

## **ABSTRACT**

SARS-CoV-2 began its outbreak in the late December of 2019 and was later declared as a global pandemic. It has led to the research of therapeutics and vaccines development for SARS-CoV-2 as a method of treatment. The target genes for the immunotherapeutic construct are usually the spike protein due to its crucial binding to the human ACE2 receptor via the RBD. Upon its entrance to the host cell, the viral antigens are presented by the HLA molecules on the T-cells and eliminated. Like every other RNA virus, however, SARS-CoV-2 has a large complex genome with high rates of mutations like the accessory proteins. The genomic feature had raised concerns regarding vaccine immunity and other development efforts for controlling and preventing the spread of SARS-CoV-2. Fortunately, constant monitoring of the mutational variants of SARS-CoV-2 using a computational tool provides insights for the effectiveness of the vaccine. This research project aims to analyze the variation of T-cell epitopes between the SARS-CoV-2 circulating strains and the ancestral strain using computational immunoinformatics approach in order to study the relevancy of current vaccines. A method called Next Generation Sequencing (NGS) was used for the retrieval of circulating SARS-CoV-2 genome for the purpose of SARS-CoV-2 variants surveillance as well as provide data for the conservancy analysis within the Indonesian population. The results showed that the SARS-CoV-2 ORF3 and ORF7a proteins had more T-cell epitopes that are not conserved, whereas, SARS-CoV-2 ORF6, ORF7b, ORF8 and ORF10 were known to be more oftenly conserved.