

# Protein Synthesis

## DNA Replication Review

- DNA is a double stranded molecule that does not leave the nucleus. DNA replication occurs exclusively in the nucleus.
- With several enzymes, 1 double stranded DNA molecule will turn into 2 double stranded molecules that are identical to each other.
- A bonds with T and C bonds with G.

Sequences of bases in the DNA called \_\_\_\_\_ can code for the production of proteins.

The process starts in the \_\_\_\_\_ and is completed at a ribosome in the \_\_\_\_\_.

Proteins may be further modified in the \_\_\_\_\_ to be incorporated in the \_\_\_\_\_ or \_\_\_\_\_ from the cell.

Proteins are composed of long chains of \_\_\_\_\_ called \_\_\_\_\_ . Proteins can be \_\_\_\_\_, hormones, \_\_\_\_\_, structural and \_\_\_\_\_.

Some protein functions include:

- 
- 
- 

What must occur before the protein can function properly?

Where are the instructions to initially build a protein?

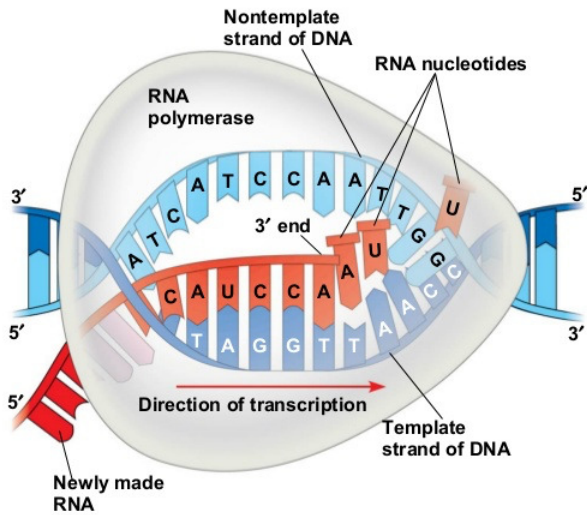
What is the role of the enzyme RNA Polymerase II?

This process is known as \_\_\_\_\_.

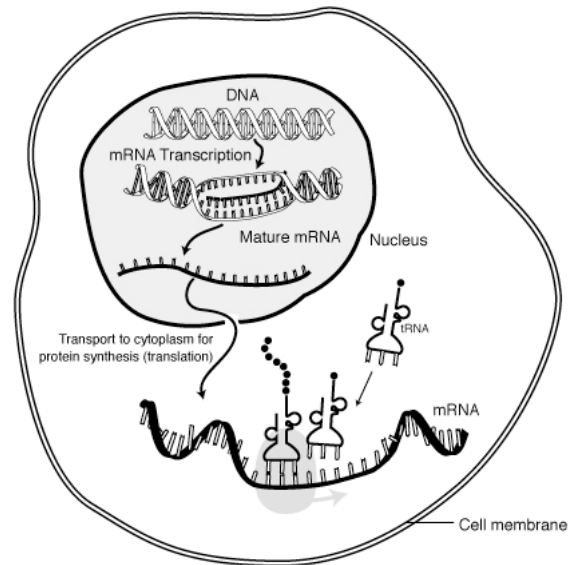
How is the base pairing of transcription different from DNA replication?

A binds with \_\_\_\_\_ instead of \_\_\_\_\_.

C to G, G to C and T to A remain the same.



DNA Replication



Transcription

Briefly describe mRNA:

\_\_\_\_\_ strand with a phosphate group, a \_\_\_\_\_ sugar and the bases \_\_\_\_\_, \_\_\_\_\_, \_\_\_\_\_ and \_\_\_\_\_.

Where will the mRNA go once it leaves the nucleus?

DNA → mRNA

T A C    T T G    C C C    G G C    A T T  
 \_\_\_\_\_

Each three base sequence is called a \_\_\_\_\_ and will code for a specific \_\_\_\_\_ . Codons are only found on mRNA. Each codon composed of \_\_\_\_\_ nucleotides will code for \_\_\_\_\_ amino acid.

### Use the Universal Genetic Code

Codon U C A  
 Amino Acid \_\_\_\_\_

Codon C U C  
 Amino Acid \_\_\_\_\_

Codon A U G  
 Amino Acid \_\_\_\_\_

Codon U G A  
 Amino Acid \_\_\_\_\_

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

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Building a polypeptide chain must begin with a \_\_\_\_\_ codon and end with a \_\_\_\_\_ codon.

START codon = \_\_\_\_\_

STOP codons = \_\_\_\_\_, \_\_\_\_\_ and \_\_\_\_\_

T A C    T T G    C C C    G G C    A T T  
A U G    A A C    G G G    C C G    U A A  
 \_\_\_\_\_

In order to start making a protein from an mRNA strand, the strand must attach to a \_\_\_\_\_ in the cytoplasm. This occurs at the START codon (\_\_\_\_\_). The ribosome will move with energy provided by \_\_\_\_\_. In reality, the ribosome covers \_\_\_\_\_ codons and will move down the length of the mRNA strand as soon as an amino acid is added. This process is known as \_\_\_\_\_

AUG GGC UUA AAG CAG UGC UAG UU...

