

GeDiPNet Cluster 55 -- 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: 2026-10-08 03:23:04. · Rows: 15 · Generated: 2026-10-07 22:41:48

GO Term	GO ID	Overlap Genes	Overlap Gene Names	Term Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
elastic fiber assembly	GO:0048251	5	ATP7A, EFEMP2, EMILIN1, COL3A1, LOX	11	82	103.59	6.506e-10	1.480e-7
blood vessel development	GO:0001568	7	COL1A1, TGFB2, ATP7A, COL3A1, LOX, TBX1, TCF7L2	70	82	22.79	2.315e-8	3.510e-6
positive regulation of extracellular matrix assembly	GO:1901203	4	AGT, SMAD3, TGFB1, EMILIN1	9	82	101.28	4.267e-8	5.925e-6
cellular response to UV-A	GO:0071492	4	MMP2, MMP9, TIMP1, MMP1	11	82	82.87	1.110e-7	1.335e-5
positive regulation of epithelial to mesenchymal transition	GO:0010718	6	AGT, COL1A1, SMAD3, TGFB1, TGFB2, TCF7L2	59	82	23.18	2.219e-7	2.406e-5
collagen fibril organization	GO:0030199	6	COL1A1, TGFB1, ATP7A, COL3A1, LOX, DPT	65	82	21.04	3.983e-7	3.894e-5
trophoblast cell migration	GO:0061450	3	SMAD3, TGFB1, MMP2	7	82	97.67	2.814e-6	1.935e-4
extracellular matrix organization	GO:0030198	7	ATP7A, MMP2, MMP9, EMILIN1, COL3A1, ELN, MMP1	145	82	11.00	3.425e-6	2.267e-4
embryonic cranial skeleton morphogenesis	GO:0048701	4	SMAD3, TGFB1, TGFB2, TBX1	31	82	29.41	9.900e-6	5.262e-4
face morphogenesis	GO:0060325	4	COL1A1, MMP2, SKI, TBX1	33	82	27.62	1.279e-5	6.406e-4
aorta development	GO:0035904	4	EFEMP2, SMAD6, COL3A1, LOX	33	82	27.62	1.279e-5	6.406e-4
response to angiotensin	GO:1990776	3	AGT, SMAD3, COL3A1	12	82	56.97	1.741e-5	8.161e-4
aortic valve morphogenesis	GO:0003180	4	TGFB2, EMILIN1, SMAD6, ELN	37	82	24.64	2.037e-5	9.253e-4
heart development	GO:0007507	8	TGFB1, TGFB2, FBN1, MMP2, CACNA1C, COL3A1, LOX, TBX1	273	82	6.68	2.622e-5	1.120e-3
cartilage development	GO:0051216	5	TGFB2, ATP7A, COL3A1, MGP, TIMP1	89	82	12.80	4.472e-5	1.689e-3