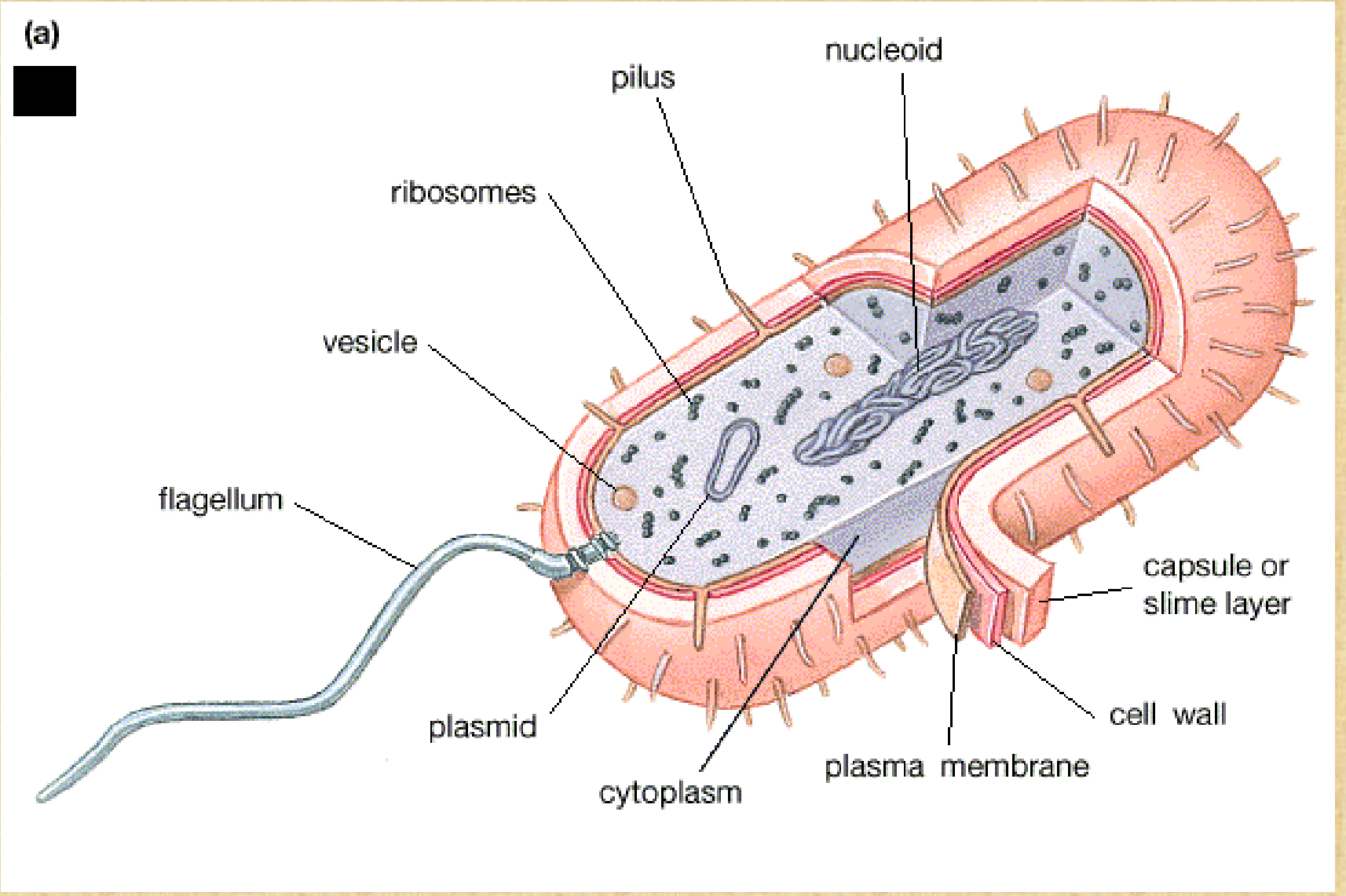
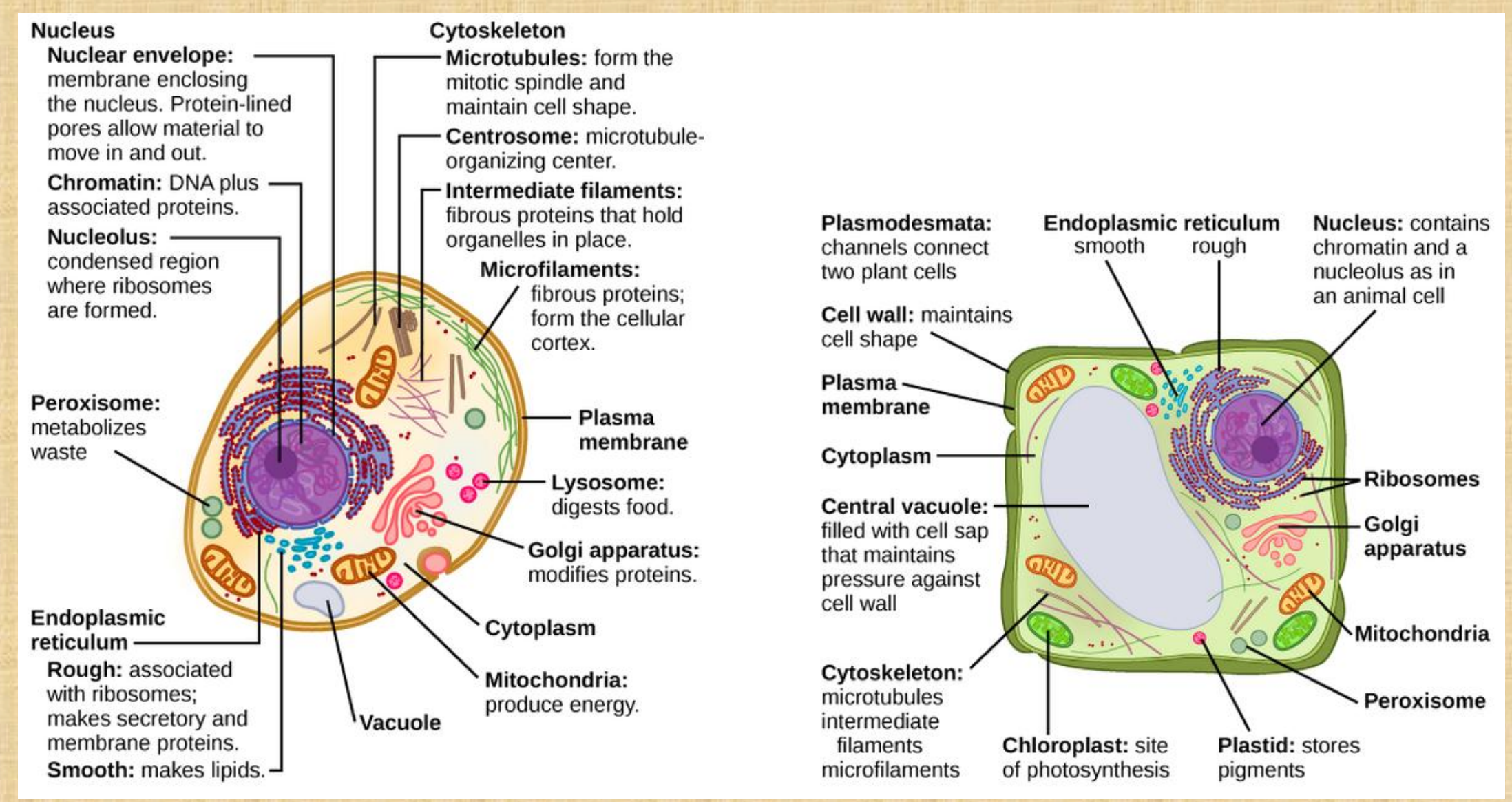
DNA: Genetic material

Dr. Ashok Kumar HG

Bacterium


(a)
pilus
nucleoid
ribosomes
vesicle
flagellum
capsule or
slime layer
plasmid
cell wall
plasma membrane
cytoplasm

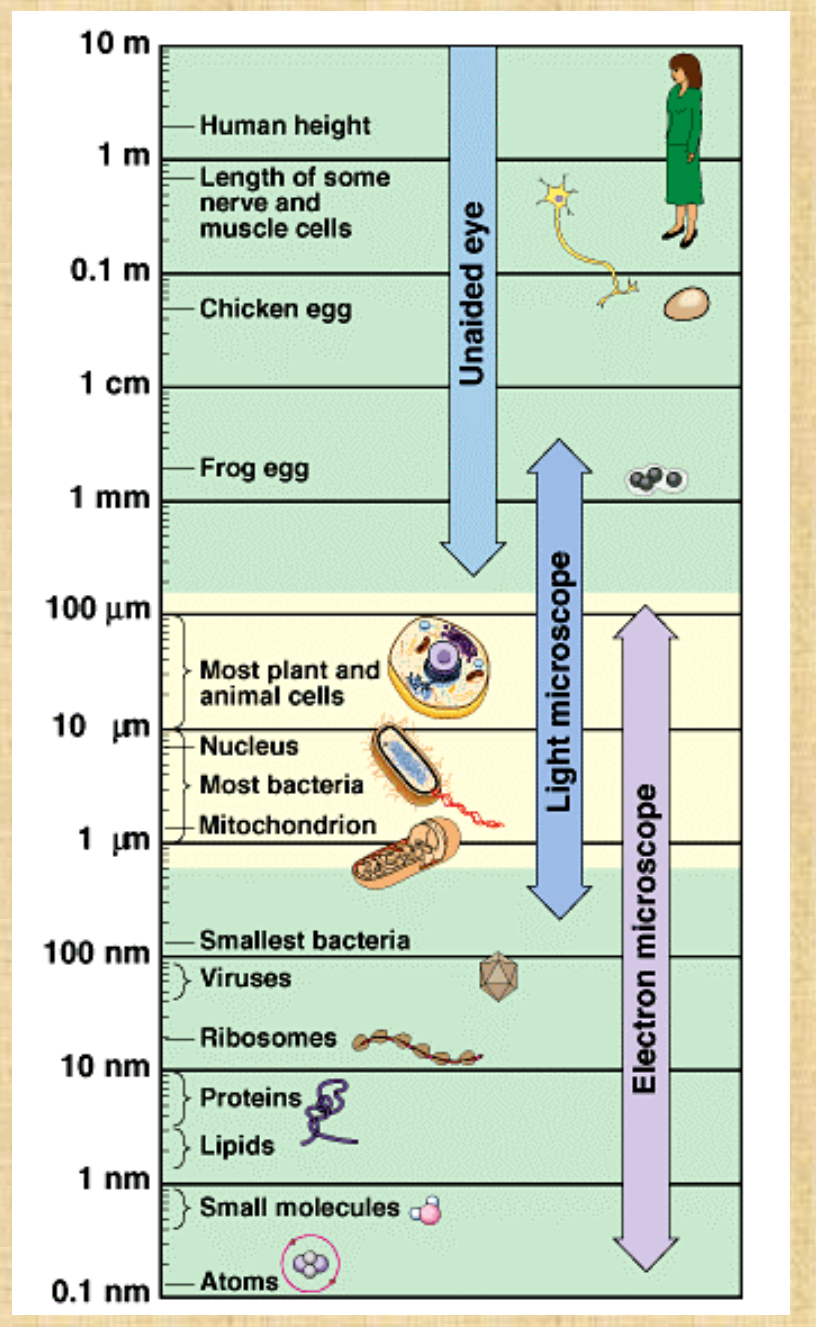
Animal and Plant Cells



Difference between Prokaryotic cell and Eukaryotic cell

	Prokaryotes	**Eukaryotes**
DNA	DNA is naked (no histones)	DNA associated with histones
	DNA is circular	DNA is linear
	Genes do not contain introns	Genes may contain introns
	DNA found in cytoplasm (nucleoid)	DNA found in nucleus
Internal Structures	No membrane-bound organelles	Have membrane-bound organelles
Ribosomes	Have 70S ribosomes	Have 80S ribosomes
Reproduction	Asexual (binary fission)	Asexual (mitosis) or sexual (meiosis)
	DNA is singular (haploid)	DNA is usually paired (diploid or more)
Average Size	Smaller (≈1 – 5 μm)	Larger (≈10 – 100 μm)

Cell size

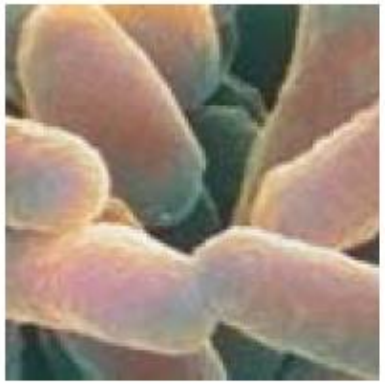

10 m
1 m
0.1 m
1 cm
1 mm
100 µm
10 µm
1 µm
100 nm
10 nm
1 nm
0.1 nm
Human height
Length of some nerve and muscle cells
Chicken egg
Frog egg
Most plant and animal cells
Nucleus
Most bacteria
Mitochondrion
Smallest bacteria
Viruses
Ribosomes
Proteins
Lipids
Small molecules
Atoms
Unaided eye
Light microscope
Electron microscope

(a)

Viruses

Proteins involved in DNA, RNA, protein synthesis
Gene regulation
Cancer and control of cell proliferation
Transport of proteins and organelles inside cells
Infection and immunity
Possible gene therapy approaches

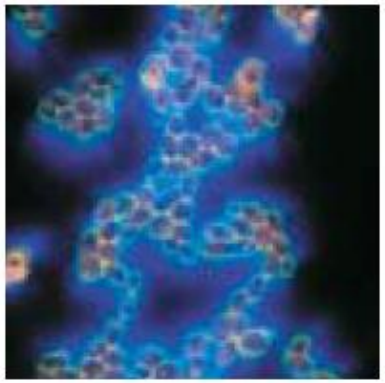
(b)



Bacteria

Proteins involved in DNA, RNA, protein synthesis, metabolism
Gene regulation
Targets for new antibiotics
Cell cycle
Signaling

(c)



Yeast (*Saccharomyces cerevisiae*)

Control of cell cycle and cell division
Protein secretion and membrane biogenesis
Function of the cytoskeleton
Cell differentiation
Aging
Gene regulation and chromosome structure

(d)

Roundworm (*Caenorhabditis elegans*)

Development of the body plan
Cell lineage
Formation and function of the nervous system
Control of programmed cell death
Cell proliferation and cancer genes
Aging
Behavior
Gene regulation and chromosome structure

Each experimental organism used in cell biology has advantages for certain types of studies. Viruses and bacteria have small genomes amenable to genetic dissection. Many insights into gene control initially came from studies with these organisms. The yeast *Saccharomyces cerevisiae* has the cellular organization of a eukaryote but is a relatively simple single-celled organism that is easy to grow and to manipulate genetically. In the nematode worm *Caenorhabditis elegans*, which has a small number of cells arranged in a nearly identical way in every worm, the formation of each individual cell can be traced. Lodish et al., 2008

(e)

Fruit fly (*Drosophila melanogaster*)

Development of the body plan
Generation of differentiated cell lineages
Formation of the nervous system, heart, and musculature
Programmed cell death
Genetic control of behavior
Cancer genes and control of cell proliferation
Control of cell polarization
Effects of drugs, alcohol, pesticides

(f)

Zebrafish

Development of vertebrate body tissues
Formation and function of brain and nervous system
Birth defects
Cancer

(g)

Mice, including cultured cells

Development of body tissues
Function of mammalian immune system
Formation and function of brain and nervous system
Models of cancers and other human diseases
Gene regulation and inheritance
Infectious disease

