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Novel Proteomics Research Information Management System (RIMS). M. Ruf¹, H. Thiele², B. Guigas³, ¹Bruker AXS Inc., 5465 East Cheryl Pkwy. Madison, Wisconsin, USA, ²Bruker Daltonik GmbH, Fahrenheitstr. 4, 28359 Bremen, Germany, ³Bruker BioSpin GmbH, Silberstreifen 4, 76287 Rheinstetten, Germany.

Proteomics RIMS is a bioinformatics solution that for the first time combines and integrates the data, information and knowledge generated in the proteomics research workflow from complementary mass spectrometry, NMR and x-ray crystallography technologies.

Proteomics RIMS combines *ProteinScape*TM for managing the workflow in expression proteomics, and *SampleTrack*TM as the backbone of a data warehousing technology providing an environment of data, programs and links to databases. Consolidating information across different experimental platforms is a key to gaining in-depth understanding and to finding relationships and information in experimental data.

Transforming experimental data into information and turning information into knowledge is a major challenge for bioinformatics, and is the key to understanding the complexities of biological and molecular clinical research. Efficient interpretation, mining and managing of the huge amounts of data generated within proteomics maximizes productivity. Having more information from expression proteomics, interaction proteomics and structural proteomics at ones fingertips enables better decision making in drug discovery and target validation.