SUPPLEMENTARY ONLINE CONTENT
Gene Therapy Restores *Mfrp* and Corrects Eye Axial Length

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Supplemental Results

Structural modeling of human MFRP mutations

It is not known how MFRP mutations cause nanophthalmos or other retinal diseases, its exact role in the cell unknown, and its crystal structure is unsolved, so to gain insight into how point mutations might affect MFRP function, we used structural modeling. This analysis predicted several domains related to signal transduction, proteolysis, and endocytosis: two globular cubulin domains (CUB1 and CUB2), two domains related to the low-density lipoprotein receptor (LDLA1 and LDLA2), and a frizzled cysteine-rich domain (CRD). Further, the MFRP N-terminal region contains a putative transmembrane domain (TM; residues 70-90), suggesting it is a type II transmembrane protein with its C-terminal region projecting out to the extracellular space.1

In the absence of a high-resolution structure for MFRP, we used structural modeling to ascertain how our patient's mutations might alter MFRP structure and function.2 We also predicted how other MFRP mutations reported in the published literature might affect predicted functions of MFRP (Table S1). MFRP, is composed of 4 distinct domains, so we used a domain-assembly strategy to model MFRP structure, based on homology to related structures: cubulin domains (CUB1 and CUB2) were modeled using the crystal structure of cubulin as a template; LDLA1 and LDLA2 domains were generated based on the LDLR structure; the CRD domain was modelled based on the XWnt8-bound Frizzled-8 structure (Fig. S2A-E). These individual domains were then assembled to generate a full-length MFRP model (Fig. S3).

Using this complete MFRP model, the mutations were mapped and found in all four domains (Fig. S3), allowing predictions as to how the mutations might affect protein function. For example, cubulin (CUB) domains are extracellular motifs comprised of ten β-strands in two five-stranded β-sheets3 that mediate protein-ligand interactions and proteolysis, like in the Tolloid proteinase family (e.g. BMP-1).3,4 Thus, although MFRP’s catalytic activity has not been demonstrated, the presence of Tolloid repeats (CUB and LDLA domains) implicate MFRP in proteolytic pathways. Mutations in these domains could affect catalytic activity (Table 2). Likewise, MFRP’s CRD contains a 40% identity to the CRDs present on SFRPs and Frizzled receptors. The CRD domain is a cysteine-rich motif in secreted frizzled receptor proteins (SFRPs) and frizzled receptors, and bind Wnt and regulate Wnt-signaling pathways.5 Although interactions between MFRP and Wnt have not been demonstrated, its role in cell fate signaling is suggested by the presence of the CRD domain.5,6 These predictions notwithstanding, since the mutations are scattered throughout several different functional domains, small-molecule therapy or highly targeted gene editing may not be feasible (Fig. S3; Table S1). Instead, either a cell-based therapy or gene replacement therapy might be more effective.

Proteomic Analysis

We first identified 20 proteins that were significantly upregulated in Mfrp<sup>ro6</sup>/Mfrp<sup>ro6</sup>. Among these proteins were thrombospondin-1 (TSP-1), argininosuccinate synthase-1 (ASS1), and cartilage oligomeric protein-1 (COMP-1). TSP-1 is a pro-angiogenic factor produced by the RPE and is believed to modulate choroidal vascular growth.7 Increased TSP-1 levels may explain the vascular leakage that contributes to cystoid macular edema.
in nanophthalmos patients (Fig. 1C). ASS1 is involved in the production of arginine and nitric oxide (NO). NO is a potent vasodilator in the central nervous system and retina. We hypothesized that increased retinal vasodilation would lead to increased intravascular leakage, causing exudative retinal detachment in nanophthalmos patients. COMP-1 is an extracellular matrix protein and a marker of collagen turnover. Increased levels of COMP-1 may promote scleral thickening, one of the pathological features of nanophthalmos. Interestingly, this protein was one of the most prominently expressed proteins in Mfpr\textsuperscript{rd6}/Mfpr\textsuperscript{rd6} mice. These proteins returned to control levels following gene therapy (Fig. 3A; Fig S4A).

