BIOCHEMISTRY
Amino Acids and Proteins

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Session 14
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Session Plan

- Characteristics of Proteins
- Amino Acids: Building Blocks for Proteins
- Essential Amino Acids
- Properties of Amino Acids
- Amino Acids as Buffers
- Cysteine – a Unique Amino Acid
- Biochemically Important Small Peptides
- Primary, Secondary, Tertiary & Quaternary Structure of Proteins
- Protein Hydrolysis
- Protein Denaturation
- Structural and Functional Classification of Proteins

Stoker 2014, Figure 20-22 p729
Functional groups in Proteins

Protein

Amino Acid

α-Carbon atom
Amino group
H₂N – C – COOH
R
Side chain
Carboxyl group
Carboxylic acid

Amine

Stoker 2014, p650
Introduction to Proteins

- Proteins are essential macronutrients which are important for life
  - Proteins are obtained mainly from animal products and other sources, such as nuts and legumes

- Proteins are also called Polypeptides and are unbranched polymers of Amino Acids (AAs)
  - The amino acid building blocks or units, are organic compounds made of carbon, hydrogen, nitrogen, oxygen or sulfur

- Next to water, proteins are the most abundant molecules in all cell
  - 15% of overall cellular mass
**Amino Acids**

- **Amino acid (AA)** = organic compound with both $-\text{NH}_2$ (Amino group) & $-\text{COOH}$ (Carboxyl group) functional groups

- All AAs found in proteins are $\alpha$-Amino acids
Amino Acids

- More than 700 different AAs are known
  - 20 standard AAs = AAs normally found in proteins

- **R group** (Side chain) = different for each amino acid
  - R groups vary in:
    - Size
    - Shape
    - Charge
    - Acidity
    - Functional groups
    - Chemical reactivity

- **20 Standard AAs are divided into 4 groups based on the properties of the R groups:**
  - Non-polar
  - Polar Neutral
  - Polar Acidic
  - Polar Basic
Classification of Amino Acids

- **Non-polar AA**
  - Hydrophobic

- **Polar Neutral AA**
  - Hydrophilic with neutral side chains

- **Polar Acidic AA**
  - Hydrophilic with acidic side chains

- **Polar Basic AA**
  - Hydrophilic with basic side chains

- **Sulphur-Containing AA**
  - Methionine, Cysteine
9 out of the 20 standard AAs.

*Are essential amino acids
*Must be obtained from the diet, as the body can not make them.

**Table 20.2** The Essential Amino Acids

<table>
<thead>
<tr>
<th>Essential Amino Acids</th>
</tr>
</thead>
<tbody>
<tr>
<td>arginine</td>
</tr>
<tr>
<td>methionine</td>
</tr>
<tr>
<td>histidine</td>
</tr>
<tr>
<td>phenylalanine</td>
</tr>
<tr>
<td>isoleucine</td>
</tr>
<tr>
<td>threonine</td>
</tr>
<tr>
<td>leucine</td>
</tr>
<tr>
<td>tryptophan</td>
</tr>
<tr>
<td>lysine</td>
</tr>
<tr>
<td>valine</td>
</tr>
</tbody>
</table>

* Arginine is required for growth in children but is not an essential amino acid for adults.
Acid-Base Properties of Amino Acids

- **Amino acids contain both:**
  - An acidic group (–COOH)
  - An alkaline/basic group (–NH₂)

![Amino acid structure diagram](image-url)
Acid-Base Properties of Amino Acids

- **In a neutral aqueous solution:**
  - Carboxyl groups donate $\text{H}^+$, producing a negatively charged ion
    $$\text{COOH} \rightarrow \text{COO}^- + \text{H}^+$$
  - Amino groups accept $\text{H}^+$ & produce a positively charged ion
    $$\text{NH}_2 + \text{H}^+ \rightarrow \text{NH}_3^+$$

- An **internal acid-base reaction** occurs on the same amino acid
  - Produces the zwitterion

