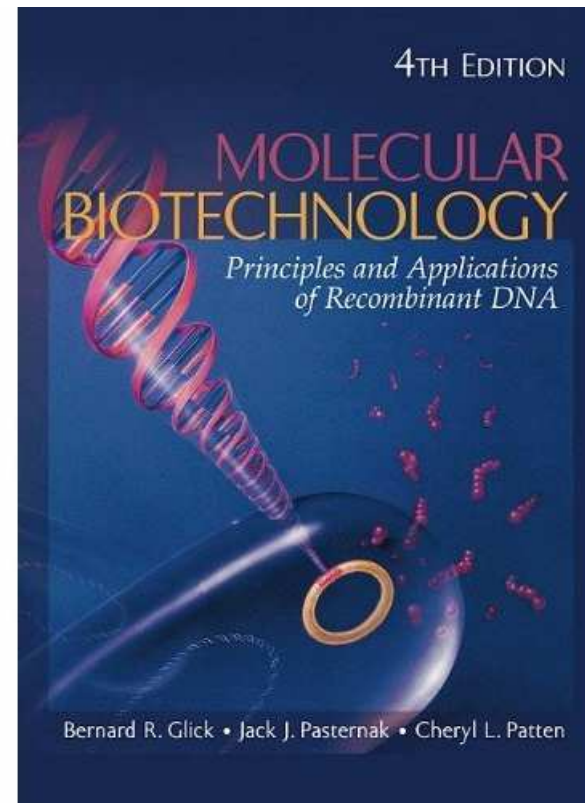


# Genetic a protein engineering

- Book: Glick, Pasternak, Molecular Biotechnology, *Principles and application of recombinant DNA*
- 4th edition 2010



MBU Třeboň  
Martin Tichý  
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Roman Sobotka  
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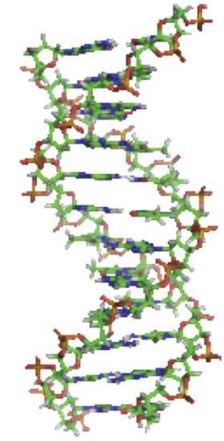
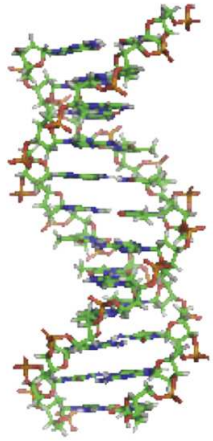
UOCHB Praha  
Iva Pichová  
iva.pichova@uochb.cas.cz

Lab  
?

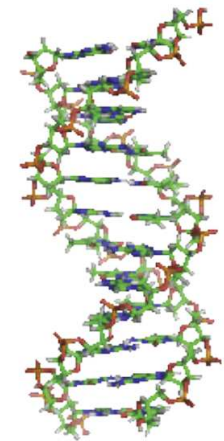
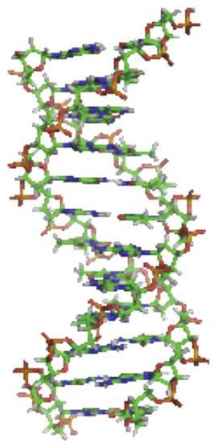
Exam  
written, 20 questions, 90 minutes



What is genetic engineering?



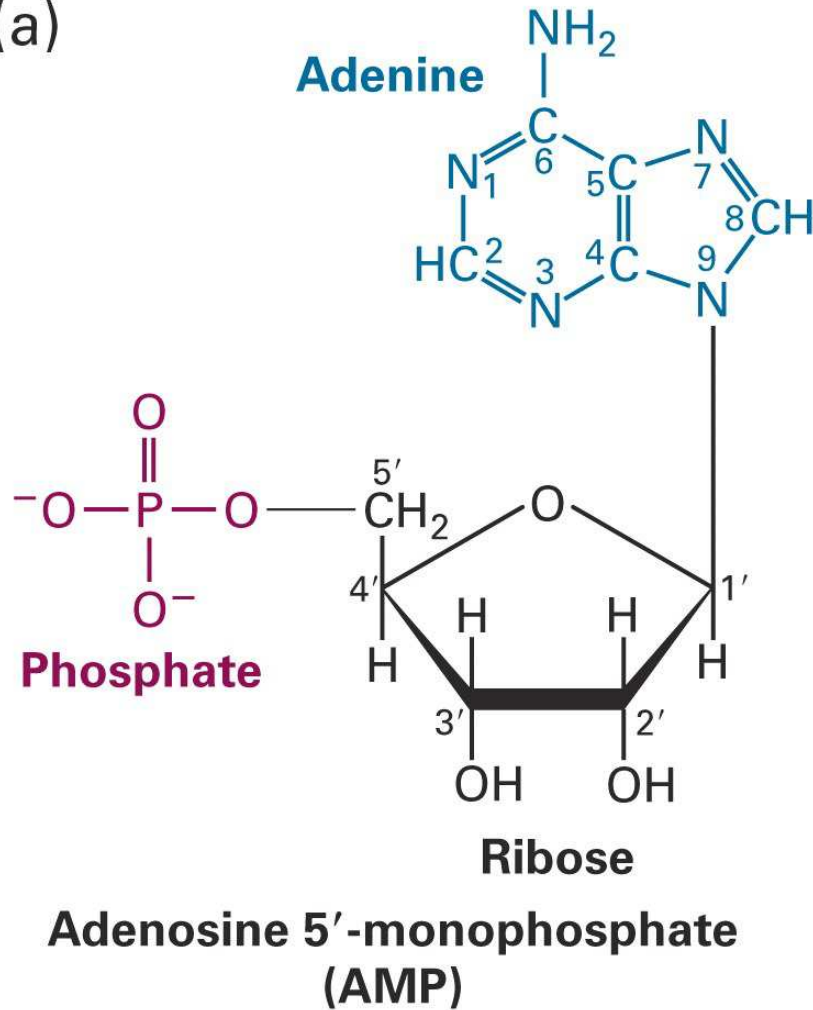
**Genetic Engineering Is  
Manipulating DNA!**



