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"In making theories, always keep a window open so that you can throw one out if necessary."- Bela Schick,
Pediatrician

Welcome to our first edition

Proteomics Resource News is a quarterly newsletter that features the work being done by the Administrative Center and Proteomics Research Centers. We will introduce the work being done under this project and supply updates through subsequent newsletters. We hope you will enjoy news regarding technologies and developments in the field of proteomics, progress on this project and relevant publications as well as activities of our members and internal groups. [Subscribe](#) to be notified of the next edition.

Systems biology and proteomics at PNNL

Exploring how proteins and other chemicals work in concert to drive the functions of living organisms is one of the most exciting, important and growing areas in science today. Some of the leading work in this exploration, within the emerging fields of systems biology and proteomics, is taking place at the Department of Energy's Pacific Northwest National Laboratory.

Systems biology at PNNL is focused on understanding complex interactions of gene, protein, and cellular components involved in cell signaling. Among PNNL's major contributions to this field are the proteomic resources developed and deployed in the William R. Wiley Environmental Molecular Sciences Laboratory, a DOE national scientific user facility located on the PNNL campus. EMSL also houses the [NCCR Proteomics Research Resource for Integrative Biology](#).

These resources are applied to a diverse range of studies, such as studies of how unique, radiation-resistant or metal-reducing organisms might be used in environmental cleanup processes, funded by the DOE's [Office of Science](#). Collaborative studies with some of the world's leading biomedical research institutions promise to significantly add to our current understanding of how diseases originate and propagate in the body. These studies are supported in part through funding from the [National Institutes of Health](#).

Recent highlights of ongoing research include studies of human blood plasma ([Plasma Proteomics Review](#) and [HUPO Discussion of the Field](#)), other health related research ([Hepatitis C virus](#), [Human Cytomegalovirus](#), [Lyme Disease](#), and [Skeletal Muscle Channels](#)), and advances in the field of microbial proteomics ([Shewanella Hypothetical Proteins](#), [Shewanella Protein Complexes](#), [Differential *Deinococcus* Proteomics](#), and [Global *Shewanella* Proteomics](#)).

The possibilities for systems-level and proteomics studies are rapidly growing across every conceivable area of biological research. Enabled by interdisciplinary research coupled with excellent scientific resources, information can be collected at unprecedented levels. These efforts will lead to solutions for some of our nation's most pressing problems – from health to energy production to biological-agent detection.



PNNL scientists can identify peptides and infer proteins from biological samples, such as *Salmonella* and Orthopox viruses using LC-FTICR MS technology. This is a next step in "going beyond the genome"

High throughput proteomics at PNNL

Mass spectrometry is the premier tool for analyzing proteins under any set of conditions, and the William R. Wiley Environmental Molecular Sciences Laboratory at PNNL houses one of the world's most diverse, powerful and unique sets of mass spectrometers located under one roof. When combined with nanoscale ultra-high pressure capillary liquid chromatography (LC) separations, these ... *continued on page 2*

Favorite Site

Cambridge Healthtech Institute

www.healthtech.com

Cambridge Healthtech Institute (CHI) is renowned for its conferences. CHI holds approximately 60 conferences throughout the US and Europe and strives to develop quality programs that provide valuable new insights and competing points of view.

"CHI events facilitate interaction with key decision-makers from leading pharmaceutical and biotech organizations."



High throughput proteomics at PNNL

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powerful mass spectrometers enable comprehensive, quantitative, and high-throughput proteome measurements. As a result, scientists can more quickly answer questions of how proteins, and thus cells, operate.

PNNL's high throughput analysis approach is similar to "shotgun" proteomics approaches in that proteins are first cleaved into peptide fragments and then analyzed by liquid chromatography-tandem mass spectrometry (LC-MS/MS) to identify peptides. However, unlike "shotgun" approaches, the results from these initial analyses are used to create a reference database that contains mass and chromatographic elution time information for each peptide; that is, a mass and time tag that serves as a unique two-dimensional marker for subsequent identifications of that particular peptide.

Once a reference database has been created, future samples from the same organism need only be analyzed by high-resolution LC-MS (such as Fourier transform ion cyclotron resonance or time-of-flight) since detected peptides can be identified by comparing mass and elution time characteristics with those in the reference database. This approach not only increases throughput by eliminating the need for routine MS/MS, but also provides both greater analytical sensitivity.

These high-throughput analyses create massive amounts of data since a single cell can express many thousands of proteins. PNNL developed the Proteomics Research Information Storage and Management System (PRISM), an easily configurable and scalable capability, to handle these ever-increasing volumes of data. PRISM not only collects data files directly from all mass spectrometers, but it also manages the storage and tracking of these data files and automates data processing to provide both intermediate results and final products.



A PNNL scientist uses a ThermoFinnigan LTQ mass spectrometer to identify peptides from living organisms such as *Salmonella* and Orthopox viruses

What's Happening ...

The [Scientific Working Group](#) (SWG), an advisory team composed of scientists with a broad range of expertise in proteomics, bioinformatics and infectious diseases, is pleased to welcome their newest member, John Belisle, Ph.D, an Associate Professor in the Department of Microbiology, Immunology and Pathology at Colorado State University. Another member of the SWG, Thomas Geisbert, Ph.D., and his lab team from Ft. Detrick, MD, were featured in the [October 2, 2005 edition of the Washington Post](#). The article recounts Dr. Geisbert's efforts to develop a vaccine for Ebola.

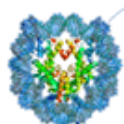


The Administrative Resource Center for Biodefense Proteomics Research Centers [presented](#) at HUPO's 4th Annual World Congress in Munich, Germany. Peter McGarvey, PIR/GU, was the Administrative Center's representative.



Cathy Wu (PIR/GU), Administrative Center and IWG member, was elected to the HUPO Council. She will serve a three-year term beginning November 1, 2005.

Upcoming Meetings ...



**Pacific Symposium on
Biocomputing 2006: Computational
Proteomics**
Grand Wailea, HI
January 3-7, 2006

Relevant Publications ...

[Structural genomics of the severe acute respiratory syndrome coronavirus: nuclear magnetic resonance structure of the protein nsP7](#) - *J Virol.* 2005 Oct; 79(20): 12905-13 [PMID: 16188992] The Scripps Research Institute

[Inhibition, escape, and attenuated growth of severe acute respiratory syndrome coronavirus treated with antisense morpholino oligomers](#) - *J Virol.* 2005 Aug; 79(15): 9665-76 [PMID: 16014928] The Scripps Research Institute

[The utility of accurate mass and LC elution time information in the analysis of complex proteomes](#) - *J Am Soc Mass Spectrom.* 2005 Aug; 16(8): 1239-49 [PMID: 15979333] Pacific Northwest National Laboratory

[Murine macrophage transcriptional responses to *Bacillus anthracis* infection and intoxication](#) - *Infect Immun.* 2005 Feb; 73(2): 1069-80 [PMID: 15664951] University of Michigan



**17th International Mass
Spectrometry Conferences**
Prague, Czech Republic
August 27-September 1, 2006