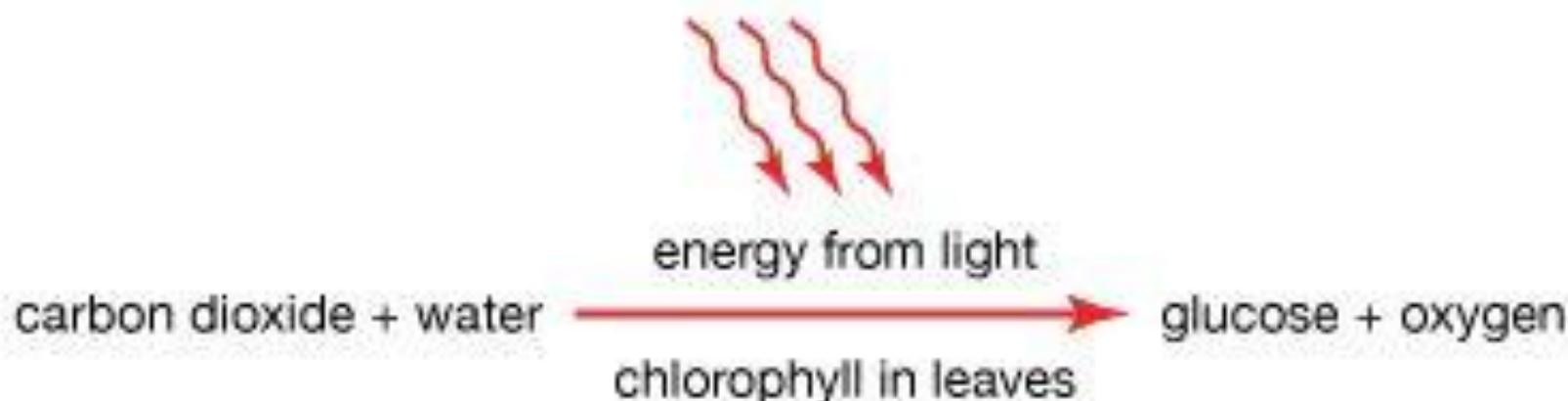




The reaction of photosynthesis

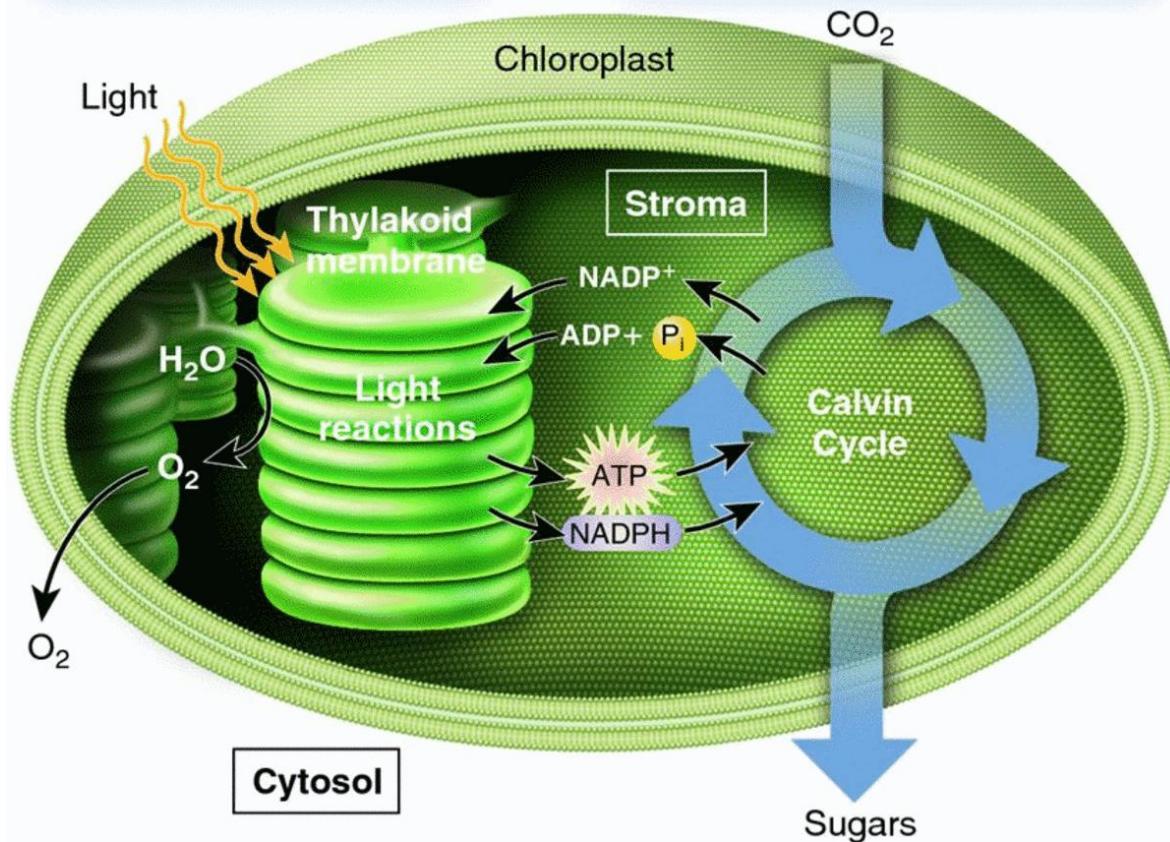


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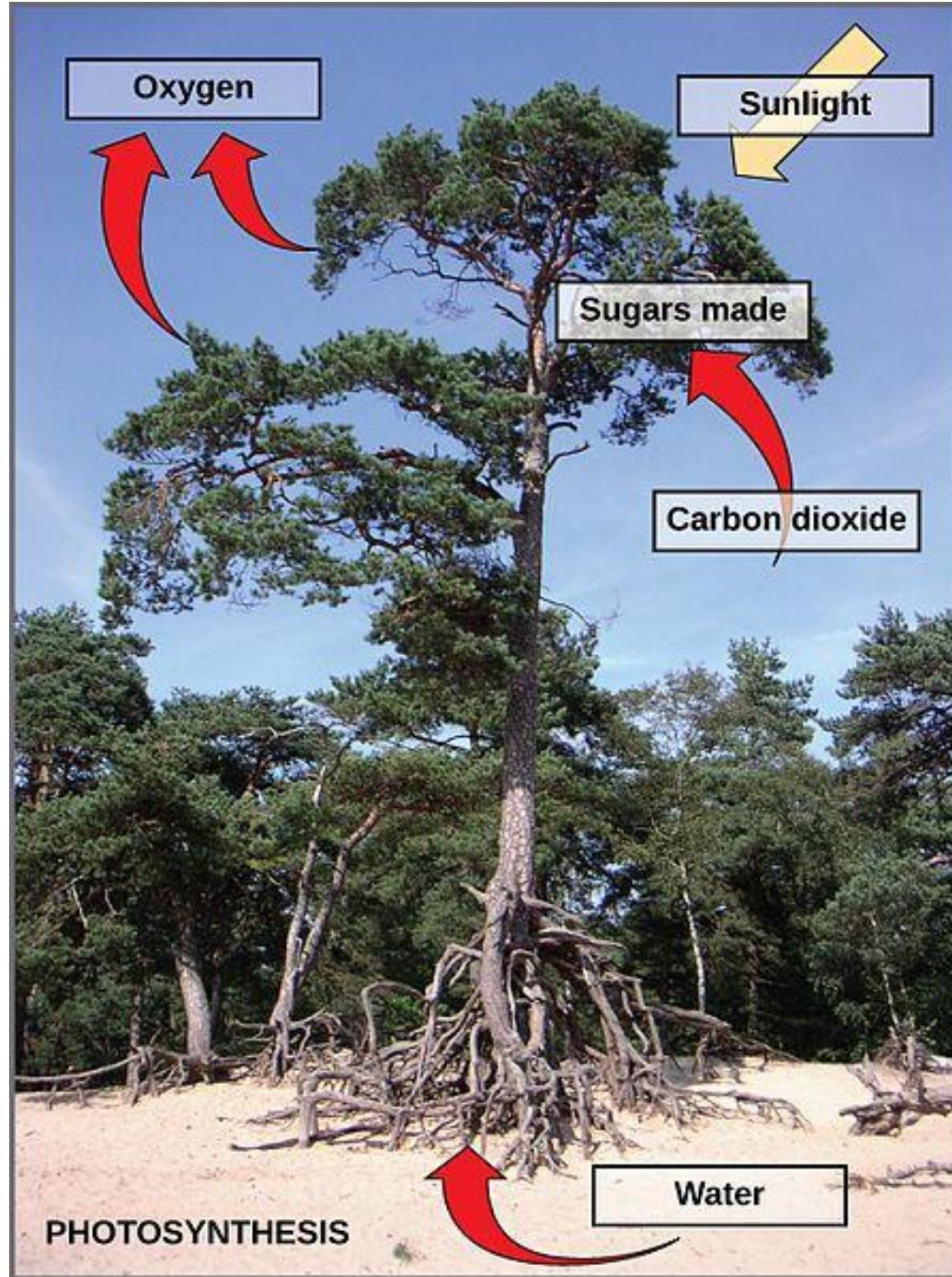
The light reactions in the thylakoid membrane produce O₂, ATP, and NADPH.

The Calvin cycle in the stroma uses CO₂, ATP, and NADPH to make carbohydrates, such as sugars.





Oxygen added
to atmosphere



Energy from sun
captured and stored
in sugar molecules

Sugar = energy used to
grow plant & keep it alive

Carbon dioxide
absorbed from
atmosphere

Water absorbed from
ground through roots

Gas exchange: plants take in CO₂ & give off O₂

- When humans grow, new tissue & cells are built from the food we eat
- When plants grow, where does the new tissue come from?
 - not from the soil: as a plant grows, the soil under it doesn't disappear
 - not from the water: bigger plants contain more water, but it doesn't account for the overall increase in solid matter
 - comes from the air! – CO₂

Carbon stays, building the molecules in the plant

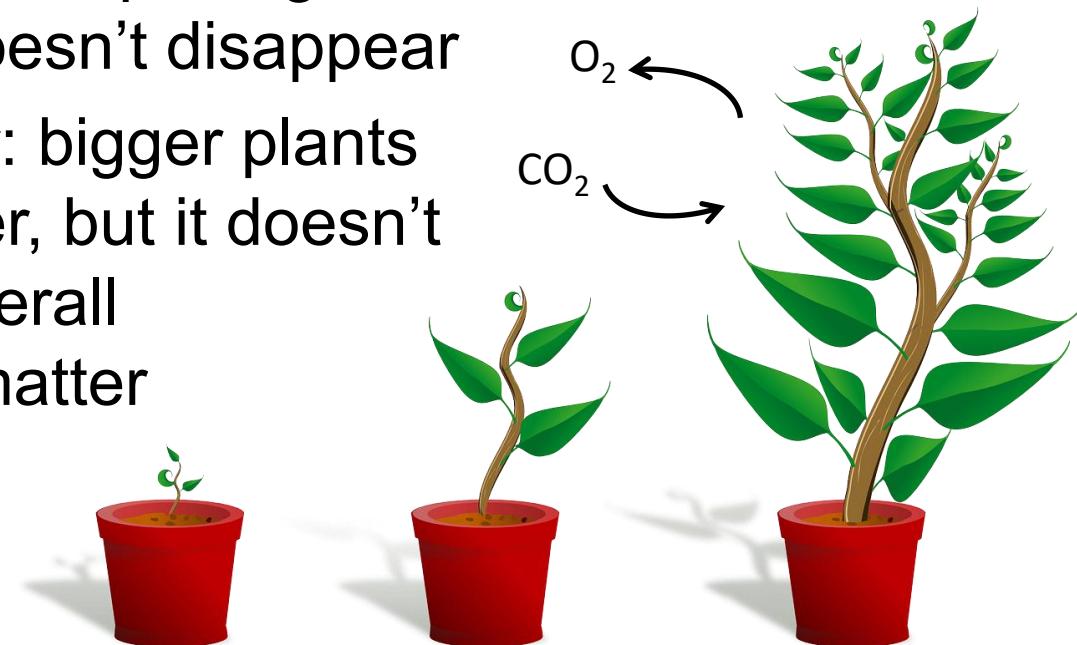


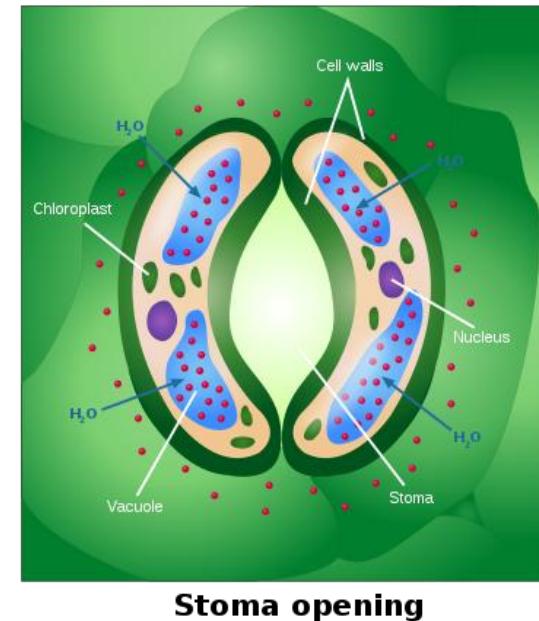
Figure: <https://pixabay.com/vectors/sapling-plant-growing-seedling-154734/>



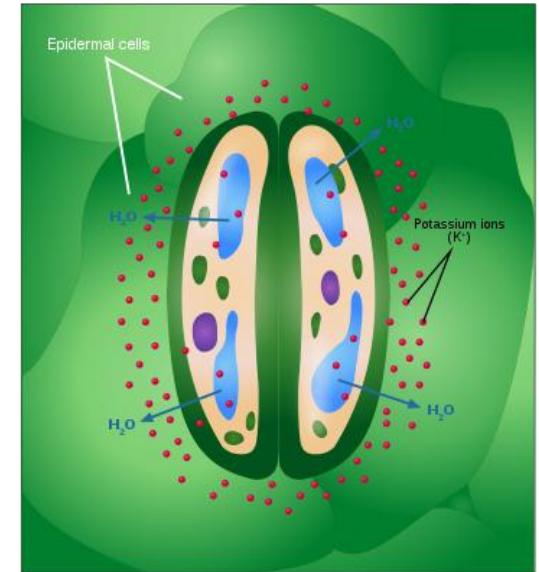
- Plants must constantly exchange gases (CO_2 & O_2) to stay healthy

- But they don't have lungs
 - Use pores in leaves instead
= **stomata**

- when stomata open, CO_2 comes in & O_2 goes out, but water also evaporates out
 - stomata close to prevent too much water loss



Stoma opening

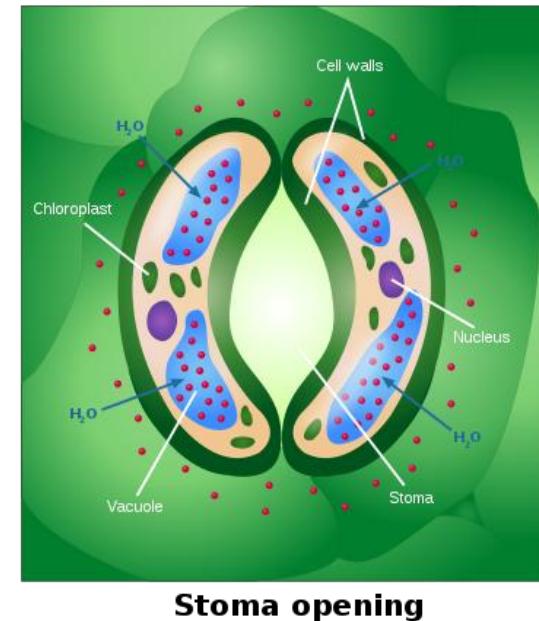


Stoma closing

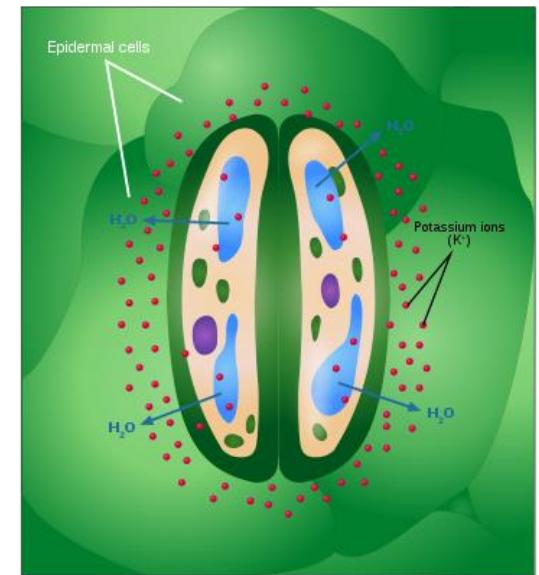
Figure: https://commons.wikimedia.org/wiki/File:Opening_and_Closing_of_Stoma.svg



- Leaves are always compromising: open stomata just enough to exchange gases, but not enough to lose too much water
 - In hot or dry environments, stomata stay closed more often to prevent water loss
 - BUT, this allows O_2 to build up inside the plant cells which can be toxic = **photorespiration**
 - **Photorespiration** = the build-up of O_2 to toxic levels: can eventually lead to death



Stoma opening



Stoma closing

Figure: https://commons.wikimedia.org/wiki/File:Opening_and_Closing_of_Stoma.svg



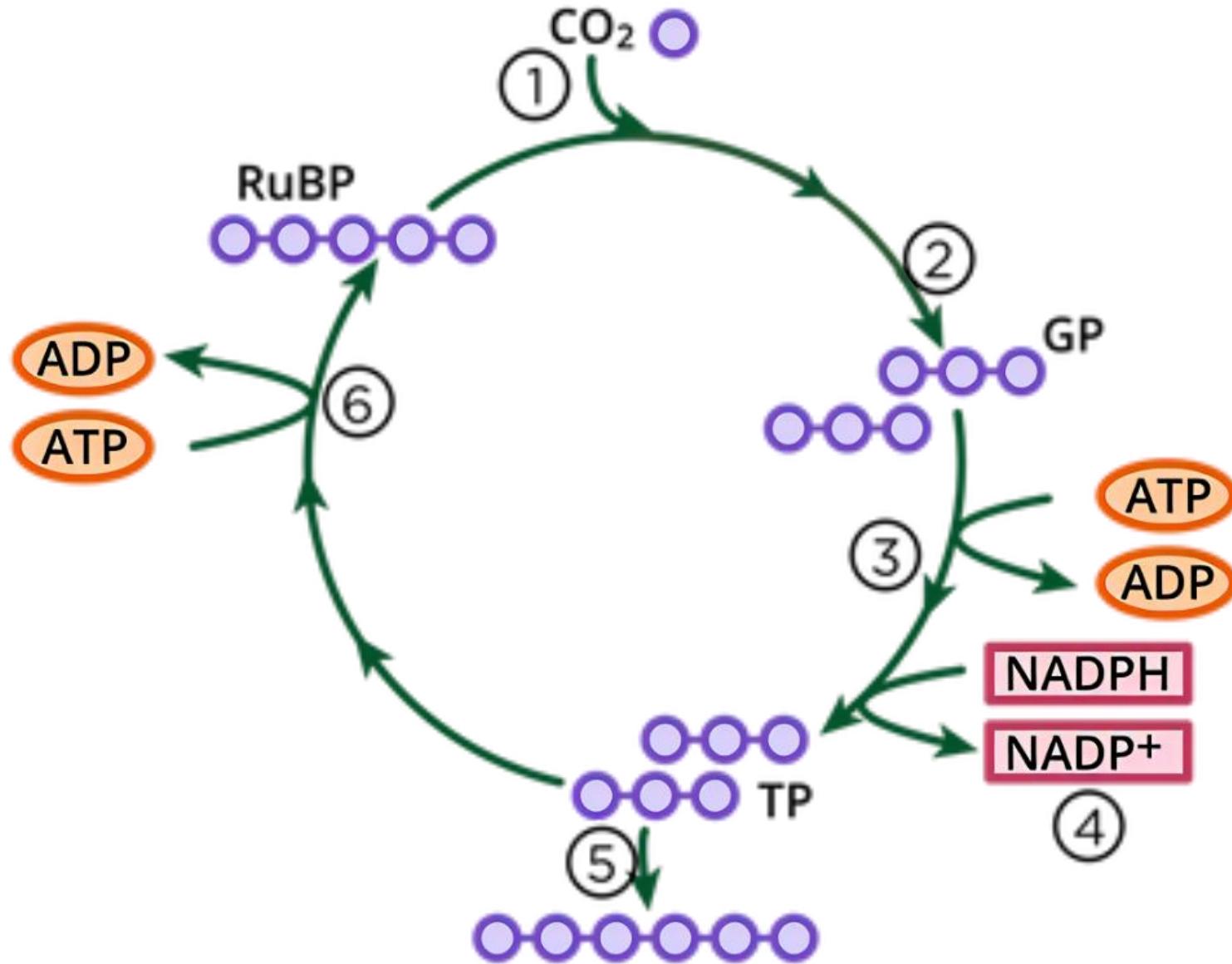
Plants in hot or dry environments are faced with a hard choice:

- 1. open stomata & dehydrate (can = death)
- 2. keep stomata closed & risk photorespiration (can = death)



C_3 plants can die of dehydration or photorespiration in hot or dry environments

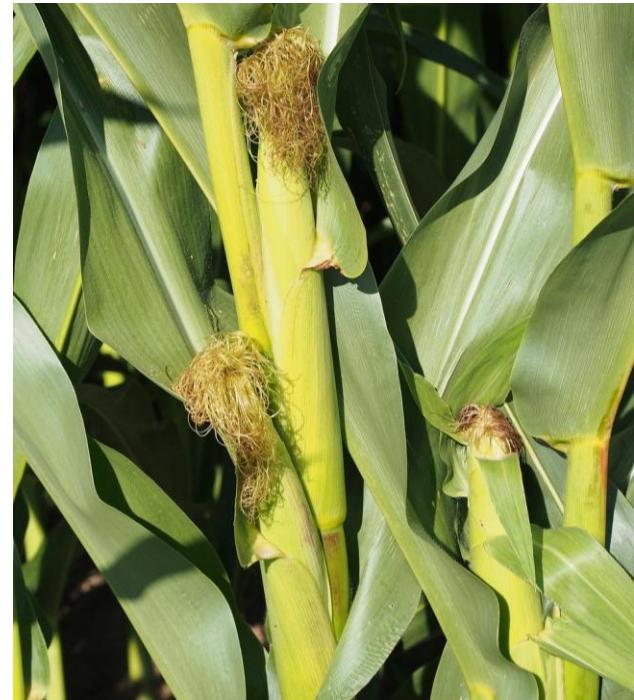
- The average plant is called a C_3 plant
 - the majority of plants on Earth are C_3 plants
 - these are at risk in hot or dry environments, because they are susceptible to photorespiration

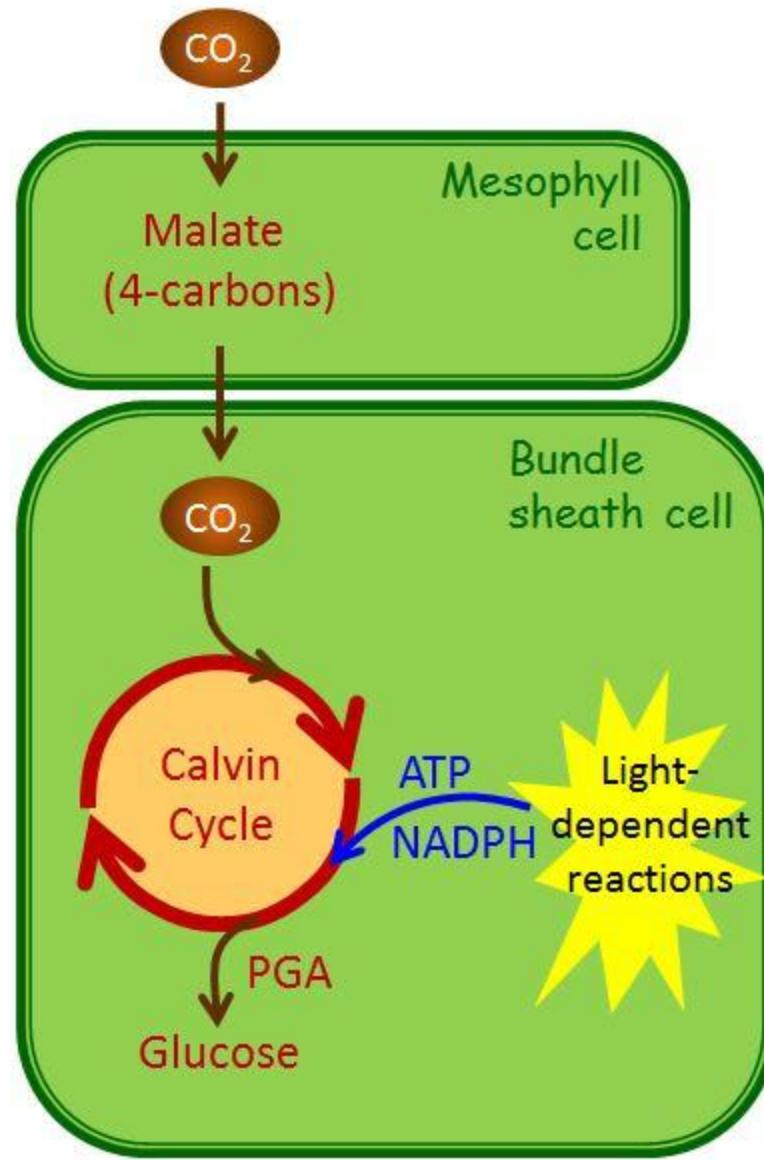




Some plants evolved a mechanism to prevent photorespiration

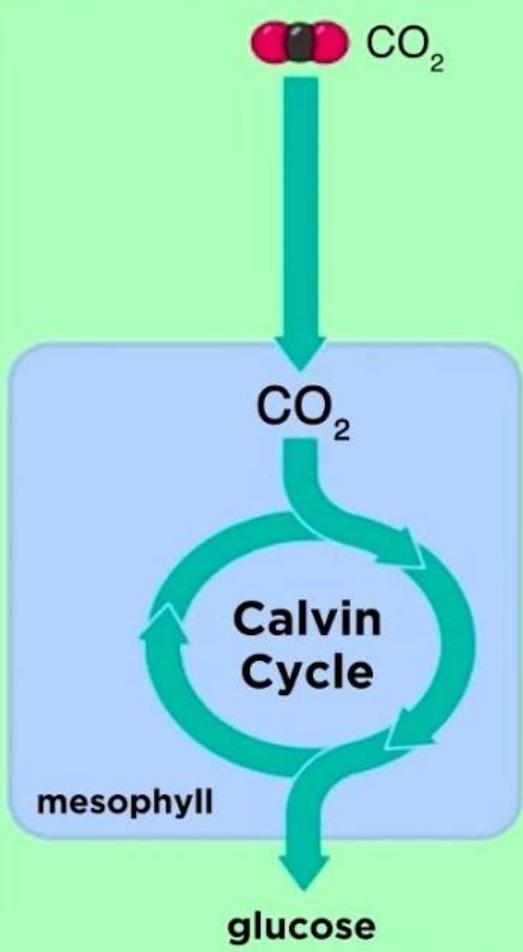
- **C₄ plants** use special cells to minimize photorespiration
 - e.g. corn & crabgrass
- **CAM plants** open stomata based on time of day
 - e.g. cacti & pineapple
 - At night stomata are open: minimal water loss
 - During the day stomata are closed: less water loss



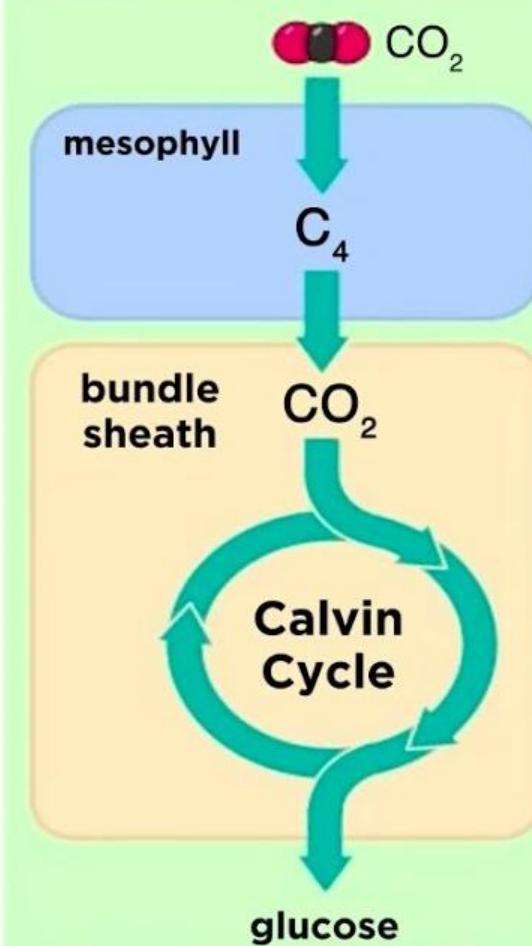




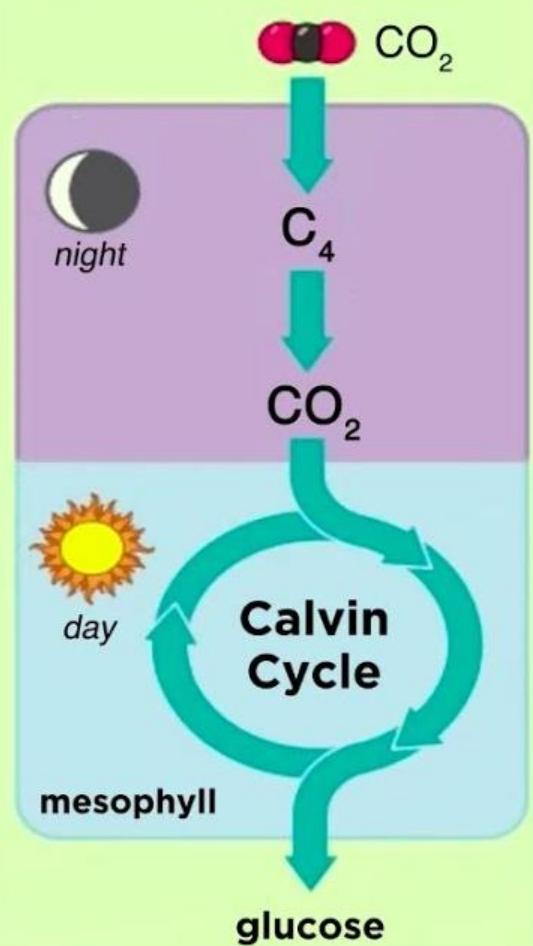
C₃ Plants



C₄ Plants

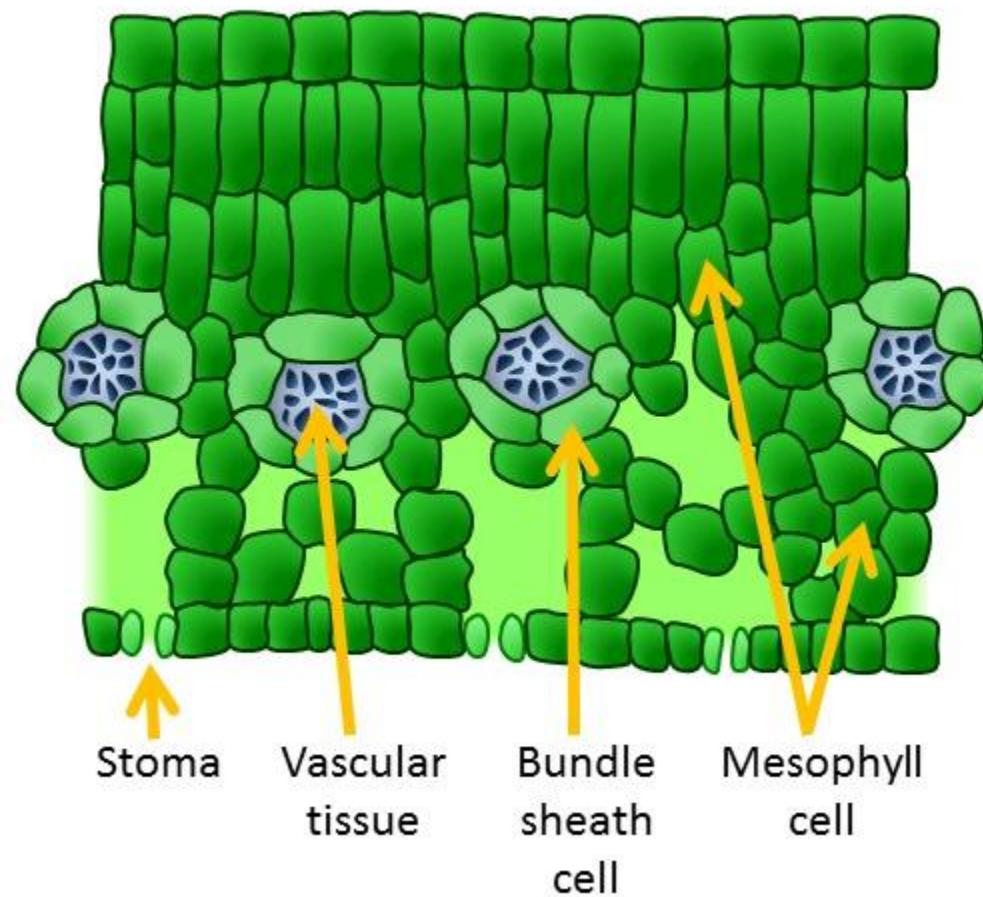


CAM Plants

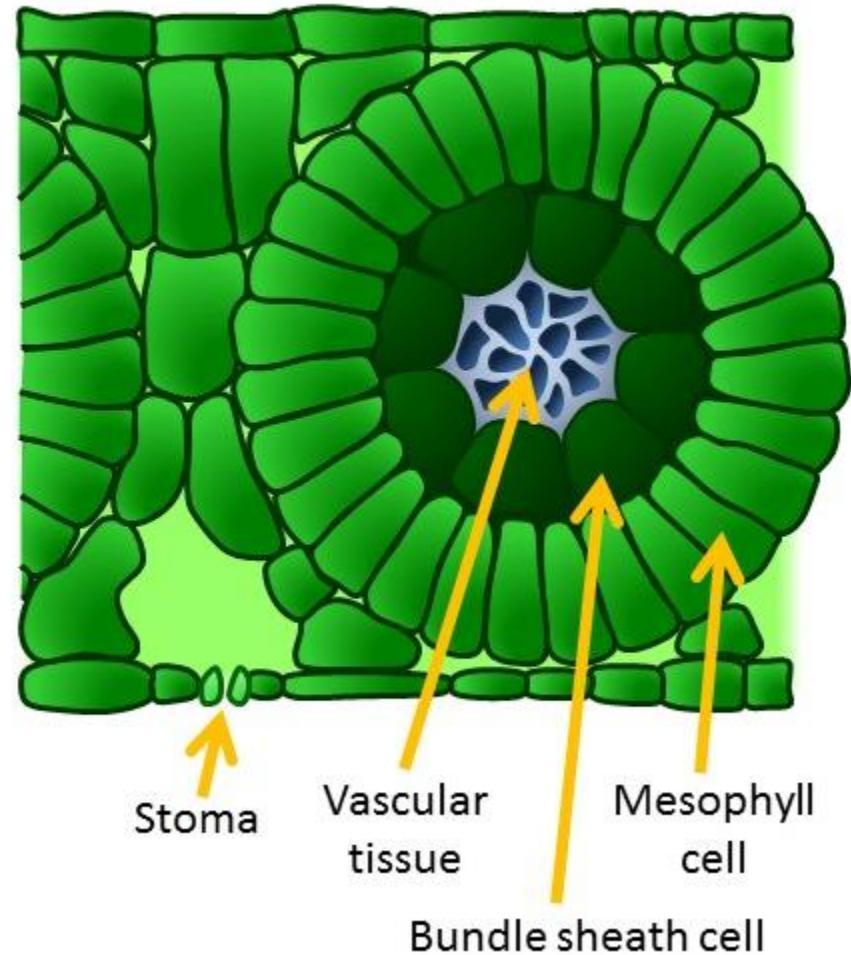




C₃ plant



C₄ plant





If C₄ & CAM plants don't have to worry about photorespiration, why haven't more plants evolved to use these strategies?

- C₄ & CAM plants use more energy than C₃ plants
 - they ONLY have an advantage in very hot or dry environments
- Where water is abundant or light levels are low, C₃ plants have the advantage
 - they do not have to use so much energy for normal functions

C₃ plants use less energy



C₄ & CAM plants need more energy to function





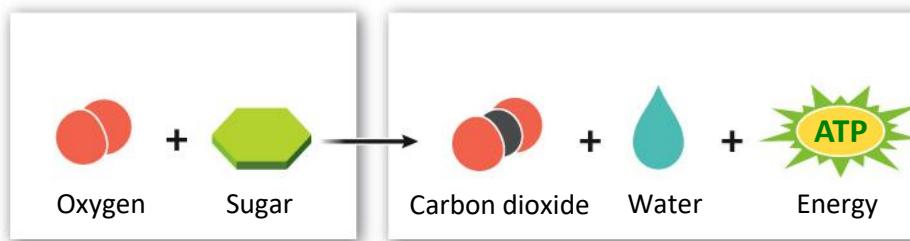
Characteristics of C₃, C₄ and CAM methods of fixing CO₂

| | C ₃ plant | C ₄ plant | CAM Plant |
|---|--|--|---|
| Cost | Photorespiration | ATP cost associated with fixing carbon twice. Carbon fixation is less efficient under cold conditions. | Reduced amount of fixed carbon, stomata only open at night |
| Benefits | Carbon fixation without using ATP | Reduced photorespiration and ability to fix Carbon under high temperatures and reduced water loss | Reduced photorespiration and reduced water loss |
| Separation of light-dependent reactions and carbon fixation | None, all of these reactions occur in the same cells | Spatial, these two sets of reactions occur in different cells | Temporal, these two sets of reactions occur at different times of day |
| Habitat | Cool and moist | Hot, not in cold environments (see cost.) | Hot and dry, large temperature differential between night and day |



How release energy trapped in molecules?