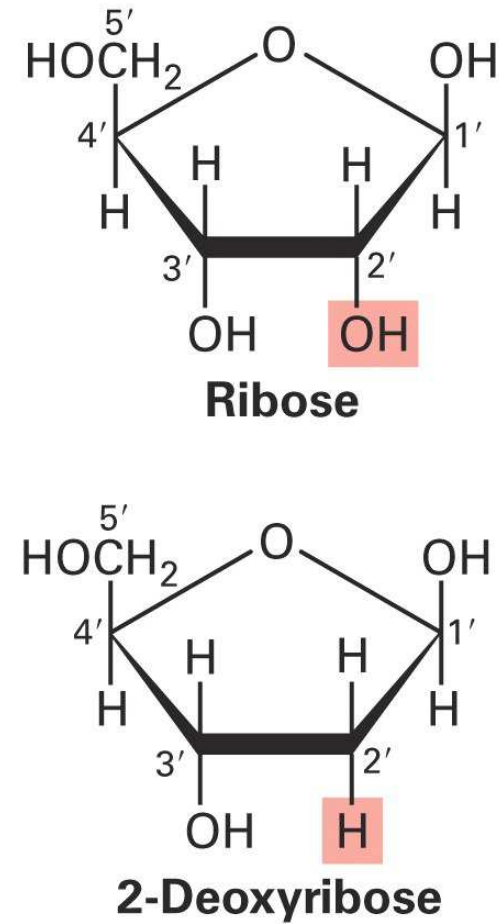


# Nucleic Acids - DNA and RNA

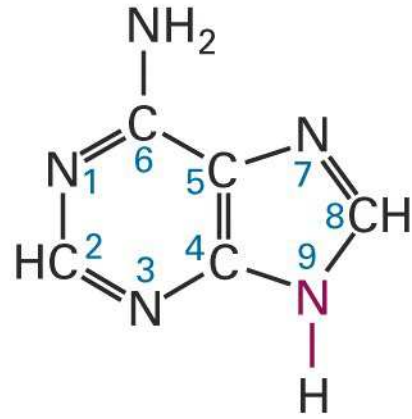
(a)



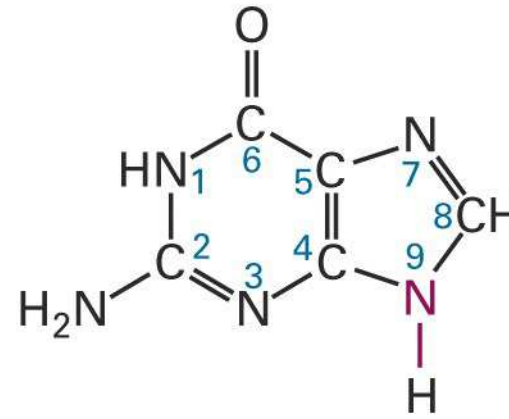
(b)



## PURINES

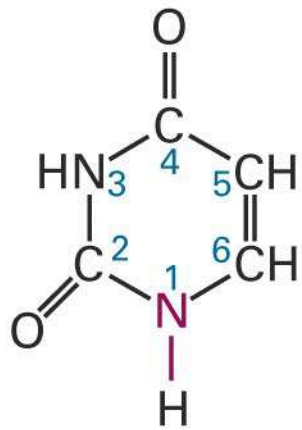


**Adenine (A)**

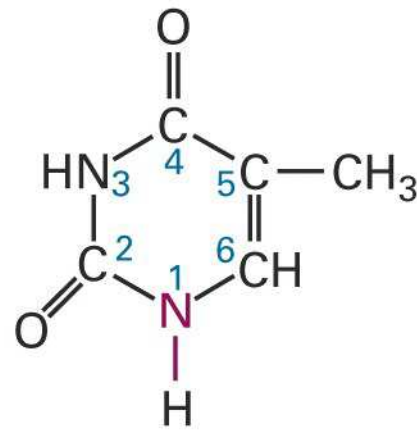


**Guanine (G)**

## PYRIMIDINES



**Uracil (U)**

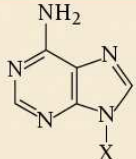
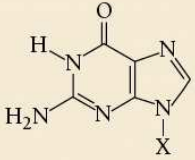
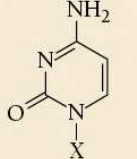
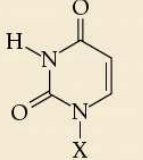
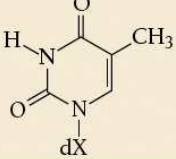


**Thymine (T)**



**Cytosine (C)**

**Table 3-1 Names and Abbreviations of Nucleic Acid Bases, Nucleosides, and Nucleotides**

Base Formula	Base (X = H)	Nucleoside (X = ribose <sup>a</sup> )	Nucleotide <sup>b</sup> (X = ribose phosphate <sup>a</sup> )
	Adenine Ade A	Adenosine Ado A	Adenylic acid Adenosine monophosphate AMP
	Guanine Gua G	Guanosine Guo G	Guanylic acid Guanosine monophosphate GMP
	Cytosine Cyt C	Cytidine Cyd C	Cytidylic acid Cytidine monophosphate CMP
	Uracil Ura U	Uridine Urd U	Uridylic acid Uridine monophosphate UMP
	Thymine Thy T	Deoxythymidine dThd dT	Deoxythymidylic acid Deoxythymidine monophosphate dTMP

