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REVIEW

Can We Name Earth's Species Before They Go Extinct?

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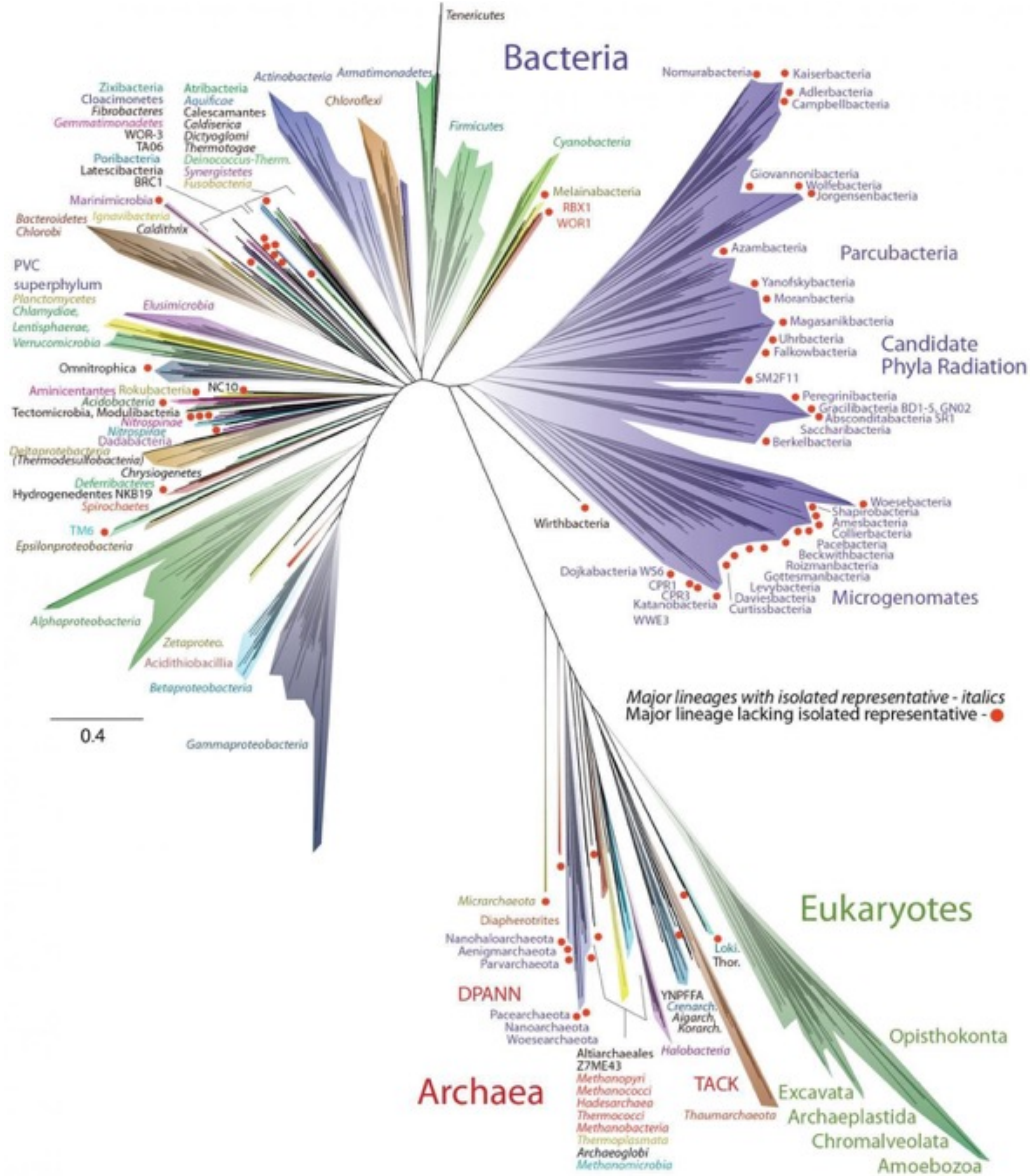
Abstract

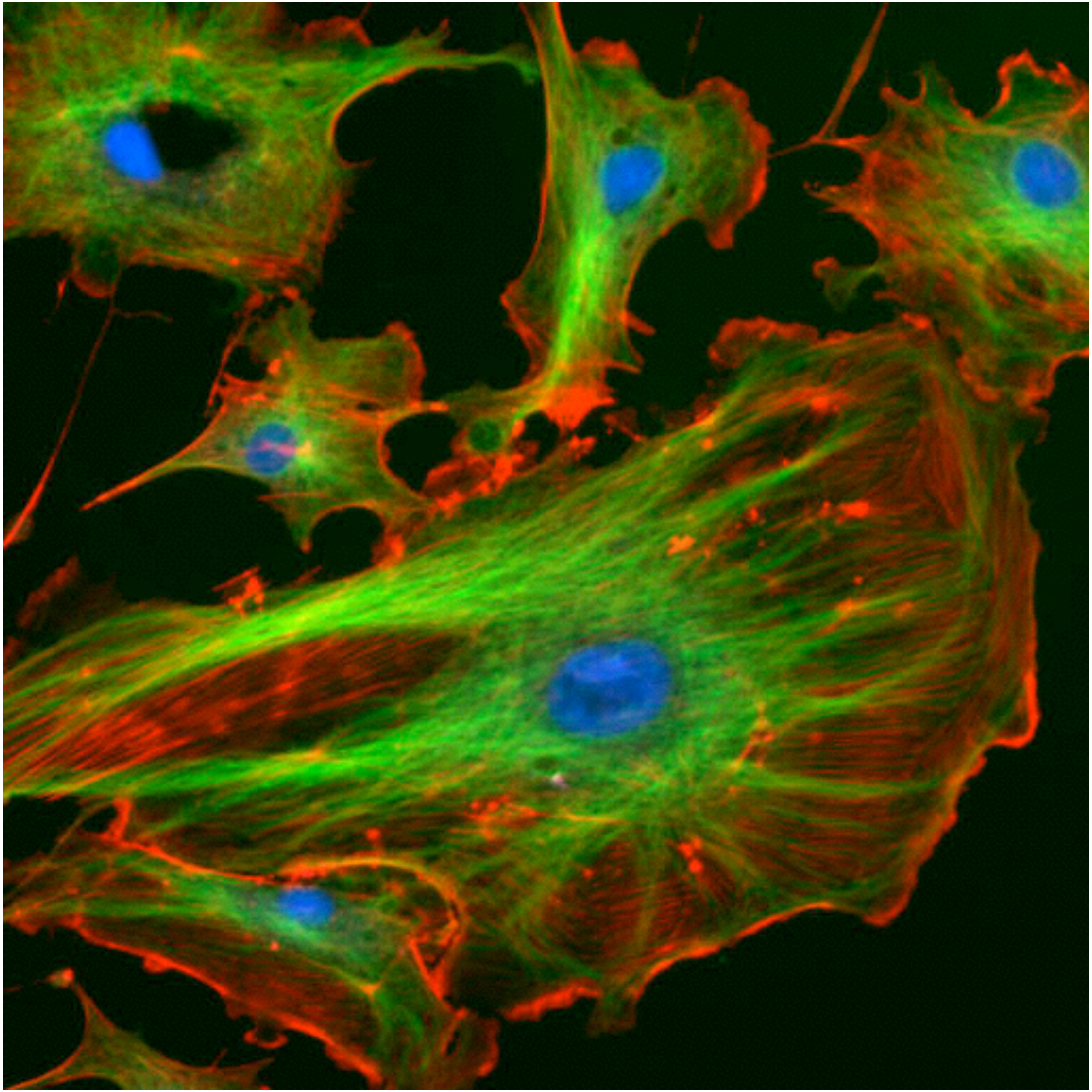
Some people despair that most species will go extinct before they are discovered. However, such worries result from overestimates of how many species may exist, beliefs that the expertise to describe species is decreasing, and alarmist estimates of extinction rates. We argue that the number of species on Earth today is 5 ± 3 million, of which 1.5 million are named. New databases show that there are more taxonomists describing species than ever before, and their number is increasing faster than the rate of species description. Conservation efforts and species survival in secondary habitats are at least delaying extinctions. Extinction rates are, however, poorly quantified, ranging from 0.01 to 1% (at most 5%) per decade. We propose practical actions to improve taxonomic productivity and associated understanding and conservation of biodiversity.

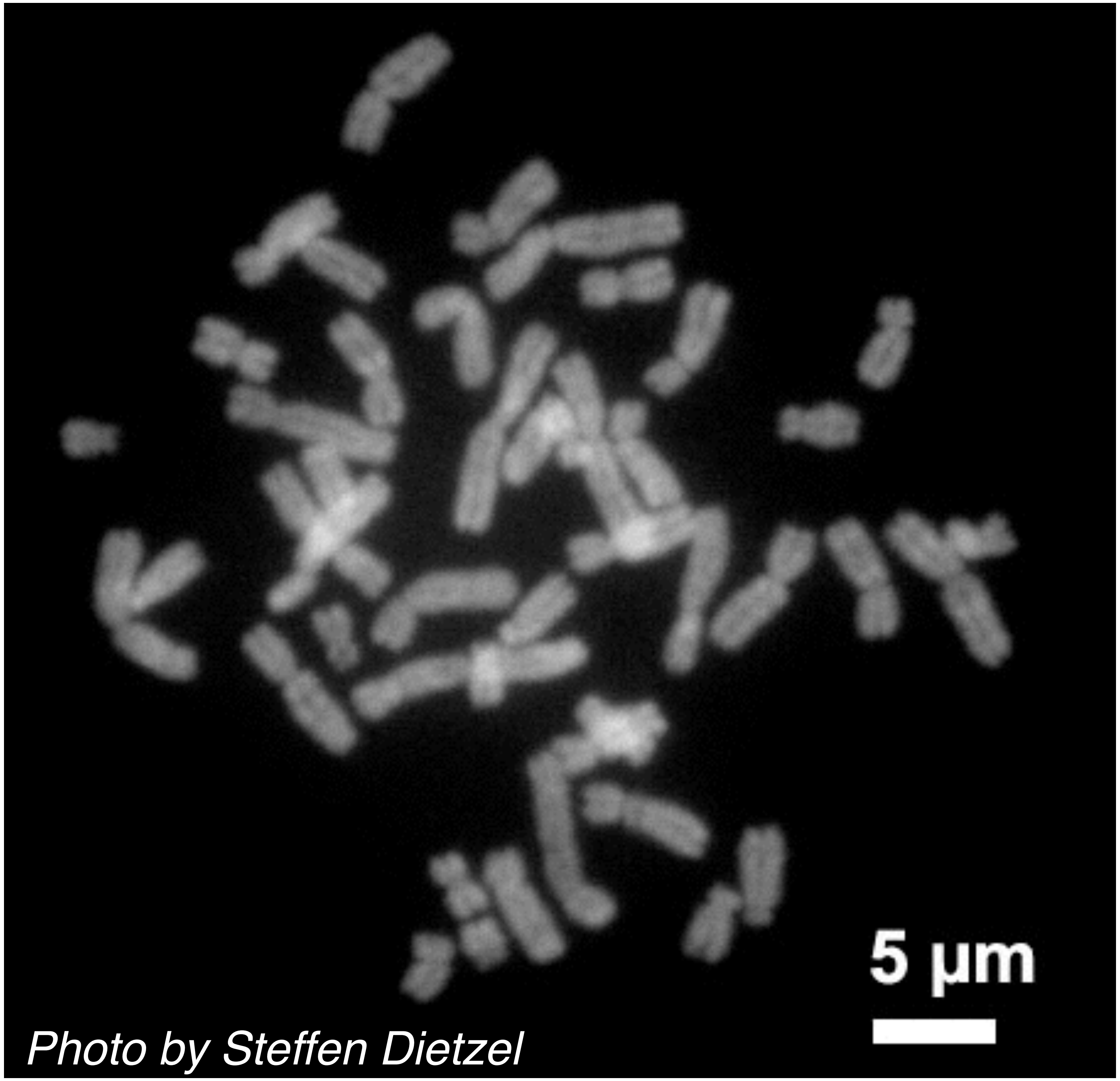

Photograph by George Grall
http://animals.nationalgeographic.com

Photograph by Beverly Joubert, from the book Relentless Enemies: Lions and Buffalo



Hug et al (2016) *Nature Microbiology*




5 µm
Photo by Steffen Dietzel

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

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 polynucleotide 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 nucleotides 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

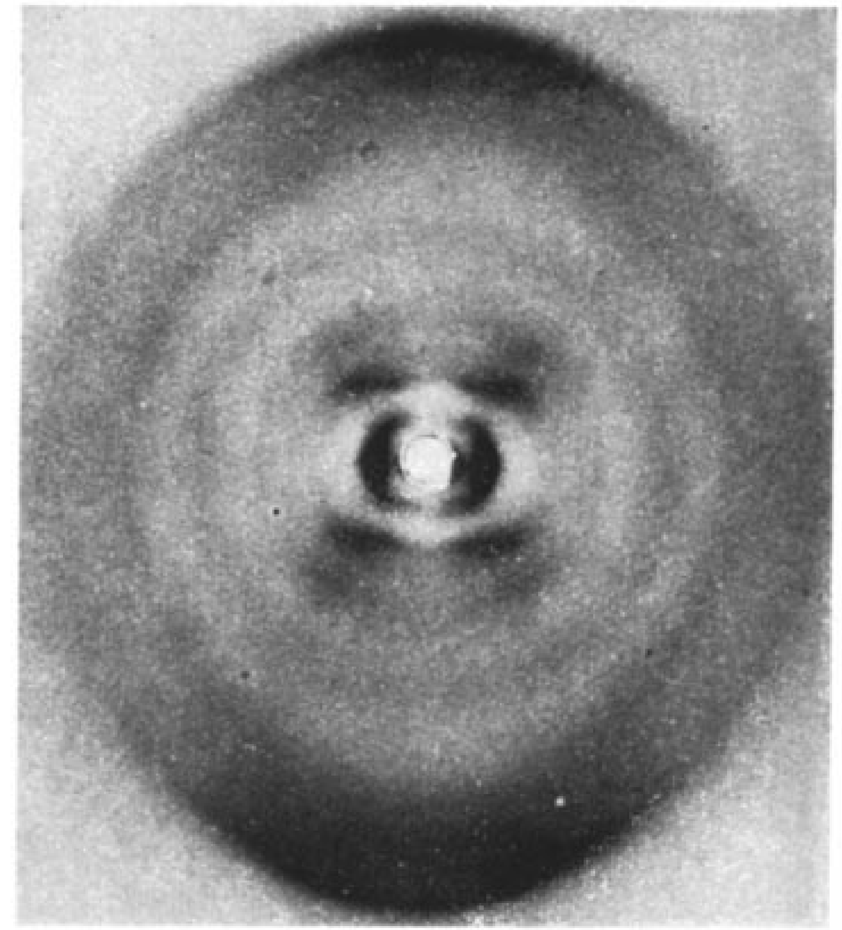


Fig. 1. Fibre diagram of deoxypentose nucleic acid from *B. coli*. Fibre axis vertical

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_0^2) 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

