

**Promega Lunchtime Seminar**

Tuesday, March 9, 12:15 – 1:30 pm

Colorado G-H (Lower Level 2), Marriott City Center Hotel

**RSVP** by sending email to [linda.link@promega.com](mailto:linda.link@promega.com).

**Improving Protein Identification and Characterization  
Through More Efficient Protease Digestion**

**Presenters**

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Dan Simpson, Ph.D., Group Leader, Research & Development, Promega Corporation

Mass spectrometry has become a standard method for the identification, quantification and characterization of proteins present over a wide dynamic range in complex biological matrices. To this end in practice proteins are most often digested into peptides, measured by mass spectrometry and matched to known sequences through algorithm-based searching. While instrumentation and bioinformatics ultimately determine the depth of complexity in which a sample can be measured, efficient digestion and high quality proteases are necessary to produce an experimental data set that will maximize the potential for correct identification and characterization. In this presentation we will discuss several parameters from “the biological side” of protein analysis to help get the most out of protein identification and characterization experiments. Our focus will be on the complimentary use of proteases, new alternative surfactants and conditions for their use with considerations specifically for in-gel and in-solution digestion.