

GeDiPNet Cluster 429 -- 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 10:43:29

Pathway	Source	Overlap Genes	Overlap Gene Names	Pathway Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
Glycine degradation	Reactome	1	DLD	4	2	1501.25	6.660e-4	9.955e-3
Vitamin C (ascorbate) metabolism	Reactome	1	CYB5R3	8	2	750.63	1.332e-3	1.681e-2
Lysine catabolism	Reactome	1	DLD	12	2	500.42	1.997e-3	2.278e-2
Biosynthesis of various nucleotide sugars	KEGG	1	CYB5R3	15	2	400.33	2.496e-3	2.686e-2
Regulation of pyruvate dehydrogenase (PDH) complex	Reactome	1	DLD	16	2	375.31	2.663e-3	2.827e-2
Lipoic acid metabolism	KEGG	1	DLD	19	2	316.05	3.162e-3	3.196e-2
Pyruvate metabolism	Reactome	1	DLD	19	2	316.05	3.162e-3	3.196e-2
Branched-chain amino acid catabolism	Reactome	1	DLD	20	2	300.25	3.328e-3	3.313e-2
Phase I - Functionalization of compounds	Reactome	1	CYB5R3	21	2	285.95	3.494e-3	3.425e-2
Signaling by Retinoic Acid	Reactome	1	DLD	21	2	285.95	3.494e-3	3.425e-2
Citric acid cycle (TCA cycle)	Reactome	1	DLD	22	2	272.95	3.660e-3	3.541e-2
Glyoxylate metabolism and glycine degradation	Reactome	1	DLD	28	2	214.46	4.658e-3	4.181e-2
Citrate cycle (TCA cycle)	KEGG	1	DLD	30	2	200.17	4.990e-3	4.365e-2
Glyoxylate and dicarboxylate metabolism	KEGG	1	DLD	30	2	200.17	4.990e-3	4.365e-2
Propanoate metabolism	KEGG	1	DLD	32	2	187.66	5.322e-3	4.557e-2