La vida, en moléculas

CdC Mérida 2016

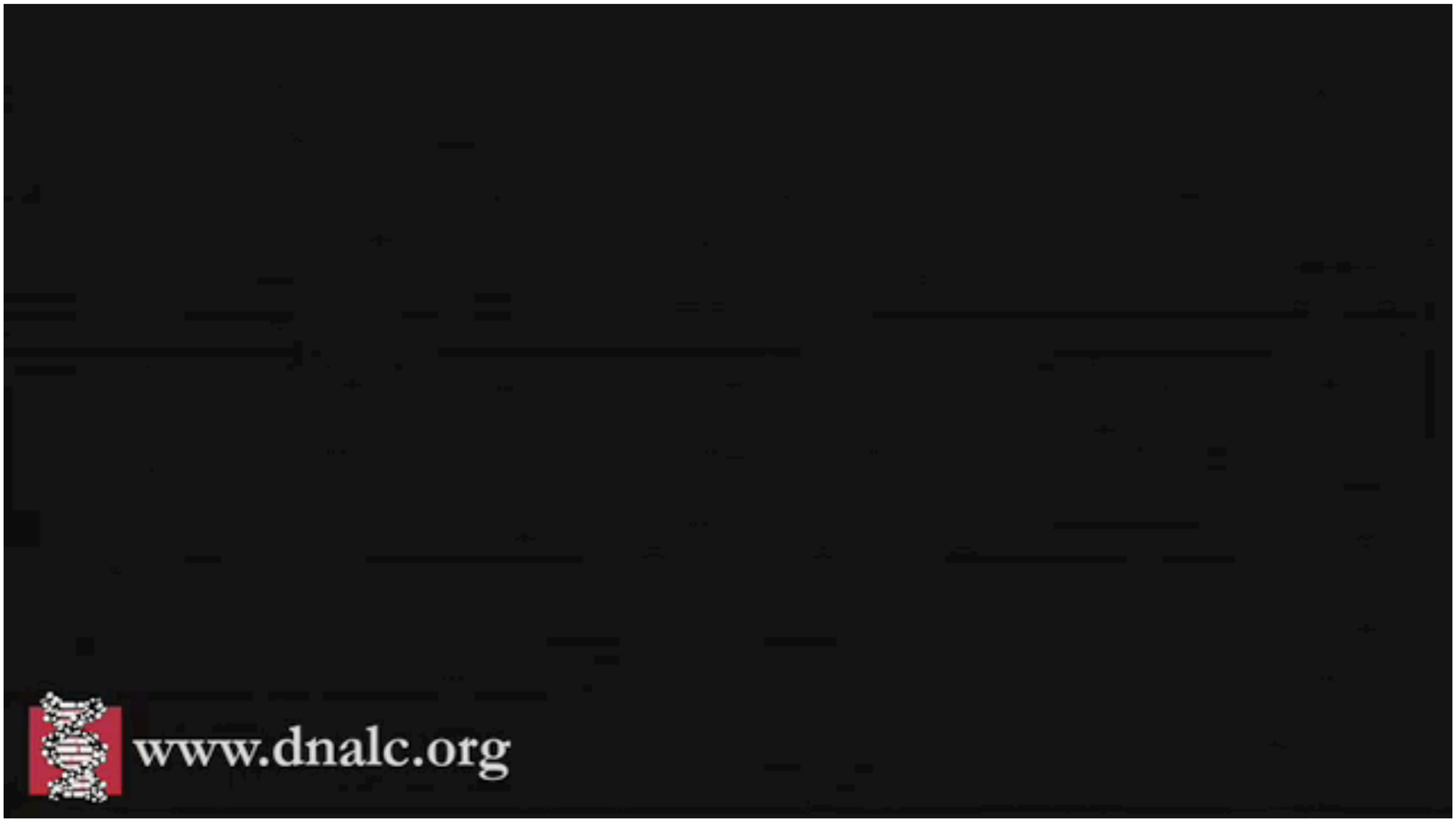
Porfirio Quintero

biología molecular

- ADN
- ARN
- proteínas
- Ingeniería genética

ácido desoxirribonucleico

ácido desoxirribonucleico



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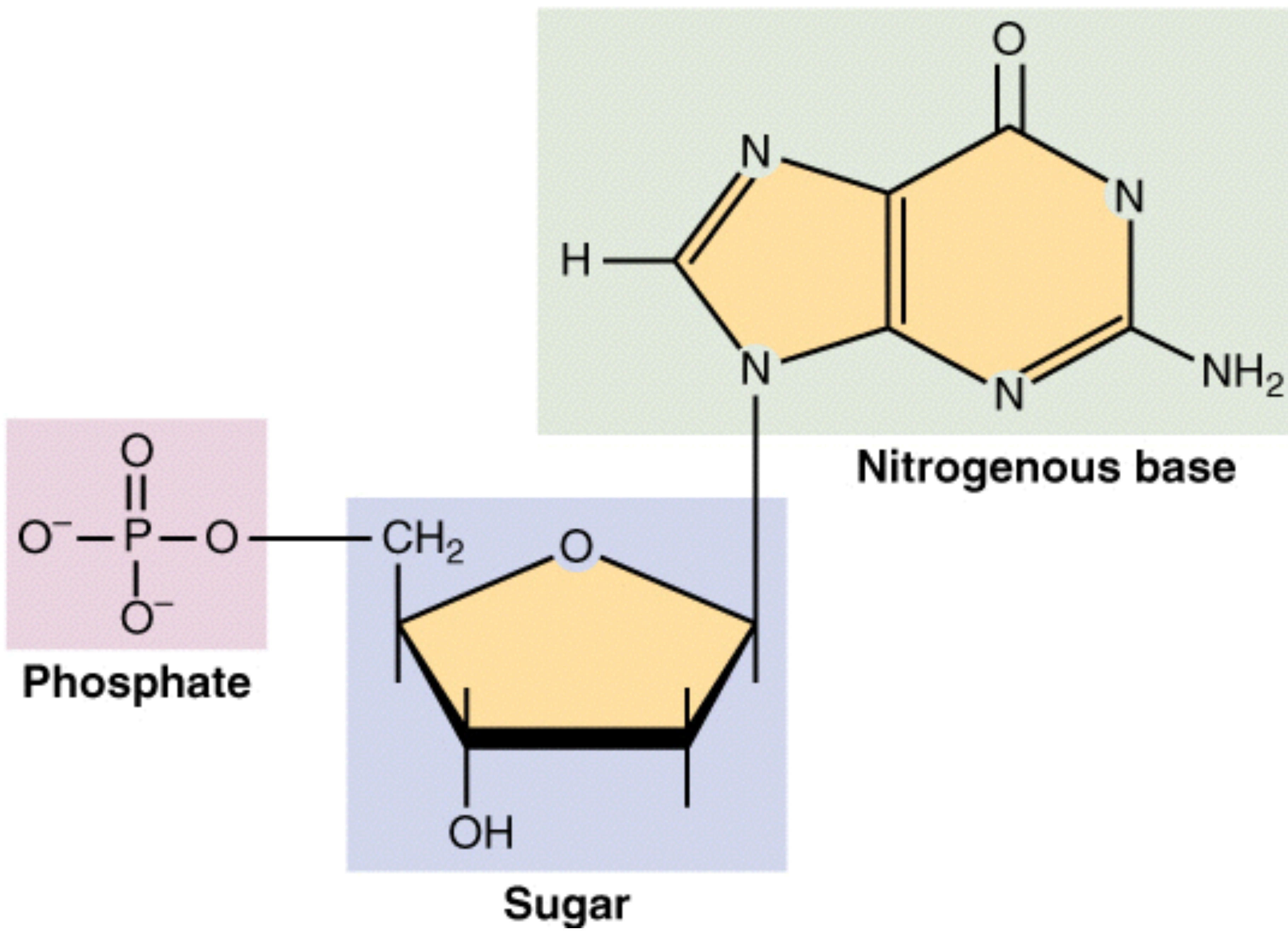

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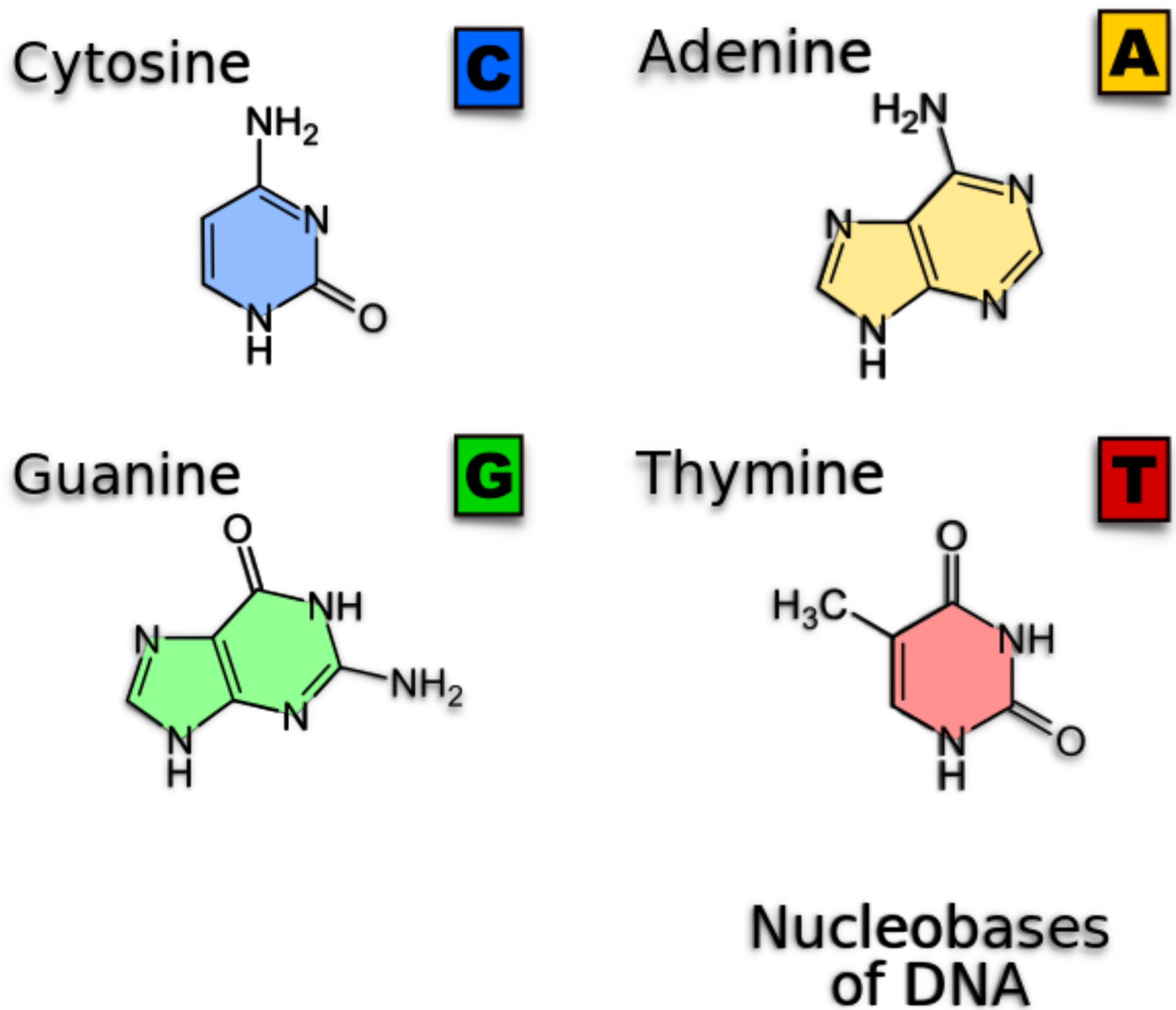

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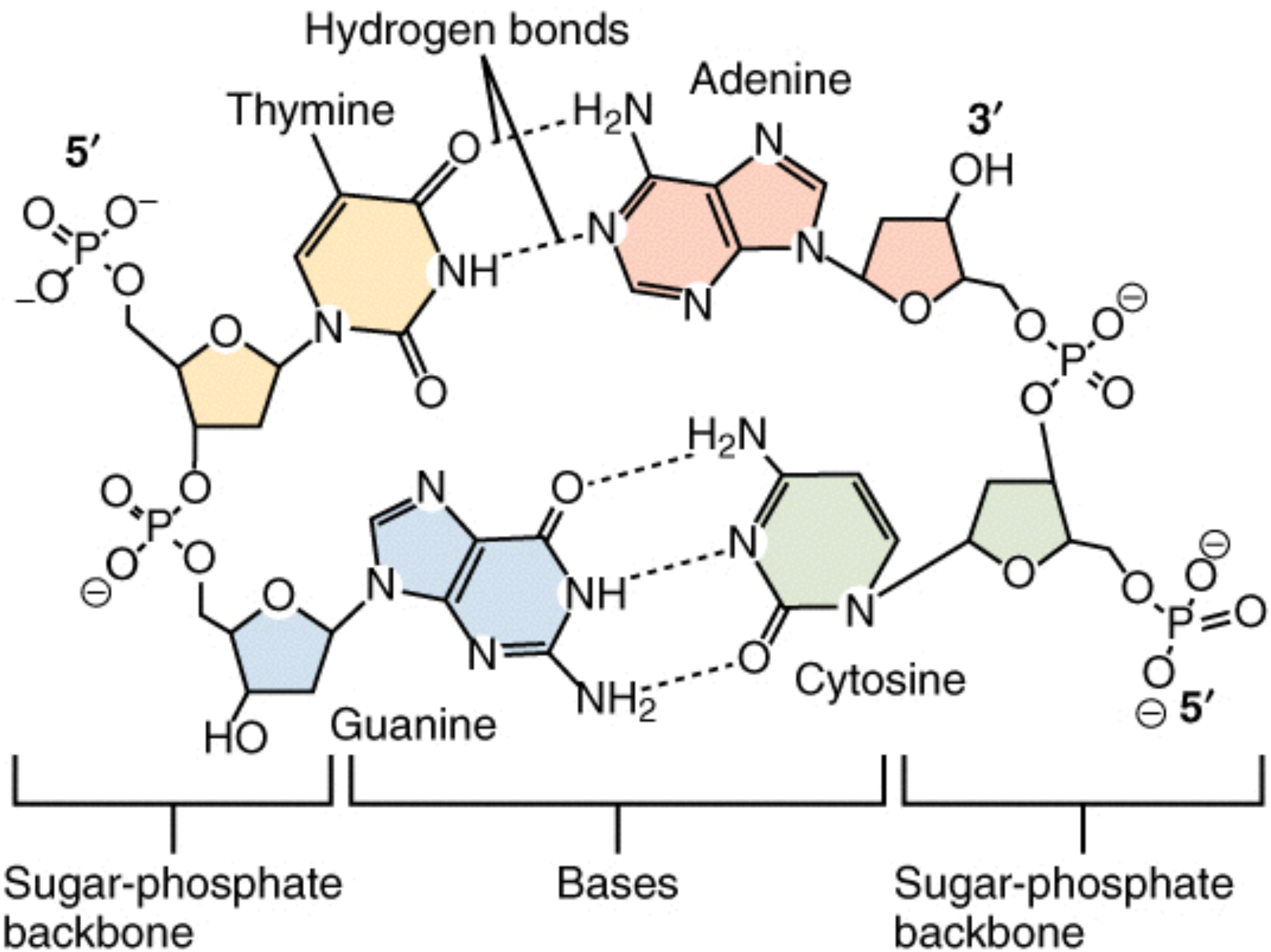

