

GeDiPNet Cluster 23 -- 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 14:59:56

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	16	CAT, MTHFR, ABCB1, MMP2, PLAT, TRPV4, CYP1A1, KCNMA1, CA9, EGR1, NOS1, NPPA	176	189	8.99	3.096e-11	1.000e-8
positive regulation of transcription by RNA polymerase II	GO:0045944	37	GLIS3, HGF, ANXA2, AR, ATF3, BMP7, ESR2, EYA1, GREM1, HOXA4, IRX6, KAT6B	1208	189	3.03	1.122e-9	2.485e-7
response to oxidative stress	GO:0006979	13	APOE, CAT, MMP2, DGKK, MPO, SOD2, RIPK1, TXNRD2, ATM, ERCC2, OGG1, WRN	146	189	8.80	3.006e-9	5.911e-7
vasodilation	GO:0042311	8	APOE, NOS3, KCNMA1, NOS1, NPPA, SOD2, TNF, ADRA2A	50	189	15.82	3.525e-8	5.032e-6
response to lipopolysaccharide	GO:0032496	12	NOS3, ABCB1, IL23R, ACP5, CYP1A1, MPO, NOS1, PCK2, SOD2, MAPK14, TNF, GPX4	161	189	7.37	9.048e-8	1.108e-5
response to nutrient levels	GO:0031667	9	ABCB1, SRD5A2, WNT11, ATF4, SOD2, PPARG, ADIPOQ, TNF, GSTP1	79	189	11.26	1.024e-7	1.232e-5
response to hyperoxia	GO:0055093	5	CAT, MMP2, CYP1A1, SOD2, TXNRD2	14	189	35.31	1.866e-7	2.042e-5
response to activity	GO:0014823	7	CAT, ANXA2, MMP2, PIK3CA, SOD2, ADIPOQ, TNF	52	189	13.31	8.822e-7	7.488e-5
positive regulation of DNA-templated transcription	GO:0045893	24	APOE, AR, BMP7, ESR2, EYA1, GREM1, IRX6, KAT6B, SP1, WNT11, ZFH3, ACTB	778	189	3.05	1.172e-6	9.419e-5
positive regulation of gene expression	GO:0010628	18	NOS3, TRPV4, AR, ATF3, BMP7, SP1, ATF4, EGR1, CUX2, PPARG, RIPK1, SFRP4	504	189	3.53	3.834e-6	2.431e-4
response to L-ascorbic acid	GO:0033591	3	CAT, SOD2, GSTP1	4	189	74.15	4.043e-6	2.534e-4
positive regulation of cholesterol efflux	GO:0010875	5	APOE, APOA1, ABCG1, PPARG, ADIPOQ	27	189	18.31	6.763e-6	3.814e-4
osteoblast differentiation	GO:0001649	9	CAT, BMP7, SND1, SP7, WNT11, ATP5F1B, ACVR1, MAPK14, ACVR2A	137	189	6.50	1.078e-5	5.521e-4
angiogenesis	GO:0001525	12	NOS3, ANXA2, MMP2, GREM1, HOXA3, PIK3CA, ATP5F1B, COL18A1, HSPA12B, MAPK14, TGFA, FN1	284	189	4.18	3.359e-5	1.334e-3
negative regulation of extrinsic apoptotic signaling pathway in absence of ligand	GO:2001240	5	COL2A1, EYA1, RIPK1, TNF, HSPA1B	37	189	13.36	3.364e-5	1.335e-3