

**STUDI *IN SILICO* DESAIN VAKSIN SUBUNIT PROTEIN
DALAM UPAYA PENGEMBANGAN VAKSIN
MONKEYPOX (MPOX)**

SKRIPSI

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Sebagai salah satu syarat untuk memperoleh gelar Sarjana Farmasi

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Kutipan atau saduran baik sebagian ataupun seluruh naskah, harus menyebut nama pengarang dan sumber aslinya, yaitu Sekolah Tinggi Farmasi Indonesia.

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ABSTRAK

Monkeypox (MPOX) merupakan penyakit zoonotik yang disebabkan oleh *monkeypox virus* (MPXV) dan masih menjadi ancaman kesehatan global. Pengembangan vaksin subunit dipandang sebagai pendekatan yang lebih aman dan efisien. Penelitian ini bertujuan merancang vaksin subunit protein fusi A35R-M1R menggunakan dua variasi *linker* fleksibel, yaitu (GGGGS)₂ dan (GGGGS)₃. Desain dilakukan secara *in silico* melalui pemodelan struktur 3D menggunakan AlphaFold, prediksi epitop sel B dengan Discotope 3.0, serta simulasi dinamika molekuler dengan perangkat lunak AMBER. Hasil menunjukkan bahwa desain vaksin dengan *linker* (GGGGS)₃ memiliki kestabilan struktural lebih tinggi dengan nilai RMSD dan RMSF yang lebih rendah dibandingkan varian (GGGGS)₂. Selain itu, prediksi epitop sel B menunjukkan distribusi yang lebih tersebar pada varian (GGGGS)₃. Simpulan dari penelitian ini adalah bahwa panjang *linker* berpengaruh terhadap kestabilan dan penyajian epitop dalam desain vaksin fusi, dan linker (GGGGS)₃ memberikan hasil yang lebih optimal.

Kata kunci : *In silico*, MPOX, vaksin subunit, linker (GGGGS)_n

ABSTRACT

Monkeypox (mpox) is a zoonotic disease caused by the monkeypox virus (MPXV) and remains a global health threat. Subunit vaccine development is considered a safer and more efficient approach. This study aimed to design a subunit vaccine based on the fusion protein A35R-M1R using two variations of flexible linkers, namely (GGGGS)₂ and (GGGGS)₃. The design was performed in silico through 3D structural modeling using AlphaFold, B-cell epitope prediction via Discotope 3.0, and molecular dynamics simulation using the AMBER software. The results showed that the vaccine design with the (GGGGS)₃ linker demonstrated higher structural stability, indicated by lower RMSD and RMSF values compared to the (GGGGS)₂ variant. In addition, B-cell epitope prediction showed a broader epitope distribution in the (GGGGS)₃ variant. It was concluded that the linker length significantly affected the structural stability and epitope presentation of the vaccine construct, with (GGGGS)₃ yielding a more optimal outcome.

Keywords : In silico, MPOX, subunit vaccine, linker (GGGGS)_n

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