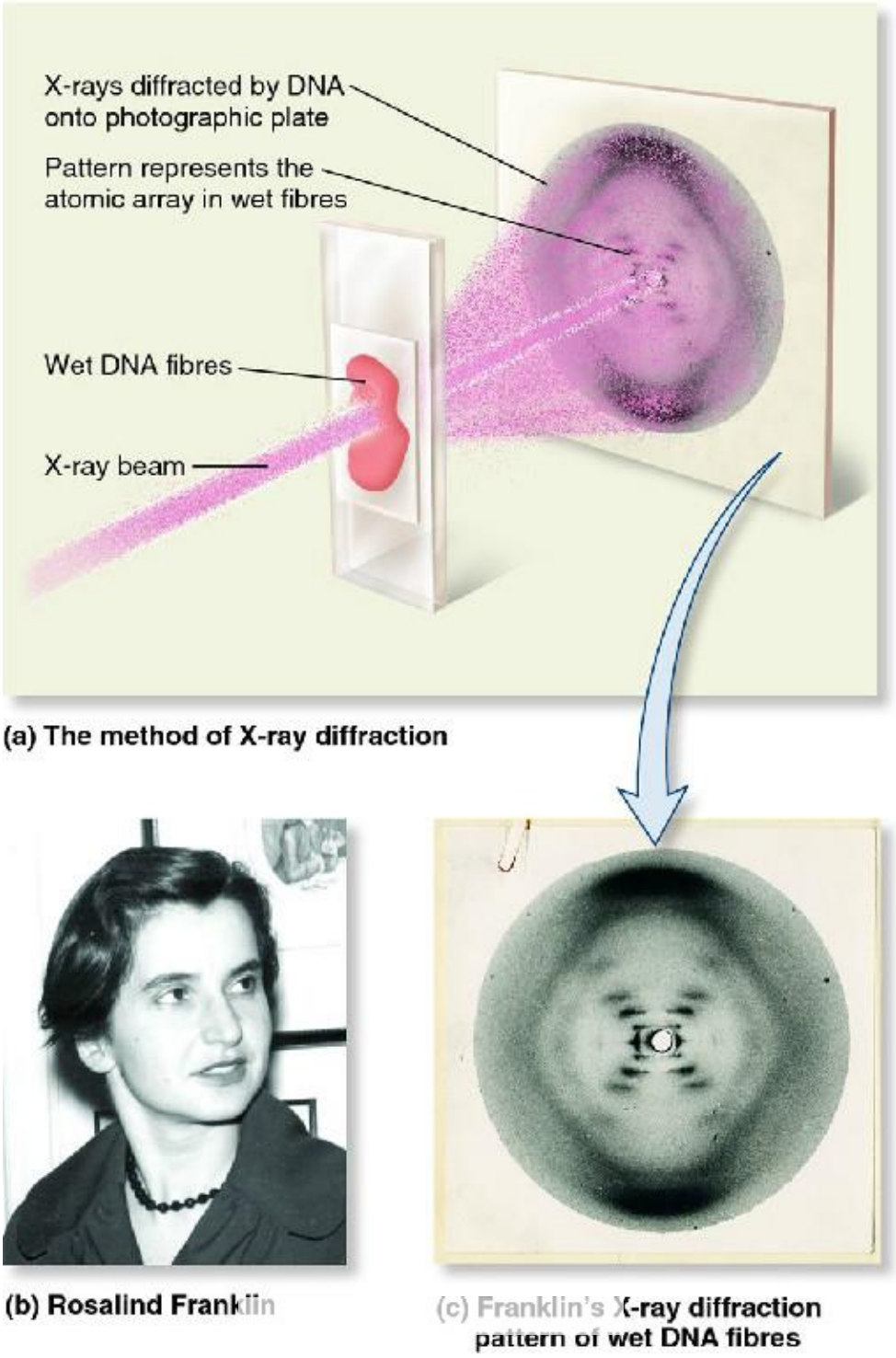
7.1 DNA Structure and Replication

Nature of Science: Making careful observations—Rosalind Franklin's X-ray diffraction provided crucial evidence that DNA is a double helix. (1.8)

β - Skill: Analysis of results of the Hershey and Chase experiment providing evidence that DNA is the genetic material.

- Watch the following animation and explanation of the Hershey-Chase experimenthttp://highered.mheducation.com/sites/9834092339/student_view0/chapter14/hershey_and_chase_experiment.html
- Do the data-based questions on page 345 to reinforce your understanding.

- **β - Application: Rosalind Franklin's and Maurice Wilkins' investigation of DNA structure by X-ray diffraction.**



http://biology-forums.com/index.php?action=gallery;sa=view;id=398

Watch the video on http://www.dnai.org/a/index.html (finding the structure > players > Rosalind Franklin) on Rosalind Franklin and read through the articles on page 345 and 346 of your text.

Describe the deductions Franklin was able to make regarding the structure of DNA.

1)

2)

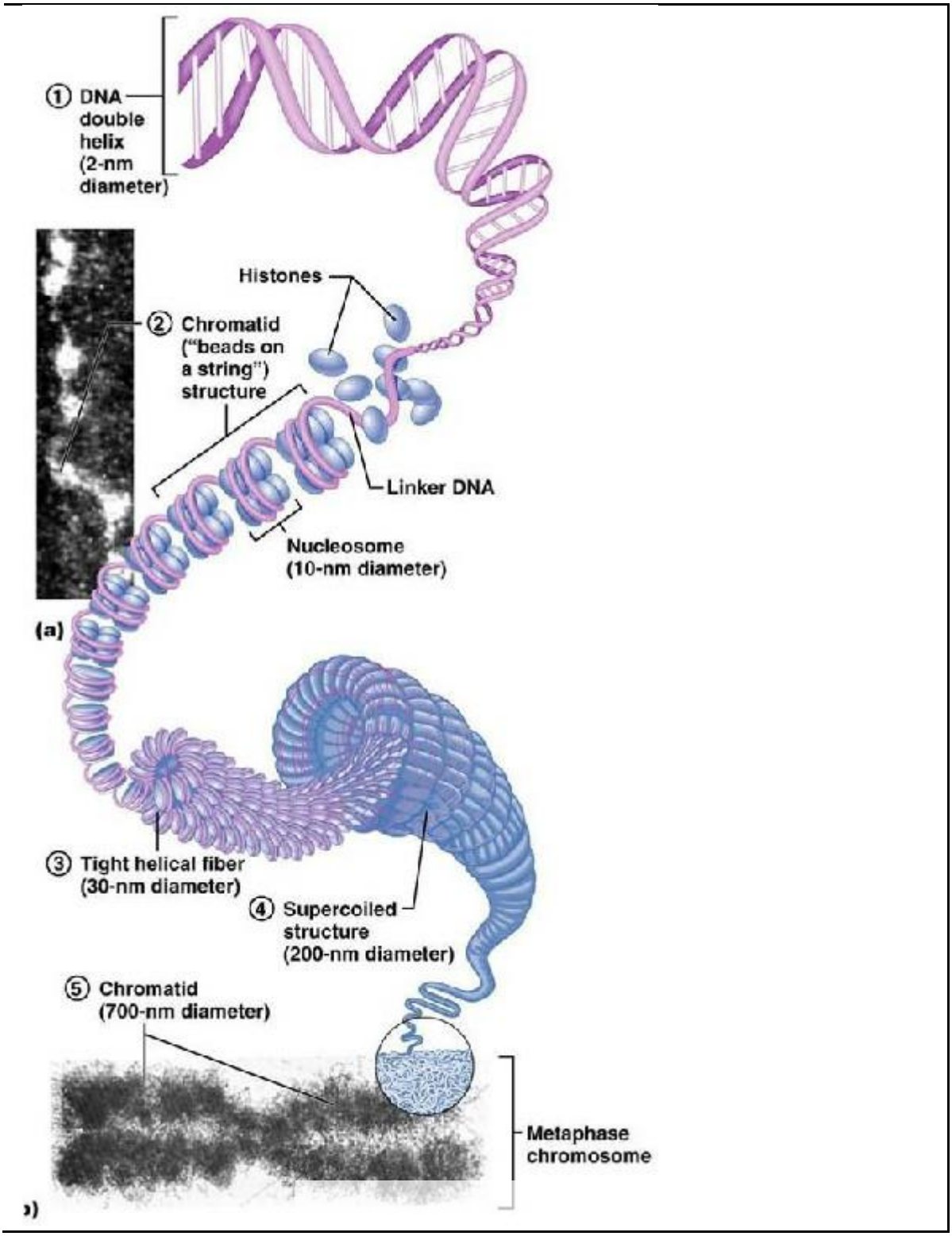
3)

4)

Understandings ∑

∑ Nucleosomes help to supercoil the DNA.

- A nucleosome consists of DNA wrapped around 8 histone proteins.
- The DNA wraps twice around the histone protein core.
- Another histone protein is attached to the outside of the DNA strand. It helps maintain the colloidal structure of the nucleosome.
- DNA, because of its negative charge is attracted to the positive charge on the amino acids of the histone proteins.
- The core of histone proteins have tails of –NH2 which is the amino side (called the N-terminus) sticking outwards from the nucleosomes
- These tails of neighboring histones, link up during chromosomal condensation, causing thenucleosomes to pull closer together.
- This is part of the supercoiling process that occurs during mitosis and meiosis
- Supercoiling in general helps regulate transcription because only certain areas of the DNA areaccessible for the production of mRNA by transcription. This regulates the production of a polypeptide.



http://apbrwww5.apsu.edu/thompsonj/Anatomy%20&%20Physiology/2010/2010%20Exam%20Reviews/Exam%201%20Review/Ch03%20The%20Nucleus.htm

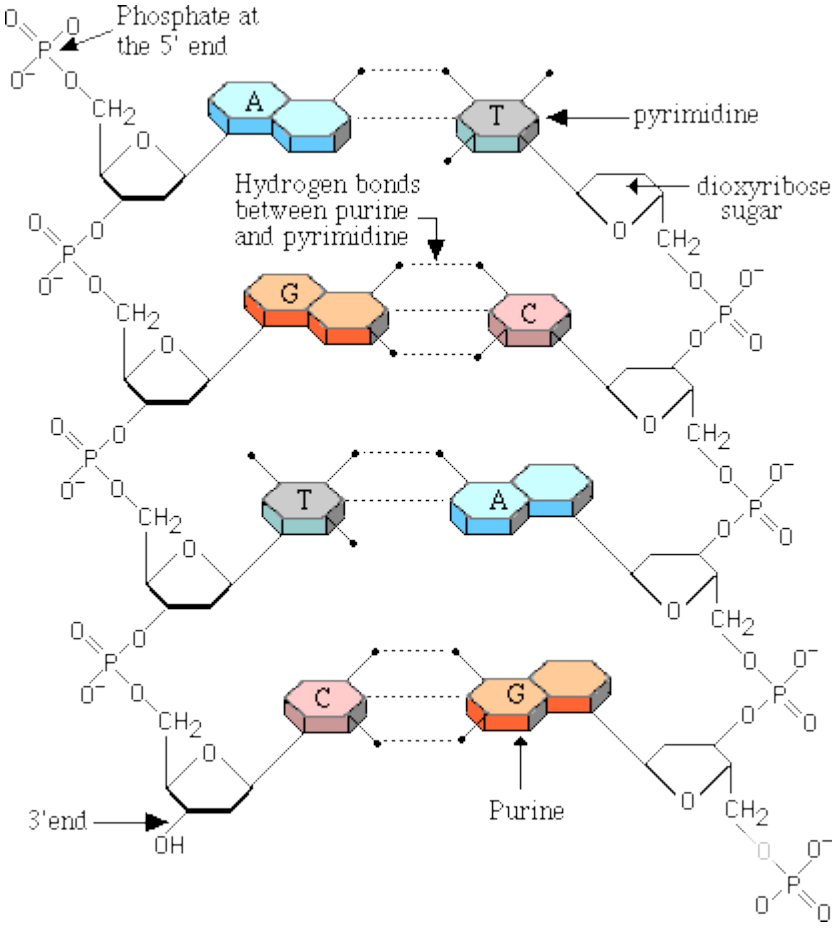
β - Skill: Utilization of molecular visualization software to analyse the association between protein and DNA within a nucleosome.

Very good molecular visualization of histone proteins and their interaction with DNA.https://www.youtube.com/watch?v=vbueAuw96zA

Do the data-based questions on page 349 of your textbook

∑ - DNA structure suggested a mechanism for DNA replication.

