

This quiz is designed to encourage you to look at protein structures. It contains 2 parts.

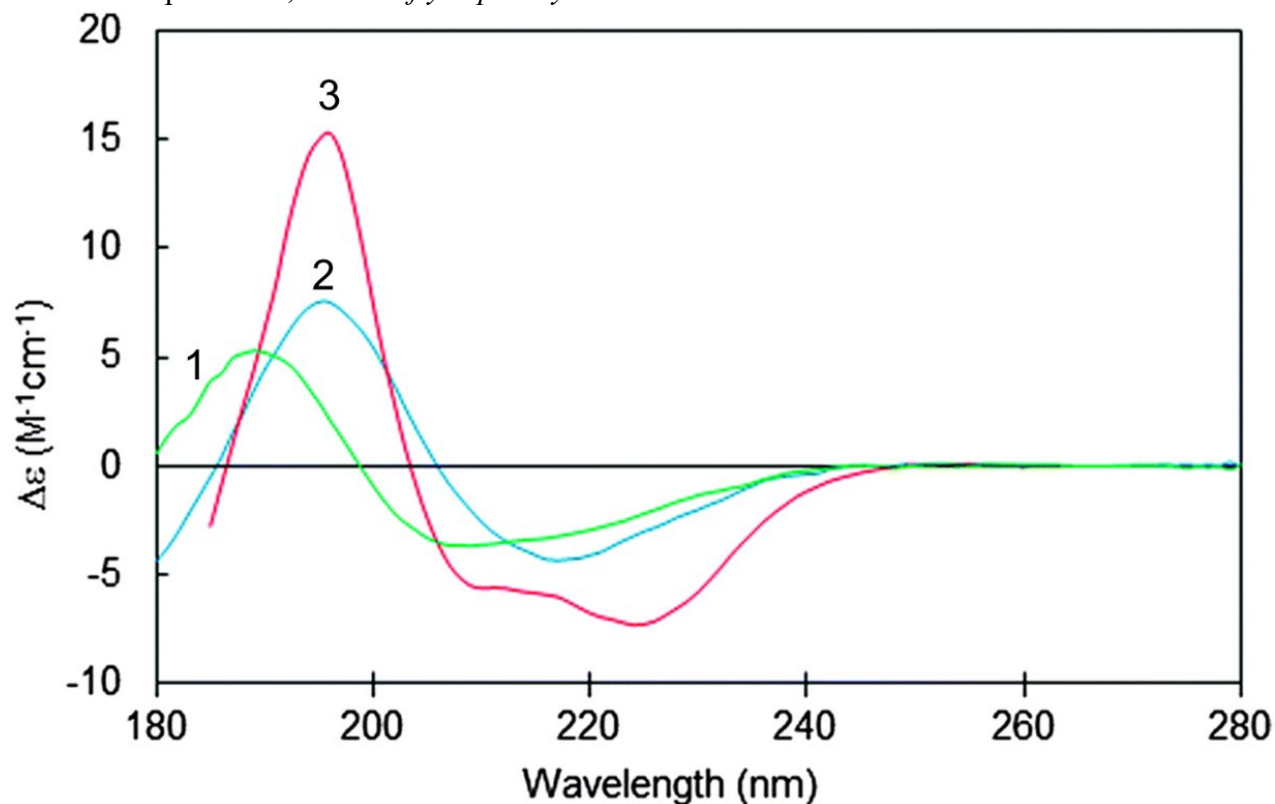
Part 1. Analyze the structures of the following five proteins, identified here by their PDB IDs: **6ZCT, 1EE6, 1NQE, 4F4L, 2TRC**. For each protein, identify the number of chains, elements of secondary structure and possibly supersecondary structure motifs, and fill out the table below.

Note: my count of the number of helices and strands is based on how the authors of the structure identified them in the protein coordinates (*.pdb) file, although in a few cases I found the same “sheet” element was listed twice, so I had to correct the total count.

Protein ID	# of chains	# of helices	# of β -strands	If β -sheets: are they parallel, antiparallel, or mixed	List structural motifs (supersecondary) that you can identify	Molecular weight*
6ZCT	protein name: Nonstructural protein 10 (nsp10) from SARS CoV-2					
	1	6	3	antiparallel	Two Zn fingers, helix-turn-helix (or helix-loop-helix)	13155 Da
1EE6	protein name: pectate lyase					
	1	0	19	parallel	beta-helix	20923 Da
1NQE	protein name: outer membrane cobalamin transporter (vitamin b12 receptor)					
	1	9	33	Antiparallel (4) and one mixed	Beta-hairpins, beta-barrel	61367 Da
4F4L	protein name: voltage gated sodium channel, ion transport protein					
	4	20 (5 per chain)	0	N/A	Maybe helix-turn(or loop)-helix.	38482 Da
2TRC	protein name: phosducin/transducin beta-gamma complex					
	3	16	$7*4+5=33$	Antiparallel (7) and one mixed	Beta-alpha-beta, beta-hairpin, beta-propeller	69164 Da

*to accurately compute the molecular weight you need to either delete all waters and ions or simply select the protein (not protein with waters or ions) and in the Action/compute menu use the option “with missing hydrogens”

Part 2. A graduate student measured circular dichroism (CD) spectra of three of these proteins; the resulting curves are shown below, labeled 1, 2, and 3. Unfortunately, the student misplaced the notebook (or maybe the dog ate it?) with the information on which spectrum belongs to which protein. Your goal is to help the student relate the CD spectra to the proteins. *Which of these proteins are likely responsible for each of the CD curves?* Some relevant information can be found on the Lecture 17 slides and in Figure 4-9 in the textbook. Your answer can be simply textual: 1 = protein X, etc. *Briefly explain your rationale.*



CD spectrum	Likely protein(s) (PDB ID)
1	6ZCT, because of significant percentage (64%) of residues in loops/unstructured regions
2	1EE6 because it is completely beta A possible runner-up is – maaayyybe – 1NQE because it's mostly beta with a very small percentage of helical residues (3+8+7+5+4+5+6+5+7 = 50 out of 594 i.e. 8%), although it contains a lot of loops, some of which are so disordered that they are “invisible” (not located) in the crystal structure
3	4F4L because it is completely alpha-helical

My answers here are based on observing characteristic CD “signatures” of a helix and a beta-sheet in the wavelength range from 205 nm and up, where the random coil’s ellipticity signal is close to zero and does not contribute significantly to the total observed CD signal.