

GeDiPNet Cluster 193 -- 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: 2026-10-09 03:23:08. · Rows: 15 · Generated: 2026-10-09 15:54:41

GO Term	GO ID	Overlap Genes	Overlap Gene Names	Term Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
skeletal muscle contraction	GO:0003009	6	CHRNA1, MYH3, TNNI1, MYH8, TNNI2, TNNT3	32	24	145.99	2.020e-12	8.592e-10
muscle contraction	GO:0006936	5	CHRNA1, MYH3, TPM2, MYH8, RYR1	85	24	45.80	6.864e-8	8.699e-6
regulation of ATP-dependent activity	GO:0043462	2	TPM2, TNNT3	2	24	778.63	1.581e-6	1.206e-4
sarcomere organization	GO:0045214	3	MYH3, MYBPC1, TNNT3	43	24	54.32	2.221e-5	9.770e-4
cardiac muscle contraction	GO:0060048	3	ACTC1, TNNI1, TNNI2	43	24	54.32	2.221e-5	9.770e-4
regulation of striated muscle contraction	GO:0006942	2	TNNI1, TNNT3	8	24	194.66	4.406e-5	1.641e-3
neuronal action potential propagation	GO:0019227	2	SCN1A, CNTNAP1	11	24	141.57	8.633e-5	2.717e-3
monoatomic ion transmembrane transport	GO:0034220	5	CHRNA1, SCN1A, NALCN, PIEZO2, RYR1	404	24	9.64	1.395e-4	3.887e-3
neuromuscular process controlling posture	GO:0050884	2	SCN1A, CNTNAP1	15	24	103.82	1.643e-4	4.402e-3
muscle filament sliding	GO:0030049	2	MYH3, MYH8	15	24	103.82	1.643e-4	4.402e-3
actin filament-based movement	GO:0030048	2	ACTC1, MYH3	21	24	74.15	3.271e-4	7.183e-3
striated muscle contraction	GO:0006941	2	TNNT3, RYR1	24	24	64.89	4.288e-4	8.652e-3
ATP metabolic process	GO:0046034	2	MYH3, MYH8	36	24	43.26	9.697e-4	1.491e-2
positive regulation of vesicle transport along microtubule	GO:1901610	1	STK11	1	24	778.63	1.284e-3	1.764e-2
neuromuscular junction development, skeletal muscle fiber	GO:0098529	1	CNTNAP1	1	24	778.63	1.284e-3	1.764e-2