- DNA is double stranded and shaped like a ladder, with the sides of the ladder made out of repeating phosphate and deoxyribose sugar molecules covalently bonded together.
- Each deoxyribose molecule has a phosphate covalently attached to a 3' carbon and a 5' carbon.
- The phosphate attached to the 5' of one deoxyribose molecule is covalently attached to the 3' of the next deoxyribose molecule forming a long single strand of DNA known as the DNA backbone.
- DNA strands run antiparallel to each other with one strand running in a 5' to 3' direction and the other strand running 3' to 5' when looking at the strands in the same direction



http://home.earthlink.net/~dayvdanls/lecw4cells6.html

- The rungs of the ladder contain two nitrogenous bases (one from each strand) that are bonded together by hydrogen bonds.

- Since these two strands are anti-parallel replication occurs in different directions on the DNA strand
- Purines are two ring nitrogenous bases and pyrimidines are single ring nitrogenous bases.
- The nitrogenous bases match up according the Chargaff's Rules in which adenine (purine) always bonds to thymine (pyrimidine), and guanine (purine) always bonds with cytosine (pyrimidine).

These three understandings are combined to explain the full process of replication.

∑ - DNA replication is continuous on the leading strand and discontinuous on the lagging strand.

∑ - DNA polymerases can only add nucleotides to the 3' end of a primer.

∑ - DNA replication is carried out by a complex system of enzymes.

- DNA replication creates two identical strands with each strand consisting of one new and one old strand (semi-conservative).
- DNA replication occurs at many different places on the DNA strand called the origins of replication (represented by bubbles along the strand).

- The DNA strand is unwound and separated (hydrogen bonds broken) by an enzyme calledhelicase.
- DNA gyrase (also called topoisomerase) is an enzyme that relieves strain on the stand as it is being unwound by the helicase
- Single-stranded binding proteins bind to the open strands and keep the strands apart long enough to prevent the strands from re-annealing before the strands are copied

- DNA replication begins at the different origins in the 5' to 3' direction at the replication fork(place where the strands split exposing the two template strands).

- RNA primase attaches to the DNA and adds a small RNA primer (5-10 RNA nucleotides) to**provide a free 3' OH starting point since DNA polymerases can only add nucleotides to the 3' end of a primer**

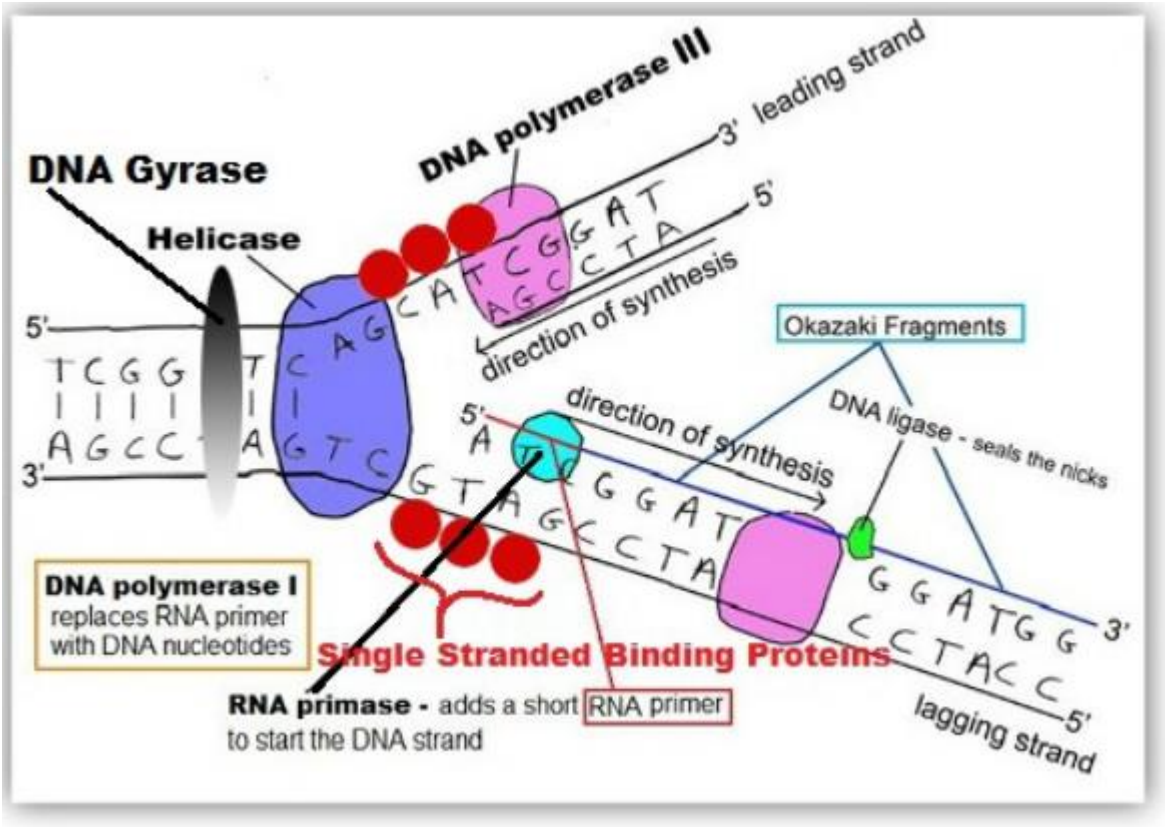
-

- DNA polymerase III adds free nucleotides found in the nucleus in the 5' to 3' direction in thedirection of the replication fork.
- These nucleotides when added are actually deoxynucleoside triphosphates (dNTP), which means the nucleotide contains 3 connected phosphate groups. As dNTP's are added, two

phosphates are lost and the energy released is used to bind the nucleotides together on the growing strand.

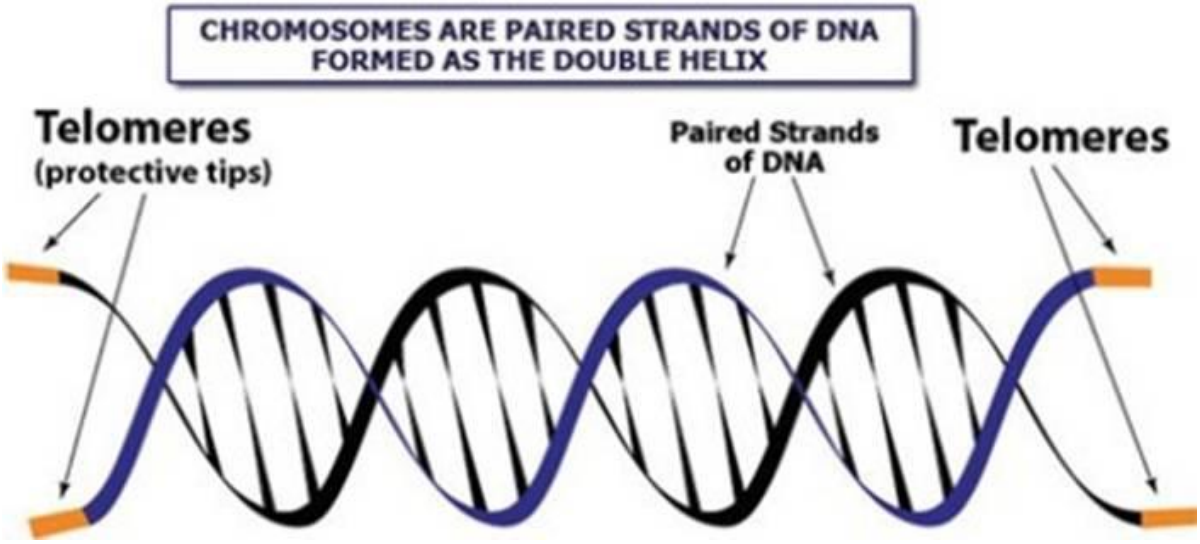
- This strand is called the **"leading strand"** because replication is **continuous** (keeps replicating until it meets another origin of replication).
- Because DNA polymerase III can only add nucleotides to a free 3' end (5'to 3' direction) the other strand is replicated in the opposite direction.
- This strand is called the **"lagging strand"** because replication is delayed until the helicase opens up available nucleotides, to allow replication "back" in the opposite direction to the leading strand. Replication in this direction is **discontinuous.**
- The lagging strand is therefore made as a series of fragments called "Okazaki fragments"

- RNA primase adds a small primer on the lagging strand of DNA.
- DNA polymerase III adds nucleotides again in the 5' to 3' direction (opposite direction of the leading strand because the stands are antiparallel)
- After the fragment is created DNA polymerase I replaces the RNA primer with DNA.
- As the strand continues to open, a new RNA primer is added and a new fragment of DNA is created away from the replication fork.
- As these fragments are made, little nicks are created between the fragments. DNA ligase forms a phosphodiester bond between 3' OH on the growing strand and the 5' phosphate on the next fragment (basically seals the nicks between the phosphates and the sugars)



∑ **- Some regions of DNA do not code for proteins but have other important functions.**

- Genes contained within DNA called coding sequences, code for polypeptides created during transcription and translation
- The majority of DNA are non-coding sequences that perform other functions such as regulators of gene expression, introns, telomeres and genes for tRNAs.
- Regulators such as **enhancers** are short DNA sequences that regulatory proteins bind to, toactivate transcription
- **Silencers** are DNA sequences that bind regulatory proteins called repressors that prevent RNA polymerase from binding to the promoter site, thereby preventing transcription
- DNA in eukaryotes also codes for the non-coding regions of mRNA called **introns**, which areremoved before leaving the nucleus
- There are specific sequences of DNA that are used as a guide for the production of tRNA and rRNA
- In DNA there are also many repetitive sequences, especially in eukaryotic DNA, that can make up 5-60% of the genome; specifically, an area of repetitive sequences that occurs on the ends of eukaryotic chromosomes.
- These repetitive sequences called telomeres, protect the DNA during replication. Since enzymes can't replicate all the way to the end of the chromosome, the parts that aren't copied are part of the telomeres. This prevents the loss of genes near the end of the chromosomes.



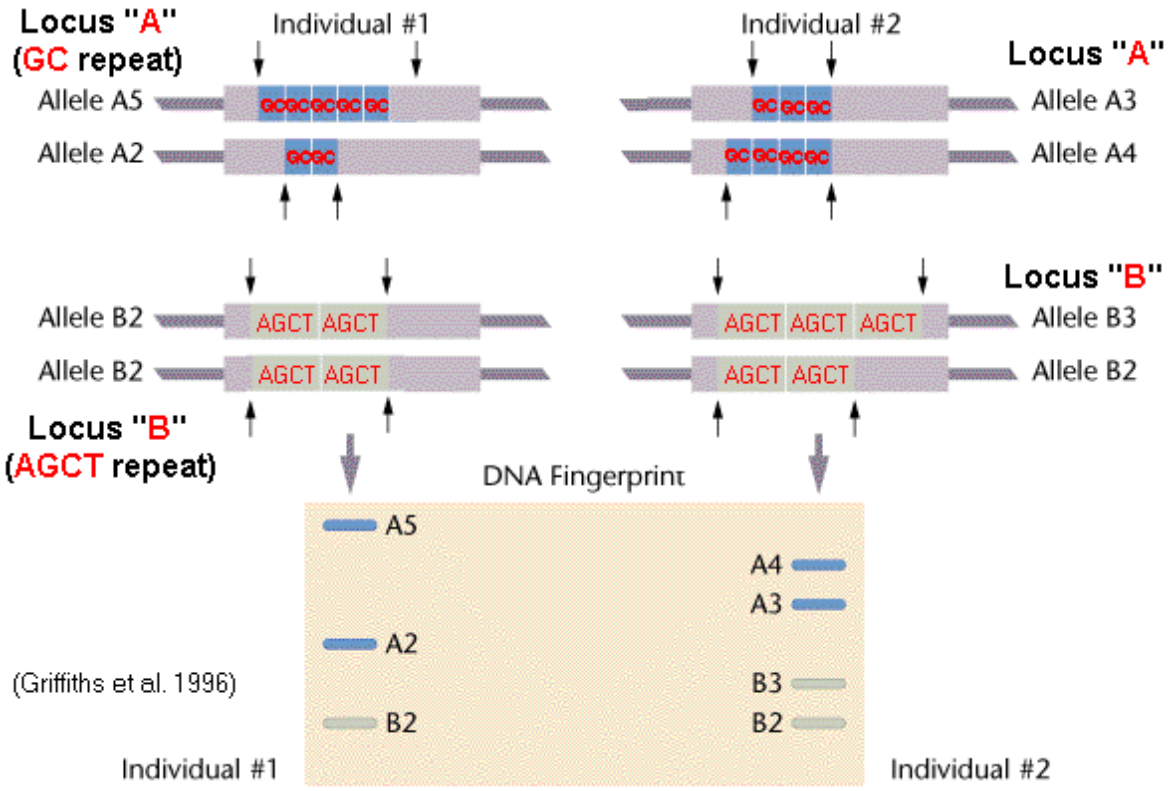
http://metro-medispa.com/wp-content/uploads/2012/02/telomeres-and-dna-chromosones.jpg

Good video on telomerase functionhttp://highered.mheducation.com/sites/9834092339/student_view0/chapter14/telomerase_function.html

β - Application: Tandem repeats are used in DNA profiling.

