

International Data Exchange and Data Representation Standards for Proteomics (PROTEOMEXCHANGE)

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Research Areas



Tool Development

Standard



Data-Sharing Enabler

At a Glance

- Status: **Completed Consortium**
- Year Launched: **2011**
- Initiating Organization: **European Commission Seventh Framework Programme (FP7)**
- Initiator Type: **Government**
- Location: **Europe**

Abstract

Over the past few years the field of mass spectrometry (MS) proteomics has evolved into a prolific data producer. As a result, various databases that collect and redistribute the acquired data were established. This simultaneous creation of multiple repositories and databases caused confusion for data submitters and users alike. Proteomics data resources such as PRIDE (European Molecular Biology Laboratory European Bioinformatics Institute, Cambridge, U.K.) and PeptideAtlas (Institute for Systems Biology, Seattle, Ore.) accepted data submissions and handled MS proteomics data for many years, but until the ProteomeXchange (PX) consortium started they had been acting independently with very limited global coordination. The overall aim of the PX Consortium is to provide a common framework and infrastructure for the cooperation of proteomics resources by defining and implementing consistent, harmonized, user-friendly data deposition and exchange procedures among the members.

Mission

The main objectives of the PX consortium are user-oriented: (a) provide a single point of data

submission to the user; (b) ensure data availability in all of the different member databases; (c) use community standard formats to represent the data, so that it becomes accessible to all regardless of data origin; and (d) provide added value through different views on the same data, from repositories to derived search tools.

With support from large-scale data producers (ISAS (Germany), University of Cambridge (U.K.), Karolinska Institute (Sweden)), industry (Pfizer, Philips, Waters), and journals (Nature Biotechnology, MCP, JPR), the consortium proposes a coordination action project to solidify an emerging informal collaboration between major repositories into a production-quality data deposition and dissemination consortium on par with the systems so successfully employed by three-dimensional structure databases and nucleotide sequence databases, among others.

Data Sharing

ProteomeXchange fully supports both MS/MS proteomics and SRM data submission. Submissions of other types of proteomics data is also possible using the partial submission mechanism.

The organization homepage contains a listing of publicly accessible ProteomeXchange datasets. Additional datasets will become visible as they are released.

Impact/Accomplishment

The major achievements of the project are as follows:

The project progressed well, in line with the planned objectives of the work packages (months 1-42). Overall, the work plan was designed to reach major milestones at month 18 of the project (Milestones 3 and 4). Through completion of a series of deliverables, the PX consortium is now fully operational. A qualitative dataset can be submitted, being received by one repository, and then automatically distributed and incorporated in other participating repositories, where it is made public, and such incorporation is reported through the resource ProteomeCentral. The PX consortium started to accept regular submissions in June 2012 (month 18). By June 30, 2014, 1,053 datasets had been submitted. Of those, 47 percent are already publicly available through the PX consortium.

The core of the standard for quantitative data (mzQuantML) was developed during the first period. During the second period, mzQuantML was extended with modules to support different quantification techniques. The second phase of the project was devoted to fine-tuning and production mode for the ProteomeXchange data flow. In addition, tracking of reprocessed datasets was developed. Since the start of the project, the consortium has published a total of 72 scientific publications acknowledging ProteomeXchange.

In June 2014, the MassIVE repository for mass spectrometry data (led by Nuno Bandeira at University of California, San Diego) became an official full member of the PX consortium (it was the first member to join that was not originally included in the grant). MassIVE's integration with the PX consortium extended the range of options for sharing for proteomics mass spectrometry data and facilitated dataset submissions from institutions within and to the United States. It is also an impressive testimony to the attraction of the ProteomeXchange concept and to its long-term viability.

Links/Social Media Feed

Other website	http://cordis.europa.eu/project/rcn/100493_en.html
Homepage	http://www.proteomexchange.org/

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