

GeDiPNet Cluster 393 -- 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 01:45:24

GO Term	GO ID	Overlap Genes	Overlap Gene Names	Term Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
snRNA pseudouridine synthesis	GO:0031120	2	DKC1, NOP10	3	4	3114.50	1.031e-7	1.239e-5
rRNA pseudouridine synthesis	GO:0031118	2	DKC1, NOP10	4	4	2335.88	2.062e-7	2.227e-5
pseudouridine synthesis	GO:0001522	2	DKC1, NOP10	16	4	583.97	4.120e-6	2.572e-4
telomere maintenance via telomerase	GO:0007004	2	DKC1, NOP10	24	4	389.31	9.470e-6	5.007e-4
DNA strand displacement	GO:0000732	1	RTEL1	1	4	4671.75	2.141e-4	5.282e-3
negative regulation of telomere maintenance in response to DNA damage	GO:1904506	1	RTEL1	1	4	4671.75	2.141e-4	5.282e-3
positive regulation of telomeric loop disassembly	GO:1904535	1	RTEL1	1	4	4671.75	2.141e-4	5.282e-3
box H/ACA sno(s)RNA metabolic process	GO:0033979	1	DKC1	1	4	4671.75	2.141e-4	5.282e-3
ribosome biogenesis	GO:0042254	2	DKC1, NOP10	122	4	76.59	2.515e-4	5.952e-3
box H/ACA sno(s)RNA 3'-end processing	GO:0000495	1	DKC1	2	4	2335.88	4.281e-4	8.586e-3
telomeric loop disassembly	GO:0090657	1	RTEL1	2	4	2335.88	4.281e-4	8.586e-3
protein localization to Cajal body	GO:1904867	1	DKC1	2	4	2335.88	4.281e-4	8.586e-3
rRNA processing	GO:0006364	2	DKC1, NOP10	162	4	57.68	4.431e-4	8.804e-3
mitotic telomere maintenance via semi-conservative replication	GO:1902990	1	RTEL1	3	4	1557.25	6.421e-4	1.127e-2
negative regulation of t-circle formation	GO:1904430	1	RTEL1	3	4	1557.25	6.421e-4	1.127e-2