

GeDiPNet Cluster 45 -- 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 00:27:00

GO Term	GO ID	Overlap Genes	Overlap Gene Names	Term Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
regulation of cell cycle	GO:0051726	18	CDKN1C, CDKN2A, PTEN, TP53, BAK1, CEBPA, IRF1, ABL1, BCR, CDK4, CDK6, BAX	262	166	7.73	2.112e-11	7.139e-9
positive regulation of transcription by RNA polymerase II	GO:0045944	34	CDKN2A, CTNNB1, PTEN, TP53, CEBPA, CEBPE, ELK3, ERG, GATA3, IKZF3, IRF1, MYB	1208	166	3.17	1.546e-9	3.303e-7
negative regulation of cell population proliferation	GO:0008285	20	SH2B3, APC, CDKN2A, CTNNB1, PTEN, TP53, BAK1, CEBPA, GATA3, IRF1, CDK6, PPM1D	444	166	5.07	2.784e-9	5.527e-7
response to gamma radiation	GO:0010332	7	TP53, BAK1, GATA3, TIGAR, BAX, CHEK2, SOD2	27	166	29.19	2.940e-9	5.794e-7
regulation of cell population proliferation	GO:0042127	14	CTNNB1, TP53, CEBPA, CSF2, STAT4, STAT6, PBX1, ABL1, CDK6, BRAF, ERBB2, TAL1	201	166	7.84	3.313e-9	6.468e-7
cell population proliferation	GO:0008283	15	CTNNB1, KRAS, TP53, CEBPA, CSF2, GATA3, PBX1, AKT1, CAV1, ERBB2, BAX, GNB1	263	166	6.42	1.357e-8	2.229e-6
regulation of gene expression	GO:0010468	18	CDKN2A, CTNNB1, CSF2, IL7, IRF1, MYB, NFKB1, FOXP1, ABL1, KMT2A, CDK4, CDK6	402	166	5.04	1.999e-8	3.117e-6
positive regulation of gene expression	GO:0010628	20	CDKN2A, CTNNB1, KRAS, TP53, CCL2, CEBPA, CEBPE, CSF2, GATA3, IL7, BCL11A, KMT2A	504	166	4.47	2.349e-8	3.584e-6
cytokine-mediated signaling pathway	GO:0019221	11	KRAS, CCL2, CEBPA, FLT3, IL7, STAT4, STAT6, TRAF3IP2, AKT1, CAV1, PTPRJ	145	166	8.54	7.068e-8	9.034e-6
response to xenobiotic stimulus	GO:0009410	13	CTNNB1, TP53, BAK1, GATA3, TRAF3IP2, ABL1, CDK4, NFE2L2, TIGAR, MDM2, CCND1, MMP2	248	166	5.90	3.454e-7	3.419e-5
embryonic hemopoiesis	GO:0035162	5	SH2B3, GATA3, PBX1, KMT2A, TAL1	18	166	31.27	4.063e-7	3.928e-5
cellular response to tumor necrosis factor	GO:0071356	9	CCL2, CD58, CEBPA, GATA3, NFKB1, FOXP1, AKT1, NFE2L2, NFKBIA	107	166	9.47	4.720e-7	4.450e-5
myeloid cell differentiation	GO:0030099	6	CDKN1C, CEBPA, CEBPE, CSF2, MYB, TAL1	35	166	19.30	5.885e-7	5.370e-5
response to muscle stretch	GO:0035994	5	NFKB1, TCAP, RYR2, NFKBIA, PIK3CA	20	166	28.14	7.248e-7	6.404e-5
signal transduction	GO:0007165	41	SH2B3, CELSR2, KRAS, ARHGAP31, CCL2, CCR6, CSF2, ELK3, ERG, GATA3, GRB10, HBS1L	2125	166	2.17	1.092e-6	8.905e-5