

## Overview of amino acids metabolism

- Amino acids serve as substrates for the synthesis of protein,
- Amino acids provide nitrogen for the synthesis of other nitrogen-containing compounds,
- Amino acids are catabolized as fuels.

### Classification of amino acids:

#### 1. Chemical classification:

- ✓ According to the **chemistry** of the side chains.
- ✓ According to **polarity** of side chains.

#### 2. Nutritional classification:

- ✓ Essential
- ✓ Non-essential

#### NOTE:

- ✓ All of the **20 amino acids** present in proteins are essential for health.
- ✓ Some clinical conditions are associated with amino acid deficiency states, such as Kwashiorkor and Marasmus diseases.
- ✓ **Kwashiorkor** is protein deficiency with adequate energy intake whereas **Marasmus** is inadequate energy intake in all forms, including protein.

### Amino acid requirements of humans

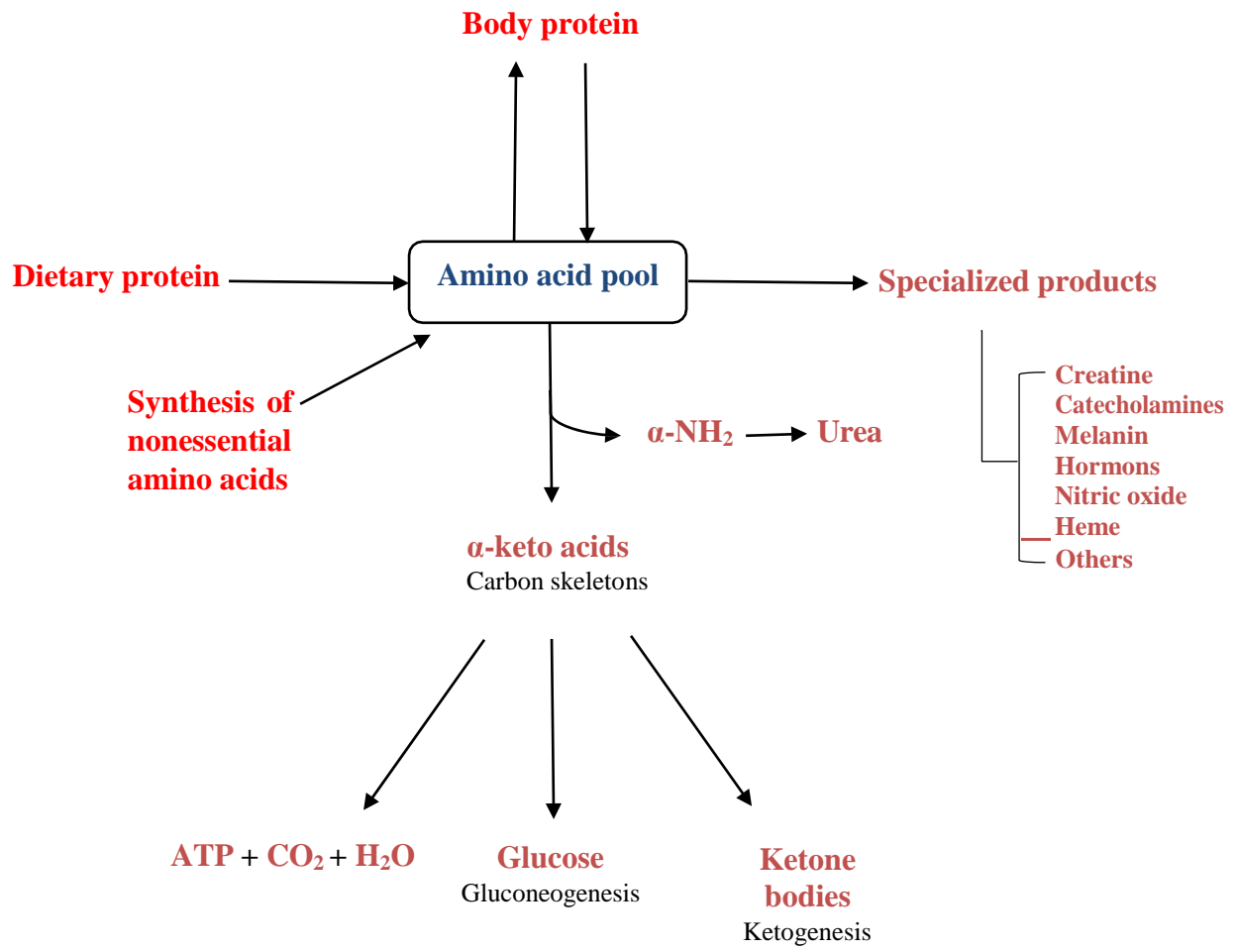
Nutritionally Essential	Nutritionally Nonessential
<b>Arginine</b> <sup>1</sup> Histidine Isoleucine Leucine <b>Lysine</b> Methionine Phenylalanine Threonine Tryptophan Valine	Alanine Asparagine Aspartate Cysteine Glutamate Glutamine Glycine Hydroxyproline <sup>2</sup> Hydroxylysine <sup>2</sup> <b>Proline</b> Serine Tyrosine

<sup>1</sup>“**Nutritionally semiessential.**” Synthesized at rates inadequate to support growth of children.

