

MECANISMOS BÁSICOS DA GENÉTICA MOLECULAR: DO GENE À PROTEÍNA (Parte 2)

Aula 3

LGN0232 – Genética Molecular

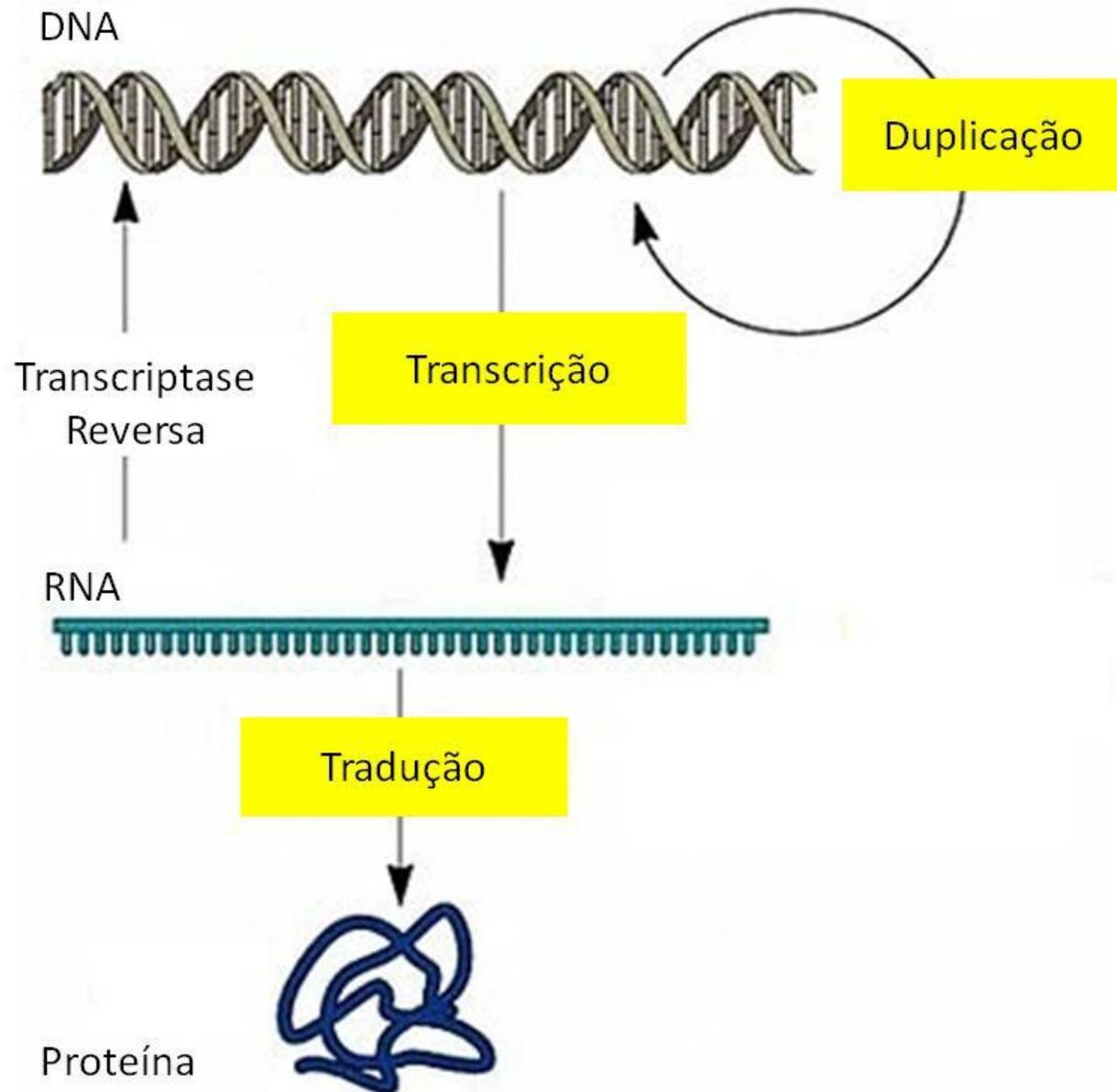


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SUMÁRIO

- Fluxo da informação genética;
- Conceito de gene;
- O processo de tradução;
- Aplicação dos conhecimentos adquiridos
- Exercício mapa conceitual.

A MAQUINARIA GENÉTICA É A MESMA



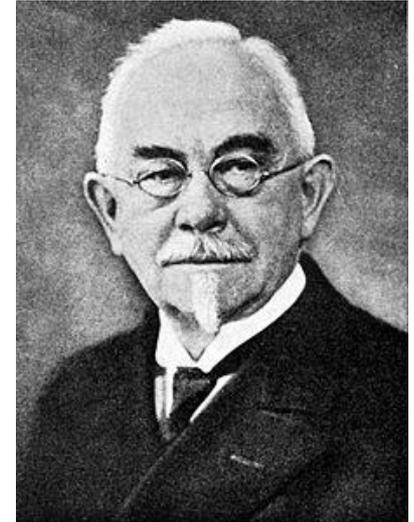
MAS O QUE É UM GENE?



DEFINIÇÃO DE GENE

Wilhelm Johannsen

1909 → gene



- ❑ Um **gene** → unidade da informação genética que controla a síntese de polipeptídios ou uma molécula de RNA estrutural

mRNA → polipeptídeo

tRNA e rRNA → RNA estrutural

- ❑ Gene inclui as regiões 5' e 3' não codificantes, que estão envolvidas na regulação da transcrição e tradução, e todos os introns dentro do gene

GENE TÍPICO DE PROCARIOTOS

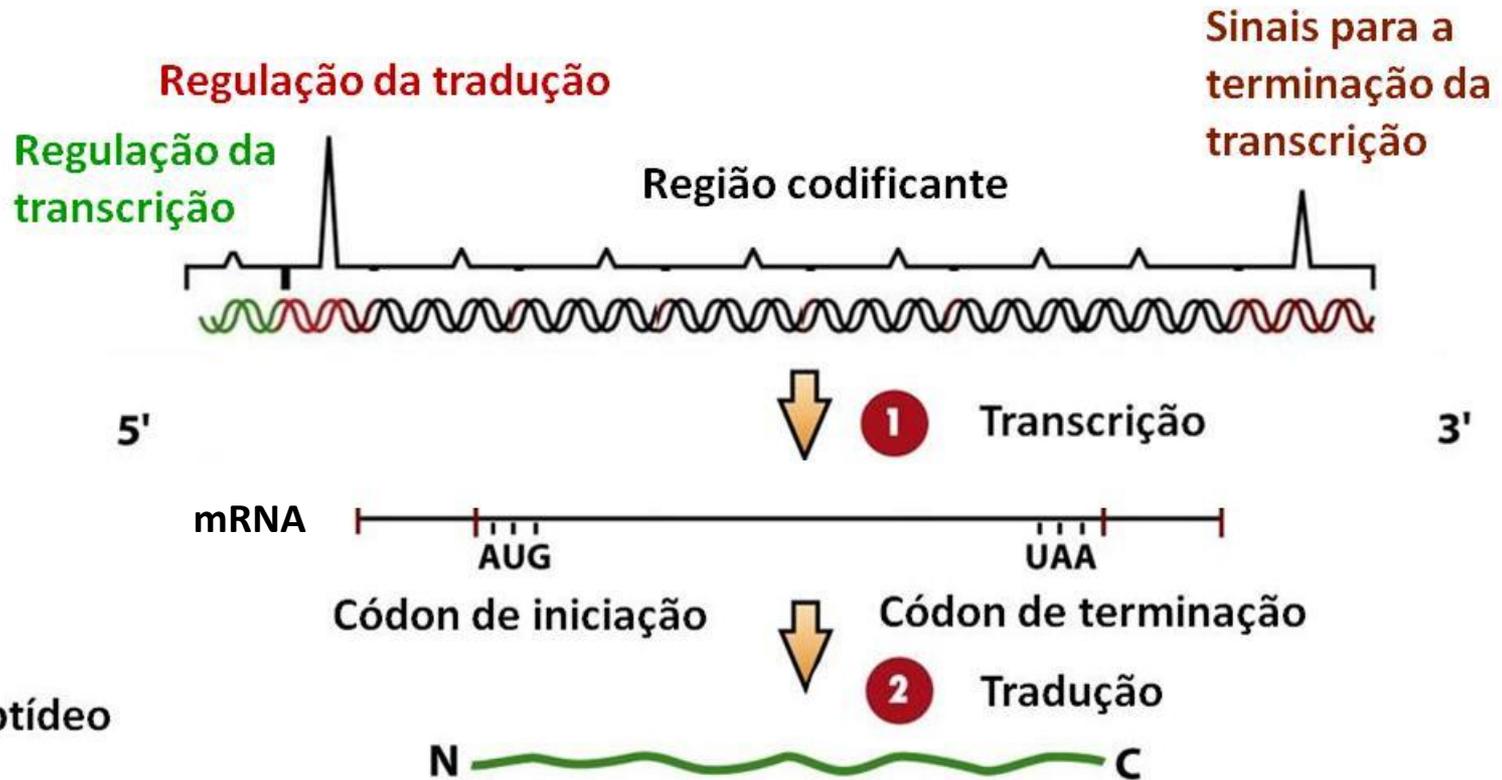
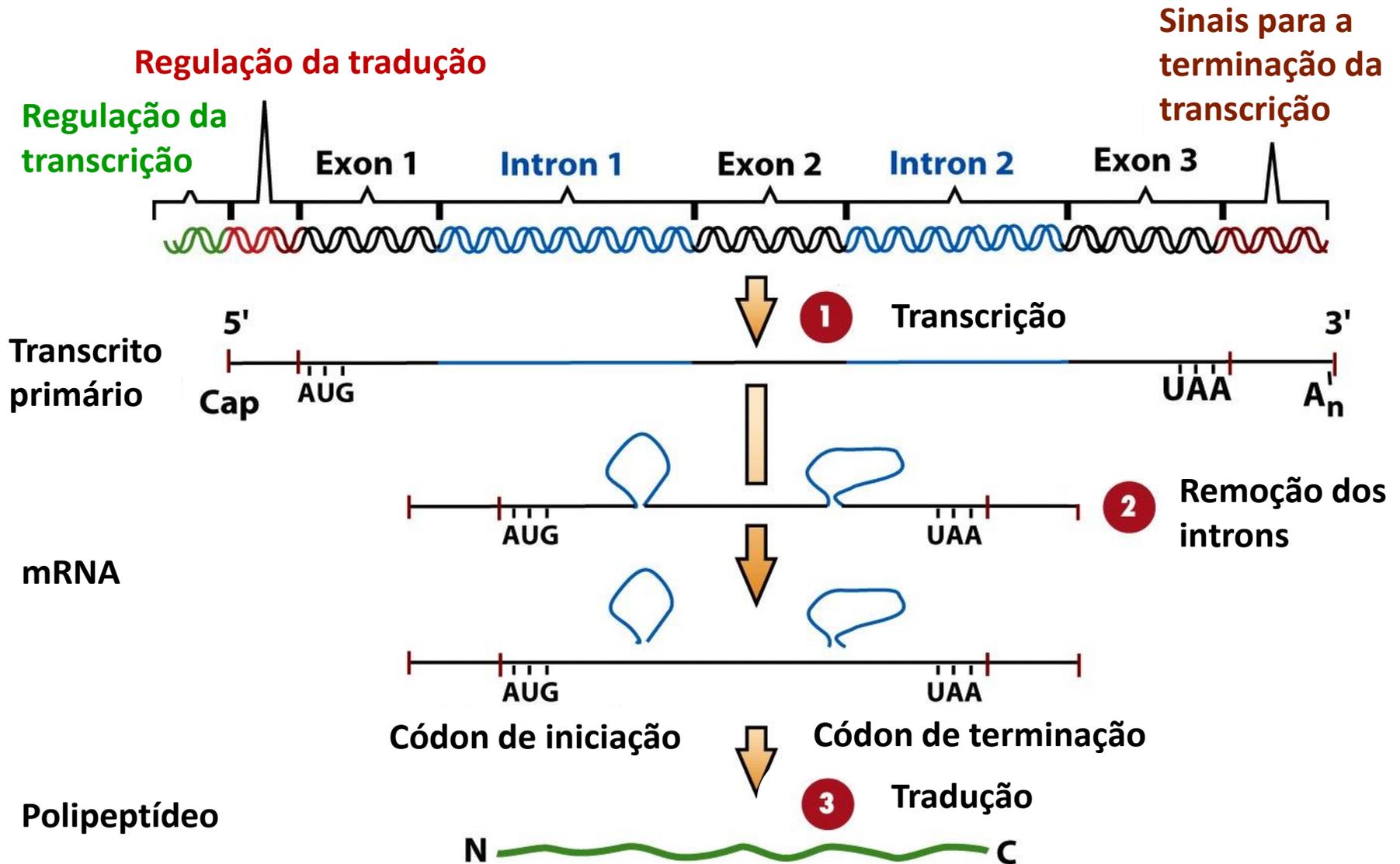
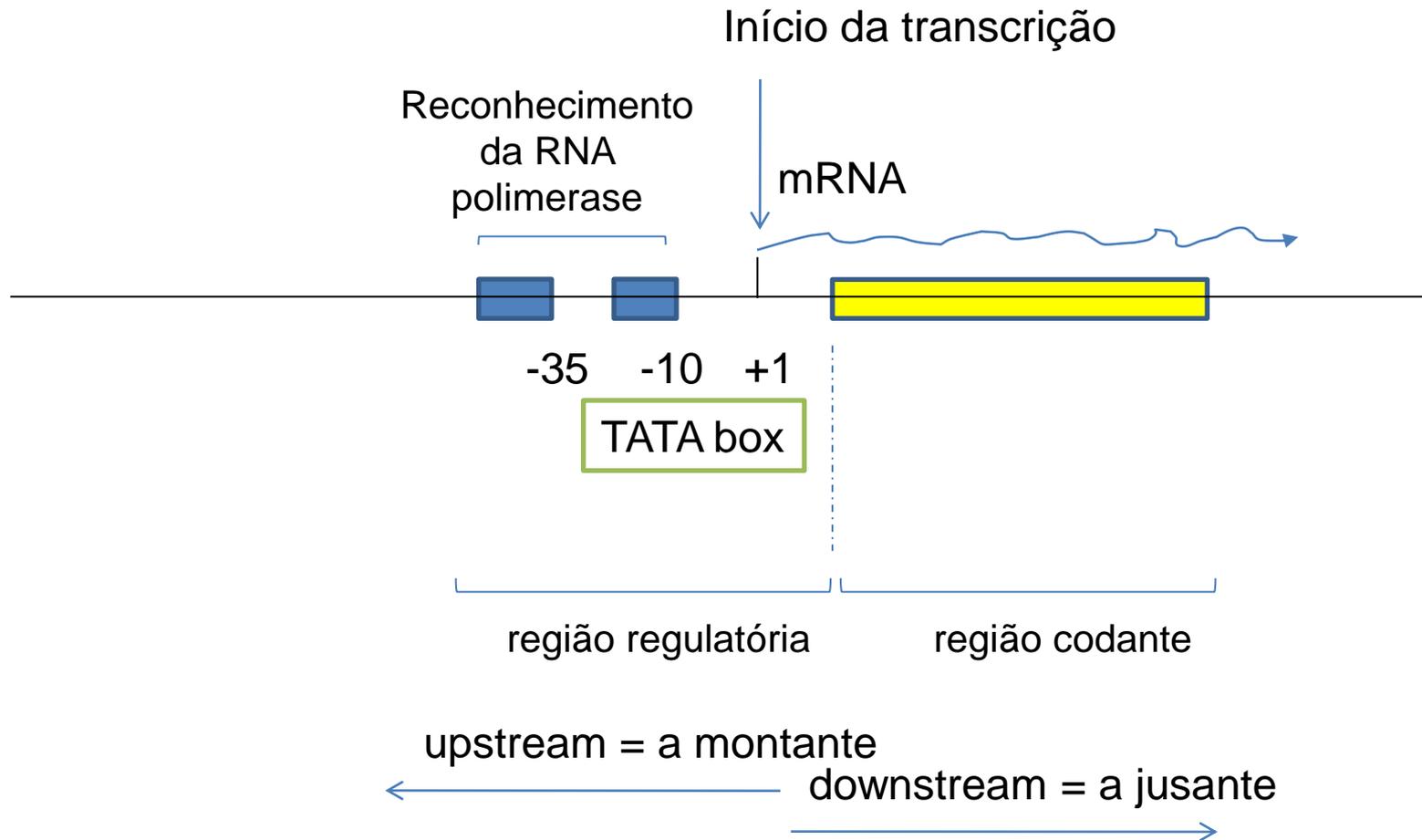


