

GeDiPNet Cluster 262 -- 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: 2026-10-08 03:30:07. · Rows: 15 · Generated: 2026-10-08 00:39:52

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	3	CP, FTL, FTH1	28	18	71.49	9.047e-6	3.159e-4
Ferroptosis	KEGG	3	CP, FTL, FTH1	42	18	47.66	3.129e-5	8.794e-4
Porphyrin metabolism	KEGG	3	CP, FTL, FTH1	46	18	43.51	4.122e-5	1.108e-3
Coenzyme A biosynthesis	Reactome	2	PANK2, COASY	8	18	166.81	5.909e-5	1.481e-3
Pantothenate and CoA biosynthesis	KEGG	2	PANK2, COASY	21	18	63.54	4.381e-4	7.350e-3
Defective SLC40A1 causes hemochromatosis 4 (HFE4) (macrophages)	Reactome	1	CP	2	18	333.61	2.995e-3	3.114e-2
Defective CP causes aceruloplasminemia (ACERULOP)	Reactome	1	CP	2	18	333.61	2.995e-3	3.114e-2
Golgi Associated Vesicle Biogenesis	Reactome	2	FTL, FTH1	56	18	23.83	3.114e-3	3.202e-2
Mineral absorption	KEGG	2	FTL, FTH1	61	18	21.88	3.685e-3	3.616e-2
Regulation of gap junction activity	Reactome	1	GJA1	3	18	222.41	4.490e-3	4.138e-2
Beta-oxidation of pristanoyl-CoA	Reactome	1	CRAT	9	18	74.14	1.341e-2	8.370e-2
Metal ion SLC transporters	Reactome	1	CP	9	18	74.14	1.341e-2	8.370e-2
Formation of annular gap junctions	Reactome	1	GJA1	11	18	60.66	1.637e-2	9.456e-2
Gap junction degradation	Reactome	1	GJA1	12	18	55.60	1.785e-2	9.951e-2
Carnitine metabolism	Reactome	1	SLC25A20	14	18	47.66	2.079e-2	1.083e-1