## This week in techniques

| Approach | Summary | Licensing status | Publication and contact information |
|---|---|---|---|
| **Drug platforms** | | | |
| Crystal structure of Selzentry maraviroc–bound HIV-1 co-receptor CC chemokine receptor 5 (CCR5; CD195) | The crystal structure of HIV-1 co-receptor CCR5 bound by the allosteric inhibitor Selzentry maraviroc could help to guide design of therapies for HIV-1 infection. The crystal structure of the complex was determined at 2.7 Å resolution and showed Selzentry bound at a site distinct from proposed recognition sites for chemokines and HIV gp120. Crystal structure–based modeling showed that different charge distributions and steric hindrances in the co-receptor ligand-binding pocket could be major determinants for HIV-1 co-receptor selectivity. Next steps include structural studies of CCR5 and CXC chemokine receptor 4 (CXCR4; NPY3R) in complex with the HIV envelope protein gp120 and CD4 to obtain more insight into the process of viral infection.<br>Selzentry is marketed by Pfizer Inc. to treat HIV/AIDS.<br>CytoDyn Inc.'s CCR5 inhibitor, PRO 140, is in Phase II trials.<br>Tobira Therapeutics Inc. has the dual CCR5 and CCR2 (CD192) antagonist cenicriviroc in Phase II trials to treat HIV/AIDS.<br><br>*SciBX* 6(39); doi:10.1038/scibx.2013.1110<br>Published online Oct. 10, 2013 | Unpatented; licensing status not applicable | Tan, Q. *et al. Science*; published online Sept. 12, 2013; doi:10.1126/science.1241475<br>**Contact:** Beili Wu, Shanghai Institute of Materia Medica, Chinese Academy of Sciences, Shanghai, China<br>e-mail: beiliwu@simm.ac.cn |