

# Transcription and translation revision

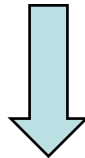
**GENOME**

**(DNA)**



**TRANSCRIPTOME**

**RNA copies of the active protein-coding genes**



**PROTEOME**

**The cell's repertoire of proteins**

# Types of RNA

- **Coding** (mRNA) and **non-coding** (rRNA and tRNA)
- **mRNA** (messenger RNA)
  - 4% of total RNA
  - Short half life
- **rRNA** (ribosomal RNA)
  - Most abundant (80%)
  - Components of the ribosome
- **tRNA** (transfer RNA)
  - Carry amino acids to the ribosomes
  - Ensure amino acids linked in correct order

DNA 5' — A-G-A-G-G-T-G-C-T — 3'  
3' — T-C-T-C-C-A-C-G-A — 5'



mRNA 5' — A-G-A-G-G-U-G-C-U — 3'

tRNAs U-C-U C-C-A C-G-A

Arginine Glycine Alanine

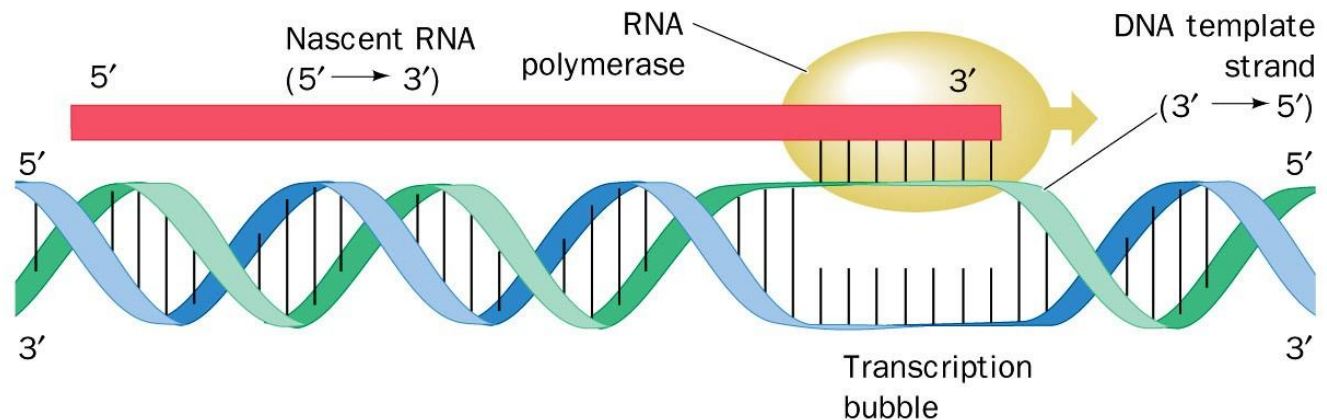


Polypeptide —Arg-Gly-Ala—

# mRNA synthesis

- Direction: 5' → 3' (Fig 5-23)
- One DNA strand transcribed at a time
  - A=U (T) ; C ≡ G
  - 10bp at a time
  - RNA polymerase

