

# Transcription and Translation

Chapter Ten

# Central Dogma

DNA



Transcription

RNA



Translation

Protein

# Definitions

**Transcription** – To copy down, within the same language

Language = Nucleic Acids

DNA to RNA

**Translation** – To translate from one language to another

From Nucleic Acids to Amino Acids

RNA to Protein

# DNA vs. RNA

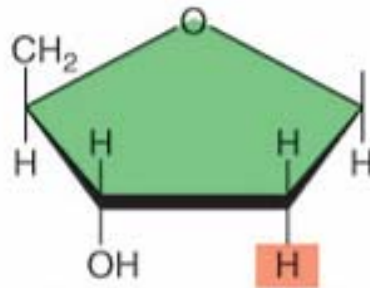


Double-stranded

b.

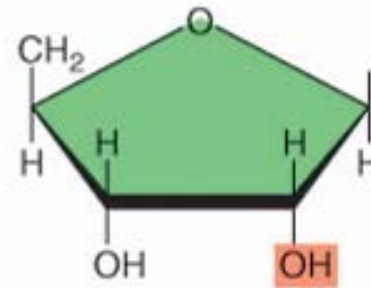


Generally single-stranded



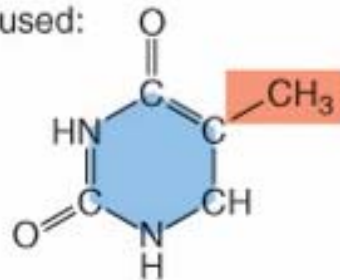
Deoxyribose as the sugar

c.



Ribose as the sugar

Bases used:



Thymine (T)

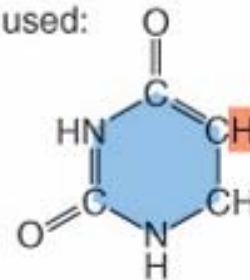
Cytosine (C)

Adenine (A)

Guanine (G)

d.

Bases used:



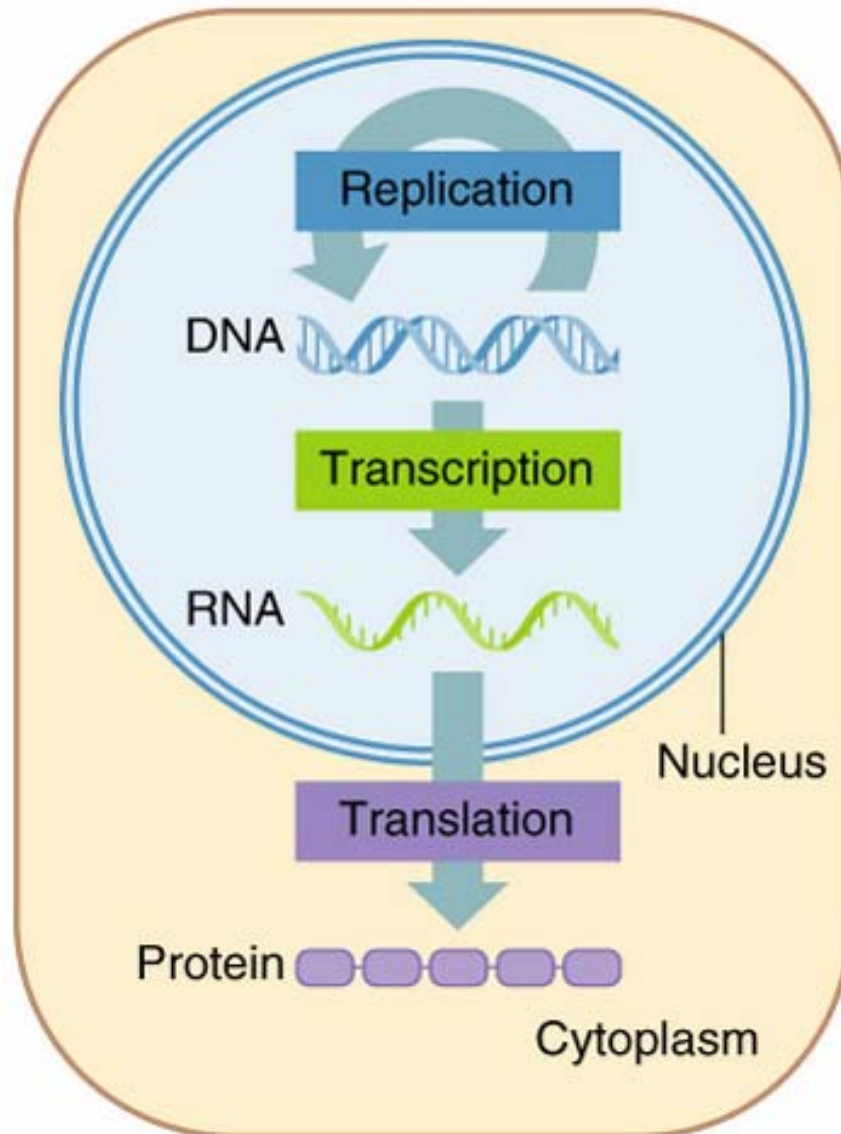
Uracil (U)

Cytosine (C)

Adenine (A)

Guanine (G)