We then identified 12 proteins were downregulated in Mfpr\textsuperscript{rd6}/Mfpr\textsuperscript{rd6} compared to controls and then restored to control levels following AAV2/8-mMfpr injection. Among these proteins were EGF-containing fibulin-like extracellular matrix protein 1 (EFEMP1), peroxiredoxin 6 (PRDX6), centrosomal protein of 97 kDa (CEP97), and ferritin (Table S4). Interestingly, mutations in EFEMP1 are known to cause a Mendelian form of macular degeneration known as Malattia Leventinese (MLVT). Patients with MLVT often display altered RPE cell ultrastructure, sub-retinal RPE deposits, and separation between the RPE and Bruch’s membrane. Notably, our Mfpr\textsuperscript{rd6}/Mfpr\textsuperscript{rd6} mice displayed similarly altered RPE morphology in our RPE wet mount, suggesting that rescue of EFEMP1 levels contributed to restored RPE morphology (Fig. S3). PRDX6 is an antioxidant protein expressed in astrocytes and Müller cells. Since oxidative stress is implicated in retinal degeneration, we hypothesize that restoration of PRDX6 levels in the RPE contributed to reduced photoreceptor cell death and normalized retinal function in AAV2/8-mMfpr mice. CEP97 is involved in regulating cilia assembly, a process that is critical to the maintenance of photoreceptor outer segments in the retina. Finally, ferritin is involved in iron storage and transport. Increased iron levels in the eye have been implicated in oxidative stress and retinal degeneration. Gene therapy rescue of ferritin may play a role in restoring iron levels in the retina and decreasing toxicity.

Finally, we identified 65 proteins that were not rescued following gene therapy. Among these proteins were lacadherin (MFGE8), basigin (BSG), monocarboxylate transporter 3 (SLC16A8), and chondroitin sulfate proteoglycan 5 (CSPG5; Table S4). MFGE8 is involved in regulating diurnal phagocytosis of photoreceptor outer segments by the RPE. Lack of synchronized retinal phagocytosis is implicated in age-related blindness. BSG is a glycoprotein that is implicated in retinal development. Knockout of Bsg in mice has been shown to cause altered retinal function, photoreceptor degeneration, and choroidal neovascularization. SLC16A8 is a proton-coupled monocarboxylate transporter involved in sub-retinal pH regulation. Interestingly, knockout of Scl16a8 in mice leads to a decrease in subretinal pH due to the accumulation of lactate and causes altered visual function. Previous genome-wide association studies (GWAS) have implicated the SLC16A8 locus in age-related macular degeneration. CSPG5 is a chondroitin-sulfate proteoglycan that has been previously found to be upregulated in mouse models of retinal degeneration (Rpe65\textsuperscript{-/-}). Although increased levels of CSPG5 have been implicated in retinal degeneration, its role in this process is poorly understood.
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Supplementary Figure 1. Fundus images and SD-OCT analysis of two patients with *MFRP* mutations.

Genotype:

