Abstract

Over the last few years, the field of proteomics has evolved into a prolific data producer. As a result, various databases that collect and redistribute the acquired data have been established. While data format standards for quantitative proteomics have now been defined and implemented with significant contribution from the recently completed EU ProDaC grant, standards for quantitative proteomics are still lacking. This simultaneous creation of multiple repositories and databases, and lack of standards for quantitative proteomics, result in a fragmentation of data and cause confusion for data submitters and users alike. Based on consortium expertise in the operation of large-scale proteomics repositories (PRIDE, PeptideAtlas, Tranche, Peptidome), we aim to implement the next step: regular data exchange among major international proteomics resources. In parallel, we will further develop standards (mzQuantML) for the dynamic field of quantitative mass spectrometry.

Mission

The main objectives of ProteomExchange are user-oriented: (i) to provide a single point of data submission to the user; (ii) to ensure data availability in all of the different member databases; (iii) to
use community standard formats to represent the data so it becomes accessible to all regardless of data origin; and (iv) to provide added value through different views on the same data, from repositories to derived search tools.

Financing

EU FP7

Other website http://cordis.europa.eu/project/rcn/100493_en.html

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Updated: 04/22/2016