

GeDiPNet Cluster 221 -- Enriched GO Terms (Biological Process)

GO term enrichment: Biological Process terms (gene2go, human/tax_id=9606 only), upper-tail hypergeometric test, fold enrichment = (overlap / cluster gene count) / (term gene count / universe size), Benjamini-Hochberg FDR-corrected. Top 15 terms per cluster by q-value. See scripts/build_cluster_go_enrichment.php on gedipnet.bicnirrh.res.in. Data as of: 2026-10-07 03:23:06. · Rows: 15 · Generated: 2026-10-07 01:46:19

GO Term	GO ID	Overlap Genes	Overlap Gene Names	Term Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
skeletal muscle myosin thick filament assembly	GO:0030241	1	TTN	3	2	3114.50	3.211e-4	7.027e-3
sarcomerogenesis	GO:0048769	1	TTN	3	2	3114.50	3.211e-4	7.027e-3
regulation of inner ear auditory receptor cell differentiation	GO:0045607	1	MYCN	4	2	2335.88	4.281e-4	8.586e-3
skeletal muscle thin filament assembly	GO:0030240	1	TTN	6	2	1557.25	6.421e-4	1.127e-2
autosome genomic imprinting	GO:0141068	1	MYCN	6	2	1557.25	6.421e-4	1.127e-2
positive regulation of gene expression	GO:0010628	2	TTN, MYCN	504	2	37.08	7.260e-4	1.228e-2
detection of muscle stretch	GO:0035995	1	TTN	7	2	1334.79	7.491e-4	1.251e-2
negative regulation of astrocyte differentiation	GO:0048712	1	MYCN	11	2	849.41	1.177e-3	1.664e-2
protein kinase A signaling	GO:0010737	1	TTN	12	2	778.63	1.284e-3	1.747e-2
cardiac muscle tissue morphogenesis	GO:0055008	1	TTN	13	2	718.73	1.391e-3	1.837e-2
cardiac myofibril assembly	GO:0055003	1	TTN	13	2	718.73	1.391e-3	1.837e-2
cardiac muscle hypertrophy	GO:0003300	1	TTN	13	2	718.73	1.391e-3	1.837e-2
muscle filament sliding	GO:0030049	1	TTN	15	2	622.90	1.605e-3	1.983e-2
positive regulation of programmed cell death	GO:0043068	1	MYCN	17	2	549.62	1.819e-3	2.147e-2
mitotic chromosome condensation	GO:0007076	1	TTN	17	2	549.62	1.819e-3	2.147e-2