

GeDiPNet Cluster 612 -- 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 23:18:43

GO Term	GO ID	Overlap Genes	Overlap Gene Names	Term Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
nucleotide-excision repair involved in interstrand cross-link repair	GO:1901255	1	ERCC4	2	2	4671.75	2.140e-4	5.314e-3
telomeric DNA-containing double minutes formation	GO:0061819	1	ERCC4	3	2	3114.50	3.211e-4	7.044e-3
negative regulation of protection from non-homologous end joining at telomere	GO:1905765	1	ERCC4	3	2	3114.50	3.211e-4	7.044e-3
DNA replication proofreading	GO:0045004	1	POLE	3	2	3114.50	3.211e-4	7.044e-3
leading strand elongation	GO:0006272	1	POLE	4	2	2335.88	4.281e-4	8.531e-3
DNA repair	GO:0006281	2	ERCC4, POLE	420	2	44.49	5.040e-4	9.548e-3
negative regulation of telomere maintenance	GO:0032205	1	ERCC4	5	2	1868.70	5.351e-4	9.880e-3
nucleotide-excision repair, DNA gap filling	GO:0006297	1	POLE	6	2	1557.25	6.421e-4	1.113e-2
DNA damage response	GO:0006974	2	ERCC4, POLE	577	2	32.39	9.518e-4	1.423e-2
negative regulation of telomere maintenance via telomere lengthening	GO:1904357	1	ERCC4	11	2	849.41	1.177e-3	1.592e-2
UV protection	GO:0009650	1	ERCC4	12	2	778.63	1.284e-3	1.669e-2
base-excision repair, gap-filling	GO:0006287	1	POLE	14	2	667.39	1.498e-3	1.821e-2
resolution of meiotic recombination intermediates	GO:0000712	1	ERCC4	17	2	549.62	1.819e-3	2.024e-2
DNA synthesis involved in DNA repair	GO:0000731	1	POLE	23	2	406.24	2.460e-3	2.361e-2
DNA biosynthetic process	GO:0071897	1	POLE	32	2	291.98	3.422e-3	2.781e-2