

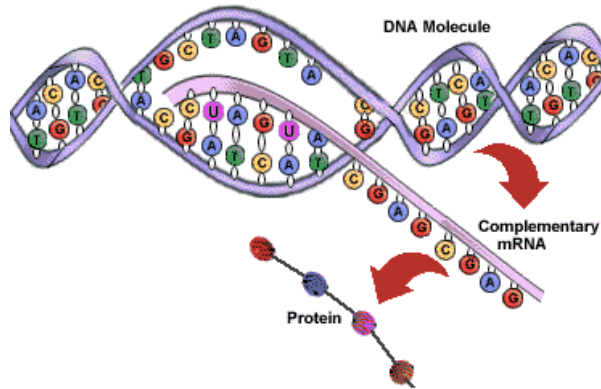
Protein Synthesis

~Biology AP~

A Meridian® Study Guide by David Guan, Jennifer Zheng [Edited by Lei Gong]

Introduction:

- DNA and RNA are essential for life because they code for enzymes, which regulate chemical reactions that's responsible for cell development, growth, and maintenance
- Two step process:
 1. transcription - use of DNA to make RNA
 2. translation - use of RNA to make proteins

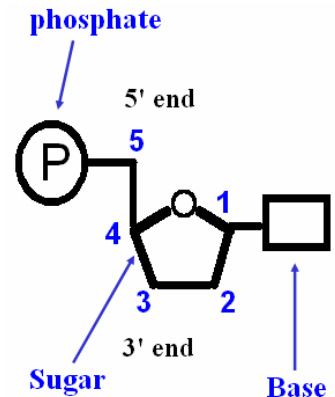


	Sugar	Nitrogen Bases	Function	Structure
DNA	deoxyribose	adenine, thymine, guanine, cytosine	contains hereditary info of the cell	double helix
RNA (3 kinds)	Ribose	adenine, uracil, guanine, cytosine	mRNA - provides information for assembling amino acids into proteins	linear
			tRNA - helps with building polypeptide chain by delivering amino acids	"clover-leaf" shaped
			rRNA - combines with proteins to form ribosomes	globular

DNA:

Structure

- made up of nucleotides (single unit of proteins)
- 5 carbon sugar, each of them have a number: number the carbons starting from right of oxygen and go around clockwise
- benefit is that it gives the nucleotide two ends
 - o 5' end is the side closer to carbon 5
 - o 3' end is the side closer to carbon 3

