

## GeDiPNet Cluster 385 -- 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: 2026-10-09 13:44:49

| GO Term                                         | GO ID      | Overlap Genes | Overlap Gene Names                                   | Term Gene Count | Cluster Gene Count | Fold Enrichment | P-value   | FDR Q-value |
|-------------------------------------------------|------------|---------------|------------------------------------------------------|-----------------|--------------------|-----------------|-----------|-------------|
| complement activation                           | GO:0006956 | 16            | C2, C4B, C8A, C8B, C9, CFB, C3, C4A, C5, C6, C7, C1S | 35              | 18                 | 474.59          | 5.904e-44 | 8.327e-40   |
| complement activation, GZMK pathway             | GO:0160257 | 11            | C2, C4B, C8A, C8B, C9, C3, C4A, C5, C6, C7, C8G      | 12              | 18                 | 951.65          | 1.575e-34 | 1.207e-30   |
| complement activation, classical pathway        | GO:0006958 | 13            | C2, C4B, C8A, C8B, C9, C3, C4A, C5, C6, C7, C1S, CFI | 37              | 18                 | 364.76          | 5.599e-33 | 4.113e-29   |
| complement activation, alternative pathway      | GO:0006957 | 10            | C8A, C8B, C9, CFB, C3, C5, C7, CFD, CFH, C8G         | 16              | 18                 | 648.85          | 2.449e-28 | 1.183e-24   |
| killing of cells of another organism            | GO:0031640 | 12            | C2, C8A, C8B, C9, CFB, C3, C4A, C5, C6, C7, C1S, C8G | 104             | 18                 | 119.79          | 8.277e-24 | 2.373e-20   |
| innate immune response                          | GO:0045087 | 16            | C2, C4B, C8A, C8B, C9, CFB, C3, C4A, C5, C6, C7, C1S | 605             | 18                 | 27.46           | 1.729e-22 | 4.092e-19   |
| immune system process                           | GO:0002376 | 16            | C2, C4B, C8A, C8B, C9, CFB, C3, C4A, C5, C6, C7, C1S | 943             | 18                 | 17.61           | 2.177e-19 | 3.185e-16   |
| activation of membrane attack complex           | GO:0001905 | 5             | C2, CFB, C3, C4A, C1S                                | 13              | 18                 | 399.29          | 5.783e-13 | 2.723e-10   |
| positive regulation of immune response          | GO:0050778 | 6             | C8A, C8B, C9, C6, C7, C8G                            | 40              | 18                 | 155.73          | 1.183e-12 | 5.302e-10   |
| opsonization                                    | GO:0008228 | 5             | C2, C4B, C3, C4A, C1S                                | 18              | 18                 | 288.38          | 3.839e-12 | 1.545e-9    |
| positive regulation of apoptotic cell clearance | GO:2000427 | 4             | C2, C4B, C3, C4A                                     | 6               | 18                 | 692.11          | 9.026e-12 | 3.350e-9    |
| complement activation, lectin pathway           | GO:0001867 | 4             | C2, C3, C4A, C5                                      | 13              | 18                 | 319.44          | 4.284e-10 | 1.065e-7    |
| protein maturation                              | GO:0051604 | 6             | C2, CFB, C3, C4A, C1S, CFD                           | 134             | 18                 | 46.49           | 2.101e-9  | 4.312e-7    |
| immune response                                 | GO:0006955 | 6             | C8A, C8B, C9, C3, C6, C7                             | 543             | 18                 | 11.47           | 8.070e-6  | 4.462e-4    |
| response to bacterium                           | GO:0009617 | 4             | C2, CFB, C3, CFD                                     | 140             | 18                 | 29.66           | 8.511e-6  | 4.657e-4    |