This week in techniques

Approach	Summary	Licensing status	Publication and contact information
Assays & screens			
Proteome-wide analysis of protein stability and turnover rates	<p>Global protein stability (GPS) profiling may be a useful platform for identifying new therapeutics to destabilize proteins that play a role in disease. Using a mammalian reporter cell library, GPS monitors the decay of any protein of interest (X) by comparing the ratio of a red fluorescent control protein with a green fluorescent protein fused to (X). This strategy can measure protein turnover in real time at the single-cell level and detect low-abundance proteins. In addition, by engineering the fusion protein constructs to include an open reading frame that could be PCR amplified and hybridized to a microarray, the levels of over 8,000 human proteins could be quantified. Researchers used this high-throughput approach to identify proteasome substrates by comparing the reporter cell library that had been treated with a proteasome inhibitor to the reporter cell library that had not been treated. Next steps include refining the approach by using better microarrays and integrating a barcode system for better data visualization.</p> <p>SciBX 1(42); doi:10.1038/scibx.2008.1031 Published online Nov. 20, 2008</p>	Patent application filed; available for licensing from the Brigham and Women's Hospital	<p>Yen, H.-C.S. <i>et al. Science</i>; published online Nov. 7, 2008; doi:10.1126/science.1160489</p> <p>Contact: Hsueh-Chi Sherry Yen, Harvard Medical School, Boston, Mass. e-mail: hyen@rics.bwh.harvard.edu</p> <p>Contact: Stephen Elledge, Harvard Medical School, Boston, Mass. e-mail: selledge@genetics.med.harvard.edu</p>