Supplementary Table 1. List of antibodies used in western blotting

Antibody name	**Company**	**Dilution**
Anti-p27	Santa Cruz Biotechnology (sc-527)	1:200
Anti- cyclin D1	Santa Cruz Biotechnology (sc-20044)	1:200
Anti-E-cadherin	Santa Cruz Biotechnology (sc-71009)	1:1000
Anti-N-cadherin	Santa Cruz Biotechnology (sc-59987)	1:1000
Anti-α Tubulin	Santa Cruz Biotechnology (sc-23948)	1:2000
Anti-Ezrin	Santa Cruz Biotechnology (sc-20773)	1:1000
Anti-Cofilin	Santa Cruz Biotechnology (sc-33779)	1:1000
Anti-pospho cofilin (ser3)	Santa Cruz Biotechnology (sc-21867-R)	1:1000
Anti-LDH-B	Santa Cruz Biotechnology (sc-133731)	1:500
Anti-β Catenin	Santa Cruz Biotechnology (sc-1496)	1:1000
Anti-pospho-Akt (ser473)	Cell Signaling (4051)	1:1000
Anti-phospho-myosin light chain 2 (ser19)	Cell Signaling (3671)	1:1000
Anti-pospho-Src (tyr416)	Cell Signaling (2101)	1:1000
Anti-pospho-p44/42 MAPK (Erk 1/2) (thr202/tyr204)	Cell Signaling (4370)	1:2000

Supplementary Table 2. Primer sequences used in the study.
Primer blast program (http://www.ncbi.nlm.nih.gov/tools/primer-blast/) was used to design specific primer sequences.

Name	Sequence	Length	Tm
Cofilin	Forward primer GTGGGCGATGTGGGCCAGAC Reverse primer CCAGGGTGCAGCGGTCCTTG	280	60°
LIMK1	Forward primer GTGCGAGATCATCGGGCGGG Reverse primer AACAGCGCACGGTGATGGGG	143	60°
ROCK1	Forward primer TGACTGGTGGTCGGTTGGGGT Reverse primer TCGGAGCGTTTCCCAAGCCC	271	60°
Vimentin	Forward primer TGGCCGACGCCATCAACACC Reverse primer CACCTCGACGCGGGCTTTGT	257	60°
E-cadherin	Forward primer ACCACCTCCACAGCCACCGT Reverse primer GTCCAGTTGGCACTCGCCCC	518	60°
N-cadherin	Forward primer ATTGTGGGTGCGGGGCTTGG Reverse primer GGGTGTGGGGCTGCAGATCG	344	60°
Snail	Forward primer CCTGCTGGCAGCCATCCCAC Reverse primer GGCAGCGTGTGGCTTCGGAT	420	60°
Slug	Forward primer ACGCCCAGCTACCCAATGGC Reverse primer AGGGCGCCCAGGCTCACATA	325	60°
Twist	Forward primer CAGCGCACCCAGTCGCTGAA Reverse primer CCAGGCCCCCTCCATCCTCC	234	60°
Profilin1	Forward primer ATGGCCGGGTGGAACGCCTA Reverse primer GAACGCCGAAGGTGGGAGGC	413	60°
Actin beta	Forward primer CCACGGCTGCTTCCAGCTCC Reverse primer GGAGGGGCCGGACTCGTCAT	422	60°
GAPDH	Forward primer GCATGGCCTTCCGTGTCCCC Reverse primer CAATGCCAGCCCCAGCGTCA	216	60°
Keratin 8	Forward primer TATTGCCAACCGCAGCCGGG Reverse primer GCGCCAGAGCCAAAGCTGGA	534	60°
Keratin 18	Forward primer TGGCCATGCGCCAGTCTGTG Reverse primer GTCCCTCTGCCCGGGTCTGT	555	60°
Keratin 19	Forward primer CGCGGCGTATCCGTGTCCTC Reverse primer GCGCCTCCGTTTCTGCCAGT	862	60°
ANXA1	Forward primer GGTGGTCCCGGATCAGCGGT Reverse primer GGCCCTTCATGGCAGCACGA	301	60°
ANXA2	Forward primer AGCGTGCCCCACCTCCAGAA Reverse primer ATCTCGCGTCCCCTTGCCCT	195	60°

ANXA3	Forward primer AGGGCGCGGGAACAAACGAA Reverse primer GCCGGCGTGTTCCTCACACA	445	60°
Transgelin	Forward primer TGCCCGAGAACCCACCCTCC Reverse primer GCCTGGGAGGCCCCTCTGTT	328	60°
CLIC1	Forward primer GCAGTGCTGTGCCCTCCCAG Reverse primer CCCGGGCGTAGGCATTGCTC	394	60°
Vinculin	Forward primer GGCTTGTGGCCGAAGGGCAT Reverse primer GTACCAACCGCAGCCGCCTT	394	60°
LDH-B	Forward primer AGCAAGAAGGGGAGAGTCGGC Reverse primer GGCAGCTGCTGGGATGAATGC	258	60°
18S	Forward primer GCCGCTAGAGGTGAAATTCTTG Reverse primer CATTCTTGGCAAATGCTTTCG	66	60°
Eplin	Forward primer GCCTGGCAGTCCGTTCCACC Reverse primer TGCAGCCAGGACACCCACCT	530	60°
Fascin	Forward primer TCCCCCGCCGAGAAGTGGAG Reverse primer AGGTCCATACCCTGGCGCGT	464	60°

Supplementary Table 3. Protein spots differentially expressed between MCF-7 and MDA-231 cell lines

Spot number	Protein name	Nominal mass (MW)	Matched Peptides	Peptides sequence	Peptide Ion		Instrument type
					m/z	z	
Spot 1	CLIC1	27248	4	K.GVTFNVTTVDTK.R	641.15	2	ESI-TRAP
				K.NSNPALNDNLEK.G	664.72	2	
				K.LAALNPESNTAGLDIFAK.F	923.06	2	
				K.VLDNYLTSPLPEEVDETSAEDEGVSQR.K	998.53	3	
Spot 2	K1C19	44079	14	R.VLDELTLAR.T	515.44	2	ESI-TRAP
				R.IVLQIDNAR.L	521.43	2	
				K.DAEAWFTSR.T	541.71	2	
				R.LEQEIATYR.S	561.94	2	
				R.MSVEADINGLR.R + Oxidation (M)	610.95	2	
				K.NHEEEISTLR.G	614.45	2	
				R.ALEAANGELEVK.I	622.87	2	
				R.SQYEVMAEQNR.K	677.99	2	
				K.AALEDTLAETEAR.F	695.55	2	
				R.QSSATSSFGGLGGGSVR.F	778.11	2	
				R.DYSHYYTTIQDLR.D	559.29	3	
				R.TLQGLEIELQSQLSMK.A + Oxidation (M)	917.84	2	
				R.SLLEGQEDHYNNLSASK.V	635.99	3	
				R.GQVGGQVSVEVDSAPGTDLAK.I	1007.71	2	
Spot 3	K1C18	48029	4	R.AQIFANTVDNAR.I	660.26	2	ESI-TRAP
				R.TVQSLEIDLDSMR.N + Oxidation (M)	761.90	2	
				R.GGMGSGGLATGIAGGLAGMGGIQNEK.E + 2 Oxidation (M)	765.23	3	
				R.YALQMEQLNGILLHLESELAQTR.A + Oxidation (M)	896.36	3	
Spot 4	GDIR2	23031	2				

				K.TLLGDGPVVTDPK.A	656.11	2	ESI-TRAP
				K.ELQEMDKDDESLIK.Y + Oxidation (M)	854.84	2	
Spot 5	2AAA	66039	6	K.LTQDQDVDVK.Y	580.61	2	ESI-TRAP
				K.ELVSDANQHVK.S	620.52	2	
				R.NLCSDDTPMVR.R	654.17	2	
				K.DNTIEHLLPLFLAQLK.D	622.23	3	
				R.QLSQSLLPAIVELAEDAK.W	642.48	3	
				R.QLSQSLLPAIVELAEDAK.W	963.4	2	
Spot 6	CH60	61157	4	R.ALMLQGVDLLADAVAVTMGPK.G + Oxidation (M)	710.44	3	ESI-TRAP
				R.TALLDAAGVASLLTTAEVVVTEIPK.E	1241.68	2	
				R.TALLDAAGVASLLTTAEVVVTEIPK.E	828.41	3	
				K.LVQDVANNTNEEAGDGTTTATVLAR.S	854.48	3	
Spot 7	GRP75 / ANXA6	73680 / 75873	13 / 8	K.GVFEVK.S	678.42	1	ESI-TRAP
				R.QAASSLQQASLK.L	616.37	2	
				K.DAGQISGLNVLR.V	622.01	2	
				K.VQQTVQDLFGR.A	646.06	2	
				R.AQFEGIVTDLIR.R	681.50	2	
				K.SDIGEVILVGGMTR.M	723.98	2	
				R.TTPSVVAFTADGER.L	725.96	2	
				R.EQQIVIQSSGGLSK.D	737.91	2	
				R.VINEPTAAALAYGLDK.S	823.54	2	
				K.NAVITVPAYFNDSQR.Q	847.98	2	
				K.MEEFKDQLPADECNK.L	618.93	3	
				R.VEAVNMAEGIIHDTETK.M	619.9	3	
				R.VEAVNMAEGIIHDTETK.M + Oxidation (HW)	625.18	3	
				/			
				K.DAISGIGTDEK.C	553.30	2	
				R.DAFVAIVQSVK.N	589.27	2	

				R.EEGGENLDQAR.E	609.34	2	
				K.SLEDALSSDTSGHFR.R	811.35	2	
				K.SLHQAIEGDTSGDFLK.A	573.57	3	
				K.SLHQAIEGDTSGDFLK.A	859.93	2	
				K.GLGTDEDTIIDIITHR.S	884.94	2	
				K.GLGTDEDTIIDIITHR.S	590.56	3	
Spot 8	PLST	70811	3	R.QFVTPADVVSGNPK.L	729.75	2	ESI-TRAP
				R.VYALPEDLVEVKPK.M	799.83	2	
				K.EGICALGGTSELSSEGTQHSYSEEEK.Y	929.17	3	
Spot 9	ENOA	47169	15	K.LMIEMDGTENK.S	640.54	2	ESI-TRAP
				K.LMIEMDGTENK.S + Oxidation (M)	648.70	2	
				K.LMIEMDGTENK.S + 2 Oxidation (M)	656.66	2	
				R.GNPTVEVDLFTSK.G	703.78	2	
				R.YISPDQLADLYK.S	713.34	2	
				K.LAQANGWGVMVSHR.S + Oxidation (M)	771.68	2	
				K.VNQIGSVTESLQACK.L	817.52	2	
				R.AAVPSGASTGIYEALELR.D	902.80	2	
				K.LAMQEFMILPVGAANFR.E	954.45	2	
				K.LAMQEFMILPVGAANFR.E + Oxidation (M)	962.54	2	
				K.DATNVGDEGGFAPNILENK.E	981.04	2	
				K.DATNVGDEGGFAPNILENK.E	654.51	3	
				R.SGETEDTFIADLVVGLCTGQIK.T	1177.01	2	
				R.SGETEDTFIADLVVGLCTGQIK.T	785.32	3	
				K.DYPVVSIEDPFDQDDWGAWQK.F	1255.50	2	
Spot 10	COF1	18719	6	R.YALYDATYETK.E	669.49	2	ESI-TRAP
				K.LGGSAVISLEGKPL.-	671.06	2	
				K.KEDLVFIFWAPESAPLK.S	996.03	2	
				K.EILVGDVGQTVDDPYATFVK.M	1083.97	2	

				K.EILVGDVGQTVDDPYATFVK.M	723.02	3	
				K.NIILEEGKEILVGDVGQTVDDPYATFVK.M	1021.87	3	
Spot 11	THIO	12015	1	K.TAFQEALDAAGDK.L	668.71	2	ESI-TRAP
Spot 12	K2C7	51386	4	R.SMQDVVEDFK.N	599.79	2	ESI-TRAP
				R.SMQDVVEDFK.N + Oxidation (M)	607.46	2	
				R.TAAENEFVVLK.K	611.26	2	
				R.GQLEALQVDGGR.L	621.99	2	
Spot 13	K2C8	53671	6	R.SLDMDSIIAEVK.A	660.61	2	ESI-TRAP
				R.SLDMDSIIAEVK.A + Oxidation (M)	668.68	2	
				R.ASLEAAIADAEQR.G	672.78	2	
				R.LEGLTDEINFLR.Q	710.31	2	
				K.LEAELGNMQGLVEDFK.N + Oxidation (M)	905.22	2	
				R.ELQSQISDTSVVLSMDNSR.S + Oxidation (M)	1063.06	2	
Spot 14	K2C8	53671	17	K.LSELEAALQR.A	1129.79	1	ESI-TRAP
				K.YEELQSLAGK.H	1137.6	1	
				R.SLDMDSIIAEVK.A	660.92	2	
				R.SLDMDSIIAEVK.A + Oxidation (M)	668.73	2	
				R.ASLEAAIADAEQR.G	672.7	2	
				R.ASLEAAIADAEQR.G	672.98	2	
				R.TEMENEFVLIK.K	676.78	2	
				R.TEMENEFVLIK.K + Oxidation (M)	684.67	2	
				R.LEGLTDEINFLR.Q	710.52	2	
				K.LEAELGNMQGLVEDFK.N	896.97	2	
				K.LEAELGNMQGLVEDFK.N + Oxidation (M)	904.99	2	
				R.SNMDNMFESYINNLR.R	924.49	2	
				R.SNMDNMFESYINNLR.R	616.76	3	

				R.SNMDNMFESYINNLR.R + Oxidation (M) R.SNMDNMFESYINNLR.R + Oxidation (M) R.ELQSQISDTSVVLSMDNSR.S R.ELQSQISDTSVVLSMDNSR.S	932.39 932.44 703.18 1054.94	2 2 3 2	
Spot 15	K2C8	53671	8	R.SLDMDSIIAEVK.A + Oxidation (M) R.ASLEAAIADAEQR.G R.LEGLTDEINFLR.Q K.LEAELGNMQGLVEDFK.N + Oxidation (M) R.SNMDNMFESYINNLR.R + 2 Oxidation (M) R.SNMDNMFESYINNLR.R + 2 Oxidation (M) R.ELQSQISDTSVVLSMDNSR.S + Oxidation (M) R.ELQSQISDTSVVLSMDNSR.S + Oxidation (M)	668.79 672.84 710.46 905.06 627.26 940.65 1062.86 709.24	2 2 2 2 3 2 2 3	ESI-TRAP
Spot 16	ANXA3	36375	5	K.GIGTDEFTLNR.I K.SDTSGDYEITLLK.I K.SLGDDISSETSGDFR.K K.GAGTNEDALIEILTTR.T R.DYPDFSPSVDAEAIQK.A	612.06 721.82 793.48 837.57 891.81	2 2 2 2 2	ESI-TRAP
Spot 17	LDHB	36900	11	K.LSGLPK.H R.VIGSGCNLDSAR.F K.MVVESAYEVIK.L K.MVVESAYEVIK.L + Oxidation (M) K.IVADKDYSVTANSK.I K.SLADELALVDVLEDK.L K.LIAPVAEEEATVPNNK.I K.SLADELALVDVLEDKLK.G K.GEMMDLQHGSLFLQTPK.I + Oxidation (M) K.GEMMDLQHGSLFLQTPK.I + 2 Oxidation (M) K.ITVVGVGQVGMACAISILGK.S + Oxidation (M)	614.76 624.68 634.18 642.32 755.86 815.42 848.23 624.48 650.04 655.17 663.60	1 2 2 2 2 2 2 3 3 3 3	ESI-TRAP

