

## GeDiPNet Cluster 98 -- 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 17:26:21

| GO Term                                                   | GO ID      | Overlap Genes | Overlap Gene Names                                                         | Term Gene Count | Cluster Gene Count | Fold Enrichment | P-value  | FDR Q-value |
|-----------------------------------------------------------|------------|---------------|----------------------------------------------------------------------------|-----------------|--------------------|-----------------|----------|-------------|
| positive regulation of peptidyl-serine phosphorylation    | GO:0033138 | 4             | IL6, BRAF, EGFR, PDCCD10                                                   | 20              | 44                 | 84.94           | 1.260e-7 | 1.486e-5    |
| heart development                                         | GO:0007507 | 8             | ENG, GLI2, OXT, NIPBL, MMP2, PKD1, PKD2, SOX17                             | 273             | 44                 | 12.45           | 2.105e-7 | 2.300e-5    |
| embryonic placenta development                            | GO:0001892 | 4             | EGFR, TTPA, PKD1, PKD2                                                     | 26              | 44                 | 65.34           | 3.848e-7 | 3.788e-5    |
| female pregnancy                                          | GO:0007565 | 5             | KRAS, GNRH1, OXT, BCL2, MMP2                                               | 80              | 44                 | 26.54           | 1.207e-6 | 9.749e-5    |
| gallbladder development                                   | GO:0061010 | 2             | NIPBL, SOX17                                                               | 2               | 44                 | 424.70          | 5.418e-6 | 3.262e-4    |
| response to glucocorticoid                                | GO:0051384 | 4             | IL6, KRAS, OXT, BCL2                                                       | 53              | 44                 | 32.05           | 7.196e-6 | 4.100e-4    |
| positive regulation of transcription by RNA polymerase II | GO:0045944 | 12            | IL6, EGFR, ENG, GLI2, NLRP3, NOTCH4, CSF3, NIPBL, KMT2D, PKD1, PKD2, SOX17 | 1208            | 44                 | 4.22            | 1.535e-5 | 7.420e-4    |
| negative regulation of apoptotic process                  | GO:0043066 | 8             | IL6, BRAF, EGFR, MAP4K4, PDCCD10, GNRH1, BCL2, MMP9                        | 524             | 44                 | 6.48            | 2.639e-5 | 1.126e-3    |
| metanephric ascending thin limb development               | GO:0072218 | 2             | PKD1, PKD2                                                                 | 4               | 44                 | 212.35          | 3.241e-5 | 1.313e-3    |
| response to steroid hormone                               | GO:0048545 | 3             | GNRH1, OXT, BCL2                                                           | 30              | 44                 | 42.47           | 4.730e-5 | 1.759e-3    |
| developmental growth                                      | GO:0048589 | 3             | GLI2, NIPBL, BCL2                                                          | 30              | 44                 | 42.47           | 4.730e-5 | 1.759e-3    |
| cellular response to virus                                | GO:0098586 | 4             | IL6, GLI2, NLRP3, IFNA2                                                    | 89              | 44                 | 19.09           | 5.642e-5 | 2.006e-3    |
| mesonephric duct development                              | GO:0072177 | 2             | PKD1, PKD2                                                                 | 6               | 44                 | 141.57          | 8.079e-5 | 2.644e-3    |
| endodermal cell differentiation                           | GO:0035987 | 3             | MMP2, MMP9, SOX17                                                          | 36              | 44                 | 35.39           | 8.236e-5 | 2.682e-3    |
| metanephros development                                   | GO:0001656 | 3             | NIPBL, BCL2, SOX17                                                         | 38              | 44                 | 33.53           | 9.700e-5 | 3.024e-3    |