

GeDiPNet Cluster 561 -- Enriched Pathways

Pathway enrichment: KEGG + Reactome, upper-tail hypergeometric test, Benjamini-Hochberg FDR-corrected. Fold enrichment = (overlap / cluster gene count) / (pathway gene count / universe size). Top 15 pathways per cluster by q-value. See scripts/build_cluster_enrichment.php on gedipnet.bicnirrh.res.in. Data as of: 2026-10-20 03:30:09. · Rows: 15 · Generated: 2026-10-20 00:02:53

Pathway	Source	Overlap Genes	Overlap Gene Names	Pathway Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
Defective SLC26A4 causes Pendred syndrome (PDS)	Reactome	1	SLC26A4	1	7	1715.71	5.828e-4	7.518e-3
Potassium transport channels	Reactome	1	KCNJ10	3	7	571.90	1.748e-3	1.725e-2
Multifunctional anion exchangers	Reactome	1	SLC26A4	9	7	190.63	5.235e-3	3.760e-2
ERBB2 Regulates Cell Motility	Reactome	1	DIAPH1	15	7	114.38	8.712e-3	5.219e-2
Insertion of tail-anchored proteins into the endoplasmic reticulum membrane	Reactome	1	OTOF	16	7	107.23	9.291e-3	5.428e-2
The canonical retinoid cycle in rods (twilight vision)	Reactome	1	MYO7A	20	7	85.79	1.160e-2	6.220e-2
Activation of G protein gated Potassium channels	Reactome	1	KCNJ10	29	7	59.16	1.678e-2	7.755e-2
Inhibition of voltage gated Ca2+ channels via Gbeta/gamma subunits	Reactome	1	KCNJ10	29	7	59.16	1.678e-2	7.755e-2
Virion - Hepatitis viruses	KEGG	1	CLDN9	48	7	35.74	2.765e-2	1.031e-1
Thyroid hormone synthesis	KEGG	1	SLC26A4	75	7	22.88	4.291e-2	1.327e-1
Gastric acid secretion	KEGG	1	KCNJ10	76	7	22.58	4.347e-2	1.336e-1
AGE-RAGE signaling pathway in diabetic complications	KEGG	1	DIAPH1	101	7	16.99	5.742e-2	1.566e-1
Leukocyte transendothelial migration	KEGG	1	CLDN9	116	7	14.79	6.570e-2	1.693e-1
RHO GTPases Activate Formins	Reactome	1	DIAPH1	140	7	12.26	7.882e-2	1.880e-1
Hepatitis C	KEGG	1	CLDN9	159	7	10.79	8.909e-2	2.019e-1