

proteins were detected with antibodies specific to Arrestin-C (1), Mn-SOD (2),  $\gamma$ -synuclein (3), E-FABP (4), Tropomyosin1a Br-1,Br-3 (5), Tropomyosin1a TM311 (6), hnRNPs A2/B1 (7), and hnRNPs C1/C2 (8). Lane P; peripheral retina, Lane M; macula.

Figure 6

*2D western blotting of Mn-SOD.*

Thirty microgram of each sample from the peripheral retina and macula were separated by 2D gel electrophoresis. After transferring to PVDF membrane, the proteins were detected with antibodies specific to Mn-SOD.

Figure 7

*Tissue localization of macula enriched proteins.*

Four micrometer paraffin section of monkey eye was stained with hematoxylin and eosin (A), other sections were labeled with antibodies specific to Arrestin-C (B), Mn-SOD (C),  $\gamma$ -synuclein (D), E-FABP (E), Tropomyosin Br-1, Br-3 (F), TM311 to Tropomyosin (G), hnRNPs A2/B1 (H), and hnRNPs C1/C2 (I). GCL, ganglion cell layer; INL, inner nuclear layer; OPL, outer plexiform layer; ONL, outer nuclear layer; PIS, photoreceptor inner segment; POS, photoreceptor outer segment; RPE, retinal pigment epithelial; Ch,

choroid. (Bar, 50  $\mu$ )

