

Figure 2

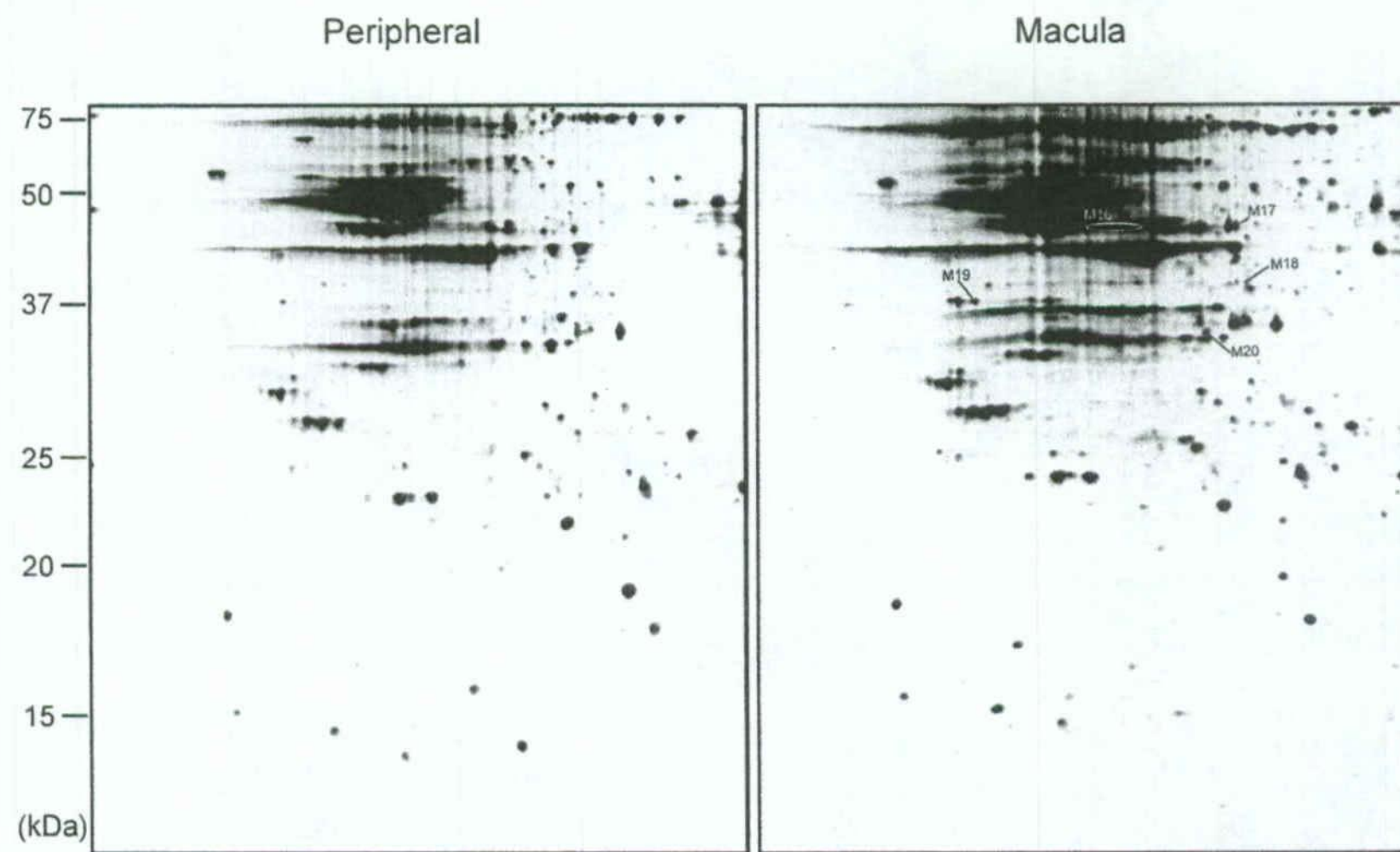


