

GeDiPNet Cluster 247 -- 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 07:49:30

Pathway	Source	Overlap Genes	Overlap Gene Names	Pathway Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
Degradation of GABA	Reactome	1	ABAT	2	25	240.20	4.159e-3	3.874e-2
Malaria	KEGG	2	LRP1, TNF	50	25	19.22	4.794e-3	4.266e-2
Cholesterol metabolism	KEGG	2	LRP1, LDLR	51	25	18.84	4.983e-3	4.365e-2
Interconversion of polyamines	Reactome	1	SAT1	3	25	160.13	6.232e-3	5.059e-2
ATF6 (ATF6-alpha) activates chaperones	Reactome	1	MBTPS2	4	25	120.10	8.301e-3	6.104e-2
CREB3 factors activate genes	Reactome	1	MBTPS2	5	25	96.08	1.037e-2	7.025e-2
Chylomicron clearance	Reactome	1	LDLR	5	25	96.08	1.037e-2	7.025e-2
Defective LFNG causes SCDO3	Reactome	1	NOTCH3	5	25	96.08	1.037e-2	7.025e-2
Tachykinin receptors bind tachykinins	Reactome	1	TAC1	5	25	96.08	1.037e-2	7.025e-2
TNFR1-mediated ceramide production	Reactome	1	TNF	6	25	80.07	1.243e-2	7.776e-2
Pre-NOTCH Processing in Golgi	Reactome	1	NOTCH3	6	25	80.07	1.243e-2	7.776e-2
Regulation of cholesterol biosynthesis by SREBP (SREBF)	Reactome	1	MBTPS2	7	25	68.63	1.448e-2	8.530e-2
TNF signaling	Reactome	1	TNF	7	25	68.63	1.448e-2	8.530e-2
Noncanonical activation of NOTCH3	Reactome	1	NOTCH3	8	25	60.05	1.654e-2	9.227e-2
Cargo recognition for clathrin-mediated endocytosis	Reactome	2	LDLR, SH3GL3	106	25	9.06	2.028e-2	1.036e-1