

GeDiPNet Cluster 7 -- 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: 2026-10-08 07:00:57

GO Term	GO ID	Overlap Genes	Overlap Gene Names	Term Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
cilium assembly	GO:0060271	77	CC2D2A, CEP290, TMEM138, TMEM216, TMEM231, TMEM237, ARL6, BBIP1, BBS1, BBS2, BBS4, BBS5	237	235	25.84	4.674e-90	5.439e-85
cell projection organization	GO:0030030	64	CC2D2A, CEP290, TMEM138, TMEM216, TMEM231, TMEM237, ARL6, BBIP1, BBS1, BBS2, BBS4, BBS5	214	235	23.78	1.517e-71	1.324e-66
non-motile cilium assembly	GO:1905515	29	CC2D2A, CEP290, TMEM216, BBS1, BBS10, BBS2, BBS4, BBS7, IFT172, IFT57, IFT74, MKKS	57	235	40.46	1.444e-40	1.528e-36
smoothened signaling pathway	GO:0007224	31	CC2D2A, TMEM231, BBS7, GLI1, GLI2, IFT172, IFT27, IFT57, WDPCP, WDR19, TTC21B, B9D1	94	235	26.22	5.363e-36	4.161e-32
regulation of smoothened signaling pathway	GO:0008589	16	ARL6, GLI1, IFT172, MKS1, RPGRIP1L, TTC21B, IFT81, TULP3, ZIC1, C2CD3, TCTN1, IFT140	29	235	43.87	1.372e-23	3.657e-20
determination of left/right symmetry	GO:0007368	20	CC2D2A, ARL6, BBS7, IFT172, IFT74, MKKS, MKS1, NPHP3, RPGRIP1L, DYNC2H1, KIF3B, SUFU	83	235	19.16	1.756e-20	2.990e-17
embryonic digit morphogenesis	GO:0042733	17	TMEM231, MKS1, WDPCP, B9D1, TBC1D32, TMEM107, TRAF3IP1, TULP3, C2CD3, IFT140, INTU, ALX4	57	235	23.72	2.455e-19	3.428e-16
positive regulation of smoothened signaling pathway	GO:0045880	14	GLI1, IFT172, KIF7, CIBAR1, DCDC2, DLG5, DYNC2H1, TXNDC15, ARMC9, EVC, INTU, RAB34	39	235	28.55	1.914e-17	1.995e-14
kidney development	GO:0001822	21	CC2D2A, CEP290, COMT, GLI2, IFT27, NPHP3, RPGRIP1L, WDPCP, DYNC2H1, TBC1D32, TRAF3IP1, PKD1	146	235	11.44	1.526e-16	1.352e-13
intraciliary transport	GO:0042073	13	BBS12, IFT172, IFT27, IFT57, IFT74, WDPCP, IFT81, KIF3B, TRAF3IP1, ARL3, IFT140, INTU	36	235	28.72	2.522e-16	2.148e-13
protein localization to cilium	GO:0061512	13	ZNF423, ARL6, BBS1, BBS4, BBS9, TTC21B, DYNC2H1, TBC1D32, TULP3, ARL3, FAM149B1, IFT140	44	235	23.49	5.185e-15	3.448e-12
neural tube patterning	GO:0021532	7	RPGRIP1L, TBC1D32, TMEM107, TRAF3IP1, ARL13B, IFT140, PTCH1	8	235	69.58	3.601e-13	1.761e-10
intraciliary anterograde transport	GO:0035720	9	IFT172, IFT27, IFT57, IFT74, IFT81, TRAF3IP1, IFT80, CLUAP1, IFT88	19	235	37.67	5.588e-13	2.622e-10
fat cell differentiation	GO:0045444	15	ARL6, BBS1, BBS12, BBS2, BBS4, BBS7, BBS9, MKKS, OSBPL8, TRIM32, TTC8, CBY1	93	235	12.83	6.510e-13	3.018e-10
heart looping	GO:0001947	13	BBS4, BBS5, BBS7, IFT172, IFT57, MKKS, NPHP3, SUFU, AHI1, ARL13B, C2CD3, CLUAP1	64	235	16.15	1.051e-12	4.728e-10