Stoker 2014, p701
Isoelectric Point (pI) or (IEP)

**Isoelectric point:**
- The pH, at which a specific amino acid exists as a zwitterion & its net charge is zero
  - At IEP the amino acid are not attracted towards applied electric field because they carry zero net charge
  - Different AAs have different IEPs
    - Dependent on the structure of the amino acid
      - Acidic and basic amino acids have very different pIs
      - Acids must gain a hydrogen to be neutral (low pH)
      - Bases must loss a hydrogen to be neutral (high pH)

<table>
<thead>
<tr>
<th>Name</th>
<th>Isoelectric Point</th>
</tr>
</thead>
<tbody>
<tr>
<td>alanine</td>
<td>6.01</td>
</tr>
<tr>
<td>arginine</td>
<td>10.76</td>
</tr>
<tr>
<td>asparagine</td>
<td>5.41</td>
</tr>
<tr>
<td>aspartic acid</td>
<td>2.77</td>
</tr>
<tr>
<td>cysteine</td>
<td>5.07</td>
</tr>
<tr>
<td>glutamic acid</td>
<td>3.22</td>
</tr>
<tr>
<td>glutamine</td>
<td>5.65</td>
</tr>
<tr>
<td>glycine</td>
<td>5.97</td>
</tr>
<tr>
<td>histidine</td>
<td>7.59</td>
</tr>
<tr>
<td>isoleucine</td>
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<tr>
<td>leucine</td>
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<tr>
<td>lysine</td>
<td>9.74</td>
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<tr>
<td>methionine</td>
<td>5.74</td>
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<td>phenylalanine</td>
<td>5.48</td>
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<td>proline</td>
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<td>serine</td>
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<td>threonine</td>
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<tr>
<td>tryptophan</td>
<td>5.88</td>
</tr>
<tr>
<td>tyrosine</td>
<td>5.66</td>
</tr>
<tr>
<td>valine</td>
<td>5.97</td>
</tr>
</tbody>
</table>

Stoker 2014, Table 20-3 p702
Zwitterion & pH Change

- Zwitterion structure changes when the pH of solution is altered

- In a solution more alkaline than the isoelectric point:
  - Zwitterion donates a H+ (from both amino and carboxyl groups) & forms a negatively charged ion
  - The amino acid behaves as an ACID.

\[
\begin{align*}
\text{H}_3\text{N}^+ - &\text{C} - \text{COO}^- + \text{OH}^- \rightarrow \text{H}_2\text{N} - &\text{C} - \text{COO}^- + \text{H}_2\text{O}
\end{align*}
\]

Zwitterion (no net charge)  \hspace{2cm} Negatively charged ion

Stoker 2014, p702
Amino Acid Forms in Solutions

- In a solution 3 different amino acid forms exist
  - The equilibrium shifts with pH change
    - Zwitterions
    - Positive ions
    - Negative ions

Alanine Zwitterion
At pI (pH=6)
Charge = 0

Alanine Positive Ion
At pH<pI
Charge = 1+

Alanine Negative Ion
At pH>pI
Charge = 1-
Cysteine – A Unique Amino Acid

- The only standard amino acid containing a **Sulfhydryl group** (−SH) (thiol group)
  - Cysteine readily oxidizes & forms a disulfide linkage with another cysteine
  - 2 Cysteine residues linked via a disulfide bond help maintain protein structure, stability & function
  - Disulfide bonds contributes to tertiary, quaternary protein structure
Amino Acid Function and Protein Classification

- Amino acids are the building block of proteins, support metabolism and are important energy source

- Proteins are classified based on chemical composition:
  - **Simple proteins**
    - Consist only of amino acids.
    - More than 1 protein subunit may be present
  
  - **Complex / Conjugated proteins**
    - Consists of 1 or more protein chains & 1 or more prosthetic groups
      - Prosthetic group: organic or inorganic non-amino acid component

