

GeDiPNet Cluster 133 -- 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 05:22:31

GO Term	GO ID	Overlap Genes	Overlap Gene Names	Term Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
inflammatory response	GO:0006954	53	IL1B, IL1RN, NFKBIA, TNF, BDKRB2, CCL1, CRP, CXCL1, CXCL2, CYBA, F2RL1, IL13	467	337	6.29	3.181e-27	1.332e-23
response to hypoxia	GO:0001666	30	ABAT, POSTN, TNF, CHRNA4, CHRNA7, CYBA, CYP1A1, EDN1, HIF1A, LEP, MMP14, NOS2	176	337	9.45	7.898e-21	1.431e-17
positive regulation of gene expression	GO:0010628	47	IL1B, TNF, VDR, ITGA3, CDKN2A, CRP, HIF1A, HSPA1A, HSPA1B, IL13, IL6, NOS3	504	337	5.17	1.448e-20	2.584e-17
positive regulation of phosphatidylinositol 3-kinase/protein kinase B signal transduction	GO:0051897	32	FLT1, IL1B, TNF, TXN, F2RL1, LEP, TGFB1, ENG, PIK3CG, IL17A, ADRA2B, CAT	217	337	8.18	3.631e-20	6.195e-17
immune response	GO:0006955	48	IL1B, IL1RN, TNF, CCL1, CD86, CD8A, CRHR1, CTLA4, CXCL1, CXCL2, DEFB1, HLA-DPB1	543	337	4.90	5.131e-20	8.427e-17
positive regulation of cell migration	GO:0030335	36	FLT1, IL1B, CCL1, EDN1, F2RL1, MMP14, TGFB1, AGER, CEACAM6, SNAI1, PLAU, IGF1R	292	337	6.84	6.746e-20	1.082e-16
positive regulation of cell population proliferation	GO:0008284	46	FLT1, HTR1A, IL1B, NANOGP8, CD86, CDKN1A, CHRNA7, EDN1, HDAC2, HTR2A, IL6, KLF5	532	337	4.79	7.974e-19	1.069e-15
positive regulation of interleukin-8 production	GO:0032757	19	IL1B, TNF, F2RL1, HSPA1A, HSPA1B, IL6, LEP, NOD2, NOS2, TLR4, CD14, TLR5	65	337	16.21	2.569e-18	3.210e-15
lung development	GO:0030324	22	ITGA3, CYP1A2, MMP14, NOS3, ABCA3, CEBPA, GLI3, CCN2, CRISPLD2, NKX2-1, PDGFRA, SPRY2	108	337	11.30	2.593e-17	2.800e-14
positive regulation of inflammatory response	GO:0050729	23	IL1B, NFKBIA, TNF, ABCC1, CCL1, HTR2A, IL12B, TGFB1, TLR4, TRPV4, TLR9, TNFRSF1A	122	337	10.45	2.984e-17	3.183e-14
positive regulation of tumor necrosis factor production	GO:0032760	22	CYBA, HDAC2, IL12B, IL6, LEP, MIF, NOD2, TGFB1, TLR4, TNFRSF8, AGER, CD14	113	337	10.80	7.214e-17	7.128e-14
positive regulation of MAPK cascade	GO:0043410	28	FLT1, IL1B, TNF, ADRB1, ADRB2, CHRNA7, EDN1, IL6, LEP, NOD2, TGFB1, TLR9	224	337	6.93	7.246e-16	5.827e-13
positive regulation of transcription by RNA polymerase II	GO:0045944	64	GRHL2, IL1B, KLF12, NFKBIA, TNF, VDR, ZNF728, ADRB2, CDKN2A, EDN1, F2RL1, FOXO3	1208	337	2.94	4.329e-15	3.022e-12
positive regulation of interleukin-6 production	GO:0032755	19	IL1B, TNF, CYBA, F2RL1, IL6, LEP, NOD2, NOS2, TGFB1, TLR4, TRPV4, AGER	103	337	10.23	2.755e-14	1.654e-11
positive regulation of ERK1 and ERK2 cascade	GO:0070374	25	IL1B, TNF, CHRNA7, F2RL1, HTR2A, ICAM1, MIF, NOD2, TGFB1, TLR4, TRPV4, AGER	201	337	6.90	3.050e-14	1.824e-11