

S003 Protein post-translational modifications related to oxidative stress

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Our laboratory engages in the development of MS-based technologies and methodologies for the identification, characterization and quantitation of a variety of protein post-translational modifications (PTMs). These include known and novel PTMs, with specific emphasis on the study of PTMs observed in the metabolic pathways associated with oxidative stress and cardiovascular disease and with protein misfolding disorders. We are applying the proteomics technologies to the characterization of clinical samples for the study of proteins and protein PTMs as a function of disease state using protocols which incorporate abundant protein depletion, robust and novel multi-dimensional protein separations and high performance mass spectrometry followed by customized analysis of MS and tandem MS data. Correlation of proteomics data (protein identification, expression levels and type and quantity of post-translational modification) with genomics data is used to gain a better understanding of the etiology of the clinical manifestation of diseases and better understanding of physiological responses to the pathogenesis of disease. The discovery of potential biomarkers should enable earlier detection and thus facilitate the diagnosis and treatment of disease.

Acknowledgements: The author thanks the following colleagues for their contributions to the work described: ME McComb, C Dauly, Y Jiang, F Lavatelli, DH Perlman, M Sethuraman, R Théberge, C Zhou, E Klings, PB O'Connor, RA Cohen. She also thanks NIH for support under P41 RR10888 and N01 NV28178.