

Combinatorial Barcoding for Protein Identification

This technology is a novel method for protein identification using combinatorial barcoding, offering a unique approach to analyze complex mixtures of proteins.

What is the Problem?

Proteins play a crucial role in various biological processes and each cell contains thousands of distinct proteins, varying in abundance. Existing methods to identify proteins, like mass spectrometry and peptide sequencing, have limitations such as the need for large protein amounts and inability to detect low-abundance proteins. Reliable protein identification is crucial for understanding cell state, antibody discovery, and protein engineering.

What is the Solution?

The technology offers a unique method for protein identification through combinatorial barcoding. This method involves attaching nucleic acid molecules to target amino acid residues in proteins, performing rounds of split-pool barcoding, sequencing the mature nucleic acid tags, and determining the frequency of the target amino acid residues. This approach allows for the assessment and identification of proteins in complex mixtures quickly and with widely available reagents and instruments.

What is the Competitive Advantage?

- Efficiency: The method allows for the rapid identification of proteins in complex mixtures.
- Cost-effective: The technology utilizes inexpensive and widely available reagents and instruments.
- Versatility: The method can be applied to a wide range of biological samples.
- High-Throughput: This approach is massively parallel, enabling high-throughput, multiplexed assays.
- Innovation: This approach uses next-generation sequencing of DNA barcodes to solve the difficult problem of protein identification.

Patent Information:

[US20240044908A1](#)

Technology ID

BDP 8390

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