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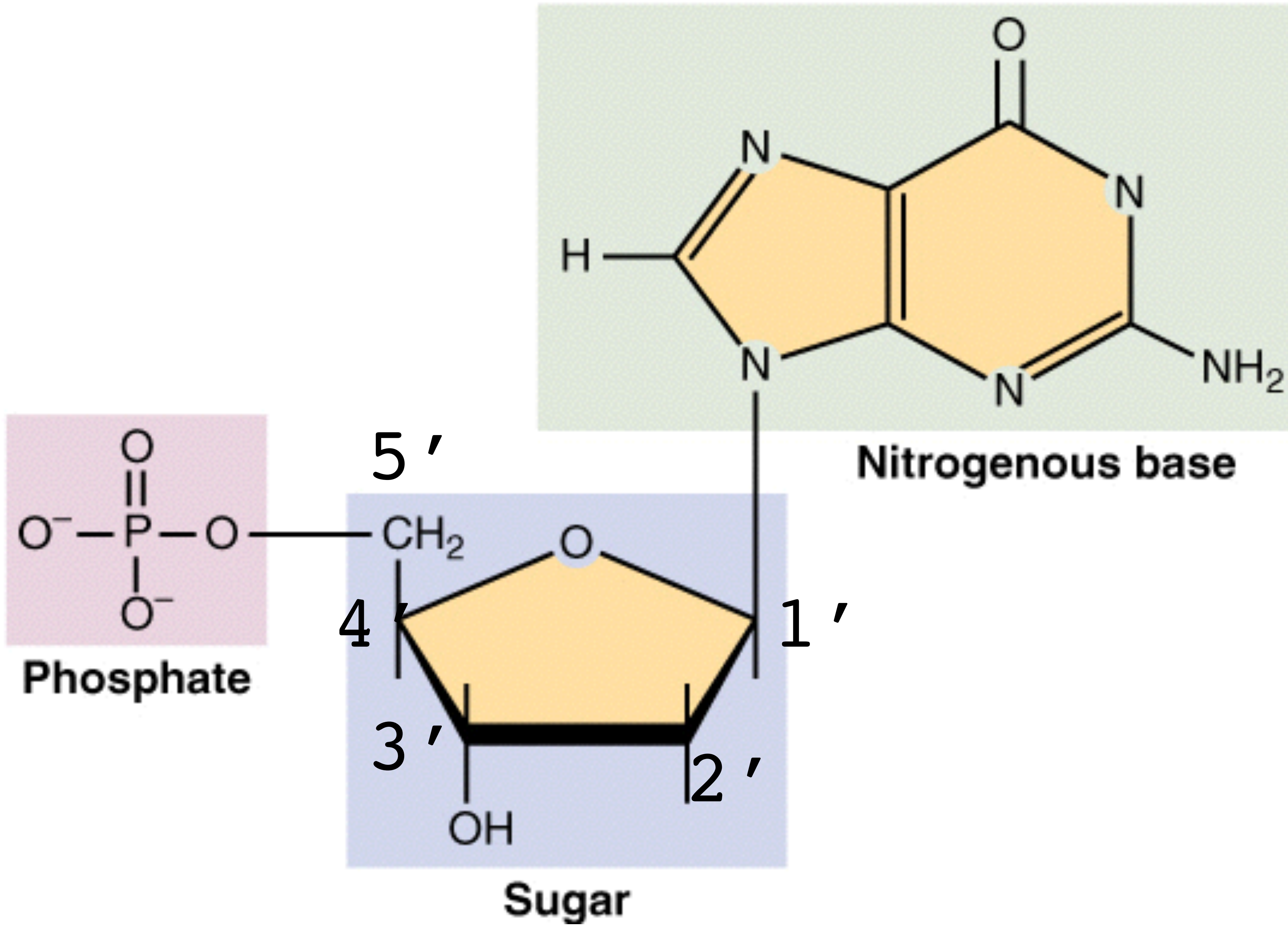

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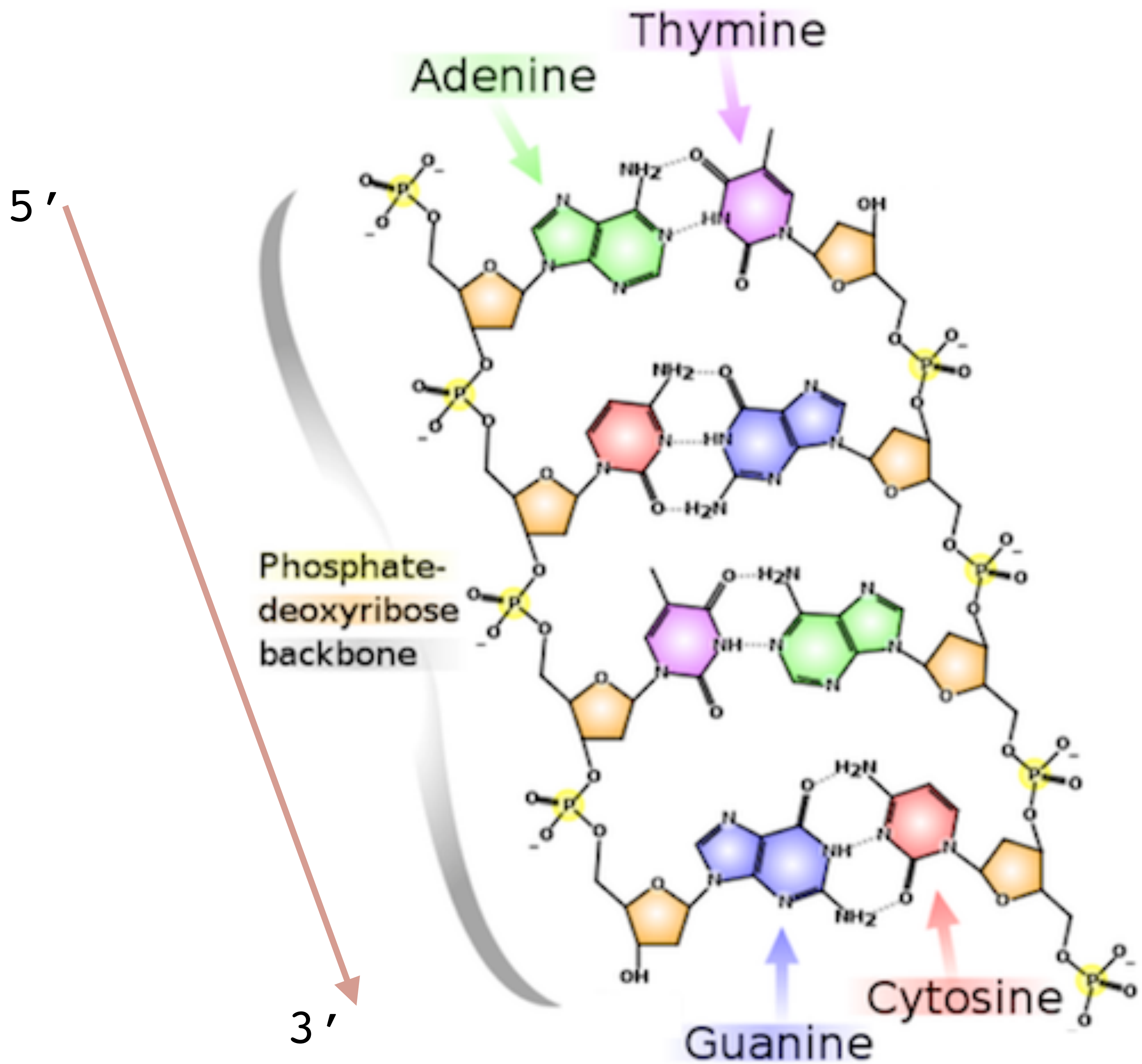
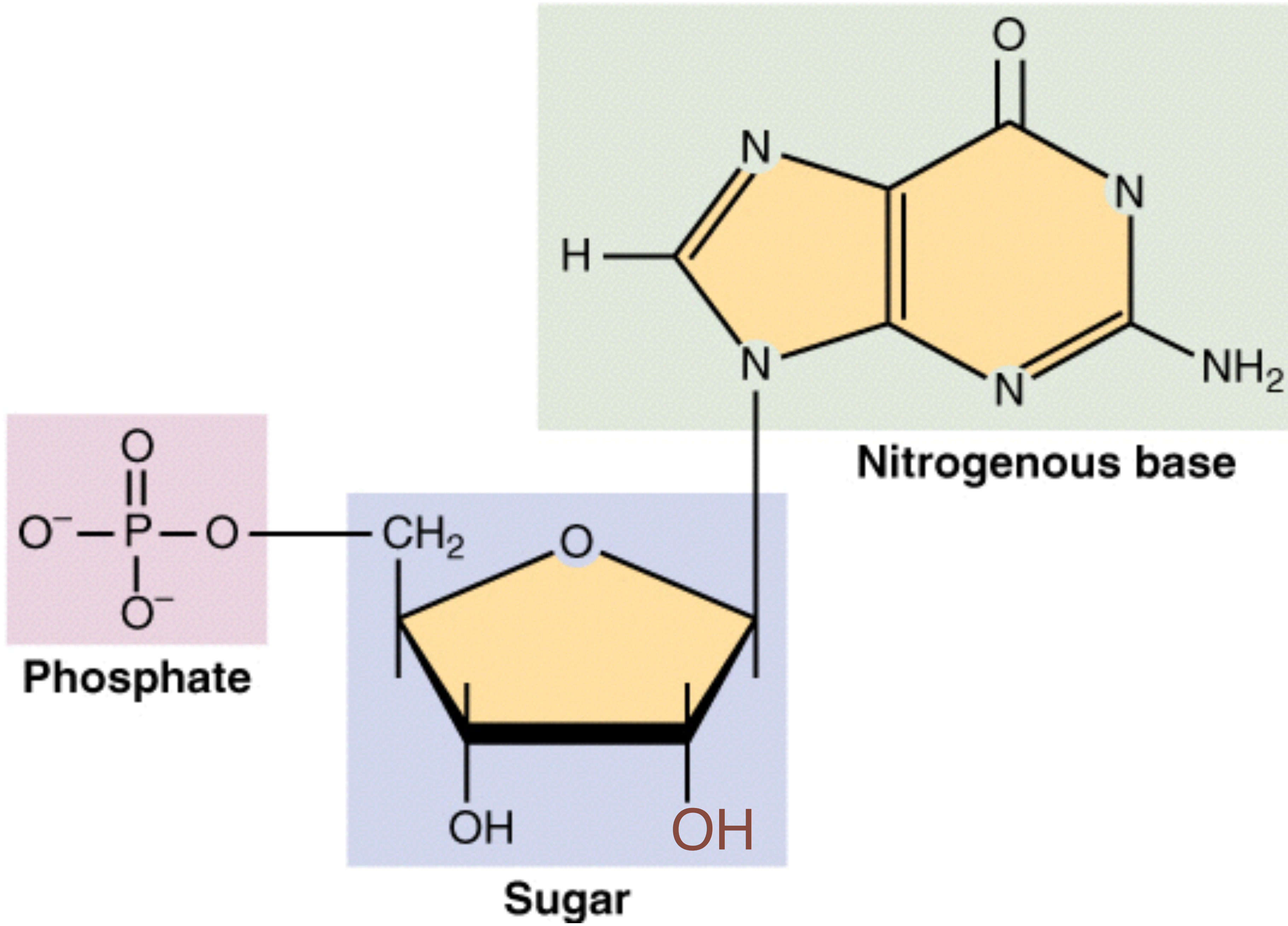


ácido desoxirribonucleico

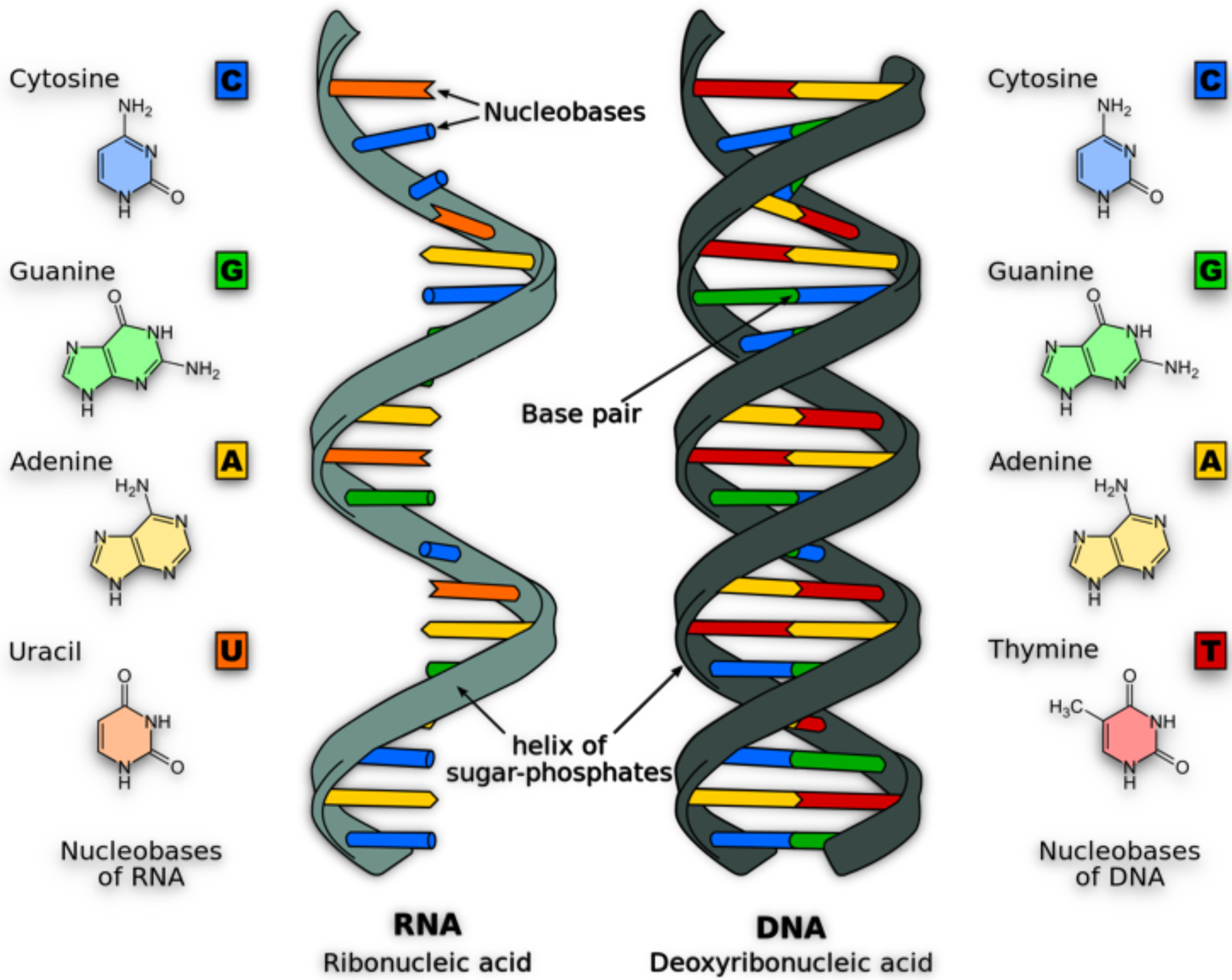
5’ atgtacgcaa 3’

ácido desoxirribonucleico

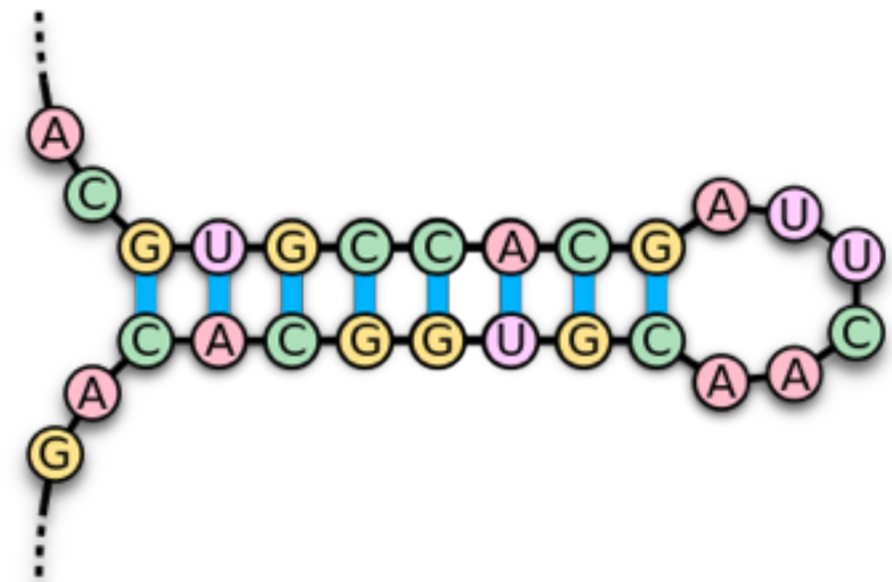
ácido ribonucleico (ARN)

