

Are Your High Throughput Expression Options Limited by Downstream Processing?

Effective techniques for micro-volume sample preparation and subsequent protein analysis following high-throughput protein expression that provide truly high-performance are seemingly elusive. What are the most effective strategies and technologies available to increase throughput, improve product and data quality, and that will unblock the sample preparation and analysis bottlenecks, opening up new avenues for efficiency?

High-Throughput Protein Expression

- Downstream success is driven by the quality of protein preparation and analysis
 - Prep Purity
 - Yield
 - Molecular Weight
 - Concentration
- Must have efficient process to monitor both expression *and* purification success

Clear Declarations of Need

Example 1: HT prescreening in structural biology

Many experiments performed for different constructs, expression conditions, etc.

Critical stage is HT purification – this step must generate the highest possible protein concentration since this drives final success.

- When applying high-throughput purification, “...A final factor to consider, once purified proteins are obtained, is that protein samples for structural studies must be of fairly high concentration.”
 - RC Stevens, Scripps Research Institute

Must have HT means of determining the success of purification and enrichment.

Clear Declarations of Need

Example 2: HT functional studies

Objective is to perform large numbers of functional assays at very small scales, requiring initial isolation of the individual proteins

As separation tools have become smaller, their overall performance has become poorer

- “...applications such as protein microarrays, multi-well solution biochemistry and the isolation of protein complexes for analysis by mass spectrometry would all benefit from improved methods for protein isolation.”
 - P. Braun & J. LaBaer, Harvard Institute of Proteomics

As before, must have HT means for determining success.