

GeDiPNet Cluster 438 -- 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 03:23:14. · Rows: 15 · Generated: 2026-10-20 00:00:46

GO Term	GO ID	Overlap Genes	Overlap Gene Names	Term Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
cell projection organization	GO:0030030	4	CC2D2A, CEP290, CPLANE1, MKS1	214	5	69.86	8.288e-8	1.086e-5
cilium assembly	GO:0060271	4	CC2D2A, CEP290, CPLANE1, MKS1	237	5	63.08	1.249e-7	1.529e-5
non-motile cilium assembly	GO:1905515	3	CC2D2A, CEP290, MKS1	57	5	196.71	2.679e-7	2.885e-5
embryonic brain development	GO:1990403	2	CC2D2A, MKS1	20	5	373.74	1.086e-5	5.797e-4
motile cilium assembly	GO:0044458	2	CC2D2A, MKS1	28	5	266.96	2.159e-5	9.799e-4
camera-type eye development	GO:0043010	2	CC2D2A, CEP290	74	5	101.01	1.535e-4	4.213e-3
determination of left/right symmetry	GO:0007368	2	CC2D2A, MKS1	83	5	90.06	1.932e-4	4.967e-3
neural tube closure	GO:0001843	2	CC2D2A, MKS1	85	5	87.94	2.027e-4	5.144e-3
regulation of superoxide dismutase activity	GO:1901668	1	SZT2	1	5	3737.40	2.676e-4	6.245e-3
smoothened signaling pathway involved in regulation of secondary heart field cardioblast proliferation	GO:0003271	1	MKS1	1	5	3737.40	2.676e-4	6.245e-3
ciliary basal body-plasma membrane docking	GO:0097711	1	CEP290	2	5	1868.70	5.351e-4	9.880e-3
kidney development	GO:0001822	2	CC2D2A, CEP290	146	5	51.20	5.970e-4	1.071e-2
ciliary transition zone assembly	GO:1905349	1	CEP290	3	5	1245.80	8.025e-4	1.283e-2
common bile duct development	GO:0061009	1	MKS1	3	5	1245.80	8.025e-4	1.283e-2
regulation of Wnt signaling pathway, planar cell polarity pathway	GO:2000095	1	MKS1	5	5	747.48	1.337e-3	1.709e-2