Semester-III

Biochemistry Notes

An Introduction to Protein Structure

by

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SEC 2 – ANALYTICAL CLINICAL BIOCHEMISTRY

Carbohydrates: Biological importance of carbohydrates, Metabolism, Cellular currency of energy (ATP), Glycolysis, Alcoholic and Lactic acid fermentations, Krebs cycle. Isolation and characterization of polysachharides.

***Proteins:* Classification, biological importance; Primary and secondary and tertiary structures of proteins: α-helix and β- pleated sheets, Isolation, characterization, denaturation of proteins.**

Enzymes: Nomenclature, Characteristics (mention of Ribozymes), and Classification; Active site, Mechanism of enzyme action, Stereospecificity of enzymes, Coenzymes and cofactors, Enzyme inhibitors, Introduction to Biocatalysis: Importance in "Green Chemistry" and Chemical Industry.

Lipids: Classification. Biological importance of triglycerides and phosphoglycerides and cholesterol; Lipid membrane, Liposomes and their biological functions and underlying applications.

Lipoproteins: Properties, functions and biochemical functions of steroid hormones. Biochemistry of peptide hormones.

Structure of DNA (Watson-Crick model) and RNA, Genetic Code, Biological roles of DNA and RNA: Replication, Transcription and Translation, Introduction to Gene therapy.

Biochemistry of disease: A diagnostic approach by blood/ urine analysis.

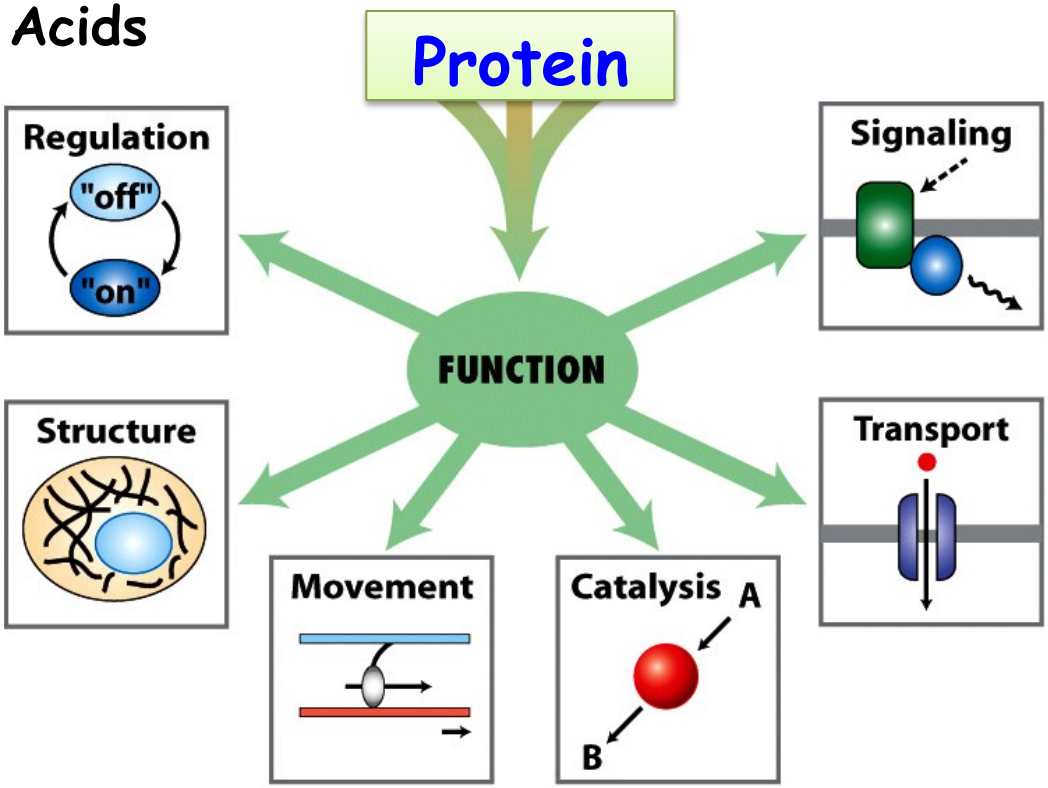
Blood: Composition and functions of blood, blood coagulation. Blood collection and preservation of samples.Anaemia, Regulation, estimation and interpretation of data for blood sugar, urea, creatinine, cholesterol and bilirubin.