Short tandem repeats (STRs), also known as variable tandem repeats (VNTRs) are regions of noncoding DNA that contain repeats of the same nucleotide sequence. These short repeats showvariations between individuals in terms of the number of times the sequences is repeated.

For example, CATACATACATACATACATACATA is a STR where the nucleotide sequence CATA is repeated six times for one individual. However, in another individual, this tandem repeat could occur only 4 times CATACATACATACATA. These variable tandem repeats are the basis for DNA profiling used in crime scene investigations and genealogical tests (paternity tests). The diagram below shows how the different number of these alleles for the VNTRs are used to create a DNA fingerprint of an individual.



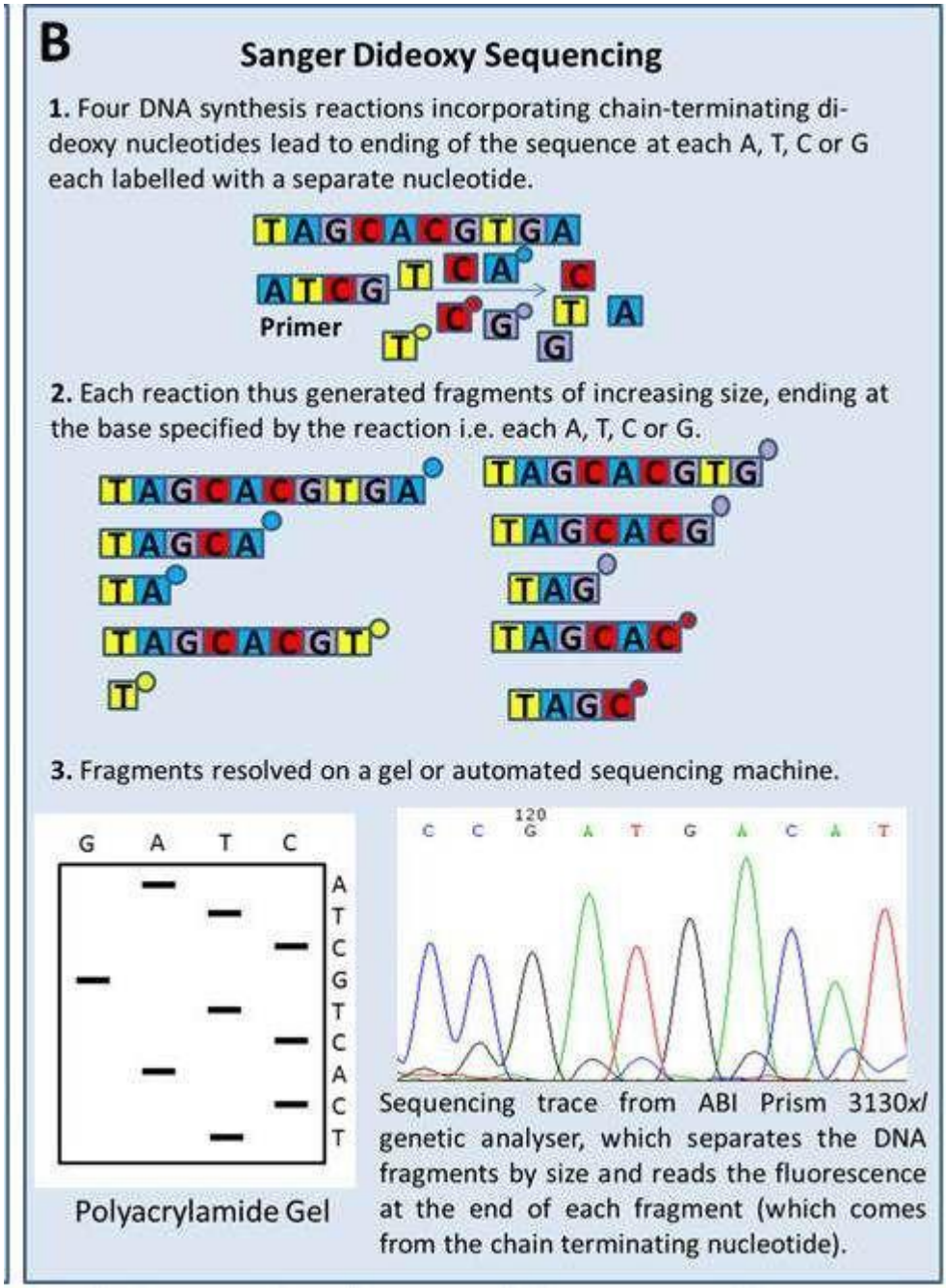
http://www.mun.ca/biology/scarr/VNTR_fingerprint_2.gif

Also look at the diagram on page 351 of your textbook to make sure you understand how tandem repeats are used in DNA profiling.

Work through the activity and questions on page 352 and 353

β - Application: Use of nucleotides containing dideoxyribonucleic acid to stop DNA replication in preparation of samples for base sequencing.

Dideoxyribonucleotides inhibit DNA polymerase during replication, thereby stopping replication from continuing. Dideoxyribonucleotides with fluorescent markers, are used and incorporated into sequences of DNA, to stop replication at the point at which they are added. This creates different sized fragmentswith fluorescent markers that can be separated by gel electrophoresis and analyzed by comparing the colour of the fluorescence with the fragment length.



http://www.oxbridgebiotech.com/review/research-and-policy/whats-so-special-about-next-generation-sequencing/

Theory of knowledge:

•Highly repetitive sequences were once classified as “junk DNA” showing a degree of confidence that it had no role. To what extent do the labels and categories used in the pursuit of knowledge affect the knowledge we obtain?

Guidance:

•Details of DNA replication differ between prokaryotes and eukaryotes. Only the prokaryotic system is expected.

•The proteins and enzymes involved in DNA replication should include helicase, DNA gyrase, single strand binding proteins, DNA primase and DNA polymerases I and III.

•The regions of DNA that do not code for proteins should be limited to regulators of gene expression, introns, telomeres and genes for tRNAs.

7.2 Transcription and Gene Expression

Nature of science: Looking for patterns, trends and discrepancies—there is mounting evidence that the environment can trigger heritable changes in epigenetic factors. (3.1)

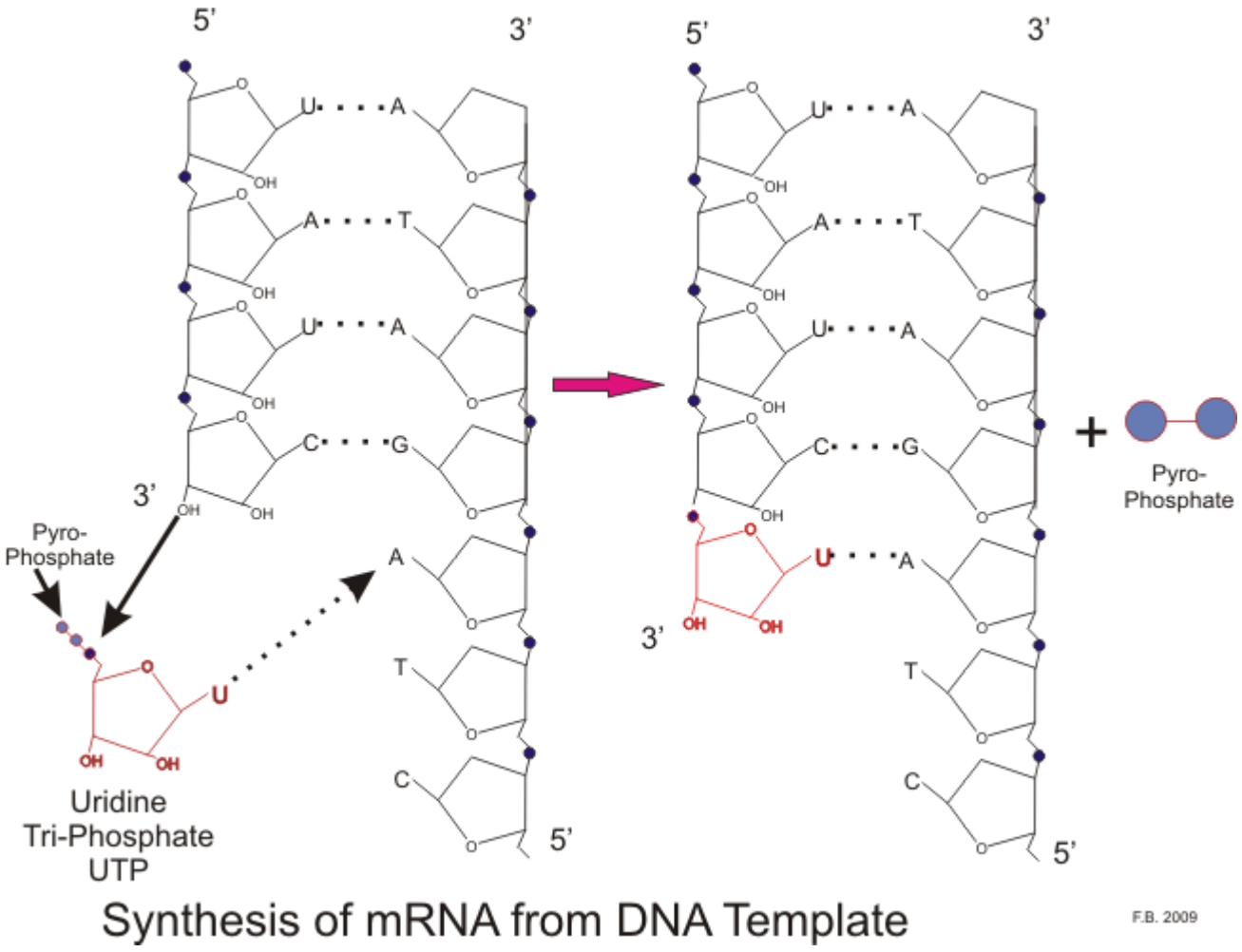
The following website is a really good introduction to the topic of gene expression and epigenetics.

Watch the videos at http://learn.genetics.utah.edu/content/epigenetics/ and complete both of the interactive explorations on ***"Gene Control" and "Lick your Rats".*** *Also read Epigenetics and Inheritance, Nutrition and the Epigenome, and Epigenetics and the Human Brain.*

∑- Understandings:

∑ - Transcription occurs in a 5' to 3' direction.