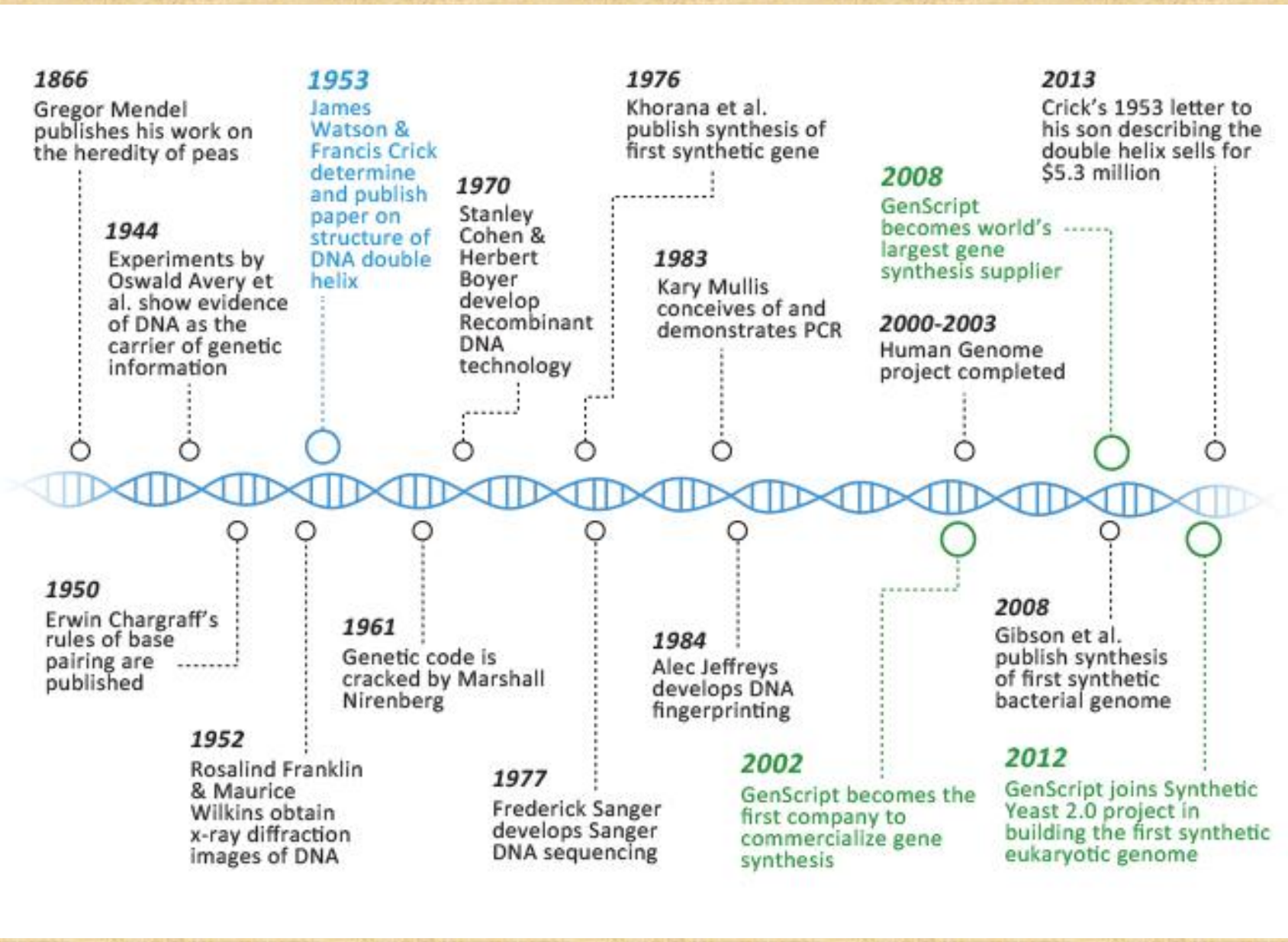
(h)

Plant (*Arabidopsis thaliana*)

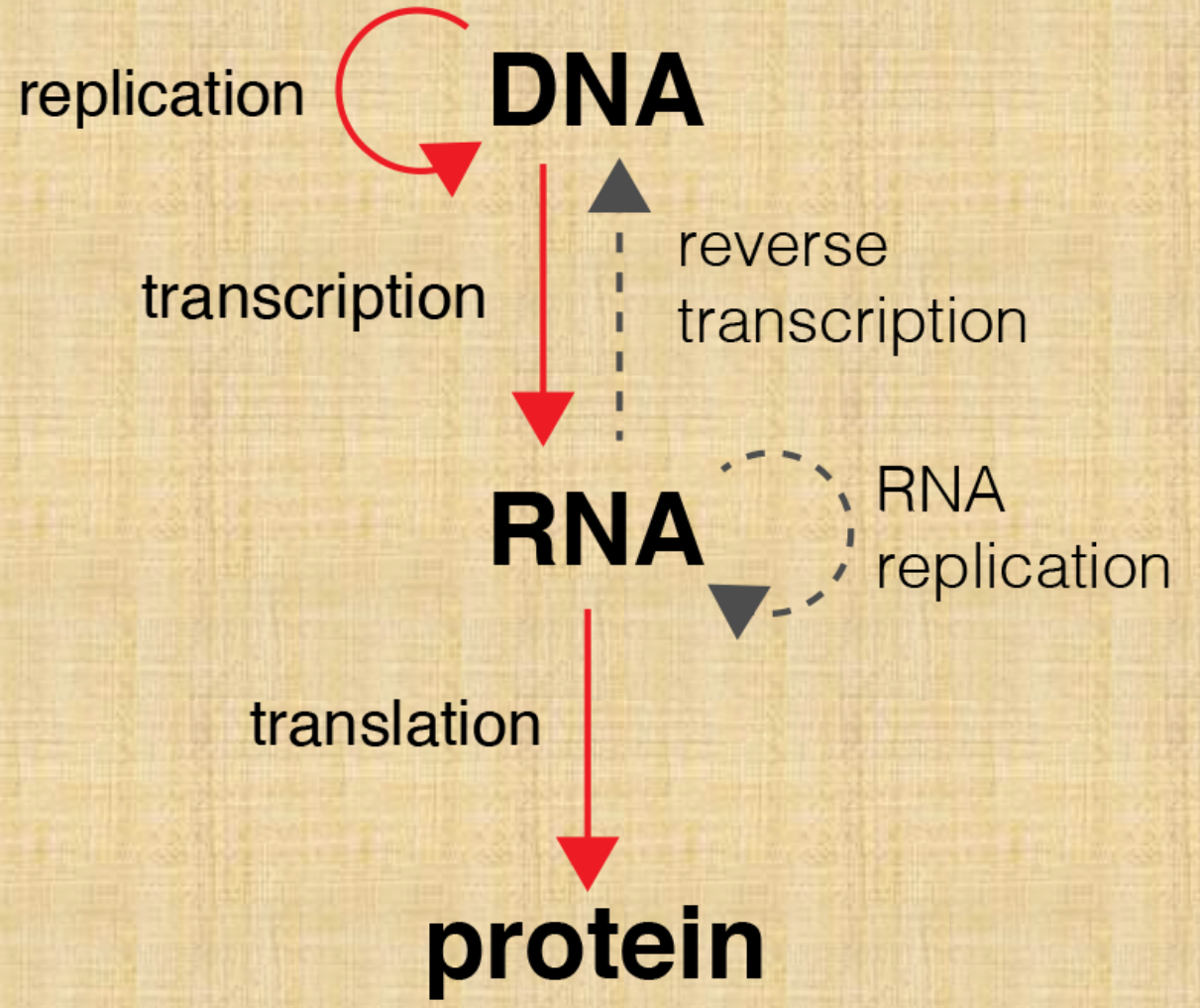
Development and patterning of tissues
Genetics of cell biology
Agricultural applications
Physiology
Gene regulation
Immunity
Infectious disease

The fruit fly *Drosophila melanogaster*, first used to discover the properties of chromosomes, has been especially valuable in identifying genes that control embryonic development. Many of these genes are evolutionarily conserved in humans. The zebrafish *Danio rerio* is used for rapid genetic screens to identify genes that control development and organogenesis. Of the experimental animal systems, mice (*Mus musculus*) are evolutionarily the closest to humans and have provided models for studying numerous human genetic and infectious diseases. The mustard-family weed *Arabidopsis thaliana*, sometimes described as the *Drosophila* of the plant kingdom, has been used for genetic screens to identify genes involved in nearly every aspect of plant life. Genome sequencing is completed for many viruses and bacterial species, the yeast *Saccharomyces cerevisiae*, the roundworm *C. elegans*, the fruit fly *D. melanogaster*, humans, and the plant *Arabidopsis thaliana*.It is mostly completed for mice and in progress for zebrafish. Other organisms, particularly frogs, sea urchins, chickens, and slime molds, continue to be immensely valuable for cell biology research. Increasingly, a wide variety of other species are used,especially for studies of evolution of cells and mechanisms.

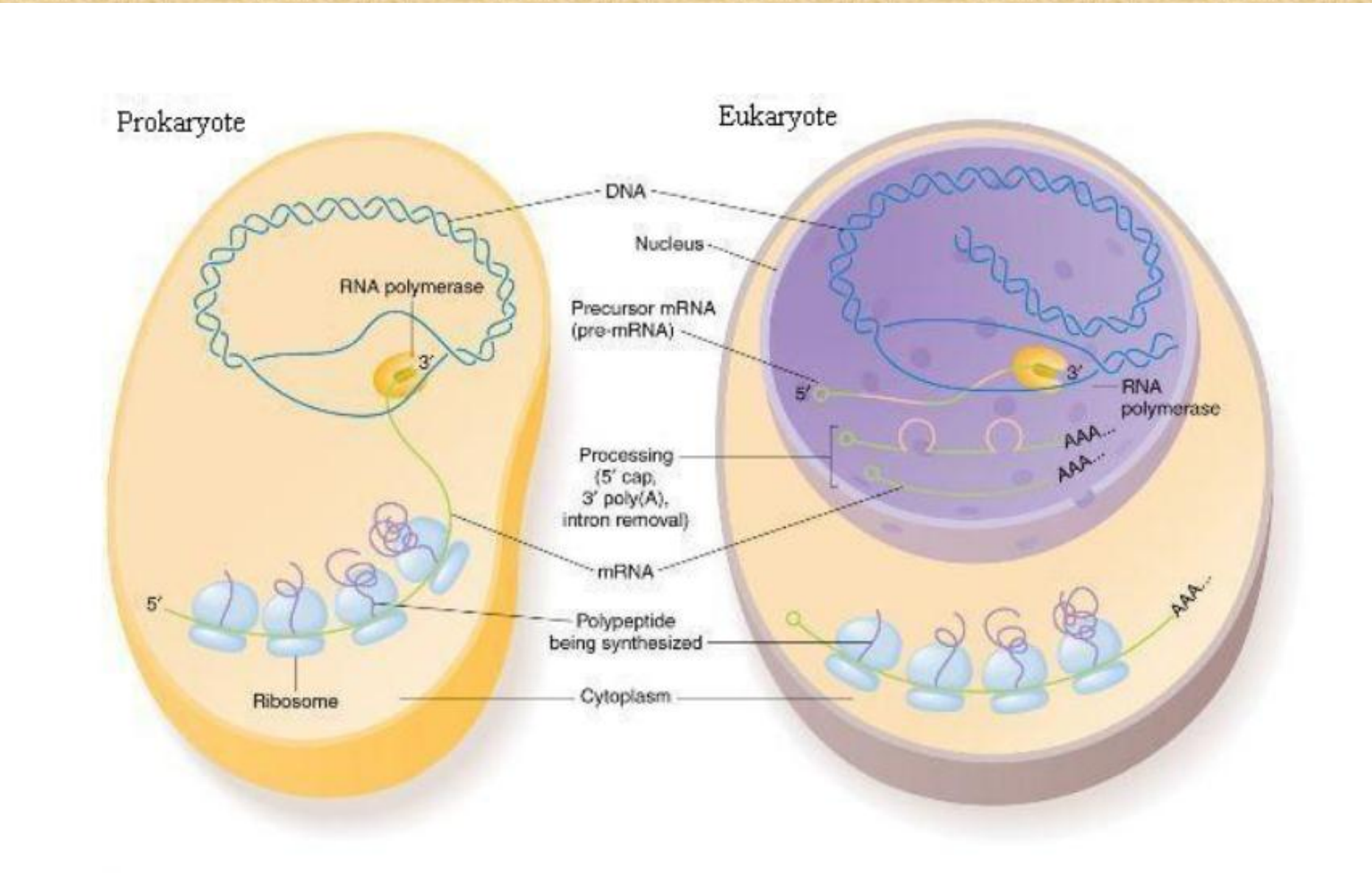
Lodish et al., 2008


1866
Gregor Mendel publishes his work on the heredity of peas
1944
Experiments by Oswald Avery et al. show evidence of DNA as the carrier of genetic information
1953
James Watson & Francis Crick determine and publish paper on structure of DNA double helix
1970
Stanley Cohen & Herbert Boyer develop Recombinant DNA technology
1976
Khorana et al. publish synthesis of first synthetic gene
1983
Kary Mullis conceives of and demonstrates PCR
2000-2003
Human Genome project completed
2008
GenScript becomes world's largest gene synthesis supplier
2013
Crick's 1953 letter to his son describing the double helix sells for $5.3 million
1950
Erwin Chargraff's rules of base pairing are published
1952
Rosalind Franklin & Maurice Wilkins obtain x-ray diffraction images of DNA
1961
Genetic code is cracked by Marshall Nirenberg
1977
Frederick Sanger develops Sanger DNA sequencing
1984
Alec Jeffreys develops DNA fingerprinting
2002
GenScript becomes the first company to commercialize gene synthesis
2008
Gibson et al. publish synthesis of first synthetic bacterial genome
2012
GenScript joins Synthetic Yeast 2.0 project in building the first synthetic eukaryotic genome