DNA + RNA

DNA + RNA

DNA + RNA

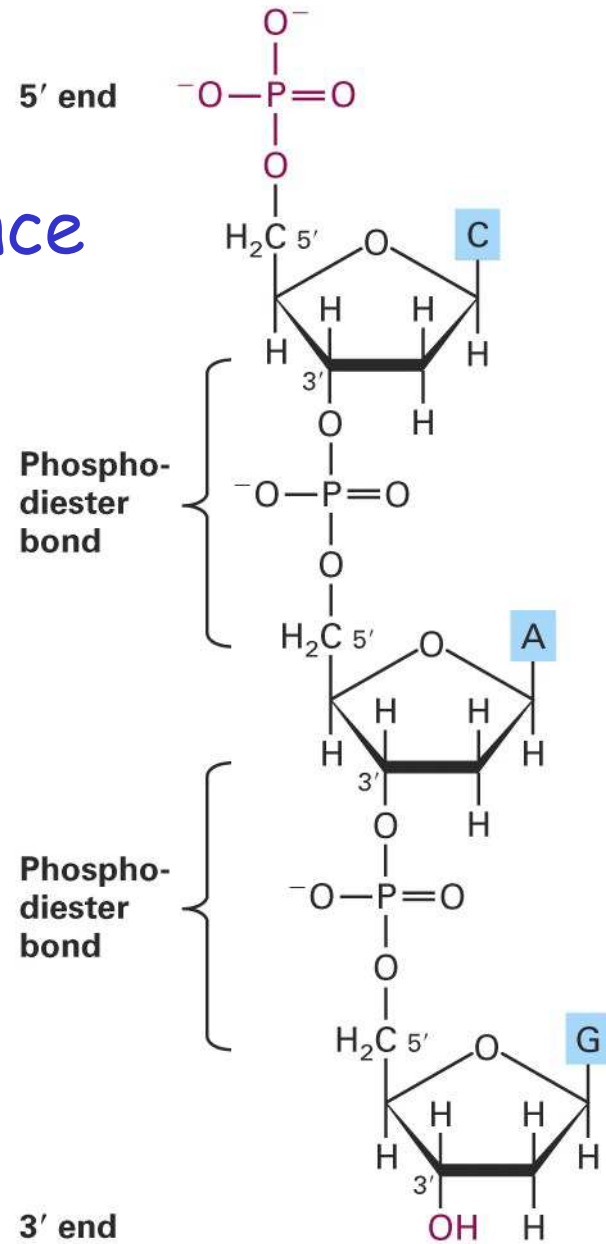
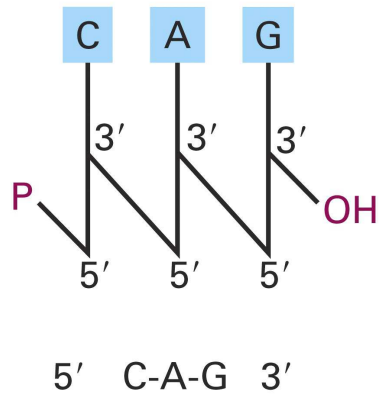
RNA ←

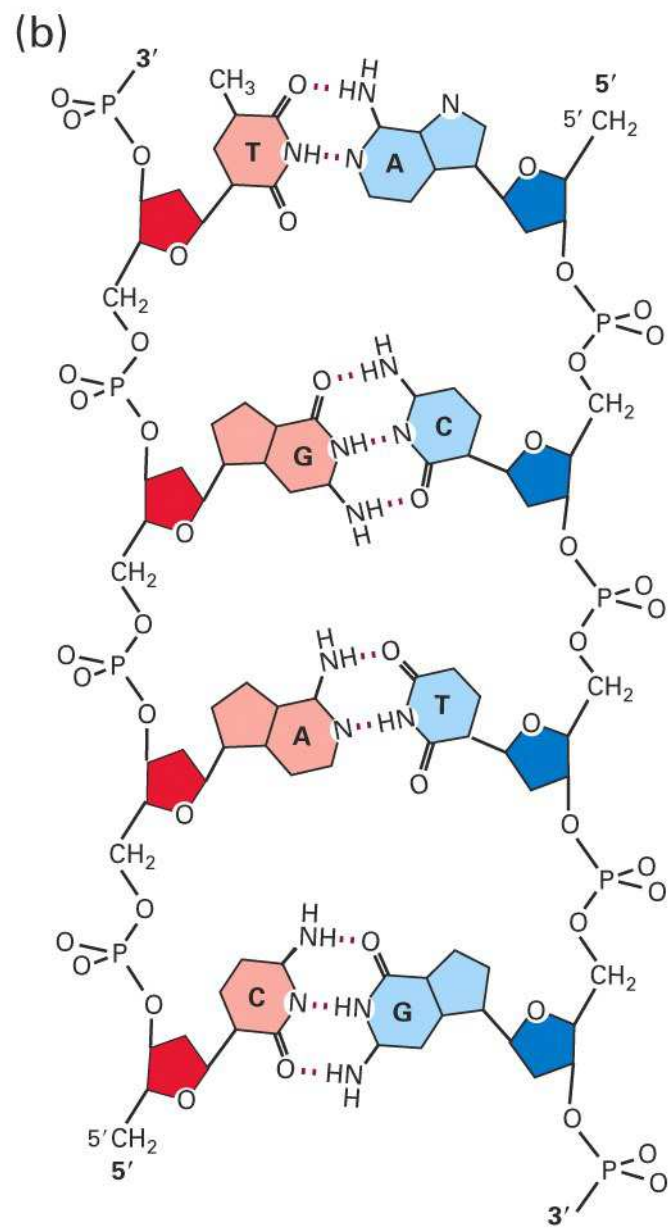
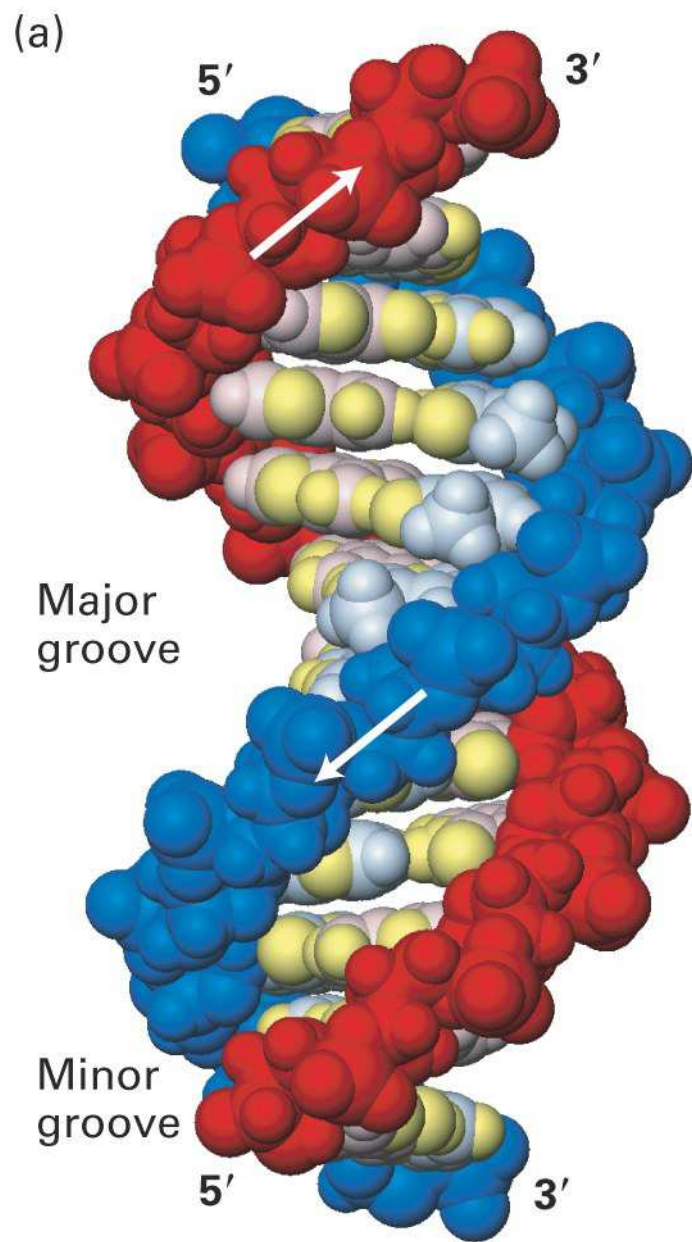
DNA ←

