Jiang et al. from the Xiangya Hospital, Changsha, analyzed the protein posttranslational modifications PTM pathway for glioma classification into distinct clusters. Comprehensive analyses compared intercluster differences in clinical outcomes, mutational landscapes, and immune microenvironment profiles. Differentially expressed genes (DEGs) were identified to construct a robust prognostic prediction model with machine learning approaches. Among the genes included in the model, TOM1L1 (Target of Myb1 Like 1 Membrane Trafficking Protein) was selected for in vitro experimental validation to assess its role in glioma progression.

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PTMs were found to influence glioma prognosis significantly. Dysregulation in specific pathways, such as glutathionylation and citrullination, was correlated with more aggressive clinical features. The prognostic model, comprising DEGs such as TOM1L1, demonstrated high predictive accuracy (c-index = 0.867)-the scores derived from the model strongly correlated with glioma progression indicators. In vitro experiments revealed that TOM1L1 facilitates malignant progression by modulating PTM pathways, confirming its functional role in glioma.

The study establishes the first comprehensive PTM atlas in gliomas, revealing subtype-specific modification patterns with clinical and therapeutic implications. TOM1L1 emerges as a promising prognostic biomarker and a potential therapeutic intervention target. Targeting PTM pathways may offer novel strategies for glioma treatment, enhancing patient outcomes <sup>1)</sup>.

## 1)

Jiang Z, Huang H, Guo Y, Wang Z, Huang H, Yin W, Huang H, Wang L, Liu W, Jiang X, Ren C. Unveiling the Role of Protein Posttranslational Modifications in Glioma Prognosis. CNS Neurosci Ther. 2025 Mar;31(3):e70330. doi: 10.1111/cns.70330. PMID: 40090864.

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TOM1L1