Figure 1

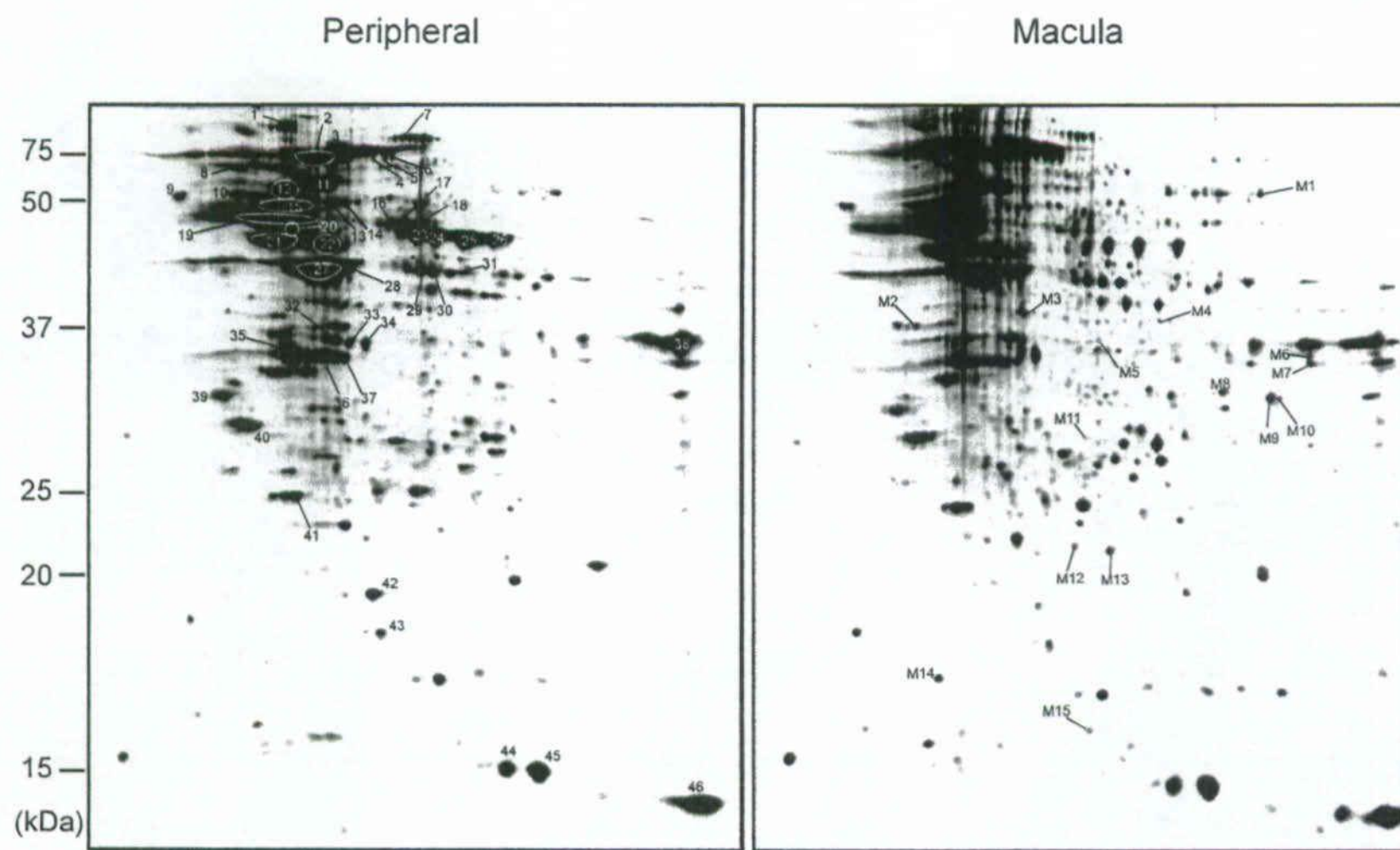


Figure 2

