

Translation



“The waltz of the polypeptides” – Cold Spring Harbor Lab, NY

Introduction

1-the genetic code

2-tRNAs codon recognition
and aminoacylation

3-Translation initiation

4-Translation elongation

5-Peptide bond formation
catalysis in the ribosome

6-Translation termination

7-Quality Control of translation

Learning outcomes:

What you need to know/understand after this chapter

Understand how the genetic code works and how tRNA decode codons

Understand aminoacyl tRNA synthetase mechanisms and how their editing activity contributes to translation fidelity

Know the global architecture of ribosome and functional sites

Understand the mechanisms of translation initiation in bacteria vs eukaryotes and how initiation can be regulated

Know the basic mechanism of translation cycle and the mechanism of peptide bond formation

Understand the mechanism of termination and the quality control mechanisms linked to translation termination

The Genetic Code

First position (5' end)	Second position				Third position (3' end)
	U	C	A	G	
U	UUU	UCU	UAU	UGU	U C A G
	UUC Phe	UCC Ser	UAC Tyr	UGC Cys	
	UUA Leu	UCA	UAA Stop	UGA Stop	
	UUG	UCG	UAG Stop	UGG Trp	
C	CUU	CCU	CAU	CGU	U C A G
	CUC Leu	CCC Pro	CAC His	CGC Arg	
	CUA	CCA	CAA Gln	CGA	
	CUG	CCG	CAG	CGG	
A	AUU	ACU	AAU	AGU	U C A G
	AUC Ile	ACC Thr	AAC Asn	AGC Ser	
	AUA	ACA	AAA Lys	AGA Arg	
	AUG Met ^b	ACG	AAG	AGG	
G	GUU	GCU	GAU	GGU	U C A G
	GUC Val	GCC Ala	GAC Asp	GGC Gly	
	GUA	GCA	GAA Glu	GGA	
	GUG	GCG	GAG	GGG	

^aNonpolar amino acid residues are tan, basic residues are blue, acidic residues are red, and polar uncharged residues are purple.

^bAUG forms part of the initiation signal as well as coding for internal Met residues.

(almost)

•Universal

The same genetic code is used in bacterial, plants, fungal or animals genomes (exceptions)

