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Proteome Software Releases Scaffold PTM

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PORTLAND, OREGON - Proteome Software today released Scaffold PTM, the premier in post-translational modification (PTM) site assignment, enhancing bioinformatics, MS/MS analysis and PTM visualization and validation for proteomics researchers.

Scaffold PTM introduces several key features for confident phosphorylation (and other PTM) site determination. It relies on the open data source format, mzIdentML (*.MZID) file type, embraced by HUPO and currently supported by Scaffold and Mascot.

Additional search engine supports enables researchers to gain access to PTM data processed by Scaffold, Mascot or any other software tool that supports the mzIdentML file format. Scaffold PTM validation at a glance allows quick comparison of the peptide modification rates from multiple samples in a data set.

Free 14-day evaluations are available at www.proteomesoftware.com. Sign up and use both Scaffold and Scaffold PTM free for 14 days.

Proteome Software was founded in 2004 in Portland, Oregon. Its products (including Scaffold, Scaffold Q+, ScaffoldBatch and MassQC) 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:

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