To note:
- **Lipoproteins** – lipid prosthetic group
- **Glycoproteins** – carbohydrate prosthetic group
- **Metalloproteins** – specific metal (Fe, Zn, Cu) prosthetic group
Amino Acids in Proteins: Peptide Bond

- Amino acids are linked together in proteins by peptide bonds
  - Covalent Amide bond found between amino acids in a peptide chain

- Peptide bond formation:
  - Carboxyl group (–COOH) of one amino acid interacts with the Amine group (–NH₂) of another amino acid
  - Produces an Amide + a molecule of H₂O

\[
\text{Acid} \quad R-C-OH + \quad \text{Amine} \quad H-N-R \quad \rightarrow \quad \text{Amide} \quad R-C-N-R + \quad H_2O
\]

Stoker 2014, p704
Amino acid chain: Peptides

**PEPTIDE**
An unbranched chain of amino acids held together by Peptide Bonds

**DIPEPTIDE**
2 amino acids linked via peptide bond

**TRIPEPTIDE**
3 amino acids linked via peptide bond

**OLIGOPEPTIDE**
10-20 amino acids linked via peptide bond

**POLYPEPTIDE**
Long unbranched chain of 20+ amino acids linked via peptide bond

---

A peptide chain has 2 different ends:

- The end carrying a free $\text{–NH}_3^+$ is called the **N-terminal end**
- The end carrying a free $\text{–COO}^-$ is called the **C-terminal end**

By convention, the sequence of AAs in a peptide is always written with N-terminal on the left & the C-terminal on the right.
Important Small Peptides

- **ANTIOXIDANTS**
  - **Glutathione**
    - Tripeptide (Glu–Cys–Gly) present in high levels in most cells
      - Protects cells from highly reactive oxygen species (peroxides & superoxides)
        - Produced during normal metabolism
        - Immune response
    - Detailed action of Glutathione is discussed in Nutritional Biochemistry.
Important Small Peptides

- **NEUROTRANSMITTERS**
  - **Enkephalins** = pentapeptide produced by the brain
    - Bind at receptor sites within the brain to reduce pain
      - Responsible for athlete’s “high” despite an injury
    - Morphine & Codeine bind to Enkephalin receptors
      - Long-lasting painkillers

- **2 best-known Enkephalins:**
  - **Met-enkephalin**: Tyr–Gly–Gly–Phe–Met
  - **Leu-enkephalin**: Tyr–Gly–Gly–Phe–Leu
Important Small Peptides

- **SMALL PEPTIDE HORMONES**
  - **Oxytocin**
  - **Vassopressin** = Antidiuretic hormone (ADH)
    - Both are Nonapeptides (9 AAs)
      - Differ in the amino acids in positions 3 & 8
  - Produced by the Hypothalamus
    - Stored in the Pituitary gland
  - 6 AA held in a loop by disulfide bonds between 2 Cysteine's

![Diagram of Oxytocin and Vassopressin peptides]
General Structure of Proteins

• The 3-D structure of all proteins (monomeric or multimeric), is more complex than that of carbohydrates or lipids

• 4 levels of protein structure:
  – Primary Structure (1°): amino acid sequence
  – Secondary Structure (2°): α-helices, β-strands, random coil (absence of 2° structure)
  – Tertiary Structure (3°): Overall arrangement of protein structure within one peptide chain
  – Quaternary Structure (4°): Overall arrangement of protein structure involving multiple peptide chains
    • Only oligomeric (multimeric) proteins have this type of structure
Primary Structure (1°) of Proteins

• Primary structure is the sequence of amino acids in a protein chain
  – Amino acids are bonded together via peptide bonds
  – Involves the number, type & order of attachment of the amino acids
  – Every protein has a different amino acid sequence

• **Insulin** was the 1st protein to have its primary structure determined
  – 51 amino acids in 2 chains, linked via disulfide bonds.
    • Chain A (21 AAs) & Chain B (30 AAs)
Secondary Structure of Proteins

