

GeDiPNet Cluster 260 -- 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: 2026-10-08 03:23:04. · Rows: 15 · Generated: 2026-10-07 23:46:14

GO Term	GO ID	Overlap Genes	Overlap Gene Names	Term Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
cellular response to caffeine	GO:0071313	2	RYR1, CACNA1S	11	2	1698.82	3.150e-7	3.206e-5
striated muscle contraction	GO:0006941	2	RYR1, CACNA1S	24	2	778.63	1.581e-6	1.211e-4
skeletal muscle fiber development	GO:0048741	2	RYR1, CACNA1S	31	2	602.81	2.663e-6	1.850e-4
release of sequestered calcium ion into cytosol	GO:0051209	2	RYR1, CACNA1S	48	2	389.31	6.461e-6	3.759e-4
muscle contraction	GO:0006936	2	RYR1, CACNA1S	85	2	219.85	2.045e-5	9.283e-4
calcium ion transmembrane transport	GO:0070588	2	RYR1, CACNA1S	149	2	125.42	6.315e-5	2.188e-3
calcium ion transport	GO:0006816	2	RYR1, CACNA1S	157	2	119.03	7.014e-5	2.373e-3
skeletal muscle adaptation	GO:0043501	1	CACNA1S	1	2	9343.50	1.070e-4	3.251e-3
monoatomic ion transmembrane transport	GO:0034220	2	RYR1, CACNA1S	404	2	46.25	4.663e-4	9.316e-3
extraocular skeletal muscle development	GO:0002074	1	CACNA1S	6	2	1557.25	6.421e-4	1.151e-2
positive regulation of muscle contraction	GO:0045933	1	CACNA1S	7	2	1334.79	7.491e-4	1.282e-2
response to caffeine	GO:0031000	1	RYR1	7	2	1334.79	7.491e-4	1.282e-2
transmembrane transport	GO:0055085	2	RYR1, CACNA1S	557	2	33.55	8.869e-4	1.431e-2
release of sequestered calcium ion into cytosol by sarcoplasmic reticulum	GO:0014808	1	RYR1	9	2	1038.17	9.630e-4	1.501e-2
monoatomic ion transport	GO:0006811	2	RYR1, CACNA1S	667	2	28.02	1.272e-3	1.789e-2