

GeDiPNet Cluster 422 -- 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: 2026-10-07 03:30:09. · Rows: 15 · Generated: 2026-10-07 21:34:14

Pathway	Source	Overlap Genes	Overlap Gene Names	Pathway Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
Oligomerization of connexins into connexons	Reactome	1	GJB1	1	3	4003.33	2.498e-4	4.644e-3
Mitochondrial ABC transporters	Reactome	1	ABCB7	4	3	1000.83	9.989e-4	1.354e-2
Reduction of cytosolic Ca++ levels	Reactome	1	ATP2B3	14	3	285.95	3.493e-3	3.425e-2
Gap junction assembly	Reactome	1	GJB1	18	3	222.41	4.490e-3	4.079e-2
ABC transporters	KEGG	1	ABCB7	45	3	88.96	1.120e-2	7.338e-2
Endocrine and other factor-regulated calcium reabsorption	KEGG	1	ATP2B3	53	3	75.53	1.318e-2	8.055e-2
Ion homeostasis	Reactome	1	ATP2B3	54	3	74.14	1.343e-2	8.139e-2
Ion transport by P-type ATPases	Reactome	1	ATP2B3	56	3	71.49	1.392e-2	8.318e-2
Mineral absorption	KEGG	1	ATP2B3	61	3	65.63	1.516e-2	8.753e-2
Salivary secretion	KEGG	1	ATP2B3	93	3	43.05	2.305e-2	1.115e-1
Aldosterone synthesis and secretion	KEGG	1	ATP2B3	98	3	40.85	2.428e-2	1.149e-1
Pancreatic secretion	KEGG	1	ATP2B3	102	3	39.25	2.527e-2	1.171e-1
Adrenergic signaling in cardiomyocytes	KEGG	1	ATP2B3	154	3	26.00	3.798e-2	1.473e-1
cGMP-PKG signaling pathway	KEGG	1	ATP2B3	166	3	24.12	4.090e-2	1.535e-1
cAMP signaling pathway	KEGG	1	ATP2B3	226	3	17.71	5.540e-2	1.807e-1