Electronic Supplementary Material (ESI) for Molecular BioSystems.

Table 1: List of proteins found to be differently expressed in the ANGII treated TK-173 cell line compared with untreated control. The gene name, accession number in Swiss-Prot, molecular weight, the peptide mass fingerprinting (PMF), MS/MS information and the sequence coverage are given. The spots where MS/MS-data are missing were only identified with PMF.

Spot Nr.	Protein Name	Gene Name	SwissProt Accession	Mol. Wt.	CPI	PMF Score	PMF Seq. Cov.	MS/MS Score	MS/MS Seq. Cov.
1	Translationally controlled tumor protein	TPT1	P13693	19595	4.84			352	14
2	Microtubule-associated protein RP/EB family member 1	MAPRE1	Q15691	29999	5.02	77	22		
3	Small ubiquitin-related modifier 2	SUMO2	P61956	10871	5.32			120	5
4	Myosin regulatory light chain 12A	MYL12A	P19105	19794	4.65			111	9
5	Prefoldin subunit 2	PFDN2	Q9UHV9	16648	6.20			114	5
6	Ferritin light chain	FTL	P02792	20020	5.50			144	7
7	Microtubule-associated protein RP/EB family member 1	MAPRE1	Q15691	29999	5.02	92	24		
8	EF-hand domain-containing protein D2	EFHD2	Q96C19	26697	5.15	105	9		
9	Peroxiredoxin-1	PRDX1	Q06830	22110	8.27			201	11
10	Peptidyl-prolyl cis-trans isomerise A	PPIA	P62937	18012	7.68	176	11		
11	Cofilin-1	CFL1	P23528	18502	8.22			134	8
12	Endoplasmin	HSP90B1	P14625	92469	4.76			76	6
13	Fibronectin	FN1	P02751	262607	5.46			574	18
14	Fibronectin	FN1	P02751	262607	5.46			707	27
15	Heat shock 70 kDa protein 4	HSPA4	P34932	94331	5.10			211	18
16	Heat shock protein HSP 90-alpha	HSP90AA 1	P07900	84660	4.94	115	12		
17	Transitional endoplasmic reticulum ATPase	VCP	P55072	89322	5.14			322	21
18	Caprin-1	CAPRIN1	Q14444	78366	5.04			69	7
19	Heat shock 70 kDa protein 1	HSPA1A	P08107	70052	5.47	64	11		
20	Stress-70 protein, mitochondrial	HSPA9	P38646	73680	5.87	114	13		
21	Lamin-B1	LMNB1	P20700	66408	5.11			82	3
22	Alpha-enolase	ENO1	P06733	47169	7.01			179	8

23	Fumarate hydratase, mitochondrial	FH	P07954	54637	8.85			42	7
24	26S protease regulatory subunit 8	PSMC5	P62195	45626	7.11			291	19
25	Cytosolic acyl coenzyme A thioester hydrolase	ACOT7	O00154	41796	8.85			261	11
26	Calponin-2	CNN2	Q99439	33697	6.94			127	6
27	Far upstream element-binding protein 2	KHSRP	Q92945	73146	6.85			124	6
28	Ras-related protein rab-11A	RAB11A	P62491	24394	6.12			159	7
29	LIM and SH3 domain protein 1	LASP1	Q14847	29717	6.61			146	8
30	Abhydrolase domain-containing protein 10, mitochondrial	ABHD10	Q9NUJ1	33933	8.81			118	9
31	Heat shock protein 105 kDa	HSPH1	Q92598	96865	5.27			66	7
32	Splicing factor 3 subunit 1	SF3A1	Q15459	88886	5.15	179	18		
33	Caprin-1	CAPRIN1	Q14444	78366	5.04			64	3
34	Peroxisome biogenesis factor 1	PEX1	O43933	142867	5.91			71	4
35	Serine/threonin protein phosphatase 2A 65 kDa	PPP2R1A	P30153	65309	5.00			63	5
36	Tubulin alpha-1A chain	TUBA1A	Q71U36	50136	4.94			70	5
37	Tubulin alpha-1B chain	TUBA1B	P68363	50152	4.94			125	8
38	Glutaredoxin-3	GLRX3	O76003	37432	5.31	63	9		
39	UBX domain-containing protein 1	UBXN1	Q04323	33325	5.23			136	11
40	N-myc-interactor	NMI	Q13287	35057	5.23	92	14		
41	Protein DJ-1	PARK7	Q99497	19891	6.32			71	5
42	Copine-1	CPNE1	Q99829	59059	5.52			68	3
43	Peptidyl-prolyl-cis trans isomerase A	PPIA	P62937	18012	7.68			80	4
44	Ubiquitin-conjugating enzymeE2 N	UBE2N	P61088	17138	6.13			82	7
45	GTP-binding nuclear protein Ran	RAN	P62826	24423	7.01			66	4
46	Superoxide dismutase (Mn), mitochondrial	SOD2	P04179	24722	8.35	116	15		
47	Malate dehydrogenase, cytoplasmic	MDH1	P40925	36426	6.91			88	6
48	Syntenin-1	SDCBP	O00560	32444	7.06			81	5
49	Glyceraldehyde-3-phosphate dehydrogenase	GAPDH	P04406	36053	8.57			104	10
50	Annexin 1	ANXA1	P04083	38714	6.57			118	6
51	Annexin 2	ANXA2	P07355	38604	7.57			175	8
52	Fructose-bisphosphate aldolase A	ALDOA	P04075	39420	8.30			149	9