![Fundus image and OCT analysis of patients with MFRP mutations](image)
Supplementary Figure 2. Individual MFRP Domain Models. (A) MFRP CUB1 domain modeled off the cubulin crystal structure (PDB: 3KQ4). (B) MFRP LDLA1 domain modeled off LDLR structure (PDB: 3P5B). (C) MFRP CUB2 domain modeled off the cubulin crystal structure (PDB: 3KQ4). (D) MFRP LDLA2 domain modeled off LDLR structure (PDB: 3P5B). (E) MFRP FZ-CRD domain modeled off the XWnt8-bound Frizzled-8 structure (PDB: 4F0A) as a template. The individual domains were joined using the homology-modeling protocol in the YASARA 15.7.25 software package to generate a MFRP model. The model was refined with an energy minimization in the YAMBER3 force field followed by a steepest descent minimization and simulated annealing.
**Supplemental Figure 3. Structural modeling of MFRP patient mutations.** (A) Schematic representation of patient mutations on the secondary structure of MFRP. The *rd6* mutation expresses in a truncated protein. The p.His384Profs*8 mutation leads to an insertion of a proline in the CUB2 domain followed by a frameshift. The p.Arg539Cys mutation adds an additional cysteine to the Frizzled cysteine-rich domain (CRD) of MFRP. The IVS10, +5, G>A is a splice donor mutation and does not affect the secondary structure. Finally, the c.492delC mutant expresses a truncated protein. (B) Homology-based model of human MFRP. (C) Predicted location of known mutations on MFRP structure. Mutations are found throughout multiple domains and are therefore predicted to affect multiple functions of the protein.
Supplemental Figure 4. RPE-choroid proteomic analysis pipeline. (A) The RPE-choroid were dissected from 9 mouse eyes. (B) Proteins were precipitated from dissected RPE-choroid using chloroform methanol and dissolved using 0.1% Rapidest detergent in 50 mM ammonium bicarbonate. Proteins were digested with trypsin. (C) Peptide intensities were analyzed by liquid chromatography-tandem mass spectrometry. Three biological replicates were analyzed using a Synapt G2 quadrupole-time-of-flight mass spectrometry (QTOF; Waters Corporation, Milford, MA). (D) The data were analyzed with MS\textsuperscript{E}/Identity\textsuperscript{E} algorithm (PLGS software Version 2.5 RC9) and Rosetta Elucidator software. Elucidator software detected 383,353 features across 27 LC/MS runs. Identifications were returned on 3,132 proteins with a PLGS score > 300 (pass 1 data only) and 4% false discovery rate. (E) Of the 3,132 proteins, 2,089 were represented by two or more peptides and used in further differential expression, ontology, and pathway analysis. Illustrations by Lucy Evans and Vinit Mahajan (acknowledgements section).
Supplemental Figure 5. Pathway analysis. Proteins in this list were interrogated using pathway analysis. The top 10 pathways are represented and are ranked by their log (p-value), obtained from the right-tailed Fisher Exact Test, and by their ratio of enrichment, which is equal to the number of observed proteins divided by the number of expected proteins from each pathway that is represented. (A) Proteins upregulated in Mfrp<sup>rd6</sup>/Mfrp<sup>rd6</sup> mice compared to controls. These proteins were restored to control levels following gene therapy (p<0.05). (B) A total of 36 proteins were upregulated in AAV2/8-mMfrp mice that were not seen in control mice or in Mfrp<sup>rd6</sup>/Mfrp<sup>rd6</sup> mice. We hypothesized that these pathways were upregulated in response to the AAV vector injection (p<0.05). (C) A total of 12 proteins were restored from Mfrp<sup>rd6</sup>/Mfrp<sup>rd6</sup> levels following gene therapy (p<0.05). Details of the individual proteins are listed in Table S4. (D) A total of 65 proteins were not rescued to control levels following gene therapy.
| Mutation  | Amino acid change | Affected Domain |
|-----------|------------------|-----------------|
| c.760G>A  | Arg54Gly         | Transmembrane   |
| c.496C>G  | Pro166Ala        | CUB1            |
| c.559G>A  | Glu187Lys        | CUB1            |
| c.602G>A  | Arg201His        | CUB1            |
| c.661C>T  | Pro221Ser        | CUB1            |
| c.664C>A  | Pro222Thr        | CUB1            |
| c.919G>A  | Gly307Cys        | CUB2            |
| c.1006G>A | Gly336Arg        | CUB2            |
| c.1115T>C | Leu372Pro        | CUB2            |
| c.1267C>T | Pro423Ser        | CUB2            |
| c.1366G>A | Gly456Ser        | LDL2            |
| c.1542G>C | Gln514His        | FZD/CRD         |
| c.1549C>T | Arg517Trp        | FZD/CRD         |
| c.1615C>T | Arg539Cys        | FZD/CRD         |
Table S2. Proteins upregulated in \textit{Mfrp}^{rd6}/\textit{Mfrp}^{rd6} mice.

