						1092.14	2	2.73	299-308	AAKDEVSESR
						992.10	2	2.54	315-322	TLEIEACR
						1565.69	2	3.25	339-352	QNADISAM*QDTINK
						1526.76	2	3.70	367-378	YLKEYQDLLNVK
						1410.67	2	3.13	379-390	M*ALDIEIAAYRK
						1075.20	2	2.60	390-398	KLLEGEETR
9	Calreticulin	P27797	48.1	4.29	15.59					
						1411.46	2	2.15	25-36	EQFLDGDGWTSR
						1131.17	2	2.25	56-64	FYGDEEKDK
						1608.78	2	4.37	74-87	FYALSASFEPFSNK
						1477.55	2	3.88	99-111	HEQNIDCGGGYVK
						1020.21	2	2.19	144-151	VHVIFNYK
						1085.28	2	2.15	154-162	NVLINKDIR
10	Protein disulfide-isomerase	P07237	57.1	4.76	5.12					
						1781.86	2	4.53	82-97	VDATEESDLAQQYGVR
						1223.42	2	2.17	317-326	LITLEEEM*TK
11	60 kDa heat shock protein, mitochondrial	P10809	61.1	5.70	15.36					
						913.14	2	3.36	293-301	VGLQVVAVK
						962.05	2	2.05	302-310	APGFGDNRK
						1647.96	2	3.35	345-359	VGEVIVTKDDAM*LLK
						902.07	2	3.18	397-405	LSDGVAVLK
						1362.47	2	4.04	406-418	VGGTSDVEVNEKK
						961.06	2	3.53	421-429	VTDALNATR
						1772.93	2	3.83	447-462	CIPALDSLTPANEDQK
						942.18	2	2.79	463-470	IGIEIIKR
11	Pyruvate kinase, isozymes M1/M2	P14618	57.8	7.95	3.58					
						1214.37	2	2.21	141-150	ITLDNAYM*EK
						996.17	2	2.76	489-497	VNFAM*NVGK
12	Vimentin	P08670	53.5	5.06	39.57					
						1429.56	2	2.47	50-63	SLYASSPGGVYATR
						1588.70	2	3.43	100-112	TNEKVELQELNDR
						1126.29	2	2.94	113-121	FANYIDKVR
						1540.83	2	3.46	129-142	ILLAELEQLKGQGK

						1217.32	2	2.63	158-167	RQVDQLTNDK
						1320.50	2	2.23	186-195	EKLQEEM*LQR
						1324.38	2	2.76	196-206	EEAENTLQSFR
						1089.14	2	2.48	207-216	QDVDNASLAR
						1662.95	3	4.29	222-235	KVESLQEEIAFLKK
						1094.16	2	3.09	294-303	FADLSEAANR
						1491.66	2	2.61	321-333	QVQSLTCEVDALK
						1767.97	2	2.28	364-377	LQDEIQNM*KEEM*AR
						1312.52	2	3.56	390-400	M*ALDIEIATYR
						933.00	2	2.14	402-409	LLEGEESR
13	Vacuolar ATP synthase subunit B, brain isoform	P21281	56.5	5.57	5.09					
						1091.20	2	2.52	83-93	SGQVLEVSGSK
						1521.70	2	4.88	94-108	AVVQVFEGTSGIDAK
14	Vacuolar ATP synthase subunit B, brain isoform	P21281	56.5	5.57	7.24					
						1091.20	2	2.67	83-93	SGQVLEVSGSK
						1521.70	2	4.13	94-108	AVVQVFEGTSGIDAK
						1309.41	2	2.86	461-471	NFIAQGPYENR
15	Tubulin alpha-3 chain	Q71U36	50.1	4.94	17.29					
						1702.93	2	3.77	65-79	AVFVDLEPTVIDEVR
						1086.26	2	2.29	113-121	EIIDLVLDR
						910.05	2	2.17	157-164	LSVDYGKK
						979.07	2	2.46	222-229	PTYTNLNR
						1016.17	2	2.82	327-336	DVNAAIATIK
						1882.12	2	4.28	374-390	AVCM*LSNTTAIAEAWAR
						1397.63	2	2.64	391-401	LDHKFDLM*YAK
15	Tubulin alpha-1 chain	P68366	49.9	4.95	14.96					
						910.05	2	2.17	157-164	LSVDYGKK
						979.07	2	2.46	222-229	PTYTNLNR
						986.15	2	3.24	327-336	DVNAAIAAIK
						1585.78	2	3.77	340-352	SIQFVDWCPTGFK
						1882.12	2	4.28	374-390	AVCM*LSNTTAIAEAWAR
						1397.63	2	2.64	391-401	LDHKFDLM*YAK
16	S-arrestin	P10523	45.1	6.14	3.70					

