

GeDiPNet Cluster 475 -- 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: 2026-10-20 03:23:14. · Rows: 15 · Generated: 2026-10-20 00:01:14

GO Term	GO ID	Overlap Genes	Overlap Gene Names	Term Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
positive regulation of telomere maintenance via telomerase	GO:0032212	3	PARN, WRAP53, DKC1	23	7	348.20	5.682e-8	7.893e-6
telomere maintenance via telomerase	GO:0007004	3	TERT, WRAP53, DKC1	24	7	333.70	6.493e-8	8.844e-6
box H/ACA sno(s)RNA 3'-end processing	GO:0000495	2	PARN, DKC1	2	7	2669.57	1.203e-7	1.482e-5
protein localization to Cajal body	GO:1904867	2	WRAP53, DKC1	2	7	2669.57	1.203e-7	1.482e-5
telomerase RNA stabilization	GO:0090669	2	PARN, DKC1	4	7	1334.79	7.214e-7	6.577e-5
regulation of telomerase RNA localization to Cajal body	GO:1904872	2	PARN, DKC1	4	7	1334.79	7.214e-7	6.577e-5
scaRNA localization to Cajal body	GO:0090666	2	WRAP53, DKC1	5	7	1067.83	1.202e-6	9.986e-5
RNA modification	GO:0009451	2	PARN, DKC1	17	7	314.07	1.631e-5	7.922e-4
telomere maintenance	GO:0000723	2	RTEL1, TERT	66	7	80.90	2.551e-4	6.036e-3
regulation of RNA stability	GO:0043487	1	PARN	1	7	2669.57	3.746e-4	7.813e-3
DNA strand displacement	GO:0000732	1	RTEL1	1	7	2669.57	3.746e-4	7.813e-3
negative regulation of telomere maintenance in response to DNA damage	GO:1904506	1	RTEL1	1	7	2669.57	3.746e-4	7.813e-3
positive regulation of telomeric loop disassembly	GO:1904535	1	RTEL1	1	7	2669.57	3.746e-4	7.813e-3
DNA strand elongation	GO:0022616	1	TERT	1	7	2669.57	3.746e-4	7.813e-3
siRNA transcription	GO:0140745	1	TERT	1	7	2669.57	3.746e-4	7.813e-3