- Once photosynthetic organisms have stored energy in the bonds of sugar, how do we release the energy in order to use it?
 - The most important exergonic reaction for life = **glucose breakdown**



- All living things (plants, animals, fungi, bacteria, etc.) must breakdown glucose molecules to release energy to stay alive



How do organisms get glucose?

- Plants & other photosynthetic organisms make it by themselves from sunlight
- Animals & other organisms eat plants (or organisms that ate plants)
 - also get it from other organic molecules (lipids, proteins, etc.) that we can convert to glucose

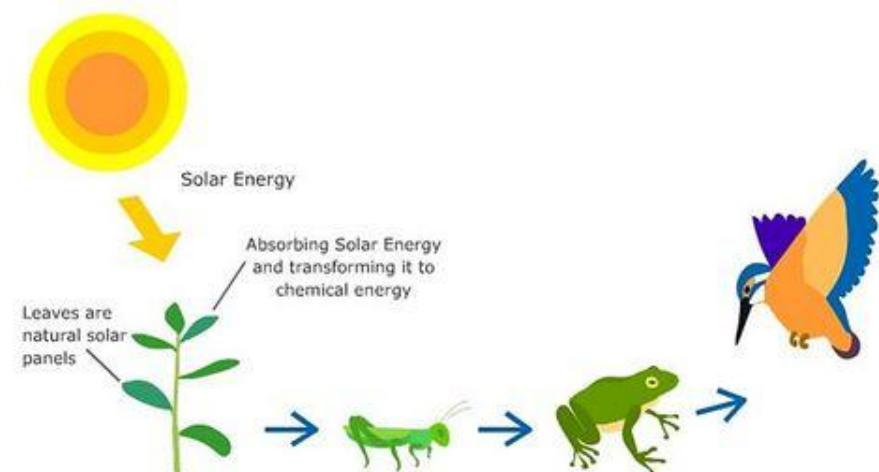
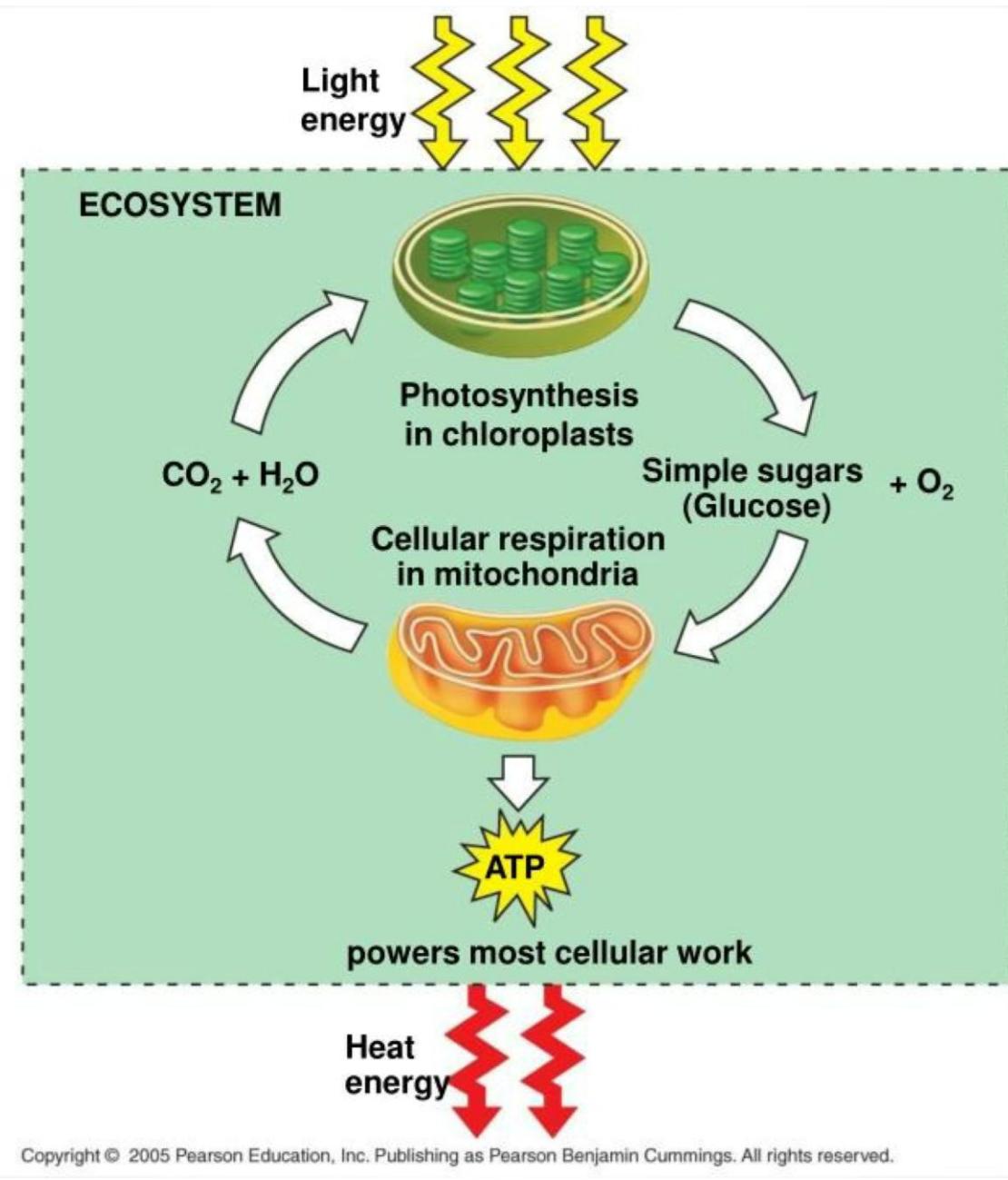


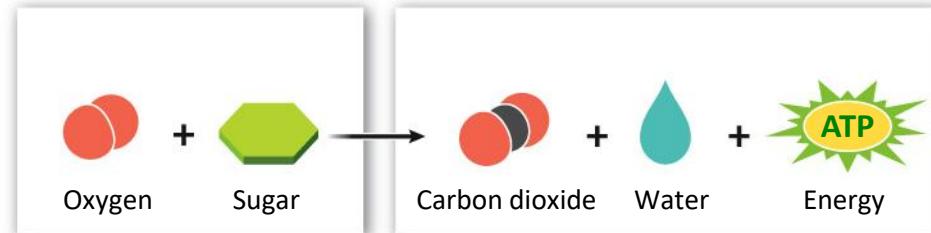
Figure: <https://www.sciencelearn.org.nz/images/2174-a-food-energy-chain>





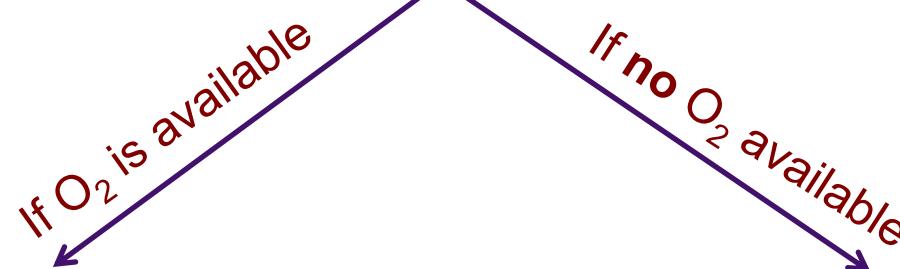
Remember: the energy in glucose can't be used directly – must first transfer it to an energy-carrier molecule like **ATP**

– we can then use ATP directly



- Glucose breakdown happens in 2 steps:

Step 1 = **glycolysis** (*in the cytoplasm of cells*)

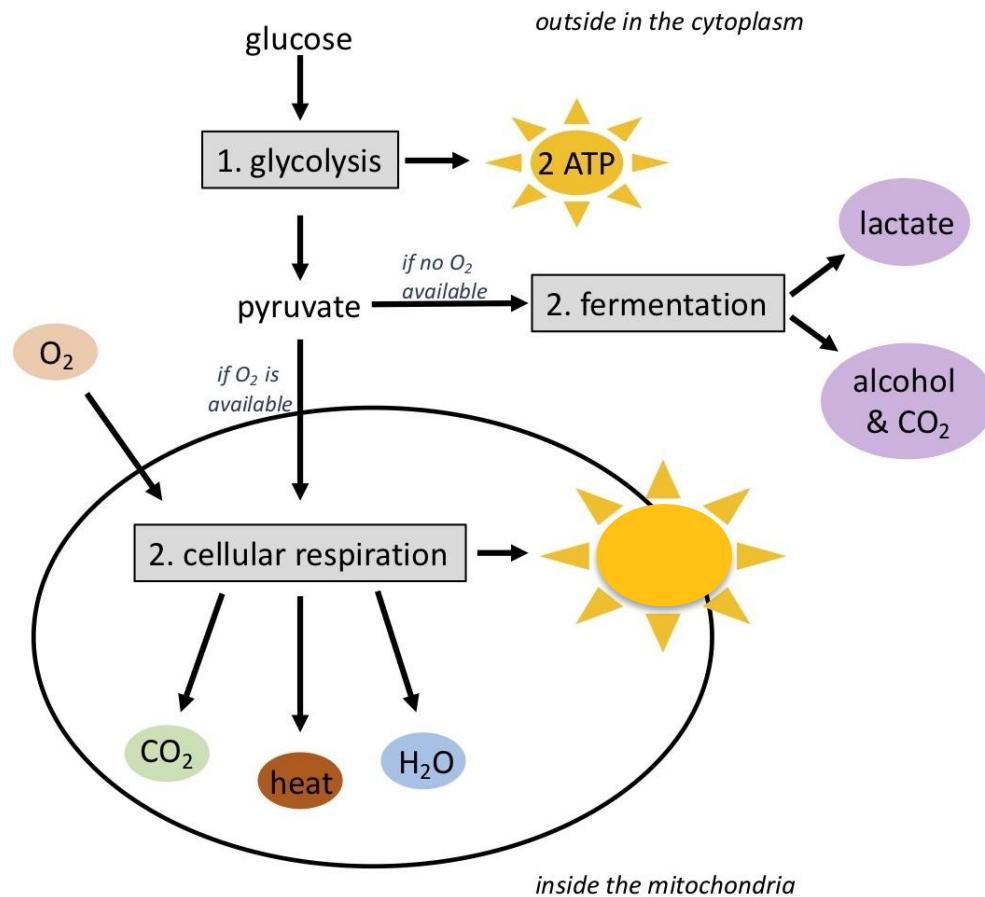


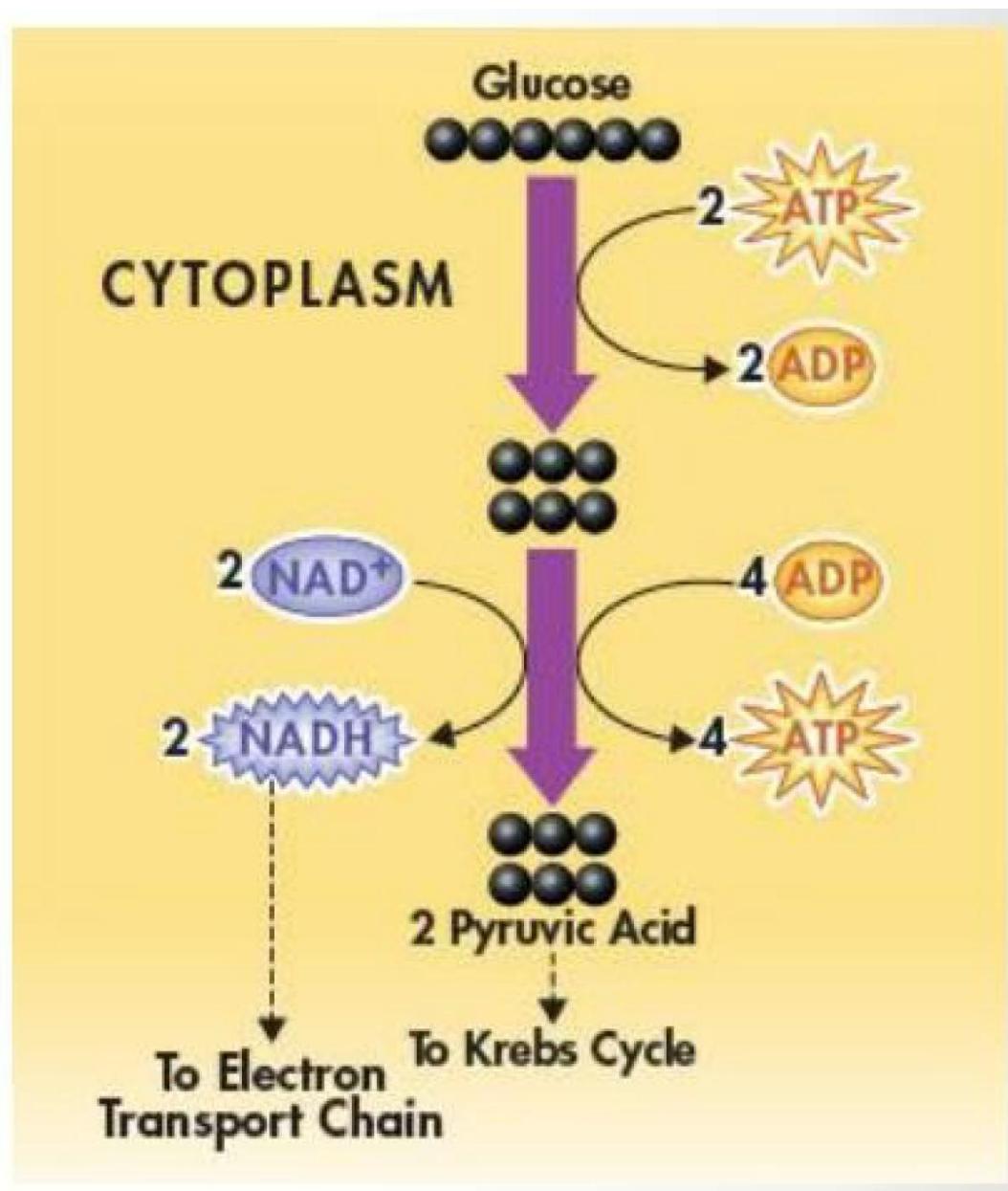
Step 2 = **cellular respiration**
(*in the mitochondria*)

Step 2 = **fermentation**
(*in the cytoplasm*)

- Step 1 is always **glycolysis** (*occurs in cytoplasm*)

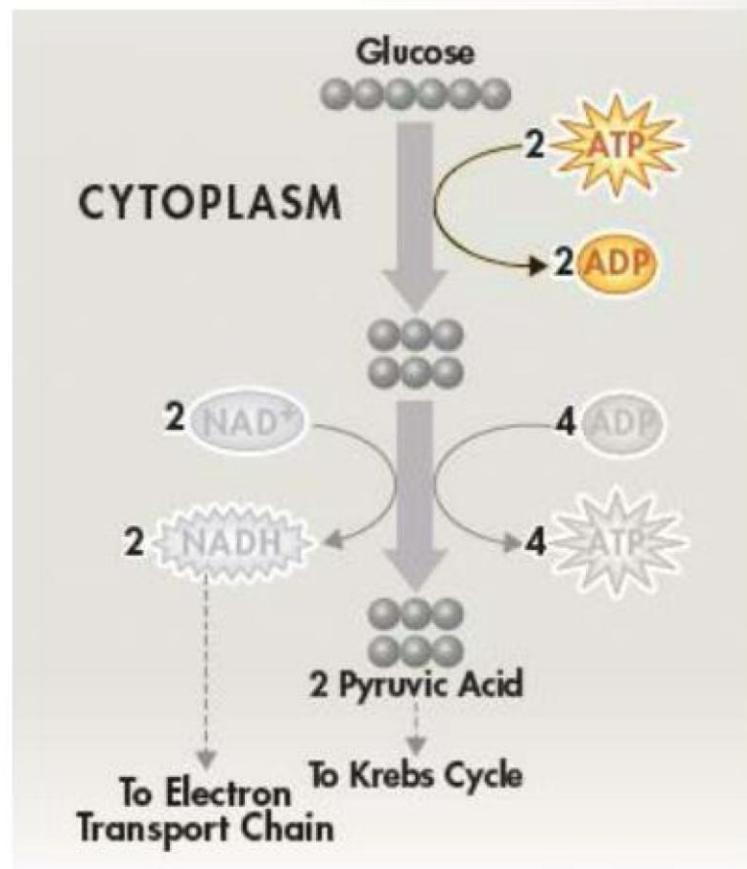
- glucose \rightarrow 2 pyruvate & 2 ATP
- breaks the 1st bond in glucose, causing the molecule to break into 2 pieces: called pyruvate
 - releases 2 ATPs (energy) by breaking the bond
- *only glucose required: no O₂ needed*





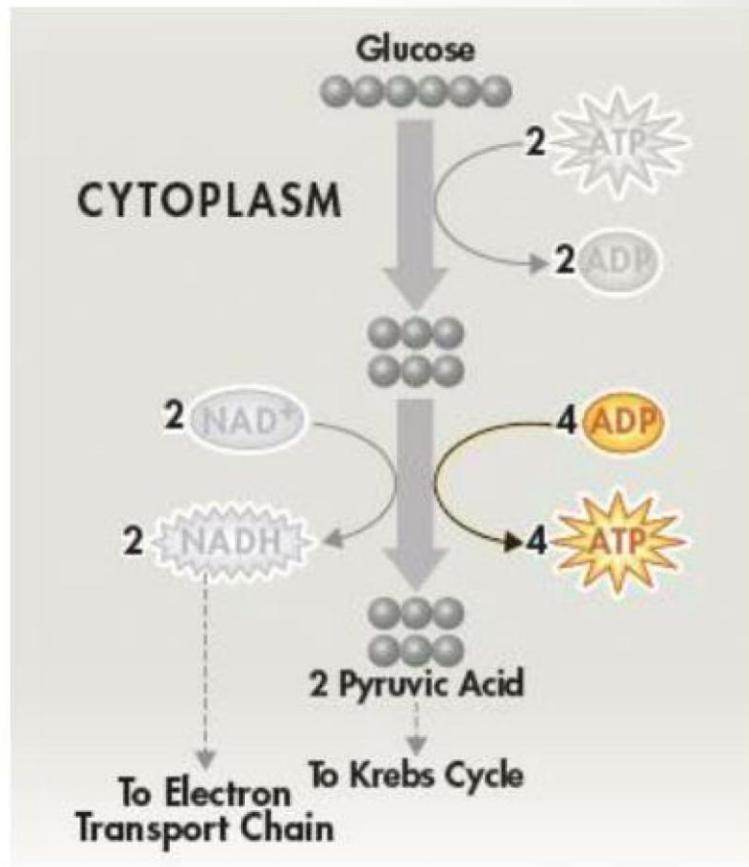
ATP Production

- 2 ATP molecules are needed to get glycolysis started.



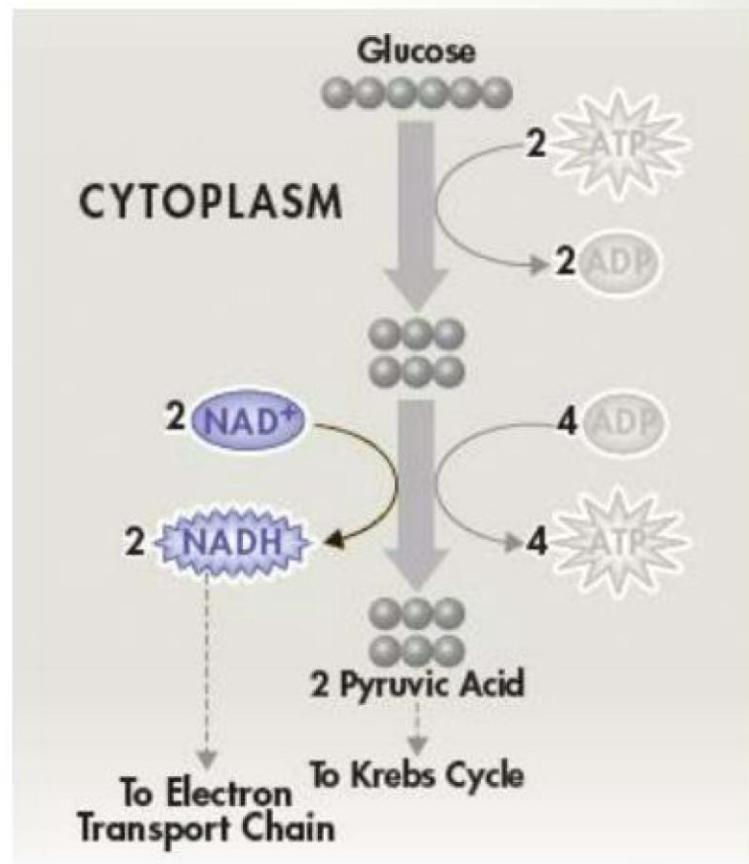
ATP Production

- Glycolysis then produces 4 ATP molecules, giving the cell a net gain of +2 ATP molecules for each molecule of glucose that enters glycolysis.



NADH Production

- During glycolysis, the electron carrier 2 **NAD⁺** become 2 NADH.
- 2 NADH molecules are produced for every molecule of glucose that enters glycolysis.



Glycolysis

- Glycolysis uses up:
 - 1 molecule of glucose (6-carbon sugar)
 - 2 molecules of ATP
 - 2 molecules of NAD⁺
- Glycolysis produces
 - 2 molecules of pyruvic acid (3-carbon acids)
 - 4 molecules of ATP
 - 2 molecules of NADH

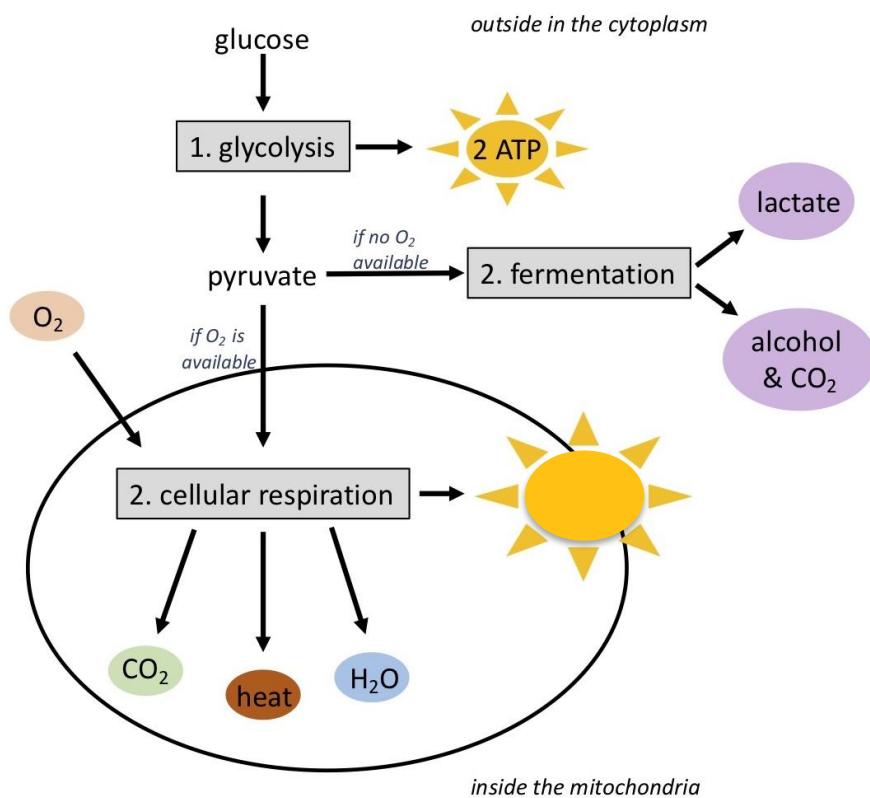
Advantages of Glycolysis

- Glycolysis produces ATP very fast, which is an advantage when the energy demands of the cell suddenly increase.
- Glycolysis does not require oxygen, so it can quickly supply energy to cells when oxygen is unavailable.



2 ATPs is not very much & there are still many more bonds to break

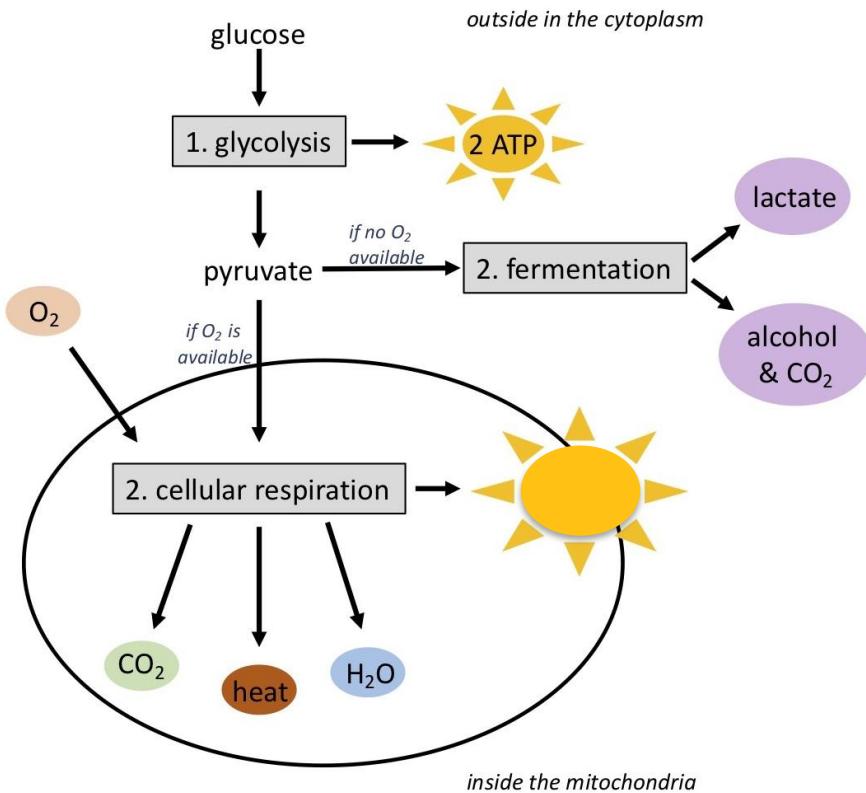
- If O₂ is available, pyruvate will get shipped into the mitochondria to have the rest of their bonds broken & to give us the most ATP
- Remember: the **mitochondria** is the powerhouse of the cell
 - its main job is to break apart glucose & store the energy in ATP





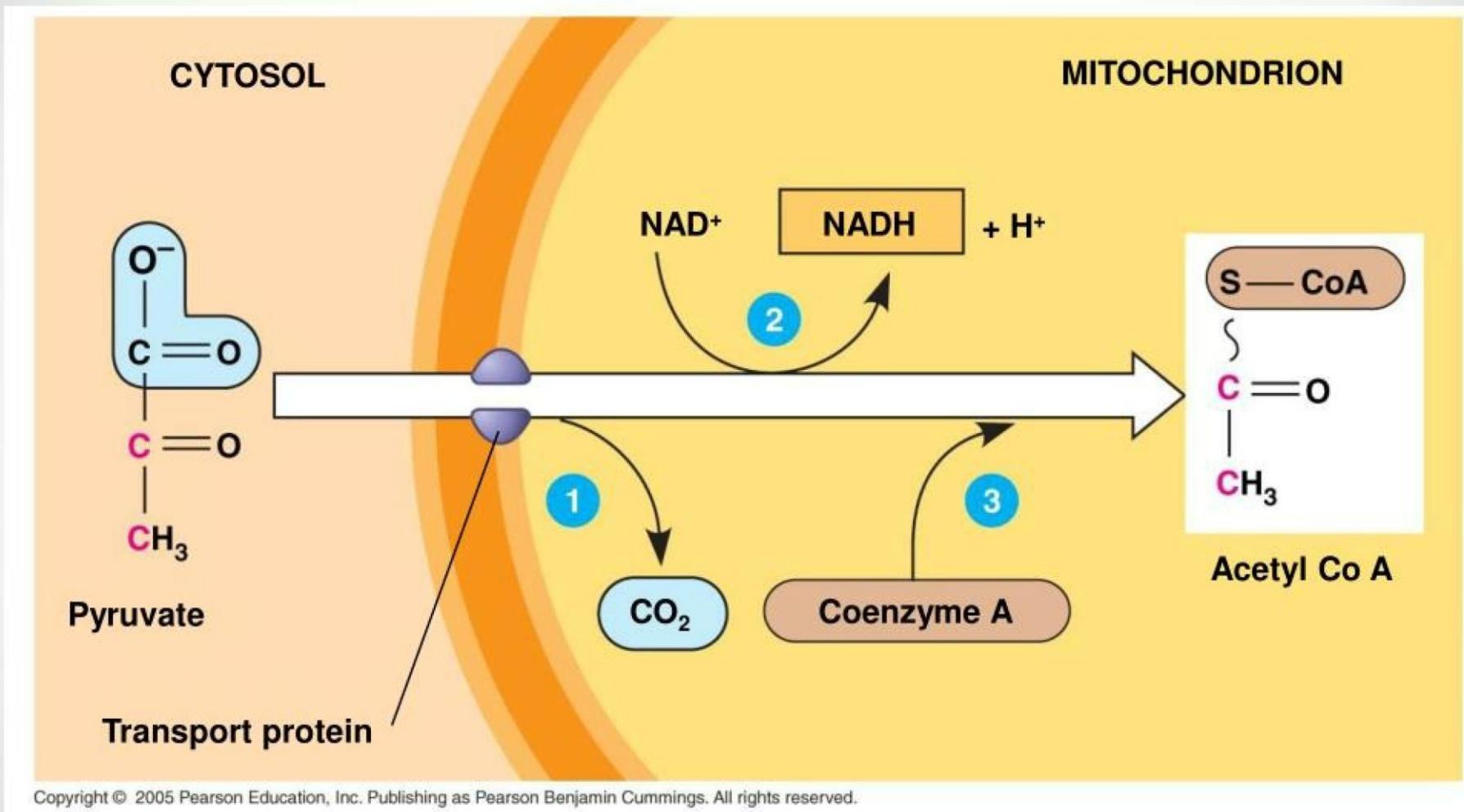
Step 2 if O₂ is available = **cellular respiration**

- Pyruvate moves into the mitochondria, which also pulls in O₂
- Because cellular respiration requires O₂ it is called **aerobic**
 - why we must breathe!



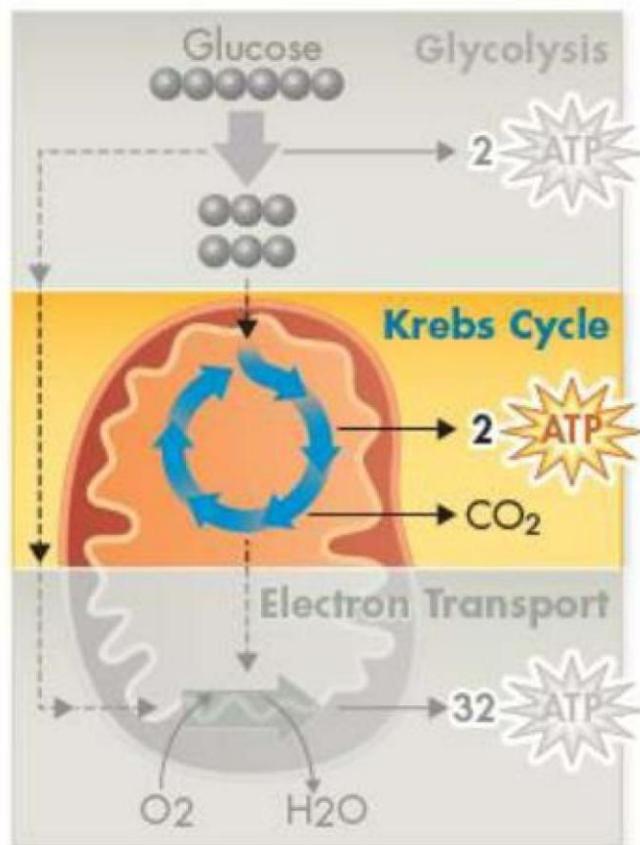
Movement to the Citric Acid Cycle

- Before the next stage can begin, pyruvic acid must first be transported inside the mitochondria.
- Pyruvic acid is combined with an enzyme called Coenzyme A. This enzyme helps with the transportation.
 - Pyruvic acid + Coenzyme A make Acetyl CoA
 - One more molecule of NADH is produced.
 - This also releases one molecule of CO₂ as a waste product.



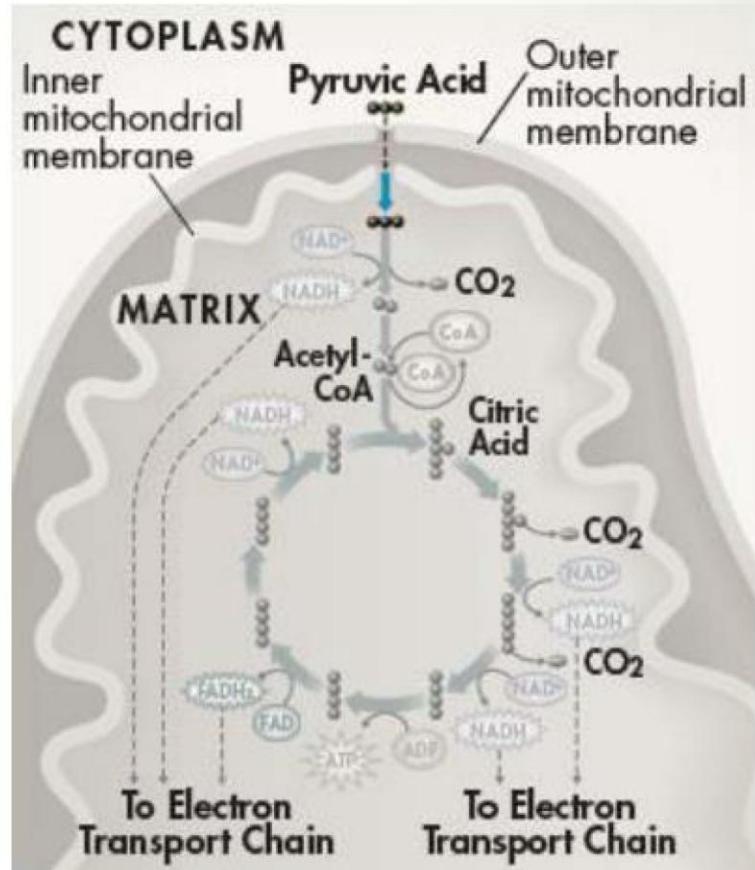
Krebs Cycle

- During the citric acid cycle, pyruvic acid produced in glycolysis is broken down into carbon dioxide and more energy is extracted.



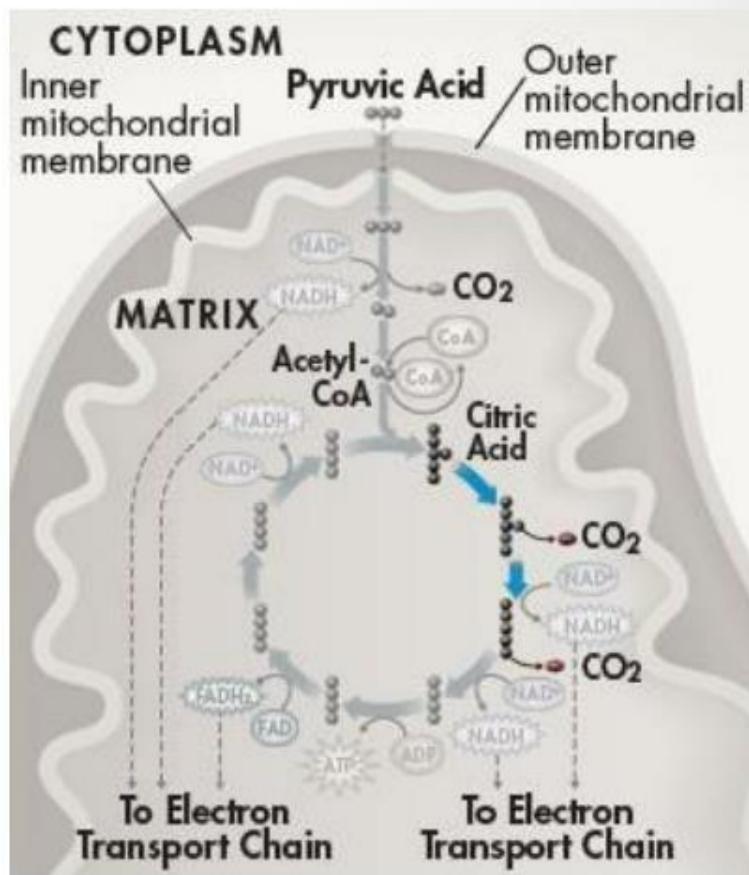
Citric Acid Cycle

- Acetyl-CoA from glycolysis enters the **matrix**, the innermost compartment of the mitochondrion.
- Once inside, the Coenzyme A is released.



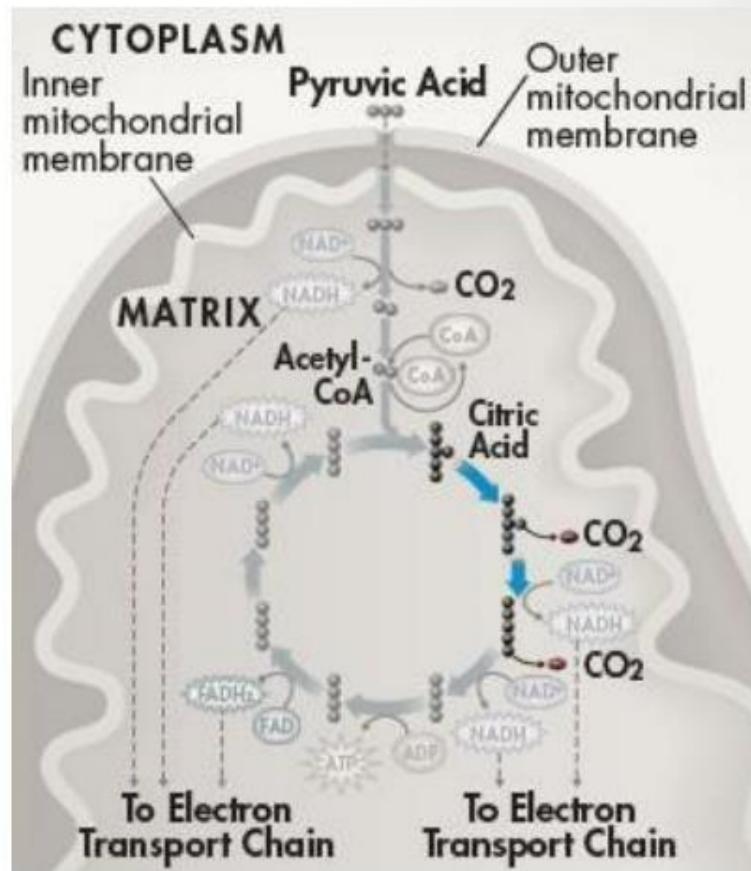
Citric Acid Cycle

- The molecule of acetate that entered from glycolysis joins up with another 4-carbon molecule already present.
- This forms citric acid.



