This week in techniques

Approach	Summary	Licensing status	Publication and contact information
Drug platforms			
Crystal structures of Middle East respiratory syndrome coronavirus (MERS-CoV) spike protein	<p>Crystal structures of the MERS-CoV spike protein in complex with its receptor could aid the development of therapeutics and vaccines against the disease. The MERS-CoV spike protein engages with dipeptidyl peptidase-4 (DPP-4; CD26) expressed on host cells. Researchers solved the crystal structures of the MERS-CoV spike protein receptor-binding domain by itself at 2.5 Å resolution and also in complex with DPP-4 at 2.7 Å resolution. The crystal structures showed that the interaction between the receptor-binding domain of the MERS-CoV spike protein and DPP-4 is mediated primarily by hydrophilic amino acid residues and that the spike protein receptor-binding motif is highly variable. Next steps could include using the crystal structures to design compounds that block the spike protein-CD26 interaction.</p> <p>SciBX 6(30); doi:10.1038/scibx.2013.806 Published online Aug. 8, 2013</p>	Patent and licensing status unavailable	<p>Lu, G. <i>et al. Nature</i>; published online July 7, 2013; doi:10.1038/nature12328 Contact: George F. Gao, Institute of Microbiology, Chinese Academy of Sciences, Beijing, China e-mail: gaof@im.ac.cn</p>