

## IDENTIFICATION OF NEW POTENTIAL DRUGS FOR LUNG ADENOCARCINOMA CAUSING PROTEIN RMB10 USING COMPUTER-AIDED DRUG DESIGN APPROACH.

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### ABSTRACT

*Lung cancer is among the most frequently diagnosed and the leading cause of cancer-related deaths worldwide. It is highly invasive, rapidly spreads, and affects both sexes. Lung cancer can be caused by mutations in various genes likewise RMB10 is commonly lacking or changed in lung adenocarcinoma, making it a possible biomarker or therapeutic target. It is a tumor suppressor gene that participates in alternative splicing. The primary goal of this study is to employ computer-aided drug design approaches to identify possible medicines for the target that might subsequently be used as a candidate therapy for the treatment of lung adenocarcinoma caused by RMB10 tumor suppressor gene absence or alteration. Plant-based molecules were downloaded, followed by ligand and target preparation. The ADMET characteristics were examined to reflect drug-likeness. The most mutated gene and the frequent type of mutation that causes a gene change and causes lung adenocarcinoma was also identified using the COSMIC database. Our findings identified three lead compounds, Vinblastine, Nabilone, and Camptothecin, that exhibited strong affinity for the RMB10, while the most mutated gene in lung adenocarcinoma is EGFR.*

**KEYWORDS:** NSCLC, RMB10, Alternative splicing, Computer-aided drug design, PyMOL, AutoDockVina, Molinspiration, DrugBank, ADMET, PubChem, COSMIC database.

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