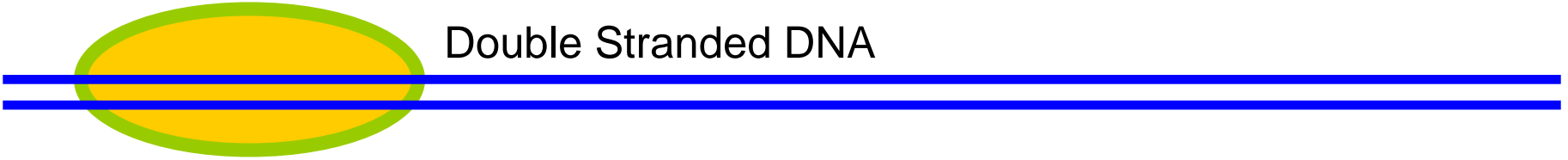
# Note **Where** Things Happen



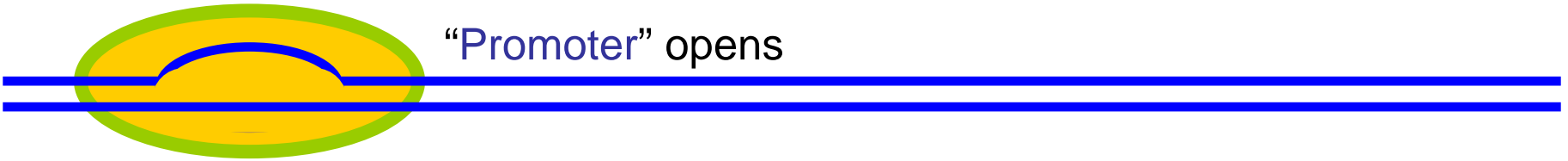
# Transcription

RNA polymerase

Double Stranded DNA



"Promoter" opens



initiation



elongation



termination



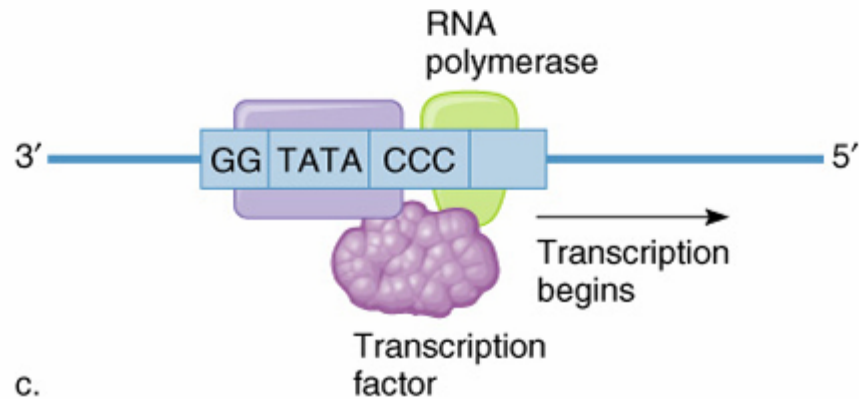
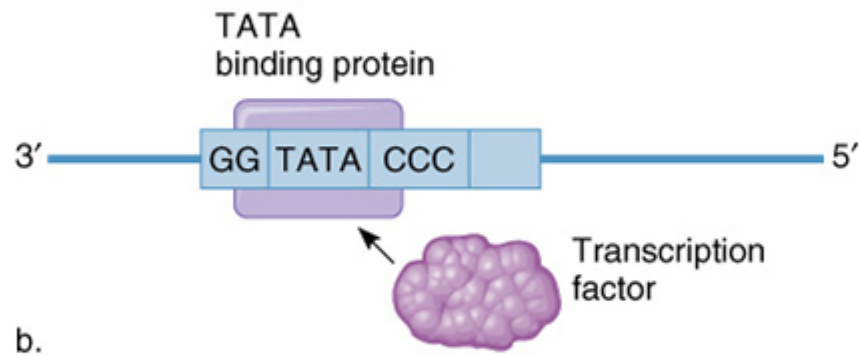
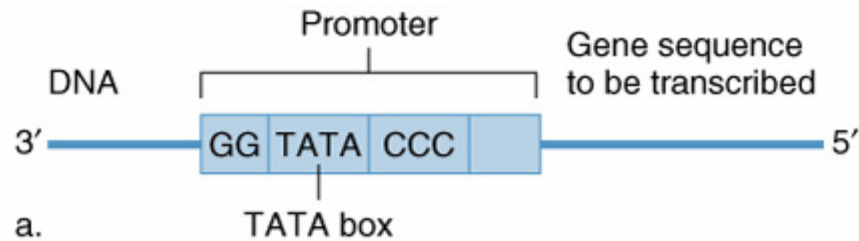
single stranded mRNA



# Important Players

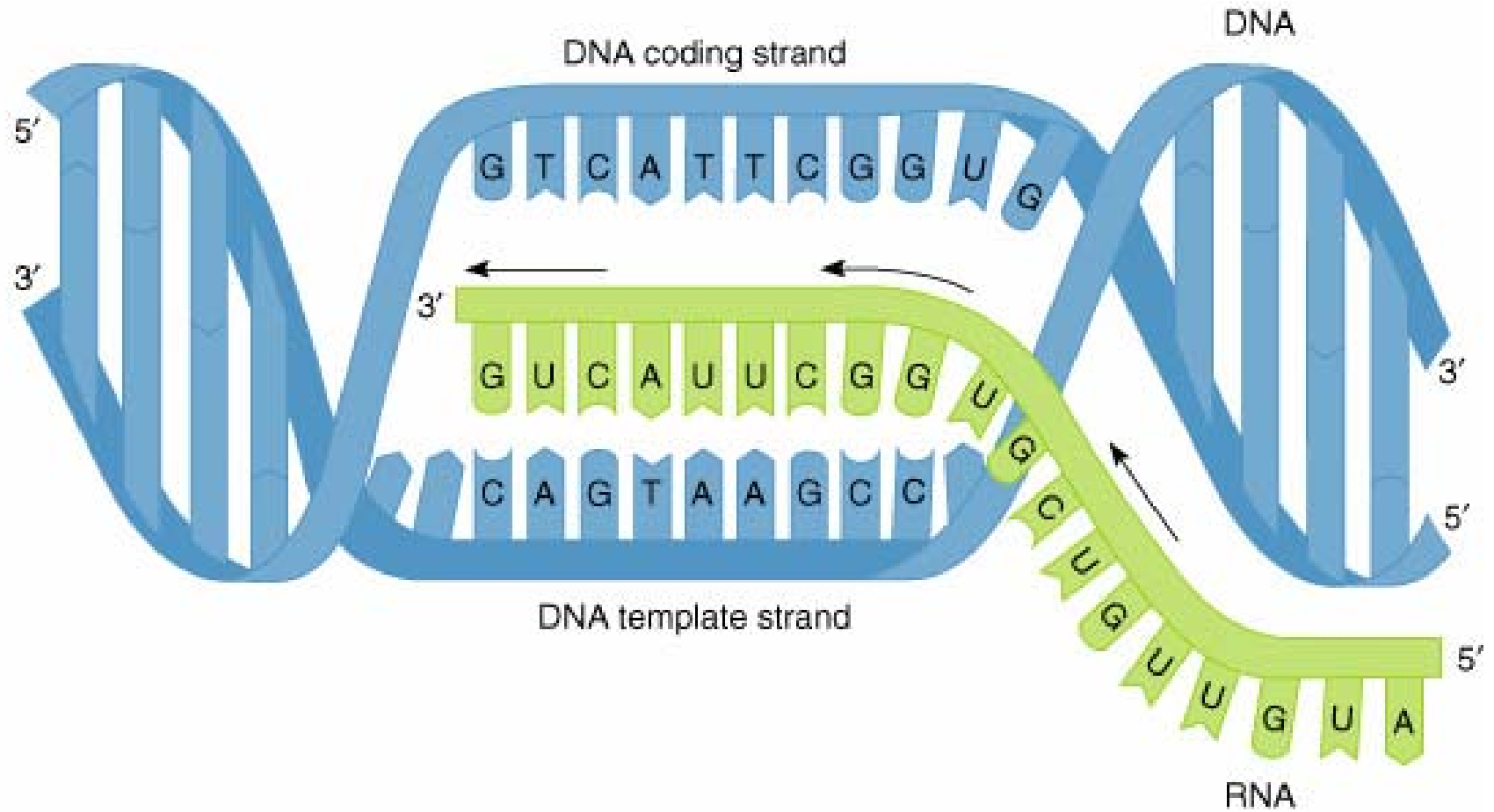
- **Template Strand** = DNA 3' to 5' direction
- **Promoter** = specific sequence of DNA that signals transcription start site
- **Transcription Factors** = proteins that attract the RNA polymerase and regulate
- **RNA Polymerase** = Enzyme that completes process of transcription
- **mRNA** = messenger RNA
  - Copy of template strand that makes protein