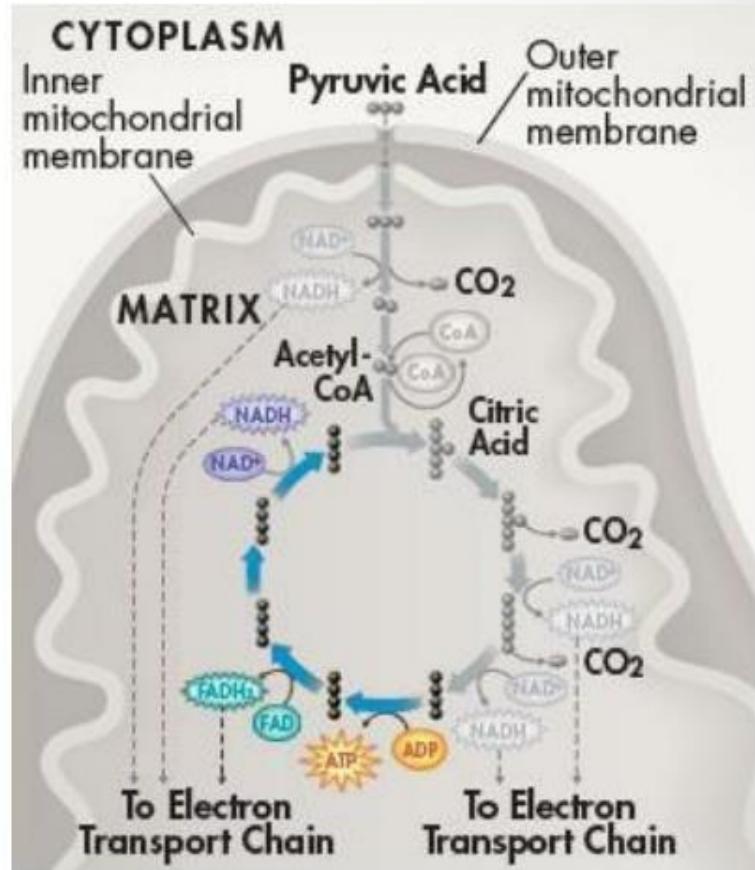
Citric Acid Cycle

- Citric acid (6-carbon molecule) is broken down one step at a time until it is a 4-carbon molecule.
- The two extra carbons are released as carbon dioxide.



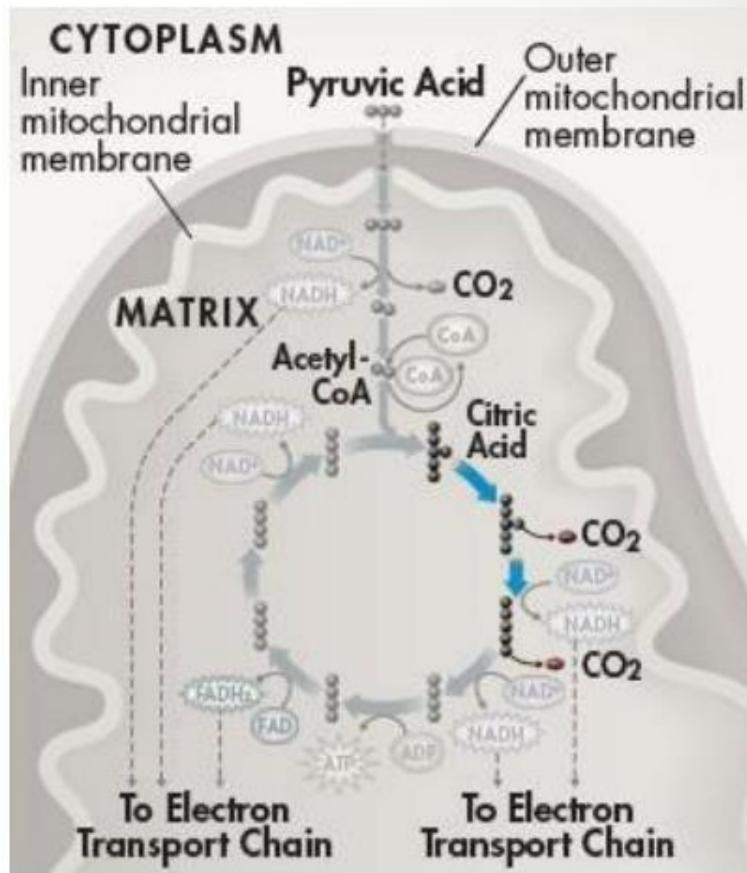
Citric Acid Cycle

- Energy released by the breaking and rearranging of carbon bonds is captured in the forms of ATP, NADH, and FADH₂.
- FADH₂ has the same purpose as NADH – to transport high-energy electrons and H⁺ ions.



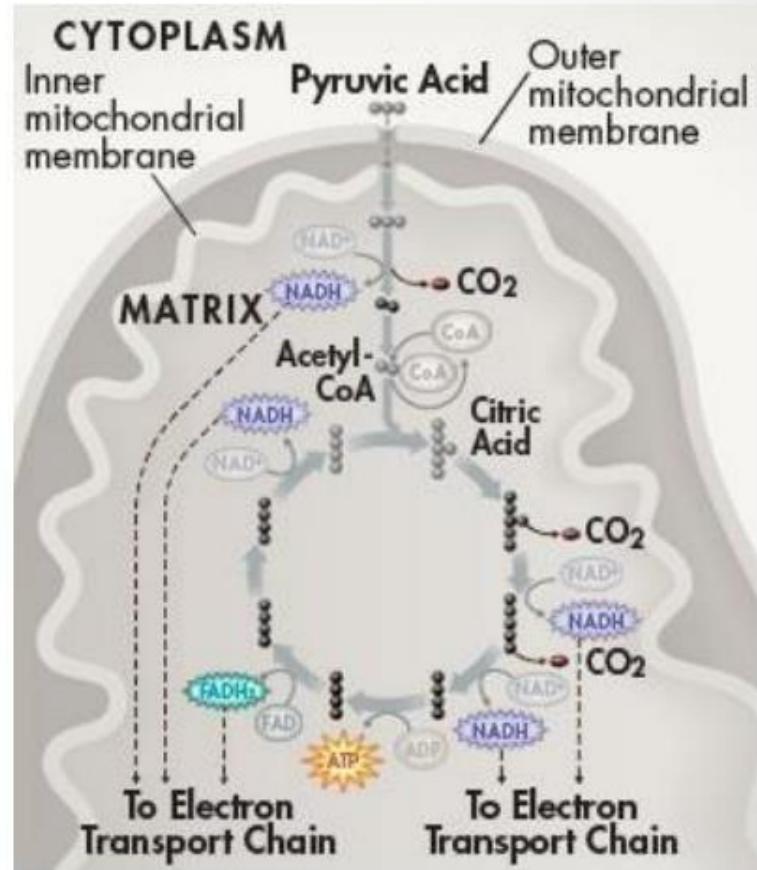
Citric Acid Cycle

- For each turn of the cycle, the following are generated:
 - 1 ATP molecule
 - 3 NADH molecules
 - 1 FADH_2 molecule



Citric Acid Cycle

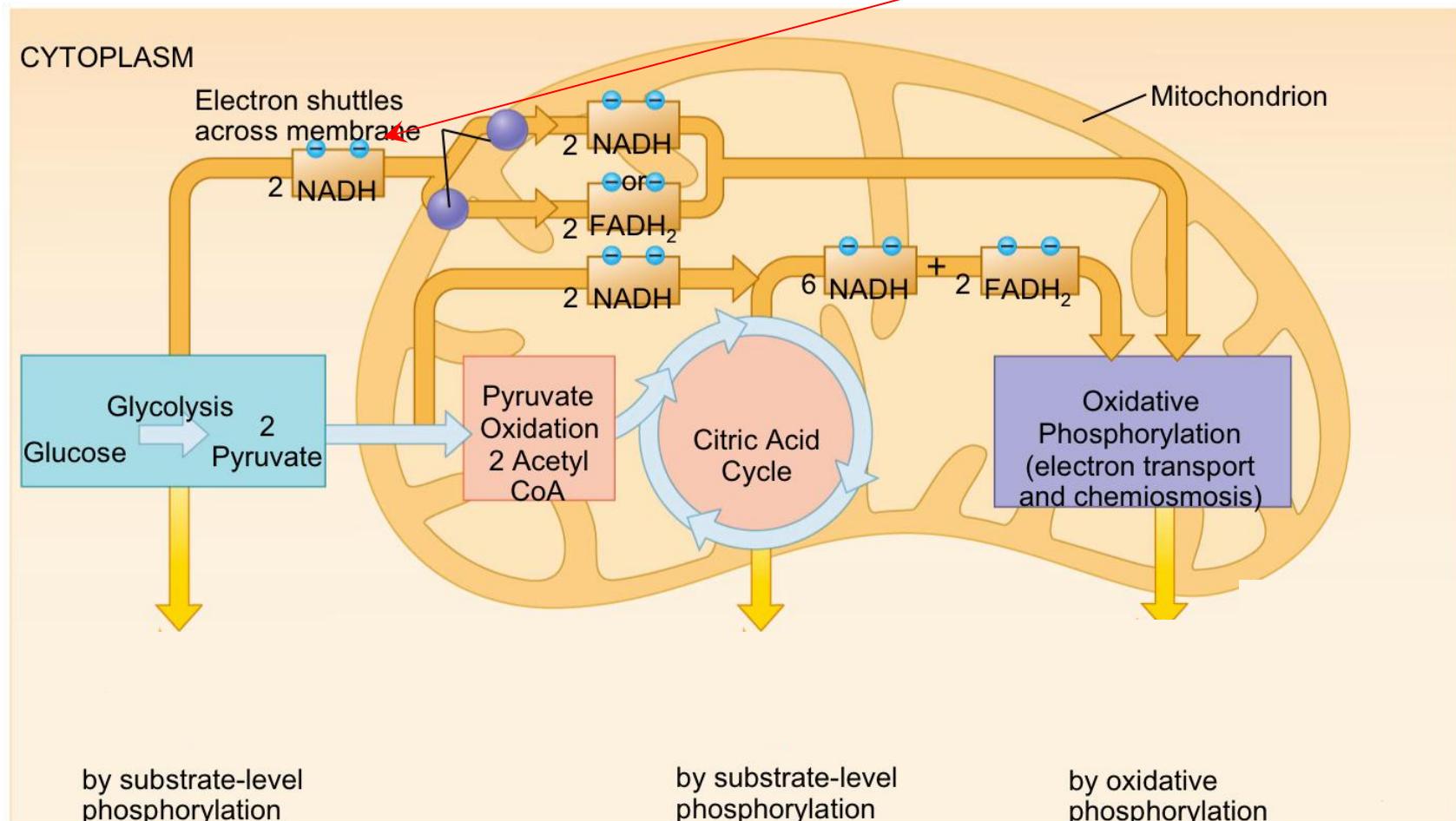
- Remember! Each molecule of glucose results in 2 molecules of pyruvic acid, which enter the Krebs cycle.
- So each molecule of glucose results in two complete “turns” of the Krebs cycle.
- Therefore, for each glucose molecule:
 - 6 CO₂ molecules,
 - 2 ATP molecules,
 - 8 NADH molecules,
 - 2 FADH₂ molecules are produced.





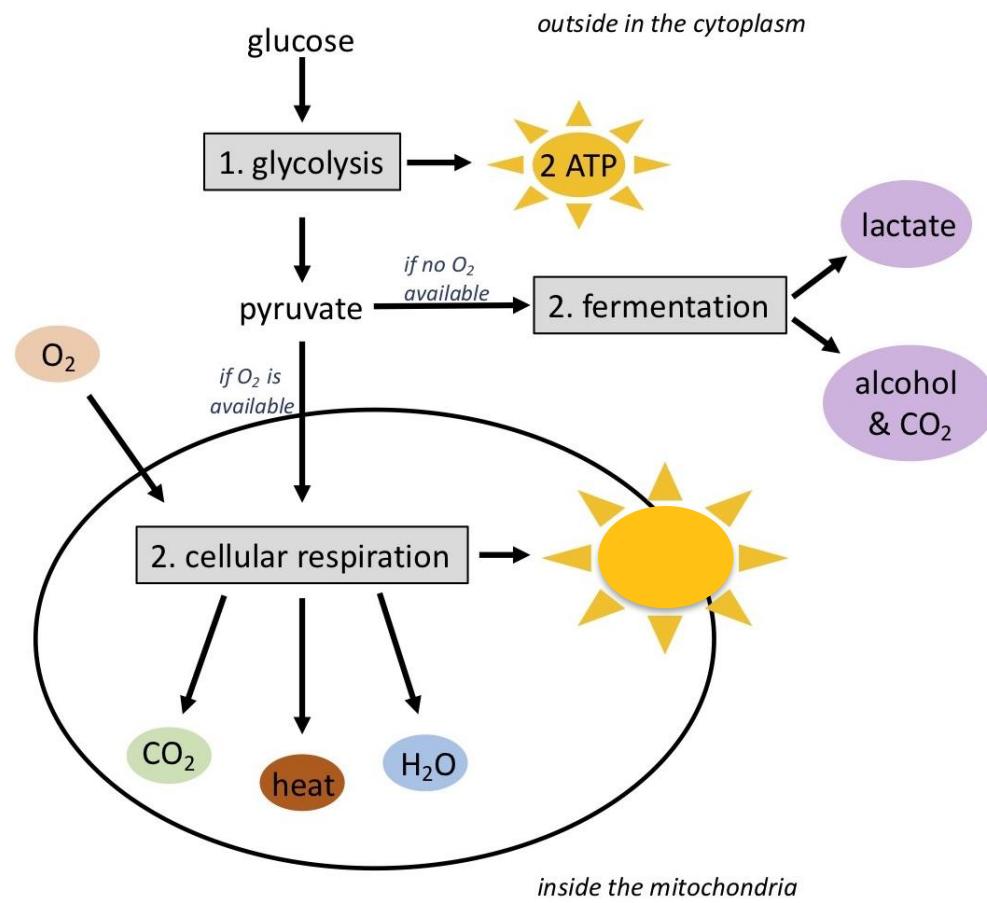
Energy Yield from the Complete Oxidation of One Molecule of Glucose

- $1 \text{ NADH} \rightarrow 2.5 \text{ ATP}$, $1 \text{ FADH}_2 \rightarrow 1.5 \text{ ATP}$
- For some cells, minus 2ATP when transporting these 2 NADH.



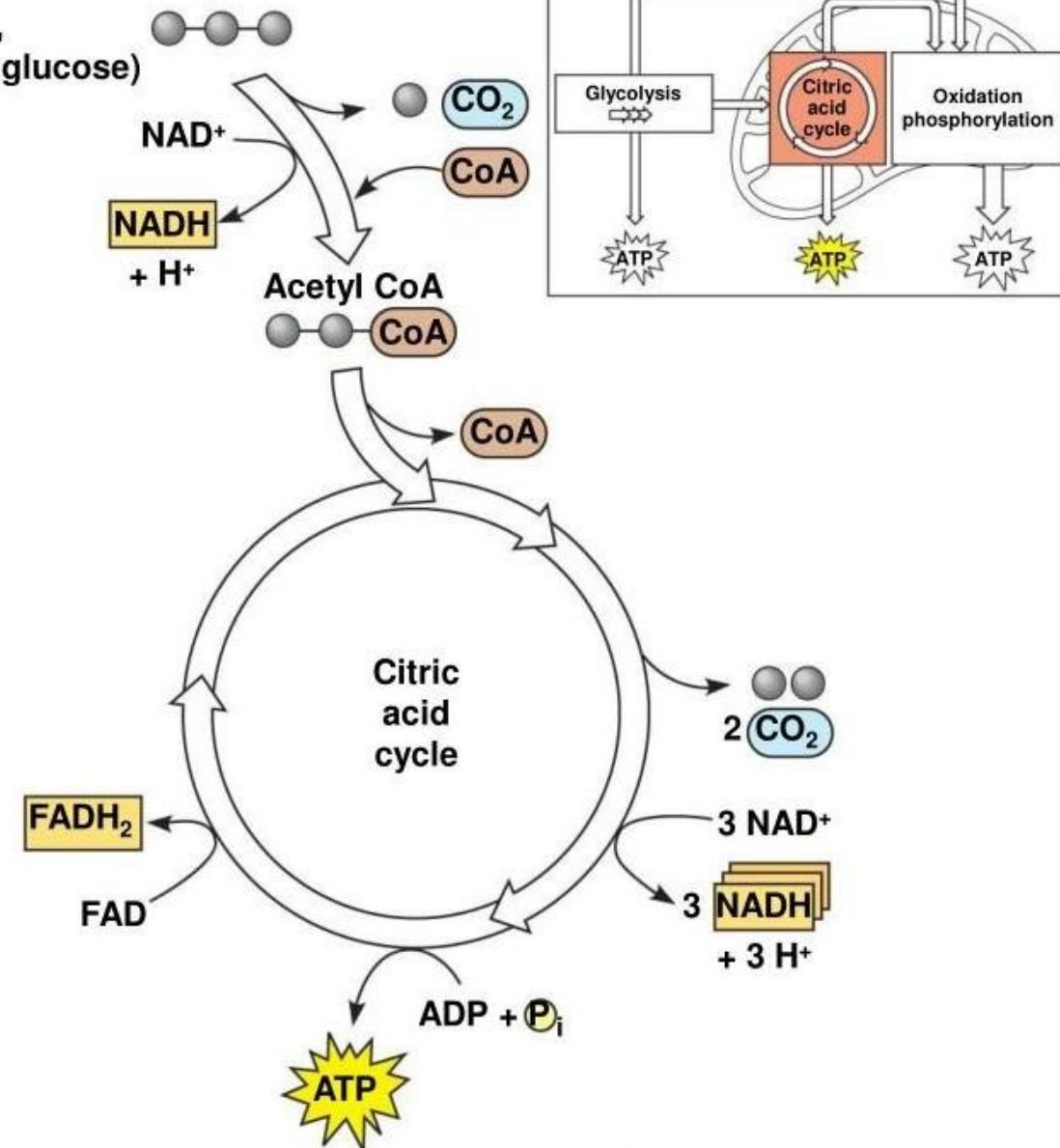


- During cellular respiration 30 ATP are created (including, using the 2 NADH from glycolysis) depending on the efficiency of the cell
- *Remember:* exergonic reactions are inefficient, so we will always have a byproduct of heat





Pyruvic acid
(from glycolysis,
2 molecules per glucose)



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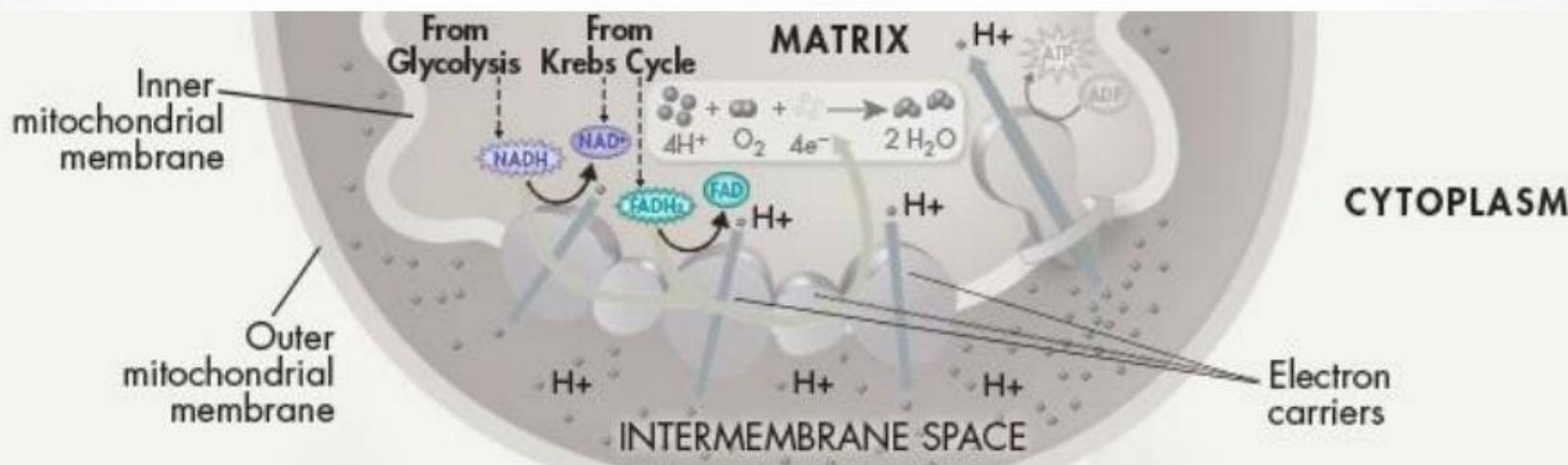
Process of ATP synthesis

Electron Transport Chain

- The electron transport chain occurs in the inner membrane of the mitochondria.
- Electrons are passed along the chain, from one protein to another.
- Each time the electron is passed, a little bit of energy is extracted from it.
- Electrons drop in energy as they go down the chain and until they end with O_2 , forming water

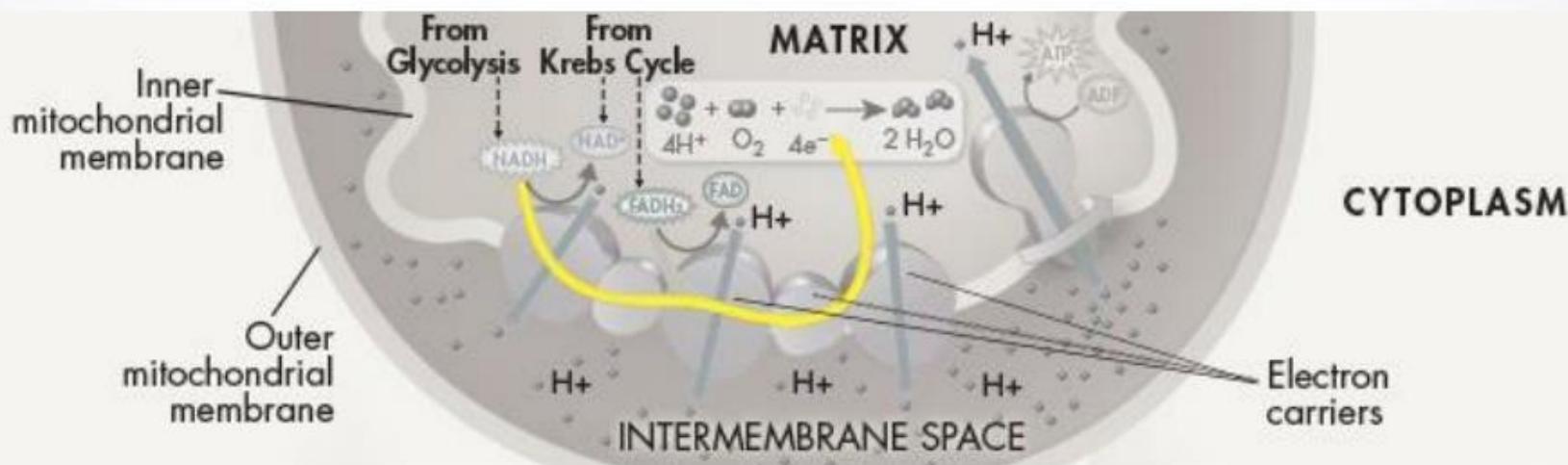
Electron Transport Chain

- NADH and FADH₂ pass their high-energy electrons to electron carrier proteins in the electron transport chain.



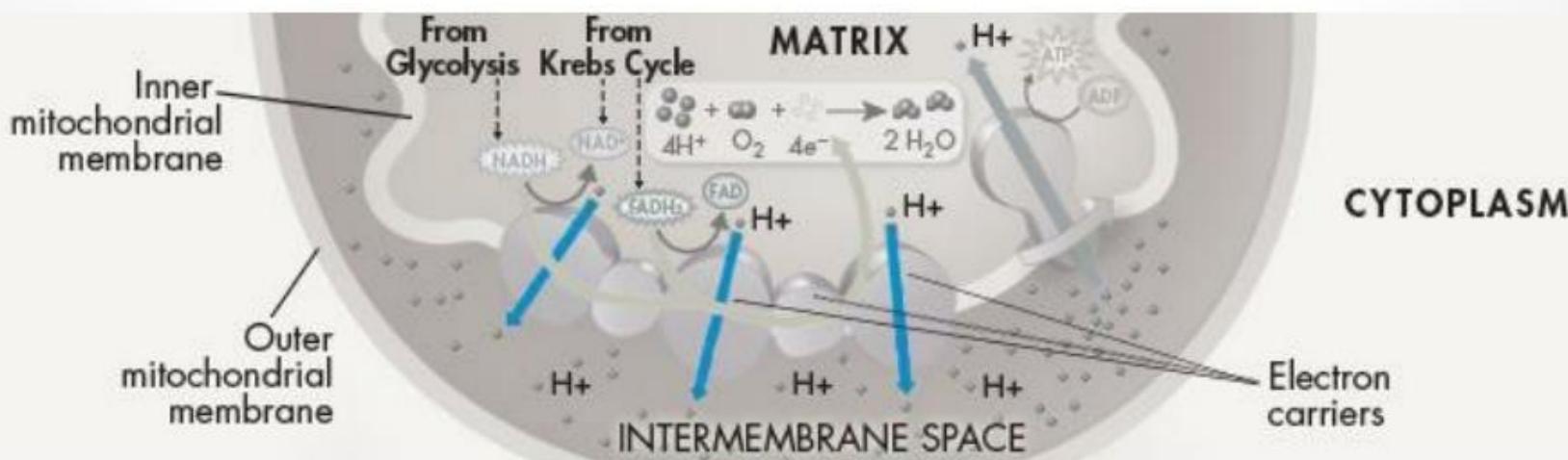
Electron Transport Chain

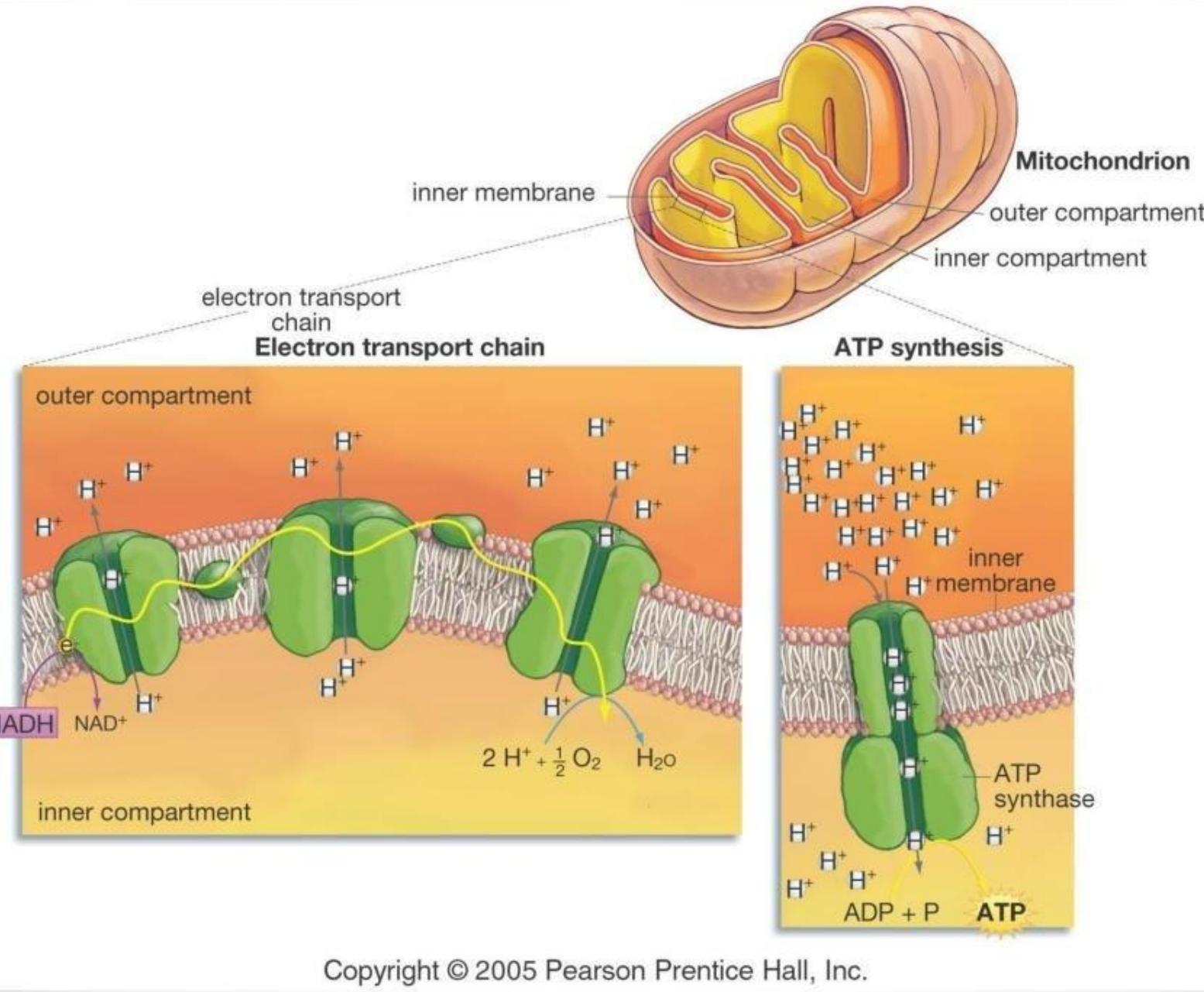
- At the end of the electron transport chain, the electrons combine with H⁺ ions and oxygen to form water.



Electron Transport Chain

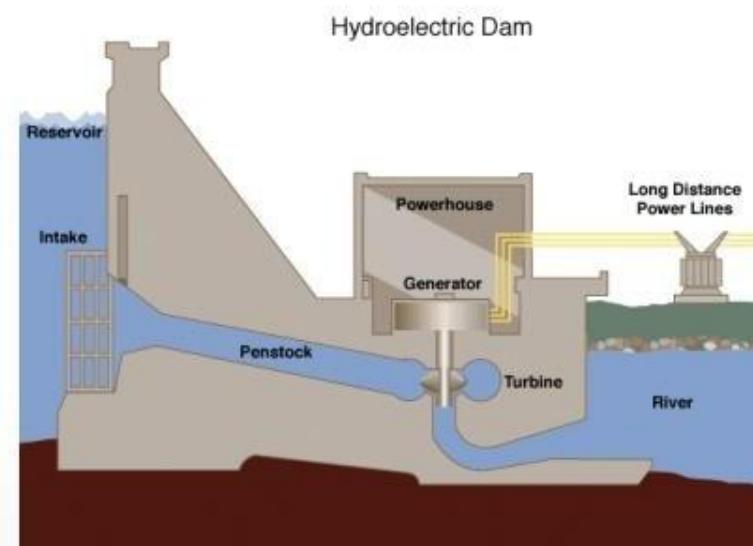
- Energy generated by the electron transport chain is used to move H⁺ ions (from NADH and FADH₂) against a concentration gradient.
- This creates a “dam” of H⁺ ions in the outer fluid of the mitochondria.





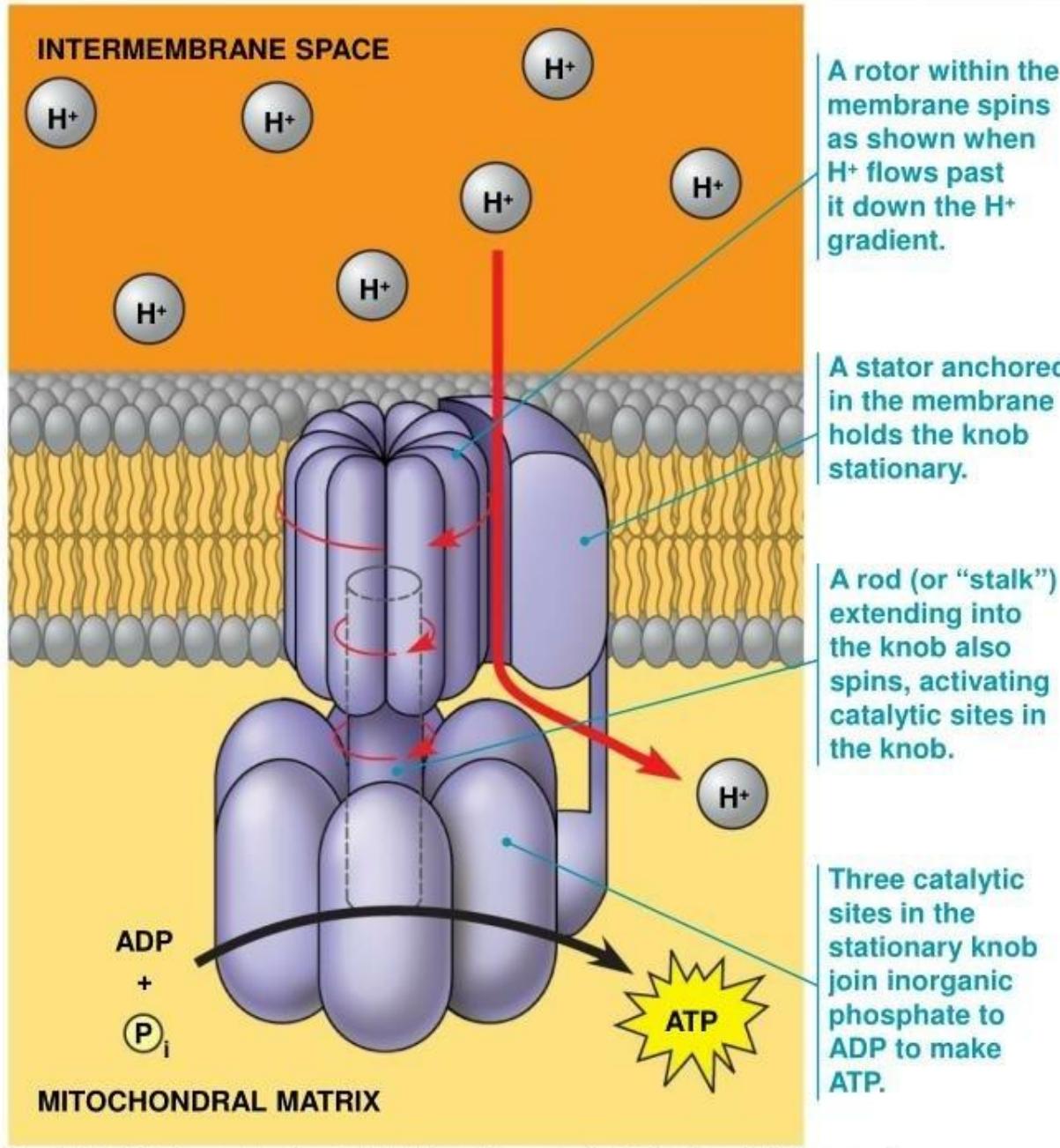
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- The electron transport chain generates no ATP
- The chain's function is to break the large free-energy drop from food to O₂ into smaller steps that release energy in manageable amounts.
- The end result is a “reservoir” of H⁺ ions that can be tapped for energy, much like a reservoir in a hydroelectric dam



Chemiosmosis

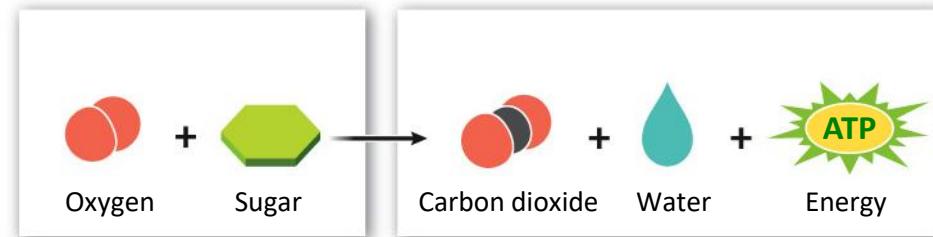
- The electron transport chain has created a high concentration of H⁺ ions in the outer fluid of the mitochondria.
- H⁺ then moves back across the membrane, into the inner fluid.
 - H⁺ ions pass through a channel protein called ATP Synthase
- ATP synthase uses this flow of H⁺ to convert ADP molecules (low energy) into ATP (high energy)





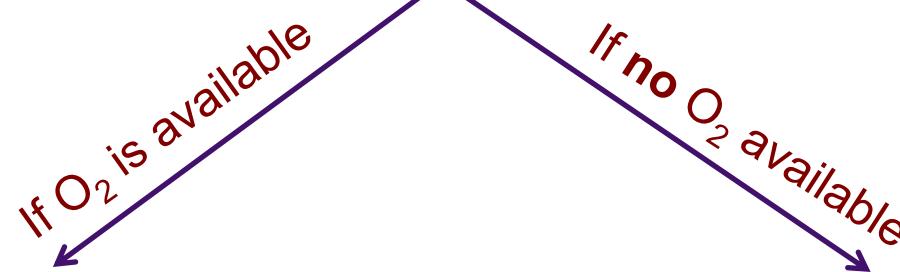
Remember: the energy in glucose can't be used directly – must first transfer it to an energy-carrier molecule like **ATP**

– we can then use ATP directly



- Glucose breakdown happens in 2 steps:

Step 1 = **glycolysis** (*in the cytoplasm of cells*)



Step 2 = **cellular respiration**
(*in the mitochondria*)

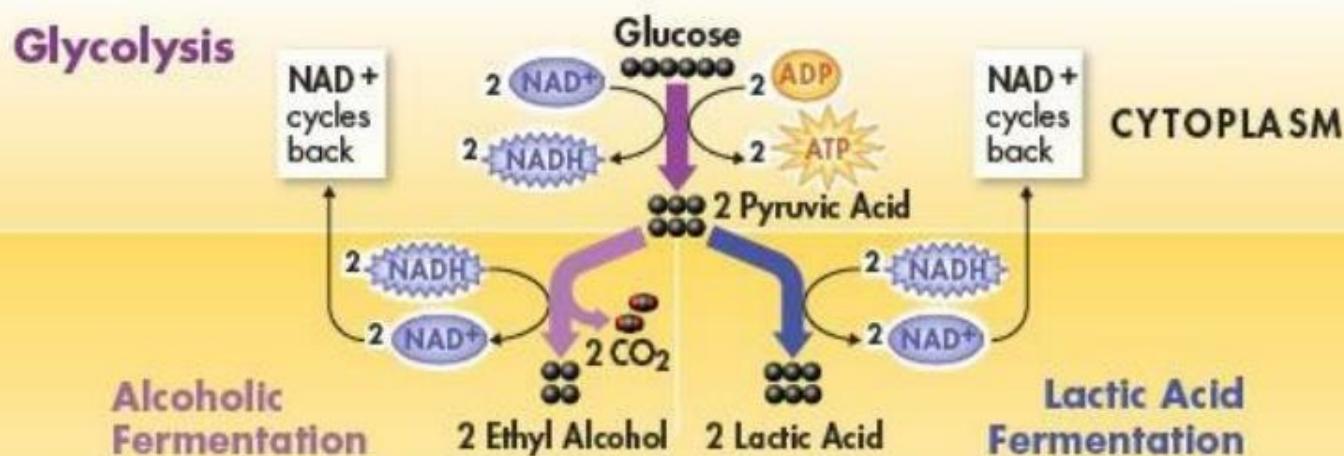
Step 2 = **fermentation**
(*in the cytoplasm*)

Fermentation

- Cellular respiration requires O_2 to produce ATP
- Glycolysis can produce ATP with or without O_2 (in aerobic or anaerobic conditions)
- In the absence of O_2 , glycolysis can couple with a process called fermentation to produce ATP.

