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DNA, RNA and Protein Synthesis

The nucleus (eukaryotic cells) or nucleoid (prokaryotic cells) is considered to be the control center (sometimes called the "brain") of the cell, because it contains the genetic information that determines what metabolic processes the cell can run, i.e., what enzymes and ribozymes the cell can make. This genetic information is stored within molecules of deoxyribonucleic acid (DNA) in the form of nucleotide (base) sequences. In order for DNA to be passed on to successive generations, it must be reproduced prior to cell division. The process by which this occurs within cells is called, is a semi-conservative process, and requires several different types of enzymes. An enzyme called
can catalyze the formation of phosphodiester bonds attaching DNA-type nucleotides to the free, 3' ends of growing nucleotide strands, and an enzyme called is used to catalyze reactions binding together (joining) the many small segments of DNA called fragments, that make up the lagging strand.
Cellular DNA molecules contain two nucleotide strands joined to one another by relatively weak hydrogen bonds . The two strands are antiparallel (up-side-down relative to one another) and complementary . If one strand of the DNA double helix contains the base sequence shown below, what will be the base sequence of the complementary strand?
DNA base sequence = TACTAGTTGAAAGTCCATGAGCCCGGGTTTATT Complementary sequence =
Ribonucleic acid (RNA) is also formed when DNA is reproduced. Each of the "fragments" named above begins with a short sequence of RNA, and the proteins involved in the production of these are called enzymes. RNA molecules (t-RNA, m-RNA, r-RNA, etc.) are made through a process called that occurs within the nucleus or nucleoid because it requires DNA as a pattern or template. This process requires a type of enzyme called, that in prokaryotic cells is a complex containing five proteins. One important component of this enzyme complex is a protein called that recognizes and binds with a specific portion of DNA
known as the site. Once this has occurred, the core enzyme can bind and begin the building process. In prokaryotic cells the synthesis of RNA molecules is said to be because each m-RNA molecule produced is a copy of multiple structural genes (cistrons).
If the DNA base sequence TYPED above were used as the template for building m-RNA, the base sequence in the m-RNA would be Messenger-RNA molecules (m-RNA) carry the information telling cells what types of polypeptides to make, and the process involved is called (also called protein synthesis, although the polypeptide made may not be a complete protein). Protein synthesis occurs in association with in all types of cells, because these bodies contain the catalyst (called) required for peptide bond formation. This catalyst is actually a type of ribosomal-RNA (r-RNA) molecule, so is actually a rather than an enzyme.
If a polypeptide were constructed using the m-RNA sequence WRITTEN above, the amino acid sequence would be

RNA? Explain why or why not below.
Individual amino acids are carried to ribosomes by another type of RNA molecule called transfer-RNA (t-RNA). Each t-RNA picks up a specific type of amino acid (from the 20-plus possible types available within cells) because the "picking up" requires the activity of another type of catalyst. This is a type of enzyme called, and each one can catalyze a reaction between a specific type of t-RNA and a specific amino acid. The nucleotide sequences of t-RNA molecules differ from one another in their anti-codon regions, and this is essential to protein synthesis because each anti-codon can form bonds with a complementary codon on the m-RNA molecule being translated.
The synthesis reactions associated with replication , transcription and translation are endergonic, i.e., require energy, so cost the cell in terms of energy expenditure. The energy required for replication and transcription is provided by
In prokaryotic cells metabolic processes are often regulated at the gene level through the interactions of proteins with regions of DNA called
(an amino acid and the end-product of the tryptophan biosynthesis pathway). Thus, this operon is said to be, i.e., transcription is "on" (will continue), unless it is "turned off" (is repressed), and repression occurs only when intracellular levels of tryptophan have increased to a certain level. In the case of the lactose utilization operon, the repressor protein is active alone, so will block (repress) transcription unless it is inactivated. This requires an (a sugar called allolactose). Because transcription of the lactose utilization genes is repressed unless allolactose is available, this operon is
(is "off", but can be turned "on"). The enzymes involved in glycolysis are essential to the function of many cells, so are, i.e., always being made in those cells. If glucose is available, these cells are better off (in terms of energy conservation) to use it, rather than making the enzymes required to utilize an alternative catabolite such as lactose. In <i>E. coli</i> cells, glucose up-take inhibits the production of a nucleotide called
by blocking the activity of an enzyme called adenylate cyclase. This regulatory nucleotide when bound to a catabolite activating protein can enhance the promoter sites of inducible operons (i.e., make them more attractive to sigma factor). Thus, glucose availability can prevent the activation of inducible operons. This regulatory mechanism is called