

GeDiPNet Cluster 519 -- 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: 2026-10-20 03:30:09. · Rows: 15 · Generated: 2026-10-20 00:03:15

Pathway	Source	Overlap Genes	Overlap Gene Names	Pathway Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
Defective SLC11A2 causes hypochromic microcytic anemia, with iron overload 1 (AHMIO1)	Reactome	1	SLC11A2	1	6	2001.67	4.996e-4	6.672e-3
Metal ion SLC transporters	Reactome	1	SLC11A2	9	6	222.41	4.489e-3	3.394e-2
Synthesis of PE	Reactome	1	LPIN2	12	6	166.81	5.981e-3	4.097e-2
Triglyceride biosynthesis	Reactome	1	LPIN2	13	6	153.97	6.478e-3	4.320e-2
Depolymerisation of the Nuclear Lamina	Reactome	1	LPIN2	15	6	133.44	7.472e-3	4.730e-2
Cytosolic tRNA aminoacylation	Reactome	1	LARS1	24	6	83.40	1.193e-2	6.320e-2
Synthesis of PC	Reactome	1	LPIN2	28	6	71.49	1.391e-2	6.943e-2
Iron uptake and transport	Reactome	1	SLC11A2	28	6	71.49	1.391e-2	6.943e-2
Ferroptosis	KEGG	1	SLC11A2	42	6	47.66	2.080e-2	8.765e-2
Collagen degradation	Reactome	1	TMPRSS6	52	6	38.49	2.570e-2	9.902e-2
Mineral absorption	KEGG	1	SLC11A2	61	6	32.81	3.010e-2	1.084e-1
Longevity regulating pathway - multiple species	KEGG	1	CLPB	62	6	32.28	3.058e-2	1.096e-1
Glycerolipid metabolism	KEGG	1	LPIN2	64	6	31.28	3.156e-2	1.114e-1
Aminoacyl-tRNA biosynthesis	KEGG	1	LARS1	66	6	30.33	3.253e-2	1.133e-1
Degradation of the extracellular matrix	Reactome	1	TMPRSS6	70	6	28.60	3.447e-2	1.168e-1