

## Chemguide – answers

### PROTEINS: STRUCTURE



It doesn't matter whether you have drawn the C=O bonds upwards or downwards, but it is common to have the N-H bonds going the opposite way. In the case of the glycine residue, you could draw the hydrocarbon group as CH<sub>2</sub> rather than separating out one of the hydrogens. And you could also show the full structure of the COOH group if you wanted to.

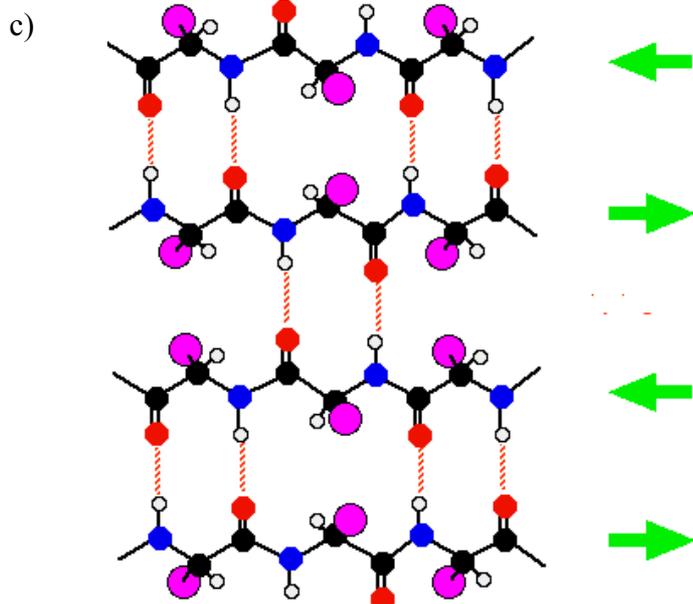
b) There will always be an NH<sub>2</sub> group at one end of a peptide chain and a COOH group at the other. The end with the NH<sub>2</sub> group is the N-terminal, and the one with the COOH group is the C-terminal. The left-hand end of the peptide chain as you have written it is always the N terminal.

c) No, it would be a different molecule. In the original Gly.Lys.Pro.Val.Val.Ala, there would be an NH<sub>2</sub> group left unreacted on the glycine residue, because the left-hand end of the peptide chain as you have written it is the N-terminal. Similarly there would be an unreacted COOH group on the alanine end.

In the the case of Ala.Val.Val.Pro.Lys.Gly the opposite is true. There is an unreacted NH<sub>2</sub> group on the alanine residue (because by convention that is what the left-hand end has), and an unreacted COOH group on the glycine residue. So the molecule is joined up entirely differently.

2. a) beta-pleated sheets

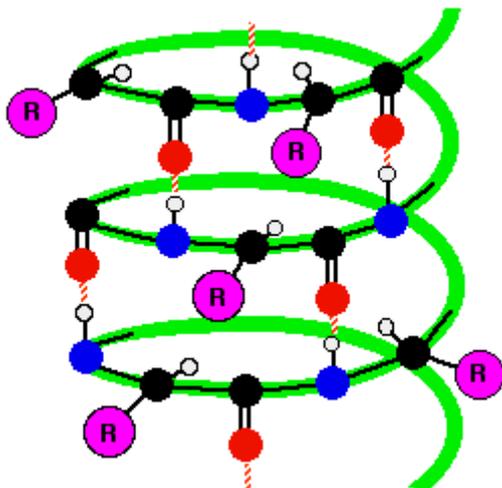
b) hydrogen bonds



## Chemguide – answers

d) alpha-helices or alpha-helices (you will find both versions of the plural)

e) hydrogen bonds



f) Simple bits of protein chain with neither beta-pleated sheets nor alpha-helices.

g) Secondary structures.

3. These are all interactions involving groups in the side-chains, not between the C=O and N-H groups as in the last question.

### ***Ionic interactions***

Some side-groups have an extra  $\text{NH}_2$  group, and some have an extra  $\text{COOH}$  group. When these come close to each other if the chain gets folded, you can get a transfer of a hydrogen ion from the  $\text{COOH}$  group to the  $\text{NH}_2$  group producing two ionic groups:  $\text{COO}^-$  and  $\text{NH}_3^+$ . The ionic attractions between these will hold the protein chain into that folded shape.

### ***Hydrogen bonds***

If side-groups contain groups like OH or  $\text{COOH}$  or  $\text{NH}_2$  or  $\text{CONH}_2$  which can hydrogen bond, then if two such groups come close to each other when the chain gets folded, the hydrogen bonds formed between them will also hold the protein chain into that folded shape.

### ***van der Waals dispersion forces***

Some amino acids have quite large side groups and so can produce quite large van der Waals forces if they come close to another big group when the chain folds. That again holds the fold in place.

### ***Sulphur-sulphur bridges***

One amino acid (cysteine) contains an SH group. If two of these get close together as the chain folds, an S-S covalent bond forms between them which locks the fold firmly into place.

In all of this, I have concentrated on the chemistry aspects of protein structure – the various types of bonding involved in the structure. If you are reading this for biology or biochemistry purposes, you will probably need much more than this.