Combined targeted and untargeted proteomics

A method to conduct simultaneous targeted and unbiased mass spectrometry-based proteomics in a sample-sparring manner.

IP Status: PCT Pending; Application number PCT/US2024/020194

Applications

- Proteomics
- Drug Discovery
- Drug Screening
- Single-cell profiling and diagnostics

Technology Overview

Researchers at the University of Minnesota have developed a method for simultaneous targeted and untargeted mass spectrometry-based proteomics. This method allows for broadly analyzing a sample of interest without a priori knowledge while allowing the targeting of a specific peptide of interest. In situations where samples are limited, such as single-cell experiments, this approach maximizes the depth of information that can be gathered. This process has been successfully implemented using pre-clinical data for the targeting of the androgen receptor (AR), a clinically relevant protein of interest normally below the detection threshold, while simultaneously still allowing for unbiased discovery that resulted in the identification of another clinically relevant protein of interest (CD326) that was not actively targeted.

Phase of Development

TRL: 5-6
The process has been successfully implemented using pre-clinical data for the targeting of the androgen receptor (AR), while identifying another, non-targeted, clinically relevant protein of interest (CD326).

Desired Partnerships

This technology is now available for:
- License
- Sponsored research
- Co-development

Please contact our office to share your business' needs and learn more.

Researchers

- **Justin Drake** Professor, Department of Pharmacology

References

Technology ID

2023-221

Category

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1. Zoi E. Sychev, Abderrahman Day, Hannah E. Bergom, Gabrianne Larson, Atef Ali, Megan Ludwig, Ella Boytim, Ilsa Coleman, Eva Corey, Stephen R. Plymate, Peter S. Nelson, Justin H. Hwang, Justin M. Drake(2024) , https://aacrjournals.org/mcr/article/22/5/452/743198/Unraveling-the-Global-Proteome-and-Phosphoproteome, Molecular Cancer Research, 22, 452–464