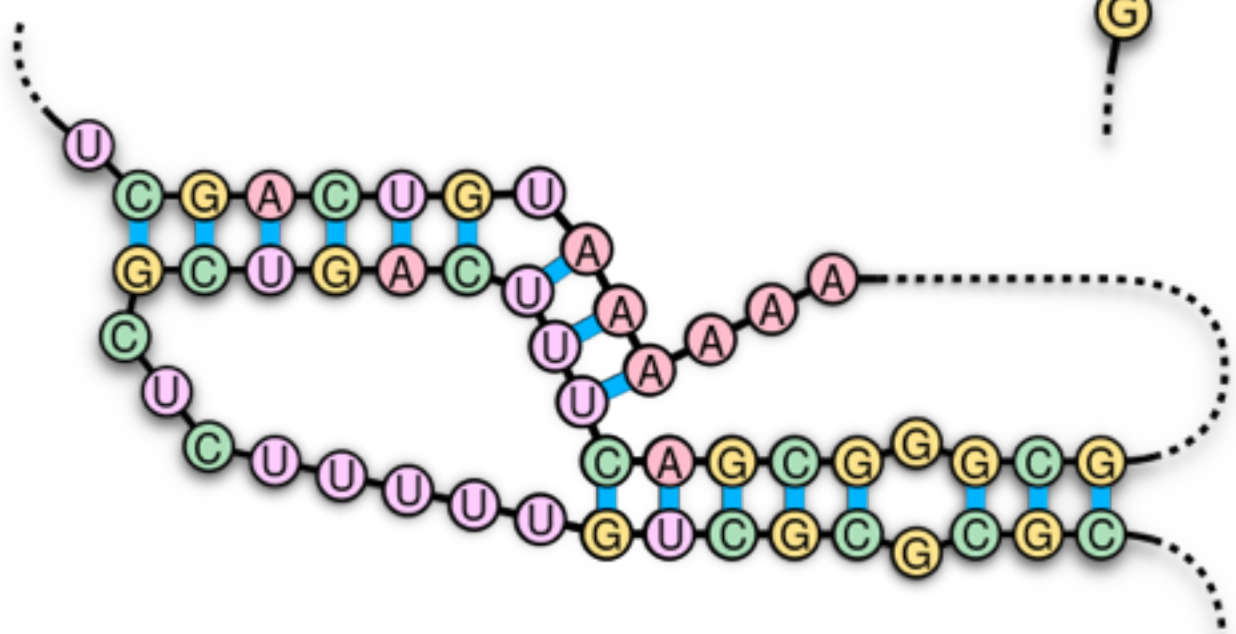


ácido ribonucleico

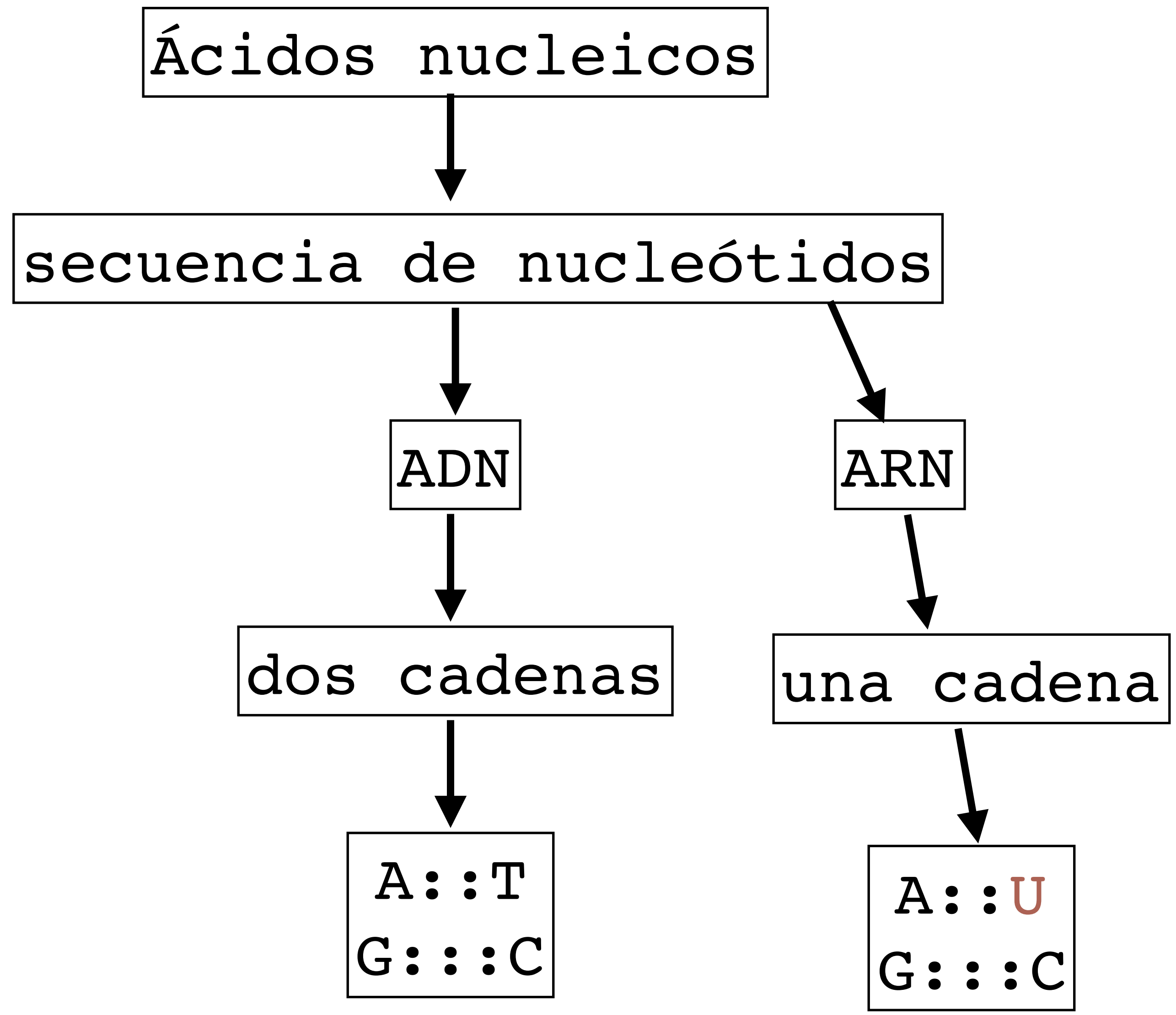


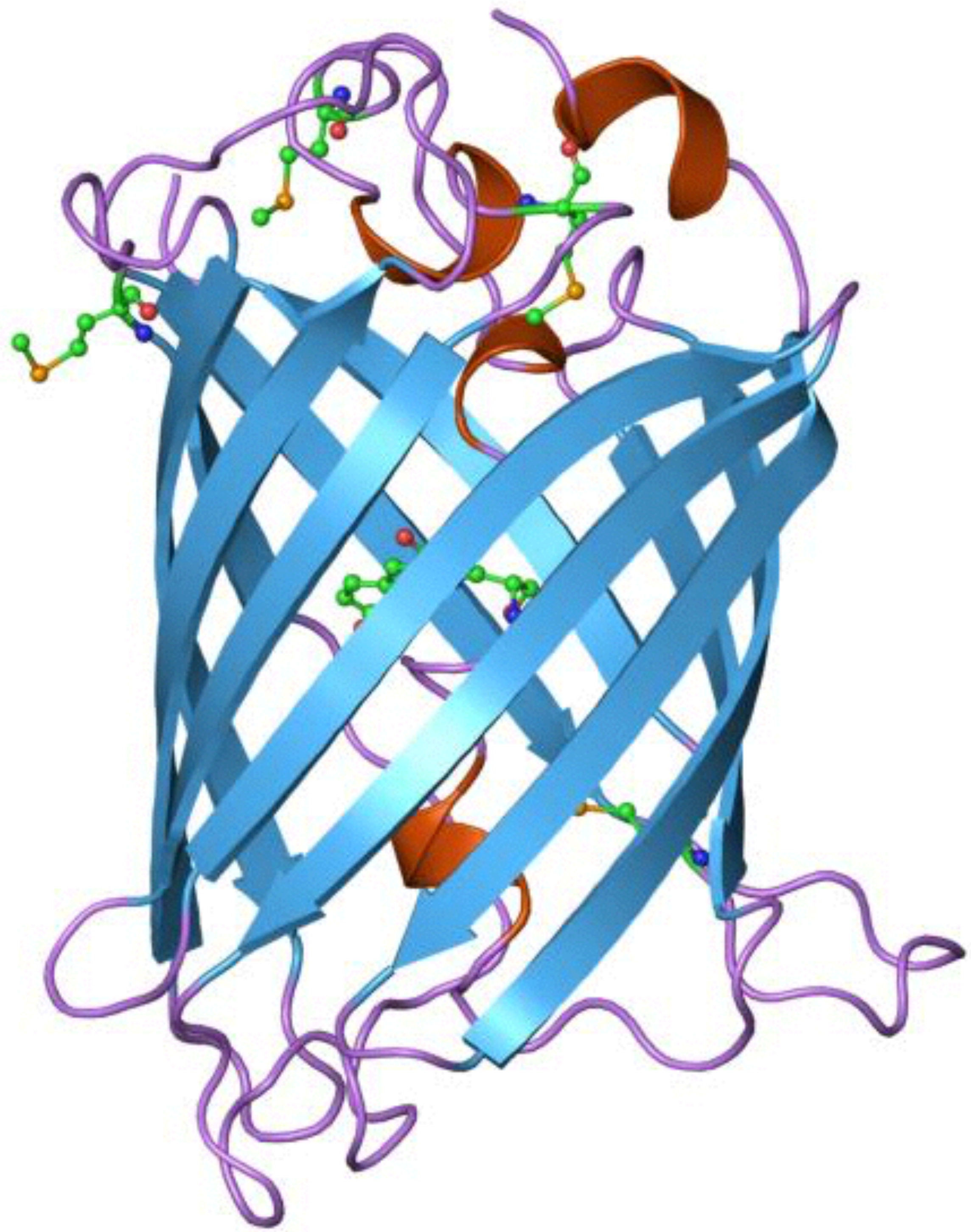
estructuras secundarias





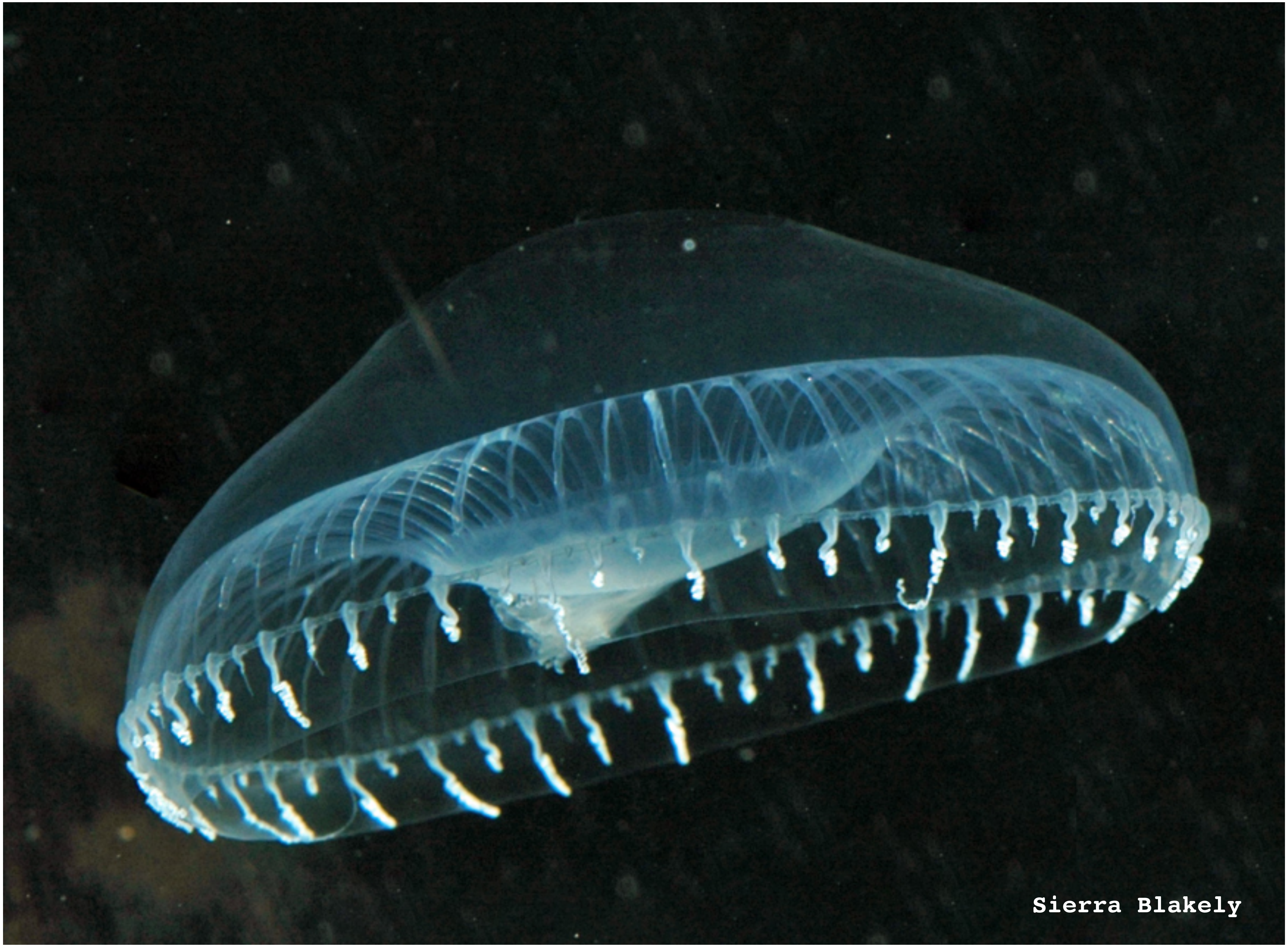
ácido desoxirribonucleico





http://www.ebi.ac.uk/

proteínas

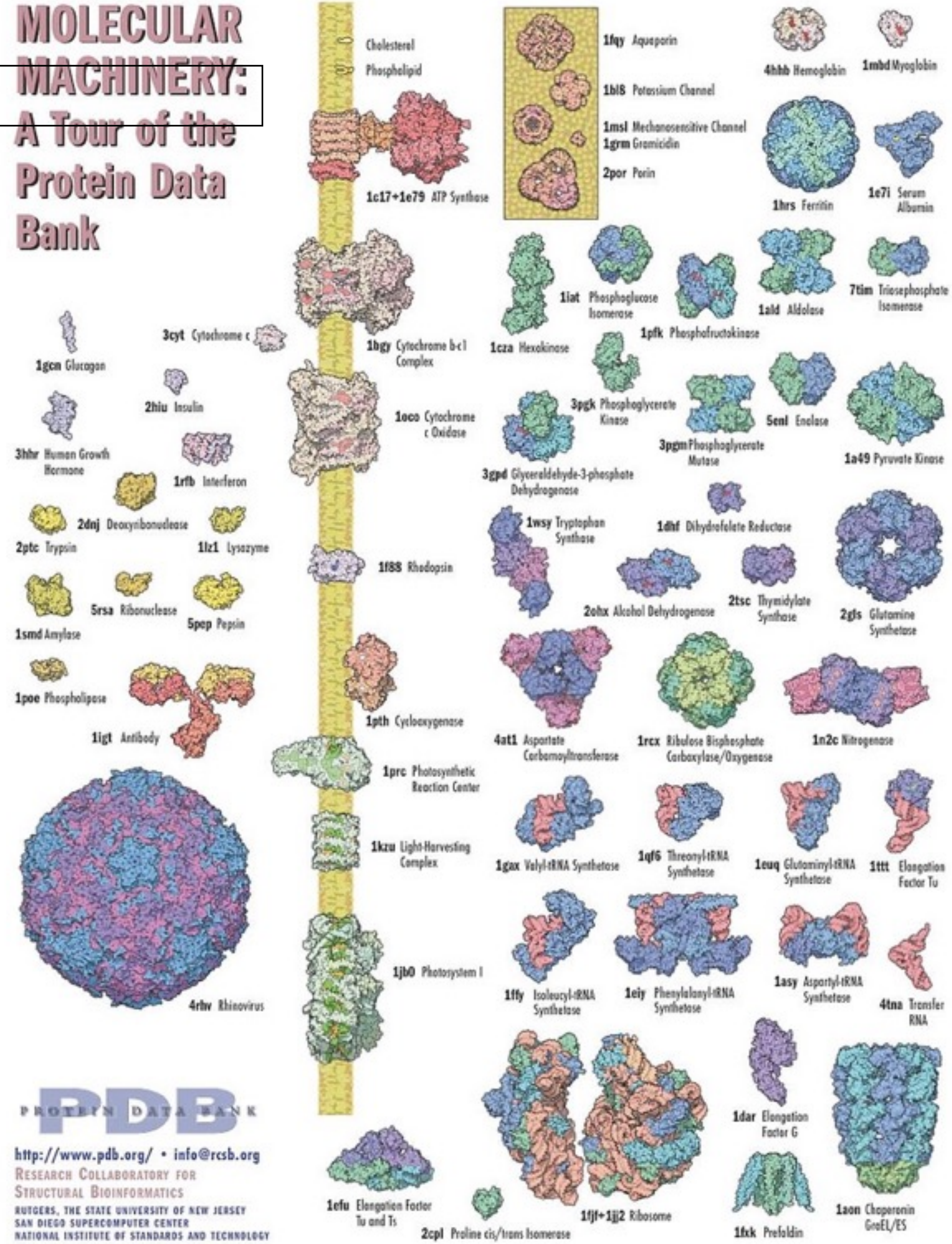


proteínas

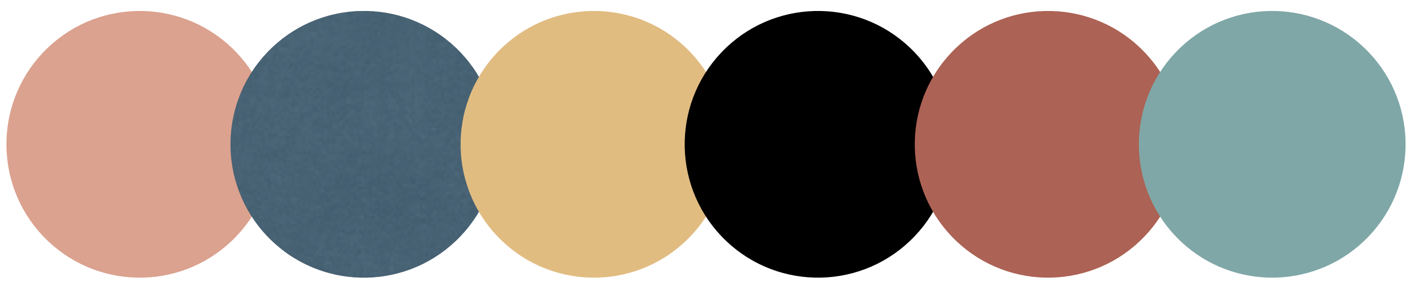
proteínas

- estructura y soporte
- metabolismo
- transporte
- señalización
- …

proteínas


MOLECULAR MACHINERY: A Tour of the Protein Data Bank
Cholesterol
Phospholipid
1c17+1e79 ATP Synthase
1fqy Aquaporin
1bl8 Potassium Channel
1msl Mechanosensitive Channel
1grm Gramicidin
2por Porin
4hhb Hemoglobin
1mbd Myoglobin
1hrs Ferritin
1e7i Serum Albumin
3cyt Cytochrome c
1gcn Glucagon
2hiu Insulin
3hhr Human Growth Hormone
1rfb Interferon
2dnj Deoxyribonuclease
2ptc Trypsin
1lz1 Lysozyme
5rsa Ribonuclease
1smd Amylase
5pep Pepsin
1poe Phospholipase
1igt Antibody
4rhv Rhinovirus
1hgy Cytochrome b-c1 Complex
1oco Cytochrome c Oxidase
1f88 Rhodopsin
1pth Cyclooxygenase
1prc Photosynthetic Reaction Center
1kzu Light-Harvesting Complex
1jb0 Photosystem I
1efu Elongation Factor Tu and Ts
1iat Phosphoglucose Isomerase
1cza Hexokinase
1pfk Phosphofructokinase
1ald Aldolase
7tim Triosephosphate Isomerase
3pgk Phosphoglycerate Kinase
3pgm Phosphoglycerate Mutase
5enl Enolase
1a49 Pyruvate Kinase
3gpd Glyceraldehyde-3-phosphate Dehydrogenase
1wsy Tryptophan Synthase
1dhf Dihydrofolate Reductase
2ohx Alcohol Dehydrogenase