Figure 3

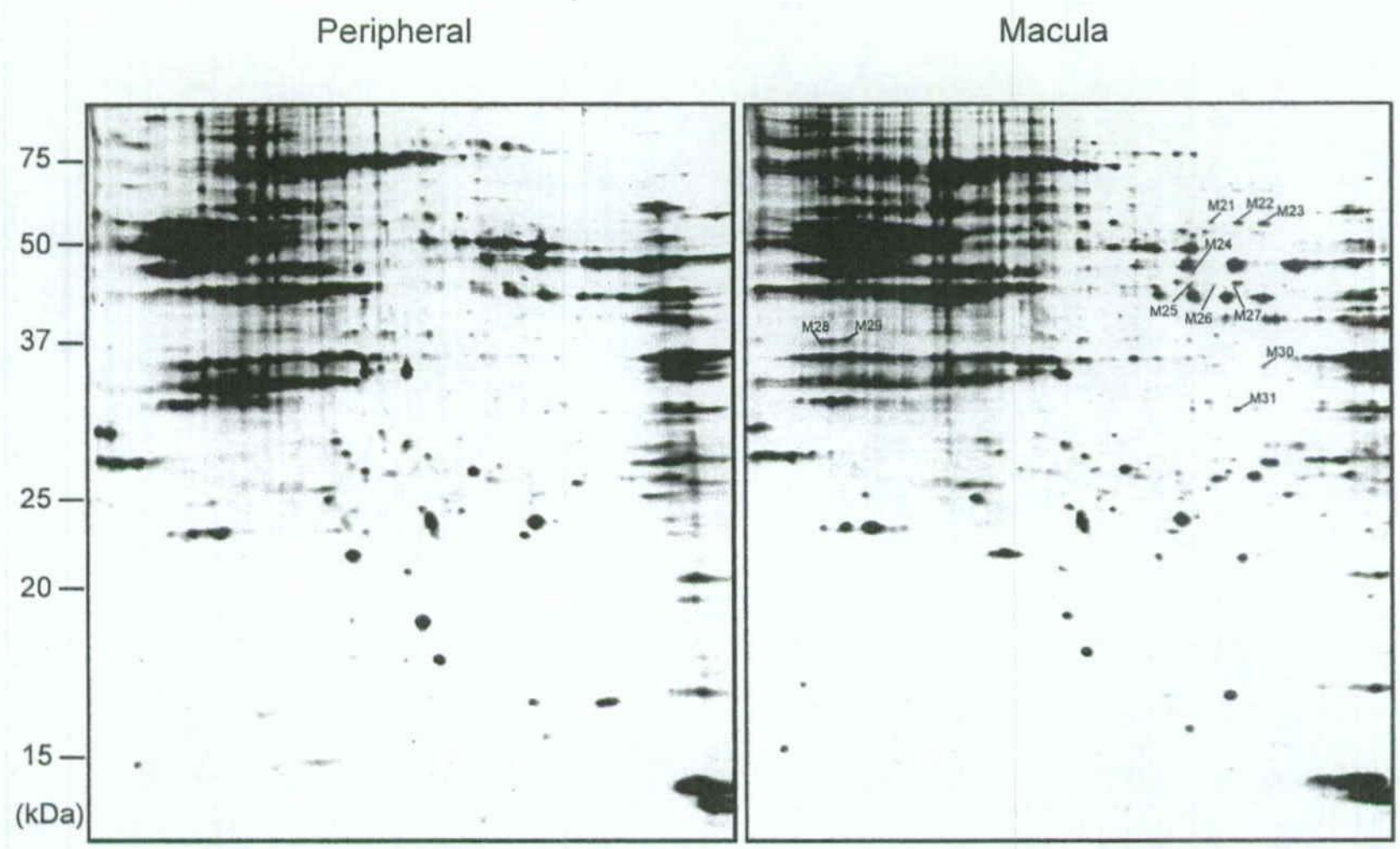


