PROTEINS

- more than 50% dry mass of cells.

★ the folding is spontaneous

★ the folding is driven by the FORMATION of various bonds between parts of the chain which depends on the ↓

SEQUENCE of AMINO ACIDS

(polar, non-polar, positive, negative, sulfur containing)

⇒ FORM & FUNCTION

→ binding to other molecules

- Antibodies
- hormones
- enzymes

Primary Structure

DICTATED by the genetic CODE !!

- assembled AT ribosomes from mRNA ∈

Secondary Structure

- COILS or FOLDS
  (α helix) (β pleated sheet)

Arising from Hydrogen Bonds between constituents of polypeptide BACKBONE, NOT (!!) the SIDE CHAINS (R-groups)

✡ - A protein can have "regions" of α helices or can be all α helices

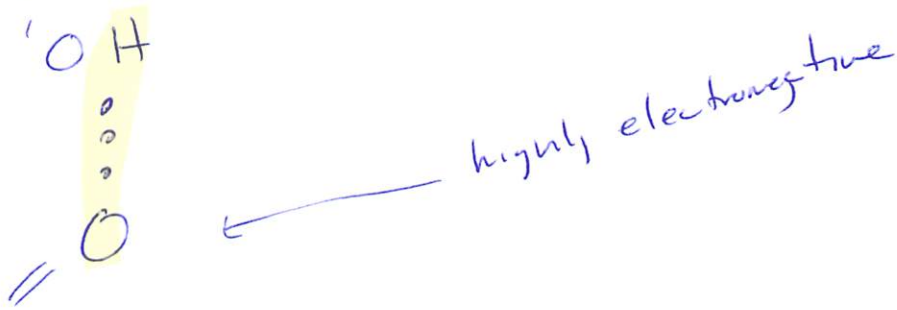
✡ - β pleated sheets composed of side by side β strands held together by Hydrogen Bonds

---

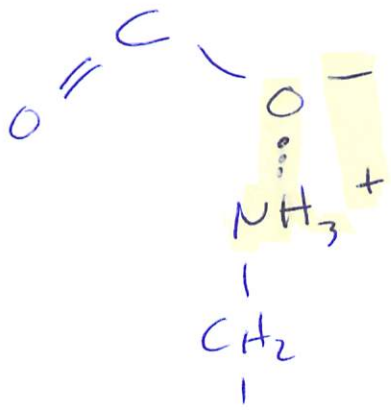
TERTIARY STRUCTURE

⇒ ARISES from INTERACTIONS among the SIDE CHAINS (R-Groups)

(1) Hydrogen Bonds



(2) Ionic Bonds

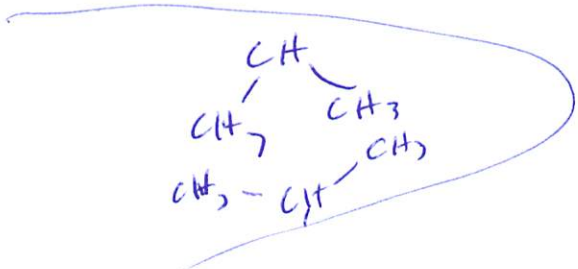


(3) Di Sulfide Bridges (cysteine)

covalent bond

- only AA with sulfur !

(4) Hydrophobic interactions & VDW's



→ clustering away from water on interior.

Quaternary Structure (some proteins)

- 2 or more polypeptide chains
- collagen – 3 units
- hemoglobin – 4 units

Sickle Cell Disease (Anemia)

- one substitution in primary structure
  VALINE for GLUTAMIC ACID
- affects structure and function of Protein.

De Naturation (A-ha!)

- pH
- ionic conditions
- heat
- non-polar solvents

> alter the protein's shape & affect FUNCTION.

- we know primary structure for 10 million
- tertiary for 20,000 LOTS of WORK left!!

Misfolding ⇒ Alzheimers, Parkinson's, mad cow