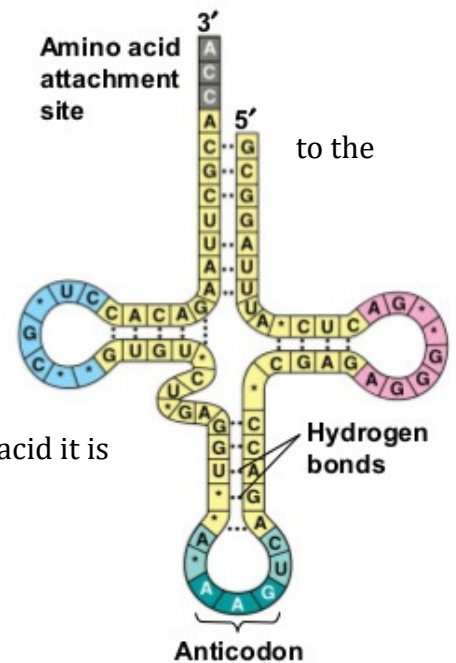
\_\_\_\_\_

Where do the amino acids come from and how do they get to the ribosome?

Once the ribosome attaches, tRNA molecules can use the instructions on the mRNA to go and retrieve the proper \_\_\_\_\_. The ribosome will move along until it is instructed to \_\_\_\_\_ off. That will happen at one of three \_\_\_\_\_ codons. At this point the ribosome will drop off. The resulting amino acid chain will \_\_\_\_\_ and form a functioning protein.

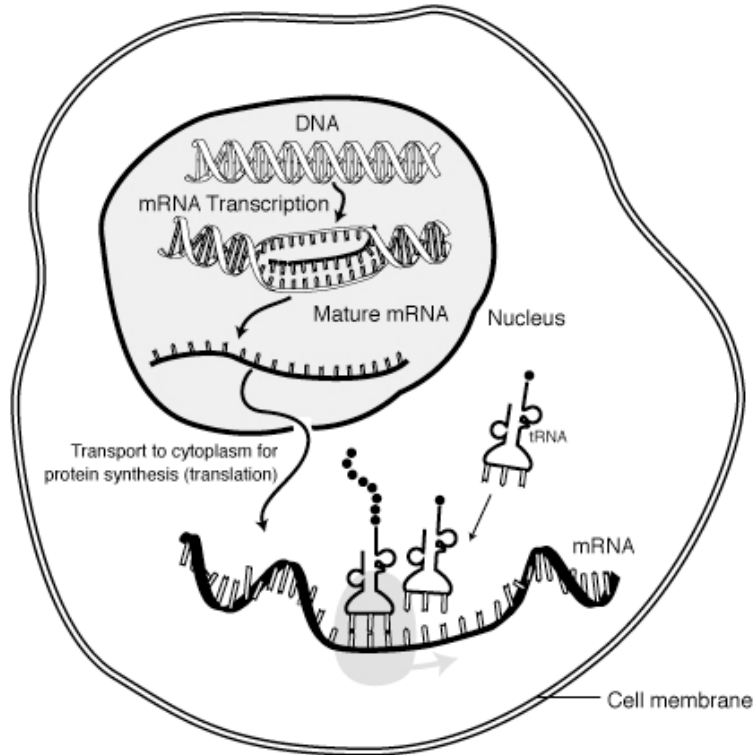
Translation

The amino acids in the \_\_\_\_\_ must be brought \_\_\_\_\_ to the \_\_\_\_\_. This is done with a molecule of \_\_\_\_\_. \_\_\_\_\_ (transfer RNA). The tRNA has a specific region called the \_\_\_\_\_ that will form a temporary bond with the mRNA. It will then release the amino acid it is carrying and move back to the cytoplasm.

