

GeDiPNet Cluster 80 -- 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 13:19:06

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	24	RELA, CDKN2A, DNMT1, HES1, HSPA1A, HSPA1B, KRAS, NFE2L2, NOTCH1, VEGFA, NGF, MAPK14	504	131	6.79	9.784e-14	5.373e-11
Notch signaling pathway	GO:0007219	13	DTX1, DTX4, HES1, HEY1, HEY2, JAG1, JAG2, NOTCH1, NOTCH3, NOTCH4, TGFB1, NR1H4	117	131	15.85	1.798e-12	7.773e-10
aortic valve morphogenesis	GO:0003180	9	HEY1, HEY2, JAG1, NOTCH1, NOS3, TGFB1, ADAMTS5, NPPA, SNAI1	37	131	34.70	3.263e-12	1.333e-9
positive regulation of transcription by RNA polymerase II	GO:0045944	33	RELA, CDKN2A, HES1, HEY1, HEY2, JAG1, NFE2L2, NOTCH1, NOTCH3, NOTCH4, OSM, VEGFA	1208	131	3.90	7.938e-12	2.976e-9
regulation of cell population proliferation	GO:0042127	15	AGTR1, CXCL11, DNMT1, JAG1, JAG2, NOTCH1, CXCL10, CXCL9, SIRT1, NOS2, TGFB1, NR5A2	201	131	10.65	1.129e-11	4.117e-9
pulmonary valve morphogenesis	GO:0003184	7	HEY1, HEY2, JAG1, NOTCH1, NOS3, ADAMTS5, TGFB2	18	131	55.47	2.112e-11	7.139e-9
response to hypoxia	GO:0001666	14	MAP3K7, VEGFA, CYGB, NOS2, TGFB1, CYBA, CYP1A1, LEP, PPARA, EDN1, NPPA, NPPC	176	131	11.35	2.413e-11	8.024e-9
negative regulation of gene expression	GO:0010629	18	DNMT1, HES1, HEY2, MAP3K7, NOTCH1, VEGFA, SIRT1, NOS2, TGFB1, AKT1, GPER1, IFNA2	339	131	7.57	2.673e-11	8.787e-9
cellular response to tumor necrosis factor	GO:0071356	11	RELA, HES1, MAP3K7, NFE2L2, SIRT1, MAPK14, AKT1, CYBA, GPER1, CCL2, EDN1	107	131	14.66	2.300e-10	6.050e-8
negative regulation of cell growth	GO:0030308	11	SIP1, CDKN2A, HSPA1A, HSPA1B, STK11, TGFB1, SESN2, NPPA, NPPB, SMAD3, TGFB2	115	131	13.64	5.037e-10	1.217e-7
inflammatory response	GO:0006954	19	RELA, AGTR1, CXCL11, MAP3K7, NFE2L2, TLR5, CXCL10, CXCL9, ITCH, MTOR, NOS2, TGFB1	467	131	5.80	6.715e-10	1.574e-7
negative regulation of transcription by RNA polymerase II	GO:0000122	27	RELA, CDKN2A, DNMT1, HES1, HEY1, HEY2, HSPA1A, NOTCH1, NOTCH3, NOTCH4, VEGFA, YEATS2	1002	131	3.84	1.238e-9	2.714e-7
negative regulation of biomineral tissue development	GO:0070168	5	HEY1, HEY2, NOTCH1, NOS3, TGFB1	10	131	71.32	3.842e-9	7.387e-7
blood vessel diameter maintenance	GO:0097746	7	AGTR1, NOS3, AGT, EDN1, NPPA, NPPB, NPPC	37	131	26.99	6.118e-9	1.116e-6
intracellular receptor signaling pathway	GO:0030522	7	AHR, NR1H2, NR1H4, NR1I2, NR1I3, NR5A2, PPARA	39	131	25.60	9.034e-9	1.569e-6