

GeDiPNet Cluster 188 -- 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 08:14:36

Pathway	Source	Overlap Genes	Overlap Gene Names	Pathway Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
Iron uptake and transport	Reactome	4	CP, SLC40A1, FTH1, TF	28	8	214.46	1.644e-9	1.730e-7
Ferroptosis	KEGG	4	CP, SLC40A1, FTH1, TF	42	8	142.98	8.952e-9	7.922e-7
Defective SLC40A1 causes hemochromatosis 4 (HFE4) (macrophages)	Reactome	2	CP, SLC40A1	2	8	1501.25	3.883e-7	2.151e-5
Defective CP causes aceruloplasminemia (ACERULOP)	Reactome	2	CP, SLC40A1	2	8	1501.25	3.883e-7	2.151e-5
Mineral absorption	KEGG	3	SLC40A1, FTH1, TF	61	8	73.83	6.857e-6	2.448e-4
Metal ion SLC transporters	Reactome	2	CP, SLC40A1	9	8	333.61	1.395e-5	4.419e-4
TGF-beta signaling pathway	KEGG	3	BMP6, HAMP, TF	108	8	41.70	3.833e-5	1.025e-3
Porphyrin metabolism	KEGG	2	CP, FTH1	46	8	65.27	3.960e-4	6.657e-3
Defective SLC40A1 causes hemochromatosis 4 (HFE4) (duodenum)	Reactome	1	SLC40A1	2	8	750.63	1.332e-3	1.681e-2
Post-translational protein phosphorylation	Reactome	2	CP, TF	108	8	27.80	2.166e-3	2.417e-2
Regulation of Insulin-like Growth Factor (IGF) transport and uptake by Insulin-like Growth Factor Binding Proteins (IGFBPs)	Reactome	2	CP, TF	125	8	24.02	2.888e-3	2.997e-2
Hormone signaling	KEGG	2	SLC40A1, HAMP	219	8	13.71	8.621e-3	6.279e-2
Transferrin endocytosis and recycling	Reactome	1	TF	31	8	48.43	2.047e-2	1.042e-1
Ovarian steroidogenesis	KEGG	1	BMP6	52	8	28.87	3.413e-2	1.388e-1
Golgi Associated Vesicle Biogenesis	Reactome	1	FTH1	56	8	26.81	3.671e-2	1.445e-1