Figure 14-1b Principles of Genetics, 4/e
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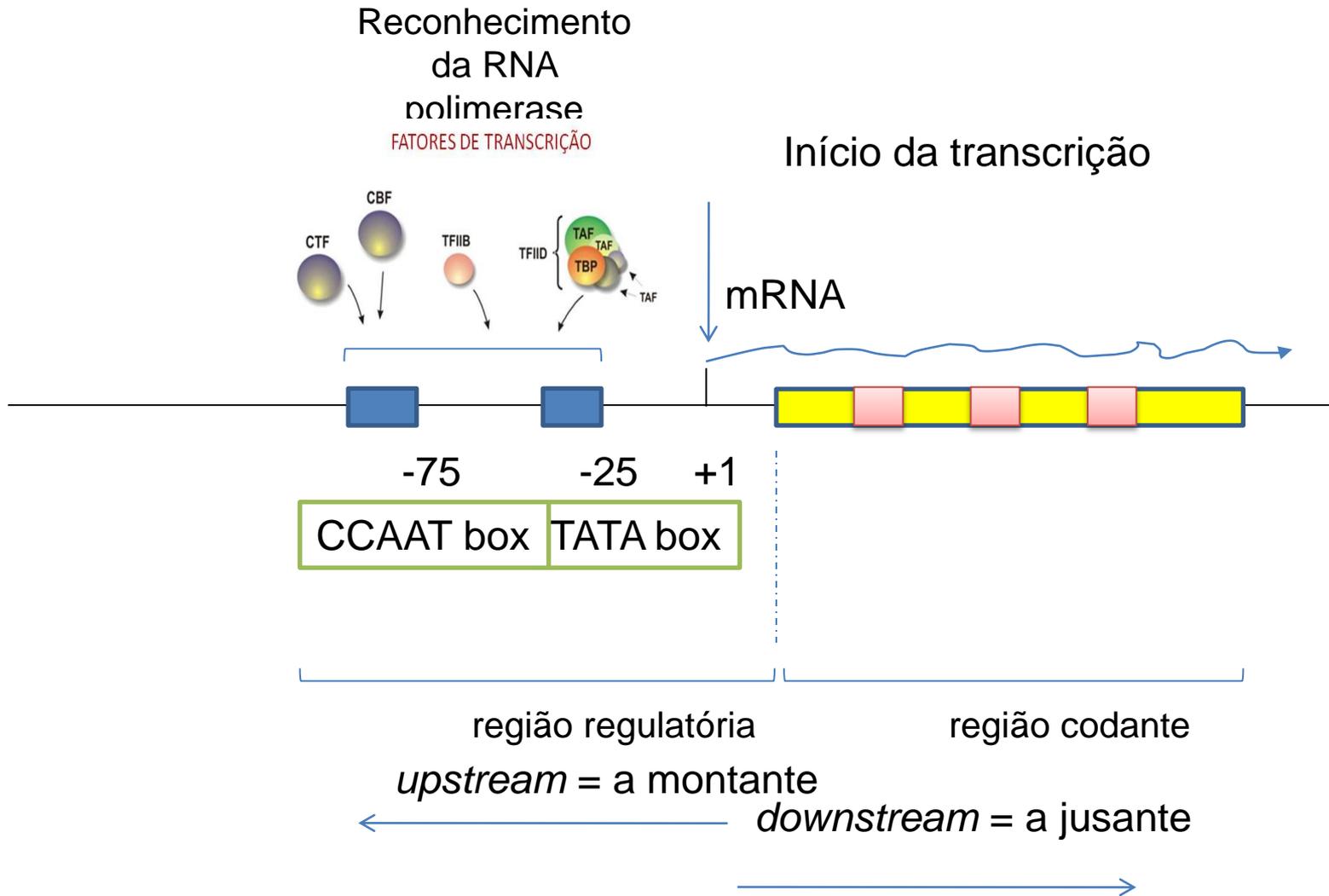
GENE TÍPICO DE EUCARIOTOS



ESTRUTURA DO PROMOTOR EM PROCARIOTOS



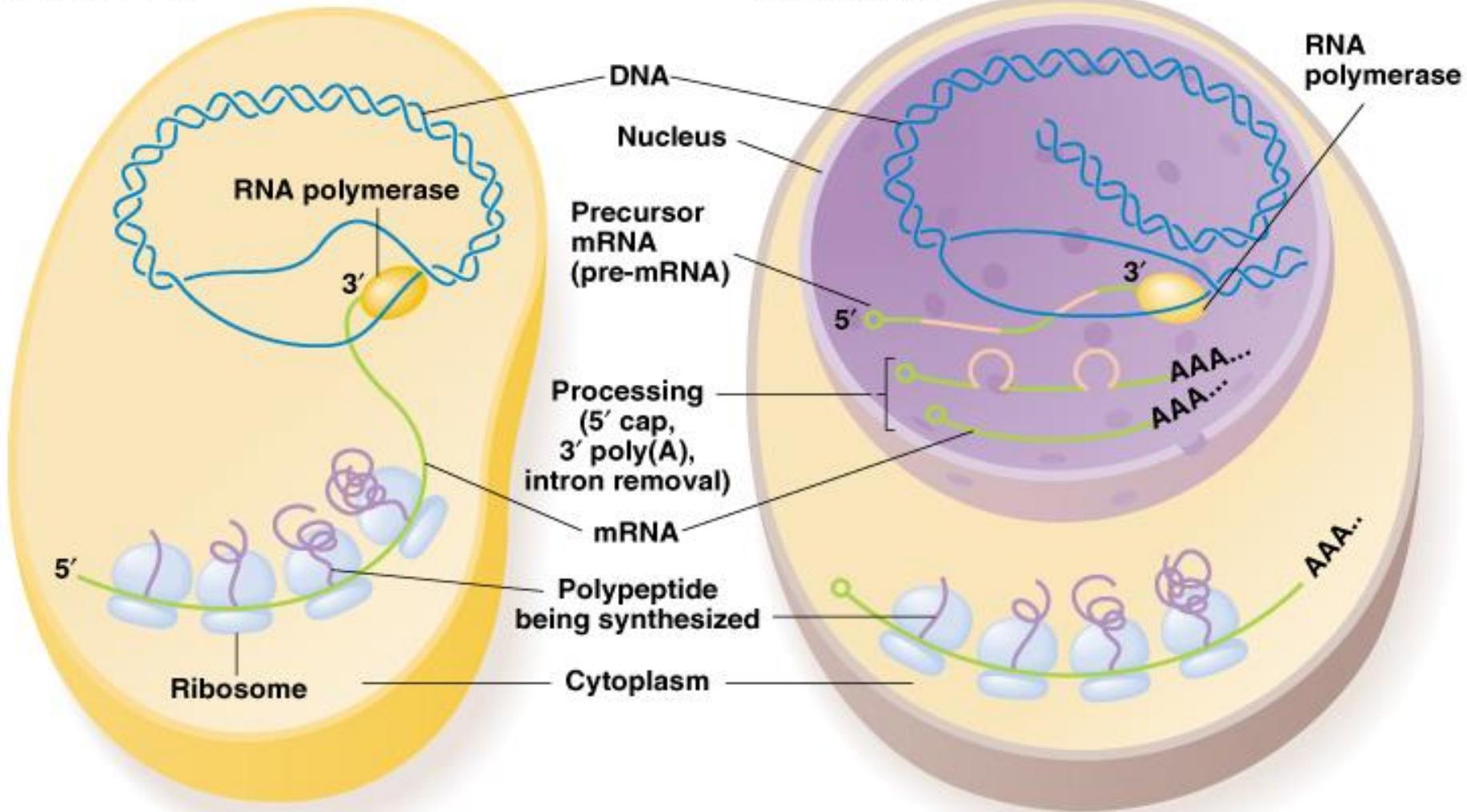
ESTRUTURA DO PROMOTOR EM EUCARIOTOS



VISÃO GERAL

a) Prokaryote

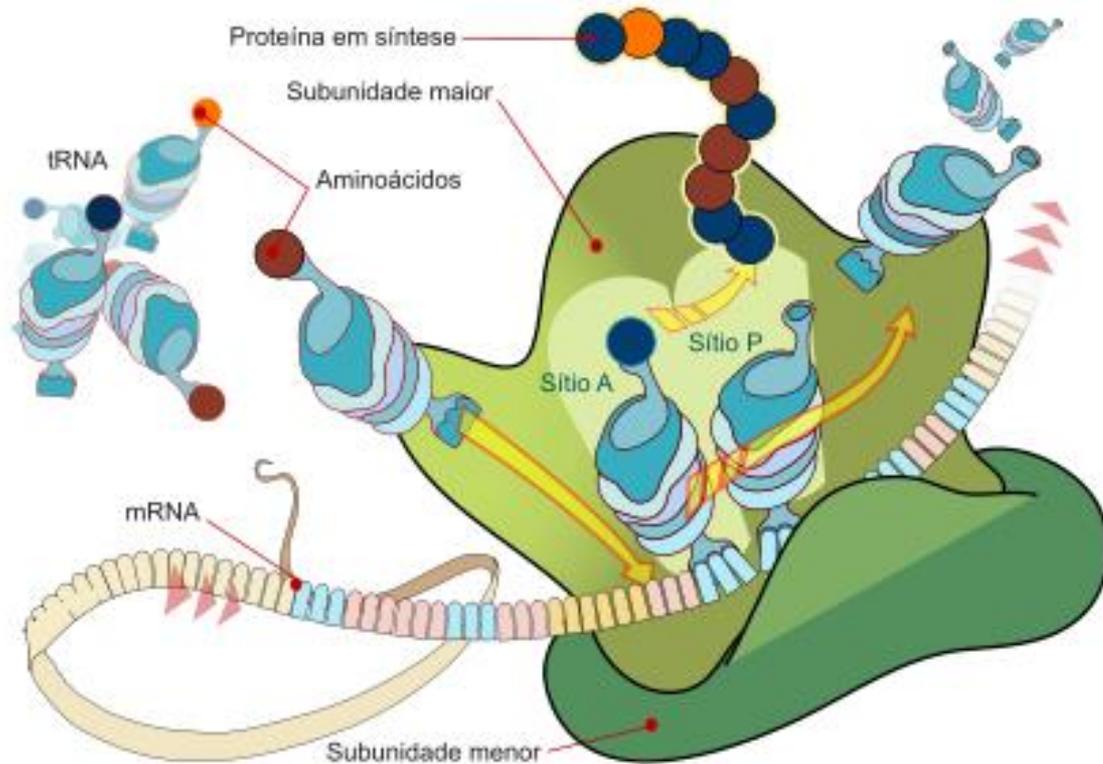
b) Eukaryote



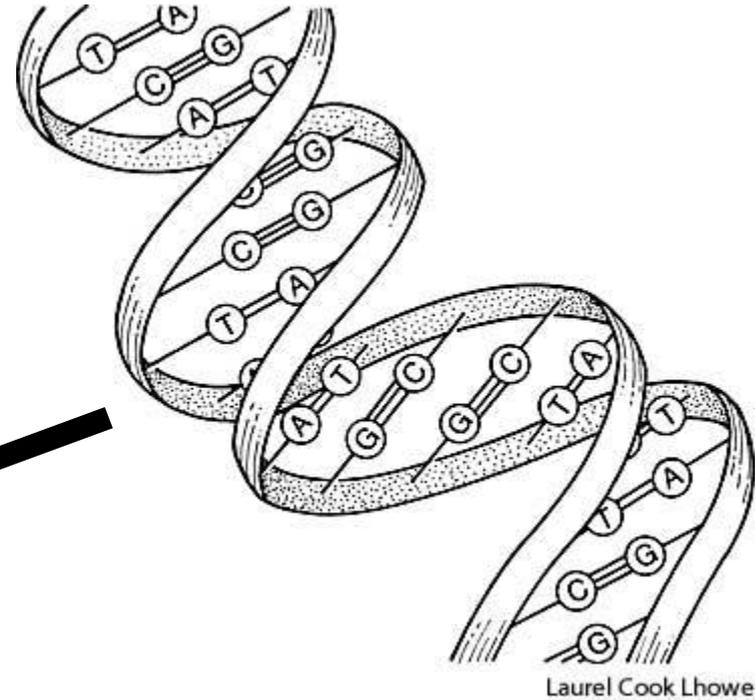
Animação: <http://www.youtube.com/watch?v=983lhh20rGY&feature=related>

TRADUÇÃO

Processo altamente conservado no qual as proteínas são sintetizadas a partir dos moldes de mRNA com auxílio de RNA estruturais.



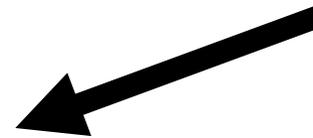
TRADUÇÃO



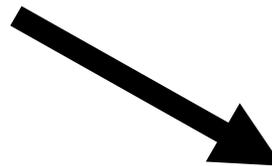
Laurel Cook Lhowe

Interpretação

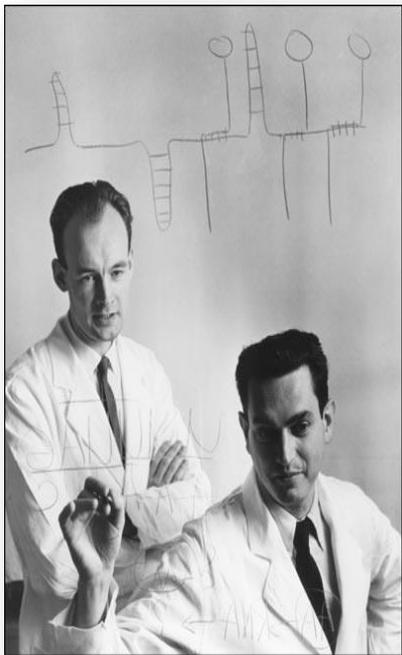
```
AAGTCCTTTTAAATAAATAATTCTAGCTATATTTGCAAC
GTTGGAAAATTAGCTATTCTAATGTTATCGAAAGAAGAA
CACAGTTACTTAGTTTCTCGGCAAACCTATATCAAAATGA
GAAGGTGAAAGAGTGGCATAATGATAAGCAAATCTGAAA
ATTTTTGGTATAATAATCTTGATTGAAATTTGAATGGA
GTAGGCTTACCAAATGTTGGTAAATCAACCTTATTTAAC
ATTATCCTTTTGC GACTATTGATCCCAATGTTGGTATGG
GACAGAATTGATTACACCTAAAAAACAGTTCCGACAAC
AAAGGTGCTTCTAGAGGGGAAGGTCTAGGAAATAAATTT
TTCATGTGGTACGTGCTTTTGGATGATGAAAATGTCATGC
TCCTATAGCAGATATTGACACTATTAATCTTGAATTAAT
TATGCGCGTGTGAAAAAATGGCACGAACTCAAAAAGAT
AAAAGATTAACCTGTTTTGGAAGATGGGAAATCAGCTA
AGTTGTTAAAGGTCTCTTTTTATTAACAACCTAACCTGT
GTTGCTAATCTAGATGGTATTGATTATGTCAAACAAATT
TAGTTGTTATCTCAGCGCGTGCAGAAGAAGAAATTTAG
GGAAGCTATCGGTCTTACTGAATCAGGCGTTGATAAATT
GGAACCTATTTTACAGCAGGTGAAAAAGAGGTTCTGTCT
AAGCTGCTGGTATTATCCATTAGATTTTGAAGAGGTT
```



Colocar em outra linguagem!!



Met -Lys -Trp...



The Nobel Prize in Physiology or Medicine 1968 was awarded jointly to Robert W. Holley, Har Gobind Khorana and Marshall W. Nirenberg "for their interpretation of the genetic code and its function in protein synthesis."

1961

Código Genético

https://history.nih.gov/exhibits/nirenberg/hs4_polyu.htm

1. Composto por trinças de bases nitrogenadas (portanto, existem 64 possibilidades - $4^3 = 64$);
2. São codificados, pelo código genético, 20 aminoácidos presentes nas proteínas;
3. Código genético é degenerado (e portanto, redundante), e linear;
4. Cada trinca (códon) codifica um único aminoácido, no entanto, um aminoácido pode ser codificado por mais do que uma trinca.

CARACTERÍSTICAS GERAIS DA TRADUÇÃO

- ✓ Todos os RNAs mensageiros são lidos na direção 5'-3';
- ✓ As cadeias polipeptídicas são sintetizadas da extremidade amina (NH_3) para a carboxila terminal (COOH) – ligação peptídica;
- ✓ A tradução é realizada nos ribossomos, com os RNA transportadores como adaptadores entre o molde de mRNA e os aminoácidos;
- ✓ Cada aminoácido é especificado por três bases (códon) no mRNA – código genético universal.

