

GeDiPNet Cluster 451 -- 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](scripts/build_cluster_enrichment.php) on gedipnet.bicnirrh.res.in. Data as of: 2026-10-20 03:30:09. · Rows: 15 · Generated: 2026-10-19 23:22:25

Pathway	Source	Overlap Genes	Overlap Gene Names	Pathway Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
Formation of annular gap junctions	Reactome	1	ACTG1	11	9	121.31	8.216e-3	5.037e-2
Cell-extracellular matrix interactions	Reactome	1	ACTG1	12	9	111.20	8.960e-3	5.313e-2
Gap junction degradation	Reactome	1	ACTG1	12	9	111.20	8.960e-3	5.313e-2
Interaction between L1 and Ankyrins	Reactome	1	ACTG1	13	9	102.65	9.703e-3	5.587e-2
Processing of SMDT1	Reactome	1	PMPCA	16	9	83.40	1.193e-2	6.320e-2
Adherens junctions interactions	Reactome	1	ACTG1	32	9	41.70	2.373e-2	9.458e-2
RHO GTPases activate IQGAPs	Reactome	1	ACTG1	32	9	41.70	2.373e-2	9.458e-2
RHO GTPases Activate WASPs and WAVES	Reactome	1	ACTG1	36	9	37.07	2.667e-2	1.010e-1
Signaling by high-kinase activity BRAF mutants	Reactome	1	ACTG1	36	9	37.07	2.667e-2	1.010e-1
EPHB-mediated forward signaling	Reactome	1	ACTG1	39	9	34.22	2.886e-2	1.057e-1
MAP2K and MAPK activation	Reactome	1	ACTG1	40	9	33.36	2.959e-2	1.073e-1
Recycling pathway of L1	Reactome	1	ACTG1	40	9	33.36	2.959e-2	1.073e-1
Signaling by moderate kinase activity BRAF mutants	Reactome	1	ACTG1	47	9	28.39	3.469e-2	1.173e-1
Paradoxical activation of RAF signaling by kinase inactive BRAF	Reactome	1	ACTG1	47	9	28.39	3.469e-2	1.173e-1
Signaling downstream of RAS mutants	Reactome	1	ACTG1	47	9	28.39	3.469e-2	1.173e-1