Most research in the life sciences requires protein based assays, underscoring the importance of characterizing protein modifications and protein interactions. Unfortunately, currently available technologies are cumbersome, expensive, and sometimes impractical. This technology offers an alternative option for scientists to study proteins. Using a high throughput approach, the proposed method would enable researchers to identify unknown proteins using fluorescent dyes. Additionally, this technology has the potential to identify protein modifications and interactions, providing a wealth of information critical for scientific research.

Identification of proteins, their modifications, and their interactions is critical in biological research, yet, few options are available to researchers. There are currently two main approaches: (1) high sensitivity methods that require a priori knowledge of the protein, and (2) low sensitivity methods that require mass spectrometry. Unfortunately, both methods are expensive and time consuming, indicating a clear need for alternative approaches. This technology uses enzymes to break down peptide bonds and fluorescent dyes to label specific amino acids that are subsequently detected by their fluorescent intensity. An amino acid sequence can then be generated and compared to protein databases to identify the unknown protein. Consequently, this proposed method is affordable and reproducible, making it an ideal tool for research.

A simulation of the technology has been tested and successfully identified up to 90% of proteins coded for in the human genome.

**Lead Inventor:**

Peter A. Sims, Ph.D.
Applications:

- Protein identification
- Protein modification identification
- Proteomics: analyzing differences in proteomic changes in disease states
- Protein-protein interaction identification

Advantages:

- Does not require a priori knowledge of the protein in question
- Higher sensitivity than mass spectrometry
- High throughput approach, increasing speed and readout

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