

GeDiPNet Cluster 105 -- 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 14:46:25

Pathway	Source	Overlap Genes	Overlap Gene Names	Pathway Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
Synaptic vesicle cycle	KEGG	3	ATP6V1B2, ATP6V1C1, CPLX1	79	11	41.46	4.352e-5	1.141e-3
Ion channel transport	Reactome	2	ATP6V1B2, ATP6V1C1	24	11	90.98	2.082e-4	4.028e-3
Oxidative phosphorylation	KEGG	3	ATP6, ATP6V1B2, ATP6V1C1	137	11	23.91	2.241e-4	4.283e-3
Insulin receptor recycling	Reactome	2	ATP6V1B2, ATP6V1C1	26	11	83.99	2.449e-4	4.576e-3
Collecting duct acid secretion	KEGG	2	ATP6V1B2, ATP6V1C1	28	11	77.99	2.846e-4	5.153e-3
Transferrin endocytosis and recycling	Reactome	2	ATP6V1B2, ATP6V1C1	31	11	70.44	3.495e-4	6.050e-3
ROS and RNS production in phagocytes	Reactome	2	ATP6V1B2, ATP6V1C1	34	11	64.22	4.211e-4	6.964e-3
Vibrio cholerae infection	KEGG	2	ATP6V1B2, ATP6V1C1	51	11	42.82	9.489e-4	1.304e-2
Amino acids regulate mTORC1	Reactome	2	ATP6V1B2, ATP6V1C1	55	11	39.70	1.103e-3	1.460e-2
Epithelial cell signaling in Helicobacter pylori infection	KEGG	2	ATP6V1B2, ATP6V1C1	71	11	30.76	1.831e-3	2.135e-2
Rheumatoid arthritis	KEGG	2	ATP6V1B2, ATP6V1C1	95	11	22.99	3.251e-3	3.259e-2
Apoptotic execution phase	Reactome	1	DNM1L	4	11	272.95	3.659e-3	3.541e-2
tRNA modification in the mitochondrion	Reactome	1	PUS1	6	11	181.97	5.484e-3	4.649e-2
Ca2+ activated K+ channels	Reactome	1	KCNN3	9	11	121.31	8.216e-3	6.072e-2
Phagosome	KEGG	2	ATP6V1B2, ATP6V1C1	155	11	14.09	8.433e-3	6.181e-2