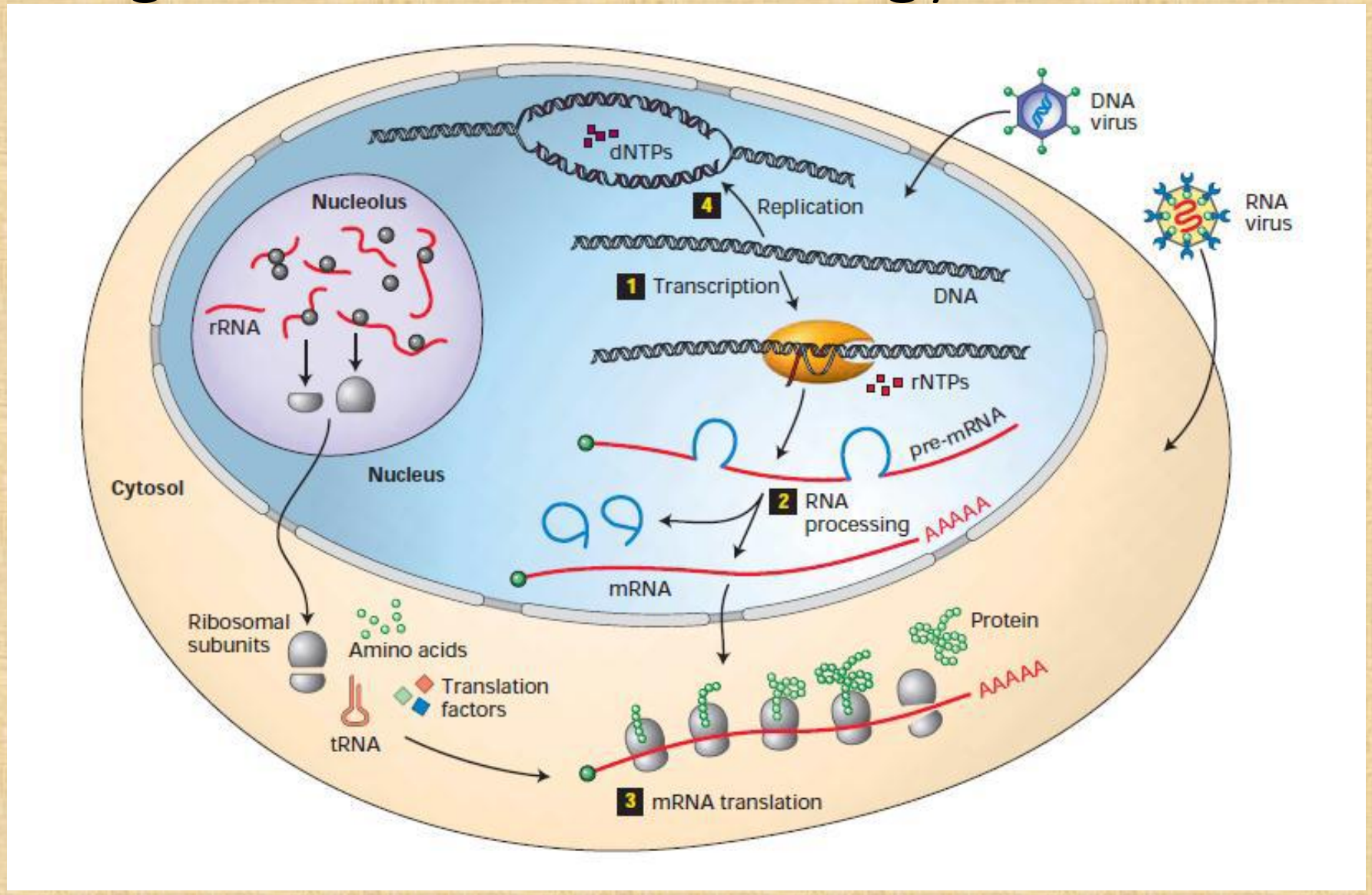
Central dogma of molecular biology



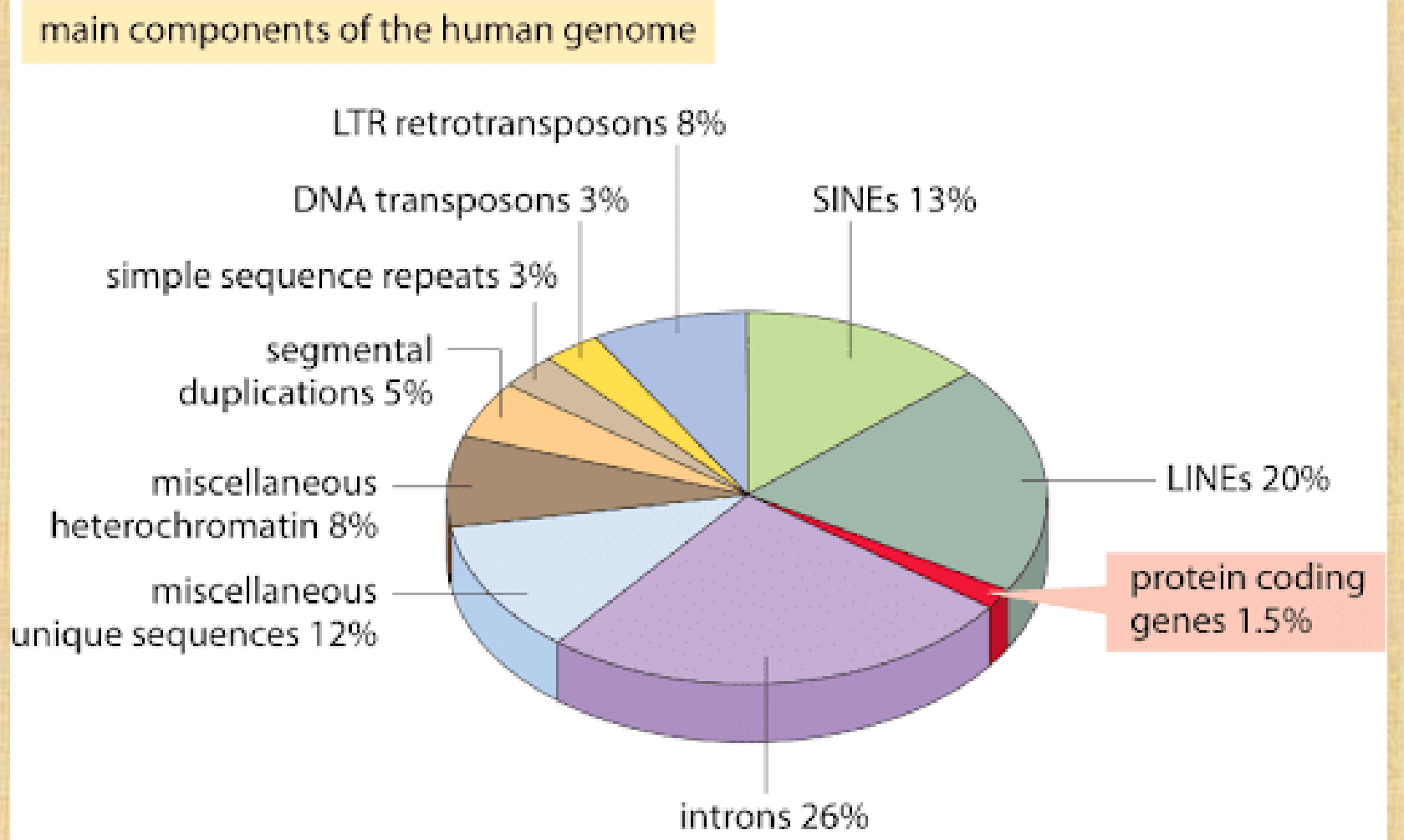
Prokaryotic and Eukaryotic Cells



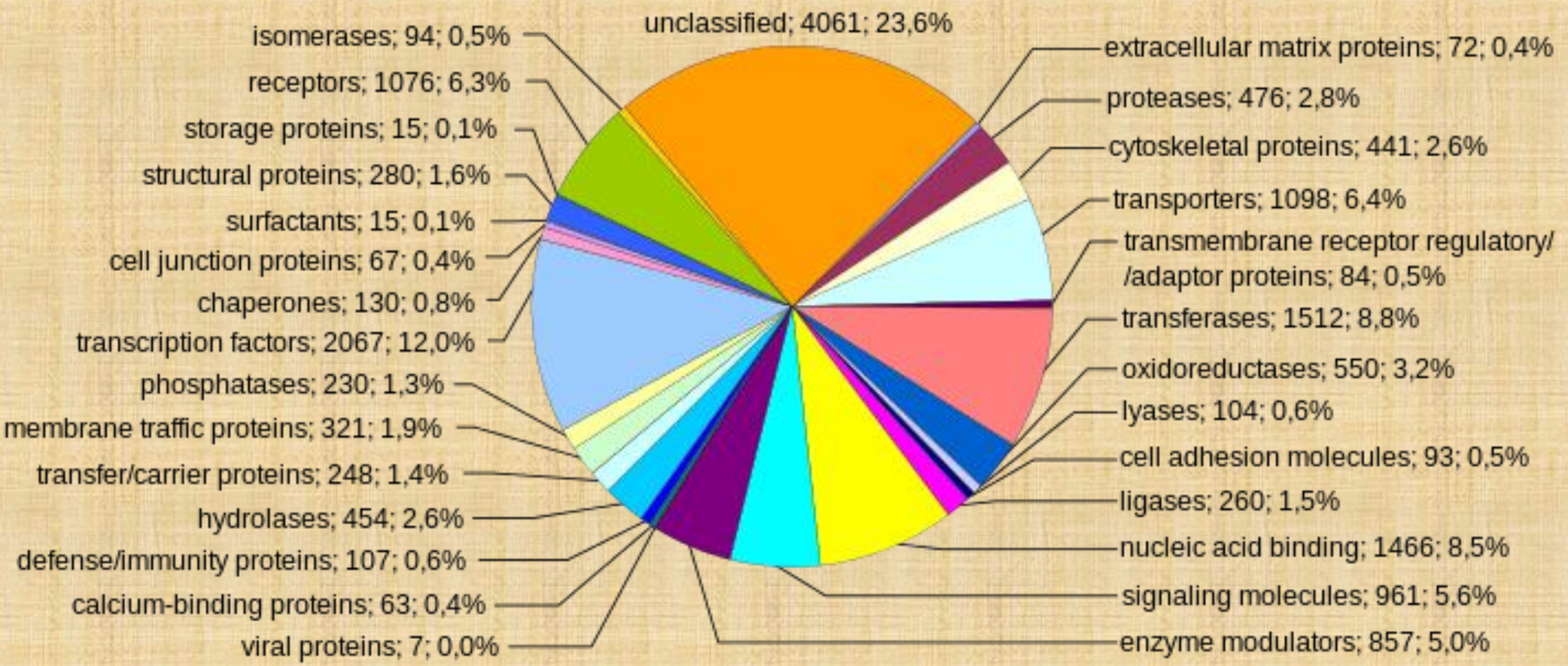
Central dogma of molecular biology



Lodish et al., 2008



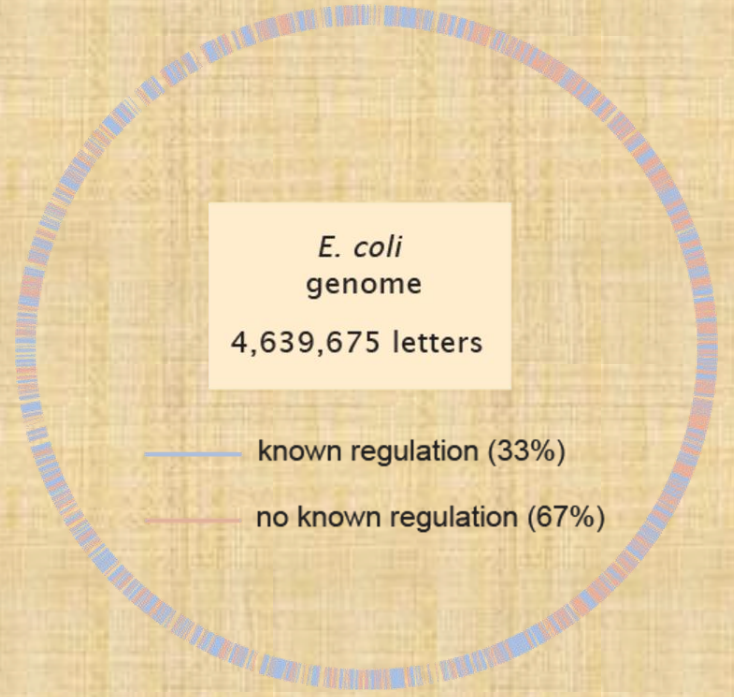
Short interspaced retrotransposable elements (SINEs), Long interspaced retrotransposable elements (LINEs)

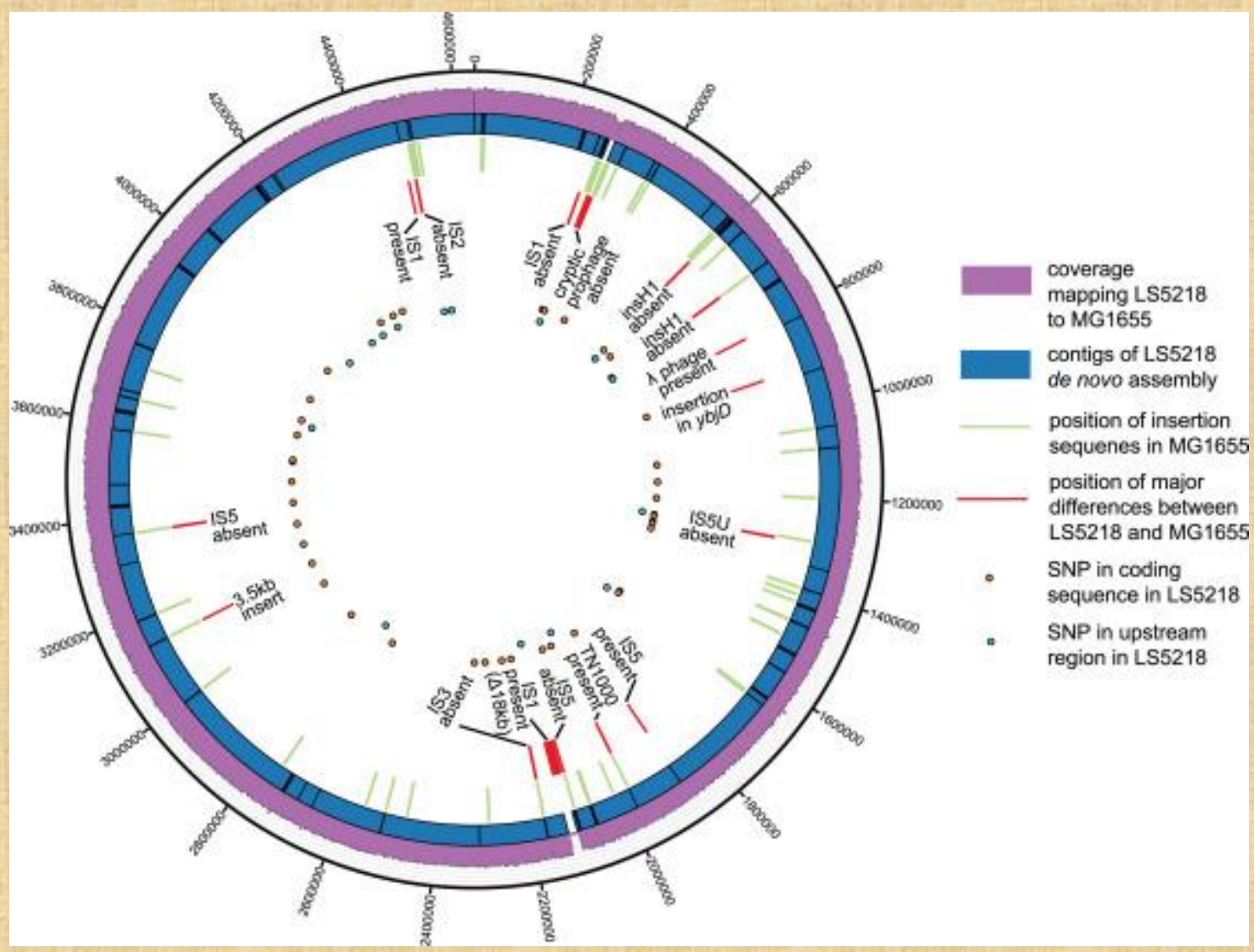


Human genes categorized by function of the transcribed proteins, given both as number of encoding genes and percentage of all genes

Examples of human protein-coding genes

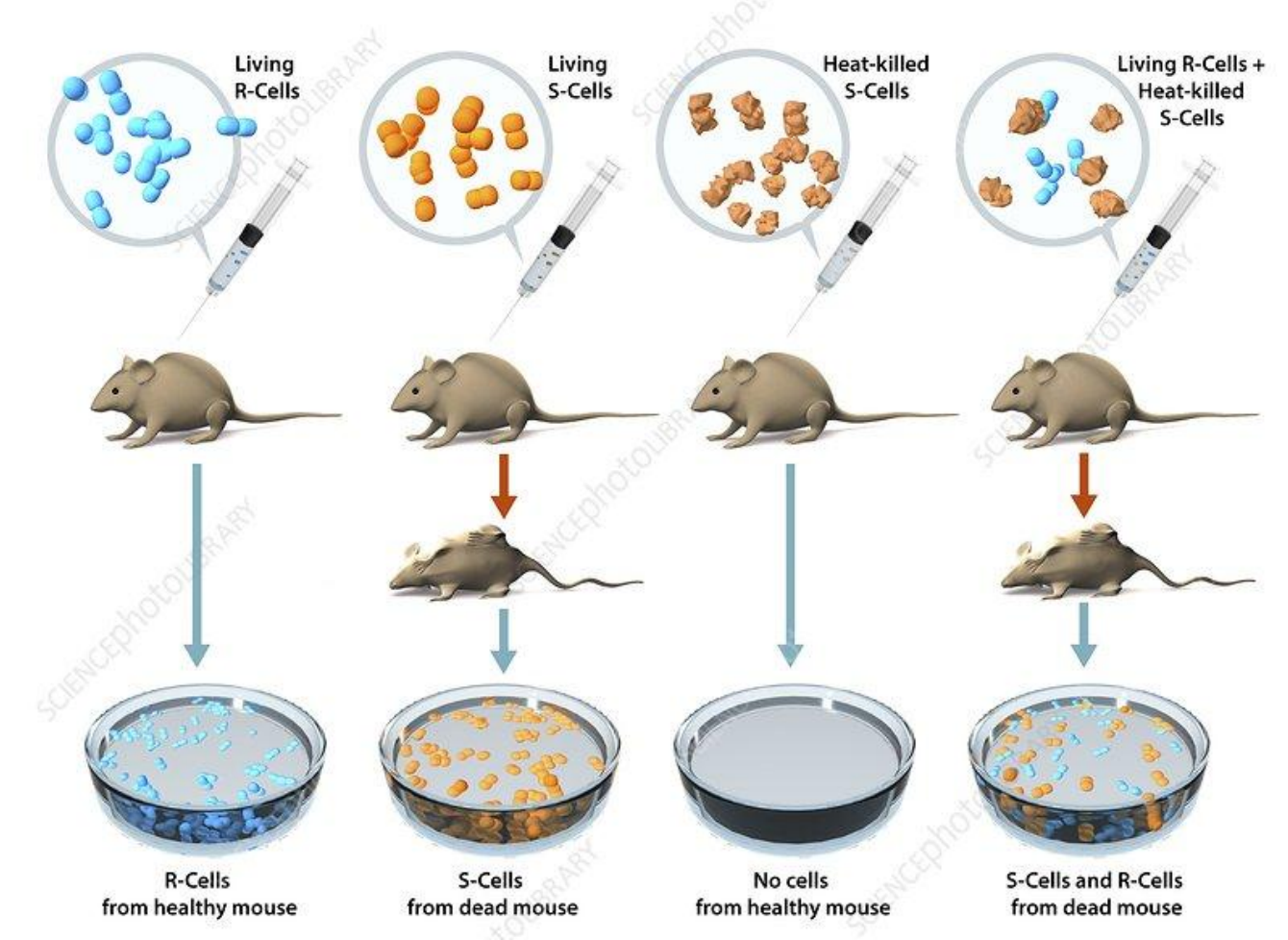
Protein	Chrom	Gene	Length	Exons	Exon length	Intron length	Alt splicing
Breast cancer type 2 susceptibility protein	13	BRCA2	83,736	27	11,386	72,350	yes
Cystic fibrosis transmembrane conductance regulator	7	CFTR	202,881	27	4,440	198,441	yes
Cytochrome b	MT	MTCYB	1,140	1	1,140	0	no
Dystrophin	X	DMD	2,220,381	79	10,500	2,209,881	yes
Glyceraldehyde-3-phosphate dehydrogenase	12	GAPDH	4,444	9	1,425	3,019	yes
Hemoglobin beta subunit	11	HBB	1,605	3	626	979	no
Histone H1A	6	HIST1H1A	781	1	781	0	no
Titin	2	TTN	281,434	364	104,301	177,133	yes





