

GeDiPNet Cluster 107 -- 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 14:48:18

Pathway	Source	Overlap Genes	Overlap Gene Names	Pathway Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
Golgi Associated Vesicle Biogenesis	Reactome	4	AP1B1, AP1S1, FTL, FTH1	56	30	28.60	1.062e-5	3.526e-4
Gap junction assembly	Reactome	3	GJA1, GJB3, GJB4	18	30	66.72	1.119e-5	3.682e-4
Iron uptake and transport	Reactome	3	CP, FTL, FTH1	28	30	42.89	4.418e-5	1.154e-3
Ferroptosis	KEGG	3	CP, FTL, FTH1	42	30	28.60	1.512e-4	3.130e-3
Coenzyme A biosynthesis	Reactome	2	PANK2, COASY	8	30	100.08	1.673e-4	3.395e-3
Porphyrin metabolism	KEGG	3	CP, FTL, FTH1	46	30	26.11	1.986e-4	3.880e-3
Nef mediated downregulation of MHC class I complex cell surface expression	Reactome	2	AP1B1, AP1S1	10	30	80.07	2.681e-4	4.916e-3
Pantothenate and CoA biosynthesis	KEGG	2	PANK2, COASY	21	30	38.13	1.230e-3	1.584e-2
Retinoid metabolism disease events	Reactome	1	RBP4	1	30	400.33	2.498e-3	2.686e-2
Lysosome Vesicle Biogenesis	Reactome	2	AP1B1, AP1S1	35	30	22.88	3.410e-3	3.374e-2
Defective SLC40A1 causes hemochromatosis 4 (HFE4) (macrophages)	Reactome	1	CP	2	30	200.17	4.990e-3	4.365e-2
Defective CP causes aceruloplasminemia (ACERULOP)	Reactome	1	CP	2	30	200.17	4.990e-3	4.365e-2
Sphingolipid de novo biosynthesis	Reactome	2	KDSR, FA2H	43	30	18.62	5.111e-3	4.437e-2
COPI-independent Golgi-to-ER retrograde traffic	Reactome	2	RAB3GAP1, PLA2G6	51	30	15.70	7.128e-3	5.536e-2
Regulation of gap junction activity	Reactome	1	GJA1	3	30	133.44	7.476e-3	5.688e-2