathway; regulation of blood coagulation; regulation of fatty acid metabolic process; regulation of nitric-oxide synthase activity; regulation of peptidase activity; regulation of smooth muscle contraction; regulation of the force of heart contraction by chemical signal; response to calcium ion; response to estrogen; response to hypoxia; response to ischemia; response to progesterone; skeletal muscle tissue development; small molecule metabolic process; structural molecule activity; triglyceride metabolic process; vasculogenesis; vasoconstriction; vesicle organization; viral process</p>	
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104	10,59	6,436000019	Q6YHK3	CD109_HUMAN	CD109 antigen OS=Homo sapiens GN=CD109 PE=1 SV=2	6	membr	CD109 antigen (150 kDa TGF-beta-1-binding protein) (C3 and PZP-like alpha-2-macroglobulin domain-containing protein 7) (Platelet-specific Gov antigen) (p180) (r150) (CD antigen CD109)	anchored component of membrane; extracellular space; negative regulation of transforming growth factor beta receptor signaling pathway; negative regulation of wound healing; plasma membrane; serine-type endopeptidase inhibitor activity; transforming growth factor beta binding	Cell membrane; Lipid-anchor &circ; GPI-anchor.
166	6,26	6,334000081	P16070	CD44_HUMAN	CD44 antigen OS=Homo sapiens GN=CD44 PE=1 SV=3	5	membr	CD44 antigen	cell adhesion; hyaluronic acid binding; membrane	
204	4,96	29,690000041	P13987	CD59_HUMAN	CD59 glycoprotein OS=Homo sapiens GN=CD59 PE=1 SV=1	4	membr	CD59 glycoprotein		
248	4	18,21999997	P60033	CD81_HUMAN	CD81 antigen OS=Homo sapiens GN=CD81 PE=1 SV=1	3	membr	CD81 antigen (Fragment)	integral component of membrane	

200	7,14	22,50999957	P60953	CDC42_HUMAN	Cell division control protein 42 homolog OS=Homo sapiens GN=CDC42 PE=1 SV=2	4	membr	Cell division control protein 42 homolog (G25K GTP-binding protein)	Fc-gamma receptor signaling pathway involved in phagocytosis; GTP binding; GTP catabolic process; GTPase activity; Golgi membrane; Golgi organization; T cell costimulation; actin cytoskeleton organization; actin filament branching; actin filament bundle assembly; adherens junction organization; apical part of cell; apolipoprotein A-I receptor binding; axon guidance; blood coagulation; canonical Wnt signaling pathway; cardiac conduction system development; cellular protein localization; cytoplasm; cytosol; epidermal growth factor receptor signaling pathway; epithelial cell-cell adhesion; epithelial-mesenchymal cell signaling; establishment of Golgi localization; establishment or maintenance of apical/basal cell polarity; establishment or maintenance of cell polarity; extracellular vesicular exosome; filopodium; filopodium assembly; hair follicle morphogenesis; hair follicle placode formation; heart contraction; identical protein binding; innate immune response; keratinization; keratinocyte development; macrophage differentiation; membrane; microtubule organizing center; midbody; mitotic spindle; multicellular organism growth; muscle cell differentiation; negative regulation of epidermal growth factor receptor signaling pathway; negative regulation of gene expression; negative regulation of protein complex assembly; neuron fate determination; neuron projection; neuronal cell body; nuclear migration; organelle transport along microtubule; plasma membrane; positive regulation of DNA replication; positive regulation of JNK cascade;	Cell membrane; Lipid-anchor; Cytoplasmic side. Cytoplasm ↔ cytoskeleton ↔ microtubule organizing center ↔ centrosome. Cytoplasm ↔ cytoskeleton ↔ spindle. Midbody.
