

GeDiPNet Cluster 621 -- 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 03:23:14. · Rows: 15 · Generated: 2026-10-19 23:19:25

GO Term	GO ID	Overlap Genes	Overlap Gene Names	Term Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
positive regulation of transcription elongation by RNA polymerase II	GO:0032968	2	CDK13, CCNK	57	4	163.92	5.463e-5	1.973e-3
regulation of signal transduction	GO:0009966	2	CDK13, CCNK	101	4	92.51	1.723e-4	4.563e-3
negative regulation of transcription by RNA polymerase III	GO:0016480	1	SETD5	4	4	1167.94	8.560e-4	1.331e-2
regulation of cell cycle	GO:0051726	2	CDK13, CCNK	262	4	35.66	1.153e-3	1.581e-2
regulation of DNA-templated transcription elongation	GO:0032784	1	SETD5	7	4	667.39	1.498e-3	1.821e-2
radial glial cell differentiation	GO:0060019	1	CCDC85C	8	4	583.97	1.711e-3	1.958e-2
regulation of chromatin organization	GO:1902275	1	SETD5	11	4	424.70	2.353e-3	2.301e-2
positive regulation of DNA-templated transcription, elongation	GO:0032786	1	CCNK	13	4	359.37	2.780e-3	2.510e-2
host-mediated suppression of viral genome replication	GO:0044828	1	CCNK	13	4	359.37	2.780e-3	2.510e-2
negative regulation of stem cell differentiation	GO:2000737	1	CDK13	18	4	259.54	3.848e-3	2.937e-2
regulation of cyclin-dependent protein serine/threonine kinase activity	GO:0000079	1	CCNK	22	4	212.35	4.701e-3	3.250e-2
alternative mRNA splicing, via spliceosome	GO:0000380	1	CDK13	25	4	186.87	5.341e-3	3.434e-2
regulation of synapse assembly	GO:0051963	1	SETD5	29	4	161.09	6.194e-3	3.697e-2
establishment of cell polarity	GO:0030010	1	CCDC85C	46	4	101.56	9.811e-3	4.606e-2
establishment of protein localization	GO:0045184	1	CCDC85C	51	4	91.60	1.087e-2	4.830e-2