This week in techniques

Approach	Summary	Licensing status	Publication and contact information
Computational models			
Database of human phosphatase-substrate interactions	A compilation of protein phosphatase-substrate interaction data could help identify new phosphatase-class drug targets. A list of phosphatases was assembled using sequence and structural information and combined with data from protein-protein interaction and gene expression databases. The data were computationally analyzed and correlated with phosphatase target-site predictions and known kinase substrates to generate a map of phosphatase-substrate interactions. Next steps could include experimental validation of predicted interactions in pathways of therapeutic interest. The human dephosphorylation database is hosted by the European Molecular Biology Laboratory and is available at http://www.koehn.embl.de/depod/ .	Unpatented; licensing status not applicable	Li, X. <i>et al. Sci. Signal.</i> ; published online May 9, 2013; doi:10.1126/scisignal.2003203 Contact: Maja Köhn, European Molecular Biology Laboratory, Heidelberg, Germany e-mail: koehn@embl.de
<p>SciBX 6(23); doi:10.1038/scibx.2013.585 Published online June 13, 2013</p>			