<sup>a</sup>The presence of a 2'-deoxyribose unit in place of ribose, as occurs in DNA, is implied by the prefixes "deoxy" or "d." For example, the deoxy-nucleoside of adenine is deoxyadenosine or dA. However, for thymine-containing residues, which rarely occur in RNA, the prefix is redundant and may be dropped. The presence of a ribose unit may be explicitly implied by the prefix "ribo."

<sup>b</sup>The position of the phosphate group in a nucleotide may be explicitly specified as in, for example, 3'-AMP and 5'-GMP.

# DNA structure -> sequence



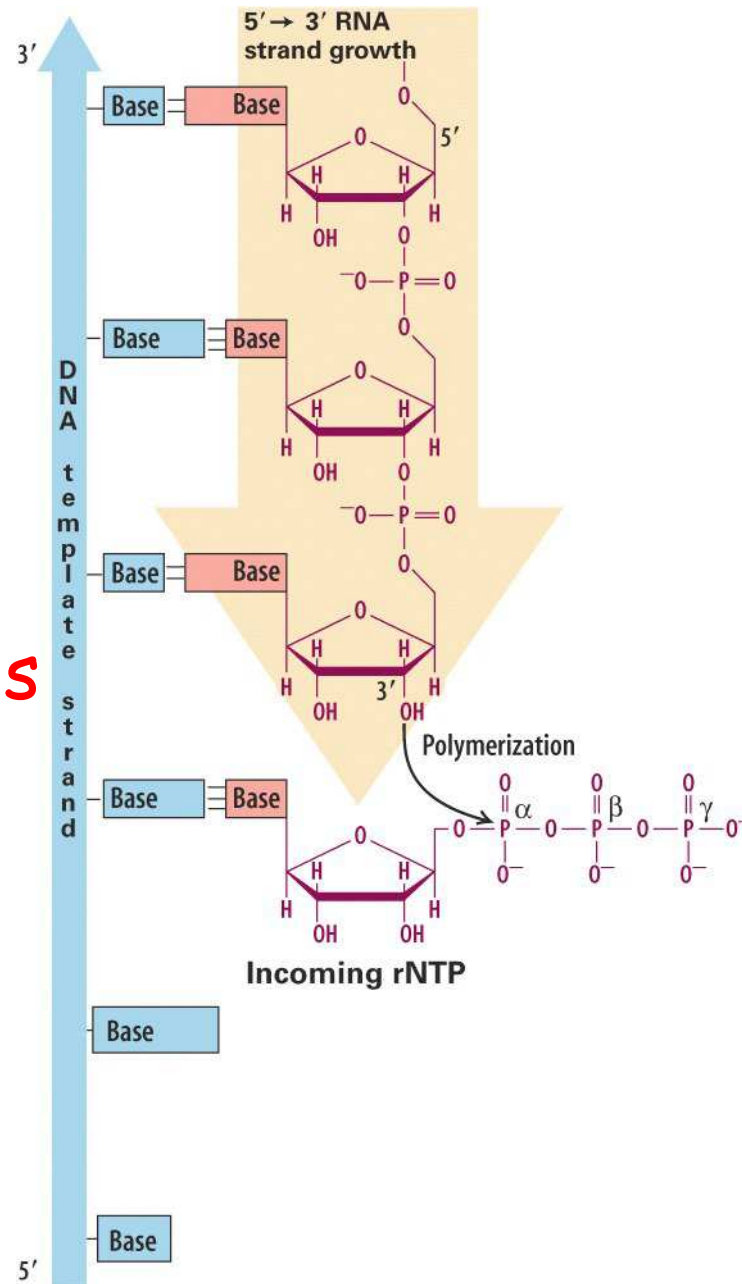


Polymerase reaction:

5' → 3'

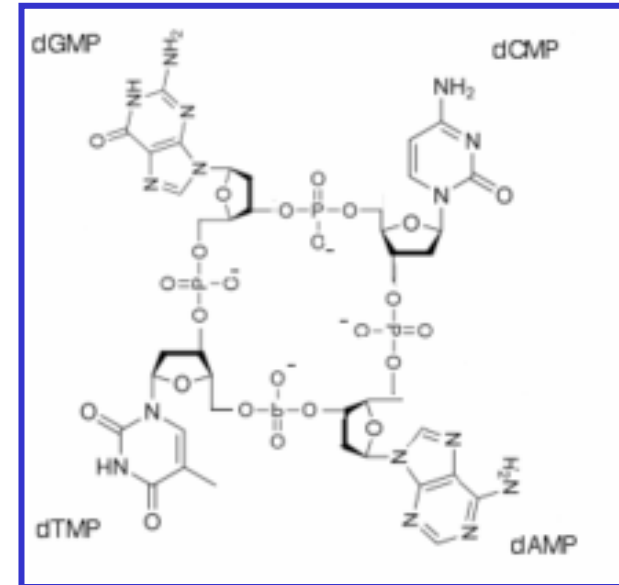
Chemical DNA synthesis

3' → 5'



# First DNA Structure

- By 1910 actual components known (nucleotides)
  - Phoebus Levene proposed a tetranucleotide structure for DNA



