

GeDiPNet Cluster 490 -- 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 23:18:20

GO Term	GO ID	Overlap Genes	Overlap Gene Names	Term Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
DNA biosynthetic process	GO:0071897	3	POLD1, POLE, POLD2	32	7	250.27	1.589e-7	1.880e-5
DNA-templated DNA replication	GO:0006261	3	POLD1, POLE, POLD2	41	7	195.33	3.410e-7	3.539e-5
DNA replication proofreading	GO:0045004	2	POLD1, POLE	3	7	1779.71	3.608e-7	3.692e-5
nucleotide-excision repair, DNA gap filling	GO:0006297	2	POLD1, POLE	6	7	889.86	1.803e-6	1.394e-4
base-excision repair, gap-filling	GO:0006287	2	POLD1, POLE	14	7	381.37	1.092e-5	5.824e-4
DNA replication	GO:0006260	3	POLD1, POLE, POLD2	131	7	61.14	1.154e-5	6.080e-4
DNA synthesis involved in DNA repair	GO:0000731	2	POLD1, POLE	23	7	232.14	3.032e-5	1.260e-3
negative regulation of cell differentiation	GO:0045596	2	SMAD7, SKIL	75	7	71.19	3.295e-4	7.164e-3
negative regulation of BMP signaling pathway	GO:0030514	2	SMAD7, SKIL	75	7	71.19	3.295e-4	7.164e-3
DNA repair	GO:0006281	3	POLD1, POLE, POLD2	420	7	19.07	3.689e-4	7.776e-3
positive regulation of chondrocyte hypertrophy	GO:1903043	1	SMAD7	1	7	2669.57	3.746e-4	7.813e-3
beta-catenin destruction complex disassembly	GO:1904886	1	SMAD7	1	7	2669.57	3.746e-4	7.813e-3
transforming growth factor beta receptor signaling pathway	GO:0007179	2	SMAD7, SKIL	112	7	47.67	7.331e-4	1.225e-2
negative regulation of T-helper 17 type immune response	GO:2000317	1	SMAD7	2	7	1334.79	7.491e-4	1.230e-2
DNA damage response	GO:0006974	3	POLD1, POLE, POLD2	577	7	13.88	9.341e-4	1.414e-2