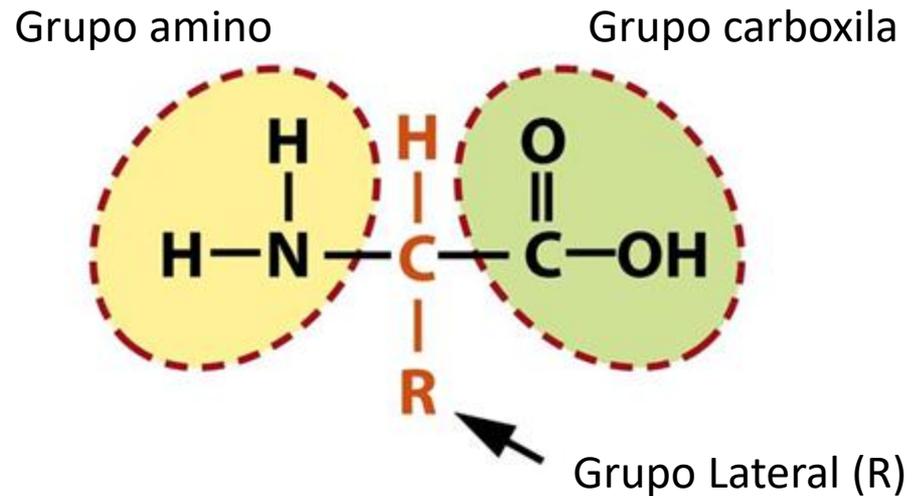
CARACTERÍSTICAS GERAIS DA TRADUÇÃO

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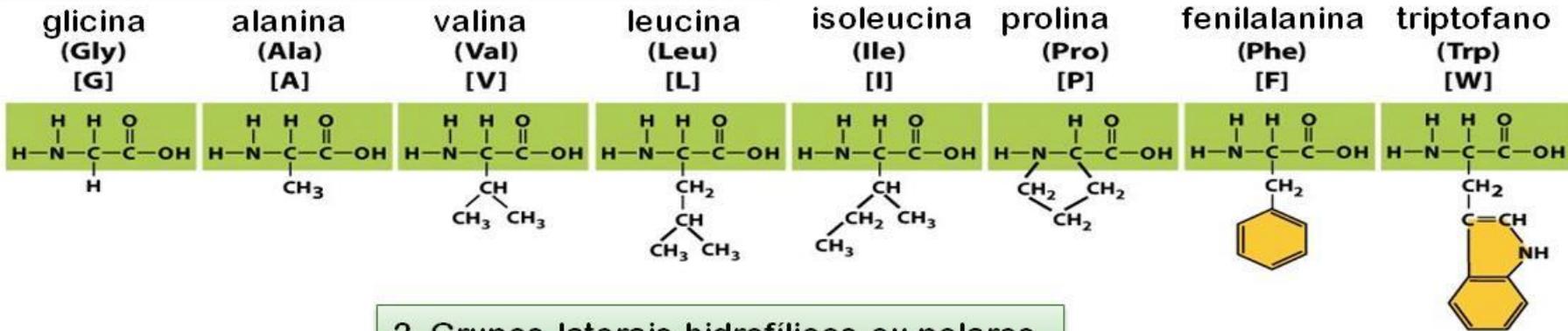
ESTRUTURA DA PROTEÍNA

Aminoácidos (20 tipo):

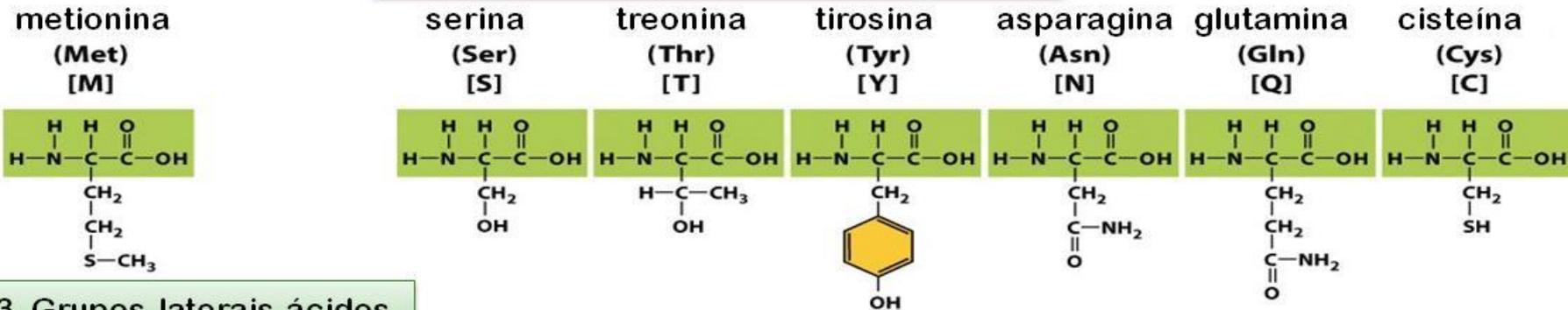
- grupo amino;
- grupo carboxila;
- grupo lateral.



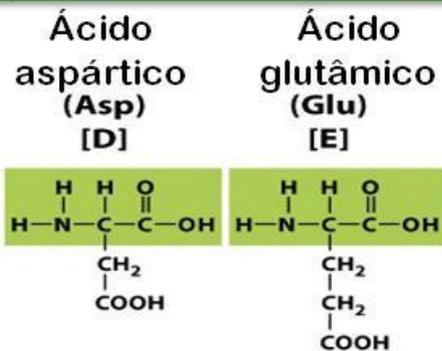
1. Grupos laterais hidrofóbicos ou não polares



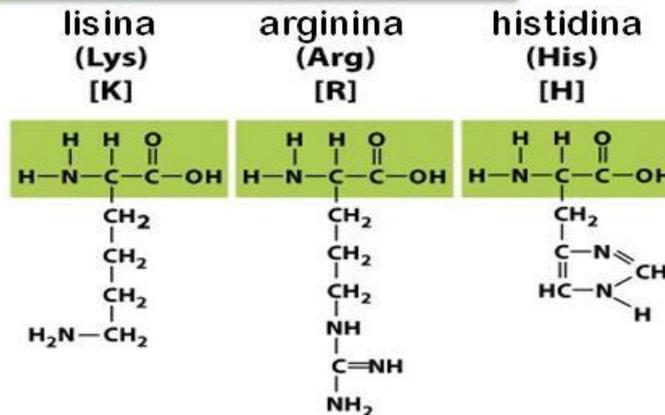
2. Grupos laterais hidrofílicos ou polares



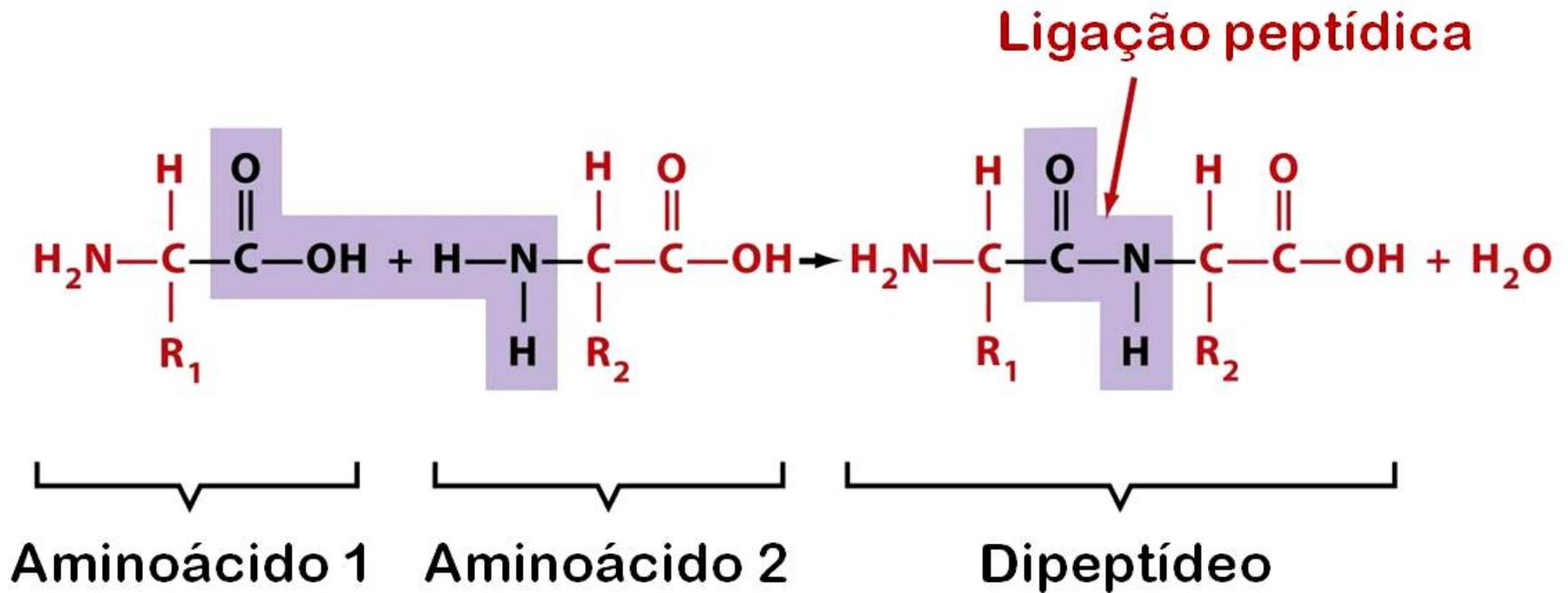
3. Grupos laterais ácidos



4. Grupos laterais básicos



LIGAÇÃO PEPTÍDICA



Proteína - direção de síntese

START CODON E STOP CODON

Início: códon de iniciação da síntese protéica

– AUG –



METIONINA

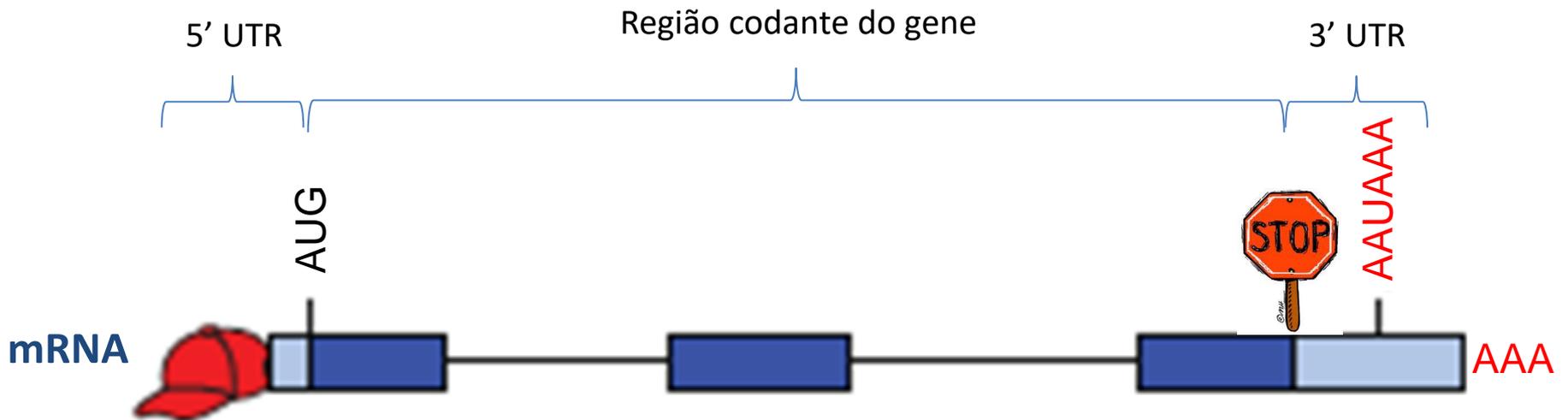
Terminação: três códons terminam a síntese protéica

– UAG – UAA – UGA –



START CODON E STOP CODON

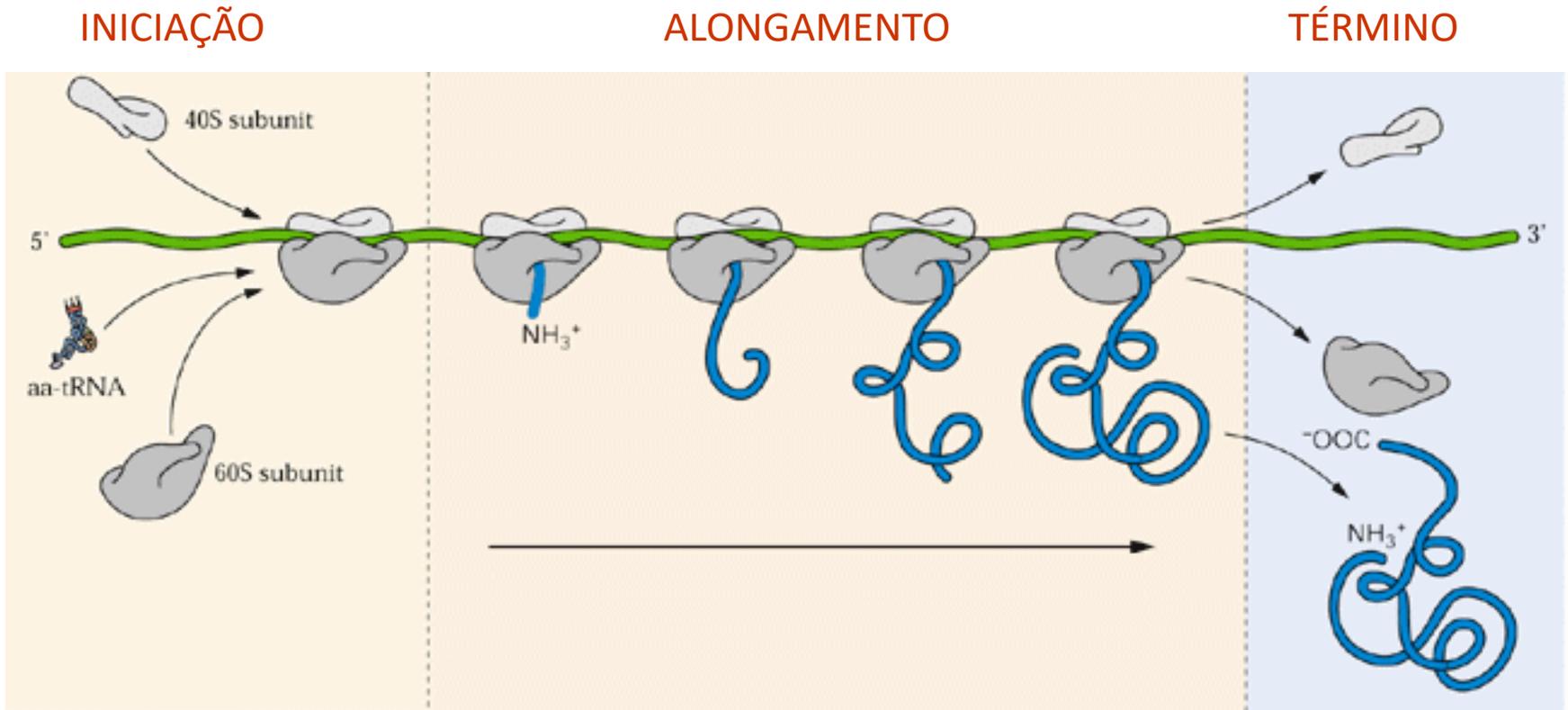
- ❖ Delimitam a região codante (região que é transcrita e traduzida!)



