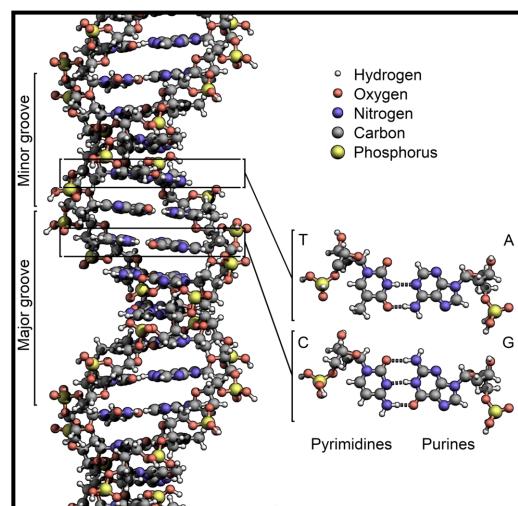
Domain 4: Information

4.1: DNA, and in some cases RNA, is the primary source of heritable information.

1. DNA Structure

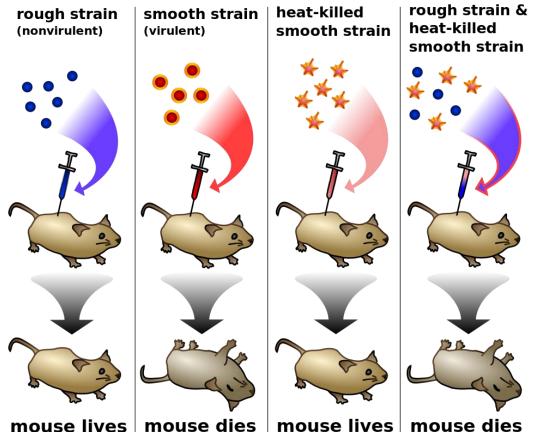
DNA is the Hereditary Molecule DNA is structured to function as the hereditary **Minor groove** molecule for all cellular life.

Many scientists contributed to this understanding



Frederick Griffith

Experiments in the 1920's suggested a molecular basis to inheritance





Avery, McCarty & MacLeod



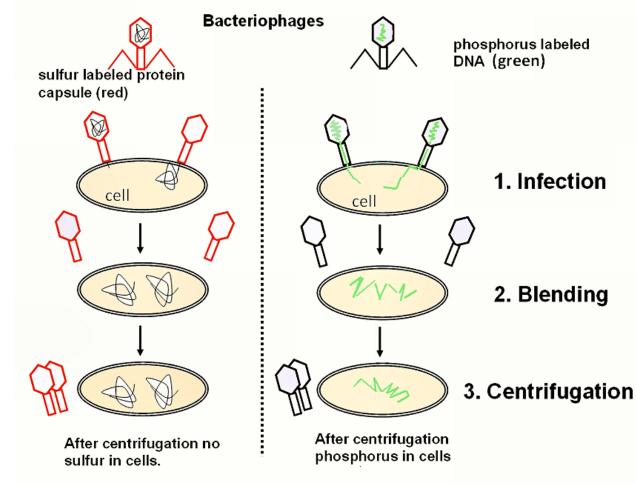


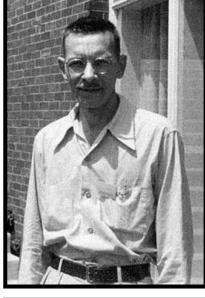
Experiments in the 1940's suggested that DNA was the bacterial heredity molecule, not protein.



Hershey & Chase

Conclusively refined the work of Avery, et. al (1952)

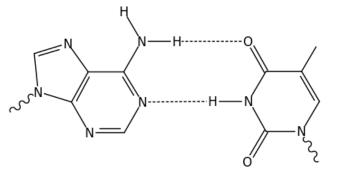






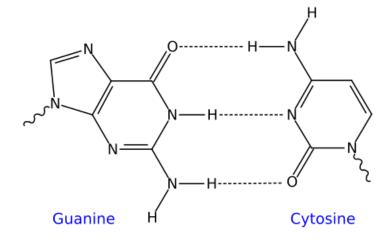
Erwin Chargaff

Demonstrated that every sample DNA had equal Adenine:Thymine and Cytosine:Guanine



Adenine

Thymine



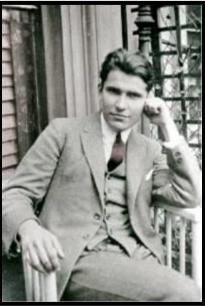
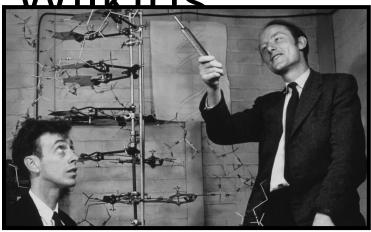


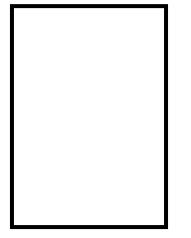
TABLE II Purine and Pyrimidine Contents of Salmon Sperm DNA The results are expressed in moles per mole of P in the hydrolysate.