53	BAG family molecular chaperone regulator 2	BAG2	O95816	23772	6.25			86	6
54	Annexin A5	ANXA5	P08758	35937	4.93	156	8		
55	Calponin-3	CNN3	Q15417	36414	5.69			65	2
56	Calponin-3	CNN3	Q15417	36414	5.69			62	6
57	Pyruvate kinase isozymes M1/M2	PKM2	P14618	57937	7.96			89	6
58	Actin, cytoplasmic 1	ACTB	P60709	41737	5.29			378	14
59	Superoxide dismutase (Cu-Zn)	SOD1	P00441	15936	5.70			88	6
60	Vimentin	VIM	P08670	53652	5.05			262	16
61	Nuclear migration protein nudC	NUDC	Q9Y266	38243	5.27			232	14
62	Proteasome subunit alpha type-3	PSMA3	P25788	28415	5.19			225	9
63	Proteasome subunit beta type-7	PSMB7	Q99436	29946	7.58			128	6
64	T-complex protein 1 subunit alpha	TCP1	P17987	60306	5.80			190	8
65	Peroxiredoxin-6	PRDX6	P30041	25035	6.00			261	9
66	Vimentin	VIM	P08670	53619	5.05			438	14
67	Hydroxymethyl glutaryl-CoA synthase, cytomplasmic	HMGCS1	Q01581	57257	5.22			516	11
68	60 kDa heat shock protein,mitochondrial	HSPD1	P10809	61016	5.70			600	19
69	Cytoplasmic dynein 1 intermediate chain 2	DYNC1I2	Q13409	71457	5.08			59	6
70	Peroxiredoxin-5, mitochondrial	PRDX5	P30044	22026	8.93			140	8
71	Nucleophosmin	NPM1	P06748	32575	4.64	60	17		
72	Prelamin-A/C	LMNA	P02545	74139	6.57			148	4
73	Annexin A5	ANXA5	P08758	35937	4.93	235	25		
74	WD repeat-containing protein 61	WDR61	Q9GZS3	33581	5.16	100	11		
75	78 kDa glucose-regulated protein	HSPA5	P11021	72333	5.07	165	12		
76	Actin, cytoplasmic 2	ACTG1	P63261	41793	5.31	70	13		
77	Collagen alpha-1 (I) chain	COL1A1	P02452	138911	5.50			83	7
78	Laminin subunit gamma-1	LAMC1	P11047	177603	5.01			61	4
79	Sex hormone-binding globulin	SHBG	P04278	43779	6.22			62	5
80	Cytoplasmic dynein 1 heavy chain 1	DYNC1H1	Q14204	532408	6.01			78	4
81	Serine hydroxymethyltransferase, mitochondrial	SHMT2	P34897	55993	8.76			164	12
82	Glutamate dehydrogenase 1, mitochondrial	GLUD1	P00367	61398	7.66			112	6
83	Ezrin	EZR	P15311	69413	5.94			85	7

84	Glial fibrallary acidic protein	GFAP	P14136	49880	5.42			77	4
85	Elongation factor 2	EEF2	P13639	95338	6.41			95	6

Table 2: List of proteins found to be differently expressed in the PDGF treated TK-173 cell line compared with untreated control. The gene name, accession number in Swiss-Prot, molecular weight, the peptide mass fingerprinting (PMF), MS/MS information and the sequence coverage are given. The spots where MS/MS-data are missing were only identified with PMF.

Spot Nr.	Protein Name	Gene Name	SwissProt Accession	Mol. Wt.	CPI	PMF Score	PMF Seq. Cov.	MS/MS Score	MS/MS Seq. Cov.
1	Actin, cytoplasmic 1	ACTB	P60709	41710	5.29			305	15
2	Actin, cytoplasmic 1	ACTB	P60709	41710	5.29			238	7
3	Elongation factor 1-delta	EEF1D	P29692	31103	4.9			388	8
4	Chromobox protein homolog 5	CBX5	P45973	22211	5.71			174	6
5	Proteasome subunit alpha type-3	PSMB3	P49720	28415	6.13			254	6
6	Tubulin beta chain	TUBB	Q9BUU9	49639	4.75	60	14		
7	Tubulin beta chain	TUBB	Q9BUU9	49639	4.75			88	8
8	Peptidyl-prolyl cis-trans isomerase A	PPIA	P62937	18001	7.68	101	11		
9	Tubulin beta chain	TUBB	Q9BUU9	49639	4.75			262	6
10	Adapter molecule crk	CRK	P46108	33810	5.38	101	13		
11	L-lactate dehydrogenase B chain	LDHB	P07195	36615	5.71	63	3		
12	Inorganic pyrophosphatase	PPA1	Q15181	32639	5.54	65	3		
13	Heat shock protein 90-beta	HSP90AB1	P08238	83212	4.96	65	2		
14	Heat shock 70 kDa protein 4	HSPA4	P34932	94271	5.10	91	4		
15	Heat shock 70 kDa protein 4	HSPA4	P34932	94271	5.10	84	4		
16	Heat shock 70 kDa protein 4	HSPA4	P34932	94271	5.10	79	3		
17	Hypoxia up-regulated protein 1	HYOU1	Q9Y4L1	111266	5.16			133	26
18	Hypoxia up-regulated protein 1	HYOU1	Q9Y4L1	111266	5.16			110	22
19	Caprin-1	CAPRIN1	Q14444	78318	5.14	114	5		
20	Heat shock 70 kDa protein 4	HSPA4	P34932	94271	5.10			292	10
21	Transitional endoplasmic reticulum ATPase	VCP	P55072	89266	5.14	90	20		
22	Transitional endoplasmic reticulum ATPase	VCP	P55072	89266	5.14	71	16		

