This week in techniques

Approach	Summary	Licensing status	Publication and contact information
Computational models			
Computational prediction of loops at protein-protein interfaces using LoopFinder	A computational approach to predict loops at protein-protein interfaces could help identify interactions amenable to pharmacological targeting. The program, LoopFinder, searches structural databases for peptide loops at protein-protein interactions, and it identified 121,086 loops. These loops were further analyzed by virtual alanine scanning to identify those that could potentially be targeted to disrupt protein-protein interactions. Next steps include experimentally testing whether compounds that mimic these potentially targetable loop structures can be used to disrupt protein-protein interactions between new targets.	Unpatented; licensing status not applicable	Gavenonis, J. <i>et al. Nat. Chem. Biol.</i> ; published online July 20, 2014; doi:10.1038/nchembio.1580 Contact: Joshua A. Kritzer, Tufts University, Medford, Mass. e-mail: joshua.kritzer@tufts.edu
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