•Degenerate

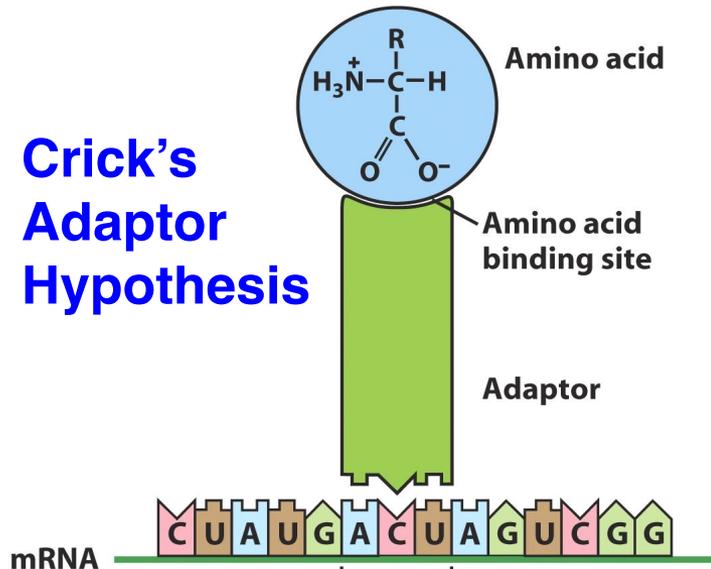
Multiple sequences code for the same AA

•Non-random

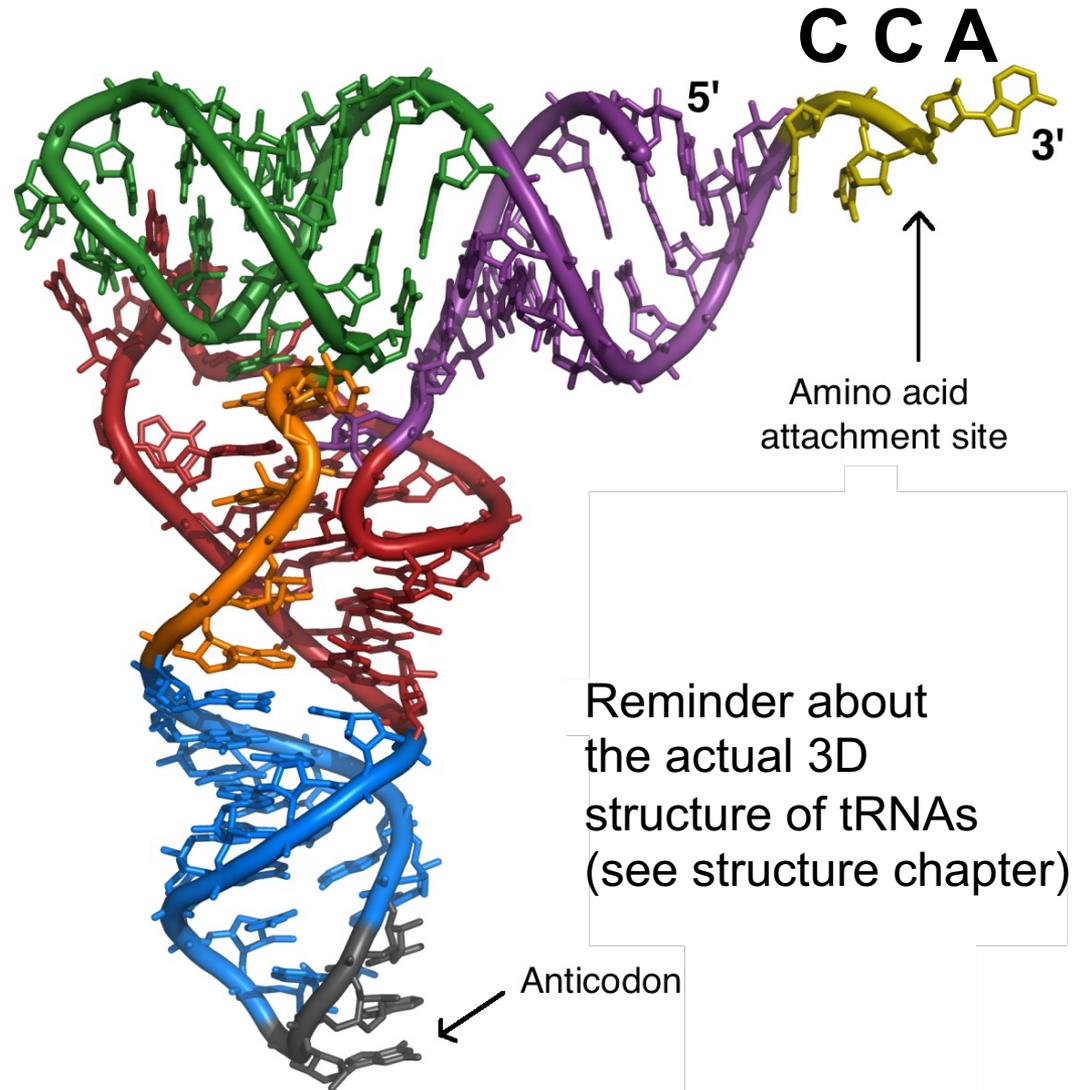
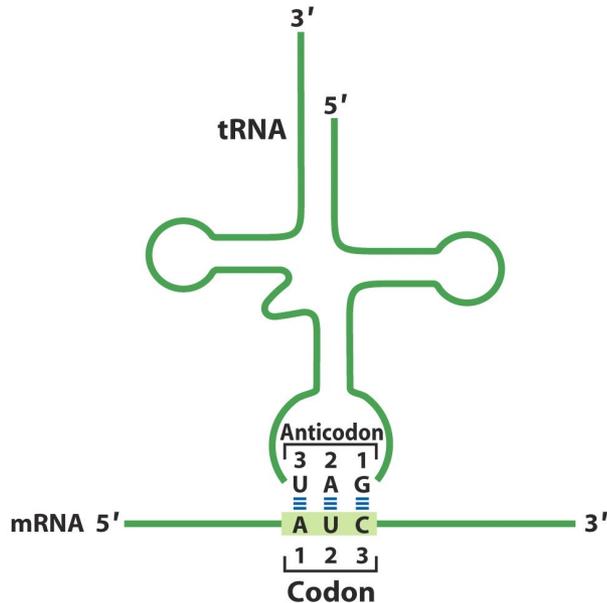
Single mutation of a codon is typically **neutral** (=> same AA) or **conservative** (results in a similar AA)

tRNAs are adaptor molecules

Crick's Adaptor Hypothesis



Nucleotide triplet coding for an amino acid



Reminder about the actual 3D structure of tRNAs (see structure chapter)