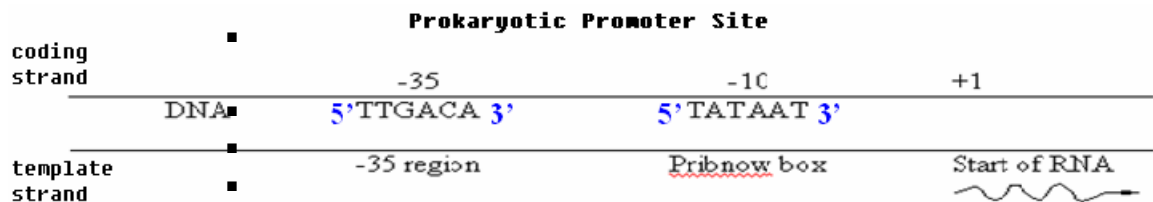


Nucleic Acid Structure

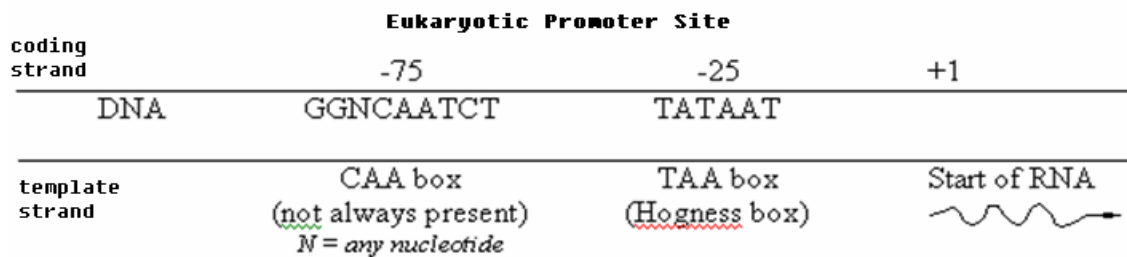
- double stranded
- hydrogen bonds occur between bases
 - o adenine pairs with thymine - causes two hydrogen bonds to form
 - o cytosine pairs with guanine - causes three hydrogen bonds to form
- strands are anti-parallel so that the bases can form hydrogen bonds
 - o coding strand - one strand runs 5' -> 3', similar to mRNA, but with thymine instead of uracil
 - o template strand - one strand runs 3' -> 5', the strand actually used to code for mRNA

Transcription

- the process of making mRNA
- Initiation
 - o Start of transcription
 - o RNA polymerase organizes promoter sequence on DNA and binds to promoter
 - o Promoter sequences
 - In prokaryotes, RNA polymerase must find following:



- REMEMBER THAT +1 is the first base in the mRNA (Note there is no +/-0 position)
- In eukaryotes, RNA polymerase must find following:



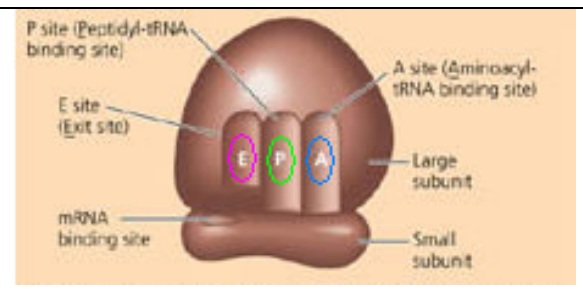
- Eukaryote genes can also have enhancer sequences from start site to help RNA polymerase bind
 - o DNA is unwound to start transcription
 - o Hydrogen bonds are broken
- Elongation
 - o How mRNA is built

- RNA polymerase brings free nucleotides over to complement with DNA template strand and catalyzes formation of covalent bonds between RNA nucleotides to form mRNA.
- Remember that:
 - Template strand is actual strand to build mRNA
 - Coding strand has almost the same sequence as RNA but doesn't help code it (like a double check)
- Termination
 - Occurs when RNA polymerase reaches special sequence of nucleotides
 - In eukaryotes, termination region contains the DNA sequence AAAA or UUUU (or any combination of these). Why?
 - With a string of A's and U's, there are fewer bonds to hold DNA template and RNA together so they separate
 - There are only TWO hydrogen bonds between A and T/U

Translation

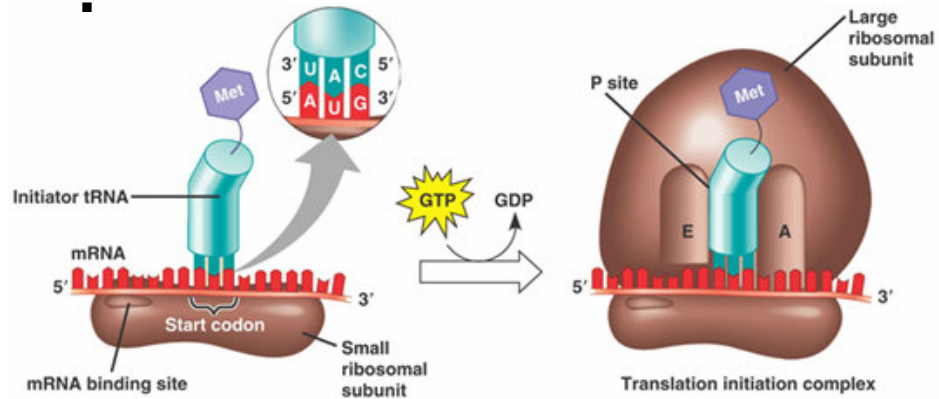
- After transcription, mRNA, tRNA, and ribosomal subunits are transported across the nuclear envelope
- using mRNA code to create appropriate protein
- occurs in cytoplasm or on rough ER
- codon is a sequence of 3 nucleotide for 64 (4^3) different combinations which codes for particular amino acids (each amino acid can be coded by more than one sequence). Why not combinations of 1 or two?
 - 1 nucleotide - only enough for 4 different amino acids
 - 2 nucleotides - only enough for 16 or (4^2) amino acids
- tRNA
 - brings correct amino acid to match with mRNA codon
 - each tRNA holds specific amino acid and has certain anticodon
- Ribosome
 - Made up of 2 subunits and composed of rRNA and proteins
 - Not specific to any particular protein - can be used to translate any RNA into any protein
 - “workbench for translation” - holds mRNA and rRNA in correct positions to assemble protein
 - 3 sites