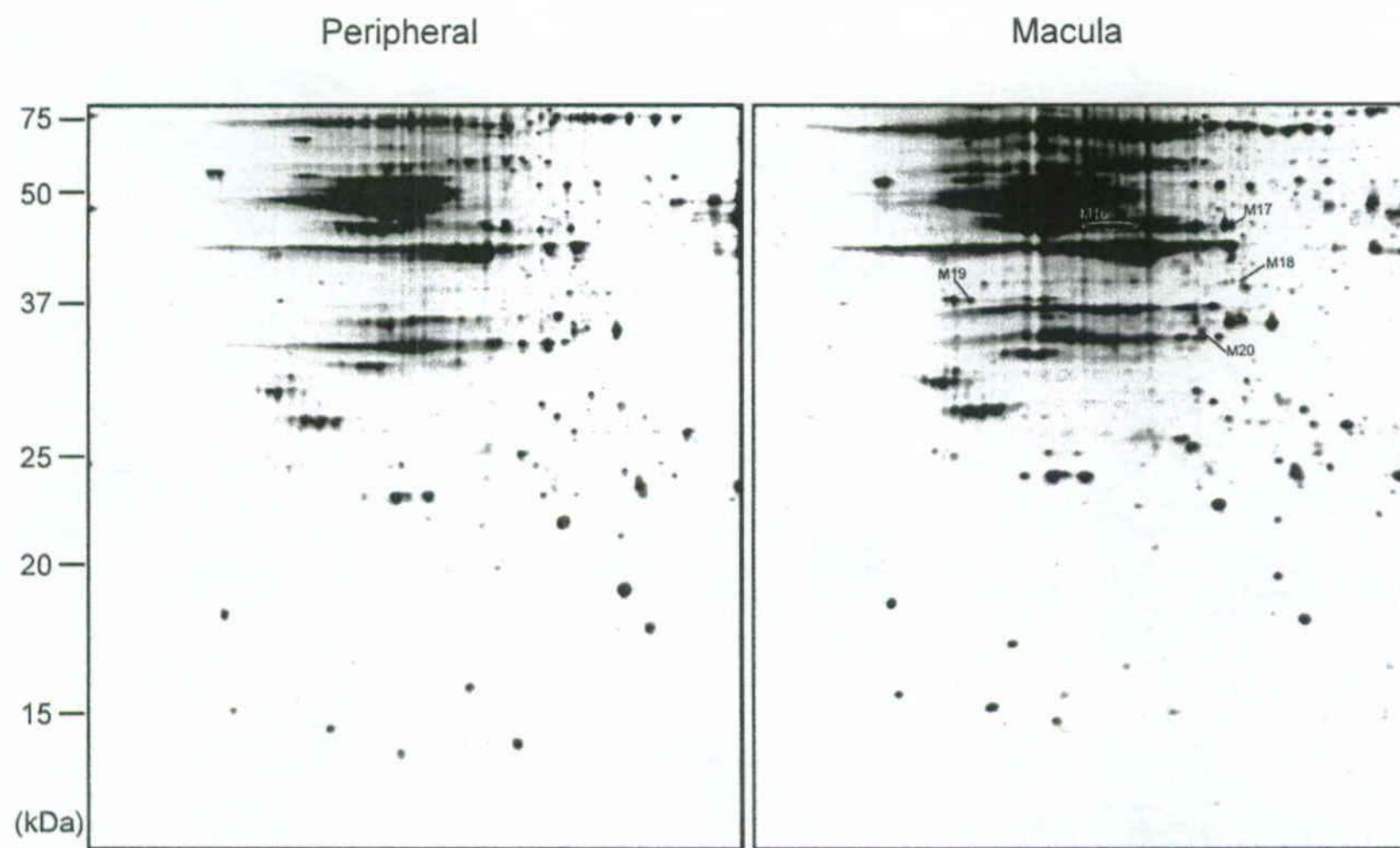




Figure 3

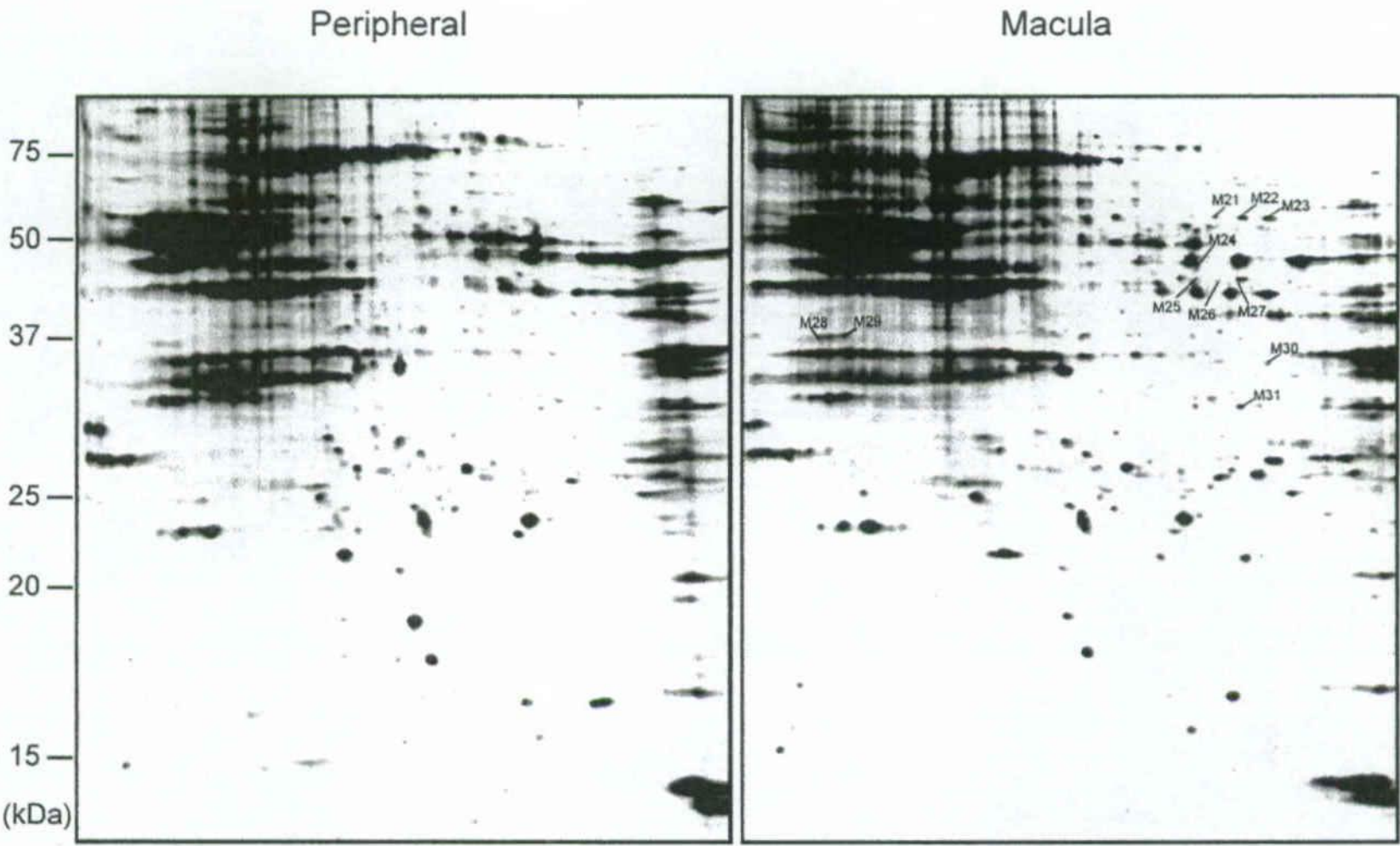