• Secondary structure is the arrangement of the primary Protein Structure in space
  – Formed by hydrogen bonds between backbone atoms
  – 2 types of structure:
    • Alpha-helix
    • Beta-pleated sheet
  – Hydrogen Bonds form between the oxygen of the C=O of one amino acid & the H of the N–H of another amino acid within the protein

KEY:
- Amino terminal = N-terminal
- Carboxyl terminal = C-terminal
- Peptide bond
- Side chain
- Alpha Carbon (central carbon)
**α-Helix**

- Shape of a coiled spring (Helix)

- Hydrogen bonds are formed between C=O (i) and NH of the 4\(^{th}\) amino acid (i+3) down the same protein chain
  - 4\(^{th}\) if C=O residue considered 1\(^{st}\)

- The R-groups stay outside of the helix

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**Arrangement of protein backbone with no detail shown.**

**Backbone arrangement with hydrogen-bonding interactions shown.**

**Backbone atomic detail shown, as well as hydrogen-bonding interactions.**

**Top view of an α helix showing that amino acid side chains (R groups) point away from the long axis of the helix.**
**β-Pleated Sheet**

- **β-Pleated Sheet** is formed between 2 protein chain segments side by side
  - Linked by Hydrogen bonds
  - The R-groups are above & below the sheet

In proteins, where **β-Pleated Sheet** involves a single protein chain, several U-turns are formed
- This “U-turn structure” is the most frequent type of **β-Pleated Sheet**
Unstructured Segments

- Most proteins have only part of the structure forming α-helix or β-sheet
  - Possible to have both α-helix & β-pleated sheet within the same protein

- **Unstructured segments**
  - Portions of a protein that have neither α-helix nor β-pleated sheet
    - Impart flexibility to proteins.

Stoker 2014, Figure 20-8 p716
Tertiary Structure of Proteins

- **Tertiary protein structure:**
  - Formed by *interactions between the side chains* (*R-groups*) *of the amino acids within a protein*
    - Result in a more complex 3-D arrangement of the protein in space

- **4 types of interactions:**
  - a) **Disulfide bonds:** The strongest interactions (covalent bond)
    - Between two cysteine’s
  - b) **Electrostatic interactions** *(Salt Bridges)*
    - Interactions between an acidic & a basic R-group (+ve/-ve charge int.)
  - c) **Hydrogen bonds:** between polar R-groups
  - d) **Hydrophobic attractions:** between non-polar R-groups
Interactions in the Tertiary Structure

a) Disulfide bond
b) Electrostatic interaction (salt bridge)
c) Hydrogen bond
d) Hydrophobic interaction

Stoker 2014, Figure 20-12 p719
Tertiary Structure of a Protein

Human insulin, a small 2-chain protein, has both intra-chain & inter-chain disulfide linkages as part of its tertiary structure.
Quaternary Structure of Proteins

Quaternary Structure of Proteins
• Highest level of protein organization

• Found only in *multimeric proteins* that have 2 or more polypeptide chains (subunits) in their structure.
  – Usually an even number of subunits (2 = dimer, 4 = tetramer,...)

• Subunits are held together by the same interactions as tertiary structure
  – Hydrogen bonds, disulfide bonds, hydrophobic & electrostatic interactions

• 4$^\circ$ structure easily disrupted by very small changes in cellular conditions
  – Protein chains fall apart, resulting in a temporary loss of protein activity
  – When normal conditions are restored the multimer automatically reforms & regains its function
Tertiary & Quaternary Structures of the Oxygen-carrying Protein Hemoglobin.

It is a Tetramer with 2 identical α-chains & 2 identical β-chains. Each chain contains a haeme group, where oxygen binds.
**PRIMARY STRUCTURE**
The sequence of amino acids present in a protein's peptide chain or chains.

