

## Report

# Towards data management of the HUPO Human Brain Proteome Project pilot phase

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The pilot phase of the Human Brain Proteome Project as a part of the Human Proteome Organisation has just been started. In two pilot studies, 18 different laboratories are analyzing mouse brains of three age stages and human brain autopsy *versus* biopsy material, respectively. The overall aim is to elucidate the portfolio of available techniques as well as to elaborate common standards. As a first step, it was decided to use the common bioinformatics platform ProteinScape™ that was introduced to the participating groups in a two day course in Bochum, Germany.

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The Human Proteome Organisation (HUPO) Human Brain Proteome Project (HBPP) has started its practical work with the initiation of a pilot phase that comprises two studies: A mouse pilot study analyzing three different age stages of mouse brain and a human pilot study comparing biopsy and autopsy tissues of human brain (see <http://www.hbpp.org/>). The samples were sent out in March and April 2004 to 18 different laboratories. It is planned that the data generated will be sent to the Human Brain Data Collection Center (DCC) in Bochum, Germany, giving all participating groups the possibility to browse, compare and review the consortia data. One aim, in addition to the scientific goals of the studies, is to reveal the technological portfolio of the participating groups. As the heterogeneous techniques will obviously deliver heterogeneous data, a standardized data file format and submission form is desirable. Most of the participating laboratories decided, therefore, to use the ProteinScape bioinformatics platform as the local database system to

manage the data. Free licences have been provided by Bruker Daltonik (Bremen, Germany) and Protagen (Dortmund, Germany).

The integrated bioinformatics platform, ProteinScape, is a database-client system with a web front end. It handles all essential steps of a proteome study: project hypothesis, sample definition, protein separation techniques, pre-mass spectrometry (MS) sample preparation, and MS (data calibration, search algorithm triggering and automatic evaluation strategies). Data from all these different steps are directly imported into the database system. Using the same local proteome database, this system gives the consortium the opportunity to provide data in a standardized way even before the Proteomics Standard Initiative (PSI) of HUPO (<http://psidev.sourceforge.net/>) has finalized data exchange formats like MIAPE (Minimum Information About a Proteomics Experiment) and mzData standards. The data exchange within the HBPP initiative will be changed to the PSI data standards as soon as they become available, and the PSI consortium will create converters for the transition of the ProteinScape formatted data into the PSI data format.

In order to familiarize pilot study participants with the software, a training course was held recently at the Medical Proteom-Center in Bochum. The participating groups

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Participants at the HUPO HBPP course.

came from Belgium, Germany, Ireland, Austria, China, Korea and Greece. Within two days, attendees received all the necessary information about installing, handling, troubleshooting and structure of ProteinScape, offering a basic understanding of the software. In addition, HUPO and the HBPP initiative were presented and the PSI standardization efforts discussed. The ProteinScape course will enable the participating groups to capture data generated during the pilot study work in a standard-

ized way, thus improving the comparability of the results produced in different laboratories. Moreover, the course which is the first of a series of courses within the HUPO HBPP training and education program, marked the end of the beginning: the pilot phase of the HUPO Human Brain Proteome Project has started.

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