23	Thioredoxin	TXN	P10599	11730	4.82	77	8		
24	Coactosin-like protein	COTL1	Q14019	15935	5.50	83	11		
25	Actin, cytoplasmic 1	ACTB	P60709	41710	5.29			210	9
26	Actin, cytoplasmic 1	ACTB	P60709	41710	5.29			217	9
27	Peroxiredoxin-1	PRDX1	Q06830	22096	8.27			174	8
28	Annexin A2	ANXA2	P07355	38580	7.57			547	16
29	Prohibitin	PHB	P35232	29786	5.57			266	7
30	Tubulin beta-4B chain	TBB4B	P68371	49799	4.79			424	18
31	Nucleoside diphosphate kinase A	NME1	P15531	17138	5.81			243	9
32	Protein DJ-1	PARK7	Q99497	19878	6.32			115	7
33	Cofilin-1	CFL1	P10668	18491	8.16			117	6
34	Superoxide dismutase [Mn], mitochondrial	SOD2	P04179	24707	8.35	90	10		
35	GTP-binding nuclear protein Ran	RAN	P62826	24408	7.01			193	5
36	Phosphoglycerate mutase 1	PGAM1	P18669	28786	6.67			112	8
37	Far upstream element-binding protein 2	KHSRP	Q92945	73101	6.85	115	19		
38	Stress-induced-phosphoprotein 1	STIP1	P31948	62599	6.40	150	35		
39	Prelamin-A/C	LMNA	P02545	74095	6.57	147	31		
40	Prelamin-A/C	LMNA	P02545	74095	6.57			44	3
41	Prelamin-A/C	LMNA	P02545	74095	6.57	169	19		
42	Prelamin-A/C	LMNA	P02545	74095	6.57			71	20
43	Heat shock protein HSP 90-beta	HSP90AB1	P08238	83212	4.96			454	12
44	Nucleolin	NCL	P19338	76568	4.60			305	13
45	Nucleolin	NCL	P19338	76568	4.60			219	9
46	Heat shock protein HSP 90-beta	HSP90AB1	P08238	83212	4.96			502	15
47	Spectrin alpha chain, brain	SPTAN1	Q13813	284364	5.22			340	19
48	Pyruvate kinase isozymes M1/M2	PKM2	P14618	57900	7.96	159	20		
49	Pyruvate kinase isozymes M1/M2	PKM2	P14618	57900	7.96	180	23		
50	Pyruvate kinase isozymes M1/M2	PKM2	P14618	57900	7.96	130	20		
51	Heterogeneous nuclear ribonuleoprotein K	HNRNPK	P61978	50944	5.39	67	13		
52	Pyruvate kinase isozymes M1/M2	PKM2	P14618	57900	7.96			201	7
53	Pyruvate kinase isozymes M1/M2	PKM2	P14618	57900	7.96			113	25

54	Pyruvate kinase isozymes M1/M2	PKM2	P14618	57900	7.96			69	15
55	TAR DNA-binding protein 43	TARDBP	Q13148	44711	5.85			166	6
56	Heterogeneous nuclear ribonucleoprotein D0	HNRNPD	Q14103	38410	7.61			98	4
57	Acetyl-CoA acetyltransferase, cytosolic	ACAT2	Q9BWD1	41324	6.46			73	6
58	Crk-like protein	CRKL	P46109	33756	6.26			63	3
59	Proliferation-associated protein 2G4	PA2G4	Q9UQ80	43759	6.13			146	9
60	Vimentin	VIM	P08670	53619	5.05			274	38
61	Aldose reductase	AKR1B1	P15121	35830	6.52			193	4
62	Poly (rC)-binding protein 1	PCBP1	Q15365	37474	6.66			104	6
63	14-3-3 protein epsilon	YWHAE	P62258	29155	4.63			95	3
64	Chloride intracellular channel protein 1	CLIC1	O00299	26906	5.09			192	5
65	Actin, cytoplasmic 1	ACTB	P60709	41710	5.29			193	8
66	Proteasome subunit alpha type-2	PSMA2	P25787	25882	6.91			229	16
67	Electron transfer flavoprotein subunit alpha, mitochondrial	ETFA	P13804	35058	8.62			235	14
68	Alpha-enolase	ENO1	P06733	47139	7.01	142	22		
69	Heterogeneous nuclear ribonucleoprotein H	HNRNPH1	P31943	49198	5.89			86	10
70	Aldehyde dehydrogenase X, mitochondrial	ALDH1B1	P30837	57202	6.36			218	18
71	Prefoldin subunit 5	PFDN5	Q99471	17317	5.94			123	9
72	Prefoldin subunit 2	PFDN2	Q9UHV9	16638	6.20			244	13
73	Thioredoxin	TXN	P10599	11730	4.82			125	4
74	Glutathione S-transferase P	GSTP1	P09211	23341	5.43	62	7		
75	Peroxiredoxin-6	PRDX6	P30041	25035	6.00			211	12
76	Protein disulfide-isomerase A3	PDIA3	P30101	56747	5.98	157	27		
77	Vimentin	VIM	P08670	53619	5.05			75	4
78	Annexin A5	ANXA2	P07355	38580	7.57			105	6
79	Elongation factor1-delta	EEF1D	P29692	31103	4.90			89	5
80	Actin, cytoplasmic 1	ACTB	P60709	41710	5.29			217	7
81	78-kDa glucose regulated protein	HSPA5	P11021	72288	5.07			117	8
82	Heat shock cognate 71 kDa protein	HSPA8	P11142	70854	5.37	73	19		
83	Heat shock cognate 71 kDa protein	HSPA8	P11142	70854	5.37	80	17		

