

GeDiPNet Cluster 238 -- 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: 2026-10-10 03:30:08. · Rows: 15 · Generated: 2026-10-10 00:14:05

Pathway	Source	Overlap Genes	Overlap Gene Names	Pathway Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
Insulin secretion	KEGG	4	ATP1A2, ATP1A3, CACNA1C, KCNN3	86	44	12.70	2.674e-4	5.042e-3
Cardiac muscle contraction	KEGG	4	ATP1A2, ATP1A3, MYH7, CACNA1C	87	44	12.55	2.796e-4	5.222e-3
cGMP-PKG signaling pathway	KEGG	5	ATP1A2, ATP1A3, MYH7, CACNA1C, INSR	166	44	8.22	3.336e-4	6.016e-3
Aldosterone-regulated sodium reabsorption	KEGG	3	ATP1A2, ATP1A3, INSR	38	44	21.55	3.539e-4	6.307e-3
Leukocyte transendothelial migration	KEGG	4	PTK2, PTPN11, ITGB1, SIPA1	116	44	9.41	8.326e-4	1.220e-2
Ion homeostasis	Reactome	3	ATP1A2, ATP1A3, ABCC9	54	44	15.16	9.989e-4	1.404e-2
Thyroid hormone signaling pathway	KEGG	4	ATP1A2, ATP1A3, MYH7, NOTCH1	122	44	8.95	1.005e-3	1.412e-2
Adrenergic signaling in cardiomyocytes	KEGG	4	ATP1A2, ATP1A3, MYH7, CACNA1C	154	44	7.09	2.369e-3	2.677e-2
Proximal tubule bicarbonate reclamation	KEGG	2	ATP1A2, ATP1A3	23	44	23.74	3.160e-3	3.272e-2
Interleukin-3, Interleukin-5 and GM-CSF signaling	Reactome	2	PTPN11, STAT5A	23	44	23.74	3.160e-3	3.272e-2
Interleukin-20 family signaling	Reactome	2	PTPN11, STAT5A	25	44	21.84	3.730e-3	3.689e-2
Insulin receptor recycling	Reactome	2	ATP6V0A1, INSR	26	44	21.00	4.032e-3	3.898e-2
Downstream signal transduction	Reactome	2	PTPN11, STAT5A	29	44	18.82	5.002e-3	4.518e-2
MET activates PTK2 signaling	Reactome	2	PTK2, ITGB1	30	44	18.20	5.346e-3	4.739e-2
Aldosterone synthesis and secretion	KEGG	3	ATP1A2, ATP1A3, CACNA1C	98	44	8.36	5.477e-3	4.816e-2