Figure 4

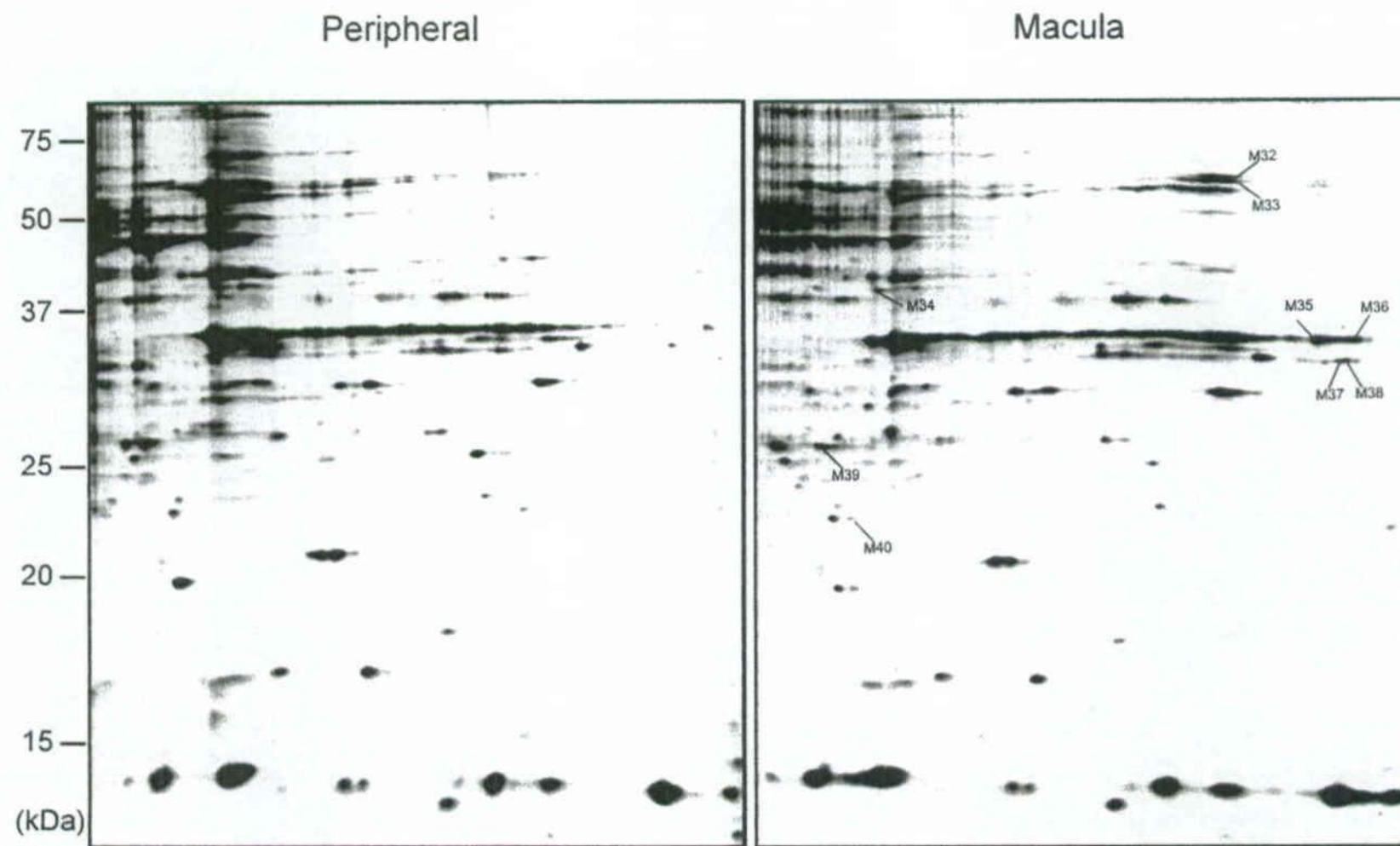