# Transcription Initiation



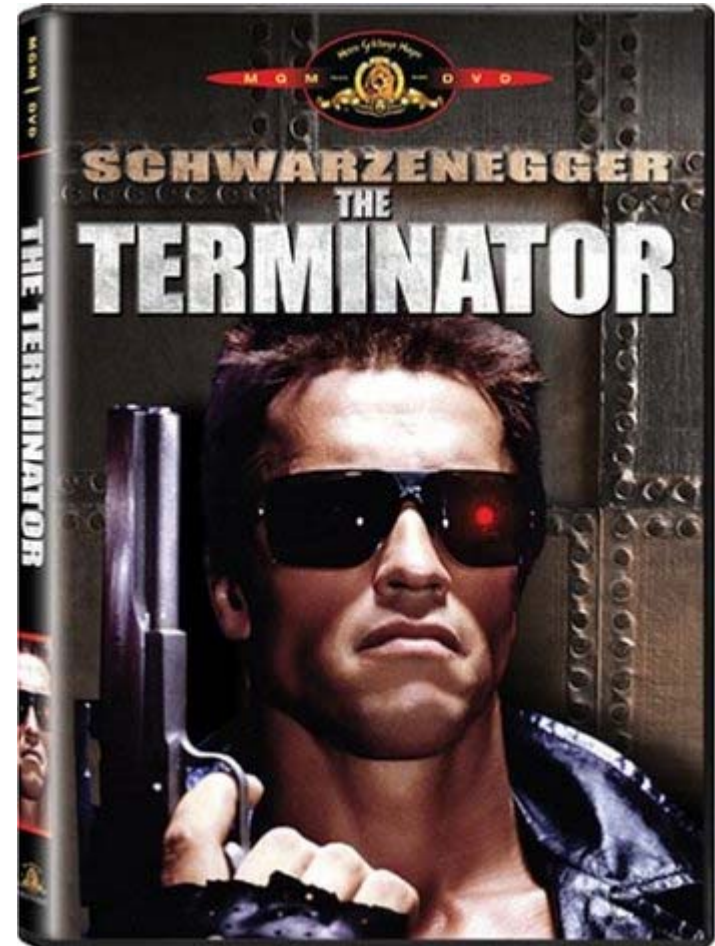


# Transcription Elongation



# Transcription Termination

- At end of gene DNA has a “terminator”
- Sequence that signals end of transcription
- RNA polymerase disassociates from DNA
- ss mRNA floats away

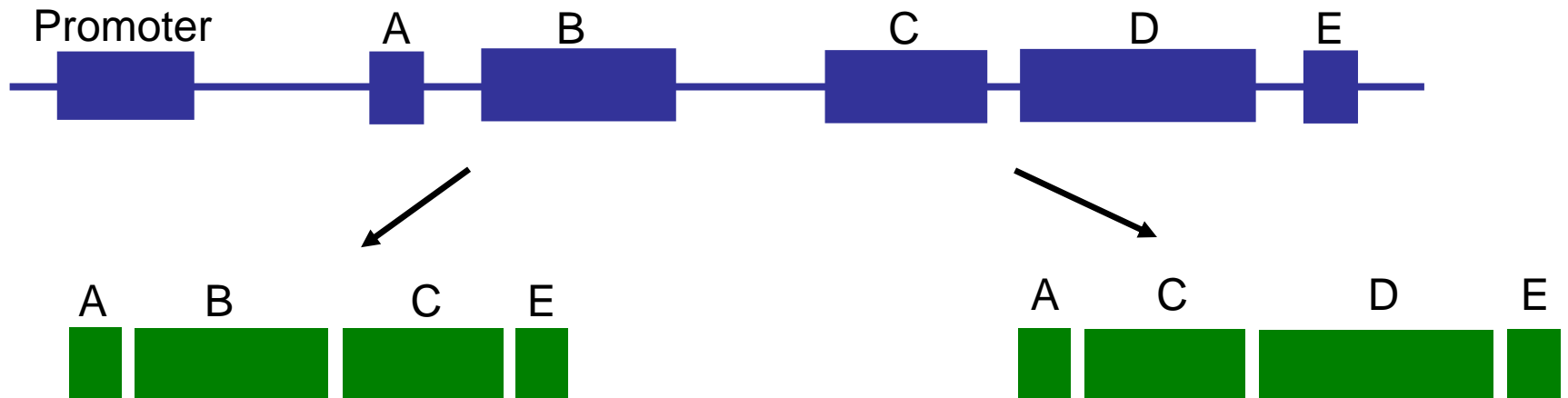


# Processing mRNA

1. 5' cap added to beginning of mRNA
  - Methyl groups are added to act as initiation site for translation
2. Poly-A tail added to end of mRNA
  - A couple hundred A's are added to end
  - Stabilizes mRNA's structure
3. Splicing out of introns
  - Introns are removed at splice sites
  - Leaving only exons for translation

# Alternative Splicing

- Many mRNA sequences can be spliced differently
- Thereby producing more than one protein from same sequence



# Translation

...AGAGCGGA**ATGGCAGAGTGGCTAAGCATGTCGTGATCGAATAAA**...



