

GeDiPNet Cluster 543 -- 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 03:23:13. · Rows: 15 · Generated: 2026-10-19 23:18:33

GO Term	GO ID	Overlap Genes	Overlap Gene Names	Term Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
sarcomere organization	GO:0045214	3	LDB3, TTN, FLNC	43	21	62.08	1.466e-5	7.310e-4
detection of muscle stretch	GO:0035995	2	TTN, CAV3	7	21	254.24	2.517e-5	1.097e-3
visual perception	GO:0007601	4	BEST1, IMPG1, IMPG2, PRPH2	215	21	16.56	8.746e-5	2.800e-3
cardiac muscle hypertrophy	GO:0003300	2	TTN, CAV3	13	21	136.90	9.312e-5	2.931e-3
muscle filament sliding	GO:0030049	2	MYH7, TTN	15	21	118.65	1.252e-4	3.632e-3
detection of light stimulus involved in visual perception	GO:0050908	2	BEST1, PRPH2	24	21	74.15	3.271e-4	7.127e-3
striated muscle contraction	GO:0006941	2	MYH7, TTN	24	21	74.15	3.271e-4	7.127e-3
cardiac muscle cell development	GO:0055013	2	TTN, CAV3	25	21	71.19	3.553e-4	7.567e-3
regulation of calcium ion transport	GO:0051924	2	BEST1, CAV3	25	21	71.19	3.553e-4	7.567e-3
positive regulation of ubiquitin-dependent protein catabolic process	GO:2000060	2	VCP, CAV3	30	21	59.32	5.134e-4	9.672e-3
skeletal muscle contraction	GO:0003009	2	MYH7, TTN	32	21	55.62	5.846e-4	1.056e-2
ATP metabolic process	GO:0046034	2	VCP, MYH7	36	21	49.44	7.405e-4	1.230e-2
regulation of heart rate	GO:0002027	2	MYH7, CAV3	39	21	45.63	8.692e-4	1.345e-2
cardiac muscle contraction	GO:0060048	2	MYH7, TTN	43	21	41.39	1.056e-3	1.514e-2
response to low light intensity stimulus	GO:0009645	1	PRPH2	1	21	889.86	1.124e-3	1.550e-2