

MicroRNA-target pairs in the rat kidney identified by microRNA microarray, proteomic, and bioinformatic analysis

Zhongmin Tian, Andrew S. Greene, Jennifer L. Pietrusz, Isaac R. Matus, and Mingyu Liang*

*correspondence: mliang@mcw.edu

Supplemental Table 1. Proteins enriched in the renal cortex compared to the renal medulla.

Supplemental Table 2. Proteins enriched in the renal medulla compared to the renal cortex.

Supplemental Table 1. Proteins enriched in the renal cortex compared to the renal medulla.

Spot IDs can be used to locate the spots in **Supplemental Figure 1**. P values are for the comparison between the cortex and the medulla. C/M ratios represent cortex/medulla ratios. Predicted isoelectric point (pI) and molecular weight (MW) were based on protein sequences. Calculated pI and MW were based on spot locations on the 2D gels. Sequence coverage, score and Expect values were from the Mascot analysis. The spots were sorted by UniProt ID and then by spot ID.

Spot ID	Common Protein Name	P Value	C/M Ratio	UniProt	Gene Symbol	Predicted pI	Predicted MW	Calculated pI	Calculated MW	Sequence coverage (%)	Score	Expect
1311	D-amino-acid oxidase	0.0039	2.2	O35078	<i>Dao1</i>	6.70	38796	6.87	40491	36	70	0.012
1519	Lactamase, beta 2	1.50E-05	2.25	O35952	<i>Lactb2</i>	6.46	28878	6.05	34622	40	97	0.00065
780	Peptidase D	0.00022	2.25	O54975	<i>Pepd</i>	5.38	69613	5.75	57020	18	78	2.20E-03
2052	cytochrome b5	4.10E-06	3.58	P00173	<i>Cyb5</i>	4.90	15215	5.03	13141	55	66	0.034
1414	Fructose-bisphosphate aldolase B (EC 4.1.2.13)	0.03	1.61	P00884	<i>Aldob</i>	8.67	39462	10.16	38202	26	77	0.0026
1446	Fructose-bisphosphate aldolase B (EC 4.1.2.13)	0.046	1.55	P00884	<i>Aldob</i>	8.67	39462	8.21	37209	30	73	0.0063
2064	alpha-2u-globulin	1.10E-06	13.52	P02761	<i>LOC259246</i>	5.48	18718	5.39	12729	62	96	3.10E-05
2065	alpha-2u-globulin	0.00044	2.37	P02761	<i>LOC259246</i>	5.48	18718	5.26	12606	60	79	0.0015
2078	alpha-2u-globulin	2.00E-06	27.31	P02761	<i>LOC259246</i>	5.48	18718	5.60	12416	53	97	2.30E-05
2095	alpha-2u-globulin	5.70E-07	18.14	P02761	<i>LOC259246</i>	5.48	18718	5.88	11617	53	90	0.00013
2190	alpha-2u-globulin	1.70E-06	9.56	P02761	<i>LOC259246</i>	5.48	18718	5.31	7772	45	66	0.031
2036	alpha-2u-globulin	2.50E-05	6.87	P02761	<i>LOC298116</i>	5.48	18718	5.40	14561	44	68	0.02
2116	alpha-2u-globulin	5.40E-07	18.27	P02761	<i>LOC298116</i>	5.48	18718	5.61	10513	58	83	0.00057
2188	alpha-2u-globulin	0.043	6	P02761	<i>LOC298116</i>	5.48	18718	5.16	7761	49	67	0.027
1025	ornithine-oxo-acid transaminase (EC 2.6.1.13) precursor	0.00046	1.53	P04182	<i>Oat</i>	5.81	44647	6.04	49161	23	63	0.059
648	Catalase (EC 1.11.1.6)	0.00055	2.3	P04762	<i>Cat</i>	7.15	59588	6.76	62135	18	58	0.031
666	Catalase (EC 1.11.1.6)	0.00097	1.61	P04762	<i>Cat</i>	7.15	59588	6.96	61878	44	216	3.10E-17
876	Alpha-enolase (EC 4.2.1.11) (Enolase 1)	3.50E-05	1.86	P04764	<i>Eno1</i>	6.16	46967	5.83	53721	27	69	0.016
467	heat shock 70kD protein 5	0.0025	3.13	P06761	<i>Hspa5</i>	5.01	70431	5.25	70879	19	82	0.023
2084	copper-zinc containing superoxide dismutase (EC 1.15.1.1)	5.70E-06	2.81	P07632	<i>Sod1</i>	5.89	15771	5.99	12279	31	79	0.0016
2093	copper-zinc containing superoxide dismutase (EC 1.15.1.1)	0.0016	3.01	P07632	<i>Sod1</i>	5.89	15771	6.12	12093	39	63	0.066
1108	acyl-CoA dehydrogenase (EC 1.3.99.3) precursor, medium-chain-specific, mitochondrial	0.00068	1.64	P08503	<i>Acadm</i>	7.68	43657	6.93	46317	27	86	0.00031
1059	argininosuccinate synthase (EC 6.3.4.5)	5.60E-06	2.73	P09034	<i>Ass</i>	7.63	46467	7.23	47685	26	93	6.30E-05
1065	argininosuccinate synthase (EC 6.3.4.5)	5.70E-08	2.36	P09034	<i>Ass</i>	7.63	46467	6.92	47818	25	65	4.00E-02
1137	argininosuccinate synthase (EC 6.3.4.5)	6.70E-05	1.56	P09034	<i>Ass</i>	7.63	46467	7.81	46061	32	80	1.30E-03
1215	argininosuccinate synthase (EC 6.3.4.5)	0.00092	3.12	P09034	<i>Ass</i>	7.63	46467	6.90	43577	24	66	3.00E-02
1105	ATP synthase subunit beta, mitochondrial [Precursor] (EC 3.6.3.14)	0.0015	2.45	P10719	<i>Atp5b</i>	4.95	51678	5.09	46704	47	192	7.70E-15
1106	ATP synthase subunit beta, mitochondrial [Precursor] (EC 3.6.3.14)	0.003	3.37	P10719	<i>Atp5b</i>	4.95	51678	5.13	46834	30	93	6.10E-05

