

Appendix 1. Mass spectrometric identification, including sequence information, of the 2D-PAGE protein spots differentially expressed in the rabbit retina.

Spot number	Protein name/ Swiss-Prot entry (Full chain length)	Peptide sequence (Amino acid numbers)	Mascot Ions score	Theoretical pI;Mr kDa	Fold change RD : Sham	Biological processes
1204	α-enolase (434) ENOA_BOVIN, fragment	IGAEVYHNLK (184-193)	79	6.99;47.0	2.24	Glycolysis; Plasminogen activation; Transcription; Transcription regulation
2204/2102	ENOA_MOUSE, fragment	IGAEVYHNLK (184-193) DATNVGDEGGFAPNILENK (203-221) SGKYDLDFK (254-262) YITPDQLADLYK (270-281) SCNCLLLK (336-343)	73/94 90/115 8/18 79/72 23/17	6.99;47.0	2.28/2.41	
1102		YITPDQLADLYK (270-281)	79	6.99;47.0	2.42	
0502	Vimentin (466) VIME_HUMAN	QVDQLTNDK (160-168) QDVNASLAR (208-217) FADLSEAANR (295-304) GTNESLER (335- 342) EYQDLLNVK (382-390) KLEGEESR (402-410) LLEGEESR (403-410) DGQVINETSQHDDLE (451-466)	72 67 46 48 40 36 25 64	5.06;53.5	2.51	Cell motion
3105/3102	Albumin (608) ALBU_RABIT, N terminal fragment	ACVADESAANCDK (76-88) DTYGDVADCCEK (106-117)	77/99 63/71	5.67;66.5	2.66/2.95	Transport; Cellular response to starvation; Maintenance of mitochondrial location; Negative regulation of apoptosis; Hemolysis of symbiont of host erythrocytes
3502		DTYGDVADCCEK (106-117)	47	5.67;66.5	3.19	
3301	Prohibitin (272) PHB_HUMAN	QVSDDLTER (149-157) QVAQQAER (187-195) AAIISAEGDSK (209-219)	27 43 25	5.57;29.8	2.72	Negative regulation of cell proliferation; Negative regulation of transcription; Regulation of apoptosis; Signal transduction; Histone deacetylation
9401	Fructose- bisphosphate aldolase A (364) ALDOA_RABIT	AAQEEYVKR (323-331)	44	8.39;39.3	0.49	ATP biosynthetic process; Fructose 1,6-bisphosphate metabolic process; Regulation of cell shape; Actin filament organisation; Striated muscle contraction; Muscle maintenance
1305	Transducin-β_1 (340) GBB1_HUMAN	LLVSASQDGK (69-78) LFVSGACDASAK (198-209) AGVLAGHDNR (305-314)	57 78 82	5.60;37.2	0.48	Hormone-mediated signaling; Muscarinic acetylcholine receptor signalling; Signal transduction; Ras protein signal transduction
1606	ATP synthase subunit β, mitochondrial (528) ATPB_BOVIN	TIAMDGTEGLVR (110-121) VALVYQMNPPGAR (265-279) ADKLAEHS (520-528)	77 100 60	5.00;51.8	0.41	Protein transport; ATP synthesis coupled proton transport; Regulation of intracellular pH; Angiogenesis
8502	Creatine kinase, ubiquitous mitochondrial (416) KCRU_BOVIN	HTTDLASK (140-148) GDLAGR (200-205)	44 7	7.31;43.1	0.38	Creatine metabolic process
8503		HTTDLASK (140-148) GTGGVDTAATGSVFDISNDR (354-374)	45 130	7.31;43.1	0.35	
1605	Tubulin β-2C chain (447) TBB2C_HUMAN	INVYYNEATGGK (47-58) NMMAACDPR (298-306) EVDEQMLNVQNK (325-336) TAVCDIPPR (351-359)	58 28 78 38	4.79;49.8	0.18	Cell motion; Microtubule-based movement; Natural killer cell mediated cytotoxicity; Protein polymerisation

Protein spots 5101, 5703, and 8605 with fold changes of 0.48, 0.43 and 0.38 respectively could not be identified. Individual Mascot ions scores greater than approximately 36 indicate identity or extensive homology ($p < 0.05$). Biological processes were taken from the Gene Ontology Consortium (www.geneontology.org). Abbreviation: RD represents retinal detachment.