84	Endoplasmin	HSP90B1	P14625	92411	4.76			156	7
85	39S ribosomal protein L12, mitochondrial	MRPL12	P52815	21335	9.05			174	5
86	Glyceraldehyde-3-phosphate dehydrogenase	GAPDH	P04406	36030	8.57			165	5
87	N(G),N(G)-dimethylarginine dimethylaminohydrolase 1	DDAH1	O94760	31102	5.53			140	6

Table 3: List of proteins found to be differently expressed in the ANGII treated HK-2 cell line compared with untreated control. The gene name, accession number in Swiss-Prot, molecular weight, the peptide mass fingerprinting (PMF), MS/MS information and the sequence coverage are given. The spots where MS/MS-data are missing were only identified with PMF.

Spot Nr.	Protein Name	Gene Name	SwissProt Accession	Mol. Wt.	CPI	PMF Score	PMF Seq. Cov.	MS/MS Score	MS/MS Seq. Cov.
1	Serine/arginine-rich splicing factor 1	SFRS1	Q07955	27728	10.37	80	12	198	13
2	Serine/arginine-rich splicing factor 1	SFRS1	Q07955	27728	10.37	91	9		
3	Glutathione S-transferase omega-1	GSTO 1	P78417	27548	6.24	68	11	112	5
4	Cathepsin D	CTSD	P07339	44524	6.10	60	11		
5	Pyridoxal kinase	PDXK	O00764	35080	5.75			122	6
6	Heat shock protein beta-1	HSPB1	P04792	22768	5.98	109	8	161	13
7	GTP-binding nuclear protein Ran	RAN	P62826	24408	7.01			164	14
8	Proteasome subunit beta type-2	PSMB2	P49721	22822	6.52			135	8
9	5'(3')-deoxyribonucleotidase, cytosolic type	NT5C	Q8TCD5	23368	6.18			156	8
10	Proteasome subunit alpha type-6	PSMA6	P60900	27382	6.34			200	13
11	S-formylglutathione hydrolase	ESD	P10768	31442	6.54	65	10	68	5
12	Protein DJ-1	PARK7	Q99497	19878	6.32			179	9
13	Peroxiredoxin-6	PRDX6	P30041	25035	6.00			148	7
14	Far upstream element-binding protein 2	KHSRP	Q92945	73101	6.85			159	14
15	Far upstream element-binding protein 1	FUBP1	Q96AE4	67518	7.18	113	13	111	5
16	C-1-tetrahydrofolate synthase, cytoplasmic	MTHFD1	P11586	101495	6.89			64	13
17	Elongation factor 2	EEF2	P13639	95277	6.41			137	6
18	Glutamate dehydrogenase 1, mitochondrial	GLUD1	P00367	61359	7.66			132	7
19	Vinculin	VCL	P18206	123722	5.50			68	16
20	Spectrin alpha chain, brain	SPTAN1	Q13813	284364	5.22	93	40		
21	Spectrin alpha chain, brain	SPTAN1	Q13813	284364	5.22			122	12
22	Spectrin alpha chain, brain	SPTAN1	Q13813	284364	5.22	103	34	139	21
23	Endoplasmin	HSP90B1	P14625	92411	4.76			447	23

