# Integrated Computational Identification and Evaluation of Novel c-Src Inhibitors as Potential Therapeutics for Colorectal Cancer

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## Abstract

Currently the third most frequent cancer in the world, colorectal cancer (CRC) is caused by malignant cell development that starts in the large intestine. The c-Src kinase is a viable therapeutic target since it is overexpressed in a number of malignancies and is essential to several signaling pathways. Nevertheless, it is still difficult to create new and specific c-Src inhibitors. In this work, we used molecular docking and E-pharmacophore-based virtual screening to find possible c-Src inhibitors. Two excellent candidates with high docking scores and interactions were chosen for additional investigation from a library of 1259 compounds that had been screened. To evaluate binding affinity and structural stability, these docked complexes underwent molecular dynamics simulations and binding free energy calculations. Density functional theory (DFT) and ADME predictions were also used to assess drug-likeness and electronic characteristics. In the end, two substances LEG 15029934 and LEG 07404577 were found to be promising leads with possible inhibitory activity against c-Src kinase. By focusing on c-Src expression, these drugs may slow the evolution of colorectal cancer. These findings highlight the effectiveness of an integrated computational approach for discovering novel c-Src inhibitors that could contribute to targeted colorectal cancer therapy.

**Keywords:** ADME prediction, Binding Free Energy, Colorectal cancer (CRC), c-Src, E-pharmacophore-based virtual screening, Molecular Dynamics Simulation.