1107	ATP synthase subunit beta, mitochondrial [Precursor] (EC 3.6.3.14)	0.00011	3.33	P10719	<i>Atp5b</i>	4.95	51678	5.17	47094	51	185	3.90E-14
1118	ATP synthase subunit beta, mitochondrial [Precursor] (EC 3.6.3.14)	0.00019	2.05	P10719	<i>Atp5b</i>	4.95	51678	6.44	46061	24	57	0.044
795	glutamate dehydrogenase [NAD(P)] (EC 1.4.1.3) precursor	2.40E-05	1.78	P10860	<i>Glud1</i>	6.71	55900	6.69	56626	22	68	0.019
809	glutamate dehydrogenase [NAD(P)] (EC 1.4.1.3) precursor	5.50E-05	1.73	P10860	<i>Glud1</i>	6.71	55900	6.74	56079	27	74	0.0052
824	Aldehyde dehydrogenase, mitochondrial (EC 1.2.1.3) (ALDH class 2)	0.00017	2.41	P11884	<i>Aldh2</i>	5.69	54333	5.97	56079	28	110	1.20E-06
843	Aldehyde dehydrogenase, mitochondrial (EC 1.2.1.3) (ALDH class 2)	0.0028	1.66	P11884	<i>Aldh2</i>	5.69	54333	6.23	55692	32	103	6.10E-06
1225	aspartate transaminase (EC 2.6.1.1)	1.20E-05	6.56	P13221	<i>Got1</i>	6.81	46268	7.17	43517	31	96	3.40E-05
1279	acetyl-Coenzyme A acyltransferase 2 (mitochondrial 3-oxoacyl-Coenzyme A thiolase)	0.0026	4.51	P13437	<i>Acaa2</i>	8.09	41844	9.36	41745	36	82	0.00083
219	Dipeptidyl peptidase 4 (EC 3.4.14.5)	0.0093	2.72	P14740	<i>Dpp4</i>	5.93	88033	5.62	84519	15	73	0.0057
242	Dipeptidyl peptidase 4 (EC 3.4.14.5)	0.0002	2.07	P14740	<i>Dpp4</i>	5.93	88033	5.73	83471	15	67	0.024
1908	glutathione transferase (EC 2.5.1.18) 8, cytosolic	0.0021	1.59	P14942	<i>Gsta4</i>	6.77	25493	6.74	22468	40	86	0.00032
1234	acyl-CoA dehydrogenase (EC 1.3.99.3) short-chain-specific precursor	0.026	1.76	P15651	<i>Acads</i>	6.38	42161	6.67	43097	27	81	0.001
1673	ATP synthase subunit alpha, mitochondrial [Precursor] (EC 3.6.3.14)	6.50E-05	2.52	P15999	<i>Atp5a1</i>	8.28	55233	8.94	29318	21	69	0.015
1934	ATP synthase subunit alpha, mitochondrial [Precursor] (EC 3.6.3.14)	0.0014	5.14	P15999	<i>Atp5a1</i>	8.28	55233	6.61	21884	41	73	0.0056
1935	ATP synthase subunit alpha, mitochondrial [Precursor] (EC 3.6.3.14)	0.0031	6.9	P15999	<i>Atp5a1</i>	8.28	55233	6.89	21733	41	80	0.0013
1169	fructose-bisphosphatase (EC 3.1.3.11),	0.0019	1.69	P19112	<i>Fbp1</i>	5.54	39453	5.45	44864	34	95	3.50E-05
1936	glutathione peroxidase (EC 1.11.1.9) precursor	6.60E-05	5.11	P23764	<i>Gpx3</i>	6.37	22868	5.65	21733	29	71	0.01
1937	glutathione peroxidase (EC 1.11.1.9) precursor	3.30E-05	4.66	P23764	<i>Gpx3</i>	6.37	22868	6.19	21643	29	64	0.05
1147	fumarylacetoacetase (EC 3.7.1.2)	6.60E-05	3.08	P25093	<i>Fah</i>	6.67	45946	6.74	45680	24	72	0.007
1244	sorbitol dehydrogenase	0.0014	3.12	P27867	<i>Sord</i>	7.14	42793	6.94	42328	39	71	0.011
1076	cytosolic NADP-dependent isocitrate dehydrogenase (IDP2)	0.0001	2.06	P41562	<i>Idh1</i>	6.53	46705	6.74	47356	33	71	0.0093
865	glutathione synthase (EC 6.3.2.3)	0.0086	1.82	P46413	<i>Gss</i>	5.48	52312	5.45	54245	27	78	0.0021
868	glutathione synthase (EC 6.3.2.3)	3.50E-05	3.16	P46413	<i>Gss</i>	5.48	52312	5.52	54320	37	169	1.50E-12
1592	3-hydroxyanthranilate 3,4-dioxygenase	0.00062	3.27	P46953	<i>Haao</i>	5.57	32561	5.54	32574	34	96	2.70E-05
1832	Triosephosphate isomerase	0.00051	2.72	P48500	<i>Tpi1</i>	7.06	26701	6.19	25033	38	56	0.049
747	lamin A	1.60E-07	2.2	P48679	<i>Lmna</i>	6.54	74279	6.37	58460	23	57	0.045
866	L-arginine-glycine amidinotransferase	0.00011	2.37	P50442	<i>Gatm</i>	6.15	44155	5.59	54320	33	93	6.60E-05
899	L-arginine-glycine amidinotransferase	9.30E-06	2.08	P50442	<i>Gatm</i>	6.15	44155	6.46	53129	50	124	4.90E-08
946	L-arginine-glycine amidinotransferase	1.40E-08	5	P50442	<i>Gatm</i>	6.15	44155	6.15	51748	25	66	0.033
947	L-arginine-glycine amidinotransferase	2.90E-05	10.4	P50442	<i>Gatm</i>	6.15	44155	6.24	51748	33	77	0.0023
948	L-arginine-glycine amidinotransferase	6.30E-06	5.85	P50442	<i>Gatm</i>	6.15	44155	6.55	51748	44	70	0.012
959	L-arginine-glycine amidinotransferase	2.30E-05	6.5	P50442	<i>Gatm</i>	6.15	44155	6.40	51533	31	96	3.00E-05
1005	L-arginine-glycine amidinotransferase	6.70E-07	3.7	P50442	<i>Gatm</i>	6.15	44155	6.25	49503	31	64	0.051
1009	L-arginine-glycine amidinotransferase	0.00059	4.82	P50442	<i>Gatm</i>	6.15	44155	6.41	49572	27	64	0.05
1035	L-arginine-glycine amidinotransferase	5.20E-05	2.26	P50442	<i>Gatm</i>	6.15	44155	6.35	48822	37	87	0.00026
1333	Alcohol dehydrogenase [NADP+] (EC 1.1.1.2) (3-DG-reducing enzyme)	0.0039	3.16	P51635	<i>Akr1a1</i>	6.81	36352	7.31	40212	44	92	7.70E-05
1340	Alcohol dehydrogenase [NADP+] (EC 1.1.1.2) (3-DG-reducing enzyme)	0.00031	4.06	P51635	<i>Akr1a1</i>	6.81	36352	6.96	40268	33	78	0.0019
1341	Alcohol dehydrogenase [NADP+] (EC 1.1.1.2) (3-DG-reducing enzyme)	0.00041	3.78	P51635	<i>Akr1a1</i>	6.81	36352	7.07	40268	35	79	0.0014
1778	Endoplasmic reticulum protein 29	0.02	1.53	P52555	<i>Erp29</i>	6.08	25593	6.16	26205	22	66	0.029
1146	beta actin	0.0062	1.77	P60711	<i>Actb</i>	5.29	41579	5.22	45553	37	96	2.70E-05
1149	beta actin	0.0038	1.7	P60711	<i>Actb</i>	5.29	41579	5.30	45365	25	70	0.0019
1151	beta actin	0.00028	2.23	P60711	<i>Actb</i>	5.29	41579	5.28	45365	32	83	0.00064
2039	beta actin	6.70E-05	4.31	P60711	<i>Actb</i>	5.29	41579	5.34	14400	22	75	0.004