| Uniprot ID | Uniprot name | Protein names |
|------------|---------------|---------------|
| O54983     | CRYM_MOUSE    | Ketimine reductase mu-crystallin (EC 1.5.1.25) (NADP-regulated thyroid-hormone-binding protein) |
| P52196     | THTR_MOUSE    | Thiosulfate sulfurtransferase (EC 2.8.1.1) (Rhodanese) |
| Q6GQT1     | A2MG_MOUSE    | Alpha-2-macroglobulin-P (Alpha-2-macroglobulin) |
| Q60634     | FLOT2_MOUSE   | Flotillin-2 (Membrane component chromosome 17 surface marker 1 homolog) |
| Q6ZWy3     | RS27L_MOUSE   | 40S ribosomal protein S27-like |
| Q8R527     | RHOQ_MOUSE    | Rho-related GTP-binding protein RhoQ (Ras-like protein TC10) |
| O88200     | CLC11_MOUSE   | C-type lectin domain family 11 member A |
| Q9R0G6     | COMP_MOUSE    | Cartilage oligomeric matrix protein (COMP) |
| Q80YQ1     | Q80YQ1_MOUSE  | Thrombospondin 1 |
| P09542     | MYL3_MOUSE    | Myosin light chain 3 |
| Q9QYR9     | ACOT2_MOUSE   | Acyl-coenzyme A thioesterase 2, mitochondrial (Acyl-CoA thioesterase 2) |
| Q9CP6      | NDUA5_MOUSE   | NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 5 |
| P33267     | CP2F2_MOUSE   | Cytochrome P450 2F2 (Naphthalene hydroxylase) |
| P32848     | PRVA_MOUSE    | Parvalbumin alpha |
| P20801     | TNNC2_MOUSE   | Troponin C, skeletal muscle (STNC) |
| Q3U9N4     | Q3U9N4_MOUSE  | Granulins (Putative uncharacterized protein) |
| P26883     | FKB1A_MOUSE   | Peptidyl-prolyl cis-trans isomerase FKBP1A (Rotamase) |
| P16460     | ASSY_MOUSE    | Argininosuccinate synthase (EC 6.3.4.5) (Citrulline--aspartate ligase) |
| P09528     | FRIH_MOUSE    | Ferritin heavy chain (Ferritin H subunit) (EC 1.16.3.1) |
| P27546     | MAP4_MOUSE    | Microtubule-associated protein 4 (MAP-4) |
| Uniprot ID | Uniprot name | Protein names |
|-----------|--------------|---------------|
| P22599    | A1AT2_MOUSE  | Alpha-1-antitrypsin 1-2 (AAT) |
| F6UXV2    | F6UXV2_MOUSE | Serine-protein kinase ATM (Fragment) |
| Q00623    | APOA1 MOUSE  | Apolipoprotein A-I |
| P49722    | PSA2_MOUSE   | Proteasome subunit alpha type-2 |
| A2AE89    | A2AE89_MOUSE | Glutathione S-transferase Mu 1 |
| A2AL18    | A2AL18_MOUSE | Rho GTPase-activating protein 11A |
| P15409    | OPSD_MOUSE   | Rhodopsin |
| P20612    | GNAT1_MOUSE  | Guanine nucleotide-binding protein G(t) subunit alpha-1 (Transducin alpha-1 chain) |
| P17879    | HS71B_MOUSE  | Heat shock 70 kDa protein 1B (Heat shock 70 kDa protein 1) (HSP70.1) |
| P45952    | ACDM_MOUSE   | Medium-chain specific acyl-CoA dehydrogenase, mitochondrial (MCAD) (EC 1.3.8.7) |
| Q61133    | GSTT2_MOUSE  | Glutathione S-transferase theta-2 (EC 2.5.1.18) (GST class-theta-2) |
| Q9D8U8    | SNX5_MOUSE   | Sorting nexin-5 |
| Q60847    | COCA1_MOUSE  | Collagen alpha-1(XII) chain |
| Q9CQG9    | TM100_MOUSE  | Transmembrane protein 100 |
| Q9Z1Q9    | SYVC_MOUSE   | Valine--tRNA ligase (EC 6.1.1.9) (Protein G7a) (Valyl-tRNA synthetase) (ValRS) |
| B1AZA7    | B1AZA7_MOUSE | Alpha-catulin |
| Q61029    | LAP2B_MOUSE  | Lamina-associated polypeptide 2 |
| P80315    | TCPD_MOUSE   | T-complex protein 1 subunit delta (TCP-1-delta) (A45) (CCT-delta) |
| Q8BG05    | ROA3_MOUSE   | Heterogeneous nuclear ribonucleoprotein A3 (hnRNP A3) |
| P63005    | LIS1_MOUSE   | Platelet-activating factor acylhydrolase IB subunit alpha |
| B2RSH2    | GNAI1_MOUSE  | Guanine nucleotide-binding protein G(i) subunit alpha-1 |
| Q8VDW0    | DX39A_MOUSE  | ATP-dependent RNA helicase DDX39A |
| Q9D552    | SPT17_MOUSE  | Spermatogenesis-associated protein 17 |
| Q8OX68    | Q8OX68_MOUSE | Citrate synthase |
| Q922J9    | FACR1_MOUSE  | Fatty acyl-CoA reductase 1 (EC 1.2.1.n2) |
| P13634    | CAH1_MOUSE   | Carbonic anhydrase 1 |
| P83882    | RL36A_MOUSE  | 60S ribosomal protein L36a (60S ribosomal protein L44) |
| Q8C726    | BTBD9_MOUSE  | BTB/POZ domain-containing protein 9 |
| Q3UIU2    | NDUB6_MOUSE  | NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 6 |
| Q6PD31    | TRAK1_MOUSE  | Trafficking kinesin-binding protein 1 |
| P51885    | LUM_MOUSE    | Lumican (Keratan sulfate proteoglycan lumican) (KSPG lumican) |
| Q9CPQ8    | ATP5L_MOUSE  | ATP synthase subunit g, mitochondrial |
| O88685    | PRS6A_MOUSE  | 26S protease regulatory subunit 6A |
| P24472    | GSTA4_MOUSE  | Glutathione S-transferase A4 |
### Table S4. Proteins rescued by gene therapy

