

GeDiPNet Cluster 564 -- 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: 2026-10-20 03:30:09. · Rows: 15 · Generated: 2026-10-20 00:02:46

Pathway	Source	Overlap Genes	Overlap Gene Names	Pathway Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
Base excision repair	KEGG	2	PNKP, APTX	44	6	90.98	1.949e-4	3.215e-3
Toxoplasmosis	KEGG	2	LAMA1, PIK3R5	112	6	35.74	1.262e-3	1.353e-2
APEX1-Independent Resolution of AP Sites via the Single Nucleotide Replacement Pathway	Reactome	1	PNKP	7	6	285.95	3.493e-3	2.829e-2
Erythropoietin activates Phosphoinositide-3-kinase (PI3K)	Reactome	1	PIK3R5	12	6	166.81	5.981e-3	4.097e-2
G beta:gamma signalling through PI3Kgamma	Reactome	1	PIK3R5	25	6	80.07	1.243e-2	6.493e-2
PI3K-Akt signaling pathway	KEGG	2	LAMA1, PIK3R5	361	6	11.09	1.247e-2	6.508e-2
Laminin interactions	Reactome	1	LAMA1	28	6	71.49	1.391e-2	6.943e-2
MET activates PTK2 signaling	Reactome	1	LAMA1	30	6	66.72	1.490e-2	7.218e-2
GPVI-mediated activation cascade	Reactome	1	PIK3R5	34	6	58.87	1.687e-2	7.778e-2
Synthesis of PIPs at the plasma membrane	Reactome	1	PIK3R5	51	6	39.25	2.522e-2	9.786e-2
Ion transport by P-type ATPases	Reactome	1	ATP8A2	56	6	35.74	2.766e-2	1.031e-1
Viral myocarditis	KEGG	1	LAMA1	70	6	28.60	3.447e-2	1.168e-1
Arrhythmogenic right ventricular cardiomyopathy	KEGG	1	LAMA1	86	6	23.28	4.221e-2	1.315e-1
ECM-receptor interaction	KEGG	1	LAMA1	89	6	22.49	4.366e-2	1.340e-1
Small cell lung cancer	KEGG	1	LAMA1	93	6	21.52	4.558e-2	1.373e-1