Urine: Collection and preservation of samples. Formation of urine.Composition and estimation of constituents of normal and pathological urine.

Introduction

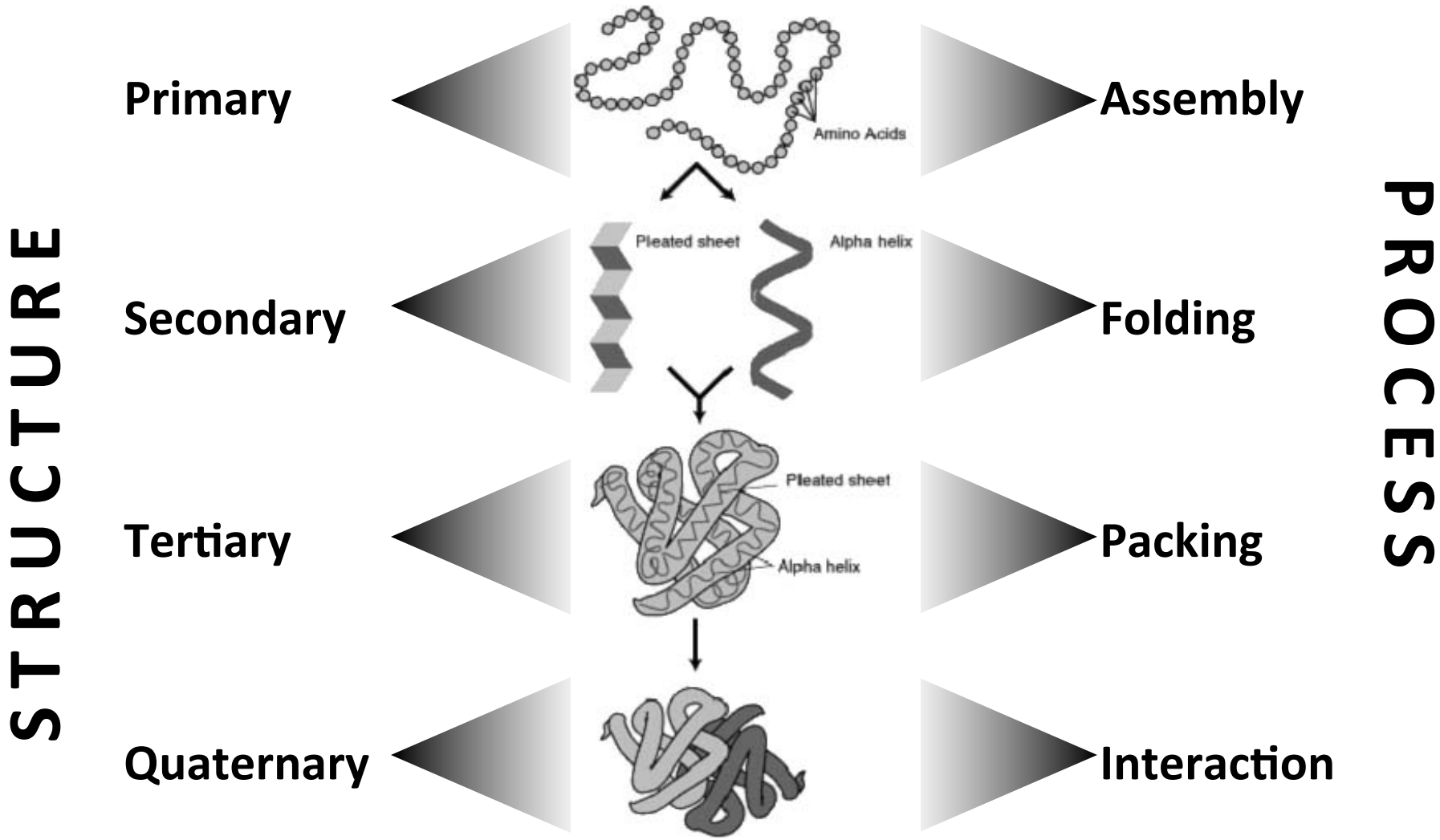
All living things are made up of four classes of large biological molecules:

