



IPI00017297.1 IPI00658109.1	MATR3 CKMT1A	matrin 3 creatine kinase, mitochondrial 1A	3.1E-04 (1) 5.0E-07 (2)	3.0E-04 (2) 6.9E-10 (1)	K.LC#SLFYTNEEVAK.N	1944.93	2.46	2	2.12E-06	3.43	0.39	[19]
<b>mRNA splicing / processing / transcription regulation</b>												
IPI00012074.3 IPI00011274.3 IPI00031556.7 IPI00479786.5	HNRNPR HNRPDL U2AF2 KHSRP	heterogeneous nuclear ribonucleoprotein R heterogeneous nuclear ribonucleoprotein D-like U2 small nuclear RNA auxiliary factor 2 KH-type splicing regulatory protein (FUSE binding protein 2)	1.5E-05 (1) 1.9E-04 (1) 5.5E-07 (1) 2.5E-07 (3)	3.3E-04 (1) 4.1E-05 (1) 1.5E-05 (1) 8.1E-09 (5)	R.GFC#FLEYEDHK.S R.FGEVDC#TIK.T  K.IQDDSGC#K.V K.C#GLVIGR.G	1815.79 1538.74  1306.60 1145.60	3.82 4.42  0.60 3.51	3 2  2 2	1.24E-04 7.86E-04  1.00E+00 1.00E+00	3.53 2.39  2.59 2.02	0.31 0.40  0.33 0.18	
IPI00021187.4 IPI00025815.2 IPI00216049.1 IPI00171903.2	RUVBL1 TARDBP HNRNPK HNRNPM	RuvB-like 1 TAR DNA binding protein heterogeneous nuclear ribonucleoprotein K heterogeneous nuclear ribonucleoprotein M	3.7E-08 (4) 2.6E-10 (1) 2.6E-07 (6) 1.0E+00 (1)	1.1E-06 (1) 6.4E-08 (1) 1.4E-08 (3) 4.5E-06 (2)	   K.DKFNEC#GHVLYADIK.M	   2180.03	   3.88	   3	   5.31E-09	   2.79	   0.36	
<b>Protein disulfide-isomerase reaction</b>												
IPI00010796.1 IPI00025252.1	P4HB PDIA3	proline 4-hydroxylase, beta polypeptide protein disulfide isomerase family A, member 3	4.8E-07 (4) 1.8E-08 (1)	1.6E-09 (3) 1.4E-07 (4)	K.KEEC#PAVR.L K.KFIQENIFGIC#PHMTEDNKDLIQGK.D K.FIQENIFGIC#PHM*TEDNKDLIQGK.D K.KFIQENIFGIC#PHM*TEDNKDLIQGK.D K.FIQENIFGIC#PHMTEDNKDLIQGK.D	1359.66 3346.65 3234.55 3362.64 3218.55	1.60 1.88 -0.41 -0.11 2.25	2 4 4 4 4	1.00E+00 1.35E-05 5.62E-03 5.37E-07 4.29E-06	2.64 4.43 2.56 4.82 2.58	0.11 0.32 0.25 0.53 0.20	[9]
IPI00299571.5	PDIA6	protein disulfide isomerase family A, member 6	1.7E-05 (2)	2.4E-05 (1)								[9]
<b>Protein folding / stress response / Protein assembly</b>												
