

GeDiPNet Cluster 415 -- 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: 9 · Generated: 2026-10-07 11:29:26

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	1	FTH1	28	4	107.23	9.294e-3	6.561e-2
Ferroptosis	KEGG	1	FTH1	42	4	71.49	1.392e-2	8.316e-2
Porphyrin metabolism	KEGG	1	FTH1	46	4	65.27	1.523e-2	8.780e-2
Golgi Associated Vesicle Biogenesis	Reactome	1	FTH1	56	4	53.62	1.852e-2	9.849e-2
Mineral absorption	KEGG	1	FTH1	61	4	49.22	2.016e-2	1.033e-1
Stimuli-sensing channels	Reactome	1	BEST1	79	4	38.01	2.606e-2	1.192e-1
Hippo signaling pathway	KEGG	1	CRB1	157	4	19.12	5.128e-2	1.737e-1
Necroptosis	KEGG	1	FTH1	159	4	18.88	5.192e-2	1.751e-1
Neutrophil degranulation	Reactome	1	FTH1	480	4	6.26	1.506e-1	3.104e-1