Figure 5

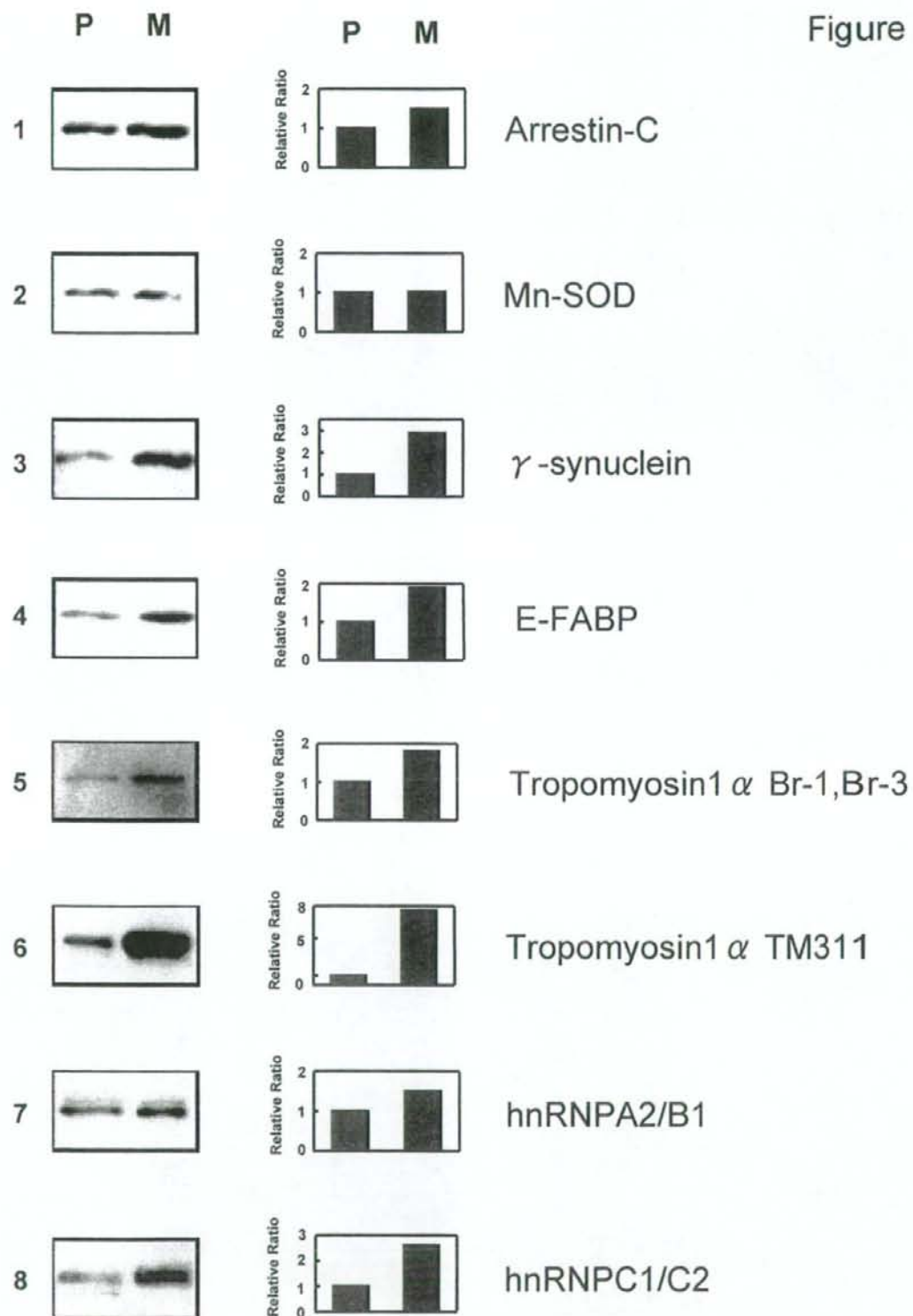


Figure 6

