

GeDiPNet Cluster 327 -- 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: 2026-10-09 03:30:08. · Rows: 15 · Generated: 2026-10-09 03:17:12

Pathway	Source	Overlap Genes	Overlap Gene Names	Pathway Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
Apelin signaling pathway	KEGG	4	CCND1, NRF1, PPARGC1A, TFAM	140	9	38.13	2.130e-6	8.893e-5
Transcriptional activation of mitochondrial biogenesis	Reactome	3	NRF1, PPARGC1A, TFAM	51	9	78.50	5.952e-6	2.114e-4
Huntington disease	KEGG	4	NRF1, PPARGC1A, TFAM, SDHB	308	9	17.33	4.828e-5	1.203e-3
Mitochondrial transcription initiation	Reactome	1	TFAM	3	9	444.81	2.247e-3	2.482e-2
Prostate cancer	KEGG	2	CCND1, MMP3	98	9	27.23	2.286e-3	2.514e-2
Interleukin-4 and Interleukin-13 signaling	Reactome	2	CCND1, MMP3	108	9	24.71	2.768e-3	2.892e-2
Ion influx/efflux at host-pathogen interface	Reactome	1	ATP7A	4	9	333.61	2.995e-3	3.054e-2
PPARA activates gene expression	Reactome	2	NRF1, PPARGC1A	115	9	23.21	3.132e-3	3.157e-2
AMPK signaling pathway	KEGG	2	CCND1, PPARGC1A	122	9	21.88	3.517e-3	3.421e-2
PTK6 Regulates Cell Cycle	Reactome	1	CCND1	6	9	222.41	4.489e-3	4.075e-2
Alcoholic liver disease	KEGG	2	CCND1, PPARGC1A	144	9	18.53	4.864e-3	4.297e-2
RUNX3 regulates WNT signaling	Reactome	1	CCND1	8	9	166.81	5.981e-3	4.934e-2
EGFR Transactivation by Gastrin	Reactome	1	MMP3	9	9	148.27	6.726e-3	5.336e-2
RUNX3 regulates p14-ARF	Reactome	1	CCND1	9	9	148.27	6.726e-3	5.336e-2
Transcriptional regulation by RUNX2	Reactome	1	CCND1	12	9	111.20	8.960e-3	6.459e-2