

GeDiPNet Cluster 97 -- 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: 2026-10-09 03:23:08. · Rows: 15 · Generated: 2026-10-09 13:21:55

GO Term	GO ID	Overlap Genes	Overlap Gene Names	Term Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
mitochondrial DNA replication	GO:0006264	5	POLG, POLG2, RRM2B, TWNK, MGME1	11	52	163.35	6.247e-11	1.922e-8
DNA biosynthetic process	GO:0071897	4	POLG, POLG2, TK2, LIG3	32	52	44.92	1.809e-6	1.347e-4
carbohydrate derivative metabolic process	GO:1901135	3	DGUOK, TK2, TYMP	18	52	59.89	1.610e-5	7.630e-4
DNA replication	GO:0006260	5	RMI2, POLG, POLG2, TWNK, LIG3	131	52	13.72	3.129e-5	1.265e-3
succinyl-CoA catabolic process	GO:1901289	2	SUCLA2, SUCLG1	6	52	119.79	1.131e-4	3.325e-3
mitochondrial DNA repair	GO:0043504	2	MGME1, LIG3	7	52	102.68	1.581e-4	4.276e-3
DNA-templated DNA replication	GO:0006261	3	POLG, POLG2, TWNK	41	52	26.30	2.011e-4	5.065e-3
mitochondrial transcription	GO:0006390	2	TWNK, TFAM	8	52	89.84	2.104e-4	5.231e-3
GMP metabolic process	GO:0046037	2	MAGI3, GUK1	12	52	59.89	4.924e-4	9.558e-3
nucleotide biosynthetic process	GO:0009165	2	DTYMK, TK2	14	52	51.34	6.765e-4	1.184e-2
base-excision repair, gap-filling	GO:0006287	2	POLG, LIG3	14	52	51.34	6.765e-4	1.184e-2
DNA repair	GO:0006281	6	RMI2, POLG, RRM2B, FANCI, MGME1, LIG3	420	52	5.13	1.057e-3	1.578e-2
cell-cell adhesion involved in neuronal-glia interactions involved in cerebral cortex radial glia guided migration	GO:0021813	1	DAB1	1	52	359.37	2.783e-3	2.756e-2
catecholamine catabolic process	GO:0042424	1	COMT	1	52	359.37	2.783e-3	2.756e-2
norepinephrine secretion	GO:0048243	1	COMT	1	52	359.37	2.783e-3	2.756e-2