

GeDiPNet Cluster 376 -- 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: 2026-10-08 03:23:04. · Rows: 15 · Generated: 2026-10-08 11:35:11

GO Term	GO ID	Overlap Genes	Overlap Gene Names	Term Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
response to hypoxia	GO:0001666	11	AGER, CASP3, CXCL12, EPO, MTHFR, PLAT, SOD2, THBS1, TNF, VEGFA, F7	176	74	15.78	9.445e-11	2.692e-8
acute-phase response	GO:0006953	7	ASS1, EPO, HP, IL1RN, F2, ORM1, INS	37	74	47.78	1.069e-10	3.025e-8
response to lipopolysaccharide	GO:0032496	9	ASS1, CASP3, EPO, FASLG, GCH1, NOS3, RELA, SOD2, TNF	161	74	14.12	1.431e-8	2.305e-6
response to nutrient levels	GO:0031667	7	ALB, SOD2, TNF, ATG7, F7, FBP1, GC	79	74	22.38	2.638e-8	3.927e-6
extrinsic apoptotic signaling pathway	GO:0097191	6	FASLG, TNF, FAS, INHBA, KRT18, KRT8	57	74	26.58	9.700e-8	1.188e-5
negative regulation of fibrinolysis	GO:0051918	4	PLAT, SERPINE1, THBS1, F2	12	74	84.18	1.095e-7	1.317e-5
response to hydrogen peroxide	GO:0042542	5	CASP3, HMOX1, HP, RELA, SOD2	39	74	32.38	4.401e-7	4.249e-5
liver development	GO:0001889	6	ASS1, RELA, SOD2, ACADM, GFER, HGF	87	74	17.42	1.229e-6	9.895e-5
positive regulation of ERK1 and ERK2 cascade	GO:0070374	8	AGER, EPO, HLA-DRB1, TNF, VEGFA, CD74, GPNMB, INHBA	201	74	10.05	1.279e-6	1.023e-4
vasodilation	GO:0042311	5	NOS3, SOD2, TNF, VEGFA, INS	50	74	25.25	1.566e-6	1.203e-4
response to amino acid	GO:0043200	4	ASS1, CASP3, MTHFR, RELA	22	74	45.91	1.570e-6	1.205e-4
negative regulation of plasminogen activation	GO:0010757	3	PLAT, SERPINE1, THBS1	7	74	108.23	2.063e-6	1.500e-4
positive regulation of cell migration	GO:0030335	9	AGER, CXCL12, SOD2, THBS1, VEGFA, F7, GPNMB, HGF, INS	292	74	7.78	2.231e-6	1.603e-4
positive regulation of canonical NF-kappaB signal transduction	GO:0043123	8	FASLG, HLA-DRB1, HMOX1, RELA, TNF, VEGFA, CD74, INS	232	74	8.71	3.725e-6	2.416e-4
tumor necrosis factor-mediated signaling pathway	GO:0033209	5	RELA, TNF, FAS, KRT18, KRT8	60	74	21.04	3.913e-6	2.514e-4