

GeDiPNet Cluster 580 -- 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: 2026-10-19 23:18:52

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	1.303e-5
rRNA pseudouridine synthesis	GO:0031118	2	DKC1, NOP10	4	4	2335.88	2.062e-7	2.318e-5
pseudouridine synthesis	GO:0001522	2	DKC1, NOP10	16	4	583.97	4.120e-6	2.713e-4
telomere maintenance via telomerase	GO:0007004	2	DKC1, NOP10	24	4	389.31	9.470e-6	5.212e-4
box H/ACA sno(s)RNA metabolic process	GO:0033979	1	DKC1	1	4	4671.75	2.141e-4	5.314e-3
ribosome biogenesis	GO:0042254	2	DKC1, NOP10	122	4	76.59	2.515e-4	5.978e-3
box H/ACA sno(s)RNA 3'-end processing	GO:0000495	1	DKC1	2	4	2335.88	4.281e-4	8.531e-3
protein localization to Cajal body	GO:1904867	1	DKC1	2	4	2335.88	4.281e-4	8.531e-3
rRNA processing	GO:0006364	2	DKC1, NOP10	162	4	57.68	4.431e-4	8.748e-3
fructose catabolic process to hydroxyacetone phosphate and glyceraldehyde-3-phosphate	GO:0061624	1	TKFC	3	4	1557.25	6.421e-4	1.113e-2
negative regulation of MDA-5 signaling pathway	GO:0039534	1	TKFC	4	4	1167.94	8.560e-4	1.331e-2
telomerase RNA stabilization	GO:0090669	1	DKC1	4	4	1167.94	8.560e-4	1.331e-2
regulation of telomerase RNA localization to Cajal body	GO:1904872	1	DKC1	4	4	1167.94	8.560e-4	1.331e-2
enzyme-directed rRNA pseudouridine synthesis	GO:0000455	1	DKC1	4	4	1167.94	8.560e-4	1.331e-2
scaRNA localization to Cajal body	GO:0090666	1	DKC1	5	4	934.35	1.070e-3	1.514e-2