

Water

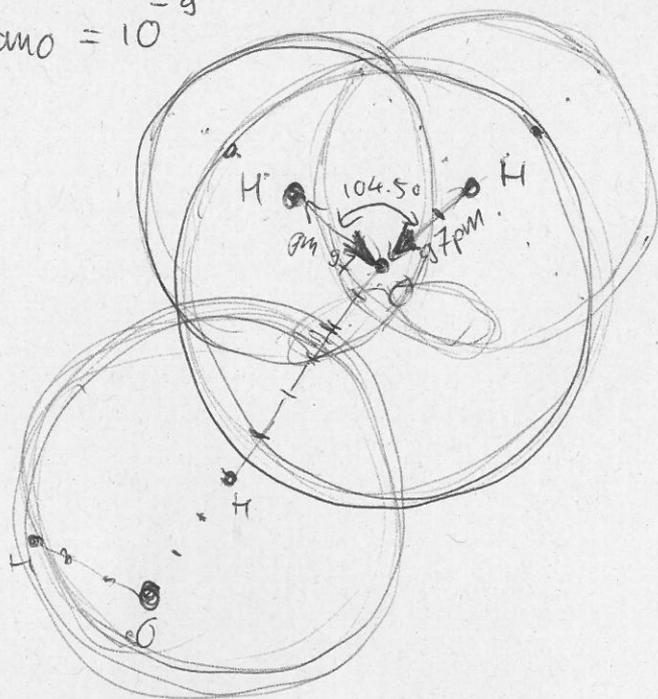
anomalous: - although water is abundant in nature, its properties are rather unique compared to other liquids

properties of a single water molecule

pico = 10^{-12}
 nano = 10^{-9}

Ångström = 10^{-10} m

O-H \approx 97 pm
 $r(O) \approx$ 150 pm
 $r(H) \approx$ 120 pm
 O...H \approx 177 pm



- tetrahedral: the non bonding e^- pairs take up space as well

- irregular tetrahedron: the non bonding e^- - pairs take up more space than the H-s

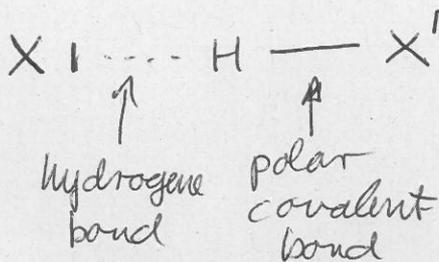
- the H-s electron cloud overlaps to a great extent with that of the O-s.

- because of the 104.5° angle and the EN difference, the water molecule has a permanent dipole moment.

the overlap between the electron clouds of the H and O atoms in a hydrogen bond is also significant

hydrogen bond

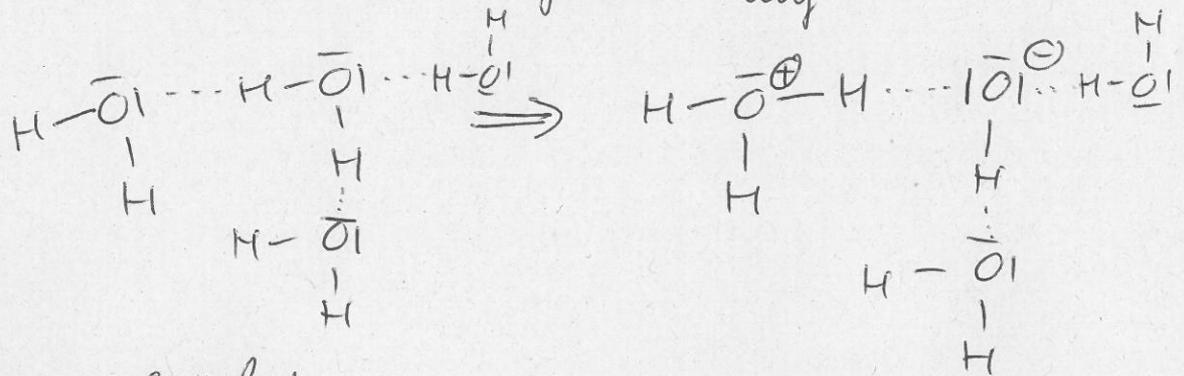
X: high EN atom
 N, O, F



a hydrogen bond can be considered a weak, polar, dative covalent bond

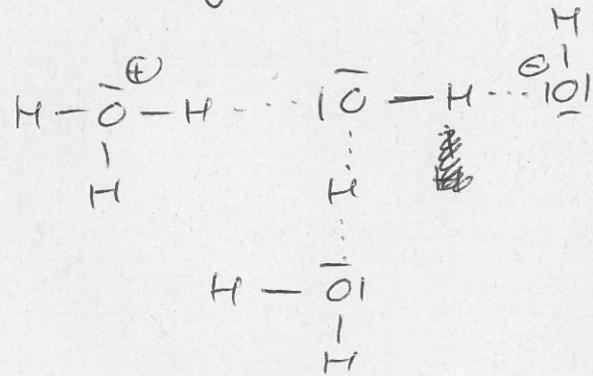
giving even more heat will melt the ice

- the tetrahedral structure will "collapse"
- the water will become more "packed"
- ~~the~~ density increases, maximum is reached at $+4^{\circ}\text{C}$
- in liquid water there is still some degree of order but it is short range, only a few or few ten ~~atoms~~ or molecules are involved
- the ordered structures are short-lived, and transform dynamically



