

GeDiPNet Cluster 178 -- 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 10:45:14

Pathway	Source	Overlap Genes	Overlap Gene Names	Pathway Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
Golgi Associated Vesicle Biogenesis	Reactome	4	AP3B1, BLOC1S3, BLOC1S6, DTNBP1	56	11	77.99	1.365e-7	8.568e-6
RAB GEFs exchange GTP for GDP on RABs	Reactome	2	HPS1, HPS4	90	11	24.26	2.923e-3	3.019e-2
Lysosome	KEGG	2	AP3B1, AP3D1	133	11	16.42	6.271e-3	5.082e-2
Signaling by BRAF and RAF fusions	Reactome	1	AP3B1	67	11	16.30	5.971e-2	1.877e-1