IPI00020984.2 IPI00010720.1 IPI00013122.1 IPI00784154.1	CANX CCT5 CDC37 HSPD1	calnexin chaperonin containing TCP1, subunit 5 (epsilon) cell division cycle 37 homolog (S. cerevisiae) heat shock 60kDa protein 1 (chaperonin)	8.1E-06 (3) 2.6E-04 (2) 6.2E-04 (1) 8.7E-10 (2)	2.9E-08 (2) 2.6E-08 (1) 2.7E-09 (1) 5.9E-08 (3)	   K.C#EFQDAYVLLSEK.K K.C#EFQDAYVLLSEK.K R.AAVEEGIVLGGG#ALLR.C [1] K.C#LELFTELAEDKENYK.F	   1972.92 1972.92 2056.08 2501.21	   0.27 0.68 3.21 0.62	   3 2 3 4	2.35E-05 3.93E-06 1.24E-05 7.19E-04	2.66 4.15 2.75 3.34	0.17 0.52 0.44 0.29	[1] [10]
IPI00382470.3 IPI00030275.5 IPI00027230.3 IPI00013894.1 IPI00003362.2 IPI00003865.1	HSP90AA1 TRAP1 HSP90B1 STIP1 HSPA5 HSPA8	heat shock protein 90kDa alpha (cytosolic), class A member 1 TNF receptor-associated protein 1 heat shock protein 90kDa beta (Grp94), member 1 stress-induced-phosphoprotein 1 (Hsp70/Hsp90-organizing protein) heat shock 70kDa protein 5 (glucose-regulated protein, 78kDa) heat shock 70kDa protein 8	6.8E-11 (4) 1.1E-08 (1) 1.2E-08 (4) 3.8E-04 (6) 3.1E-09 (2) 1.0E+00 (3)	9.5E-06 (3) 3.2E-05 (4) 2.1E-05 (6) 3.1E-05 (1) 1.2E-11 (6) 9.3E-06 (1)	   K.C#NEIINWLDKNQTAKEEFHQQK.E K.C#NEIINWLDK.N K.VC#NPIITK.L K.MEEFKDQLPADEC#NK.L K.VC#QGER.E	   3402.59 1675.80 1315.69 2224.97 1119.51	   3.35 2.56 4.22 2.41 -0.95	   4 2 2 3 2	2.33E-03 1.51E-05 3.79E-04 1.11E-08 9.99E-01	3.21 3.18 2.79 2.73 2.34	0.21 0.32 0.31 0.24 0.11	[10] [20]
IPI00007765.5	HSPA9	heat shock 70kDa protein 9 (mortalin)	3.8E-12 (13)	1.9E-10 (15)								
IPI00025512.2	HSPB1	heat shock 27kDa protein 1	4.9E-07 (4)	1.2E-08 (1)								
<b>Proteolysis</b>												
IPI00479722.2 IPI00032140.4 IPI00644196.1	PSME1 SERPINH1 SERPINB5	proteasome (prosome, macropain) activator subunit 1 (PA28 alpha) serpin peptidase inhibitor, clade H (heat shock protein 47), member 1 serpin peptidase inhibitor, clade B (ovalbumin), member 5	6.0E-05 (2) 6.2E-12 (7) 2.9E-08 (3)	7.5E-07 (1) 6.1E-08 (7) 9.1E-10 (1)								
<b>Transport</b>												
IPI00001639.2 IPI00022774.3	KPNB1 VCP	karyopherin (importin) beta 1 valosin-containing protein	9.3E-05 (1) 8.3E-05 (5)	5.6E-04 (1) 6.7E-05 (4)	K.GVLFGYPPGC#GK.T R.LGDVISIQPC#PDVK.Y	1622.79 1911.97	1.25 -0.20	2 2	1.30E-07 6.61E-06	2.45 3.75	0.41 0.56	