- Carbohydrates
- Lipids
- Protein
- Nucleic Acids

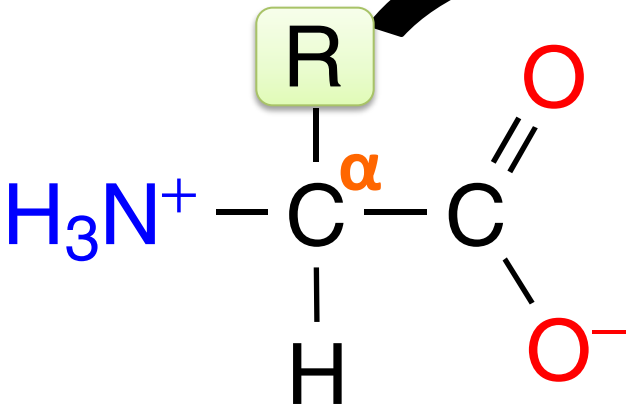


- Protein structure determines function

Biology/Chemistry of Protein Structure



Amino acids: the building block of proteins



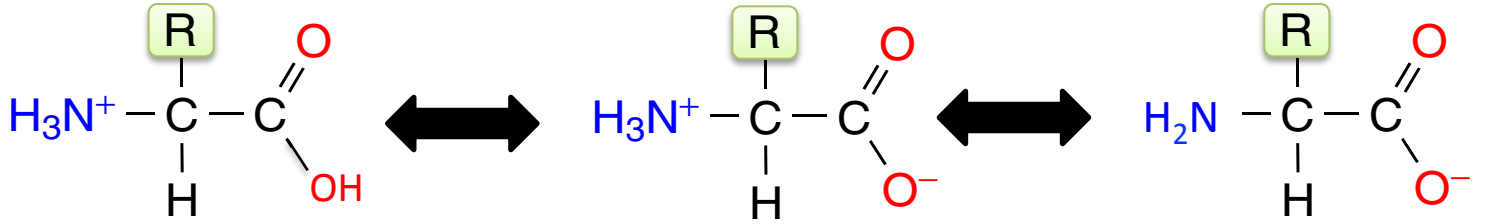
Amino acid
(20 aa)

Side chain modifications change the chemical (functional) properties of proteins

All amino acids have the same general structure but the side chain (R group) of each is different

