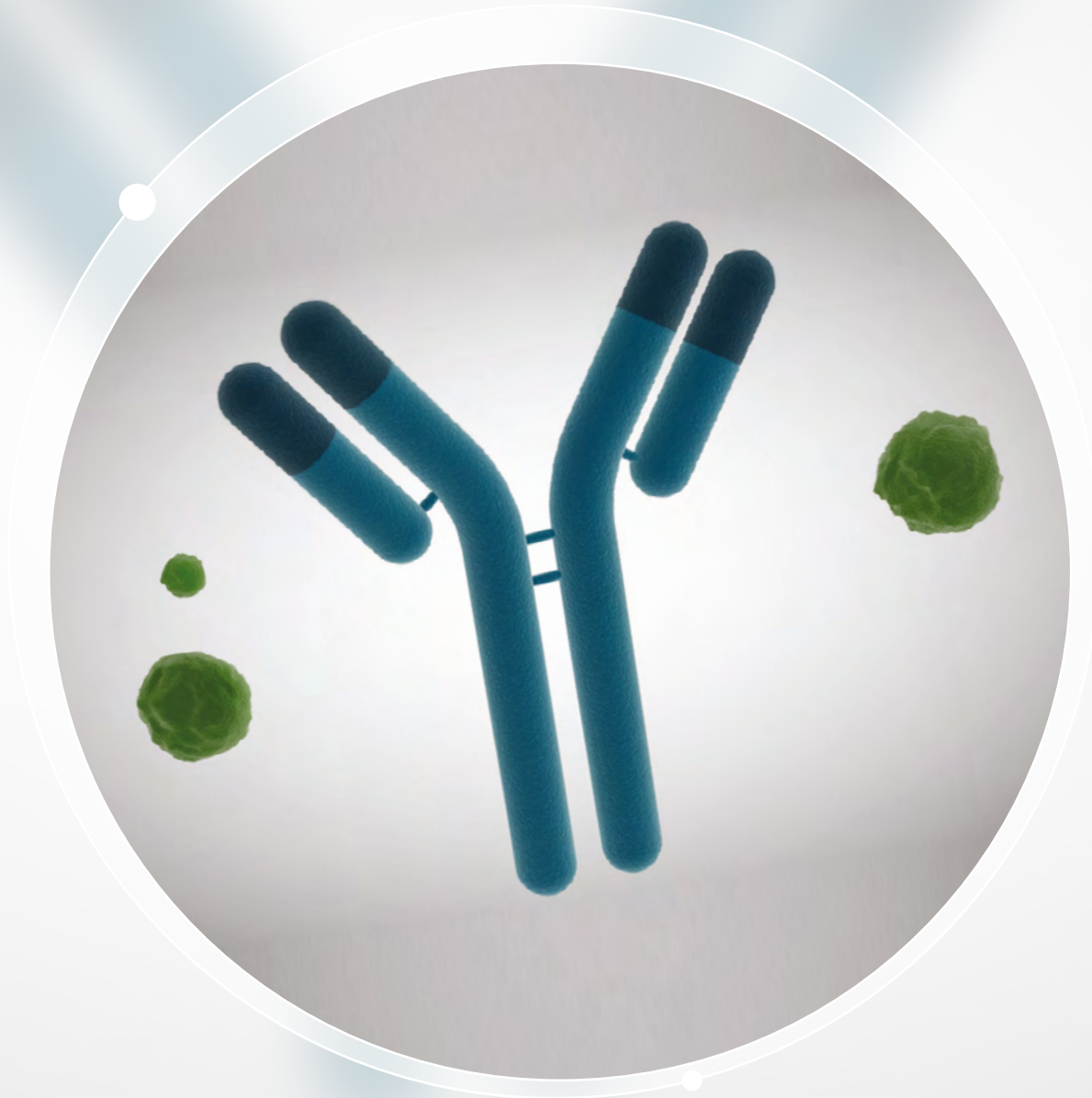


Host Cell Protein Knowledge Accelerator

Go Beyond ELISA and Learn What SWATH® LC-MS
Can do for Your Host Cell Protein Analysis



Unbeatable Sensitivity with Unbiased Host Cell Protein Detection



Host cell proteins (HCPs) can adversely affect drug safety, making it critical that these HCP contaminants can be accurately detected and identified during biotherapeutic development.

LC-MS/MS not only enables you to fully detect and characterize HCPs in a biologic preparation. Unlike polyclonal ELISA-based methods which only provide a total HCP level, the SCIEX SWATH-based method provides estimates of individual HCP quantities. SWATH® Acquisition provides unbiased sampling for detection of low-level HCPs – even those that were previously unknown.