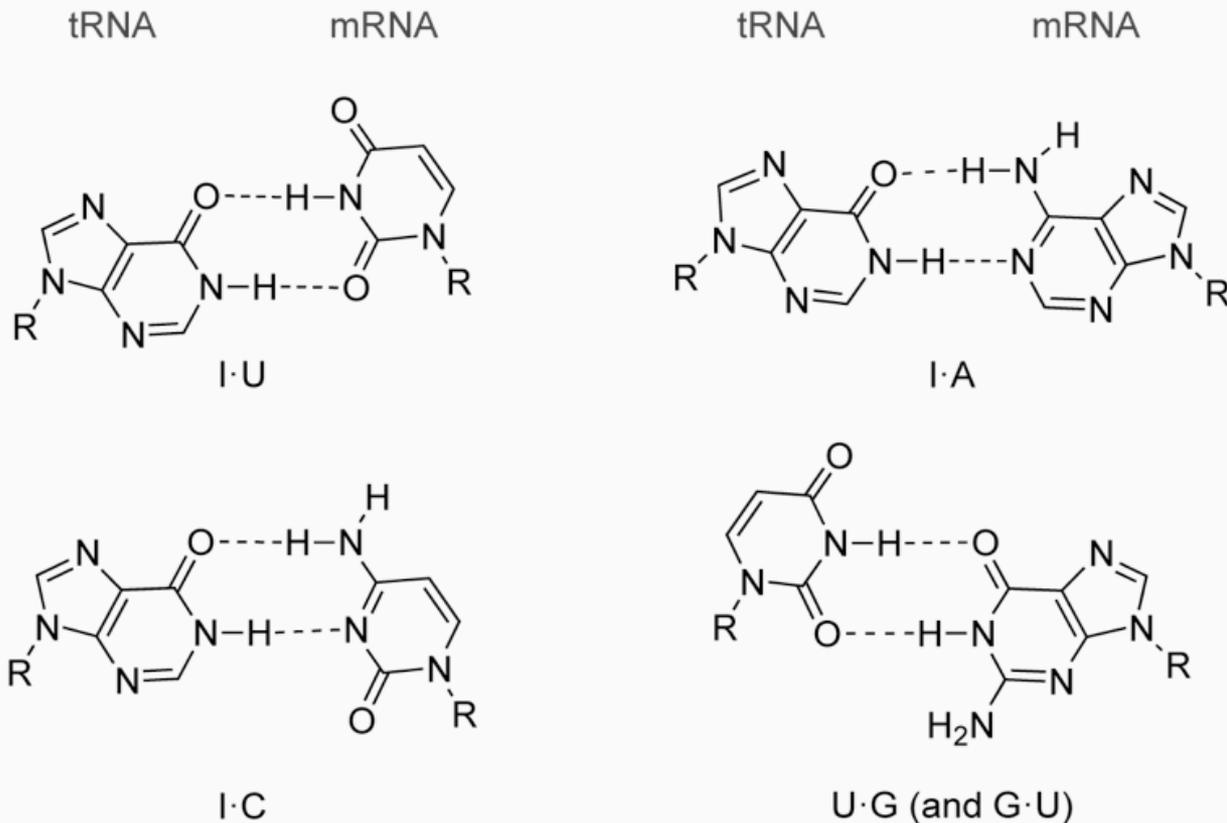
One tRNA can recognize several codons by flexibility of base pairing (“wobble”) at position 3 of the mRNA codon

<u>AntiCodon (1)</u> <u>(=tRNA)</u>	<u>Codon (3)</u> <u>(=mRNA)</u>
C can read	G
A can read	U
U can read	A, G
G can read	C, U
I can read	C, U, A

tRNA	3	2	1	tRNA	3	2	1	tRNA	3	2	1	
Anticodon	(3')	G	C	I	G	C	I	(5')	G	C	I	(5')
Codon	(5')	C	G	A	C	G	U	(3')	C	G	C	(3')
mRNA		1	2	3		1	2	3		1	2	3

CUU	CCU	CAU	His
CUC	CCC	CAC	
CUA	CCA	CAA	Gln
CUG	CCG	CAG	

Leu Pro



! The wobble rule only applies to position 3 of the codon NOT to Positions 1 and 2