

## GeDiPNet Cluster 164 -- 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 12:11:42

| GO Term                                                                                                           | GO ID      | Overlap Genes | Overlap Gene Names                                                | Term Gene Count | Cluster Gene Count | Fold Enrichment | P-value  | FDR Q-value |
|-------------------------------------------------------------------------------------------------------------------|------------|---------------|-------------------------------------------------------------------|-----------------|--------------------|-----------------|----------|-------------|
| antigen processing and presentation                                                                               | GO:0019882 | 5             | HLA-DPB1, HLA-DRB1, HLA-A, HLA-B, HLA-E                           | 48              | 28                 | 69.52           | 8.484e-9 | 1.450e-6    |
| protection from natural killer cell mediated cytotoxicity                                                         | GO:0042270 | 3             | HLA-A, HLA-B, HLA-E                                               | 6               | 28                 | 333.70          | 6.007e-8 | 7.902e-6    |
| positive regulation of T cell mediated cytotoxicity                                                               | GO:0001916 | 4             | HLA-DRB1, HLA-A, HLA-B, HLA-E                                     | 34              | 28                 | 78.52           | 1.813e-7 | 2.024e-5    |
| negative regulation of B cell apoptotic process                                                                   | GO:0002903 | 3             | IL2, BCL2, BCL6                                                   | 11              | 28                 | 182.02          | 4.931e-7 | 4.682e-5    |
| detection of bacterium                                                                                            | GO:0016045 | 3             | HLA-DRB1, HLA-A, HLA-B                                            | 12              | 28                 | 166.85          | 6.568e-7 | 5.931e-5    |
| immune response                                                                                                   | GO:0006955 | 8             | CTLA4, FCGR3A, HLA-DPB1, HLA-DRB1, HLA-A, HLA-B, IL2, HLA-E       | 543             | 28                 | 9.83            | 8.981e-7 | 7.655e-5    |
| antigen processing and presentation of endogenous peptide antigen via MHC class Ib                                | GO:0002476 | 3             | HLA-A, HLA-B, HLA-E                                               | 14              | 28                 | 143.01          | 1.085e-6 | 8.949e-5    |
| antigen processing and presentation of endogenous peptide antigen via MHC class I via ER pathway, TAP-independent | GO:0002486 | 3             | HLA-A, HLA-B, HLA-E                                               | 14              | 28                 | 143.01          | 1.085e-6 | 8.949e-5    |
| antigen processing and presentation of peptide antigen via MHC class I                                            | GO:0002474 | 3             | HLA-A, HLA-B, HLA-E                                               | 17              | 28                 | 117.78          | 2.020e-6 | 1.477e-4    |
| positive regulation of CD8-positive, alpha-beta T cell activation                                                 | GO:2001187 | 2             | HLA-A, HLA-E                                                      | 2               | 28                 | 667.39          | 2.165e-6 | 1.563e-4    |
| immune system process                                                                                             | GO:0002376 | 9             | CTLA4, FCGR3A, HLA-DPB1, HLA-DRB1, HLA-A, HLA-B, IL2, BCL6, HLA-E | 943             | 28                 | 6.37            | 5.913e-6 | 3.502e-4    |
| positive regulation of CD8-positive, alpha-beta T cell proliferation                                              | GO:2000566 | 2             | HLA-A, HLA-E                                                      | 3               | 28                 | 444.93          | 6.489e-6 | 3.771e-4    |
| adaptive immune response                                                                                          | GO:0002250 | 7             | CTLA4, HLA-DPB1, HLA-DRB1, HLA-A, HLA-B, IL2, HLA-E               | 507             | 28                 | 9.21            | 7.493e-6 | 4.241e-4    |
| CD8-positive, alpha-beta T cell activation                                                                        | GO:0036037 | 2             | HLA-A, HLA-E                                                      | 4               | 28                 | 333.70          | 1.297e-5 | 6.484e-4    |
| T cell receptor signaling pathway                                                                                 | GO:0050852 | 4             | CTLA4, HLA-DPB1, HLA-DRB1, HLA-A                                  | 121             | 28                 | 22.06           | 3.036e-5 | 1.245e-3    |