

GeDiPNet Cluster 550 -- 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: 2026-10-19 23:18:15

GO Term	GO ID	Overlap Genes	Overlap Gene Names	Term Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
branching morphogenesis of an epithelial tube	GO:0048754	2	PKHD1, PKD1	29	6	214.79	3.475e-5	1.403e-3
regulation of cell adhesion	GO:0030155	2	PKHD1, PKD1	61	6	102.11	1.559e-4	4.261e-3
metanephric distal tubule morphogenesis	GO:0072287	1	PKD1	1	6	3114.50	3.211e-4	7.044e-3
regulation of cholangiocyte proliferation	GO:1904054	1	PKHD1	1	6	3114.50	3.211e-4	7.044e-3
establishment of protein localization to endoplasmic reticulum	GO:0072599	1	RYR2	1	6	3114.50	3.211e-4	7.044e-3
negative regulation of apoptotic process	GO:0043066	3	PKHD1, CBS, BRAF	524	6	17.83	4.116e-4	8.351e-3
intracellular calcium ion homeostasis	GO:0006874	2	PKHD1, RYR2	113	6	55.12	5.351e-4	9.880e-3
Purkinje myocyte to ventricular cardiac muscle cell signaling	GO:0086029	1	RYR2	2	6	1557.25	6.421e-4	1.113e-2
nitrogen cycle metabolic process	GO:0071941	1	PKD1	2	6	1557.25	6.421e-4	1.113e-2
cysteine biosynthetic process from serine	GO:0006535	1	CBS	2	6	1557.25	6.421e-4	1.113e-2
sulfur compound biosynthetic process	GO:0044272	1	CBS	2	6	1557.25	6.421e-4	1.113e-2
animal organ morphogenesis	GO:0009887	2	BRAF, PKD1	130	6	47.92	7.073e-4	1.191e-2
kidney development	GO:0001822	2	PKHD1, PKD1	146	6	42.66	8.909e-4	1.370e-2
calcium ion transmembrane transport	GO:0070588	2	RYR2, PKD1	149	6	41.81	9.276e-4	1.406e-2
positive T cell selection	GO:0043368	1	BRAF	3	6	1038.17	9.630e-4	1.423e-2