763	ATPase, H+ transporting, V1 subunit B, isoform 2 (<i>Mus musculus</i>)	0.00017	1.95	P62815	<i>Atp6v1b2</i>	5.57	56515	5.62	57735	42	169	2.60E-13
783	ATPase, H+ transporting, V1 subunit B, isoform 2 (<i>Mus musculus</i>)	0.003	2.08	P62815	<i>Atp6v1b2</i>	5.57	56515	5.52	57257	26	67	0.025
470	dnaK-type molecular chaperone	0.029	2.2	P63018	<i>Hspa8</i>	5.37	70827	5.29	70781	25	74	0.0048
847	Hspd1 protein	0.00024	2.32	P63039	<i>Hspd1</i>	5.35	57890	5.31	55078	24	82	0.00087
1920	Abhydrolase domain containing 14b	0.011	1.69	P80299	<i>Abhd14b</i>	5.86	62300	5.60	22037	29	73	0.0063
1463	3-mercaptopyruvate sulfurtransferase (EC 2.8.1.2)	0.0011	3.62	P97532	<i>Mpst</i>	5.88	32788	6.87	36494	33	121	9.70E-08
1604	3-mercaptopyruvate sulfurtransferase (EC 2.8.1.2)	1.60E-05	1.92	P97532	<i>Mpst</i>	5.88	32788	6.04	31815	42	109	1.50E-06
788	methylmalonate-semialdehyde dehydrogenase (acylating) (EC 1.2.1.27)	7.60E-06	1.58	Q02253	<i>Aldh6a1</i>	7.54	54479	7.22	56783	23	104	4.90E-06
802	methylmalonate-semialdehyde dehydrogenase (acylating) (EC 1.2.1.27)	0.0015	1.6	Q02253	<i>Aldh6a1</i>	7.54	54479	7.08	56547	23	64	0.048
1434	senescence marker protein SMP-30	7.20E-07	3.36	Q03336	<i>Rgn</i>	5.27	33368	5.31	37676	32	100	1.20E-05
1328	Hydroxyacid oxidase 2 (EC 1.1.3.15)	0.00039	2.67	Q07523	<i>Hao2</i>	7.90	39045	8.31	40379	34	77	0.0026
1334	Hydroxyacid oxidase 2 (EC 1.1.3.15)	0.016	2.52	Q07523	<i>Hao2</i>	7.90	39045	8.50	40379	39	161	9.70E-12
1791	Biphenyl hydrolase-like (Serine hydrolase, breast epithelial mucin- associated antigen)	0.005	2.23	Q3B8N9	<i>Bphl</i>	8.94	32802	9.09	25701	29	66	0.032
1521	Aspartoacylase-3	0.0023	5	Q5M876	<i>Acy3</i>	5.42	35397	5.51	34478	35	73	0.0056
1534	Aspartoacylase-3	0.0013	3.69	Q5M876	<i>Acy3</i>	5.42	35397	5.55	34240	30	90	0.003
1378	Kif2b protein	0.0069	2.04	Q5X151	<i>Kif2b</i>	9.51	41123	6.96	39167	29	57	0.041
925	NADH dehydrogenase (Ubiquinone) flavoprotein 1	0.0013	1.64	Q5X1H3	<i>Ndufv1</i>	8.37	50699	8.11	52252	16	56	0.053
1153	keratin complex 1, acidic, gene 19	0.021	1.55	Q63279	<i>Krt1-19</i>	5.21	44609	5.34	45176	26	88	0.00019
1266	Resiniferatoxin-binding, phosphotriesterase-related protein.	0.0011	1.65	Q63530	<i>Pter</i>	6.06	38907	6.42	41803	25	74	0.0043
1268	Resiniferatoxin-binding, phosphotriesterase-related protein	2.30E-05	2.45	Q63530	<i>Pter</i>	6.06	38907	6.57	42210	36	101	9.70E-06
918	beta-alanine-pyruvate aminotransferase	4.80E-06	4.55	Q64565	<i>Agxt2</i>	7.13	52611	7.05	52762	27	103	6.10E-06
919	beta-alanine-pyruvate aminotransferase	0.0014	3.41	Q64565	<i>Agxt2</i>	7.13	52611	7.63	52689	35	71	0.0097
922	beta-alanine-pyruvate aminotransferase	0.00046	3.24	Q64565	<i>Agxt2</i>	7.13	52611	7.19	52762	35	102	7.70E-06
923	beta-alanine-pyruvate aminotransferase	6.80E-06	4.69	Q64565	<i>Agxt2</i>	7.13	52611	7.33	52689	38	110	1.20E-06
924	beta-alanine-pyruvate aminotransferase	0.00019	3.28	Q64565	<i>Agxt2</i>	7.13	52611	7.49	52689	32	124	4.90E-08
960	beta-alanine-pyruvate aminotransferase	0.031	3.38	Q64565	<i>Agxt2</i>	7.13	52611	6.80	51462	23	64	0.0089
962	beta-alanine-pyruvate aminotransferase	0.00017	3.21	Q64565	<i>Agxt2</i>	7.13	52611	6.92	51319	25	70	0.012
790	Non-specific dipeptidase (Cndp2 protein)	4.60E-05	2.2	Q66HG3	<i>Cndp2</i>	5.06	54893	5.59	56862	30	90	0.00013
821	Leucine aminopeptidase 3	3.50E-06	2.02	Q68FS4	<i>Lap3</i>	6.78	56115	6.56	56313	26	72	0.0085
1113	Kidney aminoacylase 1	5.30E-06	2.99	Q6AYS7	<i>Acy1</i>	6.03	45775	6.14	46446	51	187	2.40E-14
1589	ATPase, H+ transporting, V1 subunit E isoform 1	0.014	1.79	Q6PCU2	<i>Atp6v1e1</i>	8.44	26112	8.81	32304	35	63	0.059
1658	Nitrilase family, member 2	7.10E-05	2.39	Q7TQ94	<i>Nit2</i>	5.92	32070	6.81	29686	38	147	6.50E-09
1667	Nitrilase family, member 2	0.00012	1.53	Q7TQ94	<i>Nit2</i>	5.92	32070	6.36	29481	24	69	0.43
1505	Lambda-crystallin homolog	1.20E-05	3.69	Q811X6	<i>Cryl1</i>	5.95	35187	6.03	35251	27	76	0.003
1439	Aflatoxin B1 aldehyde reductase member 2	0.00042	2.39	Q8CG45	<i>Akr7a2</i>	8.35	40649	6.53	37676	32	71	0.0091
741	Selenium binding protein 2	8.60E-05	2.38	Q8VIF7	<i>Selenbp1</i>	6.10	52498	6.20	58460	21	63	0.061
1870	peptide methionine sulfoxide reductase or ribosyldihyronicotinamide dehydrogenase [quinone] (EC 1.10.99.2)	0.00016	2.62	Q923M1 or Q6AY80	<i>Msra</i> or <i>Nqo2</i>	8.21 or 7.10	25834 or 26144	6.80	23716	39	64	0.052
819	4-trimethylaminobutyraldehyde dehydrogenase (Tmadh)	0.00024	2.25	Q9JLJ3	<i>Aldh9a1</i>	6.57	53618	6.02	56079	21	64	0.05
1563	Voltage-dependent anion-selective channel protein 1 (VDAC-1)	0.0014	1.75	Q9Z2L0	<i>Vdac1</i>	8.63	30606	8.81	33074	46	94	0.0014