- The **P site** holds the tRNA carrying a polypeptide chain.
- The **A site** is the “waiting room,” as it holds the tRNA carrying the next amino acid.
- The **E site** is the “exit” where tRNA is discharged from the ribosome.



- Initiation

- Starts when ribosomal subunit attaches to 5' end of mRNA
- Begins translating at start codon, AUG, which codes for Met amino acid
- REMEMBER
 - AUG is NOT the same as +1 start position
 - Start LOOKING for AUG after you encounter +1 start position

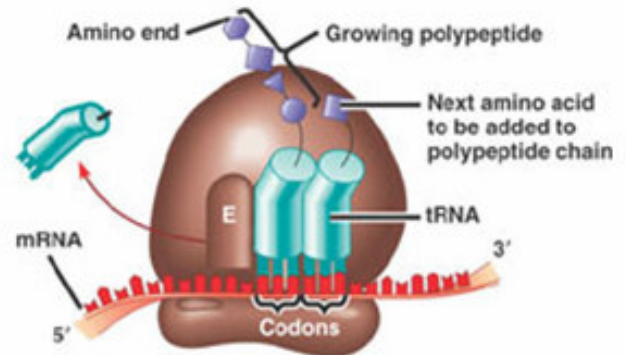


- Elongation

- Ribosome moves along 5' -> 3' direction
- When tRNA brings correct amino acid to match with mRNA codon, it forms hydrogen bonds between anticodon and codon.
- The ribosome helps tRNA attach to codon

- Termination

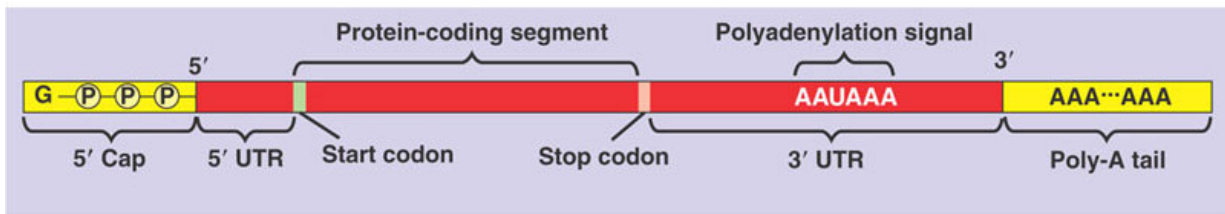
- Ribosome encounters one of the three stop codons (UAA, UAG, UGA)*
- !!!! Remember STOP is NOT a codon!!!! DO NOT write down STOP as part of your sequence.
- Completed polypeptide, last tRNA, and two ribosomal subunits are released
- Release factor binds to mRNA instead



* A useful mnemonic device in the immortal words of Ms. Tsai - U Are Awful, U Are Gross, U Go Away!