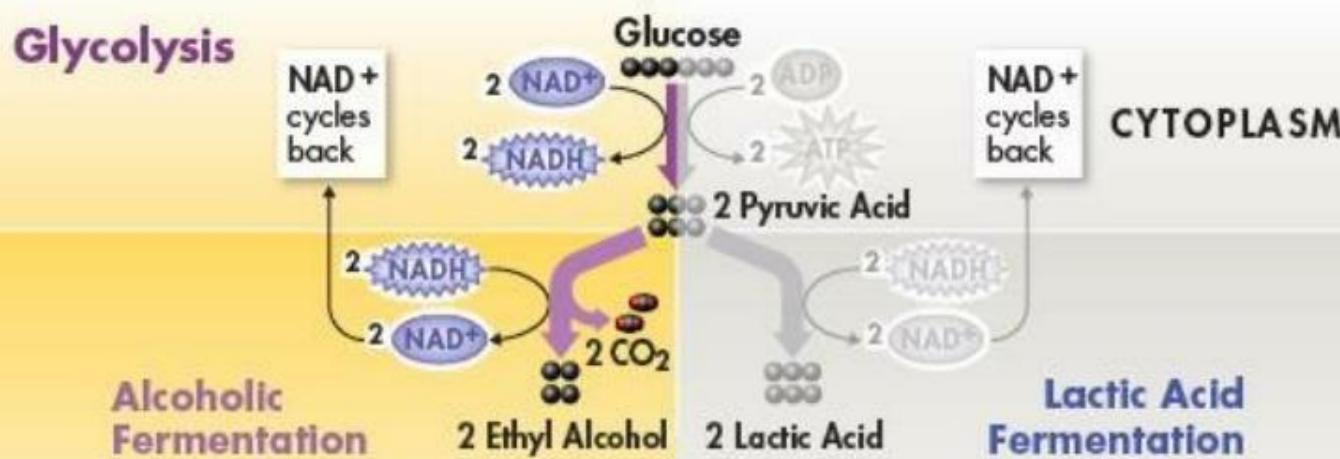
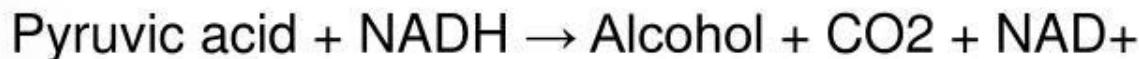
Types of Fermentation

- Fermentation consists of glycolysis + reactions that regenerate NAD⁺, which can be reused by glycolysis
- Two common types are alcohol fermentation and lactic acid fermentation



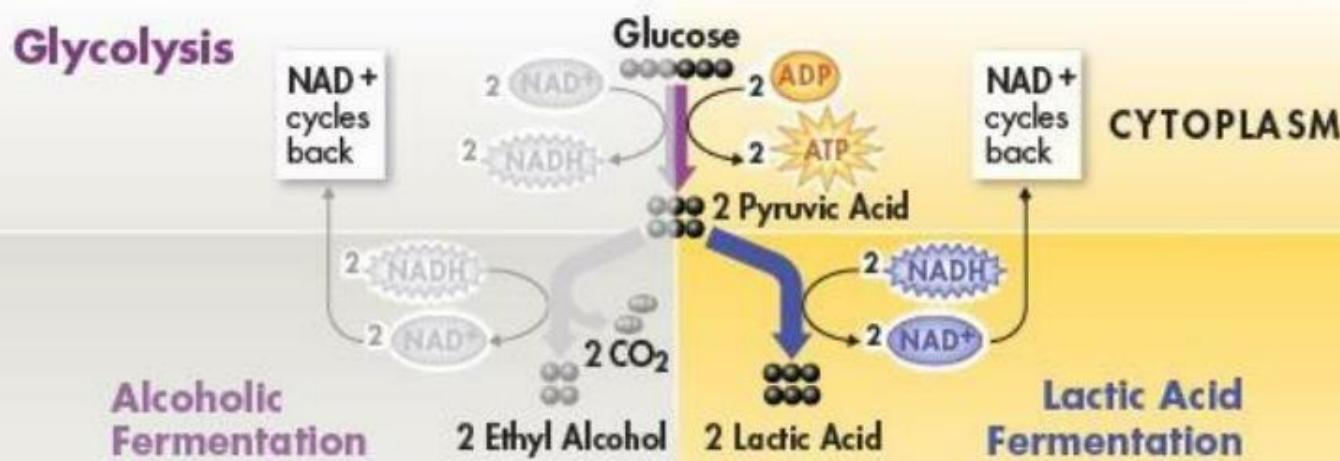
Alcohol Fermentation

- Yeast and a few other microorganisms use alcoholic fermentation that produces ethyl alcohol and carbon dioxide.
- This process is used to produce alcoholic beverages and causes bread dough to rise.



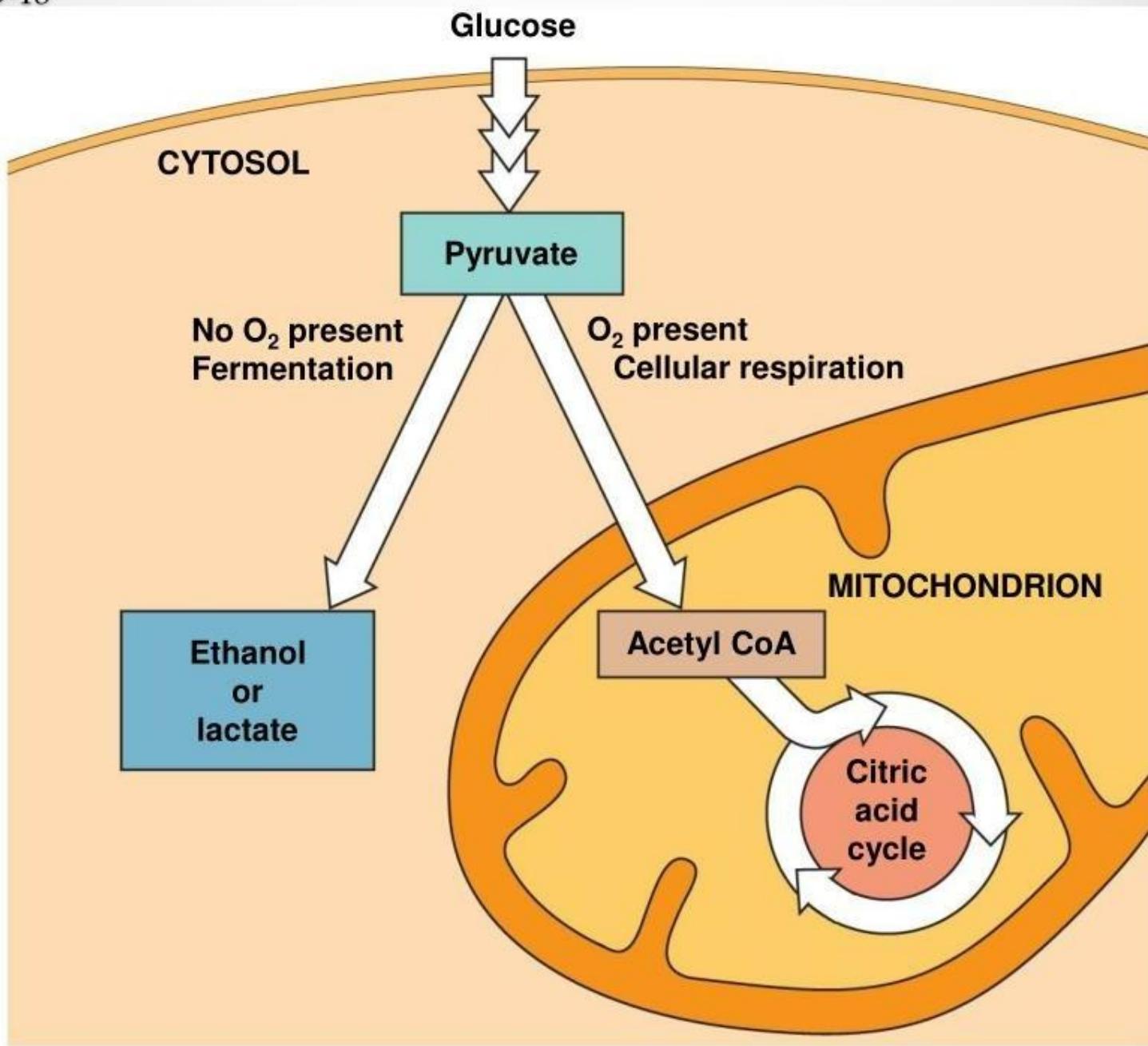
Lactic Acid Fermentation

- Most organisms, including humans, carry out fermentation using a chemical reaction that converts pyruvic acid to lactic acid.
- Pyruvic acid + NADH → Lactic acid + NAD⁺



- In lactic acid fermentation, pyruvate is reduced to NADH, the only end product is lactic acid. No carbon dioxide is released.
- Lactic acid fermentation by some fungi and bacteria is used to make cheese and yogurt
- Human muscle cells use lactic acid fermentation to generate ATP when O_2 is scarce (out of breath)
 - Result: Soreness!

- Yeast and many bacteria are facultative anaerobes, meaning that they can survive using either fermentation or cellular respiration
- Most other organisms cannot survive in the long-run using glycolysis and fermentation, they require oxygen.
 - These are obligate aerobic organisms.

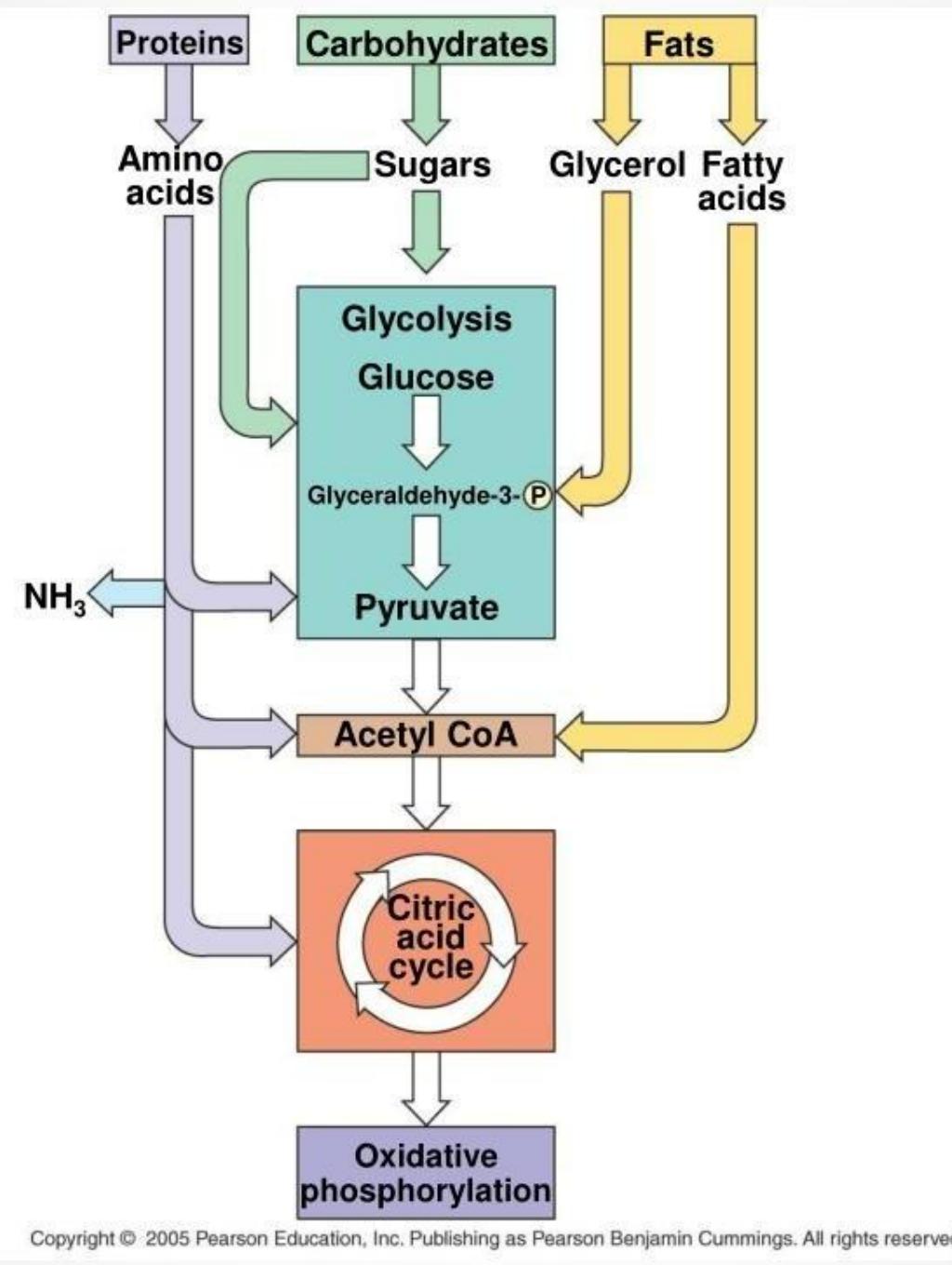


The Evolutionary Significance of Glycolysis

- Glycolysis occurs in nearly all organisms
- Glycolysis probably evolved in ancient prokaryotes before there was oxygen in the atmosphere

Other Energy Sources

- Catabolic pathways funnel electrons from many kinds of organic molecules into cellular respiration
- Glycolysis accepts a wide range of carbohydrates
- Proteins must be digested to amino acids; amino groups can feed glycolysis or the citric acid cycle
- Fats are digested to glycerol (used in glycolysis) and fatty acids (used in generating acetyl CoA)
- An oxidized gram of fat produces more than twice as much ATP as an oxidized gram of carbohydrate



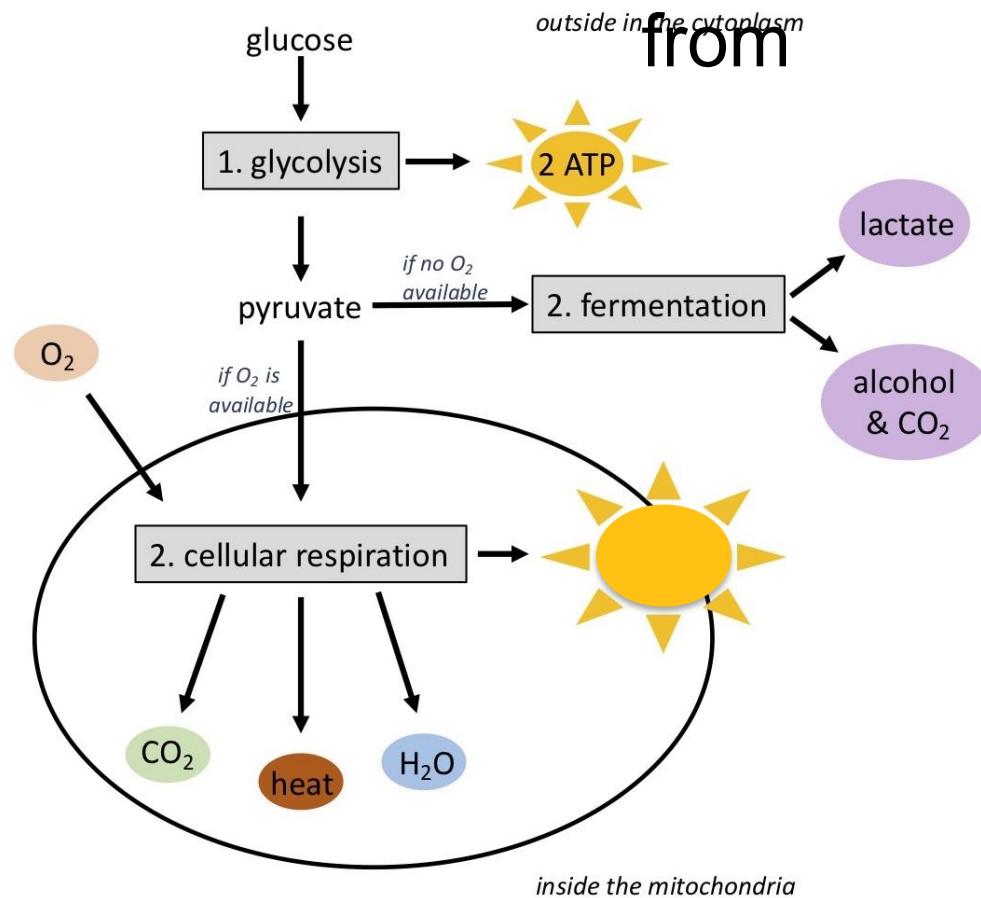


When O₂ is available:

– we got 2 ATP from glycolysis

– we got 30 ATP
cellular respiration

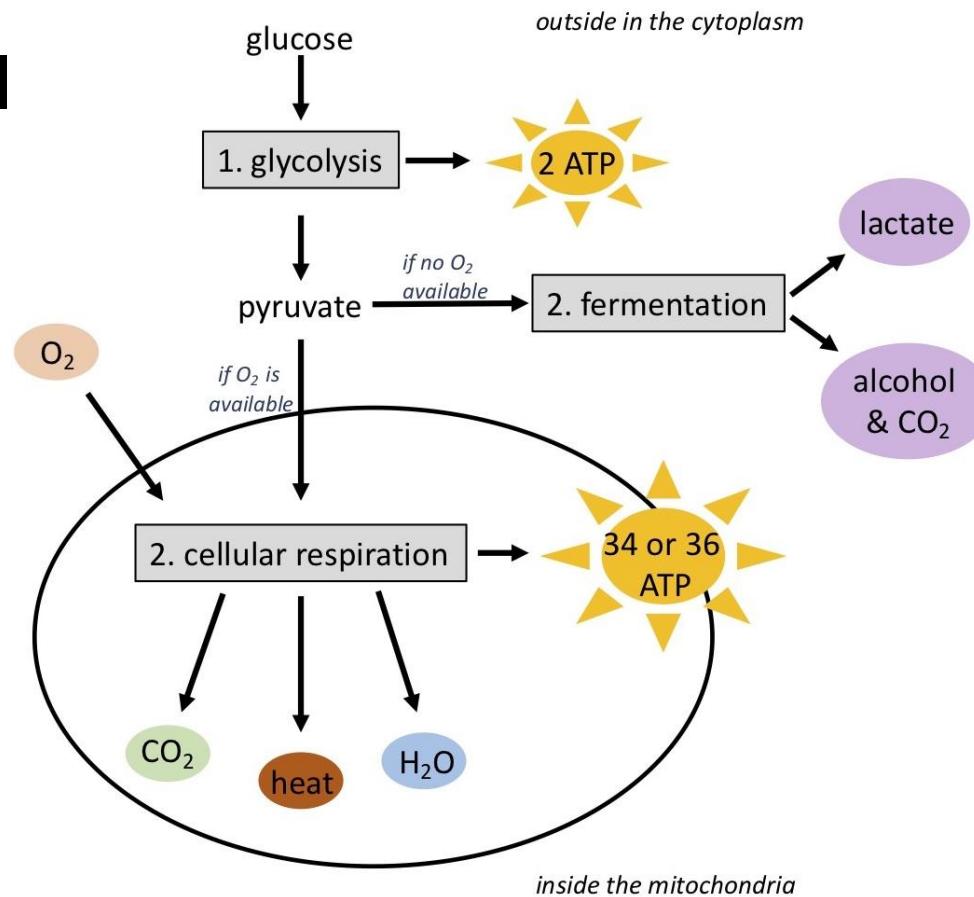
– so for each molecule
of glucose we break
down, we get a total
of **30-32 ATP**





Step 2 if O₂ is NOT available = **fermentation**

- e.g. muscles that are working hard use up O₂ very quickly → low O₂ = fermentation
- if no O₂, glycolysis still occurs (2 ATP), but pyruvate is not shipped into the mitochondria
- instead, pyruvate stays in cytoplasm & goes through fermentation



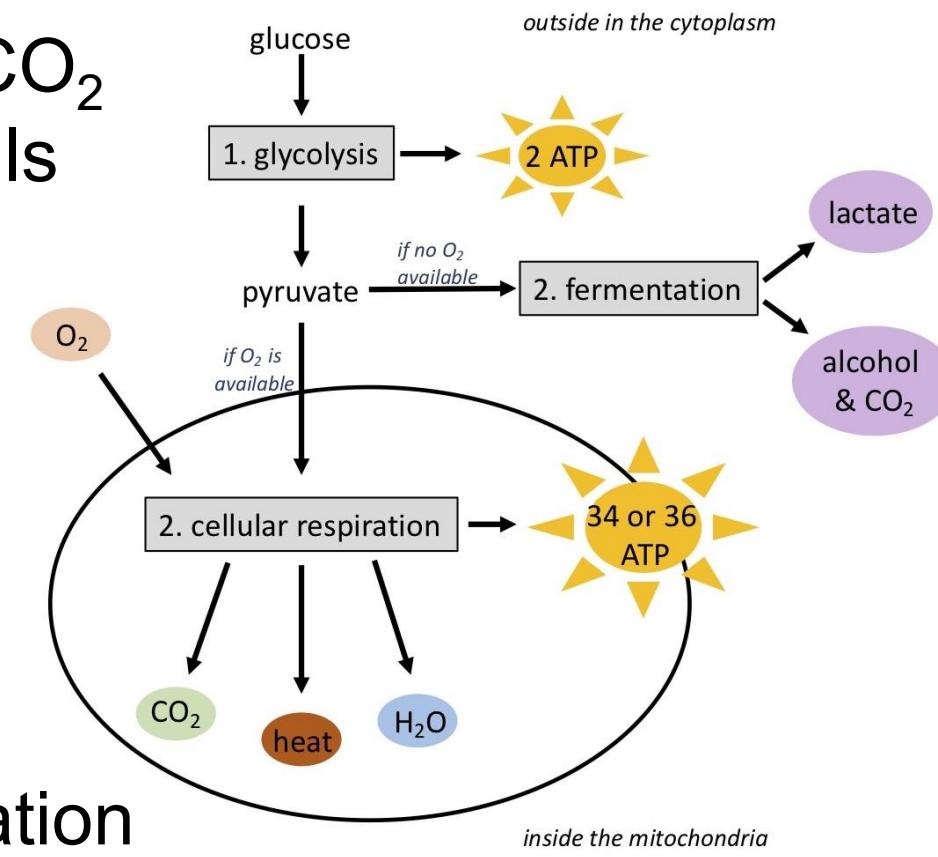


Fermentation makes no ATP

– Instead, turns pyruvate into:

- lactate (lactic acid) if in animal cells & some bacteria
- alcohol (ethanol) & CO₂ if in yeast & plant cells

– a small amount of fermentation is good: necessary to regenerate certain molecules used for cellular respiration





Lactic acid fermentation in animals

- When this builds up in muscles that are working hard, it can cause burning
 - Cleared very quickly, but athletes are experiencing this at certain times when they are “feeling the burn”

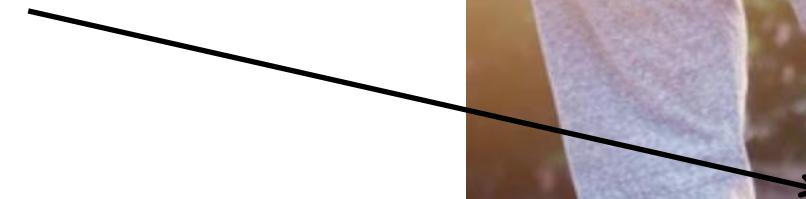


Figure: <https://www.shutterstock.com/image-photo/sore-muscles-legs-caused-exercise-1376564054>



Fermentation to make food products

- Lactic acid fermentation in bacteria is used to make foods like sauerkraut & yogurt
- Alcohol fermentation in yeast is used to make foods like beer, wine, & bread





A small amount of fermentation in cells is good, but we still need cellular respiration to function: need all that ATP energy from glucose to stay alive

- Blocking cellular respiration = unconsciousness, brain damage, & within minutes can cause death
 - e.g. stopping breathing/suffocation (*cellular respiration needs O₂ to make ATP*)
 - e.g. being poisoned with **cyanide** (*prevents O₂ from being used in the mitochondria*)
 - fastest acting poison: within minutes, just like suffocation



Lethal dose of cyanide



HOMEWORK (REPORT 6)

What is the maximum **NET** yield of ATP molecules that can be generated from a single molecule of glucose? Conversely, what is the minimum **NET** ATP output per glucose molecule?

*It should be noted that **NET** production is defined as total ATP produced minus the ATP consumed during the metabolic process.*



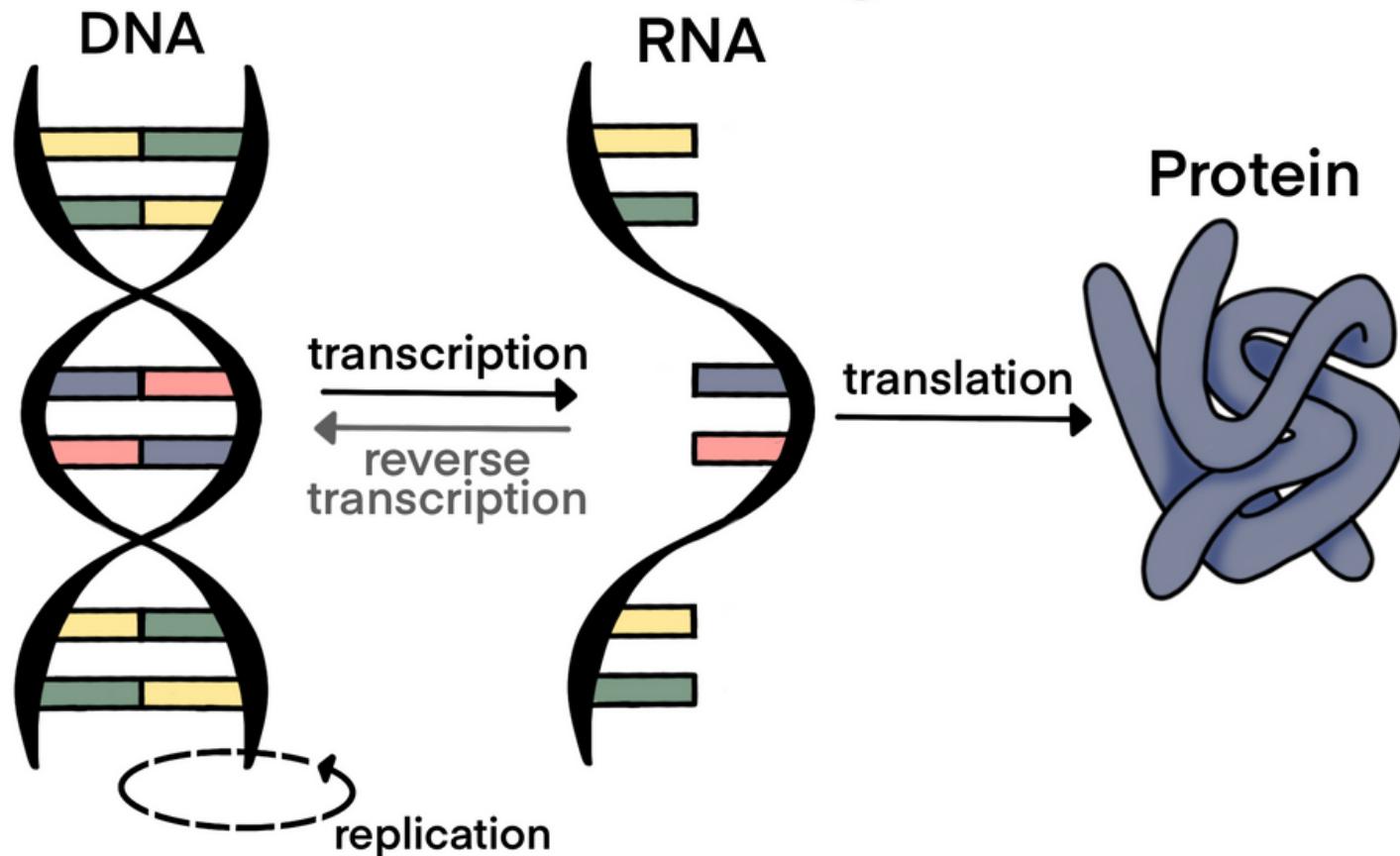
Materials of Life

Energy of Life

Information of Life



central dogma





DNA, Cell Division, & Inheritance Unit

- *Remember from chapter 1:*
 - life reproduces itself (with DNA), grows, & develops
- *Remember from chapter 3:*
 - all cells contain DNA that is duplicated & passed on
- Chapter 7 = How do we get from DNA to walking & talking us?
- Chapter 8 = How does DNA duplicate itself & how do we grow?
- Chapter 9 = How do we pass on DNA to reproduce?



Chapter 7: DNA Structure & Gene Function

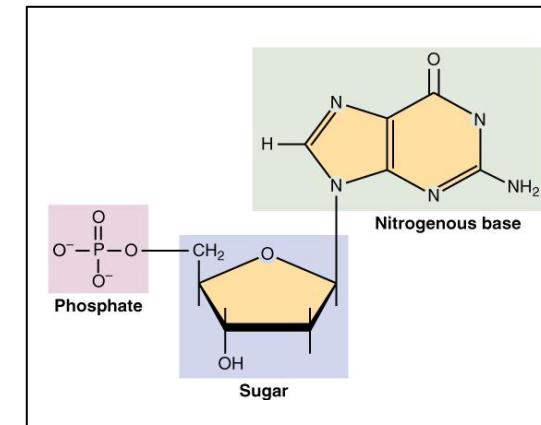
- What is the structure of DNA?
- How does DNA code for traits?
- How are genes regulated?
- How do mutations affect genes?

Corresponds with OpenStax Biology 2e Chapters 15 & 16



What is the structure of DNA?

- *Remember:* DNA (deoxyribonucleic acid) is a nucleic acid (polymer) made up of nucleotides (monomers)
- *Remember:* all nucleotides have at least 1 phosphate, a sugar, & a base
 - In DNA: always 1 phosphate & same sugar (deoxyribose)
 - Base can be any 1 of 4 though



one nucleotide

Figure: https://commons.wikimedia.org/wiki/File:0322_DNA_Nucleotides.jpg

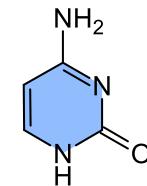


A nucleotide can have 1 of 4 bases

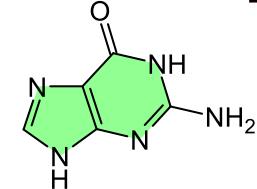
- Adenine: A
- Guanine: G
- Thymine: T
- Cytosine: C

- Even though it's only the base that changes, the entire nucleotide is often referred to by the letter representing the base (A, G, T, or C)

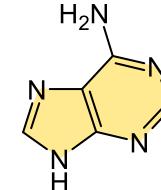
Cytosine C



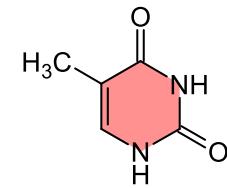
Guanine G



Adenine A



Thymine T



Nucleobases
of DNA

Figure: https://commons.wikimedia.org/wiki/File:Difference_DNA_RNA-EN.svg



The secrets of DNA function are found in the 3D structure of DNA

– DNA = a **double helix**

- **Double** = two strands connect together (like a ladder)
- **Helix** = the nucleotide strands are then twisted like a corkscrew or circular staircase

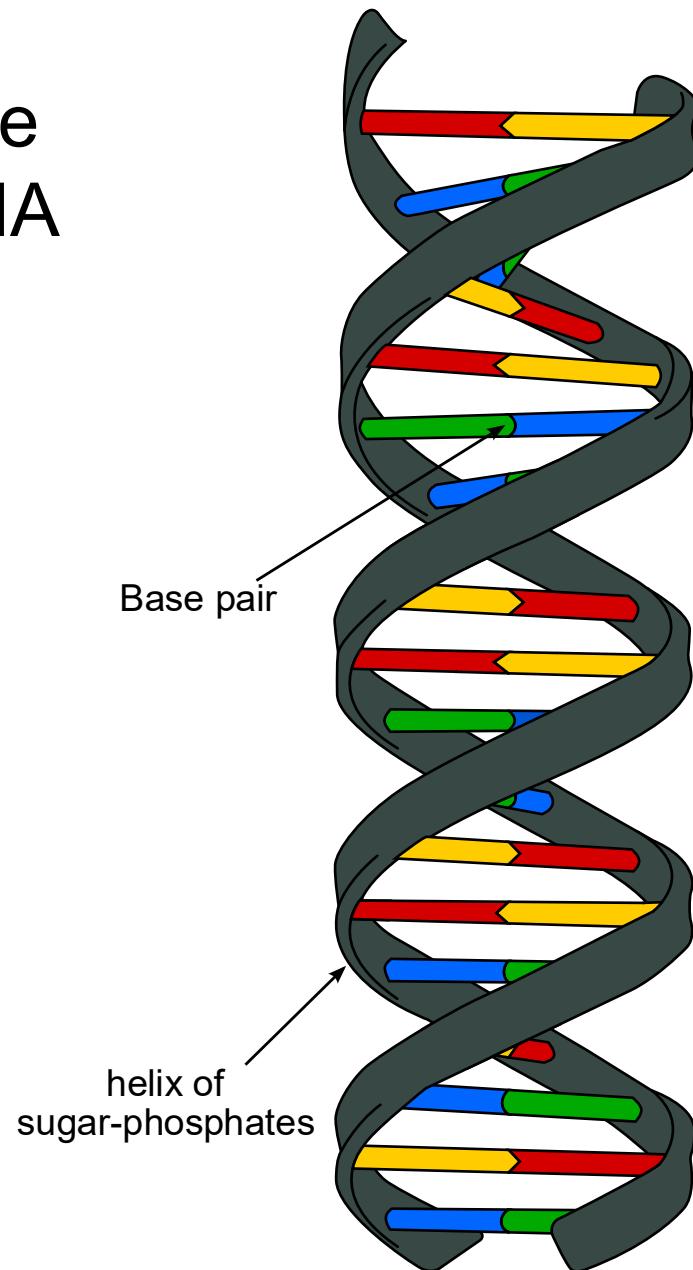


Figure: https://commons.wikimedia.org/wiki/File:Difference_DNA_RNA-EN.svg



Within each DNA strand, the phosphate group of one nucleotide binds to the sugar of the next nucleotide in the same strand

- Bond is covalent (**strong!**)
- The sugar & phosphate portions of DNA make up the **sugar-phosphate backbone**
- The 2 strands run **antiparallel** (in opposite directions)

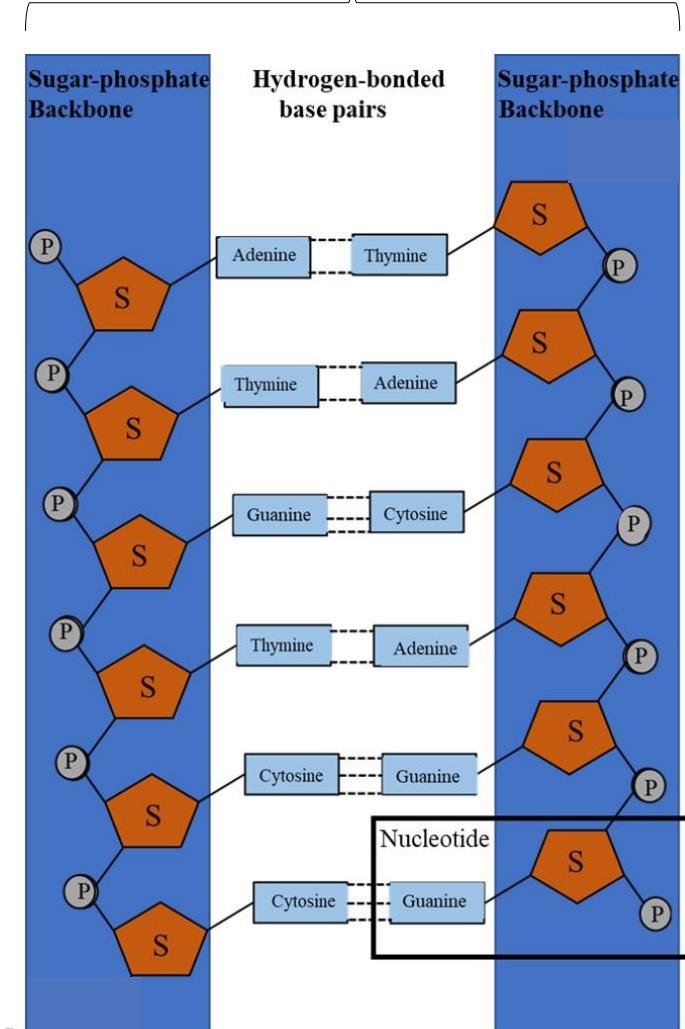
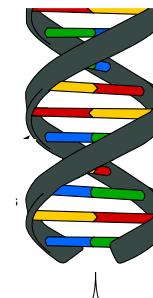


Figure: https://commons.wikimedia.org/wiki/File:DNA_molecular_structure,_showing_individual_nucleotides_and_bonds.jpg



The 2 strands are held together through bonds between the bases (making the “rungs” of the ladder)

- Hydrogen bonds hold bases together (**weak**)
- Bases pair in an exact combination: **complimentary base pairs**
 - A always binds with T
 - G always binds with C

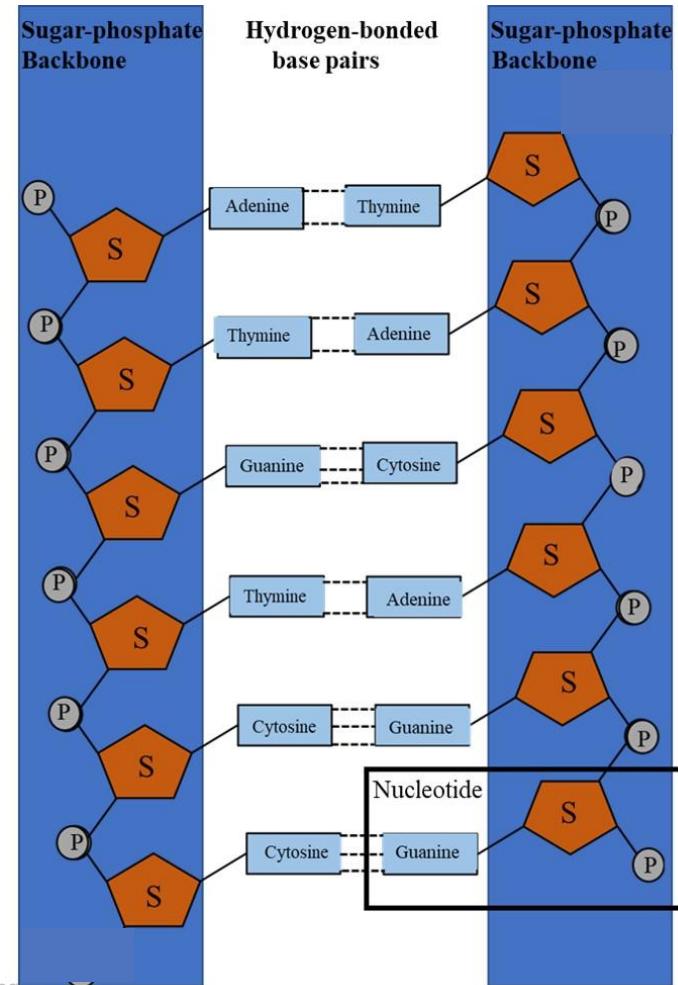


Figure: https://commons.wikimedia.org/wiki/File:DNA_molecular_structure,_showing_individual_nucleotides_and_bonds.jpg



How does DNA code for traits?