Genome sequence and analysis of *Escherichia coli*

Griffith's experiment



Griffith's Experiment

In 1928, Frederick Griffith conducted one of the first experiments to show that cells possessed genetic material

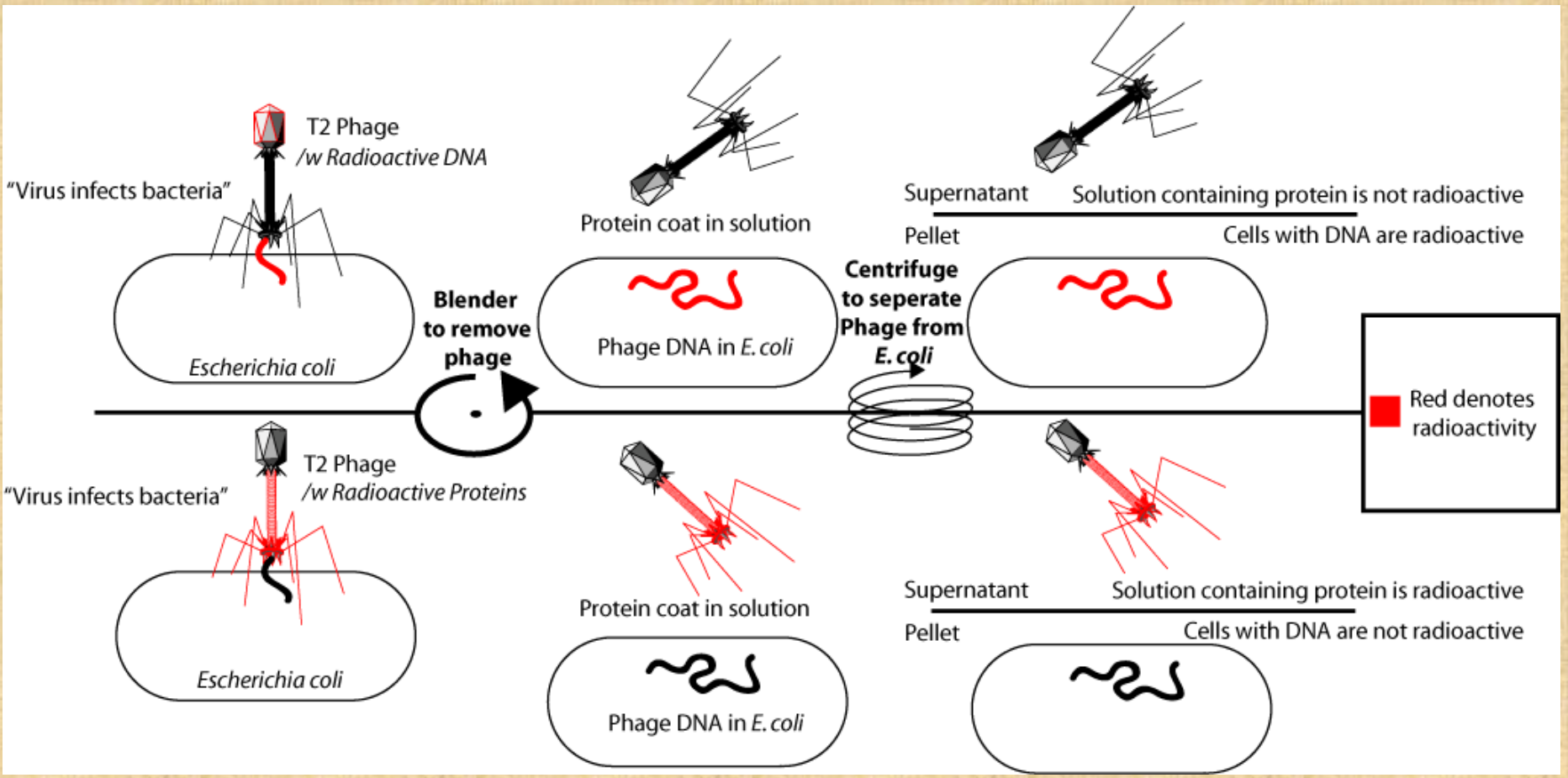
Griffith's experiment involved the use of two strains of pneumococcus – a deadly virulent strain (**S**) or a non-virulent strain (**R**)

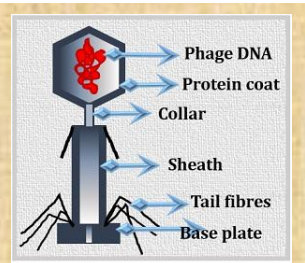
- When Griffith infected mice with the non-virulent bacteria (strain **R**), the mice survived
- When Griffith infected mice with the virulent bacteria (strain **S**), the mice died
- When Griffith infected mice with heat-killed virulent bacteria (strain **R**), the mice survived as the bacteria had been killed
- When Griffith infected mice with a mix of heat-killed strain **S** and living strain **R**, the mice were found to have died

From this Griffith's concluded that the living **R** cells had somehow been transformed into virulent **S** cells

- This indicated that there was some form of transferrable genetic material present within the cells (i.e. DNA)

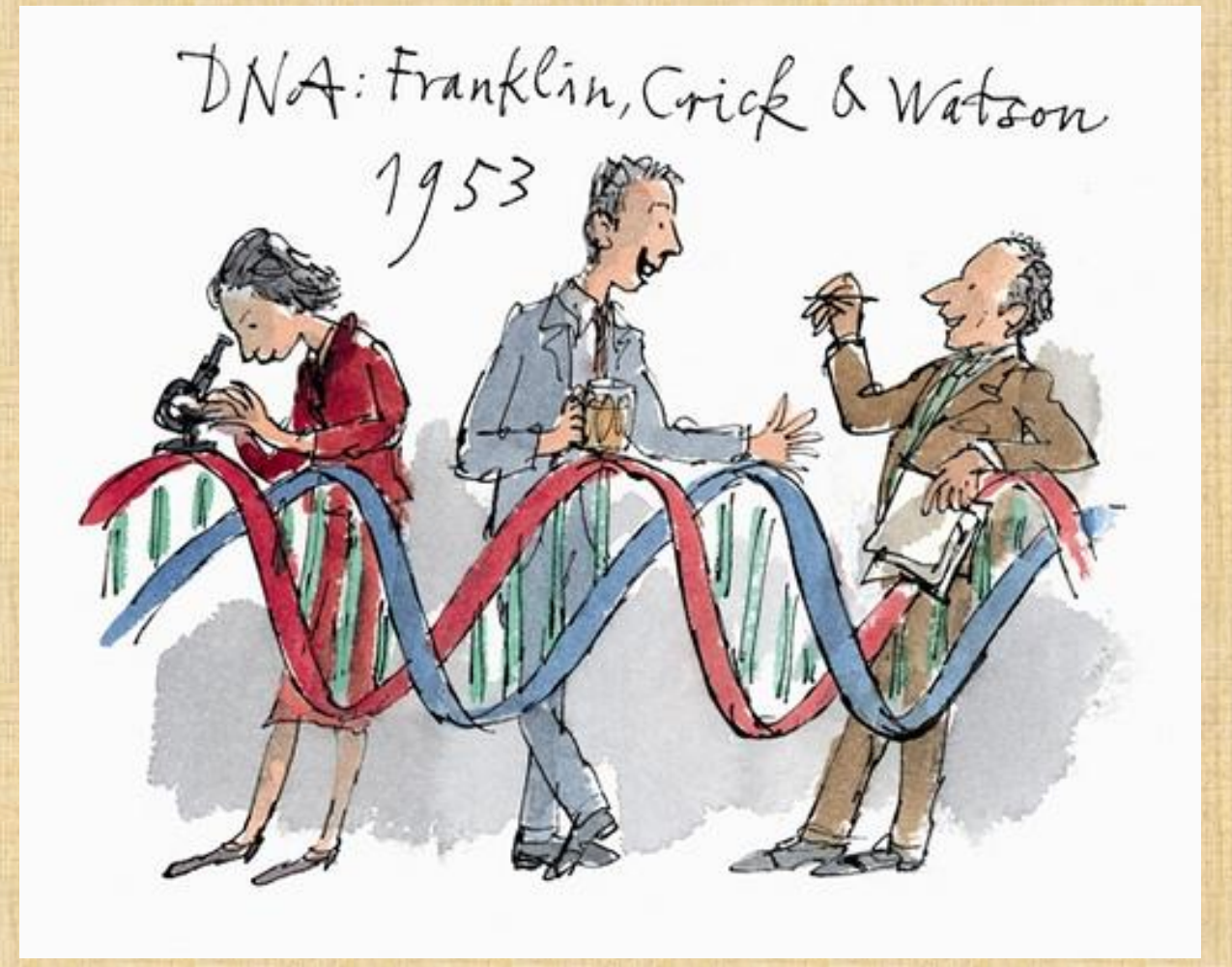
Hershey and Chase experiment



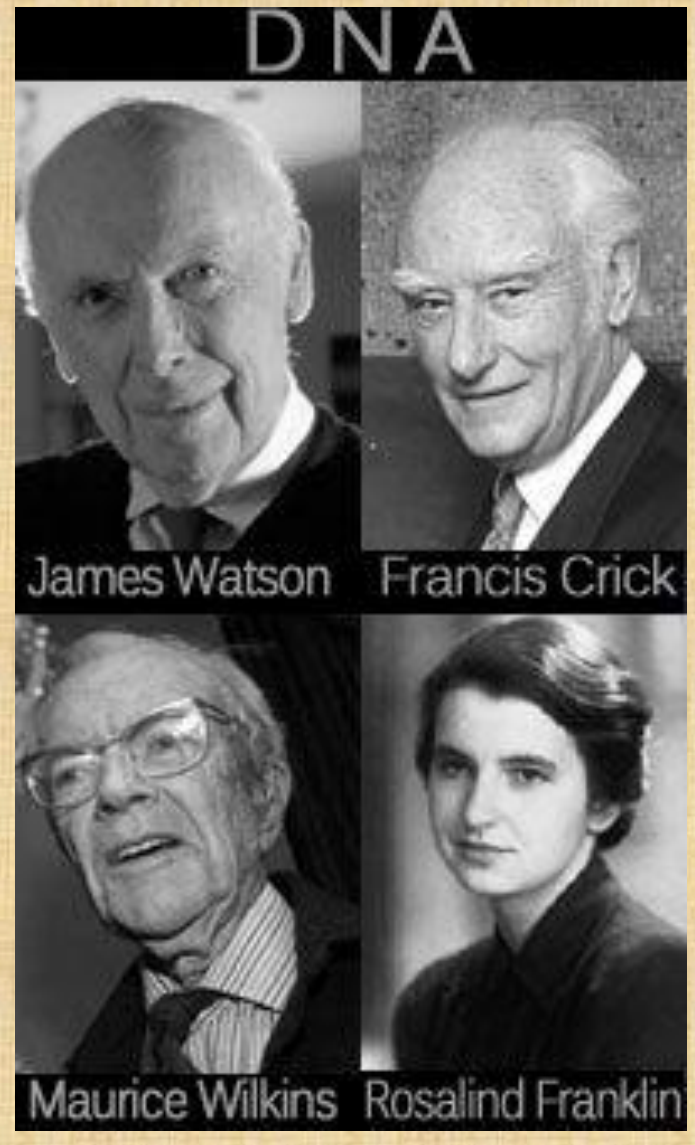


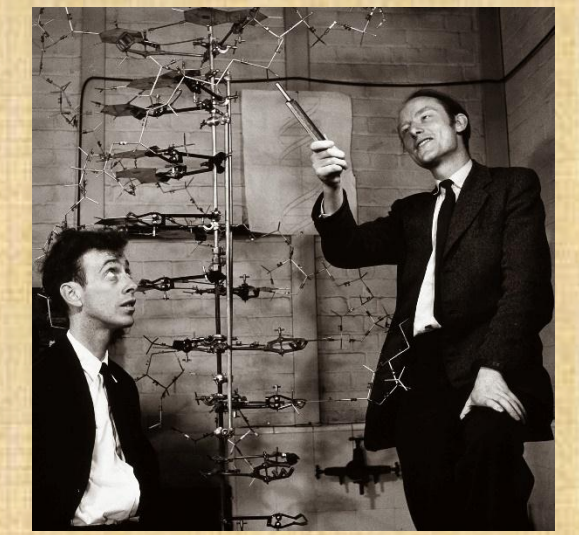
T2- BACTERIOPHAGE USED FOR THE HERSHEY AND CHASE EXPERIMENT

Hershey and Chase Experiment is a very popular experiment which provides evidence of **DNA** as "**Genetic material**". It was introduced by the two scientists **A.D. Hershey** a nd **Martha Chase** in the year **1952**. After seven years of an experiment given by the Avery, Hershey and Chase gave the further proof of DNA as genetic material by the use of **radioactive bacteriophage**.


DNA: Franklin, Crick & Watson
1953

Structure of DNA



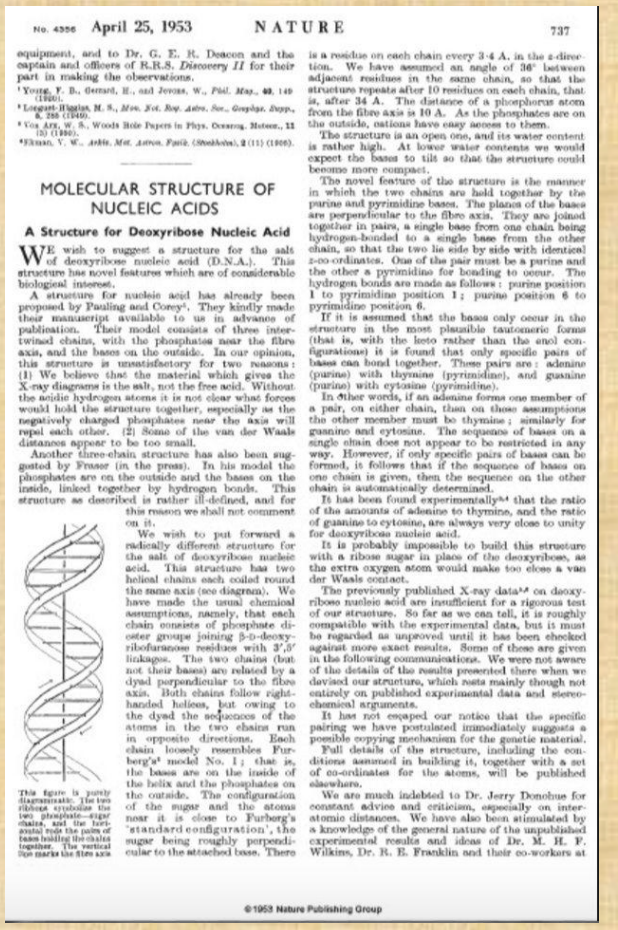


Watson & Crick

Double helix structure of DNA (1953)

X-ray diffraction pattern from B form of DNA

Structure of DNA



No. 4356 April 25, 1953 NATURE 737

equipment, and to Dr. G. E. R. Deacon and the captain and officers of R.R.S. *Discovery II* for their part in making the observations.

¹ Young, F. B., Gerrard, H., and Jevons, W., *Phil. Mag.*, **40**, 149 (1949).
² Longuet-Higgins, M. S., *Mon. Not. Roy. Astro. Soc., Geophys. Supp.*, **6**, 288 (1949).
³ Von Arx, W. S., Woods Hole Papers in Phys. Oceanog. Meteor., **11** (2) (1950).
⁴ Ekman, V. W., *Arkiv. Mat. Astron. Fysik. (Stockholm)*, **2** (11) (1906).

MOLECULAR STRUCTURE OF NUCLEIC ACIDS

A Structure for Deoxyribose Nucleic Acid

We wish to suggest a structure for the salt of deoxyribose nucleic acid (D.N.A.). This structure has novel features which are of considerable biological interest.

A structure for nucleic acid has already been proposed by Pauling and Corey[1]. They kindly made their manuscript available to us in advance of publication. Their model consists of three inter-twined chains, with the phosphates near the fibre axis, and the bases on the outside. In our opinion, this structure is unsatisfactory for two reasons: (1) We believe that the material which gives the X-ray diagrams is the salt, not the free acid. Without the acidic hydrogen atoms it is not clear what forces would hold the structure together, especially as the negatively charged phosphates near the axis will repel each other. (2) Some of the van der Waals distances appear to be too small.

Another three-chain structure has also been suggested by Fraser (in the press). In his model the phosphates are on the outside and the bases on the inside, linked together by hydrogen bonds. This structure as described is rather ill-defined, and for this reason we shall not comment on it.