2tsc Thymidylate Synthase
2gls Glutamine Synthetase
4at1 Aspartate Carbamoyltransferase
1rcx Ribulose Bisphosphate Carboxylase/Oxygenase
1n2c Nitrogenase
1gax Valyl-tRNA Synthetase
1qf6 Threonyl-tRNA Synthetase
1euq Glutaminyl-tRNA Synthetase
1ttt Elongation Factor Tu
1ffy Isoleucyl-tRNA Synthetase
1eiy Phenylalanyl-tRNA Synthetase
1asy Aspartyl-tRNA Synthetase
4tna Transfer RNA
1dar Elongation Factor G
1fxk Prefoldin
1aon Chaperonin GroEL/ES
1fjf+1jj2 Ribosome
2cpl Proline cis/trans Isomerase
PDB PROTEIN DATA BANK
http://www.pdb.org/ • info@rcsb.org
RESEARCH COLLABORATORY FOR STRUCTURAL BIOINFORMATICS
RUTGERS, THE STATE UNIVERSITY OF NEW JERSEY
SAN DIEGO SUPERCOMPUTER CENTER
NATIONAL INSTITUTE OF STANDARDS AND TECHNOLOGY

proteínas: secuencia de aminoácidos



proteínas

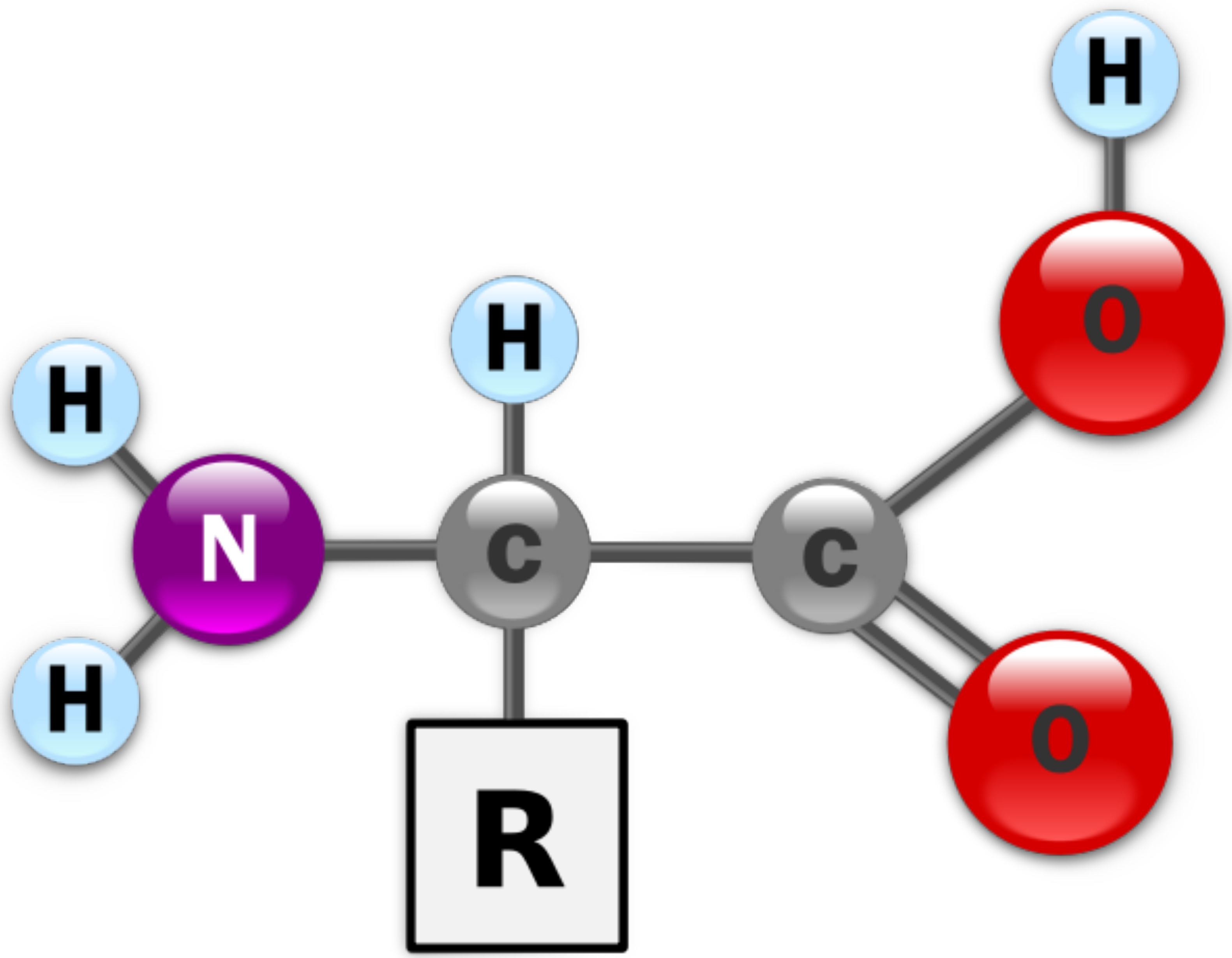
Table 2

Median protein lengths in eukaryotic, bacterial and archaeal organisms

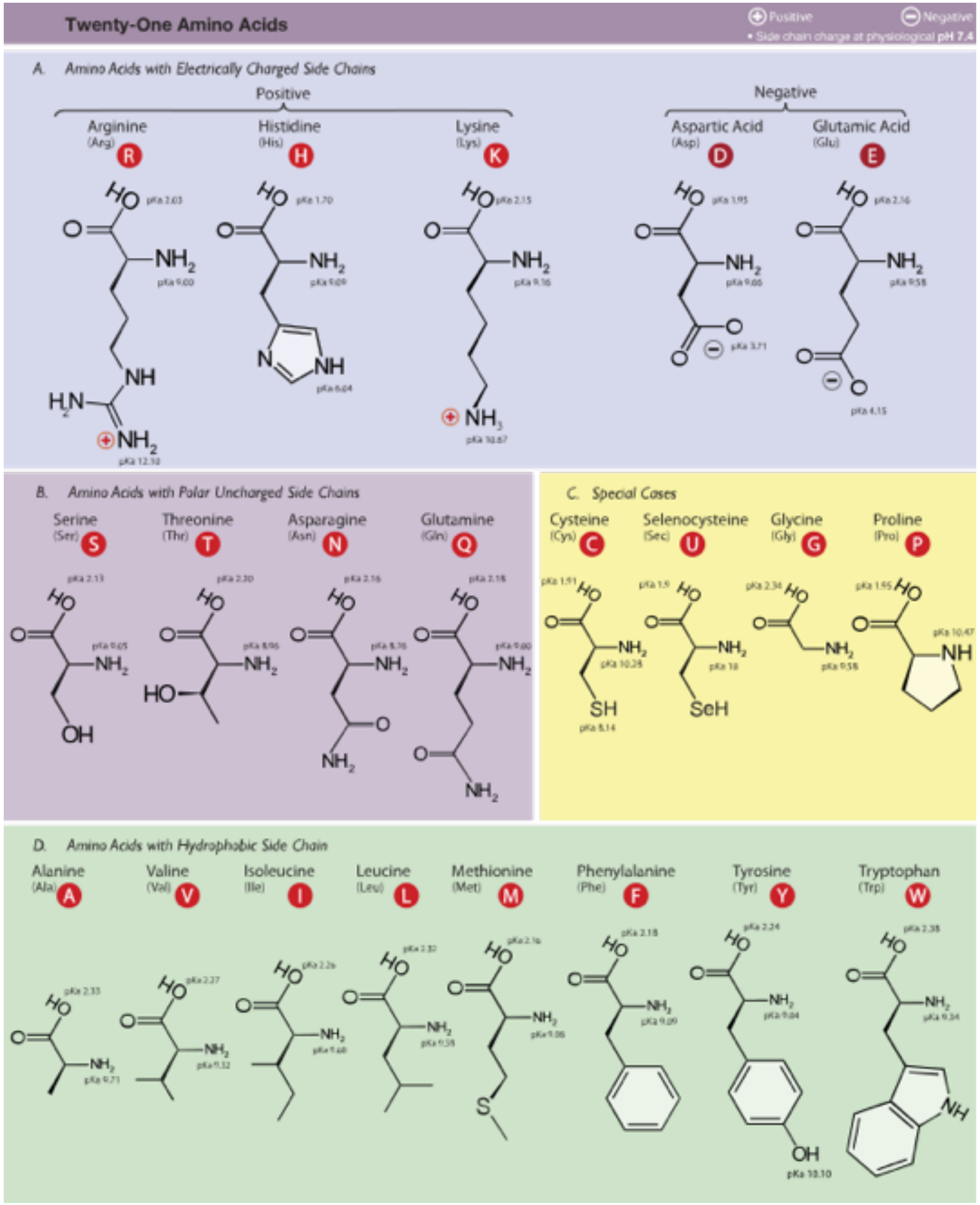
Species[a]	All species		Classified in COG		Classified in Pfan	
	Number[b]	Median[c]	Number[b]	Median[c]	Number[b]	Media
Eukarya	104 394	361	5177	471	71 584	419
HUMAN	33 869	375	–	–	21 686	416
DROME	14 226	373	3092	492	13 091	475
CAEEL	21 124	344	–	–	13 316	391
YEAST	6315	379	2085	438	3953	448
ARATH	28 860	356	–	–	19 538	407
Bacteria	191 541	267	83 513	304	131 915	306
ECOLI	4289	278	3289	309	3483	303
SALTY	4553	271	3408	303	3527	300
SALTI	4767	253	3258	300	3118	300
YERPE	4083	268	2991	299	3003	304
SHIFL	4180	261	–	–	2613	304

