Protein Production and Purification Partnership in Europe

Presentations by the Sponsors

P 2.
Protein production optimization proteins in cell lysate
Zhang, Ping - Nanotemper

NanoTemper Technologies offers a portfolio of technologies for protein characterization, that allow researchers to unlock the secrets of biomolecular interactions and protein stability. Protein production optimization is critical for drug development, whether you're looking to express antigens or drug targets, or produce proteins being used as therapeutics. High-yield production schemes that provide well-folded, active protein are critical for downstream success and efficiency.
The new Andromeda enables scientist to quickly screen for optimal expression levels and thermal stability for membrane proteins, and thereby select the best expression conditions. Follow the unfolding of your protein using a thermal ramp to check whether it is folded or stable, and test for functionality with in-lysate thermal shift assays and see how changes in your expression strategy impact protein yield. In this presentation you will get insights into the principle of the technology, and how it can be used within your production workflow, including application examples. We will also briefly cover the basic principles of our additional technologies, for the analysis of protein binding, and protein stability and aggregation.

P 5.
FIDA Technology: How to assess kinetics and sample quality directly in solution? Functional validation also in unpurified samples.
Presenter: Marion Albasini

FIDA (Flow Induced Dispersion Analysis) technology by Fidabio offers a modern approach for analyzing protein interactions in solution, crucial for protein production and purification. By measuring hydrodynamic radius changes using principles of laminar flow and Taylor dispersion, FIDA accurately determines binding kinetics (Kd, Kon, Koff). This in-solution technique prevents non-specific binding and denaturation, accommodating various pH levels, ionic strengths, and crude matrices. FIDA's high sensitivity detects minor size changes, facilitating the analysis of both strong and weak binders. Its rapid assays and minimal sample requirements enhance efficiency, making it indispensable for kinetic studies in protein research

P 6.

Advancing Biomolecular Interaction Analysis with GatorBio Biolayer Interferometry Technology

J. Schoorl[1], B. Osborn[2], H. Li[2]

1. I&L Biosystems, Waalwijk, Netherlands
2. Gator Bio, Palo Alto, United States

Presenting author: Jeroen Schoorl

Biolayer Interferometry (BLI) has evolved as an essential technique for understanding biomolecular dynamics and interactions with high sensitivity and real-time kinetics. The new GatorBio BLI technology builds upon this foundation, offering a significant advancement in this domain, offering unprecedented precision, versatility, and efficiency.

During this presentation will address the core principles and unique capabilities of the GatorBio BLI platform. We will delve into the multiple applications of this technology, spanning from Gene therapy, AAV, Nanoparticles, Small molecule characterization, Protein-Protein interactions, Epitope mapping, and more. Furthermore, we will explore recent innovations of the GatorBio BLI platform.

P 7.

The eProtein Discovery System™

Chiara Gandini, Shay Urban, Aujan Mehregan, and Vaishnavi Manoharan-Jayarajah-Nuclera

Proteins are often the cornerstone and starting point of biological research. However, obtaining the proteins of interest takes up to 6 months, many trials and failures. What if there was an easier way? Nuclera has developed the eProtein Discovery™ system, a “pipette and forget” benchtop device with the footprint of a PCR machine, that harnesses the potential of digital microfluidics and cell-free systems to enable you to go confidently from DNA to soluble, purifiable proteins in 48 hours. The presentation will include:

- How can eProtein Discovery™ help streamline your protein research?
- Description of the technologies behind eProtein Discovery™
- Case studies of challenging proteins obtained using eProtein Discovery™
- Future capabilities

P 11.

Enhance proteomics with next generation protein sequencing technology from Quantum-Si

Richard Broadhead - Quantum-Si

Quantum-Si's novel next generation protein sequencing technology allows characterisation of proteins quickly and accurately with a simple, benchtop workflow that makes proteomic data interpretation and discovery accessible. Offering single amino acid resolution through a direct protein detection method, the technique brings capabilities such as proteoform identification, antibody characterisation, discrimination of single amino acid substitutions and novel peptide barcoding based analyses within the reach of every lab.

P 13.

Revolutionizing Transient Expression with TurboCHO™: A New Era of Protein and Antibody Production

Dr. Shuting Xu - Genscript

Chinese Hamster Ovary (CHO) cell lines are widely used for the production of recombinant proteins and antibodies. At GenScript, based on our almost 20 years' experience of protein service, we have developed a revolutionary protein expression system, TurboCHO™, which boosts a significant increase in yield and a shorter production time. This makes it an excellent addition to current drug discovery and pre-evaluation pipelines. With the TurboCHO™ system, we have successfully delivered over 4,000 projects, including a wide range of antibody types, such as standard IgGs, Fab, scFv, VHH, and bi-specific antibodies, with the required quantities, purity and within the specified timeframes. For the add-on value, GenScript provides the option for protein production in Singapore and China.

Our TurboCHO™ High Throughput (HT) platform has a large capacity and can deliver purified antibodies (>90%) starting from eight business days with yield up to 1g/L. For difficult bispecific antibody and antibody fragment targets, with the joined effort of our excellent scientist team, our TurboCHO™ platform also provides a better solution by improving expression levels and purification strategies.

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