

SPECIAL ANALYTICAL SEMINAR

Thursday, March 12, 2015
12:15 p.m. in Room 1315

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“One-hour Proteomes”

For the past decade considerable effort has been invested in maturing proteomic technology to deliver information at a rate and cost commensurate to transcriptomic technologies, transforming the scope and impact of protein characterization efforts. Recently, we described the comprehensive analysis of the *saccharomyces cerevisiae* proteome (~4,000 proteins) in just over an hour of instrument analysis time. Across a 70-minute chromatographic method, we collected an average of 13,447 MS¹ and 80,460 MS² scans per run to produce 43,400 peptide spectral matches and 34,255 peptides with unique amino acid sequences. These experiments delivered an extraordinary 67 proteins per minute and demonstrate that complete analysis of the yeast proteome can be routinely performed in approximately one hour. We are applying this approach to the quantitative interrogation of over 1,000 yeast proteomes.