Spot 18	ACTB / ANXA1 / ACTC	41737 / 38714 / 42019	6 / 5 / 3	K.IWHHTFYNELR.V	758.33	2	ESI-TRAP
				K.SYELPDGQVITIGNER.F	896.06	2	
				R.VAPEEHPVLLTEAPLNPK.A	652.11	3	
				K.DLYANTVLSGGTTMYPGIADR.M + Oxidation (M)	1116.01	2	
				K.DLYANTVLSGGTTMYPGIADR.M + Oxidation (M)	744.55	3	
				R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L + Oxidation (M)	1067.41	3	
				/	/	/	
				K.TPAQFDADELR.A	631.72	2	
				K.GVDEATIIDILTK.R	694.40	2	
				K.GLGTDEDTLIEILASR.T	852.13	2	
				R.SEDFGVNEDLADSDAR.A	870.34	2	
				K.GGPGSAVSPYPTFNPSSDVAALHK.A	786.12	3	
				/	/	/	
				K.IWHHTFYNELR.V	758.33	2	
				K.ILTERGYSFVTTAER.E	581.44	3	
				K.SYELPDGQVITIGNER.F	896.06	2	
Spot 19	ANXA2	38808	9	K.DIISDTSGDFR.K	613.78	2	ESI-TRAP
				R.TNQELQEINR.V	622.8	2	
				K.SLYYYIQQDTK.G	711.37	2	
				K.SYSPYDMLESIR.K + Oxidation (M)	738.36	2	
				K.GVDEVTIVNILTNR.S	772.2	2	
				K.GLGTDEDSLIEIICSR.T	889.56	2	
				R.AEDGSVIDYELIDQDAR.D	954.93	2	
				R.RAEDGSVIDYELIDQDAR.D	1033.06	2	
				R.RAEDGSVIDYELIDQDAR.D	689.12	3	
Spot 20	VIME / TBA1B	53676 / 50804	8 / 7	R.LGDLYEEEMR.E + Oxidation (M)	635.6	2	ESI-TRAP
				K.MALDIEIATYR.K + Oxidation (M)	656.1	2	
				R.EEAENTLQSFR.Q	662.22	2	

				R.SLYASSPGGVYATR.S	714.57	2	
				R.QVQSLTCEVDALK.G	745.87	2	
				R.KVESLQEEIAFLK.K	767.33	2	
				R.ISLPLPNFSSLNLR.E	786	2	
				R.ETNLDSLPLVDTHSK.R	835.03	2	
				/	/	/	
				R.LSVDYGK.K	781.06	1	
				K.YMACCLLYR.G + Oxidation (M)	633.1	2	
				R.LISQIVSSITASLR.F	744.69	2	
				R.AVFVDLEPTVIDEVR.T	851.52	2	
				R.IHFPLATYAPVISAEK.A	878.65	2	
				K.VGINYQPPTVVPGGDLAK.V	913.38	2	
				K.TIGGGDDSFNTFFSETGAGK.H	1004.42	2	
Spot 21	VINC	124292	9	R.WIDNPTVDDR.G	616.23	2	ESI-TRAP
				R.VMLVNSMNTVK.E + Oxidation (M)	625.53	2	
				K.MTGLVDEAIDTK.S + Oxidation (M)	654.55	2	
				K.QVATALQNLQTK.T	657.65	2	
				K.AQQVSQGLDVLTAK.V	729.27	2	
				R.DPSASPGDAGEQAIR.Q	735.81	2	
				R.GILSGTSDLLLTFDEAEVR.K	679.06	3	
				R.GILSGTSDLLLTFDEAEVR.K	1018.51	2	
				K.LLAVAATAPPDAPNREEVFDER.A	794.53	3	
Spot 22	PRDX1	22324	5	R.TIAQDYGVLK.A	554.38	2	ESI-TRAP
				K.ATAVMPDGQFK.D + Oxidation (M)	590.86	2	
				R.LVQAFQFTDK.H	598.95	2	
				R.QITVNDLPVGR.S	606.49	2	
				K.KQGGLGPMNIPLVSDPK.R + Oxidation (M)	589.92	3	
Spot 23	K2C6B	60067	1	K.YEELQITAGR.H	590.60	2	ESI-TRAP

Spot 24	LMNA	74139	12	R.LSPSPTSQR.S	486.76	2	ESI-QUAD-TOF
				K.LLEGEEER.L	487.75	2	
				R.LADALQELR.A	514.79	2	
				K.EAALSTALSEK.R	560.30	2	
				K.EDLQELNDR.L	566.27	2	
				R.ITESEEVVSR.E	574.80	2	
				K.AAYEAELGDAR.K	583.28	2	
				R.TLEGELHDLR.G	591.81	2	
				R.VAVEEVDEEGK.F	602.29	2	
				R.SGAQASSTPLSPTR.I	680.35	2	
				R.IDSLSAQLSQLQK.Q	715.90	2	
				R.NSNLVGAAHEELQQSR.I	584.96	3	
Spot 25	COF1	18719	2	K.LGGSAVISLEGKPL.-	670.89	2	ESI-QUAD-TOF
				K.NIILEEGKEILVGDVGQTVDDPYATFVK.M	1021.54	3	
Spot 26	MOES	67820	5	K.ESPLLFK.F	417.25	2	ESI-QUAD-TOF
				K.APDFVFYAPR.L	591.81	2	
				R.EVWFFGLQYQDTK.G	830.92	2	
				K.KTQEQLALEMAELTAR.I + Oxidation (M)	616.66	3	
				K.IAQDLEMYGVNYFSIK.N + Oxidation (M)	953.98	2	
Spot 27	HS90A	85006	8	K.DQVANSAFVER.L	618.24	2	ESI-TRAP
				K.ADLINNLGTIAK.S	622.13	2	
				R.ELISNSSDALDK.I	645.99	2	
				K.EDQTEYLEER.R	656.13	2	
				K.EGLELPEDEEEK.K	708.62	2	
				R.GVVDSEDLPLNISR.E	757.3	2	
				R.NPDDITNEEYGEFYK.S	917.41	2	

				K.TKPIWTRNPDDITNEEYGEFYK.S	905.75	3	
Spot 28	ANXA5	35971	11	R.TPEELR.A	744.21	1	ESI-TRAP
				R.ADAETLR.K	775.32	1	
				R.QEISAAFK.T	893.51	1	
				K.NFATSLYSMIK.G	637.72	2	
				K.NFATSLYSMIK.G + Oxidation (M)	645.25	2	
				R.GTVTDFPGFDER.A	671	2	
				K.GLGTDEESILTLLTSR.S	853.11	2	
				R.SIPAYLAETLYYAMK.G + Oxidation (M)	875.41	2	
				K.YMTISGFQIEETIDR.E + Oxidation (M)	910.05	2	
				R.DPDAGIDEAQVEQDAQALFQAGELK.W	1329.61	2	
				R.DPDAGIDEAQVEQDAQALFQAGELK.W	886.81	3	

Supplementary Table 4. Biological process and molecular function of differentially expressed proteins

Swiss Prot Accession No	Biological process	Molecular function
O00299	Ion transport, transport	Chloride channel, ionic channel, voltage-gated channel
P08727	Involved in the organization of myofibers.	Structural constituent of cytoskeleton
P05783	Cell cycle, host-virus interaction	Structural molecule activity
P52566	Regulates the GDP/GTP exchange reaction of the Rho proteins by inhibiting the dissociation of GDP from them, and the subsequent binding of GTP to them.	GTPase activator activity, Rho GDP-dissociation inhibitor activity
P30153	Chromosome partition	Antigen binding, protein phosphatase type 2A regulator activity, protein serine/threonine phosphatase activity
P10809	Implicated in mitochondrial protein import and macromolecular assembly. May facilitate the correct folding of imported proteins. May also prevent misfolding and promote the refolding and proper assembly of unfolded polypeptides generated under stress conditions in the mitochondrial matrix.	ATP binding, ATPase activity, DNA replication origin binding, cell surface binding, lipopolysaccharide binding, single-stranded DNA binding
P38646 / P08133	Implicated in the control of cell proliferation and cellular aging. May also act as a chaperone / calcium ion transport, regulation of muscle contraction	ATP binding / calcium ion binding, calcium-dependent phospholipid binding
P13797	Actin-bundling protein found in intestinal microvilli, hair cell stereocilia, and fibroblast filopodia.	Calcium ion binding
P06733	Glycolysis, plasminogen activation, transcription, transcription regulation	DNA binding, magnesium ion binding, phosphopyruvate hydratase activity, sequence-specific DNA binding transcription factor activity, transcription corepressor activity
P23528	Rho protein signal transduction, actin cytoskeleton organization, anti-apoptosis, axon guidance, platelet activation, platelet degranulation, regulation of cell morphogenesis, response to virus	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. Plays a role in the regulation of cell morphology and cytoskeletal organization.
P10599	Electron transport, transcription, transcription regulation,	Electron carrier activity, peptide disulfide

	transport	oxidoreductase activity, protein disulfide oxidoreductase activity
P08729	Host-virus interaction, cytoskeleton organization	Structural molecule activity
P05787	Host-virus interaction, cytoskeleton organization	Structural molecule activity
P12429	Defense response to bacterium, hippocampus development, neutrophil degranulation, organ regeneration, phagocytosis, positive regulation of DNA metabolic process, positive regulation of angiogenesis, positive regulation of endothelial cell migration, positive regulation of sequence-specific DNA binding transcription factor activity, response to glucocorticoid stimulus, response to growth factor stimulus	Calcium ion binding, calcium-dependent phospholipid binding, phospholipase A2 inhibitor activity
P07195	Glycolysis	L-lactate dehydrogenase activity, NAD binding
P60709 / P04083 / P68032	'de novo' posttranslational protein folding, adherens junction organization, axon guidance, blood coagulation, cell junction assembly, cellular component movement, response to calcium ion / alpha-beta T cell differentiation, anti-apoptosis, arachidonic acid secretion, cell cycle, cell surface receptor signaling pathway, cellular component movement, cellular response to hydrogen peroxide, endocrine pancreas development, estrous cycle phase, gliogenesis, hepatocyte differentiation, inflammatory response, insulin secretion, keratinocyte differentiation, lipid metabolic process, negative regulation of acute inflammatory response, negative regulation of protein secretion, peptide cross-linking, positive regulation of apoptotic process, positive regulation of prostaglandin biosynthetic process, positive regulation of vesicle fusion, regulation of cell proliferation, response to X-ray, response to drug, response to estradiol stimulus, response to glucocorticoid stimulus, response to interleukin-1, response to organic cyclic compound, response to peptide hormone stimulus / apoptotic process, cardiac muscle contraction, cardiac muscle tissue morphogenesis, cardiac myofibril assembly, heart	ATP binding, structural constituent of cytoskeleton / calcium ion binding, calcium-dependent phospholipid binding, phospholipase A2 inhibitor activity, phospholipase inhibitor activity, single-stranded DNA binding, single-stranded RNA binding, structural molecule activity / ATP binding, ATPase activity

	contraction, muscle filament sliding, response to drug, response to ethanol, skeletal muscle thin filament assembly	
P07355	Angiogenesis, body fluid secretion, cellular response to acid, collagen fibril organization, fibrinolysis, positive regulation of binding, positive regulation of vesicle fusion, skeletal system development	Calcium ion binding, calcium-dependent phospholipid binding, phosphatidylinositol-4,5-bisphosphate binding, phospholipase inhibitor activity
P08670 / P68363	Cellular component disassembly involved in apoptotic process, interspecies interaction between organisms, muscle filament sliding / 'de novo' posttranslational protein folding, cell division, cytoskeleton-dependent intracellular transport, microtubule cytoskeleton organization, microtubule-based movement, microtubule-based process, protein polymerization	Structural constituent of cytoskeleton / GTP binding, GTPase activity, structural constituent of cytoskeleton, structural molecule activity
P18206	Cell adhesion	Structural molecule activity
Q06830	Cell proliferation, hydrogen peroxide catabolic process, skeletal system development	Thioredoxin peroxidase activity
P04259	Intermediate filament Keratin	Structural constituent of cytoskeleton
P02545	Activation of signaling protein activity involved in unfolded protein response, cellular component disassembly involved in apoptotic process, cellular response to hypoxia, establishment or maintenance of microtubule cytoskeleton polarity, muscle organ development, nuclear envelope organization, positive regulation of cell aging, protein localization to nucleus, regulation of apoptotic process, regulation of cell migration, spermatogenesis, sterol regulatory element binding protein import into nucleus, ventricular cardiac muscle cell development	Structural molecule activity
P26038	Leukocyte cell-cell adhesion, leukocyte migration, membrane to membrane docking, regulation of lymphocyte migration	Structural constituent of cytoskeleton
P07900	Stress response	ATP binding, ATPase activity, nitric-oxide synthase regulator activity
P08758	Blood coagulation Hemostasis	Calcium ion binding, calcium-dependent phospholipid binding, eukaryotic cell surface

binding, phospholipase inhibitor activity
Information present in this table are from http://www.uniprot.org/

