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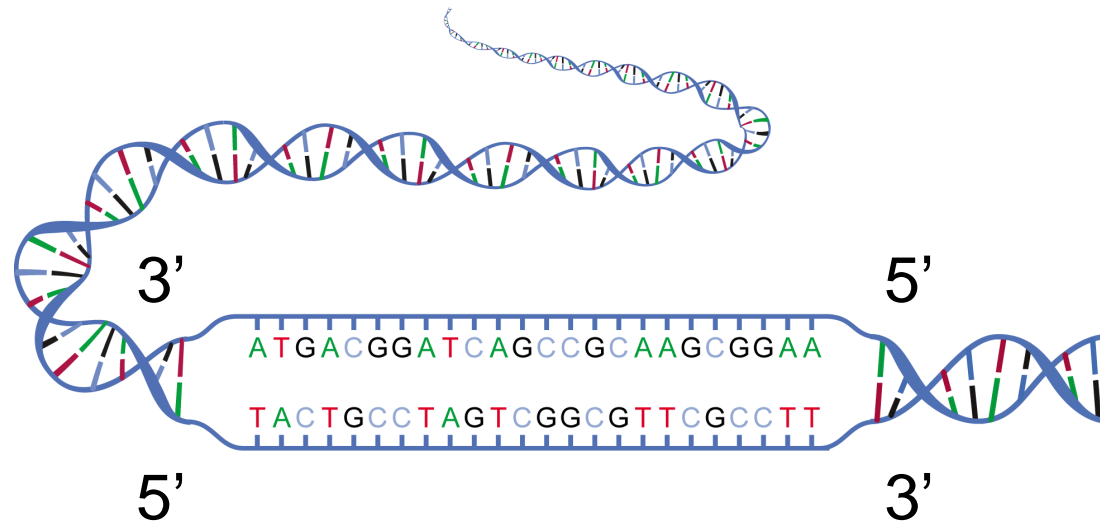
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3_ (pronounced three prime):

One end of a DNA strand. The bases in a single strand of DNA are attached to each other through chemical bonds between their sugars. The five carbon atoms of the sugar (deoxyribose) are numbered 1 through 5. The bonds linking the bases together are between carbons 3 and 5. This means that each DNA strand will have an unbonded 3 carbon at one end and an unbonded 5 carbon at the other end. The two strands of the double helix are said to be antiparallel, meaning that one strand runs in the 5_ to 3_ direction while the complementary strand runs in the 3_ to 5_ direction.

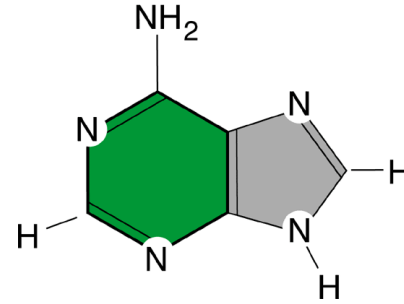


5_ (pronounced five prime):

One end of a DNA strand. The bases in a single strand of DNA are attached to each other through chemical bonds between their sugars. The five carbon atoms of the sugar (deoxyribose) are numbered 1 through 5. The bonds linking the bases together are between carbons 3 and 5. This means that each DNA strand will have an unbonded 3 carbon at one end and an unbonded 5 carbon at the other end. The two strands of the double helix are said to be antiparallel, meaning that one strand runs in the 5_ to 3_ direction while the complementary strand runs in the 3_ to 5_ direction.

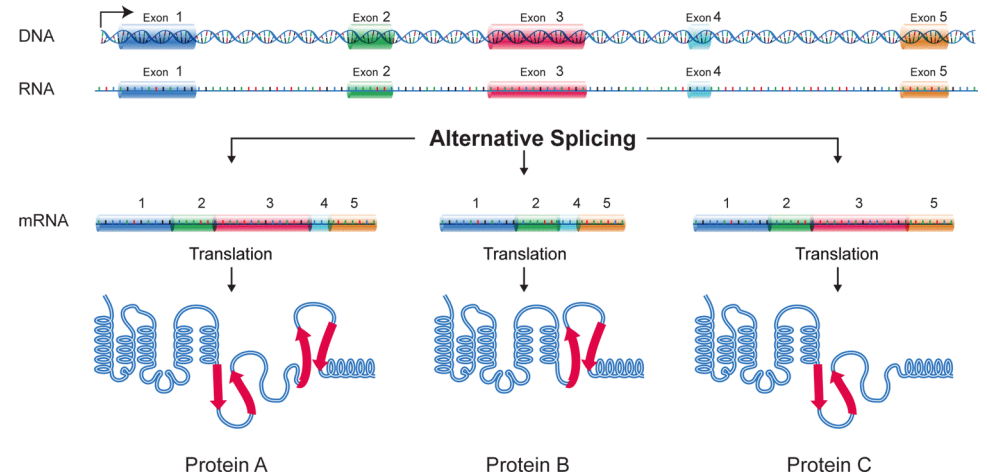
Adenine:

One of the four bases in DNA that make up the letters ATGC, adenine is the "A". The others are guanine, cytosine, and thymine. Adenine always pairs with thymine.



