This week in techniques

Computational models

Approach	Summary	Licensing status	Publication and contact information
RNA virus amino acid covariance network analysis for diagnostic and prognostic applications	Amino acid covariance network analysis may be useful for diagnosing infection and predicting responsiveness to RNA virus therapies. A complete genome analysis of 94 HCV sequences isolated from patients showed that amino acid variation patterns corresponded to groups of responders and nonresponders to standard interferon-α (IFN-α) and ribavirin combination therapy. Next steps include validating the results with an external HCV sequence data set and identifying the combination of amino acid positions with the best predictive value. Pegasys peginterferon alfa-2a, a pegylated recombinant IFN-α2a from Roche, is marketed to treat HCV infection. PEG-Intron peginterferon alfa-2b, a pegylated recombinant IFN-α2b from Enzon Pharmaceuticals Inc. and Schering-Plough Corp., is marketed for the same indication. At least 14 other companies have IFN-α-based therapeutics in Phase III or earlier to treat HCV infection. *SciBX* 2(1); doi:10.1038/scibx.2009.32 Published online Jan. 8, 2009	Patent pending covering diagnostic and prognostic uses and for identifying possible drug targets; available for licensing from the Saint Louis University Office of Innovation and Intellectual Property **Contact:** Maurice Foxworth, Saint Louis University, St. Louis, Mo. phone: 314-977-7746 e-mail: foxworth@slu.edu	Ganem, D. *et al. J. Clin. Invest.*; published online Dec. 22, 2008; doi:10.1172/JCI37085 **Contact:** Rajeev Aurora, Saint Louis University School of Medicine, St. Louis, Mo. e-mail: aurorar@slu.edu **Contact:** John E. Tavis, same affiliation as above e-mail: tavisje@slu.edu