

## GeDiPNet Cluster 99 -- 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: 2026-10-07 21:59:02

| GO Term                                                                  | GO ID      | Overlap Genes | Overlap Gene Names                            | Term Gene Count | Cluster Gene Count | Fold Enrichment | P-value  | FDR Q-value |
|--------------------------------------------------------------------------|------------|---------------|-----------------------------------------------|-----------------|--------------------|-----------------|----------|-------------|
| DNA-templated transcription                                              | GO:0006351 | 6             | POLR1C, POLR3K, POLR3B, POLR3A, ERCC2, POLR1A | 113             | 48                 | 20.67           | 4.268e-7 | 4.137e-5    |
| tRNA aminoacylation for protein translation                              | GO:0006418 | 4             | RARS1, AARS1, KARS1, EPRS1                    | 36              | 48                 | 43.26           | 2.124e-6 | 1.539e-4    |
| protein import into mitochondrial intermembrane space                    | GO:0045041 | 2             | HSPD1, AIFM1                                  | 3               | 48                 | 259.54          | 1.935e-5 | 8.876e-4    |
| lysosome organization                                                    | GO:0007040 | 4             | HEXA, TMEM63A, VPS18, TMEM106B                | 65              | 48                 | 23.96           | 2.312e-5 | 1.013e-3    |
| myelination                                                              | GO:0042552 | 4             | TMEM163, GALC, HEXA, MAL                      | 73              | 48                 | 21.33           | 3.661e-5 | 1.448e-3    |
| organelle fusion                                                         | GO:0048284 | 2             | VPS11, VPS18                                  | 4               | 48                 | 194.66          | 3.864e-5 | 1.512e-3    |
| translation                                                              | GO:0006412 | 6             | AIMP1, RARS1, AARS1, KARS1, EPRS1, AIMP2      | 310             | 48                 | 7.54            | 1.356e-4 | 3.872e-3    |
| positive regulation of interferon-beta production                        | GO:0032728 | 3             | POLR3B, POLR3A, TOMM70                        | 41              | 48                 | 28.49           | 1.583e-4 | 4.354e-3    |
| regulation of SNARE complex assembly                                     | GO:0035542 | 2             | VPS11, VPS18                                  | 12              | 48                 | 64.89           | 4.195e-4 | 8.675e-3    |
| tRNA aminoacylation                                                      | GO:0043039 | 2             | AARS1, EPRS1                                  | 13              | 48                 | 59.89           | 4.949e-4 | 9.678e-3    |
| transcription by RNA polymerase I                                        | GO:0006360 | 2             | POLR1C, POLR1A                                | 15              | 48                 | 51.91           | 6.641e-4 | 1.181e-2    |
| endosomal vesicle fusion                                                 | GO:0034058 | 2             | VPS11, VPS18                                  | 15              | 48                 | 51.91           | 6.641e-4 | 1.181e-2    |
| negative regulation of intracellular estrogen receptor signaling pathway | GO:0033147 | 2             | VPS11, VPS18                                  | 15              | 48                 | 51.91           | 6.641e-4 | 1.181e-2    |
| response to toxic substance                                              | GO:0009636 | 3             | GJC2, AIFM1, CNP                              | 83              | 48                 | 14.07           | 1.265e-3 | 1.784e-2    |
| positive regulation of macrophage activation                             | GO:0043032 | 2             | HSPD1, KARS1                                  | 21              | 48                 | 37.08           | 1.315e-3 | 1.816e-2    |