Experi-	Prepara-	Hydrolysis	Nitrogenous constituent				Recovery of nitrogenous constituents		
ment No.*	tion No.	procedure	Adenine	Guanine	Cytosine	Thymine	Purines	Pyrimi- dines	Total
1	1	1	0.27	0.18			0.45		
2		1	0.26	0.19			0.45		
3		1			0.17	0.28		0.45	
4		1			0.18	0.28		0.46	
5		2	0.28	0.20	0.21	0.27	0.48	0.48	0.96
6		2	0.30	0.22	0.20	0.29	0.52	0.49	-1.01
7		2	0.27	0.18	0.19	0.25	0.45	0.44	0.89
8		2	0.28	0.21	0.20	0.27	0.49	0.47	0.96
9	2	1	0.25	0.18			0.43		
10		1	0.29	0.20		i	0.49		
11		2	0.29	0.18	0.20	0.27	0.47	0.47	0.94
12		2	0.28	0.21	0.19	0.26	0.49	0.45	0.94
13		2	0.30	0.21	0.20	0.30	0.51	0.50	1.01

* In each experiment between twelve and twenty-four determinations of individual purines and pyrimidines were performed.

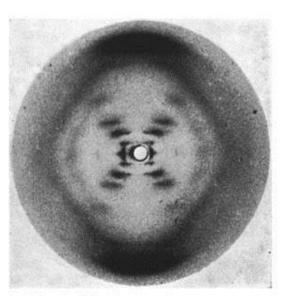
Watson, Crick, Franklin &





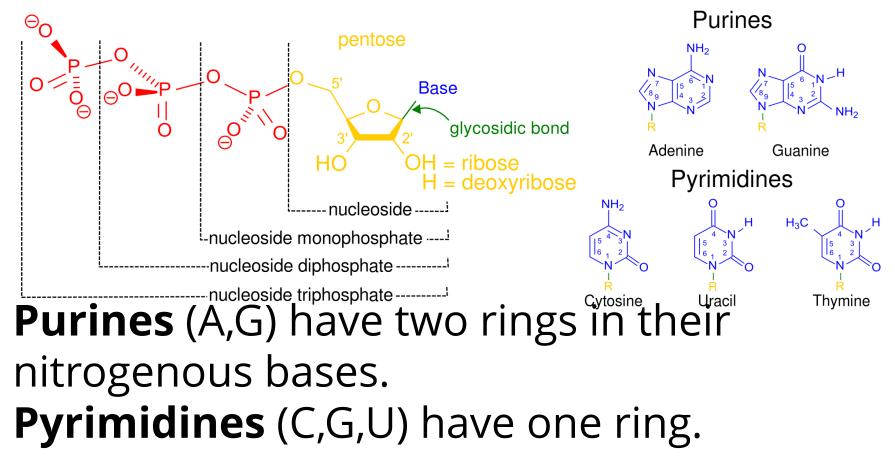


Watson & Crick: Published DNA Structure (1953) based on data generated by Rosalind Franklin, who was working in Wilkins lab.



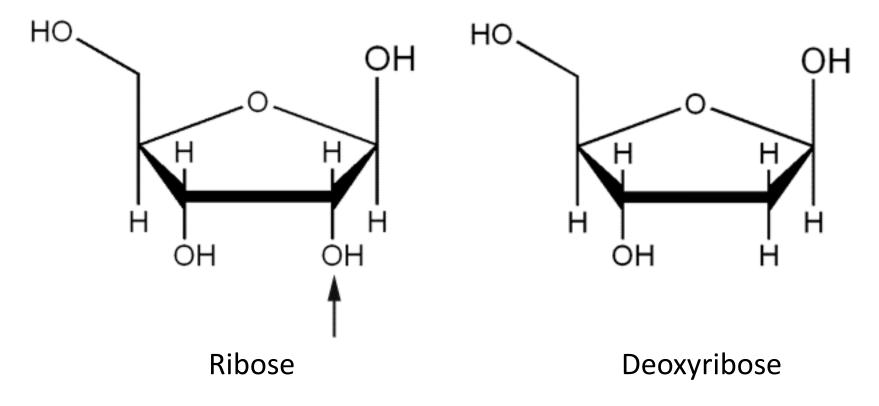
Nucleic Acids: DNA and RNA

Made of **nucleotides**, which exist in the cell as **nucleoside triphosphates** (e.g. ATP)



