

ENTREZID	Majority.p	Gene.names	Number.o	Unique.pe	Sequence.	MS.MS.co	Q.value
87	A0A024R6	ACTN1	40	25	54.3	40	0
4644	A8CDT9;G	MYO5A	29	45	28.7	56	0
2314	Q13045;Q	FLII	12	2	41.5	4	0
116143	A0A140VK	WDR92;HZGJ	8	11	43.4	14	0
7798	A0A024RA	LUZP1	7	29	35.1	34	0
22994	B2RN10;Q	AZI1;CEP131	8	28	30	30	0
8725	Q6NX55;C	C19orf2;URI1	10	17	42.5	26	0
79657	Q9H6T3;Q	RPAP3	3	16	32.3	18	0
81	A0A0S2Z3	ACTN4	12	18	45.2	27	0
10096	A0A024RA	ACTR3	20	18	64.4	25	0
10109	Q53R19;O	ARPC2	8	16	54	31	0
55075	B7ZKM6;Q	UACA	10	17	14.2	23	0
22998	D6RD46;Q	LIMCH1	26	13	18.1	15	0
4641	F5H6E2;B7	MYO1C (ikk)	14	16	22.4	20	0
55011	A0A024Q2	FLJ20643;PIH1D1	15	9	52.4	11	0
5202	B1AQP2;Q	PFDN2	2	6	44.8	12	0
10097	P61160;P6	ACTR2	6	12	37.1	17	0
10471	Q5STK2;O	PFDN6	4	7	45.7	11	0
5339	Q15149-7	PLEC;PLEC1	17	14	3.8	14	0
54442	Q9NXV2;F	KCTD5	2	6	34.2	7	0
3326	B4DMA2;E	HSP90AB1	22	8	20.1	12	0
9948	Q53GN4;C	WDR1;HEL-S-52	11	11	25.6	13	0
NA	CON_Q3S	X14	1	4	13.8	5	0
6161	D3YTB1;A	RPL32	5	10	56.4	25	0
4659	B2RAH5;O	PPP1R12A	15	9	10.5	8	0
NA	L0R819;U3	ASNSD1	6	6	70.8	9	0
51366	E7EMW7;C	UBR5	6	7	3.4	6	0
1073	Q549N0;Q	CFL2	5	4	53.6	6	0
3192	Q96BA7;B	HNRNPU;HNRPU	7	9	17	9	0
8545	Q9UFW8;C	CGGBP1	2	5	33.5	5	0
5434	E5KT65;P1	POLR2E	6	4	31	5	0
6158	H0YKD8;P2	RPL28	10	8	33.5	13	0
81572	Q9NUG6	PDRG1	1	6	47.4	10	0
284119	B4DPZ5;B2	PTRF	6	4	11.3	3	0
5756	Q12792;Q	TWF1	9	5	13.7	7	0
7511	Q5T6H7;B	XPNPEP1	8	5	16.5	4	0
6633	P62316;K7	SNRPD2	4	5	36.4	5	0
8607	B5BUB1;Q	RUVBL1	8	6	17.3	6	0
1968	P41091;Q2	EIF2S3;EIF2S3L	4	5	11.7	5	0
81873	A0A024R8	ARPC5L	3	3	20.9	5	0
26065	Q8ND56-1	LSM14A	8	5	14.5	6	0
51637	Q5RLJ0;Q5	C14orf166	6	3	13.1	3	0
506	Q0QEN7;v	ATP5B;HEL-S-271	6	5	15.7	3	0
6233	Q5RKT7;B2	RPS27A;HEL112;UBA	38	2	37.2	5	0
3964	F6V2D4;A	LGALS8	14	5	19	5	0
5074	Q96IZ0	PAWR	4	3	12.1	5	0
4638	Q15746-4	MYLK	10	5	2.7	5	0
51493	Q9Y3I0;B4	RTCB	4	4	10.9	4	0
84687	D3DTX6;Q	PPP1R9B	11	4	7.1	4	0
11078	H0Y5J9;Q5	TRIOBP	10	4	19.9	3	0
4899	A0A024R7	NRF1	7	4	7.4	4	0
6144	G3V1B3;M	RPL21	6	3	39.1	5	0
84271	Q9BY77;F5	POLDIP3;PDIP46;DK	12	4	10	4	0
79026	Q8N274;Q	AHNAK	5	4	12.6	4	0
8409	A0A0C4D	FUXT	3	3	21.3	7	0
1613	B3KSK3;B3	DAPK3	3	3	15.2	3	0
6164	A0A024R	C RPL34	2	3	14.5	4	0

