

GeDiPNet Cluster 116 -- 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 08:47:50

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	17	AKT1, BRD4, HIF1A, IL13, KDM1A, MYCN, NDP, NFE2L2, OGG1, TCF7L2, TGFB1, CASZ1	1208	59	4.46	1.114e-7	1.322e-5
glucose homeostasis	GO:0042593	7	AKT1, HIF1A, LEP, TCF7L2, FBN2, INS, POMC	134	59	16.55	2.083e-7	2.246e-5
negative regulation of oxidative stress-induced intrinsic apoptotic signaling pathway	GO:1902176	4	AKT1, HSPB1, NFE2L2, INS	18	59	70.38	2.653e-7	2.746e-5
positive regulation of blood vessel endothelial cell migration	GO:0043536	5	AKT1, HIF1A, HSPB1, NFE2L2, TGFB1	51	59	31.05	5.546e-7	5.105e-5
positive regulation of smooth muscle cell proliferation	GO:0048661	5	AKT1, HMOX1, IL13, PIK3CA, TGFB1	52	59	30.45	6.121e-7	5.553e-5
positive regulation of miRNA transcription	GO:1902895	5	HIF1A, MYCN, TGFB1, AGT, NR3C1	56	59	28.28	8.910e-7	7.539e-5
positive regulation of epithelial to mesenchymal transition	GO:0010718	5	KDM1A, TCF7L2, TGFB1, LEF1, AGT	59	59	26.84	1.159e-6	9.335e-5
glucose metabolic process	GO:0006006	5	AKT1, LEP, PIK3CA, FBN2, INS	66	59	23.99	2.035e-6	1.460e-4
cellular response to hypoxia	GO:0071456	6	HIF1A, NDP, NFE2L2, PTGS2, TGFB1, KCNK3	139	59	13.67	4.953e-6	2.982e-4
positive regulation of phosphatidylinositol 3-kinase/protein kinase B signal transduction	GO:0051897	7	LEP, NDP, PIK3CA, TCF7L2, TGFB1, AGT, INS	217	59	10.22	5.282e-6	3.137e-4
regulation of blood pressure	GO:0008217	5	LEP, PTGS2, AGT, NPPB, POMC	83	59	19.08	6.347e-6	3.628e-4
elastin metabolic process	GO:0051541	2	HIF1A, LEP	2	59	316.73	9.800e-6	5.132e-4
negative regulation of macroautophagy	GO:0016242	3	AKT1, HMOX1, PIK3CA	14	59	67.87	1.062e-5	5.454e-4
negative regulation of gene expression	GO:0010629	8	AKT1, HIF1A, LDLR, MYCN, PIK3CA, TGFB1, AGT, INS	339	59	7.47	1.070e-5	5.489e-4
retina vasculature development in camera-type eye	GO:0061298	3	HIF1A, NDP, TGFB1	15	59	63.35	1.324e-5	6.496e-4