This week in techniques

Approach	Summary	Licensing status	Publication and contact information
Disease models			
DNA sequencing of drug-resistant mammalian cells and clustered, regularly interspaced short palindromic repeats (CRISPR)-Cas9 genome editing to identify drug targets	Cell culture studies suggest high-throughput sequencing and CRISPR-Cas9 genome editing can be combined to rapidly validate drug targets. The approach uses high-throughput sequencing to identify mutations in drug-resistant clones and a CRISPR-Cas9 genome editing approach called DrugTargetSeqR to confirm the roles of the mutations in resistance. In cancer cell lines, the combination approach correctly identified the targets for two compounds in clinical trials. In another human cancer cell line, a related method correctly identified the targets and their resistance-conferring mutations for two toxic compounds. Next steps include automating the workflow of DrugTargetSeqR. SciBX 7(28); doi:10.1038/scibx.2014.840 Published online July 24, 2014	For findings from both studies, DrugTargetSeqR patented; available for licensing from The Rockefeller University Office of Technology Transfer	Kasap, C. <i>et al. Nat. Chem. Biol.</i> ; published online June 15, 2014; doi:10.1038/nchembio.1551 Contact: Tarun M. Kapoor, The Rockefeller University, New York, N.Y. e-mail: kapoor@rockefeller.edu Smurnyy, Y. <i>et al. Nat. Chem. Biol.</i> ; published online June 15, 2014; doi:10.1038/nchembio.1550 Contact: Yan Feng, Novartis Institutes for BioMedical Research, Cambridge, Mass. e-mail: yan.feng@novartis.com