

Chemical Biology

DNA \rightleftharpoons RNA \rightleftharpoons Proteins

Molecular Engineering

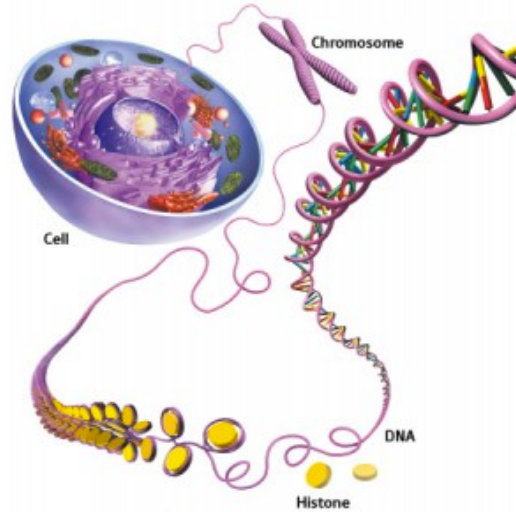
Dr. Ron Rusay

<https://www.youtube.com/watch?v=gG7uCskUOrA>



DNA & RNA: Nucleic Acids

- Store & carry genetic information.

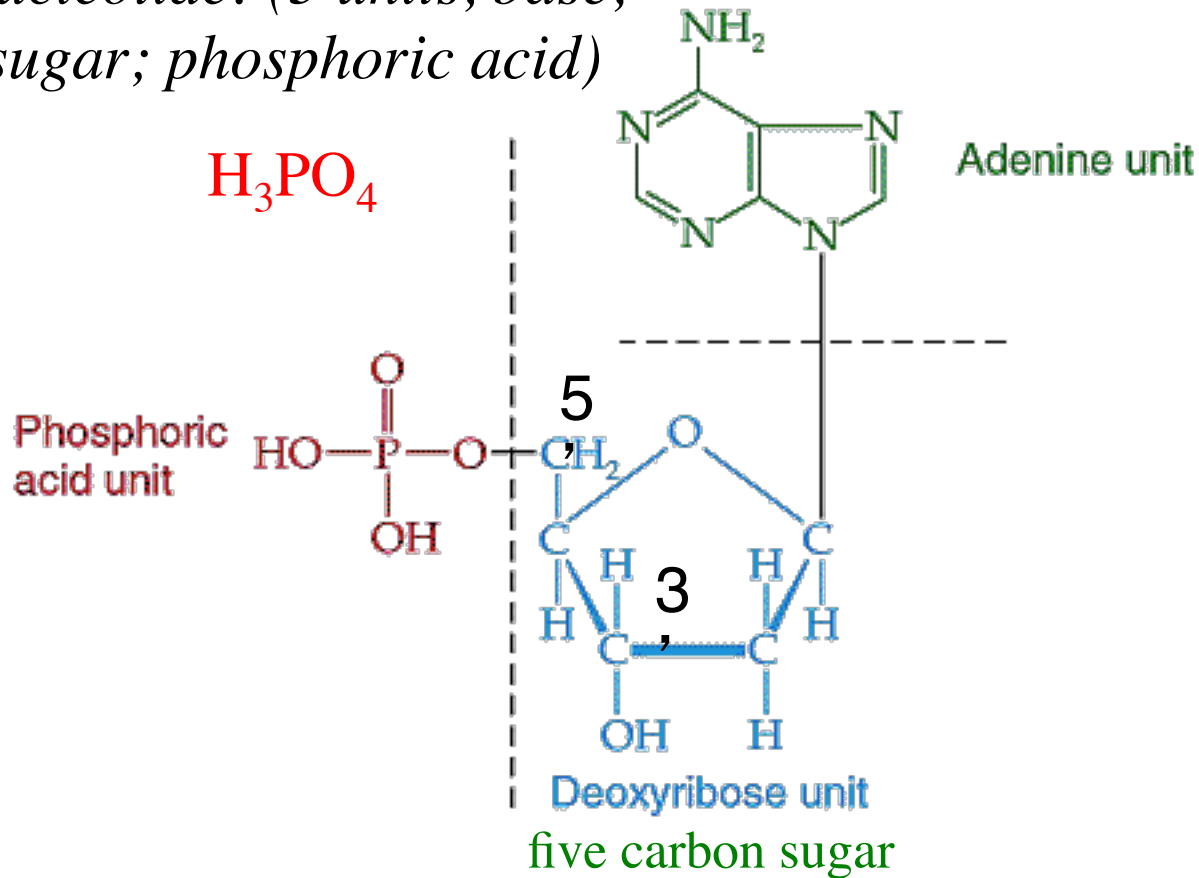


- DNA (deoxyribonucleic acids) have molecular weights $\sim 6 \times 10^6$ to 16×10^6 daltons (amu) and are found inside the nucleus of the cell.
- RNA (ribonucleic acids) have molecular weights $\sim 20,000$ to $40,000$ amu and are found in the cytoplasm outside the nucleus of the cell.

Nucleic “Acids”

*Nucleotide: (3 units, base;
sugar; phosphoric acid)*

Organic base: R-NH₂



*Nucleoside: does not
include the phosphoric acid*

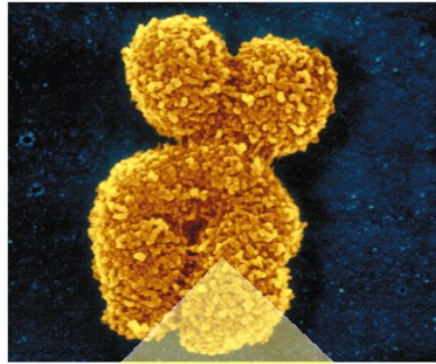
Nucleic Acids (DNA & RNA)

- DNA and RNA have different sugars (dexoyribose vs. ribose).
- There are only five bases found in DNA and RNA:
 - adenine (A),
 - guanine (G),
 - cytosine (C),
 - thymine (T found in DNA only), and
 - uracil (U found in RNA only).

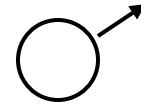
Genetics & DNA



XX



Chromosome



XY



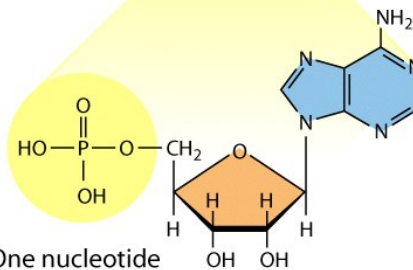
DNA double helix



Gene on a single strand of DNA

GGATATCCAAGC

Nucleotide sequence

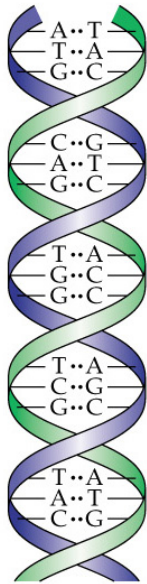


One nucleotide

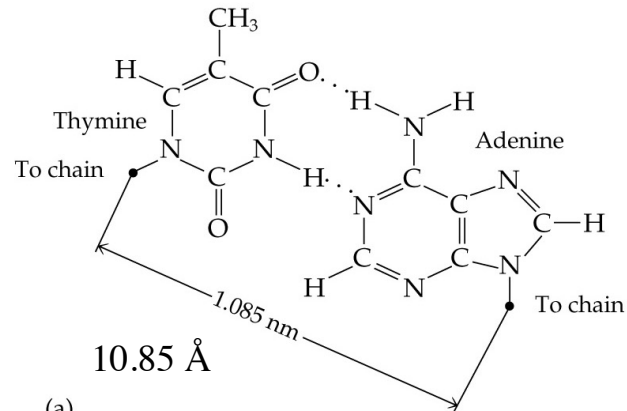
DNA: Size, Shape & Self Assembly

http://www.umass.edu/microbio/chime/beta/pe_alpha/atlas/atlas.htm

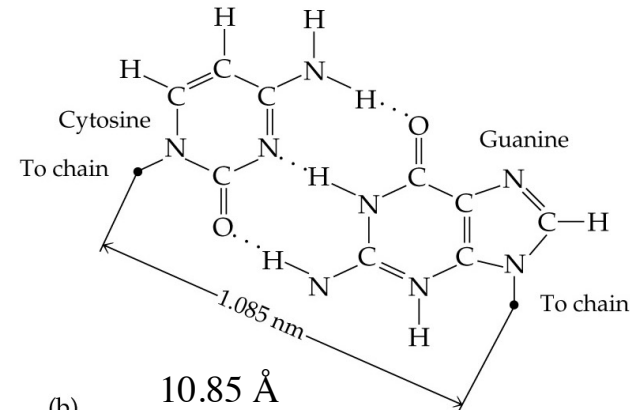
Views & Algorithms



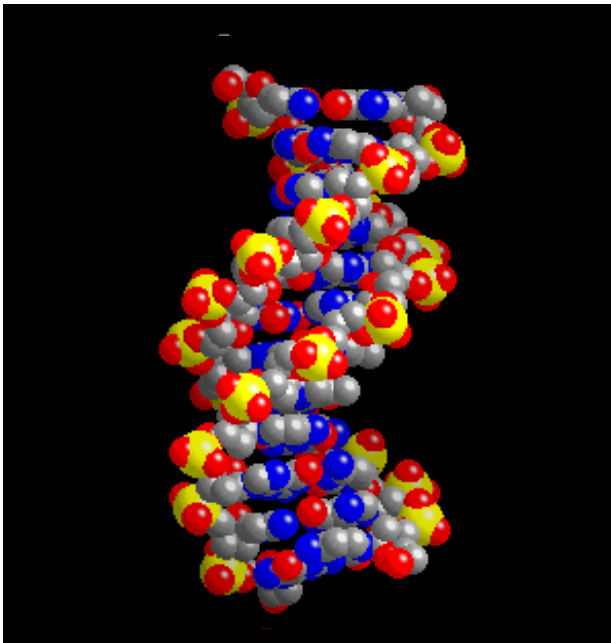
(a)



