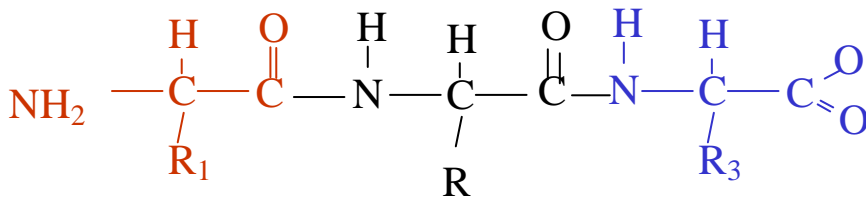Revision Übung GST

For 16 Dec 2009

All written exams will be in German. One can answer in English or German.

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

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


3. Mark the angle which is nearly planar (flat).

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

5. Name a small amino acid.

6. Name a large hydrophobic amino acid.

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

8. 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.
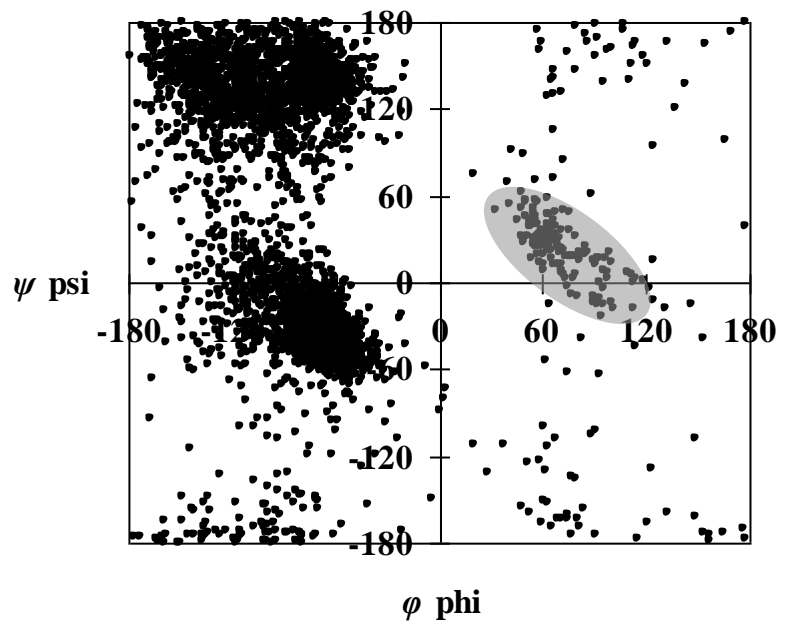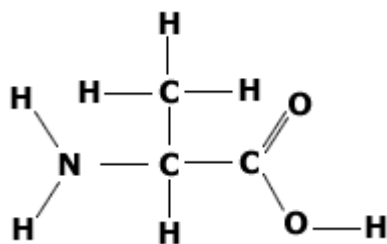

Which amino acid is this ? Why can it occupy this area ?

9. Why can proline not be part of a perfect α-helix ?

10. Name three elements, with the correct nuclei, which are relevant to biochemistry and NMR.

11. In an NMR spectrum, the hydrogen in the hydroxyl group is not normally seen.
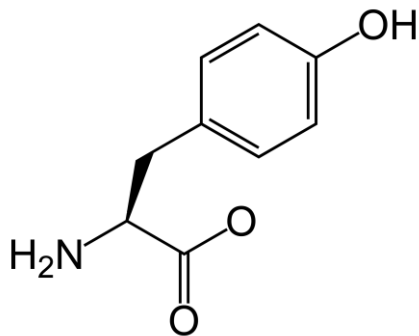
Why ?

12. In the structure of alanine, which protons would be J (spin/spin) coupled to another ?

13. When calculating a protein structure based on NMR data, what information does one get from the size of a J (spin-spin) coupling constant ?

14. Why are only some values of the coupling constant useful ?

15. You use the metric matrix method to calculate the structure of a protein, but you do not have any experimental data.

    a. What would you expect if you generate 20 structures ?

16. In a distance geometry calculation, I have a set of atoms i-j-k-l-m-n. What stops atoms i and n ending on top of each other ? If I know nothing about the angles in the structure, what is the minimum distance d_{ik} ?

17. Draw a graph that corresponds to this distance matrix

	A	B	C	D	E
A	0		4		
B		0	2	5	3
C			0	2	1
D				0	
E					0

What is the maximum distance between points D and E ?

18. What is an advantage of the variable target function method compared to the metric matrix method of distance geometry ?

19. The metric matrix method has $O(n^3)$ running time. Explain in one sentence.

20. What is the running time of the variable target function method ?

21. Write a wave equation in any format you like. Explain each term

22. Given $F_{hkl} = \sum_{j=1}^{n} e^{2\pi i (x_j + ky_j + lz_j)}$, explain what F_{hkl} is. What are x, y and z ?

23. Given $\rho_{x,y,z} = V^{-1} \sum_h \sum_k \sum_l F_{h,k,l} e^{-2\pi i (x + ky + lz)}$, explain what each of the terms are.

24. Explain why you cannot simply Fourier transform to recover $\rho_{x,y,z}$.

25. In MIR (heavy atom phasing), you have recorded data of protein alone and protein with heavy atoms. What is the first step to using this for phasing ? Describe the difference between an R factor and R_{free}.