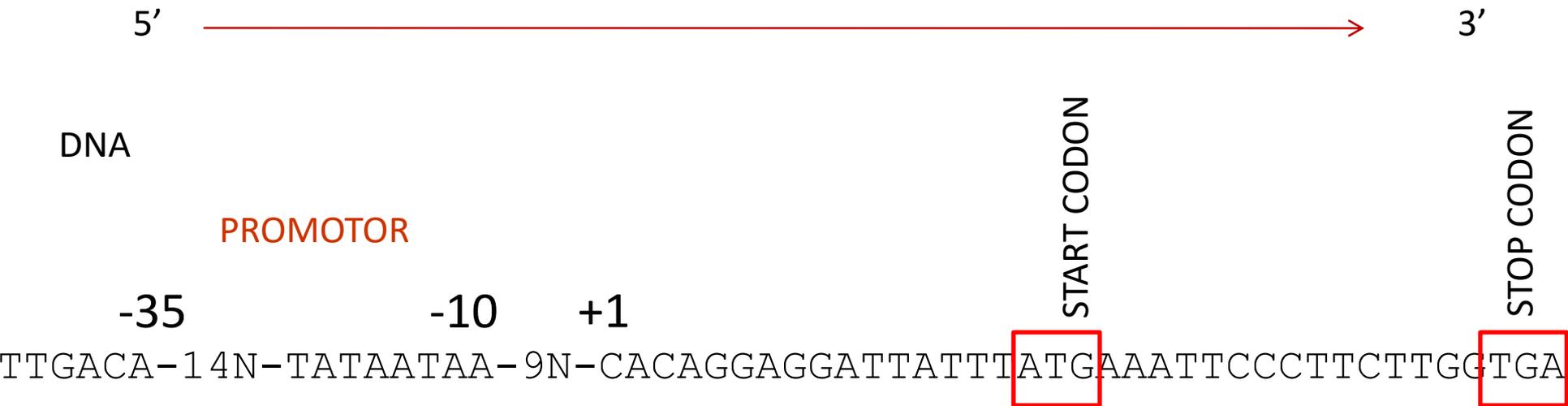
TRADUÇÃO: INÍCIO E FIM

TTCATACTTGGTTAAGACCTTTACAAGCCGACCAACGTGGTGAC
AGTGTCGTCCTTTACGCACCGAATCCCTTTATCATTGAATTAGT
AGAAGAGCGATACTTAGGACGTCTTCGG**ATG**GAATCTTGGTCCC
GTTGCCTGGAACGTCTTGAAACTGAATTCCCGCCAGAAGATGTT
CATACTTGGTTAAGACCTTTACAAGCCGACCAACGTGGTGACAG
TGTCGTCCTTTACGCACCGAATCCCTTTATCATATTGAATTAGT
AGAAGAGCGATACTTAGGACGTCTTCGGGAATTGTTATCCTATT
TCTCAGGAATACGTGAAGTAGTCCTTGCAATTGGCTCACGACCT
AAAACAACAGAACTACCCGTACCAGTAGACACTACAGGACGTTT
GTCTTCAACAGTCCCATTTAACGGAAATCTCGACACACACTATA
ACTT**TGA**TAATTTTGTGAGGGACGAAGCAATCAACTCGCTCGT
GCTGCAGCTTGGCAAGCGGCACAGAAACCGGGAGACCGTACTCA
CAACCCTCTATTGCTCTATGGTGGGACTGGTTTGGGTAAAACCC
ATTTAATGTTTGTGCTGCAGGTAACGTAATGCGGCAAGTAAACCCA
ACTTATAAAGTAATGTATCTTCGTTTCGGAACAGTTTTTTCAGCGC
CATGATAAGAGCGTACAAGATAAAAAGTATGGATCATAAGGGTAA

TRADUÇÃO



DOBRAMENTO DE PROTEÍNAS

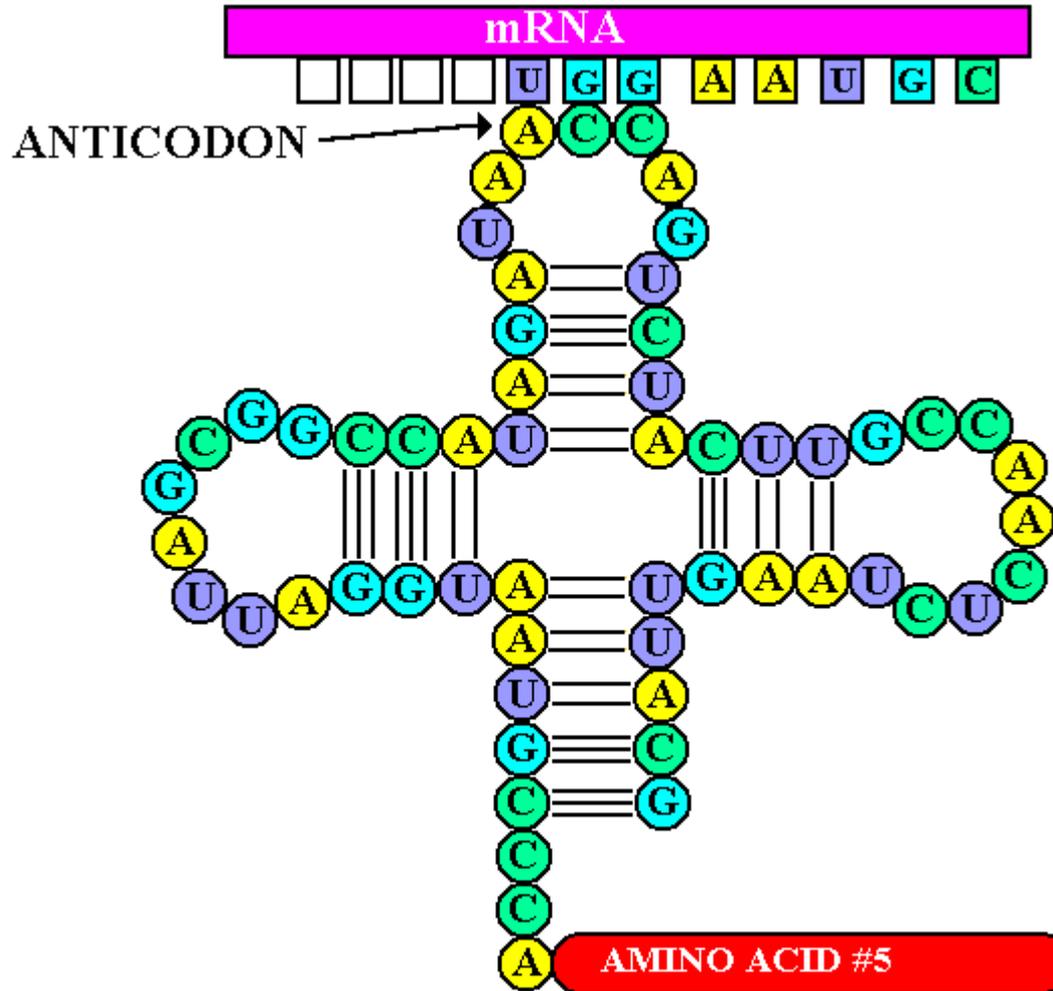


PROTEINA MET LYS PHE PRO SER TRY



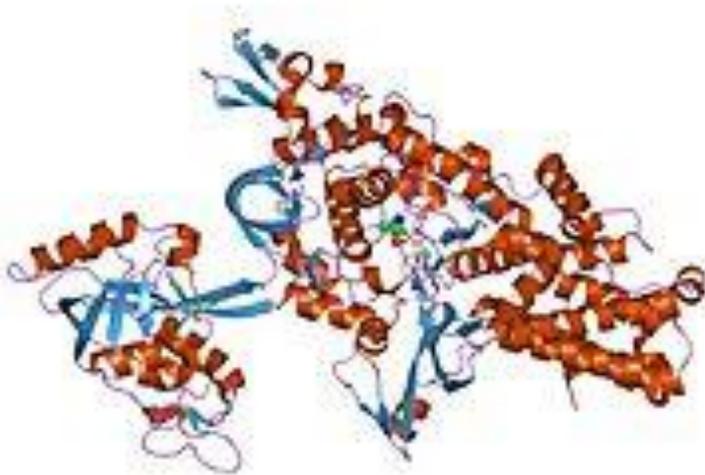
TRADUÇÃO EM PROCARIOTOS

CÓDON E ANTICÓDON

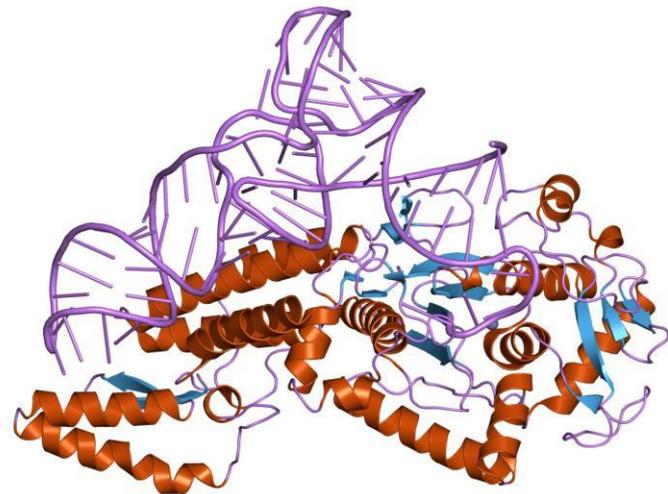


As aminoacil - tRNA sintetases:

- Para que uma molécula de tRNA se ligue ao aminoácido correto são necessárias 20 enzimas diferentes que reconheçam, especificamente, aminoácidos e seus tRNAs compatíveis.
- Cada enzima liga um aminoácido específico a seu tRNA correspondente e é capaz de reconhecer diferentes tRNAs para o mesmo aminoácido. Estas enzimas ligam o aminoácido à hidroxila 3' livre da adenosina terminal do tRNA.



LeuRS



ProRS

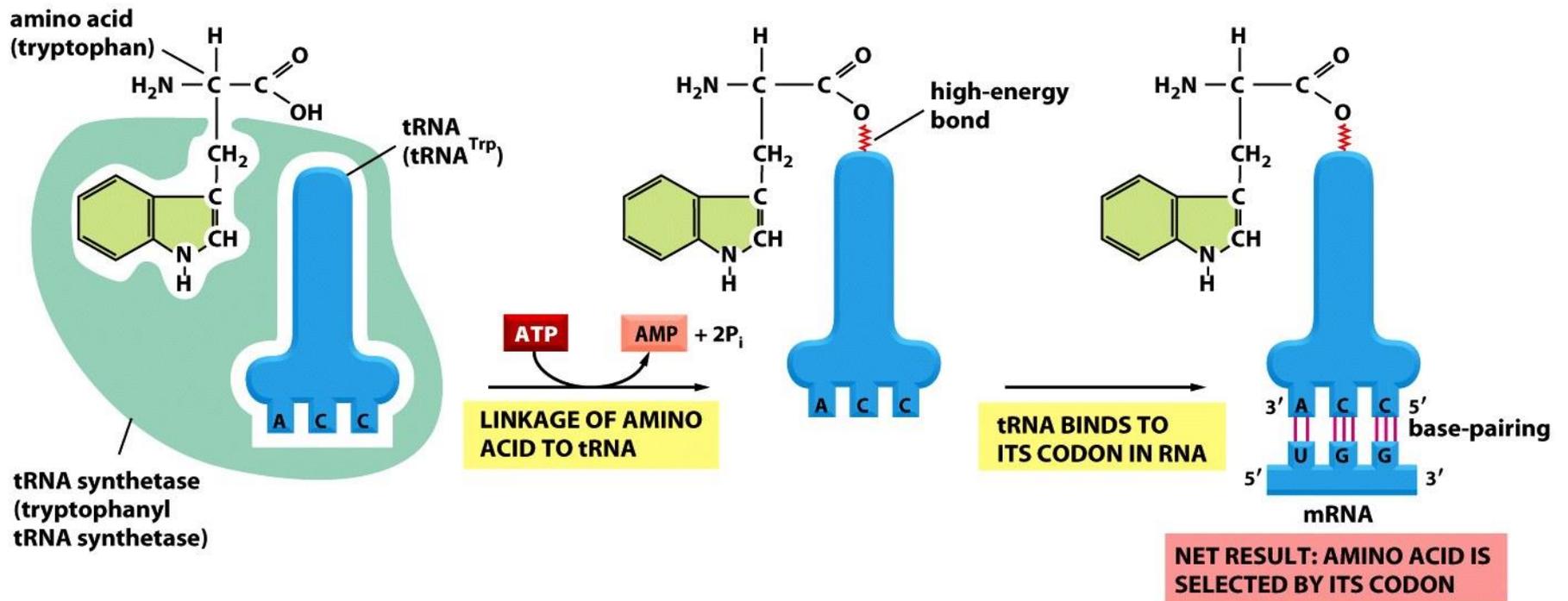


Figure 7-29 Essential Cell Biology 3/e (© Garland Science 2010)

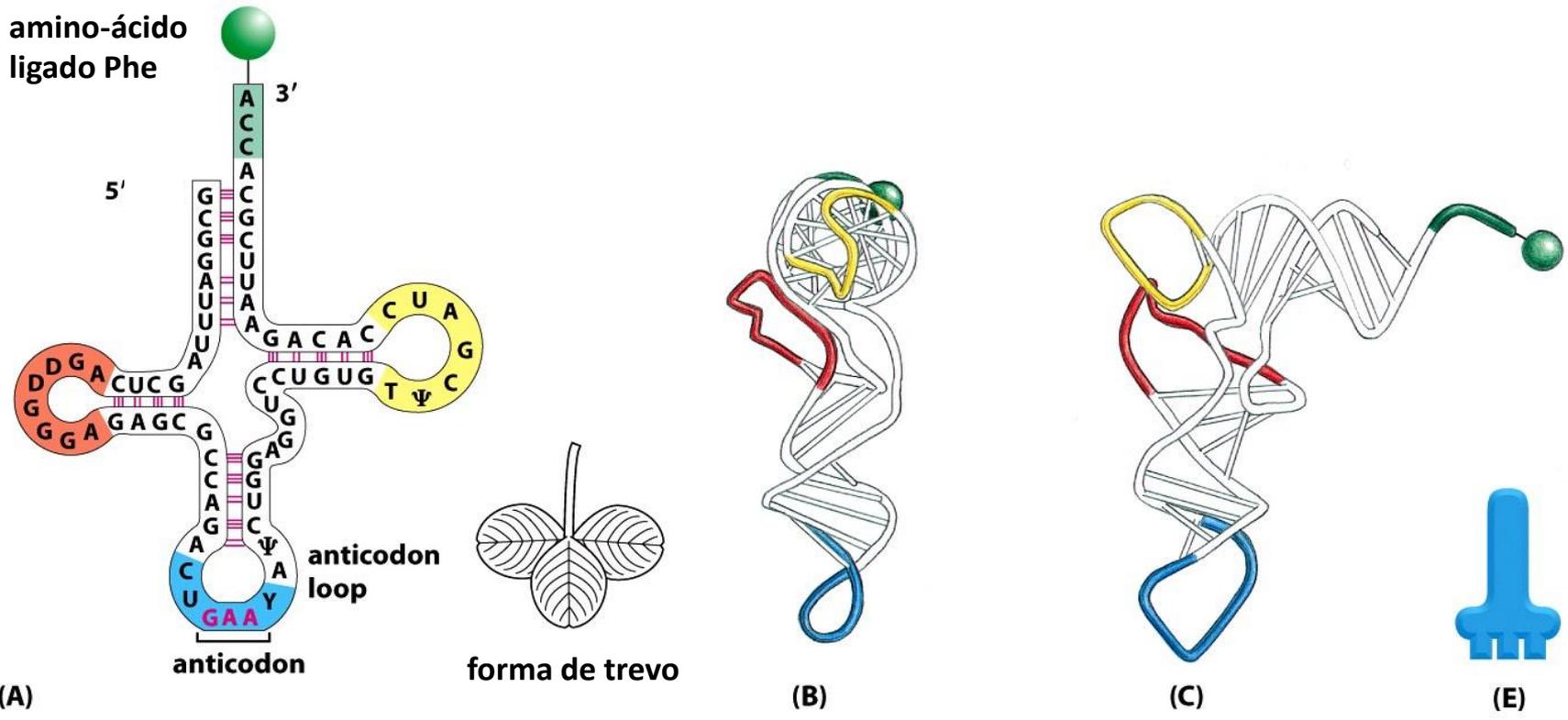


Figure 7-28 Essential Cell Biology 3/e (© Garland Science 2010)

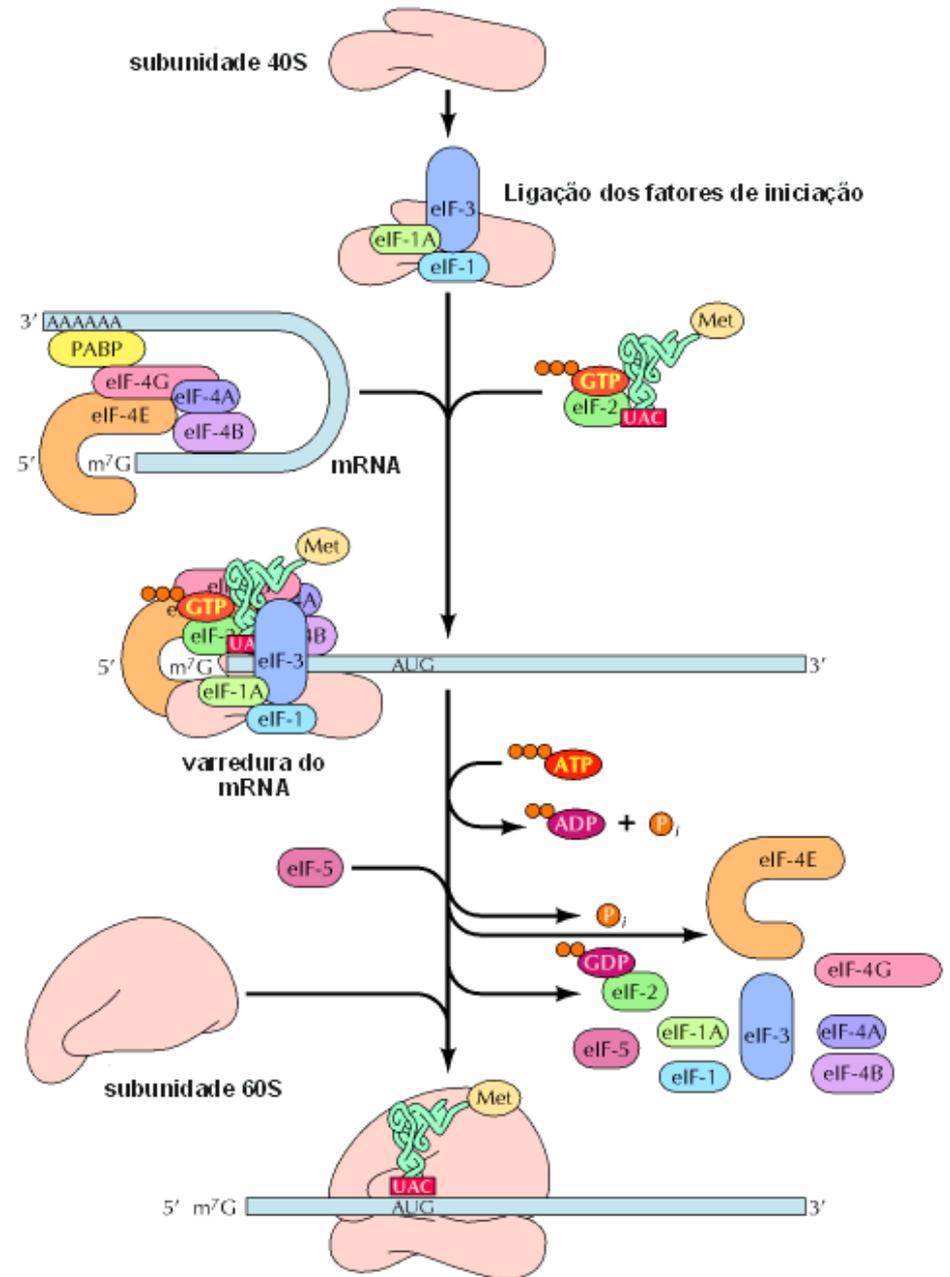
O CÓDIGO GENÉTICO É REDUNDANTE!