a) # of pep: number of peptides identified for each protein according to the criteria of XCorr values of 2.0 (2+) and 2.5 (3+),  $\Delta Cn \geq 0.1$  and  $\Delta$  mass precursor < 10 ppm (including the same peptide with different charge states).

b) C#: Cysteine modified by biotin-HPDP (+428.191567 amu); C@: Cysteine modified by MMTS (+45.98772 amu).

c) For each protein, only the biotinylated peptides with the highest score from the multiple peptide pull-downs are shown.

d) Underlined are the sequences have been reported in the literature.

Table S1B

IPI No	Gene ID	Protein name	Protein Pull-down		Peptide Pull-down									
			Run I (< 1%FP)	Run II (< 1%FP)	Biotinylated peptide	MH+	$\Delta M$	z	Prob (pep)	XC	$\Delta Cn$	Ref		
			Prob/ (pro)	# of pep									Prob (pro)	# of pep
		<b>Actin binding protein</b>												
IPI00015262.10	CNN2	calponin 2		9.27E-11(1)	K.AGQC#VIGLOMGTKN.C K.DGTILC#TLMNK.L	1847.90 1636.79	4.68 -2.18	2 2	1.24E-06 4.93E-02	2.98 2.43	0.40 0.25			
		<b>Antioxidant / free radical removal</b>												
IPI00024915.2 IPI00000874.1	PRDX5 PRDX1	Peroxiredoxin 5 peroxiredoxin 1	2.88E-04 (2)	1.09E-04 (1)	K.GVLFVGPVGAFTPGC#SK.T K.HGEVC#PAGWK.P K.HGEVC#PAGWKPGSDTIKPDVOK.S.[11]	1964.98 1511.70 2777.36	0.65 -0.63 4.19	3 3 3	7.78E-04 2.70E-02 1.85E-04	2.79 3.24 3.46	0.31 0.49 0.41			[11]
		<b>Adhesion</b>												
IPI00010697.2 IPI00219219.3	ITGA6 LGALS1	integrin, alpha 6 lectin, galactoside-binding, soluble, 1 (galectin 1)		6.58E-07 (3) 2.83E-05 (1)	K.VVTC#AHR.Y R.TGGLYSC#DITAR.G K.SC#FEYTANPAGYNPSISIVGTLEAEK.E R.FNAHGADANTIVC#NSK.D K.DSNLNC#LHFNPR.F	1213.60 1684.79 3189.49 2018.92 1857.86	-0.48 2.85 0.42 3.51 1.16	2 2 3 3 3	2.39E-04 6.89E-09 9.22E-02 2.24E-11 1.91E-05	2.12 2.77 3.53 3.67 3.00	0.20 0.53 0.35 0.66 0.40			
		<b>DNA Repair / DNA replication</b>												
IPI00220834.8 IPI00021700.3	XRCC5 PCNA	X-ray repair complementing defective repair in Chinese hamster cells 5 (double-strand-break rejoining proliferating cell nuclear antigen	3.88E-05 (1) 2.14E-07 (2)		R.HSIHWPC#R.L R.LFQC#LLHR.A K.C#AGNEDIITLR.A R.DLSHIGDAVVISC#AK.D.[2]	1463.69 1457.76 1632.79 1955.98	3.61 3.89 2.07 0.07	3 2 2 3	3.03E-05 1.16E-03 6.51E-05 1.37E-02	2.82 2.27 3.11 2.96	0.42 0.35 0.52 0.21			[2]
		<b>Ion Transport</b>												
IPI00024145.2 IPI00031804.1 IPI00010896.3 IPI00177817.4	VDAC2 VDAC3 CLIC1 ATP2A2	voltage-dependent anion channel 2 voltage-dependent anion channel 3 chloride intracellular channel 1 ATPase, Ca++ transporting, cardiac muscle, slow twitch 2		8.89E-09 (3) 4.77E-06 (1) 2.74E-08 (3) 7.80E-10 (3)	K.SC#SGVEFSTSGSSNTDTGK.V K.VC#NYGLTFTQK.W K.LHIVQVVC#K.K R.C#LALATHDNPLR.R	2278.96 1701.82 1466.80 1751.88	1.82 1.14 3.25 -2.55	2 2 3 3	2.99E-07 1.89E-02 3.09E-04 7.63E-05	4.56 2.44 2.51 4.23	0.67 0.22 0.46 0.51			[13] [13]  [1]
		<b>Metabolism</b>												
