بسم الله الرحمن الرحيم

كل هالبروتين وين يروح L

هذه المذكرة كافية تماما وهي اتمام لما بدأته قبل سنتين

هي اهداء لدفعة ٤٢٨ الرائعين J

واهداء لأغلى انسان لي في هذه الدفعة خاصة J

اهداء الى كل الدفعات القادمة . . .

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Posttranslational Modification of Polypeptide Chains:

Many polypeptide chains are **COVALENTLY** modified
either --> while they are still attached to the ribosome
or --> after their synthesis has been completed

modification occur : after translation is initiated

called : posttranslational modifications

What is posttranslation modification ?

1) removal of part of translated sequence
2) the covalent addition of one or more chemical groups required for protein activity

Types of posttranslational modifications :

A- Trimming :

- Many proteins secretion from the CELL are made as :
- large precursor molecules & not functionally active (MCQ)

- Change of protein from non active for active molecule by removed portions of the protein chain by specialized endoproteases (NOT endonuclease) (MCQ)

- Site of the cleavage reaction : 1) Endoplasmic reticulum
2) Golgi apparatus
3) secretory vesicles

- e.g : collagen are cleaved **after secetion** (MCQ)
- Zymogens (precursors of secreted enzymes) are **inactive** ,
- The zymogens become activated through cleavage when they reach their **proper sites of action** (MCQ)

The synthesis of enzymes as zymogens protects the cell from being digested by its own products (T)

B- Covalent alterations :

Proteins may be activated or inactivated by the covalent attachment of a variety of chemical groups

1) Phosphorylation :

Occurs : on the hydroxyl groups of (serine, threonine, tyrosine residues in a protein)
Catalyzed by : protein kinases
Reversed by : protein phosphatases
- the phosphorylation may **increase** or **decrease** the functional activity of protein

2) Glycosylation :

- Many of proteins -> become part of a plasma membrane , lysosome or secreted from the cell have carbohydrate chains attached to serine or threonine hydroxyl groups (O-linked) or the amide nitrogen of asparagine (N-linked)

Occurs : in the endoplasmic reticulum & golgi apparatus (MCQ)

Used to : target protein to specific organelles

e.g: enzyme destined to be incoporated into lysosomes are modified by the phosphorylation of mannose residues at C6

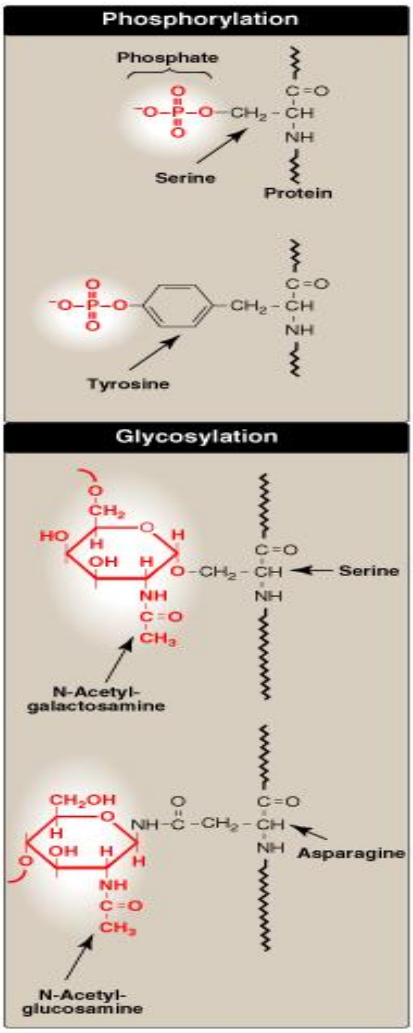


Figure 31.15 *(continued on next page)* Posttranslation modifications of some amino acid residues.