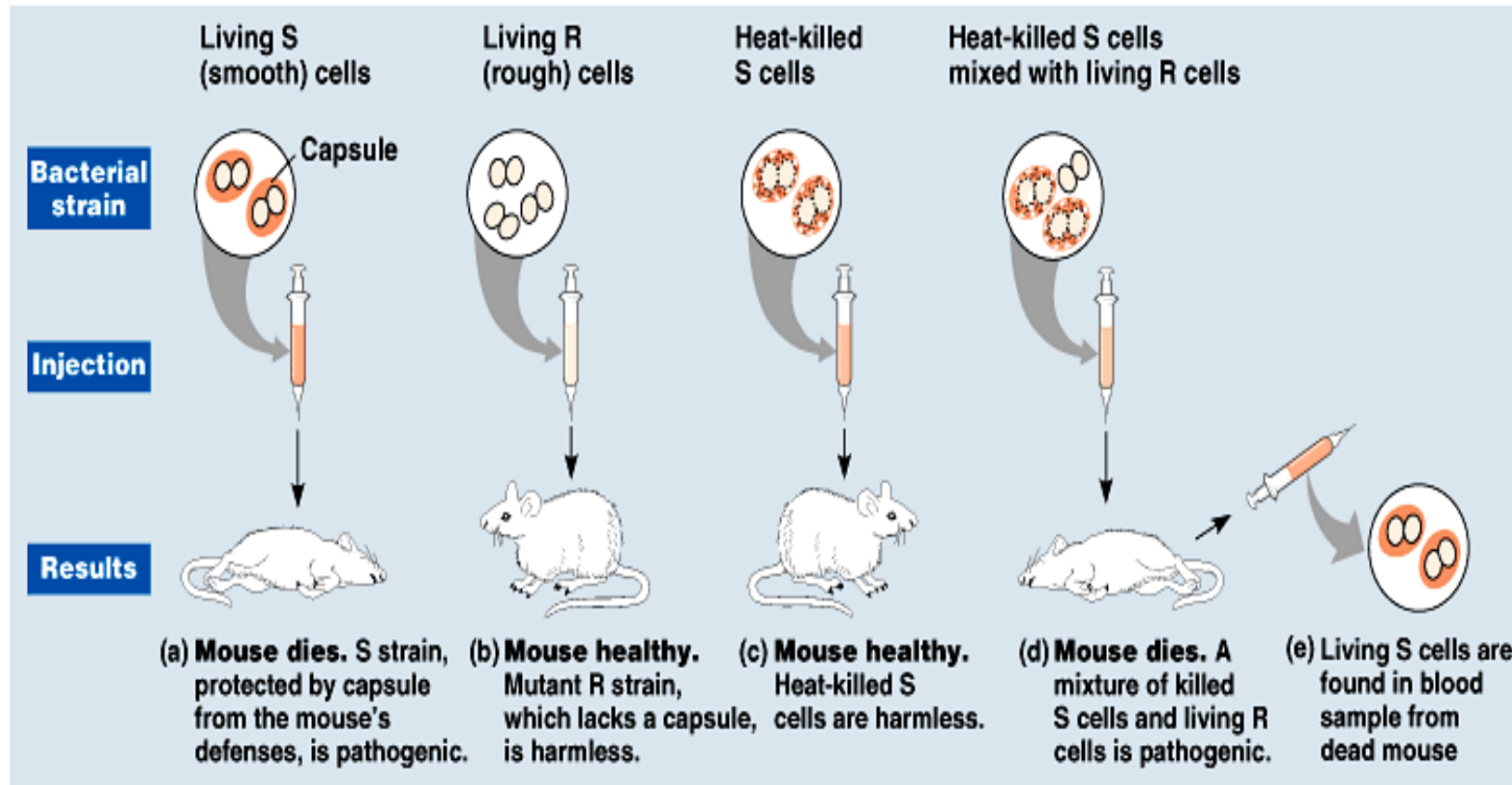
- Tetranucleotide repeat of ATCG
- Own data showed nucleotides not in 1:1:1:1 ratio
  - Differences "probably experimental error..."

# So...

- If DNA was a single covalently bonded tetranucleotide structure then it couldn't easily encode information
- Proteins, on the other hand, had 20 different amino acids and could have lots of variation
- Most geneticists focused on "transmission genetics" and passively accepted proteins as being the likely genetic material

# Frederick Griffith, 1928

## Transformation of Bacteria



Copyright © Pearson Education, Inc., publishing as Benjamin Cummings.

Heat-killed cells contain "transforming factor"

# Avery, McCarty and MacLeod (1944)

- After 10 yrs of effort published work using Griffith's approach to assay for the genetic material
  - Used
    - Cell-free extract of S cells
    - From 75 liters of cell culture obtained 10-25 mg of "active factor"
    - Proteases, RNases, DNases, etc.
  - Transforming factor is DNA

# Erwin Chargaff

- 1949-1953
- Digested many DNAs and subjected products to chromatographic separation
- Results
  - $A = T, C = G$
  - $A + G = C + T$  (purine = pyrimidine)
  - $A + T$  does not equal  $C + G$ 
    - Members of a species similar but different species vary in AT/CG ratio

