

GeDiPNet Cluster 367 -- 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 17:07:20

GO Term	GO ID	Overlap Genes	Overlap Gene Names	Term Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
heart development	GO:0007507	17	BMP2, TBX5, TGFB2, GATA4, NKX2-5, CITED2, BMP4, ISL1, PCSK5, SALL4, BMP7, IRX4	273	72	16.16	2.522e-16	2.229e-13
outflow tract septum morphogenesis	GO:0003148	9	ROBO1, TGFB2, TBX20, NKX2-5, GATA6, BMP4, ISL1, TBX2, TBX1	28	72	83.42	7.260e-16	5.871e-13
positive regulation of transcription by RNA polymerase II	GO:0045944	25	BMP2, TBX5, GATA4, TBX20, NKX2-5, CITED2, GATA6, BMP4, CHD7, ISL1, SMARCA4, TBX2	1208	72	5.37	1.156e-12	5.201e-10
heart morphogenesis	GO:0003007	9	BMP2, TGFB2, NKX2-5, BMP4, CHD7, ISL1, SOS1, TBX2, TBX1	61	72	38.29	1.649e-12	7.168e-10
endocardial cushion development	GO:0003197	6	TBX5, GATA4, CITED2, BMP4, CRELD1, FOXF1	13	72	119.79	4.442e-12	1.758e-9
atrial septum morphogenesis	GO:0060413	6	TBX5, TGFB2, GATA4, TBX20, NKX2-5, ISL1	13	72	119.79	4.442e-12	1.758e-9
positive regulation of DNA-templated transcription	GO:0045893	20	ACTL6A, BMP2, TBX5, GATA4, TBX20, NKX2-5, CITED2, GATA6, BMP4, PQBP1, SMARCA4, TBX2	778	72	6.67	7.778e-12	2.926e-9
regulation of DNA-templated transcription	GO:0006355	26	ACTL6A, BMP2, FOXP1, TBX5, GATA4, TBX20, NKX2-5, CITED2, GATA6, CHD7, ISL1, MN1	1454	72	4.64	9.786e-12	3.612e-9
aortic valve morphogenesis	GO:0003180	7	ROBO1, GATA4, TBX20, NKX2-5, BMP4, GATA5, NFATC1	37	72	49.10	8.776e-11	2.605e-8
outflow tract morphogenesis	GO:0003151	8	TGFB2, TBX20, NKX2-5, CITED2, BMP4, ISL1, TBX2, TBX1	63	72	32.96	1.064e-10	3.107e-8
pharyngeal system development	GO:0060037	6	NKX2-5, ISL1, TBX2, BMP7, NKX2-6, TBX1	21	72	74.15	1.371e-10	3.911e-8
skeletal system development	GO:0001501	10	BMP2, TGFB2, TLL1, BMP4, CHD7, BMP7, COL1A2, EVC, MMP9, RPS6KA3	151	72	17.19	3.070e-10	7.925e-8
atrioventricular canal development	GO:0036302	5	GATA4, TBX20, GATA6, CHD7, TBX2	11	72	117.97	3.345e-10	8.541e-8
endocardial cushion formation	GO:0003272	5	ROBO1, BMP2, TBX20, TBX2, BMP7	12	72	108.14	5.718e-10	1.375e-7
negative regulation of transcription by RNA polymerase II	GO:0000122	20	BMP2, FOXP1, GATA4, TBX20, NKX2-5, CITED2, GATA6, BMP4, HDAC8, ISL1, SMARCA4, TBX2	1002	72	5.18	6.981e-10	1.635e-7