<sup>2</sup>Not necessary for protein synthesis but formed during posttranslational processing of collagen.

#### 3. Metabolic classification:

- ✓ **Ketogenic** (**Leucine** and **Lysine**)
- ✓ **Both glucogenic and ketogenic** (**Isoleucine**, **Phenylalanine**, **Tryptophan**, **Tyrosine** and **Threonine**)
- ✓ **Glucogenic** (all the remaining)



## Overview of amino acid metabolism

## Amino acids pool

The amount of free amino acids distributed throughout the body is called amino acid pool. Plasma level for most amino acids varies widely throughout the day. It ranges between 4–8 mg/dl. It tends to **increase** in the **fed state** and tends to **decrease** in the **post absorptive state**.

## Sources of amino acid pool

1. Dietary protein.
2. Breakdown of tissue proteins.
3. Biosynthesis of nonessential amino acids.

## NOTE:

In general, the rate of protein synthesis equals the rate of degradation (**steady-state**). However, there is a **constant need** for dietary intake of protein because:

- ✓ Some amino acids are also used for **energy production** and **storage** and for **synthesis** of non-protein molecules.
- ✓ There are situations where protein synthesis must exceed protein degradation, such as **during growth**, **pregnancy**, and **recovery from illness**.

## Digestion of dietary proteins

- ✓ Protein digestion **begins** in the stomach.
- ✓ The **highly acidic environment** of the stomach **denatures proteins**. Denatured proteins are susceptible to proteolytic digestion.
- ✓ The **primary enzyme** involved in proteolytic digestion is **pepsin**, which catalyzes the **nonspecific hydrolysis** of peptide bonds at an optimal **pH of 2**.
- ✓ In the lumen of the small intestine, the **pancreas secretes zymogens** of **trypsin** (Trypsin cleaves peptide chains mainly at the carboxyl side of the amino acids lysine or arginine, except when either is followed by proline.), **chymotrypsin** (Chymotrypsin prefers large hydrophobic residues. Chymotrypsin preferentially catalyzes the hydrolysis of peptide bonds involving tyrosine, phenylalanine, and tryptophan), **elastase** etc.
- ✓ **Proteolytic enzymes break** the **proteins** down into **free amino acids** as well as **dipeptides** and **tripeptides**, which in turn are absorbed by the intestinal mucosa cells and subsequently are released into the blood stream where they are absorbed by other tissues.

## Turnover of cellular proteins

- ✓ **Turnover of cellular proteins** (**continuous degradation and synthesis**) occur in all forms of life.
- ✓ **Each day**, humans turn over **1% to 2%** of their total body protein, **principally muscle** protein.
- ✓ Approximately **75%** of the amino acids liberated by protein degradation are **reutilized**, the **remaining excess** free amino acids are **not stored** for future use (i.e. **amino acids not immediately incorporated into new protein are rapidly degraded**).
- ✓ The relative susceptibility of a protein to degradation is expressed as its **half-life ( $t_{1/2}$ )**.
- ✓ Half-lives of proteins may range from **under 30 minutes** to **over 150 hours**, or even the **life time of an organ**.

## Cellular functions of protein degradation

1. The **recycling** of amino acids.
2. **Elimination** of misfolded and damaged proteins (due to environmental toxins, translation errors and genetic mutations) when cannot be repaired.
3. **Regulation of cellular metabolism**, cellular growth and cell division (increase or decrease the number of enzyme molecules and regulatory substances).
4. The **generation of active proteins** (the proteolytic cleavage of the precursor generates an active enzyme).

## Pathways of protein degradation

- A. **General “non-specific” protein degradation** takes place in **lysosomes** (specialized organelles that operate at **low pH** (to denature proteins) and contain **proteases** for proteins, **lipases** for lipids, and many other **hydrolases** (~ 50 total)). By this pathway **extracellular**, **membrane-associated**, and **long-lived intracellular proteins** are degraded in lysosomes by **ATP-independent** processes.

Many **normal** and **pathological** processes involve **increased lysosomal activity**, including:

- ✓ **Disuse atrophy of muscles** and **regression of the uterus after childbirth** (the muscular mass of the uterus is reduced from about 2 kg to about 50 g in just nine days).
- ✓ **Chronic inflammatory diseases** such as rheumatoid arthritis involve extracellular release lysosomal enzymes, which attack surrounding tissues.

- B. **Controlled or programmed protein degradation involves the Ubiquitin-Proteasome system.**

Degradation of regulatory proteins with **short half-lives** and of **abnormal** or **misfolded proteins** occurs in the cytosol within the **proteasomes**, and **requires ATP** and **ubiquitin (Ub)** (a small polypeptide found in all eukaryotic cells, by which the cell distinguish between functional proteins and intracellular proteins that need to be degraded).