This figure is purely diagrammatic. The two ribbons symbolize the two phosphate–sugar chains, and the horizontal rods the pairs of bases holding the chains together. The vertical line marks the fibre axis

We wish to put forward a radically different structure for the salt of deoxyribose nucleic acid. This structure has two helical chains each coiled round the same axis (see diagram). We have made the usual chemical assumptions, namely, that each chain consists of phosphate di-ester groups joining β-D-deoxy-ribofuranose residues with 3′,5′ linkages. The two chains (but not their bases) are related by a dyad perpendicular to the fibre axis. Both chains follow right-handed helices, but owing to the dyad the sequences of the atoms in the two chains run in opposite directions. Each chain loosely resembles Furberg's[2] model No. 1; that is, the bases are on the inside of the helix and the phosphates on the outside. The configuration of the sugar and the atoms near it is close to Furberg's 'standard configuration', the sugar being roughly perpendicular to the attached base. There is a residue on each chain every 3·4 A. in the z-direction. We have assumed an angle of 36° between adjacent residues in the same chain, so that the structure repeats after 10 residues on each chain, that is, after 34 A. The distance of a phosphorus atom from the fibre axis is 10 A. As the phosphates are on the outside, cations have easy access to them.

The structure is an open one, and its water content is rather high. At lower water contents we would expect the bases to tilt so that the structure could become more compact.

The novel feature of the structure is the manner in which the two chains are held together by the purine and pyrimidine bases. The planes of the bases are perpendicular to the fibre axis. They are joined together in pairs, a single base from one chain being hydrogen-bonded to a single base from the other chain, so that the two lie side by side with identical z-co-ordinates. One of the pair must be a purine and the other a pyrimidine for bonding to occur. The hydrogen bonds are made as follows: purine position 1 to pyrimidine position 1; purine position 6 to pyrimidine position 6.

If it is assumed that the bases only occur in the structure in the most plausible tautomeric forms (that is, with the keto rather than the enol configurations) it is found that only specific pairs of bases can bond together. These pairs are: adenine (purine) with thymine (pyrimidine), and guanine (purine) with cytosine (pyrimidine).

In other words, if an adenine forms one member of a pair, on either chain, then on these assumptions the other member must be thymine; similarly for guanine and cytosine. The sequence of bases on a single chain does not appear to be restricted in any way. However, if only specific pairs of bases can be formed, it follows that if the sequence of bases on one chain is given, then the sequence on the other chain is automatically determined.

It has been found experimentally[3,4] that the ratio of the amounts of adenine to thymine, and the ratio of guanine to cytosine, are always very close to unity for deoxyribose nucleic acid.

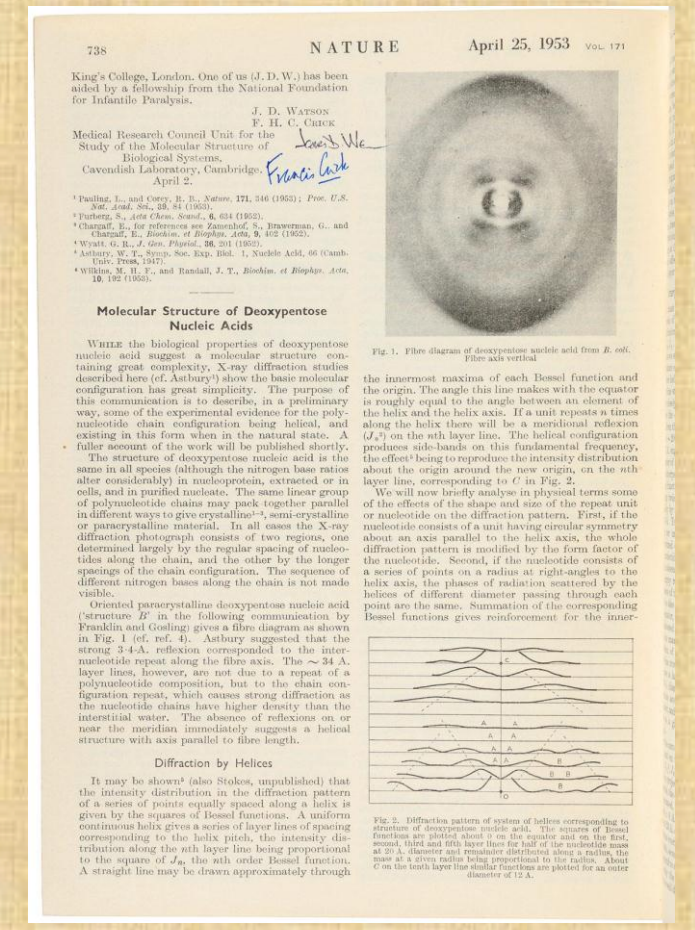
It is probably impossible to build this structure with a ribose sugar in place of the deoxyribose, as the extra oxygen atom would make too close a van der Waals contact.

The previously published X-ray data[5,6] on deoxy-ribose nucleic acid are insufficient for a rigorous test of our structure. So far as we can tell, it is roughly compatible with the experimental data, but is must be regarded as unproved until it has been checked against more exact results. Some of these are given in the following communications. We were not aware of the details of the results presented there when we devised our structure, which rests mainly though not entirely on published experimental data and stereochemical arguments.

It has not escaped our notice that the specific pairing we have postulated immediately suggests a possible copying mechanism for the genetic material.

Full details of the structure, including the conditions assumed in building it, together with a set of co-ordinates for the atoms, will be published elsewhere.

We are much indebted to Dr. Jerry Donohue for constant advice and criticism, especially on inter-atomic distances. We have also been stimulated by a knowledge of the general nature of the unpublished experimental results and ideas of Dr. M. H. F. Wilkins, Dr. R. E. Franklin and their co-workers at



738 NATURE April 25, 1953 Vol. 171

King's College, London. One of us (J. D. W.) has been aided by a fellowship from the National Foundation for Infantile Paralysis.

J. D. Watson
F. H. C. Crick

Medical Research Council Unit for the Study of the Molecular Structure of Biological Systems, Cavendish Laboratory, Cambridge.

April 2.

¹ Pauling, L., and Corey, R. B., *Nature*, **171**, 346 (1953); *Proc. U.S. Nat. Acad. Sci.*, **39**, 84 (1953).
² Furberg, S., *Acta Chem. Scand.*, **6**, 634 (1952).
³ Chargaff, E., for references see Zamenhof, S., Brawerman, G., and Chargaff, E., *Biochim. et Biophys. Acta*, **9**, 402 (1952).
⁴ Wyatt, G. R., *J. Gen. Physiol.*, **36**, 201 (1952).
⁵ Astbury, W. T., Symp. Soc. Exp. Biol. 1, Nucleic Acid, 66 (Camb. Univ. Press, 1947).
⁶ Wilkins, M. H. F., and Randall, J. T., *Biochim. et Biophys. Acta*, **10**, 192 (1953).

Molecular Structure of Deoxypentose Nucleic Acids

Fig. 1. Fibre diagram of deoxypentose nucleic acid from *B. coli*. Fibre axis vertical

While the biological properties of deoxypentose nucleic acid suggest a molecular structure containing great complexity, X-ray diffraction studies described here (cf. Astbury[1]) show the basic molecular configuration has great simplicity. The purpose of this communication is to describe, in a preliminary way, some of the experimental evidence for the poly-nucleotide chain configuration being helical, and existing in this form when in the natural state. A fuller account of the work will be published shortly.

The structure of deoxypentose nucleic acid is the same in all species (although the nitrogen base ratios alter considerably) in nucleoprotein, extracted or in cells, and in purified nucleate. The same linear group of polynucleotide chains may pack together parallel in different ways to give crystalline[1–3], semi-crystalline or paracrystalline material. In all cases the X-ray diffraction photograph consists of two regions, one determined largely by the regular spacing of nucleo-tides along the chain, and the other by the longer spacings of the chain configuration. The sequence of different nitrogen bases along the chain is not made visible.

Oriented paracrystalline deoxypentose nucleic acid ('structure B' in the following communication by Franklin and Gosling) gives a fibre diagram as shown in Fig. 1 (cf. ref. 4). Astbury suggested that the strong 3·4-A. reflexion corresponded to the inter-nucleotide repeat along the fibre axis. The ~ 34 A. layer lines, however, are not due to a repeat of a polynucleotide composition, but to the chain configuration repeat, which causes strong diffraction as the nucleotide chains have higher density than the interstitial water. The absence of reflexions on or near the meridian immediately suggests a helical structure with axis parallel to fibre length.

Diffraction by Helices

It may be shown[5] (also Stokes, unpublished) that the intensity distribution in the diffraction pattern of a series of points equally spaced along a helix is given by the squares of Bessel functions. A uniform continuous helix gives a series of layer lines of spacing corresponding to the helix pitch, the intensity distribution along the nth layer line being proportional to the square of J_n, the nth order Bessel function. A straight line may be drawn approximately through the innermost maxima of each Bessel function and the origin. The angle this line makes with the equator is roughly equal to the angle between an element of the helix and the helix axis. If a unit repeats n times along the helix there will be a meridional reflexion (J_n[2]) on the nth layer line. The helical configuration produces side-bands on this fundamental frequency, the effect[5] being to reproduce the intensity distribution about the origin around the new origin, on the nth layer line, corresponding to C in Fig. 2.

We will now briefly analyse in physical terms some of the effects of the shape and size of the repeat unit or nucleotide on the diffraction pattern. First, if the nucleotide consists of a unit having circular symmetry about an axis parallel to the helix axis, the whole diffraction pattern is modified by the form factor of the nucleotide. Second, if the nucleotide consists of a series of points on a radius at right-angles to the helix axis, the phases of radiation scattered by the helices of different diameter passing through each point are the same. Summation of the corresponding Bessel functions gives reinforcement for the inner-

Fig. 2. Diffraction pattern of system of helices corresponding to structure of deoxypentose nucleic acid. The squares of Bessel functions are plotted about 0 on the equator and on the first, second, third and fifth layer lines for half of the nucleotide mass at 20 A. diameter and remainder distributed along a radius, the mass at a given radius being proportional to the radius. About C on the tenth layer line similar functions are plotted for an outer diameter of 12 A.

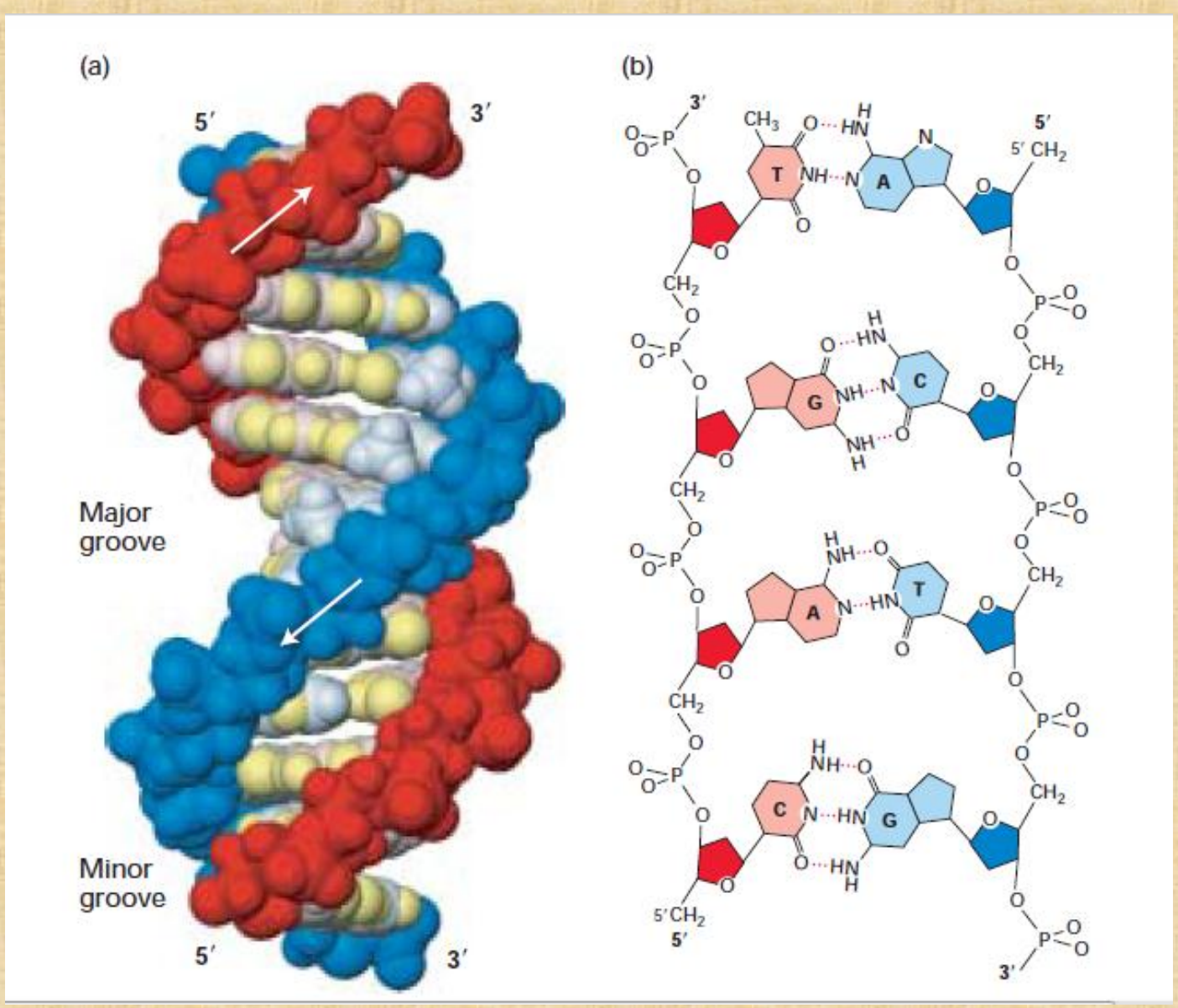
Watson and Crick (1953) developed a DNA double helix model based on Franklin's X-ray crystallography analysis and Erwin Chargaff's experiment (ratio of A and t are 1:1, and G and C are 1:1).

Watson and Crick model of DNA

Some Basic

- Nucleoside- is a compound formed by the combination of a pentose sugar and nitrogen base.
- Nucleotide-is a compound formed by the combination of nucleoside and phosphate group.
- Nucleotides building blocks of nucleic acids.
- Nucleotide have three characteristic components.

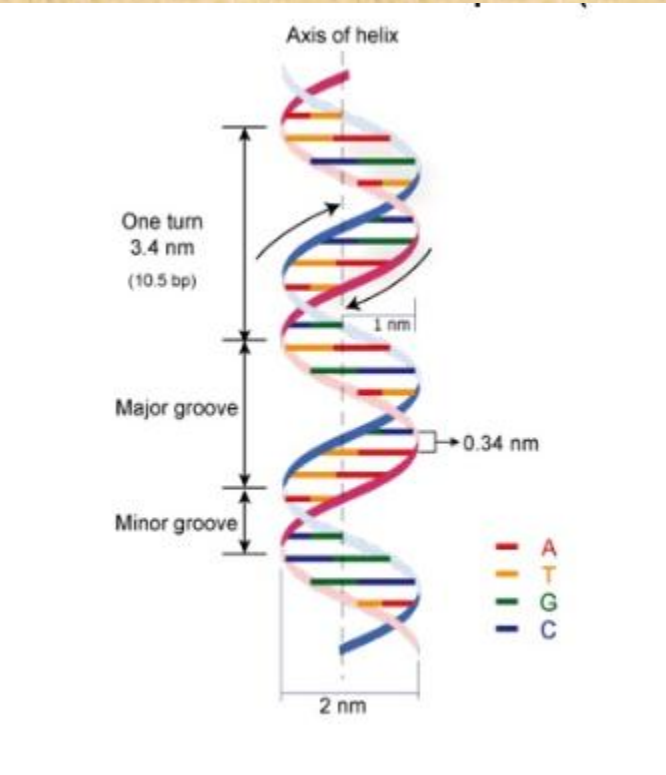
1. **A nitrogenous base**
2. **A pentose sugar**
3. **A phosphate group**

