

GeDiPNet Cluster 435 -- 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: 2026-10-20 03:23:13. · Rows: 15 · Generated: 2026-10-20 00:01:20

GO Term	GO ID	Overlap Genes	Overlap Gene Names	Term Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
kidney development	GO:0001822	13	BICC1, PKD1, PKD2, DYNC2H1, IFT88, NPHP3, PKHD1, ANKS6, AQP11, CC2D2A, CEP290, CTNNB1	146	63	26.41	1.759e-15	1.389e-12
determination of left/right symmetry	GO:0007368	11	ALG5, BICC1, IFT140, NEK8, PKD2, DYNC2H1, NPHP3, ANKS6, CC2D2A, MKKS, MKS1	83	63	39.31	3.411e-15	2.526e-12
non-motile cilium assembly	GO:1905515	8	IFT140, DYNC2H1, IFT88, NPHP3, CC2D2A, CEP290, MKKS, MKS1	57	63	41.63	1.528e-11	5.599e-9
cilium assembly	GO:0060271	12	IFT140, DYNC2H1, DZIP1L, IFT88, NPHP3, PKHD1, CC2D2A, CEP290, MKKS, MKS1, ONECUT2, ONECUT1	237	63	15.02	1.976e-11	6.996e-9
liver development	GO:0001889	8	PKD1, PKD2, PIK3CA, PRKCSH, SEC63, ONECUT2, HNF1B, ONECUT1	87	63	27.28	4.996e-10	1.285e-7
heart development	GO:0007507	11	BICC1, IFT140, NEK8, PKD1, PKD2, DYNC2H1, TSC2, ANKS6, CC2D2A, MKKS, CTNNB1	273	63	11.95	1.663e-9	3.620e-7
Wnt signaling pathway	GO:0016055	9	PKD1, PKD2, NPHP3, LRP5, MYC, DKK3, LRP6, CTNNB1, HHEX	232	63	11.51	7.932e-8	1.048e-5
embryonic brain development	GO:1990403	4	IFT140, CC2D2A, MKS1, CTNNB1	20	63	59.32	5.457e-7	5.247e-5
cell projection organization	GO:0030030	8	IFT140, DYNC2H1, IFT88, CC2D2A, CEP290, DEUP1, MKS1, MTOR	214	63	11.09	5.853e-7	5.560e-5
mesonephric duct development	GO:0072177	3	PKD1, PKD2, HNF1B	6	63	148.31	7.251e-7	6.596e-5
mesonephric tubule development	GO:0072164	3	PKD1, PKD2, HNF1B	7	63	127.12	1.266e-6	1.041e-4
post-translational protein targeting to membrane, translocation	GO:0031204	3	SEC61B, SEC63, SEC61A1	8	63	111.23	2.021e-6	1.528e-4
epidermal growth factor receptor signaling pathway	GO:0007173	5	EGFR, SRC, PIK3CA, PLCE1, CTNNB1	64	63	23.17	2.424e-6	1.774e-4
branching morphogenesis of an epithelial tube	GO:0048754	4	PKD1, PKHD1, MKS1, HNF1B	29	63	40.91	2.615e-6	1.879e-4
pancreas development	GO:0031016	4	ONECUT2, CTNNB1, HNF1B, ONECUT1	30	63	39.55	3.009e-6	2.103e-4