AGAGCGGA . **AUG** . **GCA** . **GAG** . **UGG** . **CUA** . **AGC** . **AUG** . **UCG** . **UGA** . UCGAAUAAA



**MET . ALA . GLU . TRP . LEU . SER . MET . SER . STOP**

4 Nucleotides

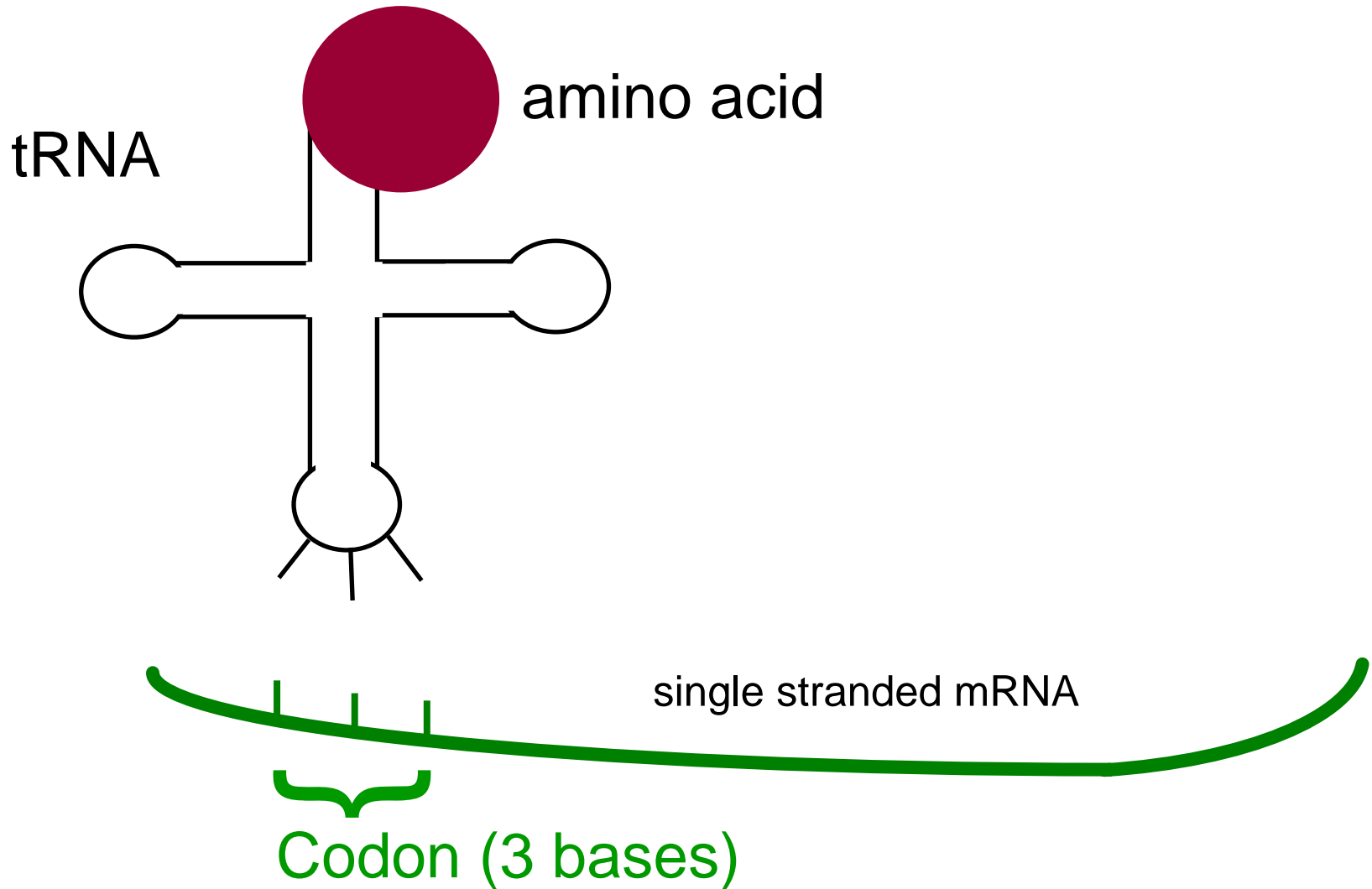
20 amino acids

1 base codon -  $4^1 = 4$  possible amino acids

2 base codon -  $4^2 = 16$  possible amino acids

3 base codon -  $4^3 = 64$  possible amino acids

# Translation



# The Genetic Code

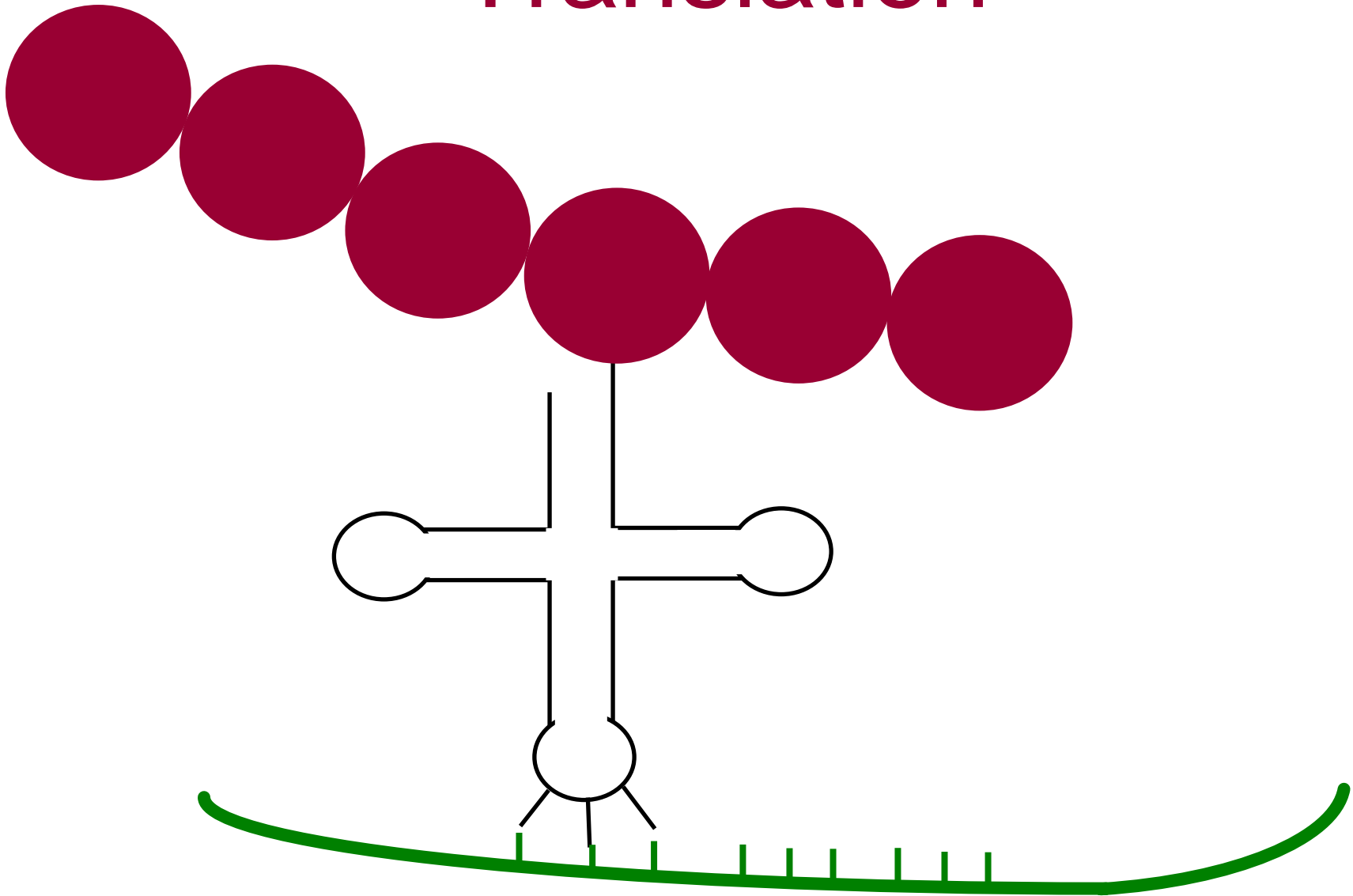
UUU	Phe	UCU	Ser	UAU	Tyr	UGU	Cys
UUC		UCC		UAC		UGC	
UUA	Leu	UCA		UAA	Stop	UGA	Stop
UUG		UCG		UAG		UGG	
CUU	Leu	CCU	Pro	CAU	His	CGU	Arg
CUC		CCC		CAC		CGC	
CUA		CCA		CAA	Gln	CGA	
CUG		CCG		CAG		CGG	
AUU	Ile	ACU	Thr	AAU	Asn	AGU	Ser
AUC		ACC		AAC		AGC	
AUA	Met	ACA		AAA	Lys	AGA	Arg
AUG		ACG		AAG		AGG	
GUU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

# Important Players

- **tRNA** = transfer RNA
  - Binds codon on one side and aa on other
- **Ribosome** = enzyme that gathers the correct tRNA and makes the peptide bond between two amino acids
- **Initiator tRNA** = aa Met; begins translation
- **Stop codons** = stop translation
- **Peptide** = the newly formed sequence of aa's



# Translation



Note: Actually a different tRNA for each different codon

# Question One:

How many bases specify one amino acid?

- 4 bases and 20 amino acids
- If a codon was only 1 base – only get 4 amino acids
- If codon was 2 bases – get 16 aa's
  - $4^2 = 16$
- If codon was 3 bases – get 64 possible aa's
  - $4^3 = 64$

# Question One:

How many bases specify one amino acid?

- Reading frame – the correct frame to read the aa's in
- Example – read sentence one letter off
- Remove one, two or three bases...
- Only by removing three bases is the reading frame unchanged

A: Therefore, a codon must be three bases.

# Question Two:

Is sequence overlapping or not?

- Easy enough to test because amino acids would always follow each other in specific order
- Ex. AUG would always be followed by an amino acid that starts with UG

A: Sequence is not overlapping.

# Question Three:

Can mRNA encode anything other than amino acids?

- Knew mRNA provides the words of the sentence
- Also, provides the punctuation as well
- Start and Stop codons

A: Yes, Start and Termination signals.

# Question Four:

Do all species use same genetic code?

- Turns out the code is “Universal”

A: Yes, all species use the same universal genetic code.

Perhaps evidence of our common evolution?

# Question Five:

Which codons specify which amino acids?

1. Build all possible mRNA codons in lab
2. Test which peptides are formed

Deciphered the entire Genetic Code

A: The genetic code is completely known.

