This week in techniques

Approach	Summary	Licensing status	Publication and contact information
Drug platforms			
Crystal structure of purinergic receptor P2Y G protein-coupled 12 (P2RY12; P2Y12) bound to an antagonist	<p><i>In vitro</i> structural studies of P2RY12 bound to an antagonist could aid antithrombotic drug design. P2RY12 is activated by nucleotide binding and regulates platelet activation and thrombus formation. A 2.6 Å-resolution crystal structure showed that antagonist-bound P2RY12 adopted a canonical seven-transmembrane bundle of helices and that the extracellular cavity of the receptor is divided into two pockets with the antagonist bound in one. <i>In silico</i> analyses predict that both pockets could be bound by dinucleotide or chemically related molecules. Next steps include understanding how binding in the two pockets impacts affinity and side effects associated with P2RY12 antagonists.</p> <p>P2RY12 antagonists marketed to treat cardiovascular disease include AstraZeneca plc and The Medicines Co.'s Brilinta ticagrelor, Daiichi Sankyo Co. Ltd. and Eli Lilly and Co.'s Effient prasugrel and Sanofi and Bristol-Myers Squibb Co.'s Plavix clopidogrel.</p> <p>At least five companies have P2RY12 antagonists in Phase III or earlier testing to treat cardiovascular disease.</p> <p>SciBX 7(14); doi:10.1038/scibx.2014.415 Published online April 10, 2014</p>	Unpatented; licensing status not applicable	<p>Zhang, K. <i>et al. Nature</i>; published online March 23, 2014; doi:10.1038/nature13083</p> <p>Contact: Qiang Zhao, Shanghai Institute of Materia Medica, Chinese Academy of Sciences, Shanghai, China e-mail: zhaoq@simm.ac.cn</p>