Case ID:M20-278L

Published: 3/10/2023

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Prediction Algorithm for MHC-bound Peptides & SARS-CoV-2 Peptides for Vaccines

T cell immunity is a fundamental component of the immune response to infections, cancer, and autoimmunity and is strongly impacted by polymorphisms in major histocompatibility complex (MHC) protein sequences. In particular, allelic MHC-I protein variants have been shown to influence patient outcomes to various viral infections, including SARS-CoV. While the influence of MHC proteins on patient outcome in viral infections has been particularly well studied, it is still difficult to identify or predict peptides which can complex with MHC proteins and induce a robust immune response.

Researchers at the Biodesign Institute of Arizona State University have developed a novel integrated algorithm, called EnsembleMHC, to improve MHC-I presentation prediction and aid in T cell-based vaccine development. EnsembleMHC integrates many different prediction algorithms to improve accuracy and confidence that are unattainable by any one algorithm alone. This approach was validated with the prediction of MHC-I peptides for SARS-CoV-2, and a set of high priority SARS-CoV-2 peptides for vaccine development and T cell immunotherapy was developed.

This technology helps identify peptides which can be used in the development of immune-based therapeutics capable of generating long lasting immunity and preventing the initial development of disease.

Potential Applications

- MHC-I presentation prediction software

- Predicting population fitness/mortality risk against SARS-CoV-2

o   Analysis of countries in general or different communities within countries

- SARS-CoV-2 peptides for vaccine development and T cell immunotherapy

Benefits and Advantages

- Combines multiple algorithms to improve accuracy and confidence

o   Provides more precise MHC-I presentation predictions through the use of

allele and algorithm-specific score thresholds and peptide confidence assignment

o   EnsembleMHC demonstrated a 3.4-fold improvement over the median precision of individual component algorithms

•   Determines allele-specific binding affinity thresholds for each algorithm at which peptides are expected to be successfully presented on the cell surface

•   EnsembleMHC allows for confidence level assignment of each peptide call made by each algorithm to allow for automated identification of high confidence MHC-I peptides

•   Reduces the number of artifacts introduced by differences in peptide isolation methods, MS acquisition and convolution of peptides in multiallelic cell lines

•   Minimizes bias toward protein expression

•   Identifies peptides based on MHC allele and algorithm-specific binding affinity thresholds to address inter-allele variation

For more information about this opportunity, please see

Wilson et al - MedRxiv - 2020

For more information about the inventor(s) and their research, please see

Dr. Anderson's departmental webpage