- Remember: the nucleus of a cell contains its chromosomes, which are made up of DNA (& proteins)

- Sequences of DNA that code for a specific protein/trait = **genes**

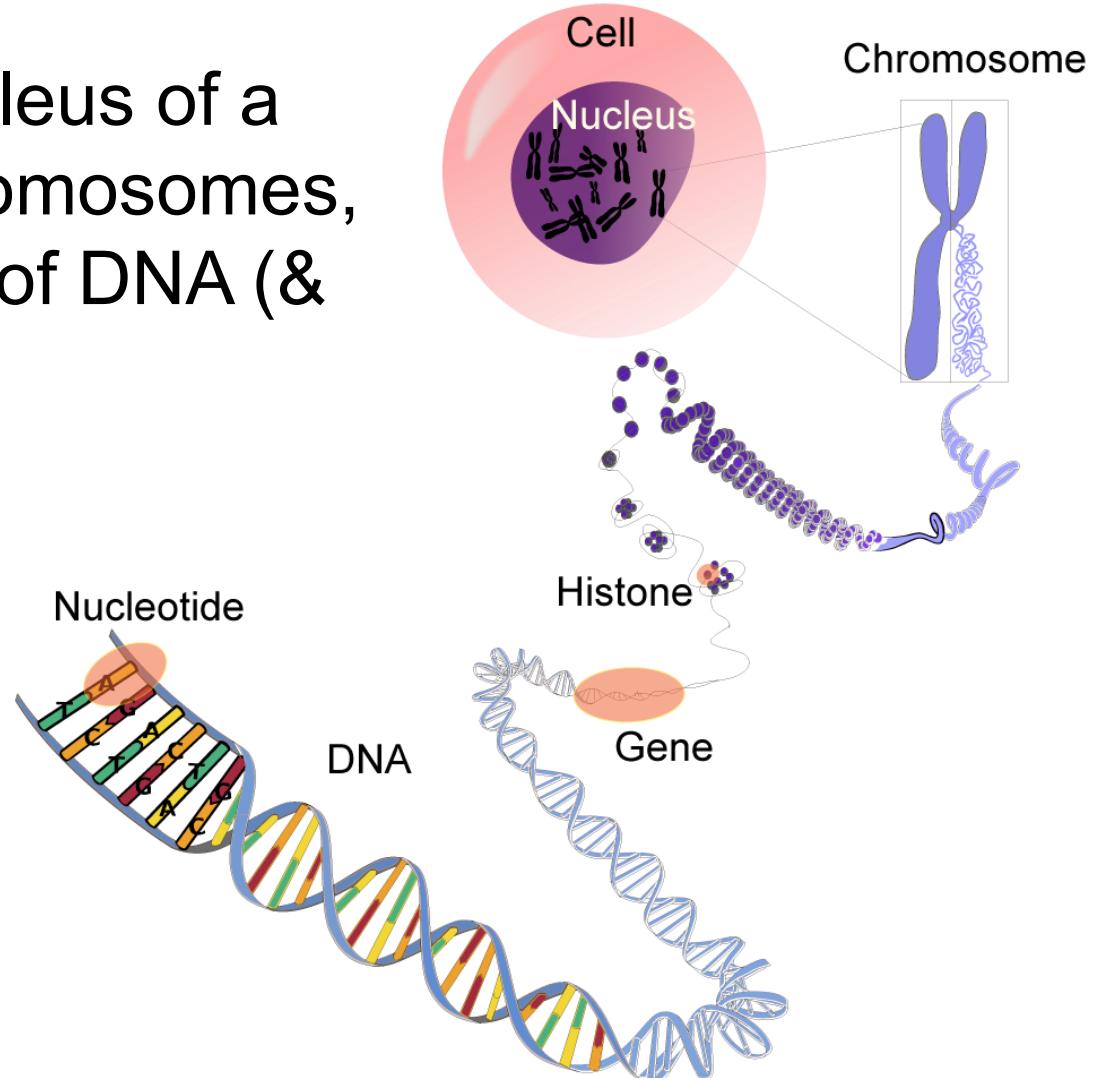


Figure: <https://commons.wikimedia.org/wiki/File:DNA-terminology.png>



- Genes are usually hundreds or thousands of nucleotides long (ATGCCTAAATCGGTA....)
- Genes code for specific proteins, which is how we get our **traits**

e.g. our skin, hair, & eye color (traits) are caused by melanin pigment proteins that are coded for by genes

e.g. our ability to see the colors red & green (a trait) is caused by a protein in the eye, which is coded for by a gene



Figure: https://commons.wikimedia.org/wiki/File:Kelly_Rowland_1.jpg

Figure: <https://pxhere.com/en/photo/903073>

Figure: https://meta.wikimedia.org/wiki/Grants:IEG/Color_blindness_content_checker



- Proteins do nearly everything, including make up us
- DNA holds the blueprints, coding the information on what kind of proteins (& how many of each) to make
 - So we know that to make up walking & talking us, there is a flow of information from DNA → proteins
 - HOWEVER, there is a problem:

- DNA is locked inside the nucleus
- Proteins are made at ribosomes & the rough ER (endoplasmic reticulum) OUTSIDE the nucleus

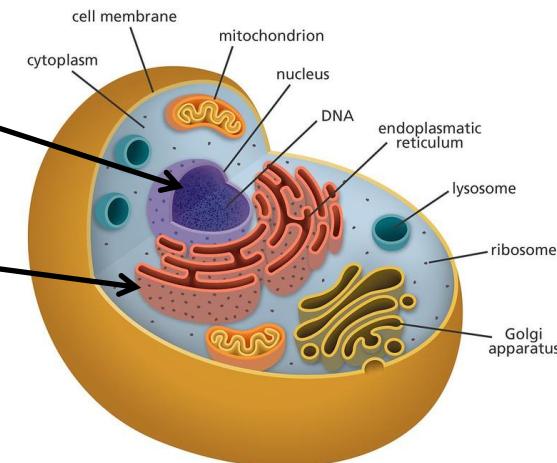


Figure: <https://www.flickr.com/photos/yourgenome/26676266160>



- We must have a middle man to take the information from DNA & transfer the instructions to proteins
 - the middle man = **RNA**

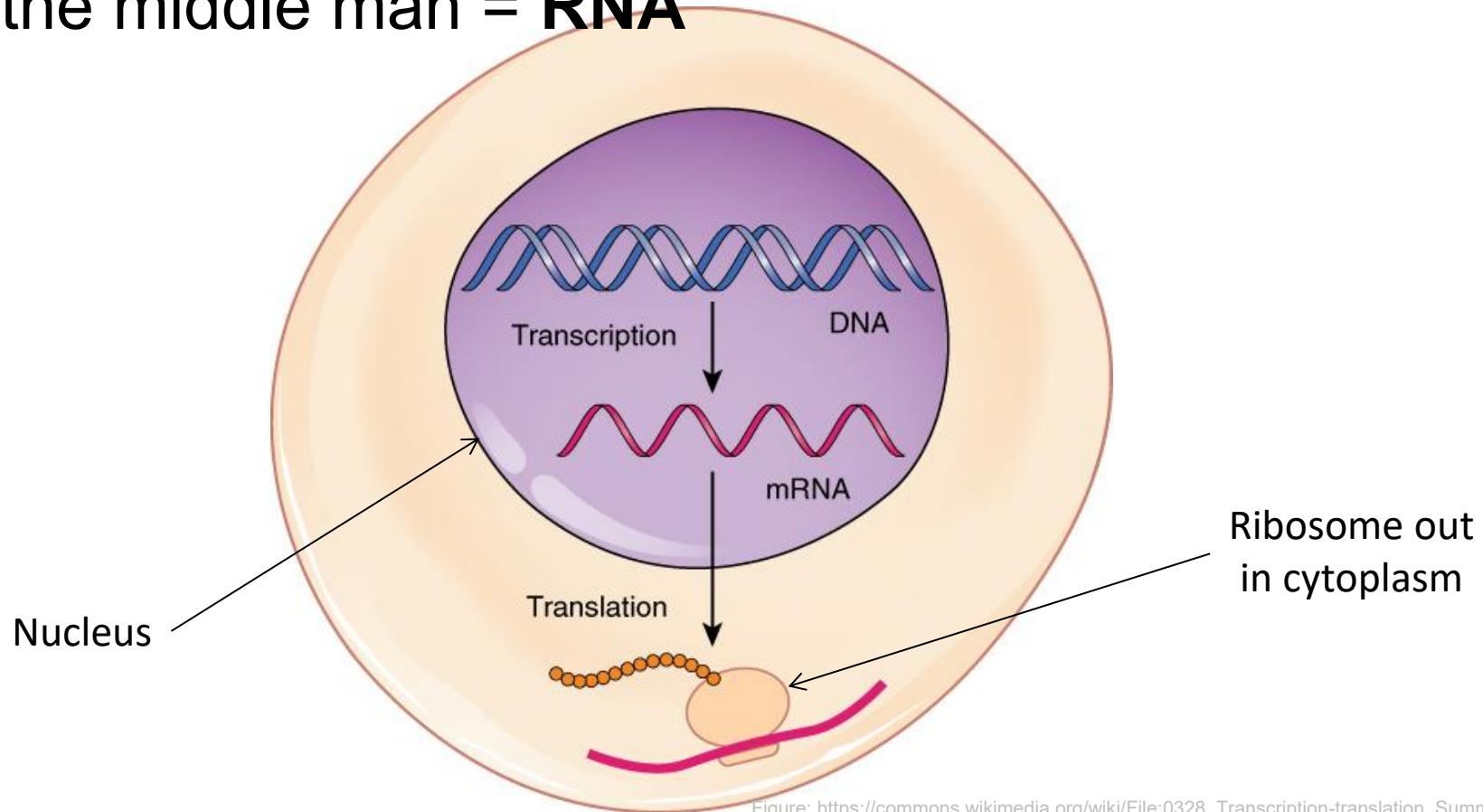


Figure: https://commons.wikimedia.org/wiki/File:0328_Transcription-translation_Summary.jpg



- **RNA** (ribonucleic acid) is a nucleic acid like DNA, but differs in a few key ways:

- has a different sugar (ribose)
- is single stranded
- does not contain the base T instead has the base U (uracil)

so RNA bases = A **U** C G

in RNA, G still pairs with C but
A pairs with U

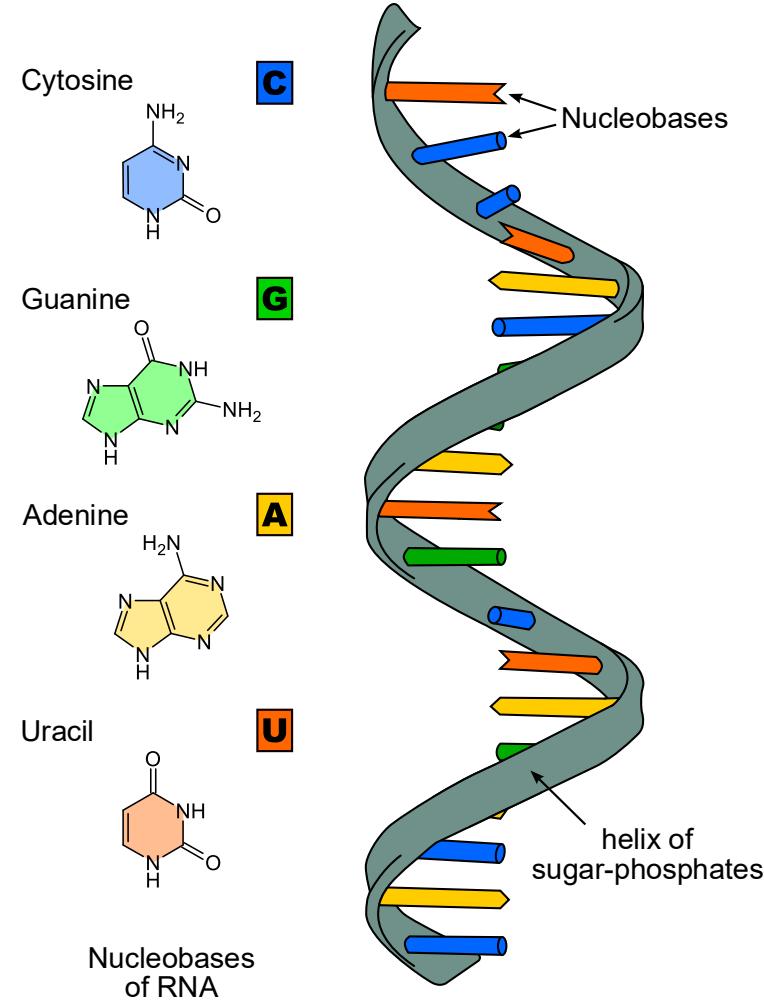
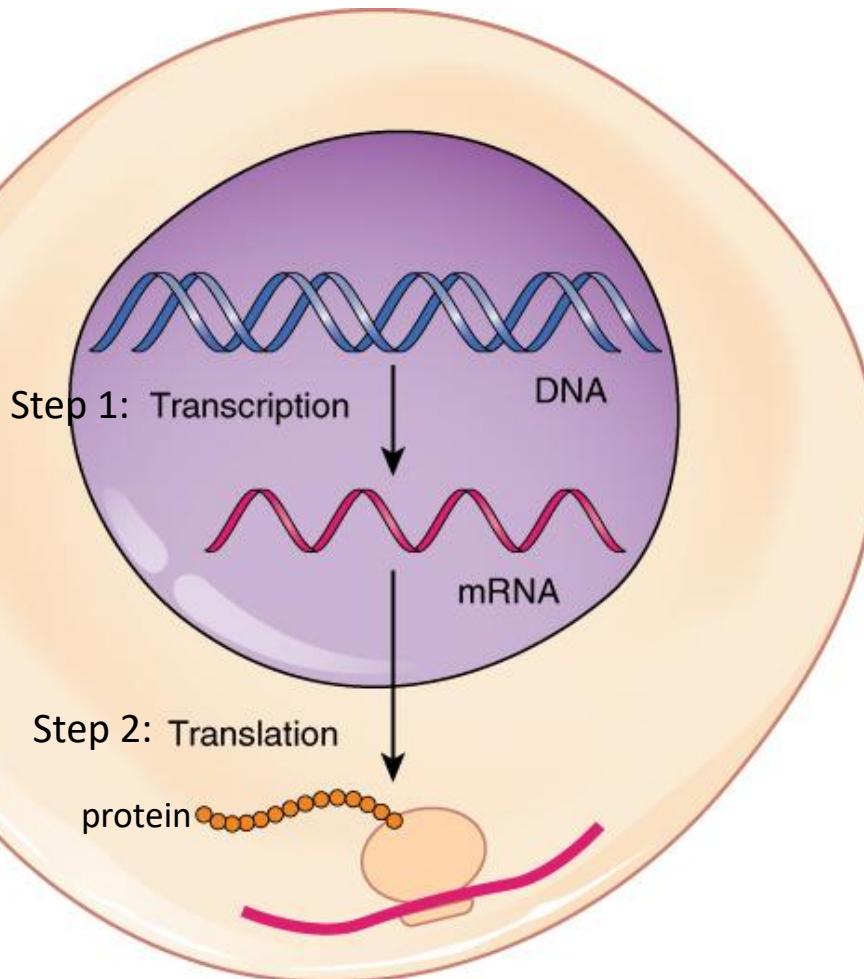


Figure: https://commons.wikimedia.org/wiki/File:Difference_DNA_RNA-EN.svg

- Getting from DNA to proteins is a 2 step process



Step 1: DNA → mRNA
is called **transcription**

Step 2: RNA → protein
is called **translation**

Figure: https://commons.wikimedia.org/wiki/File:0328_Transcription-translation_Summary.jpg



- DNA codes for proteins/traits: STEP 1 = transcription

- **Transcription = DNA → mRNA**

- the information in DNA is copied to RNA inside the nucleus
 - the RNA is acting as the middle man, so it is called **messenger RNA (mRNA)**
 - *there are other types of we'll bring up soon*

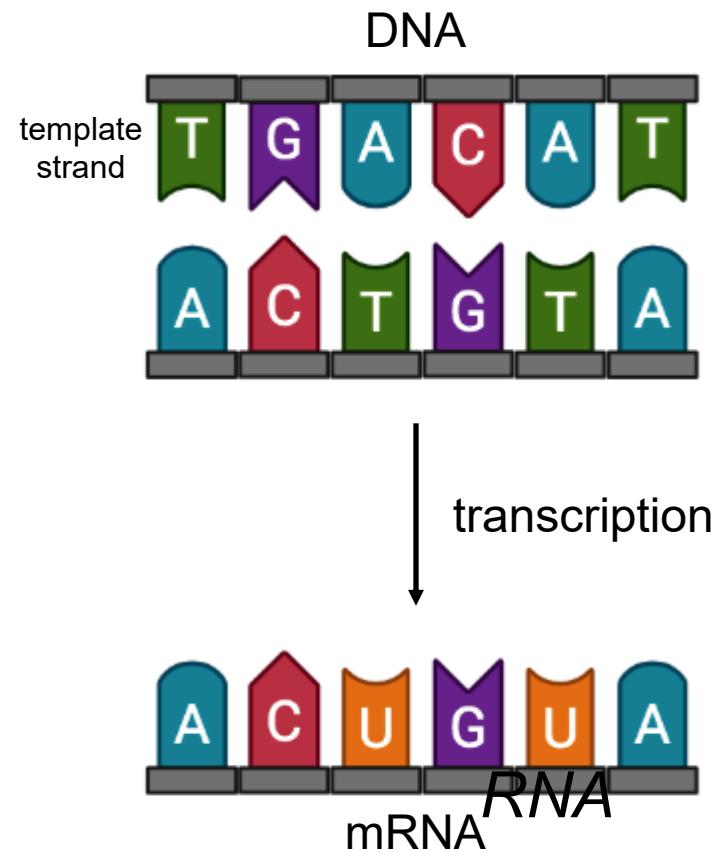


Figure made using BioRender



How do we actually transfer info from DNA to RNA?

- Transcription has 3 stages
- 1. **Initiation:** enzymes unzip the DNA double helix starting at the **promoter** (signals the start of a gene), exposing the **template strand** (the strand that will be copied)

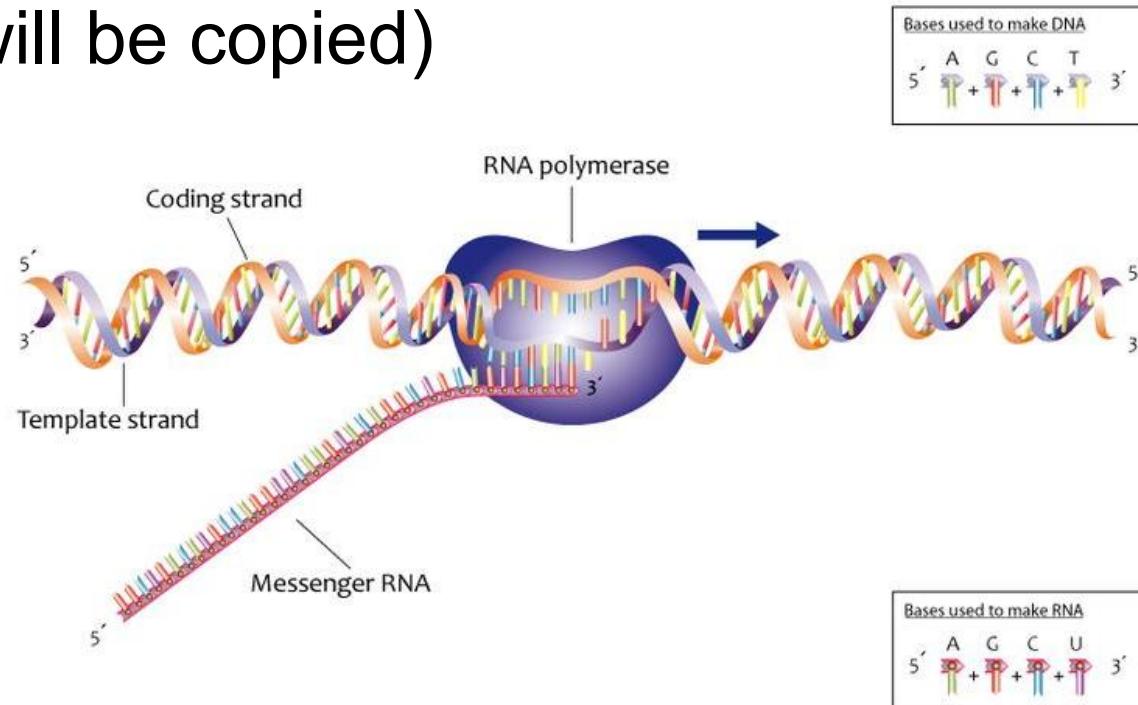


Figure: [https://commons.wikimedia.org/wiki/File:Process_of_transcription_\(13080846733\).jpg](https://commons.wikimedia.org/wiki/File:Process_of_transcription_(13080846733).jpg)



- Transcription has 3 stages

- **2. Elongation:** the enzyme **RNA polymerase** moves along the template strand pairing RNA with DNA (e.g. A with U & C with G), lengthening the mRNA strand

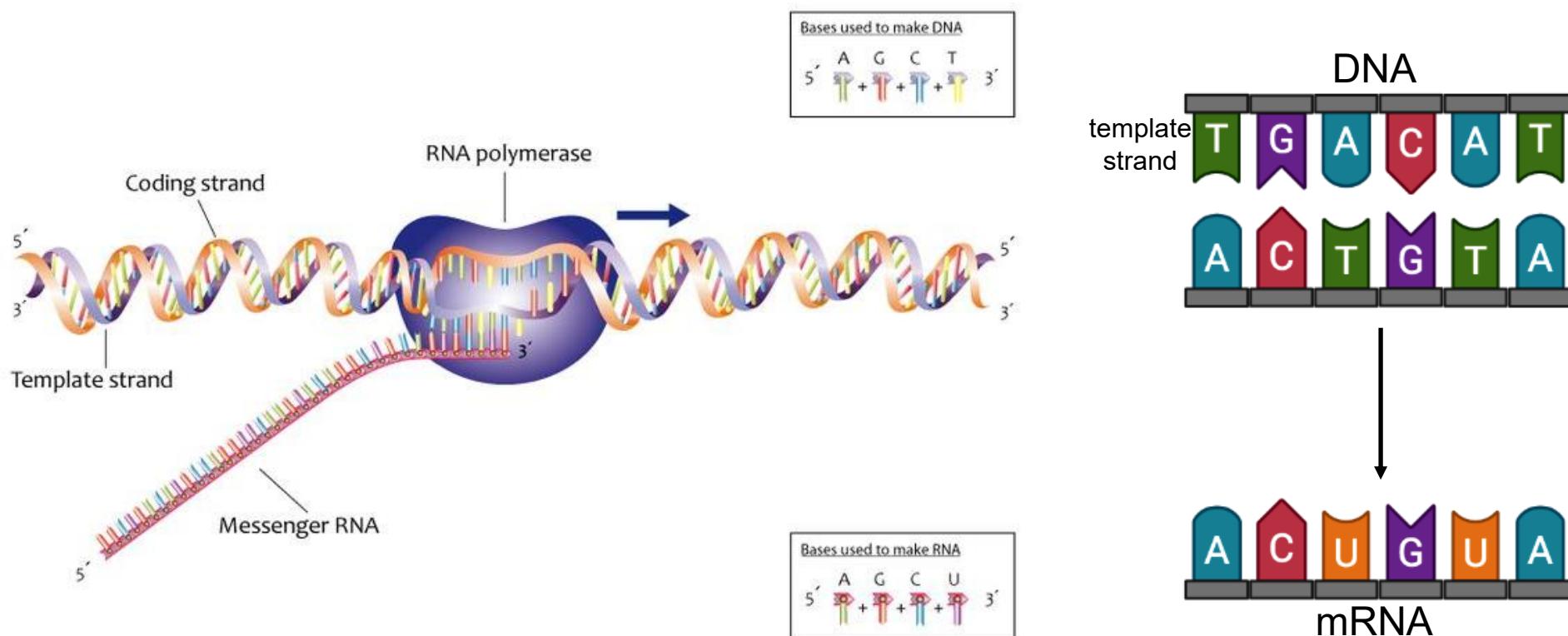
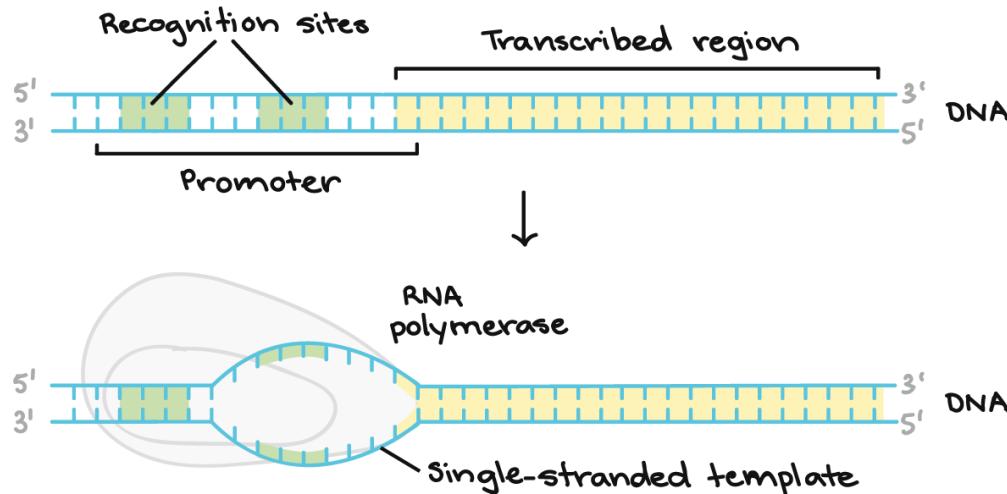


Figure: [https://commons.wikimedia.org/wiki/File:Process_of_transcription_\(13080846733\).jpg](https://commons.wikimedia.org/wiki/File:Process_of_transcription_(13080846733).jpg)



transcription initiation



transcription elongation

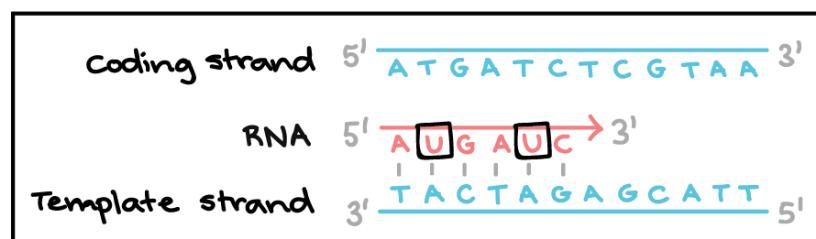
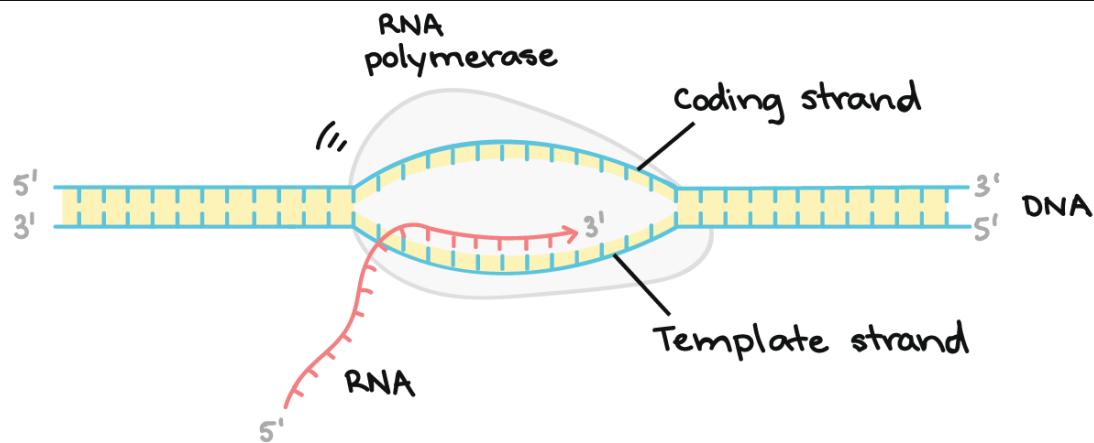


Figure: <https://www.khanacademy.org/science/biology/gene-expression-central-dogma/transcription-of-dna-into-rna/a/stages-of-transcription>



- Transcription has 3 stages
- 3. Termination: when the **terminator signal** is reached RNA, DNA, & RNA polymerase fall apart
 - DNA zips back up to a double strand
 - we now have an exact mRNA copy of a gene

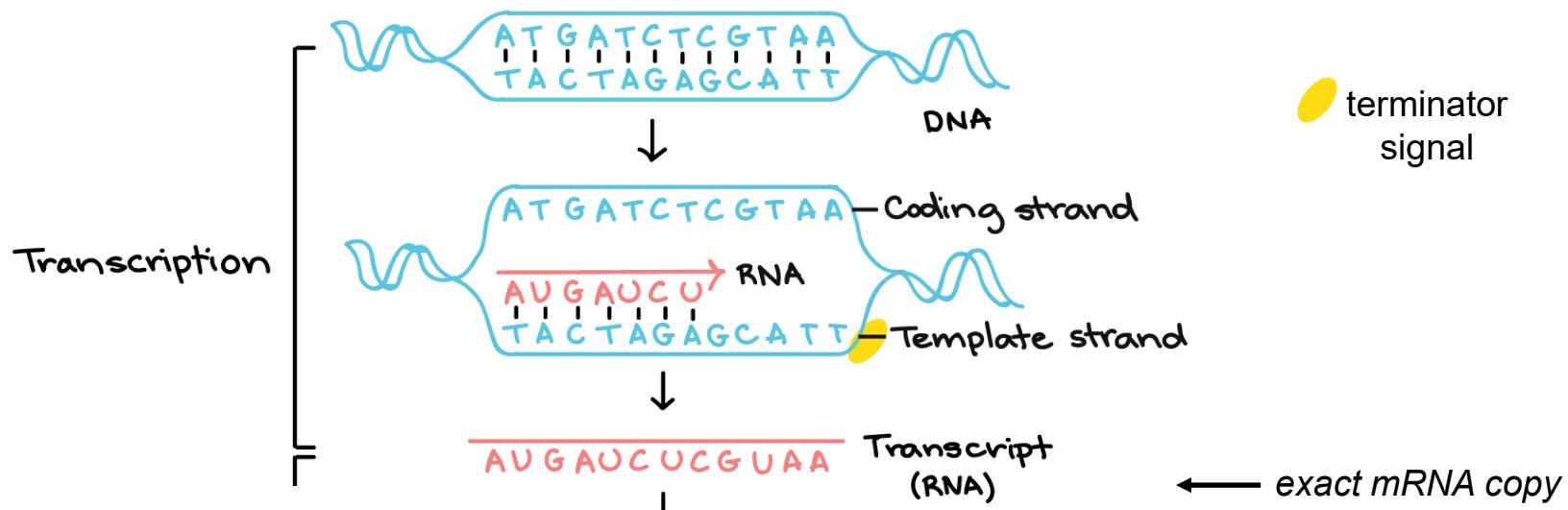
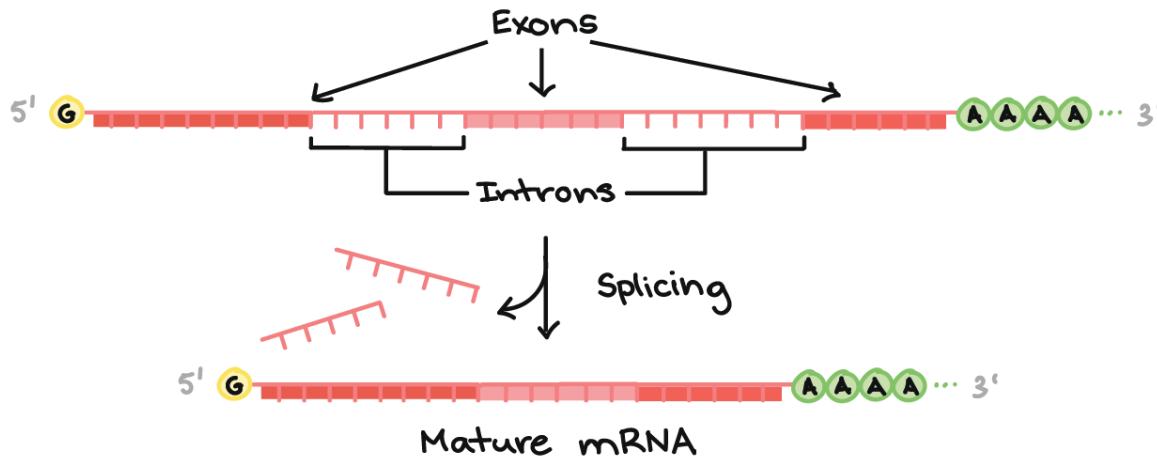


Figure: <https://www.khanacademy.org/science/biology/gene-expression-central-dogma/transcription-of-dna-into-rna/a/stages-of-transcription>



We now have an exact copy of the gene, but mRNA is not ready to leave the nucleus yet

- A gene has 2 kinds of segments: introns & exons
 - **exons** = truly coding nucleotides in DNA or RNA
 - **introns** = nucleotides that are not part of the code – must be cut out of mRNA after it's made



The process of cutting out introns = **RNA splicing**

Figure: <https://www.khanacademy.org/science/biology/gene-expression-central-dogma/transcription-of-dna-into-rna/a/eukaryotic-pre-mrna-processing>



RNA Splicing

- Immediately after transcription but before splicing, we have **pre-mRNA** – not spliced yet
- Enzymes in nucleus cut out the introns & splice together the exons to make a full strand of only coding mRNA
 - called finished or **post-mRNA**

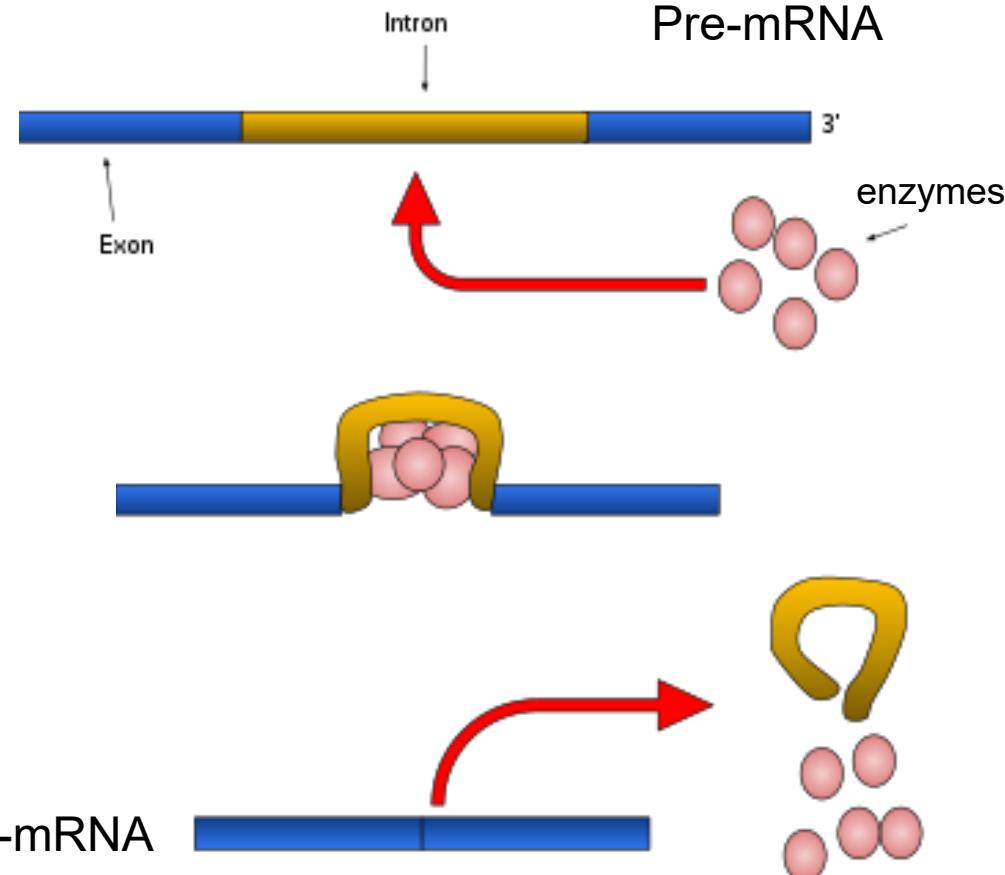


Figure: <https://en.wikipedia.org/wiki/File:Splicesome.svg>



Seems inefficient to carry around DNA we don't need – why would RNA splicing be useful?

