

MAPPING AND MEASURING PROTEOMES

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The human genome project has taught us that a complete map -in the case of the genome project the complete genomic sequence - along with computational tools to navigate the map - represent invaluable resources for experimental and theoretical biologists. A main consequence of such a complete map is that all the biological processes have to be explainable with the components that constitute the map. Proteomics, until recently, has not reached the stage that complete maps are available but the urgent need for their generation is now widely recognized.

In this presentation we will describe the first generation of complete mass spectrometric proteome reference maps, and instrumentation and methods to use the information contained in proteome maps for targeted proteomic experiments. These measurements are capable of generating complete, reproducible and quantitatively accurate datasets on differentially perturbed systems. These data are therefore ideally suited to support the generation of mathematical models in systems biology research.