

GeDiPNet Cluster 102 -- 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 09:45:19

Pathway	Source	Overlap Genes	Overlap Gene Names	Pathway Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
Cytosolic tRNA aminoacylation	Reactome	6	AIMP1, RARS1, AARS1, KARS1, EPRS1, AIMP2	24	48	62.55	3.759e-10	4.447e-8
RNA polymerase	KEGG	5	POLR1C, POLR3K, POLR3B, POLR3A, POLR1A	34	48	36.80	2.100e-7	1.198e-5
Cytosolic sensors of pathogen-associated DNA	Reactome	4	POLR1C, POLR3K, POLR3B, POLR3A	22	48	45.49	1.558e-6	6.835e-5
RNA Polymerase III Transcription Initiation From Type 2 Promoter	Reactome	4	POLR1C, POLR3K, POLR3B, POLR3A	27	48	37.07	3.684e-6	1.428e-4
RNA Polymerase III Transcription Initiation From Type 3 Promoter	Reactome	4	POLR1C, POLR3K, POLR3B, POLR3A	28	48	35.74	4.285e-6	1.622e-4
RNA Polymerase III Transcription Initiation From Type 1 Promoter	Reactome	4	POLR1C, POLR3K, POLR3B, POLR3A	28	48	35.74	4.285e-6	1.622e-4
Sphingolipid metabolism	KEGG	4	ARSA, DEGS1, GALC, HEXA	54	48	18.53	6.134e-5	1.461e-3
Aminoacyl-tRNA biosynthesis	KEGG	4	RARS1, AARS1, KARS1, EPRS1	66	48	15.16	1.350e-4	2.779e-3
RNA Polymerase I Transcription Termination	Reactome	3	POLR1C, ERCC2, POLR1A	32	48	23.46	2.739e-4	4.876e-3
Cytosolic DNA-sensing pathway	KEGG	4	POLR1C, POLR3K, POLR3B, POLR3A	83	48	12.06	3.274e-4	5.640e-3
RNA Polymerase I Transcription Initiation	Reactome	3	POLR1C, ERCC2, POLR1A	45	48	16.68	7.557e-4	1.082e-2
Glycosphingolipid metabolism	Reactome	3	ARSA, GALC, HEXA	46	48	16.32	8.062e-4	1.139e-2
Defective SLC9A6 causes X-linked, syndromic mental retardation,, Christianson type (MRXSCH)	Reactome	1	SLC9A6	1	48	250.21	3.997e-3	3.753e-2
Defective HEXA causes GM2G1	Reactome	1	HEXA	1	48	250.21	3.997e-3	3.753e-2
RNA Polymerase I Promoter Escape	Reactome	3	POLR1C, ERCC2, POLR1A	91	48	8.25	5.690e-3	4.767e-2