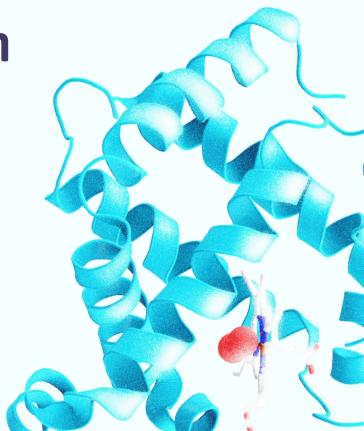
Proteins
Structure and Function

Introduction to Bioinformatics Course

Niloufar Razani
Department of Computer Engineering
Sharif University of Technology



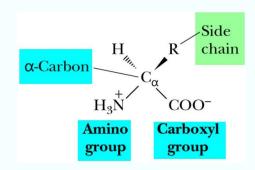
The Shape and Structure of Proteins

- Not only do proteins give the cell its shape and structure, they also carry out nearly all of its countless functions. For example:
- Enzymes promote intracellular chemical reactions by providing intricate molecular surfaces, contoured with particular bumps and crevices, that can cradle or exclude specific molecules.
- > Proteins embedded in the plasma membrane form the channels and pumps that control the passage of nutrients and other small molecules into and out of the cell.
- > Gene Regulatory Proteins bind to DNA to switch genes on or off.
- > Specialized proteins also act as antibodies, toxins, hormones, antifreeze molecules, elastic fibers, or luminescence generators. And so on ...

The multiplicity of functions carried out by proteins arises from the huge number of different shapes they adopt.

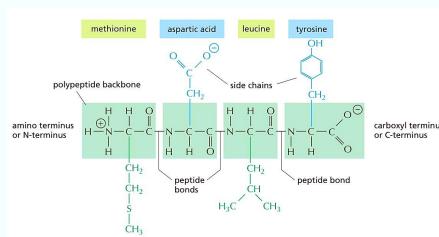
Amino Acids are the subunits of Proteins

- Proteins are assembled from a set of 20 different Amino Acids, each with different chemical properties.
- Amino acids are a varied class of molecules with one defining property: they all possess a carboxylic acid group and an amino group, both linked to the same carbon atom called the α -carbon.
- Their chemical variety comes from the **Side chain** that is also attached to the α -carbon.
- A protein molecule is made from a long chain of these amino acids, each linked to its neighbor through a **covalent peptide bond**.
- Proteins are therefore referred to as polypeptides or polypeptide chains.



Amino Acids are the subunits of Proteins

- In each type of protein, the amino acids are present in a unique order, called the **amino acid sequence**, which is exactly the same from one molecule of that protein to the next.
- Each polypeptide chain consists of a **Backbone** that supports the different amino acid side chains.
- Projecting from this repetitive backbone are any of the 20 different amino acid side chains.
- These side chains give each amino acid its unique properties.



Some of these side chains are nonpolar and hydrophobic ("water-fearing"), some are negatively or positively charged (hydrophilic), some are chemically reactive, and so on..

Twenty different amino acids

AMINO AG	SIDE CHAIN		
Aspartic acid	Asp	D	negative
Glutamic acid	Glu	Ε	negative
Arginine	Arg	R	positive
Lysine	Lys	K	positive
Histidine	His	Н	positive
Asparagine	Asn	N	uncharged polar
Glutamine	Gln	Q	uncharged polar
Serine	Ser	S	uncharged polar
Threonine	Thr	Т	uncharged polar
Tyrosine	Tyr	Υ	uncharged polar

AMINO ACID				SIDE CHAIN
	Alanine	Ala	Α	nonpolar
	Glycine	Gly	G	nonpolar
	Valine	Val	V	nonpolar
	Leucine	Leu	L	nonpolar
	Isoleucine	lle	1	nonpolar
	Proline	Pro	Р	nonpolar
	Phenylalanine	Phe	F	nonpolar
	Methionine	Met	M	nonpolar
	Tryptophan	Trp	W	nonpolar
	Cysteine	Cys	C	nonpolar