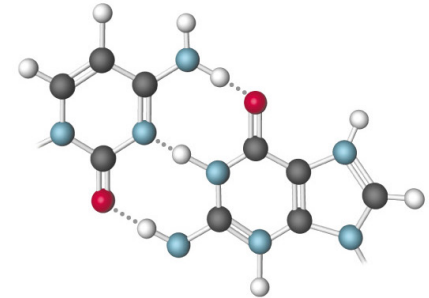
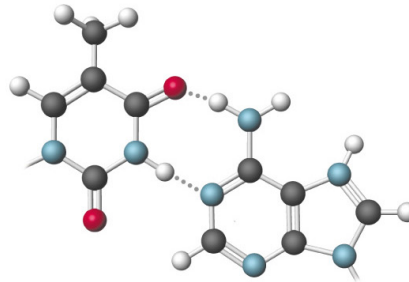
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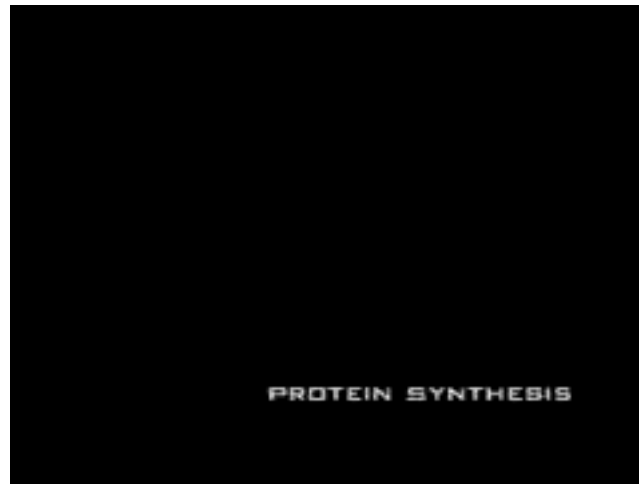
(b)



(c)



Protein Biosynthesis



<https://www.dnalc.org/resources/3d/09-how-much-dna-codes-for-protein.html>

Nucleus of cell



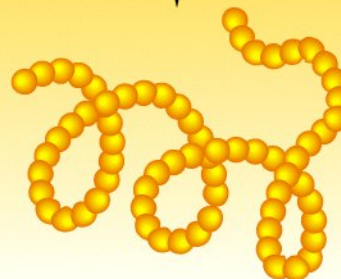
DNA

TRANSCRIPTION



RNA

TRANSLATION



Protein

~22,000 define
a human

RNA BIOLOGY

11th Annual Salk/Fondation Ipsen/Science Symposium on Biological Complexity
January 25 - 27, 2017 • Salk Institute for Biological Studies, La Jolla, CA

RNA does a lot more than simply act as a messenger between our DNA and the ribosomes that make proteins. RNA plays a role in controlling which genes are turned on or off, it provides that vital link between our DNA and the ribosomes that make proteins. This symposium is designed to help us learn more about the role of RNA in the biology of a cell, tissue, organ and a whole organism.

THE SYMPOSIUM WILL BE A SERIES OF LECTURES • **HEMATOLOGICAL "GENE" RESEARCHER** • **IMC LABORATORY OF MOLECULAR BIOLOGY, ON**

SESSION 1: RNA BIOLOGY
SPEAKER: [Name], [Institution]

SESSION 2: RNA BIOLOGY
SPEAKER: [Name], [Institution]

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ABSTRACT SUBMISSION DEADLINE: November 30, 2016 **REGISTRATION DEADLINE:** January 6, 2017

Poster design by [Name], Salk Institute

salk
Salk Institute for Biological Studies

Science
PUBLISHED BY

IPSEN

Central Dogma

DNA

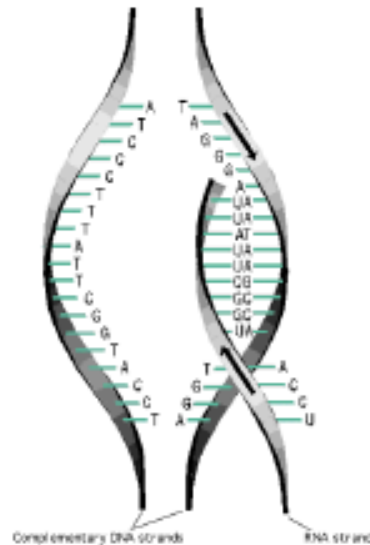


Transcription

mRNA

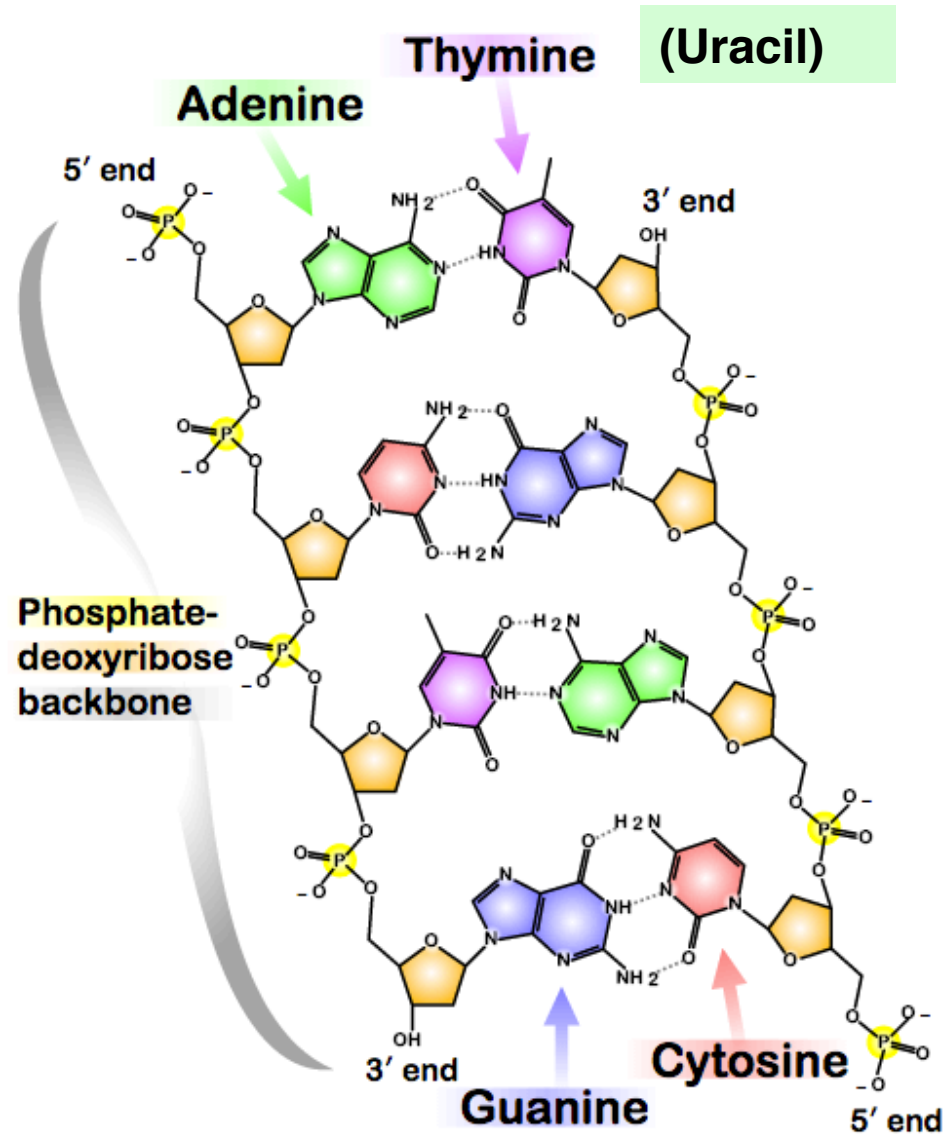
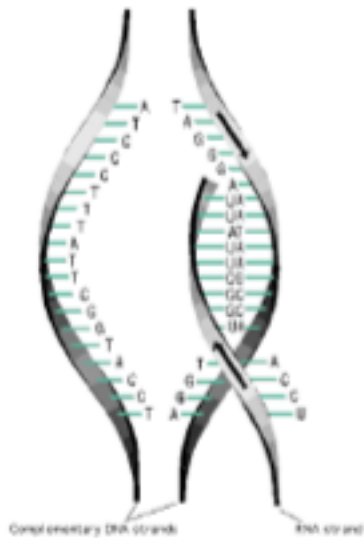
Translation

