

Comprehensive pan-cancer analysis of CDCA8: implications for prognosis and therapeutic targeting

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Using datasets from the Cancer Genome Atlas, Human Protein Atlas, and Gene Expression Omnibus, along with bioinformatics tools, we studied the implications of cell division cycle-associated 8 (CDCA8) in 33 malignancies. CDCA8 overexpression correlated with poorer survival and increased immune cell infiltration. Gene ontology enrichment analysis suggests that CDCA8 interacts with crucial proteins involved in cell cycle and mitotic control. Overall, these findings highlight CDCA8's potential as a predictive biomarker and therapeutic candidate in a broad spectrum of human malignancies.

Accordingly, we conducted a pan-cancer analysis of CDCA8, examining its expression patterns, prognostic significance, immune-related associations, and functional enrichment. The present study integrated multi-omics data from the Cancer Genome Atlas (TCGA), the Genotype-Tissue Expression (GTEx) project, and analytical platforms including Gene Expression Profiling Interactive Analysis (GEPIA), Search Tool for the Retrieval of Interacting Genes/Proteins (STRING), and Tumour Immune Estimation Resource (TIMER), along with other relevant databases.

Materials and methods

Gene expression analysis