Virtual Screening of Potential Inhibitors of APOBEC3B: a Promising Cancer Drug Target

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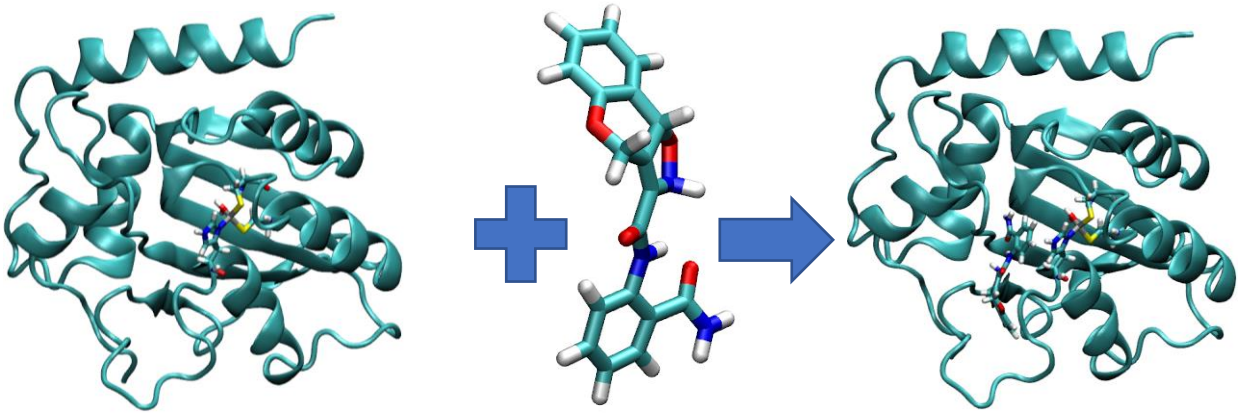
Apolipoprotein B mRNA editing enzyme catalytic polypeptide-like 3B (APOBEC3B) is a protein found in the nuclear membrane of a cell. APOBEC3B belongs to the family of proteins called cytidine deaminases; causing the cytosine to uracil transition in single strand DNA. APOBEC3B is overexpressed in many cancers such as breast, liver and colon. APOBEC3B has been implicated in an increasing number of mutations in metastatic tumors as compared to the primary cancer tumor. The movement of APOBEC3B can be studied computationally due to the recent resolution of the X-ray crystal structure. We used computational chemistry techniques to investigate the motion of APOBEC3B in the presence of many ligands (potential inhibitors). We hope to discover a molecule that is promising for future drug development to reduce the effect of APOBEC3B in the development of cancer. This work was performed using the AMBER Molecular Dynamics Software and PyRx docking software to virtually screen 7.5 million ligands from the ZINC database. The best ligands from docking were further analyzed using MMPBSA.py software to calculate the binding free energy. Preliminary results have shown some success in determination of traits that make for negative binding affinities.



APOBEC3B Protein

PDB 5CQH

Potential inhibitor

APOBEC3B-inhibitor complex