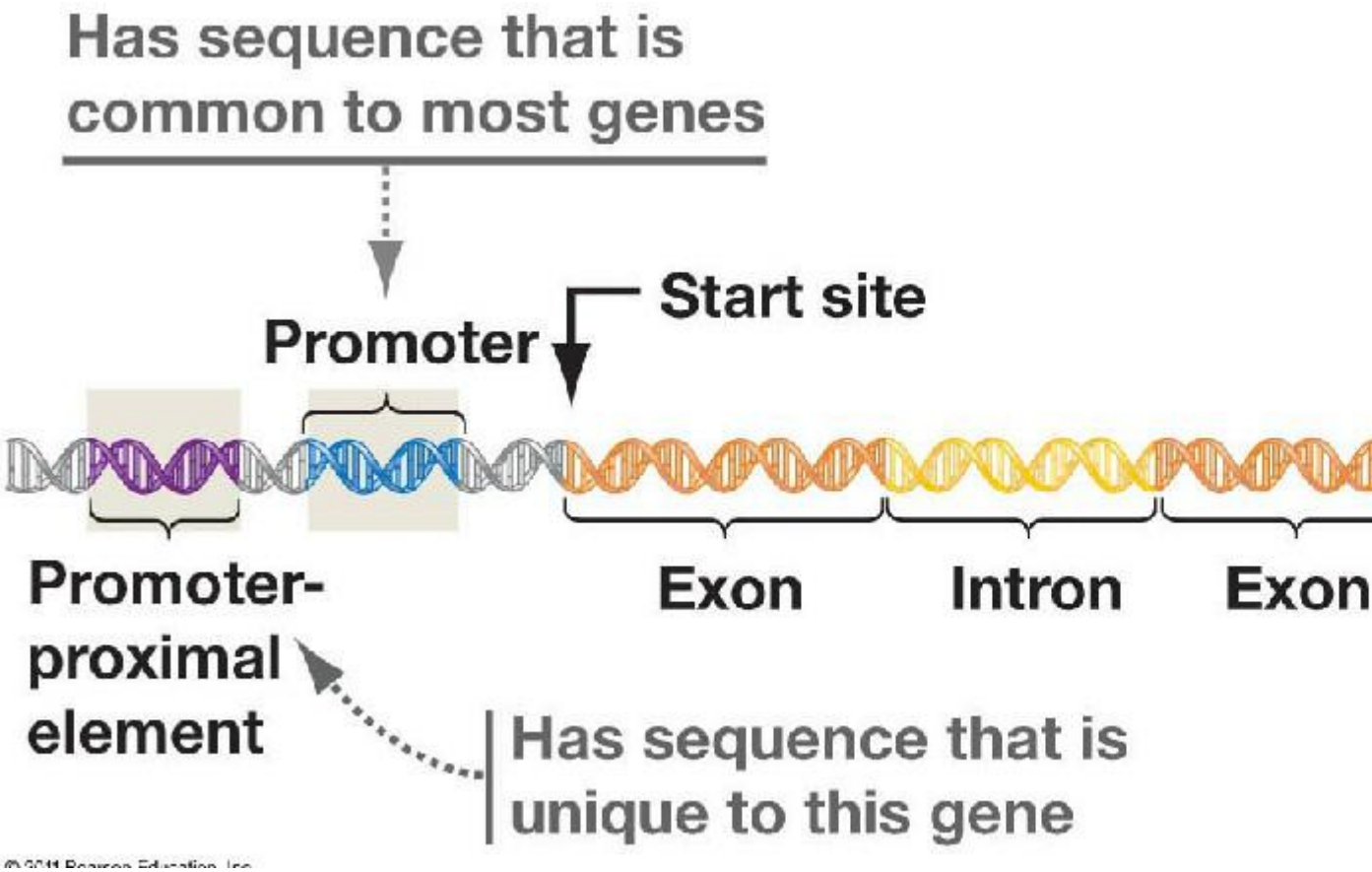
- Transcription occurs in a 5' to 3' direction where the 5' end of the free RNA nucleotide is added to the 3' end of the RNA molecule that is being synthesized.
- Transcription consists of 3 stages called initiation, elongation and termination
- Transcription begins when the RNA polymerase binds to the promoter with the help of specific binding proteins



http://upload.wikimedia.org/wikipedia/commons/2/25/Rna_syn2.png

β - Application: The promoter as an example of non-coding DNA with a function.

- The **promoter region** is a DNA sequence that initiates transcription and is an example of non-coding DNA that plays a role in gene expression.
- The promoter sequence is located near the start site of transcription and is where the RNA polymerase binds in order for transcription to take place.

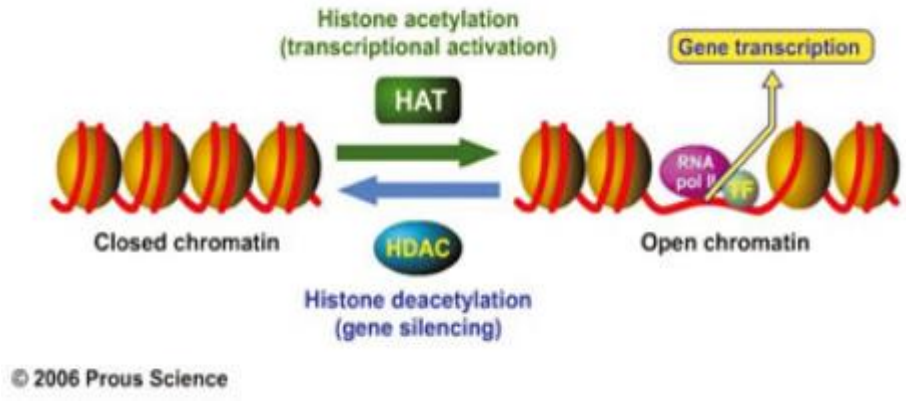


http://www.uic.edu/classes/bios/bios100/lectures/18_05_promoters-L.jpg

Good Video - https://www.youtube.com/watch?v=9AfBsTAQ8zs

∑ **- Nucleosomes help to regulate transcription in eukaryotes.**

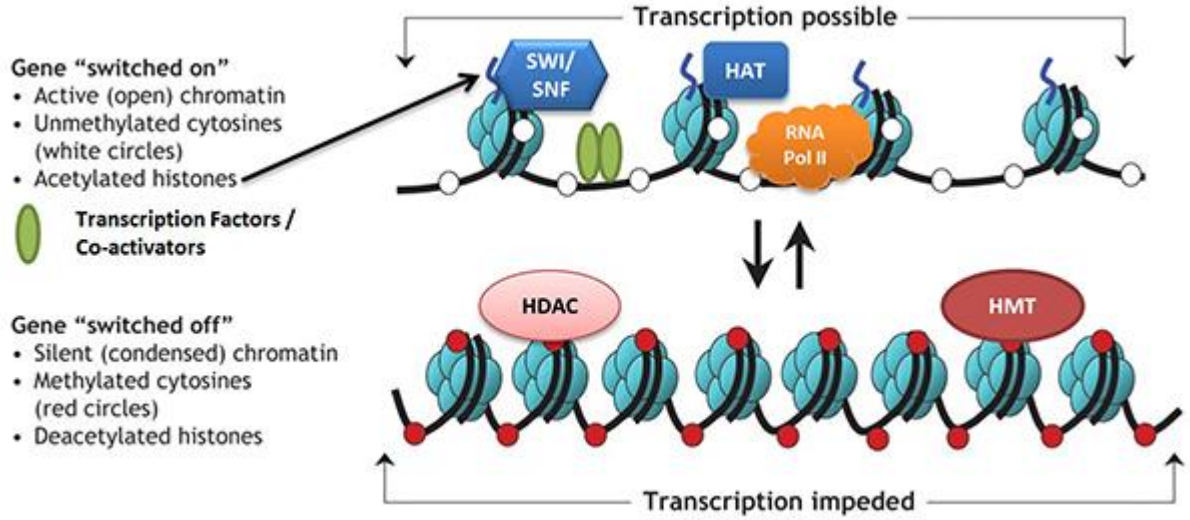
- As explained previously in 7.1 eukaryotic DNA wraps around histone proteins and supercoils
- This supercoiling helps regulate transcription because only certain areas of the DNA are accessible for the production of mRNA by transcription. This regulates the production of a polypeptide.
- One of the main ways this occurs is through the modification of the histone tails
- When acetyl groups are added to the positively charged histone tails, they become negative and the DNA repels against them. This opens up the nucleosome so the DNA is not as close to the histone anymore and chromatin remodeling can occur.
- This acetylation of the positive histone tails and opening up of the DNA structure allows the gene to be transcribed more often.
- If this does not occur, the DNA remains tightly packed and transcription is inhibited



Good video on methylation and acetylation.
https://www.youtube.com/watch?v=Tj_6DcUTRnM

β - Skill: **Analysis of changes in the DNA methylation patterns.**

- Another way gene expression can be controlled is through **methylation** (adding a methyl CH3 group) to the histone proteins.
- Methylation of the histone proteins decreases transcription of the gene
- The amount of methylation can vary over an organisms lifetime and can be affected by environmental factors

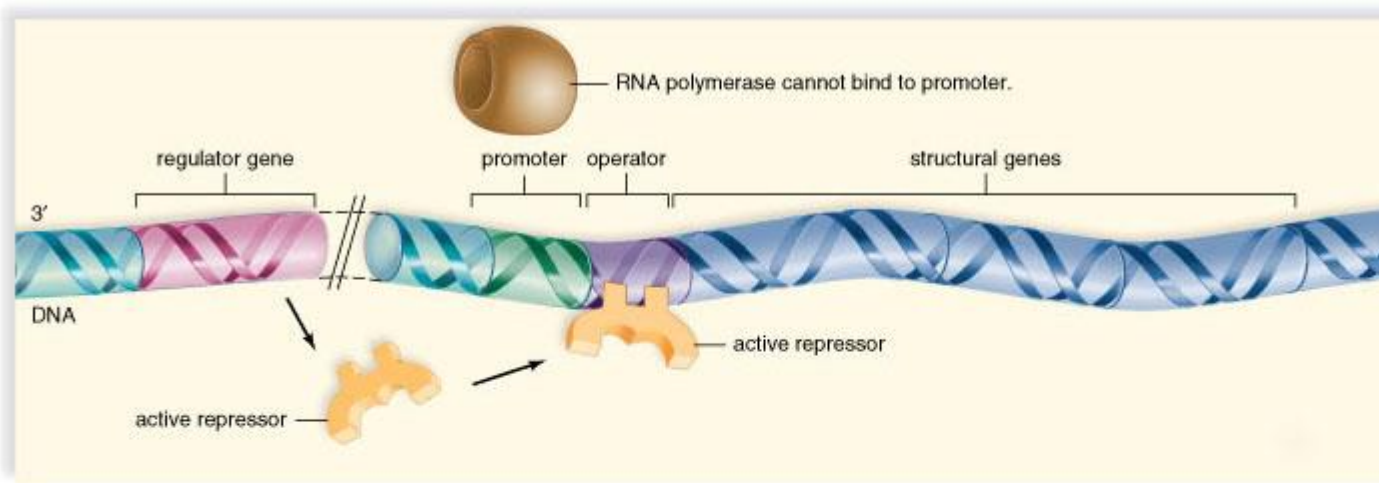


Luong, P. Basic Principles of Genetics, Connexions Web site.
[http://cnx.org/content/m26565/1.1/] (2009)

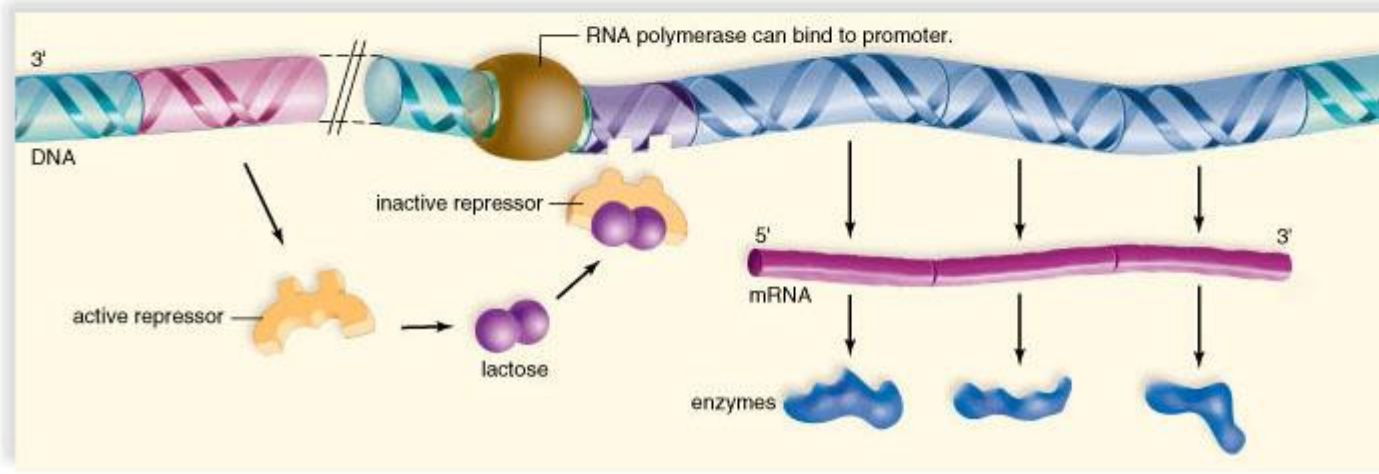
***** Complete the data based questions on page 358 of your text book*****

∑ - Gene expression is regulated by proteins that bind to specific base sequences in DNA.