3) Hydroxylation :

Proline and lysine
Endoplasmic reticulum
Prolyl or lysyl hydroxylases
e.g., Collagen

4) Other covalent modifications :

a-Carboxylation : (MCQ)

- additional carboxyl groups can be added to glutamate residues by**vit.K**
- the resulting carboxyglutamate residues are essential for the activity of several of the blood-clotting proteins

b- Biotinylated enzyme :

- biotin is covalently bound to the amino groups of lysine residues of biotin-dependent enzymes that catalyze carboxylation reactions
- *such as ->* **pyruvate carboxylase**

c- Farnesylated protein :

- help anchor proteins in membranes.

Note : many proteins are acetylated .

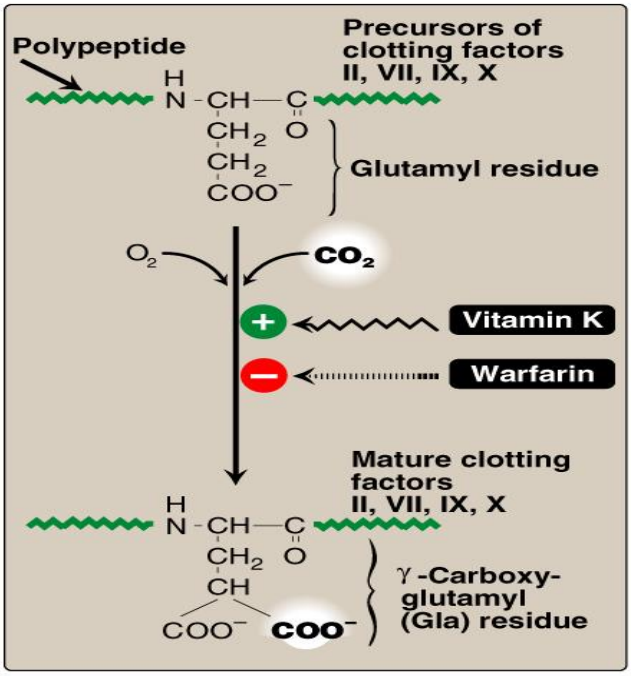
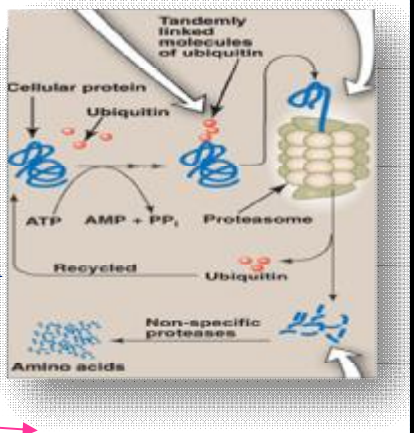


Figure 28.26
Carboxylation of glutamate to form γ-carboxyglutamate (Gla).

C.Protein degradation

Protains that are defective or destained for rapid turnover are often marked for destruction by ubiquitination

ubiquitin → **the attachment of a small, highly conserved protein**



Proteins marked in this way are:
rapidly degraded by a cellular component known as the "proteasome "

- **complex proteolytic system**
- **located in the cytosol**
- **ATP-dependent**

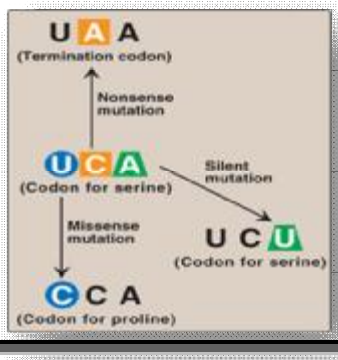
Summary

Codons → **are composed of 3 nucleotide bases presented in the mRNA language of A, G, C, and U.**
They are always written 5′→3′

three signal termination of protein synthesis (translation) + 61 code for the twenty common amino acids → Of the 64 possible three-base combina-tions

Altering the nucleotide sequence in a codon can cause

- **silent mutations** → the altered codon codes for the original amino acid
- **missense mutations** → the altered codon codes for a different amino acid
- **nonsense mutations** → the altered codon is a termination codon