24	Major vault protein	MVP	Q14764	99266	5.34			95	8
25	Endoplasmin	HSP90B1	P14625	92411	4.76			178	12
26	Endoplasmin	HSP90B1	P14625	92411	4.76	166	13		
27	Heat shock 70 kDa protein 4	HSPA4	P34932	94331	5.10			180	12
28	Heat shock 70 kDa protein 4	HSPA4	P34932	94331	5.10	78	11		
29	Endoplasmin	HSP90B1	P14625	92411	4.76			131	7
30	Fascin	FSCN1	Q16658	54496	6.84	142	20		
31	Heterogeneous nuclear ribonucleoprotein L	HNRNPL	P14866	64092	8.46	115	18	70	6
32	Bifunctional purine biosynthesis protein PURH	ATIC	P31939	64575	6.27	127	21		
33	Prelamin-A/C	LMNA	P02545	74095	6.57			141	13
34	Prelamin-A/C	LMNA	P02545	74095	6.57	98	11	153	14
35	Prelamin-A/C	LMNA	P02545	74095	6.57			145	14
36	Pre-mRNA-processing factor 19	PRPF19	Q9UMS4	55146	6.14			146	9
37	T- complex protein 1 subunit gamma	CCT3	P49368	60495	6.10			253	7
38	T-complex protein 1 subunit beta	CCT2	P78371	57452	6.01	145	19		
39	Sorting nexin-6	SNX6	Q9UNH7	46620	5.81			155	12
40	Aflatoxin B1 aldehyde reductase member 2	AKR7A2	O43488	39564	6.70			249	17
41	Sialic acid synthase	NANS	Q9NR45	40281	6.29			255	12
42	Lipocalin-1	LCN1	P31025	19238	5.38	76	6	132	7
43	Stress-70 protein	HSPA9	P38646	73635	5.87	66	13	117	8
44	Proliferation-associated protein 2G4	PA2G4	Q9UQ80	43759	6.13	92	16	158	11
45	28S ribosomal protein S22, mitochondrial	MRPS22	P82650	41254	7.70	111	15	135	9
46	Short-chain specific acyl-CoA dehydrogenase, mitochondrial	ACADS	P16219	44269	8.13	61	9	126	7
47	Heterogeneous nuclear ribonucleoproteins C1/C2	HNRNPC	P07910	33650	4.94			82	4
48	Ribose- phosphate pyrophosphokinase 1	PRPS1	P60891	34812	6.51	67	7	112	5
49	Annexin A1	ANXA1	P04083	38690	6.57	92	15		
50	RNA - binding protein 4	RBM4	Q9BWF3	40289	6.61			279	8
51	RNA - binding protein 4B	RBM4B	Q9BQ04	40124	6.28			253	9
52	78 kDa glucose-regulated protein	HSPA5	P11021	72288	5.07	188	32		
53	Thioredoxin domain- containing protein 12	TXNDC12	O95881	19194	5.25			149	10

54	Actin, cytoplasmic 1	ACTB	P60709	41710	5.29			106	14
55	Proteasome subunit beta type-4	PSMB4	P28070	29185	5.70			113	13
56	Thioredoxin-dependent peroxide reductase, mitochondrial	PRDX3	P30048	27675	7.68	185	23	133	14
57	Actin, cytoplasmic 1	ACTB	P60709	41710	5.29			105	7
58	Tubulin beta chain	TUBB	P07437	49639	4.78	75	15	198	13
59	Heterogeneous nuclear ribonucleoproteins C1/C2	HNRNPC	P07910	33650	4.94			178	9
60	Aldose reductase	AKR1B1	P15121	35830	6.52	60	14	88	6
61	Endoplasmin	HSP90B1	P14625	92411	4.76	87	20	67	4
62	Nucleoprotein TPR	TPR	P12270	267131	4.97			133	7
63	Stress-70 protein, mitochondrial	HSPA9	P38646	73635	5.87			154	11
64	Lamin- B1	LMNB1	P20700	66368	5.11	71	15	139	7
65	Peptidyl-prolyl cis-trans isomerase FKBP10	FKBP10	Q96AY3	64204	5.36			251	12
66	26S protease regulatory subunit 7	PSMC2	P35998	48603	5.71	127	23		
67	**Eukaryotic translation initiation factor 3 subunit G**	EIF3G	O75821	35589	5.87			110	5
68	**Cytochrome b-c1 complex subunit Rieske, mitochondrial**	UQCRFS1	P47985	29649	8.55			122	5
69	Omega-amidase NIT2	NIT2	Q9NQR4	30589	6.83	169	19	295	10
70	Heterogeneous nuclear ribonuclear protein L	HNRNPL	P14866	64092	8.46			249	18
71	Alpha-enolase	ENO1	P06733	47139	7.01	157	19		
72	Histone H4	HIST1H4A	P62805	11360	11.36	158	18	413	32
73	Heterogeneous nuclear ribonucleoprotein K	HNRNPK	P61978	50944	5.39	118	29	305	18
74	60 kDa shock protein, mitochondrial	HSPD1	P10809	61016	5.70			501	17
75	Cytochrome c oxidase subunit 6B1	COX6B1	P14854	10186	6.54			103	8

Table 4: List of proteins found to be differently expressed in the PDGF treated HK-2 cell line compared with untreated control. The gene name, accession number in Swiss-Prot, molecular weight, the peptide mass fingerprinting (PMF), MS/MS information and the sequence coverage are given. The spots where MS/MS-data are missing were only identified with PMF.

