

GeDiPNet Cluster 336 -- 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: 11 · Generated: 2026-10-08 04:56:50

Pathway	Source	Overlap Genes	Overlap Gene Names	Pathway Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
ATF6 (ATF6-alpha) activates chaperones	Reactome	1	MBTPS2	4	4	750.63	1.332e-3	1.729e-2
CREB3 factors activate genes	Reactome	1	MBTPS2	5	4	600.50	1.664e-3	2.040e-2
Regulation of cholesterol biosynthesis by SREBP (SREBF)	Reactome	1	MBTPS2	7	4	428.93	2.330e-3	2.607e-2
TP53 regulates transcription of several additional cell death genes whose specific roles in p53-dependent apoptosis remain uncertain	Reactome	1	PERP	14	4	214.46	4.655e-3	4.241e-2
TRP channels	Reactome	1	TRPV3	28	4	107.23	9.294e-3	6.694e-2
p53 signaling pathway	KEGG	1	PERP	75	4	40.03	2.475e-2	1.197e-1
Polycomb repressive complex	KEGG	1	YY2	83	4	36.17	2.736e-2	1.264e-1
Inflammatory mediator regulation of TRP channels	KEGG	1	TRPV3	99	4	30.33	3.257e-2	1.385e-1
ATP-dependent chromatin remodeling	KEGG	1	YY2	117	4	25.66	3.841e-2	1.513e-1
Formation of the cornified envelope	Reactome	1	PERP	130	4	23.10	4.260e-2	1.603e-1
Protein processing in endoplasmic reticulum	KEGG	1	MBTPS2	171	4	17.56	5.575e-2	1.844e-1