

This week in techniques

Approach	Summary	Licensing status	Publication and contact information
Computational models			
Enhanced signature peptide (ESP) predictor to aid in assay development and biomarker validation	<p>The ESP predictor, a computational method based on the physicochemical properties of proteins, may help identify peptide-based markers for assay development and biomarker validation. The system identified signature peptide sequences in proteins that could then be used as surrogates for protein-based biomarkers. In 10 validation data sets, the ESP predictor system had an average success rate of 89% at selecting one or more peptides per protein, which is a higher rate than previous methods used to identify signature peptide sequences. Next steps were undisclosed but could include applying the ESP predictor system to biomarker verification studies.</p> <p>SciBX 2(4); doi:10.1038/scibx.2009.163 Published online Jan. 29, 2009</p>	The software is freely available at http://www.genepattern.org/	<p>Fusaro, V.A. <i>et al. Nat. Biotechnol.</i>; published online Jan. 25, 2009; doi:10.1038/nbt.1524</p> <p>Contact: Steven A. Carr, Broad Institute of Massachusetts Institute of Technology and Harvard, Cambridge, Mass. e-mail: scarr@broad.mit.edu</p> <p>Contact: Jill P. Mesirov, same affiliation as above e-mail: mesirov@broad.mit.edu</p>