A. Suggestions

a. Implications

The proposed multimer chimeric vaccine candidate in our study, targeting the Ag85 protein complex, represents a promising avenue for addressing this challenge. This innovative approach, informed by advanced in-silico analyses, aims to enhance vaccine efficacy while considering the genetic and immunological landscape of the Indonesian population. If successful, this vaccine could significantly reduce the TB burden, providing an effective tool for both prevention and control. Moreover, the development of such a vaccine may serve as a model for other nations facing similar TB-related challenges, thus having broader global implications. Given the recent growing threat of multidrug-resistant TB and the growing barriers of current vaccine strategies, timely advancement in TB vaccine development is crucial.

Delays in addressing this issue not only prolong the morbidity and mortality associated with TB but also exacerbate the risks of further resistance and uncontrolled transmission. Therefore, the successful development and implementation of this vaccine candidate could have a transformative impact, offering a sustainable and effective solution to one of the world's most pressing infectious disease challenges.

b. Computational to Laboratory Validation

In order to translate the in-silico findings into practical applications, future studies should involve comprehensive wet lab experiments to validate and optimize the proposed vaccine candidate. Initially, the multimeric protein construct should be expressed and purified using recombinant DNA technology in a suitable expression system such as our constructed plasmid. Subsequently, in vivo studies employing established animal models, such as mice or guinea pigs, should be conducted to evaluate the immunogenicity, safety, and protective efficacy of the vaccine. Furthermore, optimization of vaccine formulation, including adjuvant selection and stability testing under varying conditions, will be critical to ensuring the scalability and translational potential of the vaccine for clinical evaluation.

B. SUPPLEMENTARY DATA

I. Multiple Sequences Alignment Result Folder: (MSA Results)

II. Table 4. Separate and combine population coverage of CTL and HTL epitopes and their corresponding MHC alleles.

Epitope	Type	Coverage		
		Class 1	Class 2	Combine
GWITPAFEW	MHC1	67.48%	-	
NERSSNLKE	MHC1	67.87%	-	
YKWELSLQW	MHC1	67.48%	-	75.50%
PVEYLQSMGRDIKVQ	MHC2	-	56.39%	
GLPVEYLQVPSASMG	MHC2	-	90.23%	
PGLPVEYLQVPSASM	MHC2	-	70.42%	90.23%
Combine				97.61%