

"The Anatomy & Taxonomy of Protein Structure" by Jane S. Richardson *Advances in Protein Chemistry* **34**, 167-339 (1981). Updated annotated web edition.

Overview:

The Richardson paper is a **classic, comprehensive review** of what was known about **protein structure** from early **crystallographic** studies. This is a beautifully written article with many elegant figures, and I think it works well as an introduction to protein structure. The web edition assigned here has several neat features: 1) it is annotated to incorporate newer results that have elaborated on, or contradicted, earlier finding and interpretations, 2) there are a number of "kinemages" included, which for viewing require your browser to be Java-enabled. Kinemages are essentially teaching figures that can be manipulated to zoom in, out and rotate elements of the picture. Note also that the review is downloadable as PDF files.

What I want you to get out of this paper:

For Friday, August 24, read the sections on Anatomy, up through the section on tight turns. For Monday, August 27, finish the rest of the Anatomy section. Refer also to the powerpoint slides for additional material/facts, plus a slightly different perspective. The powerpoint notes don't necessarily follow the reading, rather they add information not found in the Richardson article. The overall goal here is to gain **a basic understanding of the fundamental issues in protein conformation**, both backbone and side chain. There is a section called "levels of error" which discusses many aspects of the inherent uncertainties in determining protein structures experimentally. The details of this will become clearer later as the experimental aspects of crystallography are covered in week 7 or 8. For now, however, the key message is that for the most part our understanding of protein structure is only as good as our ability to experimentally determine it, and although many protein structures are known at levels of resolution high enough to measure bond angles etc. accurately, many are not. Also note that some of the material in the review, such as diagonal plots and propensities of residue types to be in certain conformations, may not be covered in class until a few lectures from now. If you don't understand something, just hang on and things will become clearer as we move along. The important thing now is to read through the review and understand what you can.

Below are a number of questions I'd like you to think about for discussion in class on **Monday, August 27:**

- >> Begin pondering why the regions of actual observed phi-psi angle combinations in proteins (Ramachandran plot) might not exactly match the distributions predicted from theories based on steric clashes. Figure 7x vs. Figure 9 in the Richardson paper.
- >>Why do you think mixed antiparallel/parallel beta-sheets are less common than pure parallel or antiparallel?
- >>Think of two reasons why proline can't be accommodated well within the body of a helix. What is the one place in a helix where it CAN be accommodated?
- >>The review notes that the classic role of tight turns to connect two adjacent antiparallel beta-strands in a "hairpin" can only be easily fulfilled by type I' and II' turns. Without worrying about in too much detail, considered why such a preference might exist.
- >>What is meant by "coil" structure in proteins?

