

# Protein database for biomedical research

June 11 2013

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As personalized medicine is on the rise, the healthcare field is discovering the opportunities of "big data" analysis. The result of a joint project between the TUM Chair of Proteomics and Bioanalytics, SAP and the SAP Innovation Center, ProteomicsDB, is a major step forward in human proteomics. It currently contains more than 11,000 datasets from human cancer cell lines, tissues and body fluids and enables real-time analysis of this highly dimensional data and creates instant value by allowing to test analytical hypothesis.

ProteomicsDB is based on the SAP HANA platform for rapid data mining and visualization. It has been built to enable public sharing of mass spectrometry-based proteomic datasets as well as to allow users to access and review data prior to publication. The database is backed with 50 TB of storage, 2 TB RAM and 160 processing units. A direct interface to the programming languages L, C++ and R allows more flexible calculations than are possible with standard SQL. The Web interface is built on a JavaScript framework for HTML5 and optimized for Google Chrome but also available under Internet Explorer and Mozilla Firefox. An easy-to-use and fast Web interface allows users to browse and upload data to the repository as well as browsing the [human proteome](#), including [protein level](#) information such as [protein function](#) and expression.

ProteomicsDB will be available free of charge. The database will be a valuable asset for researchers in the field of life sciences as well as for the pharmaceutical and [biotechnology industry](#). Insights from analyzing the inherent datasets can be used in biomedical research and for example

in developing new drugs that operate in a more targeted way without adversely influencing other cellular processes, helping to reduce side effects.

"The vast amounts of molecular data generated in biomedical research increasingly challenge the ability of scientists to see 'the forest for the trees', said Prof. Dr. Bernhard Kuester of TUM. ProteomicsDB is a significant step ahead in our research aiming at a better understanding of human disease and more informed future treatments. The software helps us and others to store, integrate and analyze experimental data in real time, allowing us to study more complex biological systems at greater depth than previously possible."

**More information:** [www.proteomicsdb.org/](http://www.proteomicsdb.org/)

Provided by Technical University Munich

Citation: Protein database for biomedical research (2013, June 11) retrieved 2 May 2024 from <https://medicalxpress.com/news/2013-06-protein-database-biomedical.html>

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