Figure 4

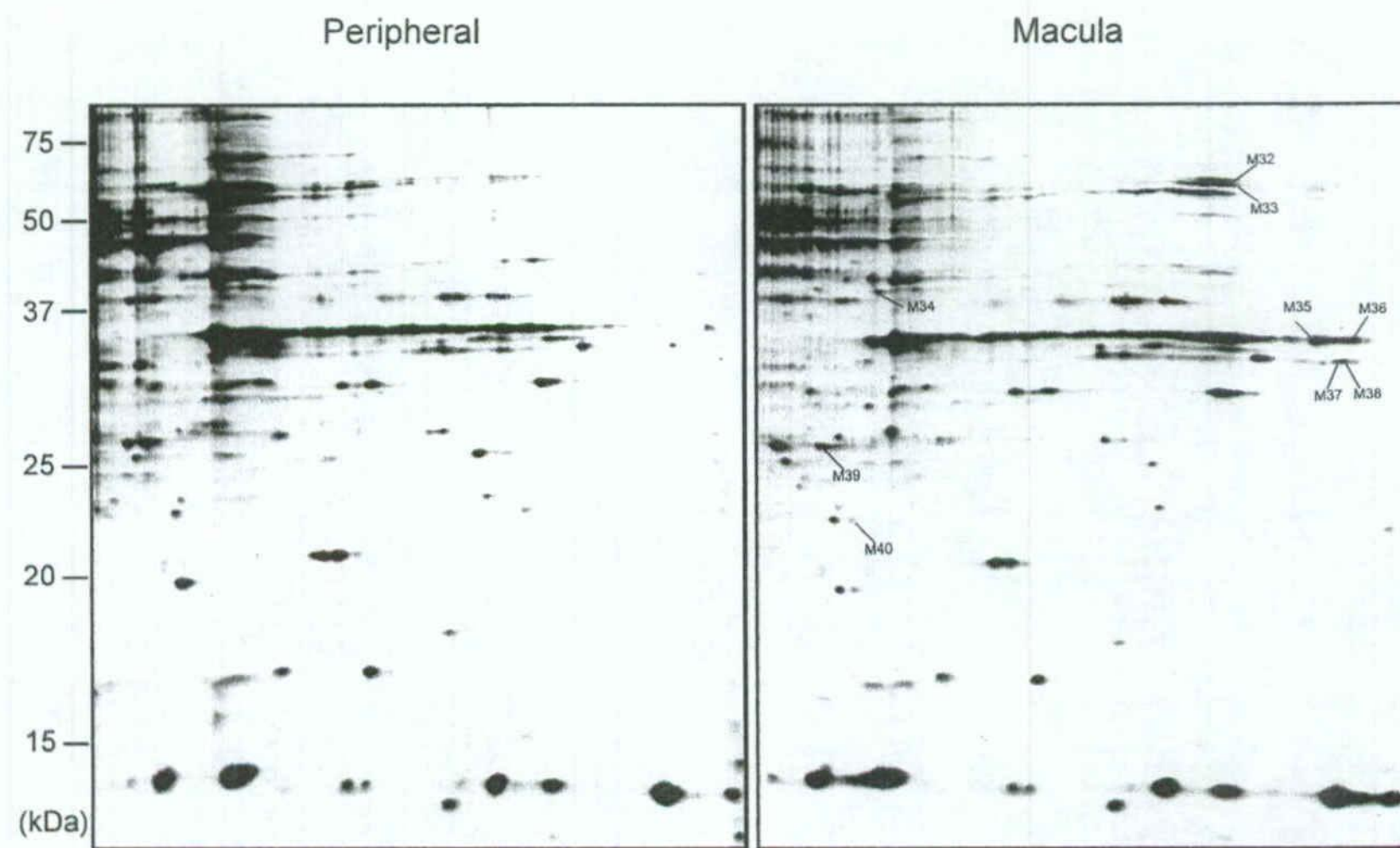


