

GeDiPNet Cluster 590 -- 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: 2026-10-19 23:22:01

Pathway	Source	Overlap Genes	Overlap Gene Names	Pathway Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
PTK6 promotes HIF1A stabilization	Reactome	1	LRRK2	6	13	153.97	6.478e-3	4.320e-2
Lysosome	KEGG	2	AP4M1, NPC2	133	13	13.89	8.765e-3	5.242e-2
Negative regulation of activity of TFAP2 (AP-2) family transcription factors	Reactome	1	WWOX	9	13	102.65	9.703e-3	5.587e-2
RHO GTPases activate KTN1	Reactome	1	KIF5B	11	13	83.99	1.185e-2	6.307e-2
Activation of the TFAP2 (AP-2) family of transcription factors	Reactome	1	WWOX	12	13	76.99	1.292e-2	6.623e-2
Insulin processing	Reactome	1	EXOC7	14	13	65.99	1.506e-2	7.270e-2
LDL clearance	Reactome	1	NPC2	18	13	51.32	1.932e-2	8.398e-2
Interleukin-37 signaling	Reactome	1	PTPN23	21	13	43.99	2.251e-2	9.162e-2
VxPx cargo-targeting to cilium	Reactome	1	EXOC7	21	13	43.99	2.251e-2	9.162e-2
Citric acid cycle (TCA cycle)	Reactome	1	ACO2	22	13	41.99	2.357e-2	9.424e-2
Nuclear signaling by ERBB4	Reactome	1	WWOX	24	13	38.49	2.568e-2	9.901e-2
Salmonella infection	KEGG	2	KIF5B, EXOC7	248	13	7.45	2.851e-2	1.051e-1
Interconversion of nucleotide di- and triphosphates	Reactome	1	DTYMK	29	13	31.86	3.095e-2	1.102e-1
Citrate cycle (TCA cycle)	KEGG	1	ACO2	30	13	30.79	3.201e-2	1.124e-1
Glyoxylate and dicarboxylate metabolism	KEGG	1	ACO2	30	13	30.79	3.201e-2	1.124e-1