

GeDiPNet Cluster 343 -- 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 12:11:40

GO Term	GO ID	Overlap Genes	Overlap Gene Names	Term Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
GPI anchor biosynthetic process	GO:0006506	9	PGAP2, PGAP3, PIGL, PIGO, PIGV, PIGW, PIGY, PIGB, PIGG	31	13	417.33	1.878e-23	4.893e-20
GPI anchor metabolic process	GO:0006505	2	PGAP3, PIGW	2	13	1437.46	4.468e-7	4.299e-5
negative regulation of transcription by RNA polymerase III	GO:0016480	1	SETD5	4	13	359.37	2.780e-3	2.776e-2
regulation of DNA-templated transcription elongation	GO:0032784	1	SETD5	7	13	205.35	4.860e-3	3.677e-2
radial glial cell differentiation	GO:0060019	1	CCDC85C	8	13	179.68	5.553e-3	3.929e-2
regulation of chromatin organization	GO:1902275	1	SETD5	11	13	130.68	7.628e-3	4.600e-2
positive regulation of DNA-templated transcription, elongation	GO:0032786	1	CCNK	13	13	110.57	9.009e-3	4.956e-2
host-mediated suppression of viral genome replication	GO:0044828	1	CCNK	13	13	110.57	9.009e-3	4.956e-2
regulation of cyclin-dependent protein serine/threonine kinase activity	GO:0000079	1	CCNK	22	13	65.34	1.520e-2	6.377e-2
regulation of synapse assembly	GO:0051963	1	SETD5	29	13	49.57	1.999e-2	7.264e-2
establishment of cell polarity	GO:0030010	1	CCDC85C	46	13	31.25	3.154e-2	9.095e-2
establishment of protein localization	GO:0045184	1	CCDC85C	51	13	28.19	3.492e-2	9.609e-2
positive regulation of transcription elongation by RNA polymerase II	GO:0032968	1	CCNK	57	13	25.22	3.895e-2	1.013e-1
cognition	GO:0050890	1	SETD5	64	13	22.46	4.363e-2	1.077e-1
cerebral cortex development	GO:0021987	1	CCDC85C	88	13	16.33	5.954e-2	1.278e-1