

Chemistry 5.08 (Spring 2016)

Recitation #7

“Stochastic but Highly Coordinated Protein Unfolding and Translocation by the ClpXP Proteolytic Machine”

Sauer and co-workers. *Cell* **2014**, *158*, 647-658.

This paper is very dense and complicated. Recitation will focus on Figures 1, 2 and 4. Please focus on these Figures and the methods/results/discussion text related to these figures.

Discussion Questions

1. What is the advantage of looking at one molecule at a time compared to a bulk analysis?
2. How can we study one molecule at a time (“single molecule” studies)?
3. What are the disadvantages of looking at one molecule at a time compared to a bulk analysis?
4. How can single-molecule studies advance our understanding of how ClpXP unfold and translocate substrates?
5. What do you find most interesting about the approach used by Sauer and co-workers?

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