Docket #: S21-090

Rapid Identification of Peptide-ligands from Protein Antigen (RIPPA)

Stanford scientists have developed a novel method to accelerate the development of T cell target probes known as Rapid Identification of Peptide-ligands from Protein Antigen (RIPPA). RIPPA aims to streamline the laborious processes involved in isolating relevant peptide/MHC-II characteristics necessary for T cell epitope discovery both experimentally and computationally. The specificity of T cell responses relies on the recognition of unique peptides presented by MHC-II molecules on the surface of antigen-presenting cells. However, the heterogeneity of MHC-II alleles and labor-intensive purification process across currently employed methods, results in lengthy screening periods often ranging between 4-6 months.

RIPPA enables a much larger panel of MHC-II alleles to be screened within a short time frame and in a cost-efficient manner. By genetically modifying an array of yeast cell clones to express a specific MHC-II allele in their native-like format, RIPPA quickly screens pathogenic peptides for their binding to tens to hundreds of MHC-II alleles over the span of a month. Characterization of relevant peptide/MHC-II characteristics will guide T cell research and therapeutic endeavors involving T cell-dependent immunity. Furthermore, RIPPA's ability to generate a vast amount of peptide/MHC-II binding data will propel computational approaches for T cell epitope discovery.

Applications

- T cell dependent therapies (e.g. vaccines and other immunotherapies)
- T cell dependent diagnostics (e.g. T cell staining)
- Structural biology research (e.g. crystallization studies)

Advantages

- Faster by eliminating lengthy repeated steps
- Cheaper by eliminating costly labor-intensive steps
- Larger data generation capability

Patents

- Published Application: 20220381793

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