

GeDiPNet Cluster 320 -- 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 07:08:09

GO Term	GO ID	Overlap Genes	Overlap Gene Names	Term Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
immune response	GO:0006955	36	C8B, CD8B, CTLA4, CXCL1, CXCR2, CXCR4, FCGR1A, IGF1R, IL1RN, OSM, SMAD3, STAT3	543	271	4.57	2.460e-14	1.491e-11
positive regulation of interleukin-17 production	GO:0032740	8	OSM, CARD9, IL2, IL21, IL23R, JAK2, TYK2, IL6	27	271	20.43	3.086e-9	6.057e-7
positive regulation of transcription by RNA polymerase II	GO:0045944	44	CREM, DDIT3, EGR1, ETV6, FOS, FOSB, FOSL2, JUN, KAT6B, KLF4, MAFF, MAML2	1208	271	2.51	1.395e-8	2.283e-6
inflammatory response	GO:0006954	25	CD14, CXCL1, CXCR2, CXCR4, FOS, FOSL2, IL1RN, OLR1, SLC11A1, STAB1, STAT3, THBS1	467	271	3.69	2.190e-8	3.379e-6
positive regulation of tumor necrosis factor production	GO:0032760	12	CD14, CLU, FCGR1A, LILRA5, STAT3, THBS1, IL1A, CARD9, JAK2, LRRK2, IL6, MIF	113	271	7.32	9.142e-8	1.117e-5
positive regulation of miRNA transcription	GO:1902895	9	EGR1, FOS, JUN, KLF4, SMAD3, STAT3, IL10, SMAD1, IL6	56	271	11.08	1.038e-7	1.245e-5
interleukin-23-mediated signaling pathway	GO:0038155	4	STAT3, IL23R, JAK2, TYK2	6	271	45.97	6.343e-7	5.714e-5
type II interferon-mediated signaling pathway	GO:0060333	5	CIITA, IRF1, JAK2, STAT1, TYK2	15	271	22.99	1.648e-6	1.236e-4
cell surface receptor signaling pathway via STAT	GO:0097696	6	STAT3, IL2, IL23R, IL6R, STAT1, IL6	28	271	14.78	2.536e-6	1.738e-4
positive regulation of T cell proliferation	GO:0042102	8	IL2, IL21, IL23R, IL2RA, JAK2, VTCN1, TYK2, IL6	67	271	8.23	5.490e-6	3.235e-4
cell surface receptor signaling pathway via JAK-STAT	GO:0007259	8	STAT3, IL23R, JAK2, STAT4, IL6R, STAT1, TYK2, IL6	67	271	8.23	5.490e-6	3.235e-4
signal transduction	GO:0007165	56	CD83, CMTM2, CREM, CTTN, CXCL1, CXCR2, CXCR4, DAPK1, DUSP1, DUSP2, DUSP4, FCGR1A	2125	271	1.82	6.279e-6	3.597e-4
response to cAMP	GO:0051591	6	AREG, DUSP1, FOS, FOSB, PER1, STAT1	34	271	12.17	8.416e-6	4.560e-4
cytokine-mediated signaling pathway	GO:0019221	11	KRAS, LILRA5, STAT3, IL1A, IL23R, JAK2, STAT4, IL2RB, IL6R, TYK2, IL6	145	271	5.23	8.867e-6	4.757e-4
positive regulation of smooth muscle cell proliferation	GO:0048661	7	FOXP1, HBEGF, NR4A3, THBS1, IL6R, STAT1, IL6	52	271	9.28	9.564e-6	5.042e-4