

GeDiPNet Cluster 73 -- 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 00:26:34

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 gene expression	GO:0010628	101	APOB, BCL3, CCL2, CCL3, CLU, CRP, HSPA1A, HSPA1B, IFNG, IL6, LDLR, NOS3	504	1218	3.07	8.834e-25	2.664e-21
response to xenobiotic stimulus	GO:0009410	64	ABCA1, ABCG5, ADIPOQ, AHR, CYBA, MTHFR, NPC1, SOD1, SOD2, TNF, EDN1, KCNK3	248	1218	3.96	4.312e-22	9.254e-19
positive regulation of transcription by RNA polymerase II	GO:0045944	161	AHR, BCL3, ESR1, IFNG, IGF2, IL6, NEUROG3, NR1H4, PARP1, PPARG, SIRT1, SMARCA4	1208	1218	2.04	5.698e-19	7.878e-16
regulation of blood pressure	GO:0008217	33	AGT, EDNRA, NOS3, NPPB, PPARG, PTGS2, SOD1, SOD2, EDN1, ACE, ATP2B1, GNB3	83	1218	6.10	3.024e-18	3.764e-15
inflammatory response	GO:0006954	84	AGER, ALOX15, ALOX5, CCL2, CCL3, CCL4, CNR2, CRP, CYBA, HDAC9, HP, HRH1	467	1218	2.76	1.049e-17	1.215e-14
kidney development	GO:0001822	43	AGT, VEGFA, ACE, AGTR1, TCF21, BICC1, HAS2, LRP2, OVOL1, SLC34A1, SOX11, UMOD	146	1218	4.52	1.410e-17	1.601e-14
lipid metabolic process	GO:0006629	122	ACACA, ABCA1, AIG1, ALOX15, ALOX5, APOA1, APOB, APOC1, APOE, CETP, CLU, CYP27A1	840	1218	2.23	2.326e-17	2.550e-14
positive regulation of phosphatidylinositol 3-kinase/protein kinase B signal transduction	GO:0051897	52	AGT, CCL3, IGF2, SIRT1, TCF7L2, TNF, VEGFA, F2, IL1B, PIK3CA, TGFB1, IL17A	217	1218	3.68	1.075e-16	1.016e-13
positive regulation of miRNA transcription	GO:1902895	26	AGT, IL6, PPARG, SMARCA4, STAT3, TNF, NOTCH3, TGFB1, IL10, NR3C1, SREBF1, TERT	56	1218	7.12	1.131e-16	1.054e-13
response to nutrient	GO:0007584	27	ABCA1, ABCG5, ADIPOQ, AGL, PPARG, VCAM1, ABCG8, BCHE, EPO, LIPG, LTA, NOD2	63	1218	6.58	3.633e-16	3.092e-13
cellular response to lipopolysaccharide	GO:0071222	47	ABCA1, CCL2, GBP3, IL6, NOS2, NR1H4, SERPINE1, TLR4, TNF, VIM, IL1B, PRPF8	187	1218	3.86	4.435e-16	3.729e-13
response to lipopolysaccharide	GO:0032496	43	CNR2, FASLG, LOXL1, MPO, NOS2, NOS3, NQO1, SOD2, TLR4, TNF, VCAM1, EDN1	161	1218	4.10	7.411e-16	5.945e-13
blood coagulation	GO:0007596	34	PLAT, F2, F5, FGA, ITGB3, PLAU, VKORC1, P2RY12, ANGPTL4, F7, FGB, GGCX	106	1218	4.92	2.011e-15	1.490e-12
negative regulation of apoptotic process	GO:0043066	85	BCL3, HSPA1A, HSPA1B, IL6, MPO, NR1H4, PTGS2, SIRT1, SOCS3, SOD1, SOD2, TNF	524	1218	2.49	3.887e-15	2.747e-12
response to hypoxia	GO:0001666	44	ADIPOQ, AGER, CBFA2T3, CYBA, EDNRA, MTHFR, NOS2, PLAT, SOD2, STAT3, TNF, VCAM1	176	1218	3.84	4.761e-15	3.292e-12