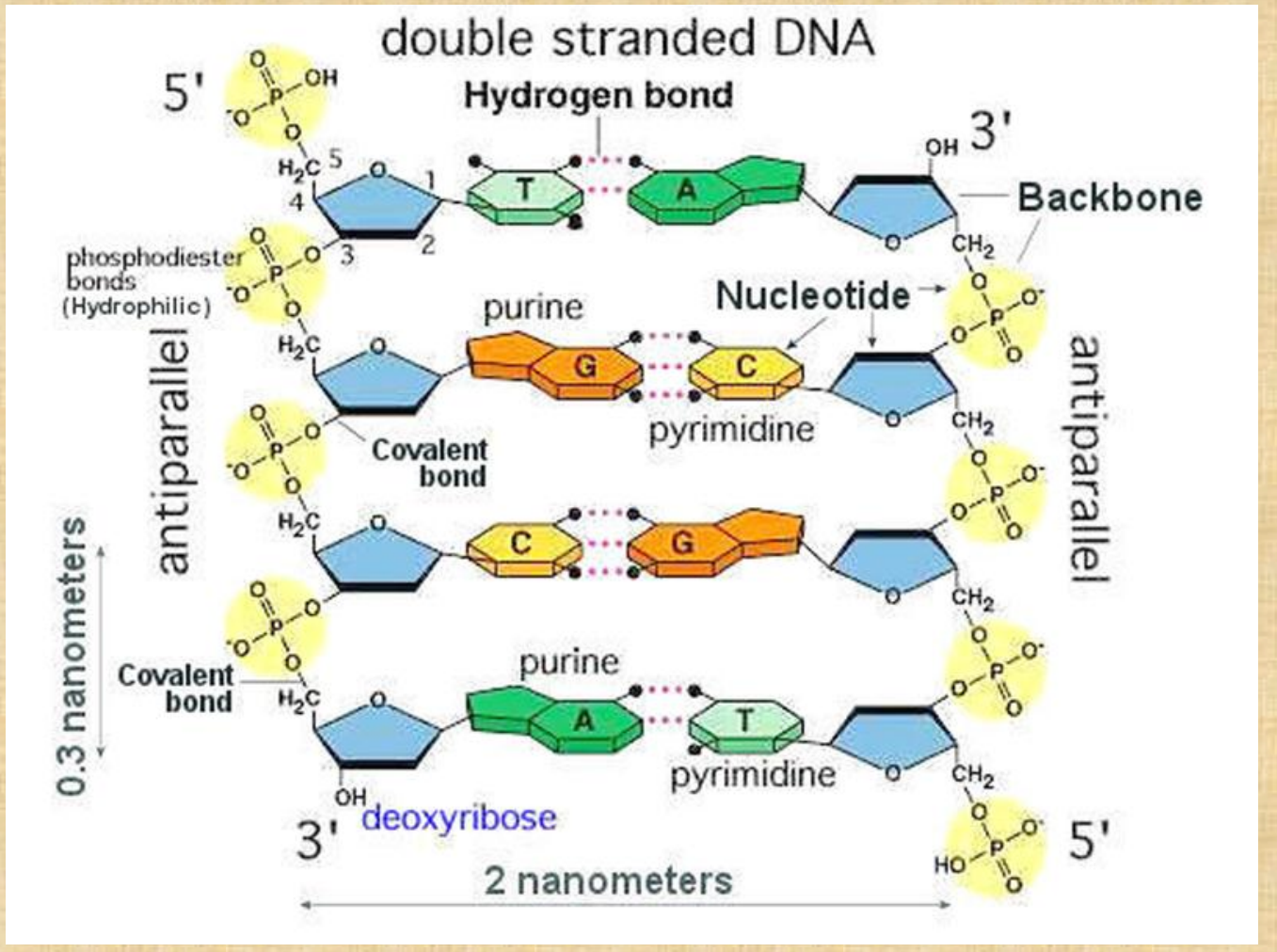


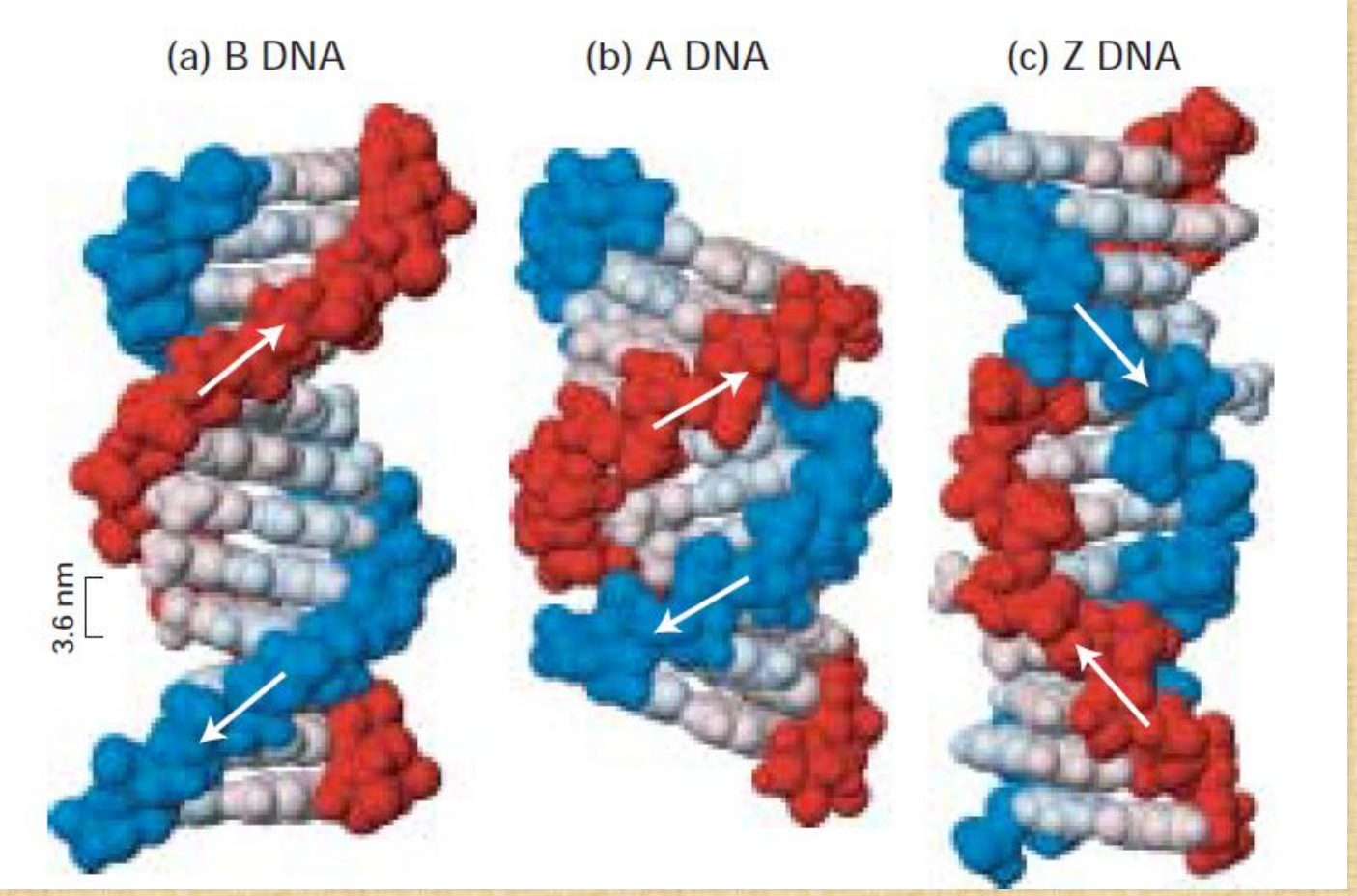
The DNA double helix. (a) Space-filling model of B DNA, the most common form of DNA in cells. The bases (light shades) project inward from the sugar-phosphate backbones (dark red and blue) of each strand, but their edges are accessible through major and minor grooves. Arrows indicate the 5'n3'direction of each strand. Hydrogen bonds between the bases are in the center of the structure. The major and minor grooves are lined by potential hydrogen bond donors and acceptors (highlighted in yellow). (b) Chemical structure of DNA double helix. This extended schematic shows the two sugar-phosphate backbones and hydrogen bonding between the Watson-Crick base pairs, AT and GC. [Part (a) from R. Wing et al., 1980, *Nature* **287**:755; part (b) from R. E. Dickerson, 1983, *Sci. Am.* **249**:94.]

Lodish et al., 2008

Structure of DNA

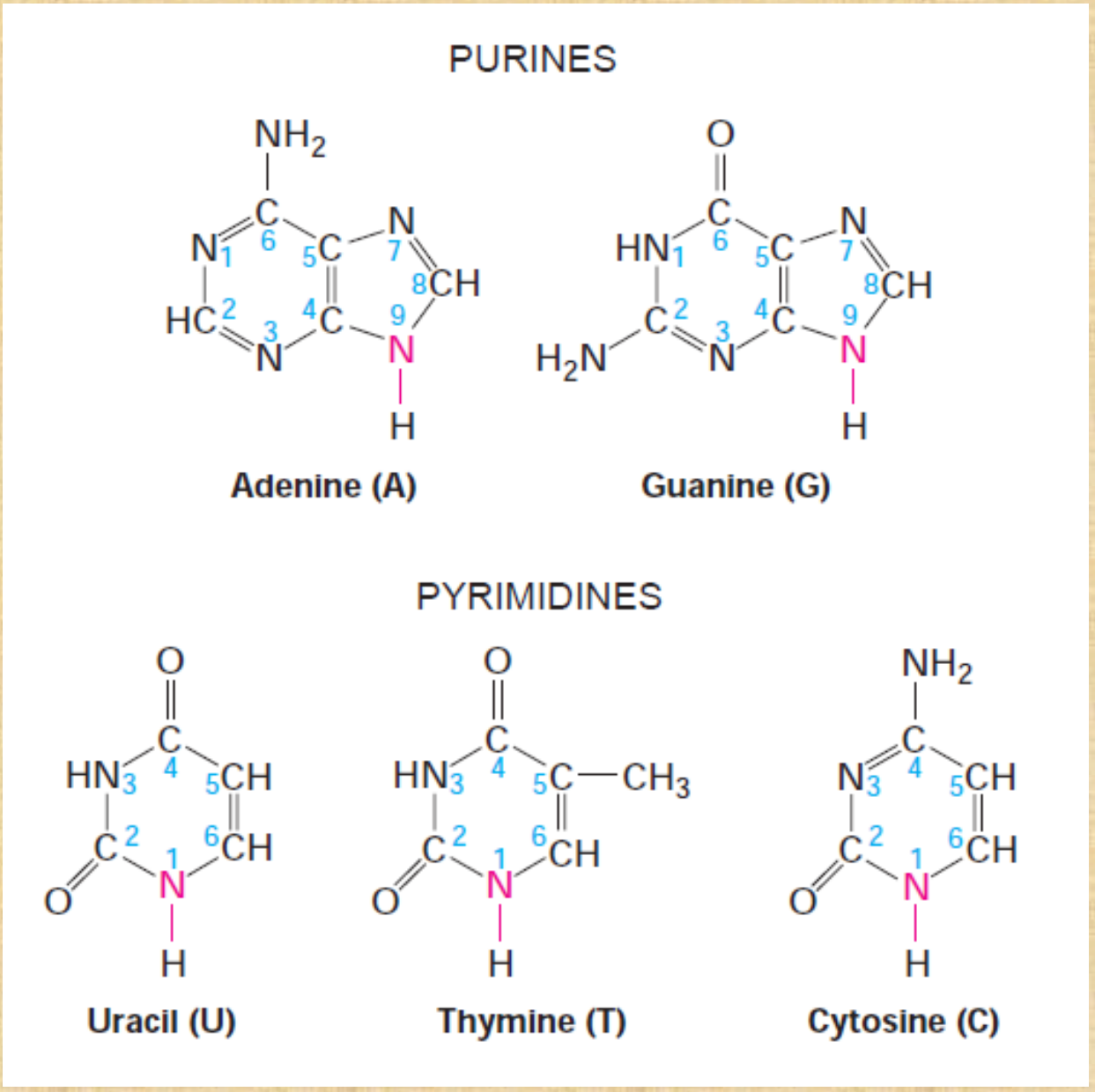






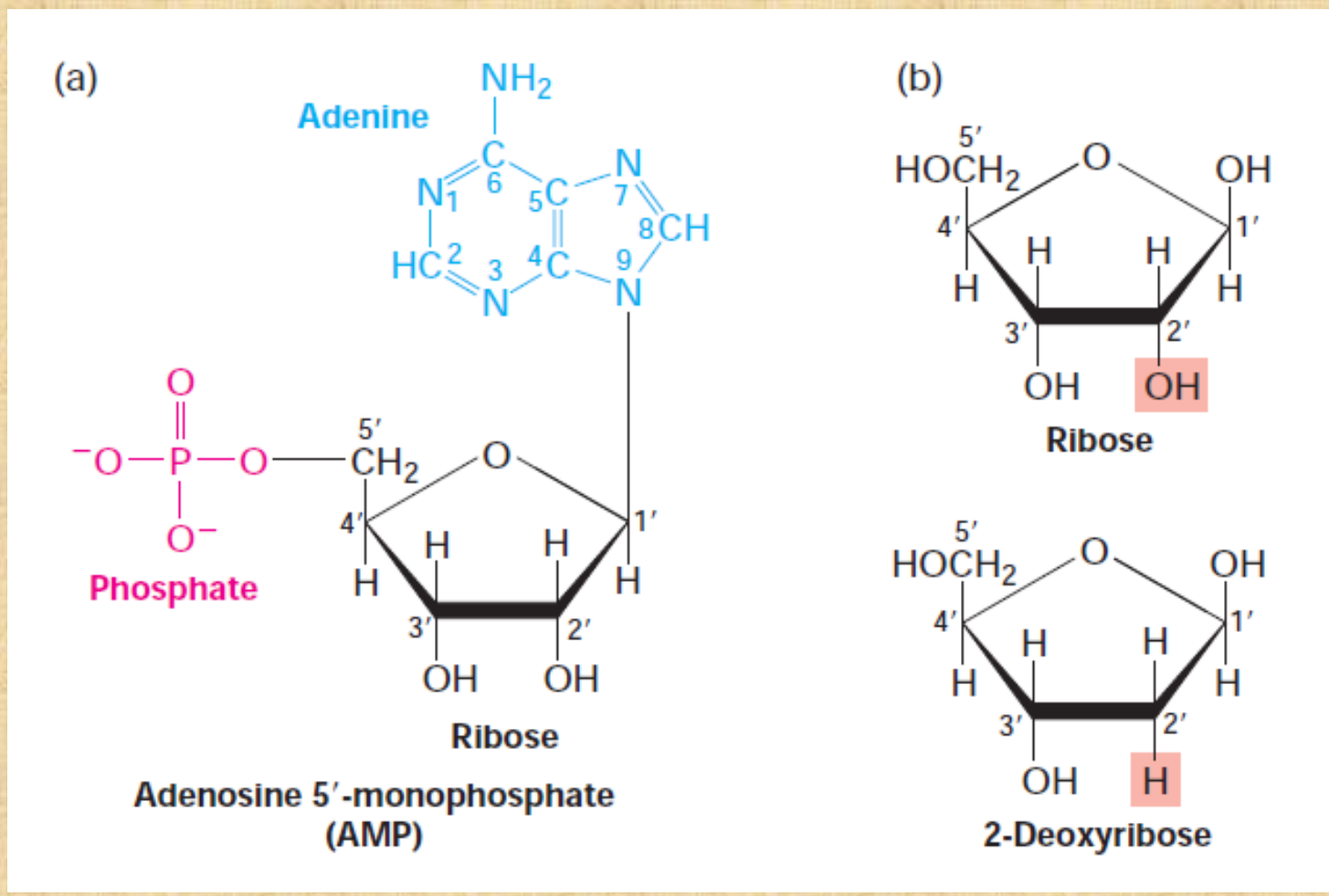
Models of various known DNA structures. The sugar-phosphate backbones of the two strands, which are on the outside in all structures, are shown in red and blue; the bases (lighter shades) are oriented inward. (a) The B form of DNA has ≈10.5 base pairs per helical turn. Adjacent stacked base pairs are 0.36 nm apart. (b) The more compact A form of DNA has11 base pairs per turn and exhibits a large tilt of the base pairs with respect to the helix axis. (c) Z DNA is a left-handed double helix.

