1.   Reading assignment 1. Preface.

Find the file "TA-PrStrPr_t1v3.rar", and within it a document. Read the Preface (pages XII to XIV) and answer the following questions.

1. What is the biggest challenge for the next generation of scientists?

   The proteins specific sequence is dictated by the genes of an organism. The genes are translated into the linear sequence of amino acids of the encoded protein through a universally conserved code. The biggest challenge is the identification of the function of the encoded proteins in different genomes (whose identification of coding regions is not completely solved).

2. What is regarded as the "Holy Grail" of biology?

   Understanding the underlying rules that let a protein (linear sequence) to spontaneously refold to its native form (three-dimensional structure), whose information that determines it resides in the chemistry of the protein's amino acid sequence.

3. For what purposes has structure prediction been used?

   To make an effective use of the large body of genetic information available for many organisms, humans included, list all their functions, and study their interplay in shaping life. The problem has an enormous relevance in many fields such as medicine, biology, biotechnology and pharmacology.

4. What would be an inadequate way to use an approximate model of a protein?

   There is no point in constructing a very approximate model of a protein and later to use it to derive detailed properties about catalytic mechanisms or interaction details; similarly, it is not wise to employ very sophisticated techniques to obtain a model of a protein that, for technical reasons, cannot be used for guiding experiments or for casting light on important biological questions.