Table 5: Spearman correlation matrix

	TBA1B/VIME	CLIC1	K1C19	K1C18	GDIR2	2AAA	RP75/ANXA	CH60	PLST	ENOA	COF1	THIO	K2C7	K2C8_1	K2C8_2	K2C8_3	ANXA3	LDHB	ACTB/ ANXA1/ACTC	ANXA2	VINC	PRDX1	K2C6B	LMNA	COF1_2	MOES	HS90A	ANXA5
TBA1B/VIME	1.000	0.986	-0.812	-0.600	0.943	0.943	0.600	-0.600	0.928	0.899	-0.829	0.706	0.829	-0.714	-0.771	-0.600	0.943	0.833	0.941	0.580	0.829	-0.829	0.880	0.714	0.829	0.794	0.580	0.600
CLIC1	0.986	1.000	-0.794	-0.667	0.986	0.986	0.580	-0.580	0.971	0.956	-0.812	0.717	0.812	-0.754	-0.812	-0.580	0.986	0.845	0.955	0.588	0.812	-0.812	0.924	0.754	0.812	0.806	0.618	0.667
K1C19	-0.812	-0.794	1.000	0.638	-0.754	-0.754	-0.812	0.812	-0.765	-0.794	0.986	-0.940	-0.986	0.580	0.580	0.812	-0.754	-0.892	-0.924	-0.794	-0.986	0.986	-0.708	-0.580	-0.986	-0.627	-0.765	-0.638
K1C18	-0.600	-0.667	0.638	1.000	-0.714	-0.714	-0.829	0.829	-0.754	-0.754	0.600	-0.794	-0.600	0.943	0.886	0.829	-0.714	-0.833	-0.698	-0.899	-0.600	0.600	-0.880	-0.943	-0.600	-0.883	-0.928	-1.000
GDIR2	0.943	0.986	-0.754	-0.714	1.000	1.000	0.543	-0.543	0.986	0.986	-0.771	0.706	0.771	-0.771	-0.829	-0.543	1.000	0.833	0.941	0.580	0.771	-0.771	0.941	0.771	0.771	0.794	0.638	0.714
2AAA	0.943	0.986	-0.754	-0.714	1.000	1.000	0.543	-0.543	0.986	0.986	-0.771	0.706	0.771	-0.771	-0.829	-0.543	1.000	0.833	0.941	0.580	0.771	-0.771	0.941	0.771	0.771	0.794	0.638	0.714
GRP75/ANXA6	0.600	0.580	-0.812	-0.829	0.543	0.543	1.000	-1.000	0.580	0.580	-0.771	0.883	0.771	-0.771	-0.714	-1.000	0.543	0.833	0.698	0.986	0.771	-0.771	0.698	0.771	0.771	0.794	0.928	0.829
CH60	-0.600	-0.580	0.812	0.829	-0.543	-0.543	-1.000	1.000	-0.580	-0.580	0.771	-0.883	-0.771	0.771	0.714	1.000	-0.543	-0.833	-0.698	-0.986	-0.771	0.771	-0.698	-0.771	-0.771	-0.794	-0.928	-0.829
PLST	0.928	0.971	-0.765	-0.754	0.986	0.986	0.580	-0.580	1.000	0.971	-0.754	0.761	0.754	-0.812	-0.812	-0.580	0.986	0.892	0.924	0.618	0.754	-0.754	0.955	0.812	0.754	0.806	0.647	0.754
ENOA	0.899	0.956	-0.794	-0.754	0.986	0.986	0.580	-0.580	0.971	1.000	-0.812	0.761	0.812	-0.754	-0.812	-0.580	0.986	0.845	0.955	0.632	0.812	-0.812	0.924	0.754	0.812	0.761	0.706	0.754
COF1	-0.829	-0.812	0.986	0.600	-0.771	-0.771	-0.771	0.771	-0.754	-0.812	1.000	-0.883	-1.000	0.543	0.600	0.771	-0.771	-0.833	-0.941	-0.754	-1.000	1.000	-0.698	-0.543	-1.000	-0.618	-0.754	-0.600
THIO	0.706	0.717	-0.940	-0.794	0.706	0.706	0.883	-0.883	0.761	0.761	-0.883	1.000	0.883	-0.706	-0.618	-0.883	0.706	0.953	0.844	0.896	0.883	-0.883	0.750	0.706	0.883	0.682	0.851	0.794
K2C7	0.829	0.812	-0.986	-0.600	0.771	0.771	0.771	-0.771	0.754	0.812	-1.000	0.883	1.000	-0.543	-0.600	-0.771	0.771	0.833	0.941	0.754	1.000	-1.000	0.698	0.543	1.000	0.618	0.754	0.600
K2C8_1	-0.714	-0.754	0.580	0.943	-0.771	-0.771	-0.771	0.771	-0.812	-0.754	0.543	-0.706	-0.543	1.000	0.943	0.771	-0.771	-0.833	-0.698	-0.812	-0.543	0.543	-0.941	-1.000	-0.543	-0.971	-0.812	-0.943
K2C8_2	-0.771	-0.812	0.580	0.886	-0.829	-0.829	-0.714	0.714	-0.812	-0.812	0.600	-0.618	-0.600	0.943	1.000	0.714	-0.829	-0.741	-0.759	-0.754	-0.600	0.600	-0.941	-0.943	-0.600	-0.971	-0.812	-0.886
K2C8_3	-0.600	-0.580	0.812	0.829	-0.543	-0.543	-1.000	1.000	-0.580	-0.580	0.771	-0.883	-0.771	0.771	0.714	1.000	-0.543	-0.833	-0.698	-0.986	-0.771	0.771	-0.698	-0.771	-0.771	-0.794	-0.928	-0.829
ANXA3	0.943	0.986	-0.754	-0.714	1.000	1.000	0.543	-0.543	0.986	0.986	-0.771	0.706	0.771	-0.771	-0.829	-0.543	1.000	0.833	0.941	0.580	0.771	-0.771	0.941	0.771	0.771	0.794	0.638	0.714
LDHB	0.833	0.845	-0.892	-0.833	0.833	0.833	0.833	-0.833	0.892	0.845	-0.833	0.953	0.833	-0.833	-0.741	-0.833	0.833	1.000	0.885	0.845	0.833	-0.833	0.885	0.833	0.833	0.810	0.798	0.833
ACTB/ ANXA1/ACTC	0.941	0.955	-0.924	-0.698	0.941	0.941	0.698	-0.698	0.924	0.955	-0.941	0.844	0.941	-0.698	-0.759	-0.698	0.941	0.885	1.000	0.708	0.941	-0.941	0.871	0.698	0.941	0.750	0.739	0.698
ANXA2	0.580	0.588	-0.794	-0.899	0.580	0.580	0.986	-0.986	0.618	0.632	-0.754	0.896	0.754	-0.812	-0.754	-0.986	0.580	0.845	0.708	1.000	0.754	-0.754	0.739	0.812	0.754	0.806	0.971	0.899
VINC	0.829	0.812	-0.986	-0.600	0.771	0.771	0.771	-0.771	0.754	0.812	-1.000	0.883	1.000	-0.543	-0.600	-0.771	0.771	0.833	0.941	0.754	1.000	-1.000	0.698	0.543	1.000	0.618	0.754	0.600
PRDX1	-0.829	-0.812	0.986	0.600	-0.771	-0.771	-0.771	0.771	-0.754	-0.812	1.000	-0.883	-1.000	0.543	0.600	0.771	-0.771	-0.833	-0.941	-0.754	-1.000	1.000	-0.698	-0.543	-1.000	-0.618	-0.754	-0.600
K2C6B	0.880	0.924	-0.708	-0.880	0.941	0.941	0.698	-0.698	0.955	0.924	-0.698	0.750	0.698	-0.941	-0.941	-0.698	0.941	0.885	0.871	0.739	0.698	-0.698	1.000	0.941	0.698	0.938	0.770	0.880
LMNA	0.714	0.754	-0.580	-0.943	0.771	0.771	0.771	-0.771	0.812	0.754	-0.543	0.706	0.543	-1.000	-0.943	-0.771	0.771	0.833	0.698	0.812	0.543	-0.543	0.941	1.000	0.543	0.971	0.812	0.943
COF1_2	0.829	0.812	-0.986	-0.600	0.771	0.771	0.771	-0.771	0.754	0.812	-1.000	0.883	1.000	-0.543	-0.600	-0.771	0.771	0.833	0.941	0.754	1.000	-1.000	0.698	0.543	1.000	0.618	0.754	0.600
MOES	0.794	0.806	-0.627	-0.883	0.794	0.794	0.794	-0.794	0.806	0.761	-0.618	0.682	0.618	-0.971	-0.971	-0.794	0.794	0.810	0.750	0.806	0.618	-0.618	0.938	0.971	0.618	1.000	0.806	0.883
HS90A	0.580	0.618	-0.765	-0.928	0.638	0.638	0.928	-0.928	0.647	0.706	-0.754	0.851	0.754	-0.812	-0.812	-0.928	0.638	0.798	0.739	0.971	0.754	-0.754	0.770	0.812	0.754	0.806	1.000	0.928
ANXA5	0.600	0.667	-0.638	-1.000	0.714	0.714	0.829	-0.829	0.754	0.754	-0.600	0.794	0.600	-0.943	-0.886	-0.829	0.714	0.833	0.698	0.899	0.600	-0.600	0.880	0.943	0.600	0.883	0.928	1.000

Table 6A

PCA Cross-Validation statistics

Principal Component	R^2X	R^2X(cum)	Eigenvalue	Q^2	limit	Q2(cum)
1	0.9380	0.9380	5.6300	0.9030	0.1950	0.9030
2	0.0387	0.9770	0.2320	0.4560	0.2290	0.9470

PCA Cross-validation statistics for the MCF7 vs MDA-MD-231 comparison. A two component model use 97.77% of X for predicting 94.70% of the response variation.

R^2X: fraction of the variation of descriptor matrix (X) explained by each Principal component (PC); **R^2X(cum)** Cumulative explained fraction of the variation of the X block; **Eigenvalue**: The number of variables (K) times R^2X; **Q^2**: Overall cross-validated R^2X for the component; **Q^2(cum)**: The cumulative Q^2 for the extracted components; **Limit:** The cross validation threshold for that component.

Table 6B

PLS-DA Cross-Validation statistics

Principal Component	**R^2X**	**R^2X(cum)**	**Eigenvalue**	**R^2Y**	**R^2Y(cum)**	**Q^2**	**limit**	**Q^2(cum)**
1	0.9380	0.938	5.630	0.9950	0.9950	0.9920	0.05	0.9920
2	0.0385	0.976	0.231	0.0049	1	0.9000	0.05	0.9990

PLS-DA Cross-validation statistics for the MCF7 vs MDA-MD-231 comparison. A two component model use 97.6 % of X variation for modelling 100 % and predicting 99.90 % of the response variation.

R^2X: fraction of the variation of descriptor matrix (X) explained by each Principal component (PC); **R^2X(cum)** Cumulative explained fraction of the variation of the X block; **Eigenvalue**: The number of variables (K) times R^2X; **R^2Y** Fraction of the Y variation modeled in that component; **R^2Y(cum)** Cumulative R^2Y up to the specified component; **Q^2**: Overall cross-validated R^2X for the component; **Limit:** The cross validation threshold for that component; **Q^2(cum)**: Cumulative Q^2 up to the specified component. Unlike R^2X(cum), Q^2(cum) is not additive

Supplementary Table 7

FKBP4	9606.ENSP00000001008	FK506 binding protein 4, 59kDa; Component of unactivated mammalian steroid receptor complexes that sediment at 8-10 S. May have a rotamase activity. May play a role in the intracellular trafficking of heterooligomeric forms of steroid hormone receptors
HSPA9	9606.ENSP00000297185	heat shock 70kDa protein 9 (mortalin); Implicated in the control of cell proliferation and cellular aging. May also act as a chaperone
SSH1	9606.ENSP00000315713	slingshot homolog 1 (Drosophila); Protein phosphatase which regulates actin filament dynamics. Dephosphorylates and activates the actin binding/depolymerizing factor cofilin, which subsequently binds to actin filaments and stimulates their disassembly. Inhibitory phosphorylation of cofilin is mediated by LIMK1, which may also be dephosphorylated and inactivated by this protein
PPP2R1A	9606.ENSP00000324804	protein phosphatase 2 (formerly 2A), regulatory subunit A, alpha isoform; The PR65 subunit of protein phosphatase 2A serves as a scaffolding molecule to coordinate the assembly of the catalytic subunit and a variable regulatory B subunit
MYL2	9606.ENSP00000228841	myosin, light chain 2, regulatory, cardiac, slow
STIP1	9606.ENSP00000305958	stress-induced-phosphoprotein 1; Mediates the association of the molecular chaperones HSC70 and HSP90 (HSPCA and HSPCB)
MOBKL3	9606.ENSP00000315702	MOB1, Mps One Binder kinase activator-like 3 (yeast)
S100B	9606.ENSP00000291700	S100 calcium binding protein B; Weakly binds calcium but binds zinc very tightly-distinct binding sites with different affinities exist for both ions on each monomer. Physiological concentrations of potassium ion antagonize the binding of both divalent cations, especially affecting high-affinity calcium-binding sites. Binds to and initiates the activation of STK38 by releasing autoinhibitory intramolecular interactions within the kinase
CALD1	9606.ENSP00000354826	caldesmon 1; 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). Stimulates actin binding of tropomyosin which increases the stabilization of actin filament structure. In muscle tissues, inhibits the actomyosin ATPase by binding to F-actin. This inhibition is attenuated by calcium-calmodulin and is potentiated by tropomyosin. Interacts with actin, myosin, two molecules of tropomyosin and with calmodulin. Also play an essential role during cellular mitos [...]
MICAL1	9606.ENSP00000351664	microtubule associated monoxygenase, calponin and LIM domain containing 1; May be a cytoskeletal regulator that connects NEDD9 to intermediate filaments
S100A9	9606.ENSP00000357727	S100 calcium binding protein A9; Calcium-binding protein. Has antimicrobial activity towards bacteria and fungi. Important for resistance to invasion by pathogenic bacteria. Up-regulates transcription of genes that are under the control of NF-kappa-B. Plays a role in the development of endotoxic shock in response to bacterial lipopolysaccharide (LPS) (By similarity). Promotes tubulin polymerization when unphosphorylated. Promotes phagocyte migration and infiltration of granulocytes at sites of wounding. Plays a role as a pro-inflammatory mediator in acute and chronic inflammation and u [...]
MYH7	9606.ENSP00000347507	myosin, heavy chain 7, cardiac muscle, beta; Muscle contraction
LMNA	9606.ENSP00000357283	lamin A/C; Lamins are components of the nuclear lamina, a fibrous layer on the nucleoplasmic side of the inner nuclear membrane, which is thought to provide a framework for the nuclear envelope and may also interact with chromatin. Lamin A and C are present in equal amounts in the lamina of mammals
TLR4	9606.ENSP00000363089	toll-like receptor 4; Cooperates with LY96 and CD14 to mediate the innate immune response to bacterial lipopolysaccharide (LPS). Acts via MYD88, TIRAP and TRAF6, leading to NF-kappa-B activation, cytokine secretion and the inflammatory response
ZYX	9606.ENSP00000324422	zyxin; Adhesion plaque protein. Binds alpha-actinin and the CRP protein. Important for targeting TES and ENA/VASP family members to focal adhesions and for the formation of actin-rich structures. May be a component of a signal transduction pathway that mediates adhesion-stimulated changes in gene expression (By similarity)
PPME1	9606.ENSP00000381461	protein phosphatase methylesterase 1; Demethylates proteins that have been reversibly carboxymethylated. Demethylates PPP2CB (in vitro)
LMNB2	9606.ENSP00000327054	lamin B2; Lamins are components of the nuclear lamina, a fibrous layer on the nucleoplasmic side of the inner nuclear membrane, which is thought to provide a framework for the nuclear envelope and may also interact with chromatin