Amino acid	3-Letter code	1-Letter code	Codons
Alanine	Ala	A	GCC, GCU, GCG, GCA
Arginine	Arg	R	CGC, CGG, CGU, CGA, AGA, AGG
Asparagine	Asn	N	AAU, AAC
Aspartic acid	Asp	D	GAU, GAC
Cysteine	Cys	C	UGU, UGC
Glutamic acid	Glu	E	GAA, GAG
Glutamine	Gln	Q	CAA, CAG
Glycine	Gly	G	GGU, GGC, GGA, GGG
Histidine	His	H	CAU, CAC
Isoleucine	Ile	I	AUU, AUC, AUA
Leucine	Leu	L	UUA, UUG, CUA, CUG, CUU, CUC
Lysine	Lys	K	AAA, AAG
Methionine	Met	M	AUG
Phenylalanine	Phe	F	UUC, UUU
Proline	Pro	P	CCU, CCC, CCA, CCG
Serine	Ser	S	UCU, UCC, UCA, UCG, AGU, AGC
Threonine	Thr	T	ACU, ACC, ACA, ACG
Tyrosine	Tyr	Y	UAU, UAC
Tryptophan	Trp	W	UGG
Valine	Val	V	GUU, GUC, GUA, GUG
"Stop"	—	—	UAA, UAG, UGA

start codon -iniciador

stop codon -terminador

**Vários
polipeptideos
auxiliam o início da
tradução!**



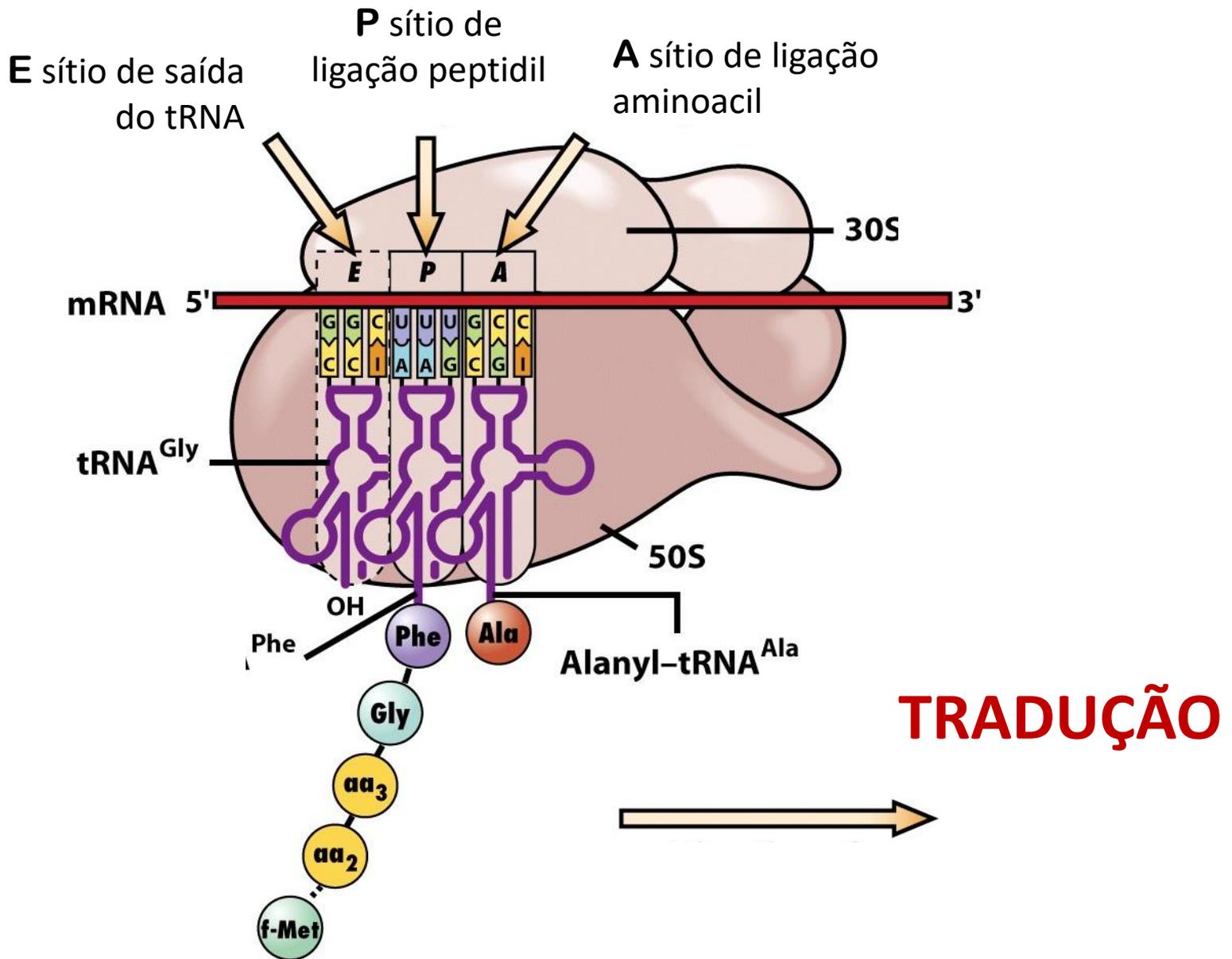
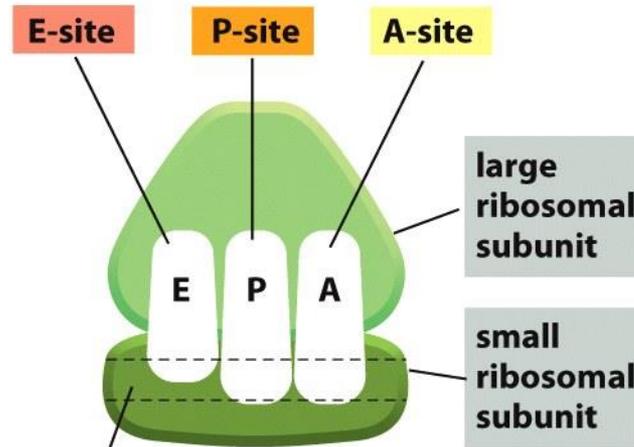
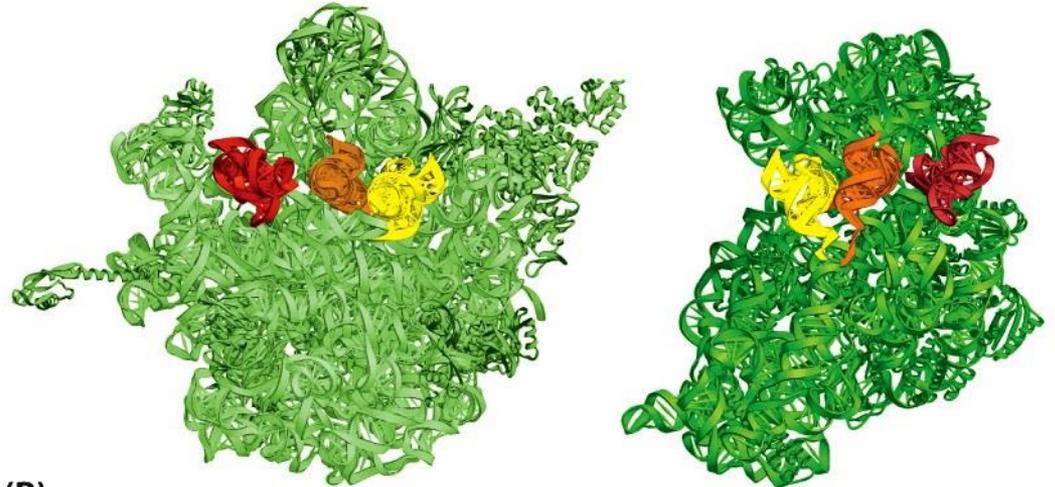
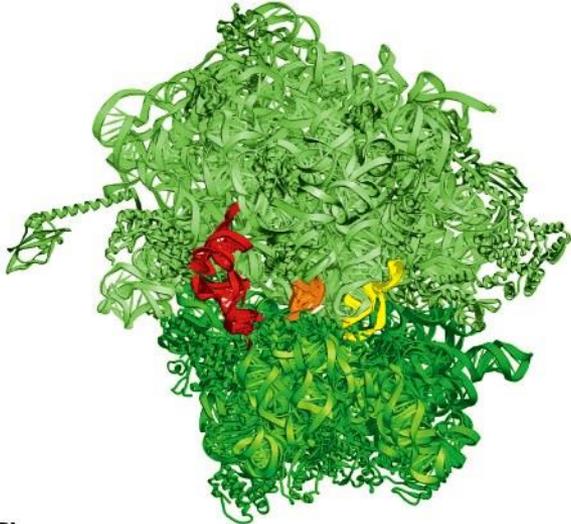
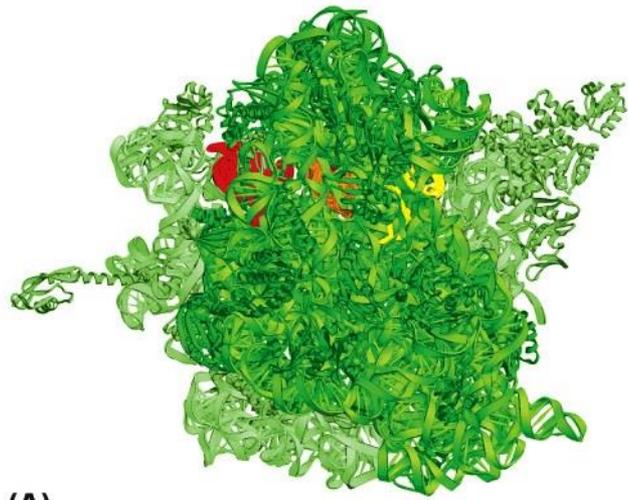


Figure 12-14a Principles of Genetics, 4/e
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(D)

Figure 7-32 Essential Cell Biology 3/e (© Garland Science 2010)

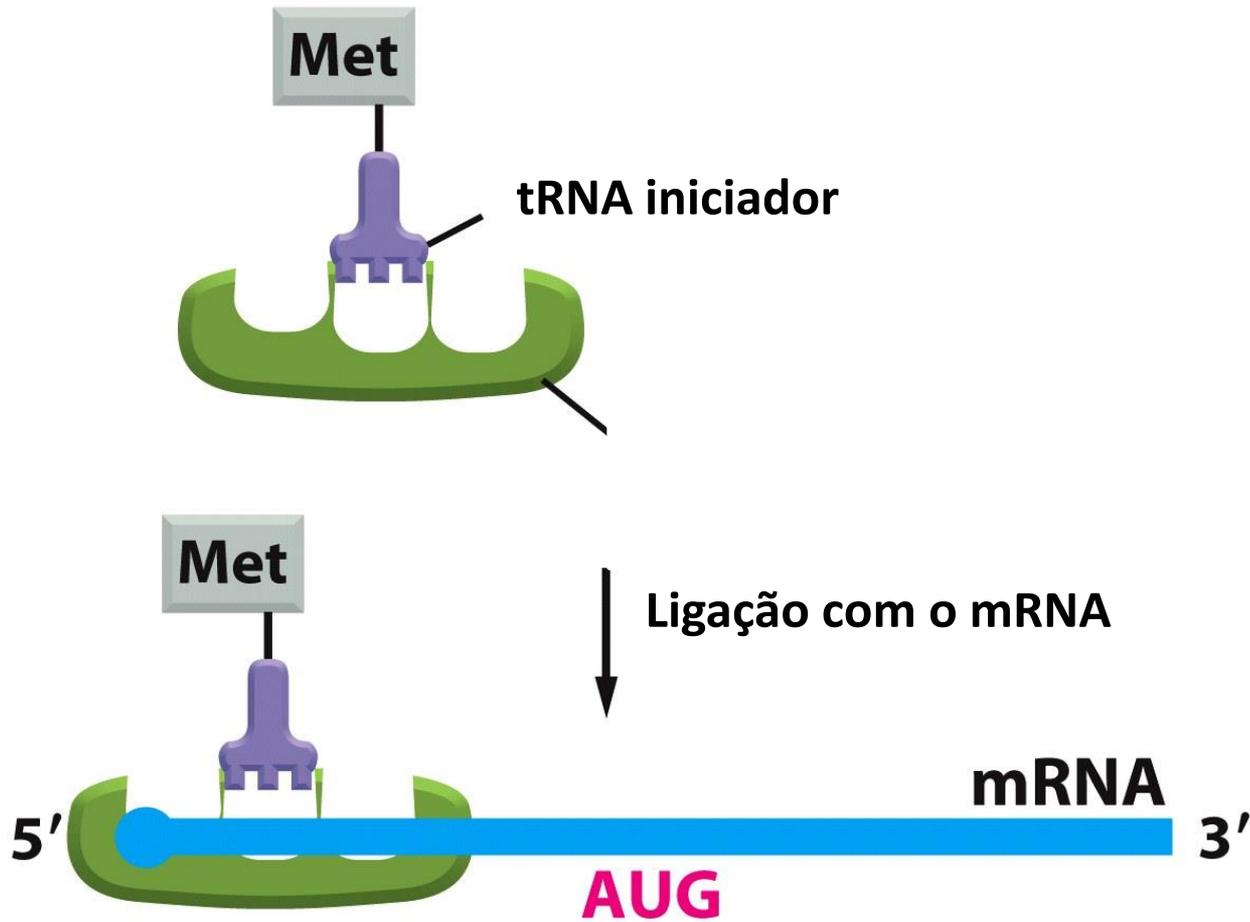


Figure 7-35 part 1 of 5 Essential Cell Biology 3/e (© Garland Science 2010)

