

GeDiPNet Cluster 101 -- 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 19:02:32

GO Term	GO ID	Overlap Genes	Overlap Gene Names	Term Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
visual perception	GO:0007601	18	COL11A1, COL1A1, COL2A1, SLITRK6, ARR3, CACNA1F, GJD2, IRX5, RDH5, SIX6, TYR, COL18A1	215	153	10.23	1.812e-13	9.482e-11
skeletal system development	GO:0001501	15	COL9A2, COMP, COL1A1, MATN3, COL2A1, BMP4, COL11A2, VCAN, BMP2, CHD7, FBN1, IGF1	151	153	12.13	1.724e-12	7.431e-10
camera-type eye development	GO:0043010	8	BMP4, SLITRK6, CHD7, FBN1, PRSS56, EFEMP1, FBN2, SLC25A25	74	153	13.20	1.603e-7	1.792e-5
sensory perception of sound	GO:0007605	10	COL11A1, COL1A1, COL2A1, COL11A2, LRP2, SLITRK6, CHD7, PGAP1, CDH23, COL4A3	162	153	7.54	8.991e-7	7.573e-5
collagen fibril organization	GO:0030199	7	COL11A1, LOXL3, COMP, COL1A1, COL2A1, COL11A2, PLOD3	65	153	13.15	1.005e-6	8.305e-5
animal organ morphogenesis	GO:0009887	9	COL9A1, COMP, BMP2, EP300, PTCH1, SIX6, VDR, COL18A1, LAMA5	130	153	8.46	1.237e-6	9.882e-5
cartilage development	GO:0051216	7	COL11A1, COMP, MATN3, COL2A1, BMP4, COL11A2, BMP2	89	153	9.61	8.445e-6	4.627e-4
heart morphogenesis	GO:0003007	6	COL11A1, COL2A1, BMP4, BMP2, CHD7, PTCH1	61	153	12.01	1.046e-5	5.436e-4
inner ear morphogenesis	GO:0042472	6	COL11A1, COL2A1, SLITRK6, CHD7, HMX2, CDH23	65	153	11.27	1.514e-5	7.256e-4
bone trabecula formation	GO:0060346	3	COL1A1, MMP2, FBN2	8	153	45.80	2.924e-5	1.206e-3
lung development	GO:0030324	7	LOXL3, BMP4, EP300, FBN1, IGF1, KDR, LAMA5	108	153	7.92	3.002e-5	1.228e-3
skeletal system morphogenesis	GO:0048705	5	COL11A1, COL1A1, COL2A1, MMP2, LAMA5	45	153	13.57	3.233e-5	1.297e-3
branching involved in ureteric bud morphogenesis	GO:0001658	5	BMP4, GZF1, BMP2, PTCH1, LAMA5	45	153	13.57	3.233e-5	1.297e-3
central nervous system development	GO:0007417	8	COL2A1, VCAN, CHD7, VPS13B, BCAN, NRCAM, PTPRZ1, SNTG2	158	153	6.18	4.798e-5	1.750e-3
prostate gland epithelium morphogenesis	GO:0060740	3	IGF1, MMP2, TNC	10	153	36.64	6.192e-5	2.119e-3