

GeDiPNet Cluster 83 -- 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 01:29:29

GO Term	GO ID	Overlap Genes	Overlap Gene Names	Term Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
telomere maintenance via telomerase	GO:0007004	9	ACD, TERT, DKC1, GAR1, NHP2, NOP10, POT1, WRAP53, RPA1	24	62	113.03	3.340e-17	3.303e-14
telomere maintenance	GO:0000723	8	ACD, NBN, TERT, CTC1, DCLRE1B, POT1, RTEL1, RPA1	66	62	36.53	4.542e-11	1.407e-8
telomere capping	GO:0016233	5	ACD, CTC1, DCLRE1B, POT1, TINF2	12	62	125.58	2.653e-10	6.760e-8
telomerase RNA localization to Cajal body	GO:0090671	4	NHP2, NOP10, WRAP53, NAF1	7	62	172.23	3.815e-9	7.165e-7
negative regulation of telomere maintenance via telomerase	GO:0032211	5	ACD, CTC1, POT1, TINF2, TP53	22	62	68.50	8.598e-9	1.465e-6
positive regulation of telomere maintenance via telomerase	GO:0032212	5	DKC1, PARN, POT1, WRAP53, NAF1	23	62	65.52	1.096e-8	1.812e-6
telomere assembly	GO:0032202	3	ACD, POT1, TINF2	3	62	301.40	3.478e-8	4.942e-6
snRNA pseudouridine synthesis	GO:0031120	3	DKC1, NHP2, NOP10	3	62	301.40	3.478e-8	4.942e-6
snoRNA guided rRNA pseudouridine synthesis	GO:0000454	3	GAR1, NHP2, NAF1	3	62	301.40	3.478e-8	4.942e-6
positive regulation of telomere maintenance	GO:0032206	5	ACD, NBN, POT1, RTEL1, TINF2	32	62	47.09	6.410e-8	8.353e-6
telomerase RNA stabilization	GO:0090669	3	DKC1, PARN, NAF1	4	62	226.05	1.388e-7	1.619e-5
rRNA pseudouridine synthesis	GO:0031118	3	DKC1, NHP2, NOP10	4	62	226.05	1.388e-7	1.619e-5
ribosome biogenesis	GO:0042254	7	SBDS, DKC1, GAR1, NHP2, NOP10, NPM1, NAF1	122	62	17.29	1.552e-7	1.776e-5
pseudouridine synthesis	GO:0001522	4	DKC1, GAR1, NOP10, NAF1	16	62	75.35	1.940e-7	2.146e-5
rRNA processing	GO:0006364	7	SBDS, DKC1, RPL5, GAR1, NHP2, NOP10, NAF1	162	62	13.02	1.065e-6	8.808e-5