- Exons aren't always spliced back together exactly
- This means the RNA splicing process can allow for 1 gene to make multiple different versions of a protein – very useful!

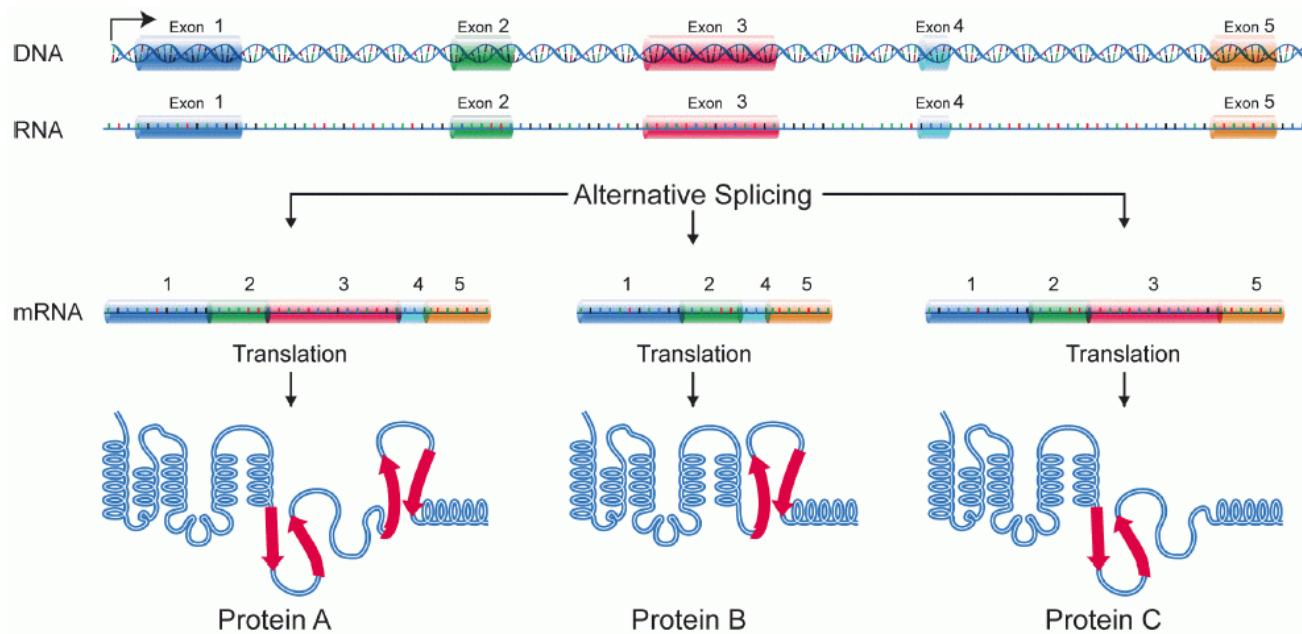


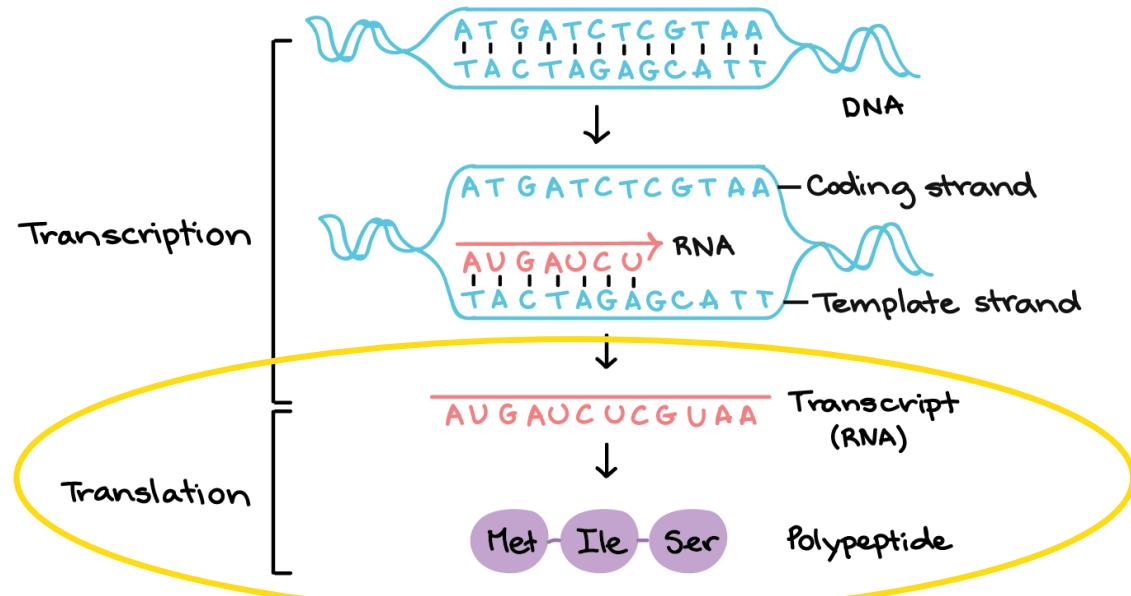
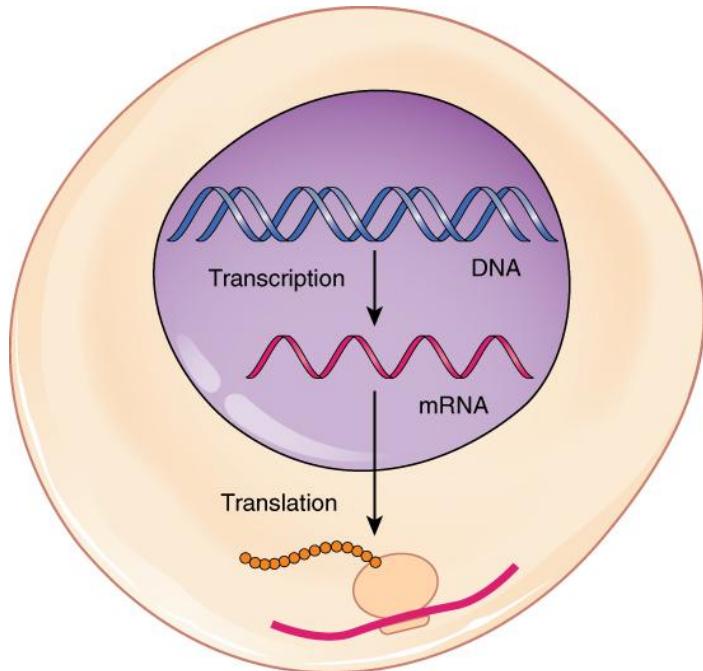
Figure: <https://www.khanacademy.org/science/biology/gene-expression-central-dogma/transcription-of-dna-into-rna/a/eukaryotic-pre-mrna-processing>



DNA codes for proteins/traits: STEP 2 = translation

– Translation = mRNA → protein

- mRNA moves out of the nucleus into the cytoplasm to direct protein synthesis (make a protein/polypeptide)





Remember: proteins (polymers) are made of amino acids (monomers)

– *Remember: there are >20 different amino acids*

- different amino acid sequence = different protein

▪ *Remember:* in transcription, 1 DNA base matches with 1 RNA base

– *Remember: there are only 4 possible bases*

▪ During **translation**, we use an mRNA sequence to build an amino acid sequence

– If there are only 4 RNA bases but 20 amino acids, we can't match up 1 base with 1 amino acid

- *we'd only use 4 amino acids & have 16 extra*



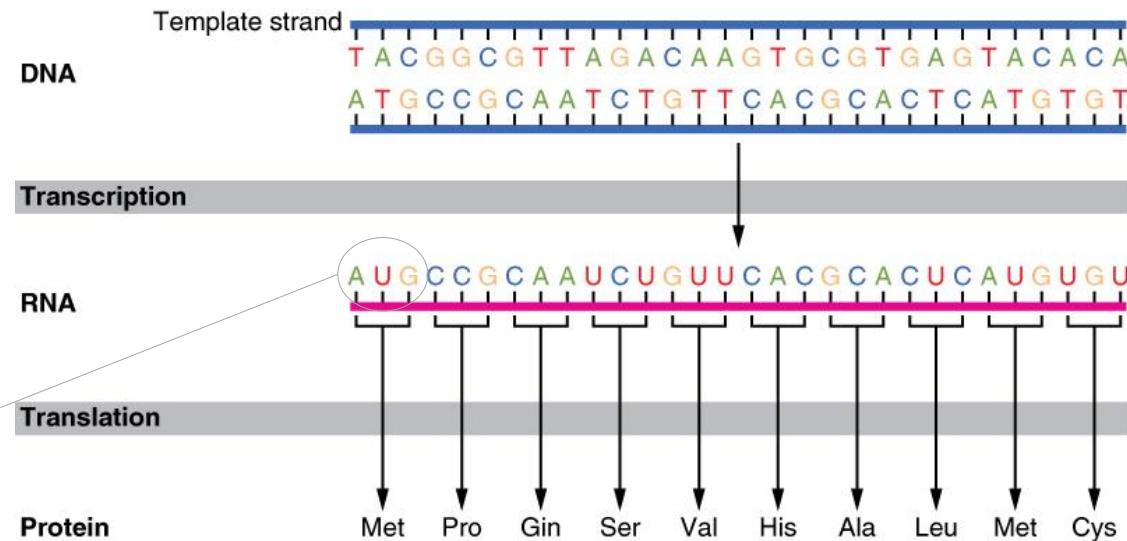
We can try to match up every 2 bases of RNA to every 1 amino acid (e.g. AG = 1 amino acid)

- there are only 16 possible 2-base combinations
 - we'd only use 16 amino acids & have 4 extra

- Must use 3 bases to code for 1 amino acid

- e.g. AUG will code for 1 amino acid

- each 3-base code is called a **codon**



Translation requires use of the genetic code

- Each **codon** specifies that a unique amino acid should be added to build the protein

| | | Second Base | | | | | | | |
|------------|---|---|--------------------------|--------------------------|---------------------------------------|------------------|--|--|--|
| | | U | C | A | G | | | | |
| First Base | U | UUU UUC UUA UUG | UCU UCC UCA UCG | UAU UAC UAA UAG | UGU UGC UGA — STOP UGG — Trp | U C A G | | | |
| | C | CUU CUC CUA CUG | CCU CCC CCA CCG | CAU CAC CAA CAG | CGU CGC CGA CGG | U C A G | | | |
| | A | AUU AUC AUA AUG — Met or Start | ACU ACC ACA ACG | AAU AAC AAA AAG | AGU AGC AGA AGG | U C A G | | | |
| | G | GUU GUC GUA GUG | GCU GCC GCA GCG | GAU GAC GAA GAG | GGU GGC GGA GGG | U C A G | | | |
| Third Base | | | | | | | | | |



Using the genetic code for translation

- Notice that one codon is a **start codon** – it signals the start of a gene/protein
- Notice that a few codons are **stop codons** – they signal the end of a gene/protein
- All other codons specify that an amino acid should be added to the growing protein

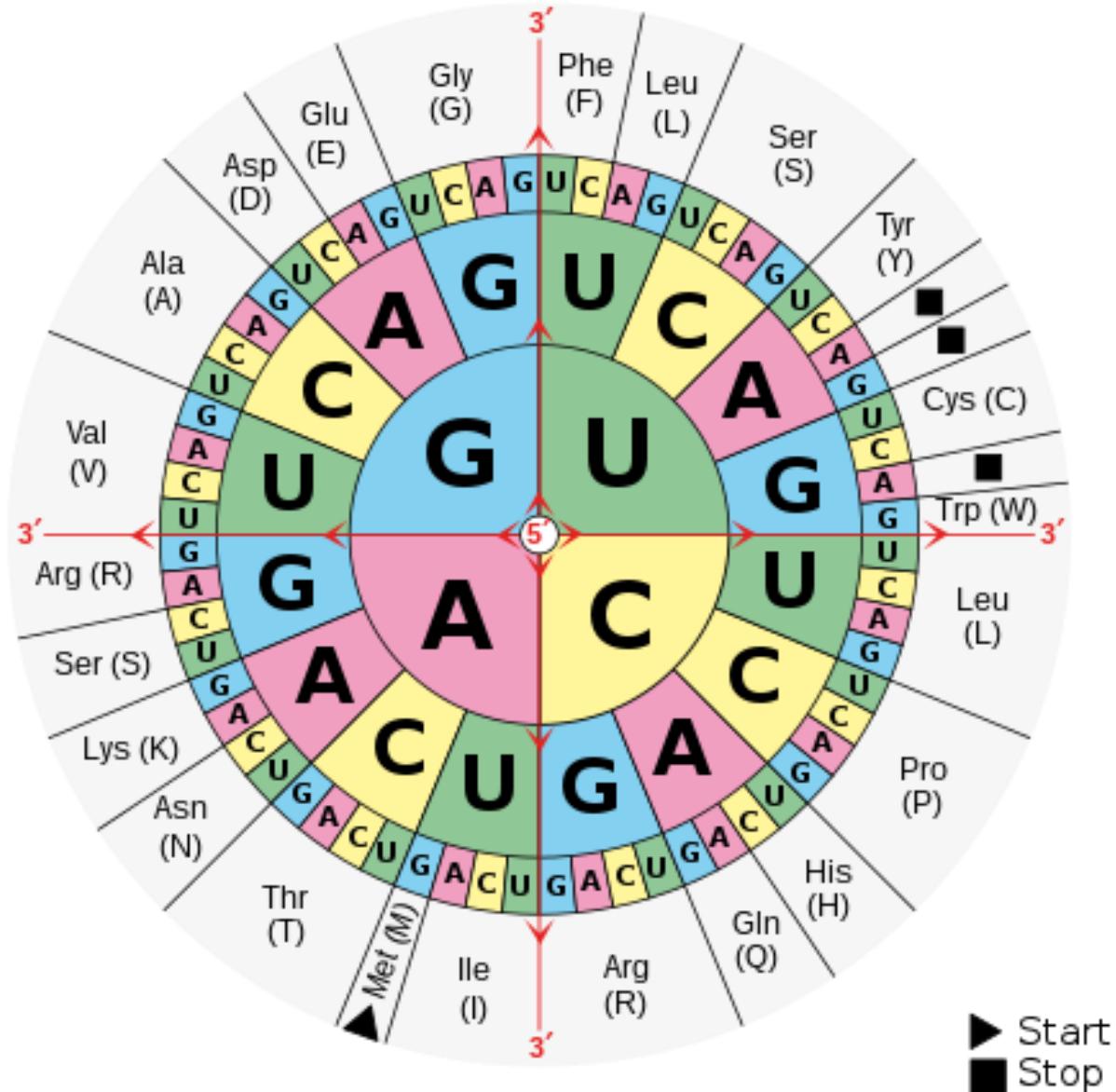
| | | Second Base | | | | | |
|------------|---|----------------------------------|--------------------------|--------------------------|-------------|--------------------------|-------------|
| | | U | C | A | G | U | C |
| First Base | U | UUU UUC UUA UUG | Phe Ser Leu Leu | UCU UCC UCA UCG | Tyr STOP | UGU UGC | Cys STOP |
| | C | CUU CUC CUA CUG | Leu Leu | CCU CCC CCA CCG | Pro | CAU CAC CAA CAG | His Arg |
| | A | AUU AUC AUA AUG — Start | Ile Met or Start | ACU ACC ACA ACG | Thr | AAU AAC AAA AAG | Asn Lys |
| | G | GUU GUC GUA GUG | Val | GCU GCC GCA GCG | Ala | GAU GAC GAA GAG | Asp Glu |
| | | Third Base | | | | U | C |
| | | U | C | A | G | U | C |

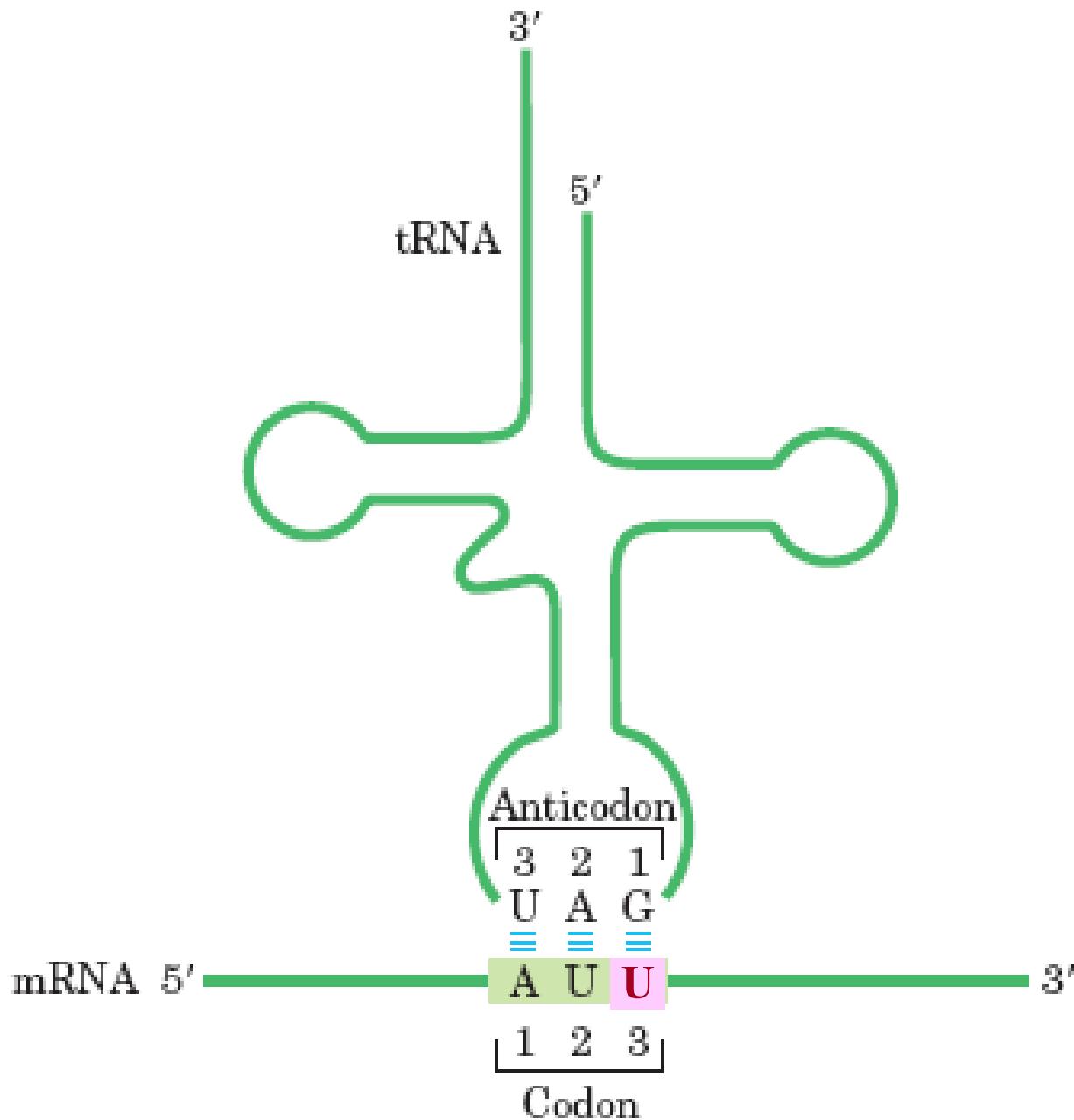


Using the genetic code for translation

- Notice that there are **64 possible codons** (*combinations of 3, like AAG*)
- But there are only **20 possible amino acids**
- This means that multiple codons code for the same amino acid
 - e.g. UUA & UUG both code for leucine
 - this means the genetic code is **redundant**

| | | Second Base | | | | |
|------------|---|--------------------------|------------|--------------------------|-----|--------------------------|
| | | U | C | A | | |
| First Base | U | UUU UUC UUA UUG | Phe Leu | UCU UCC UCA UCG | Ser | UAU UAC UAA UAG |
| | C | CUU CUC CUA CUG | Leu | CCU CCC CCA CCG | Pro | CAU CAC CAA CAG |
| | A | AUU | | ACU | | AAU |
| | T | | | | | UAU |





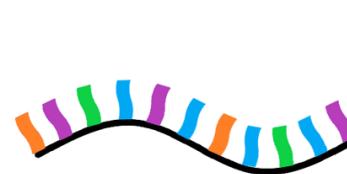


If these bases are in
first, or wobble, position of
anticodon

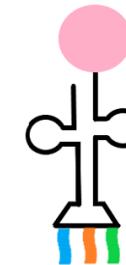
| C | A | G | U | I | |
|---|---|---|---|---|---|
| G | U | C | A | C | then tRNA may |
| | U | U | G | A | recognize codons |
| | | | | U | having these bases in third position |



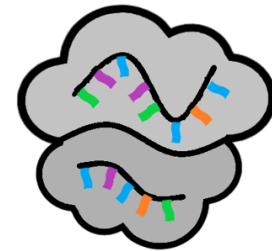
How do we physically match RNA to amino acids?



Messenger RNA



Transfer RNA



Ribosomal RNA

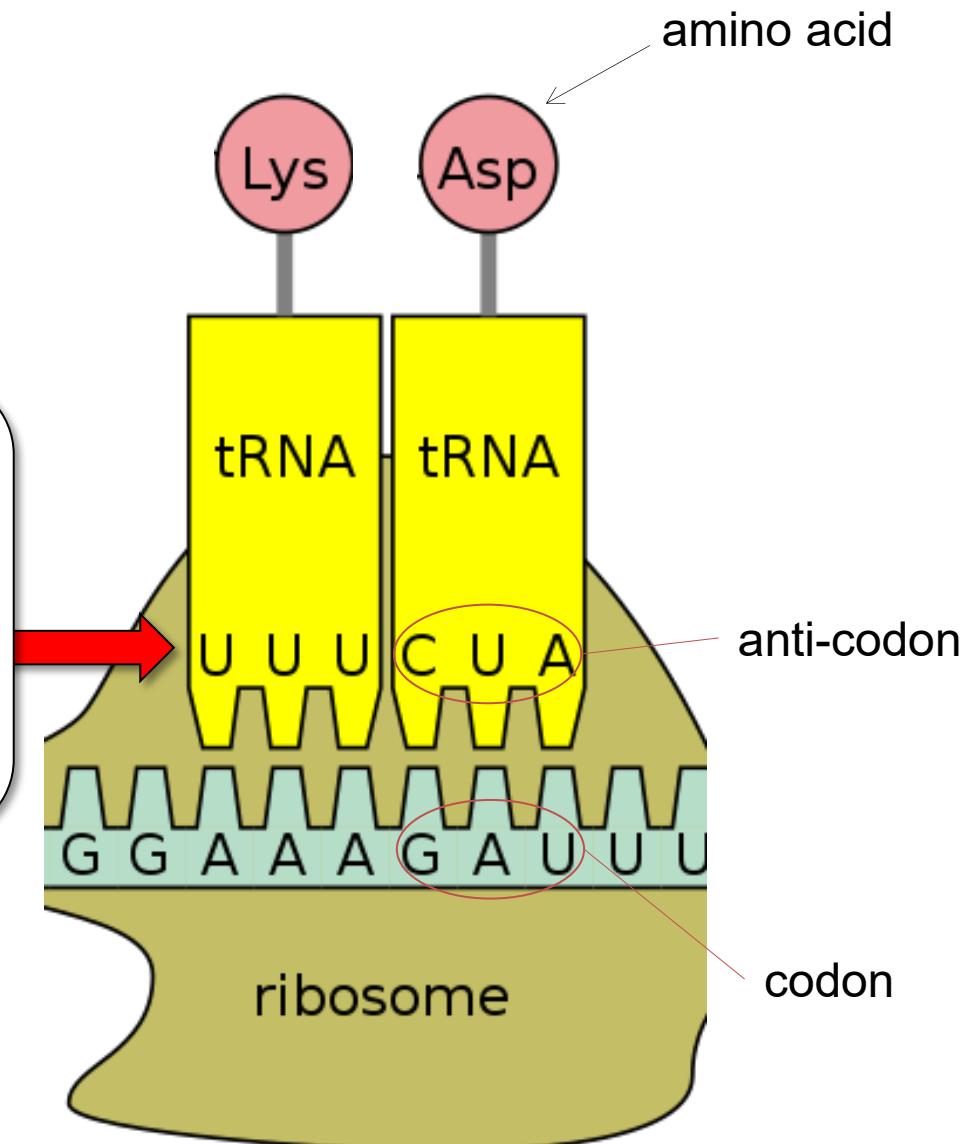
■ Key players in translation

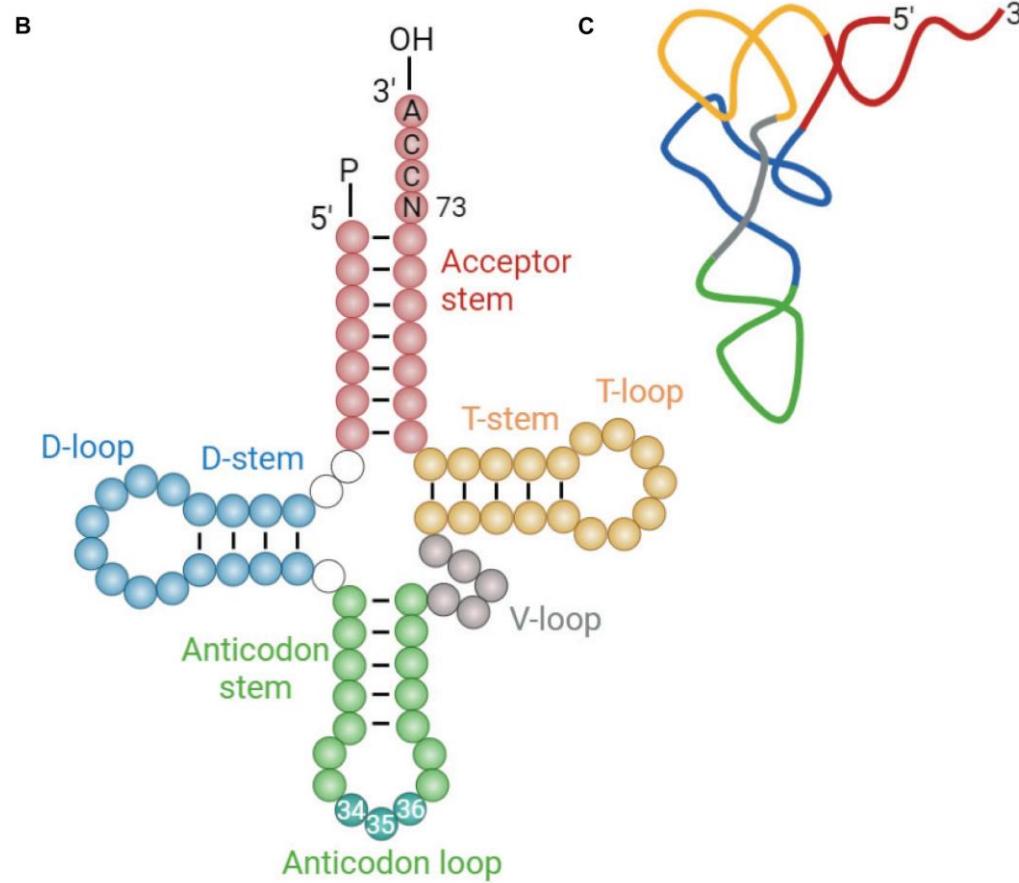
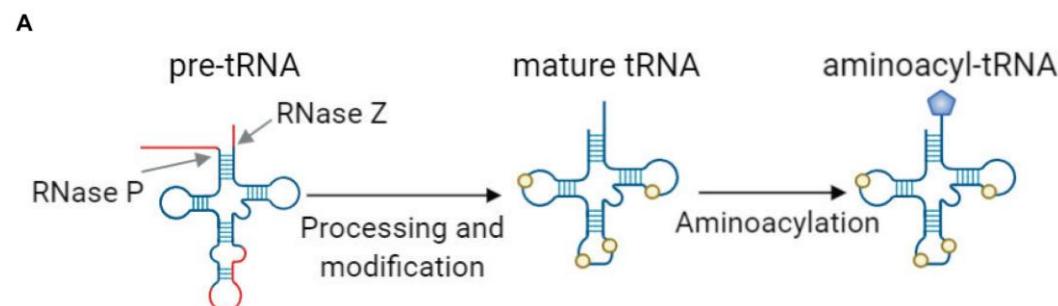
- **mRNA** (messenger RNA): brings instructions (in codons) for the amino acid sequence
- **rRNA** (ribosomal RNA): works with proteins to make **ribosomes** (on rough ER) where proteins are made
- **tRNA** (transfer RNA): helps match up each codon to the amino acid it codes for
 - can do this because it has an **anti-codon** (to bind to a codon) & each is attached to a specific amino acid

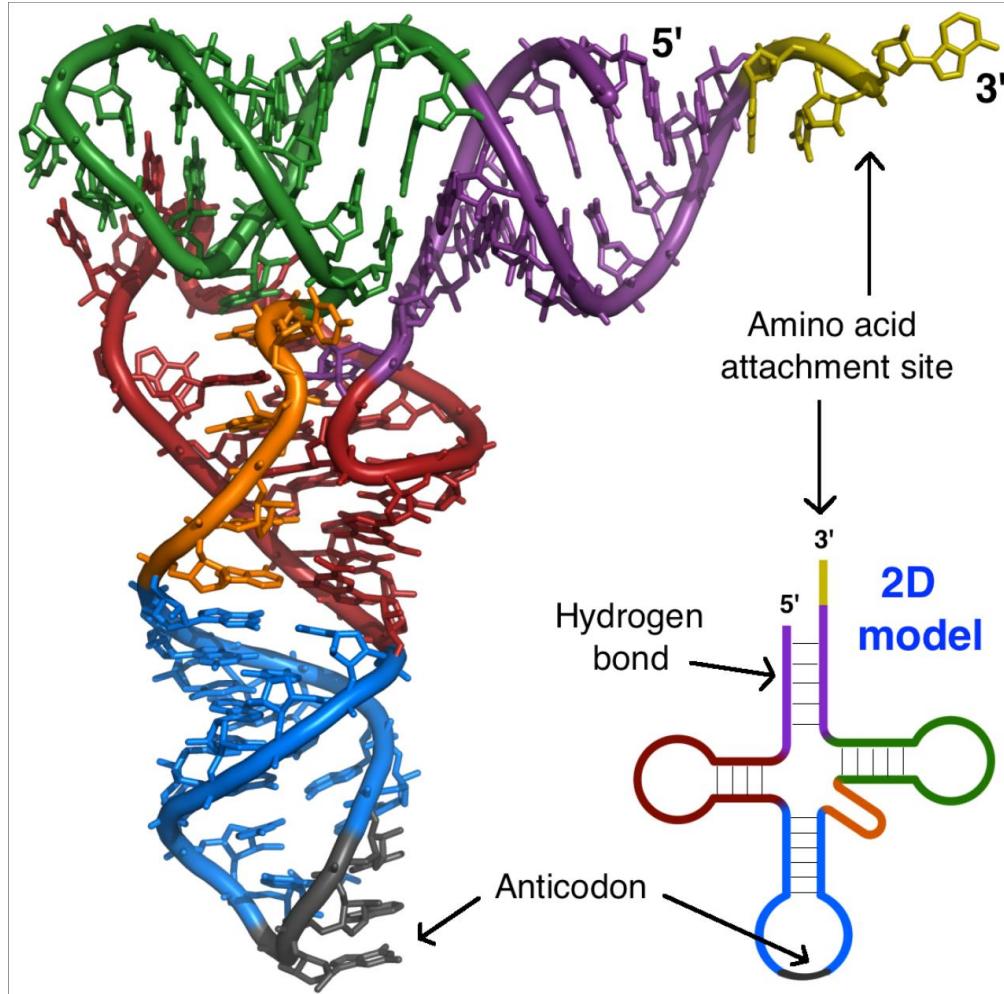
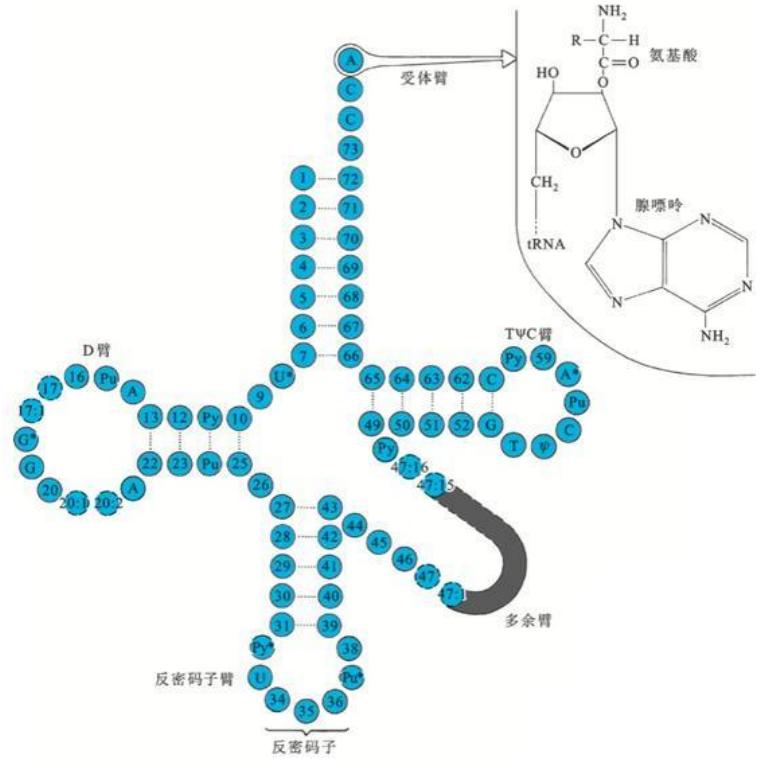


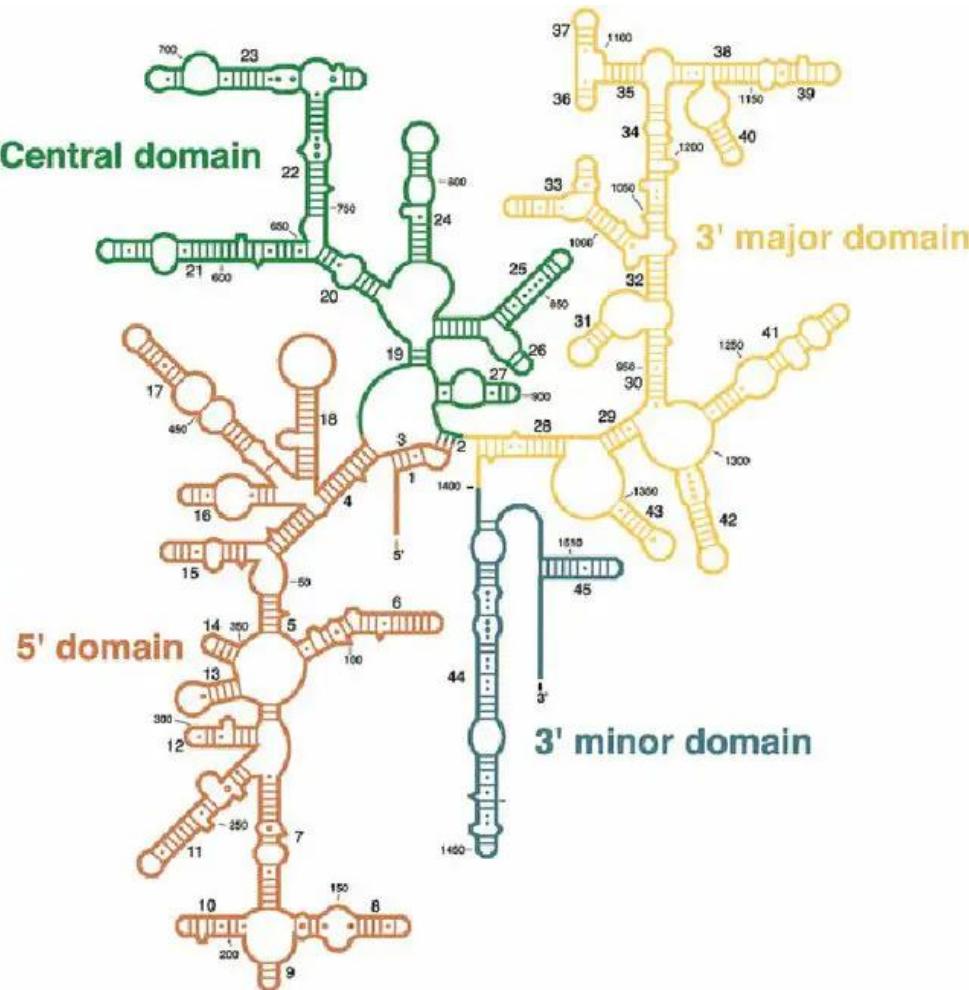
Transfer RNA (tRNA) molecules translate the mRNA code by linking specific bases on the mRNA with specific amino acids that will be used to build a protein.

The anti-codon is a 3-base sequence that matches up with the 3-base sequence on the mRNA strand. Each 3-base sequence in mRNA—called a codon—matches with a tRNA that carries one particular amino acid.