10726 Q9Y266 NUDC	4	3	11.5	4	0
2194 P49327;Q6 FASN	3	3	1.4	3	0
966 E9PNW4;C CD59	5	2	22.2	3	0
79784 Q7Z406;Q MYH14	7	2	7.6	36	0
1508 B4DL49;A6 CTSB;DKFZp686N01	18	2	7	3	0
8148 B4E312;A0 TAF15	4	2	7.8	3	0

Score	MS.MS.cot	MS.MS.cot	iBAQ	Symbol	Rank	IgG.1	rmp.1	im..IgG.1
323.31	11	29	34240000	ACTN1	156	11	29	FALSE
323.31	13	43	23183000	MYO5A	196	13	43	FALSE
323.31	0	4	876010	Q13045	483	0	4	TRUE
295.54	0	14	48109000	WDR92	125	0	14	TRUE
280.7	9	25	21173000	LUZP1	206	9	25	FALSE
275.76	0	30	20446000	AZI1	214	0	30	TRUE
246.76	0	26	1.93E+08	C19orf2	42	0	26	TRUE
199.78	0	18	24718000	RPAP3	187	0	18	TRUE
199.57	5	22	19095000	ACTN4	219	5	22	FALSE
179.64	4	21	99921000	ACTR3	80	4	21	FALSE
179.32	8	23	1.18E+08	ARPC2	66.5	8	23	FALSE
177.06	4	19	8442600	UACA	301	4	19	FALSE
156.61	3	12	7320400	LIMCH1	315	3	12	FALSE
155.98	4	16	10635000	MYO1C	280	4	16	FALSE
151.15	0	11	28946000	FLJ20643	175	0	11	TRUE
121.56	2	10	1.42E+08	PFDN2	62	2	10	FALSE
118.68	2	15	85694000	ACTR2	89	2	15	FALSE
111.08	0	11	1.37E+08	PFDN6	65	0	11	TRUE
110.12	0	14	933870	PLEC	477	0	14	TRUE
107.25	0	7	73727000	KCTD5	100	0	7	TRUE
101.86	3	9	13143000	HSP90AB1	258	3	9	FALSE
90.975	0	13	10655000	WDR1	279	0	13	TRUE
78.104	0	5	2516900	CON_Q39	416	0	5	TRUE
76.099	6	19	3.01E+08	RPL32	22	6	19	FALSE
72.109	1	7	7801800	PPP1R12A	308	1	7	FALSE
66.999	0	9	2.51E+08	ASNSD1	30	0	9	TRUE
59.096	0	6	563620	UBR5	504	0	6	TRUE
58.821	1	5	14101000	CFL2	252	1	5	FALSE
58.418	1	8	12716000	HNRNPU	264	1	8	FALSE
57.3	0	5	32120000	CGGBP1	165	0	5	TRUE
56.909	0	5	15404000	POLR2E	239	0	5	TRUE
54.259	3	10	62748000	RPL28	113	3	10	FALSE
54.052	0	10	76223000	PDRG1	96	0	10	TRUE
53.501	0	3	9170300	PTRF	295	0	3	TRUE
52.47	1	6	4476400	TWF1	355	1	6	FALSE
49.947	0	4	4988100	XPNPEP1	350	0	4	TRUE
42.087	1	4	29360000	SNRPD2	172	1	4	FALSE
40.121	0	6	4371200	RUVBL1	357	0	6	TRUE
39.529	0	5	1874400	EIF2S3	439	0	5	TRUE
38.863	1	4	62938000	ARPC5L	111	1	4	FALSE
36.492	1	5	13727000	LSM14A	254	1	5	FALSE
35.575	0	3	5632400	C14orf166	334	0	3	TRUE
35.065	0	3	3515600	ATP5B	385	0	3	TRUE
32.736	1	4	43932000	RPS27A	137	1	4	FALSE
32.655	0	5	8303000	LGALS8	302	0	5	TRUE
29.927	1	4	15201000	PAWR	243	1	4	FALSE
28.129	0	5	486350	MYLK	507	0	5	TRUE
27.494	0	4	3117300	RTCB	397	0	4	TRUE
26.97	0	4	3132000	PPP1R9B	395	0	4	TRUE
26.931	0	3	5190400	TRIOBP	342	0	3	TRUE
26.83	0	4	16338000	NRF1	232	0	4	TRUE
25.154	1	4	36472000	RPL21	149	1	4	FALSE
25.126	0	4	3264000	POLDIP3	393	0	4	TRUE
21.299	0	4	212180	AHNAK	530	0	4	TRUE
21.079	0	7	28710000	UXT	179	0	7	TRUE
20.051	0	3	12654000	DAPK3	265	0	3	TRUE
18.884	0	4	41689000	RPL34	141	0	4	TRUE