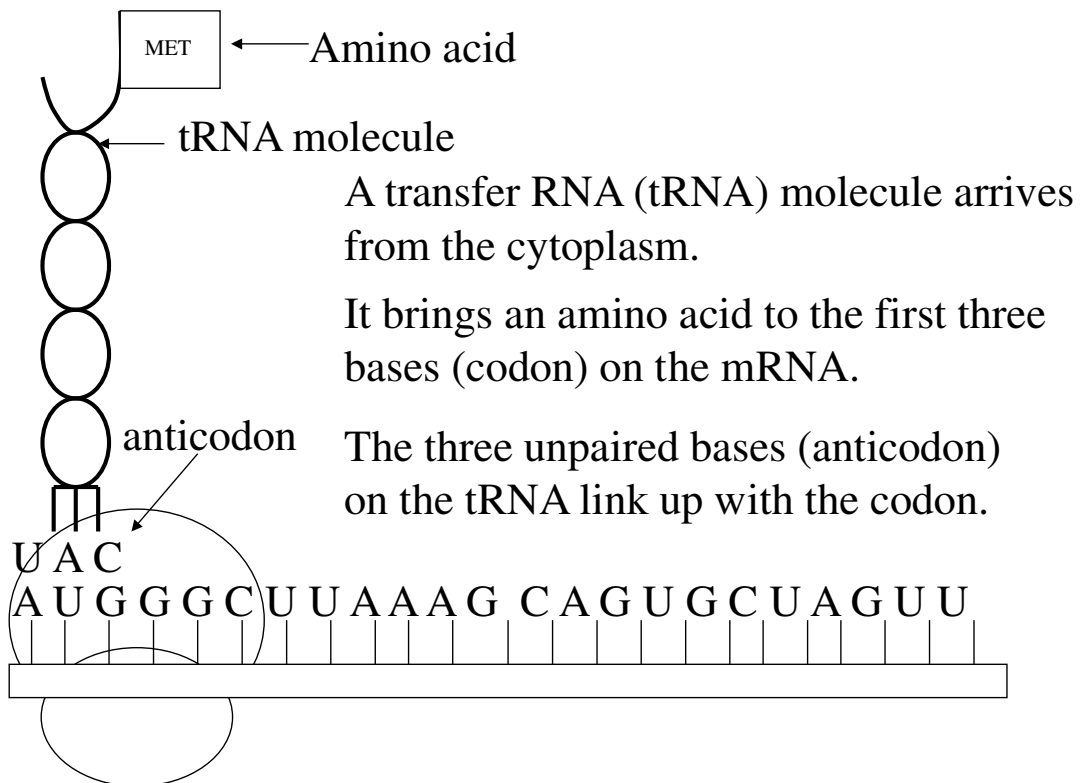


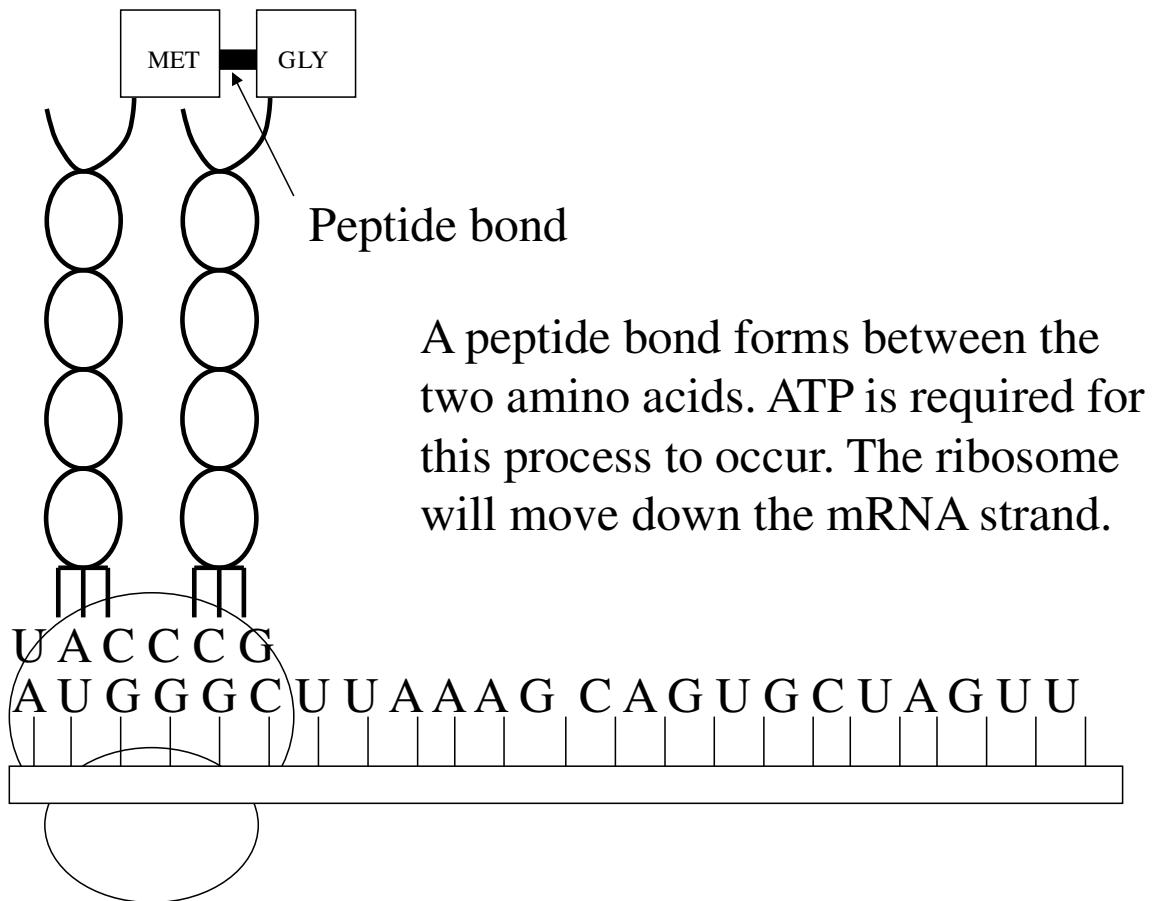
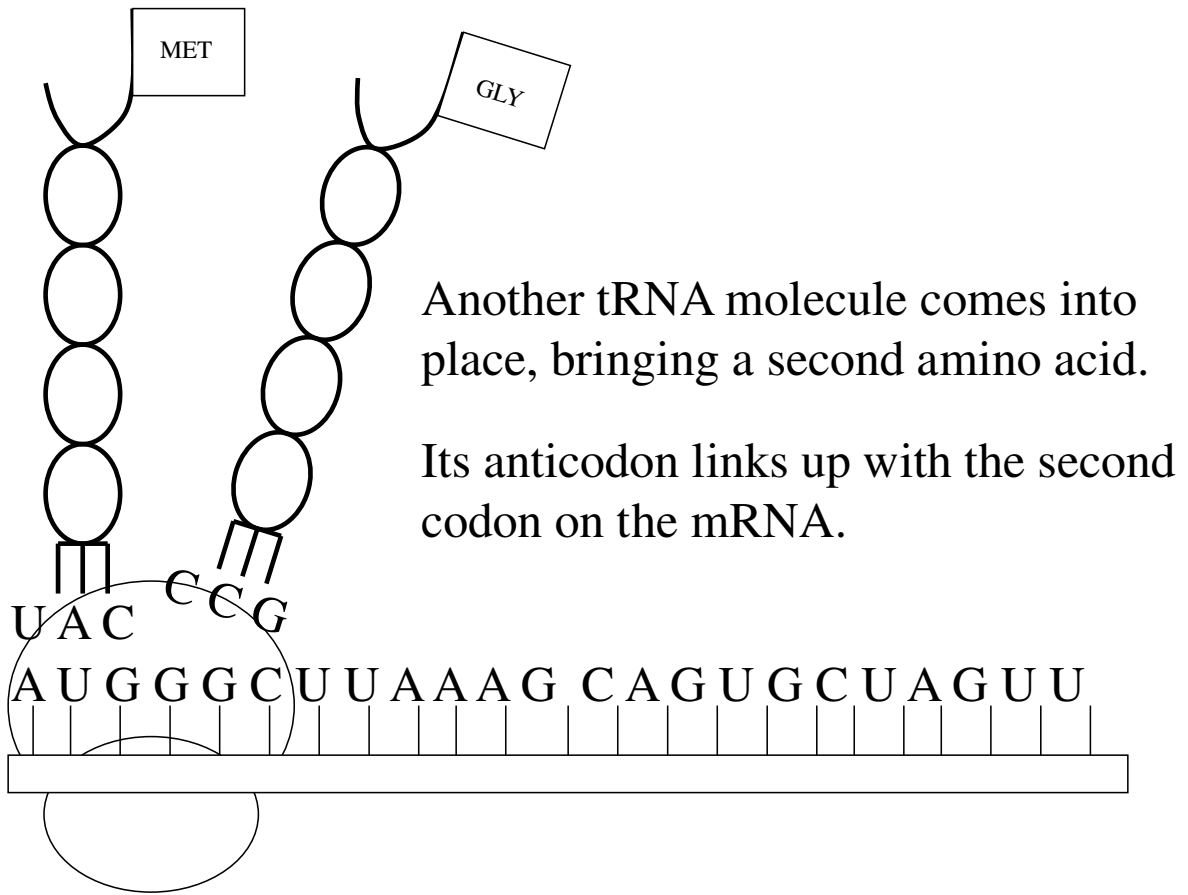
tRNA has an area for the \_\_\_\_\_ to bind as well as an area to bond with the mRNA (anticodon)

