

GeDiPNet Cluster 206 -- 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: 6 · Generated: 2026-10-09 07:16:31

Pathway	Source	Overlap Genes	Overlap Gene Names	Pathway Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
Striated Muscle Contraction	Reactome	1	TTN	36	2	166.81	5.986e-3	4.934e-2
Hypertrophic cardiomyopathy	KEGG	1	TTN	99	2	60.66	1.642e-2	9.379e-2
Dilated cardiomyopathy	KEGG	1	TTN	105	2	57.19	1.741e-2	9.711e-2
Platelet degranulation	Reactome	1	TTN	123	2	48.82	2.038e-2	1.062e-1
Transcriptional misregulation in cancer	KEGG	1	MYCN	198	2	30.33	3.270e-2	1.387e-1
Cytoskeleton in muscle cells	KEGG	1	TTN	232	2	25.88	3.826e-2	1.513e-1