

Molecular Insights into the Antidiabetic Potential of Excavatin-A as an α -Glucosidase Inhibitor: An Integrated Molecular Docking and Molecular Dynamics Study

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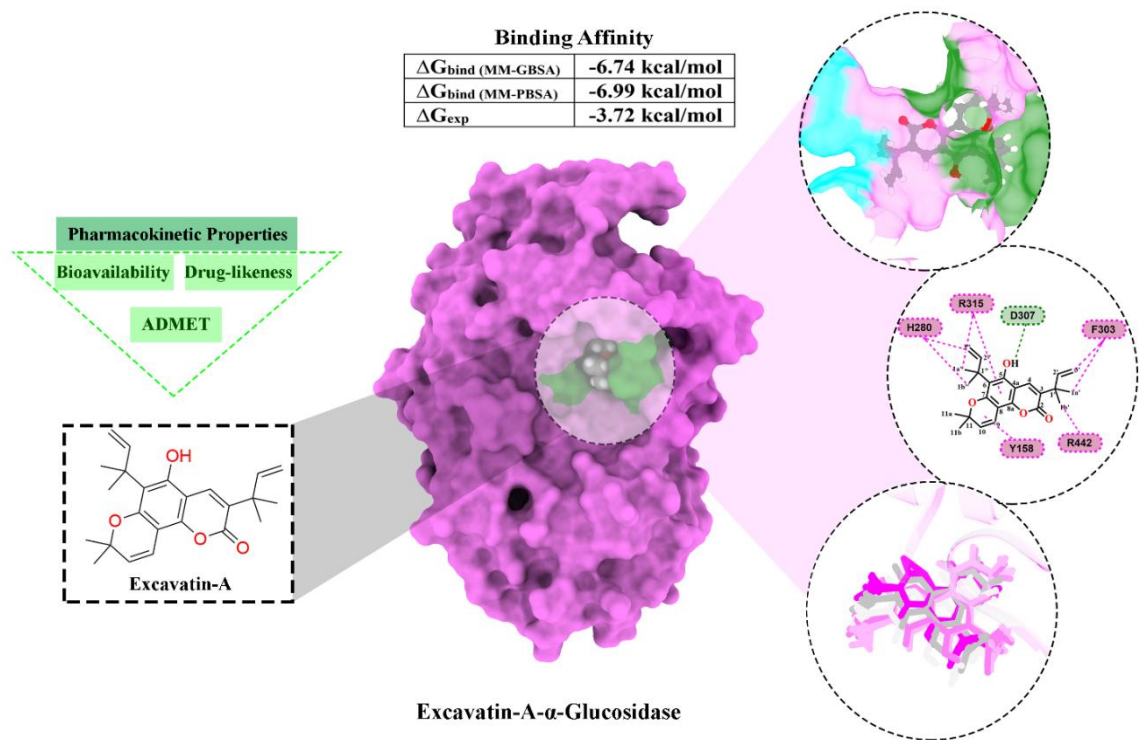
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Abstract

α -Glucosidase enzymes were targeted to hydrolyse oligosaccharides into monomers, thereby increasing blood glucose levels in people with type 2 diabetes mellitus (DM). Natural products offer diverse, accessible compounds for drug discovery. Excavatin-A (ExA) is a new compound of coumarin derivatives that has quite a structural similarity to nordentatin (Nor) and has been known as a promising α -Glucosidase inhibitor. Through a structure-based approach, the interaction of these

compounds with α -Glucosidase at the molecular level was studied. For evaluation purposes, the compounds Nordentatin and acarbose (Aca) were used as controls. The results showed that the dynamic behaviour of each system reached equilibrium over the simulation time, as indicated by stability and rigidity analyses. Meanwhile, the theoretical (ΔG_{bind}) and experimental (ΔG_{exp}) binding affinities show a good correlation, with $\text{Aca-}\alpha\text{-Glu} > \text{ExA-}\alpha\text{-Glu} > \text{Nor-}\alpha\text{-Glu}$. Moreover, the residue on the gate pocket (especially Y158) leads to stabilising ExA binding with a decomposition energy (" ΔG " _ "bind" ^ "residue"): -3.28 kcal/mol. ExA shows its potential as a promising drug candidate by meeting the Lipinski rules (only one violation), good bioavailability (0.55), good oral absorption (+Human Intestinal Absorption(HIA)), and non-toxicity (non-AMES and non-hepatotoxicity). This work provided useful molecular insights into Excavatin-A as a potential α -glucosidase inhibitor.

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Innovative Description: The first to report the potential of the new coumarin derivative Excavatin-A as a potential α -Glucosidase inhibitor through computational studies.