17	S-arrestin	P10523	45.1	6.14	19.01					
						1199.38	2	2.50	10-19	SEPNHVIFKK
						1358.60	2	3.20	60-70	KVYVTLTCAFR
						957.07	2	3.00	85-91	RDLYFSR
						959.17	2	2.37	107-114	LQESLLKK
						1339.61	2	3.45	281-292	TLTLLPLLANNR
						1670.89	2	3.05	303-317	IKHEDTNLASSTIIK
						1554.65	2	3.27	385-398	HNLKDAGEAEEGKR
18	S-arrestin	P10523	45.1	6.14	22.96					
						1199.38	2	2.63	10-19	SEPNHVIFKK
						1358.60	2	3.76	60-70	KVYVTLTCAFR
						957.07	2	2.78	85-91	RDLYFSR
						1515.74	2	2.57	92-106	VQVYPPVGAASTPTK
						1339.61	2	3.24	281-292	TLTLLPLLANNR
						1670.89	2	3.10	303-317	IKHEDTNLASSTIIK
						1334.63	2	2.54	323-334	TVLGILVSYQIK
						1279.45	2	2.29	359-369	LM*HPQPEDPAK
19	Tubulin beta-2C chain	P68371	49.8	4.79	19.55					
						1618.84	2	2.97	63-77	AVLVDLEPGTM*DSVR
						1078.16	2	2.41	155-162	IREEYPDR
						1336.58	2	3.03	163-174	IM*NTFSVVPSPK
						1131.27	2	2.70	242-251	FPGQLNADLR
						1288.59	2	2.62	252-262	KLAVNM*VPFPR
						1463.60	2	3.53	325-336	EVDEQM*LNVQNK
						1029.16	2	2.09	351-359	TAVCDIPPR
						1246.42	2	3.46	381-390	ISEQFTAM*FR
19	Tubulin beta-2 chain	P07437	49.7	4.78	18.92					
						1302.42	2	2.32	47-58	ISVYYNEATGGK
						1078.16	2	2.41	155-162	IREEYPDR
						1336.58	2	3.03	163-174	IM*NTFSVVPSPK
						1131.27	2	2.70	242-251	FPGQLNADLR
						1288.59	2	2.62	252-262	KLAVNM*VPFPR
						1463.60	2	3.53	325-336	EVDEQM*LNVQNK

						1246.42	2	3.46	381-390	ISEQFTAM*FR
19	Tubulin beta-3 chain	Q13509	50.4	4.83	16.89					
						1336.58	2	3.03	163-174	IM*NTFSVVPSPK
						1131.27	2	2.70	242-251	FPGQLNADLR
						1288.59	2	2.62	252-262	KLAVNM*VPFPR
						1917.22	2	3.49	321-336	M*SM*KEVDEQM*LAIQSK
						1407.57	2	3.39	325-336	EVDEQM*LAIQSK
						1891.14	2	2.86	363-379	M*SSTFIGNSTAIQELFK
						1246.42	2	3.46	381-390	ISEQFTAM*FR
19	Tubulin beta-6 chain	Q9BUF5	49.9	4.77	11.88					
						1062.16	2	2.43	155-162	IREEFPDR
						1384.65	2	3.19	163-174	IM*NTFSVM*PSPK
						1131.27	2	2.70	242-251	FPGQLNADLR
						1288.59	2	2.62	252-262	KLAVNM*VPFPR
						1407.57	2	3.39	325-336	EVDEQM*LAIQSK
20	ATP synthase beta chain, mitochondrial	P06576	56.6	5.26	25.90					
						1651.89	2	3.47	95-109	LVLEVAQHLGESTVR
						1279.45	2	2.74	110-121	TIAM*DGTEGLVR
						976.15	2	2.62	202-212	IGLFGGAGVGK
						1474.79	2	3.98	213-225	TVLIM*ELINNVAK
						1407.52	2	3.29	226-239	AHGGYSVFAGVGER
						1618.84	2	3.08	265-279	VALVYGQM*NEPPGAR
						1440.67	2	3.12	282-294	VALTGLTVAEYFR
						1436.60	2	3.73	311-324	FTQAGSEVSALLGR
21	Gamma-enolase	P09104	47.1	4.91	12.47					
						1131.31	2	2.83	183-192	LGAEVYHTLK
						1225.33	2	2.44	228-238	EAIDKAGYTEK
						992.18	2	2.73	335-342	ACNCLLLK
						1618.81	2	3.76	343-357	VNQIGSVTEAIQACK
						1161.20	2	2.78	412-421	IEEELGDEAR
22	Eukaryotic initiation factor 4A-II	Q14240	46.4	5.33	16.22					
						1829.05	2	2.85	47-62	GIYAYGFEKPSAIQQR
						1545.77	2	3.71	148-162	LQAEAPHIVVGTPGR