Brocchieri and Karlin (2005) *Nucleic Acids Res*

proteínas



proteínas



Twenty-One Amino Acids
Positive
Negative
• Side chain charge at physiological pH 7.4
A. Amino Acids with Electrically Charged Side Chains
Positive
Negative
Arginine (Arg) R
Histidine (His) H
Lysine (Lys) K
Aspartic Acid (Asp) D
Glutamic Acid (Glu) E
B. Amino Acids with Polar Uncharged Side Chains
Serine (Ser) S
Threonine (Thr) T
Asparagine (Asn) N
Glutamine (Gln) Q
C. Special Cases
Cysteine (Cys) C
Selenocysteine (Sec) U
Glycine (Gly) G
Proline (Pro) P
D. Amino Acids with Hydrophobic Side Chain
Alanine (Ala) A
Valine (Val) V
Isoleucine (Ile) I
Leucine (Leu) L
Methionine (Met) M
Phenylalanine (Phe) F
Tyrosine (Tyr) Y
Tryptophan (Trp) W

¿cuantas proteínas posibles?
¿cuanto espacio ocuparían?

pista: ~100 Da/aa

Biol Proced Online. 2009; 11: 32–51.
Published online 2009 May 15. doi: 10.1007/s12575-009-9008-x

Table 1

R_{min} for proteins of different mass

Protein M (kDa)	5	10	20	50	100	200	500
R_{min} (nm)	1.1	1.42	1.78	2.4	3.05	3.84	5.21

¿más o menos grande que el Universo observable?
~4e80 m^3

Respuesta:

```
In [83]: vol_sphere(3e-9) * 20**300
---------------------------------------------------------------------------
OverflowError                             Traceback (most recent call last)
<ipython-input-83-6ddc046acbb2> in <module>()
----> 1 vol_sphere(3e-9) * 20**300

OverflowError: int too large to convert to float
```

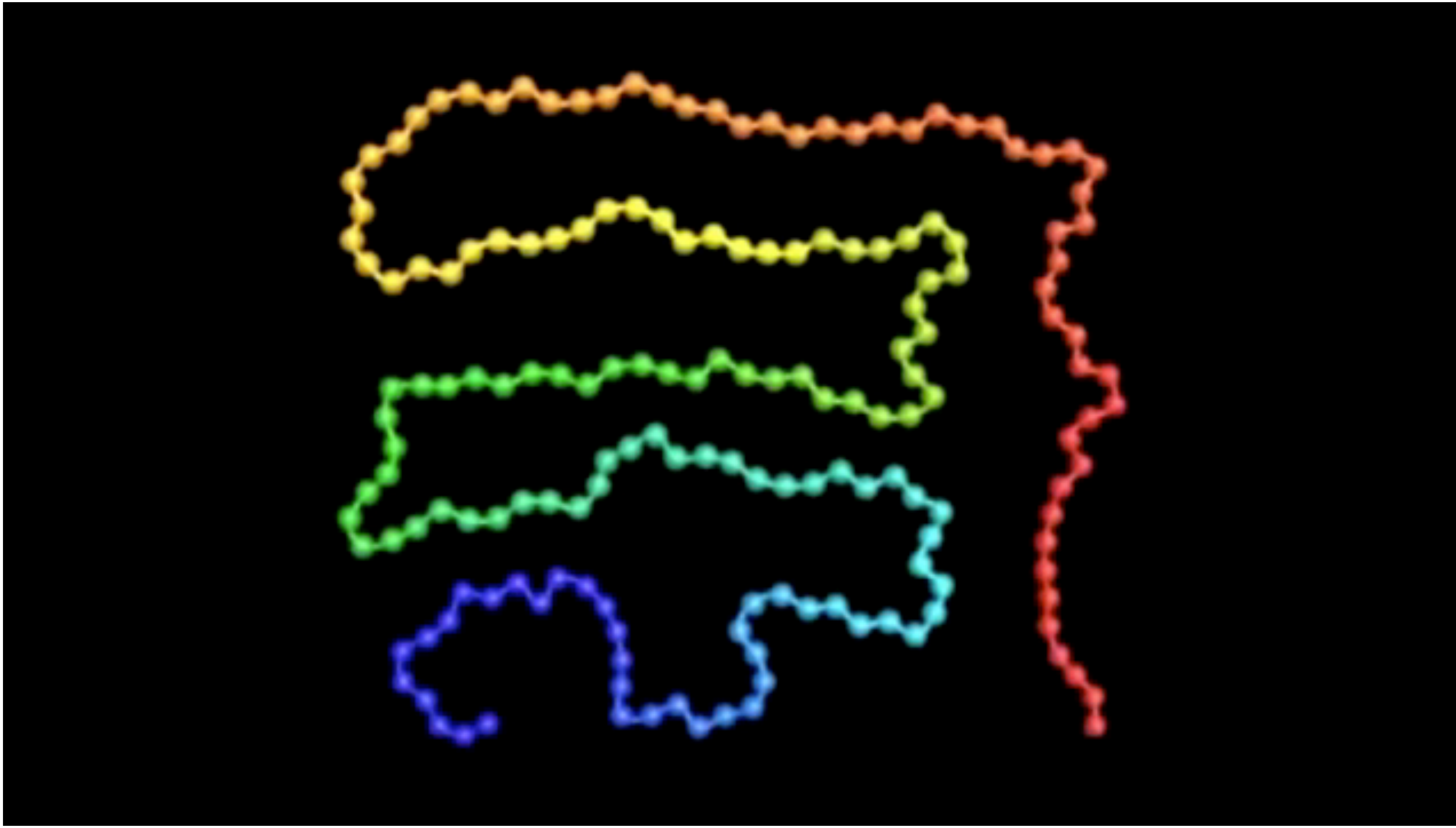
$6e{-}26m^3$ x 2e390

~1e365 posibilidades

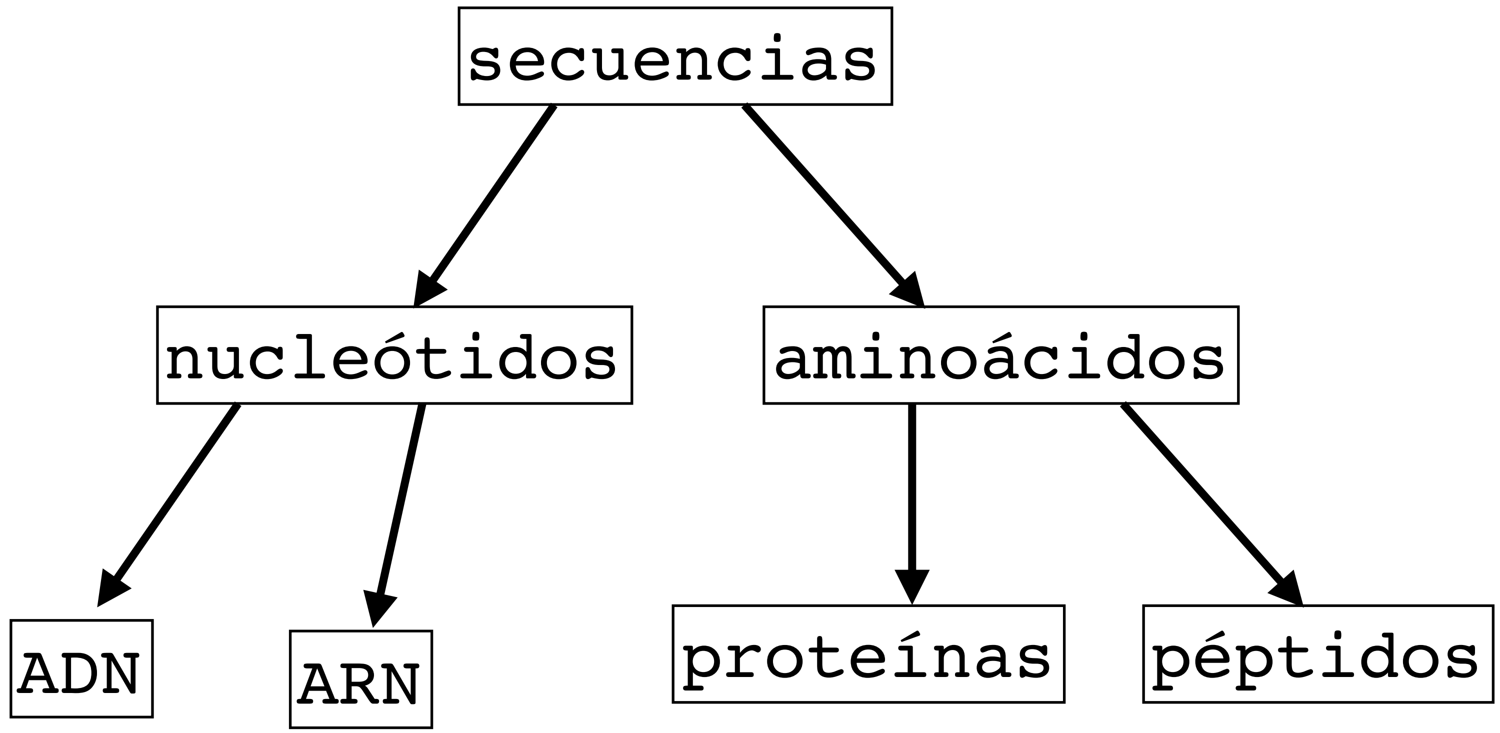
Universo observable:

~4e80 m^3

proteínas

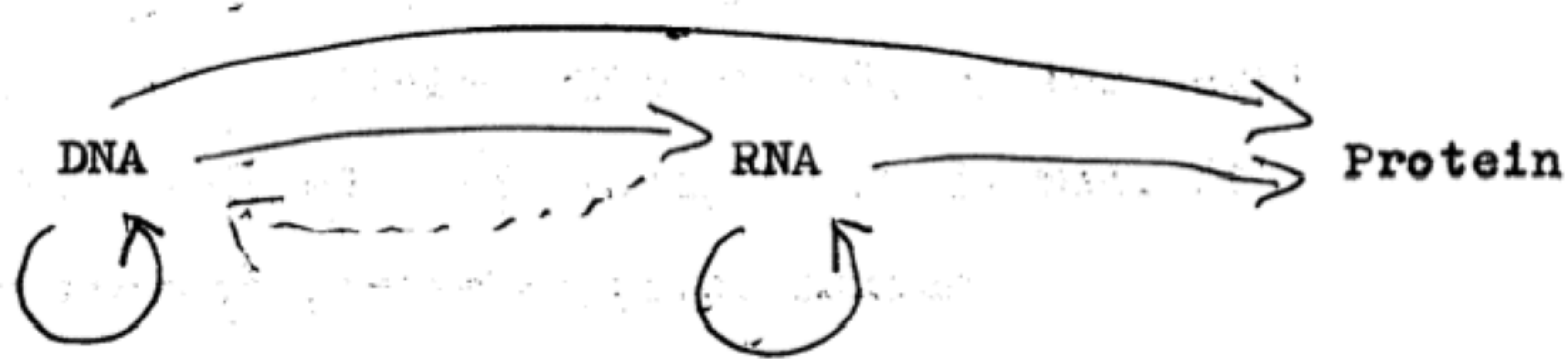


dogma central

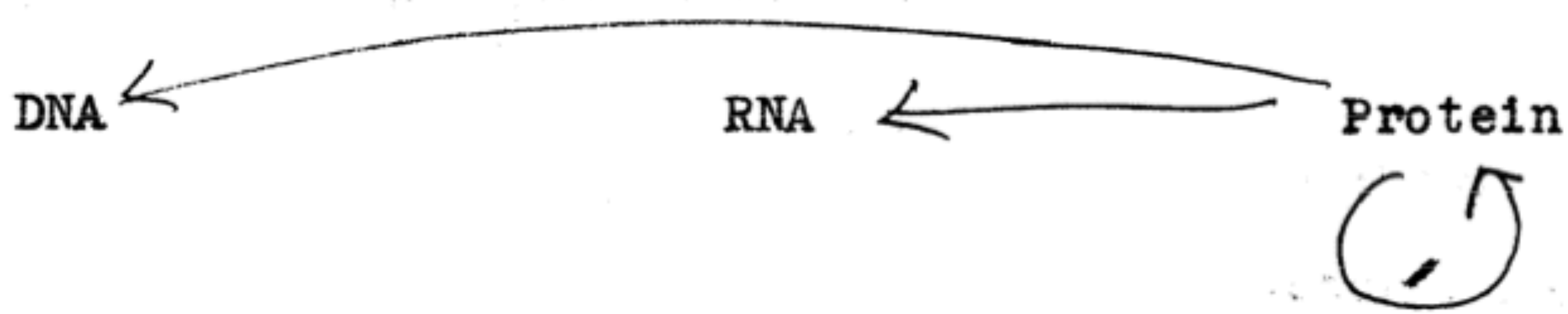


dogma central

That is, we <u>may</u> be able to have



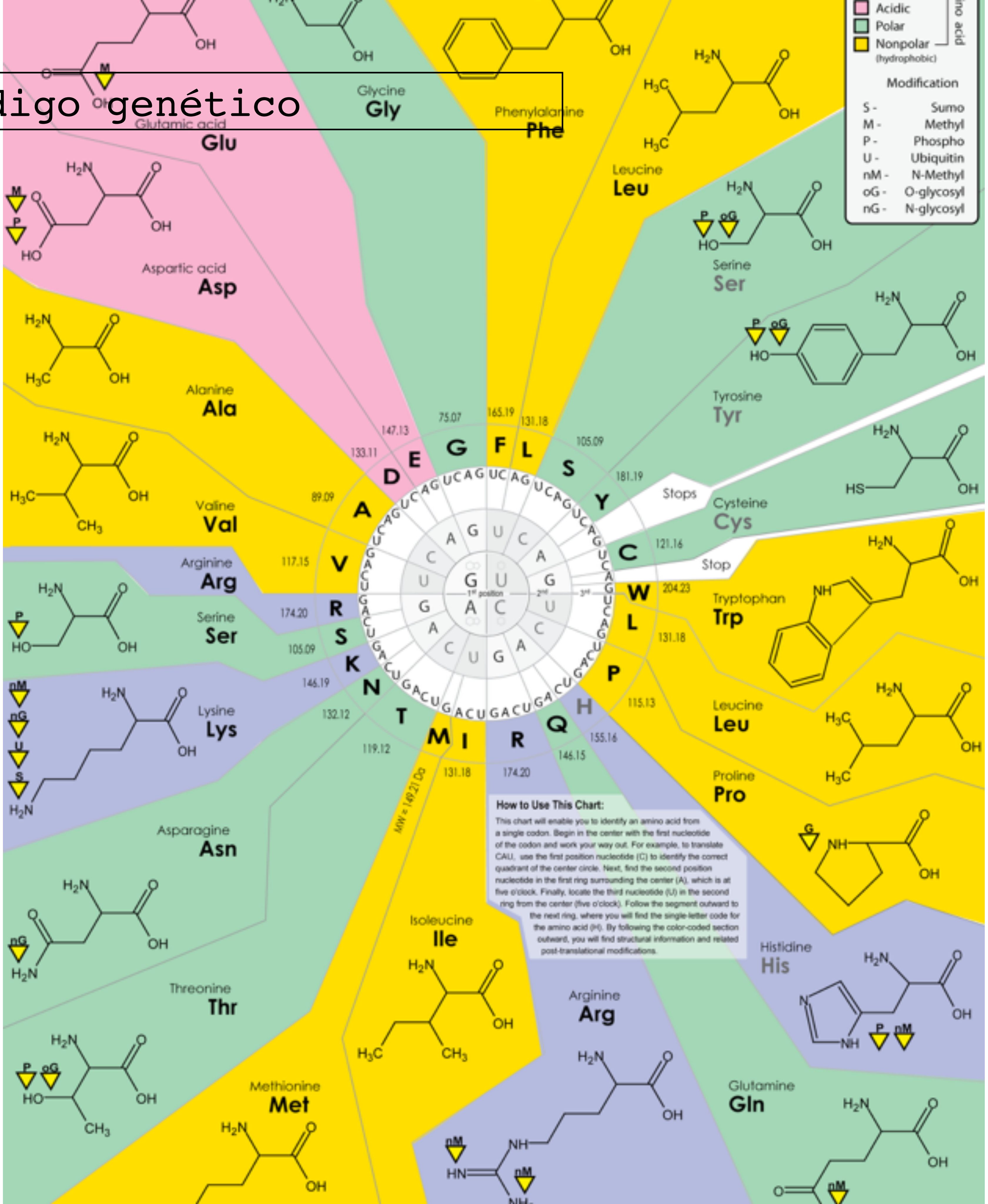
but <u>never</u>



where the arrows show <u>the transfer of information</u>.

