

GeDiPNet Cluster 89 -- 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: 2026-10-07 03:23:06. · Rows: 15 · Generated: 2026-10-07 00:26:25

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 by RNA polymerase II	GO:0045944	99	CBFB, CEBPA, ETV6, GATA2, RUNX1, APP, ASCL2, CSRN1P, DRD2, EOMES, ETS1, FLI1	1208	534	2.87	6.098e-22	1.277e-18
apoptotic process	GO:0006915	71	CHEK2, APP, BAK1, BCL2, BCL2L11, BMF, BUB1B, CASP10, CASP8, CFLAR, CLPTM1L, CSRN1P	747	534	3.33	3.100e-19	4.481e-16
positive regulation of gene expression	GO:0010628	52	CEBPA, GATA2, ACTA2, APP, ETS1, KPNA7, LEF1, MAP2K2, SMAD3, GATA3, IL13, PTPN22	504	534	3.61	9.326e-16	7.293e-13
positive regulation of DNA-templated transcription	GO:0045893	66	CEBPA, CHEK2, GATA2, RUNX1, CXXC1, EOMES, ETS1, FLI1, HLA-DRB1, IRF4, IRF8, LEF1	778	534	2.97	1.902e-15	1.416e-12
negative regulation of apoptotic process	GO:0043066	51	TERT, BCL2, CFLAR, FAS, LEF1, RPS6KB1, SMAD3, AHI1, BAD, BIRC2, BIRC3, IL2	524	534	3.41	1.887e-14	1.168e-11
negative regulation of transcription by RNA polymerase II	GO:0000122	69	CBFB, CEBPA, ETV6, GATA2, RUNX1, APP, ASCL2, EOMES, IRF8, JARID2, LEF1, NCK1	1002	534	2.41	9.619e-12	3.553e-9
macrophage differentiation	GO:0030225	13	CEBPA, CASP8, CFLAR, HLA-DRB1, GATA3, NPM1, SPI1, VEGFA, CSF1R, CSF2, CEBPE, IFNG	37	534	12.30	1.394e-11	4.956e-9
cell population proliferation	GO:0008283	31	CEBPA, BCL2, DRD2, JARID2, SMAD3, GATA3, RUNX2, BAP1, CCND1, SPHK1, KIT, KRAS	263	534	4.12	2.466e-11	8.184e-9
response to ethanol	GO:0045471	20	BAK1, CASP8, DRD2, GATA3, IL13, BIRC2, CCND1, DNMT3A, IL2, POLB, TNFRSF11A, CDO1	110	534	6.36	3.740e-11	1.183e-8
positive regulation of apoptotic process	GO:0043065	34	APP, BAK1, BCL2, BCL2L11, BMF, CASP8, FAS, IRF8, SPDEF, ABL1, EPHA7, LPAR1	326	534	3.65	7.886e-11	2.305e-8
response to gamma radiation	GO:0010332	11	CHEK2, BAK1, BCL2, GATA3, POLB, TP53, PML, BRCA2, LIG4, PARP1, SOD2	27	534	14.26	8.072e-11	2.355e-8
regulation of gene expression	GO:0010468	38	APP, BCL2, EOMES, JARID2, ABL1, MAPK3, MYOD1, RUNX2, AR, BAP1, DNMT3A, KMT2A	402	534	3.31	1.101e-10	3.132e-8
intrinsic apoptotic signaling pathway in response to DNA damage	GO:0008630	14	CHEK2, BAK1, BCL2, BCL2L11, ABL1, BAD, ATM, POLB, MYC, PML, BCL2L1, BRCA2	54	534	9.07	2.322e-10	6.099e-8
regulation of apoptotic process	GO:0042981	29	BAK1, BCL2, BCL2L11, CASP10, CASP8, CFLAR, ETS1, FAS, PHLPP1, ZBTB7A, LRP5, BAD	254	534	4.00	2.363e-10	6.195e-8
positive regulation of miRNA transcription	GO:1902895	14	GATA2, TERT, ETS1, SMAD3, GATA3, AR, WT1, IL6, TP53, SPI1, MYC, STAT3	56	534	8.75	3.942e-10	9.693e-8