						1516.72	2	3.22	192-203	GFKDQIYEIFQK
						1160.34	2	2.84	239-248	KEELTLEGIK
22	Eukaryotic initiation factor 4A-I	P60842	46.2	5.32	12.56					
						1829.05	2	2.85	46-61	GIYAYGFEKPSAIQQR
						1588.79	2	4.36	178-190	M*FVLDEADEM*LSR
						1502.70	2	3.72	191-202	GFKDQIYDIFQK
						1188.36	2	2.70	238-247	KEELTLEGIR
23	Alpha-enolase	P06733	47.0	6.99	31.41					
						1407.55	2	3.63	15-27	GNPTVEVDLFTSK
						1806.01	2	3.98	32-49	AAVPSGASTGIYEALELR
						1445.64	2	4.12	80-91	KLNVTEQEKIDK
						1669.90	2	3.20	89-102	IDKLM*IEM*DGTENK
						1144.31	2	2.75	183-192	IGAEVYHNLK
						1962.06	2	4.92	202-220	DATNVGDEGGFAPNILENK
						1557.80	2	3.78	239-252	VVIGM*DVAASEFFR
						1827.93	2	4.17	253-268	SGKYDLDFKSPDDPSR
						1426.60	2	2.90	269-280	YISPDQLADLYK
24	Alpha-enolase	P06733	47.0	6.99	24.71					
						1407.55	2	3.36	15-27	GNPTVEVDLFTSK
						1445.64	2	3.59	80-91	KLNVTEQEKIDK
						1669.90	2	3.48	89-102	IDKLM*IEM*DGTENK
						1528.73	2	2.17	92-104	LM*IEM*DGTENKSK
						1941.31	2	4.48	162-178	LAM*QEFM*ILPVGAANFR
						1144.31	2	3.10	183-192	IGAEVYHNLK
						1827.93	2	3.90	253-268	SGKYDLDFKSPDDPSR
						1426.60	2	3.30	269-280	YISPDQLADLYK
						1542.75	2	3.03	358-371	LAQANGWGVM*VSHR
25	Alpha-enolase	P06733	47.0	6.99	14.32					
						1445.64	2	4.73	80-91	KLNVTEQEKIDK
						1669.90	2	3.19	89-102	IDKLM*IEM*DGTENK
						1144.31	2	3.34	183-192	IGAEVYHNLK
						1073.18	2	2.89	253-261	SGKYDLDFK
						1426.60	2	2.46	269-280	YISPDQLADLYK

26	Alpha-enolase	P06733	47.0	6.99	22.86					
						1407.55	2	2.80	15-27	GNPTVEVDLFTSK
						1806.01	2	3.94	32-49	AAVPSGASTGIYEALELR
						1445.64	2	3.15	80-91	KLNVTEQEKIDK
						1669.90	2	3.45	89-102	IDKLM*IEM*DGTENK
						1144.31	2	2.85	183-192	IGAEVYHNLK
						1557.80	2	3.19	239-252	VVIGM*DVAASEFFR
						1073.18	2	2.98	253-261	SGKYDLDFK
						1426.60	2	2.89	269-280	YISPDQLADLYK
27	Actin, cytoplasmic 1	P60709	41.7	5.29	16.53					
						977.01	2	2.03	19-28	AGFAGDDAPR
						1955.24	2	3.09	96-113	VAPEEHPVLLTEAPLNPK
						1015.16	2	2.03	184-191	DLTDYLM*K
						1133.19	2	2.38	197-206	GYSFTTTAER
						1791.94	2	3.81	239-254	SYELPDGQVITIGNER
27	Actin, cytoplasmic 2	P63261	41.8	5.31	16.53					
						977.01	2	2.03	19-28	AGFAGDDAPR
						1955.24	2	3.09	96-113	VAPEEHPVLLTEAPLNPK
						1015.16	2	2.03	184-191	DLTDYLM*K
						1133.19	2	2.38	197-206	GYSFTTTAER
						1791.94	2	3.81	239-254	SYELPDGQVITIGNER
27	Actin, gamma-enteric smooth muscle	P63267	41.9	5.31	11.70					
						977.01	2	2.03	20-29	AGFAGDDAPR
						1015.16	2	2.03	185-192	DLTDYLM*K
						1131.22	2	3.13	198-207	GYSFVTTAER
						1791.94	2	3.81	240-255	SYELPDGQVITIGNER
27	Actin, aortic smooth muscle	P62736	42.0	5.24	11.67					
						977.01	2	2.03	21-30	AGFAGDDAPR
						1015.16	2	2.03	186-193	DLTDYLM*K
						1131.22	2	3.13	199-208	GYSFVTTAER
						1791.94	2	3.81	241-256	SYELPDGQVITIGNER
28	Creatine kinase B-type	P12277	42.6	5.34	14.17					
						1587.76	2	4.07	157-172	LAVEALSSLDGDLAGR

