ABSTRAK

Nama : Meilisa Rahmasari

Program Studi : S1 Farmasi

Judul Penelitian : Desain Vaksin HIV Berbasis Peptida Dari Matrix Protein p17 : Pendekatan Imunoinformatika

Infeksi HIV/AIDS merupakan spektrum dari penyakit infeksi sistem imun. Penularan cepat menyebabkan kesulitan dalam mengatasi penyakit ini. Penelitian ini bertujuan untuk mengetahui peptida yang berpotensi sebagai kandidat vaksin, mengetahui sifat fisikokimia dan sifat homolog dari kandidat vaksin. Penelitian ini menggunakan metode komputasi dengan pendekatan imunoinformatika dan menggunakan sampel dari sekuen matrix protein p17 dengan kode PDB 2HMX. Semua tahapan dilakukan menggunakan *webserver* dan aplikasi yang sesuai. Dari analisis sekuen didapatkan epitop Sel T dan Sel B yang terpilih. Setelah dilakukannya desain kandidat vaksin dari epitop Sel T dan Sel B langkah terakhir yaitu dilakukannya visualisasi 2D dan 3D kandidat vaksin. Hasil penelitian menunjukkan bahwa urutan peptida yang berpotensi sebagai kandidat vaksin yaitu sebagai berikut, adjuvant-**EAAAK**-GSEELRSLY-**AAY**-NNSQVSQNY-**GPGPG**-TGSEELRSLYNTIAV-**KK**-QPSLQTGSEELRS-**KK**-DVKDTKEALDK. Sifat fisikokimia dari kandidat vaksin HIV mempunyai jumlah asam amino 116, berat molekul 12871,66 g/mol, teoritis pI 9,58, jumlah residu bermuatan negatif 13, jumlah residu bermuatan positif 24, koefisien kepunahan 7825 m^2/mol, indeks kestabilan 59,77, indeks alifatik 64,74, rata-rata hidrofobisitas -0,958. Hasil dari analisis homolog kandidat vaksin matrix protein p17 menyatakan bahwa residu asam amino penyusun peptida tidak bersifat homolog atau tidak menimbulkan respon autoimun jika dijadikan kandidat vaksin.

Kata Kunci: Desain Vaksin, Epitop, HIV, Imunoinformatika

ABSTRACT

Name : Meilisa Rahmasari

Study Program : *Bachelor of Pharmacy*

Titel : *Peptide Based HIV-1 Vaccine Design From Matrix Protein p17 : imunoinformatics Approach*

*HIV/AIDS infection is a spectrum of infectious diseases of the immune system. Rapid transmission causes difficulty in overcoming this disease. This studied aims to determine potential peptides as vaccine candidates, and to determine the physicochemical properties and homologous properties of vaccine candidates. This studied used a processing method with an imunoinformatics approached and used samples from the p17 matrix protein sequence with PDB code 2HMX. All stages were carried out used the appropriate web server and application. From sequence analysis, selected T-cell and B-cell epitopes was obtained. After designing the vaccine candidate from T-cell and B-cell epitopes, the final stepped was to perform 2D and 3D visualization of the vaccine candidate. The researched shows that the peptide sequences that had potential as vaccine candidates were as follows, adjuvant-**EAAAK**-GSEELRSLY-**AAY**-NNSQVSQNY-**GPGPG**-TGSEELRSLYNTIA V-**KK**-QPSLQTGSEELRS-**KK**-DVKDTKEALDK. The physicochemical properties of the HIV vaccine candidate had a total of 116 amino acids, a molecular weight of 12871.66 g/mol, a theoretical pI of 9.58, a number of negative residues 13, a number of positively charged residues 24, the extinction coefficient was 7825 m2/mol, the stability index was 59, 77, aliphatic index 64.74, average hydrophobicity -0.958. The results of the homologous analysis of the matrix protein p17 vaccine candidate stated that the amino acid residues that made up the peptide were not homologous or did not caused an autoimmune response when used as a vaccine candidate.*

KeyWords : *Epitope, HIV, Imunoinformatics, Vaccine Design*