18.099	0	4	4839500 NUDC	352	0	4	TRUE
17.271	0	3	157850 FASN	533	0	3	TRUE
16.574	0	3	22032000 CD59	202	0	3	TRUE
12.406	6	30	63665000 MYH14	110	6	30	FALSE
11.845	0	3	3643800 CTSB	380	0	3	TRUE
11.628	0	3	6855900 TAF15	323	0	3	TRUE

im..rmp.1	IgG	rmp	fc..rmp.lgC	class..rmp.	Alias	preferred_	protein_siz	annotator
FALSE		11	29	1.022347	T	ACTN1	ACTN1	914 actinin, al
FALSE		13	43	1.348838	T	MYO5A	MYO5A	1855 myosin VA
FALSE		0	4	2.07864	T	FLII	FLII	1269 flightless I
FALSE		0	14	3.618745	T	HZGJ;WDF	WDR92	357 WD repeat
FALSE		9	25	1.080695	T	LUZP1	LUZP1	1076 leucine zip
FALSE		0	30	4.654245	T	CEP131;AZ	AZI1	1080 5-azacytid
FALSE		0	26	4.456581	T	C19orf2;UI	URI1	535 URI1, pref
FALSE		0	18	3.954978	T	RPAP3	RPAP3	665 RNA polyn
FALSE		5	22	1.642508	T	ACTN4	ACTN4	911 actinin, al
FALSE		4	21	1.842091	T	ACTR3	ACTR3	418 ARP3 actir
FALSE		8	23	1.118324	T	ARPC2	ARPC2	300 actin relate
FALSE		4	19	1.706148	T	UACA	UACA	1416 uveal auto
FALSE		3	12	1.415795	T	LIMCH1	LIMCH1	1083 LIM and ca
FALSE		4	16	1.474707	T	MYO1C	MYO1C	1063 myosin IC;
FALSE		0	11	3.302501	T	FLJ20643;F	PIH1D1	290 PIH1 dom
FALSE		2	10	1.594584	T	PFDN2	PFDN2	154 prefoldin s
FALSE		2	15	2.125467	T	ACTR2	ACTR2	399 ARP2 actir
FALSE		0	11	3.302501	T	PFDN6	NA	NA
FALSE		0	14	3.618745	T	PLEC;PLEC	PLEC	4684 plectin
FALSE		0	7	2.731651	T	KCTD5	KCTD5	234 potassium
FALSE		3	9	1.045128	T	HSP90AB1	HSP90AB1	724 heat shock
FALSE		0	13	3.520836	T	WDR1;HEL	WDR1	606 WD repeat
FALSE		0	5	2.33059	T		NA	NA
FALSE		6	19	1.220721	T	RPL32	RPL32	135 ribosomal
FALSE		1	7	1.731651	T	PPP1R12A	PPP1R12A	1030 protein ph
FALSE		0	9	3.045128	T	ASNSD1	NA	NA
FALSE		0	6	2.545013	T	UBR5	UBR5	2799 ubiquitin p
FALSE		1	5	1.33059	T	CFL2	CFL2	166 cofilin 2 (n
FALSE		1	8	1.896887	T	HNRNPU;H	HNRNPU	825 heterogen