						1866.17	2	4.78	342-358	LGFSEVELVQM*VVDGVK
						1048.24	2	2.56	359-366	LLIEM*EQR
29	Glutamine synthetase	P15104	41.9	6.42	6.45					
						957.07	2	3.34	106-113	RPAETNLR
						1003.09	2	2.36	173-180	DIVEAHYR
						995.11	2	2.24	268-275	YIEEAIEK
30	Glutamine synthetase	P15104	41.9	6.42	24.73					
						1826.07	2	3.81	25-40	VQAM*YIWIDGTGEGLR
						957.07	2	3.16	106-113	RPAETNLR
						1003.09	2	2.66	173-180	DIVEAHYR
						1064.20	2	2.03	259-267	AM*REENGLK
						1323.52	2	2.40	268-278	YIEEAIEKLSK
						914.99	2	2.42	333-339	KGYFEDR
						1934.14	2	3.36	340-356	RPSANCDPFSVTEALIR
						1930.05	2	3.96	357-372	TCLLNETGDEPFQYKN
31	Glutamine synthetase	P15104	41.9	6.42	6.45					
						957.07	2	2.95	106-113	RPAETNLR
						1930.05	2	4.01	357-372	TCLLNETGDEPFQYKN
32	L-lactate dehydrogenase B chain	P07195	36.5	5.72	7.51					
						1511.66	2	2.81	77-90	IVADKDYSVTANSK
						1284.51	2	2.51	233-243	M*VVESAYEVIK
33	L-lactate dehydrogenase B chain	P07195	36.5	5.72	27.03					
						1953.18	2	3.39	5-22	EKLIAPVAEEEATVPNNK
						1630.82	2	4.75	43-57	SLADELALVDVLEDK
						1511.66	2	3.21	77-90	IVADKDYSVTANSK
						914.13	2	2.61	91-99	IVVVTAGVR
						1249.35	2	3.70	158-169	VIGSGCNLDSAR
						1284.51	2	3.38	233-243	M*VVESAYEVIK
						1287.49	2	3.76	308-318	LKDDEVAQLKK
34	L-lactate dehydrogenase B chain	P07195	36.5	5.72	39.04					
						1953.18	2	4.08	5-22	EKLIAPVAEEEATVPNNK
						1630.82	2	4.80	43-57	SLADELALVDVLEDK
						1965.24	2	3.41	60-76	GEM*M*DLQHGSLFLQTPK

						914.13	2	2.82	91-99	IVVVTAGVR
						720.84	1	1.94	113-118	NVNVFK
						958.22	1	1.64	119-126	FIIPQIVK
						1249.35	2	2.59	158-169	VIGSGCNLDSAR
						1284.51	2	3.41	233-243	M*VVESAYEVIK
						960.11	2	2.08	299-307	GLTSVINQK
						1287.49	2	4.09	308-318	LKDDEVAQLKK
35	Cellular retinaldehyde-binding protein	P12271	36.3	4.98	22.15					
						1032.17	2	2.70	19-27	AQLEQLTTK
						975.04	2	2.79	47-54	AKDELNER
						1326.48	2	2.64	87-97	VQEKDSGFFLR
						1865.08	2	4.39	121-136	LQYPELFDSLSPEAVR
						1510.67	2	3.92	137-150	CTIEAGYPGVLSSR
						1442.65	2	3.39	222-233	M*VDM*LQDSFPAR
36	Inorganic pyrophosphatase	Q15181	32.7	5.54	11.76					
						1486.76	2	3.04	58-70	M*EIATKDPLNPIK
						1267.46	2	2.46	64-74	DPLNPIKQDVK
						1178.36	2	3.16	212-221	DKDFAIDIIK
36	Guanine nucleotide-binding protein G(I)/G(S)/G(T) beta subunit 1	P62873	37.2	5.60	6.49					
						1018.15	2	2.72	68-77	LLVSASQDGK
						1226.35	2	3.33	197-208	LFVSGACDASAK
37	Inorganic pyrophosphatase	Q15181	32.7	5.54	14.88					
						1486.76	2	3.02	58-70	M*EIATKDPLNPIK
						1267.46	2	2.30	64-74	DPLNPIKQDVK
						1807.06	2	4.83	140-155	VLGILAM*IDEGETDWK
						1178.36	2	3.34	212-221	DKDFAIDIIK
37	Guanine nucleotide-binding protein G(I)/G(S)/G(T) beta subunit 1	P62873	37.2	5.60	11.50					
						1018.15	2	2.65	68-77	LLVSASQDGK
						805.99	1	1.98	89-95	VHAIPLR
						1226.35	2	3.55	197-208	LFVSGACDASAK
						1010.09	2	2.25	304-313	AGVLAGHDNR
38	Malate dehydrogenase, mitochondrial	P40926	35.5	8.92	19.82					
						993.14	2	2.46	177-185	ANTFVAELK