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									positive regulation of cytokinesis; positive regulation of gene expression; positive regulation of hair follicle cell proliferation; positive regulation of intracellular protein transport; positive regulation of metalloenzyme activity; positive regulation of muscle cell differentiation; positive regulation of neuron apoptotic process; positive regulation of peptidyl-serine phosphorylation; positive regulation of phosphatidylinositol 3-kinase activity; positive regulation of pseudopodium assembly; positive regulation of substrate adhesion-dependent cell spreading; positive regulation of synapse structural plasticity; protein binding; protein kinase binding; regulation of attachment of spindle microtubules to kinetochore; regulation of filopodium assembly; regulation of mitosis; regulation of protein catabolic process; regulation of protein heterodimerization activity; regulation of protein kinase activity; regulation of protein stability; regulation of small GTPase mediated signal transduction; secretory granule; small GTPase mediated signal transduction; spindle midzone; sprouting angiogenesis; submandibular salivary gland formation; substantia nigra development; thioesterase binding	
118	9,5	9,649000317	P05556	ITB1_HUMAN	Integrin beta-1 OS=Homo sapiens GN=ITGB1 PE=1 SV=2	5	membr	Integrin beta-1 (Fibronectin receptor subunit beta) (Glycoprotein IIa) (GPIIA) (VLA-4 subunit beta) (CD antigen CD29)		

227	4,13	8,145999908	P26038	MOES_HUMAN	Moesin OS=Homo sapiens GN=MSN PE=1 SV=3	2	membr	Moesin (Membrane-organizing extension spike protein)	apical part of cell; apical plasma membrane; basolateral plasma membrane; blood microparticle; cell adhesion molecule binding; cellular component movement; cytoplasm; cytoskeleton; double-stranded RNA binding; establishment of endothelial barrier; extracellular vesicular exosome; extrinsic component of membrane; filopodium; leukocyte cell-cell adhesion; leukocyte migration; membrane to membrane docking; microvillus; microvillus membrane; plasma membrane; positive regulation of gene expression; protein binding; protein kinase binding; receptor binding; regulation of lymphocyte migration; structural constituent of cytoskeleton; uropod	Cell membrane; Peripheral membrane protein; Cytoplasmic side. Cytoplasmic side. Apical cell membrane; Peripheral membrane protein; Cytoplasmic side. Cell projection microvillus membrane; Peripheral membrane protein; Cytoplasmic side.
218	4,39	2,037999965	Q9NZM1	MYOF_HUMAN	Myoferlin OS=Homo sapiens GN=MYOF PE=1 SV=1	2	membr	Calcium/phospholipid-binding protein that plays a role in the plasmalemma repair mechanism of endothelial cells that permits rapid resealing of membranes disrupted by mechanical stress. Involved in endocytic recycling		
101	11,25	10,27000025	P08473	NEP_HUMAN	Neprilysin OS=Homo sapiens GN=MME PE=1 SV=2	7	membr			
420	1,72	0,709199999	Q6ZW05	PTHD4_HUMAN	Patched domain-containing protein 4 OS=Homo sapiens GN=PTCHD4 PE=2 SV=3	2	membr			

136	8,13	4,707000032	P46940	IQGA1_HUMAN	Ras GTPase-activating-like protein IQGAP1 OS=Homo sapiens GN=IQGAP1 PE=1 SV=1	4	membr	GTPase activator activity; GTPase inhibitor activity; Ras GTPase activator activity; actin filament; calcium ion binding; calmodulin binding; cell leading edge; cellular response to calcium ion; cytoplasm; energy reserve metabolic process; extracellular vesicular exosome; extrinsic component of cytoplasmic side of plasma membrane; glomerular visceral epithelial cell development; lateral plasma membrane; microtubule; midbody; negative regulation of catalytic activity; negative regulation of dephosphorylation; neuron projection; phosphatidylinositol-3,4,5-trisphosphate binding; plasma membrane; positive regulation of GTPase activity; positive regulation of protein kinase activity; protein binding; protein kinase binding; protein phosphatase binding; regulation of cytokine production; regulation of insulin secretion; ribonucleoprotein complex; signal transduction; slit diaphragm; small GTPase mediated signal transduction; small molecule metabolic process		