Characteristics of the genetic code include:

1- specificity 2- universality 3-degeneracy
4-nonoverlapping 5-commaless

Requirements for protein synthesis:

(include all the amino acids that eventually appear in the finished protein)

* for each amino acid:
  - at least one specific type of tRNA
  - one aminoacyl-tRNA synthetase
* for the protein to be synthesized
  - the mRNA coding
* for initiation, elongation, and termination of protein synthesis:
  - fully competent ribosomes
  - protein factors
* energy sources:
  - ATP and GTP

tRNA has an attachment site for a specific amino acid at it s 3′-end, and an anticodon region that can recognize the codon specifying the amino acid the tRNA is carrying

Ribosomes

large complexes of protein and rRNA
-They consist of two subunits.
- Each ribosome has three binding sites for tRNA molecules—the A, P, and E sites that cover three neighboring codons

A-site — codon binds an incoming aminoacyl-tRNA

P-site — codon is occupied by peptidyl-tRNA

E site — is occupied by the empty tRNA as it is about to exit the ribosome

Recognition of an mRNA codon is accomplished by the tRNA anticodon

The anticodon binds to the codon following the rules of complementarity and antiparallel binding.

(The nucleotide sequences of both codons and anticodons must ALWAYS be listed in the 5′→3′ order.)

wobble" hypothesis

the first (5′) base of the anticodon is not as spatially defined as the other two bases.

-Movement of that first base allows nontraditional base-pairing with the last (3′) base of the codon, thus allowing a single tRNA to recognize more than one codon for a specific amino acid.

initiation of protein synthesis

the components of the translation system are assembled, and mRNA associates with the small ribosomal subunit

- The process requires **à** initiation factors

In prokaryotes	**In eukaryotic**
-a purine-rich region of the mRNA (the Shine-Dalgarno sequence) base-pairs with a complementary sequence on 16S rRNA, resulting in the positioning of the small subunit on the mRNA so that translation can begin. **-The initiation codon is 5′-AUG-3′; N-formylmethionine is the initiating amino acid**	**-The 5′-cap on eukaryotic mRNA is used to position the small subunit on the mRNA.** **-methionine is in eukaryotes**

elongation of protein synthesis

***The polypeptide chain is elongated by :**

-the addition of amino acids to the carboxyl end of its growing chain.

***The process requires:**

-elongation factors.

***The formation of the peptide bond is catalyzed by:**

-peptidyltransferase, à which is an activity intrinsic to the rRNA of the large subunit.

***Following peptide bond formation:**

-the ribosome advances along the mRNA in the 5′→3′ direction to the next codon (translocation).

***Forming a polysome:**

-Because of the length of most mRNAs, more than one ribosome at a time can translate a message

elongation of protein synthesis

*Termination begins:

- when one of the three termination codons moves into the A site.

*These codons are recognized by:

-release factors.

*The newly synthesized protein is released from:

- the ribosomal complex.

*And the ribosome is dissociated from:

-the mRNA.

initiation | elongation | Termination

are driven by the hydrolysis of GTP

*Numerous antibiotics interfere with the process of protein synthesis.

*Many polypeptide chains are covalently modified after translation. Such modifications include,

removal of amino acids,	phosphorylation	glycosylation	hydroxylation
	which may activate or inactivate the protein,	which plays a role in protein targeting,	such as that seen in collagen.

تم بحمد الله...

إذا أغلقت الشتاء أبواب بيتك .. وحاصرتك تلال الجليد من كل مكان ..
فانتظر قدوم الربيع وافتح نوافذك لنسمات الهواء النقي .. وانظر بعيدا
فسوف ترى أسراب الطيور وقد عادت تغني .. وسوف ترى الشمس
وهي تلقي خيوطها الذهبيه فوق أغصان الشجر لتصنع لك
عمراً جديداً
وحلماً جديداً
..

وقلباً جديداً

كل الحب والود الحمد لله انتهت المهمة

مجهول ٤٢٦

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