**Fig 5-24**



**Fig 5-23**

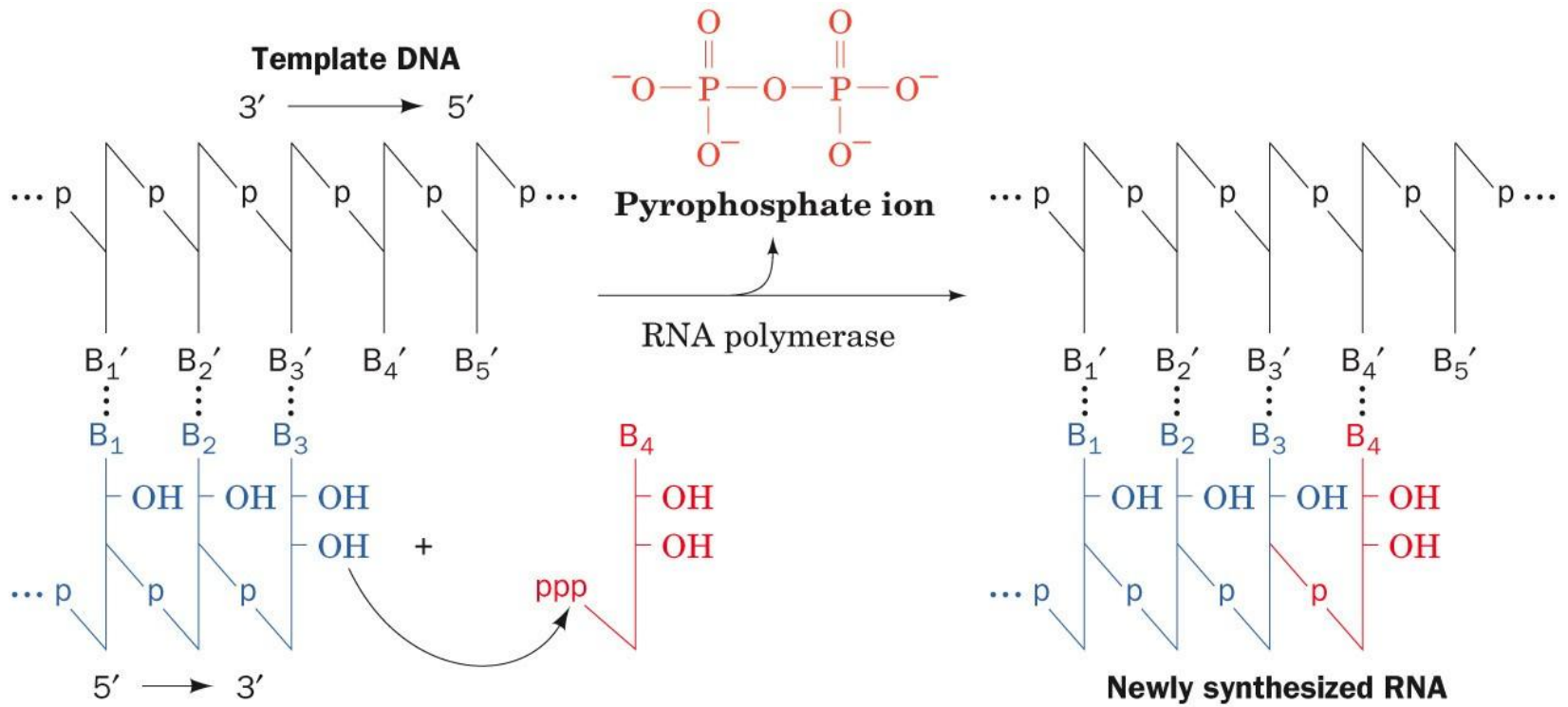
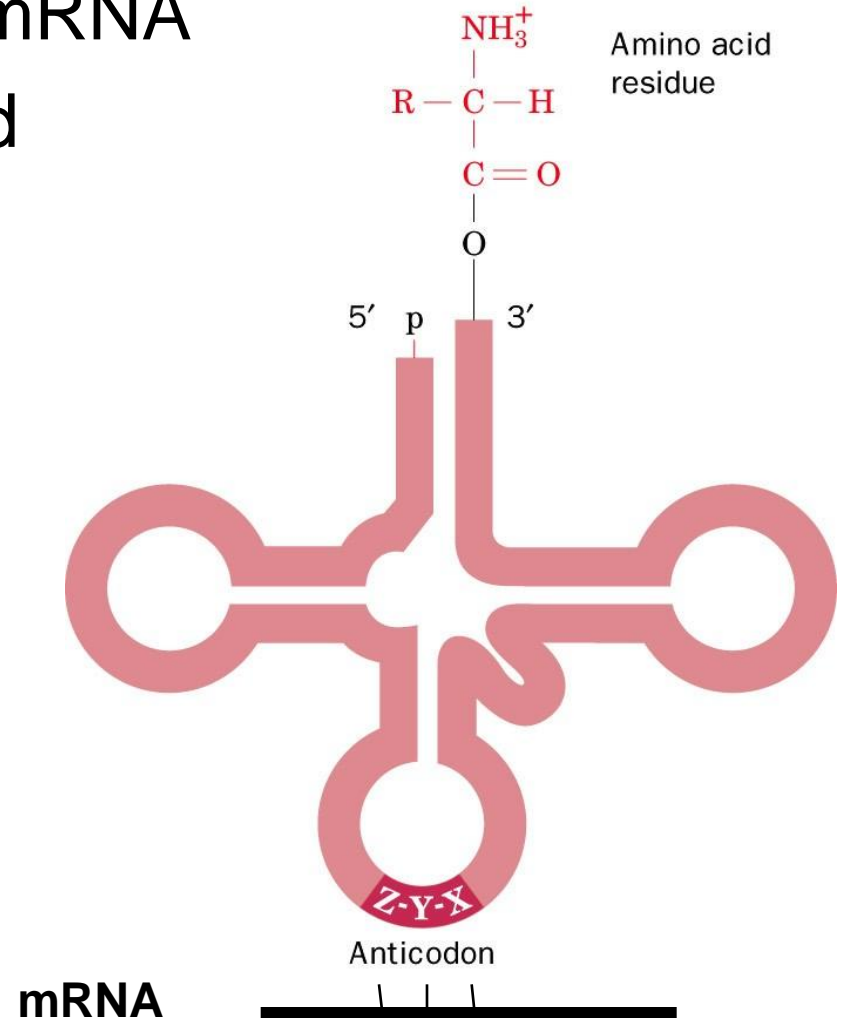