Alternative splicing:

The processing of an RNA transcript into different mRNA molecules. Eukaryotic genes are usually organized as a series of alternating exons that encode amino acids and introns that do not. After the RNA transcript is synthesized, RNA splicing enzymes remove the intron sequences and attach the exon sequences together to produce the final mRNA molecule. Sometimes an exon sequence is treated as an intron and is removed, producing an alternative form of the mRNA.



Amino acids:

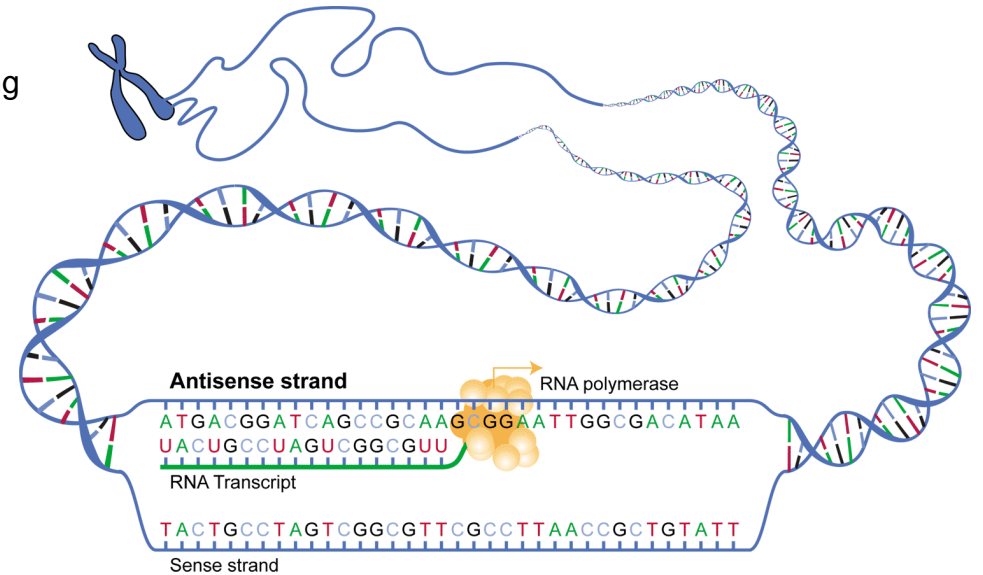
A group of 20 different kinds of small molecules that link together in long chains to form proteins. They are often referred to as the "building blocks" of proteins.

Antisense strand:

The DNA strand that serves as template for RNA polymerase during transcription. It is complementary in sequence to the sense strand.

Bioinformatics:

The study of collecting, sorting, and analyzing DNA and protein sequence information using computers and statistical techniques.



BLAST: (Basic Local Alignment Search Tool):

A computer program that searches for sequence similarities. It can be used to identify homologous genes in different organisms.

Chromosome:

One of the threadlike "packages" of genes and other DNA in the nucleus of a cell. Different kinds of organisms have different numbers of chromosomes. Humans have 23 pairs of chromosomes, 46 in all: 44 autosomes and two sex chromosomes. Each parent contributes one chromosome to each pair, so children get half of their chromosomes from their mothers and half from their fathers.

CLUSTAL:

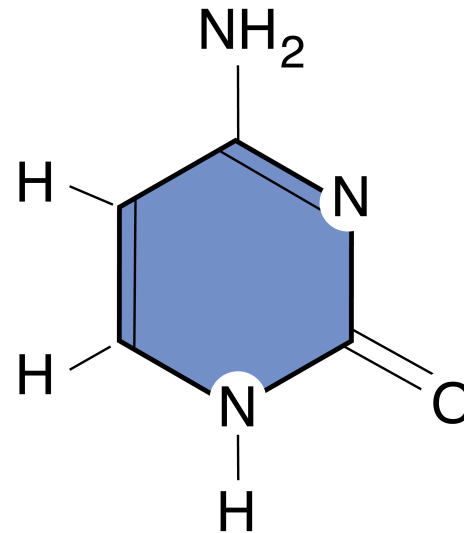
A group of computer programs that align multiple DNA or amino acid sequences to highlight their similarities and differences. Evolutionary relationships can be seen by viewing cladograms or phylogenetic trees.

