



## Proteome Software Releases Scaffold 3

April 14th, 2010

**PORTLAND, OREGON** - Proteome Software today released the next-generation of its premier proteomics/bioinformatics tool, Scaffold 3.0, for MS/MS visualization and validation.

Scaffold's new SF3 file format allows for faster data access and unlimited file size scalability. Its new and improved Venn diagram functionality makes advanced filtering and navigation quick and easy. Sophisticated statistical techniques also improve identification rates with high mass accuracy data.

Additional search engine support enables researchers to gain a deeper understanding of their proteomics experiments. Scaffold 3 also reads in the new Z-Core search engine results from Thermo's Discoverer, as well as ETD and CID data from Discoverer results. Added publish view support and Traunche repository capabilities makes Scaffold 3 an excellent choice for the research publication process.

Free 14-day evaluations of the full product are available at [www.proteomesoftware.com](http://www.proteomesoftware.com).

Proteome Software was founded in 2004 in Portland, Oregon. Its products (including MassQC, Scaffold 2, ScaffoldBatch, and Scaffold Q+) are in use in over 250 academic, public and private research facilities around the world. The company's headquarters is located in Portland and has resellers in Taiwan, the United Kingdom and Japan.

### For further information:

<http://www.proteomesoftware.com>

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