

GeDiPNet Cluster 182 -- 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 11:57:03

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 phosphatidylinositol 3-kinase/protein kinase B signal transduction	GO:0051897	34	CAT, CSF1R, FGFR3, FN1, INS, INSR, IRS1, PDGFC, RAC1, SIRT1, TCF7L2, TGFB1	217	612	4.78	2.980e-14	1.785e-11
response to hypoxia	GO:0001666	29	ADIPOQ, ASCL2, CAT, CPT1A, CYP1A1, ITGA2, KCNJ11, PML, SOD3, TFRC, TGFB1, UCP3	176	612	5.03	6.463e-13	3.080e-10
response to xenobiotic stimulus	GO:0009410	33	ABCC8, ACSL1, ADIPOQ, BCL2, CALR, CAT, CCND1, CPT1A, CYBB, CYP1A1, ITGA2, KCNJ11	248	612	4.06	7.591e-12	2.861e-9
positive regulation of MAPK cascade	GO:0043410	31	ADRB1, FGFR3, IL6, INS, INSR, KSR2, MAP3K5, SOD1, TGFB1, AR, FGF2, LEP	224	612	4.23	1.180e-11	4.291e-9
regulation of blood pressure	GO:0008217	19	ATP2B1, KCNQ1, POMC, PPARG, PTGS2, SOD1, LEP, SOD2, ACE, AGT, NOS3, GUCY1A1	83	612	6.99	1.687e-11	5.884e-9
positive regulation of cell population proliferation	GO:0008284	48	ALDH1A2, BCL2, CALR, CCND1, CCND2, CSF1R, FGFR3, FN1, HMGA2, IGF2BP1, IL6, INS	532	612	2.75	2.253e-10	5.935e-8
positive regulation of gene expression	GO:0010628	45	ALDH1A2, APOB, BCL3, CALR, CEBPB, ETS1, FN1, HFE, HMGA2, HNF1B, IL6, INS	504	612	2.73	1.176e-9	2.593e-7
regulation of insulin secretion	GO:0050796	13	CPT1A, GCK, GIPR, HNF4A, IL6, KCNJ11, MTNR1B, RFX6, TFAP2B, LEP, IFNG, GIP	46	612	8.63	1.655e-9	3.514e-7
response to glucose	GO:0009749	15	ADIPOQ, GCK, GCKR, GIPR, HNF1B, HNF4A, LPL, SLC30A8, TCF7L2, TGFB1, TXNIP, CASP3	68	612	6.74	4.013e-9	7.679e-7
positive regulation of ERK1 and ERK2 cascade	GO:0070374	25	APOE, CSF1R, FGFR3, NOTCH2, PDE8B, PDGFC, PTPN22, TGFB1, TLR4, CCN2, FGF2, GAS6	201	612	3.80	1.090e-8	1.839e-6
positive regulation of endothelial cell migration	GO:0010595	14	BCAR1, CALR, ETS1, PROX1, RAC1, FGF2, AGT, KDR, VEGFA, NRP2, SASH1, ANGPT1	66	612	6.48	2.266e-8	3.478e-6
negative regulation of apoptotic process	GO:0043066	43	BCL2, BCL3, CAT, CCND2, CSF1R, FAIM2, HMGA2, HNF1B, IL6, NOTCH2, PTGS2, SIRT1	524	612	2.51	3.350e-8	4.822e-6
positive regulation of transcription by RNA polymerase II	GO:0045944	75	ASCL2, AUTS2, BAZ1B, BCL3, BRD3, BSX, CDK12, CEBPB, CHD6, CRTCL1, ETS1, GLIS3	1208	612	1.90	6.249e-8	8.171e-6
negative regulation of neuron apoptotic process	GO:0043524	21	BCL2, CCND1, CEBPB, FAIM2, MTNR1B, SIRT1, SOD1, TFAP2B, TFAP2D, WFS1, SOD2, AXL	160	612	4.01	6.398e-8	8.344e-6
positive regulation of blood vessel endothelial cell migration	GO:0043536	12	ETS1, PLCG1, SIRT1, TGFB1, FGF2, KDR, NFE2L2, NOS3, VEGFA, PLG, ANGPT1, THBS1	51	612	7.18	6.748e-8	8.722e-6