IPI00465439.5 IPI00847989.2 IPI00383071.1 IPI00026824.2 IPI00291510.3 IPI00027497.5 IPI00017855.1 IPI00291006.2	ALDOA PKM2 TPI1 HMOX2 IMPDH2 GPI ACO2 MDH2	aldolase A, fructose-bisphosphate pyruvate kinase, muscle triosephosphate isomerase 1 heme oxygenase (decycling) 2 IMP (inosine monophosphate) dehydrogenase 2 glucose phosphate isomerase aconitase 2, mitochondrial malate dehydrogenase 2, NAD (mitochondrial)	1.75E-10 (6) 1.95E-10 (3) 5.69E-05 (1) 1.31E-05 (4) 1.00E+00 (1) 1.00E+00 (1)		R.ALANSLAC#OGK.Y R.VNVC#IGGVILFHETLYQK.A K.ALSDHHIYLEGTLTKPNM#VTPGHAC#TQK.F K.ALSDHHIYLEGTLTKPNMVTPGHAC#TQK.F R.NTGIC#TIGPASR.S.[11] R.AGKPVIC#ATOM#LESMIK.K K.PVIC#ATOM#LESMIK.K R.AGKPVIC#ATOM#LESMIK.K R.AFGSDVANAVLDGADC#HMLSGETAK.G.[1] K.C#DENILWLDYK.N R.AGKPVIC#ATOM#LESMIK.K R.AGKPVIC#ATOM#LESMIK.K K.DC#GATWVVLGHSE.R K.VPADTEVVC#APPTAYIDFAR.Q K.VAHALAEGLGVIAC#IGEKL K.GALEGSSC#PFR.T R.DIDFLKEEEHC#FLEEIM#TK.R K.M#IPC#DFLIPVQTOHPH.R R.FNHFSLLTNTNHGHILVDYSK.N K.MPC#DFLIPVQTOHPH.R K.C#TTDHISAAGPWLK.F K.GC#DVVVPAGVPR.K K.GYLQPEQLPDC#LK.G K.SQETEC#TYFSTPLLLGK.K K.VAVLGAASGGIGQPLSLLK.N	1503.75 2459.26 3518.74 3502.75 1730.88 2280.13 1991.99 2248.14 2865.31 1839.85 2264.13 2264.13 1957.91 2563.24 2179.14 1551.71 2928.32 2452.24 2457.23 2436.24 1927.92 1709.89 1860.91 2345.12 1793.09	0.62 1.28 -0.58 -5.80 2.70 1.44 3.86 1.72 2.41 1.41 2.95 2.95 2.16 4.85 1.88 3.99 3.10 0.10 1.25 -0.09 4.31 2.14 4.35 0.12 1.32	2 3 5 5 2 2 2 3 2 3 3 3 3 2 3 2 3 3 4 3 3 2 2 2	6.67E-07 2.76E-10 7.57E-04 1.16E-06 1.15E-05 2.52E-04 1.75E-06 1.29E-08 2.80E-07 1.24E-01 4.65E-08 9.50E-04 2.15E-06 9.72E-06 3.68E-03 6.49E-05 2.57E-06 7.28E-06 1.15E-04 9.72E-04 4.40E-05 1.27E-02 2.68E-08 5.35E-03 2.02E-09	2.67 3.59 2.77 3.53 3.09 4.08 3.51 4.30 3.77 2.22 4.46 2.85 3.43 3.57 3.35 2.33 3.59 3.14 3.87 2.84 3.86 2.70 2.47 2.59 5.27	0.43 0.46 0.14 0.28 0.35 0.57 0.60 0.59 0.56 0.36 0.36 0.55 0.52 0.53 0.42 0.32 0.37 0.52 0.38 0.46 0.45 0.51 0.50 0.80		[10]  [1, 10, 11]  [1,10]  [10]  [1, 10, 11, 12]	
		<b>mRNA splicing / processing / transcription</b>												
IPI00163505.2 IPI00844578.1 IPI00215965.2 IPI00054042.1 IPI00150057.6 IPI00013881.6	RBM39 DHX9 HNRNPA1 GTF2I SMARCC2 HNRNPH1	RNA binding motif protein 39 DEAH (Asp-Glu-Ala-His) box polypeptide 9 heterogeneous nuclear ribonucleoprotein A1 general transcription factor II, I SWI/SNF regulator of chromatin, subfamily c, member 2 heterogeneous nuclear ribonucleoprotein H1 (H)	8.99E-08 (2) 1.00E+00 (1) 1.50E-08 (1) 1.00E+00 (1) 1.00E+00 (1) 5.62E-05 (1)		K.C#PSIAAAIAVNALHGR.W K.SSVNC#PFSSQDMK.Y K.NFLYAWC#GK.R R.SHFEQWGLTDC#VVMR.D R.SHFEQWGLTDC#VVMR.D K.MVDQLFC#K.K R.PNIFLC#PEIEPK.L R.DLNYC#FSGMSDHR.Y	2063.07 1857.80 1529.71 2353.06 2337.06 1411.66 1827.92 1972.82	0.71 2.18 1.80 1.25 0.05 4.15 0.27 3.65	3 2 2 3 3 2 2 3	2.65E-07 1.44E-03 1.08E-04 5.10E-06 4.61E-02 1.45E-04 2.88E-04 2.76E-04	3.85 3.02 2.34 3.49 3.32 2.68 2.77 2.63	0.63 0.34 0.11 0.51 0.38 0.45 0.33 0.51			