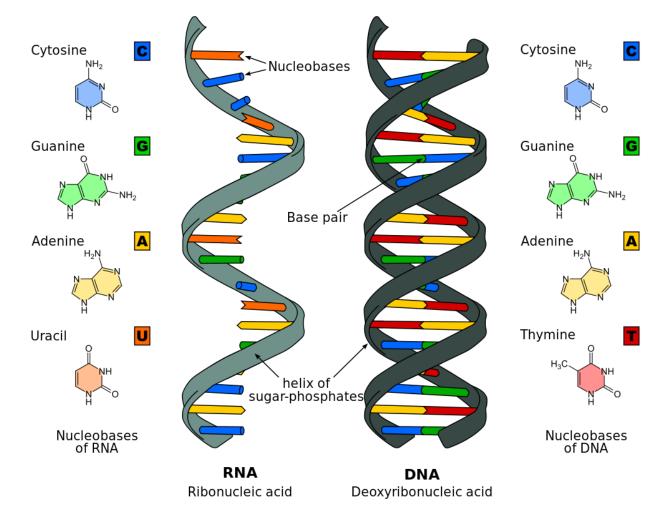
DNA vs. RNA

1. DNA sugar is **deoxyribose**, RNA is **ribose**.



DNA vs. RNA 1.DNA = ATCG 2.DNA = 2 strands

RNA = AUCG RNA = 1 Strand

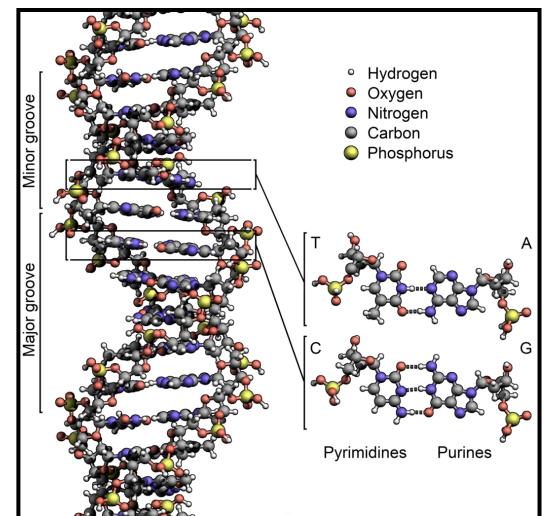


Nucleic Acid Bonding

In a strand: covalent bond between sugar and phosphate.

Between strands: H-bonds

A:T(U) = 2 H-bondsG:C = 3 H-bonds

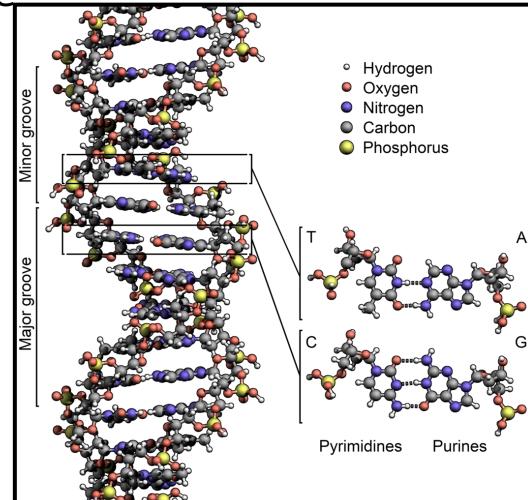


RNA can base pair due to molecular bending

Nucleic Acid Directionality

3' end = hydroxyl group **5' end** = phosphate

2 strands are "**antiparallel**" in orientation.