Property	B-DNA	A-DNA	Z-DNA
Strand	Antiparallel	Antiparallel	Antiparallel
Type of Helix	Right-handed	Right-handed	Left-handed
Overall shape	Long and narrow	Short and wide	Elongated and narrow
Base pair per turn	10	11	12
Distance between adjacent bases	0.34 nm	0.23 nm	0.38 nm
Pitch/turn of helix	3.40 nm	2.82 nm	4.56 nm
Helical Diameter	2.0 nm	2.3 nm	1.8 nm
Tilt/inclination of bp to axis	1^0	20^0	9^0



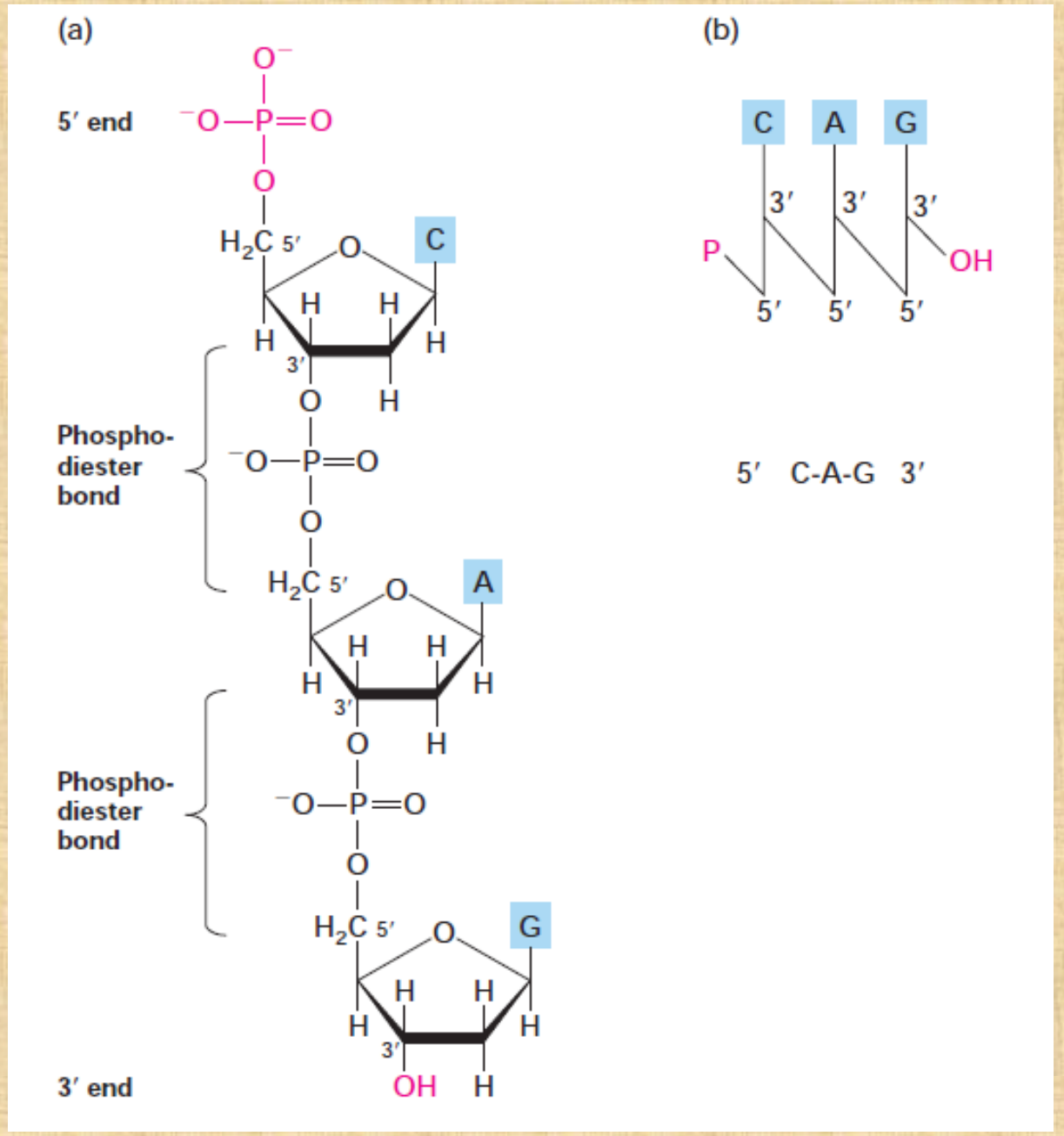
Chemical structures of the principal bases in nucleic acids. In nucleic acids and nucleotides, nitrogen 9 of purines and nitrogen 1 of pyrimidines (red) are bonded to the 1’ carbon of ribose or deoxyribose. U is only in RNA, and T is only in DNA. Both RNA and DNA contain A, G, and C.

Lodish et al., 2008



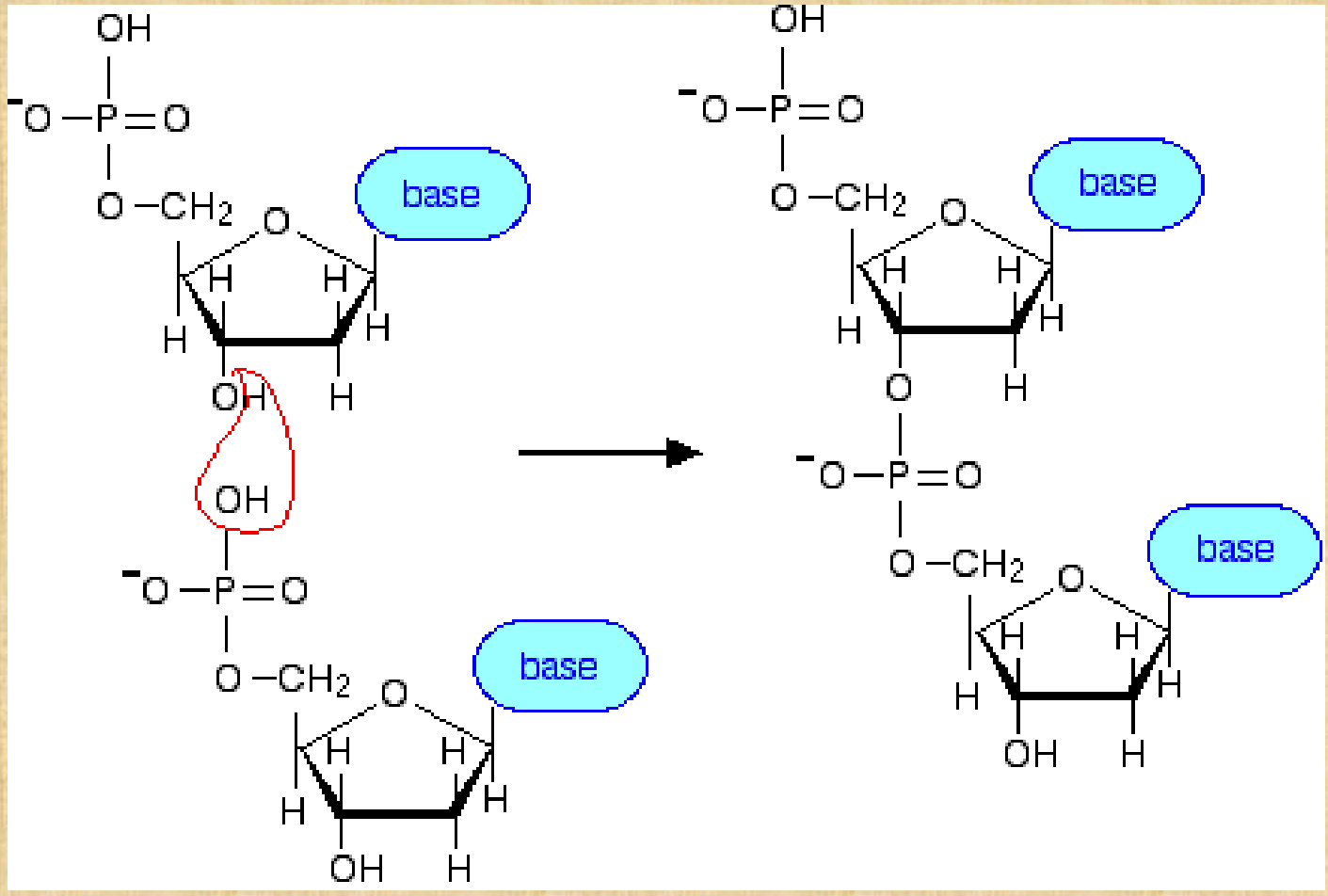
Common structure of nucleotides. (a) Adenosine 5′-monophosphate (AMP), a nucleotide present in RNA. By convention, the carbon atoms of the pentose sugar in nucleotides are numbered with primes. In natural nucleotides, the 1′ carbon is joined by a β-linkage to the base (in this case adenine); both the base (blue) and the phosphate on the 5′hydroxyl (red) extend above the plane of the furanose ring. (b) Ribose and deoxyribose, the pentoses in RNA and DNA, respectively.

Lodish et al., 2008



Alternative representations of a nucleic acid strand illustrating its chemical directionality. Shown here is a single strand of DNA containing only three bases: cytosine (C), adenine (A), and guanine (G). (a) The chemical structure shows a hydroxyl group at the 3'end and a phosphate group at the 5'end. Note also that two phosphoester bonds link adjacent nucleotides; this two-bond linkage commonly is referred to as a *phosphodiester bond*. (b) In the "stick" diagram (*top*), the sugars are indicated as vertical lines and the phosphodiester bonds as slanting lines; the bases are denoted by their single-letter abbreviations. In the simplest representation (*bottom*), only the bases are indicated. By convention, a polynucleotide sequence is always written in the 5'→3'direction (left to right) unless otherwise indicated.

Lodish et al., 2008


OH
O
P
O
O
CH2
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base
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H
OH
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OH
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CH2
O
base
H
H
H
H
OH
H
OH
O
P
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O
CH2
O
base
H
H
H
H
OH
H

TABLE 2-2 Terminology of Nucleosides and Nucleotides

		Bases			
		Purines		Pyrimidines	
		Adenine (A)	**Guanine (G)**	**Cytosine (C)**	**Uracil (U) Thymine [T]**
Nucleosides	in RNA	Adenosine	Guanosine	Cytidine	Uridine
	in DNA	Deoxyadenosine	Deoxyguanosine	Deoxycytidine	Deoxythymidine
Nucleotides	in RNA	Adenylate	Guanylate	Cytidylate	Uridylate
	in DNA	Deoxyadenylate	Deoxyguanylate	Deoxycytidylate	Deoxythymidylate
Nucleoside monophosphates		AMP	GMP	CMP	UMP
Nucleoside diphosphates		ADP	GDP	CDP	UDP
Nucleoside triphosphates		ATP	GTP	CTP	UTP
Deoxynucleoside mono-, di-, and triphosphates		dAMP, etc.			

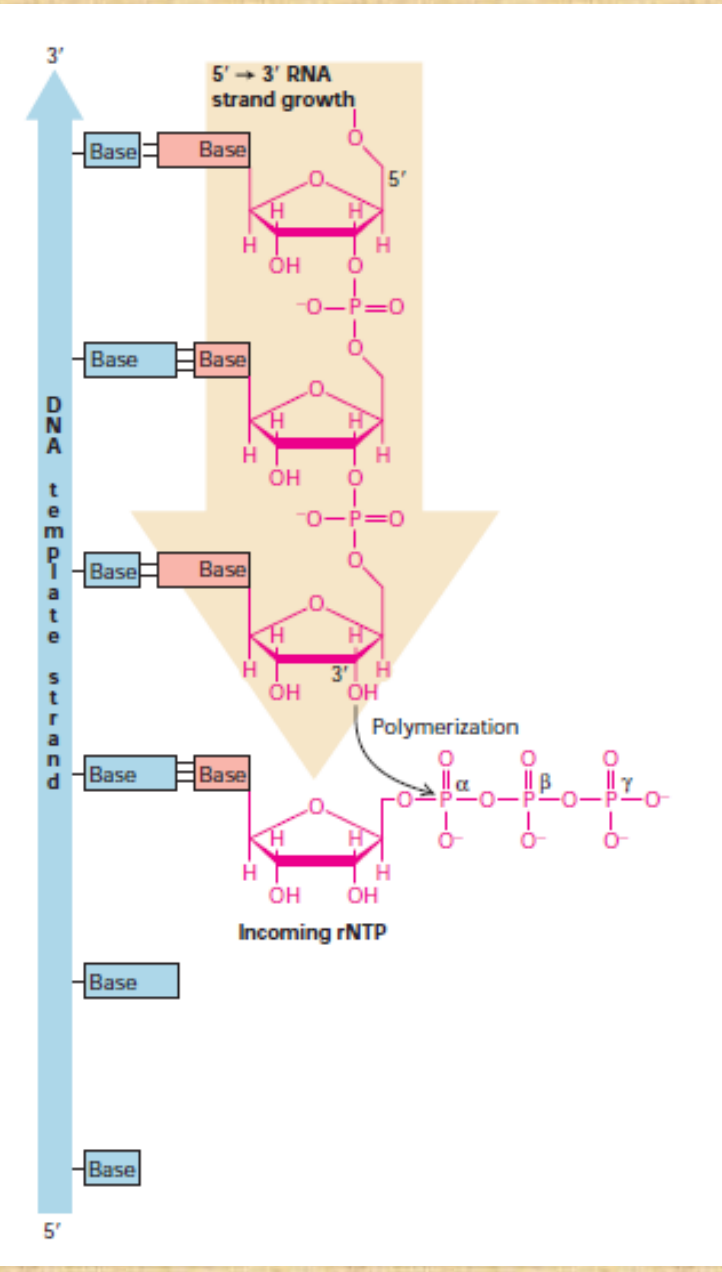
Lodish et al., 2008

TABLE 4-2 Known Deviations from the Universal Genetic Code

Codon	Universal Code	Unusual Code*	Occurrence
UGA	Stop	Trp	*Mycoplasma, Spiroplasma,* mitochondria of many species
CUG	Leu	Thr	Mitochondria in yeasts
UAA, UAG	Stop	Gln	*Acetabularia, Tetrahymena,* Paramecium, etc.
UGA	Stop	Cys	*Euplotes*

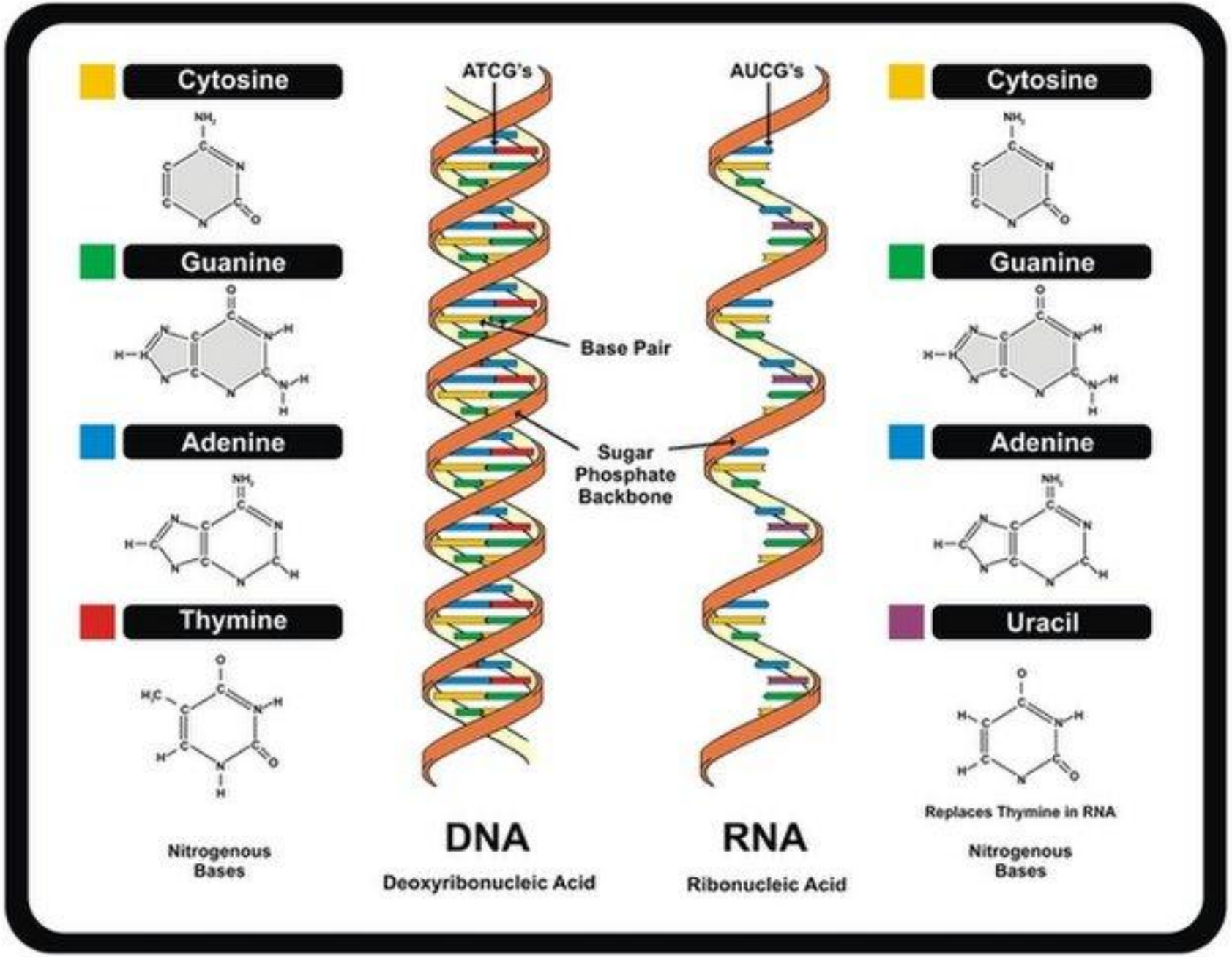
*"Unusual code" is used in nuclear genes of the listed organisms and in mitochondrial genes as indicated.
SOURCE: S. Osawa et al., 1992, *Microbiol. Rev.* 56:229.