# The Genetic Code

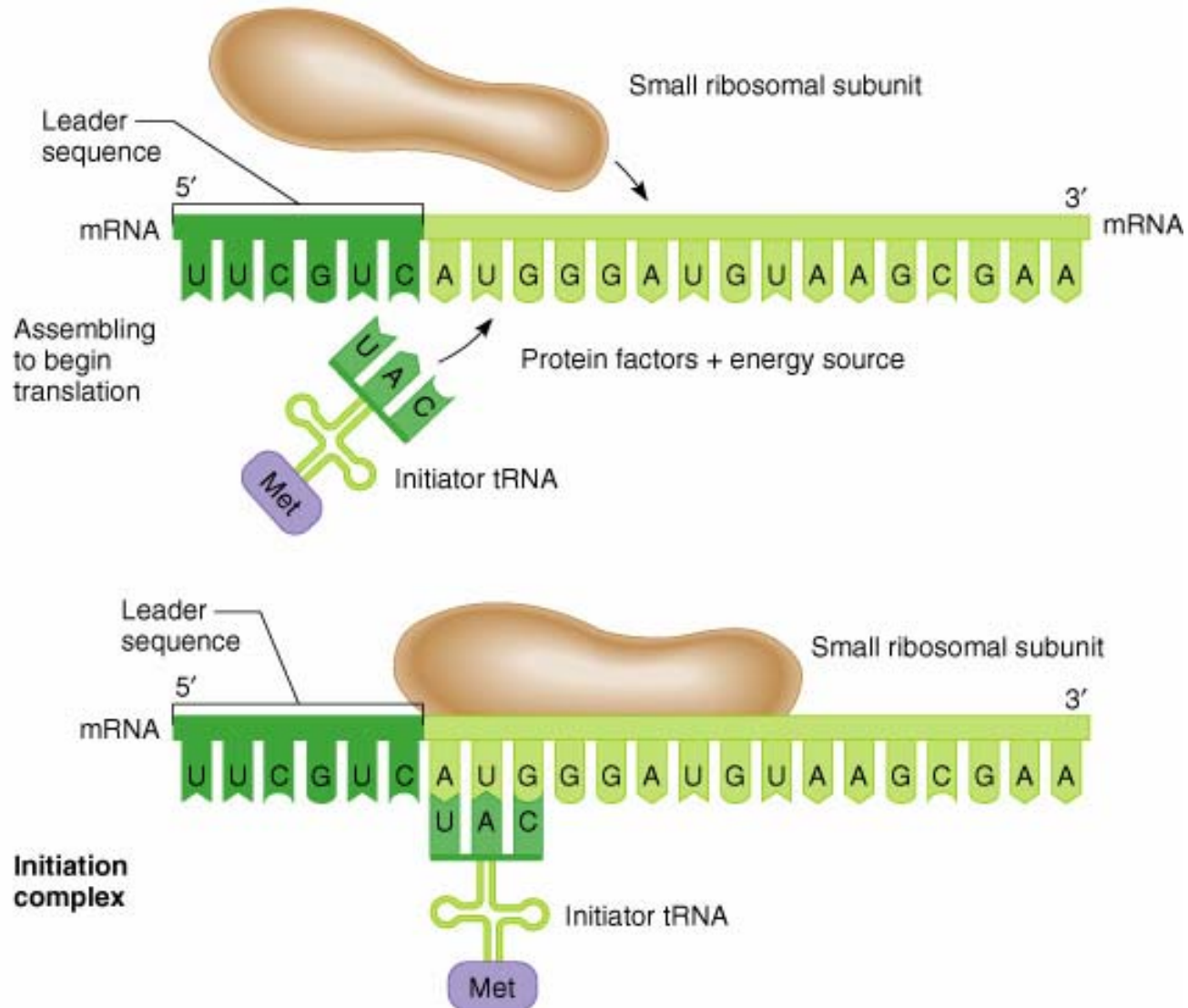
UUU	Phe	UCU	Ser	UAU	Tyr	UGU	Cys
UUC		UCC		UAC		UGC	
UUA	Leu	UCA		UAA	Stop	UGA	Stop
UUG		UCG		UAG		UGG	
CUU	Leu	CCU	Pro	CAU	His	CGU	Arg
CUC		CCC		CAC		CGC	
CUA		CCA		CAA	Gln	CGA	
CUG		CCG		CAG		CGG	
AUU	Ile	ACU	Thr	AAU	Asn	AGU	Ser
AUC		ACC		AAC		AGC	
AUA	Met	ACA		AAA	Lys	AGA	Arg
AUG		ACG		AAG		AGG	
GUU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



# Summary

1. Codons are 3 bases – encode one amino acid
2. DNA and RNA sequence is non overlapping
3. mRNA is sentence and punctuation
4. Genetic Code is universal
5. We know what amino acid every codon encodes for

# Translation Initiation

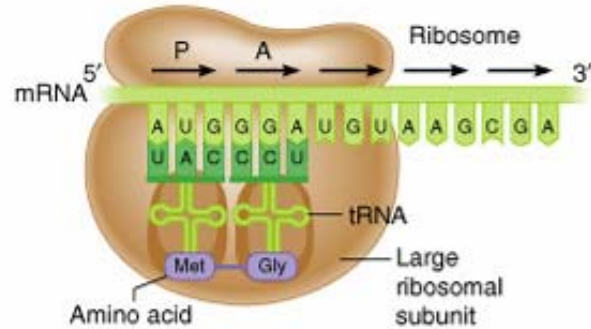


# Translation Elongation

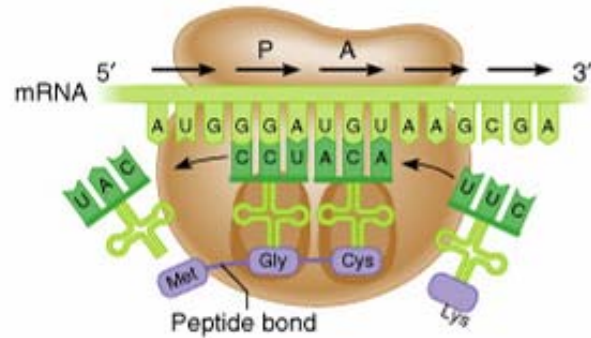
**Ribosome** – complex of proteins working together to complete process of translation

1. Brings correct tRNA to matching codon
2. Forms peptide bonds between aa's
  - **P** site – Holds growing **Peptide**
  - **A** site – **Accepts** next **Amino Acid**, and **Attaches** it to peptide

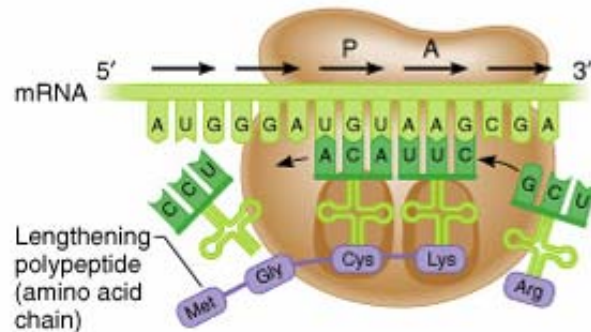
# Translation Elongation



a. Second amino acid joins initiation complex.



