

### This week in techniques

Approach	Summary	Licensing status	Publication and contact information
<b>Assays &amp; screens</b>			
Identification and quantification of peptides from high-resolution mass spectrometry data	<p>The MaxQuant software suite may be a useful computational tool for improving the accuracy of peptide identification and the quantification of proteins from high-resolution mass spectrometry proteome analysis. MaxQuant can identify and quantify peptide masses in the parts per billion range, which is a sixfold increase over standard mass spectrometry methods. Next steps could include further advances in instrumentation to allow for a more dynamic range of measurements and functional genomics experiments.</p> <p><b>SciBX 1(45); doi:10.1038/scibx.2008.1117</b>            Published online Dec. 18, 2008</p>	Patent and licensing status unavailable	<p>Cox, J. &amp; Mann, M. <i>Nat. Biotechnol.</i>; published online Nov. 30, 2008; doi:10.1038/nbt1511</p> <p><b>Contact:</b> Matthias Mann, Max-Planck Institute for Biochemistry, Martinsried, Germany            e-mail: <a href="mailto:mmann@biochem.mpg.de">mmann@biochem.mpg.de</a></p> <p><b>Contact:</b> Jürgen Cox, same affiliation as above            e-mail: <a href="mailto:cox@biochem.mpg.de">cox@biochem.mpg.de</a></p>