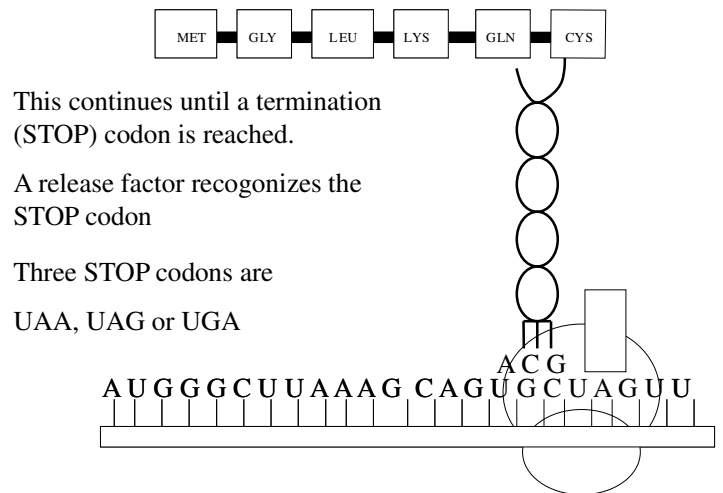
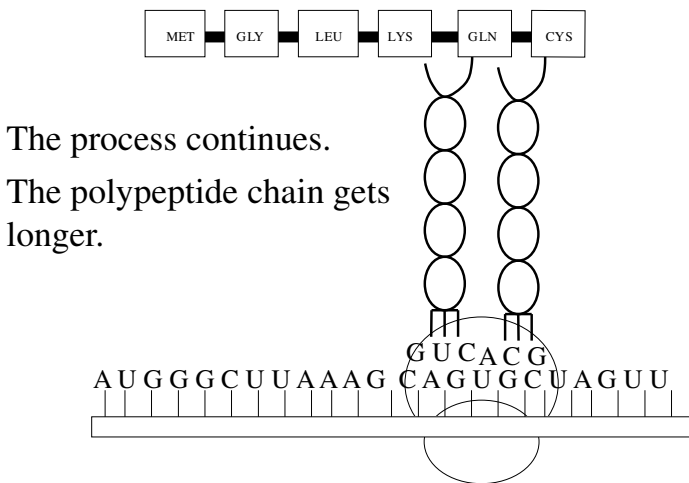
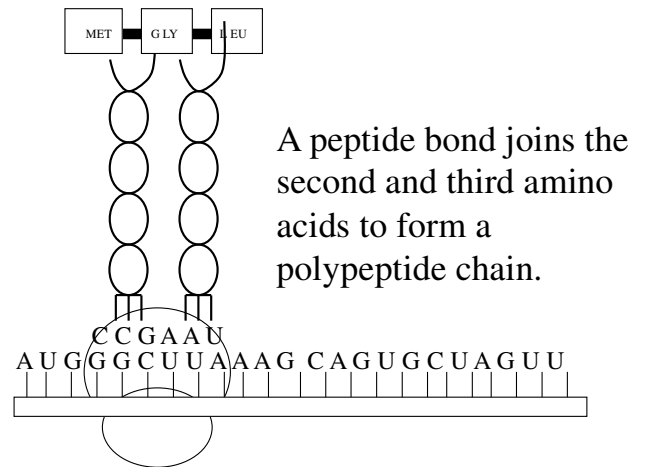
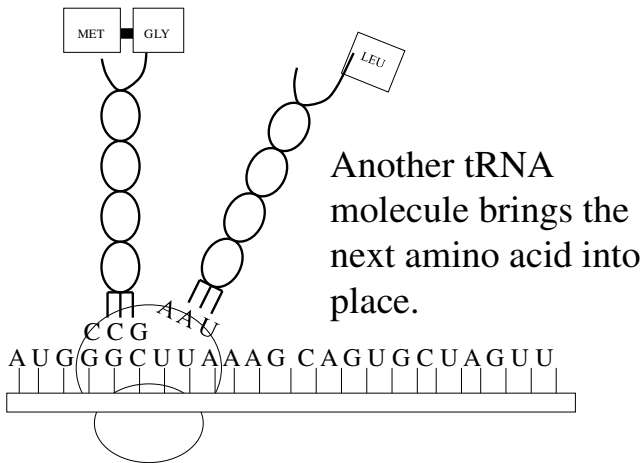
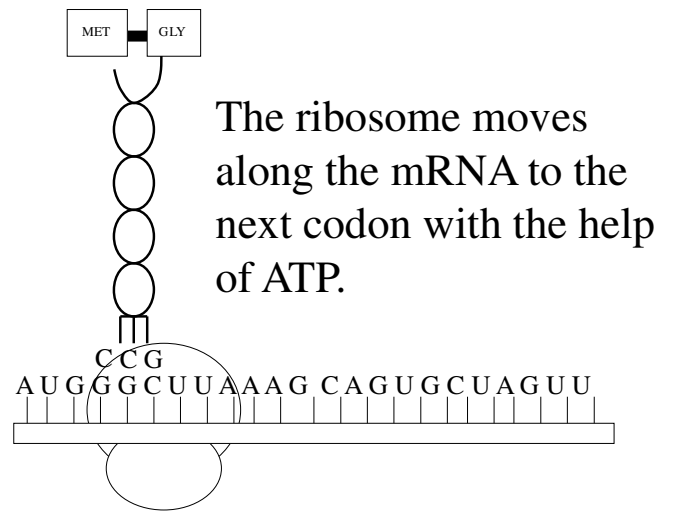
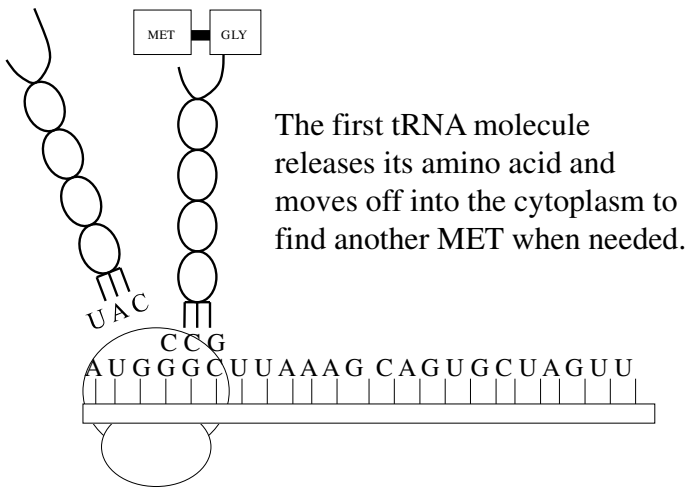
CIRCLE a codon and SQUARE an anticodon.



