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THE DISTILLERY

This week in techniques

Approach	Summary	Licensing status	Publication and contact information
Computational models			
Algorithm for creating charged antibodies to improve stability and preserve activity	*In silico* and *in vitro* studies identified a strategy to create positively charged antibodies that have better stability and lower aggregation than unmodified counterparts. A computational software package from Rosetta Genomics Ltd. was used to identify sites on an antibody in which substitution with charged amino acids would not disrupt binding function. As proof of principle, *in silico* results were used to design variants of the bacteriophage MS2 single-chain variable fragment antibody. *In vitro*, those variants showed greater stability in normal culture conditions than the wild-type antibody. When heated to 70 °C for one hour, the antibody variants showed decreased aggregation compared with the wild-type antibody and maintained 70% of their initial target-binding affinity. Next steps include validating the use of a server that applies the method to other antibodies. *SciBX* 5(19); doi:10.1038/scibx.2012.503 Published online May 10, 2012	Findings unpatented; Rosetta Genomics computational design package, protein design tools and homology modeling technology are open source; unavailable for licensing	Miklos, A.E. *et al. Chem. Biol.*; published online April 20, 2012; doi:10.1016/j.chembiol.2012.01.018 **Contact:** Andrew D. Ellington, The University of Texas at Austin, Austin, Texas e-mail: ellingtonlab@gmail.com