

## WEB WATCH

**Sharing PRIDE**

- <http://www.ebi.ac.uk/pride/>

With the rapid progress in the field of proteomics and the accumulation of vast amounts of protein information, there is an increasing need for this information to be brought together in a way that is easy to access and share. In response to this need, the European Bioinformatics Institute in the UK (which is part of the European Molecular Biology Laboratory) and the Flanders Interuniversity Institute for Biotechnology-Ghent University, Belgium, developed the Proteomics IDentifications Database.

PRIDE provides an open-source database of protein identifications and has been designed to allow researchers to store, share and compare their results. This free-to-use database aims to provide access to published, peer-reviewed, standardized data on protein identification from many different sources. PRIDE is closely linked to the Human Proteomics Organization's Proteomics Standards Initiative (HUPO-PSI) and will allow users to transfer data using the standards that are currently being developed as part of PSI.

The availability of the data in the same format allows the use of powerful computational analyses — for example, by comparing the proteins from a particular tissue under different conditions. Ultimately, this database will allow researchers to investigate how proteins are altered in many diseases, paving the way for new diagnostic and predictive methods.

The developers hope that the proteomics community will adopt PRIDE as the method of choice for making proteomics data freely available to, and exploitable by, the proteomics community. Large data sets including HUPO's Plasma Proteome project and a human platelet proteome set are currently available in PRIDE. And many more are undoubtedly on their way...

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