

GeDiPNet Cluster 570 -- 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 23:18:42

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 by RNA polymerase II	GO:0045944	23	CRTC3, FBXW7, CTNNB1, TCEA1, HRAS, TP53, ELF3, FGFR2, NFIB, HMGA2, POU5F1, PLAG1	1208	64	5.56	4.044e-12	1.682e-9
negative regulation of transcription by RNA polymerase II	GO:0000122	20	CTNNB1, USP9X, BCORL1, TP53, FGFR2, NFIB, BCOR, HMGA2, POU5F1, CHD4, SPEN, DNMT3A	1002	64	5.83	6.611e-11	2.107e-8
chromatin remodeling	GO:0006338	12	KDM6A, PWWP2A, BCOR, SETD1B, CHD4, ATM, ARID1A, ARID1B, CREBBP, SF3B1, RB1, SMARCB1	320	64	10.95	7.666e-10	1.846e-7
regulation of gene expression	GO:0010468	13	CTNNB1, KDM6A, CDH1, HMGA2, POU5F1, DNMT3A, CDKN2A, ATM, MYB, AFF4, NOTCH1, FGFR1	402	64	9.44	8.473e-10	2.009e-7
negative regulation of DNA-templated transcription	GO:0045892	14	CTNNB1, TP53, ELF3, BCOR, HMGA2, CHD4, SPEN, DNMT3A, CDKN2A, MYB, RB1, NCOR1	631	64	6.48	2.184e-8	3.477e-6
chromatin organization	GO:0006325	12	BCORL1, KDM6A, BCOR, HMGA2, SETD1B, CHD4, DNMT3A, ARID1A, ARID1B, RB1, NCOR1, SMARCB1	449	64	7.80	3.389e-8	5.106e-6
chondrocyte differentiation	GO:0002062	6	CTNNB1, NFIB, HMGA2, FGFR3, RB1, FGFR1	61	64	28.72	6.084e-8	8.372e-6
positive regulation of phospholipase activity	GO:0010518	3	FGFR2, FGFR3, FGFR1	4	64	218.99	1.529e-7	1.819e-5
negative regulation of gene expression	GO:0010629	10	FBXW7, CTNNB1, HRAS, TP53, PLAG1, CHD4, RB1, NOTCH1, FGFR1, PIK3CA	339	64	8.61	2.148e-7	2.393e-5
cell population proliferation	GO:0008283	9	CTNNB1, TP53, NFIB, KRAS, HMGA2, FGFR3, RB1, NOTCH1, FGFR1	263	64	9.99	2.648e-7	2.857e-5
glial cell proliferation	GO:0014009	4	TP53, NFIB, KRAS, RB1	18	64	64.89	3.692e-7	3.769e-5
stem cell proliferation	GO:0072089	5	CTNNB1, TP53, NFIB, HMGA2, FGFR1	54	64	27.04	1.117e-6	9.397e-5
oncogene-induced cell senescence	GO:0090402	3	HRAS, HMGA2, CDKN2A	7	64	125.14	1.328e-6	1.085e-4
regulation of G1/S transition of mitotic cell cycle	GO:2000045	5	CDKN2A, ARID1A, ARID1B, RB1, SMARCB1	57	64	25.61	1.467e-6	1.179e-4
positive regulation of cell population proliferation	GO:0008284	11	CTNNB1, LIFR, HRAS, FGFR2, HMGA2, PTEN, FGFR3, FLT4, NOTCH1, CEP43, FGFR1	532	64	6.04	1.704e-6	1.334e-4