- Gene expression can also be regulated by the environment surrounding the gene that is expressed or repressed
- Specific proteins can regulate how much transcription of a particular gene will occur
- These include proteins called enhancers, silencers and promoter-proximal elements
- These regulatory proteins are unique to a particular gene
- Regulatory sequences on the DNA that increase the rate of transcription when proteins bind to them are called **enhancers**
- Regulatory sequences on the DNA that decrease the rate of transcription when proteins bind to them are called **silencers**
- **Promoter-proximal elements** have binding sites closer to the promoter and their binding isnecessary to initiate transcription
- In prokaryotic cells such as E.coli repressor proteins block the production the enzymes needed to break down lactose in the cell.
- However, when **Lactose is present**, it will bind to the repressor protein, causing it to fall off, and allowing transcription to occur.
- As transcription occurs, these enzymes are made and lactose is broken down into glucose and galactose. Since there is small amounts of lactose now in the cell, the **repressor binds againto the operator, blocking transcription** from taking place.
- This is an example of ***negative feedback***



a. **Lactose absent.** Enzymes needed to take up and use lactose are not produced.



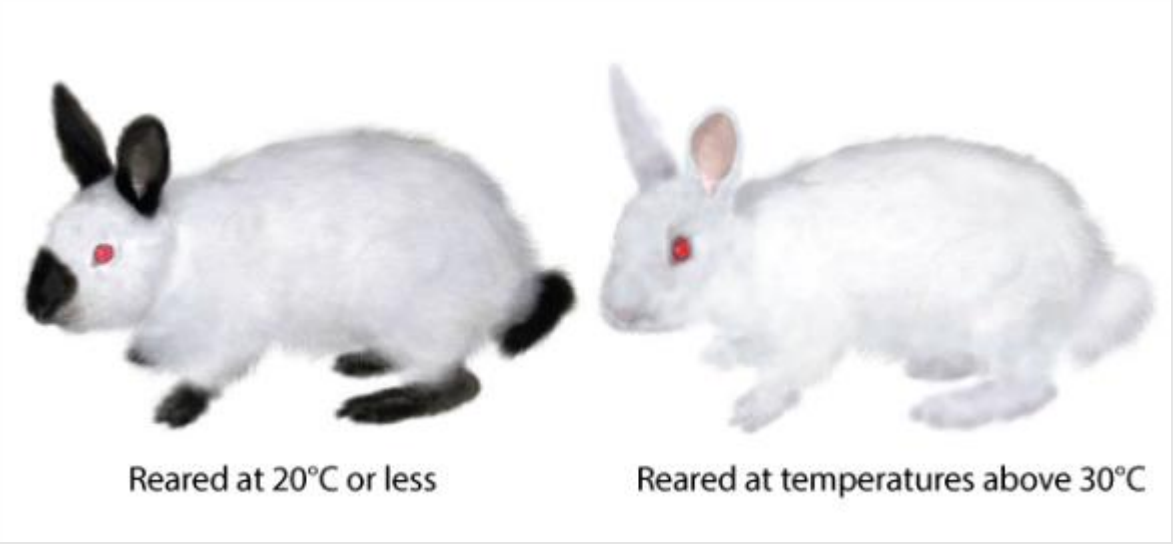
b. **Lactose present.** Enzymes needed to take up and use lactose are produced only when lactose is present.

http://classes.midlandstech.edu/carterp/Courses/bio101/chap15/chap15.htm

∑ - The environment of a cell and of an organism has an impact on gene expression.

- The external environment in which the organism is located or develops, as well as the organism's internal world, which includes such factors as its hormones and metabolism can have an impact on gene expression
- Temperature and light are external conditions which can affect gene expression in certain organisms.
- For example, Himalayan rabbits carry the C gene, which is required for the development of pigments in the fur, skin, and eyes, and whose expression is regulated by temperature (Sturtevant, 1913).
- Specifically, the C gene is inactive above 35°C, and it is maximally active from 15°C to 25°C. This temperature regulation of gene expression produces rabbits with a distinctive coat coloring. In the warm, central parts of the rabbit's body, the gene is inactive, and no pigments are produced therefore the fur color is white (picture below). In the rabbit's extremities (i.e.,

the ears, tip of the nose, and feet), where the temperature is much lower than 35°C, the C gene actively produces pigment, making these parts of the animal black.

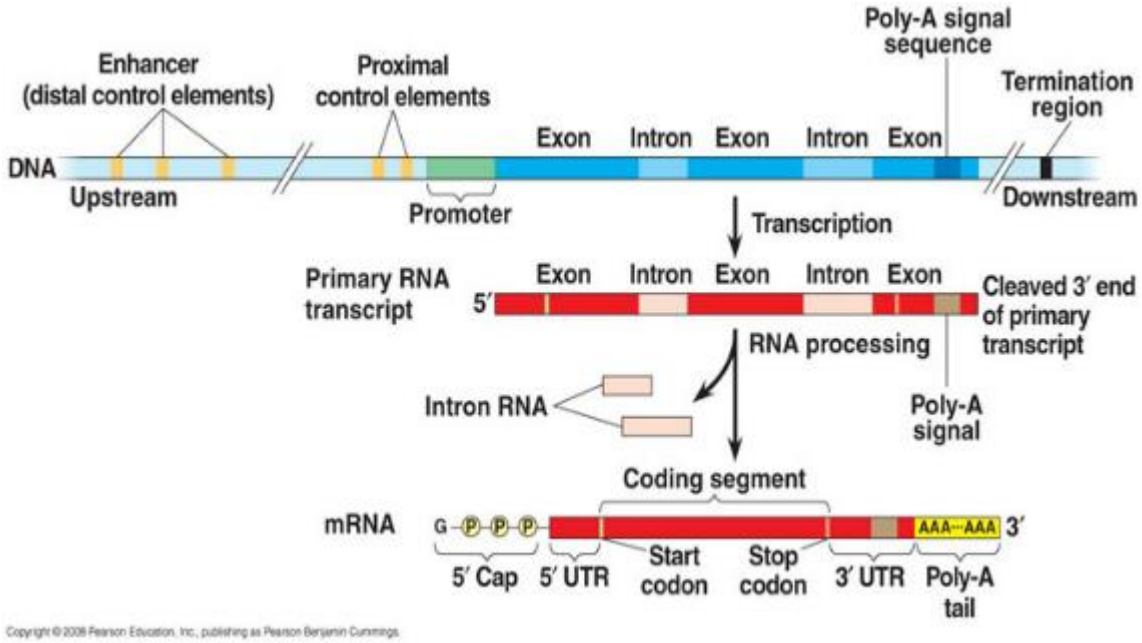


- During embryonic development embryos contain chemicals called morphogens, which canaffect gene expression and thereby affecting the fate of embryonic cells depending on their position within the embryo.
- An obvious example is how sunlight affects the production of skin pigmentation in humans
- A chemical example, was the use of Thalidomide by pregnant woman for morning sickness. It was thought it was harmless for humans but was not thoroughly tested. The drug was withdrawn too late to prevent severe developmental deformities in approximately 8,000 to 12,000 infants, many of whom were born with stunted limb development. Interestingly, despite the fact that thalidomide is dangerous during embryonic development, the drug continues to be used in certain instances yet today.

*****Do the data-based questions on page 358 of your textbook*****

∑ - Eukaryotic cells modify mRNA after transcription.

- In eukaryotes, the locations for transcription and translation are separated by the nuclear membrane. This allows for post-transcriptional modification of the mRNA.
- The first product of transcription is pre-mRNA
- As eukaryotic mRNA travels from the nucleus to the ribosomes, non-coding strands of the mRNA called introns are removed to form functional mature mRNA.
- They are removed through **RNA splicing**
- The exons are spliced together to form mature mRNA
- Also a poly A tail consisting of approximately 100-200 adenine nucleotides is added to one end of the mRNA and a 5' cap is added to the other end (these help protect the mature mRNAtranscript)



∑ **- Splicing of mRNA increases the number of different proteins an organism can produce.**

- Alternative splicing can also occur with genes that produce multiple proteins, which means that some exons may also be removed during splicing, thus producing different polypeptides
- For example, in mammals **tropomyosin** which is a protein involved in muscle contractions; however, the pre-mRNA is spliced to form 5 different forms of the protein. The mature mRNAthat codes for tropomyosin in the smooth muscle of the intestines is missing exon 3 and 10,while the mRNA that codes for tropomyosin in skeletal muscle is missing exon 2.

Guidance:

•RNA polymerase adds the 5´ end of the free RNA nucleotide to the 3´ end of the growing mRNA molecule.

Theory of knowledge:

•The nature versus nurture debate concerning the relative importance of an individual's innate qualities versus those acquired through experiences is still under discussion. Is it important for science to attempt to answer this question?

7.3 Translation

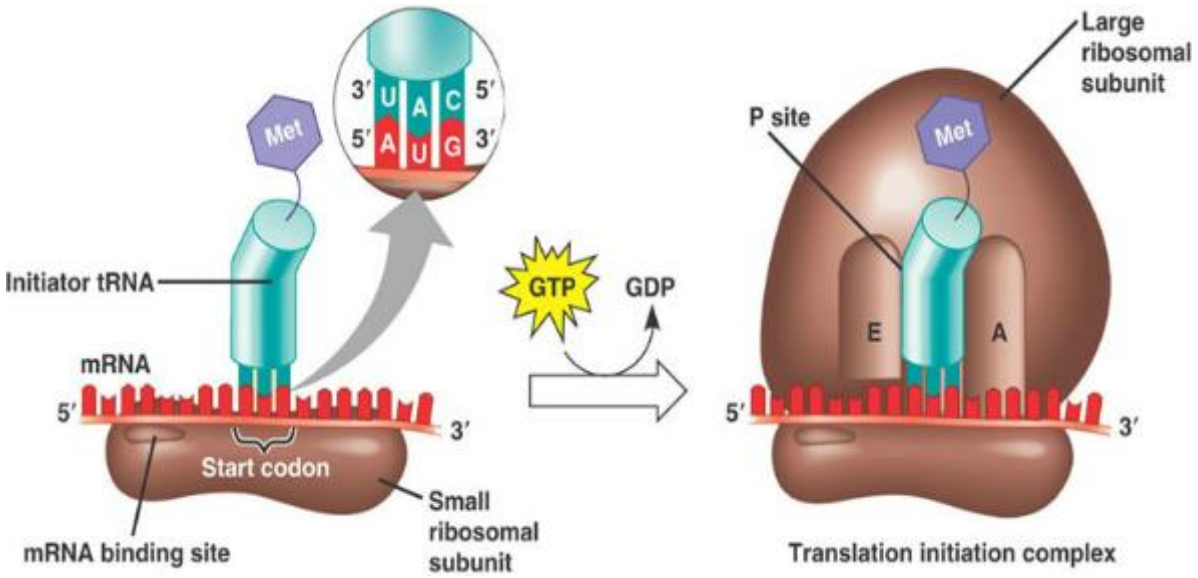
Nature of science: Developments in scientific research follow improvements in computing—the use of computers has enabled scientists to make advances in bioinformatics applications such as locating genes within genomes and identifying conserved sequences.

∑ **- Understandings:**

∑ **- Initiation of translation involves assembly of the components that carry out the process.**

Initiation

- mRNA binds to the small (30 s) ribosomal sub-unit.
- tRNA carrying Methionine with the anticodon UAC binds to the codon AUG (start codon).
- This is called the initiation complex.
- The large ribosomal subunit binds to the small ribosome, with the tRNA containing methionine binding at the p-site of large subunit.

