

GeDiPNet Cluster 146 -- 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: 2026-10-10 03:30:08. · Rows: 15 · Generated: 2026-10-10 07:03:18

Pathway	Source	Overlap Genes	Overlap Gene Names	Pathway Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
Axon guidance	KEGG	8	EPHA4, LIMK2, UNC5D, GDF7, NRP1, NTN4, SLIT3, WNT4	183	168	3.13	4.188e-3	4.006e-2
MET activates PTK2 signaling	Reactome	3	COL5A1, LAMA4, LAMA5	30	168	7.15	8.273e-3	6.273e-2
Small cell lung cancer	KEGG	5	BCL2, CKS2, LAMA4, LAMA5, RXRA	93	168	3.84	9.757e-3	6.982e-2
Purine salvage	Reactome	2	ADA, ADK	13	168	11.00	1.371e-2	8.567e-2
RAF-independent MAPK1/3 activation	Reactome	2	DUSP1, DUSP16	13	168	11.00	1.371e-2	8.567e-2
Signaling by FGFR2 amplification mutants	Reactome	1	FGFR2	1	168	71.49	1.399e-2	8.670e-2
Signaling by FGFR2 fusions	Reactome	1	FGFR2	1	168	71.49	1.399e-2	8.670e-2
Negative regulation of MAPK pathway	Reactome	3	DUSP1, DUSP16, MARK3	38	168	5.64	1.585e-2	9.382e-2
Gastric cancer	KEGG	6	BCL2, DVL2, FGFR2, RXRA, SHC3, WNT4	150	168	2.86	1.880e-2	1.036e-1
Type I diabetes mellitus	KEGG	3	IFNG, CPE, PTPRN2	44	168	4.87	2.342e-2	1.173e-1
RORA activates gene expression	Reactome	2	CHD9, RXRA	18	168	7.94	2.570e-2	1.234e-1
Elastic fibre formation	Reactome	2	FBN2, LOXL1	18	168	7.94	2.570e-2	1.234e-1
PCP/CE pathway	Reactome	2	DVL2, WNT4	18	168	7.94	2.570e-2	1.234e-1
Acetylation	Reactome	1	NAT2	2	168	35.74	2.778e-2	1.289e-1
Defective ABCC9 causes dilated cardiomyopathy 10, familial atrial fibrillation 12 and hypertrichotic osteochondrodysplasia	Reactome	1	ABCC9	2	168	35.74	2.778e-2	1.289e-1