

GeDiPNet Cluster 94 -- 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 01:34:18

Pathway	Source	Overlap Genes	Overlap Gene Names	Pathway Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
Molecules associated with elastic fibres	Reactome	6	ELN, FBLN5, EFEMP2, LTBP1, EFEMP1, LTBP4	38	27	70.23	1.871e-10	2.539e-8
Elastic fibre formation	Reactome	3	ELN, FBLN5, LOX	18	27	74.14	8.085e-6	2.805e-4
Ion channel transport	Reactome	3	ATP6V0A2, ATP6V1A, ATP6V1E1	24	27	55.60	1.987e-5	5.952e-4
Insulin receptor recycling	Reactome	3	ATP6V0A2, ATP6V1A, ATP6V1E1	26	27	51.32	2.545e-5	7.265e-4
Collecting duct acid secretion	KEGG	3	ATP6V0A2, ATP6V1A, ATP6V1E1	28	27	47.66	3.198e-5	8.808e-4
Transferrin endocytosis and recycling	Reactome	3	ATP6V0A2, ATP6V1A, ATP6V1E1	31	27	43.05	4.368e-5	1.144e-3
ROS and RNS production in phagocytes	Reactome	3	ATP6V0A2, ATP6V1A, ATP6V1E1	34	27	39.25	5.788e-5	1.439e-3
Vibrio cholerae infection	KEGG	3	ATP6V0A2, ATP6V1A, ATP6V1E1	51	27	26.17	1.964e-4	3.848e-3
Ion transport by P-type ATPases	Reactome	3	ATP7A, ATP2A2, ATP2C1	56	27	23.83	2.594e-4	4.791e-3
Glutamate and glutamine metabolism	Reactome	2	ALDH18A1, PYCR1	14	27	63.54	4.356e-4	7.151e-3
Epithelial cell signaling in Helicobacter pylori infection	KEGG	3	ATP6V0A2, ATP6V1A, ATP6V1E1	71	27	18.79	5.231e-4	8.243e-3
Synaptic vesicle cycle	KEGG	3	ATP6V0A2, ATP6V1A, ATP6V1E1	79	27	16.89	7.151e-4	1.054e-2
Rheumatoid arthritis	KEGG	3	ATP6V0A2, ATP6V1A, ATP6V1E1	95	27	14.05	1.222e-3	1.577e-2
Defective ABCC6 causes pseudoxanthoma elasticum (PXE)	Reactome	1	ABCC6	1	27	444.81	2.248e-3	2.484e-2
Resolution of D-loop Structures through Holliday Junction Intermediates	Reactome	2	MUS81, DNA2	33	27	26.96	2.462e-3	2.662e-2