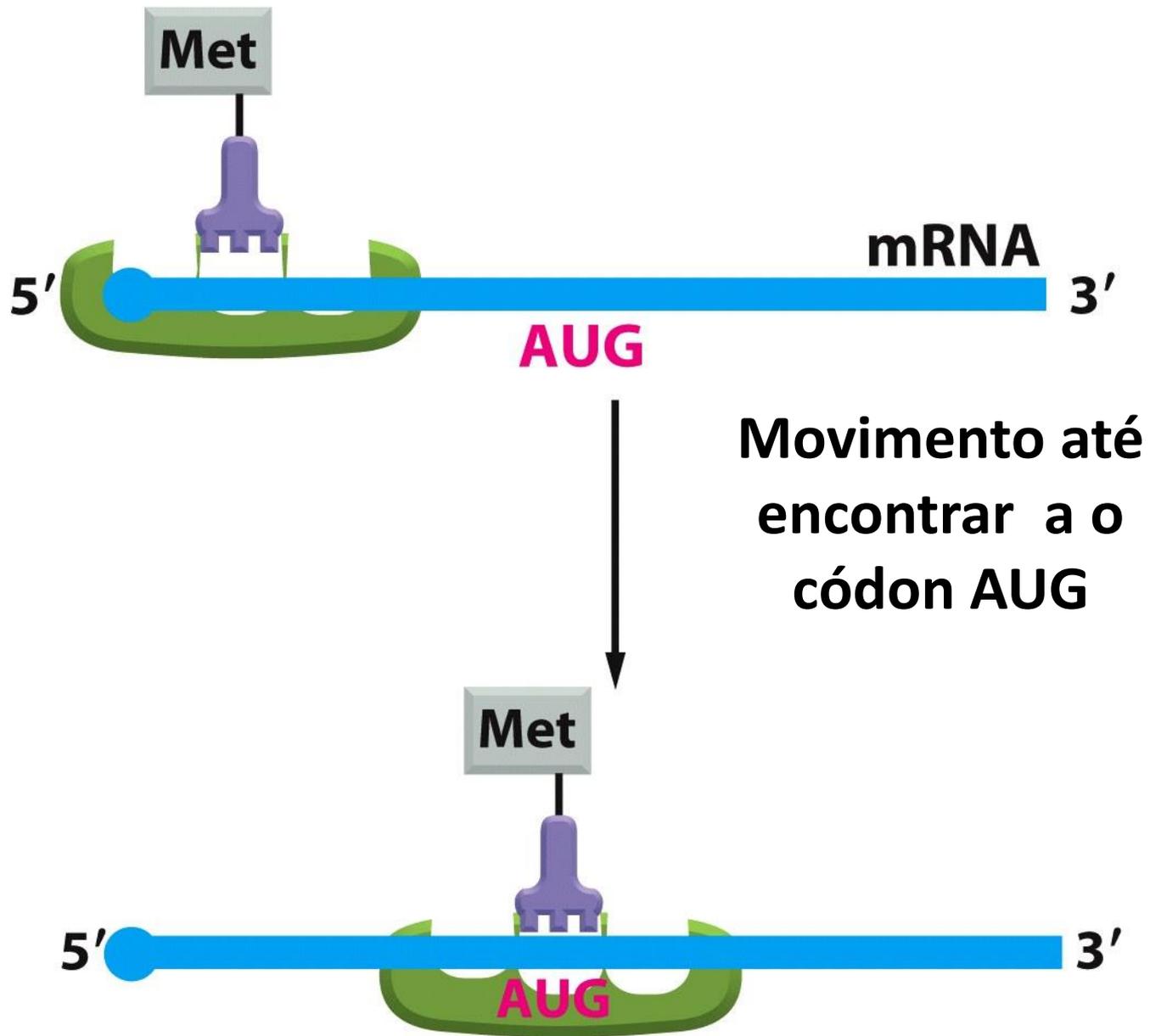


Figure 7-35 part 2 of 5 Essential Cell Biology 3/e (© Garland Science 2010)

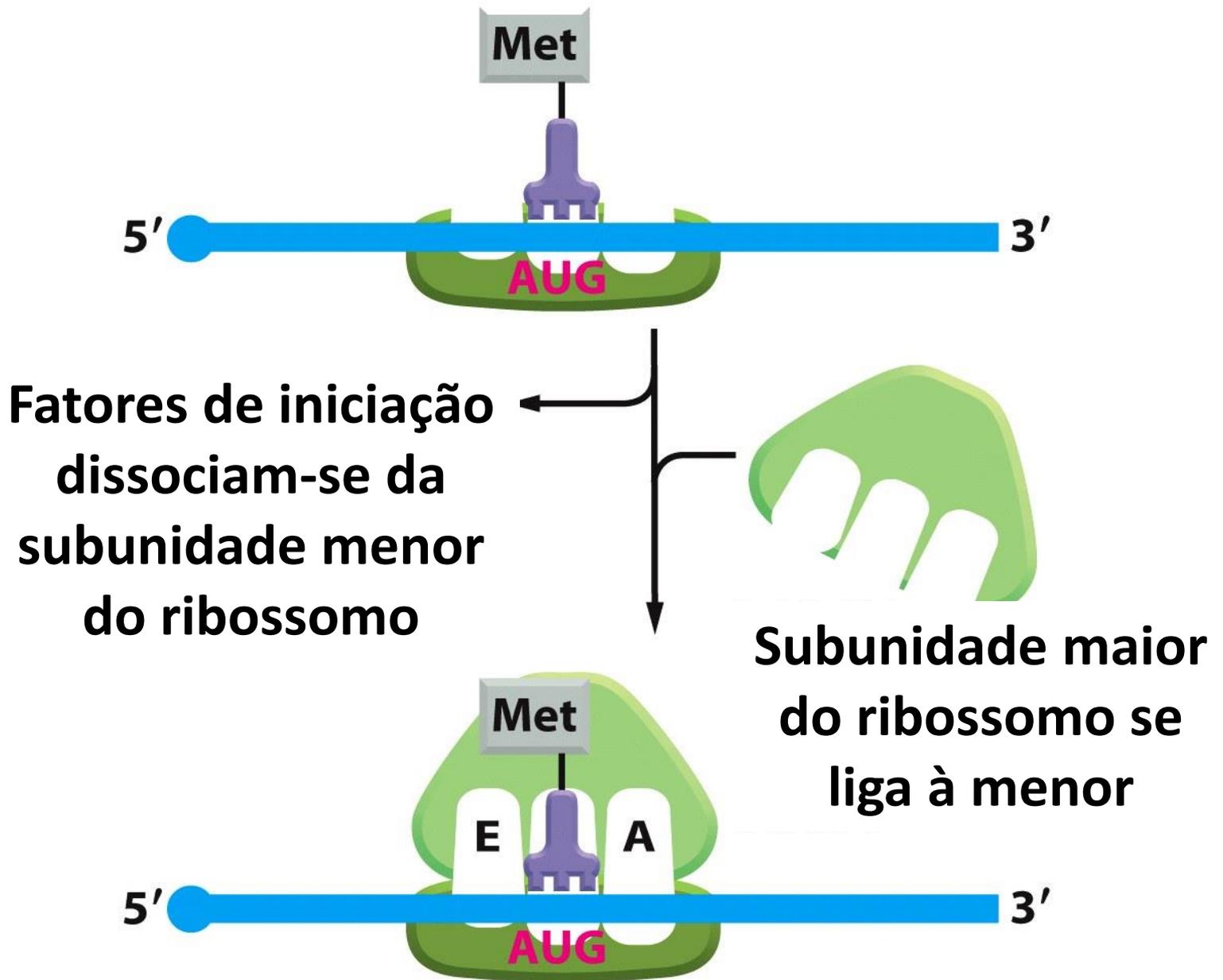


Figure 7-35 part 3 of 5 Essential Cell Biology 3/e (© Garland Science 2010)

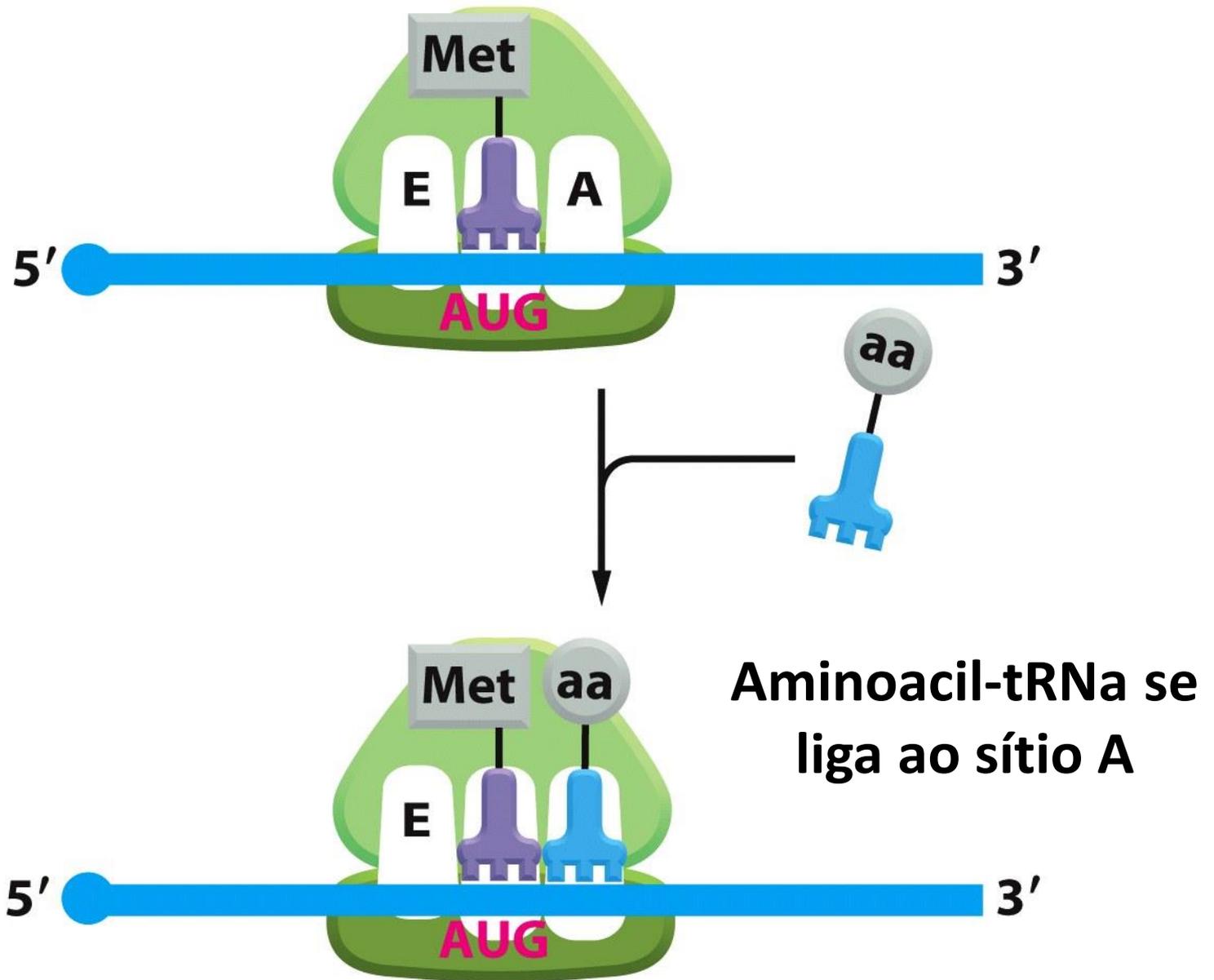


Figure 7-35 part 4 of 5 Essential Cell Biology 3/e (© Garland Science 2010)

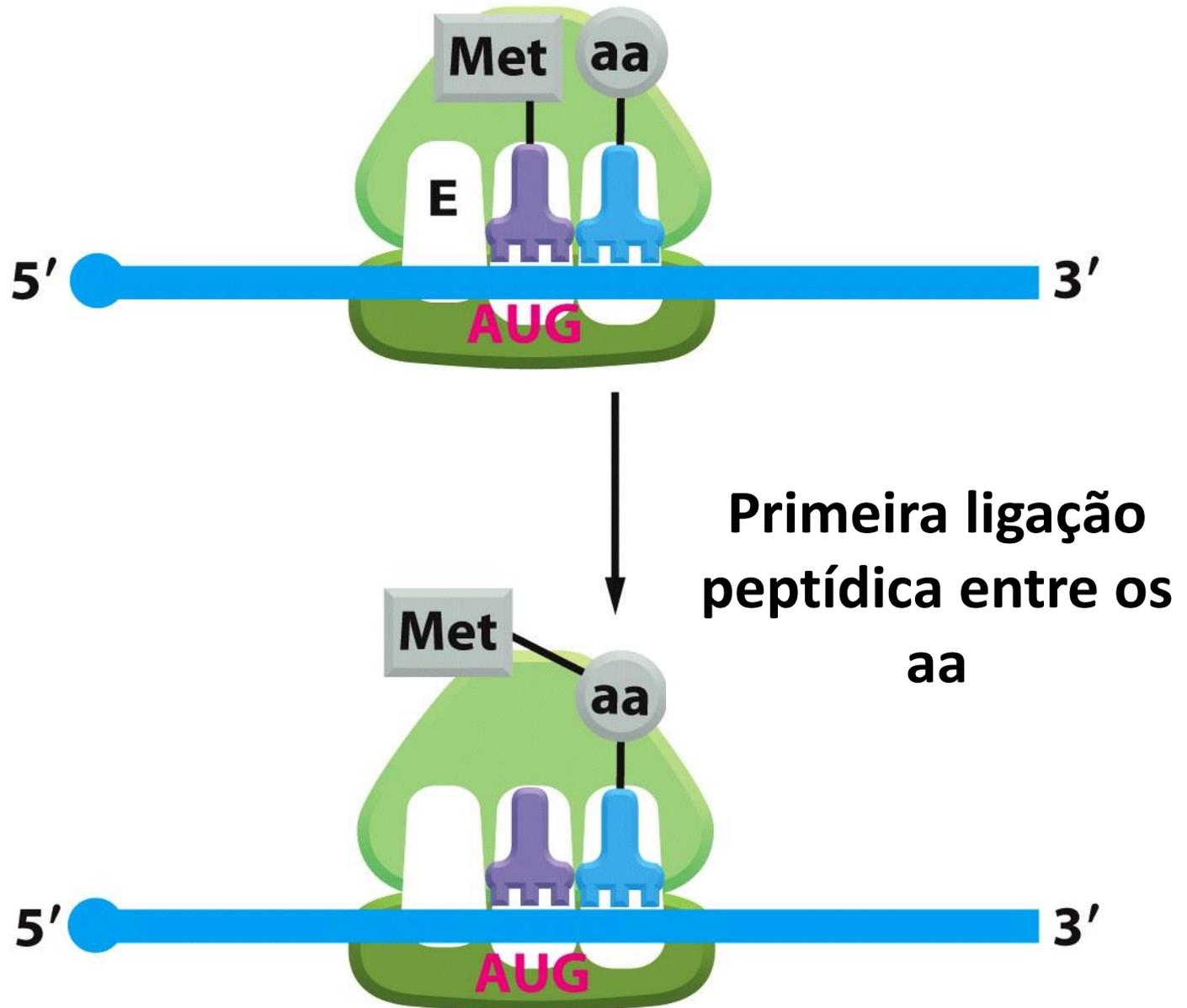
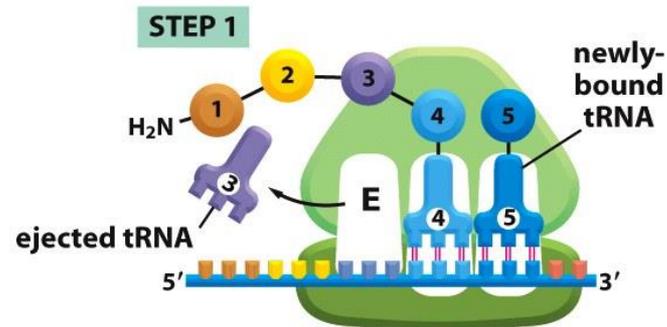
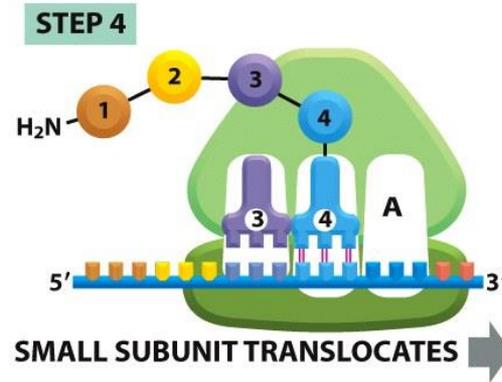
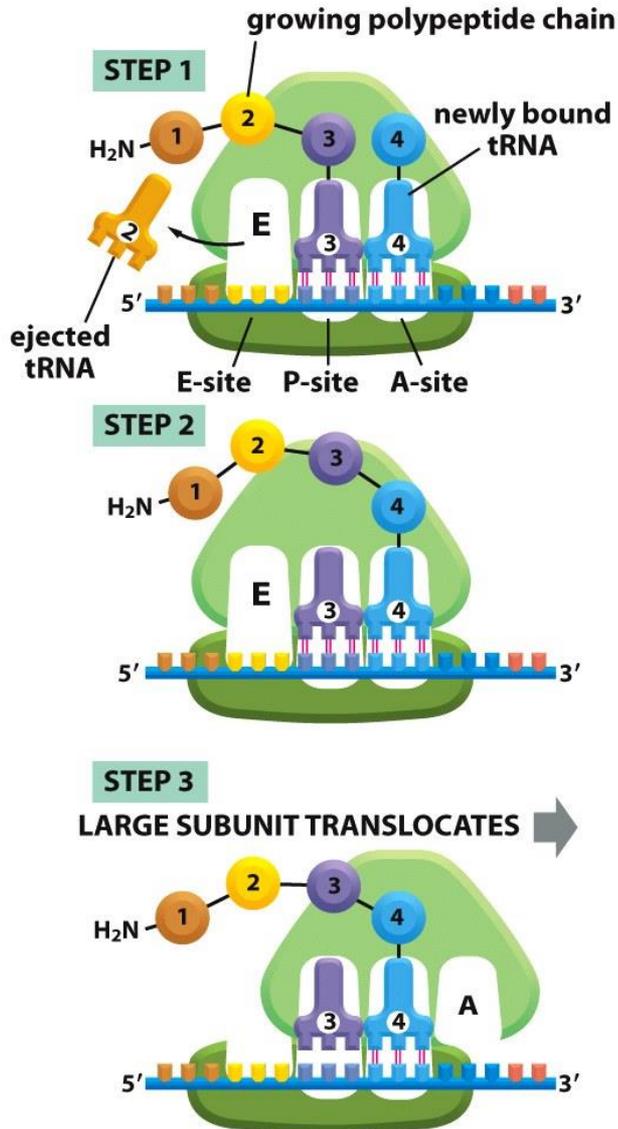


Figure 7-35 part 5 of 5 Essential Cell Biology 3/e (© Garland Science 2010)

E continuamente...