SORBS1	9606.ENSP00000355136	sorbin and SH3 domain containing 1; Plays a role in tyrosine phosphorylation of CBL by linking CBL to the insulin receptor. Required for insulin- stimulated glucose transport. Involved in formation of actin stress fibers and focal adhesions (By similarity)
SLC9A1	9606.ENSP00000263980	solute carrier family 9 (sodium/hydrogen exchanger), member 1; Involved in pH regulation to eliminate acids generated by active metabolism or to counter adverse environmental conditions. Major proton extruding system driven by the inward sodium ion chemical gradient. Plays an important role in signal transduction
TXNIP	9606.ENSP00000358323	thioredoxin interacting protein; May act as an oxidative stress mediator by inhibiting thioredoxin activity or by limiting its bioavailability. Interacts with COPS5 and restores COPS5-induced suppression of CDKN1B stability, blocking the COPS5-mediated translocation of CDKN1B from the nucleus to the cytoplasm. Functions as a transcriptional repressor, possibly by acting as a bridge molecule between transcription factors and corepressor complexes, and over- expression will induce G0/G1 cell cycle arrest. Required for the maturation of natural killer cells
GAPDH	9606.ENSP00000229239	glyceraldehyde-3-phosphate dehydrogenase; Independent of its glycolytic activity it is also involved in membrane trafficking in the early secretory pathway
PPFIA1	9606.ENSP00000253925	protein tyrosine phosphatase, receptor type, f polypeptide (PTPRF), interacting protein (liprin), alpha 1; May regulate the disassembly of focal adhesions. May localize receptor-like tyrosine phosphatases type 2A at specific sites on the plasma membrane, possibly regulating their interaction with the extracellular environment and their association with substrates
ACTN1	9606.ENSP00000377941	actinin, alpha 1; F-actin cross-linking protein which is thought to anchor actin to a variety of intracellular structures. This is a bundling protein
PKP1	9606.ENSP00000263946	plakophilin 1 (ectodermal dysplasia/skin fragility syndrome); Seems to play a role in junctional plaques. Contributes to epidermal morphogenesis
CFL1	9606.ENSP00000309629	cofilin 1 (non-muscle); Controls reversibly actin polymerization and depolymerization in a pH-sensitive manner. It has the ability to bind G- and F-actin in a 1:1 ratio of cofilin to actin. It is the major component of intranuclear and cytoplasmic actin rods
PTGES3	9606.ENSP00000262033	prostaglandin E synthase 3 (cytosolic); Molecular chaperone that localizes to genomic response elements in a hormone-dependent manner and disrupts receptor- mediated transcriptional activation, by promoting disassembly of transcriptional regulatory complexes
KRT6A	9606.ENSP00000369317	keratin 6A
PKM2	9606.ENSP00000320171	pyruvate kinase, muscle; Glycolytic enzyme that catalyzes the transfer of a phosphoryl group from phosphoenolpyruvate (PEP) to ADP, generating ATP. Stimulates POU5F1-mediated transcriptional activation. Plays a general role in caspase independent cell death of tumor cells. The ratio betwween the highly active tetrameric form and nearly inactive dimeric form determines whether glucose carbons are channeled to biosynthetic processes or used for glycolytic ATP production. The transition between the 2 forms contributes to the control of glycolysis and is important for tumor cell proliferat [...]
HSPA8	9606.ENSP00000227378	heat shock 70kDa protein 8; Chaperone. Isoform 2 may function as an endogenous inhibitory regulator of HSC70 by competing the co-chaperones
AURKB	9606.ENSP00000313950	aurora kinase B; May be directly involved in regulating the cleavage of polar spindle microtubules and is a key regulator for the onset of cytokinesis during mitosis. Component of the chromosomal passenger complex (CPC), a complex that acts as a key regulator of mitosis. The CPC complex has essential functions at the centromere in ensuring correct chromosome alignment and segregation and is required for chromatin-induced microtubule stabilization and spindle assembly. Phosphorylates 'Ser-10' and 'Ser-28' of histone H3 during mitosis
TXN	9606.ENSP00000363641	thioredoxin; Participates in various redox reactions through the reversible oxidation of its active center dithiol to a disulfide and catalyzes dithiol-disulfide exchange reactions. Plays a role in the reversible S-nitrosylation of cysteine residues in target proteins, and thereby contributes to the response to intracellular nitric oxide. Nitrosylates the active site Cys of CASP3 in response to nitric oxide (NO), and thereby inhibits caspase-3 activity
AHSA2	9606.ENSP00000349525	AHA1, activator of heat shock 90kDa protein ATPase homolog 2 (yeast); Cochaperone that stimulates HSP90 ATPase activity (By similarity)

CYCS	9606.ENSP00000307786	cytochrome c, somatic; Electron carrier protein. The oxidized form of the cytochrome c heme group can accept an electron from the heme group of the cytochrome c1 subunit of cytochrome reductase. Cytochrome c then transfers this electron to the cytochrome oxidase complex, the final protein carrier in the mitochondrial electron-transport chain
PRDX1	9606.ENSP00000262746	peroxiredoxin 1; Involved in redox regulation of the cell. Reduces peroxides with reducing equivalents provided through the thioredoxin system but not from glutaredoxin. May play an important role in eliminating peroxides generated during metabolism. Might participate in the signaling cascades of growth factors and tumor necrosis factor-alpha by regulating the intracellular concentrations of H(2)O(2). Reduces an intramolecular disulfide bond in GDPD5 that gates the ability to GDPD5 to drive postmitotic motor neuron differentiation (By similarity)
SGTA	9606.ENSP00000221566	small glutamine-rich tetratricopeptide repeat (TPR)-containing, alpha; Co-chaperone that binds directly to HSC70 and HSP70 and regulates their ATPase activity
NR3C1	9606.ENSP00000231509	nuclear receptor subfamily 3, group C, member 1 (glucocorticoid receptor); Receptor for glucocorticoids (GC). Has a dual mode of action: as a transcription factor that binds to glucocorticoid response elements (GRE) and as a modulator of other transcription factors. Affects inflammatory responses, cellular proliferation and differentiation in target tissues. Could act as a coactivator for STAT5-dependent transcription upon growth hormone (GH) stimulation and could reveal an essential role of hepatic GR in the control of body growth. Involved in chromatin remodeling. Plays a significant [...]
AIP	9606.ENSP00000279146	aryl hydrocarbon receptor interacting protein; May play a positive role in AHR-mediated (aromatic hydrocarbon receptor) signaling, possibly by influencing its receptivity for ligand and/or its nuclear targeting
TXNRD1	9606.ENSP00000412045	thioredoxin reductase 1; Isoform 1 may possess glutaredoxin activity as well as thioredoxin reductase activity and induces actin and tubulin polymerization, leading to formation of cell membrane protrusions. Isoform 4 enhances the transcriptional activity of estrogen receptors alpha and beta while isoform 5 enhances the transcriptional activity of the beta receptor only. Isoform 5 also mediates cell death induced by a combination of interferon-beta and retinoic acid
ENSG00000115541	9606.ENSP00000398885	Putative uncharacterized protein ENSP00000398885 Fragment ; Eukaryotic CPN10 homolog which is essential for mitochondrial protein biogenesis, together with CPN60. Binds to CPN60 in the presence of Mg-ATP and suppresses the ATPase activity of the latter
PTK2	9606.ENSP00000341189	PTK2 protein tyrosine kinase 2; Non-receptor protein-tyrosine kinase implicated in signaling pathways involved in cell motility, proliferation and apoptosis. Activated by tyrosine-phosphorylation in response to either integrin clustering induced by cell adhesion or antibody cross-linking, or via G-protein coupled receptor (GPCR) occupancy by ligands such as bombesin or lysophosphatidic acid, or via LDL receptor occupancy. Plays a potential role in oncogenic transformations resulting in increased kinase activity
CD93	9606.ENSP00000246006	CD93 molecule; Receptor (or element of a larger receptor complex) for C1q, mannose-binding lectin (MBL2) and pulmonary surfactant protein A (SPA). May mediate the enhancement of phagocytosis in monocytes and macrophages upon interaction with soluble defense collagens. May play a role in intercellular adhesion
CTNND1	9606.ENSP00000382004	catenin (cadherin-associated protein), delta 1; Binds to and inhibits the transcriptional repressor ZBTB33, which may lead to activation of target genes of the Wnt signaling pathway (By similarity). May associate with and regulate the cell adhesion properties of both C- and E-cadherins. Implicated both in cell transformation by SRC and in ligand-induced receptor signaling through the EGF, PDGF, CSF-1 and ERBB2 receptors. Promotes GLIS2 C-terminal cleavage
AR	9606.ENSP00000363822	androgen receptor; Steroid hormone receptors are ligand-activated transcription factors that regulate eukaryotic gene expression and affect cellular proliferation and differentiation in target tissues. Transcription factor activity is modulated by bound coactivator and corepressor proteins. Transcription activation is down-regulated by NR0B2. Activated, but not phosphorylated, by HIPK3
LMNB1	9606.ENSP00000261366	lamin B1; Lamins are components of the nuclear lamina, a fibrous layer on the nucleoplasmic side of the inner nuclear membrane, which is thought to provide a framework for the nuclear envelope and may also interact with chromatin
FLG	9606.ENSP00000357789	filaggrin; Aggregates keratin intermediate filaments and promotes disulfide-bond formation among the intermediate filaments during terminal differentiation of mammalian epidermis

KRT6C	9606.ENSP00000252250	keratin 6C
PPP2R5D	9606.ENSP00000417963	protein phosphatase 2, regulatory subunit B', delta isoform; The B regulatory subunit might modulate substrate selectivity and catalytic activity, and also might direct the localization of the catalytic enzyme to a particular subcellular compartment
RAVER1	9606.ENSP00000293677	ribonucleoprotein, PTB-binding 1; Cooperates with PTBP1 to modulate regulated alternative splicing events. Promotes exon skipping. Cooperates with PTBP1 to modulate switching between mutually exclusive exons during maturation of the TPM1 pre-mRNA (By similarity)
FKBP1A	9606.ENSP00000371138	FK506 binding protein 1A, 12kDa; May play a role in modulation of ryanodine receptor isoform-1 (RYR-1), a component of the calcium release channel of skeletal muscle sarcoplasmic reticulum. There are four molecules of FKBP12 per skeletal muscle RYR. PPIases accelerate the folding of proteins. It catalyzes the cis-trans isomerization of proline imidic peptide bonds in oligopeptides
STRN3	9606.ENSP00000350071	striatin, calmodulin binding protein 3; Binds calmodulin in a calcium dependent manner. May function as scaffolding or signaling protein
SORBS3	9606.ENSP00000240123	sorbin and SH3 domain containing 3; Vinexin alpha isoform promotes up-regulation of actin stress fiber formation. Vinexin beta isoform plays a role in cell spreading and enhances the activation of JNK/SAPK in response to EGF stimulation by using its third SH3 domain
DHFR	9606.ENSP00000396308	dihydrofolate reductase
TERT	9606.ENSP00000309572	telomerase reverse transcriptase; Telomerase is a ribonucleoprotein enzyme essential for the replication of chromosome termini in most eukaryotes. It elongates telomeres. It is a reverse transcriptase that adds simple sequence repeats to chromosome ends by copying a template sequence within the RNA component of the enzyme
PKLR	9606.ENSP00000339933	pyruvate kinase, liver and RBC; Plays a key role in glycolysis (By similarity)
PPP2R2D	9606.ENSP00000381100	protein phosphatase 2, regulatory subunit B, delta isoform; The B regulatory subunit might modulate substrate selectivity and catalytic activity, and also might direct the localization of the catalytic enzyme to a particular subcellular compartment (By similarity)
PPP2R3A	9606.ENSP00000264977	protein phosphatase 2 (formerly 2A), regulatory subunit B'', alpha; The B regulatory subunit might modulate substrate selectivity and catalytic activity, and also might direct the localization of the catalytic enzyme to a particular subcellular compartment
CASP3	9606.ENSP00000311032	caspase 3, apoptosis-related cysteine peptidase; Involved in the activation cascade of caspases responsible for apoptosis execution. At the onset of apoptosis it proteolytically cleaves poly(ADP-ribose) polymerase (PARP) at a '216-Asp-|-Gly-217' bond. Cleaves and activates sterol regulatory element binding proteins (SREBPs) between the basic helix-loop- helix leucine zipper domain and the membrane attachment domain. Cleaves and activates caspase-6, -7 and -9. Involved in the cleavage of huntingtin
PNN	9606.ENSP00000216832	pinin, desmosome associated protein; Transcriptional activator binding to the E-box 1 core sequence of the E-cadherin promoter gene; the core-binding sequence is 5'CAGGTG-3'. Capable of reversing CTBP1-mediated transcription repression. Component of a splicing-dependent multiprotein exon junction complex (EJC) deposited at splice junction on mRNAs. The EJC is a dynamic structure consisting of a few core proteins and several more peripheral nuclear and cytoplasmic associated factors that join the complex only transiently either during EJC assembly or during subsequent mRNA metabolism. P [...]
AHR	9606.ENSP00000242057	aryl hydrocarbon receptor; Ligand-activated transcriptional activator. Binds to the XRE promoter region of genes it activates. Activates the expression of multiple phase I and II xenobiotic chemical metabolizing enzyme genes (such as the CYP1A1 gene). Mediates biochemical and toxic effects of halogenated aromatic hydrocarbons. Involved in cell-cycle regulation. Likely to play an important role in the development and maturation of many tissues
SNAI2	9606.ENSP00000020945	snail homolog 2 (Drosophila); Transcriptional repressor. Involved in the generation and migration of neural crest cells
FKBP8	9606.ENSP00000222308	FK506 binding protein 8, 38kDa; Constitutively inactive PPiase, which becomes active when bound to calmodulin and calcium. Seems to act as a chaperone for BCL2, targets it to the mitochondria and modulates its phosphorylation state. The BCL2/FKBP8/calmodulin/calcium complex probably interferes with the binding of BCL2 to its targets. The active form of FKBP8 may therefore play a role in the regulation of apoptosis

