BPS2026

FEBRUARY 21–25, 2026 | SAN FRANCISCO, CALIFORNIA

Esplanade Room 157: Monday, February 23

3:30 PM – 5:00 PM
Nuclera

Unlocking the Proteome: Automated Cell-Free Expression for Structural Biology and High-Throughput PPI Validation

Protein production remains a critical bottleneck for structural analysis and interaction studies. In this two-part presentation, we introduce an automated, cell-free workflow that transforms this manual obstacle into a programmable design space.

First, Kristin Mars (Nuclera) will introduce eProtein Discovery™, a system combining cell-free protein synthesis (CFPS) and digital microfluidics. She will demonstrate how the system accelerates hit validation for difficult soluble and membrane targets, highlighting the multiplexed screening of constructs and expression conditions to generate active protein. Specifically, she will highlight workflows for the co-translational insertion of GPCRs and transporters into nanodiscs, showing how the automated screening of lipids and membrane scaffold proteins (MSPs) pinpoints conditions that yield active, homogenous receptor.

Building on this, Prof. Kliment Verba (UCSF) will discuss applying this multiplexing capability to interaction proteomics. While mass spectrometry routinely identifies protein-protein interactions (PPIs), validation is laborious. Prof. Verba will present workflows for parallel expression and co-IP analysis to rapidly map interacting motifs on intrinsically disordered proteins and validate MS-generated networks, automating the pipeline from sequence to biochemical insight.

Speakers

Kristin Mars, Key Account Manager (West Coast) in BD and Sales, Nuclera
Kliment Verba, Assistant Professor, Department of Cellular and Molecular Pharmacology, University of California, San Francisco