Vários fatores controlam a continuação da tradução!

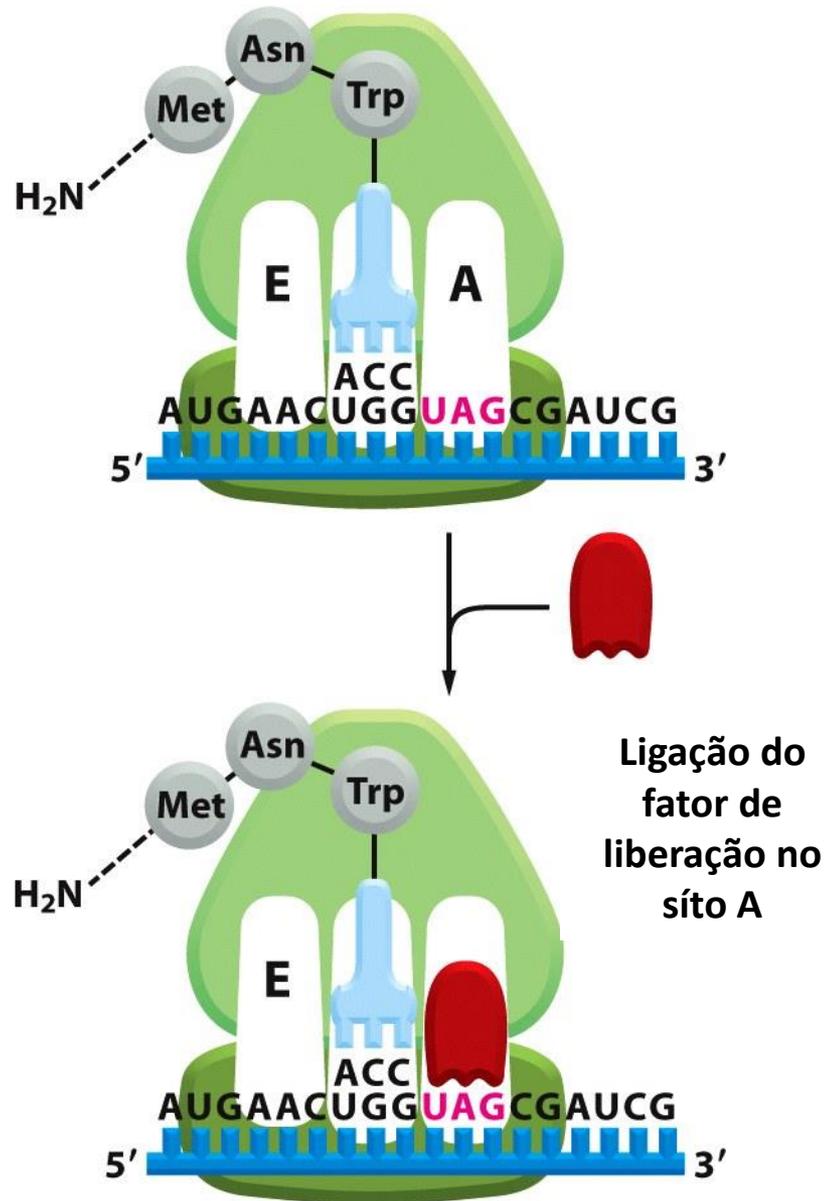
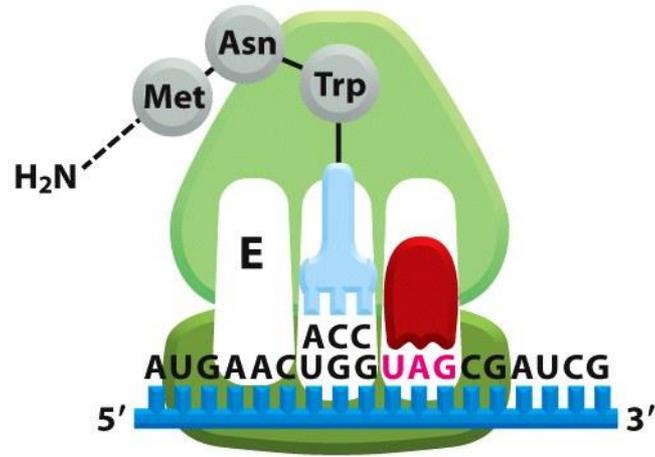


Figure 7-37 part 1 of 3 Essential Cell Biology 3/e (© Garland Science 2010)



Terminação

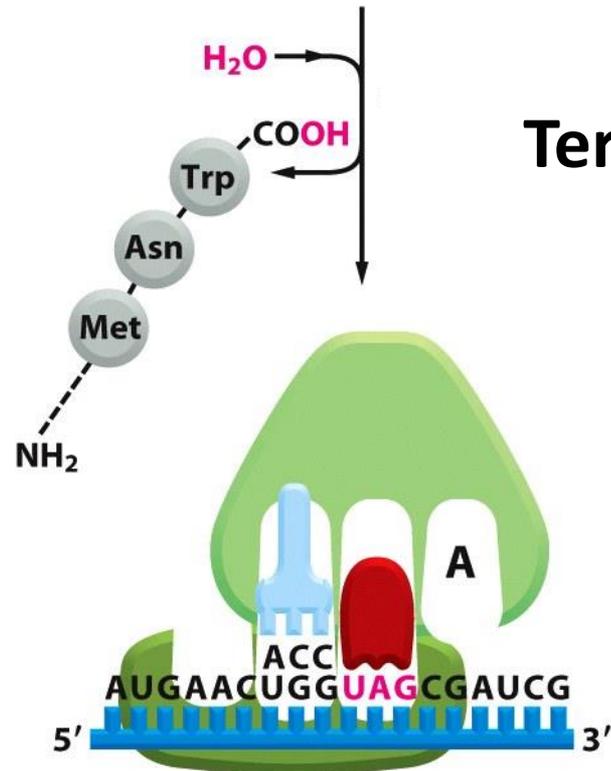


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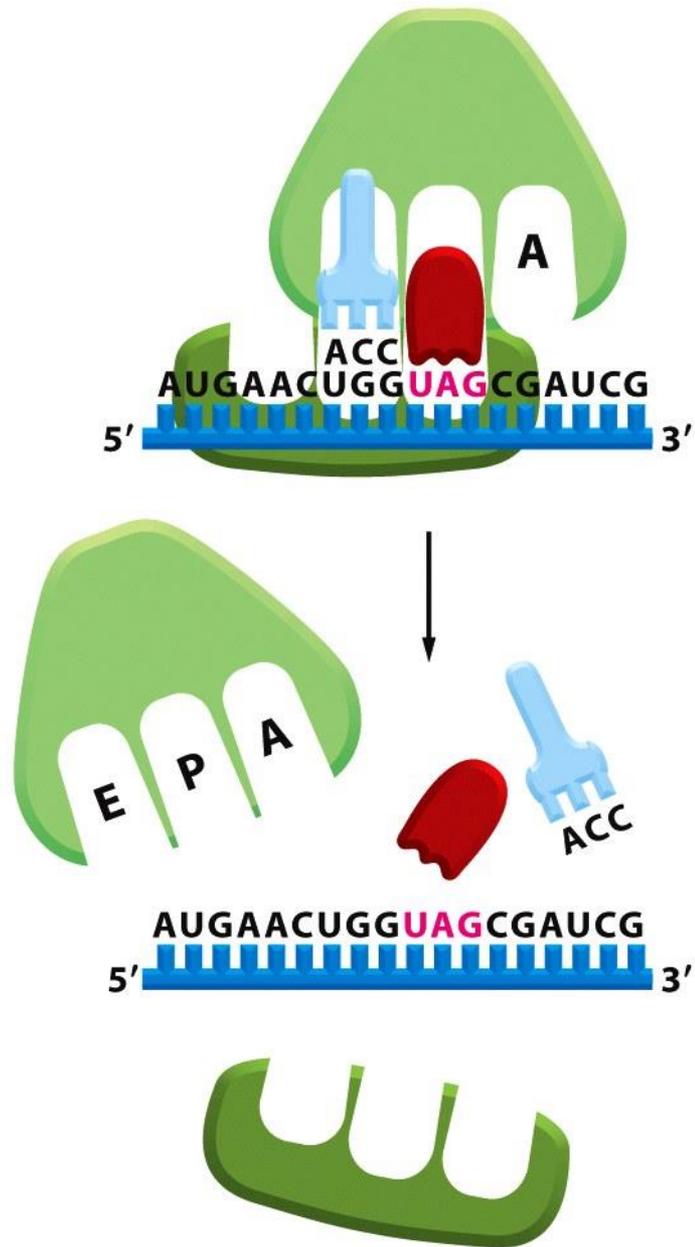
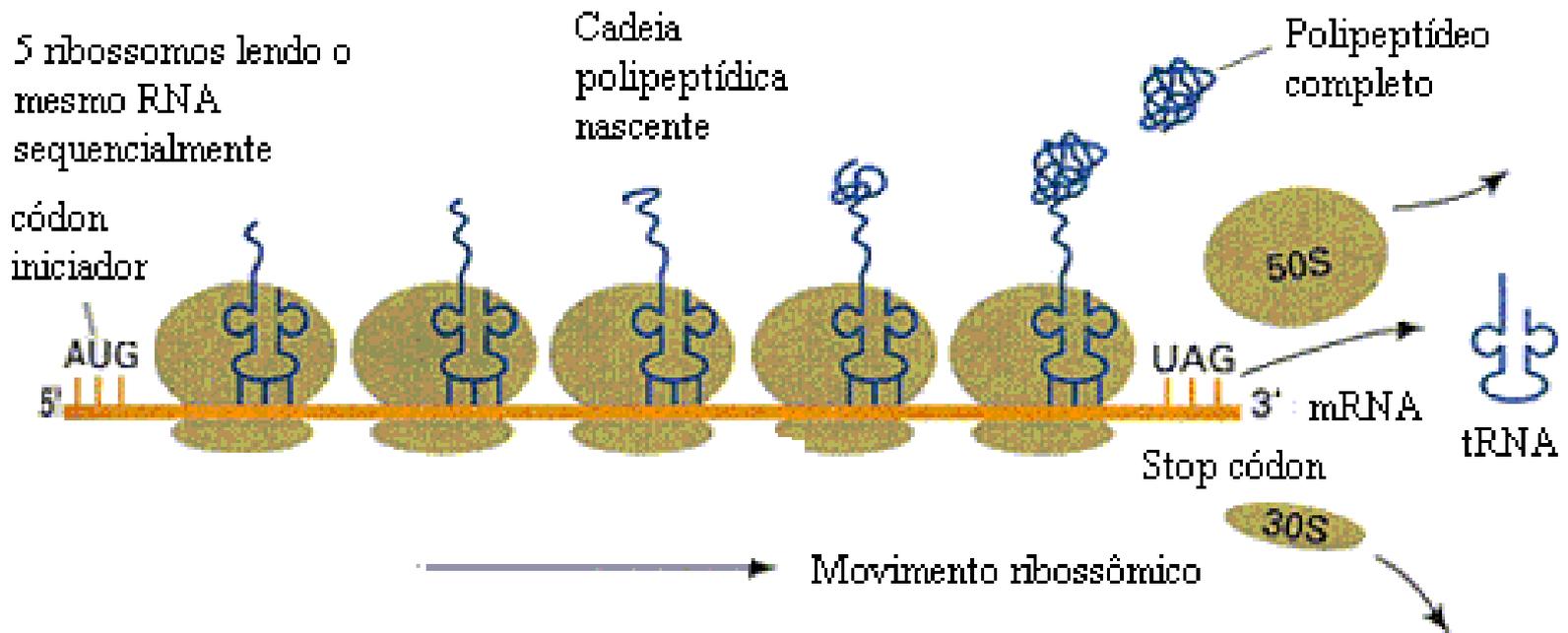
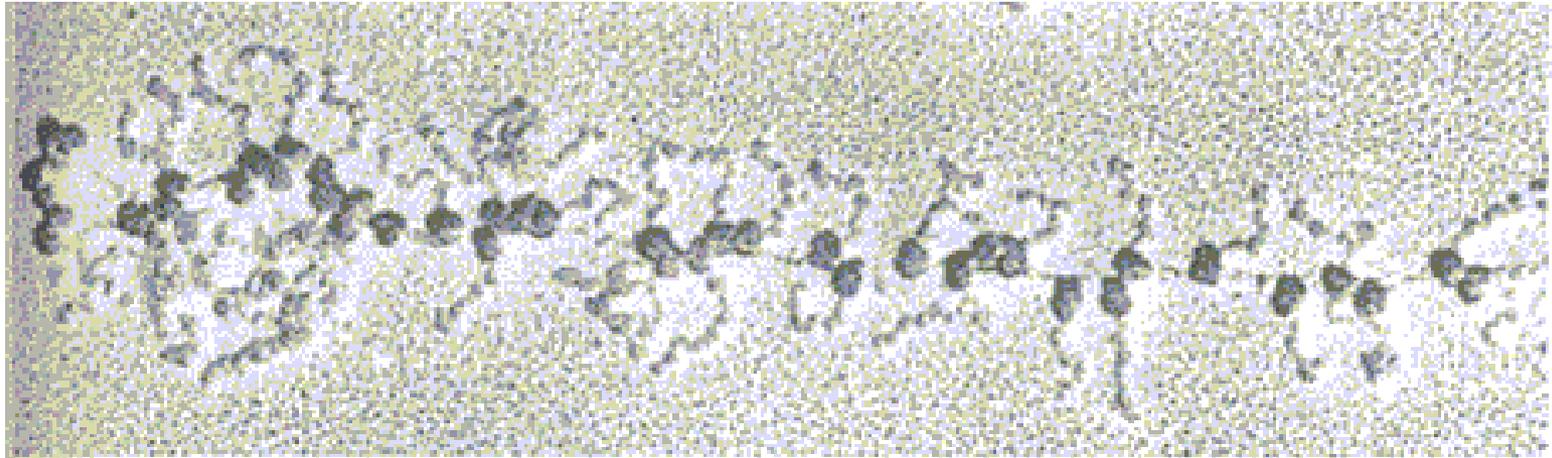
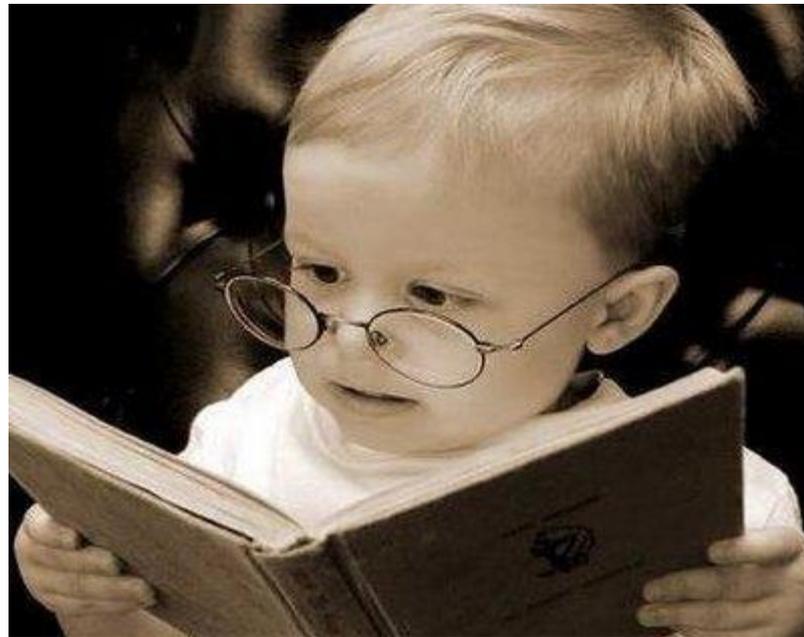


