

GeDiPNet Cluster 543 -- 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: 15 · Generated: 2026-10-20 00:02:59

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	6	LDB3, MYH7, TTN, FLNC, SPTAN1, NEB	232	21	14.79	2.073e-6	7.790e-5
Hypertrophic cardiomyopathy	KEGG	3	MYH7, TTN, CAV3	99	21	17.33	6.488e-4	8.173e-3
Dilated cardiomyopathy	KEGG	3	MYH7, TTN, CAV3	105	21	16.34	7.702e-4	9.285e-3
FGFR2 alternative splicing	Reactome	2	HNRNPA1, TIA1	26	21	43.99	9.228e-4	1.066e-2
Smooth Muscle Contraction	Reactome	2	DYSF, CAV3	34	21	33.64	1.579e-3	1.602e-2
Defective GNE causes sialuria, Nonaka myopathy and inclusion body myopathy 2	Reactome	1	GNE	1	21	571.90	1.749e-3	1.726e-2
Striated Muscle Contraction	Reactome	2	TTN, NEB	36	21	31.77	1.770e-3	1.742e-2
Amyotrophic lateral sclerosis	KEGG	4	VCP, HNRNPA1, MATR3, SQSTM1	368	21	6.22	3.432e-3	2.803e-2
Viral myocarditis	KEGG	2	MYH7, CAV3	70	21	16.34	6.547e-3	4.354e-2
Mitophagy - animal	KEGG	2	VCP, SQSTM1	105	21	10.89	1.427e-2	7.046e-2
Pexophagy	Reactome	1	SQSTM1	10	21	57.19	1.735e-2	7.882e-2
HSF1 activation	Reactome	1	VCP	12	21	47.66	2.079e-2	8.765e-2
Purine ribonucleoside monophosphate biosynthesis	Reactome	1	ADSS1	12	21	47.66	2.079e-2	8.765e-2
Cell-extracellular matrix interactions	Reactome	1	FLNC	12	21	47.66	2.079e-2	8.765e-2
Caspase-mediated cleavage of cytoskeletal proteins	Reactome	1	SPTAN1	12	21	47.66	2.079e-2	8.765e-2