Advancing Cell Biology Through Proteomics in Space and Time (PROSPECTS)*

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The term "proteomics" encompasses the large-scale detection and analysis of proteins and their post-translational modifications. Driven by major improvements in mass spectrometric instrumentation, methodology, and data analysis, the proteomics field has burgeoned in recent years. It now provides a range of sensitive and quantitative approaches for measuring protein structures and dynamics that promise to revolutionize our understanding of cell biology and molecular mechanisms in both human cells and model organisms. The Proteomics Specification in Time and Space (PROSPECTS) Network is a unique EU-funded project that brings together leading European research groups, spanning from instrumentation to biomedicine, in a collaborative five year initiative to develop new methods and applications for the functional analysis of cellular proteins. This special issue of Molecular and Cellular Proteomics presents 16 research papers reporting major recent progress by the PROSPECTS groups, including improvements to the resolution and sensitivity of the Orbitrap family of mass spectrometers, systematic detection of proteins using highly characterized antibody

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Received February 3, 2012, and in revised form, February 6, 2012 Published, MCP Papers in Press, February 6, 2012, DOI 10.1074/mcp.0112.017731 collections, and new methods for absolute as well as relative quantification of protein levels. Manuscripts in this issue exemplify approaches for performing quantitative measurements of cell proteomes and for studying their dynamic responses to perturbation, both during normal cellular responses and in disease mechanisms. Here we present a perspective on how the proteomics field is moving beyond simply identifying proteins with high sensitivity toward providing a powerful and versatile set of assay systems for characterizing proteome dynamics and thereby creating a new "third generation" proteomics strategy that offers an indispensible tool for cell biology and molecular medicine. Molecular & Cellular Proteomics 11: 10.1074/mcp.0112.017731, 1–12, 2012.

Within the postgenomics fields, proteomics has a privileged role because it deals directly with the analysis of proteins, which are the key functional units of the cell. Proteomics has developed from diverse roots, which have now coalesced into an "omics" field of study, characterized more by its diversity than a common methodological or subject orientation. Nevertheless, the current, general definition of proteomics views it as the large-scale study of proteins and their modifications. More ambitious definitions of proteomics also include the goal of analyzing the entire spectrum of protein functions, but this essentially overlaps with the goal of biological sciences in general. We suggest that the large-scale study of endogenous proteins, their post-translational modifications, interactions and dynamic behavior in space and time, are indeed the core subject area of proteomics.

Proteomics Specification in Time and Space (PROS-PECTS)¹ is a five year collaborative project that commenced early in 2008, funded by the Research Directorate of the European Commission under the 7th Research Framework Program. PROSPECTS is coordinated by Matthias Mann and brings together ten top proteomics research groups from around Europe, as well as a leading mass spectrometry in-

¹ The abbreviations used are: PROSPECTS Proteomics Specification in Space and Time; EM, electron microscopy; PCP-SILAC, protein correlation profiling-SILAC; PrEST, protein epitope tags; SIM, selected ion monitoring.

Prospects In Cell Biology

R Sandford

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