FALSE		0	5	2.33059	T	CGGBP1	CGGBP1	167 CGG triple
FALSE		0	5	2.33059	T	POLR2E	POLR2E	210 polymeras
FALSE		3	10	1.179546	T	RPL28	RPL28	169 ribosomal
FALSE		0	10	3.179546	T	PDRG1	PDRG1	133 p53 and D
FALSE		0	3	1.77318	T	CAVIN1	SKOR1	965 SKI family
FALSE		1	6	1.545013	T	TWF1	TWF1	357 twinfilin, a
FALSE		0	4	2.07864	T	XPNPEP1	XPNPEP1	666 X-prolyl ar
FALSE		1	4	1.07864	T	SNRPD2	SNRPD2	118 small nucle
FALSE		0	6	2.545013	T	RUVBL1	RUVBL1	456 RuvB-like
FALSE		0	5	2.33059	T	EIF2S3;EIF	EIF2S3	472 eukaryotic
FALSE		1	4	1.07864	T	ARPC5L	ARPC5L	153 actin relate
FALSE		1	5	1.33059	T	LSM14A	LSM14A	463 LSM14A, S
FALSE		0	3	1.77318	T	C14orf166	C14orf166	244 chromosom
FALSE		0	3	1.77318	T	ATP5B	ATP5B	529 ATP synth
FALSE		1	4	1.07864	T	UBC;UBB;L	RPS27A	156 ribosomal
FALSE		0	5	2.33059	T	LGALS8	LGALS8	359 lectin, gala
FALSE		1	4	1.07864	T	PAWR	PAWR	340 PRKC, apo
FALSE		0	5	2.33059	T	MYLK	MYLK	1914 myosin lig
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FALSE		0	4	2.07864	T	PPP1R9B	NA	NA
FALSE		0	3	1.77318	T	TRIOBP	TRIOBP	2365 TRIO and I
FALSE		0	4	2.07864	T	NRF1	NRF1	503 nuclear res
FALSE		1	4	1.07864	T	RPL21	RPL21	160 ribosomal
FALSE		0	4	2.07864	T	POLDIP3;P	POLDIP3	421 polymeras
FALSE		0	4	2.07864	T	AHNAK	AHNAK	5890 AHNAK nu
FALSE		0	7	2.731651	T	UXT	UXT	169 ubiquitous
FALSE		0	3	1.77318	T	DAPK3	DAPK3	454 death-assc
FALSE		0	4	2.07864	T	RPL34	RPL34	117 ribosomal

FALSE	0	4	2.07864 T	NUDC	NUDC	331 nuclear dis
FALSE	0	3	1.77318 T	FASN	FASN	2511 fatty acid s
FALSE	0	3	1.77318 T	CD59	CD59	128 CD59 mole
FALSE	6	30	1.84689 T	MYH14	MYH14	2036 myosin, he
FALSE	0	3	1.77318 T	CTSB;DKFZ	CTSB	339 cathepsin
FALSE	0	3	1.77318 T	TAF15	TAF15	592 TAF15 RN/

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