| Uniprot ID | Uniprot name       | Protein names                                                        |
|------------|--------------------|---------------------------------------------------------------------|
| Q00897     | A1AT4_MOUSE        | Alpha-1-antitrypsin 1-4                                             |
| Q91VB8     | Q91VB8_MOUSE       | Alpha globin                                                        |
| P01942     | HBA_MOUSE          | Hemoglobin subunit alpha                                            |
| F6ZFS0     | F6ZFS0_MOUSE       | EGF-containing fibulin-like extracellular matrix protein 1          |
| A8DUK4     | A8DUK4_MOUSE       | Beta-globin                                                         |
| Q61702     | ITIH1_MOUSE        | Inter-alpha-trypsin inhibitor heavy chain H1                        |
| D3YUE2     | D3YUE2_MOUSE       | Procollagen C-endopeptidase enhancer 1                              |
| Q91WQ3     | SYYC_MOUSE         | Tyrosine--tRNA ligase                                               |
| Q9DCS9     | NDUBA_MOUSE        | NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 10        |
| F8WHM5     | F8WHM5_MOUSE       | Golgi apparatus protein 1 (Fragment)                                |
| Q9CZ62     | CEP97_MOUSE        | Centrosomal protein of 97 kDa (Cep97)                               |
| P00920     | CAH2_MOUSE         | Carbonic anhydrase 2                                                |
| Q8K480     | MFRP_MOUSE         | Membrane frizzled-related protein                                   |
| P31725     | S10A9_MOUSE        | Protein S100-A9                                                     |
Table S5. Proteins not rescued by gene therapy