Spot Nr.	Protein Name	Gene Name	SwissProt Accession	Mol. Wt.	CPI	PMF Score	PMF Seq. Cov.	MS/MS Score	MS/MS Seq. Cov.
1	Small ubiquitin-related modifier 2	SUMO2	P61956	10864	5.32			92	6
2	Coactosin-like protein	COTL1	Q14019	15935	5.50			274	11
3	78 kDa glucose-regulated protein	HSPA5	P11021	72288	5.07			218	15
4	Sorcin	SRI	P30626	21662	5.32			191	9
5	Chloride intracellular channel protein 1	CLIC1	O00299	26906	5.09	151	18		
6	Protein DJ-1	PARK7	Q99497	19878	6.32	132	18		
7	Annexin A5	ANXA5	P08758	35914	4.93	95	9	128	10
8	Tubulin-folding cofactor B	TBCB	Q99426	27308	5.06	78	10	127	4
9	Annexin A5	ANXA5	P08758	35914	4.93	194	24		
10	Elongation factor 1-delta	EEF1D	P29692	31103	4.90			204	8
11	Peroxiredoxin 1	PRDX1	Q06830	22096	8.27	98	18	156	14
12	Serine/arginine-rich splicing factor 7	SFRS7	Q16629	27350	9.64			186	15
13	Nucleophosmin	NPM1	P06748	32555	4.64	150	19		
14	Nucleophosmin	NPM1	P06748	32555	4.64	153	17		
15	Nucleophosmin	NPM1	P06748	32555	4.64			191	8
16	Nucleophosmin	NPM1	P06748	32555	4.64			155	4
17	Heterogeneous nuclear ribonucleoprotein C1/C2	HNRNPC	P07910	33650	4.94			258	9
18	Heterogeneous nuclear ribonucleoprotein C1/C2	HNRNPC	P07910	33650	4.94	112	12	72	7
19	Serine-threonine kinase receptor associated protein	STRAP	Q9Y3F4	38414	4.98	120	16		
20	Heterogenous nuclear ribonucleoprotein C1/C2	HNRNPC	P07910	33650	4.94			159	6
21	Histidine triad nucleotide-binding protein 2, mitochondrial	HINT2	Q9BX68	17151	9.20			253	18

22	40S ribosomal protein S12	RPS12	P25398	14505	6.81			82	9
23	Cytochrome c oxidase subunit 5B, mitochondrial	COX5B	P10606	13687	9.07			237	16
24	Eukaryotic translation initiation factor 1	EIF1	P41567	12725	6.90			169	6
25	Cystatin-B	CSTB	P04080	11133	6.96			195	8
26	Prefoldin subunit 2	PFDN2	Q9UHV9	16638	6.20			164	6
27	Alpha-crystallin B chain	CRYAB	P02511	20146	6.76			140	7
28	Proteasome subunit alpha type 2	PSMA2	P25787	25882	6.91	142	15	115	5
29	Chloride intracellular channel protein 4	CLIC4	Q9Y696	28754	5.45	72	10	84	5
30	Glutathione S-transferase omega-1	GSTO1	P78417	27548	6.24			128	7
31	UMP-CMP kinase	CMPK1	P30085	22208	5.44	65	8	132	6
32	Heme-binding protein 1	HEBP1	Q9NRV9	21084	5.71	189	17	164	6
33	Calponin-3	CNN3	Q15417	36391	5.69			92	6
34	Ubiquitin-fold modifier-conjugating enzyme 1	UFC1	Q9Y3C8	19446	6.91			152	8
35	Superoxide dismutase [Mn], mitochondrial	SOD2	P04179	24707	8.35	69	9	114	7
36	Superoxide dismutase [Mn], mitochondrial	SOD2	P04179	24707	8.35			118	7
37	Delta(3,5)-Delta(2,4)-dienoyl-CoA isomerase, mitochondrial	ECH1	Q13011	35793	8.16			288	18
38	Vimentin	VIM	P08670	53619	5.05	137	33		
39	Tubulin beta -4 chain	TUBB4	P04350	49554	4.78	163	22		
40	Tubulin beta chain	TUBB	P07437	49639	4.78	71	10	154	9
41	Gamma-enolase	ENO2	P09104	47239	4.91			175	7
42	Vimentin	VIM	P08670	53619	5.05	174	35		
43	Galactokinase	GALK1	P51570	42246	6.04			136	8
44	Alpha-enolase	ENO1	P06733	47139	7.01	98	12	197	12
45	Proliferation-associated protein 2G4	PA2G4	Q9UQ80	43759	6.13			132	13
46	Heterogeneous nuclear ribonucleoprotein H3	HNRNPH3	P31942	36903	6.37			117	7
47	Eukaryotic translation initiation factor 3 subunit G	EIF3G	O75821	35589	5.87	88	11	129	5
48	Heterogeneous nuclear ribonucleoprotein D-like	HNRPDL	O14979	46409	9.59			175	8
49	Poly(rC)-binding protein 1	PCBP1	Q15365	37474	6.66			211	10
50	Heterogeneous nuclear ribonucleoprotein D0	HNRNPD	Q14103	38410	7.61			162	6
51	Medium- chain specific acyl-CoA dehydrogenase,	ACADM	P11310	46559	8.61	79	12	203	13