**SECONDARY STRUCTURE**
The regularly repeating ordered spatial arrangements of amino acids near each other in the protein chain, which result from hydrogen bonds between carbonyl oxygen atoms and amino hydrogen atoms.

**TERTIARY STRUCTURE**
The overall three-dimensional shape that results from the attractive forces between amino acid side chains (R groups) that are not near each other in the protein chain:
- Disulfide bonds
- Electrostatic interactions
- Hydrogen bonds
- Hydrophobic interactions

**QUATERNARY STRUCTURE**
The three-dimensional shape of a protein consisting of two or more independent peptide chains, which results from noncovalent interactions between R groups:
- Electrostatic interactions
- Hydrogen bonds
- Hydrophobic interactions
What types of interactions between amino acids give a single protein chain its 3D arrangement/fold?

Are the amino acids that form interactions important for folding next to each other in the amino acid sequence? Why/Why not?

Would the interactions that contribute to protein folding in one chain also allow interaction between two different protein chains?
Concept: Tertiary protein structure
Context: The tertiary interactions within a protein occur between the side chains (R-groups) of different amino acids. For example, disulfide bonds and hydrophobic interactions are examples of tertiary interactions. However, the amino acids within a protein that form tertiary interactions are not next to each other in the protein sequence.

Question: Why are the tertiary interactions important to the protein structure?

a) Tertiary interactions hold the protein chain in place when it folds back on itself, which allows the protein to adopt a complex 3D arrangement.

b) Tertiary interactions contribute to the formation of alpha helices and beta sheets.

c) Tertiary interactions ensure that each of the amino acids in the protein sequence are connected via interactions or chemical bonds.

d) Tertiary interactions hold protein structures together which contain more than one protein subunit, like haemoglobin.
Concept: Quaternary protein structure

Context: Some proteins are made up of multiple chains of amino acids (subunits). In these proteins, quaternary interactions form between the separate protein chains in order to hold together the structure of the protein. For example, haemoglobin is composed of four protein chains.

Question: Which of the following best describes the quaternary interactions that hold together multi-subunit proteins?

a) The covalent bonds that hold together two amino acids next to each other in the protein sequence

b) The interactions between the backbone of an amino acid in subunit A and the backbone of a second amino acid in subunit A

c) The interactions between the side chain and backbone within a single amino acid

d) The interactions between the side chain of one amino acid in subunit A and the side chain of a second amino acid in subunit B
Protein Hydrolysis

- Protein Hydrolysis is the reverse of peptide bond formation
  - Peptide bond is broken
    - The amine & carboxyl groups are regenerated
    - The protein splits into smaller peptides & AAs

- In the lab protein hydrolysis requires water, acid or base & heat

- In the body enzymes catalyze protein hydrolysis

Protein hydrolysis is necessary for digestion of dietary proteins
- Digestive enzymes catalyze protein hydrolysis & break the peptide bond
  - Produces free amino acids

Free amino acids are absorbed from the gut into bloodstream & transported to body cells for synthesis of new proteins

Protein hydrolysis also occurs in cells
- Old proteins are broken down to liberate amino acids
  - Used to produce new proteins
- Hydrolysis of cellular proteins & their re-synthesis is a continuous process.

Protein hydrolysis
Protein Denaturation

• Protein denaturation involves disruption of the protein’s characteristic 3-D quaternary, tertiary & secondary structures
  – Primary structure is not affected

• Protein denaturation leads to partial or complete loss of function
  – Protein function depends on protein structure
  – Small denaturation changes can be reversed & the protein does eventually “re-fold” = Renaturation
  – Major denaturation changes are irreversible
    • Denatured proteins lose their water solubility & precipitate in a solution – Coagulation.

