

Abstract

Dengue disease is one of the most prominent viral disease in Indonesia. DENV NS1 has been known to cause several pathogenic roles, especially vascular leakage in dengue infection. Structural profile analysis of the DENV NS1 of each serotype might provide correlation between the structure and sequence to the disease severity. Samples of this study were DENV NS1 amino acid sequences from Indonesia retrieved from the NCBI Genbank database. SWISS-MODEL homology modeling website was used in this study in order to construct 3D model from the retrieved DENV NS1 sequence. UCSF Chimera software was used to analyze the amino acid composition of the sequences as well as visualize the 3D models of proteins.

Keywords: Dengue Indonesia, DENV NS1, Homology Modeling, Protein Structure Analysis