

GeDiPNet Cluster 257 -- 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 14:46:36

Pathway	Source	Overlap Genes	Overlap Gene Names	Pathway Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
Tie2 Signaling	Reactome	3	TEK, KRAS, PIK3CA	18	10	200.17	3.370e-7	1.899e-5
Downstream signal transduction	Reactome	3	RASA1, KRAS, PIK3CA	29	10	124.24	1.502e-6	6.929e-5
Axon guidance	KEGG	4	RASA1, EPHB4, KRAS, PIK3CA	183	10	26.25	1.020e-5	3.410e-4
GnRH secretion	KEGG	3	GNA11, KRAS, PIK3CA	65	10	55.43	1.767e-5	5.402e-4
Signaling by FGFR3 fusions in cancer	Reactome	2	KRAS, PIK3CA	10	10	240.20	2.798e-5	7.863e-4
Ras signaling pathway	KEGG	4	RASA1, TEK, KRAS, PIK3CA	237	10	20.27	2.828e-5	7.932e-4
Signaling by FGFR4 in disease	Reactome	2	KRAS, PIK3CA	11	10	218.36	3.418e-5	9.324e-4
Signaling by PDGFRA transmembrane, juxtamembrane and kinase domain mutants	Reactome	2	KRAS, PIK3CA	12	10	200.17	4.100e-5	1.088e-3
Signaling by PDGFRA extracellular domain mutants	Reactome	2	KRAS, PIK3CA	12	10	200.17	4.100e-5	1.088e-3
PTK6 Regulates RHO GTPases, RAS GTPase and MAP kinases	Reactome	2	RASA1, KRAS	14	10	171.57	5.648e-5	1.414e-3
VEGFR2 mediated cell proliferation	Reactome	2	RASA1, KRAS	14	10	171.57	5.648e-5	1.414e-3
Constitutive Signaling by EGFRvIII	Reactome	2	KRAS, PIK3CA	15	10	160.13	6.514e-5	1.580e-3
Signaling by ERBB2 ECD mutants	Reactome	2	KRAS, PIK3CA	16	10	150.13	7.442e-5	1.760e-3
Cholinergic synapse	KEGG	3	GNA11, KRAS, PIK3CA	115	10	31.33	9.773e-5	2.209e-3
Constitutive Signaling by Ligand-Responsive EGFR Cancer Variants	Reactome	2	KRAS, PIK3CA	19	10	126.42	1.059e-4	2.357e-3