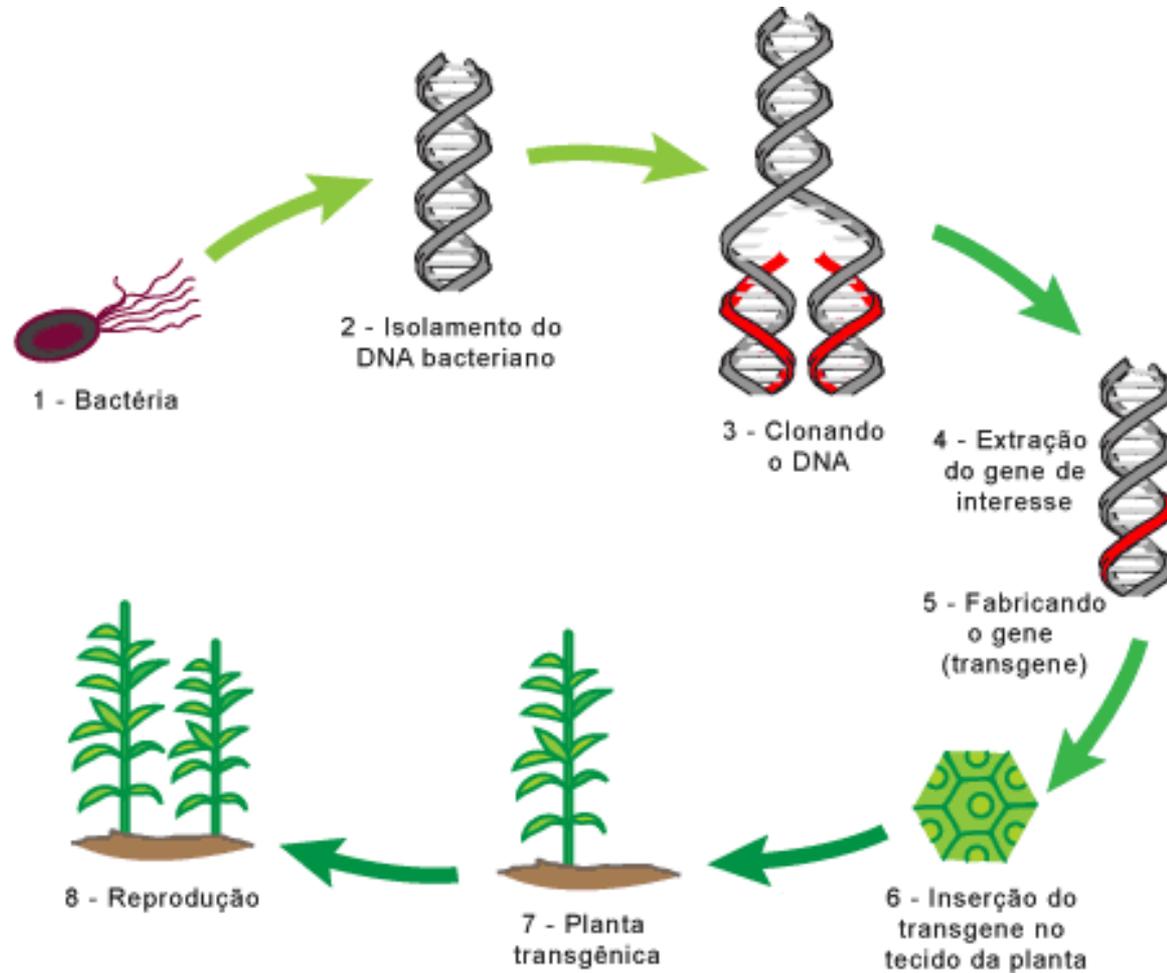
Figure 7-37 part 3 of 3 Essential Cell Biology 3/e (© Garland Science 2010)



APLICANDO O CONHECIMENTO..



OBTENÇÃO DE ORGANISMOS GENETICAMENTE MODIFICADOS



CONSTRUÇÃO PRESENTE NA SOJA RR[®]

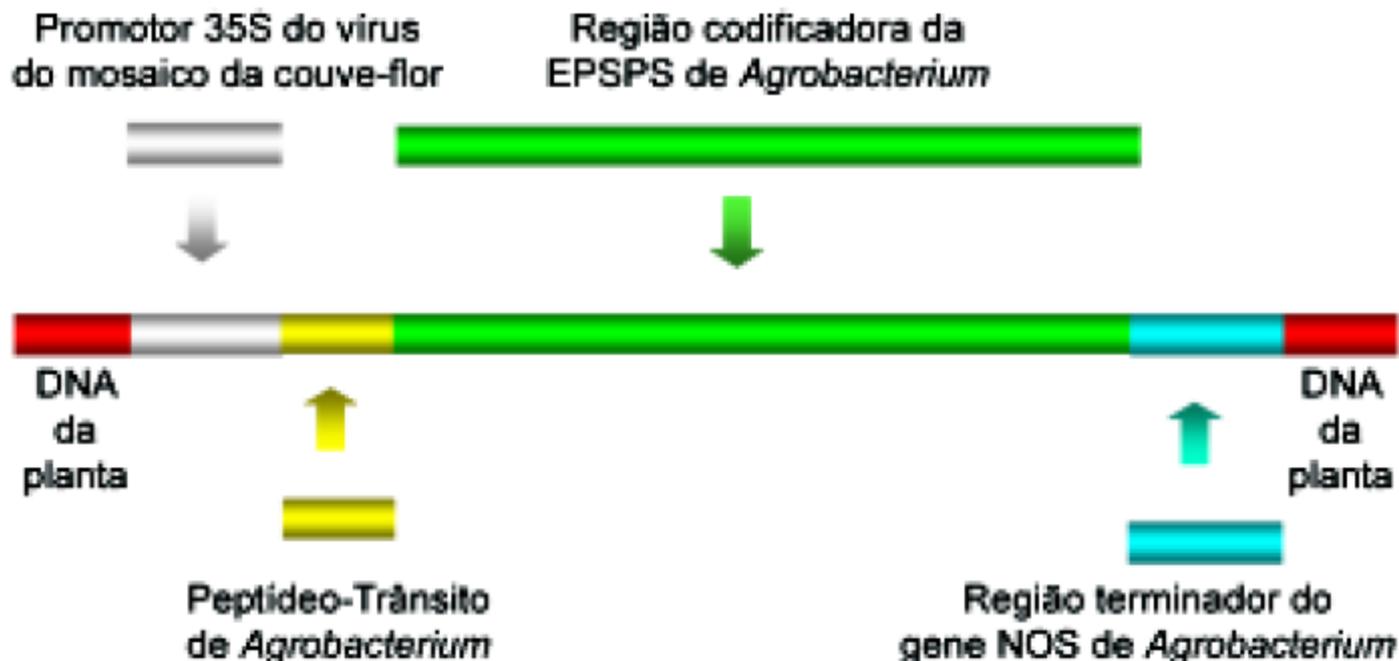


Figura 1 - Representação da construção presente na soja RR[®] (*Roundup Ready*). Região promotora 35S do vírus do mosaico da couve flor, peptídeo de trânsito de Petúnia, gene que codifica a proteína EPSPS, que confere a resistência ao herbicida, e o terminador do gene da nopalina sintase (NOS).

Codon-Optimized Fluorescent Proteins Designed for Expression in Low-GC Gram-Positive Bacteria[∇]

Inka Sastalla, Kannie Chim, Gordon Y. C. Cheung, Andrei P. Pomerantsev, and Stephen H. Leppla*

Laboratory of Bacterial Diseases, National Institute of Allergy and Infectious Diseases, National Institutes of Health, Bethesda, Maryland 20892-3202

Received 5 September 2008/Accepted 13 January 2009

Fluorescent proteins have wide applications in biology. However, not all of these proteins are properly expressed in bacteria, especially if the codon usage and genomic GC content of the host organism are not ideal for high expression. In this study, we analyzed the DNA sequences of multiple fluorescent protein genes with respect to codons and GC content and compared them to a low-GC gram-positive bacterium, *Bacillus anthracis*. We found high discrepancies for cyan fluorescent protein (CFP), yellow fluorescent protein (YFP), and the photoactivatable green fluorescent protein (PAGFP), but not GFP, with regard to GC content and codon usage. Concomitantly, when the proteins were expressed in *B. anthracis*, CFP- and YFP-derived fluorescence was undetectable microscopically, a phenomenon caused not by lack of gene transcription or degradation of the proteins but by lack of protein expression. To improve expression in bacteria with low genomic GC contents, we synthesized a codon-optimized *gfp* and constructed optimized photoactivatable *pagfp*, *cfp*, and *yfp*, which were in contrast to nonoptimized genes highly expressed in *B. anthracis* and in another low-GC gram-positive bacterium, *Staphylococcus aureus*. Using optimized GFP as a reporter, we were able to monitor the activity of the protective antigen promoter of *B. anthracis* and confirm its dependence on bicarbonate and regulators present on virulence plasmid pXO1.

Codon Bias as a Means to Fine-Tune Gene Expression

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<http://dx.doi.org/10.1016/j.molcel.2015.05.035>

The redundancy of the genetic code implies that most amino acids are encoded by multiple synonymous codons. In all domains of life, a biased frequency of synonymous codons is observed at the genome level, in functionally related genes (e.g., in operons), and within single genes. Other codon bias variants include biased codon pairs and codon co-occurrence. Although translation initiation is the key step in protein synthesis, it is generally accepted that codon bias contributes to translation efficiency by tuning the elongation rate of the process. Moreover, codon bias plays an important role in controlling a multitude of cellular processes, ranging from differential protein production to protein folding. Here we review currently known types of codon bias and how they may influence translation. We discuss how understanding the principles of codon bias and translation can contribute to improved protein production and developments in synthetic biology.

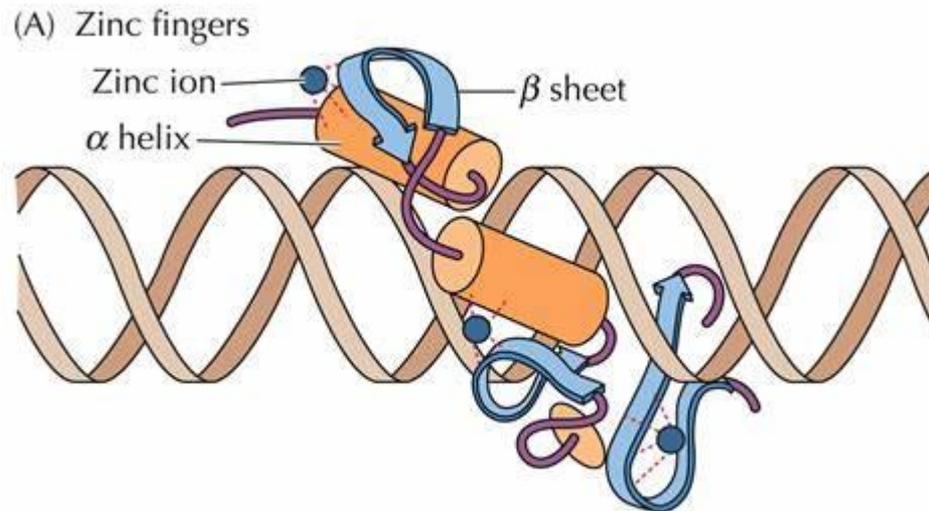
Review

Zinc-finger transcription factors in plants*

H. Takatsuji

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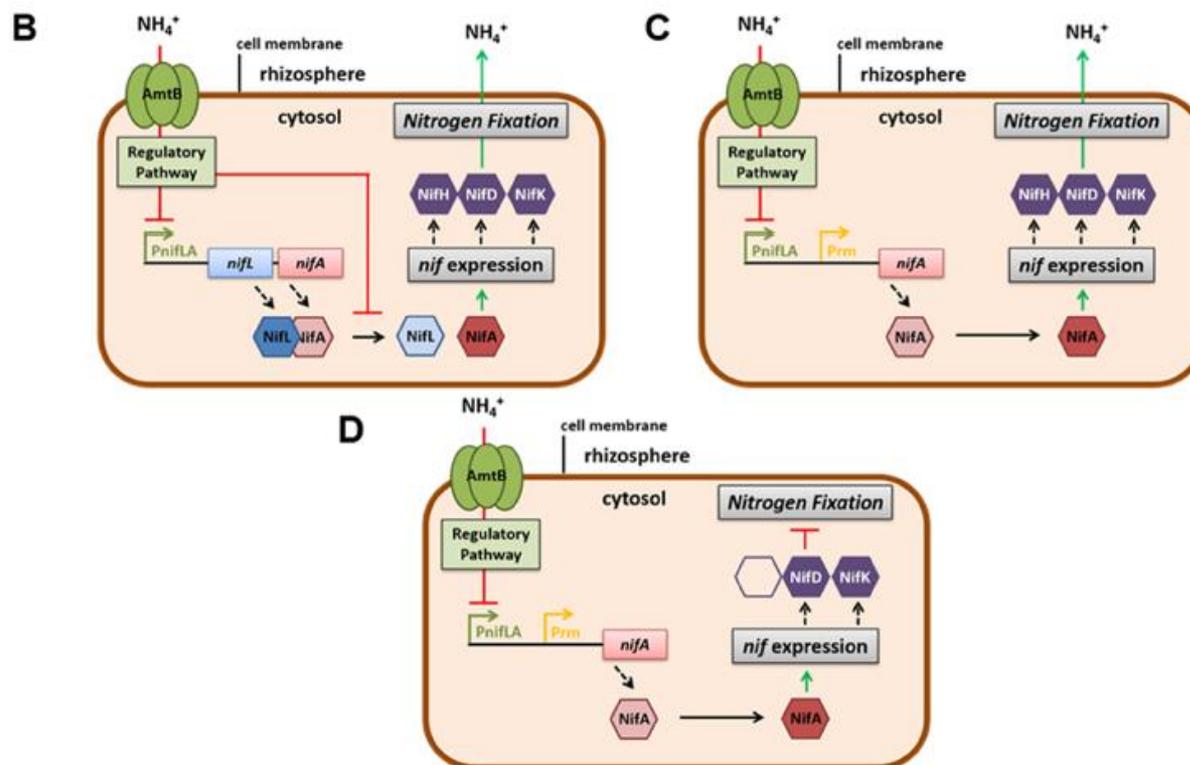


Detection of the F129L mutation in the cytochrome *b* gene in *Phakopsora pachyrhizi*

Ana C Klosowski,^{a*} Louise L May De Mio,^a Simone Miessner,^b Ronaldo Rodrigues^c and Gerd Stammler^b



Enabling Biological Nitrogen Fixation for Cereal Crops in Fertilized Fields



VISUALIZANDO O PROCESSO...

<http://www.youtube.com/watch?v=983lhh20rGY&feature=related>

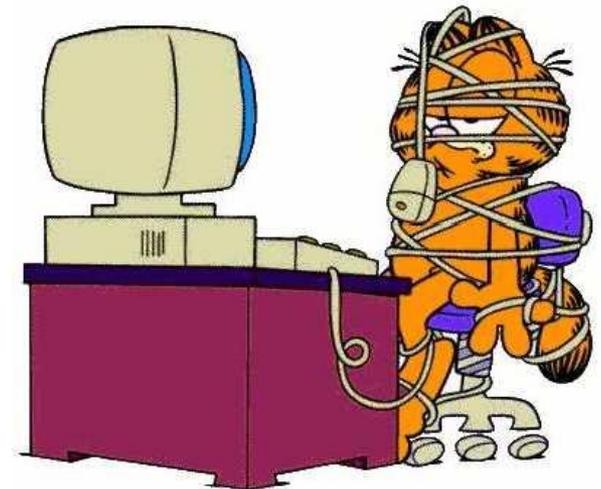
http://www.youtube.com/watch?v=-ygpqVr7_xs&feature=related

<http://qnint.s bq.org.br/qni/visualizarTema.php?idTema=33>

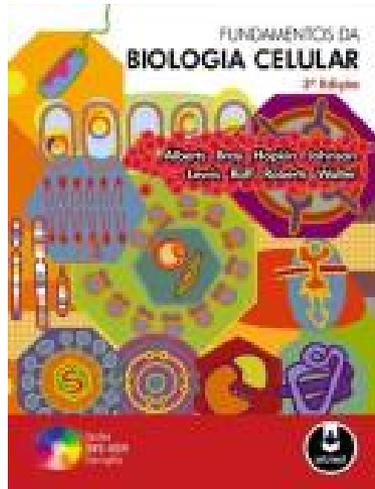
<http://www.odnavaiaescola.com.br/dna/19/bio.htm>

<http://www.youtube.com/watch?v=teV62zrm2P0>

<http://www.youtube.com/watch?v=4PKjF7OumYo>



LEITURA RECOMENDADA



FUNDAMENTOS DA BIOLOGIA CELULAR

Formato: Livro

Autor: ALBERTS, BRUCE

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Editora: ARTMED -

Assunto: CIÊNCIAS BIOLÓGICAS - BIOLOGIA

ESTUDO DIRIGIDO

1. Definição de gene;
2. Diferença na estrutura dos genes de eucariotos e procariotos;
3. Região codante: start codon e stop codon.
4. Processo de tradução

Dogma Central da Biologia
Celular - Mapa conceitual

Entrega dia 13 de Setembro!