						1471.62	2	3.51	242-257	AGAGSATLSM*AYAGAR
						1344.56	2	2.72	258-269	FVFSLVDAM*NGK
						1154.29	2	2.44	270-279	EGVVECSFVK
						1133.34	2	2.78	315-324	M*ISDAIPELK
38	Glyceraldehyde-3-phosphate dehydrogenase	P04406	35.9	8.58	10.78					
						910.01	2	2.38	107-116	AGAHLQGGAK
						1764.88	2	3.62	309-322	LISWYDNEFGYSNR
						1363.59	2	2.93	323-334	VVDLM*AHM*ASKE
39	14-3-3 protein epsilon	P62258	29.2	4.63	14.51					
						1464.63	2	2.39	30-42	VAGM*DVELTVEER
						1418.58	2	2.48	62-73	IISSIEQKEENK
						1385.51	2	2.67	131-142	YLAEFATGNDRK
40	14-3-3 protein zeta/delta	P63104	27.7	4.73	14.69					
						1549.58	2	3.39	28-41	SVTEQGAELSNEER
						1280.41	2	3.05	128-139	YLAEVAAGDDKK
						1206.44	2	2.96	213-222	DSTLIM*QLLR
40	14-3-3 protein theta	P27348	27.8	4.68	14.69					
						1533.58	2	3.62	28-41	AVTEQGAELSNEER
						1321.46	2	2.66	104-115	YLIANATNPESK
						1206.44	2	2.96	213-222	DSTLIM*QLLR
40	14-3-3 protein gamma	P61981	28.2	4.80	13.82					
						1644.72	2	3.64	28-41	NVTELNEPLSNEER
						1081.20	2	2.67	132-141	YLAEVATGEK
						1206.44	2	2.96	217-226	DSTLIM*QLLR
41	Recoverin	P35243	23.0	5.06	10.05					
						1455.64	2	3.18	43-54	ITQQQFQSIYAK
						949.11	2	2.47	131-138	M*ITPEDVK
42	Alpha crystallin A chain	P02489	19.9	5.77	16.76					
						981.21	2	2.09	71-78	FVIFLDVK
						1173.30	2	2.45	79-88	HFSPEDLTVK
						1287.40	2	3.22	89-99	VQDDFVEIHGK
43	Nucleoside diphosphate kinase A	P15531	17.1	5.83	18.42					
						985.21	2	2.11	19-27	GLVGEIIKR

						1052.16	2	2.22	106-114	GDFCIQVGR
44	Hemoglobin beta subunit	P68871	15.9	6.81	22.60					
						953.08	2	2.67	1-8	VHLTPEEK
						1315.42	2	3.36	18-30	VNVDEVGGEALGR
						1150.36	2	3.22	133-144	VVAGVANALAHK
45	Hemoglobin beta subunit	P68871	15.9	6.81	22.60					
						953.08	2	2.26	1-8	VHLTPEEK
						1315.42	2	2.52	18-30	VNVDEVGGEALGR
						1150.36	2	2.94	133-144	VVAGVANALAHK
46	Hemoglobin alpha subunit	P69905	15.1	8.73	23.40					
						1530.62	2	3.16	17-31	VGAHAGEYGAEALER
						1088.30	2	2.11	32-40	M*FLSFPTTK
						1088.29	2	2.68	91-99	LRVDPVNFK

Table 2

Proteins identified from spots detected only macular retina.

Proteins from macular unique spots by LC-MS/MS and listed.

(a)Spot ID corresponds to the numbers on gel images in figure 1 - 4.

(b)Accession no. corresponds to UniProtKB/Swiss-Prot database (Release 48.8).

(c)MW and pI are theoretical scores by Bioworks ver.3.1.

*Oxidation of methonine.

Spot no.[a]	Protein name	Database Accession no.[b]	MW (kDa)[c]	pI[c]	Sequence coverage (%)	Precursor ion MH+	Charge	XC	Residue	Sequence
M1	Pyruvate kinase, isozymes M1/M2	P14618	32.7	4.69	18.11					
						1198.35	2	3.10	32-42	LDIDSPPITAR
						1360.53	2	4.43	43-55	NTGIICTIGPASR
						1194.43	2	2.70	56-65	SVETLKEM*IK
						914.08	2	2.50	106-114	PVAVALDTK
						1119.25	2	2.86	125-135	GSGTAEVELKK
						1463.70	2	4.32	173-185	IYVDDGLISLQVK
						1780.91	2	4.61	188-205	GADFLVTEVENGGSLGSK
						1142.28	2	2.96	294-304	GDLGIEIPAEK
M2	Tropomyosin 1 alpha chain	P09493	32.7	4.69	13.73					
						1400.56	2	2.95	91-101	RIQLVEEELDR
						1728.89	2	3.24	92-105	IQLVEEELDRAQER
						1315.54	2	3.69	168-178	KLVIIESDLER
						1672.86	2	2.58	169-182	LVIIESDLERAEER
						1121.21	2	2.35	190-198	CAELEEELK
M2	Heterogeneous nuclear ribonucleoproteins C1/C2	P07910	33.7	4.95	16.67					
						1317.60	2	4.08	18-29	VFIGNLNTLVVK
						1330.47	2	4.35	51-61	GFAFVQYVNER
						1700.00	2	4.50	74-89	M*IAGQVLDINLAAEPK
						1416.60	2	3.49	205-216	QKVDSLLENLEK
M3	Transaldolase	P37837	37.5	6.36	16.62					
						1051.20	2	2.82	11-19	M*ESALDQLK
						1792.15	2	4.16	82-97	NAIDKLFVLFGAEILK
						1269.45	2	2.86	111-121	LSFDKDAM*VAR
						1234.34	2	2.50	205-215	SYEPLEDPGVK
						998.18	2	2.78	231-239	TIVM*GASFR
M3	3'(2'),5'-bisphosphate nucleotidase 1	O95861	33.4	5.46	10.06					
						1151.34	2	3.98	11-21	LVASAYSIAQK
						1243.43	2	4.16	29-40	VIAEGDLGIVEK
						914.13	2	2.84	225-232	IIQLIEGK
M4	Poly(rC)-binding protein 1	Q15365	37.5	6.66	16.85					
						1289.37	2	3.24	47-57	INISEGNCPER
						925.13	2	2.25	71-78	AFAM*IIDK

