

GeDiPNet Cluster 77 -- 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 02:40:23

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	TERT, DKC1, GAR1, NHP2, NOP10, POT1, WRAP53, ACD, RPA1	24	56	125.14	1.253e-17	1.446e-14
telomere maintenance	GO:0000723	8	NBN, TERT, CTC1, DCLRE1B, POT1, RTEL1, ACD, RPA1	66	56	40.45	1.940e-11	6.660e-9
telomere capping	GO:0016233	5	CTC1, DCLRE1B, POT1, TINF2, ACD	12	56	139.04	1.569e-10	4.311e-8
telomerase RNA localization to Cajal body	GO:0090671	4	NHP2, NOP10, WRAP53, NAF1	7	56	190.68	2.514e-9	5.054e-7
negative regulation of telomere maintenance via telomerase	GO:0032211	5	CTC1, POT1, TINF2, TP53, ACD	22	56	75.84	5.099e-9	9.492e-7
positive regulation of telomere maintenance via telomerase	GO:0032212	5	DKC1, PARN, POT1, WRAP53, NAF1	23	56	72.54	6.500e-9	1.178e-6
snRNA pseudouridine synthesis	GO:0031120	3	DKC1, NHP2, NOP10	3	56	333.70	2.549e-8	3.837e-6
telomere assembly	GO:0032202	3	POT1, TINF2, ACD	3	56	333.70	2.549e-8	3.837e-6
snoRNA guided rRNA pseudouridine synthesis	GO:0000454	3	GAR1, NHP2, NAF1	3	56	333.70	2.549e-8	3.837e-6
positive regulation of telomere maintenance	GO:0032206	5	NBN, POT1, RTEL1, TINF2, ACD	32	56	52.14	3.811e-8	5.384e-6
ribosome biogenesis	GO:0042254	7	SBDS, DKC1, GAR1, NHP2, NOP10, NPM1, NAF1	122	56	19.15	7.562e-8	9.518e-6
telomerase RNA stabilization	GO:0090669	3	DKC1, PARN, NAF1	4	56	250.27	1.017e-7	1.225e-5
rRNA pseudouridine synthesis	GO:0031118	3	DKC1, NHP2, NOP10	4	56	250.27	1.017e-7	1.225e-5
pseudouridine synthesis	GO:0001522	4	DKC1, GAR1, NOP10, NAF1	16	56	83.42	1.281e-7	1.483e-5
rRNA processing	GO:0006364	7	SBDS, DKC1, RPL5, GAR1, NHP2, NOP10, NAF1	162	56	14.42	5.245e-7	4.860e-5