

GeDiPNet Cluster 145 -- 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: 2026-10-08 03:30:07. · Rows: 15 · Generated: 2026-10-07 23:52:20

Pathway	Source	Overlap Genes	Overlap Gene Names	Pathway Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
Signaling by BMP	Reactome	3	ACVRL1, GDF2, SMAD4	28	33	38.99	5.909e-5	1.481e-3
Adherens junction	KEGG	4	KRIT1, CCM2, PDCD10, SMAD4	93	33	15.65	1.161e-4	2.553e-3
Neurotrophin signaling pathway	KEGG	4	PIK3CA, MAP3K3, MAP2K1, PSEN1	120	33	12.13	3.100e-4	5.585e-3
Apelin signaling pathway	KEGG	4	SMAD4, RYR1, RYR3, MAP2K1	140	33	10.40	5.567e-4	8.840e-3
Signaling by cytosolic FGFR1 fusion mutants	Reactome	2	PIK3CA, MYO18A	18	33	40.44	1.090e-3	1.484e-2
Pancreatic cancer	KEGG	3	PIK3CA, SMAD4, MAP2K1	77	33	14.18	1.204e-3	1.599e-2
Chronic myeloid leukemia	KEGG	3	PIK3CA, SMAD4, MAP2K1	77	33	14.18	1.204e-3	1.599e-2
Signal transduction by L1	Reactome	2	L1CAM, MAP2K1	21	33	34.66	1.488e-3	1.886e-2
Colorectal cancer	KEGG	3	PIK3CA, SMAD4, MAP2K1	87	33	12.55	1.712e-3	2.082e-2
PD-L1 expression and PD-1 checkpoint pathway in cancer	KEGG	3	PIK3CA, MAP3K3, MAP2K1	90	33	12.13	1.887e-3	2.232e-2
Defective SLC26A3 causes congenital secretory chloride diarrhea 1 (DIAR1)	Reactome	1	SLC26A3	1	33	363.94	2.748e-3	2.947e-2
Downstream signal transduction	Reactome	2	PIK3CA, RASA1	29	33	25.10	2.838e-3	3.006e-2
Human T-cell leukemia virus 1 infection	KEGG	4	PIK3CA, MAP3K3, SMAD4, MAP2K1	224	33	6.50	3.153e-3	3.234e-2
Signaling by FGFR1 in disease	Reactome	2	PIK3CA, MYO18A	33	33	22.06	3.665e-3	3.601e-2
Sterols are 12-hydroxylated by CYP8B1	Reactome	1	PTGIS	2	33	181.97	5.488e-3	4.749e-2