

GeDiPNet Cluster 13 -- 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: 2026-10-09 03:23:08. · Rows: 15 · Generated: 2026-10-09 04:51:59

GO Term	GO ID	Overlap Genes	Overlap Gene Names	Term Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
cartilage development involved in endochondral bone morphogenesis	GO:0060351	3	COL2A1, TRPV4, EXT1	9	48	129.77	1.322e-6	1.042e-4
extrinsic apoptotic signaling pathway in absence of ligand	GO:0097192	4	COL2A1, BCL2, IL1A, IL1B	36	48	43.26	2.124e-6	1.522e-4
negative regulation of extrinsic apoptotic signaling pathway in absence of ligand	GO:2001240	4	COL2A1, BCL2, IL1A, IL1B	37	48	42.09	2.377e-6	1.662e-4
glyoxylate cycle	GO:0006097	2	IDH1, IDH2	2	48	389.31	6.461e-6	3.724e-4
retina vasculature development in camera-type eye	GO:0061298	3	PDGFRA, HIF1A, LRP5	15	48	77.86	7.082e-6	4.006e-4
positive regulation of transcription by RNA polymerase II	GO:0045944	13	NR4A3, IL1A, PSMC3, IL18, IL1B, POMC, CDKN2A, HIF1A, KDM4C, LDB2, SS18, WWP2	1208	48	4.19	7.408e-6	4.155e-4
regulation of gene expression	GO:0010468	8	COL2A1, BCL2, F2, CDKN2A, HIF1A, KDM4C, VHL, RELN	402	48	7.75	7.602e-6	4.248e-4
cell morphogenesis	GO:0000902	5	EXT1, BCL2, VHL, SS18, RELN	119	48	16.36	1.324e-5	6.547e-4
positive regulation of phosphatidylinositol 3-kinase/protein kinase B signal transduction	GO:0051897	6	PDGFRA, F2, IL18, IL1B, PTPN11, RELN	217	48	10.76	1.869e-5	8.575e-4
dendritic cell apoptotic process	GO:0097048	2	NR4A3, BCL2	3	48	259.54	1.935e-5	8.815e-4
fever generation	GO:0001660	2	IL1A, IL1B	3	48	259.54	1.935e-5	8.815e-4
glucose homeostasis	GO:0042593	5	TRPV4, POMC, CDKN2A, HIF1A, PTPN11	134	48	14.53	2.352e-5	1.018e-3
negative regulation of proteolysis involved in protein catabolic process	GO:1903051	2	UFSP2, CDKN2A	4	48	194.66	3.864e-5	1.490e-3
negative regulation of ossification	GO:0030279	3	BCL2, HIF1A, LRP4	27	48	43.26	4.455e-5	1.656e-3
positive regulation of mitotic nuclear division	GO:0045840	3	IL1A, IL1B, LRP5	29	48	40.27	5.545e-5	1.955e-3