Supplemental Table 2. Proteins enriched in the renal medulla compared to the renal cortex.

Spot IDs can be used to locate the spots in **Supplemental Figure 2**. P values are for the comparison between the cortex and the medulla. M/C ratios represent medulla/cortex ratios. Predicted isoelectric point (pI) and molecular weight (MW) were based on protein sequences. Calculated pI and MW were based on spot locations on the 2D gels. Sequence coverage, score and Expect values were from the Mascot analysis. The spots were sorted by UniProt ID and then by spot ID.

Spot ID	Common Protein Name	P Value	M/C Ratio	UniProt	Gene Symbol	Predicted PI	Predicted MW	Calculated PI	Calculated MW	Sequence coverage (%)	Score	Expect
595	stress-induced phosphoprotein 1	0.00018	1.62	O35814	<i>Stip1</i>	6.40	62530	6.58	65133	30	98	2.00E-05
1478	Heterogeneous nuclear ribonucleoprotein A2/B1 (Mus musculus)	0.015	2.48	O88569	<i>Hnrpa2b1</i>	8.97	37380	8.90	36343	53	190	1.20E-14
599	myosin alpha heavy chain	8.30E-06	1.79	P02563	<i>Myh6</i>	5.59	223370	6.80	64773	12	59	0.029
380	serum albumin precursor	5.10E-07	2.99	P02770	<i>Alb</i>	5.80	65874	5.83	75440	18	66	0.027
393	serum albumin precursor	3.20E-05	1.94	P02770	<i>Alb</i>	5.80	65874	5.92	75023	22	65	0.035
428	serum albumin precursor	0.00066	2.37	P02770	<i>Alb</i>	5.80	65874	5.79	71868	21	63	0.063
451	serum albumin precursor	0.0005	2.72	P02770	<i>Alb</i>	5.80	65874	5.84	71669	27	72	0.0085
493	serum albumin precursor	0.00012	3.83	P02770	<i>Alb</i>	5.80	65874	5.79	68655	42	180	1.20E-13
500	serum albumin precursor	4.20E-05	6.43	P02770	<i>Alb</i>	5.80	65874	5.75	68750	37	170	1.20E-12
503	serum albumin precursor	2.70E-05	2.99	P02770	<i>Alb</i>	5.80	65874	5.29	68655	31	95	3.70E-05
505	serum albumin precursor	2.40E-05	2.71	P02770	<i>Alb</i>	5.80	65874	5.24	68655	21	76	0.0033
507	serum albumin precursor	4.60E-05	5.7	P02770	<i>Alb</i>	5.80	65874	5.85	68560	35	146	3.10E-10
510	serum albumin precursor	0.00044	6.1	P02770	<i>Alb</i>	5.80	65874	5.95	68465	27	133	6.10E-09
514	serum albumin precursor	0.0026	1.74	P02770	<i>Alb</i>	5.80	65874	6.54	68370	27	88	0.00018
515	serum albumin precursor	0.0013	1.63	P02770	<i>Alb</i>	5.80	65874	8.47	68276	21	63	0.063
517	serum albumin precursor	0.00045	4.92	P02770	<i>Alb</i>	5.80	65874	6.04	68370	26	96	3.20E-05
521	serum albumin precursor	7.60E-06	3.05	P02770	<i>Alb</i>	5.80	65874	5.57	68465	26	78	0.0018
523	serum albumin precursor	0.01	1.82	P02770	<i>Alb</i>	5.80	65874	6.15	68087	46	114	4.90E-07
538	serum albumin precursor	0.0043	1.84	P02770	<i>Alb</i>	5.80	65874	8.08	68181	21	69	0.016
558	serum albumin precursor	0.0012	2.65	P02770	<i>Alb</i>	5.80	65874	6.49	67429	25	71	0.0089
569	serum albumin precursor	0.00011	2.56	P02770	<i>Alb</i>	5.80	65874	5.08	65586	25	71	0.0089
601	serum albumin precursor	0.00037	2.42	P02770	<i>Alb</i>	5.80	65874	5.90	65224	26	87	0.00026
1079	serum albumin precursor	2.40E-05	1.62	P02770	<i>Alb</i>	5.80	65874	5.82	47422	21	82	0.00069
708	Protein disulfide-isomerase [Precursor]	5.90E-05	1.55	P04785	<i>P4hb</i>	4.77	54949	5.08	59688	21	77	0.0022
1198	Fructose-bisphosphate aldolase A (EC 4.1.2.13)	1.20E-07	5.37	P05065	<i>Aldoa</i>	8.40	39196	8.42	44002	33	66	0.028
1205	Fructose-bisphosphate aldolase A (EC 4.1.2.13)	0.0021	3.82	P05065	<i>Aldoa</i>	8.40	39196	8.92	43759	33	67	0.026
263	Eef2 protein	0.0022	1.86	P05197	<i>Eef2</i>	6.42	95092	6.80	81528	17	64	0.044
269	Eef2 protein	7.60E-05	1.58	P05197	<i>Eef2</i>	6.42	95092	6.71	81415	17	57	0.04