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127	8,9	34,90000069	P63000	RAC1_HUMAN	Ras-related C3 botulinum toxin substrate 1 OS=Homo sapiens GN=RAC1 PE=1 SV=1	6	membr	<p>Fc-epsilon receptor signaling pathway; Fc-gamma receptor signaling pathway involved in phagocytosis; GTP binding; GTPase activity; Golgi membrane; Rho GDP-dissociation inhibitor binding; T cell costimulation; Wnt signaling pathway, planar cell polarity pathway; actin cytoskeleton organization; actin filament polymerization; anatomical structure arrangement; anatomical structure morphogenesis; apoptotic signaling pathway; auditory receptor cell morphogenesis; axon guidance; blood coagulation; bone resorption; cell adhesion; cell motility; cell proliferation; cell-cell junction organization; cell-matrix adhesion; cellular component movement; cerebral cortex radially oriented cell migration; cochlea morphogenesis; cytosol; dendrite morphogenesis; dopaminergic neuron differentiation; embryonic olfactory bulb interneuron precursor migration; engulfment of apoptotic cell; enzyme binding; epithelial cell morphogenesis; extracellular vesicular exosome; extrinsic component of plasma membrane; hyperosmotic response; inflammatory response; innate immune response; intracellular signal transduction; lamellipodium; lamellipodium assembly;</p>		
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								<p> localization within  membrane; mast cell  chemotaxis; melanosome;  membrane; negative  regulation of interleukin-23  production; negative  regulation of receptor-  mediated endocytosis;  neurotrophin TRK receptor  signaling pathway;  phagocytic cup; plasma  membrane; platelet  activation; positive  regulation of DNA  replication; positive  regulation of Rho protein  signal transduction;  positive regulation of actin  filament polymerization;  positive regulation of  apoptotic process; positive  regulation of  lamellipodium assembly;  positive regulation of  phosphatidylinositol 3-  kinase activity; positive  regulation of protein  phosphorylation; protein  binding; regulation of cell  migration; regulation of  defense response to virus  by virus; regulation of  hydrogen peroxide  metabolic process;  regulation of respiratory  burst; response to  wounding; ruffle assembly;  ruffle membrane; ruffle  organization; semaphorin-  plexin signaling pathway;  small GTPase mediated  signal transduction;  substrate adhesion-  dependent cell spreading;  thioesterase binding; trans-  Golgi network; viral  process </p>		
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554	1,41	11,63000017	P61106	RAB14_HUMAN	Ras-related protein Rab-14 OS=Homo sapiens GN=RAB14 PE=1 SV=4	2	membr	GDP binding; GTP binding; GTP catabolic process; GTPase activity; Golgi membrane; Golgi stack; Golgi to endosome transport; cytoplasmic vesicle membrane; cytosol; early endosome; early endosome membrane; embryo development; endocytic recycling; extracellular vesicular exosome; fibroblast growth factor receptor signaling pathway; intracellular; intracellular transport; late endosome; lysosomal membrane; lysosome; membrane organization; nuclear outer membrane-endoplasmic reticulum membrane network; perinuclear region of cytoplasm; phagocytic vesicle; phagocytic vesicle membrane; plasma membrane; protein binding; protein transport; recycling endosome; regulation of protein localization; rough endoplasmic reticulum; small GTPase mediated signal transduction; trans-Golgi network transport vesicle; vesicle-mediated transport		
139	8,08	22,98000008	P04216	THY1_HUMAN	Thy-1 membrane glycoprotein OS=Homo sapiens GN=THY1 PE=1 SV=2	5	membr	Thy-1 membrane glycoprotein (Fragment)		
161	6,67	7,113999873	P14923	PLAK_HUMAN	Junction plakoglobin OS=Homo sapiens GN=JUP PE=1 SV=3	3	membr	Common junctional plaque protein		
84	14,55	27,28999853	Q92743	HTRA1_HUMAN	Serine protease HTRA1 OS=Homo sapiens GN=HTRA1 PE=1 SV=1	10	membr	Serine protease with a variety of targets, including extracellular matrix proteins such as fibronectin		

148	10,12	19,75000054	P09525	ANXA4_HUMAN	Annexin A4 OS=Homo sapiens GN=ANXA4 PE=1 SV=4	5	membr	promotes membrane fusion and is involved in exocytosis.		
484	0,88	1,685000025	Q8WWZ4	ABCAA_HUMAN	ATP-binding cassette sub-family A member 10 OS=Homo sapiens GN=ABCA10 PE=2 SV=3	2	membr	Probable transporter which may play a role in macrophage lipid homeostasis		
141	8,06	44,04999912	P80723	BASP1_HUMAN	Brain acid soluble protein 1 OS=Homo sapiens GN=BASP1 PE=1 SV=2	6	membr			
158	6,89	4,473999888	Q08554	DSC1_HUMAN	Desmocollin-1 OS=Homo sapiens GN=DSC1 PE=1 SV=2	4	membr	Component of intercellular desmosome junctions. Involved in the interaction of plaque proteins and intermediate filaments mediating cell-cell adhesion.		
