

GeDiPNet Cluster 216 -- 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: 2026-10-07 03:30:09. · Rows: 4 · Generated: 2026-10-07 06:18:56

| Pathway                                  | Source   | Overlap Genes | Overlap Gene Names | Pathway Gene Count | Cluster Gene Count | Fold Enrichment | P-value  | FDR Q-value |
|------------------------------------------|----------|---------------|--------------------|--------------------|--------------------|-----------------|----------|-------------|
| Small interfering RNA (siRNA) biogenesis | Reactome | 1             | DICER1             | 9                  | 3                  | 444.81          | 2.247e-3 | 2.484e-2    |
| SUMOylation of transcription factors     | Reactome | 1             | FOXL2              | 18                 | 3                  | 222.41          | 4.490e-3 | 4.079e-2    |
| MicroRNA (miRNA) biogenesis              | Reactome | 1             | DICER1             | 24                 | 3                  | 166.81          | 5.984e-3 | 4.925e-2    |
| MicroRNAs in cancer                      | KEGG     | 1             | DICER1             | 311                | 3                  | 12.87           | 7.570e-2 | 2.135e-1    |