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Media Contact Information:

David Chiang (Sage-N Research, Inc.)

Phone: 408-350-0475

Email: dchiang@SageNResearch.com

Website: <http://www.SageNResearch.com>

Louis Coffman (Institute for Systems Biology)

Phone: 206-732-1200

Email: lcoffman@systemsbiology.org

Website: <http://www.systemsbiology.org>

Sage-N Sorcerer™ Integrates ISB's Open Source Proteomics Tools

Plug-and-Play Appliance Provides Complete Analysis Workflow for High-throughput Proteomics

SAN JOSE, California (October 24, 2005) – Sage-N Research, Inc. and the Institute for Systems Biology (ISB) announce the integration of the Trans-Proteomic Pipeline (TPP) analysis platform into the Sorcerer appliance. For the first time, research laboratories and core facilities can replicate the power and capability of ISB's high-throughput proteomics analysis infrastructure without requiring extensive information technology (IT) support or costly cluster computers. The Sorcerer appliance can be plugged into any network to deliver high resolution, high throughput data analysis through a easy-to-use web interface. With the integration of TPP, a unified web-based tool suite can effectively identify, characterize, and quantify proteins in complex mixtures using any vendor's LC-MS/MS data.

As LC-MS/MS technology continues to become an increasingly powerful and broadly used tool to identify and quantify proteins in complex samples, the proteomics research community faces two key challenges related to the analysis of the large amounts of data generated by such studies. First, proteomics laboratories need to build a complex IT structure with sufficient computing power to process the collected data and second, the results obtained from sequence database search engines need to be statistically validated to determine the error rate of the search results. According to Dr. Ruedi Aebersold, co-founder of the Institute for Systems Biology and principal investigator for the TPP project, "Proteomics research groups and the proteomics community as a whole will greatly benefit from easily accessible systems that analyze LC-MS/MS proteomic data at high throughput with transparent algorithms and that provide an estimate of the error of the obtained data. The throughput and ease-of-use and ease-of-maintenance of the Sorcerer system with Trans-Proteomic Pipeline support will help to address these needs." The TPP software developed by ISB with Federal funds from the National Heart, Lung, and Blood Institute, National Institutes of Health, under contract No. N01-HV-28179 provides a validated tool suite based on uniform, open data standards, but it requires significant IT support and large cluster computers that limit its use in the broader community. The coupling of Sorcerer with TPP solves both the throughput and standardization challenges for even the smallest research laboratory, in order to accelerate modern proteomics research.

The Sorcerer appliance from Sage-N Research (San Jose, CA) is a compact analysis system that sets up in minutes, and requires no software installation or IT administration. Using patent-pending Pattern Match Accelerator™ hardware and systems technology, it offers processing throughput for protein identification that otherwise might require hundreds of compute nodes. The Sorcerer appliance currently supports the SEQUEST® algorithm, with additional scoring modules being planned.

The Trans-Proteomic Pipeline from the Institute for Systems Biology (Seattle, WA) is an Open Source analysis platform for unified storage and analysis of tandem mass spectrometry data based on open XML file formats. As one of the earliest comprehensive tool suites to address the requirement of the proteomics community for standardized, validated MS/MS analysis, it offers multi-vendor spectral file support, validation of identified peptides, probability-based protein scoring, and automated protein quantification.

Information on Sorcerer is available at <http://www.SageNResearch.com>. Information on TPP is published in the Molecular Systems Biology journal (A. Keller et al, "A uniform proteomics MS/MS analysis platform utilizing open XML file formats", doi:10.1038/msb4100024, Published online: 2 August 2005).

About Sage-N Research, Inc.

Sage-N Research, Inc. is a privately held corporation headquartered in San Jose, California. Sage-N Research is an industry leader in developing high-throughput, easy-to-use data analysis appliances that enable proteomics researchers to fully characterize proteins in complex biological samples. The company has developed proprietary technology based on novel software methods and hardware-optimized pattern matching algorithms. Through strategic collaborations with leading scientists, Sage-N Research advances the state of the art in ease-of-use, applications, and technology to enable world-changing discoveries in biology and medicine. For more information, please visit <http://www.SageNResearch.com>.

About the Institute for Systems Biology

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The Institute for Systems Biology (ISB) is an internationally renowned non-profit research institute dedicated to the study and application of systems biology. ISB's goal is to unravel the mysteries of human biology and identify strategies for predicting and preventing diseases such as cancer, diabetes and AIDS. The driving force behind the innovative "systems" approach is the integration of biology, computation, and technology. This approach allows scientists to analyze all of the elements in a system rather than one gene or protein at a time. Located in Seattle, Washington, the Institute has grown to 11 faculty and more than 170 staff members; an annual budget of more than \$25 million; and an extensive network of academic and industrial partners. For more information about the ISB visit: www.systemsbiology.org

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