

GeDiPNet Cluster 563 -- 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 23:18:22

GO Term	GO ID	Overlap Genes	Overlap Gene Names	Term Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
cell population proliferation	GO:0008283	7	TP53, H3-3A, CTNNB1, KRAS, STAT5B, FGFR1, RB1	263	19	26.18	4.405e-9	8.554e-7
T cell differentiation in thymus	GO:0033077	4	TP53, CTNNB1, STAT5B, BRAF	41	19	95.95	7.546e-8	1.005e-5
subtelomeric heterochromatin formation	GO:0031509	3	ATRX, EZH2, H3-3A	11	19	268.23	1.463e-7	1.756e-5
negative regulation of transcription by RNA polymerase II	GO:0000122	9	DNMT3A, TP53, EZH2, CDKN2A, CTNNB1, FOXL2, SUFU, FGFR1, RB1	1002	19	8.83	2.006e-7	2.268e-5
epidermal growth factor receptor signaling pathway	GO:0007173	4	CTNNB1, PTPN11, BRAF, PIK3CA	64	19	61.47	4.665e-7	4.595e-5
glial cell proliferation	GO:0014009	3	TP53, KRAS, RB1	18	19	163.92	7.202e-7	6.577e-5
negative regulation of gene expression	GO:0010629	6	TP53, EZH2, CTNNB1, FGFR1, PIK3CA, RB1	339	19	17.41	7.580e-7	6.835e-5
Ras protein signal transduction	GO:0007265	4	TP53, CDKN2A, KRAS, RB1	79	19	49.80	1.093e-6	9.239e-5
response to estradiol	GO:0032355	4	DNMT3A, EZH2, CTNNB1, STAT5B	84	19	46.83	1.399e-6	1.132e-4
regulation of cell population proliferation	GO:0042127	5	TP53, EZH2, CTNNB1, STAT5B, BRAF	201	19	24.47	1.409e-6	1.139e-4
negative regulation of DNA-templated transcription	GO:0045892	7	DNMT3A, TP53, EZH2, CDKN2A, CTNNB1, FOXL2, RB1	631	19	10.91	1.712e-6	1.338e-4
regulation of gene expression	GO:0010468	6	DNMT3A, EZH2, CDKN2A, CTNNB1, FGFR1, PIK3CA	402	19	14.68	2.043e-6	1.542e-4
regulation of centromere complex assembly	GO:0090230	2	H3-3A, RB1	3	19	655.68	2.936e-6	2.062e-4
multicellular organism growth	GO:0035264	4	ATRX, TP53, H3-3A, PTPN11	115	19	34.21	4.912e-6	3.131e-4
MAPK cascade	GO:0000165	4	CTNNB1, KRAS, BRAF, FGFR1	147	19	26.76	1.300e-5	6.667e-4