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Immunotherapy and Vaccine Development by DNA Sequencing

Scientists in Dr. Howard Chang's lab have developed ESCAPE-seq (Enhanced Single Chain Antigen Presentation sequencing) to identify novel neoantigen sequences for the development of immunotherapies.

A critical bottleneck in the development of effective immunotherapies is the identification of novel and physiologically relevant peptides across multiple HLA subtypes that are on antigen presenting cells. Previous methods have used mass spectrometry to identify peptides which has a high cost, requires specialized equipment, and biases the self-proteome masking clinically relevant targets. DNA oligo synthesis-based antigen profiling has allowed a higher throughput and cost-effective method in the identification of neoantigens for immunotherapies. Stanford scientists have advanced this method further by developing ESCAPE-seq which has a higher sensitivity as well as having the ability to assess various HLA subtypes. This surpasses other methods which are limited to one or two HLA variants and are prone to false negatives.

ESCAPE-seq is a cell-based assay that utilizes a modular single chain construct that allows for the combinatorial construction of peptides and HLA subtypes for screening through deep DNA sequencing. This approach can readout tens of thousands of combinations at once and provides a highly useful platform for the development of vaccines and immunotherapies.

Stage of Development
Pre-clinical

Applications

- Immunotherapy development
- Vaccine development

- CAR-T cell therapy
- TCR-T cell therapy
- T- cell engager development
- Antibody generation

Advantages

- Cost effective
- High throughput
- Combinatorial
- Multiple HLA subtype applicable

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