- Hydrophilic
  - Basic
  - Acidic
  - Non-charged
- Hydrophobic
- Special

Acid-base properties



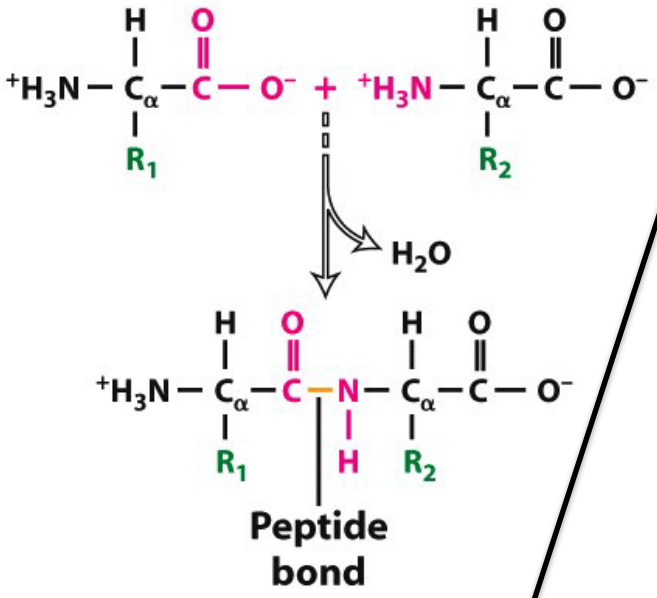
Low pH≈2

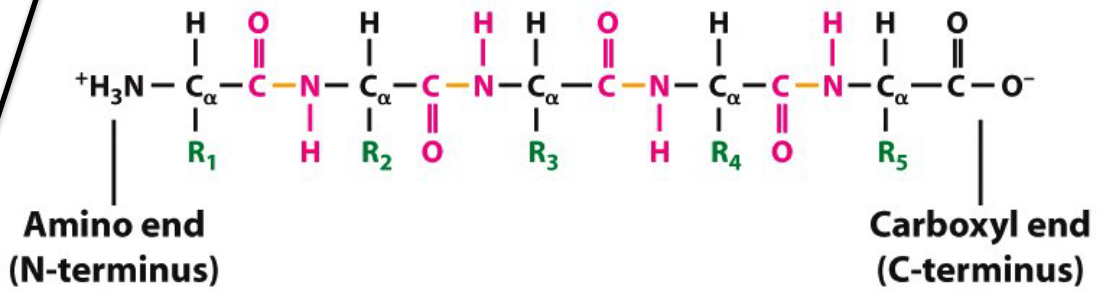
pH≈7

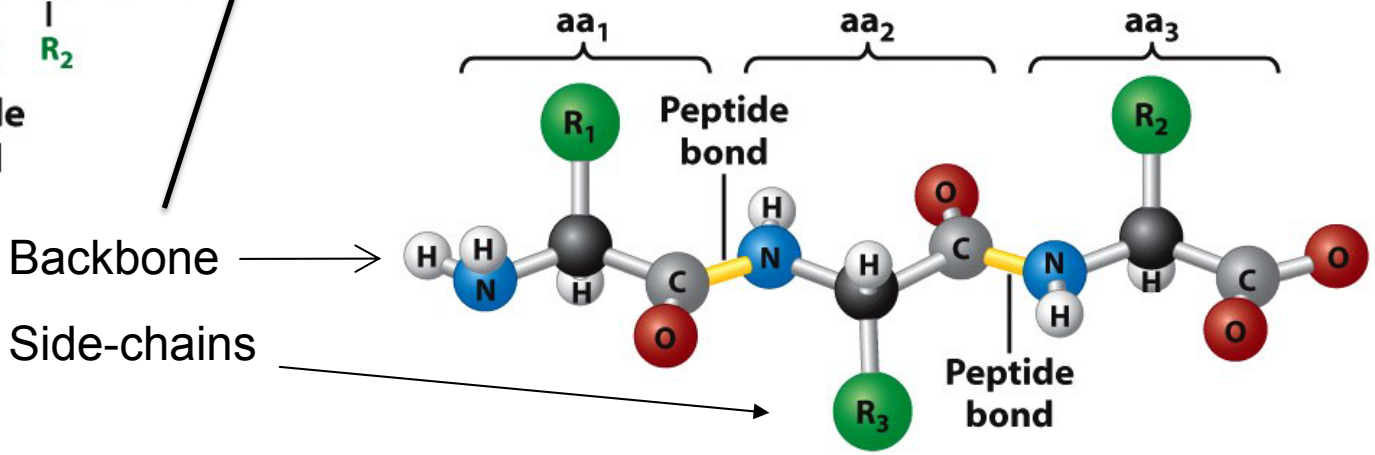
Zwitter ion

HIGH pH≈12

Peptide bonds connect amino acids into linear chains

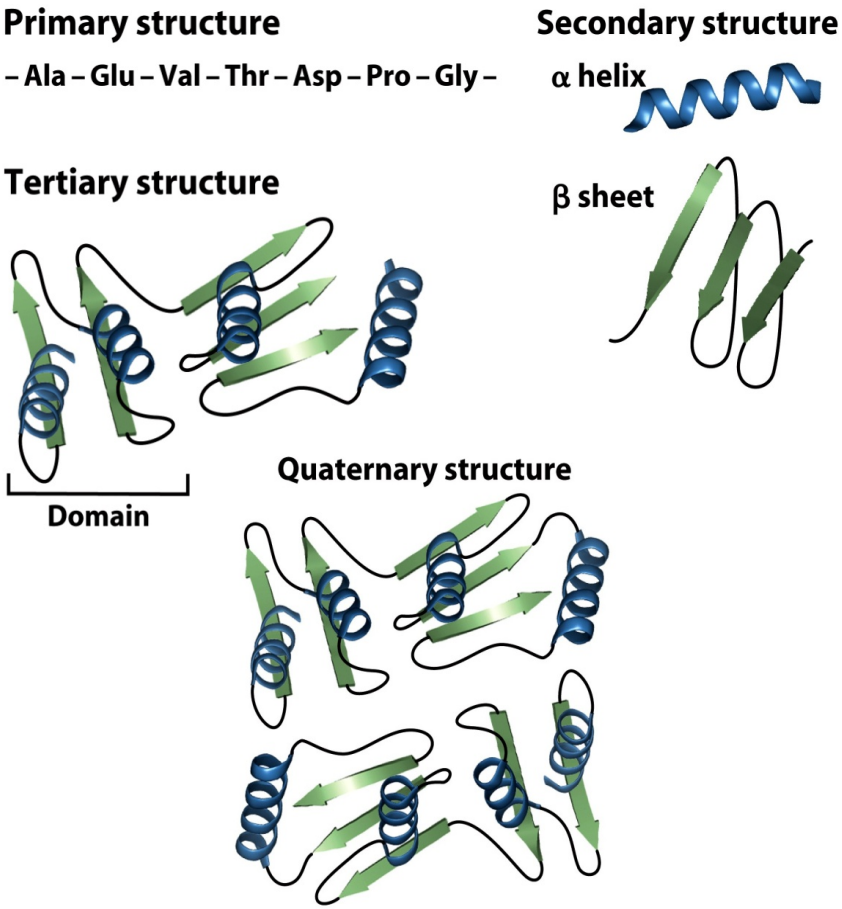






Proteins are built up by amino acids that are linked by peptide bonds to form a polypeptide chain

