

GeDiPNet Cluster 162 -- 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 10:25:19

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	6	MYPN, ANKRD1, CFL2, FLNC, TNNT1, TNNT3	43	18	144.86	1.876e-12	8.093e-10
actin filament organization	GO:0007015	5	KBTBD13, TPM2, TPM3, CFL2, LMOD3	152	18	34.15	2.622e-7	2.722e-5
regulation of ATP-dependent activity	GO:0043462	2	TPM2, TNNT3	2	18	1038.17	8.763e-7	7.442e-5
muscle contraction	GO:0006936	4	ACTA1, TPM2, TPM3, LMOD3	85	18	48.85	1.162e-6	9.352e-5
striated muscle contraction	GO:0006941	3	KLHL41, TNNT3, LMOD3	24	18	129.77	1.500e-6	1.146e-4
skeletal muscle fiber development	GO:0048741	3	ACTA1, LMOD3, KLHL40	31	18	100.47	3.317e-6	2.166e-4
skeletal muscle contraction	GO:0003009	3	TNNT1, TNNT3, TNNI1	32	18	97.33	3.658e-6	2.338e-4
skeletal muscle thin filament assembly	GO:0030240	2	ACTA1, LMOD3	6	18	346.06	1.311e-5	6.450e-4
regulation of striated muscle contraction	GO:0006942	2	TNNT3, TNNI1	8	18	259.54	2.445e-5	1.045e-3
transition between fast and slow fiber	GO:0014883	2	TNNT1, TNNI1	9	18	230.70	3.142e-5	1.265e-3
myofibril assembly	GO:0030239	2	KLHL41, LMOD3	15	18	138.42	9.133e-5	2.827e-3
regulation of muscle contraction	GO:0006937	2	TNNT1, TNNT3	16	18	129.77	1.043e-4	3.120e-3
positive regulation of calcium-dependent ATPase activity	GO:1903612	1	TNNT3	1	18	1038.17	9.632e-4	1.467e-2
slow-twitch skeletal muscle fiber contraction	GO:0031444	1	TNNT1	1	18	1038.17	9.632e-4	1.467e-2
negative regulation of muscle contraction	GO:0045932	1	TNNT1	1	18	1038.17	9.632e-4	1.467e-2