270	Eef2 protein	0.033	1.52	P05197	<i>Eef2</i>	6.42	95092	6.88	81528	18	69	0.014
547	Contrapsin-like protease inhibitor 1 [Precursor]	6.10E-05	3.51	P05545	<i>Spin2b</i>	5.31	44573	4.98	67992	25	76	0.0033
1010	creatine kinase (EC 2.7.3.2) chain B	0.00042	1.77	P07335	<i>Ckb</i>	5.39	42698	9.02	49503	40	123	6.10E-08
1016	creatine kinase (EC 2.7.3.2) chain B	0.0002	2.52	P07335	<i>Ckb</i>	5.39	42698	5.64	49366	38	126	3.10E-08
2147	Fatty acid-binding protein, heart (H-FABP)	0.021	1.85	P07483	<i>Fabp3</i>	5.92	14635	5.74	8977	46	88	0.0002
1424	Aldose reductase (EC 1.1.1.21)	0.0044	4.23	P07943	<i>Akr1b4</i>	6.28	35643	6.40	37991	37	114	4.90E-07
1428	Aldose reductase (EC 1.1.1.21)	0.00072	8.86	P07943	<i>Akr1b4</i>	6.28	35643	6.44	37833	33	110	1.20E-06
1504	Aldose reductase (EC 1.1.1.21)	0.00046	9.29	P07943	<i>Akr1b4</i>	6.28	35643	6.40	35349	31	64	0.044
1507	Aldose reductase (EC 1.1.1.21)	0.0003	4.42	P07943	<i>Akr1b4</i>	6.28	35643	6.45	35398	31	64	0.044
1846	Glutathione S-transferase Mu 2 (EC 2.5.1.18)	0.039	2.09	P08010	<i>Gstm2</i>	7.31	25555	7.54	24620	62	161	9.70E-12
1614	Tropomyosin alpha-4 chain	1.70E-05	2.63	P09495	<i>Tpm4</i>	4.66	28361	4.97	31378	45	114	4.90E-07
570	ATP synthase subunit beta, mitochondrial [Precursor] (EC 3.6.3.14)	5.00E-06	8.65	P10719	<i>Atp5b</i>	4.95	51678	5.03	66225	37	105	3.90E-06
583	ATP synthase subunit beta, mitochondrial [Precursor] (EC 3.6.3.14)	0.0017	1.72	P10719	<i>Atp5b</i>	4.95	51678	6.25	65405	26	68	0.02
640	ATP synthase subunit beta, mitochondrial [Precursor] (EC 3.6.3.14)	0.0018	1.99	P10719	<i>Atp5b</i>	4.95	51678	5.18	62222	29	77	0.0022
838	ATP synthase subunit beta, mitochondrial [Precursor] (EC 3.6.3.14)	1.60E-06	2.9	P10719	<i>Atp5b</i>	4.95	51678	5.11	55538	49	103	6.10E-06
850	ATP synthase subunit beta, mitochondrial [Precursor] (EC 3.6.3.14)	0.00046	2.47	P10719	<i>Atp5b</i>	4.95	51678	5.20	55846	46	170	1.20E-12
854	ATP synthase subunit beta, mitochondrial [Precursor] (EC 3.6.3.14)	7.00E-05	3.37	P10719	<i>Atp5b</i>	4.95	51678	5.14	51677	49	160	1.20E-11
871	ATP synthase subunit beta, mitochondrial [Precursor] (EC 3.6.3.14)	0.0012	2.17	P10719	<i>Atp5b</i>	4.95	51678	5.17	54020	46	189	1.50E-14
894	ATP synthase subunit beta, mitochondrial [Precursor] (EC 3.6.3.14)	3.50E-05	2.29	P10719	<i>Atp5b</i>	4.95	51678	5.25	53055	33	90	0.00012
1236	ATP synthase subunit beta, mitochondrial [Precursor] (EC 3.6.3.14)	8.10E-05	2.28	P10719	<i>Atp5b</i>	4.95	51678	5.19	42681	29	69	0.014
1259	ATP synthase subunit beta, mitochondrial [Precursor] (EC 3.6.3.14)	0.0009	2.34	P10719	<i>Atp5b</i>	4.95	51678	5.13	42152	41	82	0.0007
1298	ATP synthase subunit beta, mitochondrial [Precursor] (EC 3.6.3.14)	0.011	1.85	P10719	<i>Atp5b</i>	4.95	51678	5.18	40943	23	63	0.056
687	protein disulfide isomerase associated 3	0.00015	1.58	P11598	<i>Pdia3</i>	5.78	54205	5.87	61026	38	160	1.20E-11
1008	Bckdha protein (EC 1.2.4.4)	5.30E-05	1.96	P11960	<i>Bckdha</i>	5.93	45528	5.88	49298	35	76	0.0033
673	pyruvate kinase (EC 2.7.1.40) isozyme M2	3.50E-05	2.58	P11980	<i>Pkm2</i>	6.69	57650	7.70	61450	42	140	1.20E-09
2130	cytochrome c oxidase subunit VIa	0.00033	1.56	P12075	<i>Cox5b</i>	5.22	10779	5.44	9528	41	65	0.036
355	Serotransferrin [Precursor]	0.013	1.85	P12346	<i>Tf</i>	6.99	74501	6.49	76493	17	72	0.0074
372	Serotransferrin [Precursor]	0.0083	2.85	P12346	<i>Tf</i>	6.99	74501	6.71	75964	34	154	4.90E-11
375	Serotransferrin [Precursor]	0.00023	2.97	P12346	<i>Tf</i>	6.99	74501	6.81	76175	41	166	3.10E-12
995	Fumarate hydratase (EC 4.2.1.2)	0.00099	1.83	P14408	<i>Fh</i>	8.27	50007	7.60	50333	26	70	0.012
1000	Fumarate hydratase (EC 4.2.1.2)	5.10E-05	1.62	P14408	<i>Fh</i>	8.27	50007	8.13	50006	26	70	0.014
1002	Fumarate hydratase (EC 4.2.1.2)	0.012	1.51	P14408	<i>Fh</i>	8.27	50007	8.68	49917	32	84	0.0005
1073	Lipocortin V, annexin V, or actin beta	1.10E-06	1.82					5.77	47553			
1561	annexin V	2.10E-05	3.04	P14668	<i>Anxa5</i>	4.93	35591	5.16	33166	47	116	3.10E-07
1565	annexin V	0.00077	2.47	P14668	<i>Anxa5</i>	4.93	35591	5.09	33120	49	141	9.70E-10
1567	annexin V	5.80E-05	5.09	P14668	<i>Anxa5</i>	4.93	35591	5.13	35591	52	194	4.90E-15
452	propionyl-CoA carboxylase (EC 6.4.1.3) alpha chain precursor	0.00031	2.41	P14882	<i>Pcca</i>	6.08	75176	6.00	71768	27	92	8.50E-05
464	propionyl-CoA carboxylase (EC 6.4.1.3) alpha chain precursor	0.0002	1.97	P14882	<i>Pcca</i>	6.08	75176	6.07	71669	19	75	0.0035
1202	aspartate-tRNA ligase (EC 6.1.1.12)	0.014	1.59	P15178	<i>Dars</i>	6.02	57090	5.16	43638	25	63	0.057
532	ATP synthase subunit alpha, mitochondrial [Precursor] (EC 3.6.3.14)	0.0022	1.57	P15999	<i>Atp5a1</i>	8.28	55233	7.00	68087	29	76	0.0031
823	ATP synthase subunit alpha, mitochondrial [Precursor] (EC 3.6.3.14)	0.00037	1.76	P15999	<i>Atp5a1</i>	8.28	55233	8.65	56235	32	134	4.90E-09
829	ATP synthase subunit alpha, mitochondrial [Precursor] (EC 3.6.3.14)	0.00099	1.75	P15999	<i>Atp5a1</i>	8.28	55233	8.84	56157	33	114	4.90E-07

