

GeDiPNet Cluster 70 -- 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 05:57:36

Pathway	Source	Overlap Genes	Overlap Gene Names	Pathway Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
Physiological factors	Reactome	2	GATA4, TBX5	12	17	117.75	1.234e-4	2.686e-3
YAP1- and WWTR1 (TAZ)-stimulated gene expression	Reactome	2	GATA4, TBX5	14	17	100.92	1.699e-4	3.462e-3
Fatty acid degradation	KEGG	2	ACADL, ACADVL	43	17	32.86	1.646e-3	2.025e-2
Fatty acid metabolism	KEGG	2	ACADL, ACADVL	57	17	24.79	2.875e-3	3.036e-2
Regulation of gap junction activity	Reactome	1	GJA1	3	17	235.49	4.241e-3	3.983e-2
Beta oxidation of myristoyl-CoA to lauroyl-CoA	Reactome	1	ACADL	3	17	235.49	4.241e-3	3.983e-2
Beta oxidation of palmitoyl-CoA to myristoyl-CoA	Reactome	1	ACADVL	3	17	235.49	4.241e-3	3.983e-2
Beta oxidation of lauroyl-CoA to decanoyl-CoA-CoA	Reactome	1	ACADL	5	17	141.29	7.059e-3	5.613e-2
Factors involved in megakaryocyte development and platelet production	Reactome	2	GATA4, GATA6	99	17	14.27	8.440e-3	6.302e-2
mitochondrial fatty acid beta-oxidation of unsaturated fatty acids	Reactome	1	ACADL	6	17	117.75	8.465e-3	6.313e-2
Synthesis, secretion, and inactivation of Glucose-dependent Insulinotropic Polypeptide (GIP)	Reactome	1	GATA4	7	17	100.92	9.869e-3	6.949e-2
RHO GTPases activate CIT	Reactome	1	DLG4	8	17	88.31	1.127e-2	7.536e-2
WNT mediated activation of DVL	Reactome	1	DVL2	9	17	78.50	1.267e-2	8.093e-2
Formation of annular gap junctions	Reactome	1	GJA1	11	17	64.22	1.547e-2	9.134e-2
WNT5:FZD7-mediated leishmania damping	Reactome	1	DVL2	12	17	58.87	1.686e-2	9.628e-2