This week in techniques

Approach	Summary	Licensing status	Publication and contact information
Computational models			
Computational prediction of clustered, regularly interspaced short palindromic repeats (CRISPR)-associated protein 9 (Cas9) target sites	A computational method to predict CRISPR-Cas9 target cleavage could help guide the design of new disease models. CRISPR systems use a small guide RNA (sgRNA), which pairs with a target DNA sequence and Cas9 to excise the target DNA. An analysis of <i>Streptococcus pyogenes</i> Cas9 cleavage using mismatched sgRNA-DNA pairs identified determinants that affect the specificity of the cleavage process. A scoring algorithm was developed based on this information to help guide the selection of target sites for sgRNA design. Next steps could include additional characterization of Cas9 off-target activity.	Patent and licensing status unavailable; tool available at http://www.genome-engineering.org/	Hsu, P.D. <i>et al. Nat. Biotechnol.</i> ; published online July 21, 2013; doi:10.1038/nbt.2647 Contact: Feng Zhang, Broad Institute of MIT and Harvard, Cambridge, Mass. e-mail: zhang@broadinstitute.org
<i>SciBX</i> 6(32); doi:10.1038/scibx.2013.872 Published online Aug. 22, 2013			