Nucleic Acid Organization

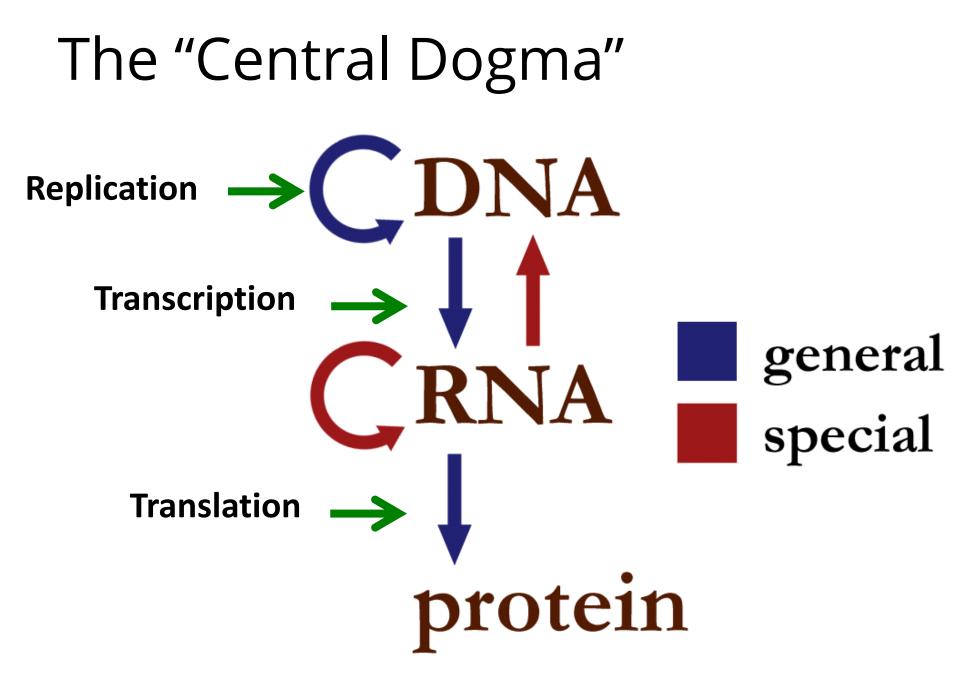
Prokaryotes: 1 circular chromosome (millions of base pairs), and usually at least one small, extra-chromosomal **plasmid** (thousands of base pairs)

Eukaryotes: multiple linear chromosomes (e.g. humans have 46 - ~3 billion base pairs)

Viruses: DNA or RNA, single or double stranded (thousands of base pairs).

4.1: DNA, and in some cases RNA, is the primary source of heritable information.

2. DNA Replication

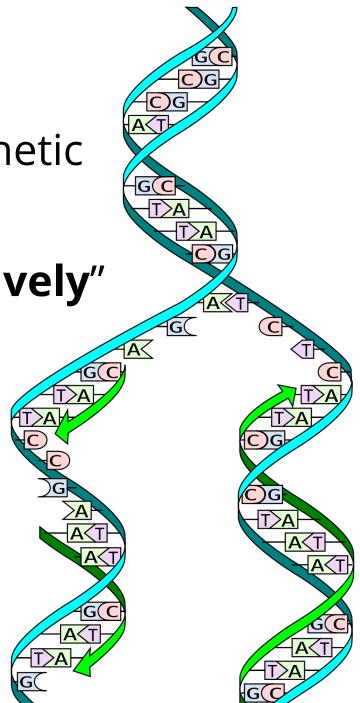


DNA Replication

Allows for heritability of genetic information.

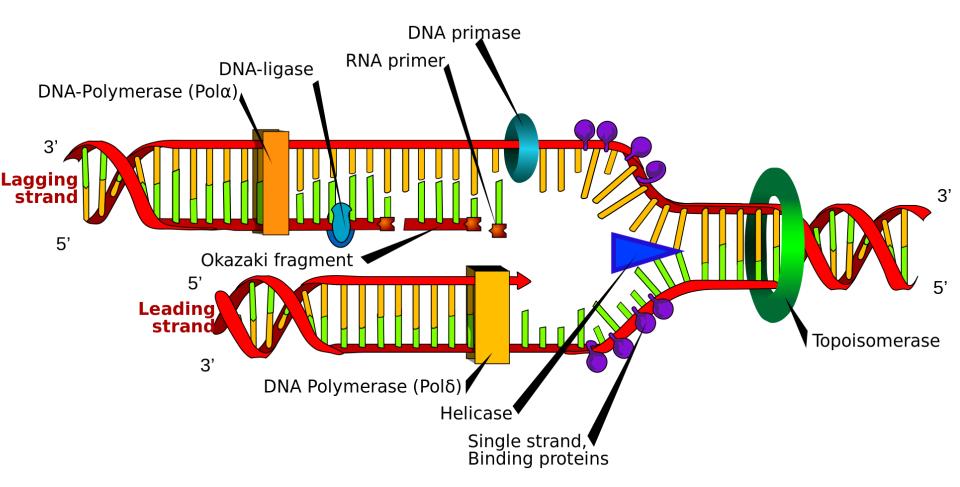
Happens "Semi-conservatively"

Each strand of an old molecule serves as a template for the synthesis of a new strand.



