This week in techniques

Approach	Summary	Licensing status	Publication and contact information
Drug platforms			
Crystal structure of inhibitor-bound resistance-nodulation-division multidrug efflux transporters AcrB and MexB, and a homology model of MexY	Structural studies identified binding sites on AcrB, MexB and MexY that could help design inhibitors to circumvent drug resistance in bacteria. AcrB, MexB and MexY are drug efflux transporters on Gram-negative bacteria that contribute to drug resistance. Crystal structures of AcrB and MexB bound to pyridopyrimidine derivatives identified a binding pocket proximal to the substrate-translocation channels of the transporters that act as a hydrophobic trap for the inhibitors. A homology model of MexY identified an indolyl side chain in the transporter's binding pocket that disrupts its interaction with the pyridopyrimidine-derivative inhibitors. Ongoing studies include using the structures to design specific inhibitors against MexB and MexY.	New protein structures unpatented; protein structures available from the Protein Data Bank	Nakashima, R. <i>et al. Nature</i> ; published online June 30, 2013; doi:10.1038/nature12300 Contact: Akihito Yamaguchi, Osaka University, Osaka, Japan e-mail: akihito@sanken.osaka-u.ac.jp
	SciBX 6(32); doi:10.1038/scibx.2013.876 Published online Aug. 22, 2013		