

GeDiPNet Cluster 541 -- 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: 2026-10-20 03:23:14. · Rows: 12 · Generated: 2026-10-20 00:01:15

GO Term	GO ID	Overlap Genes	Overlap Gene Names	Term Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
transition between fast and slow fiber	GO:0014883	2	TNNT1, TNNI1	9	3	1384.22	6.184e-7	5.802e-5
skeletal muscle contraction	GO:0003009	2	TNNT1, TNNI1	32	3	389.31	8.514e-6	4.803e-4
sarcomere organization	GO:0045214	2	TNNT1, MYPN	43	3	289.72	1.549e-5	7.629e-4
slow-twitch skeletal muscle fiber contraction	GO:0031444	1	TNNT1	1	3	6229.00	1.605e-4	4.340e-3
negative regulation of muscle contraction	GO:0045932	1	TNNT1	1	3	6229.00	1.605e-4	4.340e-3
regulation of striated muscle contraction	GO:0006942	1	TNNI1	8	3	778.63	1.284e-3	1.669e-2
regulation of muscle contraction	GO:0006937	1	TNNT1	16	3	389.31	2.567e-3	2.402e-2
dendrite self-avoidance	GO:0070593	1	MYPN	16	3	389.31	2.567e-3	2.402e-2
ventricular cardiac muscle tissue morphogenesis	GO:0055010	1	TNNI1	24	3	259.54	3.848e-3	2.937e-2
cardiac muscle contraction	GO:0060048	1	TNNI1	43	3	144.86	6.888e-3	3.897e-2
homophilic cell adhesion via plasma membrane adhesion molecules	GO:0007156	1	MYPN	167	3	37.30	2.657e-2	7.602e-2
axon guidance	GO:0007411	1	MYPN	192	3	32.44	3.051e-2	8.166e-2