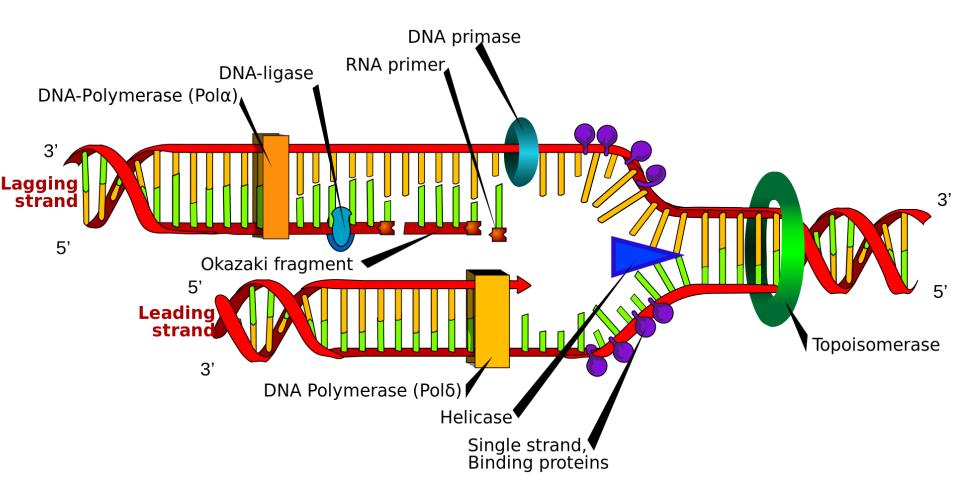
The Replisome

All of the enzymes involved in replication function together.



Helicase: Opens the helix.

Topoisomerase: Rotates the helix.

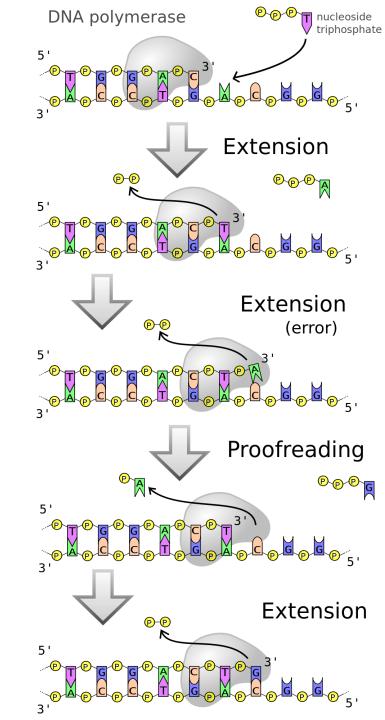


DNA Polymerase

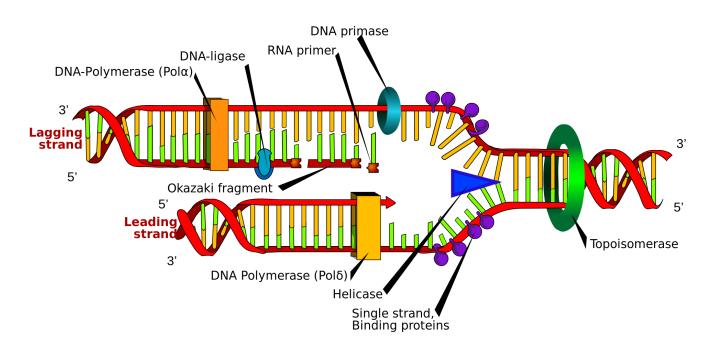
Responsible for the addition of new nucleotides to a growing strand.

Can only add nucleotides in the 5' \rightarrow 3' direction.

Makes mistakes.



Directional Synthesis $5' \rightarrow 3'$ Polymerase can only make new strands in the 5' \rightarrow 3' direction. Leading strand: synthesized continuously in 1 piece. Lagging strand: synthesized discontinuously in multiple fragments, connected by ligase.