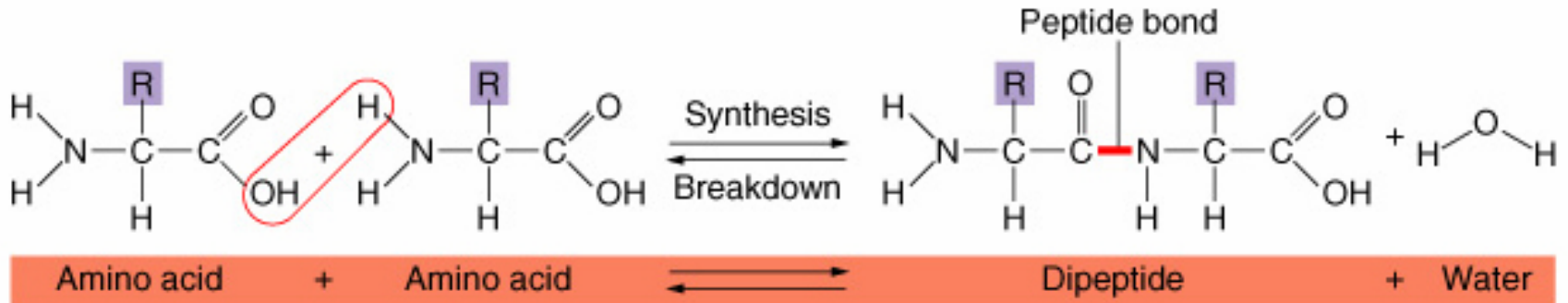
b. First peptide bond forms, as new amino acid arrives.



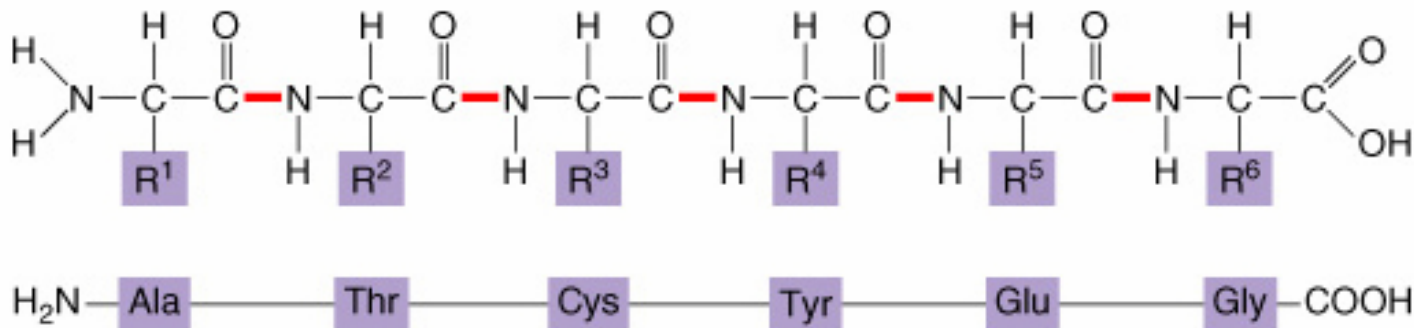
c. Amino acid chain extends.

# Peptide Bonds

- Peptide bonds form between two amino acids:

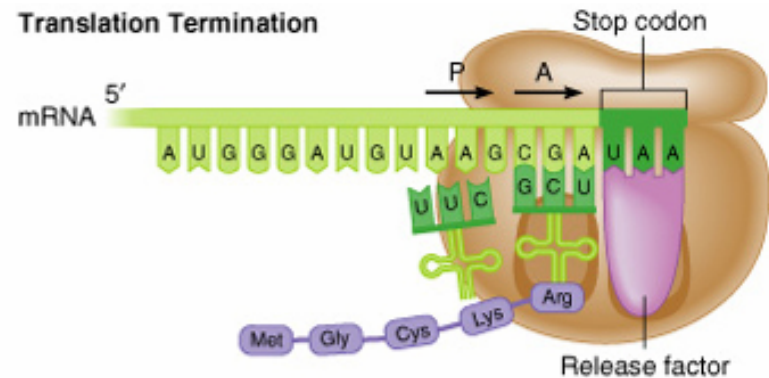


c.

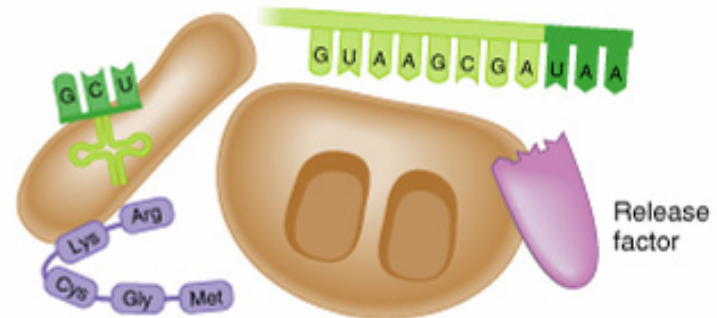


# Translation Termination

- Simple as reading a stop codon
- UAA, UAG or UGA
- Ribosome releases peptide



d. Ribosome reaches stop codon.



e. Components disassemble.

# Proteins

- Protein Sequence = order of the amino acids

Sequence



Structure



Function

# Protein Folding

Proteins are the functional part of a cell

- Cellular “machinery” or tools
- Cannot function as a flat chain of amino acids



- Instead need to fold in very specific confirmations in order to function properly



# Protein's Structure

Four levels of structure:

