ABSTRACT

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MOLECULAR DOCKING OF Vpr, A FIBRIN DEGRADING ENZYME FROM *Bacillus subtilis* G8, WITH FIBRIN
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Cardiovascular diseases such as ischemic heart disease, stroke and chronic pulmonary obstructive disease are some of the top causes of mortality. One of the reasons why those conditions occur is due to thromboembolism. Thromboembolisms may be broken down by anticoagulants known as fibrinolytic drugs. In the process of discovering a new drug, the enzyme Vpr by *Bacillus subtilis* G8 has shown fibrinolytic properties. Hence, in order to better understand the enzyme, a molecular modeling of the enzyme has been done, as well as a docking simulation with fibrin substrates. Two enzyme models were produced from the webservers Robetta and SWISS-MODEL. The Robetta model had to be manually modified in order to have a structurally accurate active site, however it also had a higher quality of model overall as compared to SWISS-MODEL. Validation tools such as VERIFY-3D, and PROSA has shown that the placement of residues for Robetta is better, however the SWISS-MODEL produced model is better in the PROCHECK result. The Robetta model was then agreed upon for the docking, and fibrin fragments with the predicted cleavage sites of Vpr was then docked by using HADDOCK. Overall, only two polypeptides were able to bind with Vpr in the correct position. This shows the successful predicted cleaving of fibrin from the enzymatic activity of Vpr. However, with many issues such as the lack of structure refinement and the manual editing of the enzyme's active site, further research needs to be done in order to have a better quality docking simulation.

Keywords : Vpr, fibrin, catalytic triad, subtilisin, *de novo* modeling, template-based modeling, structure validation tools, molecular docking.

Reference : 70 (1977 – 2021)