

Antigens and Epitopes Derived from *Mycobacterium tuberculosis*

Researchers at the La Jolla Institute for Immunology have defined novel *Mycobacterium tuberculosis* (MTB) CD4⁺ T cell epitopes using a combination of epitope predictions and high-throughput ELISPOT assays using PBMC from human donors capable of controlling MTB infection.

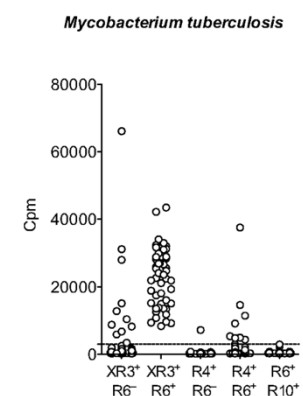
Mycobacterium tuberculosis (MTB) is the worldwide leading cause of death from infectious disease. The increasing incidence of drug resistant strains has prompted their inclusion in the list of A-C pathogens and heightened interest in the development of effective vaccines. The MTB genome encodes more than 4,000 different open reading frames (ORFs), yet only a handful of them have been reported as targets of human CD4⁺ T cells, the key cellular effector of MTB immunity. However, the availability of genomic information and recent advances in epitope prediction and validation methodologies have enabled the performance of truly unbiased genome-wide searches and have revealed an unprecedented breadth of responses to several complex pathogens.

Using these recent advances, the researchers at LJI have developed pools of predicted and validated MTB epitopes. These epitopes are useful as research tools to determine the breadth of MTB responses in humans, and they are also useful in vaccine formulations designed to protect against MTB infection.

ADVANTAGES:

- Novel predicted and validated MTB epitopes
- Useful as research tools or in vaccine compositions

Novel MTB CD4⁺ T Cell Epitopes and Antigens



T cell responses to MTB are restricted to a CKCR3⁺CCR6⁺ memory subset