

GeDiPNet Cluster 147 -- 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: 2026-10-08 03:23:04. · Rows: 15 · Generated: 2026-10-08 17:25:11

GO Term	GO ID	Overlap Genes	Overlap Gene Names	Term Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
negative regulation of apoptotic process	GO:0043066	16	DAPK1, RXFP2, CAAP1, BCL2, EGFR, ERBB2, ERBB3, ERBB4, TP53, AKT1, HIF1A, HSPB1	524	81	7.04	7.279e-10	1.631e-7
positive regulation of miRNA transcription	GO:1902895	7	EGFR, TP53, HIF1A, MYCN, TGFB1, AGT, NR3C1	56	81	28.84	4.313e-9	7.968e-7
positive regulation of epithelial cell proliferation	GO:0050679	7	EGFR, ERBB2, ERBB3, ERBB4, MYCN, TCF7L2, TGFB1	73	81	22.12	2.857e-8	4.197e-6
positive regulation of gene expression	GO:0010628	14	NWD1, ERBB2, ERBB3, KRAS, TP53, AKT1, HIF1A, IL13, LDLR, MYCN, NFE2L2, TGFB1	504	81	6.41	3.137e-8	4.544e-6
positive regulation of phosphatidylinositol 3-kinase/protein kinase B signal transduction	GO:0051897	10	EGFR, ERBB3, ERBB4, LEP, NDP, PIK3CA, TCF7L2, TGFB1, AGT, INS	217	81	10.63	3.317e-8	4.764e-6
glucose homeostasis	GO:0042593	8	NEUROD1, AKT1, HIF1A, LEP, TCF7L2, FBN2, INS, POMC	134	81	13.77	1.174e-7	1.400e-5
positive regulation of transcription by RNA polymerase II	GO:0045944	20	NEUROD1, EGFR, TP53, AKT1, BRD4, HIF1A, IL13, KDM1A, MYCN, NDP, NFE2L2, OGG1	1208	81	3.82	1.470e-7	1.699e-5
cellular response to hypoxia	GO:0071456	8	BCL2, TP53, HIF1A, NDP, NFE2L2, PTGS2, TGFB1, KCNK3	139	81	13.28	1.558e-7	1.782e-5
cell population proliferation	GO:0008283	10	BCL2, EGFR, ERBB2, KRAS, TP53, AKT1, CCND1, MYCN, NDP, TGFB1	263	81	8.77	2.007e-7	2.208e-5
neuron apoptotic process	GO:0051402	7	BCL2, ERBB3, KRAS, TP53, HIF1A, NDP, TGFB1	98	81	16.48	2.224e-7	2.410e-5
response to oxidative stress	GO:0006979	8	BCL2, KEAP1, TP53, AKT1, HMOX1, NFE2L2, OGG1, PTGS2	146	81	12.64	2.276e-7	2.460e-5
response to UV-A	GO:0070141	3	EGFR, AKT1, CCND1	4	81	173.03	3.129e-7	3.191e-5
epidermal growth factor receptor signaling pathway	GO:0007173	6	EGFR, ERBB2, ERBB3, ERBB4, AKT1, PIK3CA	64	81	21.63	3.372e-7	3.394e-5
positive regulation of MAPK cascade	GO:0043410	9	EGFR, ERBB2, ERBB3, ERBB4, LEP, TGFB1, FGF5, ADRB2, INS	224	81	9.27	5.371e-7	5.023e-5
negative regulation of oxidative stress-induced intrinsic apoptotic signaling pathway	GO:1902176	4	AKT1, HSPB1, NFE2L2, INS	18	81	51.27	9.570e-7	8.065e-5