

GeDiPNet Cluster 468 -- 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: 12 · Generated: 2026-10-20 00:03:01

Pathway	Source	Overlap Genes	Overlap Gene Names	Pathway Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
Formation of the cornified envelope	Reactome	2	PERP, KRT16	130	5	36.95	1.138e-3	1.250e-2
ATF6 (ATF6-alpha) activates chaperones	Reactome	1	MBTPS2	4	5	600.50	1.664e-3	1.665e-2
CREB3 factors activate genes	Reactome	1	MBTPS2	5	5	480.40	2.080e-3	1.956e-2
Regulation of cholesterol biosynthesis by SREBP (SREBF)	Reactome	1	MBTPS2	7	5	343.14	2.911e-3	2.492e-2
TP53 regulates transcription of several additional cell death genes whose specific roles in p53-dependent apoptosis remain uncertain	Reactome	1	PERP	14	5	171.57	5.816e-3	4.033e-2
TRP channels	Reactome	1	TRPV3	28	5	85.79	1.160e-2	6.220e-2
p53 signaling pathway	KEGG	1	PERP	75	5	32.03	3.084e-2	1.099e-1
Inflammatory mediator regulation of TRP channels	KEGG	1	TRPV3	99	5	24.26	4.055e-2	1.282e-1
Staphylococcus aureus infection	KEGG	1	KRT16	99	5	24.26	4.055e-2	1.282e-1
Estrogen signaling pathway	KEGG	1	KRT16	139	5	17.28	5.655e-2	1.554e-1
Keratinization	Reactome	1	KRT16	152	5	15.80	6.171e-2	1.631e-1
Protein processing in endoplasmic reticulum	KEGG	1	MBTPS2	171	5	14.05	6.920e-2	1.743e-1