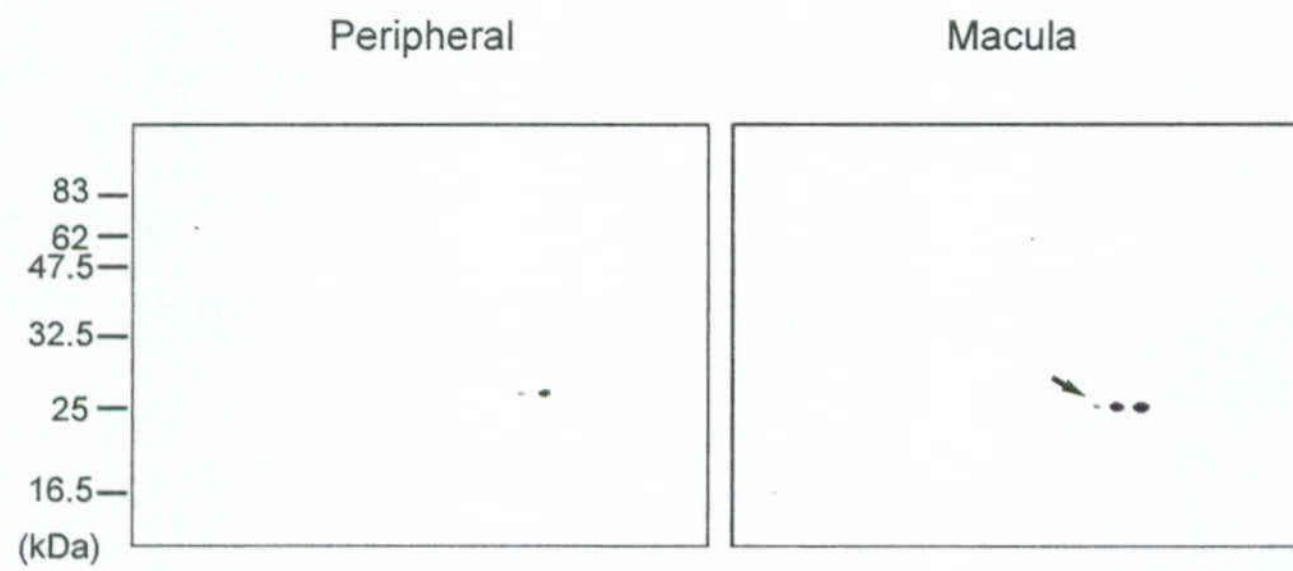
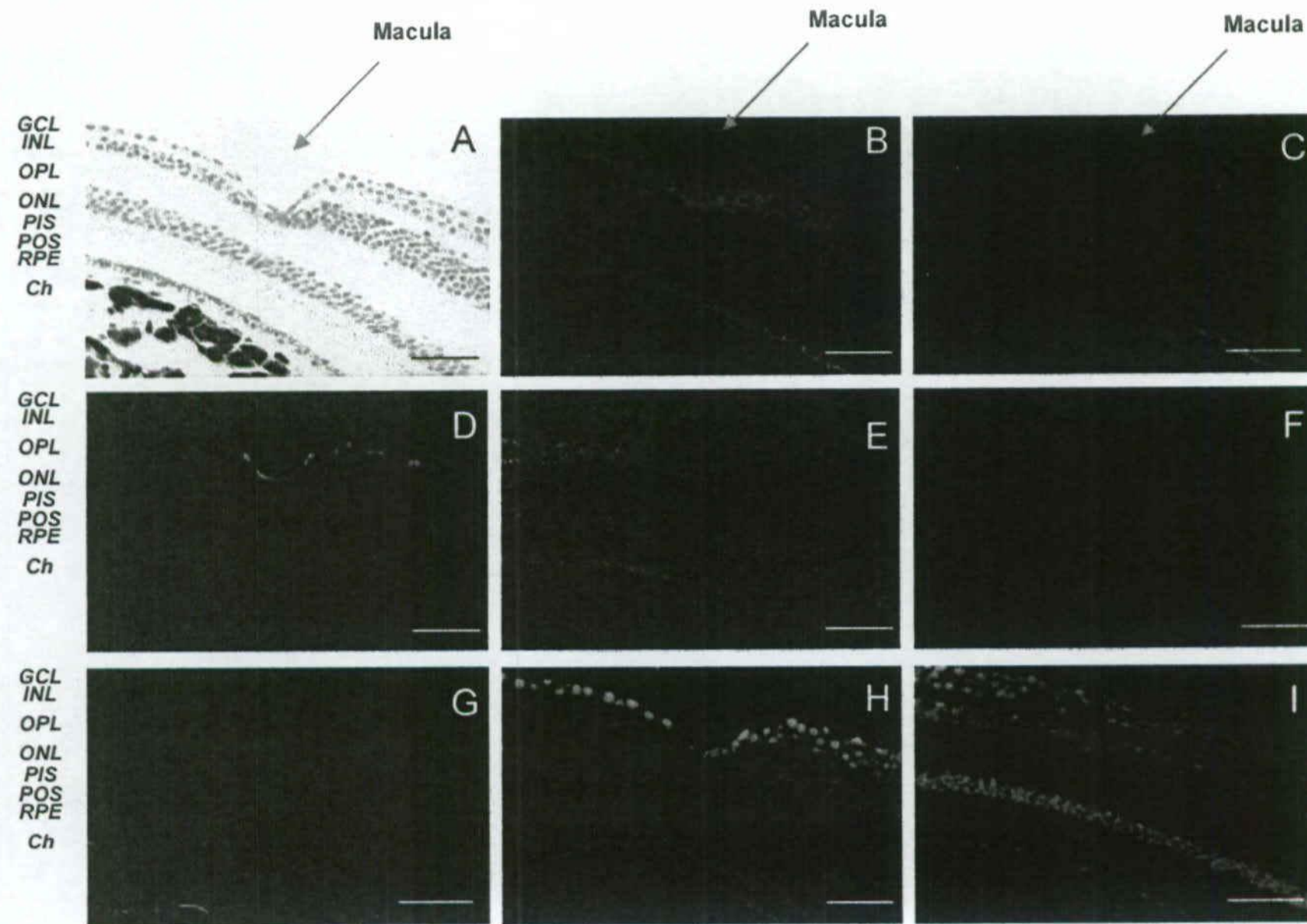