**TABLE 10.3**
**DNA BASE COMPOSITION DATA**
**(a) Chargaff's data\***

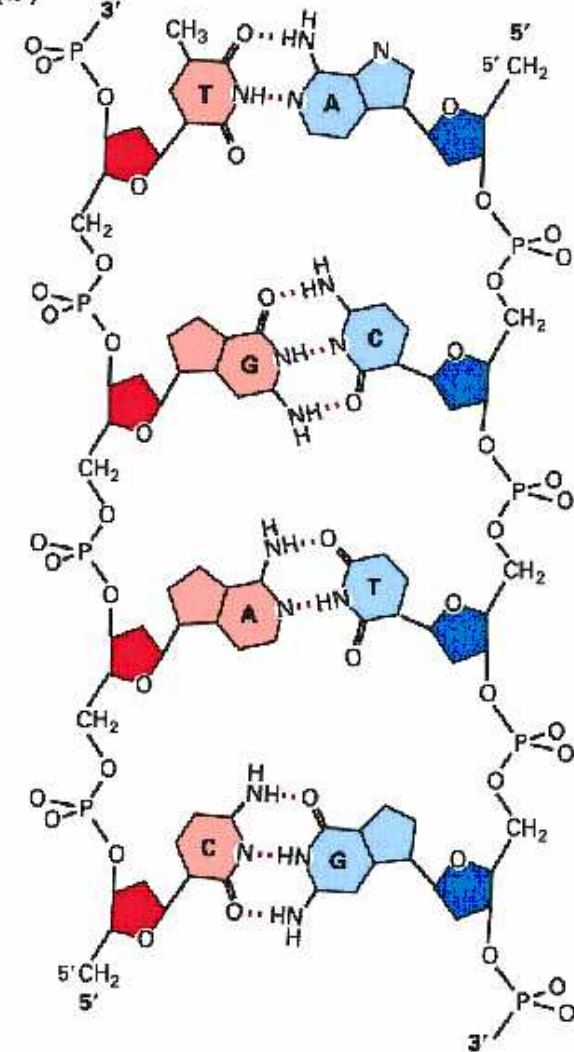
Organism's/Source	Molar proportions <sup>a</sup>			
	1 A	2 T	3 G	4 C
Ox thymus	26	25	21	16
Ox spleen	25	24	20	15
Yeast	24	25	14	13
Avian tubercle bacilli	12	11	28	26
Human sperm	29	31	18	18

**(b) Base compositions of DNAs from various sources**

Source	Base composition				Base ratio	
	1 A	2 T	3 G	4 C	5 A/T	6 G/C
Human	30.9	29.4	19.9	19.8	1.05	1.00
Sea urchin	32.8	32.1	17.7	17.3	1.02	1.02
<i>E. coli</i>	24.7	23.6	26.0	25.7	1.04	1.01
<i>Sarcina lutea</i>	13.4	12.4	37.1	37.1	1.08	1.00
T7 bacteriophage	26.0	26.0	24.0	24.0	1.00	1.00

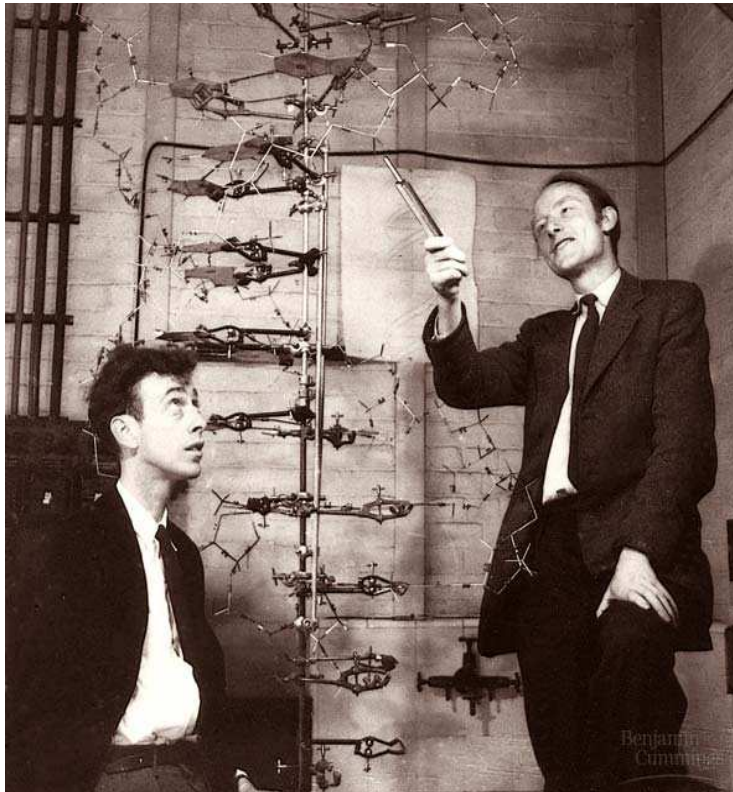
\* Source: From Chargaff, 1950.

<sup>a</sup> Moles of nitrogenous constituent per mole of P. (Often, the recovery was less than 100 percent.)

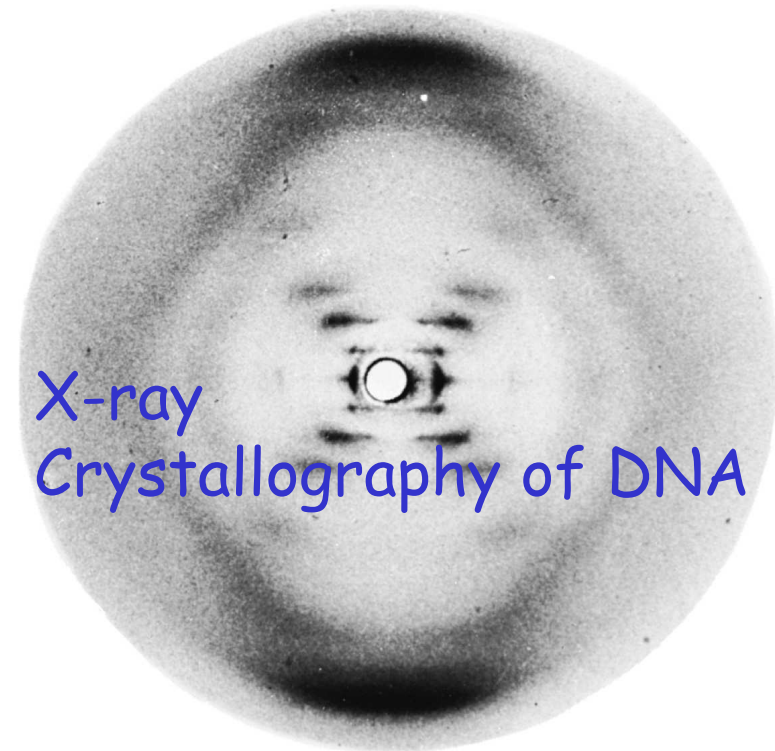
**(b)**


# Watson and Crick

- 1953 propose double helix model
  - Right-handed double helix



Method?