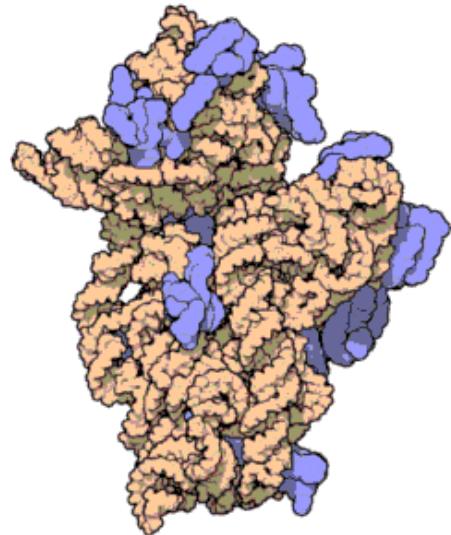




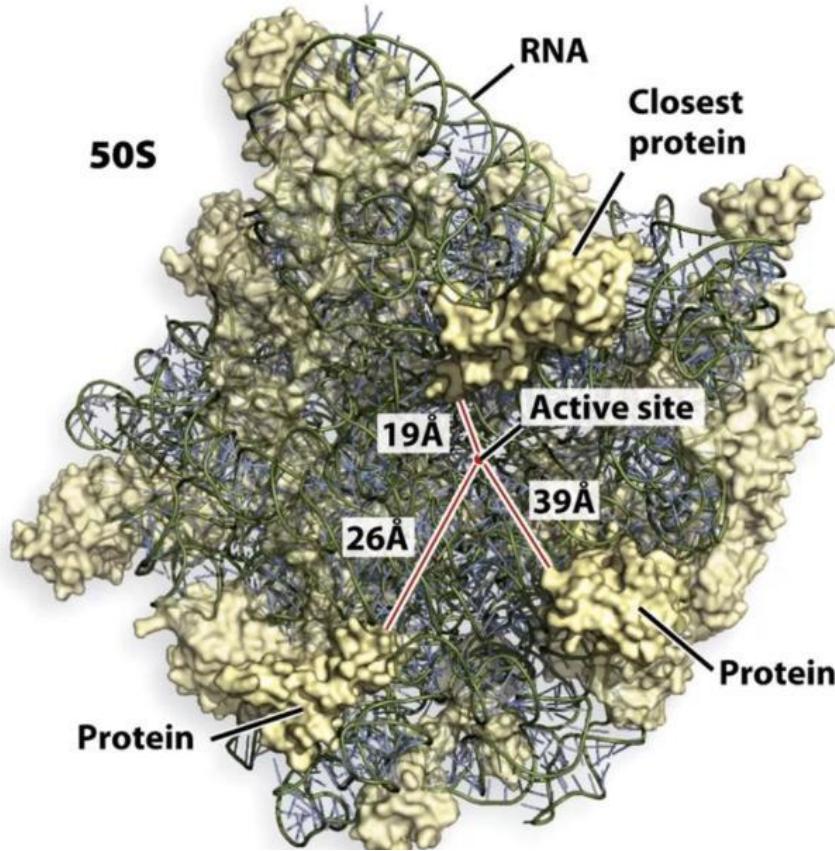


Ribosomal ribonucleic acid (rRNA) is the primary component of ribosomes and carries out protein synthesis like an enzyme; therefore also called **ribozyme**. Unlike messenger RNA, rRNA does not carry genetic information. Thus, they are non-coding RNA. Ribosomal RNA is transcribed from ribosomal DNA (rDNA).

rRNA is not a linear RNA molecule. In fact, it folds into a specific 3-D structure with stems and loops. Stems are short double-stranded RNAs formed by base-pair complementarity ($A=U$, $G\geq C$). Loops are unpaired single-stranded RNAs. This image is a secondary structure of 16S rRNA. The tertiary structure of rRNA will fold this structure up among a complex of proteins. The entire 16S rRNA gene sequence is approximately 1500 base pairs (bp).



THE RIBOSOME'S CATALYTIC SITE IS FAR FROM RIBOSOMAL PROTEINS

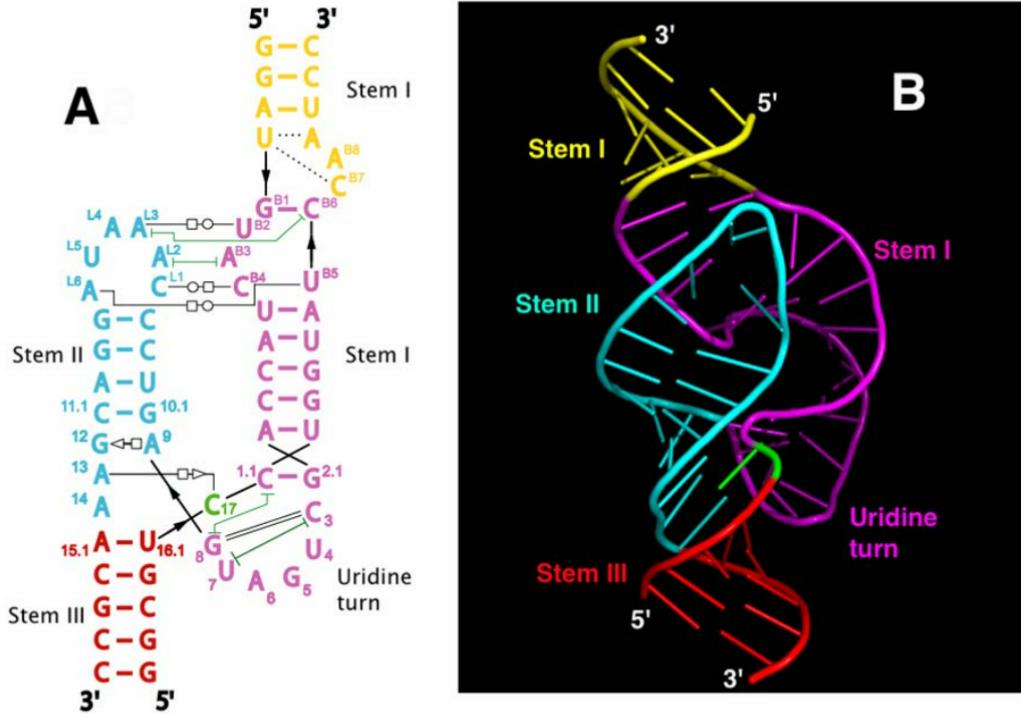


Ribosomal Catalytic Site

The active site—where the peptidyl transferase forms peptide bonds—is 18 Å away from the closest ribosomal protein (very far!). RNA is the only molecule in the active site, evidence that the ribosome is a ribozyme.

[Source: PDB ID 1Q7Y.]

What lines of evidence I've shown you suggest that RNA is the critical molecule for ribosomal function?



hammerhead ribozyme

hairpin ribozyme

Figure 1 Schematic (A) and ribbon (B) diagrams depicting the crystal structure of the full-length hammerhead ribozyme. The sequence and secondary structure in Figure A is color-coded to match the structural features shown in Figure B. The cleavage site nucleotide, C-17, is shown in green, and various helical stems and loops are denoted using several other colors. Tertiary hydrogen bonding contacts are denoted as thin black lines, and tertiary stacking interactions as thin green lines. See Figure 2 for a detailed schematic representation of the active site.

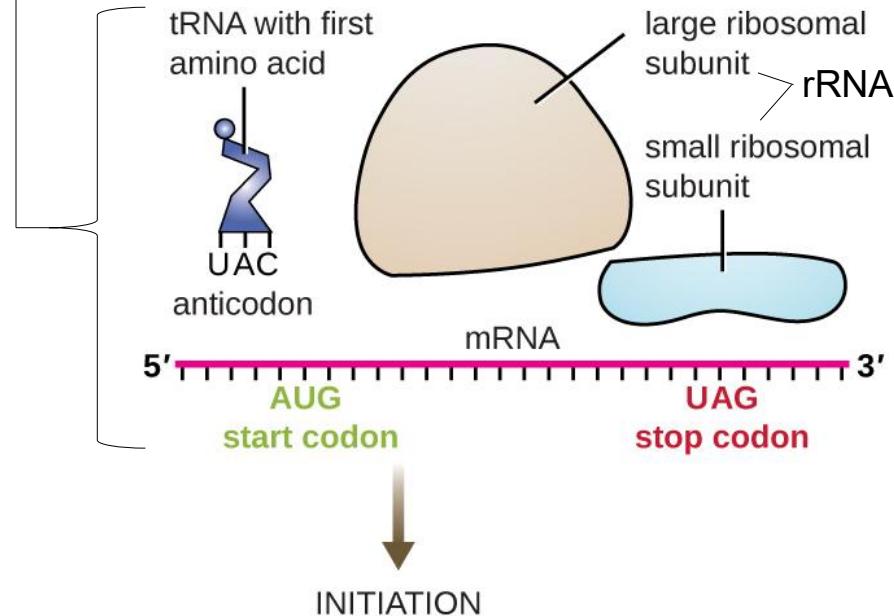


Translation has 3 stages

- 1. **Initiation:**
mRNA, tRNA, &
rRNA/ribosomes all
come together starting
at a **start codon**

- *the tRNA with the anticodon to the start codon is the first to bind inside the ribosome*

Starting components



Transitional complex forms, and tRNA brings first amino acid in polypeptide chain to bind to start codon on mRNA.

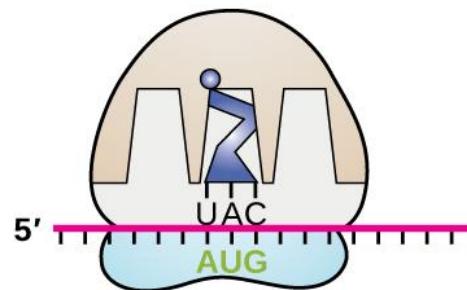
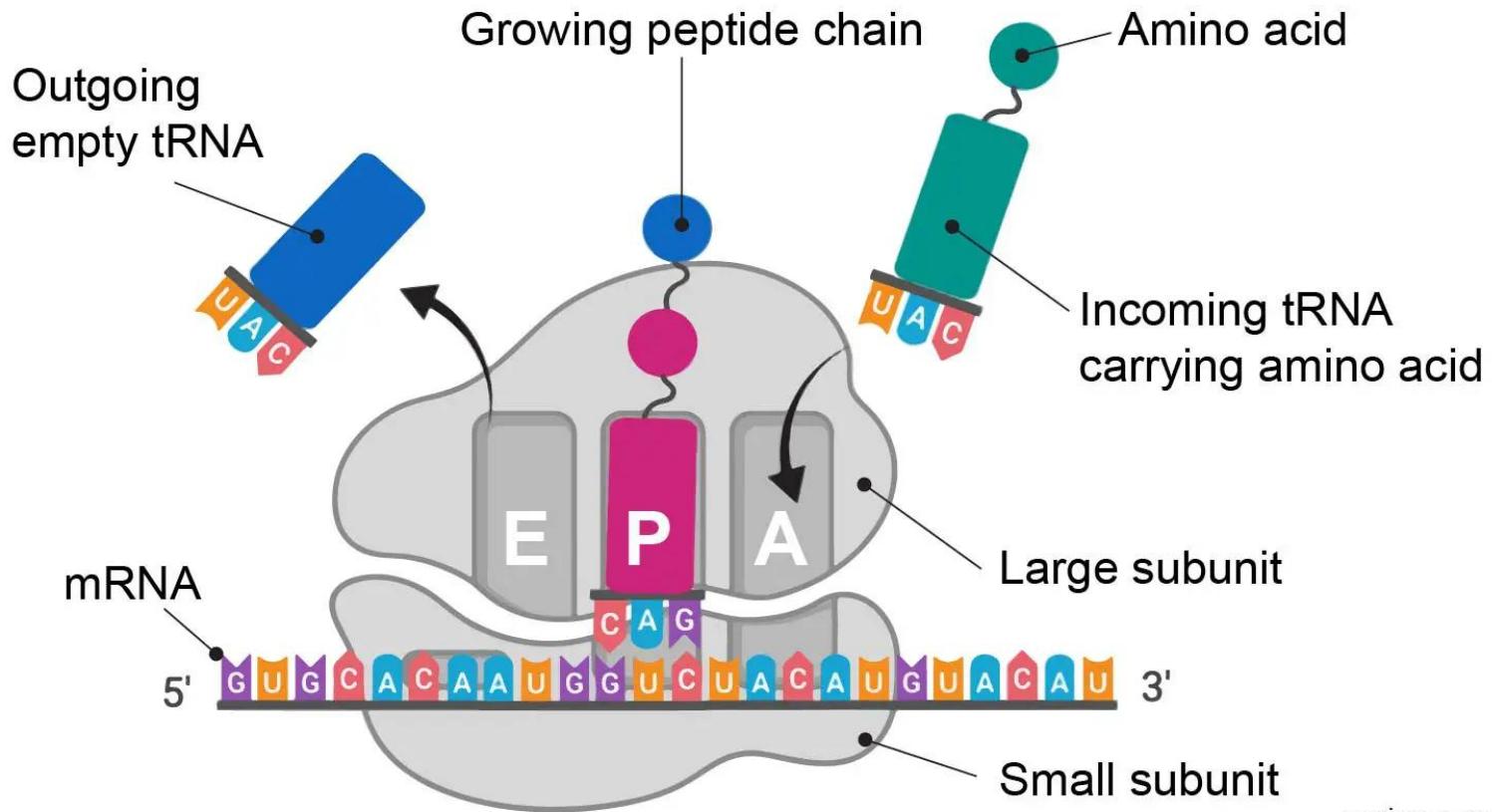


Figure: https://commons.wikimedia.org/wiki/File:OSC_Microbio_11_04_TInInit.jpg

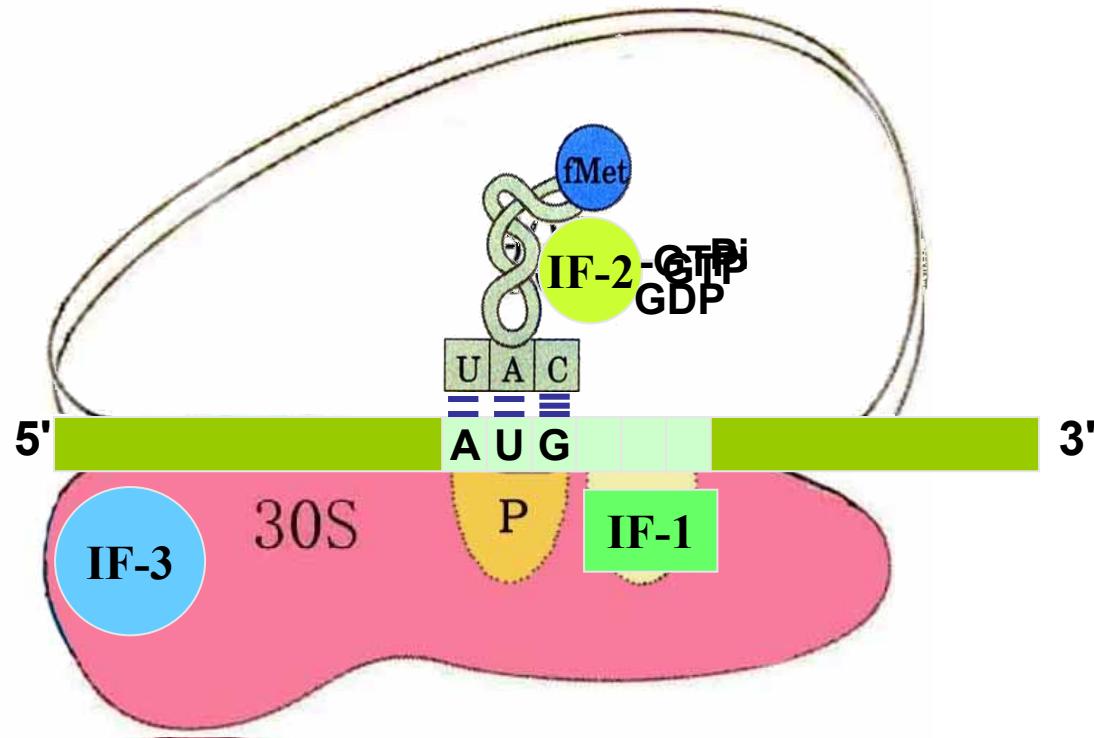


rsscience.com

A: aminoacyl site

P: peptidyl site

E: exit site





Translation has 3 stages

- **2. Elongation:** tRNAs move in & out of the ribosome, leaving their amino acid behind attached to the last amino acid
 - *each time a tRNA leaves, the mRNA shifts over, making space for a new tRNA to bind*

INITIATION

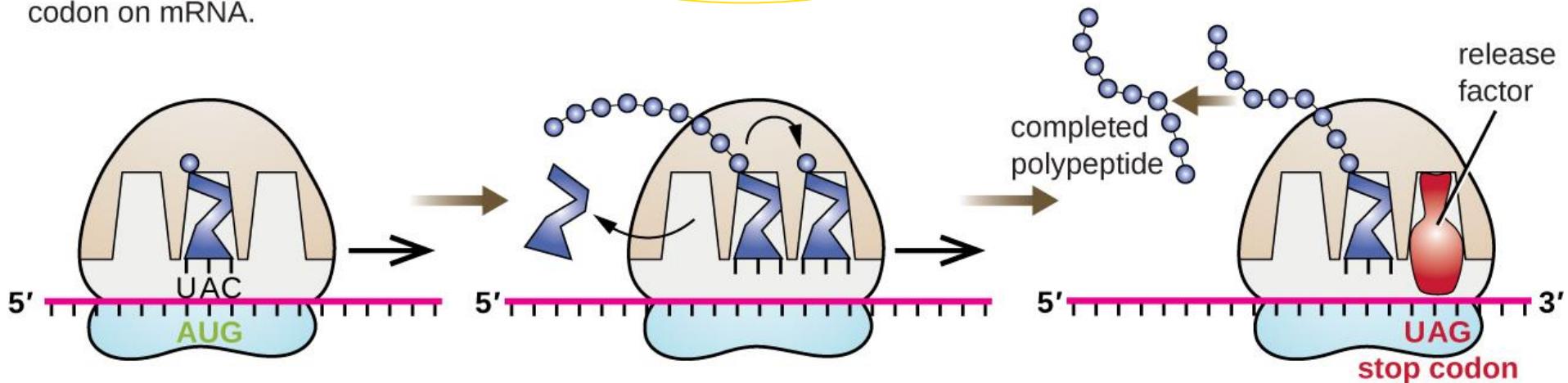
Transitional complex forms, and tRNA brings first amino acid in polypeptide chain to bind to start codon on mRNA.

ELONGATION

tRNAs bring amino acids one by one to add to polypeptide chain.

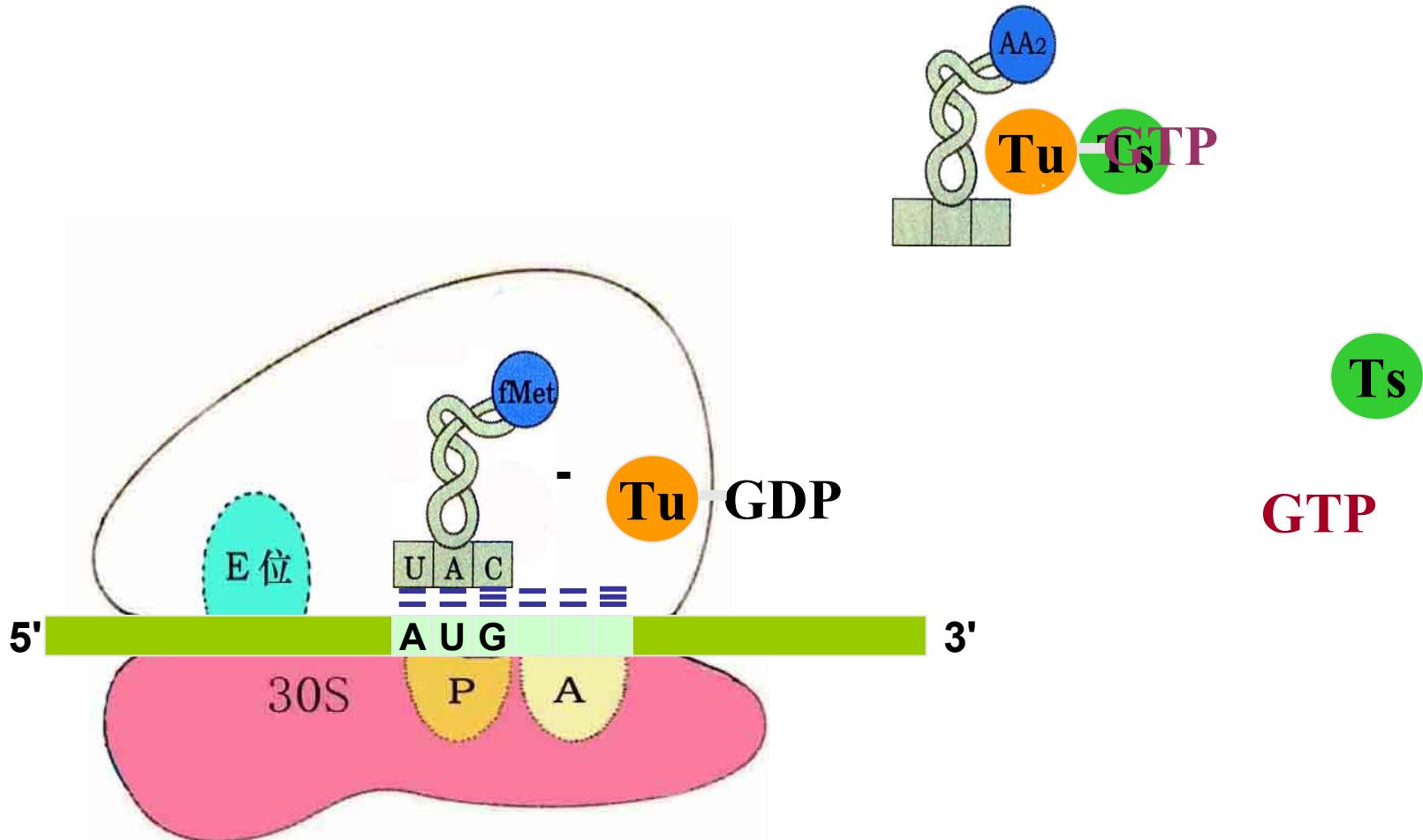
TERMINATION

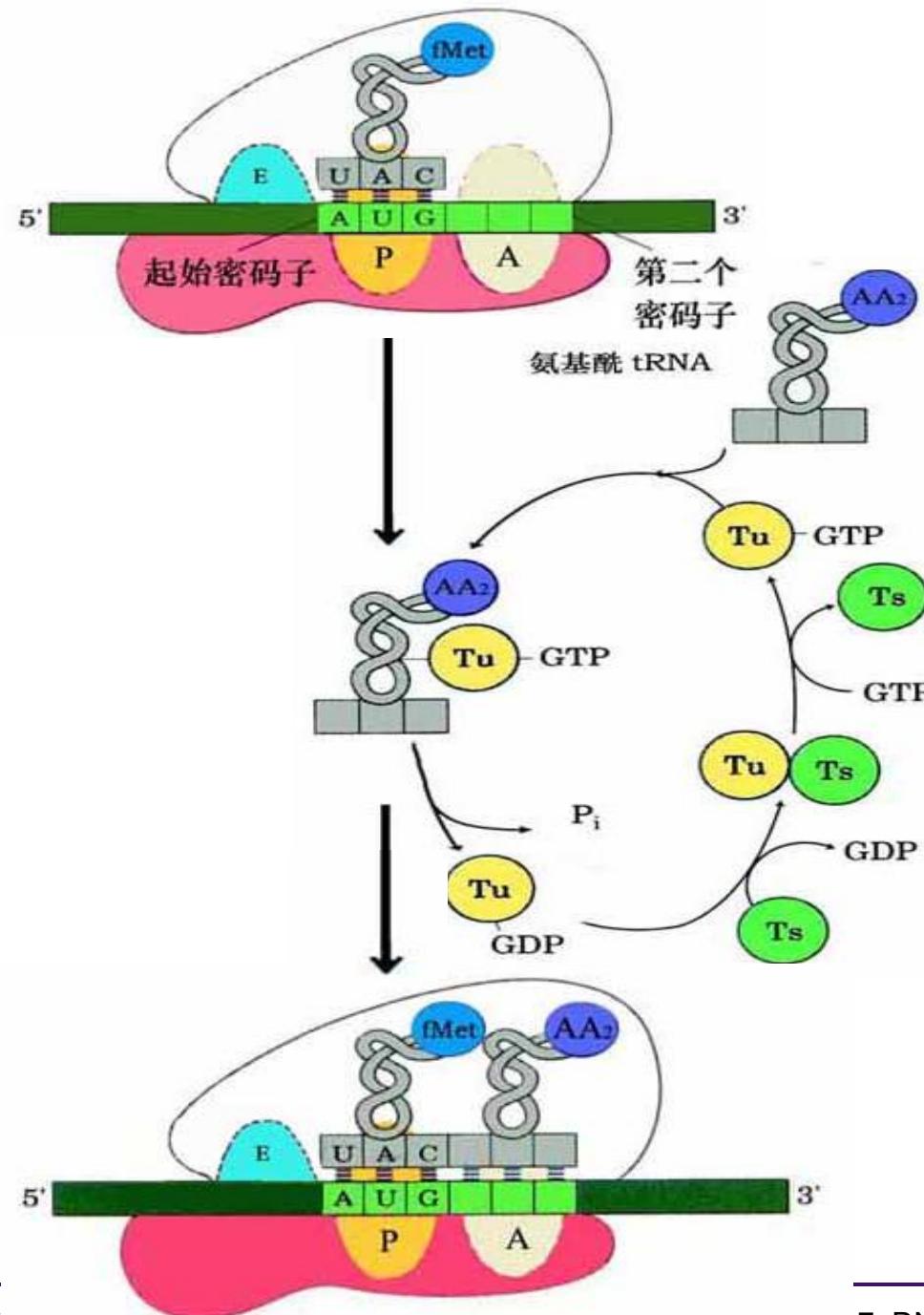
Release factor recognizes stop codon, translational complex dissociates, and completed polypeptide is released.





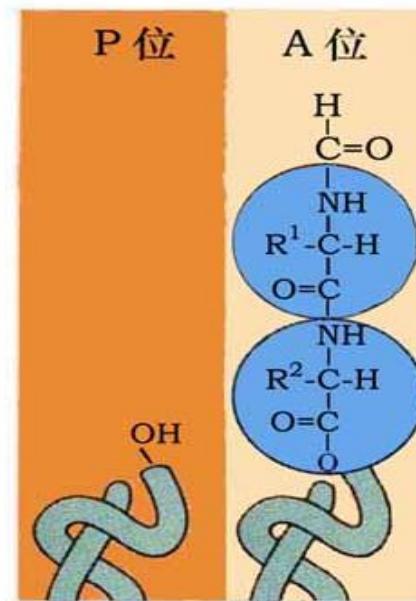
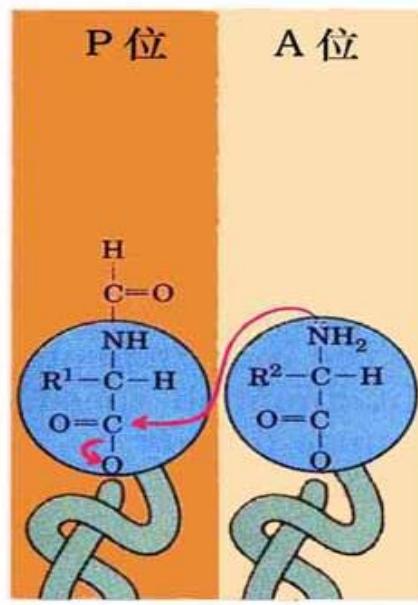
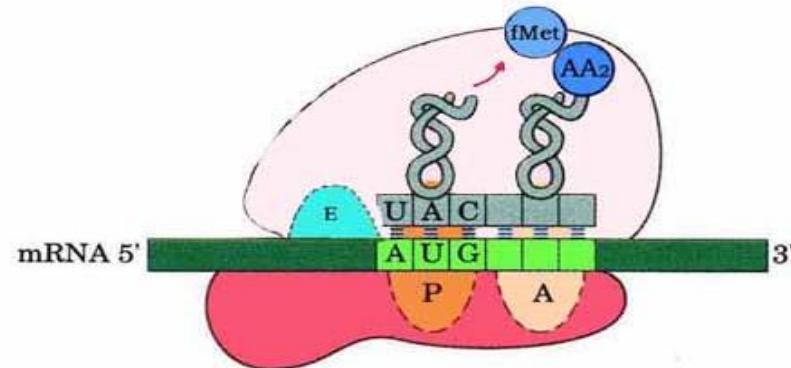
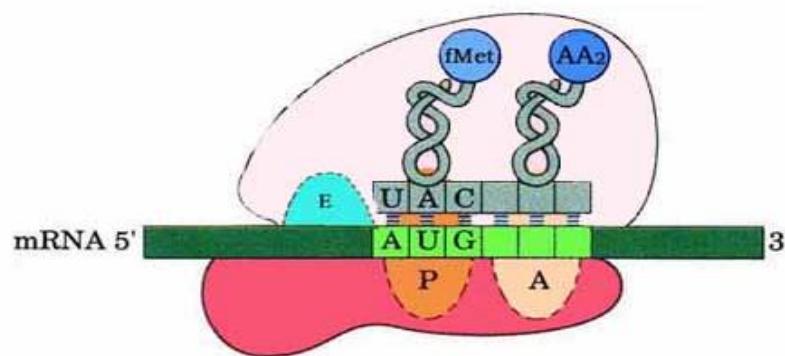
2.1 entrance





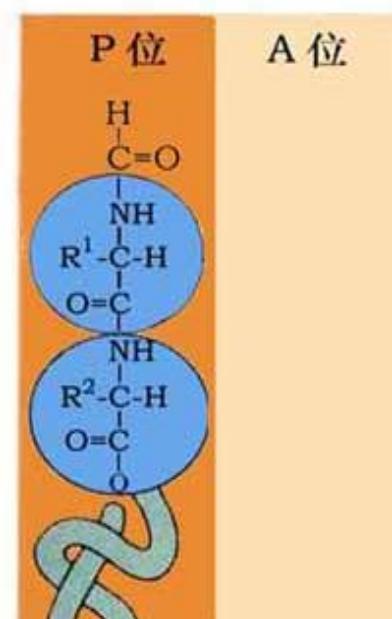
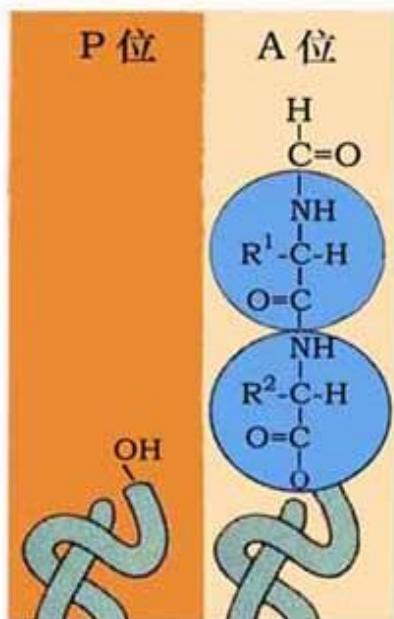
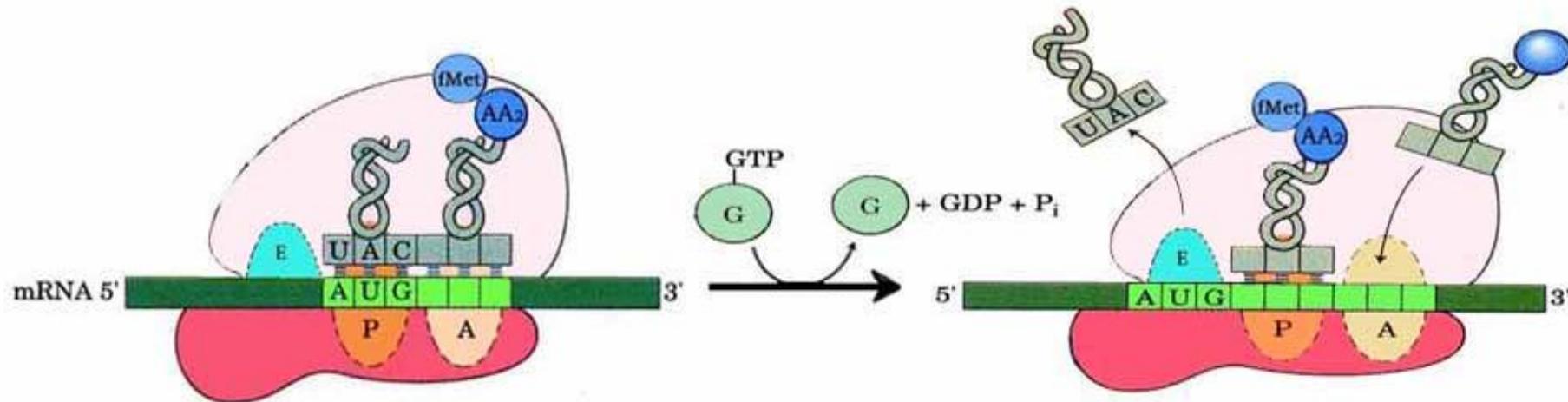


2.2 peptide bond formation



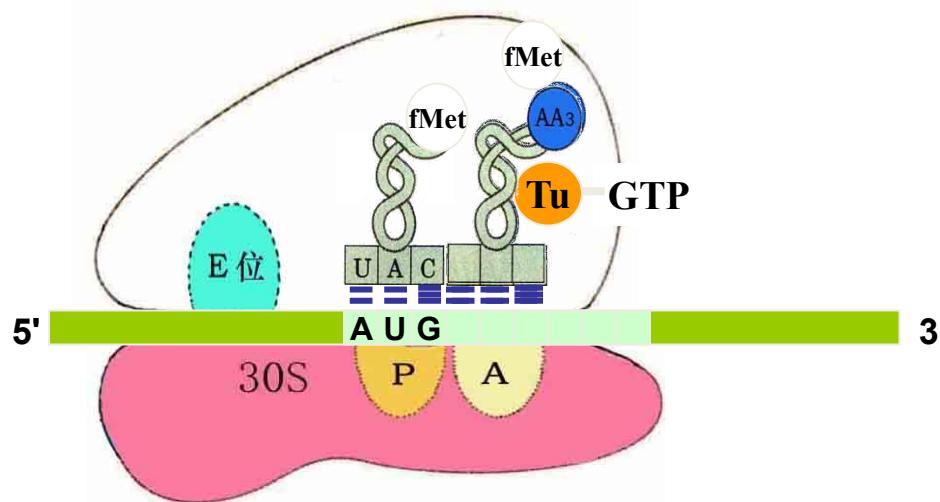


2.3 translocation





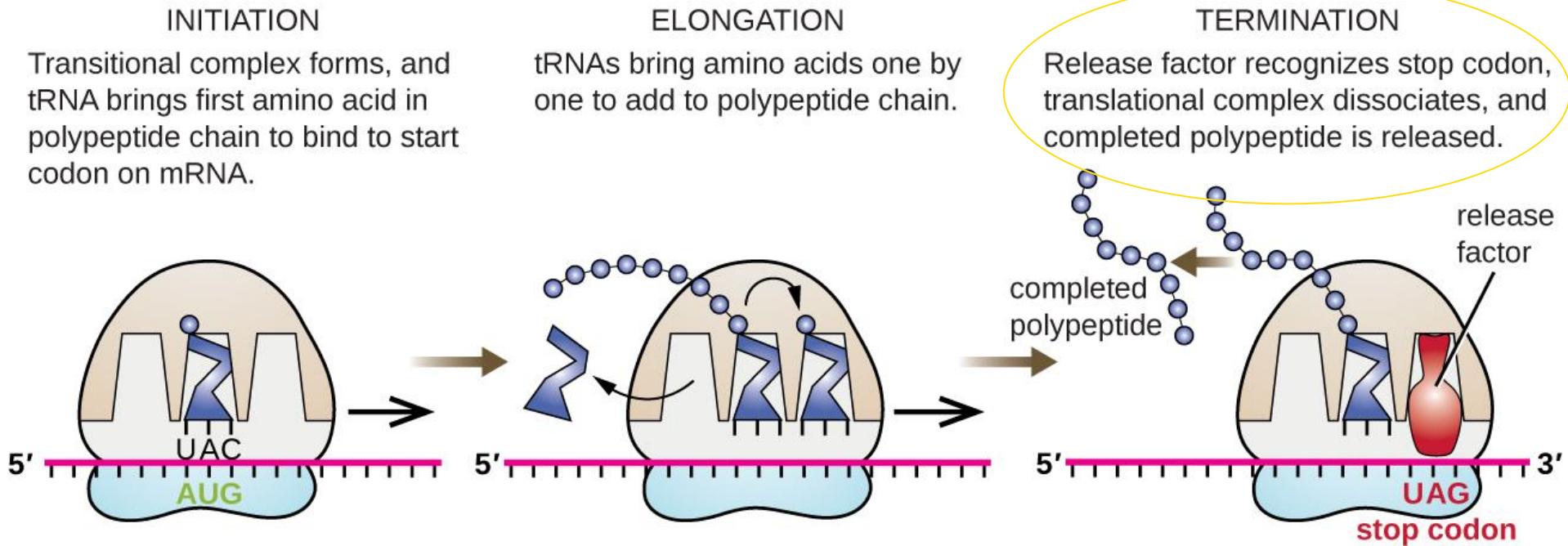
2.4 repeatcontinuousl

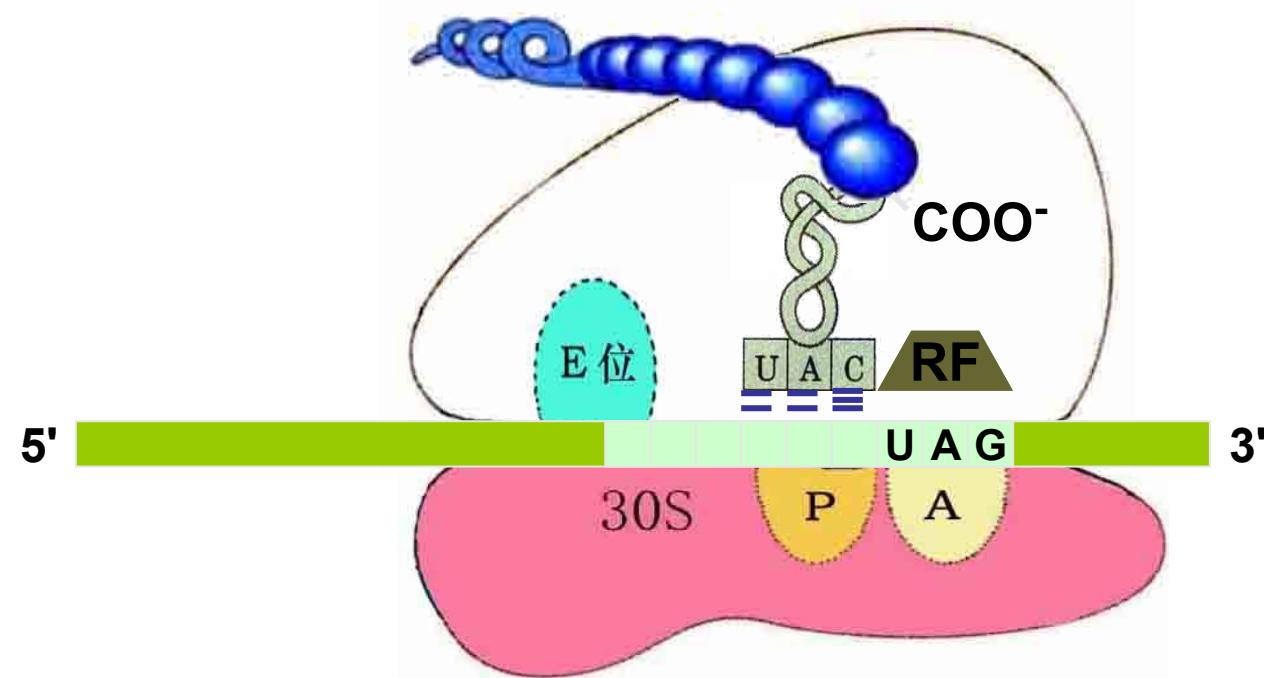




Translation has 3 stages

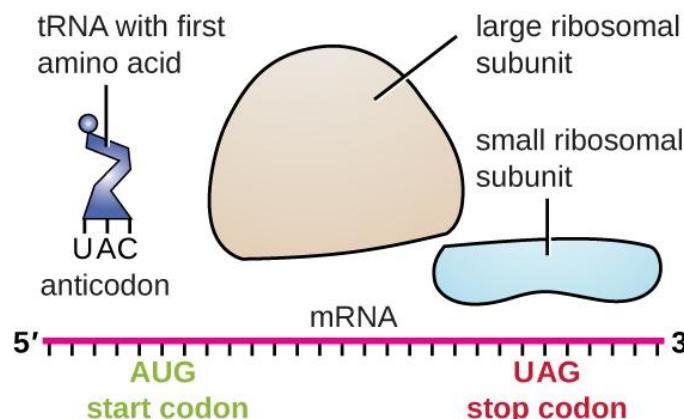
- **3. Termination:** when a **stop codon** is reached, all components separate & the amino acid chain will move through the rough ER & golgi apparatus to be folded & functional







The mRNA strand can be translated over & over again before it is degraded – can produce dozens or even hundreds more proteins



INITIATION

Transitional complex forms, and tRNA brings first amino acid in polypeptide chain to bind to start codon on mRNA.