Four levels of structure determines the shape of proteins



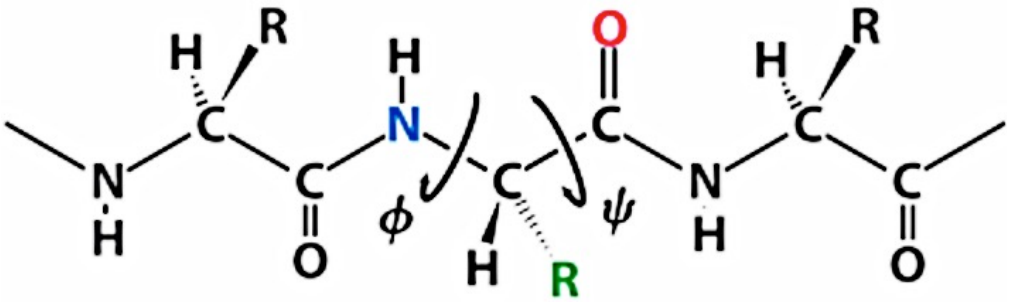
Primary: Linear sequence of amino acids (Peptide bond)

Secondary: Localized organization of parts of a polypeptide chain (e.g. α-helix or β-sheet)
Backbone H-bonds

Tertiary: Three dimensional arrangement of the polypeptide chain
Hydrophobic interactions, H-bonds, S-bridges

