

## GeDiPNet Cluster 238 -- 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: 2026-10-07 03:23:06. · Rows: 15 · Generated: 2026-10-07 01:45:21

| GO Term                                                   | GO ID      | Overlap Genes | Overlap Gene Names                                                                      | Term Gene Count | Cluster Gene Count | Fold Enrichment | P-value   | FDR Q-value |
|-----------------------------------------------------------|------------|---------------|-----------------------------------------------------------------------------------------|-----------------|--------------------|-----------------|-----------|-------------|
| visual perception                                         | GO:0007601 | 26            | ABCA4, HMCN1, AIPL1, RDH5, TRPM1, EYS, CDH3, BBS10, BEST1, CNGA3, FSCN2, PRPH2          | 215             | 209                | 10.81           | 1.377e-19 | 2.093e-16   |
| complement activation                                     | GO:0006956 | 10            | CFHR1, CFI, C2, C3, C9, CFB, CFH, CFHR4, CFHR5, CFHR3                                   | 35              | 209                | 25.55           | 3.551e-12 | 1.434e-9    |
| complement activation, alternative pathway                | GO:0006957 | 5             | C3, C9, CFB, CFH, CFHR5                                                                 | 16              | 209                | 27.94           | 6.592e-7  | 5.902e-5    |
| retina development in camera-type eye                     | GO:0060041 | 8             | BBS10, CNGA3, PRPH2, CRB1, NDP, RHO, RD3, RP1                                           | 85              | 209                | 8.42            | 4.926e-6  | 2.967e-4    |
| detection of light stimulus involved in visual perception | GO:0050908 | 5             | EYS, BEST1, PRPH2, CRB1, RPE65                                                          | 24              | 209                | 18.63           | 5.963e-6  | 3.453e-4    |
| phototransduction, visible light                          | GO:0007603 | 4             | ABCA4, AIPL1, RHO, RP1                                                                  | 13              | 209                | 27.51           | 1.004e-5  | 5.240e-4    |
| photoreceptor cell maintenance                            | GO:0045494 | 6             | ABCA4, BBS10, ERCC6, CRB1, RHO, RP1                                                     | 45              | 209                | 11.92           | 1.031e-5  | 5.337e-4    |
| glutathione metabolic process                             | GO:0006749 | 6             | SOD2, GSTM1, GSTP1, GSTT1, GSR, NDP                                                     | 49              | 209                | 10.95           | 1.706e-5  | 7.925e-4    |
| retina homeostasis                                        | GO:0001895 | 4             | AIPL1, ARMS2, CDH3, RPE65                                                               | 15              | 209                | 23.84           | 1.884e-5  | 8.557e-4    |
| photoreceptor cell outer segment organization             | GO:0035845 | 4             | PRPH2, TOPORS, CRB1, RP1                                                                | 15              | 209                | 23.84           | 1.884e-5  | 8.557e-4    |
| positive regulation of apoptotic process                  | GO:0043065 | 14            | ALDH1A2, BARD1, MMP9, TGFB1, HTRA1, MMP2, SQSTM1, TNFRSF10A, AIFM1, APAF1, CASP3, CASP9 | 326             | 209                | 3.84            | 1.923e-5  | 8.709e-4    |
| cellular response to light stimulus                       | GO:0071482 | 4             | TRPM1, CRB1, RHO, RP1                                                                   | 16              | 209                | 22.35           | 2.490e-5  | 1.059e-3    |
| response to hypoxia                                       | GO:0001666 | 10            | SOD2, MTHFR, VEGFA, ERCC2, MMP2, ND4, APAF1, CASP3, CASP9, NDP                          | 176             | 209                | 5.08            | 2.986e-5  | 1.216e-3    |
| reverse cholesterol transport                             | GO:0043691 | 4             | ABCA1, APOE, CETP, LIPC                                                                 | 17              | 209                | 21.04           | 3.228e-5  | 1.292e-3    |
| extracellular matrix organization                         | GO:0030198 | 9             | MMP9, ELN, ERCC2, MMP2, FBLN5, DNAJB6, COL4A2, TNR, TNXB                                | 145             | 209                | 5.55            | 3.761e-5  | 1.451e-3    |