

GeDiPNet Cluster 586 -- 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: 2026-10-20 03:30:09. · Rows: 15 · Generated: 2026-10-20 00:02:44

Pathway	Source	Overlap Genes	Overlap Gene Names	Pathway Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
POU5F1 (OCT4), SOX2, NANOG activate genes related to proliferation	Reactome	1	SALL1	13	5	184.77	5.401e-3	3.839e-2
Deadenylation of mRNA	Reactome	1	EIF4A3	24	5	100.08	9.953e-3	5.666e-2
RNA Polymerase I Transcription Termination	Reactome	1	POLR1A	32	5	75.06	1.325e-2	6.742e-2
RNA polymerase	KEGG	1	POLR1A	34	5	70.65	1.408e-2	6.986e-2
RNA Polymerase I Transcription Initiation	Reactome	1	POLR1A	45	5	53.38	1.860e-2	8.214e-2
mRNA 3'-end processing	Reactome	1	EIF4A3	58	5	41.41	2.392e-2	9.492e-2
RNA Polymerase II Transcription Termination	Reactome	1	EIF4A3	67	5	35.85	2.759e-2	1.031e-1
ISG15 antiviral mechanism	Reactome	1	EIF4A3	72	5	33.36	2.962e-2	1.074e-1
Transport of Mature mRNA derived from an Intron-Containing Transcript	Reactome	1	EIF4A3	75	5	32.03	3.084e-2	1.099e-1
RNA Polymerase I Promoter Escape	Reactome	1	POLR1A	91	5	26.40	3.732e-2	1.224e-1
B-WICH complex positively regulates rRNA expression	Reactome	1	POLR1A	91	5	26.40	3.732e-2	1.224e-1
mRNA surveillance pathway	KEGG	1	EIF4A3	103	5	23.32	4.216e-2	1.314e-1
Nucleocytoplasmic transport	KEGG	1	EIF4A3	108	5	22.24	4.417e-2	1.348e-1
Nonsense Mediated Decay (NMD) enhanced by the Exon Junction Complex (EJC)	Reactome	1	EIF4A3	115	5	20.89	4.698e-2	1.396e-1
Spliceosome	KEGG	1	EIF4A3	162	5	14.83	6.566e-2	1.692e-1