RRM2B	9606.ENSP00000251810	ribonucleotide reductase M2 B (TP53 inducible); Plays a pivotal role in cell survival by repairing damaged DNA in a p53/TP53-dependent manner. Supplies deoxyribonucleotides for DNA repair in cells arrested at G1 or G2. Contains an iron-tyrosyl free radical center required for catalysis. Forms an active ribonucleotide reductase (RNR) complex with RRM1 which is expressed both in resting and proliferating cells in response to DNA damage
ZMPSTE24	9606.ENSP00000361845	zinc metallopeptidase (STE24 homolog, S. cerevisiae); Proteolytically removes the C-terminal three residues of farnesylated proteins. Acts on lamin A/C
S100A4	9606.ENSP00000346294	S100 calcium binding protein A4
PPP2R2A	9606.ENSP00000370113	protein phosphatase 2 (formerly 2A), regulatory subunit B, alpha isoform; The B regulatory subunit might modulate substrate selectivity and catalytic activity, and also might direct the localization of the catalytic enzyme to a particular subcellular compartment
ANXA2	9606.ENSP00000346032	annexin A2 pseudogene 1; Calcium-regulated membrane-binding protein whose affinity for calcium is greatly enhanced by anionic phospholipids (By similarity). It binds two calcium ions with high affinity (By similarity). May be involved in heat-stress response (By similarity)
PPP2R2C	9606.ENSP00000335083	protein phosphatase 2 (formerly 2A), regulatory subunit B, gamma isoform; The B regulatory subunit might modulate substrate selectivity and catalytic activity, and also might direct the localization of the catalytic enzyme to a particular subcellular compartment
SRC	9606.ENSP00000350941	v-src sarcoma (Schmidt-Ruppin A-2) viral oncogene homolog (avian)
PRDX5	9606.ENSP00000265462	peroxiredoxin 5; Reduces hydrogen peroxide and alkyl hydroperoxides with reducing equivalents provided through the thioredoxin system. Involved in intracellular redox signaling
EGF	9606.ENSP00000265171	epidermal growth factor (beta-urogastrone); EGF stimulates the growth of various epidermal and epithelial tissues in vivo and in vitro and of some fibroblasts in cell culture. Magnesiotropic hormone that stimulates magnesium reabsorption in the renal distal convoluted tubule via engagement of EGFR and activation of the magnesium channel TRPM6
MSN	9606.ENSP00000353408	moesin; Probably involved in connections of major cytoskeletal structures to the plasma membrane
SLC9A3R1	9606.ENSP00000262613	solute carrier family 9 (sodium/hydrogen exchanger), member 3 regulator 1; Scaffold protein that connects plasma membrane proteins with members of the ezrin/moesin/radixin family and thereby helps to link them to the actin cytoskeleton and to regulate their surface expression. Necessary for recycling of internalized ADRB2. Was first known to play a role in the regulation of the activity and subcellular location of SLC9A3. Necessary for cAMP-mediated phosphorylation and inhibition of SLC9A3. May enhance Wnt signaling. May participate in HTR4 targeting to microvilli (By similarity)
TRAPPC2	9606.ENSP00000352708	trafficking protein particle complex 2; Prevents MBP1-mediated transcriptional repression and antagonizes MBP1-mediated cell death. May play a role in vesicular transport from endoplasmic reticulum to Golgi
C1QBP	9606.ENSP00000225698	complement component 1, q subcomponent binding protein; Not known. Binds to the globular "heads" of C1Q thus inhibiting C1 activation
ERBB2	9606.ENSP00000269571	v-erb-b2 erythroblastic leukemia viral oncogene homolog 2, neuro/glioblastoma derived oncogene homolog (avian); Essential component of a neuregulin-receptor complex, although neuregulins do not interact with it alone. GP30 is a potential ligand for this receptor. Not activated by EGF, TGF- alpha and amphiregulin
STUB1	9606.ENSP00000219548	STIP1 homology and U-box containing protein 1; Modulates the activity of several chaperone complexes, including Hsp70, Hsc70 and Hsp90. Has E3 ubiquitin-protein ligase activity and targets misfolded chaperone substrates towards proteasomal degradation. Mediates transfer of non-canonical short ubiquitin chains to HSPA8 that have no effect on HSPA8 degradation
SGOL1	9606.ENSP00000263753	shugoshin-like 1 (S. pombe); Plays a central role in chromosome cohesion during mitosis by preventing premature dissociation of cohesin complex from centromeres after prophase, when most of cohesin complex dissociates from chromosomes arms. May act by preventing phosphorylation of the STAG2 subunit of cohesin complex at the centromere, ensuring cohesin persistence at centromere until cohesin cleavage by ESPL1/separase at anaphase
FAM40A	9606.ENSP00000358810	family with sequence similarity 40, member A
AHSA1	9606.ENSP00000216479	AHA1, activator of heat shock 90kDa protein ATPase homolog 1 (yeast); Cochaperone that stimulates HSP90 ATPase activity (By similarity). May affect a step in the endoplasmic reticulum to Golgi trafficking

PGR	9606.ENSP00000325120	progesterone receptor; The steroid hormones and their receptors are involved in the regulation of eukaryotic gene expression and affect cellular proliferation and differentiation in target tissues. Progesterone receptor isoform B (PRB) is involved activation of c-SRC/MAPK signaling on hormone stimulation
LIMK2	9606.ENSP00000339916	LIM domain kinase 2; Displays serine/threonine-specific phosphorylation of myelin basic protein and histone (MBP) in vitro
TNS1	9606.ENSP00000171887	tensin 1; May be involved in cell migration, cartilage development and in linking signal transduction pathways to the cytoskeleton
ESR1	9606.ENSP00000206249	estrogen receptor 1; Nuclear hormone receptor. The steroid hormones and their receptors are involved in the regulation of eukaryotic gene expression and affect cellular proliferation and differentiation in target tissues
DNAJC7	9606.ENSP00000406463	DnaJ (Hsp40) homolog, subfamily C, member 7
GDPD5	9606.ENSP00000337972	glycerophosphodiester phosphodiesterase domain containing 5; Promotes neurite formation. Cooperates with PRDX1 to drive postmitotic motor neuron differentiation. The glycerophosphodiester phosphodiesterase activity may be required for its role in neuronal differentiation. May contribute to the osmotic regulation of cellular glycerophosphocholine
ARHGDIB	9606.ENSP00000228945	Rho GDP dissociation inhibitor (GDI) beta; Regulates the GDP/GTP exchange reaction of the Rho proteins by inhibiting the dissociation of GDP from them, and the subsequent binding of GTP to them
KRT18	9606.ENSP00000373487	keratin 18; Involved in the uptake of thrombin-antithrombin complexes by hepatic cells (By similarity). When phosphorylated, plays a role in filament reorganization. Involved in the delivery of mutated CFTR to the plasma membrane. Together with KRT8, is involved in interleukin-6 (IL-6)-mediated barrier protection
PLS3	9606.ENSP00000348163	plastin 3 (T isoform); Actin-bundling protein found in intestinal microvilli, hair cell stereocilia, and fibroblast filopodia
STAT3	9606.ENSP00000264657	signal transducer and activator of transcription 3 (acute-phase response factor); Transcription factor that binds to the interleukin-6 (IL-6)-responsive elements identified in the promoters of various acute-phase protein genes. Activated by IL31 through IL31RA
KRT8	9606.ENSP00000293308	keratin 8; Together with KRT19, helps to link the contractile apparatus to dystrophin at the costameres of striated muscle
CTNNA1	9606.ENSP00000304669	catenin (cadherin-associated protein), alpha 1, 102kDa; Associates with the cytoplasmic domain of a variety of cadherins. The association of catenins to cadherins produces a complex which is linked to the actin filament network, and which seems to be of primary importance for cadherins cell-adhesion properties. May play a crucial role in cell differentiation
NARF	9606.ENSP00000309899	nuclear prelamin A recognition factor
BANF1	9606.ENSP00000310275	barrier to autointegration factor 1; Plays fundamental roles in nuclear assembly, chromatin organization, gene expression and gonad development. May potently compress chromatin structure and be involved in membrane recruitment and chromatin decondensation during nuclear assembly. Contains 2 non-specific dsDNA-binding sites which may promote DNA cross-bridging. Exploited by retroviruses for inhibiting self-destructing autointegration of retroviral DNA, thereby promoting integration of viral DNA into the host chromosome. EMD and BAF are cooperative cofactors of HIV-1 infection. Associat [...]
PPP2CB	9606.ENSP00000221138	protein phosphatase 2 (formerly 2A), catalytic subunit, beta isoform; PP2A can modulate the activity of phosphorylase B kinase casein kinase 2, mitogen-stimulated S6 kinase, and MAP-2 kinase. Can dephosphorylate SV40 large T antigen and p53. Dephosphorylates SV40 large T antigen, preferentially on serine residues 120, 123, 677, and perhaps 679. The C subunit was most active, followed by the AC form, which was more active than the ABC form, and activity of all three forms was strongly stimulated by manganese, and to a lesser extent by magnesium. Dephosphorylation by the AC form, but not [...]
TMPO	9606.ENSP00000266732	thymopoietin; May help direct the assembly of the nuclear lamina and thereby help maintain the structural organization of the nuclear envelope. Possible receptor for attachment of lamin filaments to the inner nuclear membrane. May be involved in the control of initiation of DNA replication through its interaction with NAKAP95
MAP3K5	9606.ENSP00000351908	mitogen-activated protein kinase kinase kinase 5; Component of a protein kinase signal transduction cascade. Phosphorylates and activates MAP2K4 and MAP2K6, which in turn activate the JNK and p38 MAP kinases, respectively. Overexpression induces apoptotic cell death

PPP2R5A	9606.ENSP00000261461	protein phosphatase 2, regulatory subunit B', alpha isoform; The B regulatory subunit might modulate substrate selectivity and catalytic activity, and also might direct the localization of the catalytic enzyme to a particular subcellular compartment
PFN1	9606.ENSP00000225655	profilin 1; Binds to actin and affects the structure of the cytoskeleton. At high concentrations, profilin prevents the polymerization of actin, whereas it enhances it at low concentrations. By binding to PIP2, it inhibits the formation of IP3 and DG
FPR2	9606.ENSP00000340191	formyl peptide receptor 2; Low affinity receptor for N-formyl-methionyl peptides, which are powerful neutrophils chemotactic factors. Binding of FMLP to the receptor causes activation of neutrophils. This response is mediated via a G-protein that activates a phosphatidylinositol-calcium second messenger system. The activation of LXA4R could result in an anti-inflammatory outcome counteracting the actions of proinflammatory signals such as LTB4 (leukotriene B4)
MYC	9606.ENSP00000367207	v-myc myelocytomatosis viral oncogene homolog (avian); Participates in the regulation of gene transcription. Binds DNA in a non-specific manner, yet also specifically recognizes the core sequence 5'-CAC[GA]TG-3'. Seems to activate the transcription of growth-related genes
CDK4	9606.ENSP00000257904	cyclin-dependent kinase 4; Probably involved in the control of the cell cycle
PPP2R5B	9606.ENSP00000164133	protein phosphatase 2, regulatory subunit B', beta isoform; The B regulatory subunit might modulate substrate selectivity and catalytic activity, and also might direct the localization of the catalytic enzyme to a particular subcellular compartment
FPR1	9606.ENSP00000302707	formyl peptide receptor 1; High affinity receptor for N-formyl-methionyl peptides, which are powerful neutrophils chemotactic factors. Binding of FMLP to the receptor causes activation of neutrophils. This response is mediated via a G-protein that activates a phosphatidylinositol-calcium second messenger system
AKT1	9606.ENSP00000270202	v-akt murine thymoma viral oncogene homolog 1; General protein kinase capable of phosphorylating several known proteins. Phosphorylates TBC1D4. Signals downstream of phosphatidylinositol 3-kinase (PI(3)K) to mediate the effects of various growth factors such as platelet-derived growth factor (PDGF), epidermal growth factor (EGF), insulin and insulin-like growth factor I (IGF-I). Plays a role in glucose transport by mediating insulin-induced translocation of the GLUT4 glucose transporter to the cell surface. Mediates the antiapoptotic effects of IGF-I. Mediates insulin-stimulated protei [...]
PPP2R2B	9606.ENSP00000336591	protein phosphatase 2 (formerly 2A), regulatory subunit B, beta isoform; The B regulatory subunit might modulate substrate selectivity and catalytic activity, and also might direct the localization of the catalytic enzyme to a particular subcellular compartment. Within the PP2A holoenzyme complex, isoform 2 is required to promote proapoptotic activity (By similarity). Isoform 2 regulates neuronal survival through the mitochondrial fission and fusion balance (By similarity)
TLN1	9606.ENSP00000316029	talin 1; Probably involved in connections of major cytoskeletal structures to the plasma membrane. High molecular weight cytoskeletal protein concentrated at regions of cell-substratum contact and, in lymphocytes, at cell-cell contacts (By similarity)
IKBKB	9606.ENSP00000339151	inhibitor of kappa light polypeptide gene enhancer in B-cells, kinase beta; Acts as part of the IKK complex in the conventional pathway of NF-kappa-B activation and phosphorylates inhibitors of NF-kappa-B thus leading to the dissociation of the inhibitor/NF- kappa-B complex and ultimately the degradation of the inhibitor. Also phosphorylates NCOA3
HSPB1	9606.ENSP00000248553	heat shock 27kDa protein 1; Involved in stress resistance and actin organization
CTSB	9606.ENSP00000342070	cathepsin B; Thiol protease which is believed to participate in intracellular degradation and turnover of proteins. Has also been implicated in tumor invasion and metastasis
VCL	9606.ENSP00000211998	vinculin; Involved in cell adhesion. May be involved in the attachment of the actin-based microfilaments to the plasma membrane. May also play important roles in cell morphology and locomotion
TBPL2	9606.ENSP00000247219	TATA box binding protein like 2; Transcription factor required in complex with TAF3 for the differentiation of myoblasts into myocytes. The complex replaces TFIID at specific promoters at an early stage in the differentiation process (By similarity)
ANXA5	9606.ENSP00000296511	annexin A5; 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

ANXA1	9606.ENSP00000257497	annexin A1; Calcium/phospholipid-binding protein which promotes membrane fusion and is involved in exocytosis. This protein regulates phospholipase A2 activity. It seems to bind from two to four calcium ions with high affinity
OSBP2	9606.ENSP00000332576	oxysterol binding protein 2; Binds 7-ketocholesterol
F3	9606.ENSP00000334145	coagulation factor III (thromboplastin, tissue factor); Initiates blood coagulation by forming a complex with circulating factor VII or VIIa. The [TF:VIIa] complex activates factors IX or X by specific limited protolysis. TF plays a role in normal hemostasis by initiating the cell-surface assembly and propagation of the coagulation protease cascade
ANXA3	9606.ENSP00000264908	annexin A3; Inhibitor of phospholipase A2, also possesses anti- coagulant properties. Also cleaves the cyclic bond of inositol 1,2-cyclic phosphate to form inositol 1-phosphate
TCHP	9606.ENSP00000324404	trichoplein, keratin filament binding; May act as a 'capping' or 'branching' protein for keratin filaments in the cell periphery. May regulate K8/K18 filament and desmosome organization mainly at the apical or peripheral regions of simple epithelial cells
SF3A2	9606.ENSP00000221494	splicing factor 3a, subunit 2, 66kDa; Subunit of the splicing factor SF3A required for 'A' complex assembly formed by the stable binding of U2 snRNP to the branchpoint sequence (BPS) in pre-mRNA. Sequence independent binding of SF3A/SF3B complex upstream of the branch site is essential, it may anchor U2 snRNP to the pre-mRNA. May also be involved in the assembly of the 'E' complex
GDI1	9606.ENSP00000394071	GDP dissociation inhibitor 1; Regulates the GDP/GTP exchange reaction of most Rab proteins by inhibiting the dissociation of GDP from them, and the subsequent binding of GTP to them
HSPA4	9606.ENSP00000302961	heat shock 70kDa protein 4
FPR3	9606.ENSP00000341821	formyl peptide receptor 3; Low affinity receptor for N-formyl-methionyl peptides, which are powerful neutrophils chemotactic factors. Binding of FMLP to the receptor causes activation of neutrophils. This response is mediated via a G-protein that activates a phosphatidylinositol-calcium second messenger system
ANXA6	9606.ENSP00000346550	annexin A6; May associate with CD21. May regulate the release of Ca(2+) from intracellular stores
FN1	9606.ENSP00000346839	fibronectin 1; Fibronectins bind cell surfaces and various compounds including collagen, fibrin, heparin, DNA, and actin. Fibronectins are involved in cell adhesion, cell motility, opsonization, wound healing, and maintenance of cell shape
HIF1A	9606.ENSP00000338018	hypoxia inducible factor 1, alpha subunit (basic helix-loop-helix transcription factor); Functions as a master transcriptional regulator of the adaptive response to hypoxia. Under hypoxic conditions activates the transcription of over 40 genes, including, erythropoietin, glucose transporters, glycolytic enzymes, vascular endothelial growth factor, and other genes whose protein products increase oxygen delivery or facilitate metabolic adaptation to hypoxia. Plays an essential role in embryonic vascularization, tumor angiogenesis and pathophysiology of ischemic disease. Binds to core DNA [...]
RHOA	9606.ENSP00000400175	ras homolog gene family, member A; Regulates a signal transduction pathway linking plasma membrane receptors to the assembly of focal adhesions and actin stress fibers. Serves as a target for the yopT cysteine peptidase from Yersinia pestis, vector of the plague, and Yersinia pseudotuberculosis, which causes gastrointestinal disorders. May be an activator of PLCE1. Activated by ARHGEF2, which promotes the exchange of GDP for GTP
TPM1	9606.ENSP00000267996	tropomyosin 1 (alpha); Binds to actin filaments in muscle and non-muscle cells. Plays a central role, in association with the troponin complex, in the calcium dependent regulation of vertebrate striated muscle contraction. Smooth muscle contraction is regulated by interaction with caldesmon. In non-muscle cells is implicated in stabilizing cytoskeleton actin filaments
VASP	9606.ENSP00000245932	vasodilator-stimulated phosphoprotein; Ena/VASP proteins are actin-associated proteins involved in a range of processes dependent on cytoskeleton remodeling and cell polarity such as axon guidance, lamellipodial and filopodial dynamics, platelet activation and cell migration. VASP promotes actin filament elongation. It protects the barbed end of growing actin filaments against capping and increases the rate of actin polymerization in the presence of capping protein. VASP stimulates actin filament elongation by promoting the transfer of profilin- bound actin monomers onto the barbed end [...]

