

GeDiPNet Cluster 17 -- 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 10:06:03

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	29	DYNC2H1, DYNC2I1, DYNC2I2, DYNC2LI1, DYNLT2B, IFT140, IFT172, IFT52, INTU, KIAA0586, KIAA0753, NEK1	237	71	32.21	7.318e-37	6.451e-33
intraciliary retrograde transport	GO:0035721	12	DYNC2H1, DYNC2I1, DYNC2I2, DYNC2LI1, DYNLT2B, IFT140, TTC21B, WDR19, WDR35, CILK1, IFT122, IFT43	14	71	225.60	3.070e-28	1.444e-24
intraciliary transport	GO:0042073	15	DYNC2I1, DYNC2I2, IFT140, IFT172, IFT52, INTU, WDR35, CILK1, IFT122, FUZ, IFT27, IFT74	36	71	109.67	5.335e-28	2.475e-24
cell projection organization	GO:0030030	23	DYNC2H1, DYNC2I1, DYNC2LI1, IFT140, IFT52, INTU, KIAA0586, NEK1, WDR19, WDR35, CILK1, IFT122	214	71	28.29	1.110e-27	5.016e-24
intraciliary anterograde transport	GO:0035720	10	IFT172, IFT52, IFT80, CILK1, IFT122, IFT27, IFT74, IFT81, IFT88, TRAF3IP1	19	71	138.52	2.909e-20	4.861e-17
non-motile cilium assembly	GO:1905515	12	DYNC2H1, IFT140, IFT172, IFT52, INTU, IFT80, IFT122, C2CD3, FUZ, IFT74, IFT88, BBS10	57	71	55.41	2.105e-18	2.577e-15
smoothened signaling pathway	GO:0007224	11	IFT172, IFT52, INTU, KIAA0586, TTC21B, WDR19, IFT80, B9D1, EVC2, IFT27, EVC	94	71	30.80	5.708e-14	3.316e-11
regulation of smoothened signaling pathway	GO:0008589	7	IFT140, IFT172, INTU, TTC21B, C2CD3, FUZ, IFT81	29	71	63.53	1.232e-11	4.456e-9
embryonic digit morphogenesis	GO:0042733	7	IFT140, IFT52, INTU, B9D1, C2CD3, FLVCR1, TRAF3IP1	57	71	32.32	1.919e-9	3.968e-7
negative regulation of keratinocyte proliferation	GO:0010839	5	IFT172, IFT52, INTU, IFT80, IFT74	24	71	54.83	2.757e-8	4.028e-6
regulation of cilium assembly	GO:1902017	6	DYNC2LI1, DYNLT2B, IFT140, INTU, FUZ, IFT88	52	71	30.37	4.301e-8	5.873e-6
positive regulation of smoothened signaling pathway	GO:0045880	5	DYNC2H1, IFT172, INTU, RAB34, EVC	39	71	33.74	3.573e-7	3.516e-5
protein localization to cilium	GO:0061512	5	DYNC2H1, IFT140, TTC21B, WDR35, IFT122	44	71	29.91	6.641e-7	5.919e-5
determination of left/right symmetry	GO:0007368	6	DYNC2H1, DYNC2LI1, IFT140, IFT172, IFT52, IFT74	83	71	19.03	7.269e-7	6.368e-5
protein processing	GO:0016485	6	BMP1, PSEN1, PSEN2, DYNC2H1, IFT172, C2CD3	95	71	16.62	1.615e-6	1.227e-4