

GeDiPNet Cluster 312 -- 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: 2026-10-08 23:31:23

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	6	DCDC2, TMEM67, CC2D2A, INPP5E, OFD1, RPGRIP1L	237	8	59.14	1.071e-10	3.121e-8
cell projection organization	GO:0030030	4	DCDC2, TMEM67, CC2D2A, OFD1	214	8	43.66	1.129e-6	9.190e-5
axoneme assembly	GO:0035082	2	CC2D2A, OFD1	33	8	141.57	8.412e-5	2.668e-3
non-motile cilium assembly	GO:1905515	2	CC2D2A, RPGRIP1L	57	8	81.96	2.530e-4	5.959e-3
camera-type eye development	GO:0043010	2	CC2D2A, RPGRIP1L	74	8	63.13	4.265e-4	8.639e-3
determination of left/right symmetry	GO:0007368	2	CC2D2A, RPGRIP1L	83	8	56.29	5.364e-4	1.008e-2
lipid export from cell	GO:0140353	1	SAR1B	2	8	1167.94	8.560e-4	1.377e-2
negative regulation of fibroblast growth factor receptor signaling pathway involved in neural plate anterior/posterior pattern formation	GO:2000314	1	OFD1	2	8	1167.94	8.560e-4	1.377e-2
negative regulation of protein localization to cilium	GO:1903565	1	INPP5E	3	8	778.63	1.284e-3	1.764e-2
kidney development	GO:0001822	2	CC2D2A, RPGRIP1L	146	8	32.00	1.646e-3	2.051e-2
response to inositol	GO:1902140	1	INPP5E	4	8	583.97	1.711e-3	2.101e-2
negative regulation of centrosome duplication	GO:0010826	1	TMEM67	5	8	467.18	2.139e-3	2.370e-2
regulation of lipid transport	GO:0032368	1	SAR1B	5	8	467.18	2.139e-3	2.370e-2
regulation of COPII vesicle coating	GO:0003400	1	SAR1B	5	8	467.18	2.139e-3	2.370e-2
protein localization to ciliary transition zone	GO:1904491	1	CC2D2A	6	8	389.31	2.566e-3	2.639e-2