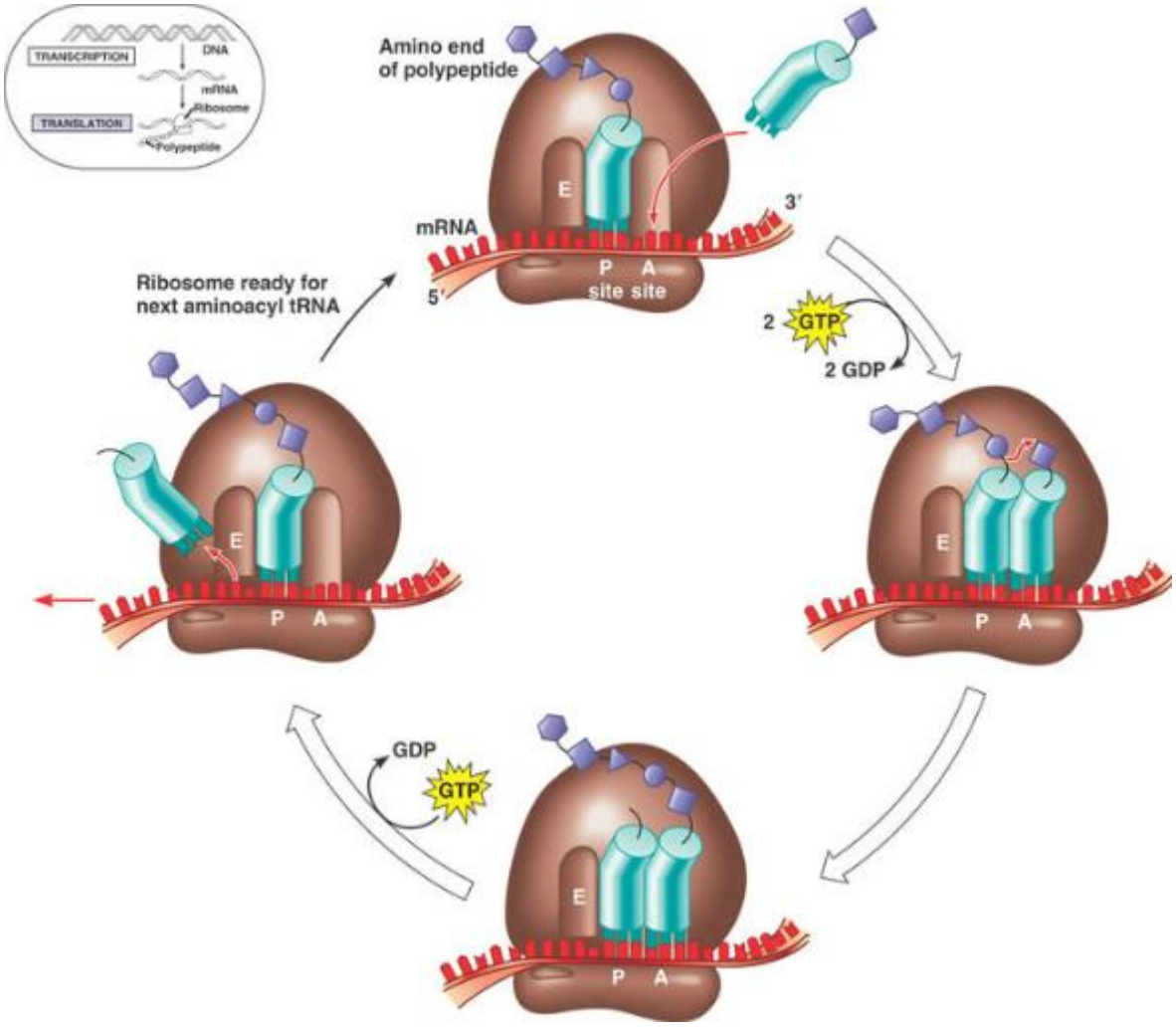


http://kvhs.nbed.nb.ca/gallant/biology/translation_initiation.html

∑ **- Synthesis of the polypeptide involves a repeated cycle of events.**

Elongation

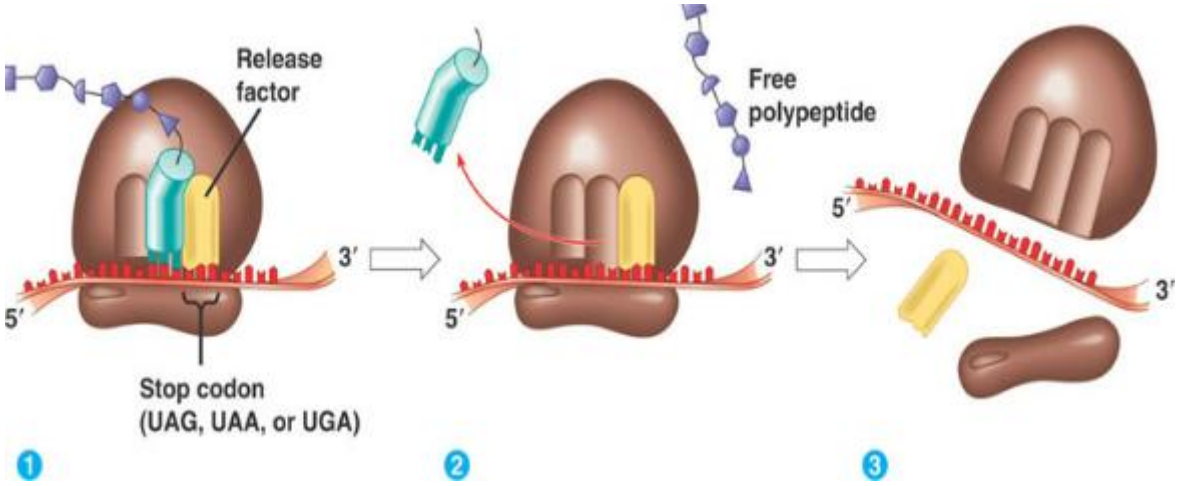
- While the first tRNA is still attached, a second tRNA attaches to the mRNA at the A site on the ribosome, carrying the amino acid that corresponds to the mRNA codon.
- The methionine amino acid at the P site binds to the amino acid carried by the second tRNA located at the A site.
- The two amino acids are joined together through a condensation reaction that creates a peptide bond between the two amino acids.
- The ribosome moves along the mRNA one codon shifting the tRNA that was attached to methionine to the E site.
- The tRNA is released back into the cytoplasm from the E site, allowing it to pick up another amino acid (methionine) to build another polypeptide.
- Another tRNA moves into the empty A site bringing the next amino acid corresponding to themRNA codon.
- Again, the amino acid is attached to the polypeptide forming a peptide bond, the ribosome slides across one codon and tRNA at the P site moves into the E site releasing it back into the cytoplasm.
- The ribosome continues to move along the mRNA adding amino acids to the polypeptide chain.
- This process continues until a stop codon is reached.



∑ **- Disassembly of the components follows termination of translation.**

Termination

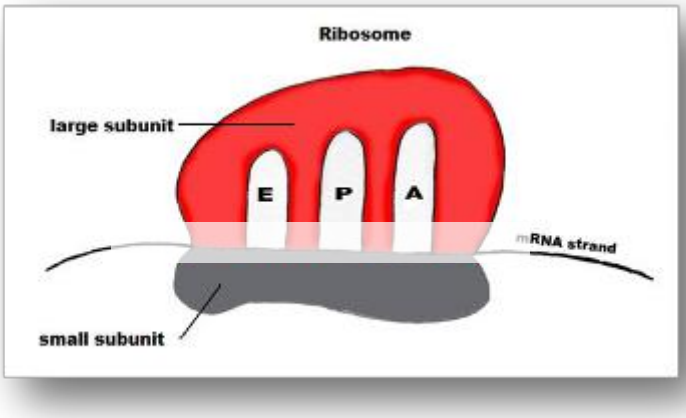
- **Termination begins when 1 of the 3 stop codons (UAA, UGA, UAG)** moves into the A site.
- These tRNA have no attached amino acids.
- When the stop codon is reached the ribosome dissociates and the polypeptide is released.



http://bio1151.nicerweb.com/Locked/media/ch17/translation-termination.html

β - Skill: The use of molecular visualization software to analyse the structure of eukaryotic ribosomes and a tRNA molecule.

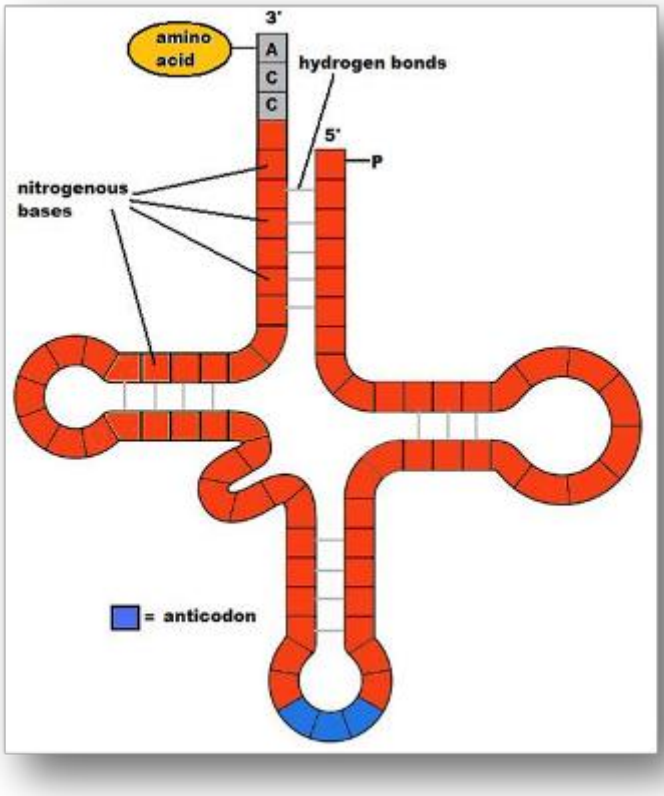
- Ribosomes are organelles made from protein and RNA that catalyze the assembly of amino acids into polypeptides during translation.
- Ribosomes consist of two sub-units; a large sub-unit and a small sub unit.
- The large sub-unit consists of 3 binding sites for tRNA molecules called the A site (The A site binds an aminoacyl-tRNA (tRNA bound to an amino acid); the P site binds a peptidyl-tRNA (tRNA bound to the peptide being synthesized); and the E site binds a free tRNA (no amino acid attached) before it exits the ribosome.
- The order of the sites in the ribosomes is E P A.
- There is a binding site for the mRNA on the surface of the ribosome
- The small subunit of the ribosome contains the binding site for the mRNA strand.
- The space between the two sub-units of the ribosome is where the polypeptide is assembled during translation.



Go to http://www.rcsb.org/pdb/explore/jmol.do?structureId=4W2F&bionumber=1 to check out the three dimensional shape of a ribosome and its binding sites. When looking at the ribosome,

you can right click on the image to change different aspects of how you view the 3D shape of the ribosome.

- **tRNA i**s a type of RNA molecule that transfers a specific amino acid to a growing polypeptidechain during translation (protein synthesis) at the ribosomes.
- Sections of the tRNA become double stranded through hydrogen bonds formed between base pairs creating loops
- A triplet of bases form the anticodon which will bind to the corresponding triplet codon on the mRNA strand
- The base sequence of CCA at the 3' end forms the amino acid binding site

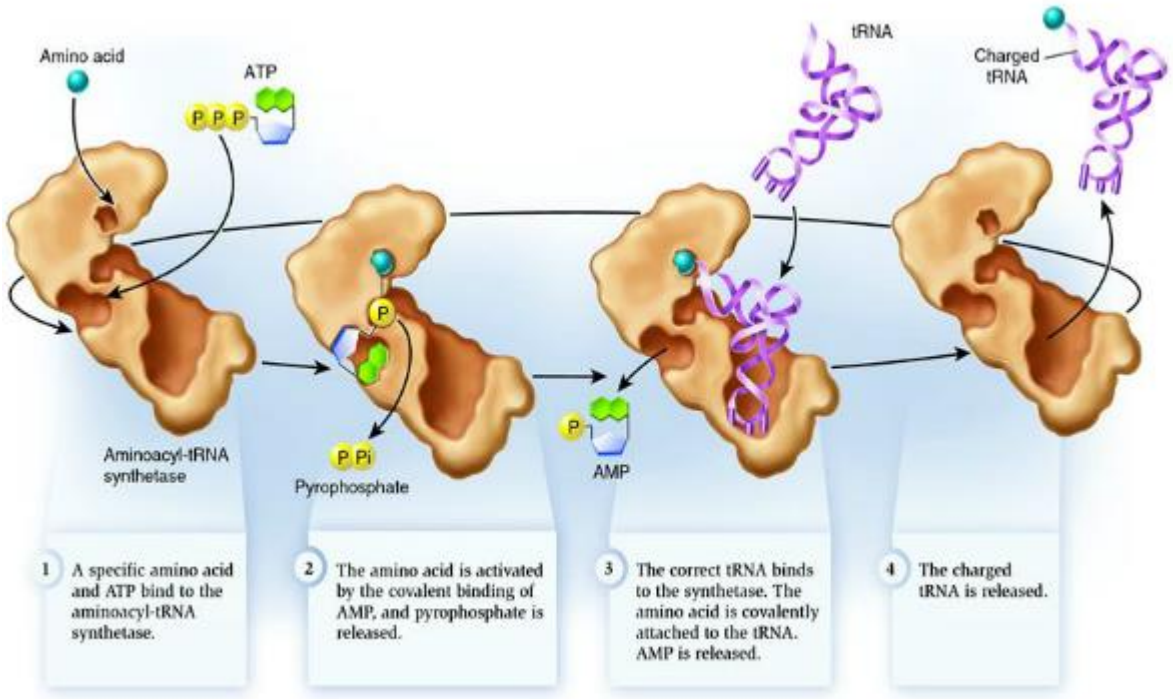


Go to the PDB and search for a tRNA molecule. Explore the structure of the tRNA using the 3D molecular visualization software

- http://www.rcsb.org/pdb/101/motm.do?momID=15&evtc=Suggest&evta=Moleculeof%20the%20Month&evtl=OtherOptions

β – Application - tRNA-activating enzymes illustrate enzyme–substrate specificity and the role of phosphorylation.