	mitochondrial								
52	Mannose-1-phosphate guanyltransferase alpha	GMPPA	Q96IJ6	46262	6.73			140	5
53	Fascin	FSCN1	Q16658	54496	6.84	78	14	212	12
54	LIM and SH3 domain protein 1	LASP1	Q14847	29698	6.61	115	16	146	12
55	PDZ and LIM domain protein 1	PDLIM1	O00151	36049	6.56			252	12
56	Mitotic checkpoint protein BUB3	BUB3	O43684	37131	6.36			122	7
57	Isocitrate dehydrogenase [NADP], cytoplasmic	IDH1	O75874	46630	6.53			247	11
58	Actin, cytoplasmic 1	ACTB	P60709	41710	5.29	158	13		
59	Actin, cytoplasmic 1	ACTB	P60709	41710	5.29	162	33		
60	Thioredoxin	TXN	P10599	11730	4.82	143	17	152	8
61	Protein S100-A6	S100A6	P06703	10173	5.32	82	8	107	4
62	Protein S100-A11	S100A11	P31949	11733	6.56	159	11	69	4
63	Endoplasmic reticulum resident protein 29	ERP29	P30040	28975	6.77	118	18		
64	26S proteasome non-ATPase regulatory subunit 10	PSMD10	O75832	24412	5.71	150	16		
65	Peroxiredoxin-4	PRDX4	Q13162	30521	5.86	79	13	111	7
66	Src substrate cortactin	CTTN	Q14247	61549	5.24	101	22	153	8
67	Heat shock cognate 71 kDa protein	HSPA8	P11142	70854	5.37	96	18		
68	Macrophage-capping protein	CAPG	P40121	38494	5.82	176	24		
69	Galactokinase	GALK1	P51570	42246	6.04	113	27	76	4
70	Sialic acid synthase	NANS	Q9NR45	40281	6.29	95	16	110	4
71	Thioredoxin-dependent peroxide reductase, mitochondrial	PRDX3	P30048	27675	7.68	145	18		
72	78 kDa glucose-regulated protein	HSPA5	P11021	72288	5.07	222	30		
74	Lamin-B1	LMNB1	P20700	66368	5.11	112	26		
75	Transitional endoplasmic reticulum ATPase	VCP	P55072	89266	5.14	197	37		
76	Protein disulfide-isomerase A3	PDIA3	P30101	56747	5.98	131	22		
77	Isocitrate dehydrogenase [NADP], cytoplasmic	IDH1	O75874	46630	6.53	97	19	143	8
78	Aldose reductase	AKR1B1	P15121	35830	6.52	120	12	176	8
79	Prelamin-A/C	LMNA	P02545	74095	6.57	74	26	198	10
80	Endoplasmin	HSP90B1	P14625	92411	4.76	82	22		
81	Endoplasmin	HSP90B1	P14625	92411	4.76			152	14

82	60 kDa heat shock protein, mitochondrial	HSPD1	**P10809**	61016	5.70	80	20		
83	Tubulin beta chain	TUBB	**P07437**	49639	4.78	110	18		
84	Actin, cytoplasmic 1	ACTB	**P60709**	41710	5.29	104	18		
85	Vimentin	VIM	**P08670**	53619	5.05	149	27		
86	Heterogeneous nuclear ribonucleoproteins C1/C2	HNRNPC	**P07910**	33650	4.95	68	14	75	6
87	Annexin A3	ANXA3	**P12429**	36353	5.62	77	17	193	11

Table 5: List of proteins identified from immunoprecipitation of the WT-DJ-1 transfected TK-173 and HK-2 cell lysates using anti-DJ-1 antibody and G-protein agarose matrix. The gene name, accession number in Swiss-Prot, protein mass, and MS/MS information are given.

Spot Nr.	Protein Name	Gene Name	SwissProt Accession	Mol. Wt.	CPI	MS/MS Score	MS/MS Seq. Cov.
1	Myosin regulatory light chain 12A	MYL12A	P19105	19781	4.65	139	4
2	Protein DJ-1	PARK7	Q99497	19878	6.32	118	6
3	Peroxiredoxin-1	PRDX1	Q06830	22096	8.27	108	5
4	Peroxiredoxin-6	PRDX6	P30041	25035	6.00	88	4
5	Prohibitin	PHB	P35232	29786	5.57	99	8
6	ADP/ATP translocase 2	SLC25A5	P05141	32831	9.71	126	6
7	Annexin A5	ANXA5	P08758	35914	4.93	167	8
8	Glyceraldehyde-3-phosphate dehydrogenase	GAPDH	P04406	36030	8.57	335	10
9	L-lactate dehydrogenase A chain	LDHA	P00338	36665	8.44	100	5
10	Annexin A2	ANXA2	P07355	38580	7.57	580	12
11	Annexin A1	ANXA1	P04083	38690	6.57	304	11
12	Actin, cytoplasmic 1	ACTB	P60709	41710	5.29	258	9
13	Actin, cytoplasmic 2	ACTG1	P63261	41766	5.31	140	6
14	Alpha-enolase	ENO1	P06733	47139	7.01	390	11
15	Tubulin beta chain	TUBB	P07437	49639	4.78	259	13
16	Vimentin	VIM	P08670	53619	5.05	574	21
17	Pyruvate kinase isozymes M1/M2	PKM	P14618	57900	7.96	179	6
18	Heterogeneous nuclear ribonucleoprotein L	HNRNPL	P14866	64092	8.46	98	4
19	Ezrin	EZR	P15311	69370	5.94	149	7
20	Heat shock cognate 71 kDa protein	HSPA8	P11142	70854	5.37	372	9
21	Heat shock 70 kDa protein 6	HSPA6	P17066	70984	5.81	153	6
22	78 kDa glucose-regulated protein	HSPA5	P11021	72288	5.07	347	8

23	Heat shock protein HSP 90-beta	HSP90AB1	P08238	83212	4.96	522	14
24	Elongation factor 2	EEF2	P13639	95277	6.41	110	5
25	Poly [ADP-ribose] polymerase 1	PARP1	P09874	113012	8.99	148	5
26	Clathrin heavy chain 1	CLTC	Q00610	191493	5.48	190	6
27	Filamin-A	FLNA	P21333	280564	5.70	776	20
28	Filamin-C	FLNC	Q14315	290841	5.65	420	16

Table 6: List of proteins identified from immunoprecipitation of the mutant E18Q-DJ-1 in TK-173 and HK-2 cell lysates using the QIA express Ni-NTA Fast Start assay. The gene name, accession number in Swiss-Prot, protein mass, and MS/MS information are given.

