

GeDiPNet Cluster 61 -- 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: 15 · Generated: 2026-10-07 15:32:40

Pathway	Source	Overlap Genes	Overlap Gene Names	Pathway Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
Phospholipase D signaling pathway	KEGG	3	ADCY6, DNM2, PIP5K1C	149	22	10.99	2.424e-3	2.629e-2
Assembly of collagen fibrils and other multimeric structures	Reactome	2	COL6A3, DST	51	22	21.41	3.868e-3	3.684e-2
Synthesis of PIPs at the plasma membrane	Reactome	2	PIP5K1C, MTM1	51	22	21.41	3.868e-3	3.684e-2
Endocrine and other factor-regulated calcium reabsorption	KEGG	2	ADCY6, DNM2	53	22	20.60	4.171e-3	3.882e-2
Inositol phosphate metabolism	KEGG	2	PIP5K1C, MTM1	73	22	14.96	7.781e-3	5.861e-2
NOSTRIN mediated eNOS trafficking	Reactome	1	DNM2	5	22	109.18	9.127e-3	6.495e-2
GRB7 events in ERBB2 signaling	Reactome	1	ERBB3	5	22	109.18	9.127e-3	6.495e-2
NOTCH2 intracellular domain regulates transcription	Reactome	1	MAMLD1	7	22	77.99	1.276e-2	7.893e-2
Activation of NIMA Kinases NEK9, NEK6, NEK7	Reactome	1	NEK9	7	22	77.99	1.276e-2	7.893e-2
Circadian entrainment	KEGG	2	ADCY6, RYR1	97	22	11.26	1.343e-2	8.139e-2
Phosphatidylinositol signaling system	KEGG	2	PIP5K1C, MTM1	98	22	11.14	1.369e-2	8.238e-2
Fc gamma R-mediated phagocytosis	KEGG	2	DNM2, PIP5K1C	98	22	11.14	1.369e-2	8.238e-2
PI5P, PP2A and IER3 Regulate PI3K/AKT Signaling	Reactome	2	PIP5K1C, ERBB3	103	22	10.60	1.505e-2	8.714e-2
SEMA3A-Plexin repulsion signaling by inhibiting Integrin adhesion	Reactome	1	PIP5K1C	10	22	54.59	1.817e-2	9.770e-2
Adenylate cyclase activating pathway	Reactome	1	ADCY6	10	22	54.59	1.817e-2	9.770e-2