- Each tRNA binds with a specific amino acid in the cytoplasm in a reaction catalyzed by a specific tRNA-activating enzyme (21 specific enzymes for the 21 different amino acids).
- Each specific amino acid binds covalently to the 3'- terminal nucleotide (CCA) at the end of the tRNA molecule.
- The binding of the specific amino acid to the tRNA requires energy from ATP.



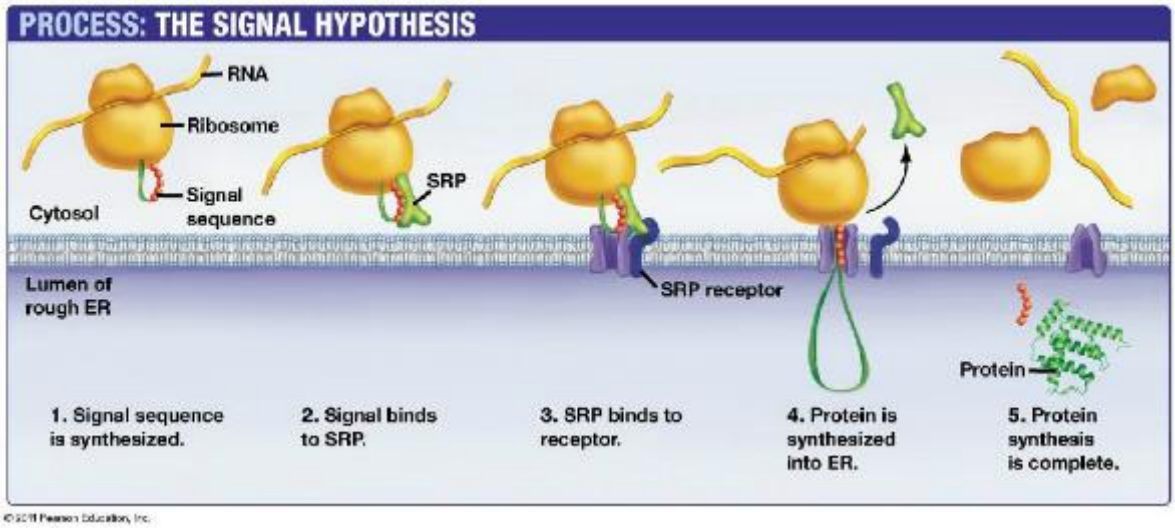
http://biomoocnews.blogspot.ca/2014/09/daily-newsletter-september-10-2014.html

∑ **- Free ribosomes synthesize proteins for use primarily within the cell.**

- Free ribosomes in the cytoplasm synthesize proteins that will be used inside the cell in the cytoplasm, mitochondria and chloroplasts (in autotrophs)

∑ **- Bound ribosomes synthesize proteins primarily for secretion or for use in lysosomes.**

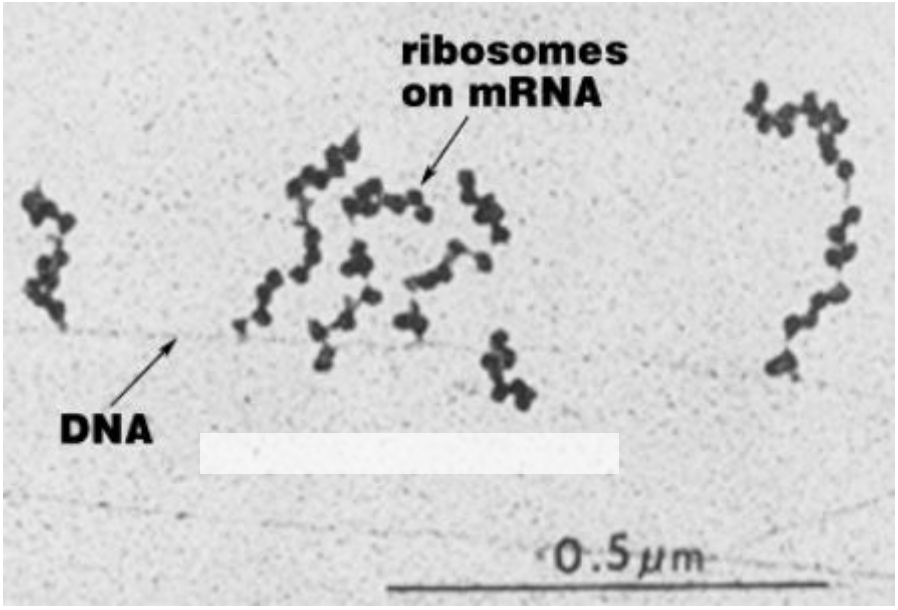
- Ribosomes attached to ER create proteins that are secreted from the cell by exocytosis or are used in lysosomes.
- Proteins perform many functions within specific compartments of the cell or in other parts of the body after they are secreted out of the cell
- Proteins that are destined to be used in lysosomes, ER, Golgi Apparatus, the plasma membrane or secreted by the cell are made by ribosomes bound by the endoplasmic reticulum
- Ribosomes that become bound to the ER are directed here by a signal sequence that is part of that specific polypeptide
- This signal sequence on the polypeptide binds to a signal recognition protein (SRP)
- The SRP guides the polypeptide and ribosome to the ER where it binds to an SRP receptor
- Translation can now continue and the polypeptide is deposited into the lumen of the ER as its created for transportation to the correct location



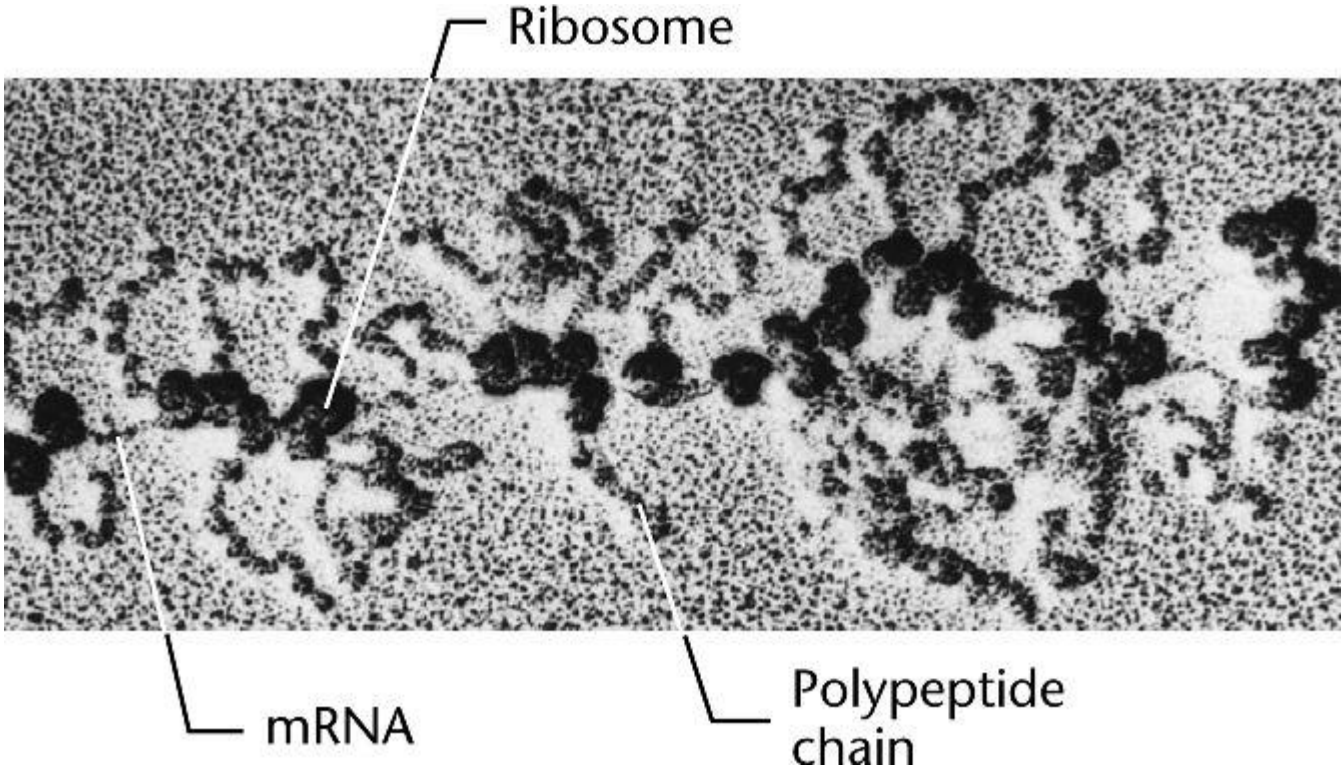
∑ - Translation can occur immediately after transcription in prokaryotes due to the absence of a nuclear membrane.

- Since prokaryotic DNA is not compartmentalized into a nucleus, once transcription begins creating a strand of mRNA, translation can begin immediately as the mRNA strand is created
- In eukaryotes, the completed mRNA has to be transported from the nucleus, through the nuclear pore to the ribosome on the ER or in the cytosol

β - Skill: Identification of polysomes in electron micrographs of prokaryotes and eukaryotes.



- In prokaryotes, several ribosomes can attach themselves to the growing mRNA chains to form a polysome while the mRNA chains are still attached to the DNA



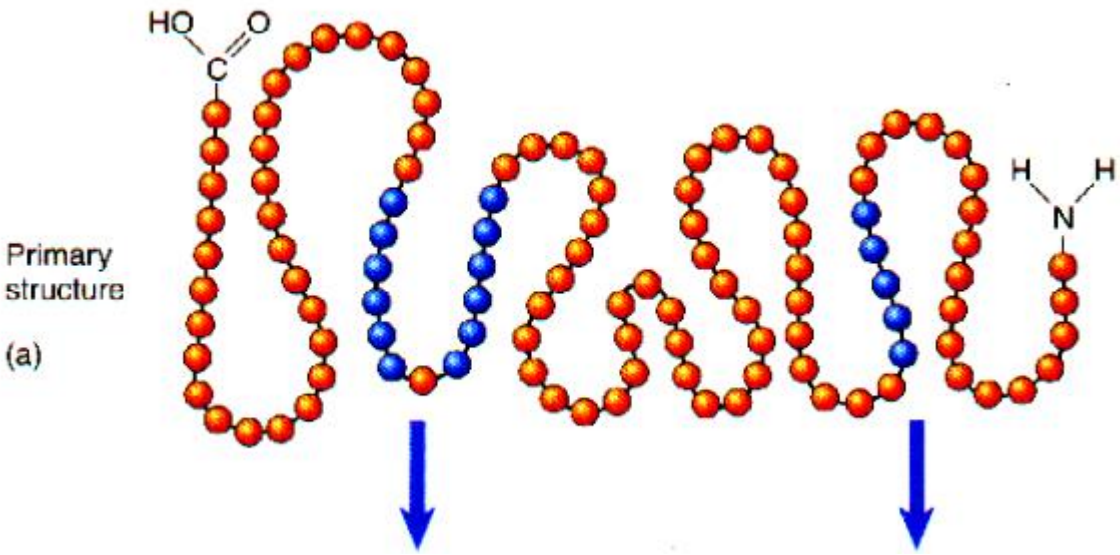
- In eukaryotes, the mRNA detaches from the DNA and is then transported through pores in the nuclear envelope to the ribosomes in the cytoplasm. Once in the cytosol, eukaryote mRNA can also form polysomes

Protein Structure

∑ **- The sequence and number of amino acids in the polypeptide is the primary structure.**

