SIMULATION ON THE UREASE INHIBITION BY BENZIMIDAZOLE

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AUTHOR'S DECLARATION

I declare that the work in this case study was carried out in accordance with the regulations of Universiti Teknologi MARA. It is original and is the results of my own work, unless otherwise indicated or acknowledge as referred work. This thesis has not been submitted to any other academic institution or non-academic institution for any degree or qualification.

I, hereby, acknowledge that I have been supplied with the Academic Rules and Regulations for Post-Graduate, Universiti Teknologi MARA, regulating the conduct of my study and research.

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ABSTRACT

The theoretical research is done to learn more and gain a better idea of what substance would work best as a urease inhibitor. Plants, soils, and bacteria all have urease enzymes. Due to its necessity for plant development and growth, this enzyme is crucial to the nitrogen cycle where a nickel-dependent metalloenzyme called urease catalyzes the breakdown of urea to release ammonia and carbon dioxide. Currently, pharmaceutical research and development (R&D) are active in looking for new and potent urease inhibitors. So, the interaction between benzimidazole which acts as a urease inhibitor, the characteristics, and structures of binding interactions between urease and benzimidazole are also analyzed. The geometry optimization is investigated using xTB method which is more reliable and accurate by detecting the necessary structures for less polar compounds, polar and highly hydrogen bonded systems. Next, the OH on benzimidazole was deformed from its initial location after geometries optimization where OH in P1 shifted to the active site while P2 is vice versa. The value of interaction energy is determined from the binding energy between urease and inhibitor. Comparing the interaction energy, P1 has discovered the higher total energy which more stable. For Wiberg bond order, nickels positively charged in the absence of the inhibitor. The inhibitor has altered the interactions and charges. So, P1 has been chosen as the stable complex due to the greater bond order. In electron localization function, the isosurface map demonstrates that the oxygens and nitrogens near to the nickels still have lone pairs linked to them, instead of exposing the bonding to Ni88 and Ni89. Thus, these obtained results of this research are supported as evidence of the use of benzimidazole as a urease inhibitor by knowing their arrangement of structure and

its energy. It has been found that benzimidazole can interact favorably with the nickel-containing active sites of urease and the contact is not of a covalent type. The interaction energies of system P1 and P2 are weaker like the flavone compound.

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