ELONGATION

tRNAs bring amino acids one by one to add to polypeptide chain.

TERMINATION

Release factor recognizes stop codon, translational complex dissociates, and completed polypeptide is released.

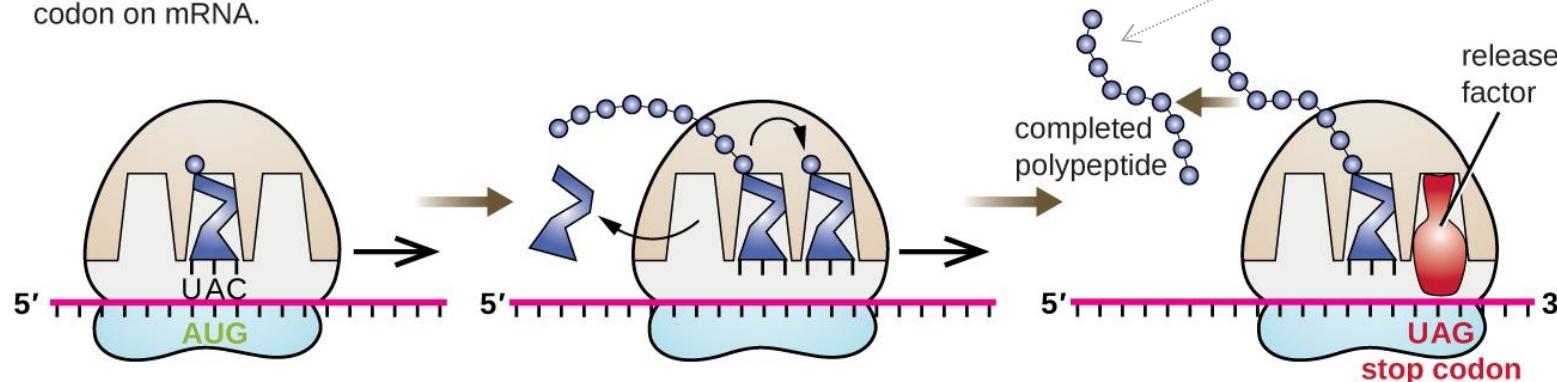
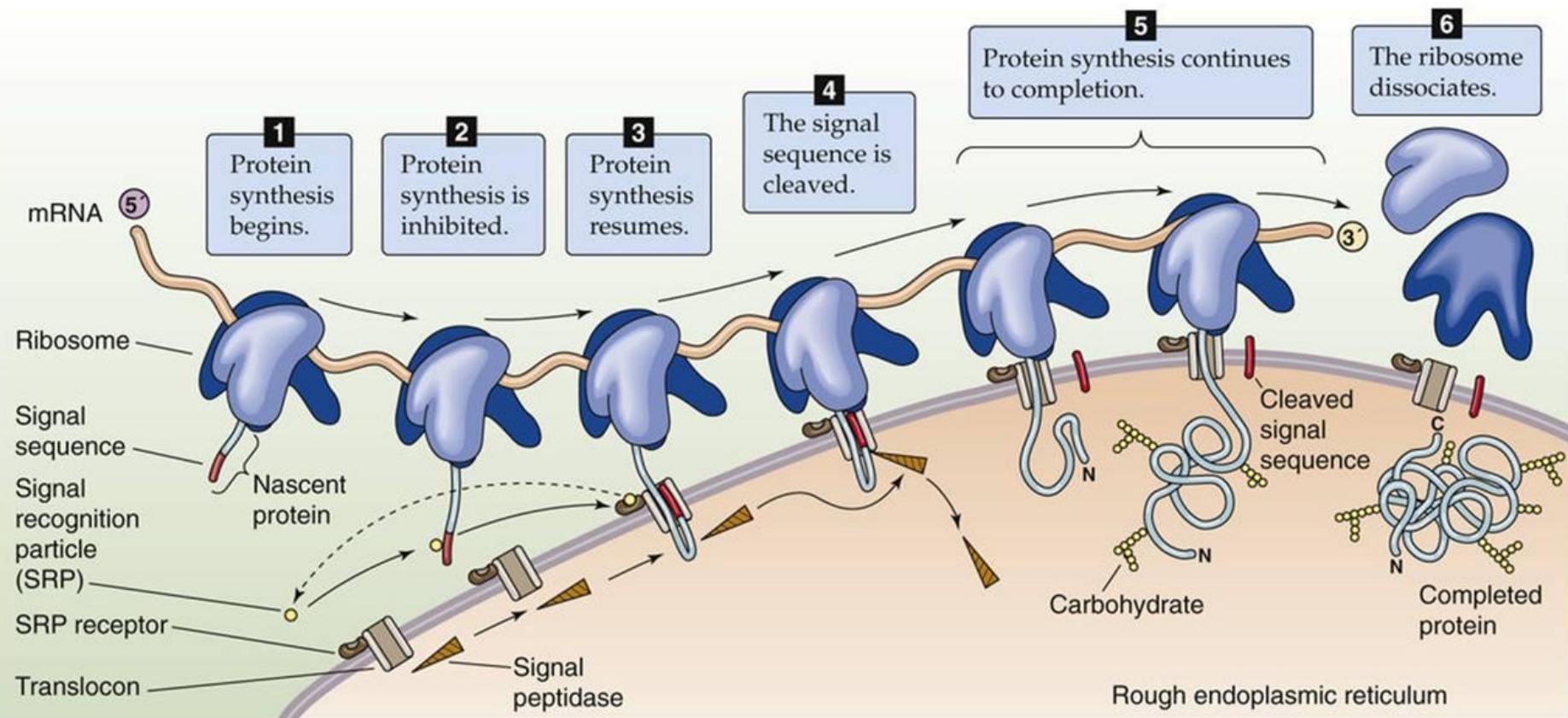


Figure: https://commons.wikimedia.org/wiki/File:OSC_Microbio_11_04_TlInit.jpg

The newly formed amino acid sequence will become folded into a functional protein



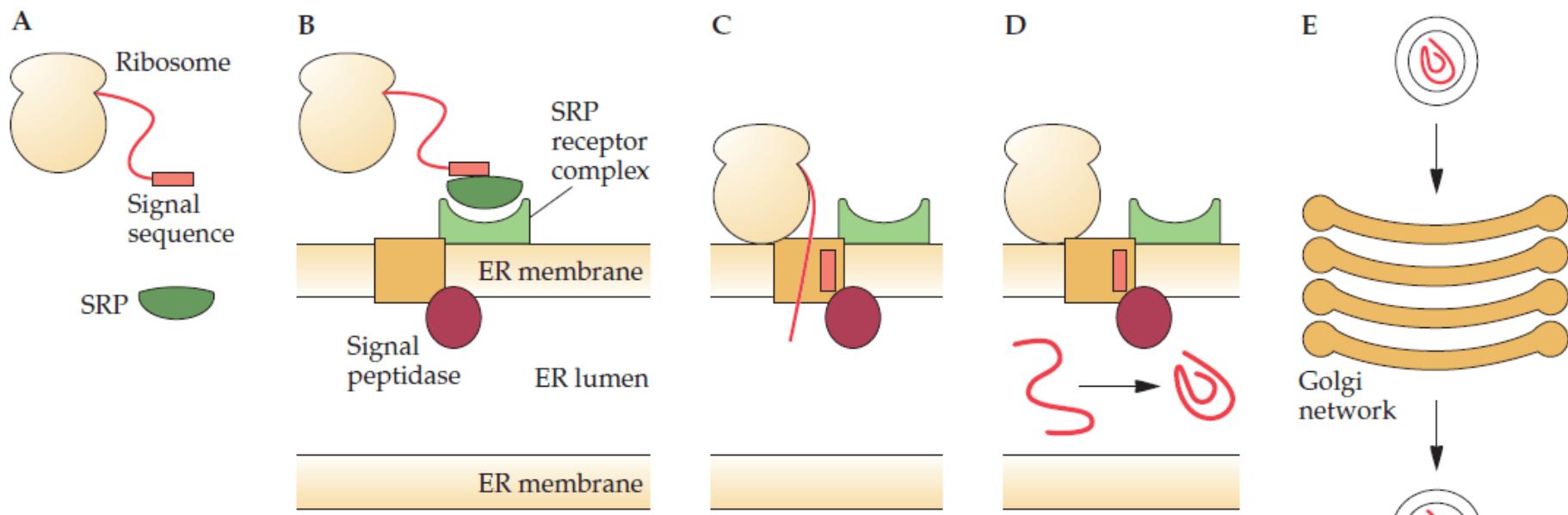
Protein Secretion Pathways



<https://doctorlib.info/physiology/medical/medical.files/image045.jpg>



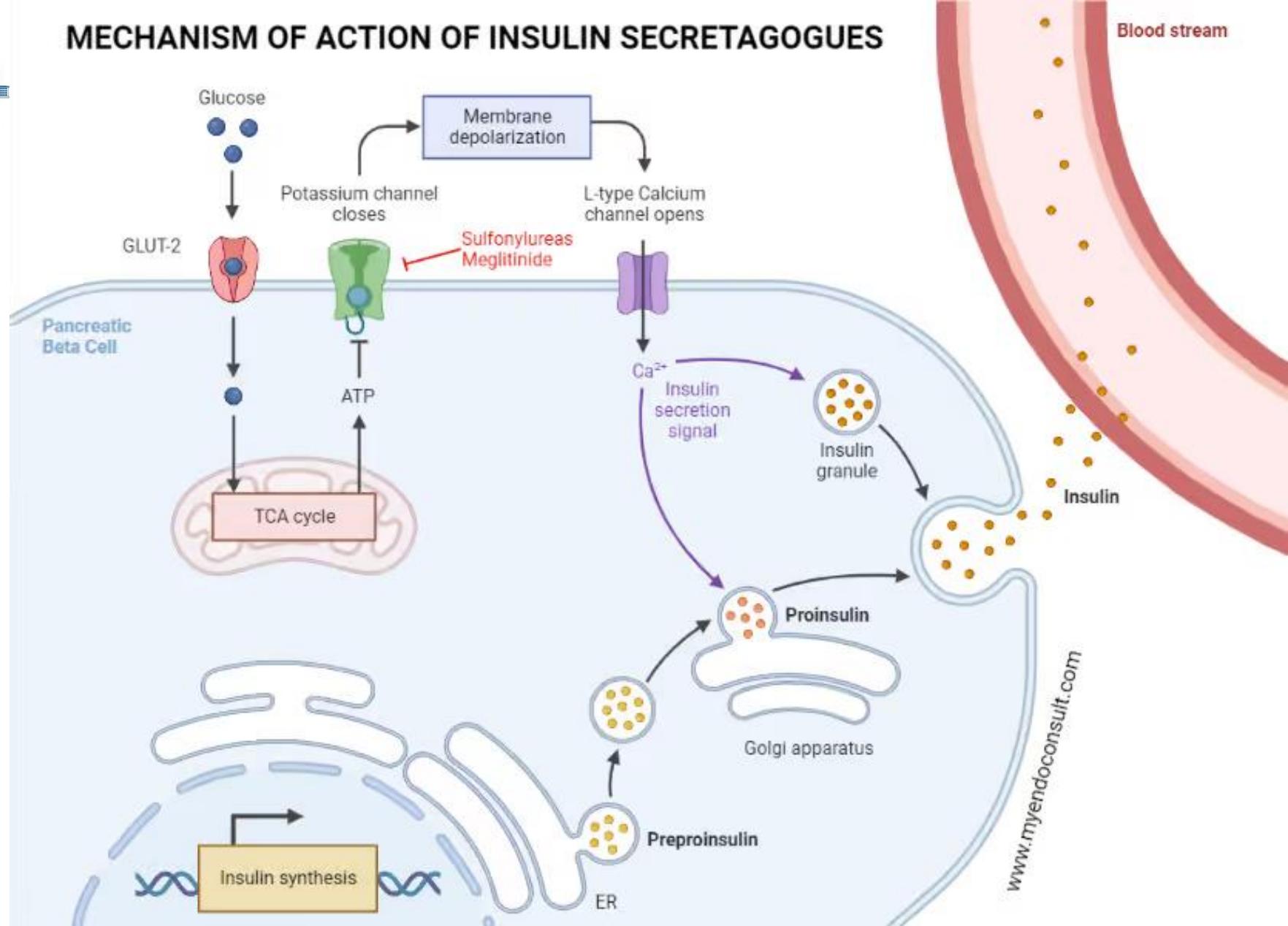
Protein Secretion Pathways



(A) A signal recognition particle (SRP) binds to the signal sequence of a secretory protein. (B) The SRP attaches to an SRP receptor on the endoplasmic reticulum (ER) membrane. (C) The secretory protein is translocated into the lumen of the ER, and a signal peptidase removes the signal sequence. (D) The secretory protein is folded, partially modified, and packaged in a transport vesicle intended for the Golgi network. (E) The ER-released vesicle carrying the secretory protein enters the Golgi network at the cis face and passes through the Golgi stack, where it is further modified; after it is sorted, a plasma membrane-specific vesicle is formed at the trans face of the Golgi network. The secretory transport vesicle fuses with the plasma membrane and releases the secretory protein to the extracellular environment.



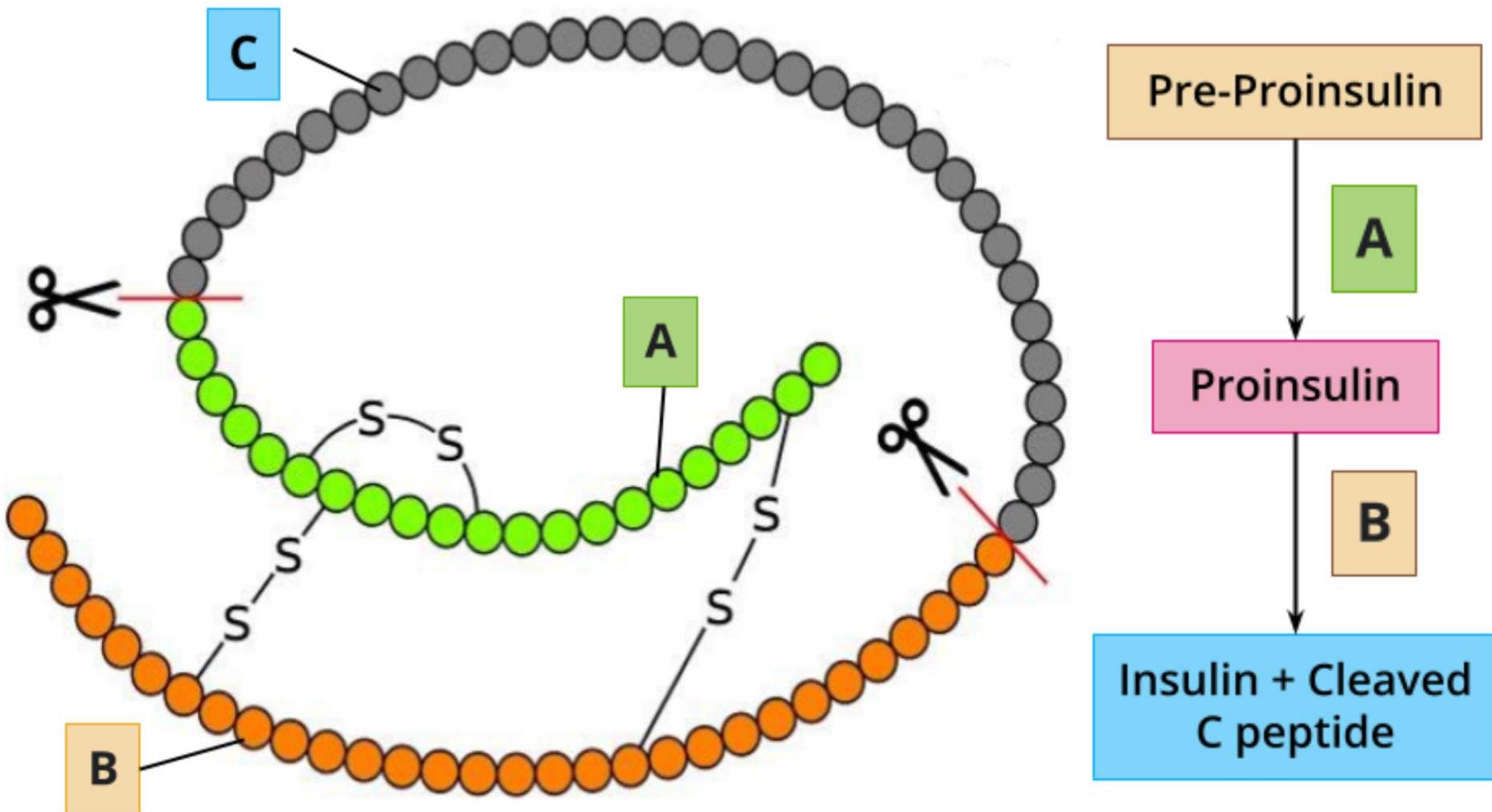
MECHANISM OF ACTION OF INSULIN SECRETAGOGUES



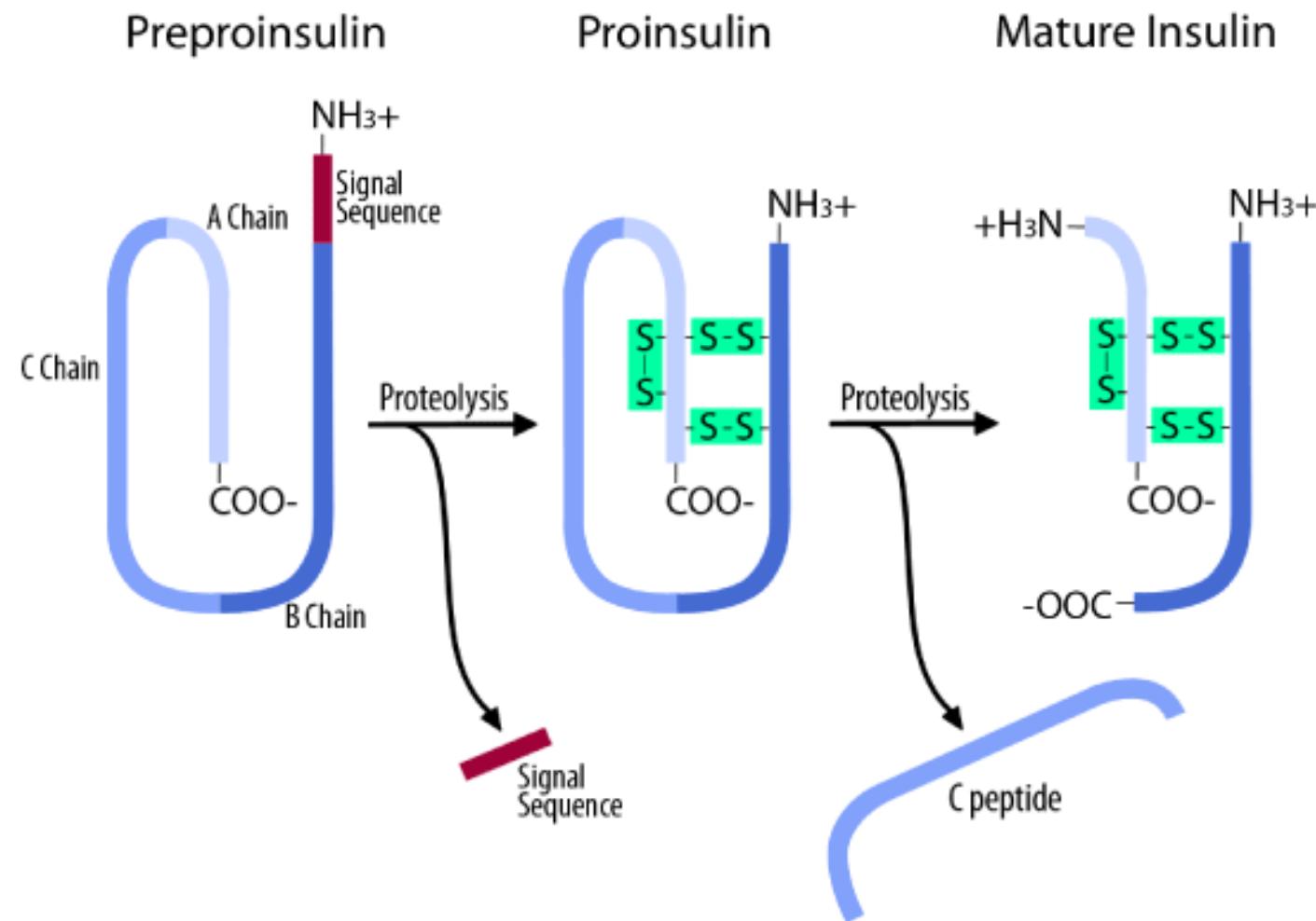
<https://myendoconsult.com/learn/insulin-physiology-and-clinical-applications/>



Protein processing



Biotechnology in medicine — lesson. Science State Board, Class 10.



<https://www.omicsonline.org/articles-images/2161-1459-3-138-g001.gif>



How are genes regulated?

- We now see how our DNA codes for our traits, making us who we are
- BUT: not all of our genes are expressed at all times
 - Humans have around 25,000 pairs of genes (1 from each parent) spread across 23 pairs of chromosomes

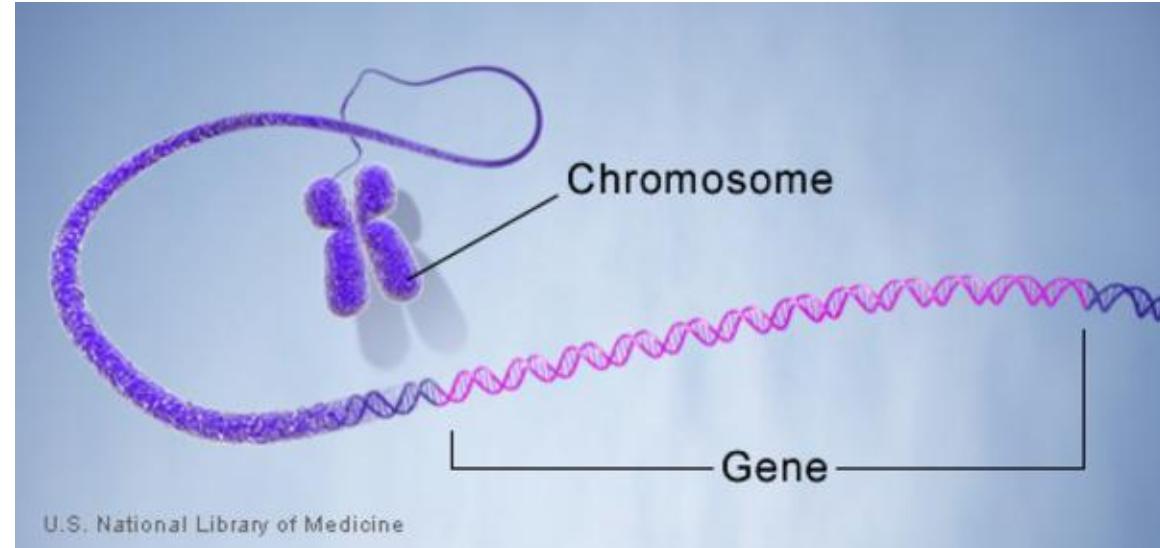


Figure: <https://medlineplus.gov/genetics/understanding/basics/gene/>



Gene expression:

- Some genes are only expressed at certain times
 - e.g. every human has 2 genes that code for milk proteins during lactation, but only some people produce these proteins at only specific times
- Some are never used by a cell
 - e.g. skin cells never need hemoglobin (for blood)
- Some are always expressed in every cell
 - e.g. cellular respiration / mitochondria enzymes
 - (all cells need ATP)

- Cells can regulate gene expression at 3 levels

- **Level 1: Transcription**

- cells control which genes are actually transcribed from DNA → RNA

- no transcription = no expression at all (e.g. milk proteins in cells that aren't lactating)

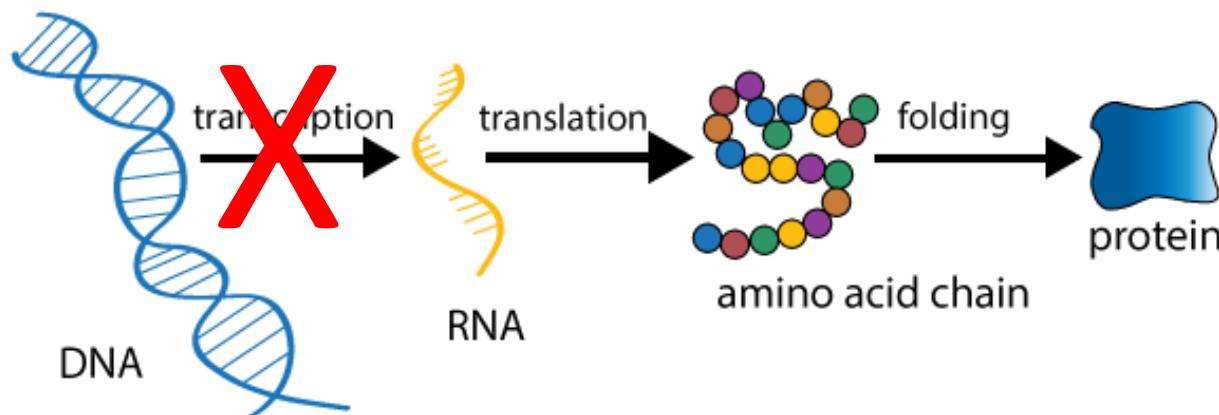


Figure: <https://biosocialmethods.isr.umich.edu/research-support/videos-tutorials/epigenetics-tutorial/>



■ RNA splicing

- Exons aren't always spliced back together exactly
- This means the RNA splicing process can allow for 1 gene to make multiple different versions of a protein – very useful!

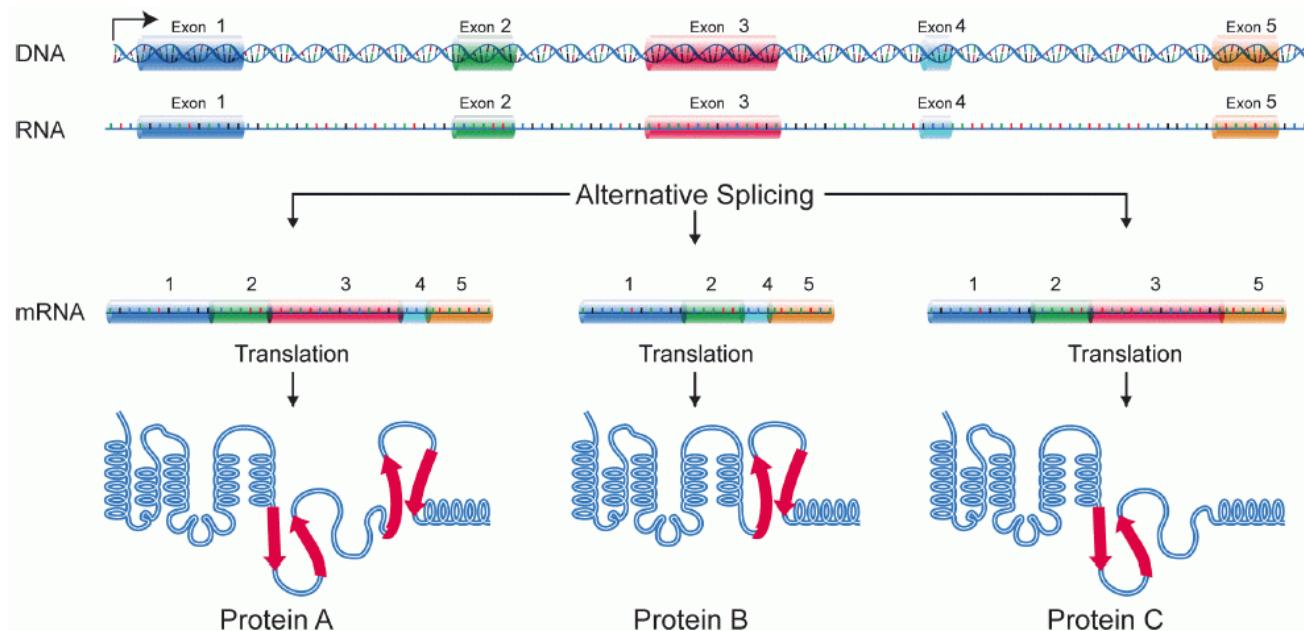


Figure: <https://www.khanacademy.org/science/biology/gene-expression-central-dogma/transcription-of-dna-into-rna/a/eukaryotic-pre-mrna-processing>

- Cells can regulate gene expression at 3 levels

- **Level 2: Translation**

- cells control how many proteins are made from mRNA after transcription

- does 1 mRNA strand make 1 protein & stop, or should it make 100 proteins?

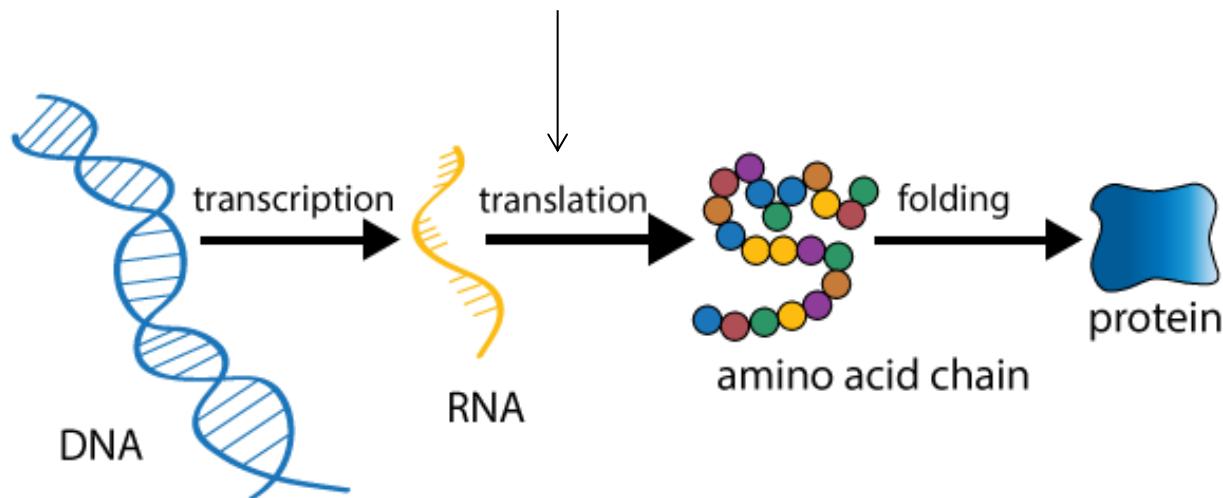
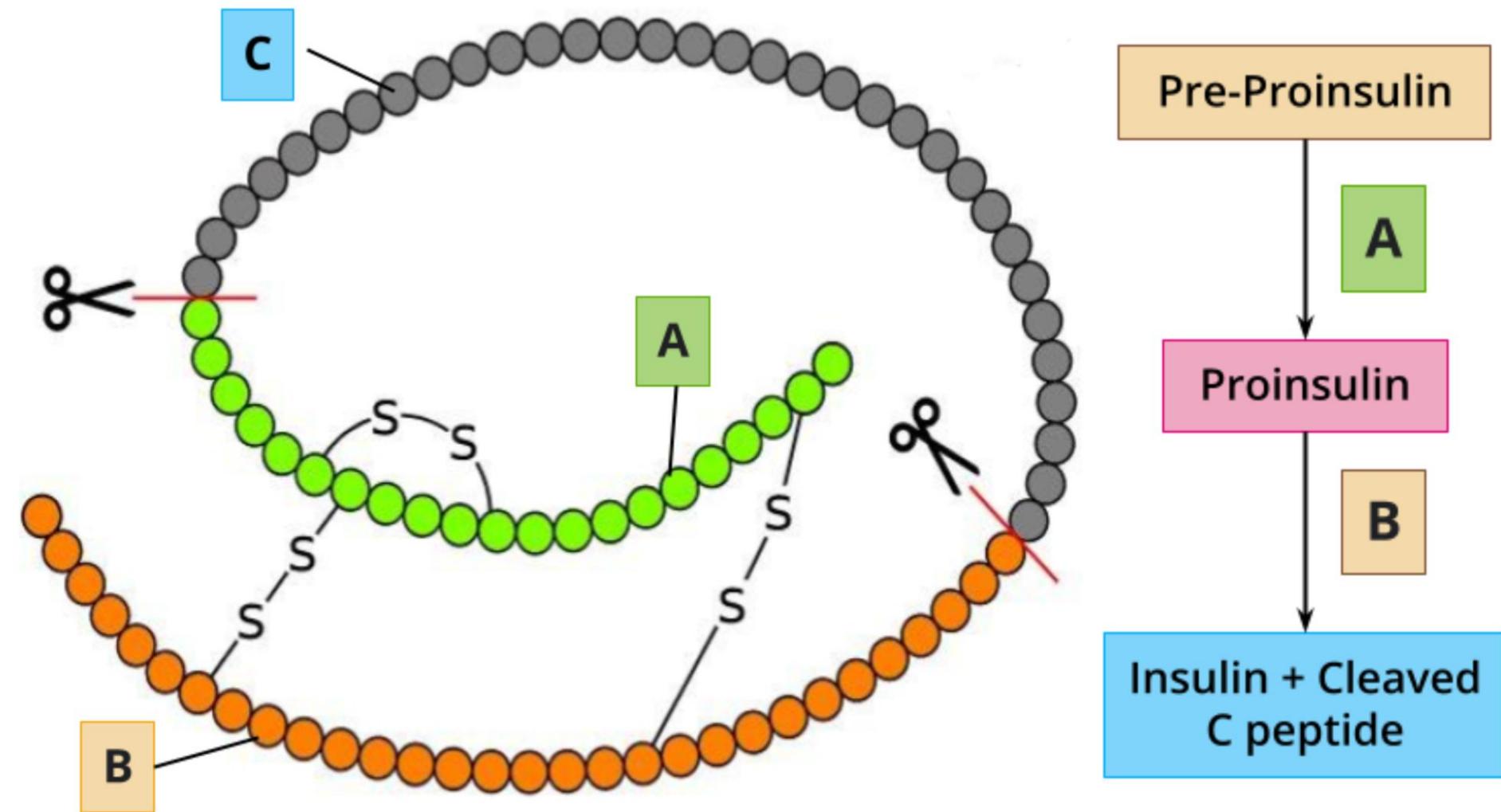


Figure: <https://biosocialmethods.isr.umich.edu/research-support/videos-tutorials/epigenetics-tutorial/>



Protein processing



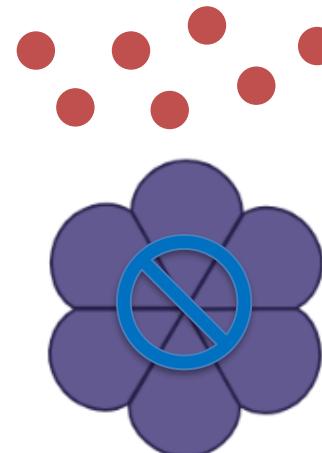
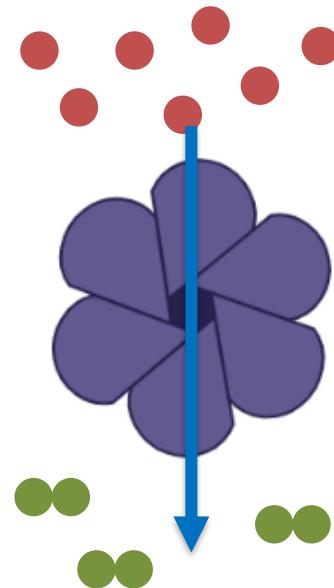
Biotechnology in medicine — lesson. Science State Board, Class 10.

- Cells can regulate gene expression at 3 levels

- **Level 3: Protein activity**

- *Remember:* cells can control metabolism by activating or inactivating proteins that have already been made

A regularly functioning protein



A protein that has been inactivated