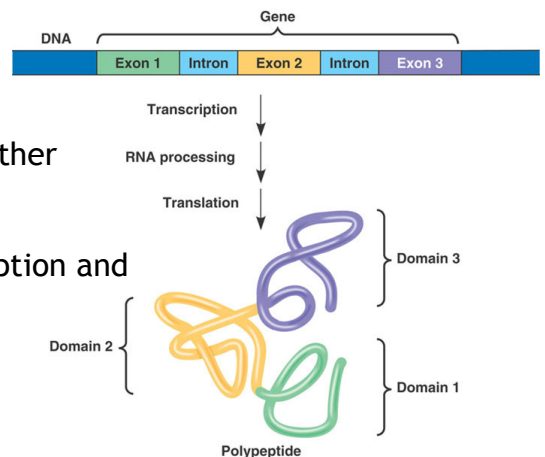
PROTEIN SYNTHESIS: Prokaryotes vs. Eukaryotes

- ❖ **PROTEIN TARGETTING (In Eukaryotes)**
 - Signal peptide (part of protein to be bound to Signal Recognition Particle) directs secretory protein to ER
 - Ribosome translates amino acids of signal peptide
 - Signal peptide is recognized by SRP and bound to it
 - Protein goes into ER as it is made.
 - Signal sequence is removed by enzyme in ER
- **Protein Synthesis in Eukaryotes**
 - RNA processing occurs between transcription and translation
 - Pre-mRNA is modified
- **5' (G) cap is added**
 - Helps mRNA bind to ribosome
 - Protects RNA from enzymes
- **Poly A tail is added**
 - NOT a termination sequence
 - Stabilizes RNA



- **RNA Splicing**
 - Introns - (“Junk DNA”) are cut out
 - Exons - (coding portions) are joined together

- **Protein Synthesis in Prokaryotes**
 - The absence of a nucleus allows transcription and translation to occur concurrently



Mutations

- **Mutations** are changes in the DNA of a gene.
- **Point Mutations** are mutations that occur in just one base pair of a gene.
- **Wild Type** is the normal DNA sequence.

TYPES OF POINT MUTATIONS	
Base-pair Substitution	<p>Wild type</p> <p>mRNA 5' AUGAAGUUUGGCUA 3'</p> <p>Protein Met Lys Phe Gly Stop</p> <p>Amino end Carboxyl end</p> <p>Base-pair substitution</p> <p>No effect on amino acid sequence</p> <p>U instead of C</p> <p>AUGAAGUUUGUUA</p> <p>Met Lys Phe Gly Stop</p> <p>➤ Only one nucleotide and its partner are replaced, therefore there is no effect on the amino sequence.</p> <p>➤ Also called a <i>silent mutation</i>.</p>
Missense	<p>Wild type</p> <p>mRNA 5' AUGAAGUUUGGCUA 3'</p> <p>Protein Met Lys Phe Gly Stop</p> <p>Amino end Carboxyl end</p> <p>Missense</p> <p>A instead of G</p> <p>AUGAAGUUUAAGCUAA</p> <p>Met Lys Phe Ser Stop</p> <p>➤ Altered codon codes for an alternate amino acid that has similar functions.</p>
Nonsense	<p>Wild type</p> <p>mRNA 5' AUGAAGUUUGGCUA 3'</p> <p>Protein Met Lys Phe Gly Stop</p> <p>Amino end Carboxyl end</p> <p>Nonsense</p> <p>U instead of A</p> <p>AUGUAGUUUGGCUA</p> <p>Met Stop</p> <p>➤ Codon is altered into a stop codon, therefore terminating translation prematurely – frequently results in nonfunctional proteins.</p>
FRAMESHIFT MUTATIONS (Insertion/Deletion)	
Wild type	<p>Base-pair insertion or deletion</p> <p>Frameshift causing immediate nonsense</p> <p>Extra U</p> <p>AUGUAAGUUUGGCUA</p> <p>Met Stop</p> <p>➤ An extra nucleotide pair is added, causing immediate nonsense.</p>