Protein



Amanda Ruby

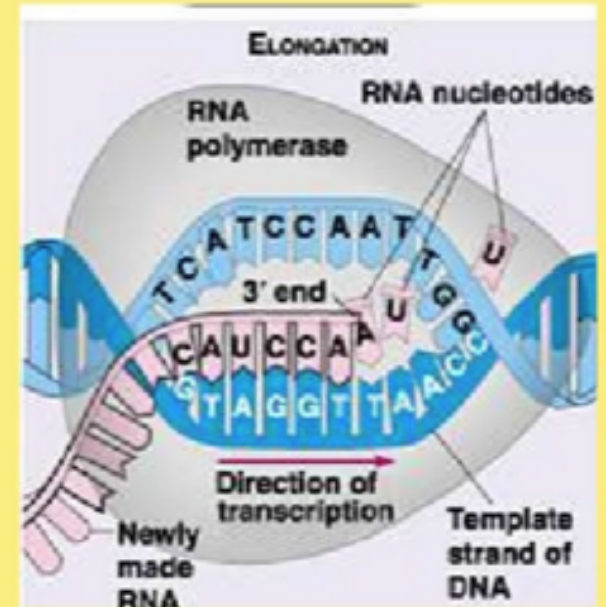
mRNA



Control secondary (DNA strands)

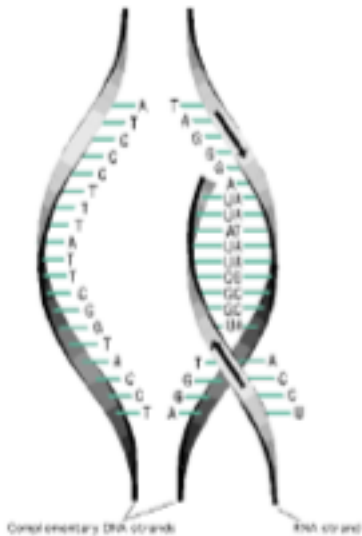
RNA strand

- **Sense strand** - the “other” strand, not transcribed.
- **Antisense strand** - the one mRNA attaches to, and is complimentary to.
- mRNA is similar to the sense strand, except T→U.



Antisense DNA from the left: GTAGGT...
mRNA: CAUCCA...

mRNA



DNA	Coding Strand (Codons)	5' >>> ----- T T C ----- >>> 3'
	Template Strand (Anti-codons)	3' <<< ----- A A G ----- <<< 5'
mRNA	Message (Codons)	5' >>> ----- U U C ----- >>> 3'
tRNA	Transfer (Anti-codons)	3' <<< A A G <<< 5'
Protein	Amino Acid	Amino >>> Phenylalanine >>> Carboxy

Coding Strand = Antisense strand: TTC

Anti-coding = Sense strand

mRNA:

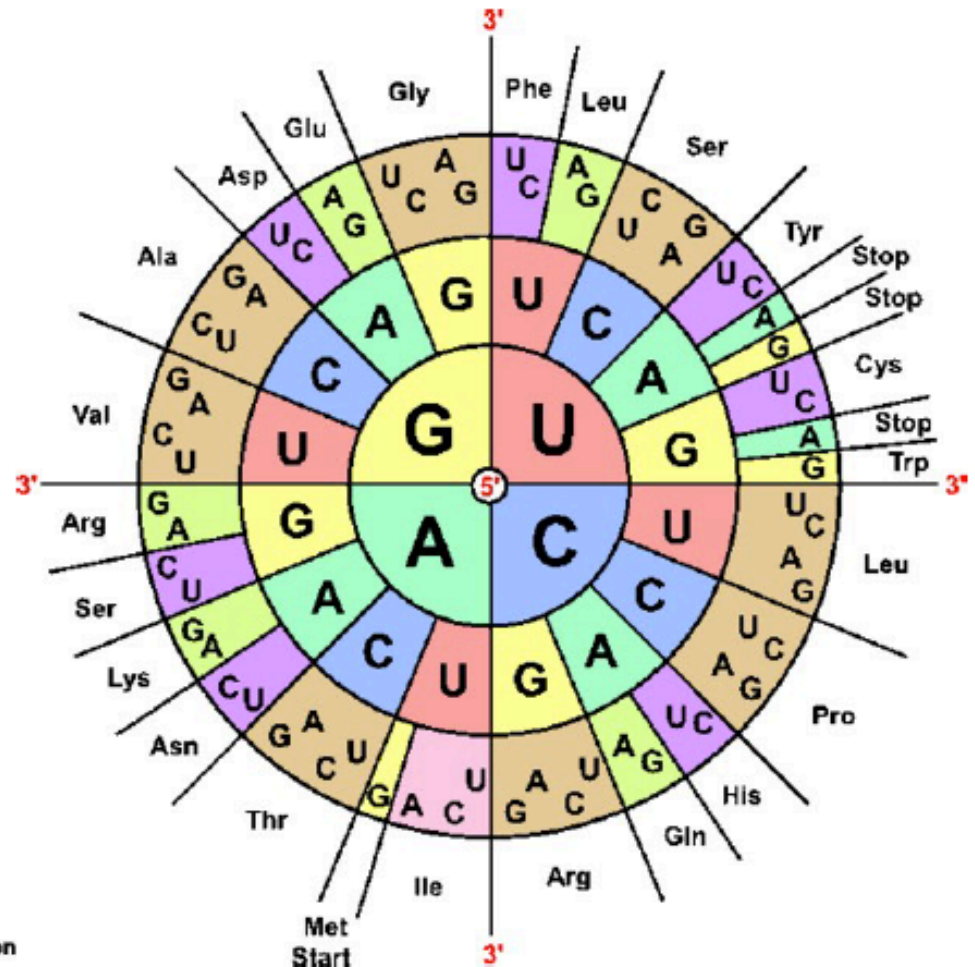
UUC

Protein Biosynthesis

Codons

- mRNA is translated in “chunks” of three, called **codons**
- The starting nucleotide is determined using bioinformatics to find the **reading frame**
- The genetic code is **degenerate**

(similar, but not identical)



→

5' AUG CAA CCC GAC UCC AGC 3' ← Codon
3' UAC GUU GGG CUG AGG UAG 5' ← AntiCodon
Met-Gln-Pro-Asp-Phe-Ser ← Amino Acids

Protein Biosynthesis

Codon Chart

		Second Letter					
		U	C	A	G		
1st letter	U	UUU Phe UUC UUA Leu UUG	UCU UCC Ser UCA UCG	UAU Tyr UAC UAA Stop UAG Stop	UGU Cys UGC UGA Stop UGG Trp	U C A G	3rd letter
	C	CUU CUC Leu CUA CUG	CCU CCC Pro CCA CCG	CAU His CAC CAA Gln CAG	CGU CGC Arg CGA CGG	U C A G	
	A	AUU AUC Ile AUA AUG Met	ACU ACC Thr ACA ACG	AAU Asn AAC AAA Lys AAG	AGU Ser AGC AGA Arg AGG	U C A G	
	G	GUU GUC Val GUA GUG	GCU GCC Ala GCA GCG	GAU Asp GAC GAA Glu GAG	GGU GGC Gly GGA GGG	U C A G	

Central Dogma

DNA

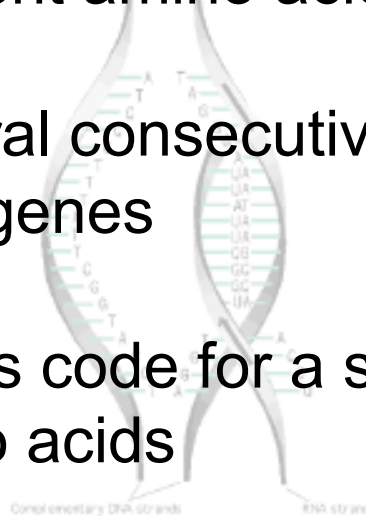
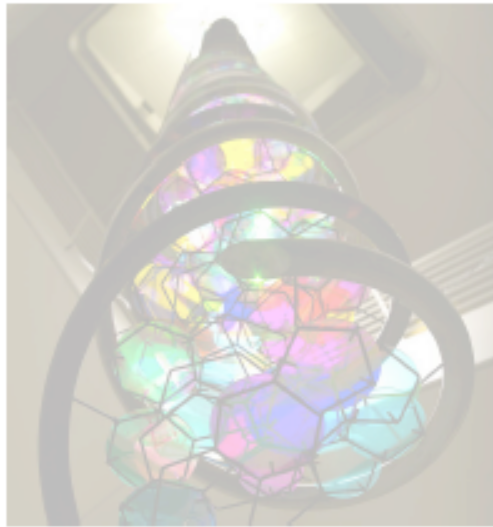
Several nucleic acids linked together form DNA

Three nucleic acids in a row form a codon, which codes for different amino acids

Several consecutive codons form genes

Genes code for a sequence of amino acids

Several amino acids linked together form proteins



Protein



~22,000 define a human

1865

DNA: Genetics & Genomics

Timelines

The screenshot shows a web browser window with the URL `unlockinglifescode.org/timeline?tid=4`. The page features a navigation bar with links: EXPLORE, ABOUT, LEARN, TRAVELING EXHIBIT, MEDIA, and CONNECTIONS. A prominent orange box on the left reads "TIMELINE OF THE HUMAN GENOME". Below this is a circular portrait of Gregor Mendel, with a "VIEW DETAILS" link underneath. To the right, a detailed diagram illustrates Mendel's pea plant experiment. It shows a P generation of a purple flower (PP) crossed with a white flower (pp). The resulting F1 generation consists of all purple flowers (Pp). One F1 plant (Pp) is then self-crossed, leading to the F2 generation, which shows a 3:1 phenotypic ratio of purple (PP or Pp) to white (pp) flowers. The diagram includes Punnett squares for both the P and F1 generations. An orange box at the bottom right of the diagram area contains the text: "1865 | Gregor Mendel, the father of modern genetics, presents his research on experiments in plant hybridization".

