

GeDiPNet Cluster 302 -- 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: 2026-10-08 03:23:04. · Rows: 15 · Generated: 2026-10-08 06:35:46

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	SMC1A, NIPBL, RAD21, SMC3	7	13	821.41	4.921e-12	1.937e-9
mitotic sister chromatid cohesion	GO:0007064	4	SMC1A, HDAC8, NIPBL, SMC3	16	13	359.37	2.550e-10	6.522e-8
establishment of meiotic sister chromatid cohesion	GO:0034089	3	SMC1A, RAD21, SMC3	4	13	1078.10	1.052e-9	2.272e-7
sister chromatid cohesion	GO:0007062	3	SMC1A, RAD21, SMC3	20	13	215.62	2.978e-7	3.062e-5
ear morphogenesis	GO:0042471	2	NIPBL, CHD7	5	13	574.98	4.462e-6	2.790e-4
replication-born double-strand break repair via sister chromatid exchange	GO:1990414	2	NIPBL, RAD21	6	13	479.15	6.691e-6	3.861e-4
chromatin organization	GO:0006325	5	BRD4, HDAC8, KMT2A, ARID1B, CHD7	449	13	16.01	8.595e-6	4.726e-4
cognition	GO:0050890	3	NIPBL, KMT2A, CHD7	64	13	67.38	1.069e-5	5.583e-4
DNA damage response	GO:0006974	5	SMC1A, BRD4, NIPBL, RAD21, SMC3	577	13	12.46	2.890e-5	1.202e-3
chromatin looping	GO:0140588	2	NIPBL, RAD21	14	13	205.35	4.046e-5	1.563e-3
chromatin remodeling	GO:0006338	4	BRD4, NIPBL, ARID1B, CHD7	320	13	17.97	5.340e-5	1.928e-3
regulation of gene expression	GO:0010468	4	NIPBL, KMT2A, AFF4, CHD7	402	13	14.30	1.293e-4	3.745e-3
positive regulation of multicellular organism growth	GO:0040018	2	NIPBL, CHD7	34	13	84.56	2.475e-4	5.973e-3
mitotic sister chromatid segregation	GO:0000070	2	SMC1A, NIPBL	38	13	75.66	3.097e-4	7.021e-3
transcription initiation-coupled chromatin remodeling	GO:0045815	2	KMT2A, ARID1B	41	13	70.12	3.608e-4	7.811e-3