- the $\text{H}-\text{O}$ covalent bonds transform rapidly into $\text{H} \cdots \text{O}$ hydrogen bonds

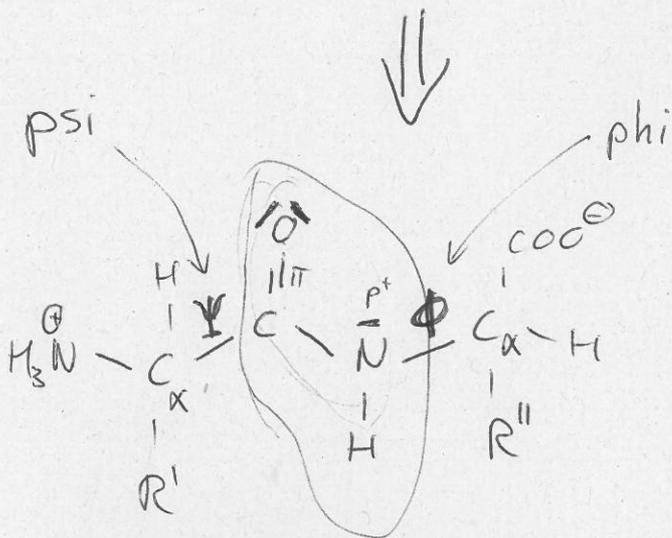
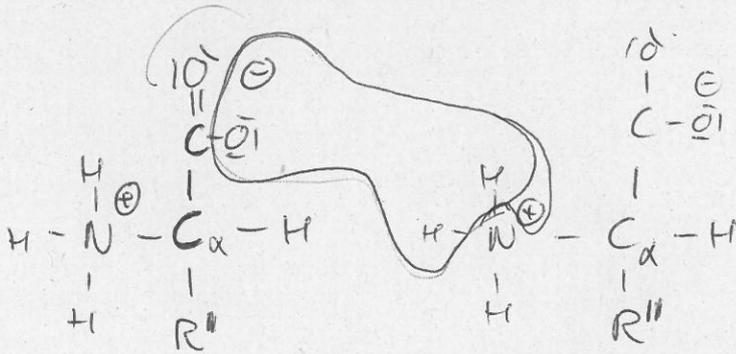
- hydrogen bonds break up and re-form very quickly (10^{10} times/s)



- the organized structure in liquid water is e.g. the water cluster

Proteins

- directed ~~hetero~~ heteropolymers of the 20 (+2) proteinogenic amino acids



peptide bond with delocalized electrons

all atoms involved in the delocalization will be in the same plane

COPLANAR

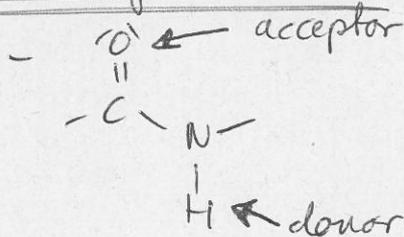
- no free rotation about the $\overset{\ominus}{\text{O}} \parallel \text{C} - \overset{\oplus}{\text{N}} \text{ bond}$

- only the Ψ and Φ torsional angles allow relatively free rotation. \rightarrow protein structure
- there is a hierarchy in protein structure

primary structure:

- the amino acid sequence = constitution
- stabilized by covalent (peptide) bonds
- chemical methods, sequencing

secondary structure:



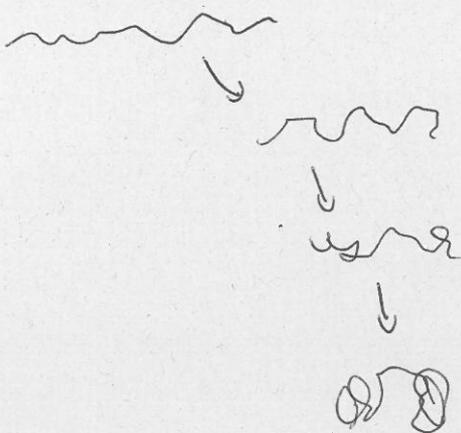
- local order in the size of ψ and ϕ torsional angles involving at least 3 amino-acid residues (units)
- it is stabilized by hydrogen bonds between the polypeptid backbone N and O

- possible angle combinations are shown in the RAMACHANDRAN plot

- typical examples:
- α helix (right handed)
 - β -sheet (parallel & anti parallel)
 - β -turn

tertiary structure:

- complete protein conformation
- 3D-structure
- stabilized by hydrophobic interactions
- the process of the formation of this structure is called protein folding.



~~tertiary~~

quaternary structure

- proteins consisting of several subunits : polypeptide chains
- hydrophobic interaction

Nucleic acids

primary structure: → nucleotide sequence

secondary structure: → double helix

- A, B, Z

- stabilized by base pairing

tertiary structure: → nucleosome formation
super helix



chromosome