

Robert Chalkey, PhD: Robert's research interests are in the analysis of challenging protein post-translational modifications using mass spectrometry. In addition to method improvement he also manages the development of the Protein Prospector suite of proteomic tools. He was one of the first to characterize O-GlcNAcylation using mass spectrometry, and has published on a wide variety of modifications from methylation to sulfation. His more recent emphasis has been on the analysis of intact glycopeptides, and also cross-linked peptide analysis. He helped develop an effective lectin-based enrichment protocol for glycopeptides and has adapted Protein Prospector to be able to analyze the resulting data, which has resulted in many of the largest glycopeptide datasets to date. He has made Protein Prospector one of the leading software tools for cross-linked peptide analysis, and has helped teach a US HUPO short course on cross-linking for the last five years. Robert also has a heavy focus on community proteomic data analysis performance and reliability, having managed several studies while chairing the proteome informatics research group of ABRF, and also being a driving force behind journal proteomic publication guidelines.