| Uniprot ID | Uniprot name     | Protein names                                           |
|------------|------------------|--------------------------------------------------------|
| P46425     | GSTP2_MOUSE      | Glutathione S-transferase P 2                           |
| P04344     | CRGB_MOUSE       | Gamma-crystallin B                                      |
| D3YX34     | D3YX34_MOUSE     | Dynactin subunit 1                                      |
| Q6VYI4     | Q6VYI4_MOUSE     | TAR DNA-binding protein 43                              |
| P24622     | CRYAA_MOUSE      | Alpha-crystallin A chain                                |
| Q9QZF2     | GPC1_MOUSE       | Glypican-1                                              |
| G3UZI2     | G3UZI2_MOUSE     | Heterogeneous nuclear ribonucleoprotein Q               |
| Q62417     | SRBS1_MOUSE      | Sorbin and SH3 domain-containing protein 1              |
| Q9CZ44     | NSF1C_MOUSE      | NSFL1 cofactor p47 (p97 cofactor p47)                   |
| P17710     | HXK1_MOUSE       | Hexokinase-1                                            |
| Q91WJ8     | FUBP1_MOUSE      | Far upstream element-binding protein 1 (FBP)            |
| O08599     | STXB1_MOUSE      | Syntaxin-binding protein 1                              |
| P09405     | NUCL_MOUSE       | Nucleolin (Protein C23)                                 |
| P56546     | CTBP2_MOUSE      | C-terminal-binding protein 2 (CtBP2)                    |
| O35945     | AL1A7_MOUSE      | Aldehyde dehydrogenase, cytosolic 1                     |
| Q62148     | AL1A2_MOUSE      | Retinal dehydrogenase 2                                 |
| P63011     | RAB3A_MOUSE      | Ras-related protein Rab-3A                              |
| P15105     | GLNA_MOUSE       | Glutamine synthetase                                    |
| Q99JR1     | SFXN1_MOUSE      | Sideroflexin-1                                          |
| Q80U72     | SCRIB_MOUSE      | Protein scribble homolog (Scribble) (Protein LAP4)      |
| E9Q1Z0     | E9Q1Z0_MOUSE     | Keratin 90                                             |
| P11438     | LAMP1_MOUSE      | Lysosome-associated membrane glycoprotein 1             |
| Q8C9S4     | CC186_MOUSE      | Coiled-coil domain-containing protein 186              |
| H3BLG5     | H3BLG5_MOUSE     | Syntenin-1 (Fragment)                                   |
| Q8VCH7     | RDH10_MOUSE      | Retinol dehydrogenase 10                               |
| Q61171     | PRDX2_MOUSE      | Peroxiredoxin-2                                         |
| Q61553     | FSCN1_MOUSE      | Fascin                                                  |
| O54984     | ASNA_MOUSE       | ATPase Asna1                                            |
| E9Q2W9     | E9Q2W9_MOUSE     | Alpha-actinin-4                                         |
| O55240     | RDH1_MOUSE       | 11-cis retinol dehydrogenase                            |
| P61089     | UBE2N_MOUSE      | Ubiquitin-conjugating enzyme E2 N                       |
| Q61990     | PCBP2_MOUSE      | Poly(rC)-binding protein 2                              |
| Q9CQ19     | MYL9_MOUSE       | Myosin regulatory light polypeptide 9                   |
| Q62132     | PTPRR_MOUSE      | Receptor-type tyrosine-protein phosphatase R             |
| Uniprot ID | Organism   | Protein Name                                                                 |
|-----------|------------|------------------------------------------------------------------------------|
| Q71M36    | CSPG5_MOUSE| Chondroitin sulfate proteoglycan 5                                           |
| P97427    | DYPY1_MOUSE| Dihydropyrimidinase-related protein 1                                       |
| P21956    | MFGM_MOUSE | Lactadherin (MFGM)                                                          |
| H3BL49    | H3BL49_MOUSE| T-complex protein 1 subunit theta                                              |
| O35308    | MOT3_MOUSE | Monocarboxylate transporter 3                                                |
| Q8BMF3    | MAON_MOUSE | NADP-dependent malic enzyme, mitochondrial                                   |
| Q80TB8    | VAT1L_MOUSE| Synaptic vesicle membrane protein VAT-1 homolog-like                          |
| Q9QXC6    | Q9QXC6_MOUSE| Beta-A3/A1 crystallin protein                                                 |
| Q60737    | CSK21_MOUSE| Casein kinase II subunit alpha                                               |
| P43275    | H11_MOUSE  | Histone H1.1 (H1 VAR.3)                                                      |
| P29812    | TYRP2_MOUSE| L-dopachrome tautomerase                                                     |
| P18572    | BASI_MOUSE | Basigin                                                                      |
| Q9D0M5    | DYL2_MOUSE | Dynein light chain 2, cytoplasmian                                           |
| P62696    | CRBB2_MOUSE| Beta-crystallin B2                                                           |
| Q9Z275    | RLBP1_MOUSE| Retinaldehyde-binding protein 1                                              |
| Q91ZQ5    | RPE65_MOUSE| Retinoid isomerohydrolase                                                    |
| Q00915    | RET1_MOUSE | Retinol-binding protein 1                                                    |
| Q99M71    | EPDR1_MOUSE| Mammalian ependymin-related protein 1                                        |
| Q9JI60    | LRAT_MOUSE | Lecithin retinol acyltransferase                                              |
| Q91XU3    | PI42C_MOUSE| Phosphatidylinositol 5-phosphate 4-kinase type-2 gamma                      |
| Q9Z0P5    | TWF2_MOUSE | Twinfilin-2 (A6-related protein)                                             |
| P19246    | NFH_MOUSE  | Neurofilament heavy polypeptide (NF-H)                                       |
| E9Q4P0    | E9Q4P0_MOUSE| KxDL motif-containing protein 1                                              |
| F2Z468    | F2Z468_MOUSE| Matrilin-4                                                                  |
| Q9EQ80    | NIF3L_MOUSE| NIF3-like protein 1                                                          |
| Q9Z1T2    | TSP4_MOUSE | Thrombospondin-4                                                             |
| Q505F5    | LRC47_MOUSE| Leucine-rich repeat-containing protein 47                                    |
| Q9R0H0    | ACOX1_MOUSE| Peroxisomal acyl-coenzyme A oxidase 1 (AOX)                                  |
| P50171    | DHB8_MOUSE | Estradiol 17-beta-dehydrogenase 8                                            |
| P47964    | RL36_MOUSE | 60S ribosomal protein L36                                                     |
| A2ATI9    | A2ATI9_MOUSE| Golgi reassembly stacking protein 2, isoform CRA_d                           |