Figure 5

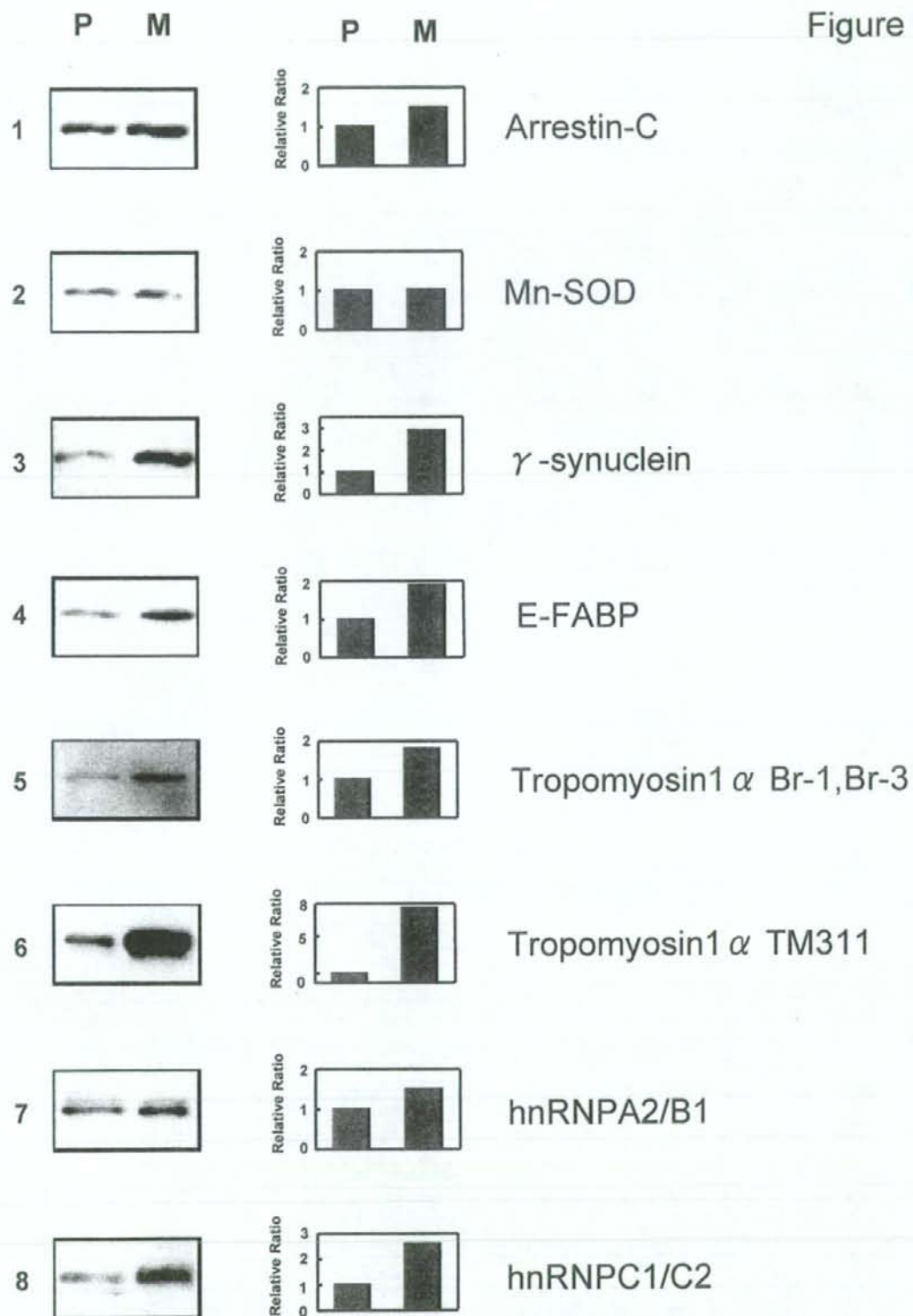