• Egg white (a concentrates solution of protein Albumin) forms a white solid when heated
  – Cooking food denatures the protein but doesn’t change protein nutritional value
    • Easy for digestive enzymes to hydrolyse the protein
      & kills microorganisms by denaturing their proteins
**Protein Denaturation by Heat and Chemicals**

- **Cauterization**: heat used in surgery to seal blood vessels or small wounds

- **Sterilization** of surgical instruments, at high temperature & high pressure, in autoclave denatures bacterial proteins & enzymes

- **Canning** foods

- **Fever**
  - Body temperature may rise to 40°C without serious consequences
  - Temperature greater than 40°C, can inactivate enzymes, esp. in CNS, leading to dysfunction & death

- **Change in pH**
  - In the stomach Hydrochloric acid denatures proteins
  - In yoghurt Lactic acid produced by fermenting bacteria denatures milk proteins

- **Alcohol** denatures bacterial proteins
  - Used as disinfectant >>> hence swabbing skin prior to injection

- **Agitation** stretches peptide chains until weak bonds break
  - Whipping egg whites

- **Heavy metals** (Hg\(^{2+}\), Pb\(^{2+}\)) & **reducing agents** disrupt disulfide bonds, changing the tertiary structure of proteins
Protein denaturation involves loss of the protein’s 3-D structure. Complete loss of such structure produces a random-coil protein strand.

Table 20.5 Selected Physical and Chemical Denaturing Agents

<table>
<thead>
<tr>
<th>Denaturing Agent</th>
<th>Mode of Action</th>
</tr>
</thead>
<tbody>
<tr>
<td>heat</td>
<td>disrupts hydrogen bonds by making molecules vibrate too violently; produces coagulation, as in the frying of an egg</td>
</tr>
<tr>
<td>microwave radiation</td>
<td>causes violent vibrations of molecules that disrupt hydrogen bonds</td>
</tr>
<tr>
<td>ultraviolet radiation</td>
<td>operates very similarly to the action of heat (e.g., sunburning)</td>
</tr>
<tr>
<td>violent whipping or shaking</td>
<td>causes molecules in globular shapes to extend to longer lengths, which then entangle (e.g., beating egg white into meringue)</td>
</tr>
<tr>
<td>detergent</td>
<td>affects R-group interactions</td>
</tr>
<tr>
<td>organic solvents (e.g., ethanol, 2-propanol, acetone)</td>
<td>interferes with R-group interactions because these solvents also can form hydrogen bonds; quickly denatures proteins in bacteria, killing them (e.g., the disinfectant action of 70% ethanol)</td>
</tr>
<tr>
<td>strong acids and bases</td>
<td>disrupts hydrogen bonds and salt bridges; prolonged action leads to actual hydrolysis of peptide bonds</td>
</tr>
<tr>
<td>salts of heavy metals (e.g., salts of Hg^{2+}, Ag^{+}, Pb^{2+})</td>
<td>metal ions combine with —SH groups and form poisonous salts</td>
</tr>
<tr>
<td>reducing agents</td>
<td>reduces disulfide linkages to produce —SH groups</td>
</tr>
</tbody>
</table>
What can cause a protein to denature?

After protein denaturation, which of the four levels of protein structure remain in tract/are broken down?

Will the protein be functional/non-functional after denaturation? Why/why not?
Concept: Function of native proteins vs denatured proteins

Context: Each different protein present in the human body performs its own specific role (function). For example, collagen is a major structural component of skin and bone. Under conditions such as high temperature, proteins denature which affects their capacity to perform their function.

Question: Which of the following accurately describes the function of a protein in its native form before denaturation?

a) The protein remains functional despite the drastic shape changes caused by the breakdown of the protein’s structure

b) The protein is non-functional due to the drastic shape change caused by the breakdown of the protein’s structure

c) The protein can perform its function as all of the levels of protein structure are intact, meaning the protein adopts the shape needed to perform its role

d) The protein will be partially functional, but it will not perform its role as well as a protein that has undergone denaturation
Concept: Function of native proteins vs denatured proteins

Context: Each different protein present in the human body performs its own specific role (function). For example, collagen is a major structural component of skin and bone. Under conditions such as high temperature, proteins denature which affects their capacity to perform their function.