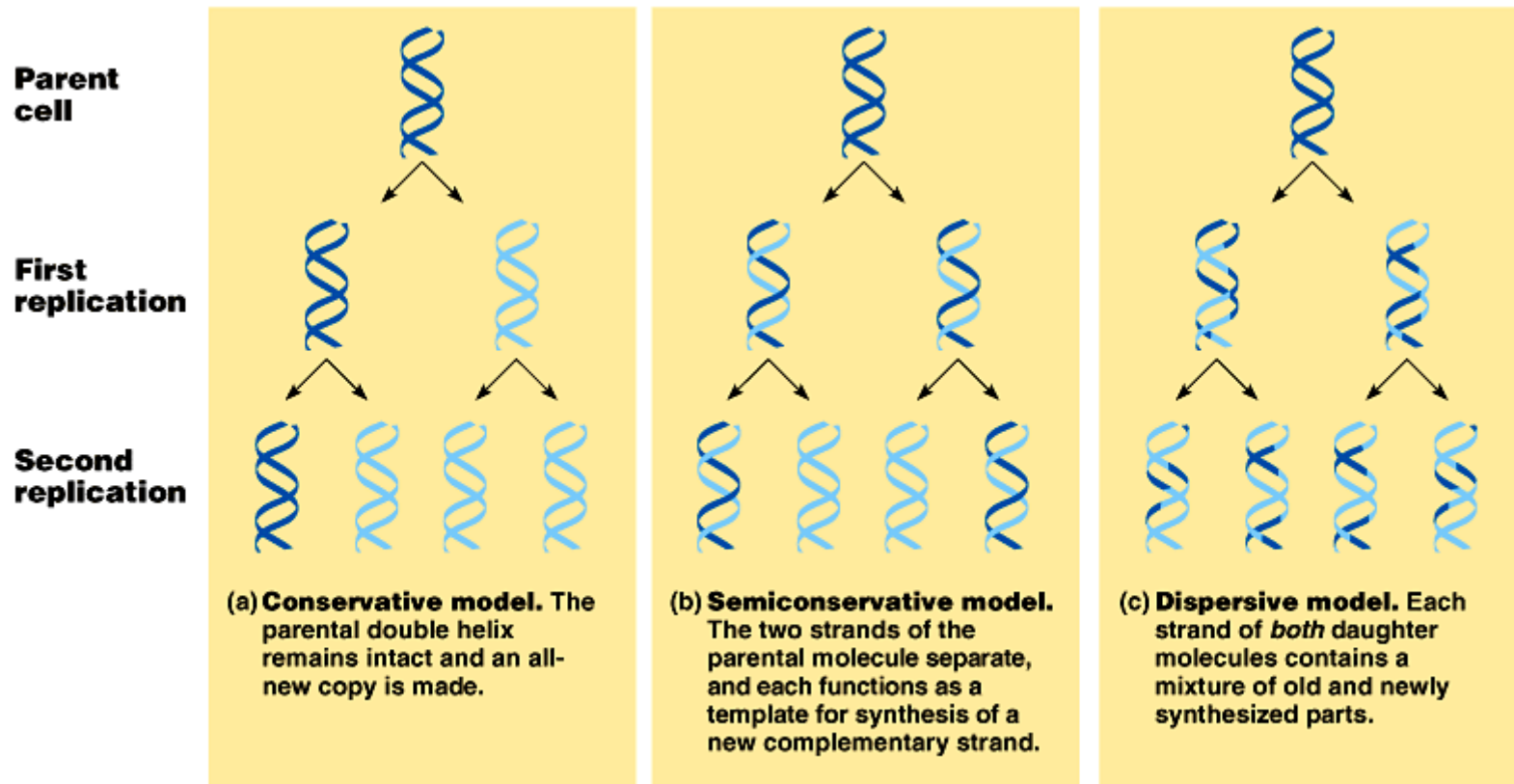


X-ray  
Crystallography of DNA

# Impact

- *Article in Nature*
  - "It has not escaped our notice that the specific pairing we have postulated immediately suggests a possible copy mechanism for the genetic material"
    - Second paper 2 months later describes semiconservative replication and that mutations must change bases in DNA (information encoded in the bases and their order)
- DNA became the genetic material...

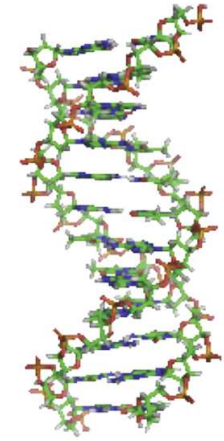
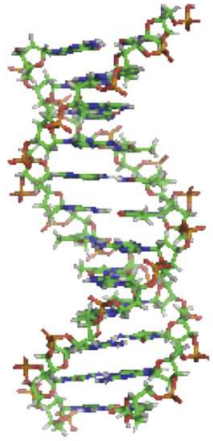
# DNA Replication



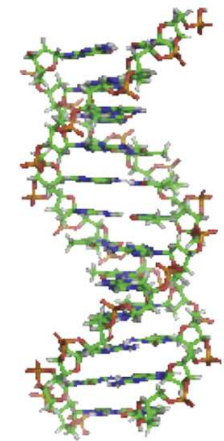
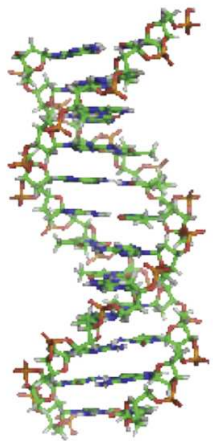
Nobel Prize in 1962.

The Nobel Committee noted that the discovery had "no immediate practical application, but determining the molecular structure of the substance that is responsible for the forms that life takes is a discovery of tremendous importance".

The understatement of the year?



**We Live in  
The Age of DNA!**



## We Live in the Era of....

- Genes & DNA
  - Genomics & Genome Sequencing
  - Genetic Engineering of Microbes, Plants, & Animals
  - Biotechnology Using Genetic Engineering Technology
  - Synthetic Microbes Made by "Man"
  - Personalized Genomes and Ability to Identify Any Individual Using DNA
  - Mammalian Reproduction, Stem Cells & Cloning
- And the SYNTHESIS of These Technologies!!