Codon:

Three bases in a DNA or RNA sequence which specify a single amino acid or a stop signal.

Cytosine:

One of the four bases in DNA that make up the letters ATGC, cytosine is the "C". The others are adenine, guanine, and thymine. Cytosine always pairs with guanine.



DNA sequencing:

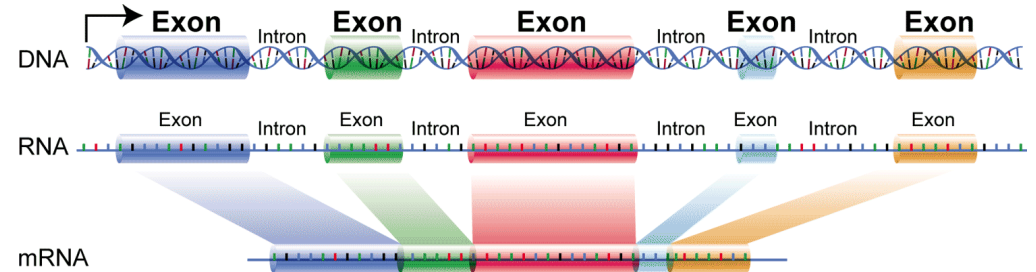
Determining the exact order of the base pairs in a segment of DNA.

Enzyme:

A molecule, usually a protein, that encourages a biochemical reaction, usually speeding it up. Organisms could not function if they had no enzymes.

Exon:

The region of a gene that contains the code for producing the gene's protein. Each exon codes for a specific portion of the complete protein. In some species (including humans), a gene's exons are separated by long regions of DNA (called introns or sometimes "junk DNA") that have no apparent function.



Frameshift:

A type of mutation characterized by insertions or deletions that change the identities of the codons following the mutation. Often this creates stop codons that cause premature termination of the protein.

Gene:

The functional and physical unit of heredity passed from parent to offspring. Genes are pieces of DNA, and most genes contain the information for making a specific protein.

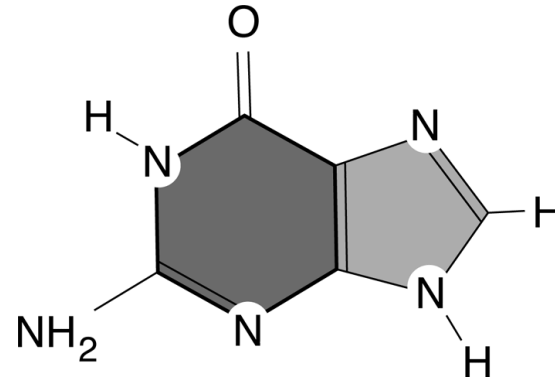
Genetic code:

The instructions in a gene that tell the cell how to make a specific protein. A, T, G, and C are the "letters" of the DNA code; they stand for the chemicals adenine, thymine, guanine, and cytosine, respectively, that make up the nucleotide bases of DNA. Each gene's code combines the four chemicals in various ways to spell out 3-letter "words" that specify which amino acid is needed at every step in making a protein.

1st position	2nd position				3rd position
	U	C	A	G	
U	Phe Phe Leu Leu	Ser Ser Ser Ser	Tyr Tyr stop stop	Cys Cys stop Trp	U C A G
C	Leu Leu Leu Leu	Pro Pro Pro Pro	His His Gln Gln	Arg Arg Arg Arg	U C A G
A	Ile Ile Ile Met	Thr Thr Thr Thr	Asn Asn Lys Lys	Ser Ser Arg Arg	U C A G
G	Val Val Val Val	Ala Ala Ala Ala	Asp Asp Glu Glu	Gly Gly Gly Gly	U C A G

Guanine:

One of the four bases in DNA that make up the letters ATGC, guanine is the "G". The others are adenine, cytosine, and thymine. Guanine always pairs with cytosine.

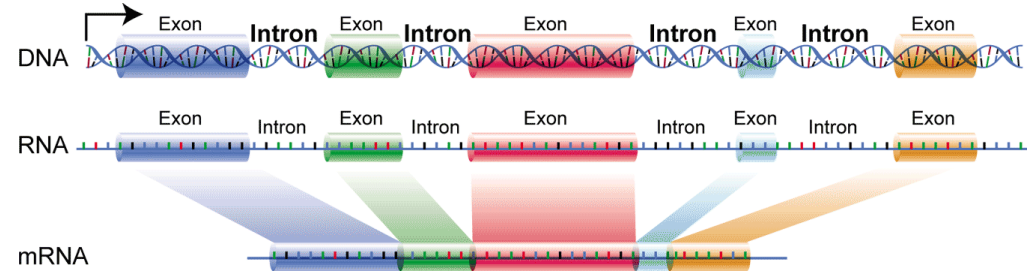


Human Genome Project:

An international research project begun in 1990 and completed in 2003 that mapped and sequenced the three billion DNA bases of the human genome.