845	ATP synthase subunit alpha, mitochondrial [Precursor] (EC 3.6.3.14)	0.0057	1.77	P15999	<i>Atp5a1</i>	8.28	55233	8.50	56079	38	146	3.10E-10
149	alpha II spectrin	0.00064	4.9	P16086	<i>Spna2</i>	5.20	284462	5.51	90960	14	68	0.021
422	Hemopexin	0.0018	1.92	P20059	<i>Hpx</i>	7.33	48911	5.66	72468	21	73	0.0063
425	Hemopexin	0.0066	1.87	P20059	<i>Hpx</i>	7.33	48911	5.75	72067	23	68	0.017
2011	Alpha crystallin B chain	0.0049	3.53	P23928	<i>Cryab</i>	6.76	20076	6.97	18583	44	78	0.0022
602	t-complex protein 1	0.00034	1.86	P28480	<i>Tcp1</i>	5.86	60322	6.00	64773	25	80	0.0011
1003	Vimentin	0.016	2.1	P31000	<i>Vim</i>	5.06	53569	5.02	49572	33	99	1.60E-05
1220	Vimentin	0.0016	1.91	P31000	<i>Vim</i>	5.06	53569	4.99	43397	27	65	0.006
396	Ezrin	0.0021	1.55	P31977	<i>Vil2</i>	5.83	69217	5.99	74711	27	79	0.0014
397	Ezrin	6.10E-06	1.77	P31977	<i>Vil2</i>	5.83	69217	6.07	74608	25	80	0.0013
1158	Ubiquinol-cytochrome c reductase core protein II	0.00015	3.03	P32551	<i>Uqcrc2</i>	8.83	46722	8.78	45114	31	96	2.80E-05
346	Heat shock protein HSP 90-beta	4.30E-06	2.54	P34058	<i>Hsp90ab1</i>	4.97	83098	5.19	76493	27	100	1.20E-05
369	Heat shock protein HSP 90-beta	0.015	1.83	P34058	<i>Hsp90ab1</i>	4.97	83098	5.23	76070	23	67	0.022
1180	40S ribosomal protein SA	0.046	1.74	P38983	<i>Rpsa</i>	4.80	32672	5.08	44740	38	72	0.0069
1389	L-lactate dehydrogenase B chain (EC 1.1.1.27)	5.80E-05	2.79	P42123	<i>Ldhd</i>	5.70	36458	5.75	38950	38	111	9.70E-07
591	dihydropyrimidinase-related protein 2	0.0015	4.28	P47942	<i>Dpysl2</i>	5.95	62239	6.21	65224	24	68	0.018
701	dihydropyrimidinase-related protein 2	0.0016	2.42	P47942	<i>Dpysl2</i>	5.95	62239	5.65	59771	24	75	0.0042
463	lamin A	0.0059	1.78	P48679	<i>Lmna</i>	6.54	74279	6.71	72267	24	85	0.00039
585	lamin A	5.30E-05	1.78	P48679	<i>Lmna</i>	6.54	74279	6.96	64953	25	58	0.036
597	lamin A	0.0071	1.66	P48679	<i>Lmna</i>	6.54	74279	6.54	65043	27	83	0.00064
604	lamin A	0.00057	1.63	P48679	<i>Lmna</i>	6.54	74279	6.67	64863	24	68	0.019
421	HSP-70 protein, mitochondrial precursor	0.0018	1.89	P48721	<i>HSPA9</i>	5.51	68801	5.71	72167	22	65	0.04
1476	Pyruvate dehydrogenase (Lipoamide) beta	3.50E-05	2.07	P49432	<i>Pdhb</i>	5.29	35818	5.47	36242	32	72	0.007
542	Transketolase	1.00E-06	1.66	P50137	<i>Tkt</i>	7.22	67601	7.45	67992	29	82	0.00072
1480	Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta 2	0.0062	1.98	P54313	<i>Gnb2</i>	5.60	37176	5.57	36042	23	66	0.031
1562	Annexin A4	0.00043	1.94	P55260	<i>Anxa4</i>	5.32	35695	5.44	33212	56	178	1.90E-13
190	beta actin	0.00026	1.6	P60711	<i>Actb</i>	5.29	41579	5.39	86533	28	82	0.00087
388	beta actin	0.00019	1.51	P60711	<i>Actb</i>	5.29	41579	5.37	75335	32	70	0.012
998	beta actin	2.90E-05	1.9	P60711	<i>Actb</i>	5.29	41579	5.37	50055	25	67	0.024
1021	beta actin	1.10E-05	4.11	P60711	<i>Actb</i>	5.29	41579	5.55	49298	25	66	0.03
1061	beta actin	0.00086	1.68	P60711	<i>Actb</i>	5.29	41579	5.21	47619	23	70	0.013
1064	beta actin	0.00015	2.41	P60711	<i>Actb</i>	5.29	41579	5.26	47619	22	68	0.021
1070	beta actin	0.014	1.9	P60711	<i>Actb</i>	5.29	41579	5.31	47356	25	86	0.00034
1071	beta actin	3.10E-06	1.77	P60711	<i>Actb</i>	5.29	41579	5.67	47290	30	69	0.015
1074	beta actin	1.40E-06	2.01	P60711	<i>Actb</i>	5.29	41579	5.87	47422	38	67	0.023
1084	beta actin	5.70E-05	1.56	P60711	<i>Actb</i>	5.29	41579	5.95	47290	25	68	0.018
1090	beta actin	0.00082	1.62	P60711	<i>Actb</i>	5.29	41579	6.06	47159	30	65	0.006
1141	beta actin	0.00018	3.04	P60711	<i>Actb</i>	5.29	41579	5.96	45807	22	68	0.021
1756	Beta-actin FE-3	0.0004	3.11	Q99NC6				5.34	26423	55	67	0.026
1787	Beta-actin FE-3	0.0035	1.63	Q99NC6				5.51	25808	55	66	0.029
606	heterogeneous nuclear ribonucleoprotein K	0.00037	1.73	P61980	<i>Hnrpk</i>	5.39	50944	5.34	64237	33	95	3.90E-05
1703	14-3-3 zeta protein	0.002	1.68	P63102	<i>Ywhaz</i>	4.73	27754	5.03	28085	36	75	0.0041