IPI00027834.3	HNRNPL	heterogeneous nuclear ribonucleoprotein L	7.68E-06 (1)		K.LC#FSTAQHAS	1492.67	4.47	2	4.79E-07	2.25	0.49	[2]	
		<b>Proteolysis</b>											
IPI00220857.3	CAST	calpastatin (proteolysis)	1.98E-04 (1)		K.AAAPADPVEAVC#R.T K.KPADDODPIDALSGDLSDSC#PSTTETSQNTAK.D	1669.82 3648.63	-0.25 2.91	2 3	2.02E-09 5.34E-08	2.83 6.15	0.59 0.66		
		<b>Protein biosynthesis/ translational regulation</b>											
IPI00297982.7	EIF2S3	eukaryotic translation initiation factor 2, subunit 3 gamma, 52kDa	6.18E-08 (1)	5.06E-06 (2)	K.YNIEVVC#EYIVK.K	1899.94	4.18	2	2.67E-04	2.83	0.46	[8]	
IPI00186290.6	EEF2	eukaryotic translation elongation factor 2	2.03E-10 (3)		K.STLTDLSLVC#K.A	1494.74	0.60	2	1.60E-05	2.41	0.38		
					K.IWC#FGPDGTGPNILTDITK.G	2476.21	7.35	3	6.70E-01	3.03	0.38		
					R.C#ELLYEGPPDDEAAMGK.S	2379.07	4.48	3	4.89E-04	3.06	0.38		
IPI00000494.6	RPL5	ribosomal protein L5	1.00E+00 (1)		R.IEGDM*IVC#AAYAHELK.Y	2304.09	2.87	3	6.43E-02	3.63	0.31		
					K.VGLTNYAAAYC#TGLLAR.R	2298.18	-0.08	3	2.27E-04	2.69	0.35		
					R.IEGDMIVC#AAYAHELK.Y	2288.09	1.33	3	3.69E-07	3.02	0.27		
IPI00027107.5	TUFM	Tu translation elongation factor, mitochondrial	1.00E+00 (1)		K.KGDEC#ELLGHSK.N	1743.82	1.20	4	6.09E-06	3.05	0.40		
IPI00011253.3	RPS3	ribosomal protein S3	1.00E+00 (1)		R.GLC#AIAOAFSLR.Y [1, 11]	1659.84	2.45	2	1.83E-06	3.29	0.47		
IPI00025874.2	RPN1	ribophorin I	2.34E-05 (2)		K.VAC#ITEQVTLVVK.R	1959.05	2.36	2	9.15E-05	3.99	0.45		
IPI00025447.8	EEF1A1	eukaryotic translation elongation factor 1 alpha 1	9.96E-01 (1)	K.SGDAAIWDM*VPGKPMC#VEFESDYPPILGR.F [2] K.SGDAAIWDM*VPGKPMC#VEFESDYPPILGR.F [2] K.SGDAAIWDM*VPGKPMC#VEFESDYPPILGR.F [2]	3382.56 3382.56 3398.56	-1.31 -3.18 5.18	3 4 3	6.16E-07 1.31E-02 1.29E-09	3.01 2.95 3.61	0.36 0.41 0.53	[2, 8, 10, 11]		
		<b>Protein folding / stress reponse / complex assembly</b>											
IPI00002966.2	HSPA4	heat shock 70kDa protein 4	1.17E-09 (2)		R.KFDEVLVNHF#EEFGK.K R.KFDEVLVNHF#EEFGK.K	2369.11 2369.11	-0.41 2.00	4 3	2.35E-08 1.35E-04	3.58 3.11	0.40 0.20	[10]	
IPI00414676.6	HSP90AB1	heat shock protein 90kDa alpha (cytosolic), class B member 1	6.26E-13 (5)		K.C#LELFSELAEDKENYK.K K.C#LELFSELAEDKENYK.F	2359.10 2487.20	0.10 -0.95	3 3	2.35E-05 4.89E-05	3.56 4.29	0.44 0.43	[10]	
IPI00302927.6	CCT4	chaperonin containing TCP1, subunit 4 (delta)	1.93E-04 (1)		K.TGC#NVLIIQK.S	1516.80	0.51	2	1.07E-04	2.46	0.11	[11]	
IPI00290566.1	TCP1	t-complex 1	1.50E-08 (4)		K.ITGC#ASPGK.T K.VLC#ELADLQD.K R.IC#DDELIIJK.N [11]	1261.61 1674.83 1602.83	2.63 2.56 2.37	2 2 2	8.33E-01 1.36E-06 3.79E-03	2.40 3.49 2.31	0.17 0.31 0.24	[2, 11]	
IPI00290770.3	CCT3	chaperonin containing TCP1, subunit 3 (gamma)	2.65E-05 (2)		R.WSSLAC#NIALDAVK.M K.IPGGIIFDSC#VLR.G [2]	1918.96 1799.92	3.01 2.81	2 2	3.79E-05 2.64E-07	2.15 3.25	0.38 0.48	[2]	
IPI00018465.1	CCT7	chaperonin containing TCP1, subunit 7 (eta)	1.24E-05 (1)		R.YNFFTGK#PK.A R.QLC#DNAGDFATNLLK.L	1504.68 2165.02	1.12 1.66	2 3	3.58E-03 2.09E-05	2.20 3.95	0.22 0.32	[11]	
