

GeDiPNet Cluster 21 -- 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 18:06:09

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 transcription by RNA polymerase II	GO:0045944	378	ALX4, AP3D1, AR, ATF1, ATXN1, AUTS2, BCL11A, BMP4, BMP7, CASZ1, CBFB, CDC5L	1208	3697	1.58	5.623e-23	1.385e-19
positive regulation of DNA-templated transcription	GO:0045893	239	AR, ATF7IP, BICRA, BMP4, BMP7, CASZ1, CITED4, CLOCK, CTNNB1, EPC1, FOXE1, FOXF2	778	3697	1.55	8.188e-14	4.573e-11
negative regulation of transcription by RNA polymerase II	GO:0000122	277	AR, ATF7IP, ATXN1, BCL11A, BHLHE40, BMP4, CBFB, CBX5, CIC, CTNNB1, CUX1, DNMT3B	1002	3697	1.40	4.248e-10	1.040e-7
negative regulation of DNA-templated transcription	GO:0045892	188	ATF7IP, ATXN1, BHLHE40, BMP4, BMP7, CBX5, CDYL2, CIC, CLOCK, CTNNB1, EPC1, FOXF2	631	3697	1.51	6.575e-10	1.550e-7
stem cell proliferation	GO:0072089	31	CDKN2C, CTNNB1, PBX1, RUNX2, TGFB1, WNT3, WNT7B, ZNRF3, TP53, BRCA2, CD34, FGF10	54	3697	2.90	1.184e-9	2.610e-7
odontogenesis of dentin-containing tooth	GO:0042475	30	BMP4, BMP7, CTNNB1, EDA, EDAR, GLI2, HAND1, NFIC, RUNX2, TGFB1, WNT6, BCL2L11	56	3697	2.71	1.976e-8	3.084e-6
axon guidance	GO:0007411	70	BMP7, CRPPA, ECE1, FYN, GLI2, LHX2, NOG, NRP2, OPHN1, WNT3, BOC, ALCAM	192	3697	1.84	4.987e-8	6.767e-6
positive regulation of miRNA transcription	GO:1902895	29	AR, MYB, SMAD3, TEAD1, TGFB1, MRTFB, SMAD6, TERT, TP53, EGFR, KLF4, MRTFA	56	3697	2.62	9.125e-8	1.115e-5
DNA damage response	GO:0006974	166	BABAM2, BCL2, CBX5, CDC5L, CLOCK, CRADD, DYRK2, ETAA1, HMGB1, MAPT, RAD51B, REV3L	577	3697	1.45	9.254e-8	1.129e-5
embryonic organ development	GO:0048568	24	CTNNB1, PBX1, SYF2, TEAD1, UTP25, WNT7B, TP53, FGFR2, PALB2, PKD2, PTCH1, ZFPM2	42	3697	2.89	1.006e-7	1.213e-5
heart development	GO:0007507	90	BMP4, BMP7, CTNNB1, ECE1, GLI2, HAND1, HDAC9, HOPX, KAT2B, NRP2, SH3PXD2B, TGFB1	273	3697	1.67	1.639e-7	1.833e-5
regulation of gene expression	GO:0010468	122	AFF3, AR, BCL2, BMP4, CLOCK, CTNNB1, DNMT3B, GLI2, IRF1, ITCH, KAT2B, KLF15	402	3697	1.53	2.248e-7	2.392e-5
cell-cell adhesion	GO:0098609	75	BCL2, BMP7, CDON, CTNNB1, JUP, LRP6, BOC, CDH1, COL19A1, BAIAP2, BAIAP2L1, CD34	218	3697	1.74	2.615e-7	2.716e-5
inner ear morphogenesis	GO:0042472	31	FGFR2, CDH23, FGF10, TBX1, TBX3, FOXI1, KCNQ1, MAFB, NTN1, PAX8, FGFR1, ATOH1	65	3697	2.41	3.690e-7	3.621e-5
regulation of transcription by RNA polymerase II	GO:0006357	394	ALX4, AR, ATF1, BBX, BCL11A, BHLHE40, BICRA, CBFB, CDC5L, CIC, CLOCK, CTNNB1	1602	3697	1.24	4.710e-7	4.442e-5