**Young Researcher Presentation 8**

# IDENTIFYING POTENTIAL INHIBITORS OF HUMAN HEXOKINASE II FOR THE DEVELOPMENT OF ANTI-DENGUE THERAPEUTICS *VIA* VIRTUAL SCREENING APPROACHES

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The human hexokinase II (HK2) has been suggested as a potential therapeutic target for the development of drugs against dengue virus (DENV) infection. In this paper, compounds with potential HK2 inhibitory activity have been identified using ligand-based and structure-based virtual screening approaches. Ligand-based drug design was performed by using Ultra-Fast Shape Recognition with Atom Types (UFSRAT) and Ultrafast Shape Recognition with CREDO Atom Types (USRCAT) programmes by utilising 2-Deoxyglucose (2-DG) as the query molecule, which is a known HK2 inhibitor. The molecules identified from the programmes showed great similarity to 2-DG with scores ranged from 0.78-0.85 and 0.88-0.97 for UFSRAT and USRCAT, respectively. The analogues were docked against the crystal structure of HK2 (PDB ID: 2NZT) in complex with alpha-D-glucose (GLC) and beta-D-glucose-6-phosphate (BG6) by using AutoDock Vina programme, on both A and B chains where the active sites were located. The docking hits for molecules from UFSRAT showed binding energies ranged from -7.1 to -4.8 kcal/mol when docked on chain A, while the hits for chain B showed scores ranged from -6.7 to -4.8 kcal/mol. On the other hand, the binding energies for molecules from USRCAT when docked on both A and B chains were similar, which ranged from -7.0 to -5.2 kcal/mol. The hits bind firmly at the cavities, where both GLC and BG6 were oriented towards the active sites of HK2. Taken together, this study has successfully discovered compounds which have potentials as potent inhibitors of HK2, thus pave the path towards the development of dengue therapeutics.