Let's Put It All Together





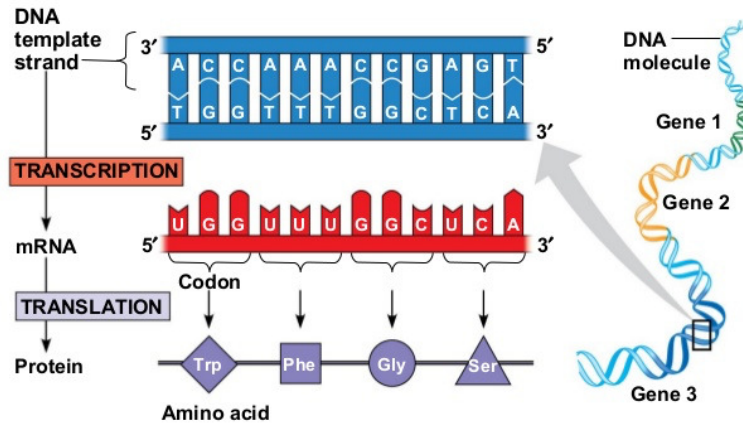


What happens when the STOP codon is reached?

Now that the polypeptide chain is released from the ribosome, what must occur before the protein can function?

## REVIEW

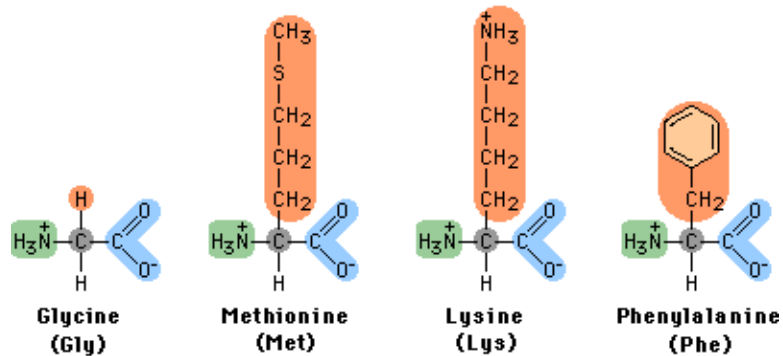
DNA BASE SEQUENCE → AMINO ACID SEQUENCE → PROTEIN SHAPE → PROTEIN FUNCTION → TRAIT



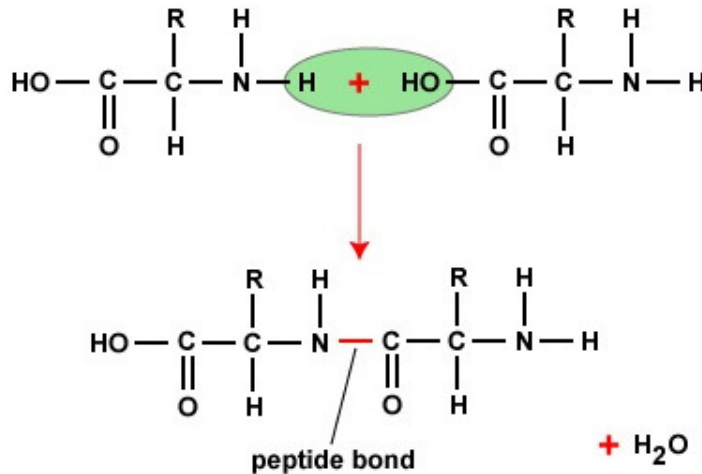
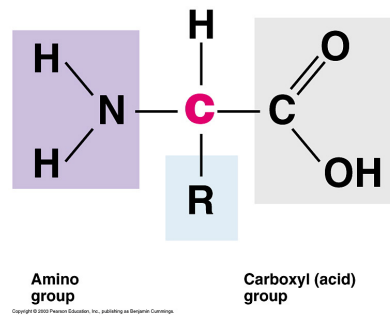
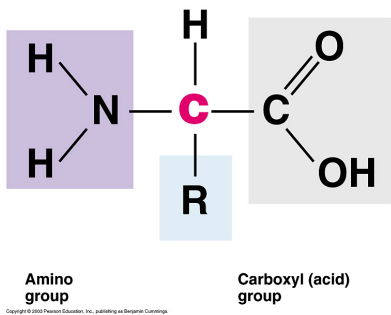
## THE PEPTIDE BOND-DEHYDRATION SYNTHESIS

Amino acids all have the same basic structure. The only difference is the functional \_\_\_\_ group.

The \_\_\_\_\_ of one amino acid will form a bond with the \_\_\_\_\_ of a different amino acid. This will release a \_\_\_\_\_ molecule in a process known as \_\_\_\_\_.







WHAT IF THERE IS A PROBLEM WITH THE DNA????

\_\_\_\_\_ are a permanent change in the \_\_\_\_\_. These mutations can alter the \_\_\_\_\_ of a protein encoded by the gene.

CAUSES:

- Genetic-\_\_\_\_\_ the mutation from your parents.
- Caused by \_\_\_\_\_ such as ultra-violet rays from the sun, X-rays or gamma radiation from nuclear material.
- \_\_\_\_\_ mistake during DNA replication.

Cystic Fibrosis is an \_\_\_\_\_ disease found on chromosome \_\_\_\_ that affects the \_\_\_\_\_ and \_\_\_\_\_ system.

The effect is to produce a \_\_\_\_\_ which clogs the lungs. This will cause a serious \_\_\_\_\_.

Under normal conditions the CFTR sequence is shown with the amino acid phenylalanine.

An individual suffering from CF has a change at the \_\_\_\_\_ position, missing the Phe.

This change has a drastic effect on the protein. It does not function causing mucous to build up in and on the lungs.

CFTR Sequence:					
Nucleotide	ATC	ATC	C T T	GGT	GTT
Amino Acid	Ile	Ile	Phe	Gly	Val
	506		508		510
			Deleted in $\Delta F508$		

$\Delta F508$ CFTR Sequence:				
Nucleotide	ATC	ATT	GGT	GTT
Amino Acid	Ile	Ile	Gly	Val
	506			

## Types of Mutations

Mutations can be classified as a \_\_\_\_\_, an \_\_\_\_\_ or a \_\_\_\_\_. In each case there can be little to no effect or the effect can be so severe that the protein does not function properly.

### Deletion

Here one base is removed causing all of the remaining bases to shift. This is called a frame shift and the amino acid sequence will be so badly altered that the new protein will not fold correctly and not function.

### Insertion

Here one base is added causing all of the remaining bases to shift. This is called a frame shift and the amino acid sequence will be so badly altered that the new protein will not fold correctly and not function.

