

This week in techniques

Approach	Summary	Licensing status	Publication and contact information
Assays & screens			
High throughput small hairpin RNA-based genetic interaction mapping in human cells	<p>A high throughput method to analyze genetic interactions in human cells could help identify new disease pathways and targets. A library of shRNAs was synthesized against all annotated human protein-coding genes that carried, on average, 25 independent shRNAs per target. In cultured human cells treated with the library, quantification of shRNA levels by deep sequencing identified shRNAs against a series of targets, including HMG-CoA reductase, which decreased ricin toxicity compared with control shRNA. In a secondary screen of positive shRNA hits, a library containing every pairwise combination of two shRNAs identified synergistic or suppressive genetic interactions, which led to the identification of multiple putative protein pathways or complexes that affect ricin sensitivity. Next steps include using the method to analyze genetic interactions in cancer cells.</p> <p>SciBX 6(6); doi:10.1038/scibx.2013.146 Published online Feb. 14, 2013</p>	Patent and licensing status undisclosed	<p>Bassik, M.C. <i>et al. Cell</i>; published online Feb. 7, 2013; doi:10.1016/j.cell.2013.01.030 Contact: Martin Kampmann University of California, San Francisco, Calif. e-mail: martin.kampmann@ucsf.edu Contact: Michael C. Bassik, same affiliation as above e-mail: bassik@cmp.ucsf.edu</p>