1716	14-3-3 protein, theta subtype	0.0016	1.56	P68255	<i>Ywhaq</i>	4.69	27761	4.99	27545	36	63	0.056
726	Tubb5 protein	0.0012	2.37	P69897	<i>Tubb2c</i>	4.78	49639	5.15	58785	25	111	9.70E-07
504	lamin B	2.90E-07	2.82	P70615	<i>Lmnb1</i>	5.16	66435	5.31	68465	19	68	0.019
1619	Tropomyosin 5	7.20E-06	2.09	P97726	<i>Tpm3_v1</i>	4.72	28930	5.00	31204	36	139	4.10E-08
492	Heat shock 70 kDa protein 1A/1B	3.50E-06	3.81	Q07439	<i>Hspa1a</i> , <i>Hspa1b</i>	5.60	70142	5.71	68941	43	204	4.90E-16
513	Heat shock 70 kDa protein 1A/1B	0.02	3.4	Q07439	<i>Hspa1a</i> , <i>Hspa1b</i>	5.60	70142	6.07	68465	32	130	1.20E-08
383	Inner membrane protein, mitochondrial	2.30E-05	1.93	Q3KR86	<i>Immt</i>	5.57	67135	5.45	75649	27	78	0.0019
385	Inner membrane protein, mitochondrial	1.70E-05	2.03	Q3KR86	<i>Immt</i>	5.57	67135	5.41	75440	27	97	2.60E-05
603	Guanosine diphosphate dissociation inhibitor 1	8.30E-07	6.78	Q499U0	<i>Gdi1</i>	5.00	50504	5.21	64773	36	103	6.10E-06
1228	Ndufa10 protein	1.60E-05	1.89	Q561S0	<i>Ndufa10</i>	5.96	36820	6.07	43457	43	131	9.70E-09
1116	Suc1g2 protein	1.80E-05	1.8	Q5EBA9	<i>Suc1g2</i>	5.64	41980	5.73	41980	21	68	0.021
423	Methylcrotonoyl-Coenzyme A carboxylase 1 (Alpha)	0.0036	1.99	Q5I0C3	<i>Mccc1</i>	6.66	79279	6.43	72267	19	70	0.013
424	Methylcrotonoyl-Coenzyme A carboxylase 1 (Alpha)	0.016	1.59	Q5I0C3	<i>Mccc1</i>	6.66	79279	6.54	72468	25	89	0.00016
426	Methylcrotonoyl-Coenzyme A carboxylase 1 (Alpha)	0.00034	1.69	Q5I0C3	<i>Mccc1</i>	6.66	79279	6.62	72368	21	64	0.05
576	Serine/cysteine proteinase inhibitor, clade C, member 1	4.80E-05	2.93	Q5M7T5	<i>Serpinc1</i>	6.18	52201	5.10	65224	28	71	0.0091
579	Serine/cysteine proteinase inhibitor, clade C, member 1	6.10E-06	4.44	Q5M7T5	<i>Serpinc1</i>	6.18	52201	5.13	65405	43	96	2.90E-05
596	Serine/cysteine proteinase inhibitor, clade C, member 1	2.60E-08	4.31	Q5M7T5	<i>Serpinc1</i>	6.18	52201	5.17	65043	32	101	9.70E-06
609	Serine/cysteine proteinase inhibitor, clade C, member 1	9.80E-09	3.38	Q5M7T5	<i>Serpinc1</i>	6.18	52201	5.25	64148	35	115	3.90E-07
621	Serine/cysteine proteinase inhibitor, clade C, member 1	9.20E-05	1.75	Q5M7T5	<i>Serpinc1</i>	6.18	52201	5.30	64237	25	64	0.045
989	Eukaryotic translation initiation factor 4A1 (Mus musculus)	1.30E-05	2.17	Q5RK11	<i>Eif4a1</i>	5.33	46373	5.44	50403	34	90	0.00013
927	thioredoxin domain containing 4	0.0021	1.6	Q5VLR5	<i>Txndc4</i>	5.09	46848	5.30	52543	39	130	1.20E-08
1757	Rho GDP dissociation inhibitor (GDI) alpha	0.00076	2.01	Q5XI73	<i>Arhgdia</i>	5.12	23393	5.24	26241	33	81	0.001
206	2-oxoglutarate dehydrogenase E1 component, mitochondrial [Precursor]	8.80E-05	1.74	Q5XI78	<i>LOC360975</i>	6.00	111615	6.24	84989	17	70	0.013
213	2-oxoglutarate dehydrogenase E1 component, mitochondrial [Precursor]	4.60E-05	2.09	Q5XI78	<i>LOC360975</i>	6.00	111615	6.17	84636	14	79	0.0015
1168	Pyruvate dehydrogenase kinase 1	0.044	1.77	Q63065	<i>Pdk1</i>	6.46	46285	9.04	44927	23	56	0.05
633	Calcium binding protein	0.00033	2.14	Q63083	<i>Nucb1</i>	5.01	50888	5.20	62828	36	89	0.00016
855	vacuolar ATPase NG38, Bat1	0.00087	2.26	Q63413	<i>Bat1a</i>	5.44	49004	5.63	55384	27	66	0.032
1708	Proteasome (Prosome, macropain) 28 subunit	0.00093	1.51	Q63797	<i>Psme1</i>	5.77	28559	5.64	27968	41	90	0.00012
182	Vinculin (Mus musculus)	8.20E-07	3.3	Q64727	<i>Vcl_predicted</i>	5.77	116513	6.02	86894	20	78	0.0019
298	Tumor rejection antigen gp96 (Predicted)	0.0013	2.11	Q66HD0	<i>Tra1_predicted</i>	5.02	74162	5.06	80852	22	90	0.00012
410	NADH dehydrogenase	7.90E-06	1.8	Q66HF1	<i>Ndufs1</i>	5.28	76811	5.41	73581	21	82	0.00087
316	Gelsolin	1.00E-05	4.31	Q68FP1	<i>Gsn</i>	5.75	86014	5.76	79079	16	77	0.0027
320	Gelsolin	2.30E-05	5.41	Q68FP1	<i>Gsn</i>	5.75	86014	5.69	78970	16	60	0.02
944	Ubiquinol-cytochrome c reductase core protein I	0.0001	1.87	Q68FY0	<i>Uqcrc1</i>	5.22	49350	5.40	51892	25	78	0.0018
1160	Capping protein (Actin filament), gelsolin-like (Predicted)	0.00025	1.69	Q6AYC4	<i>Capg</i>	6.11	38775	6.08	44864	25	74	0.0053
1163	Capping protein (Actin filament), gelsolin-like (Predicted)	8.90E-05	2.61	Q6AYC4	<i>Capg</i>	6.11	38775	6.23	44864	25	74	0.0051
698	Rattus norvegicus tubulin, alpha 6,	0.041	1.68	Q6AYZ1	<i>Tuba6</i>	4.96	49905	5.31	59688	28	67	0.023
703	Rattus norvegicus tubulin, alpha 6	0.0016	1.81	Q6AYZ1	<i>Tuba6</i>	4.96	49905	5.25	59194	35	113	6.10E-07
715	Rattus norvegicus tubulin, alpha 6	0.00077	2.05	Q6AYZ1	<i>Tuba6</i>	4.96	49905	5.21	59112	27	80	0.0014

