Technology Overview

To combat spread of viruses such as CoV and HIV, it is necessary to design therapeutic antibodies that specifically stop the entry of the virus into a cell. One critical method is the identification of amino acids involved in the interaction between a viral protein and the respective antibody. Dr. Overbaugh has developed a technology that maps protein residues using a combination of deep mutation scanning (DMS) and high throughput screening. This method, known as Phage-DMS, replaces each amino acid of a given protein with all other possible amino acids, thus determining the effects of each substitution. This technology rapidly facilitates mapping of antibody epitopes and identifies optimal protein binding with the candidate molecule.

Applications

- Tests efficacy of antibody binding to viral surface proteins
- Identifies mutations impacting protein and binding molecule interactions
- Identifies antibody epitopes responsible for antibody resistance, defines residues [e.g., ligands] and designated targets [e.g., HIV, CoV]
- Can be applied to bacterial, fungal proteins, and cancer antigens

Advantages

- Does not rely on molecular barcodes to tag peptides, functional assays to determine protein interactions, and works using small amounts of virus
- Utilizes bacteriophage to generate libraries, reducing immunogenicity and is optimal for scalability

Market Overview

By 2027, the global next-generation sequencing market is predicted to be worth USD 23.7 billion, with a compound annual growth rate (CAGR) of 11.7%. Particular advantages offered by high throughput sequencing compared to other genetic technologies drive growth in this market. Increasing availability of low input DNA sampling methods should decrease overall operational costs and accelerate use of sequencing across various research and clinical applications by 2027.