

**Docket #:** S23-312

# **Methods for Ultra-High-Throughput Profiling of Nucleic Acid Binding or Modifying Proteins**

Researchers at Stanford have developed a novel method for the mapping of nucleic acid binding or modifying proteins in a massively multiplexed manner.

Next generation sequencing (NGS) has allowed for sequence-agnostic sequencing and has revolutionized every area of biomedical science. One application of NGS is assaying the nucleic acid binding or modifying for a single protein interacting with thousands to millions of sequences simultaneously. However, increasing the number of proteins assayed has been difficult, costly, and labor-intensive. In another vein, microfluidics platforms have allowed for the parallel assessment of binding affinities of a several sequences with hundreds of transcription factors (TFs). Microfluidic technology has not yet been leveraged to assay the binding of many TFs to many sequences in parallel.

## **Stage of Development**

Research - in vivo

## **Stage of Research**

The inventors have developed a novel approach to assay many sequences and many proteins binding affinity at the same time. Specifically, they use a barcode and print approach that links particular members of pooled sequenced libraries to specific protein variants that interact with the particular library members. Briefly, a barcoded library of sequences and a library of proteins that are imprinted at discrete locations to provide a barcode of sorts for the protein variant are created and pooled. These libraries are then put through a microfluidic device separately such that each microfluidic droplet contains one protein variant and one sequence. These are then incubated with a capture agent that binds to variant proteins and the captured sequences bound to the variant proteins are sequenced. This allows for the

assessment of many different protein-sequence binding partners in a single assay.

## **Applications**

- High throughput assessment of many different protein-sequence interactions in the same assay.

## **Advantages**

- Can produce measurements of 100,000+ protein-sequence interactions in a single day.
- Reduces costs associated with performing many assays vs one assay with the proposed method.

## **Patents**

- Published Application: [WO2025137217](#)

## **Innovators**

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