Francis Crick (1956) Ideas on Protein Syn

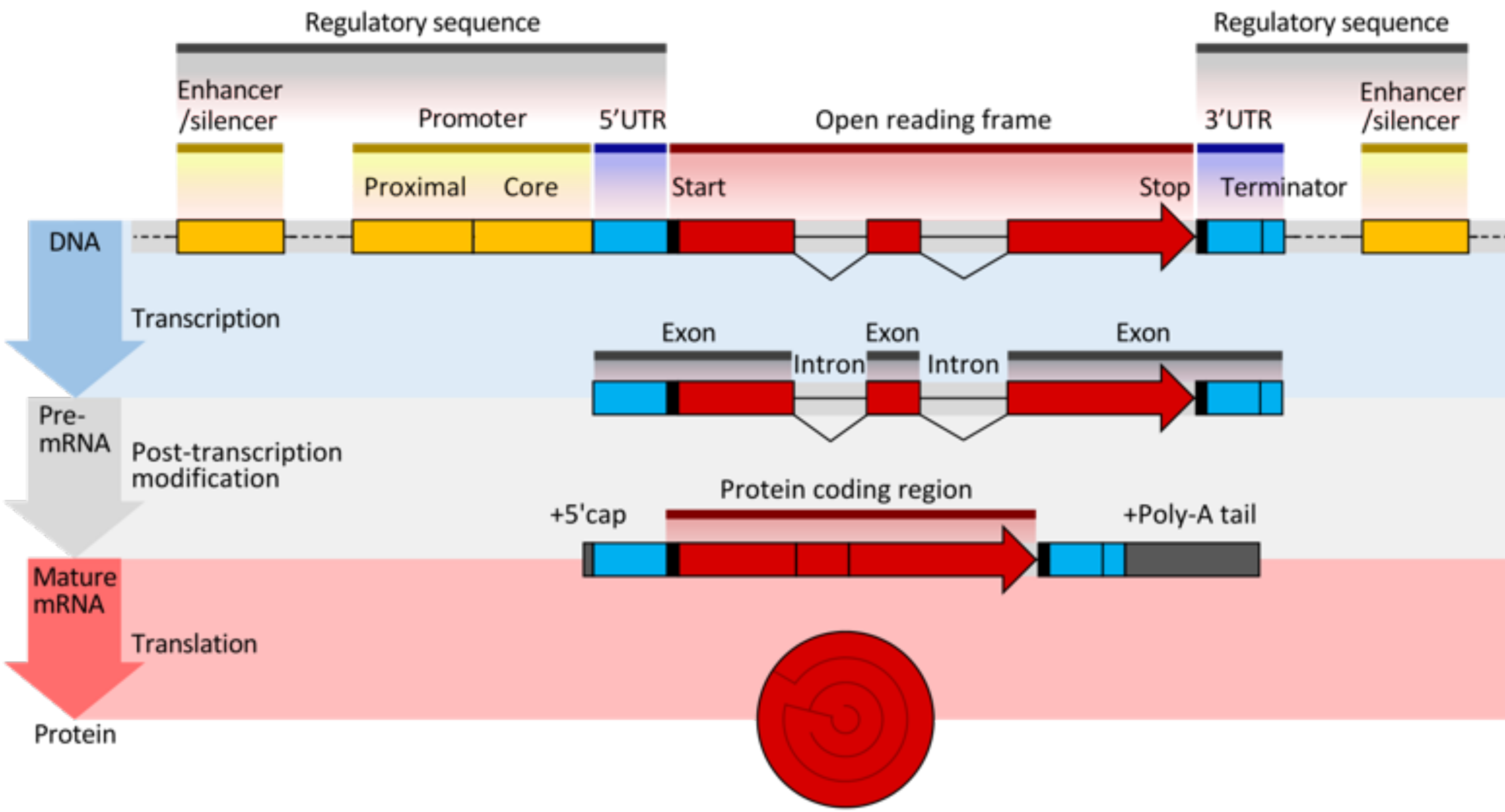
código genético



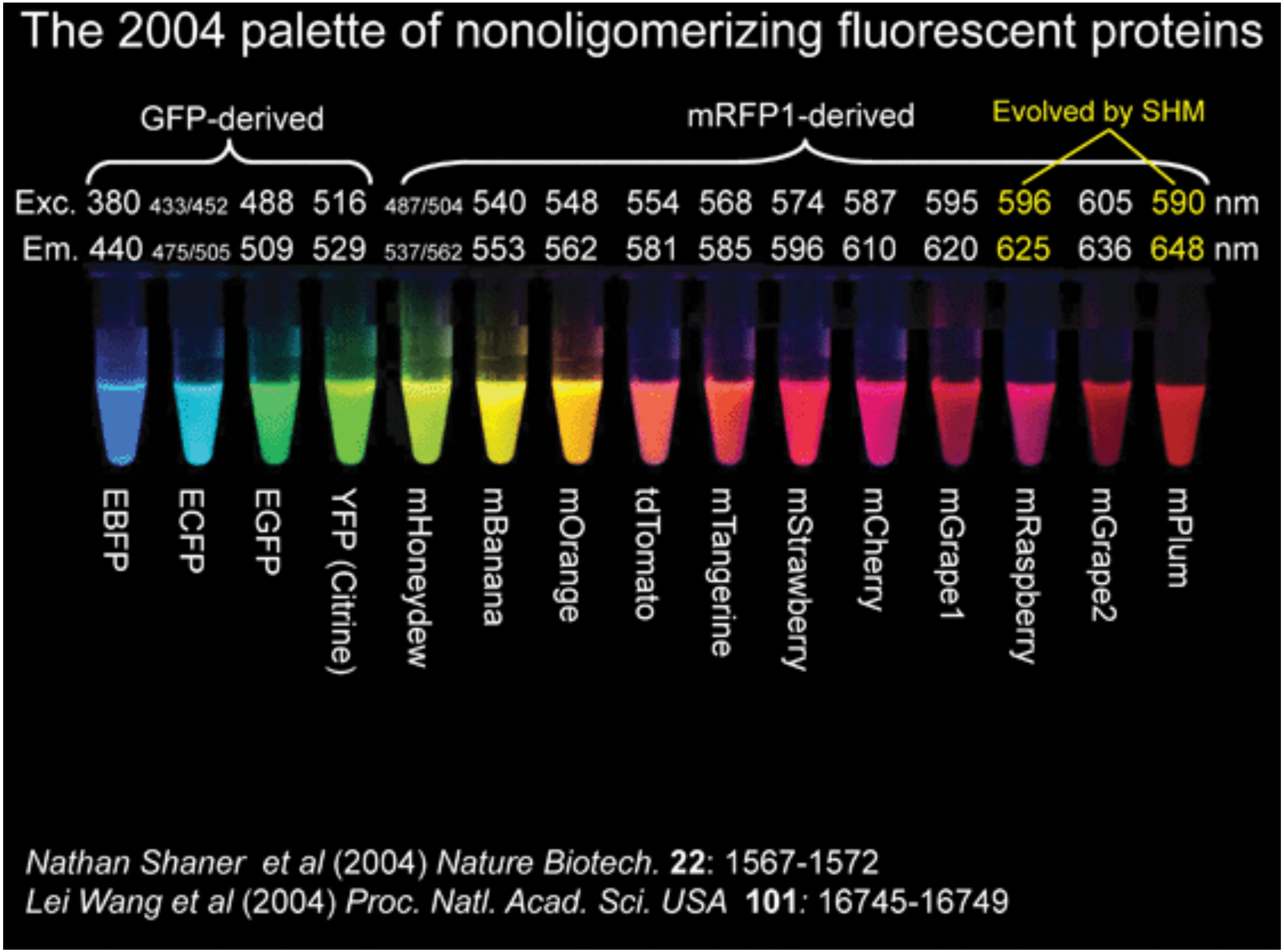
código genético

5’ atg tac gca aac cgc ctc tcc tag 3’

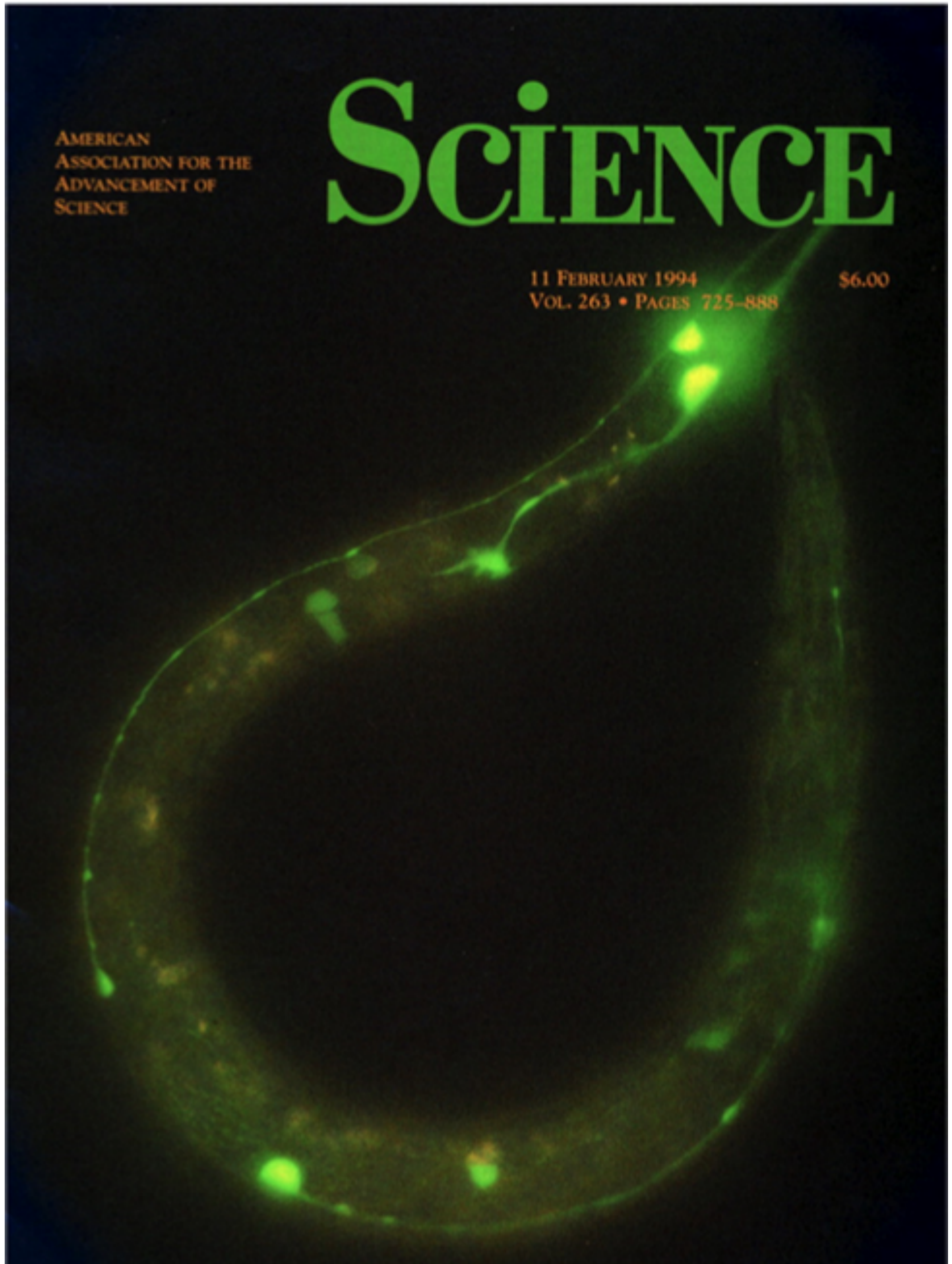
Módulos de ADN



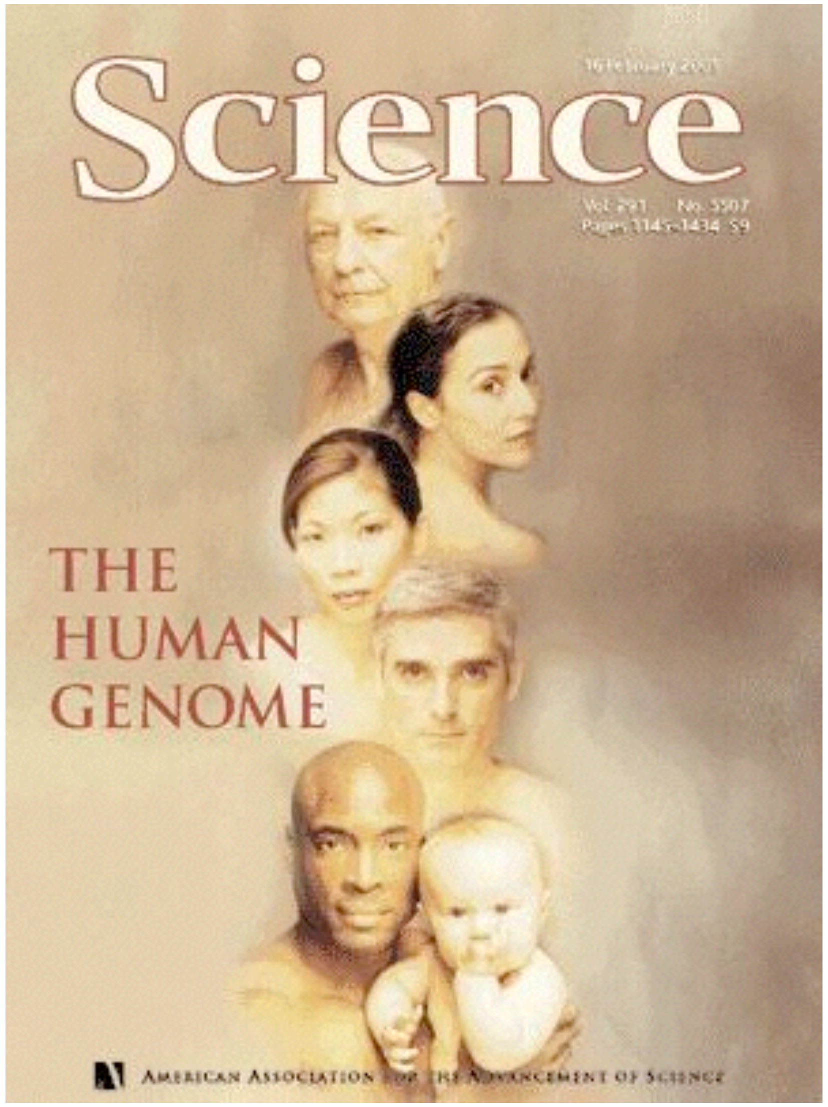
ingeniería genética


The 2004 palette of nonoligomerizing fluorescent proteins
GFP-derived
mRFP1-derived
Evolved by SHM
Exc. 380 433/452 488 516 487/504 540 548 554 568 574 587 595 596 605 590 nm
Em. 440 475/505 509 529 537/562 553 562 581 585 596 610 620 625 636 648 nm
EBFP
ECFP
EGFP
YFP (Citrine)
mHoneydew
mBanana
mOrange
tdTomato
mTangerine
mStrawberry
mCherry
mGrape1
mRaspberry
mGrape2
mPlum
Nathan Shaner et al (2004) Nature Biotech. 22: 1567-1572
Lei Wang et al (2004) Proc. Natl. Acad. Sci. USA 101: 16745-16749

