

GeDiPNet Cluster 241 -- 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 14:37:34

Pathway	Source	Overlap Genes	Overlap Gene Names	Pathway Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
Cytoskeleton in muscle cells	KEGG	11	ACTA1, MYPN, NEB, TPM2, TPM3, ANKRD1, FLNC, TNNT1, TNNT3, LMOD3, TNNI1	232	18	31.64	3.118e-15	9.998e-13
Striated Muscle Contraction	Reactome	7	ACTA1, NEB, TPM2, TPM3, TNNT1, TNNT3, TNNI1	36	18	129.74	3.636e-14	9.515e-12
Motor proteins	KEGG	7	ACTA1, TPM2, TPM3, MYO18B, TNNT1, TNNT3, TNNI1	194	18	24.08	7.051e-9	6.205e-7
Smooth Muscle Contraction	Reactome	2	TPM2, TPM3	34	18	39.25	1.157e-3	1.552e-2
Cardiac muscle contraction	KEGG	2	TPM2, TPM3	87	18	15.34	7.361e-3	5.766e-2
Hypertrophic cardiomyopathy	KEGG	2	TPM2, TPM3	99	18	13.48	9.444e-3	6.764e-2
Dilated cardiomyopathy	KEGG	2	TPM2, TPM3	105	18	12.71	1.057e-2	7.262e-2
Cell-extracellular matrix interactions	Reactome	1	FLNC	12	18	55.60	1.785e-2	9.951e-2
Adrenergic signaling in cardiomyocytes	KEGG	2	TPM2, TPM3	154	18	8.67	2.185e-2	1.115e-1
Cholesterol biosynthesis	Reactome	1	MVK	21	18	31.77	3.103e-2	1.350e-1
Terpenoid backbone biosynthesis	KEGG	1	MVK	23	18	29.01	3.394e-2	1.416e-1
Neddylation	Reactome	2	KBTBD13, KLHL41	234	18	5.70	4.712e-2	1.690e-1
Thyroid cancer	KEGG	1	TPM3	37	18	18.03	5.406e-2	1.817e-1
Activation of gene expression by SREBF (SREBP)	Reactome	1	MVK	42	18	15.89	6.115e-2	1.934e-1
Antigen processing: Ubiquitination & Proteasome degradation	Reactome	2	KBTBD13, KLHL41	309	18	4.32	7.702e-2	2.187e-1