Figure 6

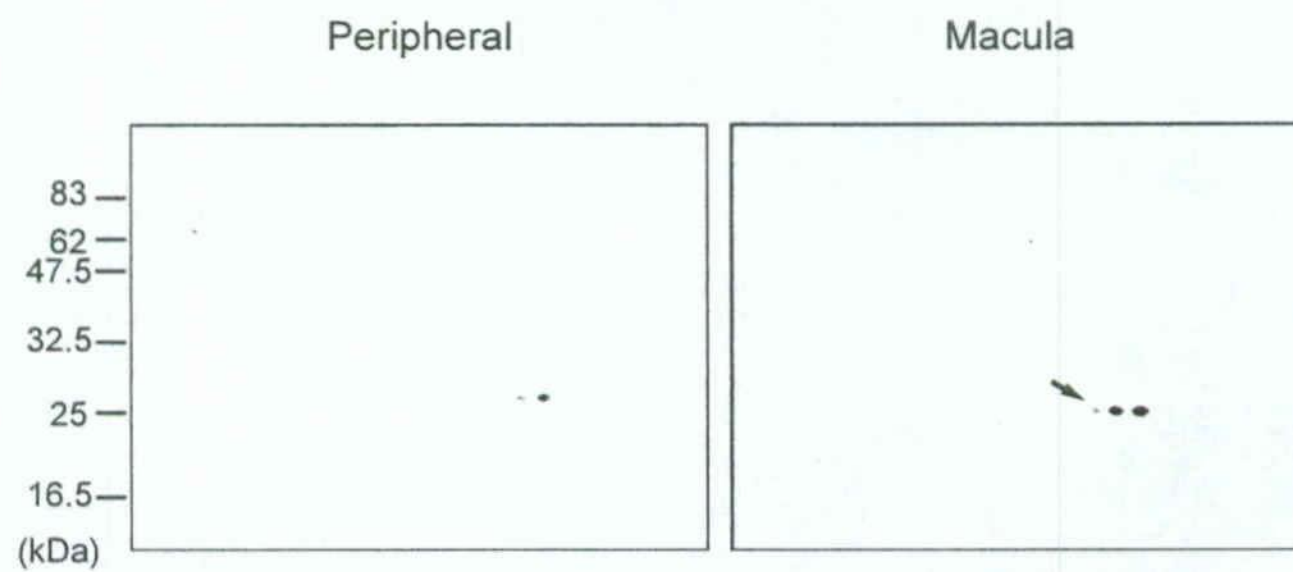
