

GeDiPNet Cluster 501 -- 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 00:01:22

GO Term	GO ID	Overlap Genes	Overlap Gene Names	Term Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
negative regulation of sodium ion transport	GO:0010766	2	WNK4, WNK1	5	3	2491.60	1.718e-7	1.992e-5
negative regulation of pancreatic juice secretion	GO:0090188	2	WNK4, WNK1	5	3	2491.60	1.718e-7	1.992e-5
intracellular chloride ion homeostasis	GO:0030644	2	WNK4, WNK1	10	3	1245.80	7.730e-7	6.937e-5
homeostatic process	GO:0042592	2	WNK4, WNK1	19	3	655.68	2.936e-6	2.062e-4
negative regulation of protein localization to plasma membrane	GO:1903077	2	WNK4, WNK1	25	3	498.32	5.151e-6	3.245e-4
regulation of blood pressure	GO:0008217	2	WNK4, WNK1	83	3	150.10	5.830e-5	2.071e-3
sodium ion transmembrane transport	GO:0035725	2	WNK4, WNK1	134	3	92.97	1.524e-4	4.192e-3
positive regulation of termination of RNA polymerase II transcription	GO:1904595	1	WNK1	1	3	6229.00	1.605e-4	4.340e-3
aldosterone secretion	GO:0035932	1	WNK4	1	3	6229.00	1.605e-4	4.340e-3
potassium ion transmembrane transport	GO:0071805	2	WNK4, WNK1	150	3	83.05	1.910e-4	4.926e-3
distal tubule morphogenesis	GO:0072156	1	WNK4	2	3	3114.50	3.211e-4	7.044e-3
negative regulation of cell-cell adhesion mediated by integrin	GO:0033633	1	WNK1	2	3	3114.50	3.211e-4	7.044e-3
chemokine (C-C motif) ligand 21 signaling pathway	GO:0038116	1	WNK1	3	3	2076.33	4.816e-4	9.241e-3
regulation of potassium ion export across plasma membrane	GO:1903764	1	WNK4	3	3	2076.33	4.816e-4	9.241e-3
protein phosphorylation	GO:0006468	2	WNK4, WNK1	258	3	48.29	5.645e-4	1.029e-2