

GeDiPNet Cluster 615 -- 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: 2026-10-20 03:23:14. · Rows: 15 · Generated: 2026-10-20 00:01:10

| GO Term                                                | GO ID      | Overlap Genes | Overlap Gene Names | Term Gene Count | Cluster Gene Count | Fold Enrichment | P-value  | FDR Q-value |
|--------------------------------------------------------|------------|---------------|--------------------|-----------------|--------------------|-----------------|----------|-------------|
| response to cytokine                                   | GO:0034097 | 3             | IL6R, RELB, IL6ST  | 56              | 7                  | 143.01          | 8.846e-7 | 7.747e-5    |
| ciliary neurotrophic factor-mediated signaling pathway | GO:0070120 | 2             | IL6R, IL6ST        | 5               | 7                  | 1067.83         | 1.202e-6 | 9.986e-5    |
| interleukin-11-mediated signaling pathway              | GO:0038154 | 2             | IL6R, IL6ST        | 7               | 7                  | 762.73          | 2.524e-6 | 1.827e-4    |
| B cell differentiation                                 | GO:0030183 | 3             | MS4A1, CR2, ADAM17 | 80              | 7                  | 100.11          | 2.612e-6 | 1.877e-4    |
| neutrophil mediated immunity                           | GO:0002446 | 2             | IL6R, ADAM17       | 11              | 7                  | 485.38          | 6.605e-6 | 3.941e-4    |
| positive regulation of leukocyte chemotaxis            | GO:0002690 | 2             | IL6R, ADAM17       | 13              | 7                  | 410.70          | 9.363e-6 | 5.169e-4    |
| T-helper 17 cell lineage commitment                    | GO:0072540 | 2             | IL6R, IL6ST        | 13              | 7                  | 410.70          | 9.363e-6 | 5.169e-4    |
| positive regulation of platelet aggregation            | GO:1901731 | 2             | IL6R, IL6ST        | 13              | 7                  | 410.70          | 9.363e-6 | 5.169e-4    |
| interleukin-6-mediated signaling pathway               | GO:0070102 | 2             | IL6R, IL6ST        | 16              | 7                  | 333.70          | 1.440e-5 | 7.220e-4    |
| cell surface receptor signaling pathway via STAT       | GO:0097696 | 2             | IL6R, IL6ST        | 28              | 7                  | 190.68          | 4.526e-5 | 1.713e-3    |
| B cell proliferation                                   | GO:0042100 | 2             | MS4A1, CR2         | 38              | 7                  | 140.50          | 8.402e-5 | 2.716e-3    |
| B cell activation                                      | GO:0042113 | 2             | MS4A1, CR2         | 44              | 7                  | 121.34          | 1.129e-4 | 3.378e-3    |
| positive regulation of chemokine production            | GO:0032722 | 2             | IL6R, ADAM17       | 49              | 7                  | 108.96          | 1.403e-4 | 3.937e-3    |
| cell surface receptor signaling pathway via JAK-STAT   | GO:0007259 | 2             | IL6R, IL6ST        | 67              | 7                  | 79.69           | 2.629e-4 | 6.179e-3    |
| positive regulation of osteoblast differentiation      | GO:0045669 | 2             | IL6R, IL6ST        | 78              | 7                  | 68.45           | 3.563e-4 | 7.582e-3    |