

GeDiPNet Cluster 170 -- 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: 2026-10-09 03:30:08. · Rows: 10 · Generated: 2026-10-09 07:17:12

Pathway	Source	Overlap Genes	Overlap Gene Names	Pathway Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
Recycling of eIF2:GDP	Reactome	5	EIF2B1, EIF2B2, EIF2B3, EIF2B4, EIF2B5	8	7	1072.32	5.650e-16	2.016e-13
Herpes simplex virus 1 infection	KEGG	5	EIF2B1, EIF2B2, EIF2B3, EIF2B4, EIF2B5	182	7	47.14	1.550e-8	1.207e-6
Regulation of cytoskeletal remodeling and cell spreading by IPP complex components	Reactome	1	ARHGEF6	8	7	214.46	4.655e-3	4.170e-2
Initiation of Nuclear Envelope (NE) Reformation	Reactome	1	ANKLE2	19	7	90.30	1.102e-2	7.366e-2
G beta:gamma signalling through CDC42	Reactome	1	ARHGEF6	20	7	85.79	1.160e-2	7.601e-2
NRAGE signals death through JNK	Reactome	1	ARHGEF6	55	7	31.19	3.163e-2	1.361e-1
Pancreatic cancer	KEGG	1	ARHGEF6	77	7	22.28	4.404e-2	1.631e-1
G alpha (12/13) signalling events	Reactome	1	ARHGEF6	80	7	21.45	4.572e-2	1.666e-1
Rho GTPase cycle	Reactome	1	ARHGEF6	138	7	12.43	7.773e-2	2.214e-1
Regulation of actin cytoskeleton	KEGG	1	ARHGEF6	232	7	7.40	1.277e-1	2.886e-1