Intron:

A noncoding sequence of DNA that is initially copied into RNA but is cut out of the final RNA transcript.



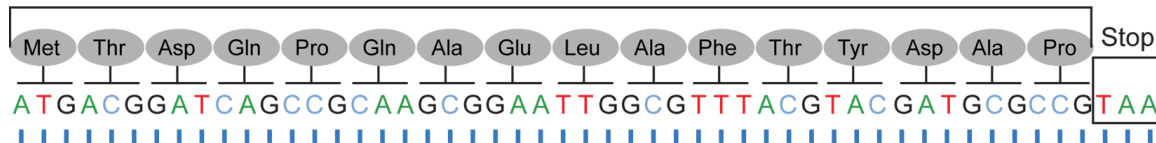
Nucleic acid:

A large polymer consisting of a linear stretch of nucleotides, as in DNA and RNA.

Open reading frame (ORF):

A stretch of DNA that when translated into an amino acid sequence doesn't contain an internal stop codon. An ORF can be evidence that a DNA sequence is part of a gene.

Open reading frame



Protein:

A large complex molecule made up of one or more chains of amino acids. Proteins perform a wide variety of activities in the cell.

Query sequence:

A nucleic acid or amino acid sequence that is entered into the BLAST computer program. BLAST searches a database to locate identical or similar sequences.

Reading frame:

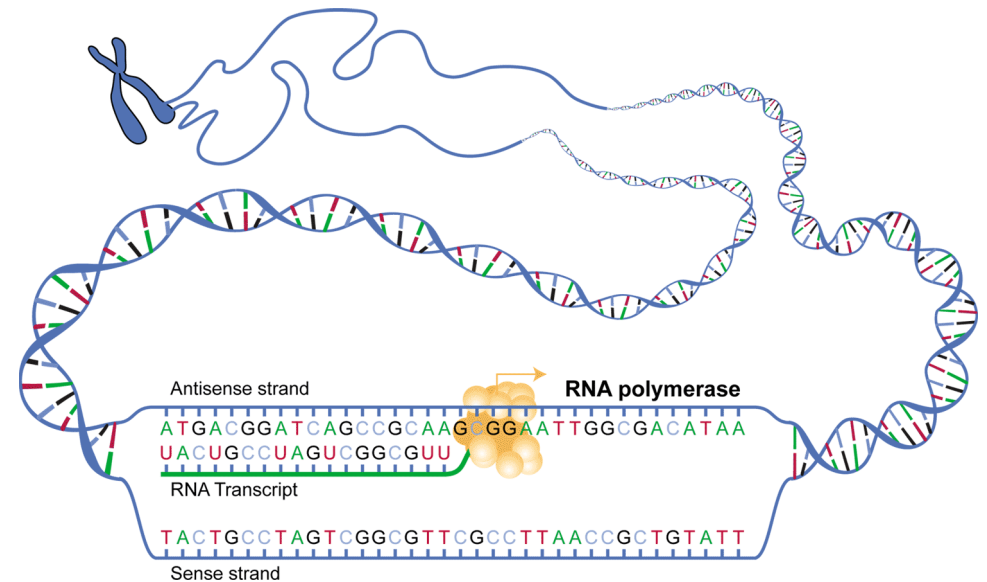
The way an mRNA is read as a series of triplet codons during translation. There are three possible reading frames for any mRNA, and the correct reading frame is set by recognition of the AUG initiation codon.