CHEK1	9606.ENSP00000278916	CHK1 checkpoint homolog (S. pombe); Required for checkpoint mediated cell cycle arrest in response to DNA damage or the presence of unreplicated DNA. May also negatively regulate cell cycle progression during unperturbed cell cycles. Recognizes the substrate consensus sequence [R-X-X- S/T]. Binds to and phosphorylates CDC25A, CDC25B and CDC25C. Phosphorylation of CDC25A at 'Ser-178' and 'Thr-507' and phosphorylation of CDC25C at 'Ser-216' creates binding sites for 14-3-3 proteins which inhibit CDC25A and CDC25C. Phosphorylation of CDC25A at 'Ser-76', 'Ser-124', 'Ser-178', 'Ser-279' and [...]
TPM4	9606.ENSP00000345230	tropomyosin 4; Binds to actin filaments in muscle and non-muscle cells. Plays a central role, in association with the troponin complex, in the calcium dependent regulation of vertebrate striated muscle contraction. Smooth muscle contraction is regulated by interaction with caldesmon. In non-muscle cells is implicated in stabilizing cytoskeleton actin filaments. Binds calcium
S100A10	9606.ENSP00000357799	S100 calcium binding protein A10; Because S100A10 induces the dimerization of ANXA2/p36, it may function as a regulator of protein phosphorylation in that the ANXA2 monomer is the preferred target (in vitro) of tyrosine- specific kinase
ALDOA	9606.ENSP00000336927	aldolase A, fructose-bisphosphate
NFKB1	9606.ENSP00000226574	nuclear factor of kappa light polypeptide gene enhancer in B-cells 1; NF-kappa-B is a pleiotropic transcription factor which is present in almost all cell types and is involved in many biological processed such as inflammation, immunity, differentiation, cell growth, tumorigenesis and apoptosis. NF- kappa-B is a homo- or heterodimeric complex formed by the Rel-like domain-containing proteins RELA/p65, RELB, NFKB1/p105, NFKB1/p50, REL and NFKB2/p52 and the heterodimeric p65-p50 complex appears to be most abundant one. The dimers bind at kappa-B sites in the DNA of their target genes and [...]
PRDX2	9606.ENSP00000301522	peroxiredoxin 2; Involved in redox regulation of the cell. Reduces peroxides with reducing equivalents provided through the thioredoxin system. It is not able to receive electrons from glutaredoxin. May play an important role in eliminating peroxides generated during metabolism. Might participate in the signaling cascades of growth factors and tumor necrosis factor-alpha by regulating the intracellular concentrations of H(2)O(2)
ETV5	9606.ENSP00000306894	ets variant 5; Binds to DNA sequences containing the consensus nucleotide core sequence GGAA
RRM1	9606.ENSP00000300738	ribonucleotide reductase M1; Provides the precursors necessary for DNA synthesis. Catalyzes the biosynthesis of deoxyribonucleotides from the corresponding ribonucleotides (By similarity)
ME1	9606.ENSP00000358719	malic enzyme 1, NADP(+)-dependent, cytosolic
VCAM1	9606.ENSP00000294728	vascular cell adhesion molecule 1; Important in cell-cell recognition. Appears to function in leukocyte-endothelial cell adhesion. Interacts with the beta-1 integrin VLA4 on leukocytes, and mediates both adhesion and signal transduction. The VCAM1/VLA4 interaction may play a pathophysiologic role both in immune responses and in leukocyte emigration to sites of inflammation
S100A11	9606.ENSP00000271638	S100 calcium binding protein A11; Facilitates the differentiation and the cornification of keratinocytes
MYH6	9606.ENSP00000348634	myosin, heavy chain 6, cardiac muscle, alpha; Muscle contraction
SPN	9606.ENSP00000353238	sialophorin; One of the major glycoproteins of thymocytes and T lymphocytes. Plays a role in the physicochemical properties of the T-cell surface and in lectin binding. Presents carbohydrate ligands to selectins. Has an extended rodlike structure that could protrude above the glycocalyx of the cell and allow multiple glycan chains to be accessible for binding. Is a counter receptor for SN/Siglec-1 (By similarity). During T-cell activation is actively removed from the T-cell-APC (antigen-presenting cell) contact site thus suggesting a negative regulatory role in adaptive immune response [...]
ENO1	9606.ENSP00000234590	enolase 1, (alpha); Multifunctional enzyme that, as well as its role in glycolysis, plays a part in various processes such as growth control, hypoxia tolerance and allergic responses. May also function in the intravascular and pericellular fibrinolytic system due to its ability to serve as a receptor and activator of plasminogen on the cell surface of several cell-types such as leukocytes and neurons. Stimulates immunoglobulin production
TPD52	9606.ENSP00000368391	tumor protein D52
PRKCA	9606.ENSP00000284384	protein kinase C, alpha; This is a calcium-activated, phospholipid-dependent, serine- and threonine-specific enzyme. May play a role in cell motility by phosphorylating CSPG4
CDC37	9606.ENSP00000222005	microRNA 1181; Co-chaperone that binds to numerous kinases and promotes their interaction with the Hsp90 complex, resulting in stabilization and promotion of their activity

CD46	9606.ENSP00000313875	CD46 molecule, complement regulatory protein; Acts as a cofactor for complement factor I, a serine protease which protects autologous cells against complement-mediated injury by cleaving C3b and C4b deposited on host tissue. May be involved in the fusion of the spermatozoa with the oocyte during fertilization. Also acts as a costimulatory factor for T- cells which induces the differentiation of CD4+ into T-regulatory 1 cells. T-regulatory 1 cells suppress immune responses by secreting interleukin-10, and therefore are thought to prevent autoimmunity. A number of viral and bacterial pa [...]
KRT5	9606.ENSP00000252242	keratin 5
ACTC1	9606.ENSP00000290378	actin, alpha, cardiac muscle 1; Actins are highly conserved proteins that are involved in various types of cell motility and are ubiquitously expressed in all eukaryotic cells (By similarity)
HSF1	9606.ENSP00000332698	heat shock transcription factor 1; DNA-binding protein that specifically binds heat shock promoter elements (HSE) and activates transcription. In higher eukaryotes, HSF is unable to bind to the HSE unless the cells are heat shocked
ACTN2	9606.ENSP00000355537	actinin, alpha 2; F-actin cross-linking protein which is thought to anchor actin to a variety of intracellular structures. This is a bundling protein
KRT19	9606.ENSP00000355124	keratin 19; Involved in the organization of myofibers. Together with KRT8, helps to link the contractile apparatus to dystrophin at the costameres of striated muscle
PPP2CA	9606.ENSP00000418447	protein phosphatase 2 (formerly 2A), catalytic subunit, alpha isoform; PP2A can modulate the activity of phosphorylase B kinase casein kinase 2, mitogen-stimulated S6 kinase, and MAP-2 kinase. Can dephosphorylate SV40 large T antigen and p53. Dephosphorylates SV40 large T antigen, preferentially on serine residues 120, 123, 677, and perhaps 679. The C subunit was most active, followed by the AC form, which was more active than the ABC form, and activity of all three forms was strongly stimulated by manganese, and to a lesser extent by magnesium. Dephosphorylation by the AC form, but no [...]
LAMA2	9606.ENSP00000400365	laminin, alpha 2; Binding to cells via a high affinity receptor, laminin is thought to mediate the attachment, migration and organization of cells into tissues during embryonic development by interacting with other extracellular matrix components
PCNA	9606.ENSP00000368438	proliferating cell nuclear antigen; This protein is an auxiliary protein of DNA polymerase delta and is involved in the control of eukaryotic DNA replication by increasing the polymerase's processibility during elongation of the leading strand (By similarity)
UCK2	9606.ENSP00000356853	uridine-cytidine kinase 2; Phosphorylates uridine and cytidine to uridine monophosphate and cytidine monophosphate. Does not phosphorylate deoxyribonucleosides or purine ribonucleosides. Can use ATP or GTP as a phosphate donor. Can also phosphorylate cytidine and uridine nucleoside analogs such as 6-azauridine, 5-fluorouridine, 4- thiouridine, 5-bromouridine, N(4)-acetylcytidine, N(4)-benzoylcytidine, 5-fluorocytidine, 2-thiocytidine, 5- methylcytidine, and N(4)-anisoylcytidine
CHUK	9606.ENSP00000359424	conserved helix-loop-helix ubiquitous kinase; Acts as part of the IKK complex in the conventional pathway of NF-kappa-B activation and phosphorylates inhibitors of NF-kappa-B thus leading to the dissociation of the inhibitor/NF- kappa-B complex and ultimately the degradation of the inhibitor. As part of the non-canonical pathway of NF-kappa-B activation, the MAP3K14-activated CHUK/IKKA homodimer phosphorylates NFKB2/p100 associated with RelB, inducing its proteolytic processing to NFKB2/p52 and the formation of NF-kappa-B RelB-p52 complexes. Also phosphorylates NCOA3. Phosphorylates 'S [...]
KRT16	9606.ENSP00000301653	keratin 16
EZR	9606.ENSP00000338934	ezrin; Probably involved in connections of major cytoskeletal structures to the plasma membrane. In epithelial cells, required for the formation of microvilli and membrane ruffles on the apical pole. Along with PLEKHG6, required for normal macropinocytosis
RUVBL1	9606.ENSP00000318297	RuvB-like 1 (E. coli); Possesses single-stranded DNA-stimulated ATPase and ATP-dependent DNA helicase (3' to 5') activity. Component of the NuA4 histone acetyltransferase complex which is involved in transcriptional activation of select genes principally by acetylation of nucleosomal histones H4 and H2A. This modification may both alter nucleosome - DNA interactions and promote interaction of the modified histones with other proteins which positively regulate transcription. This complex may be required for the activation of transcriptional programs associated with oncogene and proto-o [...]

KAT5	9606.ENSP00000340330	K(lysine) acetyltransferase 5; Catalytic subunit of the NuA4 histone acetyltransferase complex which is involved in transcriptional activation of select genes principally by acetylation of nucleosomal histones H4 and H2A. This modification may both alter nucleosome-DNA interactions and promote interaction of the modified histones with other proteins which positively regulate transcription. This complex may be required for the activation of transcriptional programs associated with oncogene and proto-oncogene mediated growth induction, tumor suppressor mediated growth arrest and replicat [...]
APAF1	9606.ENSP00000353059	apoptotic peptidase activating factor 1; Oligomeric Apaf-1 mediates the cytochrome c-dependent autocatalytic activation of pro-caspase-9 (Apaf-3), leading to the activation of caspase-3 and apoptosis. This activation requires ATP. Isoform 6 is less effective in inducing apoptosis
VIM	9606.ENSP00000224237	vimentin; Vimentins are class-III intermediate filaments found in various non-epithelial cells, especially mesenchymal cells
TMSB4X	9606.ENSP00000370007	thymosin beta 4, X-linked; Plays an important role in the organization of the cytoskeleton (By similarity). Binds to and sequesters actin monomers (G actin) and therefore inhibits actin polymerization
LDHB	9606.ENSP00000229319	lactate dehydrogenase B
EIF2AK1	9606.ENSP00000199389	eukaryotic translation initiation factor 2-alpha kinase 1; Mediates down-regulation of protein synthesis in response to various stress conditions by the phosphorylation of EIF2S1 at 'Ser-48' and 'Ser-51'. Protein synthesis is inhibited at the level of initiation (By similarity)
S100A1	9606.ENSP00000292169	S100 calcium binding protein A1; Weakly binds calcium but binds zinc very tightly-distinct binding sites with different affinities exist for both ions on each monomer. Physiological concentrations of potassium ion antagonize the binding of both divalent cations, especially affecting high-affinity calcium-binding sites
CASP7	9606.ENSP00000298700	caspase 7, apoptosis-related cysteine peptidase; Involved in the activation cascade of caspases responsible for apoptosis execution. Cleaves and activates sterol regulatory element binding proteins (SREBPs). Proteolytically cleaves poly(ADP-ribose) polymerase (PARP) at a '216-Asp-|-Gly- 217' bond. Overexpression promotes programmed cell death
HSP90AA1	9606.ENSP00000335153	heat shock protein 90kDa alpha (cytosolic), class A member 1; Molecular chaperone. Has ATPase activity (By similarity)
PPP2R5E	9606.ENSP00000337641	protein phosphatase 2, regulatory subunit B', epsilon isoform; The B regulatory subunit might modulate substrate selectivity and catalytic activity, and also might direct the localization of the catalytic enzyme to a particular subcellular compartment
KRT7	9606.ENSP00000329243	keratin 7; Blocks interferon-dependent interphase and stimulates DNA synthesis in cells. Involved in the translational regulation of the human papillomavirus type 16 E7 mRNA (HPV16 E7)
ICAM3	9606.ENSP00000160262	intercellular adhesion molecule 3; ICAM proteins are ligands for the leukocyte adhesion protein LFA-1 (integrin alpha-L/beta-2). ICAM3 is also a ligand for integrin alpha-D/beta-2
ACTB	9606.ENSP00000349960	actin, beta; Actins are highly conserved proteins that are involved in various types of cell motility and are ubiquitously expressed in all eukaryotic cells (By similarity)
IKBKG	9606.ENSP00000358622	inhibitor of kappa light polypeptide gene enhancer in B-cells, kinase gamma; Regulatory subunit of the IKK core complex which phosphorylates inhibitors of NF-kappa-B thus leading to the dissociation of the inhibitor/NF-kappa-B complex and ultimately the degradation of the inhibitor. Also considered to be a mediator for TAX activation of NF-kappa-B. Could be implicated in NF-kappa- B-mediated protection from cytokine toxicity (By similarity)
TTN	9606.ENSP00000348444	titin
SLMAP	9606.ENSP00000295951	sarcolemma associated protein; May play a role during myoblast fusion (By similarity)
RRM2	9606.ENSP00000302955	ribonucleotide reductase M2; Provides the precursors necessary for DNA synthesis. Catalyzes the biosynthesis of deoxyribonucleotides from the corresponding ribonucleotides. Inhibits Wnt signaling
GPI	9606.ENSP00000348877	glucose phosphate isomerase; Besides it's role as a glycolytic enzyme, mammalian GPI can function as a tumor-secreted cytokine and an angiogenic factor (AMF) that stimulates endothelial cell motility. GPI is also a neurotrophic factor (Neuroleukin) for spinal and sensory neurons