Figure 7



## Tables

### Table 1

Proteins identified macular and peripheral retina.

Abundant proteins in macular and peripheral retina are identified by LC-MS/MS and listed.

<sup>(a)</sup> Spot numbers correspond to the numbers on gel images in figure 1.

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

<sup>(c)</sup> MW and pI is theoretical score by Bioworks ver.3.1.

\*Oxidation of methionine.

Spot no. <sup>(a)</sup>	Protein name	Database Accession no. <sup>(b)</sup>	MW (kDa) <sup>(c)</sup>	pI <sup>(d)</sup>	Sequence coverage (%)	Precursor ion MH+	Charge	XC	Residue	Sequence
1	Heat shock protein HSP 90-alpha	P07900	84.5	4.94	10.53	1243.44	2	3.66	100-111	ADLINNLGTIAK
						1152.24	2	3.03	283-291	YIDQEELNK
						1834.87	2	4.55	299-313	NPDDITNEEYGEFYK
						1265.40	2	3.09	345-354	RAPFDLFENR
						1169.23	2	2.23	446-455	LGIHEDSQNR
						1225.38	2	2.85	489-498	HIYYITGETK
						1236.32	2	3.23	499-509	DQVANSFVER
1	Heat shock protein HSP 90-beta	P08238	83.1	4.97	6.09	1545.72	2	2.34	41-54	ELISNASDALDKIR
						1040.11	2	2.43	55-63	YESLTDPSK
						1243.44	2	3.66	95-106	ADLINNLGTIAK
						1152.24	2	3.03	275-283	YIDQEELNK
2	Heat shock cognate 71 kDa protein	P11142	70.9	5.37	29.41	1488.58	2	2.96	37-49	TTPSYVAFTDTER
						1666.84	2	4.15	57-71	NQVAM*NPTNTVFDAK
						1271.38	2	2.13	78-88	FDDAVVQSDM*K
						1181.32	2	3.19	103-112	VQVEYKGETK
						1633.85	2	3.48	113-126	SFYPEEVSSM*VLTK
						1269.49	2	3.69	127-137	M*KEIAEAYLGK
						1200.37	2	3.82	160-171	DAGTIAGLNVLK
						1789.07	2	4.31	172-188	IINEPTAAAIAYGLDKK
						1252.47	2	3.36	237-246	M*VNHFAIEFK
						1254.37	2	2.60	302-311	FEELNADLFR
						1482.67	2	3.92	329-342	SQIHDIVLVGGSTR
						1082.23	2	2.37	349-357	LLQDFFNK
						773.86	1	1.80	452-458	DNNLLGK
						1018.15	2	2.43	501-509	ITITNDKGR
						990.09	2	2.54	510-517	LSKEDIK
1142.31	2	2.30	518-526	M*VQEAKEYK						
1320.45	2	3.71	540-550	NSLESYAFNM*K						