ingeniería genética



ingeniería genética



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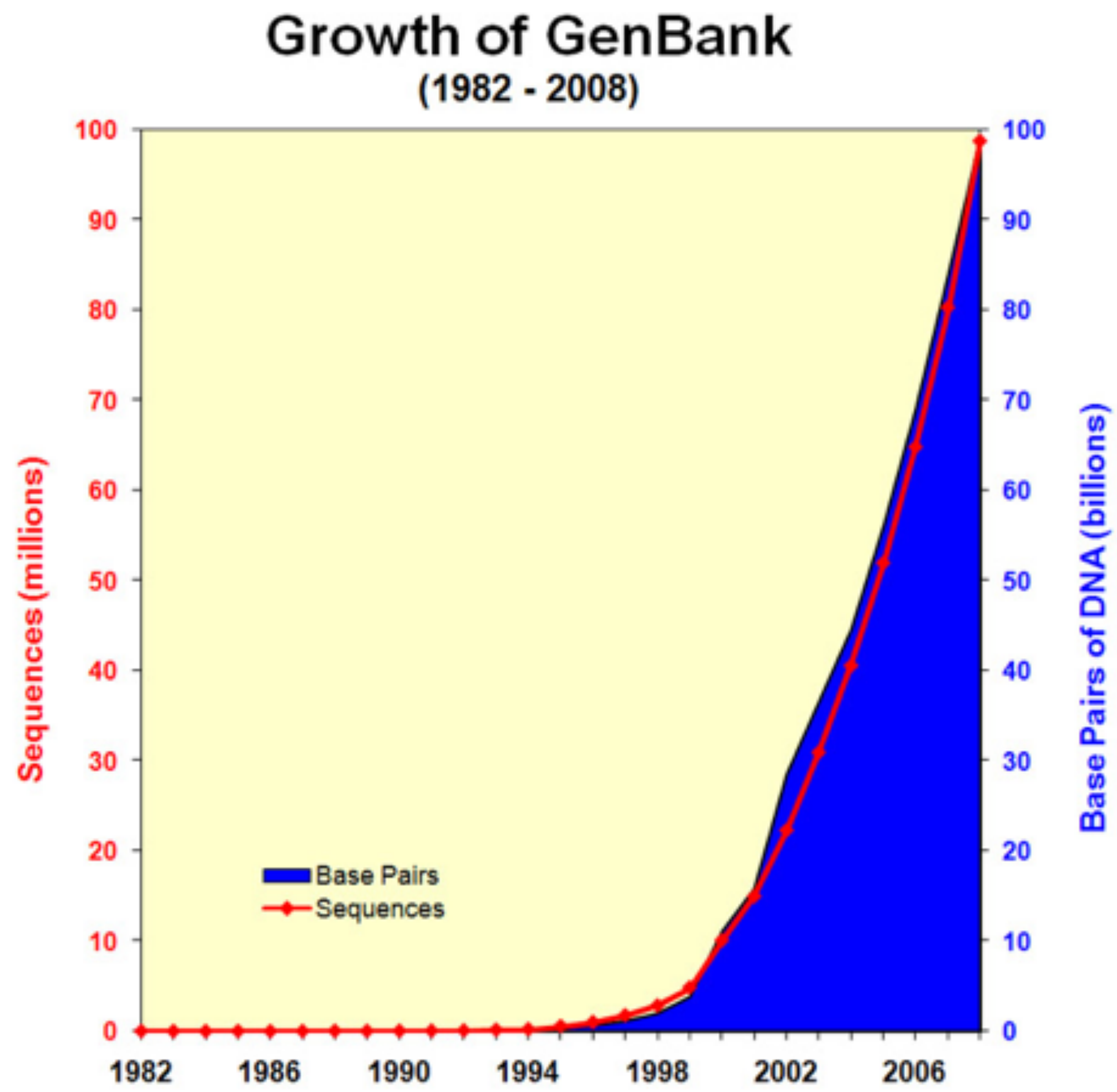

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cggactacctgaaact
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gttacccaggactcct
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tccggttatgcagaaa
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aaatcaaaatgcgtct
gaaactgaaagacggtggtcacta aaaccg
gttcagctgccgggtg
cttacaaaaccgacatcaaactgga tgaaca
gtacgaacgtgctgaa

http://www.ncbi.nlm.nih.gov/genbank/genbankstats.html

ggtcgtcactccaccggtgcttaataacgctgatagtgctagtgtagatcgctactagagccag
gcatcaaataaaacga
aaggctcagtcgaaagactgggcctttcgttttatctgttgtttgtcggtgaacgctctctact
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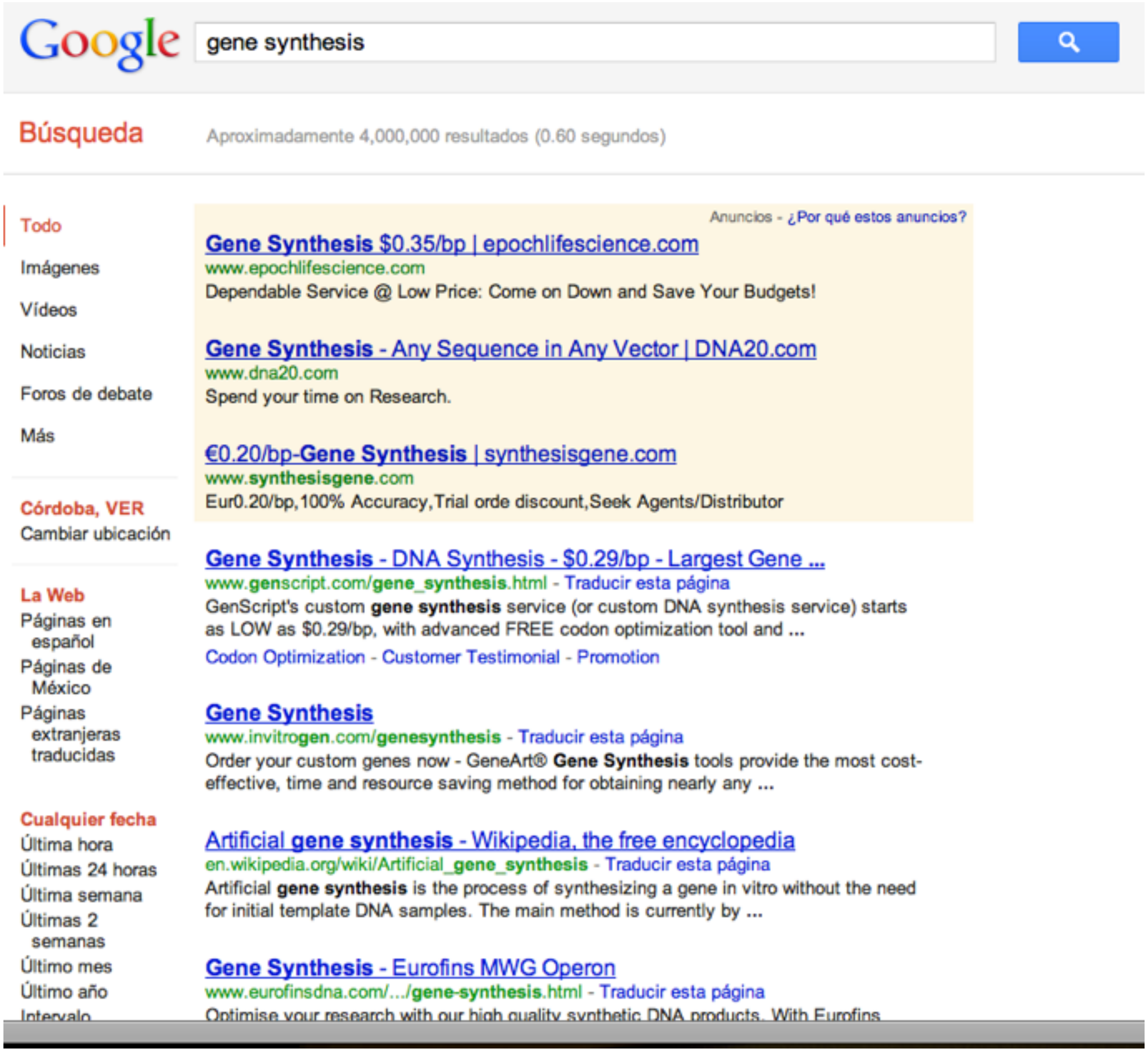
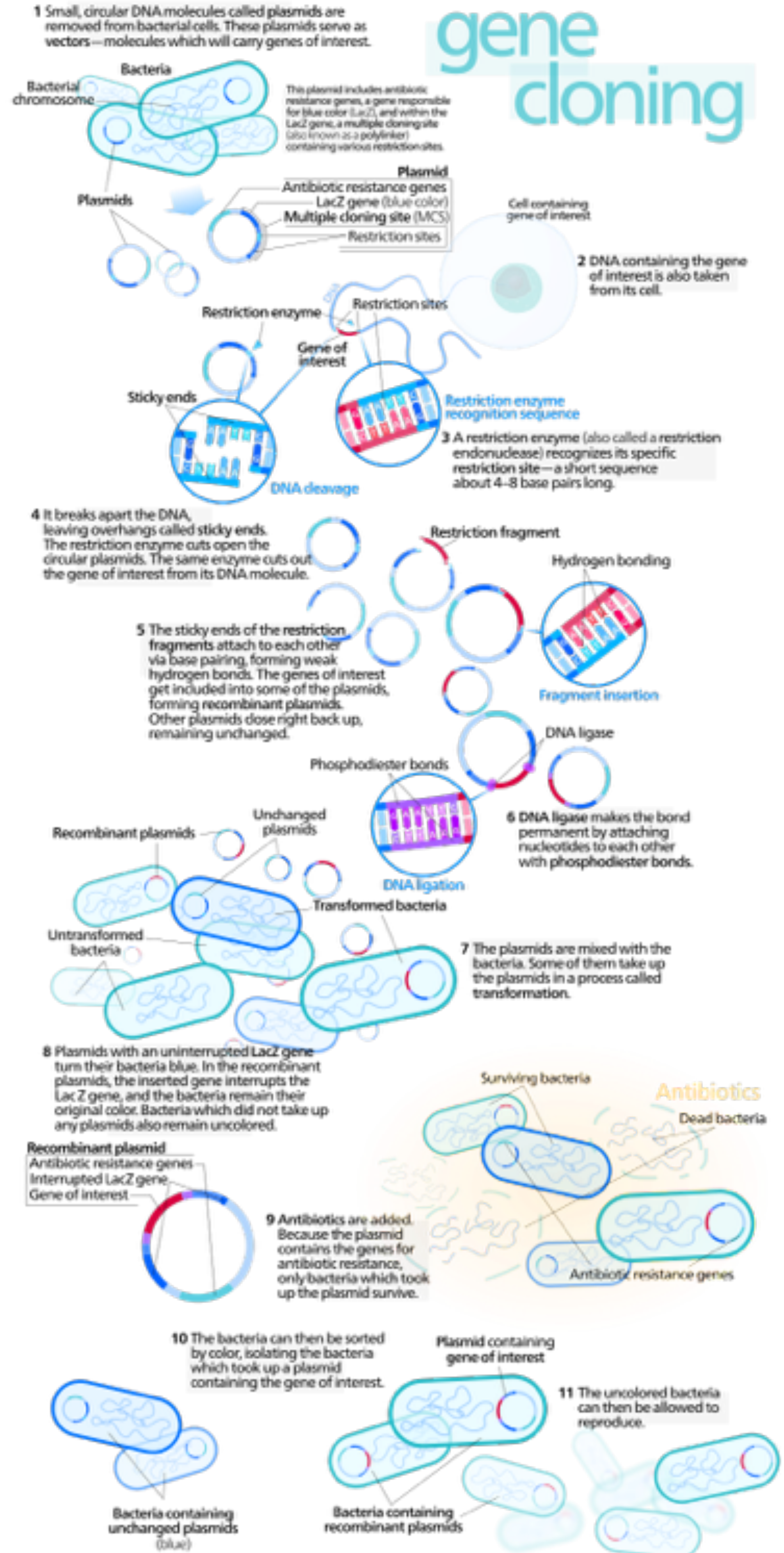
ingeniería genética

ingeniería genética





gene cloning
1 Small, circular DNA molecules called plasmids are removed from bacterial cells. These plasmids serve as vectors—molecules which will carry genes of interest.
Bacteria
Bacterial chromosome
This plasmid includes antibiotic resistance genes, a gene responsible for blue color (LacZ), and within the LacZ gene, a multiple cloning site (also known as a polylinker) containing various restriction sites.
Plasmids
Plasmid
Antibiotic resistance genes
LacZ gene (blue color)
Multiple cloning site (MCS)
Restriction sites
Cell containing gene of interest
2 DNA containing the gene of interest is also taken from its cell.
Restriction enzyme
Restriction sites
Gene of interest
Sticky ends
Restriction enzyme recognition sequence
DNA cleavage
3 A restriction enzyme (also called a restriction endonuclease) recognizes its specific restriction site—a short sequence about 4–8 base pairs long.
4 It breaks apart the DNA, leaving overhangs called sticky ends. The restriction enzyme cuts open the circular plasmids. The same enzyme cuts out the gene of interest from its DNA molecule.
Restriction fragment
Hydrogen bonding
5 The sticky ends of the restriction fragments attach to each other via base pairing, forming weak hydrogen bonds. The genes of interest get included into some of the plasmids, forming recombinant plasmids. Other plasmids close right back up, remaining unchanged.
Fragment insertion
DNA ligase
Phosphodiester bonds
6 DNA ligase makes the bond permanent by attaching nucleotides to each other with phosphodiester bonds.
DNA ligation
Recombinant plasmids
Unchanged plasmids
Transformed bacteria
Untransformed bacteria
7 The plasmids are mixed with the bacteria. Some of them take up the plasmids in a process called transformation.
8 Plasmids with an uninterrupted LacZ gene turn their bacteria blue. In the recombinant plasmids, the inserted gene interrupts the Lac Z gene, and the bacteria remain their original color. Bacteria which did not take up any plasmids also remain uncolored.
Surviving bacteria
Antibiotics
Dead bacteria
Recombinant plasmid
Antibiotic resistance genes
Interrupted LacZ gene
Gene of interest
9 Antibiotics are added. Because the plasmid contains the genes for antibiotic resistance, only bacteria which took up the plasmid survive.
Antibiotic resistance genes
10 The bacteria can then be sorted by color, isolating the bacteria which took up a plasmid containing the gene of interest.
Plasmid containing gene of interest
11 The uncolored bacteria can then be allowed to reproduce.
Bacteria containing unchanged plasmids (blue)
Bacteria containing recombinant plasmids