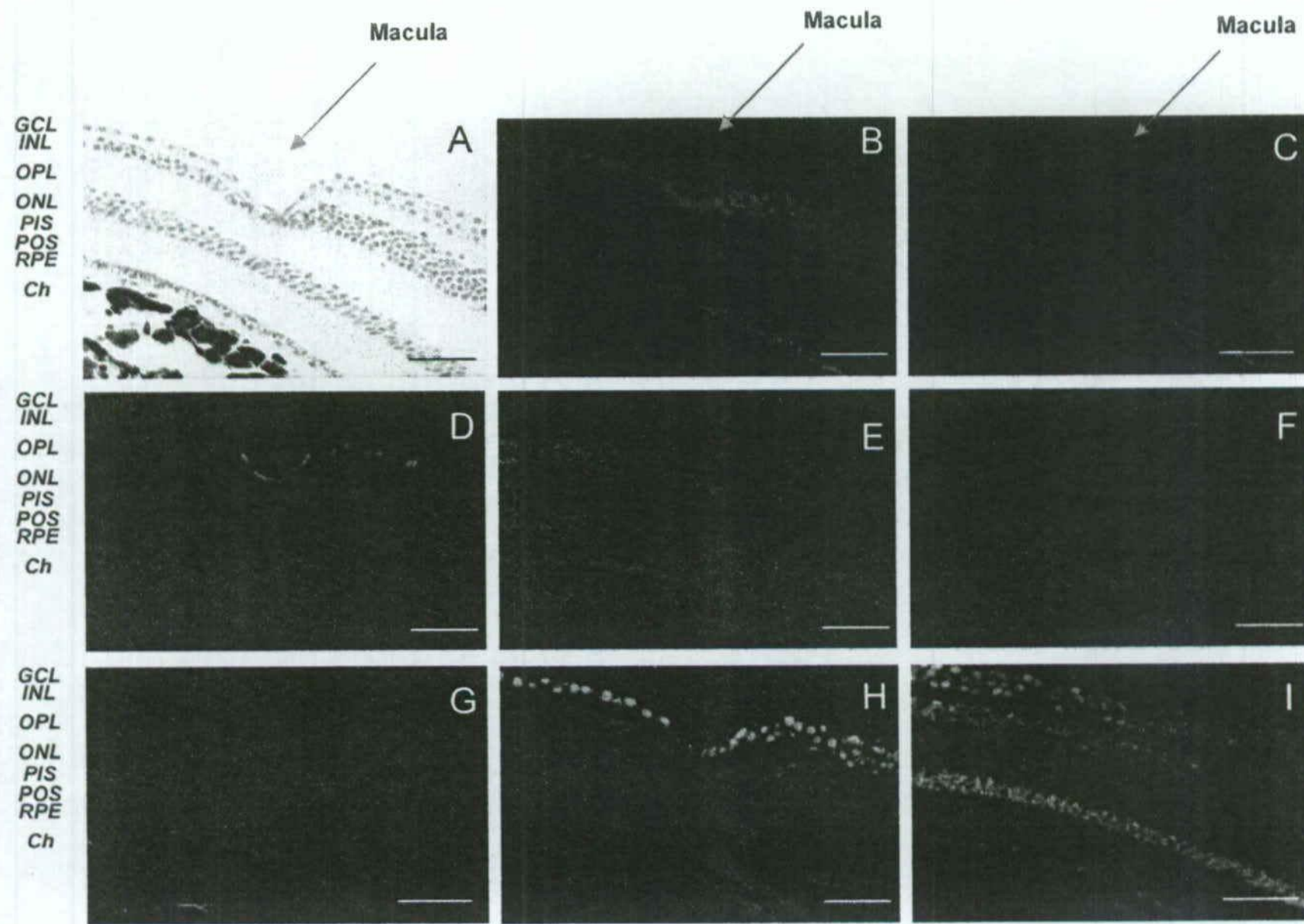