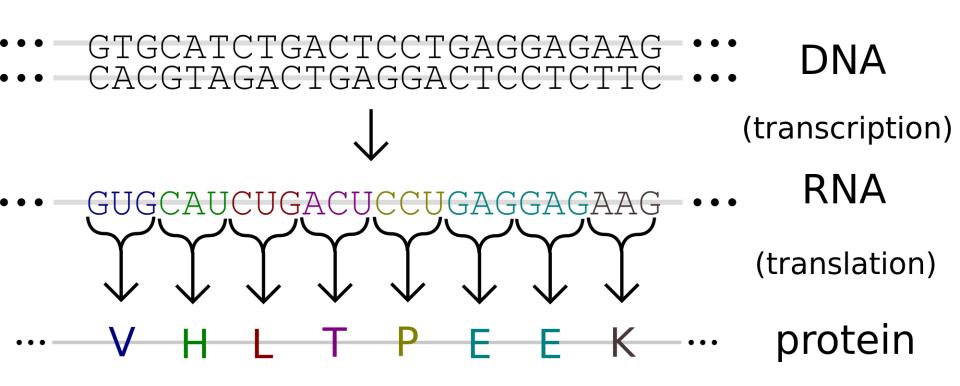


4.1: DNA, and in some cases RNA, is the primary source of heritable information.

3. Protein Synthesis

Protein Synthesis

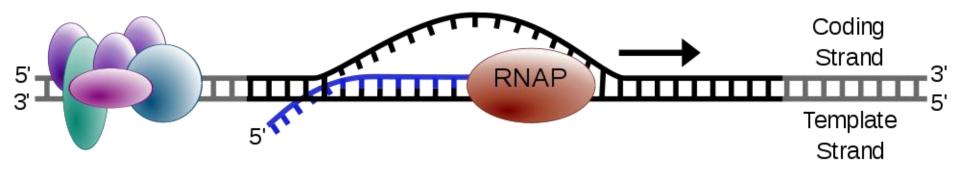
The process by which information stored in DNA is used to produce proteins.



Transcription

Converts DNA sequence information into RNA sequence information.

RNA Polymerase: Enzyme that catalyzes the 5' \rightarrow 3' synthesis of an RNA strand from a single DNA strand.



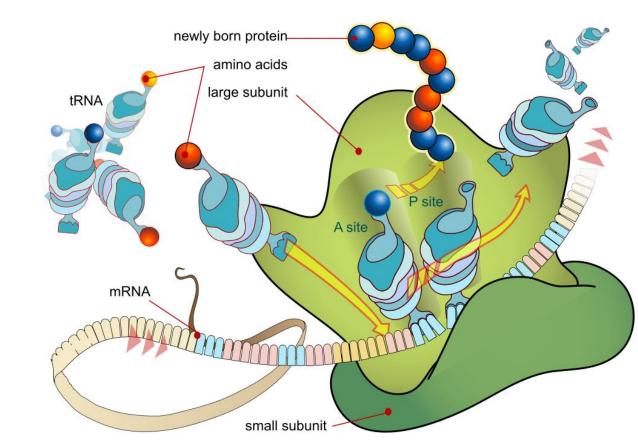
Roles of RNA

mRNA: RNA sequence of a DNA segment that specifies a polypeptides amino acid sequence.

tRNA: Molecules that bring specific amino newly born protein acids to the ribosome, as amino acids large subunit dictated by the mRNA tRNA sequence. P site **rRNA:** Structural A site components of ribosome subunits. mRNA **Regulatory RNA:** Control gene expression. small subunit

Translation

Converts mRNA sequence information in to polypeptide sequences. Occurs at the ribosome.



