Independent Project

Your objective is to produce a presentation on one of the proteins selected from the list on the last page. The choice of which structure you will present is up to you, but the decision must be finalized by 5 PM on Friday, October 8 (the last day before the midsemester break). Each protein can be presented by only one student, who will be assigned the protein on a first-come first-served basis - you email your choice to me, and my reply to that email, indicating that your choice is acceptable, constitutes the final decision.

This presentation will include the following:

1. A Powerpoint presentation describing the biological function of the chosen protein. This presentation (and the next one) should be considered as an outline of a paper on the topic, with the paragraphs of the (nonexistent) paper corresponding to pages of the presentation. The presentation on the protein function should be suitable for advanced students. You may obtain initial information about the subject from an introductory biology text book, and more detailed information from either a biochemistry textbook (Stryer is recommended) or cell biology text (Alberts et al is recommended). These sources will also provide you references to reviews and the most important primary literature, all of which you should pursue. A final major source will be references in the opening paragraphs of the paper describing the structure. From all of these sources, and accessory materials to which they lead, you will provide a description of what the protein does in sufficient detail to pose the molecular mechanism questions which the structure will address.

2. A second Powerpoint presentation describing the structure of the protein. This presentation will consist of an exegesis of the paper, or papers, describing the structure of the protein. In some cases, there are many structures and papers, and some judgement will be required to select the most fundamental, most complete, or most central of these for presentation. The presentation should include ample illustrations; these should not be taken from the papers, but rather should be created by you using Protein Explorer or Cn3D. In each case, you should include a small text box (probably in smaller font) describing how the illustration was created. The presentation pages will probably contain more explanatory text than are found in lecture notes from class, since they must be complete and self-contained. This presentation should address the various questions posed in the first presentation.

3. An *annotated* bibliography. This bibliography should include all of the references which you consulted during the preparation of the presentation, whether or not any of their contents made it into the final products. With each reference, you should include a sentence (or maybe two) summarizing the relevance of the contents to the overall subject.

The results of your work can be submitted electronically by Email, or delivered on a PC-format memory stick. The presentations should be in Microsoft Powerpoint, the bibliography in either

Word or WordPerfect format. If you operate on a Mac system, you should consult with me well before the due date to straighten out potential compatibility problems. A rough draft of both presentations must be in my hands before Thanksgiving break, , in preparation for a meeting with me that must be scheduled at least one week before your presentation day. A final version of all required materials must be received and acknowledged by me before the end of the third day of finals (Monday, December 20).

Project Proteins

1. **Argonaute:** A new structure (1UO4) about one of the hottest topics in current molecular biology - the engine at the center of the small inhibitory RNA process.

2. **Nucleosome**: The original structure (1AOI) has been supplemented by high resolution structures, and by a structure from yeast (1ID3).

3. **Nuclear Export Complex:** The most recent contribution to the structural characterization of nuclear import and export processes appeared a couple of summers ago (3GJX).

4. **Nitrogenase**: Also examined in pieces, a combined structure can be found in 1N2C.

5. **Acetylcholine receptor**: The epitome of electron crystallography (1OED), combined with modeling help from an X-ray structure of a homologous protein (1I9B).

6. **Lac permease**: A classic protein, studied in immense detail biochemically before its structure was determined (1PV6).

7. **Signal Recognition Particle**. An RNA/protein complex whose structure is not completely known, but chunks of it are, with lots of different functions. (2V3C)

8. **ABC ATPases**. Membrane ATPases associated with transport functions. A great collection of structures, a problematic function. (1L7V).

9. **Protein translocation channel**. Sec61, a channel that gets proteins either across or into membranes at the time of their translation.(1RH5)

10. **Proteasome**. For such an awesome (aweful?) structure, this one has been determined many times, from many organisms. A moderately complete and complex structure from yeast has been determined at high resolution. (1RYP)

11. **Nuclear receptors**: Lots of these have been crystallized. At first glance, they are all pretty much the same, but it turns out the differences between them tell the story of how they work. (1BY4)

12. **Fatty acid synthase**: A classic rotating tether model (featured in Bio 30 for years) finally gets a high resolution structure. (2UVB)

13. **Rhomboid protease**: These do a fairly routine thing in a very non-routine location, which

turns out to be interesting for some important corners of biology. (2ICB)

14. **E2 protein**: Ubiquitination is a big deal in current research circles, and E2 proteins are central to the process which adds ubiquitin to some proteins, and not others. (2BF8)

15. **Cyclin/CDK/p27:** Cyclin-mediated regulation of the cell cycle is a central process in understanding regulation of growth and cancer. (1JSU)

16. **Nonribosomal peptide synthetase**: Proteins don't need ribosomal RNA or mRNA to make other proteins, as long as the product proteins are little, and this is a machine that can do it. (2VSQ)

17. **Influenza virus**: Viruses are big, but often the structure of the virion is just a magnificent three dimensional stack of a single or a few proteins. The influenza virus is rather more complicated, and a recent structure from cryo-EM (the PDB code given here) was complemented by a standard crystallographic analysis in the same issue of science (3IVN).

18. **Coatamer**: Formation of vesicles in eukaryotic cells, part of the process of membrane trafficking, requires formation of a lattice surrounding the incipient vesicle. This structure identifies many of the principles of the construction of such lattices (3MKQ).