Spot Nr.	Protein Name	Gene Name	SwissProt Accession	Mol. Wt.	CPI	MS/MS Score	MS/MS Seq. Cov.
1	60S ribosomal protein L31	RPL31	P62899	14454	10.54	59	4
2	Peptidyl-prolyl cis-trans isomerase A	PPIA	P62937	18001	7.68	59	5
3	Cofilin-1	CFL1	P23528	18491	8.22	44	4
4	Protein DJ-1	PARK7	Q99497	19878	6.32	52	6
5	Ferritin light chain	FTL	P02792	20007	5.50	46	4
6	Peroxiredoxin-1	PRDX1	Q06830	22096	8.27	43	4
7	Peptidyl-prolyl cis-trans isomerase B	PPIB	P23284	23728	9.42	104	8
8	Ras-related protein Rab-11A	RAB11A	P62491	24378	6.12	67	6
9	Superoxide dismutase [Mn], mitochondrial	SOD2	P04179	24707	8.35	68	7
10	Malate dehydrogenase, mitochondrial	MDH2	P40926	35481	8.92	76	4
11	Annexin A5	ANXA5	P08758	35914	4.93	334	10
12	Glyceraldehyde-3-phosphate dehydrogenase	GAPDH	P04406	36030	8.57	197	4
13	Annexin A2	ANXA2	P07355	38580	7.57	289	12
14	Annexin A1	ANXA1	P04083	38690	6.57	141	5
15	Actin, cytoplasmic 1	ACTB	P60709	41710	5.29	202	6
16	Actin, cytoplasmic 2	ACTG1	P63261	41766	5.31	191	12
17	Alpha-enolase	ENO1	P06733	47139	7.01	68	7
18	Serine hydroxymethyltransferase, mitochondrial	SHMT2	P34897	55958	8.76	92	9
19	Protein disulfide-isomerase	P4HB	P07237	57081	4.76	72	5
20	Pyruvate kinase isozymes M1/M2	PKM2	P14618	57900	7.96	206	15
21	Glutamate dehydrogenase 1, mitochondrial	GLUD1	P00367	61359	7.66	69	5
22	78 kDa glucose-regulated protein	HSPA5	P11021	72288	5.07	131	7
23	Heat shock protein HSP 90-alpha	HSP90AA1	P07900	84607	4.94	99	6

24	Endoplasmin	HSP90B1	P14625	92411	4.76	130	7

Table 7: List of proteins identified from immunoprecipitation of the mutant E18D-DJ-1 in TK-173 and HK-2 cell lysates using the QIA express Ni-NTA Fast Start assay. The gene name, accession number in Swiss-Prot, protein mass, and MS/MS information are given.

Spot Nr.	Protein Name	Gene Name	SwissProt Accession	Mol. Wt.	CPI	MS/MS Score	MS/MS Seq. Cov.
1	Profilin-1	PFN1	P07737	15045	8.44	40	3
2	Peptidyl-prolyl cis-trans isomerase A	PPIA	P62937	18001	7.68	53	4
3	Lipocalin-1	LCN1	P31025	19238	5.38	98	3
4	Peroxiredoxin-2	PRDX2	P32119	21878	5.66	147	12
5	Peroxiredoxin-1	PRDX1	Q06830	22096	8.27	89	5
6	Ras-related protein Rab-2A	RAB2A	P61019	23531	6.08	54	6
7	Superoxide dismutase [Mn], mitochondrial	SOD2	P04179	24707	8.35	64	4
8	Peroxiredoxin-6	PRDX6	P30041	25035	6.00	83	9
9	Triosephosphate isomerase	TPI1	P60174	30772	5.65	55	4
10	1-acyl-sn-glycerol-3-phosphate acyltransferase alpha	AGPAT1	Q99943	31696	9.48	68	6
11	Enoyl-CoA delta isomerase 1, mitochondrial	ECI1	P42126	32795	8.80	88	7
12	Annexin A2	ANXA2	P07355	38580	7.57	319	8
13	Fructose-bisphosphate aldolase A	ALDOA	P04075	39395	8.30	44	7
14	Actin, cytoplasmic 1	ACTB	P60709	41710	5.29	65	10
15	Serpin H1	SERPINH1	P50454	46411	8.75	212	7
16	Protein disulfide-isomerase A6	PDIA6	Q15084	48091	4.95	87	4
17	Acyl-coenzyme A thioesterase 9, mitochondrial	ACOT9	Q9Y305	49870	8.81	137	10
18	Tubulin alpha-1B chain	TUBA1B	P68363	50120	4.94	166	5
19	ATP synthase subunit beta, mitochondrial	ATP5B	P06576	56525	5.26	205	5
20	EH domain-containing protein 2	EHD2	Q9NZN4	61123	6.02	99	3
21	78 kDa glucose-regulated protein	HSPA5	P11021	72288	5.07	235	18
22	Stress-70 protein, mitochondrial	HSPA6	P38646	73635	5.87	62	3

23	Endoplasmin	HSP90B1	P14625	92411	4.76	120	9
24	Alpha-actinin-1	ACTN1	P12814	102993	5.25	64	4
25	Carboxypeptidase D	CPD	O75976	152835	5.68	61	3