TIMELINE OF THE HUMAN GENOME

1865 | Gregor Mendel, the father of modern genetics, presents his research on experiments in plant hybridization

Gregor Mendel (1822-1884)

<https://www2.edc.org/weblabs/Mendel/MendelMenu.html>

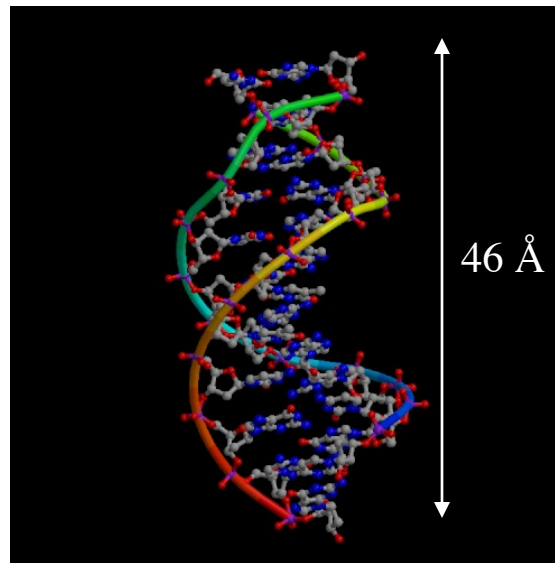
1953

DNA: Molecular Discovery

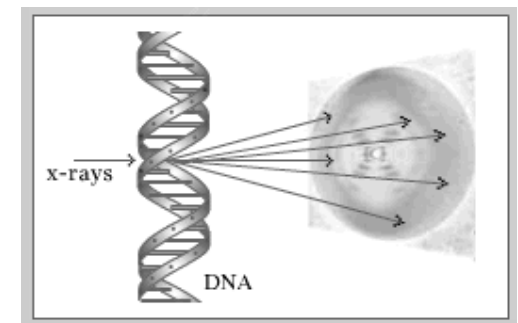
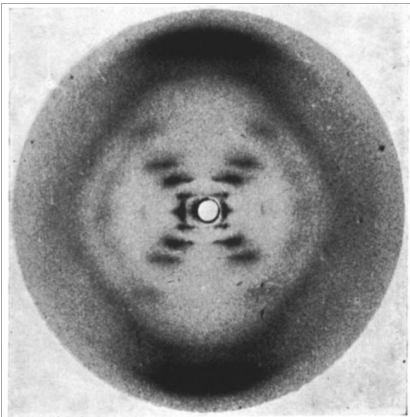
X-Ray Crystal Structure

<http://info.bio.cmu.edu/courses/03231/ProtStruc/ProtStruc.htm>

β -DNA: Rosalind Franklin



12 base sequence



http://molvis.sdsc.edu/pdb/dna_b_form.pdb

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

²Young, F. E., Gerrard, H., and Jensen, W., *Phil. Mag.*, **40**, 149 (1925).

³Langseth-Higgins, M. S., *Mon. Not. Roy. Astr. Soc., Geophys. Supp.*, **8**, 288 (1950).

⁴Van der Waals, W. S., *Woods Hole Papers in Phys. Oceanogr. Meteor.*, **11** (3) (1950).

⁵Ekman, V. W., *Archiv. Mat. Astron. Fysik. (Stockholm)*, **2** (11) (1905).

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 Corey¹. They kindly made their manuscript available to us in advance of publication. Their model consists of three intertwined 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.

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 diester groups joining β -D-deoxyribofuranose 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 Furbert's 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 Furbert's 'standard configuration', the sugar being roughly perpendicular to the attached base. There

is a residue on each chain every 3.4 Å. 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 Å. The distance of a phosphorus atom from the fibre axis is 10 Å. 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^{2,3} 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^{4,5} on deoxyribose 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 it 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 interatomic 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

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.

¹Pauling, L., and Corey, R. B., *Nature*, **157**, 546 (1953); *Proc. U.S. Nat. Acad. Sci.*, **28**, 81 (1953).

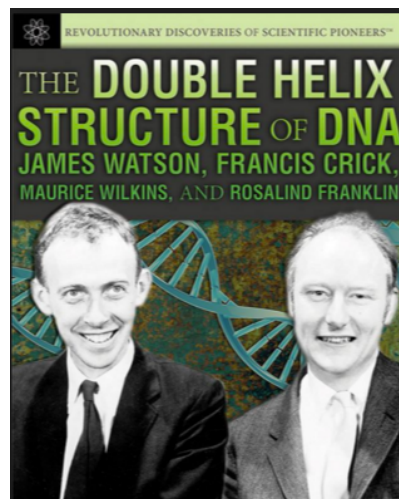
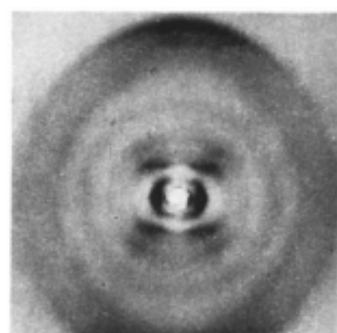
²Furberg, S., *Acta Chem. Scand.*, **6**, 684 (1952).

³Chargaff, E., for references see *Excerpta Med.*, **8**, 402 (1952).

⁴Wyatt, G. R., *J. Gen. Physiol.*, **26**, 201 (1952).

⁵Astbury, M. T., *Synop. Soc. Exp. Biol.*, **1**, Nucleic Acid, 66 (Camb. Univ. Press, 1947).

⁶Wilkins, M. H. F., and Randall, J. T., *Biochim. et Biophys. Acta*, **20**, 182 (1953).



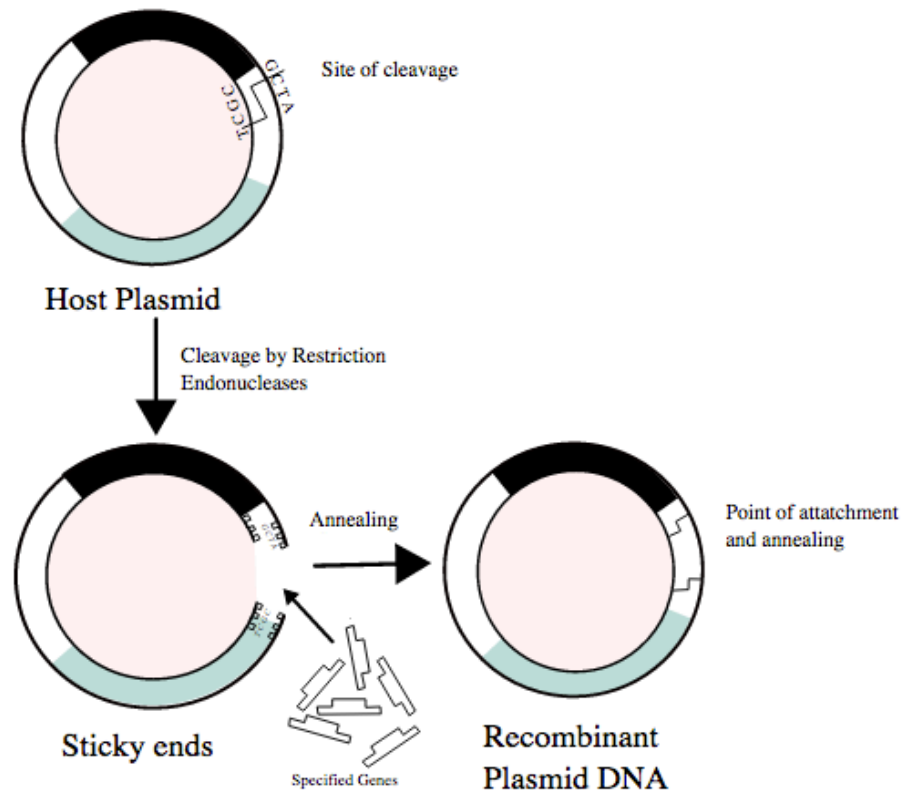
This figure is purely diagrammatic. The two ribbons symbolize the two phosphate-sugar chains, and the horizontal rods the pairs of bases holding the chains together. The vertical line marks the fibre axis.

