This week in techniques

Approach	Summary	Licensing status	Publication and contact information
Chemistry			
Hydrophobic cross-linking of peptides to create inhibitors of protein-protein interactions	Hydrophobic cross-linking of peptides at critical binding residues could help generate stable, peptide-based inhibitors of protein-protein interactions involving irregular, non–alpha helical interfaces. X-ray crystallography of the interaction between *Pseudomonas aeruginosa* exoenzyme S (exoS) and human 14-3-3 protein identified critical binding residues in an 11-amino-acid peptide sequence of exoS. Replacement of two exoS residues with non-natural amino acids followed by cross-linking via a hydrophobic bridge increased the peptide's binding affinity for 14-3-3 compared with the natural peptide sequence. *In vitro*, the best-modified cross-linked peptide decreased the binding interaction between exoS and 14-3-3 more than the natural peptide. Next steps include optimizing the peptides for cell membrane permeability and cellular activity. *SciBX* 7(12); doi:10.1038/scibx.2014.355 Published online March 27, 2014	Patent filed by the Max Planck Society; available for licensing	Glas, A. *et al. Angew. Chem. Int. Ed.*; published online Feb. 6, 2014; doi:10.1002/anie.201310082 **Contact:** Tom N. Grossmann, Chemical Genomics Centre of the Max Planck Society, Dortmund, Germany e-mail: tom.grossmann@cgc.mpg.de **Contact:** Christian Ottmann, Eindhoven University of Technology, Eindhoven, the Netherlands e-mail: c.ottmann@tue.nl