

Webinar:

Harnessing the power of TMT11plex sample multiplexing and improved phosphopeptide enrichment to gain new insights into signaling pathways

CONTINUING EDUCATION (CME/CE/CEU) CREDITS: P.A.C.E. CE | Florida CE



Speaker: Ryan Bomgarden, Ph.D. Senior R & D Staff Scientist, Protein and Cell Analysis Thermo Fisher Scientific

Biography: Ryan Bomgarden received his bachelor's degree from Coe College with majors in chemistry and molecular biology. He received his Ph.D. at Stanford University under Dr. Karlene Cimprich where he worked on biochemical characterization of the checkpoint kinase ATR DNA binding activity and signaling in UV-sensitive human cell lines. Since joining Thermo Fisher Scientific in protein biology R & D, he has worked on the development of key protein research reagents including photo-reactive crosslinkers, SILAC metabolic labeling kits and subcellular protein fractionation kits. Currently Dr. Bomgarden is in the mass spectrometry R & D group where his development work includes tandem Mass Tag reagents for relative quantitation of proteomic samples, HeLa protein digest standards for LC-MS QC, MS-cleaveable crosslinkers for protein structure analysis, heavy protein IVT kits for production of stable isotope-labeled proteins; and Thermo Scientific[™] ActivX[™] probes for kinase, GTPase and serine hydrolase inhibitor profiling and detection. In addition to his work at Thermo Fisher Scientific, Dr. Bomgarden is also an adjunct professor at the University of Illinois College of Medicine where he teaches courses on biochemical techniques, drug design and ethics. Dr. Bomgarden is also heavily involved in STEM education, creating and performing science demonstrations for local schools and nonprofit organizations.

Abstract:

Mass spectrometry (MS) has become the predominant technology to analyze proteins due to its ability to identify and characterize proteins and their modifications with high sensitivity and selectivity. Increasing the number of samples analyzed simultaneously in a single mass

spectrometry experiment is essential for increased sample throughput, fewer missing measurements between samples, and increased statistical power among replicates. Thermo Scientific™ Tandem Mass Tag TMT Reagents are one technology which enables concurrent identification and multiplexed quantitation of different samples using tandem mass spectrometry. Recently, we have extended the multiplexing capabilities of TMT Reagents from 6 to 11 without an increase in the tag size or structure by utilizing the mass difference between 13C and 15N isotopes in the reporter region. We have also developed new phosphopeptide enrichment workflows with improved phosphopeptide yield, selectivity and identification rates. Overall, these additions to the TMT workflow enable higher sample multiplexing and provide in depth quantification of protein post-translational modifications.

Learning objectives — in this webinar you will learn the following information:

- Understand the basics of how tandem mass tags can be used for protein multiplexing.
- Discuss how the multiplexing capabilities of TMT Reagents were extended from 6 to 11 without an increase in the tag size or structure.
- Identify the differences between Fe-NTA and TiO2 and how to use sequentially for maximum phosphopeptide enrichment.

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