### Base Substitution-NEUTRAL

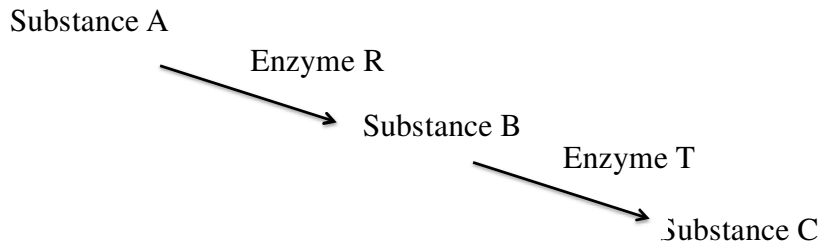
Here, one base is swapped with another base but the order of amino acids does not change. In this case, the protein function will be unaffected.

### Base Substitution-MISSENSE

Here, one base is swapped with another base but the number of amino acids does change. In this case, the protein may not function properly or not at all.

### Base Substitution-NONSENSE

Here, one base is swapped with another base and resulting codon is a STOP codon. In this case, the protein will be too short and not function at all.



If the DNA is altered/mutated, Enzyme T does not function properly and the cell will be unable to create substance C.

Let's start with a piece of DNA with no mutations.

DNA code    T A C    G G C    A C C    T T T    G A T    A A A    A T T

mRNA code

Amino Acid    \_\_\_\_\_    \_\_\_\_\_    \_\_\_\_\_    \_\_\_\_\_    \_\_\_\_\_    \_\_\_\_\_    \_\_\_\_\_

**EXAMPLE #1**

DNA code    T A C    G G C    A C C    T T T    G A A    T A A    A A T

mRNA code

Amino Acid    \_\_\_\_\_    \_\_\_\_\_    \_\_\_\_\_    \_\_\_\_\_    \_\_\_\_\_    \_\_\_\_\_    \_\_\_\_\_

Insertion	Deletion		
Substitution	NONSENSE	MISSENSE	NEUTRAL
Affected	TOO LONG	TOO SHORT	
Not Affected			

**EXAMPLE #2**

DNA code    T A C    G G C    A C C    T T C    G A T    A A A    A T T

mRNA code

Amino Acid    \_\_\_\_\_    \_\_\_\_\_    \_\_\_\_\_    \_\_\_\_\_    \_\_\_\_\_    \_\_\_\_\_    \_\_\_\_\_

Insertion	Deletion		
Substitution	NONSENSE	MISSENSE	NEUTRAL
Affected	TOO LONG	TOO SHORT	
Not Affected			

**EXAMPLE #3**

DNA code    T A C    G G C    A C T    T T T    G A T    A A A    A T T

mRNA code

Amino Acid    \_\_\_\_\_    \_\_\_\_\_    \_\_\_\_\_    \_\_\_\_\_    \_\_\_\_\_    \_\_\_\_\_

Insertion      Deletion

Substitution    NONSENSE            MISSENSE            NEUTRAL

Affected        TOO LONG            TOO SHORT

Not Affected

**EXAMPLE #4**

DNA code    T A C    G G C    A C C    T T A    G A T    A A A    A T T

mRNA code

Amino Acid    \_\_\_\_\_    \_\_\_\_\_    \_\_\_\_\_    \_\_\_\_\_    \_\_\_\_\_    \_\_\_\_\_

Insertion      Deletion

Substitution    NONSENSE            MISSENSE            NEUTRAL

Affected        TOO LONG            TOO SHORT

Not Affected

**EXAMPLE #5**

DNA code    T A C    G G A    C C T    T T G    A T A    A A A    T T C

mRNA code

Amino Acid    \_\_\_\_\_    \_\_\_\_\_    \_\_\_\_\_    \_\_\_\_\_    \_\_\_\_\_    \_\_\_\_\_

Insertion      Deletion

Substitution    NONSENSE            MISSENSE            NEUTRAL

Affected        TOO LONG            TOO SHORT

Not Affected



Name \_\_\_\_\_

Use the Universal Genetic Code Chart to answer the questions below.

**Universal Genetic Code Chart**  
Messenger RNA Codons and Amino Acids for Which They Code

		Second base				
		U	C	A	G	
F i r s t  b a s e	U	UUU } PHE UUC } UUA } LEU UUG }	UCU } UCC } SER UCA } UCG }	UAU } TYR UAC } UAA } STOP UAG }	UGU } CYS UGC } UGA } STOP UGG } TRP	U C A G
	C	CUU } CUC } LEU CUA } CUG }	CCU } CCC } PRO CCA } CCG }	CAU } HIS CAC } CAA } GLN CAG }	CGU } CGC } ARG CGA } CGG }	U C A G
	A	AUU } AUC } ILE AUA } AUG } MET or START	ACU } ACC } THR ACA } ACG }	AAU } ASN AAC } AAA } LYS AAG }	AGU } SER AGC } AGA } ARG AGG }	U C A G
	G	GUU } GUC } VAL GUA } GUG }	GCU } GCC } ALA GCA } GCG }	GAU } ASP GAC } GAA } GLU GAG }	GGU } GGC } GLY GGA } GGG }	U C A G

Species A	DNA strand: TAC CGA CCT TCA mRNA strand: AUG GCU GGA AGU Amino acid sequence: _____
Species B	DNA strand: TAC TTT GCA GGA mRNA strand: _____ Amino acid sequence: MET LYS ARG PRO
Species C	DNA strand: _____ mRNA strand: AUG UUU UGU CCC Amino acid sequence: MET PHE CYS PRO
Species D	DNA strand: TAC GTA GTT GCA mRNA strand: AUG CAU CAA CGU Amino acid sequence: MET HIS GLN ARG
Species E	DNA strand: TAC TTC GCG GGT mRNA strand: AUG AAG CGC CCA Amino acid sequence: MET LYS ARG PRO

According to the information, which two species are most closely related. Support your answer.