SIDE CHAIN

AMINO ACID

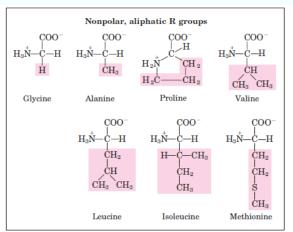
POLAR AMINO ACIDS

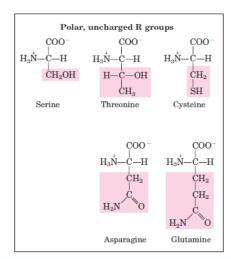
(hydrophilic)

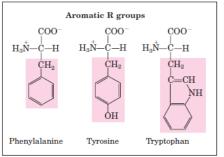
NONPOLAR AMINO ACIDS (hydrophobic)

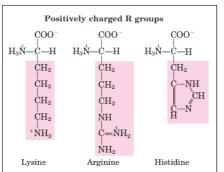
Twenty different amino acids

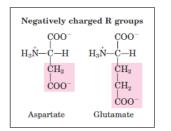
- Nonpolar/Aliphatic amino acids contain R groups which are nonpolar and hydrophobic. Aliphatic R groups can be linear or branched.
- Nonpolar/Aromatic R groups contain ring structures.
- ➤ Polar/Uncharged amino acids contain more electronegative atoms like oxygen or nitrogen.
- Positively charged amino acids have R groups that are protonated at physiological pH.
- ➤ Negatively charged amino acids contain R groups with a deprotonated carboxyl group, giving them a negative charge.





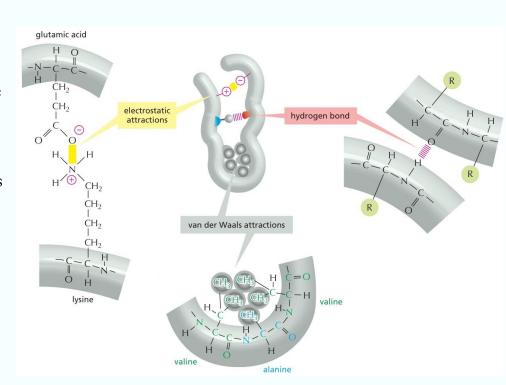






The Shape of a Protein is Specified by its amino acid Sequence

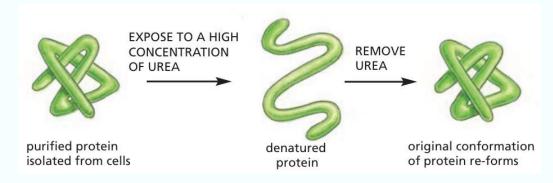
- Long polypeptide chains are very flexible and therefore proteins can in principle **fold** in an enormous number of ways.
- Each folded chain is constrained by many different sets of weak noncovalent bonds that form within proteins.
- These bonds include hydrogen bonds, electrostatic attractions, and van der Waals attractions.



Proteins fold into a conformation of lowest energy

- Each type of protein has a particular 3D structure, which is determined by the order of the amino acids in its chain.
- A protein generally folds into the shape in which the free energy is minimized.

When proteins fold incorrectly, they sometimes form aggregates that can damage cells and even whole tissues.

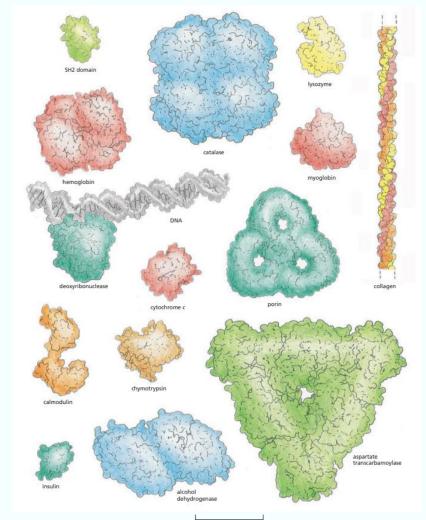


The fact that a renatured protein can, on its own, regain the correct conformation indicates that all the information necessary to specify the three-dimensional shape of a protein is contained in its amino acid sequence.

