

GeDiPNet Cluster 108 -- 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 02:36:44

| GO Term                                                                    | GO ID      | Overlap Genes | Overlap Gene Names | Term Gene Count | Cluster Gene Count | Fold Enrichment | P-value  | FDR Q-value |
|----------------------------------------------------------------------------|------------|---------------|--------------------|-----------------|--------------------|-----------------|----------|-------------|
| regulation of complement-dependent cytotoxicity                            | GO:1903659 | 2             | CFH, IL10          | 8               | 19                 | 245.88          | 2.732e-5 | 1.153e-3    |
| negative regulation of autophagy                                           | GO:0010507 | 3             | WNK1, IL10, SLC7A5 | 73              | 19                 | 40.42           | 5.299e-5 | 1.917e-3    |
| negative regulation of heterotypic cell-cell adhesion                      | GO:0034115 | 2             | WNK1, IL10         | 11              | 19                 | 178.82          | 5.357e-5 | 1.929e-3    |
| liver regeneration                                                         | GO:0097421 | 2             | IL10, SLC7A5       | 29              | 19                 | 67.83           | 3.912e-4 | 8.279e-3    |
| complement activation                                                      | GO:0006956 | 2             | CFH, CFI           | 35              | 19                 | 56.20           | 5.712e-4 | 1.070e-2    |
| complement activation, classical pathway                                   | GO:0006958 | 2             | CFI, CD46          | 37              | 19                 | 53.16           | 6.386e-4 | 1.151e-2    |
| response to low light intensity stimulus                                   | GO:0009645 | 1             | PRPH2              | 1               | 19                 | 983.53          | 1.017e-3 | 1.554e-2    |
| negative regulation of chronic inflammatory response to antigenic stimulus | GO:0002875 | 1             | IL10               | 1               | 19                 | 983.53          | 1.017e-3 | 1.554e-2    |
| negative regulation of cytokine activity                                   | GO:0060302 | 1             | IL10               | 1               | 19                 | 983.53          | 1.017e-3 | 1.554e-2    |
| regulation of response to wounding                                         | GO:1903034 | 1             | IL10               | 1               | 19                 | 983.53          | 1.017e-3 | 1.554e-2    |
| regulation of complement activation, alternative pathway                   | GO:0030451 | 1             | CFH                | 1               | 19                 | 983.53          | 1.017e-3 | 1.554e-2    |
| positive regulation of L-leucine import across plasma membrane             | GO:1905534 | 1             | SLC7A5             | 1               | 19                 | 983.53          | 1.017e-3 | 1.554e-2    |
| positive regulation of termination of RNA polymerase II transcription      | GO:1904595 | 1             | WNK1               | 1               | 19                 | 983.53          | 1.017e-3 | 1.554e-2    |
| tissue development                                                         | GO:0009888 | 2             | GATA5, NOTCH4      | 51              | 19                 | 38.57           | 1.212e-3 | 1.736e-2    |
| sequestering of extracellular ligand from receptor                         | GO:0035581 | 1             | CD46               | 2               | 19                 | 491.76          | 2.033e-3 | 2.335e-2    |