						903.02	2	3.29	121-129	GVNVSALSR
						1317.52	2	3.10	221-232	LPANHPLLTGQR
						1051.16	2	2.45	281-289	GNEM*SEVLR
						1397.53	2	2.25	290-301	DFPELTM*EVDGK
						1532.75	2	4.18	309-323	TALVANTSNM*PVAAR
						1799.00	2	3.81	365-381	LAEM*PADSGYPAYLGAR
						1869.18	2	3.94	537-552	TVGM*LSNM*IAFYDM*AR
						1248.41	2	2.11	586-596	FKDPLKDGEAK
						1817.96	2	3.68	599-613	SDYAQLLEDM*QNAFR
2	Lamin B2	Q03252	67.7	5.29	17.67					
						1427.67	2	3.18	46-57	ALELENDRIILK
						1192.30	2	2.94	58-67	ISEKEEVTR
						1238.33	2	3.58	74-84	ALYESELADAR
						1089.18	2	2.77	152-161	GLESVAELR
						1434.50	2	3.60	271-284	LSSDQNDKAASAAR
						1770.05	2	3.50	292-306	M*RLESLSYQLSGLQK
						1453.69	2	2.67	362-373	LALDM*EINAYRK
						975.04	2	2.10	374-381	LLEGEEER
						1520.69	2	4.09	542-555	TVLVNADGEEVAM*R
2	Heat shock 70 kDa protein 1	P08107	70.1	5.48	16.54					
						1488.58	2	2.96	37-49	TTPSYVAFTDTER
						1659.83	2	4.00	57-71	NQVALNPQNTVFDK
						1688.91	2	4.24	172-187	IINEPTAAAAYGLDR
						1676.68	2	3.22	221-236	ATAGDTHLGGEDFDNR
						1110.25	2	2.57	349-357	LLQDFNGR
						1018.15	2	2.43	501-509	ITITNDKGR
						1004.12	2	2.44	510-517	LSKEEIER
						1142.31	2	2.30	518-526	M*VQEAKEYK
						1304.46	2	2.81	540-550	NALESYAFNM*K
2	Stress-70 protein, mitochondrial	P38646	73.7	5.87	9.57					
						1570.88	2	3.07	160-173	LYSPSQIGAFVLM*K
						1243.40	2	3.54	207-218	DAGQISGLNVLK
						1646.87	2	4.48	219-234	VINFPTAAAIAYGI DK





						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	ILIAFI FOI KGQK



					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	DVNAIAAIK
					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*LNQNK
						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	EVDEOM*LNQNK



19	Tubulin beta-3 chain	Q13509	50.4	4.83	16.89	1246.42	2	3.46	381-390	ISEQFTAM*FR
						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
19	Tubulin beta-6 chain	Q9BUF5	49.9	4.77	11.88	1246.42	2	3.46	381-390	ISEQFTAM*FR
						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
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						
21	Gamma-enolase	P09104	47.1	4.91	12.47	1436.60	2	3.73	311-324	FTQAGSEVSALLGR
						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
1545.77	2	3.71	148-162	LQAEAPHIVGTPGR						

					1516.72	2	3.22	192-203	GFKDQIYEIFQK
					1160.34	2	2.84	239-248	KEELTLEGIK
22	Eukaryotic initiation factor 4A-1	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	AAVPSGASTGIYEALRL
					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	LAQANGWGVV*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	YISPDQI ADI YK



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	AAVPSGASTGIYEALRLR
						1445.64	2	3.15	80-91	KLNVTEQEKIDK
						1669.90	2	3.45	89-102	IDKLM*LEM*DG TENK
						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	EKLIAPVAEEEEATVPNNK
					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	EKLIAPVAEEEEATVPNNK
					1630.82	2	4.80	43-57	SLADELALVDVLEDK
					1965.24	2	3.41	60-76	GEM*M*DLQHGSLFLQTPK