

Macromolecular Structure and Biophysical Analysis (MB&B 420a/720a)

Protein secondary structures and interfaces, part II

Review reading:

Kuriyan, Konforti and Wemmer:

Chapter 4, All of sections C

Additional Reading:

Lohman and Fazio, "How Does a Helicase Unwind DNA? Insights from RecBCD Helicase",
Bioessays **40**, 1800009 (2018)

PMID: 29603305, DOI: 10.1002/bies.201800009

Due by 4:00pm, September 17, 2018:

The structure referred to in reference 21 of Lohman and Fazio as having "melted" is the no-ATP structure deposited as 1W36. Download the pse file I have left for you on canvas called RECBCD.pse. When you open it, you will see I have predefined some relevant selections for you on the right. The view of the pin you see on opening the pse file is also stored as Scene F1, just in case.

Now look at the top two ATP-free states depicted in Lohman and Fazio in Figure 3.

Write a summary of Lohman and Fazio that is < 300 words, is accompanied by a figure stored as Scene F2 in an uploaded pse file and which talks around these two questions:

- a) Which of the two ATP free states in Figure 3 do you think Lohman means is the melted state?
- b) Which of these two ATP-free states do you think is best represented by 1W36 and why?

There is no right answer here. Your grade comes from the clarity of your reasoning and your ability to illustrate your point using a stored pymol "Scene".

No more than 300 words in your narrative please.