

Proteomics Links Protein Chemistry to Biology

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Proteomics is an important experimental approach that provides new kinds of information in quantities that were unimaginable 10 to 15 years ago. It has been made possible by recent advances in DNA and protein sequencing, the application of mass spectrometry to biological macromolecules permitting the identification of hundreds of proteins per day and the building and maintenance of data banks. As is true for all new experimental approaches it permits one to ask questions that never have been asked before, obtain information that never was available before and it has problems that also have never arisen before. Some of these problems are technical and we can expect that solutions will be forthcoming soon. Others are conceptual and new approaches will be necessary to circumvent them. For example it is not correct to interpret an increase in the level of a protein in a cell extract as an increase in gene "expression", if the rate of degradation was not measured. When proteomics is used to compare two biological stages, increases or decreases in specific proteins cannot be interpreted to be the result of causal relationships. Thus, successful proteomic experiments do not "close" questions but rather give rise to new and different experiments which provide new kinds of data that confirm and extend the proteomic data. The considerations will be illustrated by examples of research carried out by our graduate students and with our collaborators who used the 2 DE proteomic approach to study: (1) the differentiation and maturation of human monocytes to mature dendritic cells, (2) the progression of mouse melanocytes to melanoma cells and (3) the effect of cisplatin on human melanoma cells.

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