Section 9: CRISPR Off-Target Prediction

The two readings both address the practical application of CRISPR gene editing, specifically, the problem of guiding the nuclease to the correct target site.

, seeking to better understand the molecular composition of proteins. The first, by Dill et al., is a review paper describing the task of understanding and predicting protein folding. The second, by Bowman et al., introduces MSMBUILDER, a python application and library for automating the construction of Markov state models (MSMs). Both papers describe recent advances in protein modeling and demonstrate the value of computational methods in understanding the nature of proteins.

Shengdar et al. begin by d

The paper by Alexendar et al. presents GuideScan, a software system for designing CRISPR guide RNA (gRNA) libraries.

* Shengdar Q. Tsai and J. Keith Joung (2016) Defining and improving the genomewide specificities of CRISPR–Cas9 nucleases. [PDF](http://www.nature.com/nrg/journal/v17/n5/pdf/nrg.2016.28.pdf)
* Alexendar R Perez et al. (2017) GuideScan software for improved single and paired CRISPR guide RNA design. [PDF](http://www.nature.com/nbt/journal/vaop/ncurrent/pdf/nbt.3804.pdf)