						1087.17	2	2.54	315-325	IANPVEGSSGR
M5	Crk-like protein	P46109	33.8	6.26	7.59					
						1229.45	2	3.50	254-265	TALALEVGDIVK
						1318.33	2	2.79	293-303	IFDPQNPDENE
M6	Heterogeneous nuclear ribonucleoproteins A2/B1	P22626	37.4	8.97	4.53					
						1800.00	2	4.85	23-38	LFIGGLSFETTEESLR
M7	Heterogeneous nuclear ribonucleoproteins A2/B1	P22626	37.4	8.97	11.90					
						1928.18	2	4.47	22-38	KLFIGGLSFETTEESLR
						1189.34	2	3.72	138-147	IDTIEIITDR
						1696.80	2	3.17	154-168	GFGFVTFDDHDPVDK
M8	Voltage-dependent anion-selective channel protein 2	P45880	38.1	6.32	9.80					
						941.03	2	2.25	193-200	NNFAVGYR
						1722.92	2	3.22	263-278	VNNSSLIGVGYTQTLR
						1017.20	2	2.81	283-292	LTLSALVDGK
M9	Voltage-dependent anion-selective channel protein 1	P21796	30.6	8.63	7.80					
						1415.52	2	2.03	224-235	YQIDPDACFSAK
						1031.23	2	3.29	256-265	LTLSALLDGK
M10	Voltage-dependent anion-selective channel protein 1	P21796	30.6	8.63	15.60					
						1960.99	2	5.74	34-52	SENGLEFTSSGSANTETTK
						1529.68	2	3.53	96-109	LTFDSSFSPNTGKK
						1214.35	2	3.32	163-173	VTQSNFAVGYK
M11	Endoplasmic reticulum protein ERp29	P30040	29.0	6.77	27.59					
						1325.54	2	2.88	37-48	GALPLDTVTFYK
						1248.32	2	2.61	60-69	FDTQYPYGEK
						1321.51	2	2.43	113-122	ESYPVFYLFR
						1609.72	2	3.64	123-137	DGDFENPVPYTGAVK
						1725.86	2	4.72	209-223	ILDQGEDFPASEM*TR
						1135.34	2	3.65	244-253	SLNILTAFQK
M12	Guanylate kinase	Q16774	21.6	6.11	13.27					
						1069.24	2	2.84	5-16	PVVLSGPSGAGK
						1675.78	2	3.85	44-57	PGEENGKDYYFVTR
M13	Guanylate kinase	Q16774	21.6	6.11	19.39					
						1069.24	2	3.39	5-16	PVVLSGPSGAGK
						1675.78	2	4.23	44-57	PGEENGKDYYFVTR
						1387.60	2	3.71	96-107	ICVLDVDLQGVR

						1674.84	2	4.65	81-96	TVEEAENIAVTSGVVR
M15	Fatty acid-binding protein, epidermal	Q01469	15.0	6.80	21.64					
						928.11	2	2.22	24-32	ELGVGIALR
						1272.38	2	2.94	61-71	TTQFSCTLGEK
						1026.04	2	2.25	72-80	FEETTADGR
M16	Arrestin-C	P36575	42.8	5.53	14.95					
						1402.72	2	3.74	48-58	KLFVM*LTCAFR
						1654.85	2	4.47	59-72	YGRDDLEVIGLTFR
						1654.75	2	3.41	145-158	SFCAENPEETVSKR
						1952.20	2	4.11	167-185	KVQFAPPEAGPGPSAQTIR
M17	Arrestin-C	P36575	42.8	5.53	4.64					
						1824.03	2	4.66	168-185	VQFAPPEAGPGPSAQTIR
M18	Isocitrate dehydrogenase [NAD] subunit alpha	P50213	39.6	6.46	22.40					
						1607.90	2	2.90	101-115	TPIAAGHPSM*NLLLR
						1392.58	2	3.70	135-146	TPYTDVNIVTIR
						975.13	2	2.74	170-178	LITEGASKR
						1217.36	2	3.94	179-188	IAEFAFEYAR
						1055.23	2	2.38	206-214	M*SDGLFLQK
						1896.29	2	4.58	300-316	DM*ANPTALLLSAVM*M*LR
						1124.30	2	3.03	327-336	IEAACFATIK
M18	Transaldolase	P37837	37.5	6.36	15.73					
						1051.20	2	2.54	11-19	M*ESALDQLK
						1250.55	2	2.65	87-97	LFVLFGAEILK
						1234.34	2	2.34	205-215	SYEPLEDPGVK
						998.18	2	2.35	231-239	TIVM*GASFR
						1393.60	2	3.77	246-258	ALAGCDFLTISPK
M19	Tropomyosin 1 alpha chain	P09493	32.7	4.69	14.79					
						1885.07	3	4.05	91-105	RIQLVEEELDRAQER
						1977.23	3	5.13	134-149	AQKDEEKM*EIQEIQLK
						1315.54	2	3.66	168-178	KLVIIESDLER
M19	Heterogeneous nuclear ribonucleoproteins C1/C2	P07910	33.7	4.95	12.75					
						1317.60	2	3.87	18-29	VFIGNLNTLVVK
						1330.47	2	3.69	51-61	GFAFVQYVNER
						1700.00	2	5.06	74-89	M*IAGQVLDINLAAEPK
M20	Pyruvate dehydrogenase E1 component beta subunit	P11177	39.2	6.20	31.75					

