

GeDiPNet Cluster 220 -- 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 06:18:50

Pathway	Source	Overlap Genes	Overlap Gene Names	Pathway Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
Inhibition of TSC complex formation by PKB	Reactome	1	TSC1	3	9	444.81	2.247e-3	2.484e-2
TP53 regulates transcription of additional cell cycle genes whose exact role in the p53 pathway remain uncertain	Reactome	1	CNOT3	20	9	66.72	1.489e-2	8.659e-2
Deadenylation of mRNA	Reactome	1	CNOT3	24	9	55.60	1.785e-2	9.668e-2
Laminin interactions	Reactome	1	LAMC3	28	9	47.66	2.079e-2	1.050e-1
Energy dependent regulation of mTOR by LKB1-AMPK	Reactome	1	TSC1	29	9	46.02	2.153e-2	1.074e-1
MET activates PTK2 signaling	Reactome	1	LAMC3	30	9	44.48	2.227e-2	1.093e-1
Human papillomavirus infection	KEGG	2	TSC1, LAMC3	333	9	8.01	2.426e-2	1.148e-1
PI3K-Akt signaling pathway	KEGG	2	TSC1, LAMC3	361	9	7.39	2.820e-2	1.247e-1
TBC/RABGAPs	Reactome	1	TSC1	46	9	29.01	3.396e-2	1.385e-1
Nuclear Receptor transcription pathway	Reactome	1	NR4A2	52	9	25.66	3.831e-2	1.480e-1
Macroautophagy	Reactome	1	TSC1	68	9	19.62	4.983e-2	1.710e-1
Non-small cell lung cancer	KEGG	1	KIF5C	73	9	18.28	5.341e-2	1.781e-1
RNA degradation	KEGG	1	CNOT3	78	9	17.11	5.697e-2	1.835e-1
TP53 Regulates Metabolic Genes	Reactome	1	TSC1	86	9	15.52	6.265e-2	1.927e-1
ECM-receptor interaction	KEGG	1	LAMC3	89	9	14.99	6.477e-2	1.963e-1