

GeDiPNet Cluster 96 -- 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 14:57:43

GO Term	GO ID	Overlap Genes	Overlap Gene Names	Term Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
smoothened signaling pathway	GO:0007224	27	B9D1, CC2D2A, CD3E, CDON, CTNNA1, DISP1, DYRK2, FOXF1, GLI1, GLI2, GLI3, HHAT	94	76	70.63	3.400e-44	4.995e-40
determination of left/right symmetry	GO:0007368	15	FGF8, FOXH1, CC2D2A, DISP1, FOXF1, IFT172, IFT52, NME7, SMO, SUFU, DLL1, NODAL	83	76	44.44	3.117e-21	6.006e-18
heart looping	GO:0001947	13	FGF8, FOXH1, C2CD3, IFT172, IFT52, IHH, SMO, SUFU, TGFB2, DLL1, NODAL, SHH	64	76	49.94	3.154e-19	4.431e-16
dorsal/ventral pattern formation	GO:0009953	11	FGF8, DISP1, GLI1, GLI3, HHIP, IFT172, IFT52, PTCH1, SMO, SHH, TGIF1	47	76	57.55	3.668e-17	3.695e-14
negative regulation of smoothened signaling pathway	GO:0045879	10	CD3E, GLI3, GLIS2, HHIP, IFT172, PTCH1, PTCH2, RB1, SUFU, TULP3	35	76	70.25	1.133e-16	1.068e-13
lung development	GO:0030324	11	FGF8, PDGFRA, FOXF1, GLI1, GLI2, GLI3, TGFB2, FGFR1, LAMA5, NODAL, SHH	108	76	25.04	5.977e-13	2.799e-10
embryonic digit morphogenesis	GO:0042733	9	B9D1, C2CD3, GLI3, IFT52, IHH, TMEM231, TULP3, SHH, LMBR1	57	76	38.82	1.436e-12	6.313e-10
positive regulation of smoothened signaling pathway	GO:0045880	8	CTNNA1, GLI1, IFT172, IHH, NDST1, SMO, STK36, SHH	39	76	50.44	2.849e-12	1.183e-9
cilium assembly	GO:0060271	13	B9D1, C2CD3, CC2D2A, IFT172, IFT52, IFT88, KIF3A, NME7, RAB23, STK36, TMEM17, TMEM231	237	76	13.49	1.190e-11	4.312e-9
regulation of smoothened signaling pathway	GO:0008589	7	C2CD3, GLI1, GLI3, IFT172, PTCH1, TULP3, GAS1	29	76	59.35	2.015e-11	6.938e-9
in utero embryonic development	GO:0001701	13	PDGFRA, B9D1, C2CD3, FOXF1, GLI3, IHH, PTCH1, SMO, TGFB2, TMEM231, FGFR1, NODAL	252	76	12.68	2.572e-11	8.661e-9
cell population proliferation	GO:0008283	13	FGF8, KIT, GLI3, HIPK1, HIPK2, IHH, NDST1, RB1, SMO, FGFR1, NODAL, SHH	263	76	12.15	4.387e-11	1.392e-8
spinal cord dorsal/ventral patterning	GO:0021513	5	GLI2, GLI3, SMO, SUFU, SHH	8	76	153.68	5.399e-11	1.691e-8
brain development	GO:0007420	12	C2CD3, GLI3, IFT172, NME7, PTCH1, STK36, TGFB2, TULP3, FGFR1, NODAL, SIX3, ZIC2	244	76	12.09	2.778e-10	7.288e-8
camera-type eye development	GO:0043010	8	B9D1, CC2D2A, GLI3, IHH, TMEM231, SHH, SIX3, TWSG1	74	76	26.58	6.231e-10	1.484e-7