

GeDiPNet Cluster 417 -- 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: 2026-10-08 12:25:40

GO Term	GO ID	Overlap Genes	Overlap Gene Names	Term Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
tRNA-type intron splice site recognition and cleavage	GO:0000379	3	TSEN2, TSEN34, TSEN54	3	11	1698.82	1.517e-10	4.126e-8
tRNA splicing, via endonucleolytic cleavage and ligation	GO:0006388	3	TSEN2, TSEN34, TSEN54	13	11	392.03	4.326e-8	5.993e-6
tRNA processing	GO:0008033	3	TSEN2, TSEN34, TSEN54	107	11	47.63	2.913e-5	1.210e-3
muscle cell proliferation	GO:0033002	1	MEGF10	1	11	1698.82	5.886e-4	1.091e-2
regulation of skeletal muscle tissue development	GO:0048641	1	MEGF10	2	11	849.41	1.177e-3	1.702e-2
chromosomal DNA methylation maintenance following DNA replication	GO:0141119	1	DNMT1	2	11	849.41	1.177e-3	1.702e-2
negative regulation of vascular associated smooth muscle cell differentiation involved in phenotypic switching	GO:1905931	1	DNMT1	2	11	849.41	1.177e-3	1.702e-2
mRNA processing	GO:0006397	3	TSEN2, TSEN34, TSEN54	410	11	12.43	1.517e-3	1.970e-2
skeletal muscle satellite cell activation	GO:0014719	1	MEGF10	3	11	566.27	1.765e-3	2.164e-2
epigenetic programming of gene expression	GO:0043045	1	DNMT1	3	11	566.27	1.765e-3	2.164e-2
cardiac muscle thin filament assembly	GO:0071691	1	NEB	3	11	566.27	1.765e-3	2.164e-2
muscle organ development	GO:0007517	2	NEB, MEGF10	114	11	29.80	1.957e-3	2.286e-2
cellular response to bisphenol A	GO:1903926	1	DNMT1	4	11	424.70	2.353e-3	2.546e-2
myoblast development	GO:0048627	1	MEGF10	4	11	424.70	2.353e-3	2.546e-2
somatic muscle development	GO:0007525	1	NEB	4	11	424.70	2.353e-3	2.546e-2