		<b>Protein phosphorylation</b>											
IPI00783271.1	LRPPRC	leucine-rich PPR-motif containing	2.54E-04 (1)	2.01E-06 (4) 1.17E-07 (5)	R.C#VANNOVETLEK.L	1775.85	-0.65	2	8.73E-04	4.04	0.52	[22]	
IPI00006167.1	PPM1G	protein phosphatase 1G (formerly 2C),				K.C#SGDGVGAPR.L	1346.60	2.82	2	1.00E+00	2.37		0.27
IPI00018274.1	EGFR	epidermal growth factor receptor				R.AC#GADSYEM*EEDGVR.K K.YSFGATC#VK.K K.NLC#YANTINWK.K	2075.82 1403.65 1767.84	5.17 1.59 4.03	2 2 2	3.64E-08 8.67E-07 9.26E-06	4.44 2.39 3.47		0.72 0.46 0.41
		<b>Structure and motility</b>											
IPI00215743.3	RRBP1	ribosome binding protein 1 homolog 180kDa		3.76E-06 (4)	R.ELC#HTOSSHASLR.A K.LTAEFEAEQTSAC#R.L	1896.89 1983.90	-0.69 -0.31	3 3	7.59E-04 1.38E-04	2.59 3.07	0.44 0.41	[13]	
IPI00010779.4	TPM4	tropomyosin 4	1.23E-07 (2)	3.06E-04 (1)	K.C#GDLLEELK.N	1463.66	2.26	2	8.08E-04	2.79	0.35	[14, 23]	
IPI00013808.1	ACTN4	actinin, alpha 4			K.IC#DQWDALGSLTHSR.R	2129.99	1.69	3	1.71E-08	5.37	0.65	[10, 11]	
					K.AC#LISLGYDVENDR.Q	1995.93	5.44	2	2.80E-06	3.22	0.67		
IPI00178352.5	FLNC	filamin C, gamma (actin binding protein 280)	1.00E+00 (1)		K.GAGTGGLGLTVEGPC#EAK.I K.GAGTGGLGLTVEGPC#EAK.I	2044.99 2044.99	-0.59 2.85	3 2	4.69E-02 9.40E-04	2.54 3.60	0.41 0.53	[2]	
IPI00007750.1	TUBA4A	tubulin, alpha 4a	3.20E-08 (7)		R.SIQEVDWC#PTGFK.V [1] R.SIQEVDWC#PTGFK.V [1] R.AVC#M*LSNTTAAIAFAWAR.L [1] K.AYHEQISVAFITNAC#FFPANOM*VK.C [1] K.TIGGGDDSFITFFC#ETGAGK.H R.AVC#MLSNTTAAIAFAWAR.L [1] R.AVC#MLSNTTAAIAFAWAR.L [1] R.AVC#MLSNTTAAIAFAWAR.L [1]	1955.92 1955.92 2252.07 3137.46 2439.07 2236.07 2236.07 2252.07	0.64 1.27 5.12 3.34 0.68 1.60 2.40 3.01	3 3 3 3 3 3 2 2	3.01E-07 1.07E-07 4.66E-09 2.67E-05 6.50E-04 4.60E-05 6.00E-10 1.56E-06	4.07 3.25 3.15 3.66 2.76 3.92 4.61 3.63	0.54 0.62 0.38 0.48 0.50 0.35 0.55 0.50	[1, 8, 10]	
		<b>Signal transduction</b>											
IPI00018146.1	YWHAQ	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, theta polypeptide	4.20E-08 (2)			R.YLAEVAC#GDDR.K	1639.73	3.22	2	3.20E-06	2.76	0.51	[3]
		<b>Unclassified</b>											
IPI00550069.3	RNH1	ribonuclease/angiogenin inhibitor 1	2.93E-05 (1)		6.40E-05 (4)	R.LDDC#GLTEAR.C	1520.69	5.32	2	6.06E-05	2.88	0.41	[2]
						K.LGDVGMALC#PGLHPSSR.L	2380.16	-1.02	3	3.68E-08	3.25	0.44	
IPI00021812.2	AHNAK	AHNAK nucleoprotein (desmoyokin)		K.VDVEC#PDVNIEGPEGK.W K.LEGDLTGPSVGVVDPDVELEC#PDAK.L		2127.98 2996.43	2.62 2.64	2 3	4.83E-07 3.72E-09	3.76 4.49	0.56 0.49		
				K.GPFVAEVDPDVELEC#PDAK.L		2458.13	-0.56	3	2.40E-01	2.90	0.34		
IPI00008530.1	RPLP0	ribosomal protein, large, P0	8.44E-06 (6)	K.C#FIVGADNVGSK.Q		1637.78	2.48	2	2.23E-06	3.95	0.43	[2, 11]	
IPI00219018.7	GAPDH	glyceraldehyde-3-phosphate dehydrogenase	4.62E-08 (1)	R.VPTANVSWDLIC#R.L [2] R.VPTANVSWDLIC#R.L [2]		1901.96 1901.96	-0.06 2.74	3 2	4.86E-03 5.57E-13	2.62 4.11	0.44 0.58	[1, 2, 8, 11, 13, 15]	