Primary Structure

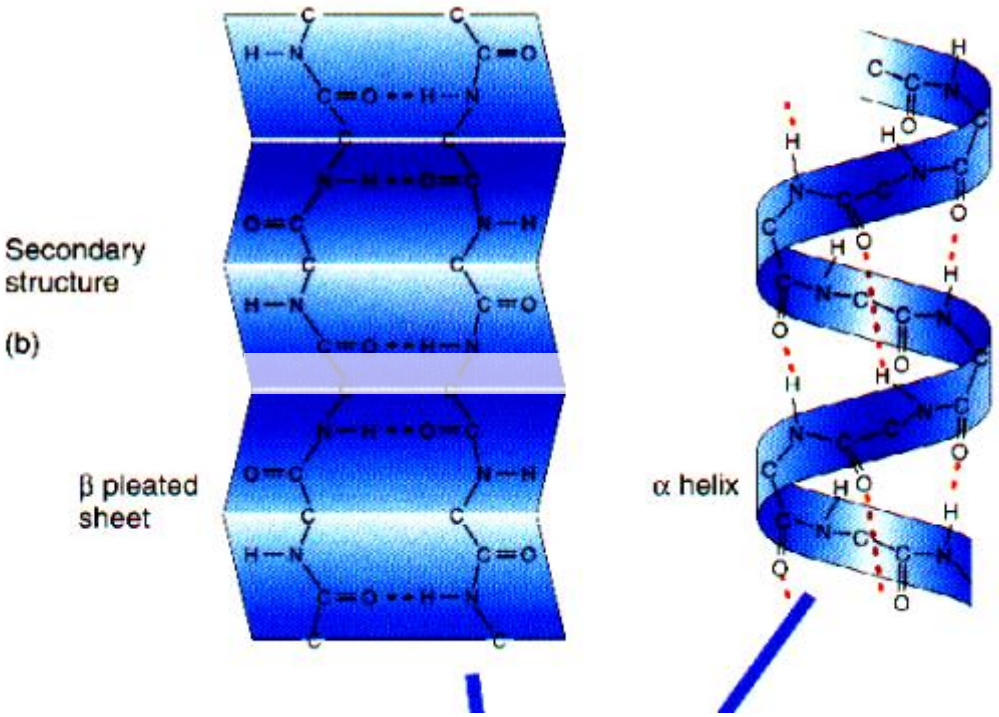
- Is the amino acid sequence of the polypeptide chain attached together by peptide bonds
- The sequence can consist of any of the 21 amino acids and is coded for by a gene in the DNA.
- The sequence of amino acids can determine the shape of the other three levels of protein structure.



∑ - The secondary structure is the formation of alpha helices and beta pleated sheets stabilized by hydrogen bonding.

Secondary Structure

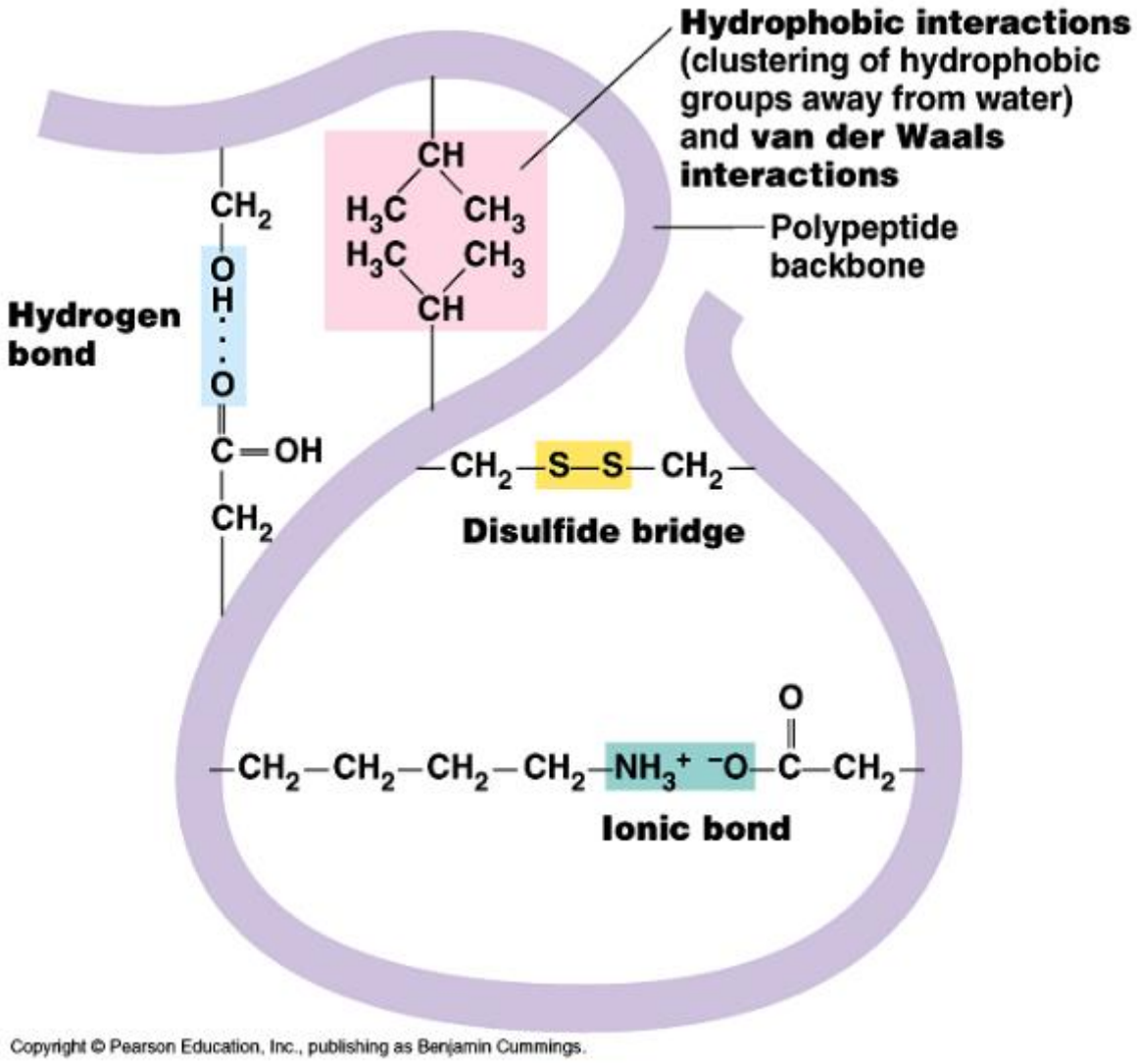
- Secondary structure is created when the hydrogen bonds are formed between the main peptide groups in amino acids (not the R groups) in the polypeptide.
- The two main structures formed are the alpha helix and the beta pleated sheets which are locally defined, which means there can be many different secondary structures present in a single protein molecule.
- Proteins with secondary structure are generally structural in nature like the secondary structure in silk.

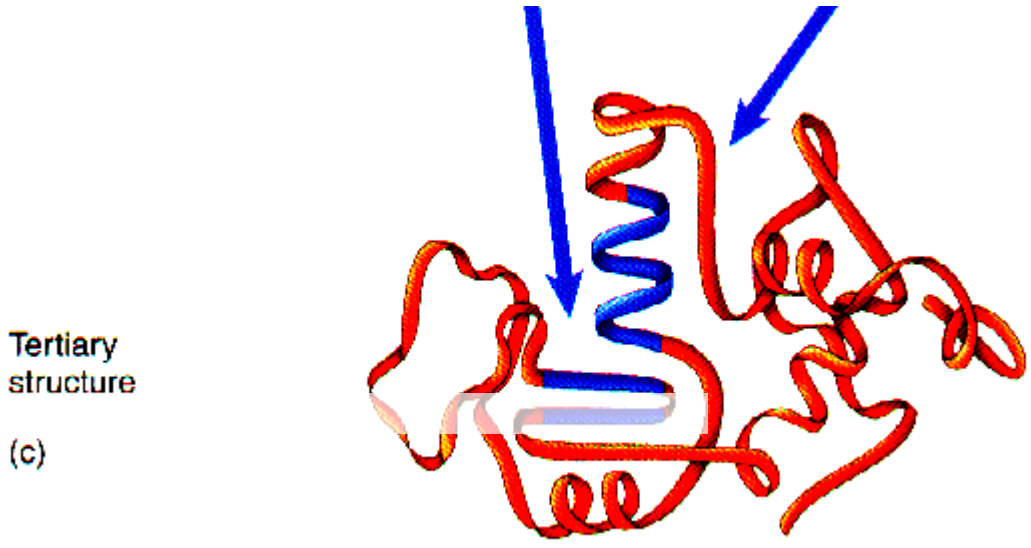


∑ - The tertiary structure is the further folding of the polypeptide stabilized by interactions between R groups.

Tertiary Structure

- Tertiary structure is the third level of protein organization.
- Tertiary structure develops a three dimensional shape because of the interactions that occur between the R groups.
- Disulphide bridges form between sulphur atoms on the R-groups from the amino acid cysteine.
- Hydrogen bonds form between polar R-groups and other polar R-groups.
- Ionic Bonds are also formed between some R-groups
- Hydrophobic R-groups turn inwards away from water and hydrophilic R-groups face outwardstowards the water.
- Protein is globular in nature.

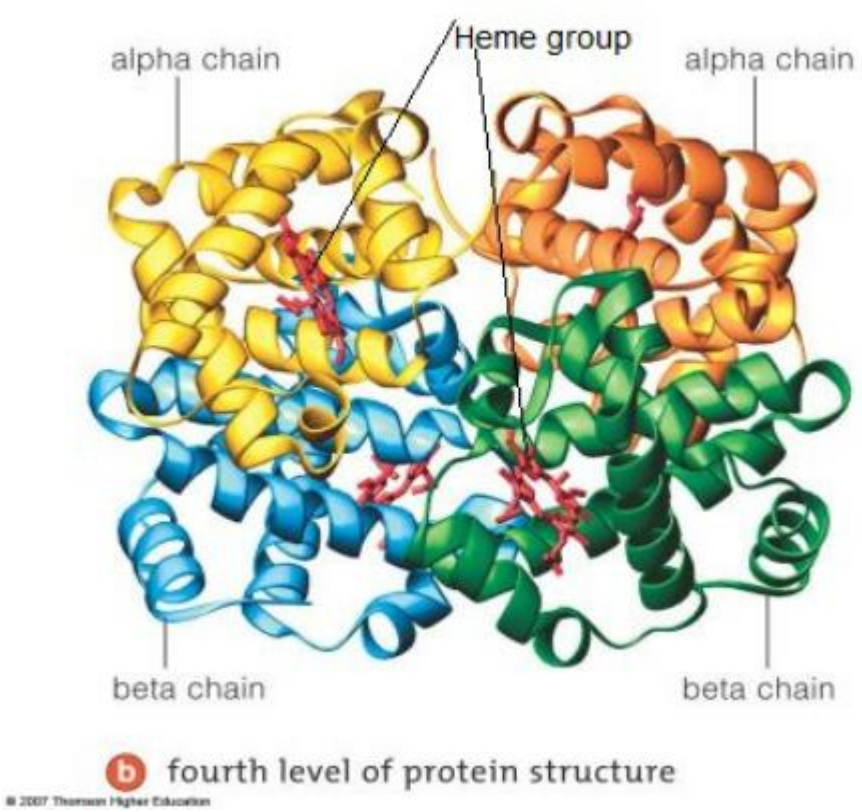




∑ - The quaternary structure exists in proteins with more than one polypeptide chain.

Quaternary Structure

- Protein consisting of more than one polypeptide chain.
- Quaternary structure exists in many proteins such as hemoglobin (4 polypeptide chains).
- Hemoglobin also contains a prosthetic group (non-polypeptide structure). The prosthetic group in hemoglobin is iron. Hemoglobin contains 4 iron molecules.
- Proteins with prosthetic groups are called conjugated proteins.



***** Do the data-based questions on page 369 and 371 of your textbook*****

Nature of science: Developments in scientific research follow improvements in computing—developments in bioinformatics, such as the interrogation of databases, have facilitated research into metabolic pathways. (3.8)

- Read the paragraph on Bioinformatics on page 368 to familiarize yourself with what this means.

Guidance:

•Names of the tRNA binding sites are expected as well as their roles.

•Examples of start and stop codons are not required.

•Polar and non-polar amino acids are relevant to the bonds formed between R groups.

•Quaternary structure may involve the binding of a prosthetic group to form a conjugated protein

Topic 1 - Cells
Topic 2 - Molecular Biology
Topi 3 - Genetics
Topic 4 - Ecology
Topic 5 - Evolution&Biodiversity
Topic 6- Human Health and Physiology
Topic 7 - Nucleic Acids
7.1 DNA Structure and Replication
7.2 Transcription and Gene Expression
7.3 Translation
Topic 8 - Respiration and Photosynthesis (AHL)
Topic 9 - Plant Biology (AHL)
Topic 10 - Genetics and Evolution (AHL)
Topic 11 - Physiology (AHL)