

GeDiPNet Cluster 558 -- 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 00:02:39

Pathway	Source	Overlap Genes	Overlap Gene Names	Pathway Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
Virion - Ebolavirus, Lyssavirus and Morbillivirus	KEGG	1	NPC1	12	12	83.40	1.193e-2	6.320e-2
LDL clearance	Reactome	1	NPC1	18	12	55.60	1.785e-2	8.027e-2
Adherens junctions interactions	Reactome	1	CDH18	32	12	31.28	3.152e-2	1.113e-1
Cholesterol metabolism	KEGG	1	NPC1	51	12	19.62	4.981e-2	1.444e-1
Hedgehog signaling pathway	KEGG	1	SUFU	56	12	17.87	5.456e-2	1.520e-1
Hedgehog 'off' state	Reactome	1	SUFU	56	12	17.87	5.456e-2	1.520e-1
Degradation of GLI1 by the proteasome	Reactome	1	SUFU	57	12	17.56	5.551e-2	1.537e-1
GLI3 is processed to GLI3R by the proteasome	Reactome	1	SUFU	60	12	16.68	5.836e-2	1.579e-1
Basal cell carcinoma	KEGG	1	SUFU	63	12	15.89	6.119e-2	1.624e-1
Hedgehog 'on' state	Reactome	1	SUFU	70	12	14.30	6.777e-2	1.721e-1
PRC2 methylates histones and DNA	Reactome	1	JARID2	73	12	13.71	7.058e-2	1.764e-1
Polycomb repressive complex	KEGG	1	JARID2	83	12	12.06	7.989e-2	1.893e-1
Lysosome	KEGG	1	NPC1	133	12	7.53	1.251e-1	2.471e-1
Signaling pathways regulating pluripotency of stem cells	KEGG	1	JARID2	144	12	6.95	1.348e-1	2.583e-1
Protein processing in endoplasmic reticulum	KEGG	1	SIL1	171	12	5.85	1.582e-1	2.852e-1