CDH1	9606.ENSP00000261769	cadherin 1, type 1, E-cadherin (epithelial); Cadherins are calcium-dependent cell adhesion proteins. They preferentially interact with themselves in a homophilic manner in connecting cells; cadherins may thus contribute to the sorting of heterogeneous cell types. CDH1 is involved in mechanisms regulating cell-cell adhesions, mobility and proliferation of epithelial cells. Has a potent invasive suppressor role. It is a ligand for integrin alpha-E/beta-7
LIMK1	9606.ENSP00000336740	LIM domain kinase 1; Protein kinase which regulates actin filament dynamics. Phosphorylates and inactivates the actin binding/depolymerizing factor cofilin, thereby stabilizing the actin cytoskeleton. Isoform 3 has a dominant negative effect on actin cytoskeletal changes. May be involved in brain development
ZNF239	9606.ENSP00000307774	zinc finger protein 239; May be involved in transcriptional regulation
SUGT1	9606.ENSP00000367208	SGT1, suppressor of G2 allele of SKP1 (S. cerevisiae); May play a role in ubiquitination and subsequent proteosomal degradation of target proteins
HSPE1	9606.ENSP00000233893	heat shock 10kDa protein 1 (chaperonin 10); Eukaryotic CPN10 homolog which is essential for mitochondrial protein biogenesis, together with CPN60. Binds to CPN60 in the presence of Mg-ATP and suppresses the ATPase activity of the latter
PPP2R5C	9606.ENSP00000333905	protein phosphatase 2, regulatory subunit B', gamma isoform; The B regulatory subunit might modulate substrate selectivity and catalytic activity, and also might direct the localization of the catalytic enzyme to a particular subcellular compartment
TUBA1B	9606.ENSP00000336799	tubulin, alpha 1b; Tubulin is the major constituent of microtubules. It binds two moles of GTP, one at an exchangeable site on the beta chain and one at a non-exchangeable site on the alpha-chain (By similarity)
CLIC1	9606.ENSP00000408094	chloride intracellular channel 1; Can insert into membranes and form chloride ion channels. Channel activity depends on the pH. Membrane insertion seems to be redox-regulated and may occur only under oxydizing conditions
STRN4	9606.ENSP00000375777	striatin, calmodulin binding protein 4; Binds calmodulin in a calcium dependent manner. May function as scaffolding or signaling protein
SRXN1	9606.ENSP00000371388	sulfiredoxin 1 homolog (S. cerevisiae); Contributes to oxidative stress resistance by reducing cysteine-sulfinic acid formed under exposure to oxidants in the peroxiredoxins PRDX1, PRDX2, PRDX3 and PRDX4. Does not act on PRDX5 or PRDX6. May catalyze the reduction in a multi-step process by acting both as a specific phosphotransferase and a thioltransferase
CDK1	9606.ENSP00000306043	cyclin-dependent kinase 1; Plays a key role in the control of the eukaryotic cell cycle. It is required in higher cells for entry into S-phase and mitosis. p34 is a component of the kinase complex that phosphorylates the repetitive C-terminus of RNA polymerase II
CTNNB1	9606.ENSP00000344456	catenin (cadherin-associated protein), beta 1, 88kDa; Involved in the regulation of cell adhesion and in signal transduction through the Wnt pathway
DNAJA1	9606.ENSP00000369127	DnaJ (Hsp40) homolog, subfamily A, member 1; Co-chaperone of Hsc70. Seems to play a role in protein import into mitochondria
PPP4C	9606.ENSP00000279387	protein phosphatase 4 (formerly X), catalytic subunit; Protein phosphatase that is involved in many processes such as microtubule organization at centrosomes, maturation of spliceosomal snRNPs, apoptosis, tumor necrosis factor (TNF)-alpha signaling, activation of c-Jun N-terminal kinase MAPK8, regulation of histone acetylation, DNA damage checkpoint signaling, NF-kappa- B activation and cell migration. The PPP4C-PPP4R1 PP4 complex may play a role in dephosphorylation and regulation of HDAC3. The PPP4C-PPP4R2-PPP4R3A PP4 complex specifically dephosphorylates H2AFX phosphorylated on Ser- [...]
PHB	9606.ENSP00000300408	prohibitin; Prohibitin inhibits DNA synthesis. It has a role in regulating proliferation. As yet it is unclear if the protein or the mRNA exhibits this effect. May play a role in regulating mitochondrial respiration activity and in aging
TRPM7	9606.ENSP00000320239	transient receptor potential cation channel, subfamily M, member 7; Essential ion channel and serine/threonine-protein kinase. Divalent cation channel permeable to calcium and magnesium. Has a central role in magnesium ion homeostasis and in the regulation of anoxic neuronal cell death. The kinase activity is essential for the channel function. May be involved in a fundamental process that adjusts plasma membrane divalent cation fluxes according to the metabolic state of the cell. Phosphorylates annexin A1 (ANXA1)

RUVBL2	9606.ENSP00000221413	RuvB-like 2 (E. coli); Possesses single-stranded DNA-stimulated ATPase and ATP-dependent DNA helicase (5' to 3') activity. Component of the NuA4 histone acetyltransferase complex which is involved in transcriptional activation of select genes principally by acetylation of nucleosomal histones H4 and H2A. This modification may both alter nucleosome - DNA interactions and promote interaction of the modified histones with other proteins which positively regulate transcription. This complex may be required for the activation of transcriptional programs associated with oncogene and proto-o [...]
MDH2	9606.ENSP00000327070	malate dehydrogenase 2, NAD (mitochondrial)
CDC42	9606.ENSP00000314458	cell division cycle 42 (GTP binding protein, 25kDa); Plasma membrane-associated small GTPase which cycles between an active GTP-bound and an inactive GDP-bound state. In active state binds to a variety of effector proteins to regulate cellular responses. Involved in epithelial cell polarization processes. Causes the formation of thin, actin-rich surface projections called filopodia
CDC37L1	9606.ENSP00000371278	cell division cycle 37 homolog (S. cerevisiae)-like 1; Co-chaperone that binds to numerous proteins and promotes their interaction with Hsp70 and Hsp90 (By similarity)
TPI1	9606.ENSP00000379933	triosephosphate isomerase 1
CRK	9606.ENSP00000300574	v-crk sarcoma virus CT10 oncogene homolog (avian); The Crk-I and Crk-II forms differ in their biological activities. Crk-II has less transforming activity than Crk-I. Crk- II mediates attachment-induced MAPK8 activation, membrane ruffling and cell motility in a Rac-dependent manner. Involved in phagocytosis of apoptotic cells and cell motility via its interaction with DOCK1 and DOCK4
HSPD1	9606.ENSP00000340019	heat shock 60kDa protein 1 (chaperonin); Implicated in mitochondrial protein import and macromolecular assembly. May facilitate the correct folding of imported proteins. May also prevent misfolding and promote the refolding and proper assembly of unfolded polypeptides generated under stress conditions in the mitochondrial matrix
MYL3	9606.ENSP00000292327	myosin, light chain 3, alkali; ventricular, skeletal, slow; Regulatory light chain of myosin. Does not bind calcium
PPP2R4	9606.ENSP00000351885	protein phosphatase 2A activator, regulatory subunit 4; Reversibly stimulates the variable phosphotyrosyl phosphatase activity of PP2A core heterodimer in presence of ATP and Mg(2+) (in vitro)
TP53	9606.ENSP00000269305	tumor protein p53; Acts as a tumor suppressor in many tumor types; induces growth arrest or apoptosis depending on the physiological circumstances and cell type. Involved in cell cycle regulation as a trans-activator that acts to negatively regulate cell division by controlling a set of genes required for this process. One of the activated genes is an inhibitor of cyclin-dependent kinases. Apoptosis induction seems to be mediated either by stimulation of BAX and FAS antigen expression, or by repression of Bcl-2 expression. Implicated in Notch signaling cross-over
APEX1	9606.ENSP00000216714	APEX nuclease (multifunctional DNA repair enzyme) 1; Repairs oxidative DNA damages in vitro. May have a role in protection against cell lethality and suppression of mutations. Removes the blocking groups from the 3'-termini of the DNA strand breaks generated by ionizing radiations and bleomycin
PLG	9606.ENSP00000308938	plasminogen; Plasmin dissolves the fibrin of blood clots and acts as a proteolytic factor in a variety of other processes including embryonic development, tissue remodeling, tumor invasion, and inflammation; in ovulation it weakens the walls of the Graafian follicle. It activates the urokinase-type plasminogen activator, collagenases and several complement zymogens, such as C1 and C5. It cleaves fibrin, fibronectin, thrombospondin, laminin and von Willebrand factor. Its role in tissue remodeling and tumor invasion may be modulated by CSPG4
PPID	9606.ENSP00000303754	peptidylprolyl isomerase D; PPIases accelerate the folding of proteins. It catalyzes the cis-trans isomerization of proline imidic peptide bonds in oligopeptides (By similarity)
PLAT	9606.ENSP00000220809	plasminogen activator, tissue; Converts the abundant, but inactive, zymogen plasminogen to plasmin by hydrolyzing a single Arg-Val bond in plasminogen. By controlling plasmin-mediated proteolysis, it plays an important role in tissue remodeling and degradation, in cell migration and many other physiopathological events. Play a direct role in facilitating neuronal migration
RAC2	9606.ENSP00000249071	ras-related C3 botulinum toxin substrate 2 (rho family, small GTP binding protein Rac2); Plasma membrane-associated small GTPase which cycles between an active GTP-bound and inactive GDP-bound state. In active state binds to a variety of effector proteins to regulate cellular responses, such as secretory processes, phagocytose of apoptotic cells and epithelial cell polarization. Seems to be involved in the regulation of the NADPH oxidase

GOT1	9606.ENSP00000359539	glutamic-oxaloacetic transaminase 1, soluble (aspartate aminotransferase 1)
CSNK2A1	9606.ENSP00000217244	casein kinase 2, alpha 1 polypeptide pseudogene; Casein kinases are operationally defined by their preferential utilization of acidic proteins such as caseins as substrates. The alpha and alpha' chains contain the catalytic site. Participates in Wnt signaling. CK2 phosphorylates 'Ser-392' of p53/TP53 following UV irradiation
CALM1	9606.ENSP00000349467	calmodulin 1 (phosphorylase kinase, delta); Calmodulin mediates the control of a large number of enzymes and other proteins by Ca(2+). Among the enzymes to be stimulated by the calmodulin-Ca(2+) complex are a number of protein kinases and phosphatases. Together with CEP110 and centrin, is involved in a genetic pathway that regulates the centrosome cycle and progression through cytokinesis
MAPK14	9606.ENSP00000229794	mitogen-activated protein kinase 14; Responds to activation by environmental stress, pro- inflammatory cytokines and lipopolysaccharide (LPS) by phosphorylating a number of transcription factors, such as ELK1 and ATF2 and several downstream kinases, such as MAPKAPK2 and MAPKAPK5. Plays a critical role in the production of some cytokines, for example IL-6. May play a role in stabilization of EPO mRNA during hypoxic stress. Isoform Mxi2 activation is stimulated by mitogens and oxidative stress and only poorly phosphorylates ELK1 and ATF2. Isoform Exip may play a role in the early onset o [...]
CASP6	9606.ENSP00000265164	caspase 6, apoptosis-related cysteine peptidase; Involved in the activation cascade of caspases responsible for apoptosis execution. Cleaves poly(ADP-ribose) polymerase in vitro, as well as lamins. Overexpression promotes programmed cell death
ZNF148	9606.ENSP00000353863	zinc finger protein 148; Involved in transcriptional regulation. Represses the transcription of a number of genes including gastrin, stromelysin and enolase. Binds to the G-rich box in the enhancer region of these genes
CD44	9606.ENSP00000278385	CD44 molecule (Indian blood group); Receptor for hyaluronic acid (HA). Mediates cell-cell and cell-matrix interactions through its affinity for HA, and possibly also through its affinity for other ligands such as osteopontin, collagens, and matrix metalloproteinases (MMPs). Adhesion with HA plays an important role in cell migration, tumor growth and progression. Also involved in lymphocyte activation, recirculation and homing, and in hematopoiesis. Altered expression or dysfunction causes numerous pathogenic phenotypes. Great protein heterogeneity due to numerous alternative splicing a [...]
RHOH	9606.ENSP00000371219	ras homolog gene family, member H; Negative regulator of hematopoietic progenitor cell proliferation, survival and migration. Critical regulator of thymocyte development and T-cell antigen receptor (TCR) signaling by mediating recruitment and activation of ZAP70. Required for phosphorylation of CD3Z, membrane translocation of ZAP70 and subsequent activation of the ZAP70-mediated pathways. Essential for efficient beta-selection and positive selection by promoting the ZAP70-dependent phosphorylation of the LAT signalosome during pre-TCR and TCR signaling. Crucial for thymocyte maturation [...]
EMD	9606.ENSP00000358857	emerin; Stabilizes and promotes the formation of a nuclear actin cortical network. Stimulates actin polymerization in vitro by binding and stabilizing the pointed end of growing filaments. Inhibits beta-catenin activity by preventing its accumulation in the nucleus. Acts by influencing the nuclear accumulation of beta- catenin through a CRM1-dependent export pathway. Links centrosomes to the nuclear envelope via a microtubule association. EMD and BAF are cooperative cofactors of HIV-1 infection. Association of EMD with the viral DNA requires the presence of BAF and viral integrase. The [...]
COL2A1	9606.ENSP00000369889	collagen, type II, alpha 1; Type II collagen is specific for cartilaginous tissues. It is essential for the normal embryonic development of the skeleton, for linear growth and for the ability of cartilage to resist compressive forces
TNNI3	9606.ENSP00000341838	troponin I type 3 (cardiac); Troponin I is the inhibitory subunit of troponin, the thin filament regulatory complex which confers calcium-sensitivity to striated muscle actomyosin ATPase activity
RAF1	9606.ENSP00000251849	v-raf-1 murine leukemia viral oncogene homolog 1; Involved in the transduction of mitogenic signals from the cell membrane to the nucleus. Part of the Ras-dependent signaling pathway from receptors to the nucleus. Protects cells from apoptosis mediated by STK3
STRN	9606.ENSP00000263918	striatin, calmodulin binding protein; Calmodulin-binding protein which may function as scaffolding or signaling protein and may play a role in dendritic Ca(2+) signaling
FKBP5	9606.ENSP00000338160	FK506 binding protein 5; Interacts with functionally mature heterooligomeric progesterone receptor complexes along with HSP90 and TEBP