1975

Restriction Enzymes / Recombinant DNA

Berg, Boyer, Cohen, and many others

<http://nar.oxfordjournals.org/content/early/2013/10/18/nar.gkt990.full>



1989

PCR: Polymerase Chain Reaction

Kary Mullis, Cetus-Chiron-Roche, Emeryville

The Nobel Prize in Chemistry 1993

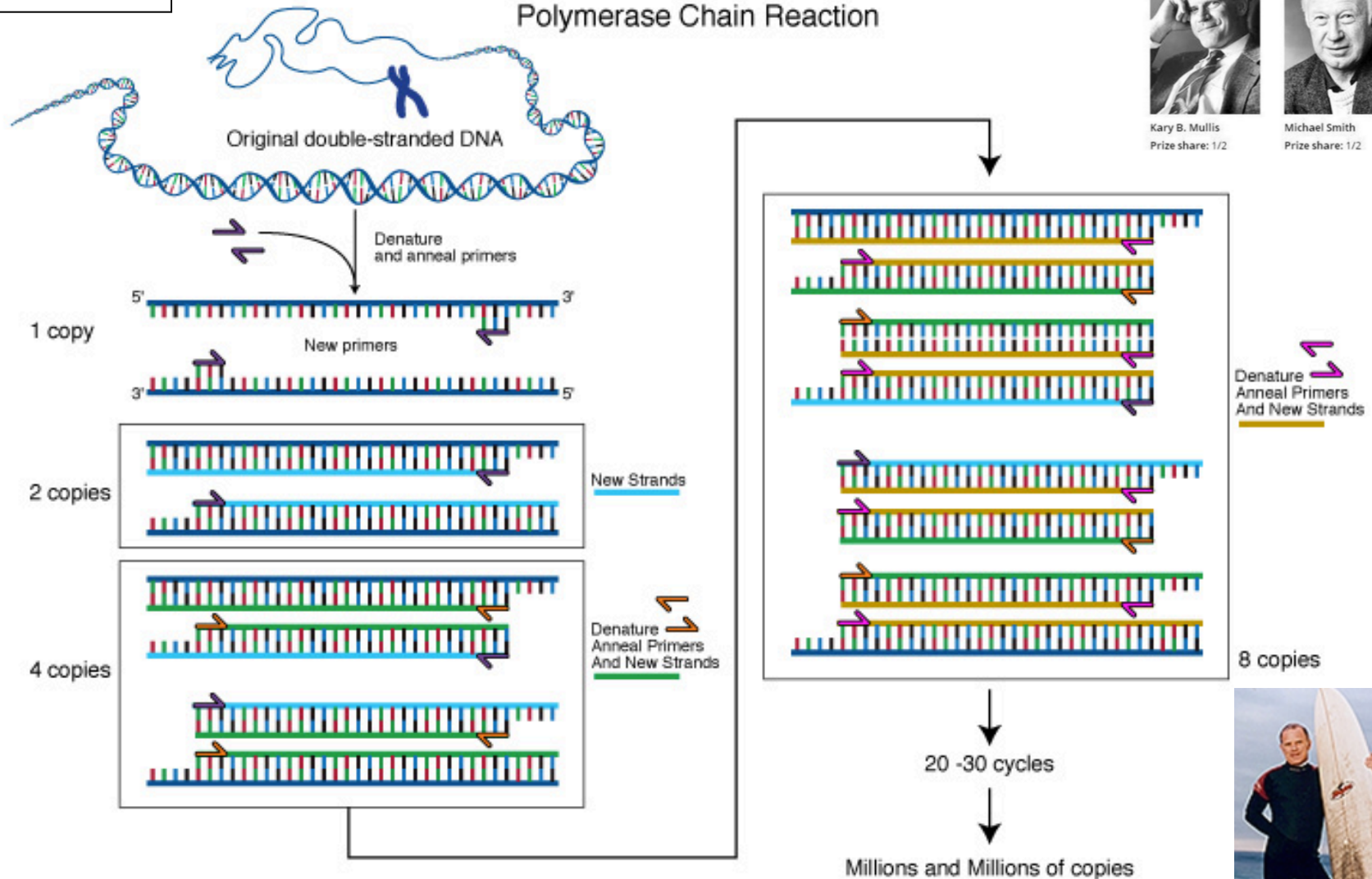


Kary B. Mullis
Prize share: 1/2



Michael Smith
Prize share: 1/2

Polymerase Chain Reaction



The Human Genome Project:

Exploring our Molecular Selves.

[DYNAMIC TIMELINE](#)[QUICK SEARCH](#)

3D
Animation



Laura
screen



EXIT

[BACK](#)[MORE INFORMATION](#)[MORE ON THIS YEAR](#)

1994 FLAYR SAVR tomato



The FDA approved the sale of the first genetically modified food — the FLAYR SAVR tomato, deeming it as safe as conventionally-bred tomatoes.

The FDA's decision on the FLAYR SAVR tomato — marketed by Calgene, Inc. of Davis, California — marked the first time the agency evaluated a food that was genetically engineered. FLAYR SAVR tomatoes are modified to stay firm after harvest, so they can be left on the vine longer before shipping. The FDA decided the change in the tomatoes was not great enough to warrant mandated labeling describing the alteration.



Roger
Salquist
Chairman
CEO
Calgene



Genes, Variation
& Human History 7



The Future of
Research & Medicine



How to Sequence
a Genome 10



ELSI 11



Glossary 12

1995

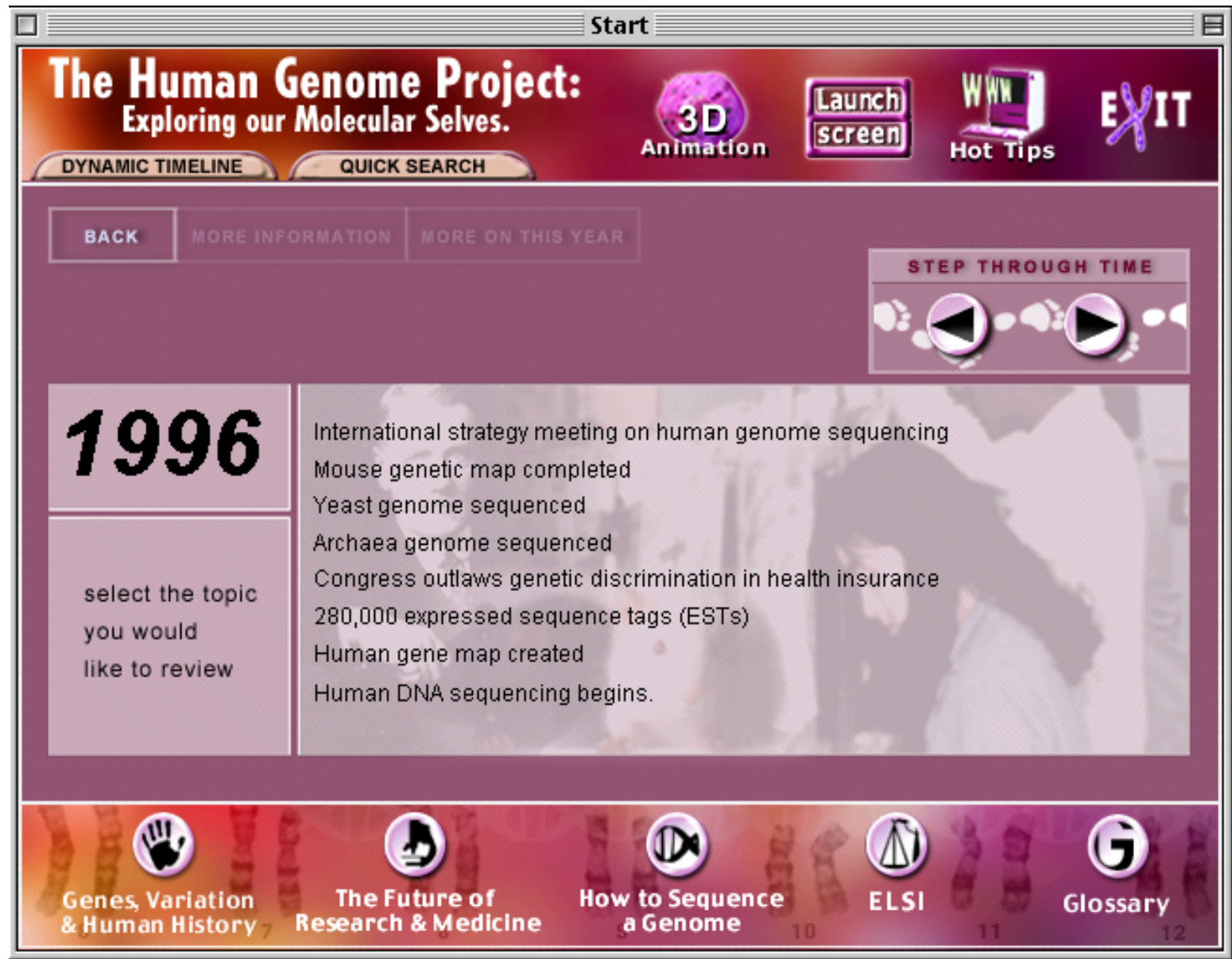
Genetic Fingerprinting



Blood on glove found on Simpson's property appeared to contain genetic markers of Simpson and both victims.



