

Structure-guided identification of Baicalin exhibiting anti-Alzheimer's effects via CLK1 inhibition

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Motivation and Aim: Alzheimer's disease (AD) is a rapidly increasing neurodegenerative disorder, projected to affect 78 million people by 2050 [1]. Current treatments provide only modest symptomatic relief [2]. Tau protein hyperphosphorylation is a key pathological feature of AD, and evidence suggests that targeting tau phosphorylation through the inhibition of protein kinases, particularly CLK1 (CDC2-like kinase 1), could reduce tau aggregation and neuronal death [3]. This study aims to investigate the potential of Baicalin as a CLK1 inhibitor, offering a novel therapeutic approach for AD and other tauopathies.

Methods and Algorithms: We employed structure-based molecular docking to predict the binding affinity of Baicalin to CLK1. Molecular dynamics simulations were conducted to analyze the stability and interactions of the Baicalin-CLK1 complex. Fluorescence spectroscopy was used to confirm the binding mechanism. Additionally, a kinase inhibition assay was performed to determine the inhibitory potential of Baicalin on CLK1, quantified by IC₅₀ values.

Results: Our molecular docking studies revealed a strong binding affinity of Baicalin to CLK1. Molecular dynamics simulations confirmed the stability of the Baicalin-CLK1 complex. Fluorescence spectroscopy validated the binding interactions between Baicalin and CLK1. The kinase inhibition assay demonstrated that Baicalin significantly inhibits CLK1 activity, with an IC₅₀ value of 12.04 μ M.

Conclusion: Baicalin exhibits significant potential as a CLK1 inhibitor, effectively reducing CLK1 activity *in vitro*. These findings position Baicalin as a promising lead molecule for developing specific CLK1 inhibitors, offering a novel therapeutic strategy for AD and other tauopathies. Further research and clinical trials are necessary to validate these findings and explore the therapeutic efficacy of Baicalin *in vivo*.

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References

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