

An Open, Application Driven LIMS for Proteomic Facilities

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Managing proteomic samples and experiments is complex, as vast amounts of data are generated. It presents significant challenges in data integration, analysis, storage, and querying; and thus underscores the need for proteomic application driven Laboratory Information Management Systems (LIMS). However, most commercially available LIMS are not designed specifically for the proteomic laboratory. To fill this need, we developed an open and integrated LIMS solution (Proteus) customized for proteomic research. Our software is built on an open architecture and can interface with various gel pickers, imaging systems, MS instruments, analysis software, and search engines from different vendors. Proteus consists of four major components: (1) a centralized laboratory information management system that tracks samples throughout different proteomic workflows such as 1D/2D gel, 2D DIGE, ICAT/iTRAQ, SILAC, PMF, and MuPIT based experiments, providing histories for particular samples. Researchers can search across data at the project or sample level to easily access information stored in the LIMS database; (2) a web module for secure on-line communication and sample submission and results sharing; (3) a result comparison function for comparing protein identification results from different search engines; (4) a reporting feature that allows researchers to generate reports on projects, samples, and activities. Using gel and LC/MS/MS workflow, we demonstrate that Proteus is able to seamlessly integrate data from different instrumentations, analysis software, and search engines; thus allowing researchers to centralize proteomic data and then visualize and compare protein identification results.