147	Spna2 protein	0.00024	2.34	Q6IRK8	<i>Spna2</i>	5.19	282206	5.23	91339	9	78	0.0017
717	Tubulin beta-2C chain	4.10E-05	2.57	Q6P9T8	<i>Tubb2c</i>	4.79	49769	5.19	59030	31	117	2.40E-07
765	Tubulin beta-2C chain	0.00013	2.33	Q6P9T8	<i>Tubb2c</i>	4.79	49769	5.11	57655	28	76	0.0027
343	aconitase 2, mitochondrial	8.10E-05	2.31	Q9ER34	<i>Aco2</i>	7.15	82410	7.73	76493	32	123	6.10E-08
344	aconitase 2, mitochondrial	7.20E-05	2.29	Q9ER34	<i>Aco2</i>	7.15	82410	7.95	76493	36	125	3.90E-08
357	aconitase 2, mitochondrial	0.0035	2.85	Q9ER34	<i>Aco2</i>	7.15	82410	6.99	76387	23	87	0.00026
359	aconitase 2, mitochondrial	6.00E-05	2.31	Q9ER34	<i>Aco2</i>	7.15	82410	7.58	76493	31	165	3.90E-12
360	aconitase 2, mitochondrial	6.60E-05	2.4	Q9ER34	<i>Aco2</i>	7.15	82410	8.23	76387	29	131	9.70E-09
364	aconitase 2, mitochondrial	6.60E-05	2.43	Q9ER34	<i>Aco2</i>	7.15	82410	7.12	76493	37	173	6.10E-13
366	aconitase 2, mitochondrial	0.00049	2.2	Q9ER34	<i>Aco2</i>	7.15	82410	7.33	82410	35	175	3.90E-13
384	aconitase 2, mitochondrial	0.0006	2.3	Q9ER34	<i>Aco2</i>	7.15	82410	8.43	75754	29	129	1.50E-08
386	aconitase 2, mitochondrial	0.033	1.73	Q9ER34	<i>Aco2</i>	7.15	82410	8.74	75127	26	98	1.80E-05
525	Apoptosis-inducing factor	0.00011	2.28	Q9JM53	<i>Pdcd8</i>	6.63	55481	8.31	68087	26	62	0.014
536	Apoptosis-inducing factor	0.00024	1.65	Q9JM53	<i>Pdcd8</i>	6.63	55481	7.29	67992	23	69	0.016
543	Apoptosis-inducing factor	1.20E-05	1.92	Q9JM53	<i>Pdcd8</i>	6.63	55481	7.64	67898	28	92	7.50E-05
288	Alpha actinin 4	7.90E-05	2.29	Q9QXQ0	<i>Actn4</i>	5.24	104720	5.37	80852	23	109	1.50E-06
289	Alpha actinin 4	5.90E-05	2.97	Q9QXQ0	<i>Actn4</i>	5.24	104720	5.40	80965	19	89	0.00017
1395	F-actin capping protein alpha-2 subunit (CapZ alpha-2)	1.10E-05	1.75	Q9WUV6	<i>Capza2</i>	7.59	34985	5.67	37833	41	74	0.0048