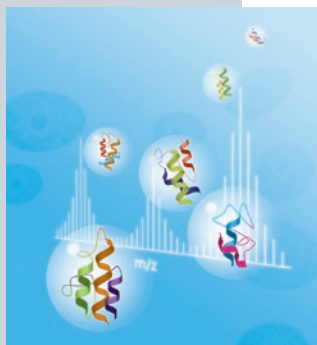


Focus on mass spectrometry in proteomics

A user's guide



Artistic interpretation of mass spectrometry-based proteomics by Erin Boyle.

Mass spectrometry is rapidly maturing as a powerful tool for proteomics applications as new sample-preparation approaches, instrumentation developments and bioinformatics tools for analyzing data become increasingly available. No one other technology can now match both the throughput and the molecular information content that mass spectrometry provides. This is an exciting time for proteomics.

Historically, however, mass spectrometry has been a tool for chemists and is not routinely taught to biologists. In conversations with proteomics researchers, we became aware that this 'technology gap' between mass spectrometrists and the would-be end-users—cell biologists—is still fairly sizable. The idea for a focus issue on mass spectrometry grew out of these discussions, as it became clear that mass spectrometrists and cell biologists must understand each others' needs to take full advantage of the technology.

Some cell biologists have managed to successfully integrate mass spectrometry into their research, and thus provide a unique perspective on how it can and should be done (see Commentary on p. 783). Another Commentary explores both the potential of and the challenges specific to making mass spectrometry a clinical research tool (p. 785).

Applications in proteomics are as diverse as the methods themselves, and we could not hope to provide a comprehensive overview of the field in a single issue. We aimed to cover some of the best-established, state-of-the-art mass spectrometry approaches to proteomics (pp. 787, 798, 807) as well as some exciting emerging applications (pp. 817, 822, 828). We hope that these pieces will help cell biologists understand both the power of the technology but also its present limitations, so that they might engage in productive collaborations with mass spectrometrists.

Additionally, we invite you to visit our Focus website, which contains a glossary of acronyms and a collection of relevant papers published in the *Nature* titles in the past two years. We extend our sincerest thanks to our authors and referees as well as to others who helped define the scope of this special issue.

Allison Doerr

CONTENTS

- 783 The protein microscope: incorporating mass spectrometry into cell biology**
A W Bell, T Nilsson, R E Kearney & J J M Bergeron
- 785 Proteomics from the clinical perspective: many hopes and much debate**
L Beretta
- 787 Analysis and validation of proteomic data generated by tandem mass spectrometry**
A I Nesvizhskii, O Vitek & R Aebersold
- 798 Mapping protein post-translational modifications with mass spectrometry**
E S Witze, W M Old, K A Resing & N G Ahn
- 807 Mass spectrometry-based functional proteomics: from molecular machines to protein networks**
T Köcher & G Superti-Furga
- 817 Decoding protein modifications using top-down mass spectrometry**
N Siuti & N L Kelleher
- 822 Activity-based protein profiling for the functional annotation of enzymes**
K T Barglow & B F Cravatt
- 828 MALDI imaging mass spectrometry: molecular snapshots of biochemical systems**
D S Cornett, M L Reyzer, P Chaurand & R M Caprioli

Editor, *Nature Methods*
Veronique Kiermer

Focus Editor Allison Doerr

Design Erin Boyle

Senior Copy Editor Irene Kaganman

Copy Editor Anita Gould

Marketing Amy Maurer,
Eric Claiborne

Senior Production Editor

Ingrid McNamara

Production Editors Brandy Moyer,
Amy Silver