						1803.01	2	3.07	53-68	VFLLGEEVAQYDGAYK
						1845.16	2	4.59	130-145	TYYM*SGGLQPVPIVFR
						1352.49	2	2.48	259-269	EGVECEVINM*R
						1901.22	2	3.37	270-285	TIRPM*DM*ETIEASVM*K
						1765.03	2	4.39	309-324	IM*EGPAFNFLDAPAVR
						1265.46	2	3.43	325-336	VTGADVPM*PYAK
						1256.43	2	3.25	337-347	ILEDNSIPQVK
M21	Glucose-6-phosphate 1-dehydrogenase	P11413	59.1	6.44	5.84					
						1174.34	2	2.75	182-191	LSNHISSLFR
						1265.53	2	2.37	205-214	EM*VQNLM*VLR
						1192.30	2	2.39	498-507	VGFQYEGTYK
M22	Glucose-6-phosphate 1-dehydrogenase	P11413	59.1	6.44	9.73					
						1139.33	2	2.58	95-103	LKLEDFFAR
						1174.34	2	3.07	182-191	LSNHISSLFR
						1265.53	2	2.35	205-214	EM*VQNLM*VLR
						1274.41	2	3.75	246-256	GGYFDEFGIIR
						1192.30	2	2.42	498-507	VGFQYEGTYK
M23	Glucose-6-phosphate 1-dehydrogenase	P11413	59.1	6.44	12.65					
						1011.16	2	2.36	81-88	KQSEPFFK
						1174.34	2	2.91	182-191	LSNHISSLFR
						1265.53	2	2.24	205-214	EM*VQNLM*VLR
						1274.41	2	3.44	246-256	GGYFDEFGIIR
						1944.13	3	3.81	370-385	LQFHDVAGDIFHQQCK
						1192.30	2	2.72	498-507	VGFQYEGTYK
M24	26S proteasome non-ATPase regulatory subunit 11	O00231	47.3	6.09	23.04					
						1517.58	2	4.24	33-45	DIQENDEEAVQVK
						1401.63	2	3.41	46-58	EQSILELGSLLAK
						1158.33	2	3.13	59-70	TGQAAELGGLLK
						1324.55	2	3.14	71-81	YVRPFLNSISK
						1086.26	2	2.30	132-140	LVSLYFDTK
						1342.61	2	3.28	163-174	ALLVEVQLLESK
						1731.99	2	4.86	258-273	IM*LNTPEDVQALVSGK
						1267.50	2	3.15	344-354	VQIEHISSLIK
M25	Elongation factor Tu	P49411	49.5	7.26	10.62					
						1674.84	2	4.58	105-120	GITINAAHVEYSTAAR

						1186.30	2	3.31	316-327	AEAGDNLGALVR
						1150.35	2	3.50	352-361	VEAQVYILSK
M26	Elongation factor Tu	P49411	49.5	7.26	4.87					
						1186.30	2	3.66	316-327	AEAGDNLGALVR
						1150.35	2	3.14	352-361	VEAQVYILSK
M27	Alpha-centractin	P61163	42.6	6.19	8.78					
						1868.04	2	4.98	239-255	AQYYLPDGSTIEIGPSR
						1684.96	2	3.94	293-308	TLFSNIVLSGGSTLFK
M28	Heterogeneous nuclear ribonucleoproteins C1/C2	P07910	33.7	4.95	16.01					
						1317.60	2	3.56	18-29	VFIGNLNTLVVK
						1124.27	2	3.16	30-39	KSDVEAIFSK
						1330.47	2	4.23	51-61	GFAFVQYVNER
						1700.00	2	4.11	74-89	M*IAGQVLDINLAAEPK
M29	Heterogeneous nuclear ribonucleoproteins C1/C2	P07910	33.7	4.95	22.55					
						1317.60	2	3.72	18-29	VFIGNLNTLVVK
						996.10	2	2.73	31-39	SDVEAIFSK
						1330.47	2	4.45	51-61	GFAFVQYVNER
						1700.00	2	5.44	74-89	M*IAGQVLDINLAAEPK
						1229.45	2	3.27	188-198	LKGDDLQAIKK
						1160.30	2	3.51	207-216	VDSLLENLEK
M30	Heterogeneous nuclear ribonucleoprotein H3	P31942	36.9	6.37	11.27					
						1272.39	2	3.88	56-67	STGEAFVQFASK
						1920.12	2	4.95	206-222	ATENDIANFFSPLNPIR
						1053.15	2	2.76	223-232	VHIDIGADGR
M31	Voltage-dependent anion-selective channel protein 1	P21796	30.6	8.63	19.50					
						1960.99	2	4.52	34-52	SENGLEFTSSGSANTETTK
						1401.50	2	4.13	96-108	LTFDSSFSPNTGK
						1214.35	2	3.33	163-173	VTQSNFAVGYK
						1415.52	2	3.13	224-235	YQIDPDACFSAK
M31	Esterase D	P10768	31.5	6.54	4.61					
						1402.53	2	4.63	186-198	KAFSGYLGTDQSK
M32	Pyruvate kinase, isozymes M1/M2	P14618	57.8	7.95	33.21					
						1198.35	2	3.32	32-42	LDIDSPPITAR
						1360.53	2	3.86	43-55	NTGIICTIGPASR
						1885.03	3	4.35	73-88	LNFSHGTHEYHAETIK