Resources



High Sensitivity Host Protein Quantitation in an IgG1 Monoclonal Antibody Preparation via Data-Independent Acquisition

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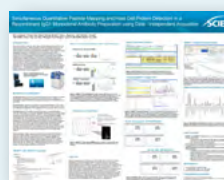
MS/MS^{ALL} with SWATH® Acquisition

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The Optimization of Host-Cell Protein Detection Using Data Independent SWATH MS

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Simultaneous Quantitative Peptide Mapping and Host Cell Protein Detection in a Recombinant IgG1 Monoclonal Antibody Preparation using Data-Independent Acquisition

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Dr. Thomas Kofoed

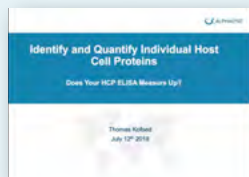
CEO, Alphalyse



“Mass spec is going to be the gold-standard for HCP analysis, as it provides more detailed information about individual HCPs compared to ELISA assays. Adding SWATH Acquisition for unbiased identification and quantification of proteins leads to high reproducibility and sensitivity. With this solution, standardization of the methods to any given set of biotherapeutic samples becomes possible, providing us with a huge advantage.”

[Read the full Customer Profile](#)

Webinars



Identify and Quantify Individual Host Cell Proteins – Does Your HCP ELISA Measure Up?

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SWATH-MS HCPs Profiling and Absolute Quantification of Key Impurities

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Single Digit PPM Level Identification of Host Cell Protein Contaminants Using a Simple One Hour SWATH Acquisition Method

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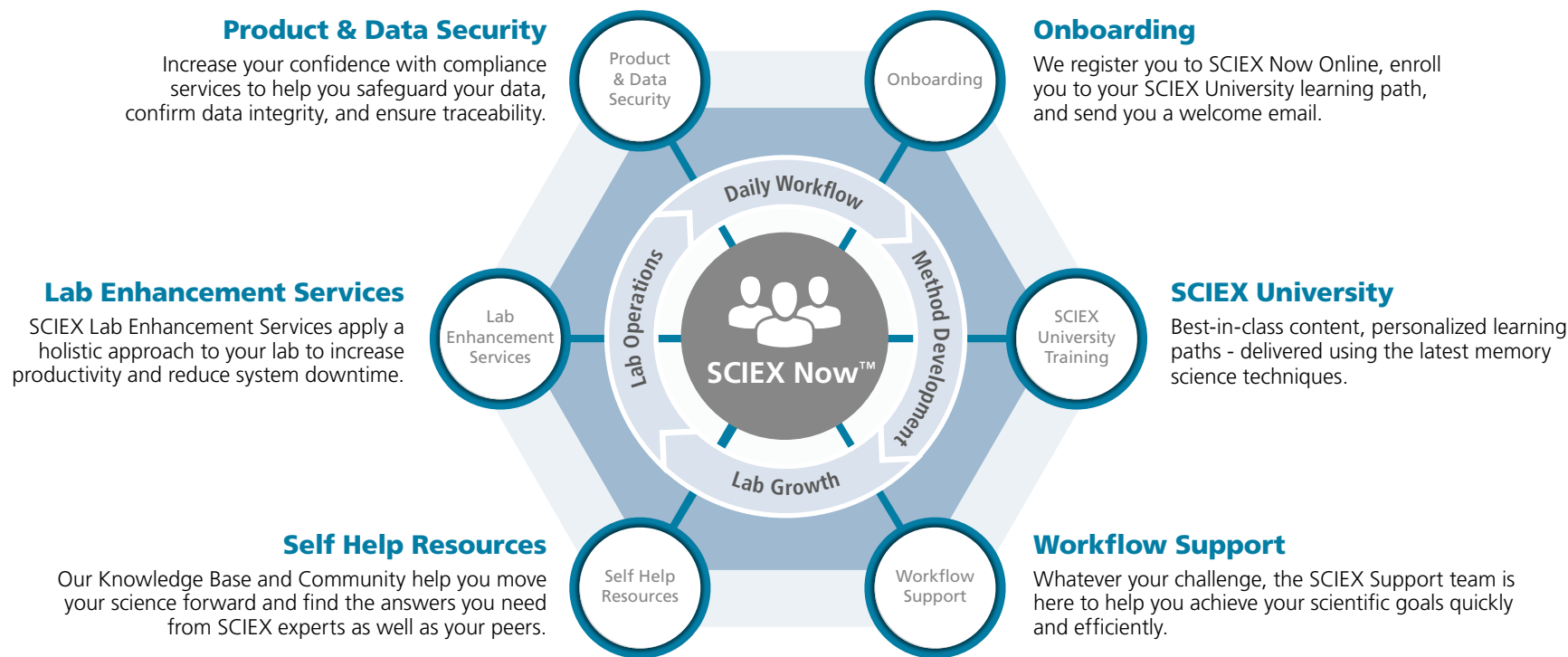


Characterization of Host-Cell Proteins Using Mass Spectrometry Enables Effective Purification Optimization

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