Fig 5-27

# Structure of tRNA

- tRNA **anticodon** binds to mRNA
  - Amino acids transferred

tRNA



# Template binding

- RNA synthesis is initiated at specific sites on the DNA template
  - Anti-sense (3'→5'') DNA transcribed
- RNA polymerase binds to initiating site via promotor
- Two highly conserved consensus sequences in promotor (Fig 31-10)
  - Pribnow box (hexamer at -10): **TATAAT**
  - **TTGACA** hexamer at -35
  - **16-19 bp** between the two conserved sequences
- Initiation site (+1) for transcription: **A or G**



# DNA anti-sense

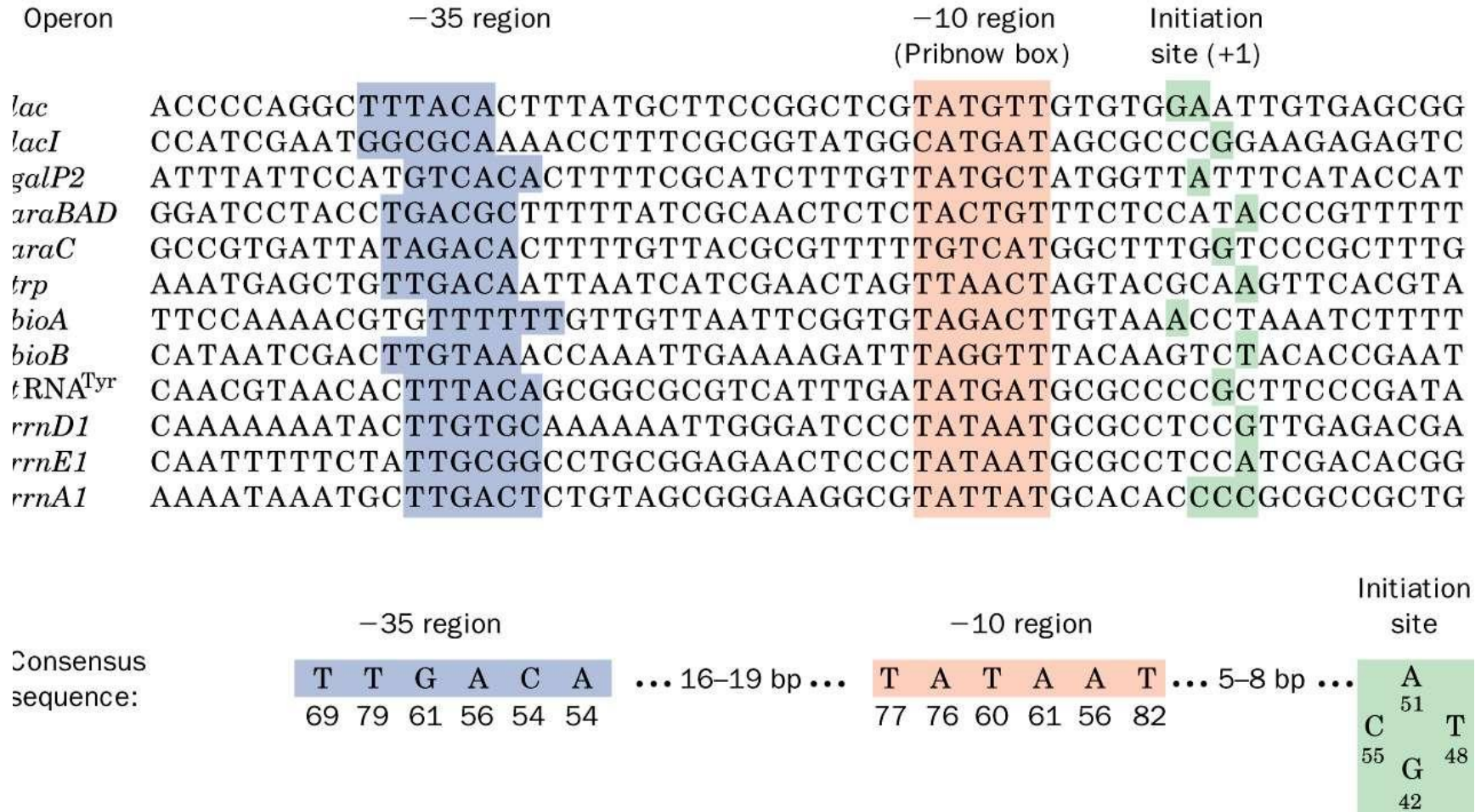
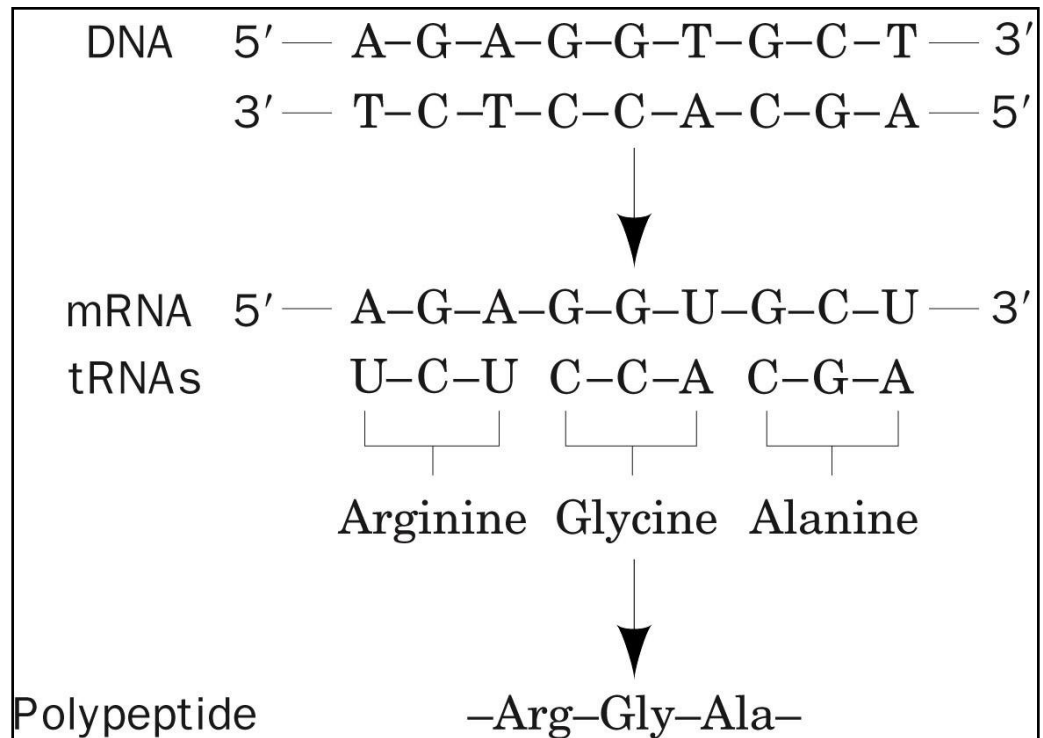
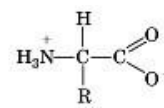