Species \_\_\_\_\_ and \_\_\_\_\_

Because \_\_\_\_\_

\_\_\_\_\_

Name \_\_\_\_\_ Protein Synthesis

Use the mRNA strand to correctly synthesis a protein. Below each codon, write the amino acid (**bolded**) it codes for and the corresponding letter or word to complete a sentence. Carefully note what happens if the base sequence is altered. These alterations can cause mutations in the protein.

**BASE SUBSTITUTION:** The original base is replaced by one of the other three bases. This may or may not lead to an amino acid substitution/mutation. If there is no affect, it is called a **NEUTRAL SUBSTITUTION**.

**BASE DELETION:** A base is missing. This can result in a shift in the reading frame (also known as a frameshift mutation). If the normal protein code is THE FAT CAT ATE THE BIG RAT, the protein code resulting from deleting the E in THE would be THF ATC ATA TET HEB IGR AT. This mutation could affect the end protein, possibly making it nonfunctional.

**BASE INSERTION:** An extra base has been added. This can result in a shift in the reading frame (frameshift mutation). If the normal protein code is THE FAT CAT ATE THE BIG RAT, the protein code resulting from insertion of an extra initial E would be THE EFA TCA TAT ETH EBI GRA T. This mutation could affect the end protein, possibly making it nonfunctional.

**NONSENSE MUTATION:** If a codon is changed to a "STOP" codon (UAA, UAG, or UGA) translation of mRNA would be prematurely terminated. These are called nonsense mutations because the protein is nonfunctional.

**Universal Genetic Code Chart**  
**Messenger RNA Codons and Amino Acids for Which They Code**

		Second base				
		U	C	A	G	
First base	U	UUU } PHE UUC } UUA } LEU UUG }	UCU } UCC } SER UCA } UCG }	UAU } TYR UAC } UAA } STOP UAG }	UGU } CYS UGC } UGA } STOP UGG } TRP	U C A G
	C	CUU } CUC } LEU CUA } CUG }	CCU } CCC } PRO CCA } CCG }	CAU } HIS CAC } CAA } GLN CAG }	CGU } CGC } ARG CGA } CGG }	U C A G
	A	AUU } AUC } ILE AUA } AUG } MET or START	ACU } ACC } THR ACA } ACG }	AAU } ASN AAC } AAA } LYS AAG }	AGU } SER AGC } AGA } ARG AGG }	U C A G
	G	GUU } GUC } VAL GUA } GUG }	GCU } GCC } ALA GCA } GCG }	GAU } ASP GAC } GAA } GLU GAG }	GGU } GGC } GLY GGA } GGG }	U C A G

Below are amino acids in the cytoplasm.

<b>HIS</b> I	<b>TYR</b> AROUND	<b>PRO</b> THIS	<b>LYS</b> TODAY
	<b>ASN</b> LOVE	<b>MET</b> START	<b>ARG</b> UP
<b>GLY</b> CORN	<b>ILE</b> MEET	<b>ALA</b> CLASS	<b>LEU</b> DOWN

Below is a functioning mRNA. Determine the amino acid sequence which could form a sentence.

**A U G C A C A A U C C G G C C U A A A**

_____	_____	_____	_____	_____	_____
_____	_____	_____	_____	_____	_____

The next four sequences have been mutated in some way. Determine the amino acid sequence/sentence and record which mutation occurred. Circle the end result of the mutation.

**A U G C A C A A U C C G G C C U A A A**

A U G C A C A A U C C G G C C U A G A

_____	_____	_____	_____	_____	_____
_____	_____	_____	_____	_____	_____

**Mutation:** Base Substitution    Neutral Substitution    Insertion    Deletion    Nonsense

**Result:** None    Affected    Nonfunctional



**A U G C A C A A U C C G G C C U A A A**

A U G C A C A G U C C G G C C U A A A

\_\_\_\_\_

\_\_\_\_\_

**Mutation:** Base Substitution    Neutral Substitution    Insertion    Deletion    Nonsense

**Result:** None    Affected    Nonfunctional

**A U G C A C A A U C C G G C C U A A A**

A U G C A C A A U C C G G C U A A A

\_\_\_\_\_

\_\_\_\_\_

**Mutation:** Base Substitution    Neutral Substitution    Insertion    Deletion    Nonsense

**Result:** None    Affected    Nonfunctional

**A U G C A C A A U C C G G C C U A A A**

A U G C A C A A A U C C G G C C U A A A

\_\_\_\_\_

\_\_\_\_\_

**Mutation:** Base Substitution    Neutral Substitution    Insertion    Deletion    Nonsense

**Result:** None    Affected    Nonfunctional

**A U G C A C A A U C C G G C C U A A A**

A U G C A C U A G C C G G C C U A U A

\_\_\_\_\_

\_\_\_\_\_

**Mutation:** Base Substitution    Neutral Substitution    Insertion    Deletion    Nonsense

**Result:** None    Affected    Nonfunctional

Which mutation seems to have the most affect on the function of a protein? Explain your answer.

Describe what happens if no STOP codon is present.

Describe what happens if a STOP codon is in the wrong place (too close to the beginning of the protein).