Figure 7



## 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	DQVANSAFVER
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*NPTNTVFDK
						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	DAGTIAGLNVL
						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	SQIHDIIVLVGGSTR
						1082.23	2	2.37	349-357	LLQDFFNGK
						773.86	1	1.80	452-458	DNNLLGK
						1018.15	2	2.43	501-509	ITITNDKGR
						990.09	2	2.54	510-517	LSKEDIER
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	ALELENDRLLLK
					1192.30	2	2.94	58-67	ISEKEEVTR
					1238.33	2	3.58	74-84	ALYESELADAR
					1089.18	2	2.77	152-161	GLESDVAELR
					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	LLEGEER
					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	NOVALNPQNTVFDK
					1688.91	2	4.24	172-187	IINEPTAAAIAYGLDR
					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	DAGQISGLNVL
					1646.87	2	4.48	219-234	VINFPTAAAIAYGI DK

3	Stress-70 protein, mitochondrial	P38646	73.7	5.87	8.25	1291.44	2	3.38	395-405	VQQTVDLFR
						1243.40	2	2.60	207-218	DAGQISGLNVL
						1646.87	2	4.44	219-234	VINEPTAAALAYGLDK
						1291.44	2	2.51	395-405	VQQTVDLFR
3	Serum albumin	P02768	69.4	5.92	6.90	1809.96	2	2.32	469-485	SQVFSTAADGQTQVEIK
						1150.31	2	2.76	66-75	LVNEVTEFAK
						961.14	2	2.44	427-434	FQNALLVR
						1512.73	2	2.34	439-452	VPQVSTPTLVEVSR
4	Serum albumin	P02768	69.4	5.92	6.90	1129.38	2	2.83	549-558	KQTALVELVK
						1651.88	2	3.32	250-264	AEFAEVSKLVTDLTK
						1640.88	2	2.71	348-360	DVFLGM*FLYEYAR
						1512.73	2	2.82	439-452	VPQVSTPTLVEVSR
5	Serum albumin	P02768	69.4	5.92	7.39	1150.31	2	2.70	66-75	LVNEVTEFAK
						1658.78	2	3.62	414-426	QNCLEFEQLGEYK
						1512.73	2	3.13	439-452	VPQVSTPTLVEVSR
						1129.38	2	2.98	549-558	KQTALVELVK
6	Serum albumin	P02768	69.4	5.92	3.94	1150.31	2	2.55	66-75	LVNEVTEFAK
						1512.73	2	2.78	439-452	VPQVSTPTLVEVSR
7	Serotransferrin	P02787	77.1	6.81	3.72	1274.41	2	2.88	226-236	HSTIFENLANK
						1883.00	2	3.38	237-251	ADRDQYELLCLDNTR
8	Neurofilament triplet L protein	P07196	61.4	4.64	23.99	1073.14	2	2.30	91-99	AQLQDLNDR
						1125.22	2	2.35	107-115	VHELEQQNK
						1155.41	2	3.43	116-125	VLEAELLVLR
						1062.11	2	2.99	147-156	LAAEDATNEK
						1025.09	2	2.90	177-184	YEEEVLSR
						1002.11	2	2.53	196-205	KGADEAALAR

						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	KLEGEETR
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	VGLQVAVK
						962.05	2	2.05	302-310	APGFQDNRK
						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	IGIEIKR
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	EKLOEEM*LQR
					1324.38	2	2.76	196-206	EEAENTLQSFR
					1089.14	2	2.48	207-216	QDVNASLAR
					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	EIIDLVLDLDR
					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*LSNTTAAIEAWAR
					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*LSNTTAAIEAWAR
					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	KVYVTLCAFR
						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	KVYVTLCAFR
						957.07	2	2.78	85-91	RDLYFSR
						1515.74	2	2.57	92-106	VQVYPPVGAASPTK
						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	EVDEQM*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	IREEFDR
						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
20	ATP synthase beta chain, mitochondrial	P06576	56.6	5.26	25.90	1407.57	2	3.39	325-336	EVDEQM*LAIQSK
						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	VALVYQGM*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	VNOIGSVTEAIQACK
22	Eukaryotic initiation factor 4A-II	Q14240	46.4	5.33	16.22	1161.20	2	2.78	412-421	IEEELGDEAR
						1829.05	2	2.85	47-62	GIYAYGFKPSAIQQR
						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-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	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	KLVNTEQEKIDK
						1669.90	2	3.45	89-102	IDKLM*IEI*DGTEIENK
						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*DLQHGSFLQTPK

						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	LQYPELFDLSPEAVR
						1510.67	2	3.92	137-150	CTIEAGYPGVLSSR
						1442.65	2	3.39	222-233	M*VDM*LQDSFFAR
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	DKDFAIDIHK
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*IDEGETDVK
						1178.36	2	3.34	212-221	DKDFAIDIHK
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	EGWVECSFVK
					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	VVGLM*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	IISIEQKEENK
					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	GI VGFIIKR

44	Hemoglobin beta subunit	P68871	15.9	6.81	22.60	1052.16	2	2.22	106-114	GDFCIQVGR
						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
						1530.62	2	3.16	17-31	VGAHAGEYGAEALER
46	Hemoglobin alpha subunit	P69905	15.1	8.73	23.40	1088.30	2	2.11	32-40	M*FLSFPTTK
						1088.29	2	2.68	91-99	LRVDPVNFK