

Macromolecular Structure and Biophysical Analysis

(MB&B 420a/720a)

Protein secondary structures and interfaces

Review reading:

Kuriyan, Konforti and Wemmer:
Chapter 4, All of sections A and B

Additional Reading:

To be assigned on Tuesday.

Due by 5:00pm, September 12, 2018:

1a) Align 6BXX and 6BWZ using the “pair fitting” wizard and selecting only atoms contained in Y2 and Y38 respectively.

1b) Which residues on the two proteins (other than Y2 and Y38) become aligned after this procedure?

1c) Which torsional angle(s) is (are) most responsible for the imperfect alignment of the backbone? (Use the measurement tool set to “dihedrals” to be more specific and make better illustrations).

NOTE: In answering 1a and 1c, save a pose or two in Pymol using the “Store” function to illustrate your points. Upload a saved session (.pse file) as part of this homework. No need for figures in your narrative. Instead, just direct us to which “Scene” you want us to “Recall”.

2) PDB IDs: 1FBI and 2DQJ are each cocrystal structures of lysozyme with a monoclonal antibody. The lysozymes are the same, but the monoclonals are different and yet bind to the same epitope on lysozyme.

2a) Spend no more than 5 to 10 minutes trying to align the structures using only backbone atoms of the lysozymes. Try this yourself, store a pose, save a session and upload. Be sure to direct us to the stored pose in the narrative of your homework. This is not straightforward. For 2a, effort counts, not success.

2b) Load the pse file I have provided for you on canvas called “PreAligned_1FBI_2DQJ.pse”. You will find the lysozyme structures aligned, but also you will find some independently named selections so that you can conveniently change the lysozyme or the antibody in each of the respective chains.

Pick one and only one of the following amino acids in lysozyme, Y20, N93, K97 and N77. For this amino acid, write a narrative (and make a figure or two stored in a pse file) that compares and contrasts the interactions with the corresponding antibody. Imagine you are trying to decide if you can use mutation to reengineer the two antibodies into a super antibody that combines the best interactions for each of the interfaces.

Keep yourself to under 500 words and one or two poses. Two or three of you will be presenting your interpretation in class, so keep your pse files safe.

You are strongly encouraged to work together. If you do so, please be sure each member of the study group works on a different one of the 4 amino acids.