

GeDiPNet Cluster 434 -- 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: unknown. · Rows: 0 · Generated: 2026-10-08 12:58:02

| Pathway | Source | Overlap Genes | Overlap Gene Names | Pathway Gene Count | Cluster Gene Count | Fold Enrichment | P-value | FDR Q-value |
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