Question: Which of the following accurately describes the function of a completely denatured protein?

a) The protein remains functional despite the drastic shape changes caused by the breakdown of the protein’s structure

b) The protein is non-functional due to the drastic shape change caused by the breakdown of the protein’s structure

c) It depends on what type of protein has been denatured, the protein may either be functional or non-functional

d) The protein will be partially functional, but will not perform it’s role as well as a protein that has not undergone denaturation
Classification of Proteins based on shape

- Protein classification is based on molecular shape
  - Determined by tertiary & quaternary structures

3 types:
- **Fibrous Proteins**
  - Protein molecules with elongated shape
  - **Structural proteins**
    - Provide support & protection
  - Most abundant in the body
    - Total mass is greater than globular proteins
  - Tend to aggregate together to form macromolecular structures, e.g., hair, nails

- **Globular Proteins**
  - Molecules with peptide chains folded into spherical or globular shapes
  - More numerous than Fibrous proteins
  - **Functional proteins**
    - Involved in metabolism, enzymes, transport & regulatory molecules, intracellular signaling molecules

- **Membrane proteins**
  - Associated with cell membranes
    - Non-polar R-groups are outside & polar R-groups inside of the molecule
  - Generally water-insoluble
  - Help in transport of molecules across the membrane
<table>
<thead>
<tr>
<th>Name</th>
<th>Occurrence and Function</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Fibrous proteins (insoluble)</strong></td>
<td></td>
</tr>
<tr>
<td>keratins</td>
<td>found in wool, feathers, hooves, silk, and fingernails</td>
</tr>
<tr>
<td>collagens</td>
<td>found in tendons, bone, and other connective tissue</td>
</tr>
<tr>
<td>elastins</td>
<td>found in blood vessels and ligaments</td>
</tr>
<tr>
<td>myosins</td>
<td>found in muscle tissue</td>
</tr>
<tr>
<td>fibrin</td>
<td>found in blood clots</td>
</tr>
<tr>
<td><strong>Globular proteins (soluble)</strong></td>
<td></td>
</tr>
<tr>
<td>insulin</td>
<td>regulatory hormone for controlling glucose metabolism</td>
</tr>
<tr>
<td>myoglobin</td>
<td>involved in oxygen storage in muscles</td>
</tr>
<tr>
<td>hemoglobin</td>
<td>involved in oxygen transport in blood</td>
</tr>
<tr>
<td>transferrin</td>
<td>involved in iron transport in blood</td>
</tr>
<tr>
<td>immunoglobulins</td>
<td>involved in immune system responses</td>
</tr>
</tbody>
</table>
α-Keratin structure in hair

Collagen

- Collagen is the most abundant protein in the body (30% of total proteins)
  - Main structural protein in connective tissues, bones, tendons, skin, cartilage, ligaments, blood vessels etc.

- **Triple helix** – formed by 3 peptide chains wrapping around each other
  - Rich in Proline (up to 20%), Glycine, Hydroxyproline & Hydroxylysine

- Many triple helices combine into collagen fibrils
  - Cross-linking of fibrils gives collagen its strength

- The greater the cross-linking, the more rigid the fibril
  - Stiffening of collagen associated with ageing.
Collagen

Electron micrograph of collagen fibers.

