

GeDiPNet Cluster 130 -- 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: 2026-10-09 03:23:08. · Rows: 15 · Generated: 2026-10-08 23:31:35

| 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             | BRAF, EGFR, PDCD10, IL6                          | 20              | 28                 | 133.48          | 1.921e-8 | 2.966e-6    |
| negative regulation of apoptotic process                        | GO:0043066 | 7             | HMGA2, BRAF, EGFR, MAP4K4, PDCD10, IL6, MITF     | 524             | 28                 | 8.92            | 9.293e-6 | 4.978e-4    |
| MAPK cascade                                                    | GO:0000165 | 4             | BRAF, EGFR, KRAS, MAP4K4                         | 147             | 28                 | 18.16           | 6.497e-5 | 2.196e-3    |
| positive regulation of T-helper 2 cell cytokine production      | GO:2000553 | 2             | NLRP3, IL6                                       | 9               | 28                 | 148.31          | 7.744e-5 | 2.507e-3    |
| positive regulation of gene expression                          | GO:0010628 | 6             | HMGA2, BRAF, KRAS, PDCD10, IL6, MITF             | 504             | 28                 | 7.95            | 8.491e-5 | 2.684e-3    |
| synaptic vesicle clustering                                     | GO:0097091 | 2             | CDH2, SYN3                                       | 12              | 28                 | 111.23          | 1.416e-4 | 3.931e-3    |
| regulation of synaptic transmission, GABAergic                  | GO:0032228 | 2             | KRAS, SYN3                                       | 14              | 28                 | 95.34           | 1.948e-4 | 4.961e-3    |
| regulation of cell population proliferation                     | GO:0042127 | 4             | BRAF, EGFR, ENG, MITF                            | 201             | 28                 | 13.28           | 2.173e-4 | 5.342e-3    |
| positive regulation of protein serine/threonine kinase activity | GO:0071902 | 2             | HMGA2, PDCD10                                    | 15              | 28                 | 88.99           | 2.246e-4 | 5.465e-3    |
| positive regulation of transcription by RNA polymerase II       | GO:0045944 | 8             | HMGA2, EGFR, ENG, GLI2, NLRP3, NOTCH4, IL6, MITF | 1208            | 28                 | 4.42            | 2.886e-4 | 6.577e-3    |
| cellular response to virus                                      | GO:0098586 | 3             | GLI2, NLRP3, IL6                                 | 89              | 28                 | 22.50           | 3.139e-4 | 6.994e-3    |
| striated muscle cell differentiation                            | GO:0051146 | 2             | CDH2, KRAS                                       | 20              | 28                 | 66.74           | 4.045e-4 | 8.316e-3    |
| epithelial tube branching involved in lung morphogenesis        | GO:0060441 | 2             | HMGA2, KRAS                                      | 20              | 28                 | 66.74           | 4.045e-4 | 8.316e-3    |
| positive regulation of glial cell proliferation                 | GO:0060252 | 2             | KRAS, IL6                                        | 22              | 28                 | 60.67           | 4.909e-4 | 9.546e-3    |
| stress fiber assembly                                           | GO:0043149 | 2             | BRAF, PDCD10                                     | 24              | 28                 | 55.62           | 5.855e-4 | 1.075e-2    |