Possible Exam Questions

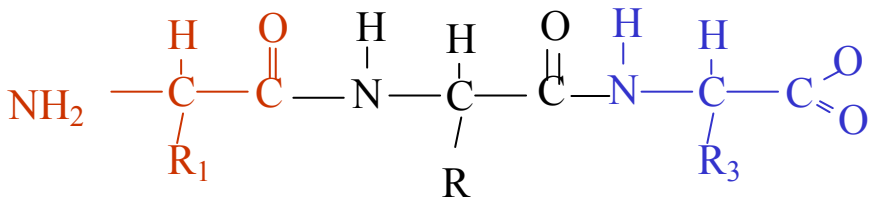
GST 00.908 Jan 2008

The exams will be in German and English. Sie durfen auf Englisch oder Deutsch anworten.

* What order of magnitude is a chemical bond (in Å) ?

* On the diagram, mark the two backbone angles which can rotate in a normal protein. You only need do this for one residue.

Mark the angle which is nearly planar (flat).



* Why can I not have a short α-helix which is only 2 residues long ?

* Name a small amino acid.

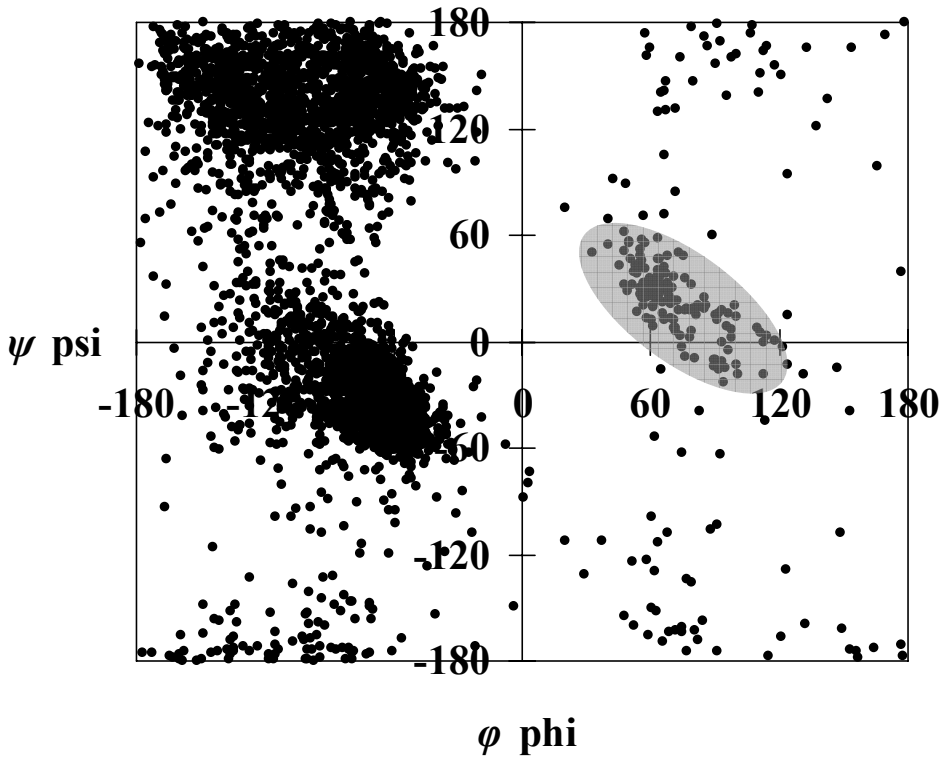
* Name a large hydrophobic amino acid.

* Name the amino acid which often forms covalent bonds from its side-chain.

* If you consider a ramachandran plot for a protein, there is a region where only one amino acid is found, marked on the diagram by the grey oval.

Which amino acid is this ?

Why can it occupy this area ?



* If you see the formula: $\rho_x = 1/a \sum_h |F_h| \cos(2\pi h - \alpha_h)$ it tells you you can calculate the electron density in one dimension given some observed structure factors. Which term is the phase angle ?

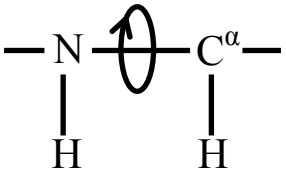
* In the method known as multiple isomorphous replacement, one uses heavy atoms to solve the phase problem. Give an outline of the method.

* A protein data bank file contains columns of "B-Factors". In physical terms, what do these mean ?

* Explain the difference between static and dynamic disorder.

* Name two types of nuclei which are important in structure determination using NMR data. You must get the isotope correct.

* What are the most important kinds of information / measurements which come from NMR for determining macromolecular structure ?

* There is a relationship between torsion angle and the *J* coupling measured between the amide (N) H and the proton bound to the C^{α}.  It is not usually possible to calculate the angle simply from a measurement of the measure *J* coupling. Why ? Draw a diagram if it is helpful.

* If you have a set of particles in space and a set of distances, you might try to use simple trigonometry to calculate the coordinates. Why is this not going to work for protein coordinates based on NMR data ?

* For three points, draw a diagram with distances between the points which do not obey the triangle inequality.

* If you want to calculate a structure from NMR data, you may turn the problem into a distance geometry problem. The experimental information is not enough to define the location of points in space. You know the sequence of a protein. What other information can be added ?

* Describe in words or pseudocode a method which will let you find the tightest bound between any two atoms in a protein.

* Why may chirality be a problem in a structure solved, based on NMR data using the metric matrix method ?

* What are two reasonable ways to define / recognise secondary structure in proteins ?

* You use two different programs to recognise (label) secondary structure in a protein. Both are based on recognising hydrogen bonds, but they give slightly different answers. What is a likely reason (aside from programming errors) ?

* Describe a sensible definition of protein domains.

* I have a pair of proteins with 25 % sequence identity. I want to guess whether they have similar structures. What else do I need to know in order to judge this ? Why ?

* Over the course of evolution, which changes faster – protein sequence or structure ? Give a reason why this may be the case.

* Some protein structure classifications impose a hierarchy on proteins. Why may this be a reasonable thing to do ?

* Give an argument why a hierarchical classification may not be appropriate for many proteins.

* Why is it fundamentally difficult to superimpose two protein structures if they are not the same size ?

* Write in pseudocode a method which may work to find the similar region between two proteins.

* I have two proteins and an effective algorithm to find the common region between two protein structures. When I run the program I find the following alignment:

	residues			
protein 1	1-10	11-60		61-90
protein 2		1-50	51-70	71-100

So, for example, residues 11-60 in protein 1 are aligned to 1 to 50 in protein 2. Draw a diagram of what the structures could look like. Mark in the residue numbers.

* I have two models of one protein, but they are rather different. Describe an algorithm with pseudo-code to find the more similar regions of the structures.

* You would like to align protein structures of different sizes and you would like to turn the problem into a classic dynamic programming formulation. Describe one method for this.

* Similarity of protein structures is often measured using the root mean square difference of coordinates. Draw an example to show why this may not be a good measure.

* Describe a measure of protein similarity which is quantitative (in Å), but is not the root mean square difference (rmsd) of Cartesian coordinates. Why may it be better than rmsd of Cartesian coordinates.

* You have built an initial structural model for a sequence. You have a very simple model for the energy of the system. Describe a method to find a reasonable arrangement of side-chains.

* You want to use distance geometry to generate possible conformations of a loop in a protein. You have endpoints for the loops. Describe how you would cast this into a problem suitable for the metric matrix method.