Table 20.7 The Collagen Content of Selected Body Tissues

<table>
<thead>
<tr>
<th>Tissue</th>
<th>Collagen (% dry mass)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Achilles tendon</td>
<td>86</td>
</tr>
<tr>
<td>aorta</td>
<td>12–24</td>
</tr>
<tr>
<td>bone (mineral-free)</td>
<td>88</td>
</tr>
<tr>
<td>cartilage</td>
<td>46–63</td>
</tr>
<tr>
<td>cornea</td>
<td>68</td>
</tr>
<tr>
<td>ligament</td>
<td>17</td>
</tr>
<tr>
<td>skin</td>
<td>72</td>
</tr>
</tbody>
</table>

Stoker 2014, Figure 20-22 p729

Stoker 2014, Table 20-7 p728
Haemoglobin

- Haemoglobin is a globular protein that transports oxygen in blood from lungs to tissues

- Haemoglobin is a tetrameric protein (4 protein chains) with 4 Haeme groups, each containing an Fe atom
  - Fe ion interacts with oxygen
  - Each Haemoglobin molecule can transport up to 4 oxygen molecules at a time

Stoker 2014, p729
<table>
<thead>
<tr>
<th>Class</th>
<th>Prosthetic Group</th>
<th>Specific Example</th>
<th>Function of Example</th>
</tr>
</thead>
<tbody>
<tr>
<td>hemoproteins</td>
<td>heme unit</td>
<td>hemoglobin, myoglobin</td>
<td>carrier of $O_2$ in blood, oxygen binder in muscles</td>
</tr>
<tr>
<td>lipoproteins</td>
<td>lipid</td>
<td>low-density lipoprotein (LDL), high-density lipoprotein (HDL)</td>
<td>lipid carrier</td>
</tr>
<tr>
<td>glycoproteins</td>
<td>carbohydrate</td>
<td>gamma globulin, mucin, interferon</td>
<td>antibody, lubricant in mucous secretions, antiviral protection</td>
</tr>
<tr>
<td>phosphoproteins</td>
<td>phosphate group</td>
<td>glycogen phosphorylase</td>
<td>enzyme in glycogen phosphorylation</td>
</tr>
<tr>
<td>nucleoproteins</td>
<td>nucleic acid</td>
<td>ribosomes, viruses</td>
<td>site for protein synthesis in cells, self-replicating, infectious complex</td>
</tr>
<tr>
<td>metalloproteins</td>
<td>metal ion</td>
<td>iron–ferritin, zinc–alcohol dehydrogenase</td>
<td>storage complex for iron, enzyme in alcohol oxidation</td>
</tr>
</tbody>
</table>
Functional Classification of Proteins

- Proteins play crucial roles in most biochemical processes.

- The diversity of functions exhibited by proteins far exceeds the role of other biochemical molecules.

  *The functional versatility of proteins stems from:*
  - Ability to bind small molecules specifically & strongly to themselves.
  - Ability to bind other proteins & form fiber-like structures.
  - Ability to bind & be integrated into cell membranes.
Functional Classification of Proteins

- **Catalytic proteins** = *Enzymes*
  - Every biochemical reaction in the body requires an enzyme

- **Defense proteins** = *Immunoglobulins / Antibodies*
  - Vital for immune system function

- **Transport proteins**
  - Transport small molecules elsewhere in the body & release them on demand
    - E.g. *Haemoglobin, Lipoproteins*

- **Messenger proteins**
  - Transmit signals to coordinate biochemical processes between different cells, tissues & organs
    - E.g. hormones: *Insulin, Glucagon, human growth hormone*

- **Contractile proteins**
  - Required for movement
    - E.g. *Actin & Myosin* proteins in muscles
Functional Classification of Proteins

• **Structural proteins**
  – Provide structural support
  – E.g. *Collagen* (cartilage, tendons) & *Keratin* (skin, hair, nails)

• **Trans-membrane proteins**
  – Help control the movement of small molecules & ions across the cell membrane
    • E.g. Ion channels

• **Storage proteins**
  – Bind & store small molecules or atoms
    • E.g. Ferritin (Fe-storing protein), Myoglobin (oxygen-storing protein)

• **Regulatory proteins**
  – Form *receptors* to which messenger molecules bind, usually on the exterior of cell membrane

• **Nutrient proteins**
  – Particularly important in the early stages of life from embryo to infant
    • E.g. *Casein* (milk), *Ovalbumin* (egg white)
Readings & Resources
