SciBX
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THE DISTILLERY

This week in techniques

Approach	Summary	Licensing status	Publication and contact information
Computational models			
Computational approach for prioritizing potential cancer targets	A computational approach that predicts the druggability of cancer-associated proteins could help prioritize targets in small molecule discovery programs. The computational approach integrates target class, bioactivity data, protein structural information and homology modeling to estimate a protein's druggability. From a list of 479 genes known to be altered in cancer, the method identified 29 oncogenes and 16 tumor suppressors predicted to be druggable but for which few or no small molecule ligands had yet been reported. Next steps include incorporating additional cancer genomic data and could include prioritizing additional types of gene lists such as those from synthetic lethal screens in cancer cell lines. The computational method is freely available through the canSAR database hosted by The Institute of Cancer Research. *SciBX* 6(6); doi:10.1038/scibx.2013.150 Published online Feb. 14, 2013	Unpatented; licensing status not applicable	Patel, M.N. *et al. Nat. Rev. Drug Discov.*; published online Dec. 31, 2012; doi:10.1038/nrd3913 **Contact:** Bissan Al-Lazikani, The Institute of Cancer Research, London, U.K. e-mail: bissan.al-lazikani@icr.ac.uk **Contact:** Paul Workman, same affiliation as above e-mail: paul.workman@icr.ac.uk