Proteins come in a wide Variety of complicated Shapes

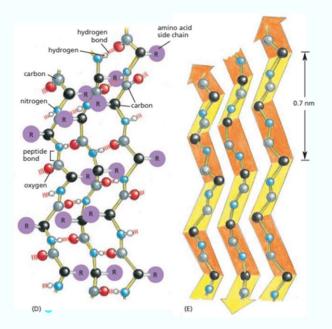
- ➤ Proteins are the most structurally diverse macromolecules in the cell.
- The vast majority of proteins are between 50 and 2000 amino acids long.
- Proteins can be Globular, Membrane or Fibrous; they can form filaments, sheets, rings, or spheres.
- To discover the precise folding pattern of any protein is by experiment, using either X-ray crystallography or nuclear magnetic resonance (NMR) spectroscopy.

AlphaFold is an artificial intelligence program developed by DeepMind which performs predictions of protein structure.

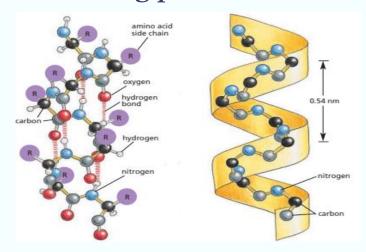


The α helix and the β Sheet are common folding patterns

Although the overall conformation of each protein is unique, two regular folding patterns are often present:
 α helix and β Sheet



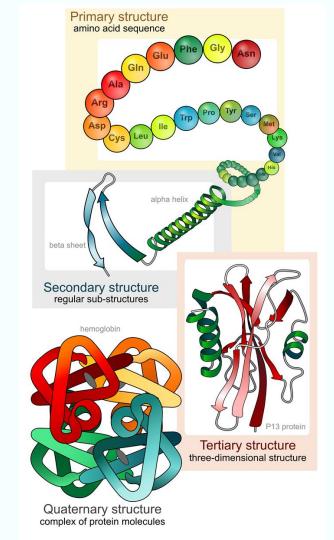
These two folding patterns are particularly common because they result from hydrogen bonds that form between the N–H and C=O groups in the polypeptide backbone.



Because the amino acid side chains are not involved in forming these hydrogen bonds,
 α helices and β sheets can be generated by many different amino acid sequences.

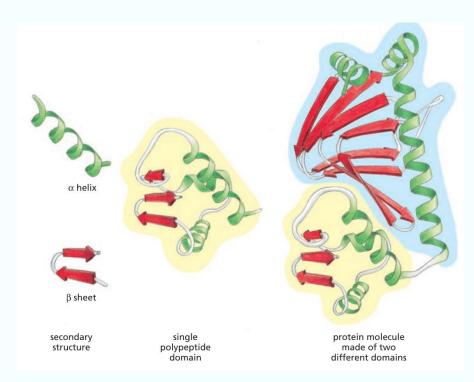
Proteins have Several levels of organization

- A protein's structure begins with its amino acid sequence, which is thus considered its **primary structure**.
- The next level of organization includes the α helices and β sheets that form within certain segments of a polypeptide chain; these folds are elements of the protein's secondary structure.
- The full, three-dimensional conformation formed by an entire polypeptide chain—including the α helices, β sheets, random coils, and any other loops and folds that form between the N-and C-termini—is referred to as the tertiary structure.
- Finally, if a particular protein molecule is formed as a complex of more than one polypeptide chain, then the complete structure is designated its **quaternary structure**.



Proteins have Several levels of organization

- A **Domain** is a part of a polypeptide chain that is independently stable or could undergo movements as a single entity with respect to the entire protein.
- A domain usually consists of 100–250 amino acids, and it is the modular unit from which many larger proteins are constructed.
- The different domains of a protein are often associated with different functions.
- Small protein molecules, such as the oxygen-carrying muscle protein myoglobin, contain only a single domain



Few of the Many possible polypeptide chains will Be useful

- In theory, a vast number of different polypeptide chains could be made. Because each of the 20 amino acids is chemically distinct and each can, in principle, occur at any position in a protein chain.
- ➤ However, only a very small fraction of this unimaginably large number of polypeptide chains would fold into a stable, well-defined three-dimensional conformation.
- why do most proteins present in cells adopt unique and stable conformations?
- ➤ a protein with many different conformations and variable properties would not be biologically useful, for it would be like a tool that unexpectedly changes its function.

RESOURCES

- ➤ Alberts, Bruce, et al. Essential cell biology, Chapter2, Chemical Components of Cells.
- ➤ Alberts, Bruce, et al. Essential cell biology, Chapter 4, Protein Structure and Function.