

## GeDiPNet Cluster 551 -- 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: 2026-10-19 23:18:59

| GO Term                                                                                   | GO ID      | Overlap Genes | Overlap Gene Names                  | Term Gene Count | Cluster Gene Count | Fold Enrichment | P-value  | FDR Q-value |
|-------------------------------------------------------------------------------------------|------------|---------------|-------------------------------------|-----------------|--------------------|-----------------|----------|-------------|
| innate immune response                                                                    | GO:0045087 | 5             | C2, TRIM10, TRIM31, TRIM40, CR2     | 605             | 11                 | 14.04           | 1.375e-5 | 6.966e-4    |
| antigen processing and presentation of peptide or polysaccharide antigen via MHC class II | GO:0002504 | 2             | HLA-DPA1, HLA-DPB1                  | 15              | 11                 | 226.51          | 3.294e-5 | 1.347e-3    |
| peptide antigen assembly with MHC class II protein complex                                | GO:0002503 | 2             | HLA-DPA1, HLA-DPB1                  | 16              | 11                 | 212.35          | 3.763e-5 | 1.487e-3    |
| host-mediated suppression of symbiont invasion                                            | GO:0046597 | 2             | TRIM10, TRIM31                      | 24              | 11                 | 141.57          | 8.633e-5 | 2.773e-3    |
| immune system process                                                                     | GO:0002376 | 5             | C2, HLA-DPA1, HLA-DPB1, TRIM31, CR2 | 943             | 11                 | 9.01            | 1.159e-4 | 3.442e-3    |
| antigen processing and presentation of exogenous peptide antigen via MHC class II         | GO:0019886 | 2             | HLA-DPA1, HLA-DPB1                  | 31              | 11                 | 109.60          | 1.451e-4 | 4.037e-3    |
| complement activation, classical pathway                                                  | GO:0006958 | 2             | C2, CR2                             | 37              | 11                 | 91.83           | 2.075e-4 | 5.215e-3    |
| positive regulation of immune response                                                    | GO:0050778 | 2             | HLA-DPA1, HLA-DPB1                  | 40              | 11                 | 84.94           | 2.427e-4 | 5.824e-3    |
| positive regulation of T cell activation                                                  | GO:0050870 | 2             | HLA-DPA1, HLA-DPB1                  | 45              | 11                 | 75.50           | 3.076e-4 | 6.904e-3    |
| antigen processing and presentation                                                       | GO:0019882 | 2             | HLA-DPA1, HLA-DPB1                  | 48              | 11                 | 70.78           | 3.501e-4 | 7.487e-3    |
| negative regulation of interleukin-2-mediated signaling pathway                           | GO:1902206 | 1             | PTPN2                               | 1               | 11                 | 1698.82         | 5.886e-4 | 1.058e-2    |
| negative regulation of positive thymic T cell selection                                   | GO:1902233 | 1             | PTPN2                               | 1               | 11                 | 1698.82         | 5.886e-4 | 1.058e-2    |
| erythrocyte differentiation                                                               | GO:0030218 | 2             | TRIM10, PTPN2                       | 65              | 11                 | 52.27           | 6.421e-4 | 1.113e-2    |
| positive regulation of T cell proliferation                                               | GO:0042102 | 2             | HLA-DPA1, HLA-DPB1                  | 67              | 11                 | 50.71           | 6.821e-4 | 1.167e-2    |
| positive regulation of type II interferon production                                      | GO:0032729 | 2             | HLA-DPA1, HLA-DPB1                  | 77              | 11                 | 44.13           | 8.998e-4 | 1.379e-2    |