

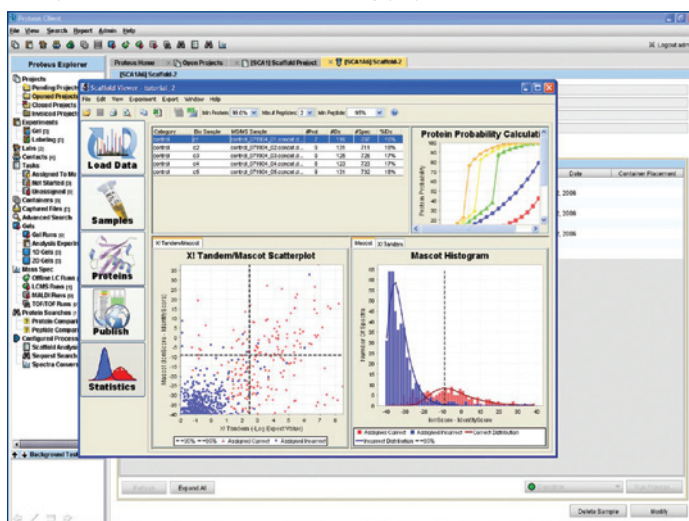
Seamlessly Integrating Proteus and ScaffoldBatch

Proteus-Analytics™ is an integrated software solution for proteomics lab management and data integration, with key protein ID validation and visualization capabilities. Proteus-Analytics is the seamless integration of GenoLogics' best-in-class Proteus lab and data management system with Proteome Software's ScaffoldBatch Analysis System. ScaffoldBatch is launched from within Proteus-Analytics as part of a proteomics workflow and bioinformatics pipeline, with validated results automatically captured and normalized into the Proteus DB for querying, reporting and data mining. This integrated solution provides end-to-end workflow, data management, and bioinformatics support required in today's cutting edge proteomics research environments.

Automated Bioinformatics Pipelining

GenoLogics' Automated Informatics (AI) Framework™ enables automatic bioinformatics pipelining of proteomics data, and facilitates Proteus' close integration with the ScaffoldBatch Analysis System.

- Using the AI Framework, Proteus™ queues protein search results data from Mascot and X!Tandem protein search engines into the ScaffoldBatch Analysis System. Scaffold uses statistical scoring models to provide improved confidence in validating peptide data.



Proteus-Analytics seamlessly integrates Proteus and ScaffoldBatch Analysis System

- Scaffold's validation tactics include visually checking for repeatability of the proteins across samples, peptides within proteins across samples, and the spectral fragmentation peaks across peptides. Another visual validation tool confirms that the peptide's amino acids and post translational modifications are consistent with the fragmentation peaks in the spectra.
- Proteus automatically captures analysis results and parses them into its database. Users can then launch Scaffold Viewer for results viewing and dissemination to collaborators. The finalized results are integrated into the Proteus database for queries and data mining.

Protein Search Results Analysis

Proteus integrates with multiple protein search engines, including Mascot, ABI, SEQUEST, Peaks, Phenyx, Spectrum Mill, BioWorks, X!Tandem and others, and allows labs to track samples back to specific proteins and expression profiles.

- Go beyond point analysis, and easily compare proteomic results across numerous samples and conditions
- Extended support for multiple protein search engines
- Compare the outcomes of multiple protein search engine results, across multiple samples, projects, biosources, mass spec runs

Enhanced Proteomic Data Views: Peptide-Centric Results and Comparison

Following protein identification validation by ScaffoldBatch, Proteus' new peptide data and comparison views allow for comparison of peptide hits across protein searches, samples, etc. This view has two modes of operation for different needs; users can easily switch between protein-grouped and peptide-centric data and comparison views.

- Peptide-centric view lets researchers view and perform comparison analysis on peptides across samples, fractions, and protein hits
- GenoLogics' LabLink web collaboration system collects protein sequence data from public repositories and overlays matched peptide hits onto the protein sequence
- Proteus now normalizes protein search parameters, which are associated with proteomic search results, and may be queried by numerous filter options
- Easily search on, view, and analyze peptide charge states, modifications, and elution times

Proteus-Analytics: A Comprehensive Lab and Data Management Solution

In addition to the integrated ScaffoldBatch protein identification validation component, Proteus-Analytics automates lab management and sample tracking, with the associated contact management, task assignment, and lab scheduling. This improves efficiency, increases throughput, ensures quality, and manages resources, allowing researchers to focus on proteomics research while the Proteus lab and data management component of Proteus-Analytics handles workflows and the large volumes of data generated in proteomics research.

Project Management

Lab Management

Proteus tracks outside research and clinical labs, including contact data and linkages to projects, experiments, and samples. For each project, permissions may be edited by qualified users, ensuring projects and associated data are only accessed and altered by authorized users. Proteus supports bar codes, and samples (including gels, vials, well trays, and MALDI target plates), instruments, and stations within the lab may each be identified with a unique barcode.

LabLink Web Collaboration System

Proteus' LabLink web interface provides a secure communication channel for information sharing and results dissemination.

Workflow and Data Management

Proteus' feature-rich java client provides a high degree of usability. The GUI provides quick overviews of full sample workflows and a fully traceable sample history, including detailed sample genealogies. Proteus users can predefine and reuse workflow definitions and protocols.

Configurable Processes

Proteus is a robust and flexible system that can accommodate a lab's unique methods, techniques, protocols, and workflow changes. Configurable research processes enable process parameter tracking, and allow users to associate research processes to particular instruments, software or reagents, in order to define novel research techniques.

Instrument Integrations

Researchers can rest assured that their laboratory instruments can be linked with each other through Proteus, reducing complexity, streamlining processes, and encouraging research collaboration on a common platform. Proteus integrates with a broad selection of mass spectrometers, utilizing driver files to create standards for file naming, linking and contextually associating proteomics data. Proteus' Automated Data Capture (ADC) ensures seamless data integration from mass spectrometers, robotic spot pickers, and gel equipment.

Enhanced Quantitation Analysis

Proteus now offers enhanced quantitation analysis with the Trans Proteomic Pipeline (TPP), a result of GenoLogics' partnership with the Institute for Systems Biology (ISB). The TPP integration provides Proteus users with protein identification, results validation, and quantitation, all within an automated bioinformatics pipeline. Proteus works with any of the three existing ISB open data formats - mzXML, pepXML, or protXML.

Advanced Query Functionality

Users can access archived experiment data to provide historical validation of a research project and underlying processes. Proteus features advanced search capabilities, including the ability to search on user defined data fields, enabling users to submit complex scientific queries to their data to determine commonalities and differences among samples and various analyses, and reveal critical data elements.

OMIX™ Lab Informatics Platform

Proteus' open standards architecture enables integration to a variety of instrumentation, bioinformatics software, and IT environments. The Proteus workflow is based on input and output of standardized data that collaborating researchers can easily read, verify, and duplicate.

GenoLogics' Open, Collaborative Approach

GenoLogics is focused on creating best-in-class solutions that address the challenges of lab management, sample tracking, instrument integration and automation – and most importantly contextual scientific data integration. GenoLogics is committed to collaborating with genomics and proteomics analysis companies to address the bioinformatics requirements customers are asking for, with the goal of providing end-to-end solutions on one open, integrated, automated, and configurable platform.



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