

GeDiPNet Cluster 533 -- 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 03:23:13. · Rows: 15 · Generated: 2026-10-20 00:01:22

GO Term	GO ID	Overlap Genes	Overlap Gene Names	Term Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
establishment of mitotic sister chromatid cohesion	GO:0034087	4	NIPBL, RAD21, SMC1A, SMC3	7	14	762.73	6.889e-12	2.711e-9
mitotic sister chromatid cohesion	GO:0007064	4	HDAC8, NIPBL, SMC1A, SMC3	16	14	333.70	3.568e-10	9.511e-8
establishment of meiotic sister chromatid cohesion	GO:0034089	3	RAD21, SMC1A, SMC3	4	14	1001.09	1.338e-9	3.000e-7
sister chromatid cohesion	GO:0007062	3	RAD21, SMC1A, SMC3	20	14	200.22	3.787e-7	3.848e-5
chromatin organization	GO:0006325	6	BRD4, HDAC8, KMT2A, ARID1B, CHD7, BRD3	449	14	17.84	4.746e-7	4.665e-5
chromatin remodeling	GO:0006338	5	BRD4, NIPBL, ARID1B, CHD7, BRD3	320	14	20.86	2.517e-6	1.825e-4
ear morphogenesis	GO:0042471	2	NIPBL, CHD7	5	14	533.91	5.205e-6	3.268e-4
replication-born double-strand break repair via sister chromatid exchange	GO:1990414	2	NIPBL, RAD21	6	14	444.93	7.805e-6	4.506e-4
cognition	GO:0050890	3	NIPBL, KMT2A, CHD7	64	14	62.57	1.358e-5	6.892e-4
DNA damage response	GO:0006974	5	BRD4, NIPBL, RAD21, SMC1A, SMC3	577	14	11.57	4.381e-5	1.672e-3
chromatin looping	GO:0140588	2	NIPBL, RAD21	14	14	190.68	4.719e-5	1.771e-3
regulation of gene expression	GO:0010468	4	NIPBL, KMT2A, AFF4, CHD7	402	14	13.28	1.780e-4	4.678e-3
protein localization to chromatin	GO:0071168	2	RAD21, BRD3	31	14	86.12	2.394e-4	5.762e-3
positive regulation of multicellular organism growth	GO:0040018	2	NIPBL, CHD7	34	14	78.52	2.884e-4	6.594e-3
mitotic sister chromatid segregation	GO:0000070	2	NIPBL, SMC1A	38	14	70.25	3.608e-4	7.643e-3