87	14,09	10,96000001	Q02413	DSG1_HUMAN	Desmoglein-1 OS=Homo sapiens GN=DSG1 PE=1 SV=2	9	membr	Component of intercellular desmosome junctions. Involved in the interaction of plaque proteins and intermediate filaments mediating cell-cell adhesion.		
79	14,85	3,203999996	P15924	DESP_HUMAN	Desmoplakin OS=Homo sapiens GN=DSP PE=1 SV=3	7	membr	Major high molecular weight protein of desmosomes		
153	7,12	19,51999962	Q9NZN4	EHD2_HUMAN	EH domain-containing protein 2 OS=Homo sapiens GN=EHD2 PE=1 SV=2	5	membr	ATP- and membrane-binding protein that controls membrane reorganization/tubulation upon ATP hydrolysis		
175	6,09	3,908000141	P08648	ITA5_HUMAN	Integrin alpha-5 OS=Homo sapiens GN=ITGA5 PE=1 SV=2	3	membr			
52	21,37	40,04999995	Q08431	MFGM_HUMAN	Lactadherin OS=Homo sapiens GN=MFGE8 PE=1 SV=2	13	membr	cell adhesion		

86	14,33	36,66999936	Q6NZI2	PTRF_HUMAN	Polymerase I and transcript release factor OS=Homo sapiens GN=PTRF PE=1 SV=1	10	membr	caveola; cytoplasm; cytosol; endoplasmic reticulum; gene expression; mitochondrion; nucleoplasm; nucleus; poly(A) RNA binding; protein binding; rRNA primary transcript binding; regulation of transcription, DNA-templated; termination of RNA polymerase I transcription; transcription from RNA polymerase I promoter; transcription initiation from RNA polymerase I promoter		
420	1,72	0,643800013	Q9Y5G6	PCDG7_HUMAN	Protocadherin gamma-A7 OS=Homo sapiens GN=PCDHGA7 PE=2 SV=1	2	membr			
193	5,35	17,92999953	P61224	RAP1B_HUMAN	Ras-related protein Rap-1b OS=Homo sapiens GN=RAP1B PE=1 SV=1	4	membr	GTP binding; GTP catabolic process; membrane; small GTPase mediated signal transduction		
193	3,21	11,9599998	A6NIZ1	RP1BL_HUMAN	Ras-related protein Rap-1b-like protein OS=Homo sapiens PE=2 SV=1	3	membr			
576	7,14	26,94000006	P08134	RHOC_HUMAN	Rho-related GTP-binding protein RhoC OS=Homo sapiens GN=RHOC PE=1 SV=1	6	membr	GTP binding; apical junction assembly; cytosol; nucleus; plasma membrane; small GTPase mediated signal transduction		
206	4,86	13,30000013	Q15019	SEPT2_HUMAN	Septin-2 OS=Homo sapiens GN=SEPT2 PE=1 SV=1	3	membr	GTP binding; cell cycle; cell surface; ciliary membrane; cilium assembly; enzyme regulator activity; exocyst; neuron projection development; perinuclear region of cytoplasm; regulation of L-glutamate transport; regulation of protein localization; septin complex; smoothened signaling pathway; synapse		

130	8,65	32,12000132	P61586	RHOA_HUMAN	Transforming protein RhoA OS=Homo sapiens GN=RHOA PE=1 SV=1	7	membr	Regulates a signal transduction pathway linking plasma membrane receptors to the assembly of focal adhesions and actin stress fibers.		