OJ Simpson and the bloody glove.



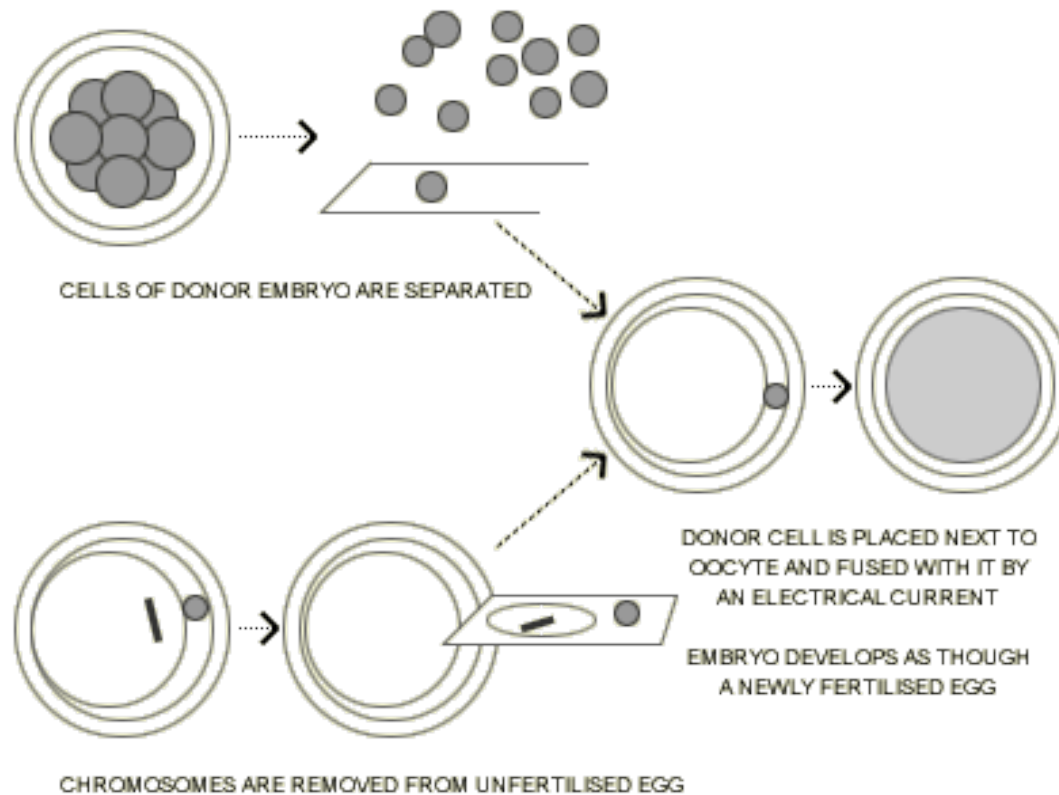
<http://www.genome.gov/25019879>
<http://unlockinglifescode.org/timeline?tid=4>

1996



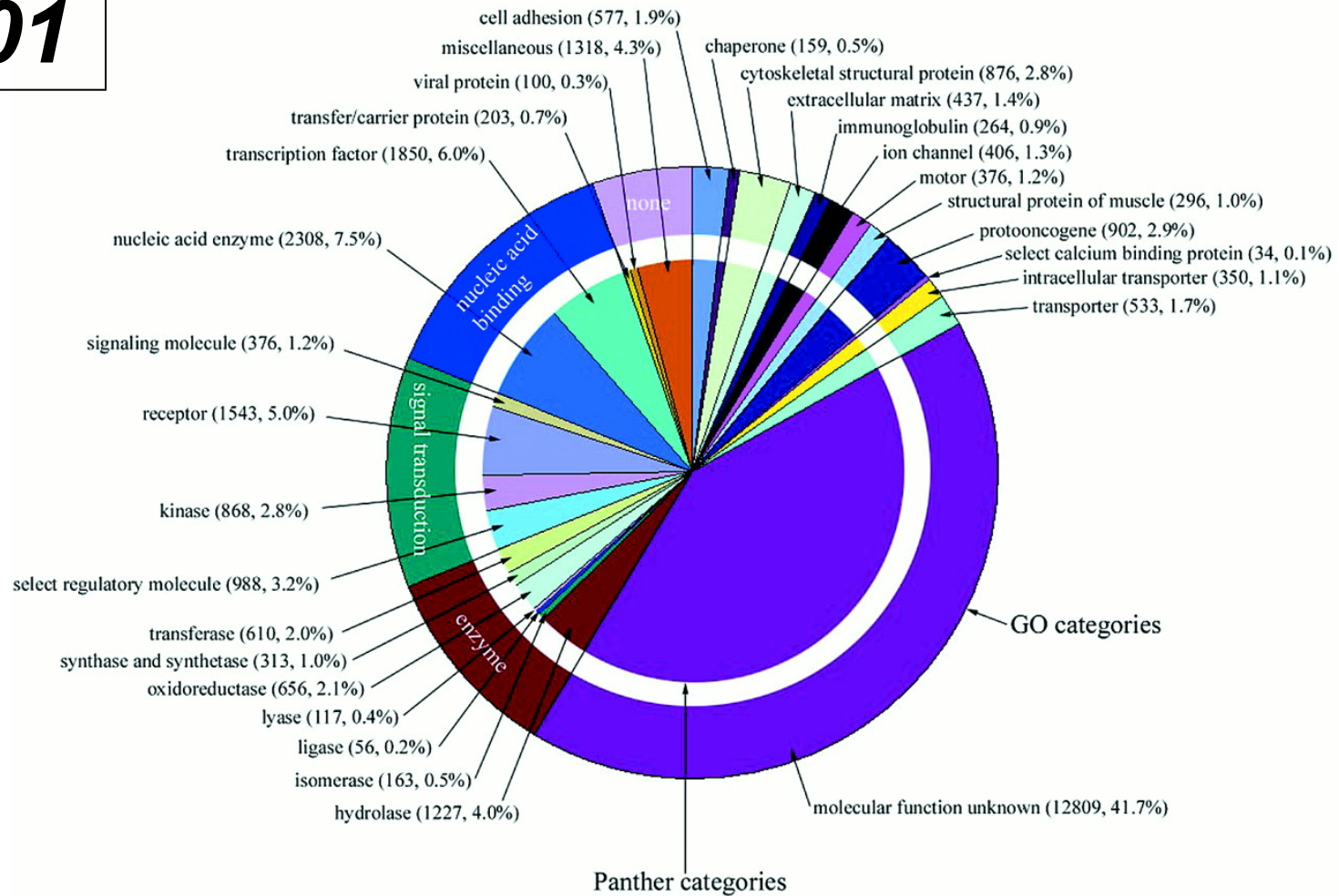
CLONING

*Hello
Dolly!*



Human Genome: Distribution of the molecular functions of 26,383 human genes.

2001

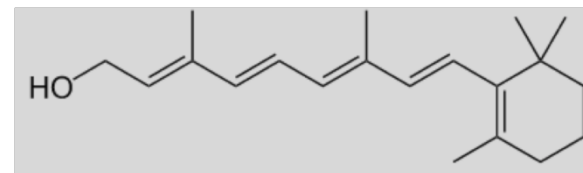
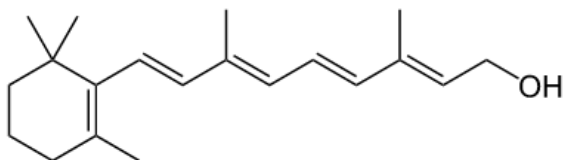


J. Craig Venter et al. Science 2001;291:1304-1351

2001

Golden Rice

<http://www.goldenrice.org/>



Hunan Study 2008

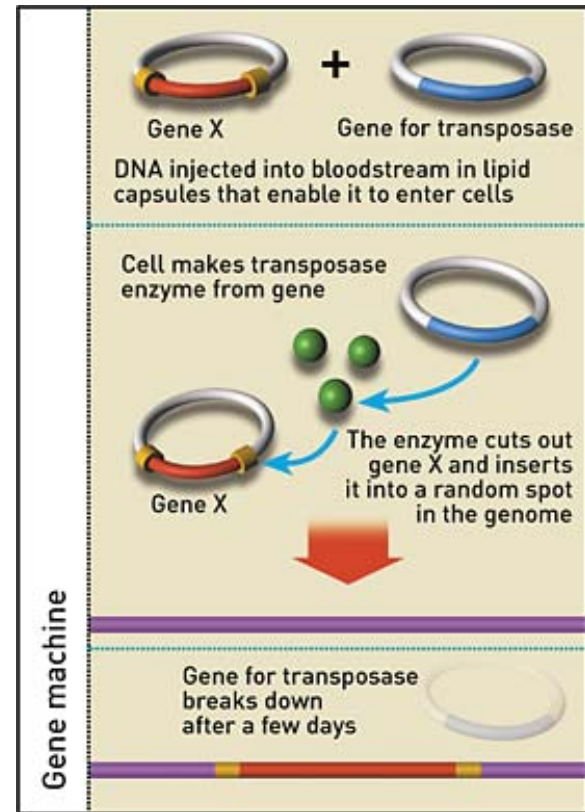
Golden Rice Paper 2012

Patents for Humanity Awards 2015

<http://news.sciencemag.org/asiapacific/2013/09/golden-rice-not-so-golden-tufts>

Transgenic Crops

Genetically Modified Organisms (GMOs)



