

GeDiPNet Cluster 396 -- 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 02:44:45

GO Term	GO ID	Overlap Genes	Overlap Gene Names	Term Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
skeletal system development	GO:0001501	8	TP63, COL11A2, HAPLN1, HOXA11, HOXD12, HOXD13, TBX3, TGFB2	151	23	43.05	6.672e-12	2.559e-9
cranial skeletal system development	GO:1904888	4	FGFR2, IRF6, TP63, TGFB2	18	23	180.55	5.274e-9	9.777e-7
embryonic digit morphogenesis	GO:0042733	5	HOXA11, HOXD12, HOXD13, SALL1, TBX3	57	23	71.27	7.120e-9	1.276e-6
embryonic limb morphogenesis	GO:0030326	5	TP63, HOXA11, HOXD13, SALL4, TGFB2	59	23	68.85	8.499e-9	1.486e-6
embryonic forelimb morphogenesis	GO:0035115	4	TP63, CACNA1C, HOXA11, TBX3	33	23	98.48	6.967e-8	8.942e-6
hair follicle morphogenesis	GO:0031069	4	FGFR2, GORAB, TP63, TGFB2	34	23	95.59	7.890e-8	9.862e-6
regulation of extracellular matrix organization	GO:1903053	3	PRDM5, ZNF469, TGFB2	12	23	203.12	3.557e-7	3.508e-5
prostate gland development	GO:0030850	3	TP63, HOXA11, HOXD13	16	23	152.34	9.026e-7	7.624e-5
regulation of transcription by RNA polymerase II	GO:0006357	11	CHUK, ERCC2, IRF6, SOD2, HOXA11, HOXD11, HOXD12, HOXD13, SALL1, SALL4, TBX3	1602	23	5.58	9.106e-7	7.686e-5
squamous basal epithelial stem cell differentiation involved in prostate gland acinus development	GO:0060529	2	FGFR2, TP63	2	23	812.48	1.449e-6	1.114e-4
positive regulation of transcription by RNA polymerase II	GO:0045944	9	PRDM5, CHUK, FGFR2, IRF6, TP63, HOXD13, SALL1, SALL4, TBX3	1208	23	6.05	6.832e-6	3.848e-4
heart development	GO:0007507	5	SOD2, CACNA1C, SALL1, SALL4, TGFB2	273	23	14.88	1.740e-5	8.038e-4
positive regulation of cell cycle	GO:0045787	3	FGFR2, TBX3, TGFB2	44	23	55.40	2.087e-5	9.286e-4
branching involved in ureteric bud morphogenesis	GO:0001658	3	HOXA11, HOXD11, SALL1	45	23	54.17	2.234e-5	9.788e-4
prostate epithelial cord arborization involved in prostate glandular acinus morphogenesis	GO:0060527	2	FGFR2, HOXD13	7	23	232.14	3.032e-5	1.230e-3