

## GeDiPNet Cluster 38 -- Enriched GO Terms (Biological Process)

GO term enrichment: Biological Process terms (gene2go, human/tax\_id=9606 only), upper-tail hypergeometric test, fold enrichment = (overlap / cluster gene count) / (term gene count / universe size), Benjamini-Hochberg FDR-corrected. Top 15 terms per cluster by q-value. See scripts/build\_cluster\_go\_enrichment.php on gedipnet.bicnirrh.res.in. Data as of: 2026-10-08 03:23:04. · Rows: 15 · Generated: 2026-10-08 10:54:28

| GO Term                                       | GO ID      | Overlap Genes | Overlap Gene Names                                                                 | Term Gene Count | Cluster Gene Count | Fold Enrichment | P-value   | FDR Q-value |
|-----------------------------------------------|------------|---------------|------------------------------------------------------------------------------------|-----------------|--------------------|-----------------|-----------|-------------|
| lens development in camera-type eye           | GO:0002088 | 22            | CRYAA, CRYAB, CRYBB1, CRYBB3, CRYGC, CRYGD, CRYGS, FOXE3, GJA8, LIM2, MIP, PAX6    | 48              | 223                | 38.41           | 3.546e-30 | 1.719e-26   |
| visual perception                             | GO:0007601 | 22            | BFSP2, COL18A1, COL2A1, CRYAA, CRYBB1, CRYBB3, CRYGC, CRYGD, CRYGS, MIP, PAX6, RHO | 215             | 223                | 8.57            | 1.376e-14 | 8.592e-12   |
| camera-type eye development                   | GO:0043010 | 14            | BMP4, CRYAA, CRYAB, FOXE3, GJA8, JAG1, LIM2, MITF, PAX6, PITX2, CRYBA4, CRYBB2     | 74              | 223                | 15.85           | 1.911e-13 | 9.913e-11   |
| lens fiber cell differentiation               | GO:0070306 | 5             | CRYGD, HSF4, PITX3, TDRD7, MAF                                                     | 15              | 223                | 27.93           | 6.304e-7  | 5.725e-5    |
| eye development                               | GO:0001654 | 7             | CPAMD8, FOXE3, PAX6, CRYGB, SIPA1L3, CRYGA, SIX6                                   | 49              | 223                | 11.97           | 1.760e-6  | 1.324e-4    |
| lens fiber cell development                   | GO:0070307 | 4             | BFSP2, VIM, BFSP1, CRYGB                                                           | 9               | 223                | 37.24           | 2.373e-6  | 1.684e-4    |
| lens morphogenesis in camera-type eye         | GO:0002089 | 4             | CRYAA, PITX3, TDRD7, NECTIN3                                                       | 15              | 223                | 22.35           | 2.430e-5  | 1.055e-3    |
| gap junction-mediated intercellular transport | GO:1990349 | 3             | GJA8, MIP, GJA3                                                                    | 6               | 223                | 41.90           | 3.266e-5  | 1.322e-3    |
| axon ensheathment                             | GO:0008366 | 3             | PPARD, QKI, PRX                                                                    | 7               | 223                | 35.91           | 5.665e-5  | 2.008e-3    |
| maintenance of lens transparency              | GO:0036438 | 3             | MIP, GCNT2, CHMP4B                                                                 | 8               | 223                | 31.42           | 8.984e-5  | 2.859e-3    |
| lens fiber cell morphogenesis                 | GO:0070309 | 3             | CRYAA, EPHA2, CRYGB                                                                | 8               | 223                | 31.42           | 8.984e-5  | 2.859e-3    |
| iris morphogenesis                            | GO:0061072 | 3             | FOXE3, PAX6, PITX2                                                                 | 9               | 223                | 27.93           | 1.336e-4  | 3.829e-3    |
| embryonic eye morphogenesis                   | GO:0048048 | 3             | MFAP5, RARB, FBN1                                                                  | 11              | 223                | 22.85           | 2.578e-4  | 6.151e-3    |
| protein refolding                             | GO:0042026 | 4             | CRYAA, CRYAB, HSPA1A, HSPA1L                                                       | 27              | 223                | 12.41           | 2.792e-4  | 6.495e-3    |
| cell population proliferation                 | GO:0008283 | 11            | BMP4, CDKN2C, CNTNAP2, FGF18, FGFR3, HMGA2, OCA2, PAX6, PPARD, RARB, TYR           | 263             | 223                | 3.50            | 3.338e-4  | 7.384e-3    |