

GeDiPNet Cluster 34 -- 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 01:43:25

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 transcription by RNA polymerase II	GO:0045944	407	ABLIM1, ACVR2A, AGRN, AKIRIN2, AP3D1, ARNT2, ASH1L, ATXN1, BAZ1B, BCAS3, BCL3, BSX	1208	3802	1.66	2.032e-29	9.872e-26
regulation of blood pressure	GO:0008217	59	ACE, ADRA1A, AGT, ATP2B1, CORIN, EDN1, EMILIN2, EXT1, GNA12, KCNQ1, MYH6, NOS3	83	3802	3.49	2.575e-23	6.722e-20
response to xenobiotic stimulus	GO:0009410	117	ADRA1A, DNMT3A, EDN1, GATA4, GNA12, HDAC3, HDAC5, HSPG2, MTHFR, MYO6, NPC1, P2RX7	248	3802	2.32	1.449e-21	2.847e-18
angiogenesis	GO:0001525	120	ADAM15, ANGPT1, APOLD1, ARHGAP24, BCAM, BCAS3, CAV1, ENPEP, EPAS1, FGFR2, GJA5, HAND2	284	3802	2.08	2.527e-17	2.754e-14
negative regulation of apoptotic process	GO:0043066	188	ANGPT1, ANXA4, ARHGAP10, ARNT2, BCL3, BNIP1, CCND2, DSG2, ERBB2, ERBB4, FOXO1, HDAC3	524	3802	1.76	4.638e-17	4.800e-14
positive regulation of phosphatidylinositol 3-kinase/protein kinase B signal transduction	GO:0051897	98	AGT, ANGPT1, ERBB4, EXTL3, FERMT2, FGFR3, HBEGF, IGF1R, INSR, MERTK, PRKD1, PTK2	217	3802	2.22	1.094e-16	1.026e-13
positive regulation of DNA-templated transcription	GO:0045893	251	AGT, ARNT2, BCL3, BICRA, CAND2, CASZ1, CHD4, CREB5, CREBBP, DOT1L, DTX3L, EBF2	778	3802	1.59	9.969e-16	7.715e-13
response to hypoxia	GO:0001666	83	ARNT2, CAV1, CIAO3, CREBBP, EDN1, EPAS1, HIGD1C, HSPG2, ITPR2, KCNA5, MTHFR, MYOCD	176	3802	2.32	1.085e-15	8.323e-13
heart development	GO:0007507	112	BBS7, CDKN1A, CXADR, EDN1, EEF1AKMT4-ECE2, ERBB2, ERBB4, GATA4, GATA5, GJA1, GJA5, HAND2	273	3802	2.02	3.613e-15	2.579e-12
positive regulation of MAPK cascade	GO:0043410	97	ADRA1A, BANK1, CAV2, EDN1, ERBB2, ERBB4, FGF5, FGFR2, FGFR3, FRS2, GHR, IGF1R	224	3802	2.13	4.392e-15	3.060e-12
negative regulation of cell population proliferation	GO:0008285	160	ADGRB1, ADRA1A, AGBL4, ALDH1A2, ARID2, CAV1, CDH13, CDK6, CDKN1A, DLC1, DLEC1, DLG5	444	3802	1.77	6.768e-15	4.509e-12
regulation of heart rate by cardiac conduction	GO:0086091	31	ACE, ANK2, CACNA1D, CAMK2D, CAV1, CTNNA3, DSG2, GJA5, HCN4, ISL1, KCNA5, KCND3	43	3802	3.54	3.729e-13	1.853e-10
blood coagulation	GO:0007596	55	ANGPT1, F5, GNA12, HPS6, ITPK1, JMJD1C, PTPRJ, VWF, HGFAC, PLG, FGB, GNAQ	106	3802	2.55	5.329e-13	2.585e-10
positive regulation of angiogenesis	GO:0045766	72	EMILIN2, GATA4, HMGA2, ISL1, NOS3, PIK3CD, PLCG1, PRKD1, RUNX1, SIRT1, STIM1, TNFSF12	159	3802	2.23	1.039e-12	4.775e-10
negative regulation of transcription by RNA polymerase II	GO:0000122	294	ANXA4, ATXN1, CAV1, CBX6, CBX8, CDK6, CHD4, CREBBP, CUX1, CUX2, DNMT3A, E2F6	1002	3802	1.44	2.110e-12	9.001e-10