This week in techniques

Approach	Summary	Licensing status	Publication and contact information
Computational models			
Cluster expansion and linear programming-based analysis of specificity and stability (CLASSY) for modeling protein-protein interactions	<p>A computational framework for modeling protein-protein interactions, dubbed CLASSY, should allow for the <i>in silico</i> design of peptides with high stability and specificity for therapeutic targets. The method was used to design interacting peptides specific for 19 highly similar DNA binding proteins. Next steps include improving the computational model of protein-protein interactions and expanding the method to the design of therapeutic peptides.</p> <p>SciBX 2(16); doi:10.1038/scibx.2009.677 Published online April 23, 2009</p>	Method unpatented; unavailable for licensing	<p>Grigoryan, G. <i>et al. Nature</i>; published online April 15, 2009; doi:10.1038/nature07885</p> <p>Contact: Amy E. Keating, Massachusetts Institute of Technology, Cambridge, Mass. e-mail: keating@mit.edu</p>