SRF	9606.ENSP00000265354	serum response factor (c-fos serum response element-binding transcription factor); SRF is a transcription factor that binds to the serum response element (SRE), a short sequence of dyad symmetry located 300 bp to the 5' of the site of transcription initiation of some genes (such as FOS). Required for cardiac differentiation and maturation
PXN	9606.ENSP00000228307	paxillin; Cytoskeletal protein involved in actin-membrane attachment at sites of cell adhesion to the extracellular matrix (focal adhesion)
PPP2R3B	9606.ENSP00000375080	protein phosphatase 2 (formerly 2A), regulatory subunit B'', beta; The B regulatory subunit might modulate substrate selectivity and catalytic activity, and also might direct the localization of the catalytic enzyme to a particular subcellular compartment
TUBB2C	9606.ENSP00000341289	tubulin, beta 2C; Tubulin is the major constituent of microtubules. It binds two moles of GTP, one at an exchangeable site on the beta chain and one at a non-exchangeable site on the alpha-chain (By similarity)
CASP8	9606.ENSP00000351273	caspase 8, apoptosis-related cysteine peptidase; Most upstream protease of the activation cascade of caspases responsible for the TNFRSF6/FAS mediated and TNFRSF1A induced cell death. Binding to the adapter molecule FADD recruits it to either receptor. The resulting aggregate called death- inducing signaling complex (DISC) performs CASP8 proteolytic activation. The active dimeric enzyme is then liberated from the DISC and free to activate downstream apoptotic proteases. Proteolytic fragments of the N-terminal propeptide (termed CAP3, CAP5 and CAP6) are likely retained in the DISC. Clea [...]
HDAC6	9606.ENSP00000334061	histone deacetylase 6; Responsible for the deacetylation of lysine residues on the N-terminal part of the core histones (H2A, H2B, H3 and H4). Histone deacetylation gives a tag for epigenetic repression and plays an important role in transcriptional regulation, cell cycle progression and developmental events. Histone deacetylases act via the formation of large multiprotein complexes (By similarity). Plays a central role in microtubule-dependent cell motility via deacetylation of tubulin
NOS3	9606.ENSP00000297494	nitric oxide synthase 3 (endothelial cell); Produces nitric oxide (NO) which is implicated in vascular smooth muscle relaxation through a cGMP-mediated signal transduction pathway. NO mediates vascular endothelial growth factor (VEGF)-induced angiogenesis in coronary vessels and promotes blood clotting through the activation of platelets
GDI2	9606.ENSP00000369538	GDP dissociation inhibitor 2; Regulates the GDP/GTP exchange reaction of most Rab proteins by inhibiting the dissociation of GDP from them, and the subsequent binding of GTP to them

Function

Feature	**Genes in the network**	**Genes in the genome with the function**
protein phosphatase type 2A complex	12	15
protein serine/threonine kinase activity	35	283
axon guidance	24	294
regulation of cysteine-type endopeptidase activity	20	131
protein serine/threonine phosphatase complex	7	32
response to growth factor stimulus	22	212
regulation of cysteine-type endopeptidase activity involved in apoptotic process	19	128
regulation of innate immune response	11	182
pattern recognition receptor signaling pathway	9	103
innate immune response-activating signal transduction	9	106
MyD88-dependent toll-like receptor signaling pathway	8	74
activation of innate immune response	9	108
heat shock protein binding	12	28
muscle system process	26	195
regulation of endopeptidase activity	11	198
protein folding	23	111
regulation of peptidase activity	20	205
cellular response to growth factor stimulus	20	204
small GTPase mediated signal transduction	12	264
intracellular receptor mediated signaling pathway	19	170
positive regulation of innate immune response	9	129
muscle structure development	11	222
fibroblast growth factor receptor signaling pathway	15	129
muscle contraction	24	176
TRIF-dependent toll-like receptor signaling pathway	7	62
toll-like receptor signaling pathway	8	95
response to fibroblast growth factor stimulus	9	136
cellular response to fibroblast growth factor stimulus	9	136
actin filament-based process	26	293
regulation of defense response	12	295
toll-like receptor 3 signaling pathway	7	66
MyD88-independent toll-like receptor signaling pathway	7	66
cellular component disassembly involved in apoptosis	14	68

toll-like receptor 1 signaling pathway	7	69
regulation of protein serine/threonine kinase activity	20	249
de novo' protein folding	14	42
toll-like receptor 2 signaling pathway	7	72
nucleotide-binding domain, leucine rich repeat containing receptor signaling pathway	6	43
activation of cysteine-type endopeptidase activity	13	72
activation of cysteine-type endopeptidase activity involved in apoptotic process	13	72
immune response-activating signal transduction	10	201
platelet activation	24	207
immune response-regulating signaling pathway	10	208
activation of cysteine-type endopeptidase activity involved in apoptotic process by cytochrome c	4	10
Toll signaling pathway	7	78
cell-substrate adherens junction	7	79
positive regulation of defense response	9	165
protein phosphatase binding	10	51
cell-substrate junction	7	83
toll-like receptor 4 signaling pathway	7	83
positive regulation of cysteine-type endopeptidase activity	14	84
positive regulation of cysteine-type endopeptidase activity involved in apoptotic process	14	84
positive regulation of endopeptidase activity	14	87
activation of immune response	10	232
activation of MAPKK activity	5	30
positive regulation of peptidase activity	14	92
Ras protein signal transduction	8	135
protein phosphatase 2A binding	4	14
H4/H2A histone acetyltransferase complex	4	14
protein phosphatase type 2A regulator activity	11	14
NuA4 histone acetyltransferase complex	4	14
epidermal growth factor receptor signaling pathway	8	148
response to topologically incorrect protein	17	103
de novo' posttranslational protein folding	11	37
adherens junction	20	108
actin-myosin filament sliding	11	38
muscle filament sliding	11	38
positive regulation of immune response	10	272
actin-mediated cell contraction	11	39
nerve growth factor receptor signaling pathway	17	216
cellular component disassembly	9	220
myofibril	14	74
anchoring junction	21	116

contractile fiber part	14	77
protein domain specific binding	19	292
focal adhesion	19	77
induction of apoptosis by intracellular signals	11	79
phosphatase binding	11	84
muscle cell differentiation	7	130
contractile fiber	14	85
actin filament-based movement	11	50
unfolded protein binding	12	53
cytoplasmic pattern recognition receptor signaling pathway	4	26
nucleotide-binding oligomerization domain containing signaling pathway	4	26
basolateral plasma membrane	21	147
negative regulation of cellular protein metabolic process	8	205
response to unfolded protein	15	98
cellular senescence	4	29
IkappaB kinase complex	3	10
cellular component disassembly at cellular level	8	217
regulation of muscle cell differentiation	5	63
protein phosphatase regulator activity	11	31
sarcomere	12	64
histone modification	8	228
G1/S transition of mitotic cell cycle	7	169
chaperone-mediated protein complex assembly	8	12
I band	4	34
negative regulation of protein metabolic process	8	232
covalent chromatin modification	8	233
regulation of MAP kinase activity	14	173
positive regulation of muscle cell differentiation	4	37
actin binding	12	122
phosphatase regulator activity	11	38
regulation of reactive oxygen species metabolic process	4	39
activation of protein kinase activity	7	184
actin cytoskeleton organization	20	252
platelet degranulation	13	80
DNA replication	15	191
negative regulation of hydrolase activity	7	191
structural constituent of muscle	9	42
cytosolic part	6	134
negative regulation of cysteine-type endopeptidase activity	4	45
response to biotic stimulus	20	272
anti-apoptosis	19	202
regulation of peptidyl-tyrosine phosphorylation	5	87
cell junction	26	273
gluconeogenesis	4	46
cell junction assembly	18	143
cell aging	4	47

protein serine/threonine/tyrosine kinase activity	3	18
activation of MAPK activity	5	90
protein complex binding	14	146
smooth muscle cell differentiation	3	19
response to virus	6	150
androgen receptor signaling pathway	4	50
regulation of I-kappaB kinase/NF-kappaB cascade	6	150
heart morphogenesis	12	96
regulation of transcription involved in G1/S phase of mitotic cell cycle	3	20
MAPK cascade	8	293
cellular response to peptide hormone stimulus	7	220
cell junction organization	18	154
positive regulation of protein serine/threonine kinase activity	13	154
chromatin modification	8	299
muscle organ development	13	158
internal protein amino acid acetylation	5	101
cellular response to insulin stimulus	6	160
hexose biosynthetic process	4	55
negative regulation of proteolysis	3	22
response to peptide hormone stimulus	7	230
response to insulin stimulus	6	164
regulation of cyclin-dependent protein kinase activity	4	57
aging	4	57
negative regulation of phosphorus metabolic process	4	58
negative regulation of phosphate metabolic process	4	58
regulation of muscle system process	4	60
Wnt receptor signaling pathway	6	171
protein acetylation	5	110
heart development	14	173
I-kappaB kinase/NF-kappaB cascade	13	174
cardiac muscle tissue development	10	62
microtubule-based process	7	247
Z disc	3	26
protein acylation	5	116
peptidyl-tyrosine phosphorylation	5	116
peptidyl-lysine modification	5	117
structural constituent of cytoskeleton	10	65
monosaccharide biosynthetic process	4	65
histone deacetylation	3	27
chaperone binding	3	27
peptidyl-tyrosine modification	5	118
filopodium	3	28
ATP catabolic process	9	67
positive regulation of MAP kinase activity	5	121

positive regulation of I-kappaB kinase/NF-kappaB cascade	5	124
histone acetyltransferase complex	4	70
cardiac muscle tissue morphogenesis	9	31
negative regulation of blood coagulation	3	31
signal transduction in response to DNA damage	5	128
protein deacetylation	3	31
negative regulation of hemostasis	3	31
nitric oxide biosynthetic process	3	31
extrinsic to membrane	4	74
protein deacylation	3	32
muscle organ morphogenesis	9	33
negative regulation of coagulation	3	33
cysteine-type endopeptidase activity	3	33
muscle tissue morphogenesis	9	33
proteolysis involved in cellular protein catabolic process	7	283
intracellular steroid hormone receptor signaling pathway	4	77
peptidyl-serine phosphorylation	4	77
cellular response to hormone stimulus	16	283
internal side of plasma membrane	4	78
nuclear chromosome	6	208
endopeptidase activity	5	138
base-excision repair	3	35
ATP metabolic process	10	80
cellular protein catabolic process	7	292
reactive oxygen species metabolic process	4	81
alcohol biosynthetic process	4	82
insulin receptor signaling pathway	5	143
intermediate filament cytoskeleton	16	83
peptidyl-serine modification	4	83
adherens junction organization	3	37
regulation of cell growth	7	183
negative regulation of intracellular protein kinase cascade	5	90
cellular response to light stimulus	3	24
peroxidase activity	3	24
cell growth	8	238
oxidoreductase activity, acting on peroxide as acceptor	3	24
regulation of stress fiber assembly	3	24
transcription regulatory region DNA binding	8	235
regulatory region nucleic acid binding	8	236
regulatory region DNA binding	8	236
protein localization in membrane	4	52
plasma membrane organization	4	51
regulation of nitric oxide biosynthetic process	3	23
positive regulation of organelle organization	6	132
secretory granule	6	130
vesicle lumen	4	49
muscle tissue development	6	127

cytoplasmic membrane-bounded vesicle lumen	4	49
secretory granule lumen	4	49
regulation of ATPase activity	3	22
cell-cell adherens junction	3	22
positive regulation of glucose metabolic process	3	22
cellular component disassembly	8	220
muscle structure development	8	222
platelet alpha granule lumen	4	47
regulation of MAPK cascade	8	223
cellular response to UV	3	21
peptidyl-proline modification	3	21
regulation of cytoskeleton organization	7	172
striated muscle contraction	4	45
cellular component disassembly at cellular level	8	217
regulation of protein import into nucleus	5	80
macrophage activation	3	20
actin filament bundle assembly	4	46
endothelial cell migration	5	79
nitric oxide metabolic process	4	42
peptidyl-prolyl cis-trans isomerase activity	3	18
protein peptidyl-prolyl isomerization	3	18
response to estradiol stimulus	3	18
response to steroid hormone stimulus	5	76
receptor complex	6	117
positive regulation of actin filament bundle assembly	3	19
positive regulation of nitric oxide biosynthetic process	3	19
cis-trans isomerase activity	3	19
striated muscle tissue development	6	119
positive regulation of cellular component movement	7	154
cadherin binding	3	17
positive regulation of epithelial cell proliferation	5	72
dephosphorylation	8	204
antioxidant activity	4	41
negative regulation of lipid metabolic process	4	41
cell-substrate junction assembly	4	39
anatomical structure homeostasis	6	108
positive regulation of locomotion	7	153
positive regulation of cell motility	7	148
apical junction assembly	4	38
response to interleukin-1	4	38
monosaccharide metabolic process	8	196
phospholipid binding	7	149
steroid hormone mediated signaling pathway	3	15
positive regulation of cell migration	7	145
cell-matrix adhesion	6	91
protein import into nucleus	7	131
cellular carbohydrate catabolic process	6	92
regulation of cell morphogenesis	8	177

nuclear import	7	134
heart contraction	5	60
vasculature development	10	281
regulation of cell division	4	33
heart process	5	61
tissue morphogenesis	8	182
regulation of lipid metabolic process	7	137
myosin binding	3	14
cell-cell junction organization	6	99
blood vessel morphogenesis	9	239
carbohydrate catabolic process	6	101
protein localization in plasma membrane	4	36
FK506 binding	3	15
positive regulation of monooxygenase activity	3	15
positive regulation of stress fiber assembly	3	15
macrolide binding	3	15
establishment of protein localization in membrane	4	27
actin filament bundle	4	27
actomyosin structure organization	4	27
response to other organism	10	257
hexose metabolic process	8	162
cardiac chamber development	5	52
cell-substrate adhesion	7	122
regulation of tumor necrosis factor biosynthetic process	3	11
Hsp90 protein binding	3	11
tumor necrosis factor biosynthetic process	3	11
blood vessel development	10	263
stress fiber assembly	4	29
cell-cell junction assembly	5	55
actin filament organization	7	126
regulation of protein localization	9	218
negative regulation of MAPK cascade	5	57
positive regulation of nitric-oxide synthase activity	3	10
regulation of heart rate	3	10
protein dephosphorylation	7	117
angiogenesis	9	203
stress fiber	4	26
establishment of protein localization in plasma membrane	4	26
regulation of cell adhesion	8	158
myofibril assembly	4	23
regulation of establishment of protein localization	9	191
regulation of transmembrane transport	8	148
cardiac chamber morphogenesis	5	47
alcohol catabolic process	6	77
positive regulation of cellular component organization	11	297
regulation of endopeptidase activity	9	198

protein localization to nucleus	8	155
regulation of cellular component biogenesis	9	200
cardiac ventricle development	5	43
protein maturation	6	72
cellular protein complex assembly	9	174
glucose metabolic process	8	134
hexose catabolic process	6	66
cell adhesion molecule binding	5	40
monosaccharide catabolic process	6	69
cardiac ventricle morphogenesis	5	38
regulation of establishment of protein localization in plasma membrane	4	19
exocytosis	9	168
regulation of oxidoreductase activity	6	57
cell-cell junction	9	158
glucose catabolic process	6	52
regulation of locomotion	12	278
actomyosin	5	31
response to reactive oxygen species	6	54
beta-catenin binding	6	45
protein import	10	173
regulation of cell motility	12	262
regulation of nitric-oxide synthase activity	5	28
cellular response to reactive oxygen species	6	43
glycolysis	6	43
ventricular cardiac muscle tissue development	5	23
response to oxidative stress	9	125
regulation of cell migration	12	245
inflammatory response	12	239
ventricular cardiac muscle tissue morphogenesis	5	23
regulation of cellular component movement	13	275
regulation of monooxygenase activity	6	38
actin cytoskeleton	13	255
nucleobase-containing small molecule interconversion	5	18
cellular response to oxidative stress	8	64
calcium-dependent phospholipid binding	5	14
protein refolding	5	10
cell-substrate adherens junction	13	79
cell-substrate junction	13	83
intermediate filament	12	44