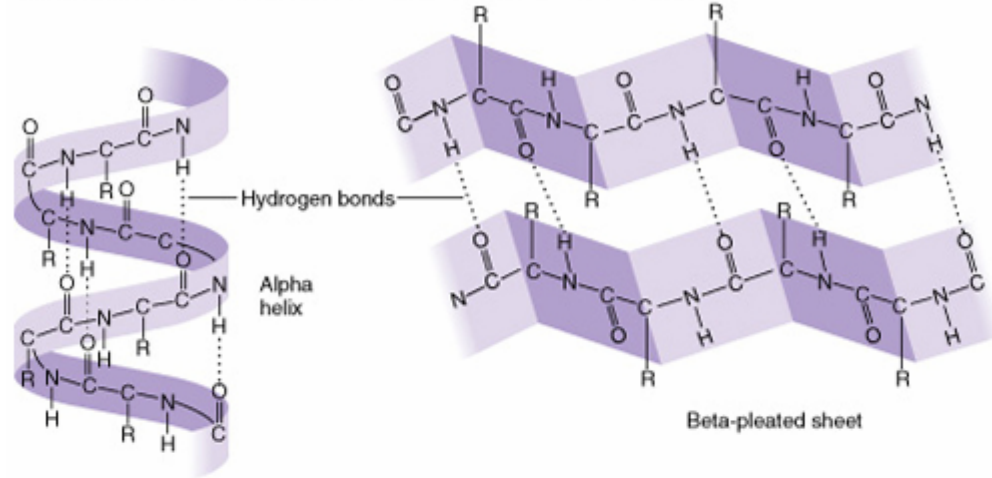
1. Primary ( $1^\circ$ ) = amino acid sequence (order)
2. Secondary ( $2^\circ$ ) = loops, helixes, pleats, etc.
  - Caused by interactions between aa's
3. Tertiary ( $3^\circ$ ) = overall structure of entire protein
  - Caused by interactions with water
4. Quaternary ( $4^\circ$ ) = peptide subunits come together

# Protein Structure

1°



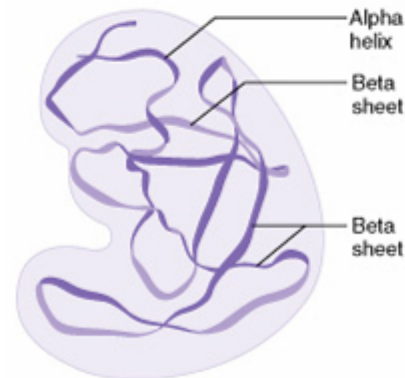
a. **Primary structure**—the sequence of amino acids in a polypeptide chain



2°

b. **Secondary structure**—loops, coils, sheets or other shapes formed by hydrogen bonds between nonadjacent carboxyl and amino groups

3°



c. **Tertiary structure**—three-dimensional forms shaped by bonds between R groups, interactions between R groups and water



d. **Quaternary structure**—proteins formed by bonds between separate polypeptides

4°

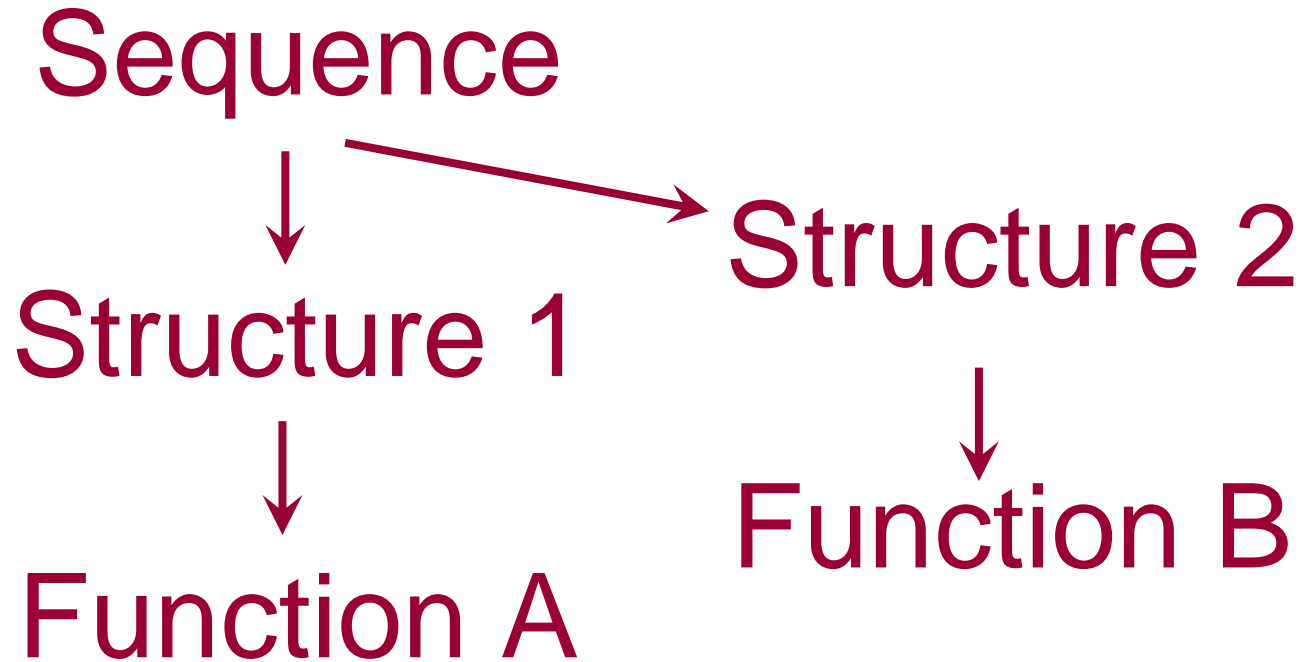
# Quality Control

Misfolded proteins can cause disease and death

1. Chaperone proteins
2. Countless enzymes
3. Ubiquitin
  - A tag added to a misfolded protein
  - Identifies that the protein is wrong
  - Attracts Proteasome
  - Proteasome degrades misfolded protein

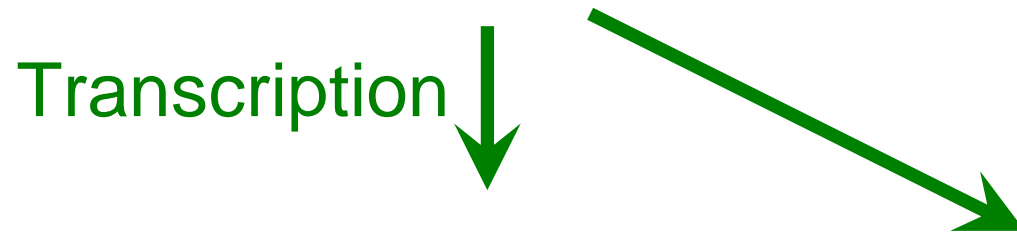
# Proteins

- Sometimes protein sequence can fold in more than one way



# Central Dogma

DNA



RNA

RNA2



Protein

Protein2

Protein3



# Next Class:

- Read Chapter Eleven
- Homework - Chapter Ten Problems;
  - Review: 1,3,4,6,7,9,12,14,18,19
  - Applied: 2,4,15