

GeDiPNet Cluster 368 -- 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 11:55:30

GO Term	GO ID	Overlap Genes	Overlap Gene Names	Term Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
cell population proliferation	GO:0008283	5	BAP1, ERCC1, FGF9, KITLG, BRCA2	263	12	29.61	3.884e-7	3.780e-5
male gonad development	GO:0008584	4	DMRT1, ERCC1, FGF9, KITLG	117	12	53.24	6.950e-7	6.181e-5
telomeric DNA-containing double minutes formation	GO:0061819	2	ERCC1, ERCC4	3	12	1038.17	1.134e-6	9.164e-5
negative regulation of protection from non-homologous end joining at telomere	GO:1905765	2	ERCC1, ERCC4	3	12	1038.17	1.134e-6	9.164e-5
nucleotide-excision repair	GO:0006289	3	ERCC1, ERCC4, BRCA2	42	12	111.23	2.290e-6	1.605e-4
negative regulation of telomere maintenance	GO:0032205	2	ERCC1, ERCC4	5	12	622.90	3.776e-6	2.400e-4
DNA repair	GO:0006281	5	ERCC1, ERCC4, BRCA2, MBD4, CHEK2	420	12	18.54	3.894e-6	2.460e-4
establishment of protein localization to telomere	GO:0070200	2	BRCA2, POT1	7	12	444.93	7.924e-6	4.343e-4
telomere maintenance	GO:0000723	3	ERCC1, ERCC4, POT1	66	12	70.78	9.049e-6	4.829e-4
developmental process involved in reproduction	GO:0003006	2	DMRT1, KITLG	10	12	311.45	1.696e-5	7.891e-4
DNA damage response	GO:0006974	5	ERCC1, ERCC4, BRCA2, MBD4, CHEK2	577	12	13.49	1.825e-5	8.340e-4
double-strand break repair	GO:0006302	3	ERCC1, BRCA2, CHEK2	87	12	53.70	2.080e-5	9.261e-4
UV protection	GO:0009650	2	ERCC1, ERCC4	12	12	259.54	2.486e-5	1.058e-3
male sex determination	GO:0030238	2	DMRT1, FGF9	12	12	259.54	2.486e-5	1.058e-3
replicative senescence	GO:0090399	2	ERCC1, CHEK2	16	12	194.66	4.514e-5	1.669e-3