

GeDiPNet Cluster 391 -- 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 03:05:02

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 cell migration	GO:0030335	14	BMP2, CCL2, COL1A1, IL1B, ITGB1, JAK2, MMP2, NOTCH1, PDGFB, PDGFRB, SNAI2, TGFB1	292	66	13.58	1.417e-12	6.306e-10
positive regulation of ERK1 and ERK2 cascade	GO:0070374	11	BMP2, EPO, FGF23, IL1B, NOTCH1, PDGFB, PDGFRB, PYCARD, TGFB1, TNF, HTR2B	201	66	15.50	1.086e-10	3.096e-8
response to macrophage colony-stimulating factor	GO:0036005	4	ALPL, BGLAP, SPP1, TNF	4	66	283.14	1.419e-10	3.936e-8
response to xenobiotic stimulus	GO:0009410	11	BGLAP, CASP3, COL18A1, COL1A1, LCN2, MMP2, TGFB1, TNF, TP53, GABRG3, HTR2B	248	66	12.56	1.017e-9	2.272e-7
positive regulation of apoptotic process	GO:0043065	12	BMP2, CASP3, ITGB1, JAK2, LCN2, MMP2, MMP9, NOTCH1, PYCARD, TGFB1, TNF, TP53	326	66	10.42	1.376e-9	2.985e-7
skeletal system development	GO:0001501	9	AHSG, ALPL, BGLAP, BMP2, COL18A1, COL1A1, MMP9, COL1A2, FGFR1	151	66	16.88	2.889e-9	5.709e-7
positive regulation of cell population proliferation	GO:0008284	14	BMP2, EPO, FGF23, IL1B, JAK2, NOTCH1, PDGFB, PDGFRB, PTPN6, TGFB1, TIMP1, FGFR1	532	66	7.45	3.854e-9	7.408e-7
positive regulation of phosphatidylinositol 3-kinase/protein kinase B signal transduction	GO:0051897	10	IL18, IL1B, ITGB1, JAK2, PDGFB, PDGFRB, PTPN6, TGFB1, TNF, FGFR1	217	66	13.05	4.336e-9	8.198e-7
positive regulation of DNA-templated transcription	GO:0045893	16	BMP2, COL1A1, EPO, FGF23, IL1B, NOTCH1, NR1I2, PDGFB, RIPK3, SPP1, TGFB1, TNF	778	66	5.82	8.514e-9	1.486e-6
response to vitamin D	GO:0033280	5	ALPL, BGLAP, KL, SPP1, TGFB1	21	66	67.41	9.173e-9	1.589e-6
positive regulation of smooth muscle cell proliferation	GO:0048661	6	IL18, MMP2, PDGFB, PDGFRB, TGFB1, TNF	52	66	32.67	2.757e-8	4.095e-6
positive regulation of reactive oxygen species metabolic process	GO:2000379	5	LCN2, PDGFB, PDGFRB, RIPK3, TP53	34	66	41.64	1.211e-7	1.413e-5
smooth muscle adaptation	GO:0014805	3	IL1B, PDGFB, PDGFRB	4	66	212.35	1.679e-7	1.871e-5
positive regulation of gene expression	GO:0010628	12	BMP2, CCL2, IL18, IL1B, LCN2, NOTCH1, NR1I2, PDGFB, TGFB1, TNF, TP53, CDK6	504	66	6.74	1.704e-7	1.893e-5
apoptotic process	GO:0006915	14	CASP3, EPO, GALNT3, IL1B, ITGB2, JAK2, LCN2, MMP9, NOTCH1, PYCARD, RIPK3, TGFB1	747	66	5.31	2.646e-7	2.743e-5