- ✓ **Three different enzymes** add progressively more **Ub molecules**, in tandem chains, an energy-requiring process (**ATP**). **The more Ub molecules attached, the more rapid the degradation.**
- ✓ Carboxyl terminal of Ub is attached to the  $\epsilon$ -amino groups of lysyl residues in the target protein (isopeptide bond).
- ✓ The residue present at its amino terminus affects whether a protein is ubiquitinated. Amino terminal **Met**, or **Ser residues** retard, whereas **Asp**, or **Arg accelerate ubiquitination.**
- ✓ Subsequent **degradation of Ub-tagged proteins takes place** in the **proteasome**, a macromolecule that also is ubiquitous in eukaryotic cells.

<p>The diagram illustrates the biochemical steps of ubiquitination. It begins with Ubiquitin (Ub) and E1 (ubiquitin-activating enzyme). ATP is hydrolyzed to AMP + PP<sub>i</sub> to form a thioester bond between Ub and E1. Ub is then transferred to E2 (ubiquitin-conjugating enzyme), forming another thioester bond. E2 then transfers Ub to E3 (ubiquitin-ligase), which facilitates the attachment of Ub to a lysine residue (LYS) on a protein (Pr). This process repeats, leading to the formation of a polyubiquitin chain (Ub<sub>4</sub>) attached to the protein.</p>	<p>The diagram shows the structure of a proteasome, a barrel-shaped complex. It consists of a central 'Core particle' and two 'Regulatory particle' rings at the top and bottom. The top regulatory ring has a 'Gated pore' that allows 'polyubiquitinated proteins' (represented by a chain of Ub molecules) to enter the core. Inside the core, 'Active sites' are visible where degradation occurs. The bottom regulatory ring also has a 'Gated pore'.</p>
<p><b>Reactions involved in the attachment of ubiquitin (Ub) to proteins</b></p>	<p><b>Representation of the structure of a proteasome</b></p> <p><i>The upper ring is gated to <b>permit only polyubiquitinated proteins</b> to enter the <b>proteasome</b>, where immobilized internal proteases degrade them to peptides.</i></p>

### What controls the rate of protein degradation?

Different proteins are degraded at different rates. **Abnormal proteins** are **quickly degraded**, whereas the **rate of degradation of normal proteins may vary widely depending on their functions**. **Enzymes** at important **metabolic control points** may be **degraded much faster** than those enzymes whose activity is largely constant under all physiological conditions.

**Degradation of normal proteins with comparable functions depends on:**

- ✓ **N-terminal residue**, the residue present at its amino terminal affects whether a protein is ubiquitinated and subsequently degraded. Amino terminal **Met** or **Ser** **retards** whereas **Asp** or **Arg** **accelerates** ubiquitination.
- ✓ **PEST sequences**, regions rich in **proline (P)**, **glutamate (E)**, **serine (S)**, and **threonine (T)**, target **some** proteins for **rapid degradation**.

## Interorgan exchange of amino acids

The net balance between release from endogenous protein stores and utilization by various tissues keeps the steady-state concentrations of circulating plasma amino acids between meals.

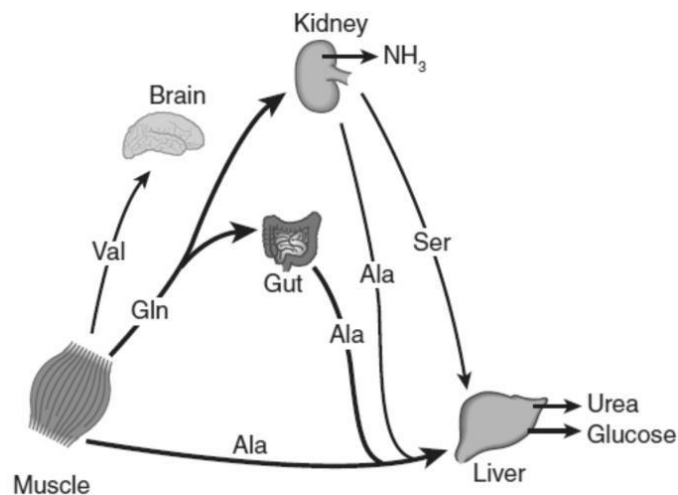
✚ In the **postabsorptive state**, free amino acids, particularly **alanine** and **glutamine**, are released from **muscle** into the circulation.

**Alanine** is extracted primarily by the **liver**, and **glutamine** is extracted by the **gut** and the **kidney**, both of which convert a significant portion to **alanine**. **Alanine** is a **key gluconeogenic amino acid**, and the rate of hepatic gluconeogenesis from alanine is far higher than from all other amino acids.

**Glutamine** also serves as a **source of ammonia** for excretion by the **kidney**.

**Branched-chain amino acids**, particularly **valine**, are released by **muscle** and taken up predominantly by the **brain**.

The **kidney** provides a **major source of serine** for uptake by peripheral tissues, including liver and muscle.



### Interorgan amino acid exchange in normal postabsorptive humans

✚ In the **fed state** (following a protein-rich meal), the splanchnic tissues release amino acids while the peripheral muscles extract amino acids.