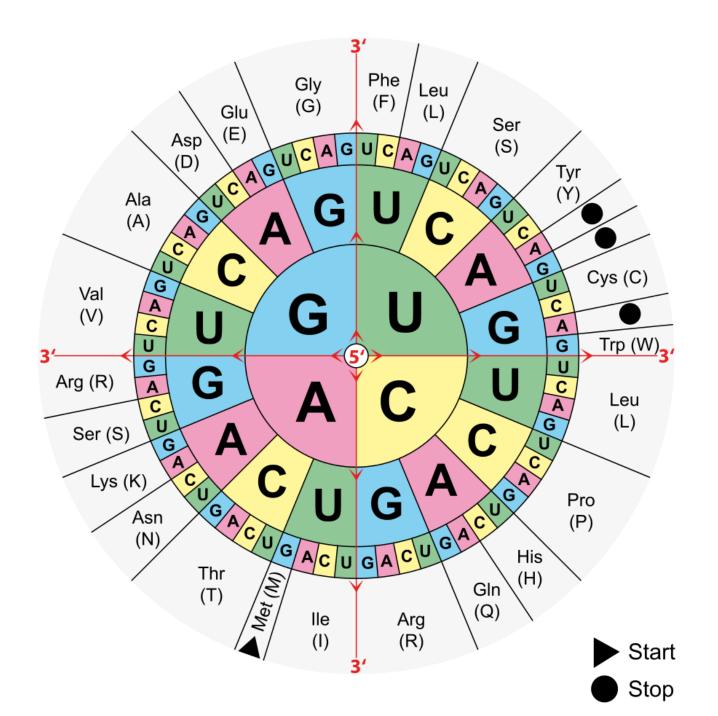
The Genetic Code

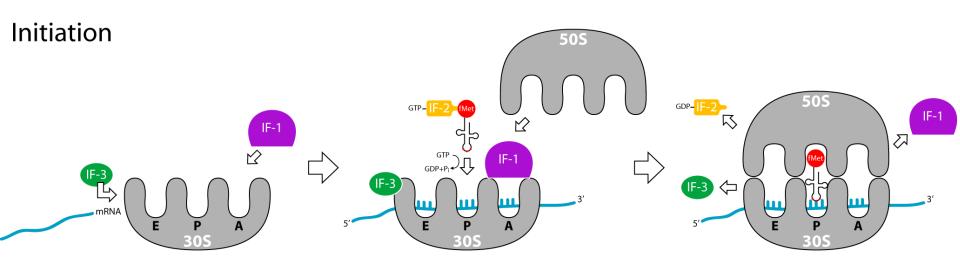
The genetic code is interpreted as a series of 3nucleotide codons. 64 possible codons, which code for all 20 amino acids, along with 1 **START** codon and 3 **STOP** codons.

"Redundant, Unambiguous, Punctuated"

	U		с		А		G		
U	UUU	Phenylalanine	UCU	Serine	UAU	Tyrosine	UGU	Cysteine	U
	UUC	Phenylalanine	UCC	Serine	UAC	Tyrosine	UGC	Cysteine	C
	UUA	Leucine	UCA	Serine	UAA	Stop	UGA	Stop	A
	UUG	Leucine	UCG	Serine	UAG	Stop	UGG	Tryptophan	G
с	CUU	Leucine	CCU	Proline	CAU	Histidine	CGU	Arginine	U
	CUC	Leucine	CCC	Proline	CAC	Histidine	CGC	Arginine	C
	CUA	Leucine	CCA	Proline	CAA	Glutamine	CGA	Arginine	A
	CUG	Leucine	CCG	Proline	CAG	Glutamine	CGG	Arginine	G
А	AUU	Isoleucine	ACU	Threonine	AAU	Asparagine	AGU	Serine	U
	AUC	Isoleucine	ACC	Threonine	AAC	Asparagine	AGC	Serine	C
	AUA	Isoleucine	ACA	Threonine	AAA	Lysine	AGA	Arginine	A
	AUG	Methionine (Start)	ACG	Threonine	AAG	Lysine	AGG	Arginine	G
G	GUU	Valine	GCU	Alanine	GAU	Aspartic Acid	GGU	Glycine	U
	GUC	Valine	GCC	Alanine	GAC	Aspartic Acid	GGC	Glycine	C
	GUA	Valine	GCA	Alanine	GAA	Glutamic Acid	GGA	Glycine	A
	GUG	Valine	GCG	Alanine	GAG	Glutamic Acid	GGG	Glycine	G

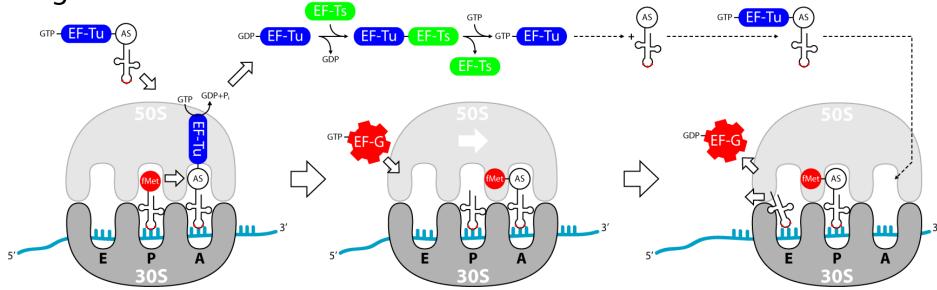
1st base





The mRNA interacts with the ribosome to begin translation at the START (AUG) codon closest to the 5' end of the mRNA.