Ribosome:

A cellular organelle that is the site of protein synthesis

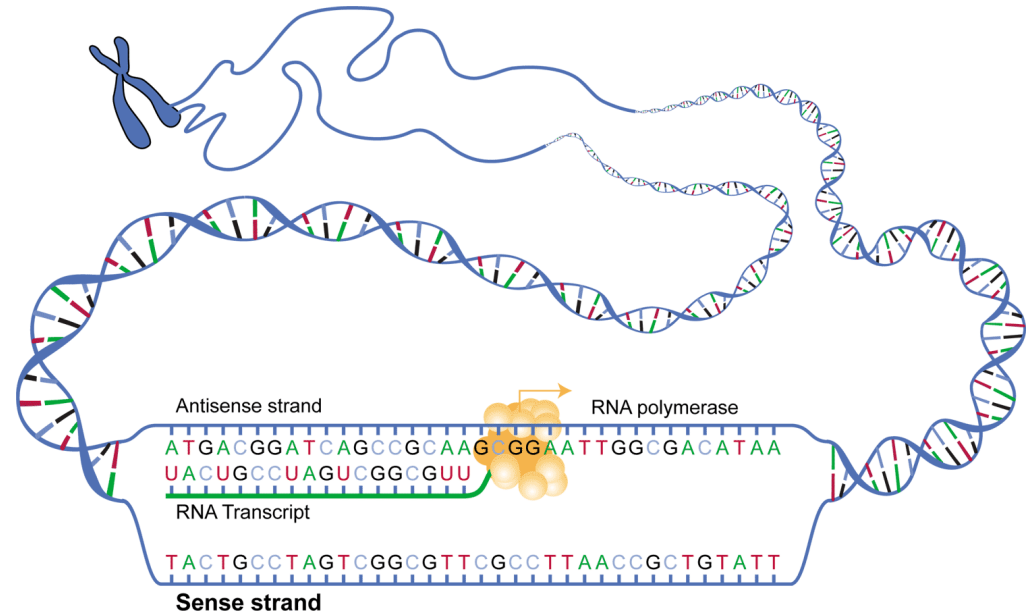
RNA polymerase:

The enzyme used during transcription. RNA polymerase reads the DNA sequence on the template (antisense strand) and makes a complementary RNA transcript.



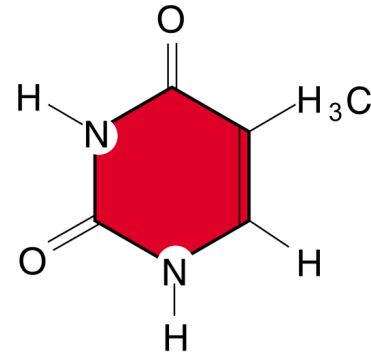
Sense strand:

The DNA strand of a gene that is complementary in sequence to the template (antisense) strand, and identical to the transcribed mRNA sequence (except that DNA contains T where RNA has U). Gene sequences found in databases are always of the sense strand, in the 5' to 3' direction.



Thymine:

One of the four bases in DNA that make up the letters ATGC, thymine is the "T". The others are adenine, guanine, and cytosine. Thymine always pairs with adenine.

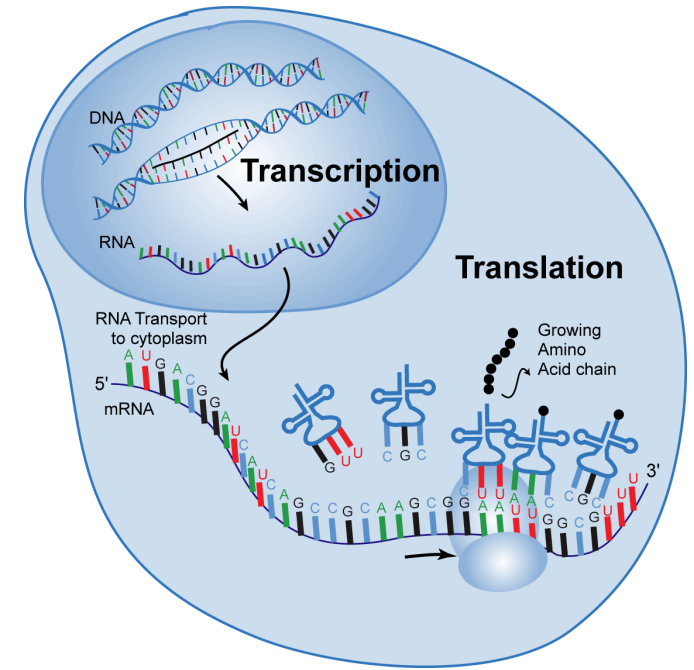


Transcription:

The process by which RNA polymerase assembles an RNA molecule complementary to the template strand (antisense) of the DNA. The product may be messenger RNA, transfer RNA or ribosomal RNA.

Translation:

The process by which messenger RNA directs a ribosome to assemble a polypeptide. As specified in the genetic code each codon in the mRNA corresponds to an amino acid. The assembly of the protein stops when the ribosome encounters one of three possible stop codons.



Uracil:

One of the four bases in RNA. The others are adenine, guanine, and cytosine. Uracil replaces thymine, which is the fourth base in DNA. Like thymine, uracil always pairs with adenine.

