1.

(a) From the length of C-N bond in peptide linkage, we can speculate that the strength of peptide bond is between double bond and single bond, and peptide bond is special bond which have properties of both double and single bond.

(b) The observations indicate that it is not easy for peptide bond to rotate because four atoms attached to the C-N bond group are located in the same plane and to α-carbon atoms are always trans to each other.

2.

(a) Wool fiber is constituted by alpha-keratin whose main secondary structure is alpha-helix. Steam and stretch can break hydrogen bonds which maintain the structure of alpha-helix, so the conformation is convert to beta conformation.

Two alpha-keratin strands twisted into a coiled coil produce the 5.2Ǻ.

(b) Silk fiber is constituted by beta-keratin rather than alpha-keratin. Hydrogen bond in beta-keratin is between parallel peptide fragments but not between different residue of one fragment. So breaking hydrogen bonds of beta-keratin cannot enlarge the space of repeating structural units.

5.

(a) Disulfide bond is a kind of covalent bond between Cys residues in peptide chain. From the properties of covalent bonds, it is much harder to break than noncovalent interactions. So, the structure of protein which is rich in disulfide bonds is much more stable than protein doesn’t have much.

(b) Disulfide bond cannot be break by heating. As noncovalent bonds are broken, disulfide bonds can stabilize a basic spatial relation of peptide chain. Thus, the protein contain multiple disulfide bond is more stable in heating, and is easy to achieve proper conformation when cooling the solution.

Cystine can, depending on their location in the protein structure, prevent or restrict the movement of folded protein domains, block access of solvent water to the interior of the protein, and prevent the complete of unfolding protein.

12.

(a) In each peptide, only the N-terminal residue can be marked by 2,4-FDNP. So we can calculate the amount of DNP-Val and amount of protein and their ratio is the unit the protein have.

(b) Mr (DNP-Val) =283, Mr (protein)=132,000, m (DNP-Val) =0.0055g m (protein) =0.66g

This protein contains 4 subunits.

(c) We can use SDS-PAGE to detect the number of subunits. SDS and reducing agents can break quaternary structure of protein and each band on gel indicate a single subunit or some subunits. By check these bands and their Mr, we can know the number of subunits the protein has.

13.

(a) is more likely to take up an alpha-helix because (b) have some proline and glycine residues which will break the structure of alpha-helix.