



Antibody validation with immunoprecipitation/mass spectrometry and orthogonal methods



Speaker: John Rogers, PhD, Thermo Fisher Scientific

Biography: John is a Senior R&D Manager at Thermo Scientific where he manages the development of new reagents and kits for protein mass spectrometry research. John has an undergraduate degree in Biochemistry and Computer Science, and a PhD in Pharmacology from the University of Washington. John managed a bioinformatics group at Pfizer and a proteomics group at Abbott before joining Thermo Fisher Scientific in 2007. Since that time, John has led the development of new MS standards and calibrants, protein sample preparation reagents, and reagents for quantitative proteomic analysis, including Tandem Mass Tag reagents.

Abstract

Antibodies are used in a broad range of research and diagnostic applications for the enrichment, detection, and quantitation of proteins and their modifications. Hundreds of thousands of antibodies are commercially available against thousands of proteins and their modifications. Unfortunately, many antibodies are poorly characterized, resulting in wasted time and cost as well as potentially flawed research conclusions. To verify the performance and specificity of Thermo Scientific antibodies, we have created a comprehensive workflow to assess antibody specificity using immunoprecipitation (immunocapture) combined with mass spectrometry (IP-MS). This strategy includes the selection of protein targets, antibody candidates, and cell models, as well as the characterization of cell models by LC-MS, IP-MS sample preparation and analysis, and bioinformatic analysis. In this webinar we will highlight new data demonstrating the power of this new workflow.