

GeDiPNet Cluster 27 -- 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 05:34:16

Pathway	Source	Overlap Genes	Overlap Gene Names	Pathway Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
Cohesin Loading onto Chromatin	Reactome	2	WAPL, NIPBL	10	39	61.59	4.549e-4	7.403e-3
Retinoid cycle disease events	Reactome	2	LRAT, RBP4	13	39	47.38	7.836e-4	1.133e-2
Aminoacyl-tRNA biosynthesis	KEGG	3	AARS1, DARS2, AARS2	66	39	14.00	1.258e-3	1.610e-2
The canonical retinoid cycle in rods (twilight vision)	Reactome	2	LRAT, RBP4	20	39	30.79	1.881e-3	2.179e-2
Mtb iron assimilation by chelation	Reactome	1	LTF	1	39	307.95	3.247e-3	3.258e-2
Retinoid metabolism disease events	Reactome	1	RBP4	1	39	307.95	3.247e-3	3.258e-2
Retinoid metabolism and transport	Reactome	2	LRAT, RBP4	41	39	15.02	7.779e-3	5.861e-2
ARL13B-mediated ciliary trafficking of INPP5E	Reactome	1	INPP5E	3	39	102.65	9.711e-3	6.740e-2
Biosynthesis of protectins	Reactome	1	CYP1A1	4	39	76.99	1.293e-2	7.946e-2
Ion homeostasis	Reactome	2	ATP2B1, RYR1	54	39	11.41	1.322e-2	8.070e-2
Hippo signaling pathway	KEGG	3	BMP4, BMP5, WNT3	157	39	5.88	1.420e-2	8.426e-2
Lysine degradation	KEGG	2	NSD2, PLOD2	63	39	9.78	1.772e-2	9.637e-2
Basal cell carcinoma	KEGG	2	BMP4, WNT3	63	39	9.78	1.772e-2	9.637e-2
Metal sequestration by antimicrobial proteins	Reactome	1	LTF	6	39	51.32	1.933e-2	1.009e-1
Collagen biosynthesis and modifying enzymes	Reactome	2	COL5A1, PLOD2	67	39	9.19	1.989e-2	1.025e-1