						914.08	2	2.85	106-114	PVAVALDTK
						1214.37	2	2.87	141-150	ITLDNAYM*EK
						1463.70	2	4.50	173-185	IYVDDGLISLQVK
						1780.91	2	6.10	188-205	GADFLVTEVENGGSLGSK
						1766.03	2	4.67	206-223	KGVNLPGAAVDLPAVSEK
						1682.88	2	4.25	279-293	FDEILEASDGIM*VAR
						1142.28	2	3.10	294-304	GDLGIEIPAEK
						1020.12	2	2.56	367-375	GDYPLEAVR
						996.17	2	2.76	489-497	VNFAM*NVGK
						1084.19	2	3.01	516-525	PGSGFTNTM*R
M33	Pyruvate kinase, isozymes M1/M2	P14618	57.8	7.95	29.43					
						1360.53	2	4.10	43-55	NTGIICTIGPASR
						1571.71	2	4.07	92-105	TATESFASDPILYR
						914.08	2	2.69	106-114	PVAVALDTK
						1214.37	2	3.10	141-150	ITLDNAYM*EK
						1463.70	2	4.43	173-185	IYVDDGLISLQVK
						1780.91	2	5.94	188-205	GADFLVTEVENGGSLGSK
						1637.86	2	4.16	207-223	GVNLPGAAVDLPAVSEK
						954.02	2	2.69	270-277	IENHEGVR
						1682.88	2	3.17	279-293	FDEILEASDGIM*VAR
						1142.28	2	3.04	294-304	GDLGIEIPAEK
						1020.12	2	2.57	367-375	GDYPLEAVR
						996.17	2	2.90	489-497	VNFAM*NVGK
						1084.19	2	2.89	516-525	PGSGFTNTM*R
M34	Aspartate aminotransferase	P17174	46.1	6.57	8.74					
						1357.54	2	3.39	86-98	LALGDDSPALKEK
						1428.62	2	4.00	99-113	RVGGVQSLGGTGALR
						1013.09	2	2.45	259-266	NFGLYNER
M35	Heterogeneous nuclear ribonucleoproteins A2/B1	P22626	37.4	8.97	9.92					
						1058.21	2	2.21	4-12	TLETVPLER
						1800.00	2	4.67	23-38	LFIGGLSFETTEESLR
						1189.34	2	2.67	138-147	IDTIEIITDR
M36	Heterogeneous nuclear ribonucleoproteins A2/B1	P22626	37.4	8.97	9.92					
						1058.21	2	2.28	4-12	TLETVPLER
						1800.00	2	4.99	23-38	LFIGGLSFETTEESLR

M37	Heterogeneous nuclear ribonucleoproteins A2/B1	P22626	37.4	8.97	7.37					
						1800.00	2	4.40	23-38	LFIGGLSFETTEESLR
						1189.34	2	2.81	138-147	IDTIEIITDR
M38	Heterogeneous nuclear ribonucleoproteins A2/B1	P22626	37.4	8.97	7.37					
						1800.00	2	4.06	23-38	LFIGGLSFETTEESLR
						1189.34	2	2.99	138-147	IDTIEIITDR
M39	Phosphoglycerate mutase 1	P18669	28.7	6.75	8.30					
						1060.19	2	2.48	90-99	HYGGLTGLNK
						1151.34	2	3.16	180-190	VLIAAHGNSLR
M40	Superoxide dismutase [Mn]	P04179	24.7	8.35	10.36					
						1425.66	2	3.68	76-89	GDVTAQIALQPALK
						1029.22	2	2.59	115-123	GELLEAIKR

(Neurobiology of Disease)

Expression of Mutated Optineurin Leads to Normal Tension Glaucoma in Mice by the Disruption of Optineurin-Rab8 Interaction

Abbreviated title: Mutated optineurin leads to normal tension glaucoma in mice

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