Lodish et al., 2008



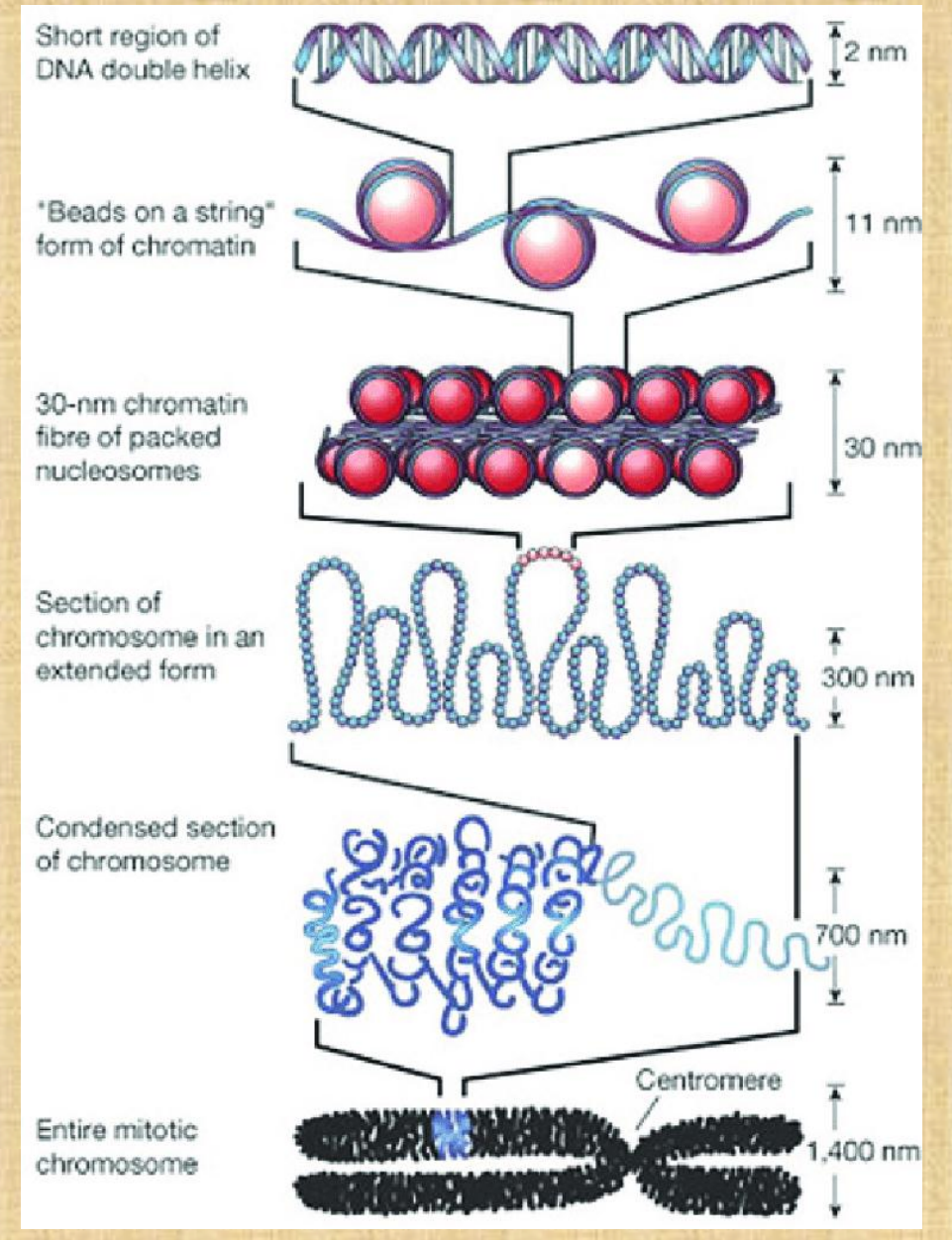
Polymerization of ribonucleotides by RNA polymerase during transcription. The ribonucleotide to be added at the 3 end of a growing RNA strand is specified by base pairing between the next base in the template DNA strand and the complementary incoming ribonucleoside triphosphate (rNTP). A phosphodiester bond is formed when RNA polymerase catalyzes a reaction between the 3 O of the growing strand and the phosphate of a correctly base-paired rNTP. RNA strands always are synthesized in the 5n3 direction and are opposite in polarity to their template DNA strands.

Lodish et al., 2008

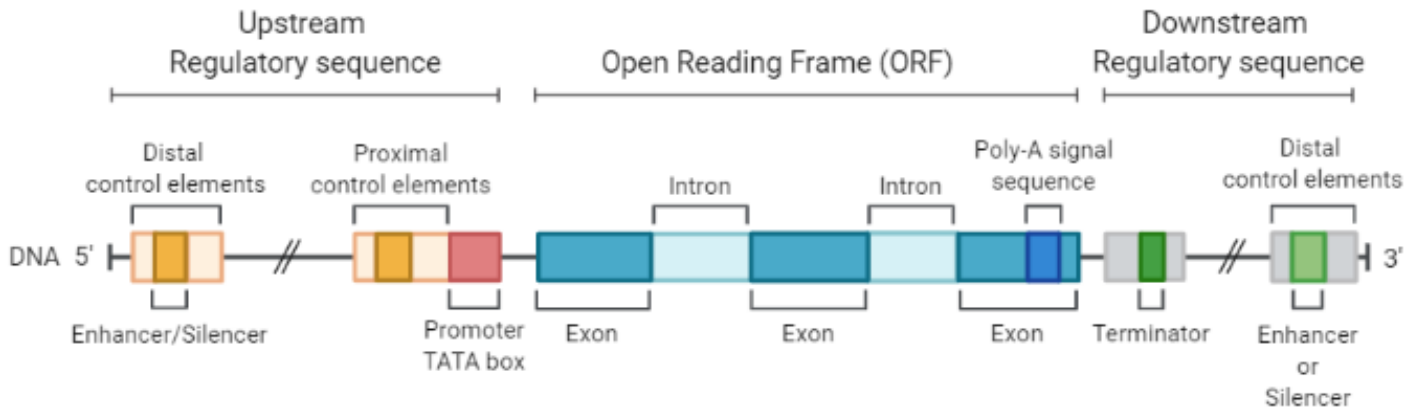

Cytosine
Guanine
Adenine
Thymine
Nitrogenous Bases
ATCG's
AUCG's
Base Pair
Sugar Phosphate Backbone
DNA
Deoxyribonucleic Acid
RNA
Ribonucleic Acid
Cytosine
Guanine
Adenine
Uracil
Replaces Thymine in RNA
Nitrogenous Bases

Sl.No.	Organism	Chromosome Number	Genome Size (MB)	Number of genes
1	*Escherichia coli*	1	4.6	4288
2	*Saccharomyces cerevisiae*	16	13	6034
3	*Drosophila melanogaster*	8	180	13600
4	*Arabidopsis thaliana*	10	125	26000
5	*Oryza sativa*	24	390	38000
6	*Homo sapiens*	46	2900	25000

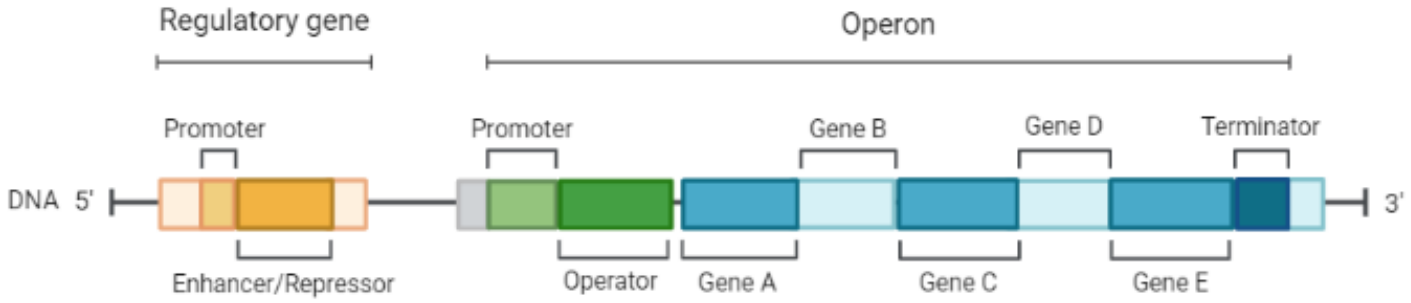
Eukaryotic chromosome organization



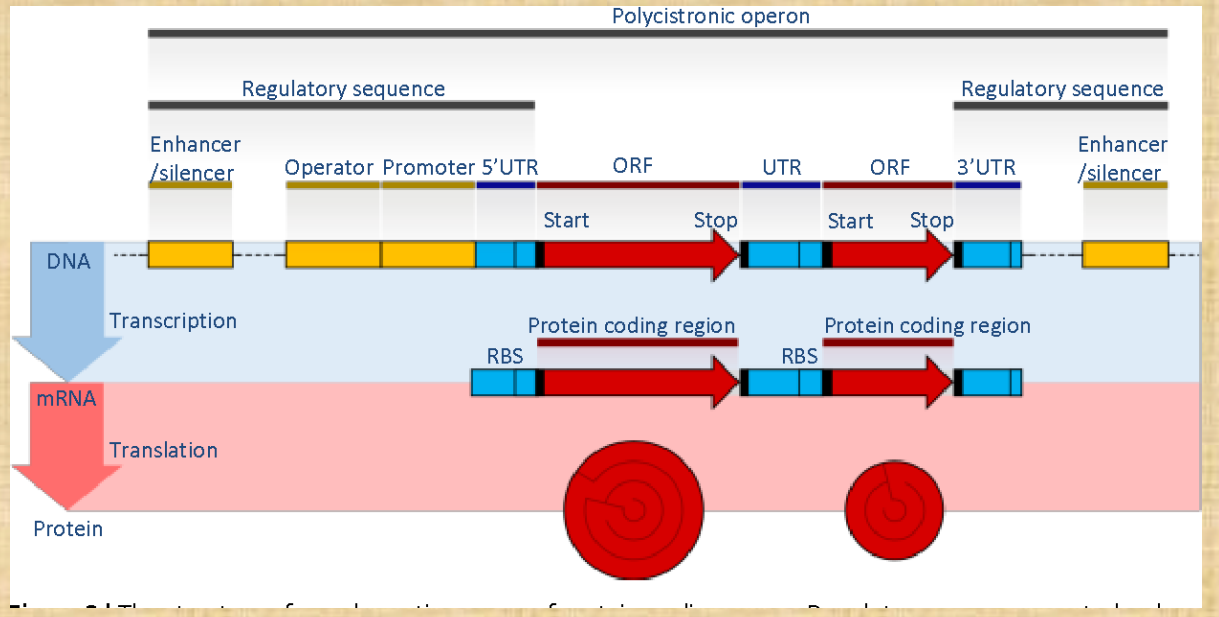
Eukaryotic Gene Structure

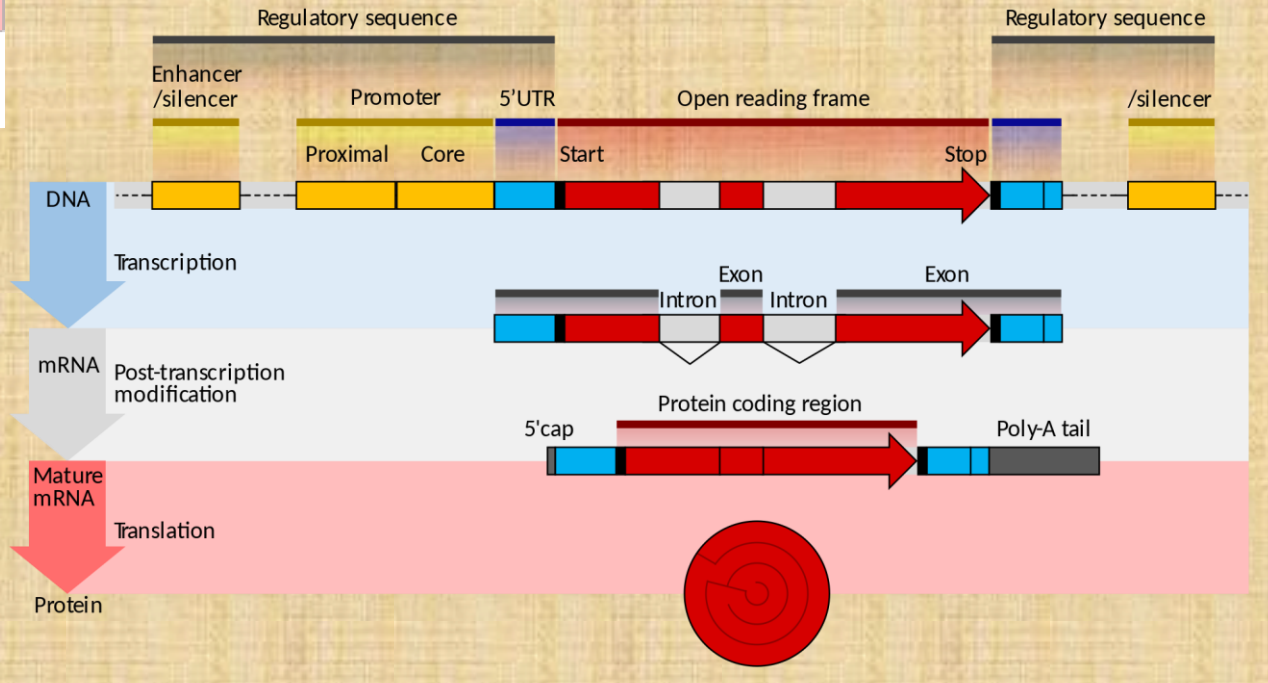


Prokaryotic Gene Structure



Prokaryotic and Eukaryotic gene structure



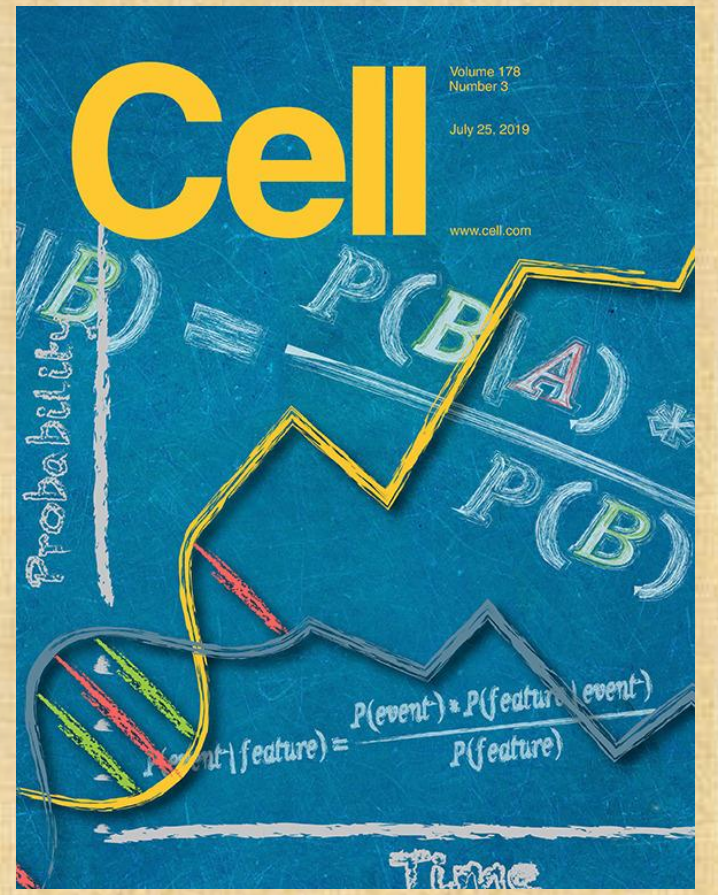


Publisher: Nature Research (subsidiary of Springer Nature) (United Kingdom)

Impact factor: 43.070 (2019)

Publisher: American Association for the Advancement of Science (United States)

Impact factor: 42 (2019)



Publisher: Cell Press

Impact factor: 36.637 (2019)

Herbert Boyer (pictured) and Stanley Cohen created the first genetically modified organism, a bacteria resistant to the antibiotic kanamycin in 1973.

Rudolf Jaenisch created the first genetically modified animal, a mouse in 1974

Simian Virus 40 DNA Sequences in DNA of Healthy Adult Mice Derived from Preimplantation Blastocysts Injected with Viral DNA

Rudolf Jaenisch and Beatrice Mintz

PNAS April 1, 1974 71 (4) 1250-1254; https://doi.org/10.1073/pnas.71.4.1250

Mary-Dell Chilton: produced the first genetically modified plants using Agrobacterium carrying the disarmed Ti plasmid (**1983**)

A chimaeric antibiotic resistance gene as a selectable marker for plant cell transformation

Michael W. Bevan, Richard B. Flavell & Mary-Dell Chilton

Nature **304**, 184–187 (1983) | Download Citation