Fig 31-10

# The Genetic code

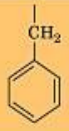
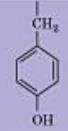


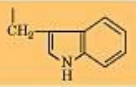
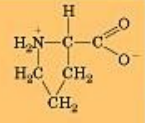
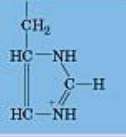
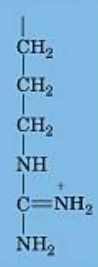
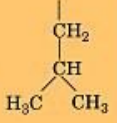
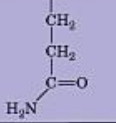

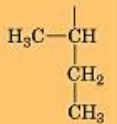
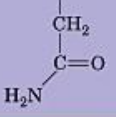
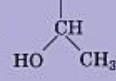
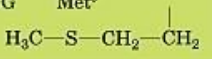
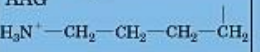
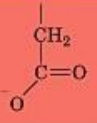
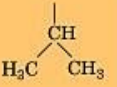


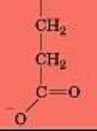
- Specifies how mRNA is translated into a polypeptide
  - Each codon = three nucleotides (on mRNA)
  - Highly degenerate





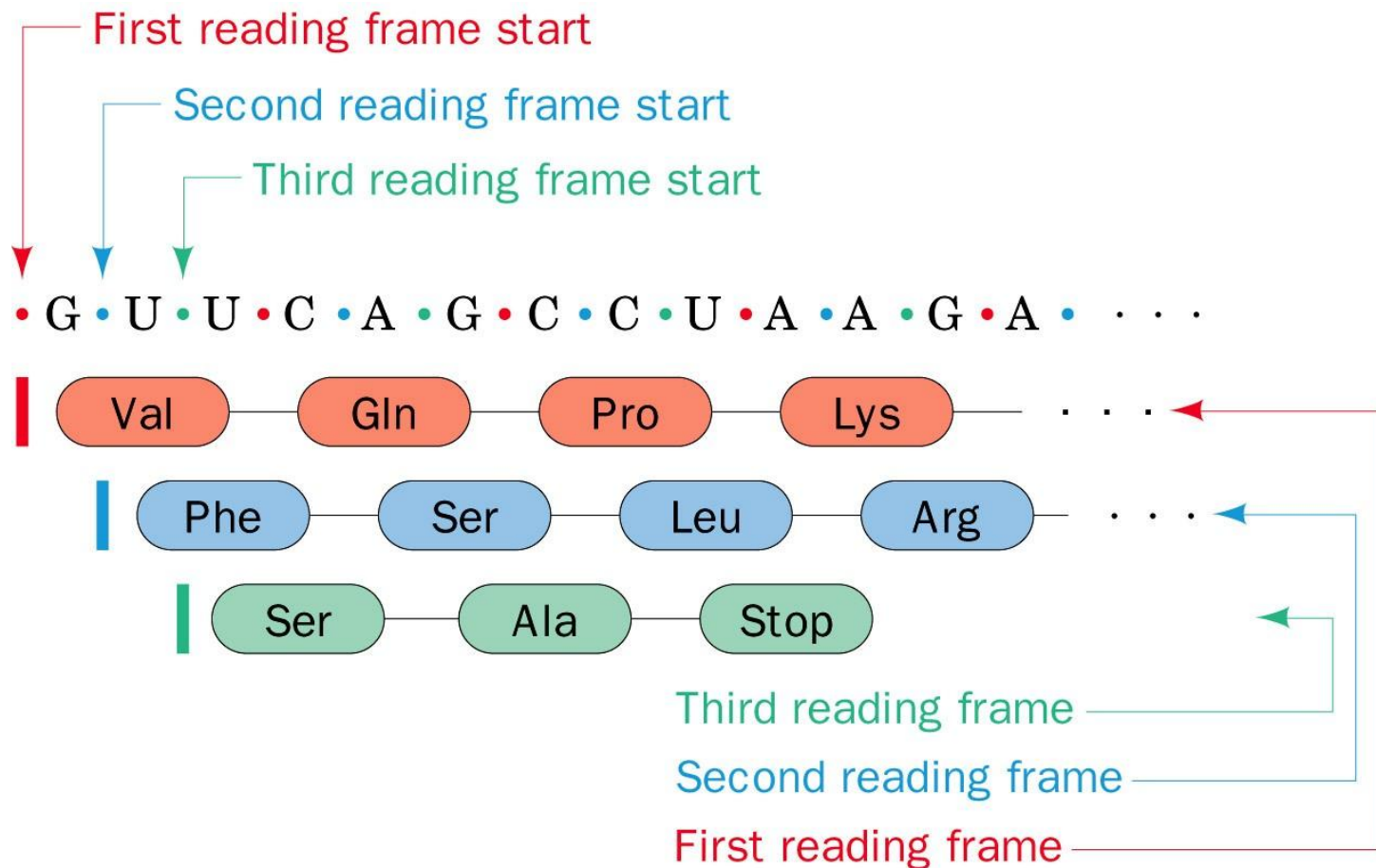
**Table 5-3**

**Genetic code**

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

<sup>a</sup>Nonpolar amino acid residues are tan, basic residues are blue, acidic residues are red, and polar uncharged residues are purple.  
<sup>b</sup>AUG forms part of the initiation signal as well as coding for internal Met residues.

- Ribosomes read mRNA in 5' → 3' direction
  - Reading frame must be correct (Fig 5-30)
  - AUG (usually) sets reading frame = **Start codon**



# Translation

- Initiation of translation: 5'-AUG-3' on mRNA
  - Codes for methionine –**START**
- **Termination:** 5'UAG3'/ 5'UAA3'/5'UGA3'
- Translational initiation site specified by more than just initiation codon
  - AUG codons that are not initiation sites are masked via mRNA secondary structure
  - Shine-Dalgarno sequence
- Polypeptide grows from N-terminus to C-terminus

# Shine Dalgarno sequence

- **Purine**-rich tract of 3-10 nucleotides on mRNA
  - ~10 nucleotides upstream from START codon (AUG)
  - Binds to 16S rRNA (which has pyrimidine-rich segment at 3' end)
  - Helps ribosome select correct initiation codon

Figure 32-43

