

GeDiPNet Cluster 99 -- Enriched Pathways

Pathway enrichment: KEGG + Reactome, upper-tail hypergeometric test, Benjamini-Hochberg FDR-corrected. Fold enrichment = (overlap / cluster gene count) / (pathway gene count / universe size). Top 15 pathways per cluster by q-value. See scripts/build\_cluster\_enrichment.php on gedipnet.bicnirrh.res.in. Data as of: 2026-10-08 03:30:07. · Rows: 15 · Generated: 2026-10-08 06:18:54

| Pathway                                                                                     | Source   | Overlap Genes | Overlap Gene Names                       | Pathway Gene Count | Cluster Gene Count | Fold Enrichment | P-value   | FDR Q-value |
|---------------------------------------------------------------------------------------------|----------|---------------|------------------------------------------|--------------------|--------------------|-----------------|-----------|-------------|
| Cytosolic tRNA aminoacylation                                                               | Reactome | 6             | AIMP1, RARS1, AARS1, KARS1, EPRS1, AIMP2 | 24                 | 48                 | 62.55           | 3.759e-10 | 4.470e-8    |
| RNA polymerase                                                                              | KEGG     | 5             | POLR1C, POLR3K, POLR3B, POLR3A, POLR1A   | 34                 | 48                 | 36.80           | 2.100e-7  | 1.253e-5    |
| Cytosolic sensors of pathogen-associated DNA                                                | Reactome | 4             | POLR1C, POLR3K, POLR3B, POLR3A           | 22                 | 48                 | 45.49           | 1.558e-6  | 7.122e-5    |
| RNA Polymerase III Transcription Initiation From Type 2 Promoter                            | Reactome | 4             | POLR1C, POLR3K, POLR3B, POLR3A           | 27                 | 48                 | 37.07           | 3.684e-6  | 1.501e-4    |
| RNA Polymerase III Transcription Initiation From Type 3 Promoter                            | Reactome | 4             | POLR1C, POLR3K, POLR3B, POLR3A           | 28                 | 48                 | 35.74           | 4.285e-6  | 1.706e-4    |
| RNA Polymerase III Transcription Initiation From Type 1 Promoter                            | Reactome | 4             | POLR1C, POLR3K, POLR3B, POLR3A           | 28                 | 48                 | 35.74           | 4.285e-6  | 1.706e-4    |
| Sphingolipid metabolism                                                                     | KEGG     | 4             | ARSA, DEGS1, GALC, HEXA                  | 54                 | 48                 | 18.53           | 6.134e-5  | 1.524e-3    |
| Aminoacyl-tRNA biosynthesis                                                                 | KEGG     | 4             | RARS1, AARS1, KARS1, EPRS1               | 66                 | 48                 | 15.16           | 1.350e-4  | 2.888e-3    |
| RNA Polymerase I Transcription Termination                                                  | Reactome | 3             | POLR1C, ERCC2, POLR1A                    | 32                 | 48                 | 23.46           | 2.739e-4  | 5.055e-3    |
| Cytosolic DNA-sensing pathway                                                               | KEGG     | 4             | POLR1C, POLR3K, POLR3B, POLR3A           | 83                 | 48                 | 12.06           | 3.274e-4  | 5.831e-3    |
| RNA Polymerase I Transcription Initiation                                                   | Reactome | 3             | POLR1C, ERCC2, POLR1A                    | 45                 | 48                 | 16.68           | 7.557e-4  | 1.122e-2    |
| Glycosphingolipid metabolism                                                                | Reactome | 3             | ARSA, GALC, HEXA                         | 46                 | 48                 | 16.32           | 8.062e-4  | 1.181e-2    |
| Defective SLC9A6 causes X-linked, syndromic mental retardation,, Christianson type (MRXSCH) | Reactome | 1             | SLC9A6                                   | 1                  | 48                 | 250.21          | 3.997e-3  | 3.823e-2    |
| Defective HEXA causes GM2G1                                                                 | Reactome | 1             | HEXA                                     | 1                  | 48                 | 250.21          | 3.997e-3  | 3.823e-2    |
| RNA Polymerase I Promoter Escape                                                            | Reactome | 3             | POLR1C, ERCC2, POLR1A                    | 91                 | 48                 | 8.25            | 5.690e-3  | 4.868e-2    |