

GeDiPNet Cluster 91 -- 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: 2026-10-09 03:30:08. · Rows: 15 · Generated: 2026-10-09 07:57:47

Pathway	Source	Overlap Genes	Overlap Gene Names	Pathway Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
Lysosome	KEGG	4	MCOLN1, GNPTAB, GNPTG, NEU1	133	8	45.15	9.723e-7	4.572e-5
Glycerophospholipid catabolism	Reactome	1	PNPLA6	3	8	500.42	1.997e-3	2.277e-2
Defective NEU1 causes sialidosis	Reactome	1	NEU1	3	8	500.42	1.997e-3	2.277e-2
Other glycan degradation	KEGG	1	NEU1	18	8	83.40	1.193e-2	7.721e-2
Negative regulators of DDX58/IFIH1 signaling	Reactome	1	RNF216	27	8	55.60	1.785e-2	9.870e-2
TRP channels	Reactome	1	MCOLN1	28	8	53.62	1.850e-2	1.006e-1
Transferrin endocytosis and recycling	Reactome	1	MCOLN1	31	8	48.43	2.047e-2	1.064e-1
Sialic acid metabolism	Reactome	1	NEU1	33	8	45.49	2.178e-2	1.102e-1
Glycosphingolipid metabolism	Reactome	1	NEU1	46	8	32.64	3.024e-2	1.326e-1
Sphingolipid metabolism	KEGG	1	NEU1	54	8	27.80	3.542e-2	1.448e-1
Viral myocarditis	KEGG	1	SGCB	70	8	21.45	4.570e-2	1.666e-1
Arrhythmogenic right ventricular cardiomyopathy	KEGG	1	SGCB	86	8	17.46	5.589e-2	1.861e-1
Hypertrophic cardiomyopathy	KEGG	1	SGCB	99	8	15.16	6.409e-2	1.995e-1
Glycerophospholipid metabolism	KEGG	1	PNPLA6	102	8	14.72	6.598e-2	2.027e-1
Dilated cardiomyopathy	KEGG	1	SGCB	105	8	14.30	6.786e-2	2.058e-1