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Short Commentary
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Effects of ESCO2 or Its Methylation on the Prognosis, Clinical Characteristics, Immune Microenvironment, and Pathogenesis of Low-Grade Glioma

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Short Commentary

In this short commentary, we made a brief introduction to the advantages of using public databases to research the pathogenesis of LGG and summarized the main research results of this study. Finally, we make a prospect for the use of public data and the significance of our article.

The current system of basic research is well established, and if we focus on a single molecule in a glioma, we can demonstrate its biological function from different dimensions. However, how to step out of the comfort zone and look for undiscovered targets in glioma pathology is a challenge for future researchers [1,2]. Nowadays, bioinformatics analysis based on public databases makes it easier to mine new targets, and has become an important field of glioma research [3]. Compared to the time and cost of sequencing clinical samples, gradually increasing data are available in open databases, allowing researchers to quickly access the omics analysis.

As a landmark cancer genome project, The Cancer Genome Atlas (TCGA) database contains the 2.5 petabytes data on molecular signatures of more than 20,000 primary cancer samples from 33 tumor types, making it a useful tool for researchers to conduct omics studies [4]. This study was by mining the well-known TCGA database, which led us to identify ESCO2 as a significant target of glioma patients. More importantly, data from the Chinese Glioma Genome Atlas (CGGA) sequencing and microarray database were included in the study [5], which on the one hand eliminates bias in results that may result from a single database, and on the other hand identifies glioma marker on Chinese cohort, being more conducive for us to reach to clinical applications.

The article firstly elucidates the relationship between ESCO2 with prognosis of LGG patients and malignant characteristics of LGG, which revealed that high expression of ESCO2 led to poor prognosis of LGG patients and was an independent risk factor for LGG. At the same time, the GSEA analysis was performed to predict the potential cell signaling pathways that ESCO2 involved in LGG [6]. Of even greater caliber is the article's broader inclusion of the concepts of methylation and immune infiltration in glioma research, providing comprehensive insight into the effect of ESCO2 on malignant process of LGG.

The main significance of this paper is to provide an example of a novel prognostic target for LGG and predict the potential mechanism of its involvement in LGG pathological process, which was a successful experiment using public databases to discover part of the pathogenesis of LGG. Therefore, finding key loci in the pathological mechanism of LGG through data analysis can give researchers more innovative scientific ideas and provide a whole new avenue for possible solutions to LGG. It is hoped that future researchers will be able to unearth more targets and continue the work of their predecessors, further combining mechanism studies on molecular levels to decipher cancer black boxes at an early date.

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