Quaternary: Association of two or more polypeptides into a multi-subunit complex

Backbone degrees of freedom

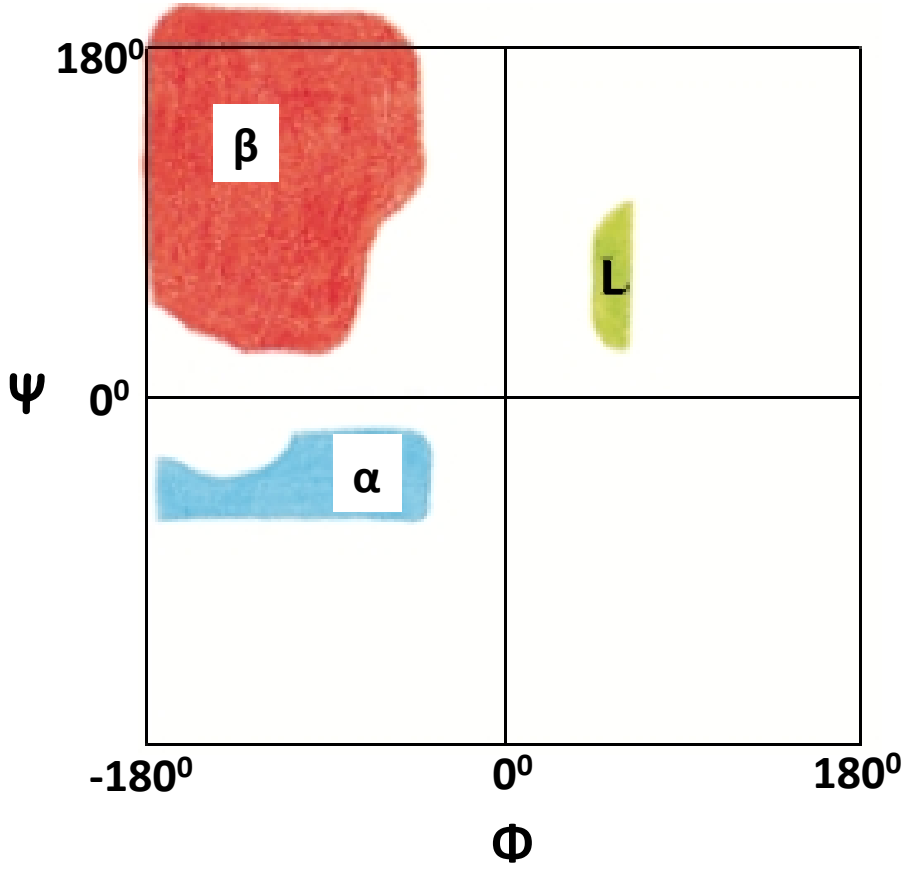


Φ: Torsion angle rotating about the N-Cα bond

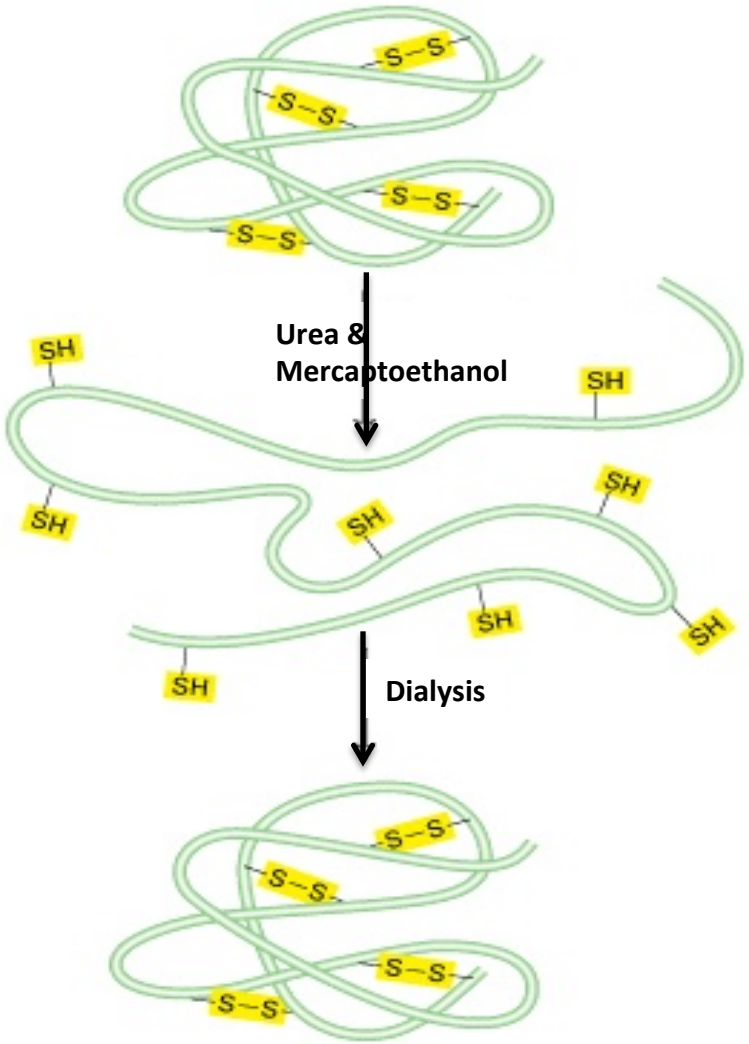
Ψ: Torsion angle rotating about the Cα-C bond

Ramachandran Plot

- Visualize dihedral angles ψ against Φ of amino acid residues in protein structure
- Many combinations of angles in a polypeptide chain are forbidden because of steric collisions between atoms.



Information for protein folding is encoded in the sequence



- Many proteins fold spontaneously to their native structure
- Protein folding is relatively fast (nsec–sec)
- Chaperones speed up folding, but do not alter the structure

Anfinsen's dogma

All the necessary information for the 3-dimensional structure of an enzyme is contained in the primary structure or sequence of the amino acids

Levinthal's Paradox

If a chain of a hundred amino acids is considered and it assumed each amino acid can exist in one of three conformations, extended, helical or loop, then there are 3100 possible ways to arrange this chain.

The protein sequence contains all information needed to create a correctly folded protein