177	6,05	9,424000233	P10809	CH60_HUMAN	60 kDa heat shock protein, mitochondrial OS=Homo sapiens GN=HSPD1 PE=1 SV=2	3	mito	60 kDa heat shock protein, mitochondrial (60 kDa chaperonin) (Chaperonin 60) (CPN60) (Heat shock protein 60) (HSP-60) (Hsp60) (HuCHA60) (Mitochondrial matrix protein P1) (P60 lymphocyte protein)	'de novo' protein folding; ATP binding; ATP catabolic process; ATPase activity; B cell activation; B cell cytokine production; B cell proliferation; DNA replication origin binding; MyD88-dependent toll-like receptor signaling pathway; T cell activation; activation of cysteine-type endopeptidase activity involved in apoptotic process; cell surface; chaperone binding; chaperone-mediated protein complex assembly; coated pit; coated vesicle; cytoplasm; cytosol; double-stranded RNA binding; early endosome; extracellular space; extracellular vesicular exosome; isotype switching to IgG isotypes; lipopolysaccharide binding; lipopolysaccharide receptor complex; mitochondrial inner membrane; mitochondrial matrix; mitochondrion; negative regulation of apoptotic process; p53 binding; plasma membrane; poly(A) RNA binding; positive regulation of T cell activation; positive regulation of T cell mediated immune response to tumor cell; positive regulation of apoptotic process; positive regulation of interferon-alpha production; positive regulation of interferon-gamma production; positive regulation of interleukin-10 production; positive regulation of interleukin-12 production; positive regulation of interleukin-6 production; positive regulation of macrophage activation; protein binding; protein complex; protein maturation; protein refolding; protein stabilization; response to unfolded protein; secretory	

									granule; single-stranded DNA binding; unfolded protein binding; viral process	
281	3,01	7,413999736	P25705	ATPA_HUMAN	ATP synthase subunit alpha, mitochondrial OS=Homo sapiens GN=ATP5A1 PE=1 SV=1	3	mito	ATP synthase subunit alpha, mitochondrial		
165	6,35	14,5600006	P06576	ATPB_HUMAN	ATP synthase subunit beta, mitochondrial OS=Homo sapiens GN=ATP5B PE=1 SV=3	3	mito			
108	10,45	18,12999994	P31930	QCR1_HUMAN	Cytochrome b-c1 complex subunit 1, mitochondrial OS=Homo sapiens GN=UQCRC1 PE=1 SV=3	5	mito	Cytochrome b-c1 complex subunit 7 (Complex III subunit 7) (Complex III subunit VII) (QP-C) (Ubiquinol-cytochrome c reductase complex 14 kDa protein)	aerobic respiration; cellular metabolic process; mitochondrial electron transport, ubiquinol to cytochrome c; mitochondrial inner membrane; mitochondrial respiratory chain; mitochondrial respiratory chain complex III; oxidation-reduction process; oxidative phosphorylation; respiratory electron transport chain; small molecule metabolic process	Mitochondrion inner membrane.
147	7,81	16,779999943	P22695	QCR2_HUMAN	Cytochrome b-c1 complex subunit 2, mitochondrial OS=Homo sapiens GN=UQCRC2 PE=1 SV=3	5	mito	Cytochrome b-c1 complex subunit 2, mitochondrial (Complex III subunit 2) (Core protein II) (Ubiquinol-cytochrome-c reductase complex core protein 2)	aerobic respiration; cellular metabolic process; metal ion binding; metalloendopeptidase activity; mitochondrial inner membrane; mitochondrial respiratory chain complex III; mitochondrion; oxidative phosphorylation; protein binding; respiratory electron transport chain; small molecule metabolic process	Mitochondrion inner membrane; Peripheral membrane protein; Matrix side.
100	11,31	61,33000255	P20674	COX5A_HUMAN	Cytochrome c oxidase subunit 5A, mitochondrial OS=Homo sapiens GN=COX5A PE=1 SV=2	7	mito	Cytochrome c oxidase subunit 5A, mitochondrial (Cytochrome c oxidase polypeptide Va)	cellular metabolic process; cytochrome-c oxidase activity; electron carrier activity; hydrogen ion transmembrane transport; metal ion binding; mitochondrial inner membrane; respiratory electron transport chain; small molecule metabolic process	Mitochondrion inner membrane.

321	2,19	27,91000009	P10606	COX5B_HUMAN	Cytochrome c oxidase subunit 5B, mitochondrial OS=Homo sapiens GN=COX5B PE=1 SV=2	3	mito	Cytochrome c oxidase subunit 5B, mitochondrial (Cytochrome c oxidase polypeptide Vb)	cellular metabolic process; cytochrome-c oxidase activity; hydrogen ion transmembrane transport; metal ion binding; mitochondrial inner membrane; respiratory electron transport chain; respiratory gaseous exchange; small molecule metabolic process	Mitochondrion inner membrane.
