

Towards Comprehensive Proteomic Analysis of Cells and Tissues

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A component to understanding biological processes involves identifying the proteins expressed in cells as well as their modifications. A recent approach to identifying protein mixtures is direct analysis of the proteolytically digested proteins using liquid separation techniques and tandem mass spectrometry/database searching. As peptide mixtures become more complex better separation techniques are required to resolve the peptide components for tandem mass spectrometry. We have an approach to separate complex peptide mixtures using microcolumn LC/LC in conjunction with tandem mass spectrometry. We are able to identify proteins, identify modifications and on membrane enriched fractions we are able to identify proteins and determine protein folding topology. Results on studies of yeast protein complexes, human tissues, and rat organelles will be discussed.