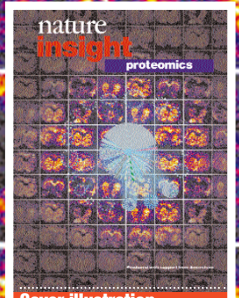
nature insight proteomics



Cover illustration
Interactions among proteins encoded by the yeast genome (Tyers and Mann, this issue), set against a background of mass profiles of transverse sections of rat brain showing different protein signals (courtesy of S. Hanash).

We are only just beginning to appreciate the power and limitations of the genomics revolution, yet hard on its heels proteomics promises an even more radical transformation of biological and medical research. Encoded proteins carry out most biological functions, and to understand how cells work, one must study what proteins are present, how they interact with each other and what they do.

The term proteome defines the entire protein complement in a given cell, tissue or organism. In its wider sense, proteomics research also assesses protein activities, modifications and localization, and interactions of proteins in complexes. It is very much a technology-driven enterprise, and this collection of reviews reflects the progress made and future developments needed to identify proteins and protein complexes in biological samples comprehensively and quantitatively with both high sensitivity and fidelity.

By studying global patterns of protein content and activity and how these change during development or in response to disease, proteomics research is poised to boost our understanding of systems-level cellular behaviour. Clinical research also hopes to benefit from proteomics by both the identification of new drug targets and the development of new diagnostic markers.

Like genomics, the sheer scale of proteomics research makes it a community effort with the Human Proteome Organisation (HUPO) playing an important role in coordinating proteomics projects worldwide. The wealth of information produced poses challenges for data management, and necessitates publicly accessible databases that use agreed standards to describe protein data, allowing data comparison and integration. Furthermore, the expense and scale of proteomics technologies restricts their access, and solutions must be found that allow the widespread use of proteomics tools. In this spirit, in a commentary published in today's issue of *Nature* (**422,** 115–116; 2003), Ruedi Aebersold proposes a community-wide strategy that could help shift proteomics research towards a 'browsing mode' of searching through existing information.

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Barbara Marte **Senior Editor**