286	2,89	33,7199986	P14854	CX6B1_HUMAN	Cytochrome c oxidase subunit 6B1 OS=Homo sapiens GN=COX6B1 PE=1 SV=2	2	mito	Cytochrome c oxidase subunit 6B1 (Cytochrome c oxidase subunit VIb isoform 1) (COX VIb-1)	cellular metabolic process; cytochrome-c oxidase activity; hydrogen ion transmembrane transport; mitochondrial inner membrane; mitochondrial intermembrane space; respiratory electron transport chain; small molecule metabolic process; substantia nigra development	Mitochondrion intermembrane space.
277	3,12	27,70999968	P14406	CX7A2_HUMAN	Cytochrome c oxidase subunit 7A2, mitochondrial OS=Homo sapiens GN=COX7A2 PE=1 SV=1	2	mito	Cytochrome c oxidase subunit 7A2, mitochondrial (Cytochrome c oxidase subunit VIIa polypeptide 2) (Cytochrome c oxidase subunit VIIa polypeptide 2 (Liver), isoform CRA_a)	cytochrome-c oxidase activity; mitochondrial respiratory chain	
447	4,93	7,955999672	P34931	HS71L_HUMAN	Heat shock 70 kDa protein 1-like OS=Homo sapiens GN=HSPA1L PE=1 SV=2	4	mito	Molecular chaperone implicated in a wide variety of cellular processes, including protection of the proteome from stress, folding and transport of newly synthesized polypeptides, activation of proteolysis of misfolded proteins and the formation and dissociation of protein complexes.		
447	4,96	7,955999672	P08107	HSP71_HUMAN	Heat shock 70 kDa protein 1A/1B OS=Homo sapiens GN=HSPA1A PE=1 SV=5	4	mito			
326	2,15	5,541000143	Q16891	IMMT_HUMAN	Mitochondrial inner membrane protein OS=Homo sapiens GN=IMMT PE=1 SV=1	2	mito	Mitochondrial inner membrane protein (Cell proliferation-inducing gene 4/52 protein) (Mitofilin) (p87/89)	integral component of membrane; mitochondrial calcium ion homeostasis; mitochondrial inner membrane; mitochondrion; poly(A) RNA binding; protein binding; response to cold	Mitochondrion inner membrane.
419	1,74	6,617999822	P35232	PHB_HUMAN	Prohibitin OS=Homo sapiens GN=PHB PE=1 SV=1	2	mito	Prohibitin inhibits DNA synthesis. It has a role in regulating proliferation		

251	3,92	7,842999697	Q00796	DHSO_HUMAN	Sorbitol dehydrogenase OS=Homo sapiens GN=SORD PE=1 SV=4	2	mito			
282	2,96	5,649000034	P49748	ACADV_HUMAN	Very long-chain specific acyl-CoA dehydrogenase, mitochondrial OS=Homo sapiens GN=ACADVL PE=1 SV=1	2	mito	activation of signaling protein activity involved in unfolded protein response; acyl-CoA dehydrogenase activity; cellular lipid metabolic process; cellular protein metabolic process; endoplasmic reticulum unfolded protein response; energy derivation by oxidation of organic compounds; epithelial cell differentiation; fatty acid beta-oxidation; fatty acid beta-oxidation using acyl- CoA dehydrogenase; flavin adenine dinucleotide binding; long-chain-acyl- CoA dehydrogenase activity; mitochondrial inner membrane; mitochondrial matrix; mitochondrial nucleoid; mitochondrion; negative regulation of fatty acid biosynthetic process; negative regulation of fatty acid oxidation; regulation of cholesterol metabolic process; small molecule metabolic process; temperature homeostasis		
56	18,99	50,18000007	P21796	VDAC1_HUMAN	Voltage-dependent anion- selective channel protein 1 OS=Homo sapiens GN=VDAC1 PE=1 SV=2	10	mito	Forms a channel through the mitochondrial outer membrane and also the plasma membrane.		
137	8,12	25,51000118	P45880	VDAC2_HUMAN	Voltage-dependent anion- selective channel protein 2 OS=Homo sapiens GN=VDAC2 PE=1 SV=2	7	mito			