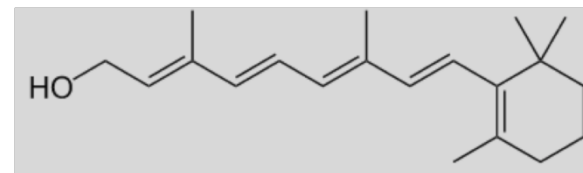
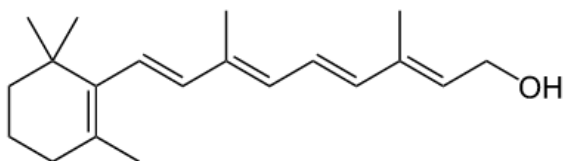
<http://www.greenpeace.org/international/Global/international/publications/agriculture/2013/458%20-%20Golden%20Illusion-GE-goldenrice.pdf>

<http://www.i-sis.org.uk/rice.php>

2015

Golden Rice

<http://www.goldenrice.org/>



Hunan Study 2008

WITHDRAWN July 2015

Patents for Humanity Awards 2015

<http://news.sciencemag.org/asiapacific/2013/09/golden-rice-not-so-golden-tufts>

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β -Carotene in Golden Rice is as good as β -carotene in oil at providing vitamin A to children^{1,2,3,4}

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This Article

First published August
1, 2012, doi: 10.3945/
ajcn.111.030775

WITHDRAWN:

For lack of evidence that all human participants provided full consent

supported

by Massachusetts Court (August 3, 2015)

(0.3 mg), GR β -carotene (0.6 mg), and spinach β -carotene (1.4 mg) to retinol were 2.0, 2.3, and 7.5 to 1 by weight, respectively.

Conclusions: The β -carotene in GR is as effective as pure β -carotene in oil and better than that in spinach at providing vitamin A to children. A bowl of ~100 to 150 g cooked GR (50 g dry weight) can provide ~60% of the Chinese Recommended Nutrient Intake of vitamin A for 6-8-y-old children. This trial was registered at www.clinicaltrials.gov as [NCT00680212](https://clinicaltrials.gov/ct2/show/study/NCT00680212).

+ Google Scholar
+ PubMed
+ Agricola
- Social Bookmarking

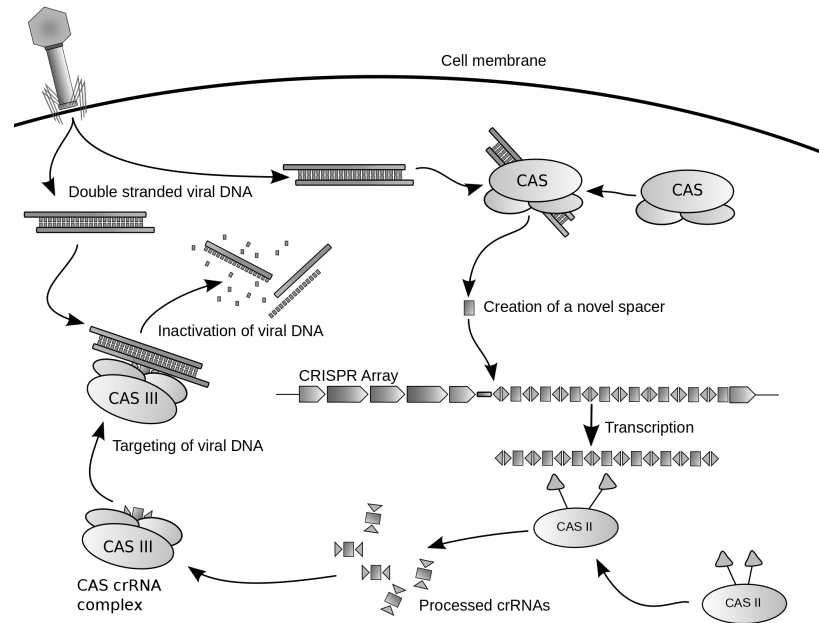


2012

Genome Editing / CRISPR-Cas9

<https://www.youtube.com/watch?v=2pp17E4E-O8>

<https://www.youtube.com/watch?v=SuAxDVBt7kQ>

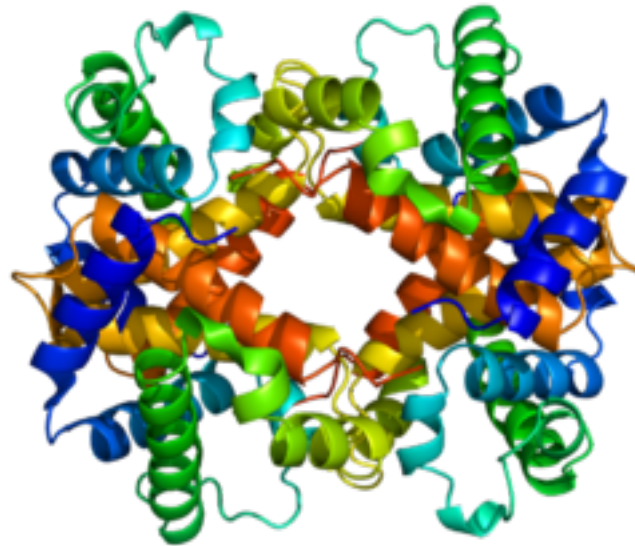


2016

Genome Editing / CRISPR-Cas9

Target

β -Thalassemia: Shortage of β -globin Protein



Normal β -globin

<https://www.dnalc.org/resources/3d/17-sickle-cell.html>

2016

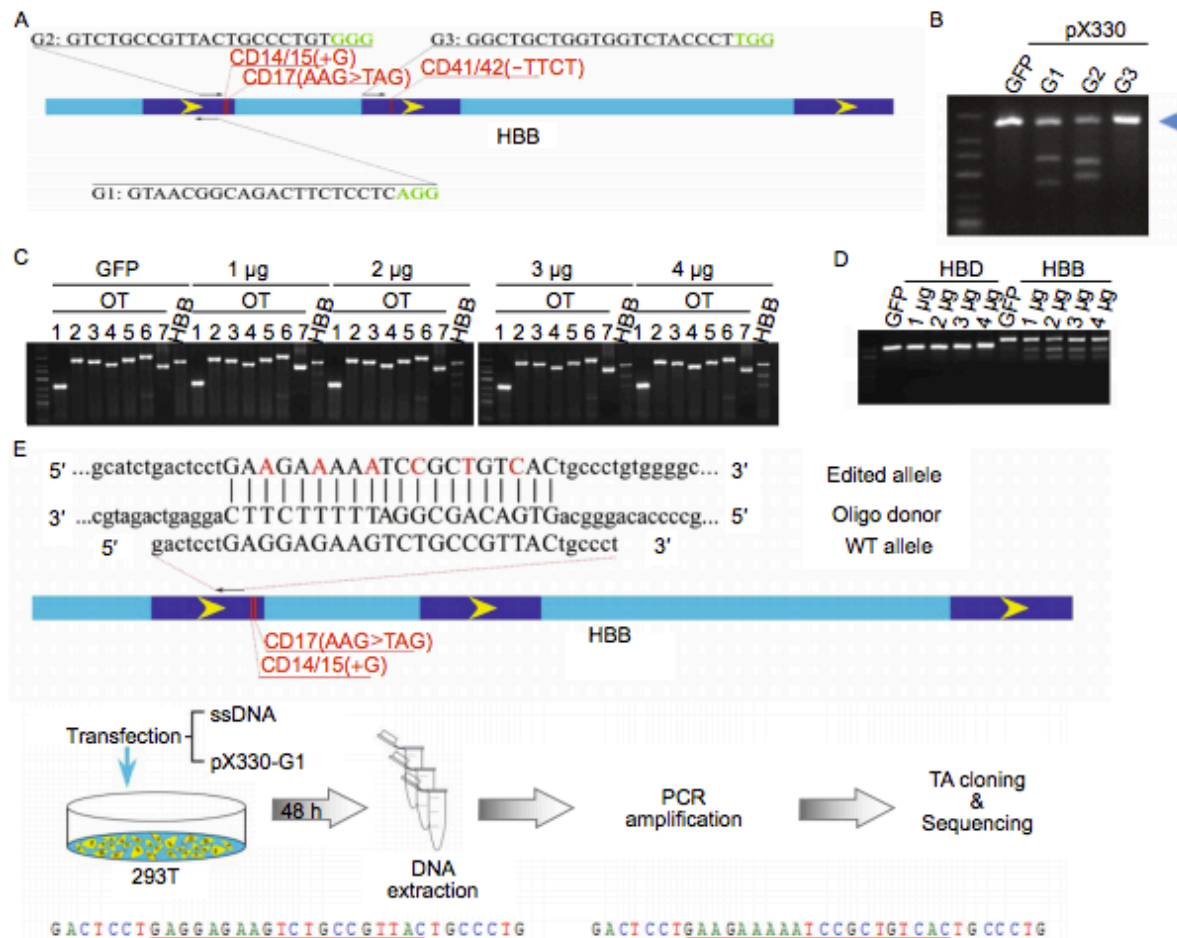
Genome Editing / CRISPR-Cas9

β -Thalassemia / Human Embryo Research

<http://chemconnections.org/general/chem121/Gene%20Editing/Gene%20Editing%202015-0153.pdf>

CRISPR/Cas9-mediated gene editing in human tripronuclear zygotes

RESEARCH ARTICLE



Protein & Cell

Genetic Fingerprinting

1985

**500
nanograms**

Amount of DNA needed for fingerprinting when the technique was first published in 1985. It corresponds to about one drop of blood or 100,000 cells.

