

GeDiPNet Cluster 35 -- 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 07:38:52

GO Term	GO ID	Overlap Genes	Overlap Gene Names	Term Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
glucose homeostasis	GO:0042593	19	PPARG, GCK, HNF4A, INS, PDX1, STAT3, ADIPOQ, FBN1, GCG, HNF1A, IL6, INSR	134	205	12.93	4.644e-16	3.868e-13
regulation of insulin secretion	GO:0050796	12	KCNJ11, GCK, HADH, HNF4A, GCG, IL6, LEP, NEUROD1, SLC16A1, TNF, IL1B, RFX6	46	205	23.78	6.168e-14	3.520e-11
glucose metabolic process	GO:0006006	12	KCNJ11, GCK, INS, PDX1, ADIPOQ, FBN1, IRS2, LEP, TNF, AKT2, IGF2, ONECUT1	66	205	16.57	6.443e-12	2.477e-9
response to xenobiotic stimulus	GO:0009410	19	KCNJ11, ABCC8, LTA, MMP2, SOD2, TP53, HADH, GATA4, PDX1, SCNN1B, SNCA, ADIPOQ	248	205	6.98	3.532e-11	1.123e-8
endocrine pancreas development	GO:0031018	8	HNF1B, MNX1, PDX1, IL6, NEUROD1, RFX6, NKX2-2, ONECUT1	22	205	33.15	5.127e-11	1.580e-8
response to nutrient levels	GO:0031667	12	GSTP1, PPARG, PRL, SOD2, PDX1, ADIPOQ, CD40, LEP, SOD1, PTPN1, TNF, G6PC1	79	205	13.85	5.917e-11	1.792e-8
cellular response to insulin stimulus	GO:0032869	13	GSTP1, PPARG, UCP2, GCK, ADIPOQ, INSR, IRS2, LEP, SP1, IRS1, PTPN1, AKT2	102	205	11.62	9.038e-11	2.617e-8
positive regulation of D-glucose import	GO:0046326	9	INS, ADIPOQ, INSR, IRS2, NFE2L2, TERT, IRS1, AKT2, APPL1	38	205	21.59	2.389e-10	6.250e-8
positive regulation of glycogen biosynthetic process	GO:0045725	7	GCK, INS, INSR, IRS2, IRS1, AKT2, IGF2	17	205	37.53	3.058e-10	7.785e-8
type B pancreatic cell differentiation	GO:0003309	6	PDX1, PAX4, RFX6, GATA6, NKX2-2, ONECUT1	10	205	54.69	3.280e-10	8.296e-8
response to oxidative stress	GO:0006979	14	APOE, HMOX1, MMP2, SOD2, TP53, GPX1, NFE2L2, NQO1, PRDX4, PTGS2, SOD1, LIAS	146	205	8.74	7.924e-10	1.821e-7
positive regulation of DNA-templated transcription	GO:0045893	30	AGT, APOE, PPARG, TP53, HNF4A, GATA4, HNF1B, NEUROG3, PDX1, PTF1A, STAT3, CASZ1	778	205	3.52	1.990e-9	4.114e-7
positive regulation of angiogenesis	GO:0045766	14	HMOX1, GATA4, STAT3, ADM, CCL11, CD40, NFE2L2, NOS3, PRKCB, SP1, TERT, IL1B	159	205	8.03	2.437e-9	4.923e-7
response to lipopolysaccharide	GO:0032496	14	ABCC8, FASLG, LTA, SOD2, TLR4, IL13, SNCA, CNR2, GPX1, NOS3, NQO1, LIAS	161	205	7.93	2.870e-9	5.678e-7
response to glucose	GO:0009749	10	UCP2, GCK, HNF4A, HNF1B, PDX1, ADIPOQ, GPX1, IRS2, NEUROD1, NKX2-2	68	205	13.41	3.387e-9	6.601e-7