



Key Investigator

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Field

- Structural biology
- Pharmaceutical research
- Biotechnology
- Drug development

Technology

- Protein folding
- In-cell footprinting
- Protein conformation

Advantages

- High temporal and molecular resolution
- Real-time analysis of protein folding
- Study of proteins in native cellular environments

Status

Available for licensing

Patent Status

PCT/US2019/024691 Patent

UMB Docket Reference

LJ-2018-104

External Reference

Grand View Research,
[Proteomics Market Size, Growth & Trends Report, 2022-2030](#)
(grandviewresearch.com)
MIT Technology Review,
[DeepMind's protein-folding AI has solved a 50-year-old grand challenge of biology | MIT Technology Review](#)
Coherent Market Insights,
[Protein Stability Analysis Market Size & Share Analysis - Industry Research Report - Growth Trends](#)
(coherentmarketinsights.com)

Device and Method for Measuring In-Cell Protein Folding

Summary

The 'Device and Method for Measuring In-Cell Protein Folding' introduces the pcIC-FPOP technique, a novel method combining pulse-chase experiments with in-cell protein footprinting and mass spectrometry. This innovation provides high-resolution, real-time insights into protein folding within the cellular environment, addressing critical needs in various scientific fields.

Market

The patent for measuring in-cell protein folding using the pcIC-FPOP method has broad commercial potential across several fields. This technology is particularly relevant for structural biology, biophysics, molecular biology, pharmaceutical research, biotechnology, drug development, and personalized medicine. Its ability to provide high-resolution, real-time insights into protein folding pathways within the native cellular environment addresses critical needs in these areas.

The proteomics market, valued at USD 22.30 billion in 2021, is projected to reach USD 70.56 billion by 2030, driven by demand for personalized medicine, advancements in mass spectrometry, and rising chronic diseases. A shift towards automation and miniaturization in protein analysis workflows enhances efficiency and reduces costs. Traditional protein analysis methods are often slow, creating demand for efficient techniques like pcIC-FPOP that provide real-time insights into complex protein-protein interactions and folding pathways.

Technology

The patent describes a novel method for studying protein folding in the native cellular environment. This innovation, referred to as pulse-chase in-cell fast photochemical oxidation of proteins (pcIC-FPOP), integrates pulse-chase experiments with in-cell protein footprinting and mass spectrometry. This combination allows for high-resolution analysis of protein folding and mis-folding pathways, offering a significant advancement over existing techniques.

The pcIC-FPOP method uses a multi-well plate housed within an incubator, where cells expressing the protein of interest undergo a carefully timed pulse-chase treatment. This process involves perfusing the cells with both labeled and unlabeled media, followed by treatment with hydrogen peroxide, irradiation with a laser to generate hydroxyl radicals, and quenching the reaction. The resulting protein modifications are then analyzed using mass spectrometry. This sequence allows for the capture of detailed information on protein folding at various stages, filling gaps in the understanding of protein folding mechanisms and their implications for diseases.

A key aspect of this technology is its ability to provide high temporal and molecular resolution. The method can probe protein folding intermediates and interactions with chaperones, which are essential for understanding the folding pathways that determine protein function and stability. Unlike traditional methods, which often rely on isolated proteins in artificial environments, pcIC-FPOP enables the study of protein folding within the native cellular context. This is crucial for obtaining accurate insights into how proteins behave in their natural state, influenced by the complex milieu of cellular components and conditions.