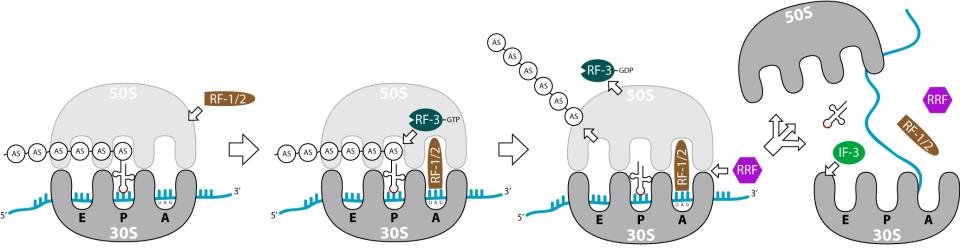




Subsequent amino acids are brought to the ribosome as specified by subsequent, adjacent codons.

Each amino acid is transferred to a growing polypeptide chain.

Termination

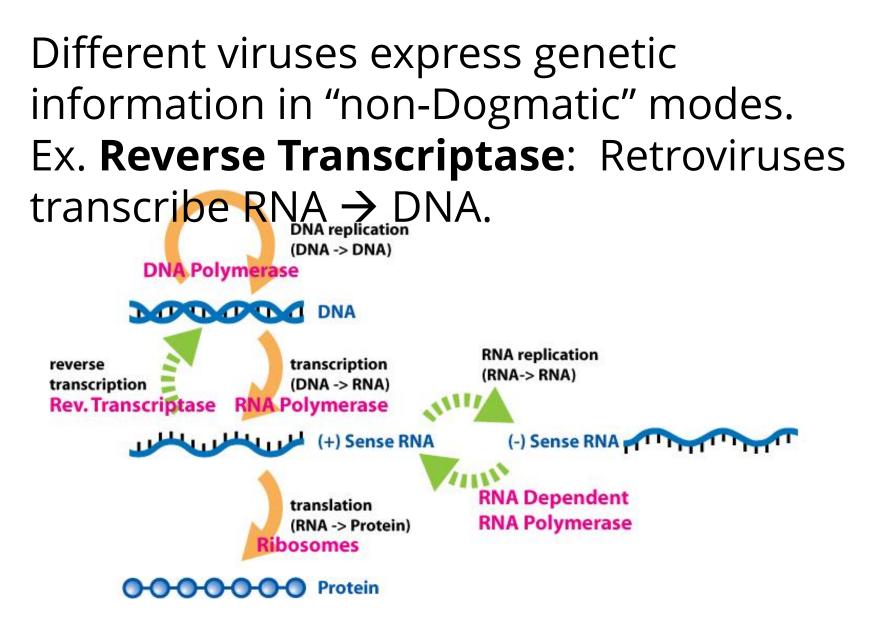


This process continues until the first STOP codon is reached, which triggers the release of the polypeptide and the disassembly of the ribosome.

4.1: DNA, and in some cases RNA, is the primary source of heritable information.

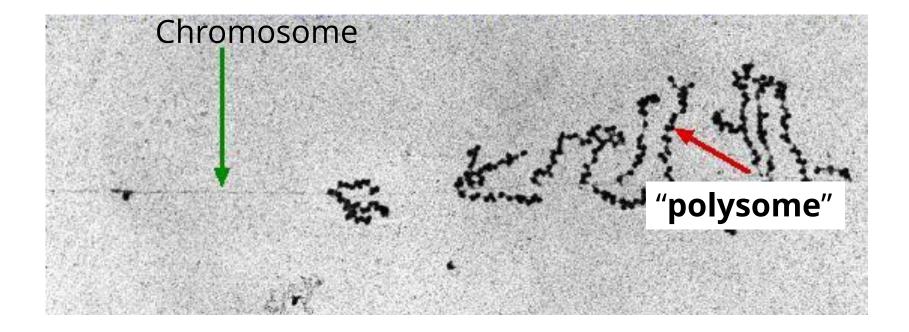
4. Genetic Information Processing & Variation

Viral RNA Processing



Prokaryotic RNA Processing

The lack of a nucleus allows for simultaneous transcription and translation, leading to multiple ribosomes translating a single mRNA



Eukaryotic Gene Processing

Eukaryotes extensively process RNA transcripts prior to their export from the nucleus to the ribosome.

1.Poly-Adenylation: a chain of Adenine residues is added to the 3' end of the transcript.

2.5' capping: a modified nucleotide is added to the 5' end of the transcript.

20000	0000000	00000	0000000	
		Nascent RNA		RNA Polymerase II
5' Cap	AAUAAA	CA	— UUGUGUGUUG ——	
	Polyadenylation Signal	Cleavage Signal	GU-rich Sequence	

1.Exon splicing: Many segments of the transcript ("**introns**") are removed, and the remaining segments ("**exons**") are spliced together to produce a mature transcript.