**WHEN DNA IS
LYING**

**0.1
nanogram**

The amount that, in some cases, suffices today. It corresponds to about 20 cells, a number that could be found in a fingerprint.

2016

- Forensics
- Paternity
- Military-ID
- Food
- Wine
- Anthropology
- Medical
Diagnosis



Fig 1. Storing the total amount of information encoded in DNA in the biosphere, 5.3×10^{31} megabases (Mb), would require approximately 1021 supercomputers with the average storage capacity of the world's four most powerful supercomputers.

5.3×10^{31} Megabases of DNA

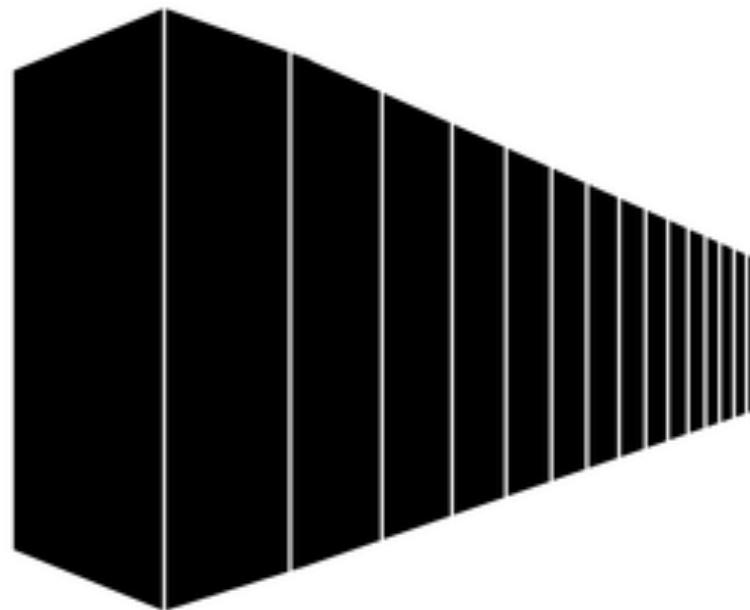
=

10^{21} Supercomputers

2016



=



<http://journals.plos.org/plosbiology/article?id=10.1371/journal.pbio.1002168#pbio-1002168-g001>

Landenmark HKE, Forgan DH, Cockell CS (2015) An Estimate of the Total DNA in the Biosphere. PLoS Biol 13(6): e1002168. doi:10.1371/journal.pbio.1002168

<http://127.0.0.1:8081/plosbiology/article?id=info:doi/10.1371/journal.pbio.1002168>

Table 1. The total DNA content in the biosphere

	DNA amount (Mb)
Prokaryotes	$1.6 (1.1) \times 10^{31}$
Unicellular eukaryotes	$1.3 (0.9) \times 10^{29}$
Fungi	$1.7 (3.4) \times 10^{27}$
Animals	$4.2 (1.5) \times 10^{29}$
Plants	$3.6 (3.4) \times 10^{31}$
Viruses	$4.0 (3.4) \times 10^{29}$
Total	$5.3 (3.6) \times 10^{31}$

doi:10.1371/journal.pbio.1002168.t001

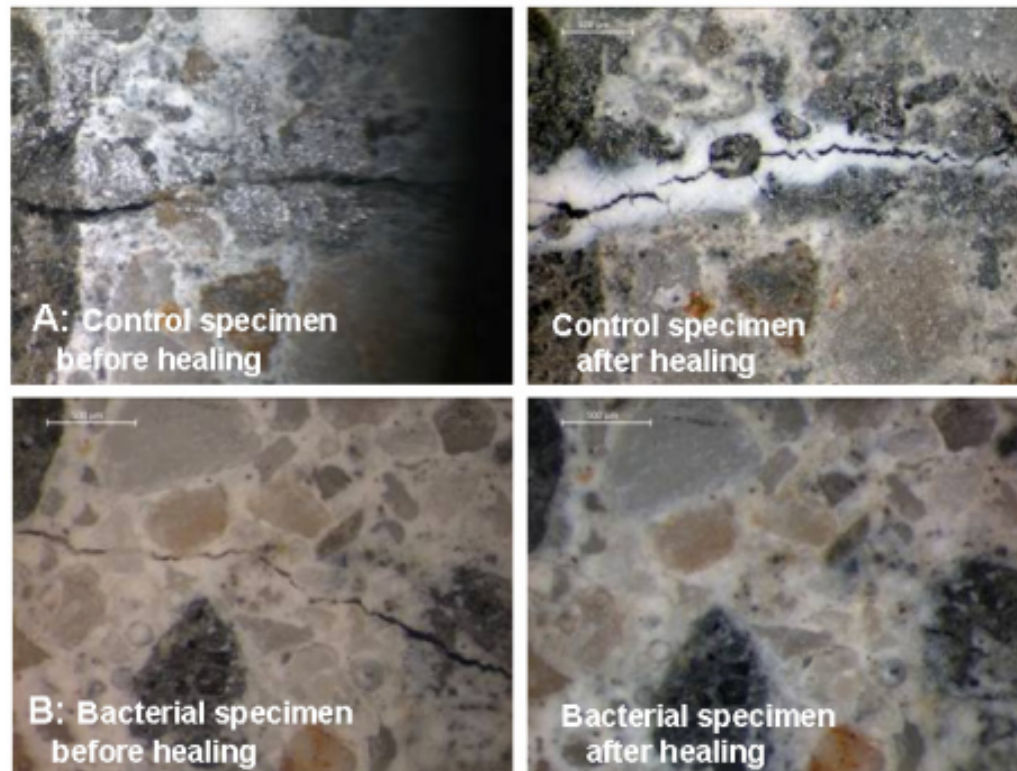
Landenmark HKE, Forgan DH, Cockell CS (2015) An Estimate of the Total DNA in the Biosphere. PLoS Biol 13(6): e1002168. doi:10.1371/journal.pbio.1002168

<http://127.0.0.1:8081/plosbiology/article?id=info:doi/10.1371/journal.pbio.1002168>

2016

Bioengineering:
Structural Materials & Molecules
Bacteria & Yeast
Healing Concrete

<http://heronjournal.nl/56-12/1.pdf>

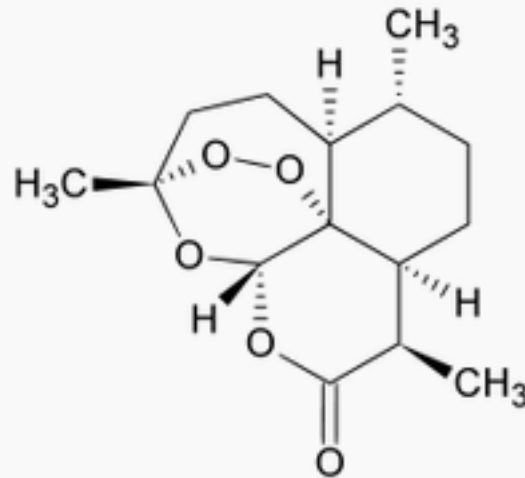


**2017-
2019**

Bioengineering: Bacteria, Yeast & Chemical Synthesis

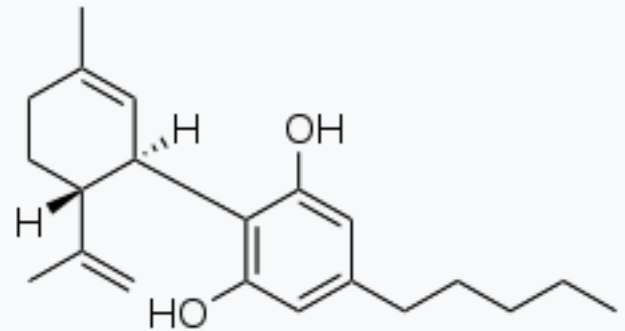
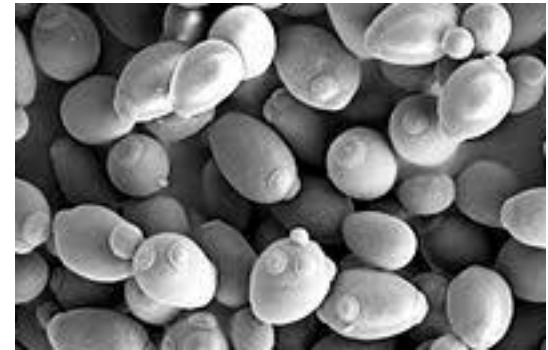


Chinese Wormwood
(*Artemisia annua*)



anti-malarial

Brewer's Yeast
(*Saccharomyces cerevisiae*)



cannabadiol (CBD)