

GeDiPNet Cluster 14 -- 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 02:44:38

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	185	CCL2, CCL20, CCL21, CD40, CXCR2, IL17A, IL18R1, IL18RAP, IL1R1, IL23R, IL27, IL2RA	467	3075	2.41	7.615e-34	5.328e-30
immune response	GO:0006955	197	CCL2, CCL20, CCL21, CCR6, CD244, CD28, CTLA4, CXCR1, CXCR2, ETS1, FAS, HLA-B	543	3075	2.20	6.031e-30	3.149e-26
response to lipopolysaccharide	GO:0032496	76	CD6, CSF2RB, CYP1A1, IL10, IL12RB2, IL23R, IRAK1, LITAF, MAPK3, NOS2, NOTCH1, PTPN22	161	3075	2.87	7.171e-20	1.145e-16
positive regulation of transcription by RNA polymerase II	GO:0045944	319	ACTR2, AHR, ASCL2, CD28, CD40, CREM, CYTL1, EOMES, ETS1, GRHL3, HHEX, IGF2	1208	3075	1.60	7.487e-20	1.190e-16
cytokine-mediated signaling pathway	GO:0019221	69	CCL2, CSF2RB, IFNGR2, IFNLR1, IL12RB2, IL1R1, IL1R2, IL23R, IL6, IL6R, IL7R, IRAK1	145	3075	2.89	2.087e-18	2.654e-15
cell surface receptor signaling pathway via JAK-STAT	GO:0007259	40	CCL2, CD40, CSF2RB, IL12B, IL15RA, IL23R, IL6, IL6R, JAK2, STAT3, TNFRSF1A, TYK2	67	3075	3.63	1.404e-15	1.059e-12
positive regulation of type II interferon production	GO:0032729	43	CD226, CD244, IL12B, IL12RB2, IL18R1, IL1R1, IL2, IL21, IL23R, IL27, JAK2, PTPN22	77	3075	3.39	3.560e-15	2.546e-12
positive regulation of canonical NF-kappaB signal transduction	GO:0043123	87	CARD9, CCL21, CD40, HLA-DRB1, IL1R1, INAVA, IRAK1, LITAF, LTBR, LURAP1L, NDFIP1, NOD2	232	3075	2.28	7.105e-15	4.698e-12
cellular response to lipopolysaccharide	GO:0071222	72	CCL2, CD40, IL10, IL12B, IL6, IRAK1, IRGM, JAK2, LITAF, NFKB1, NOD2, NOS2	187	3075	2.34	3.261e-13	1.651e-10
response to hypoxia	GO:0001666	68	ASCL2, CYP1A1, HIF3A, MTHFR, NOS2, PLAU, SMAD3, STAT3, CRYAA, EGR1, SOD2, TGFB2	176	3075	2.35	1.216e-12	5.503e-10
positive regulation of cytokine production	GO:0001819	41	CARD9, CD28, IL10, IL21, JAK2, PTGER4, IFNG, TNF, AGER, BATF, CD14, GATA3	81	3075	3.08	1.253e-12	5.662e-10
positive regulation of ERK1 and ERK2 cascade	GO:0070374	74	ACTA2, CARD9, CCL21, HLA-DRB1, MAPK3, NOD2, NOTCH1, PDE8A, PDGFB, PTPN22, TLR4, BMP4	201	3075	2.24	2.107e-12	8.998e-10
positive regulation of T cell activation	GO:0050870	28	CCL2, CD28, CORO1A, HLA-DQA1, HLA-DQB1, HLA-DRB1, NR5A2, PRKCQ, B2M, CCR2, ADA, CARD11	45	3075	3.78	6.161e-12	2.373e-9
positive regulation of DNA-templated transcription	GO:0045893	200	AHR, EOMES, ETS1, GRHL3, HHEX, HLA-DRB1, IL10, IL6, IRF1, KDM5A, KPNB1, MYRF	778	3075	1.56	1.327e-11	4.750e-9
positive regulation of interleukin-6 production	GO:0032755	46	CARD9, IFIH1, IL17A, IL6, IL6R, INAVA, NOD2, NOS2, STAT3, TLR4, IFNG, TNF	103	3075	2.71	1.561e-11	5.486e-9