

GeDiPNet Cluster 505 -- 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: 10 · Generated: 2026-10-20 00:03:16

Pathway	Source	Overlap Genes	Overlap Gene Names	Pathway Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
Galactose metabolism	KEGG	4	GALT, GALM, GALE, GALK1	32	4	375.31	4.150e-11	5.441e-9
Galactose catabolism	Reactome	3	GALT, GALE, GALK1	5	4	1801.50	1.386e-10	1.559e-8
Biosynthesis of nucleotide sugars	KEGG	3	GALT, GALE, GALK1	37	4	243.45	1.074e-7	5.957e-6
Amino sugar and nucleotide sugar metabolism	KEGG	3	GALT, GALE, GALK1	38	4	237.04	1.166e-7	6.405e-6
Metabolic pathways	KEGG	4	GALT, GALM, GALE, GALK1	1563	4	7.68	2.859e-4	4.343e-3
Defective GALE can cause Epimerase-deficiency galactosemia (EDG)	Reactome	1	GALE	1	4	3002.50	3.331e-4	4.876e-3
Defective GALK1 can cause Galactosemia II (GALCT2)	Reactome	1	GALK1	1	4	3002.50	3.331e-4	4.876e-3
Defective GALT can cause Galactosemia	Reactome	1	GALT	1	4	3002.50	3.331e-4	4.876e-3
Glycolysis / Gluconeogenesis	KEGG	1	GALM	67	4	44.81	2.213e-2	9.093e-2
Prolactin signaling pathway	KEGG	1	GALT	71	4	42.29	2.344e-2	9.406e-2