

GeDiPNet Cluster 403 -- 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: 2026-10-07 03:23:06. · Rows: 15 · Generated: 2026-10-07 02:36:26

GO Term	GO ID	Overlap Genes	Overlap Gene Names	Term Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
regulation of G1/S transition of mitotic cell cycle	GO:2000045	2	PKD1, CCND1	57	5	131.14	9.088e-5	2.818e-3
liver development	GO:0001889	2	PKD1, CCND1	87	5	85.92	2.123e-4	5.265e-3
metanephric distal tubule morphogenesis	GO:0072287	1	PKD1	1	5	3737.40	2.676e-4	6.199e-3
nitrogen cycle metabolic process	GO:0071941	1	PKD1	2	5	1868.70	5.351e-4	9.981e-3
lymph vessel morphogenesis	GO:0036303	1	PKD1	3	5	1245.80	8.025e-4	1.302e-2
metanephric proximal tubule development	GO:0072237	1	PKD1	3	5	1245.80	8.025e-4	1.302e-2
response to UV-A	GO:0070141	1	CCND1	4	5	934.35	1.070e-3	1.569e-2
re-entry into mitotic cell cycle	GO:0000320	1	CCND1	4	5	934.35	1.070e-3	1.569e-2
calcium-independent cell-matrix adhesion	GO:0007161	1	PKD1	4	5	934.35	1.070e-3	1.569e-2
metanephric ascending thin limb development	GO:0072218	1	PKD1	4	5	934.35	1.070e-3	1.569e-2
succinate metabolic process	GO:0006105	1	SDHB	5	5	747.48	1.337e-3	1.795e-2
mitochondrial electron transport, succinate to ubiquinone	GO:0006121	1	SDHB	5	5	747.48	1.337e-3	1.795e-2
Wnt signaling pathway	GO:0016055	2	PKD1, CCND1	232	5	32.22	1.497e-3	1.912e-2
response to vitamin E	GO:0033197	1	CCND1	6	5	622.90	1.605e-3	1.983e-2
mesonephric duct development	GO:0072177	1	PKD1	6	5	622.90	1.605e-3	1.983e-2