IPI00141318.2	CKAP4	cytoskeleton-associated protein 4		1.04E-09 (1)	K.IISNASC#TTNC#LAPLAK.V [1,2,11] K.SSSSSASAAAAAASSSASC#SR.R K.SSSSSASAAAAAASSSASC#SR.R	2194.06 2461.08 2461.08	5.95 4.29 3.34	2 2 3	2.38E-07 7.89E-11 1.02E-12	2.67 3.79 3.89	0.50 0.65 0.60	[2] [1]
IPI00645078.1	UBA1	ubiquitin-like modifier activating enzyme 1	1.48E-09 (4)		K.DNPGVVC#LDEAR.H	1816.84	2.23	2	1.69E-06	3.52	0.62	
IPI00029656.1	DFNA5	deafness, autosomal dominant 5	3.82E-05 (3)		R.NEVLG#VLTKQ.I	1574.81	3.61	2	3.85E-05	2.80	0.44	

a) # of pep: number of peptides identified for each protein according to the criteria of XCorr values of 2.0 (2+) and 2.5 (3+),  $\Delta Cn \geq 0.1$  and  $\Delta$  mass precursor < 10 ppm (including the same peptide with different charge states).

b) C#: Cysteine modified by biotin-HPDP (+428.191567 amu); C@: Cysteine modified by MMTS (+45.98772 amu).

c) For each protein, only the biotinylated peptides with the highest score from the multiple peptide pull-downs are shown.

d) Underlined are the sequences have been reported in the literature.

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