# Genetic Engineering Can Now Be Used To Synthesize Entire Chromosomes From Chemicals and Create Synthetic Microbes in a Test Tube

2 JULY 2010 VOL 329 SCIENCE www.sciencemag.org

## Creation of a Bacterial Cell Controlled by a Chemically Synthesized Genome

May 20, 2010

### Researchers Say They Created a 'Synthetic Cell'

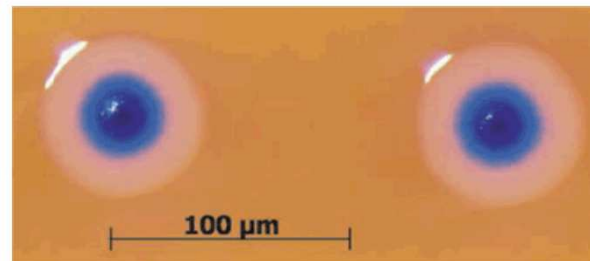
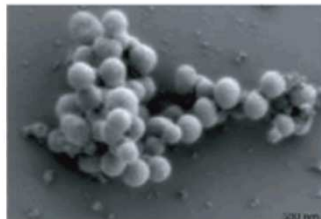
By NICHOLAS WADE

The genome pioneer J. Craig Venter has taken another step in his quest to create synthetic life, by synthesizing an

J. Craig Venter  
*Mycoplasma genitalium*

Why did they choose this Pathogenic organism?

582,970 bp genome  
Low GC content ~ 30%



# Chemical gene and chromosome synthesis

## HOW TO MAKE ARTIFICIAL LIFE

**1** Entire DNA of *Mycoplasma mycoides*, a bug that usually infects goats, is decoded.

**2** Researchers buy fragments of DNA from a mail order catalogue. Each of the four bottles contains a section of the code.

**3** The fragments are put into yeast, which 'stitches' them together, gradually building a synthetic copy of the original DNA.

**4** The artificial DNA is put into a recipient bacterium, which then grows and divides, creating two daughter cells, one with the artificial DNA and one with the natural DNA.

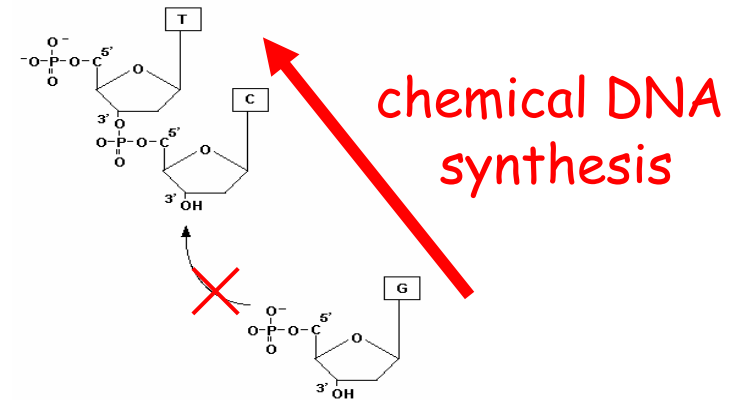
**5** Antibiotics in the petri dish kill the bacterium with the natural DNA, leaving the one with the synthetic DNA to multiply.

**6** Within just a few hours, all traces of the recipient bug are wiped out and bugs with artificial DNA thrive. New life has been created.

**7** Possible uses are bugs capable of producing clean fuels and sucking carbon dioxide out of the atmosphere. Also microbes capable of mopping up oil slicks (above) or generating drugs, including the flu vaccine.

Maverick: Dr Craig Venter

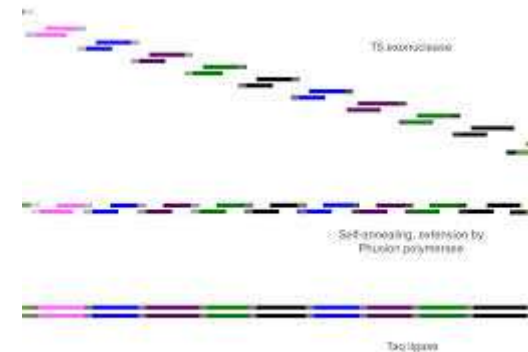
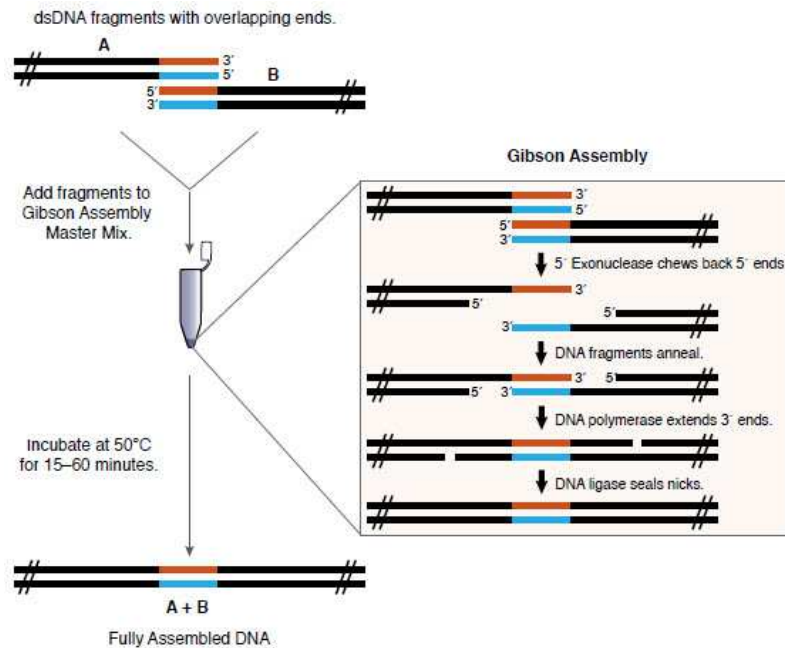
Graphic by John Lawson



Gene synthesis from \$0.35/bp

Scientist accused of playing God

# Gibson assembly



Taq ligase

Example of synthetic biology

# DNA can be used to look into the past

## RESEARCH ARTICLE

*Science*, May 7, 2010 (328, 710-722)

### A Draft Sequence of the Neanderthal Genome

From a 45,000 Year-Old Bone



Reconstruction by Kennis & Kennis / Photograph by Joe McNally

For the first time, a Neanderthal female peers from the past in a reconstruction informed by both fossil anatomy and ancient DNA. At least some of her kind carried a gene for red hair and pale skin.

# 2014

1 Genetic variants in 846 people of non-African heritage, 176 people from sub-Saharan Africa, and a 50,000-year-old Neanderthal

Areas with reduced Neanderthal ancestry tend to cluster on the X chromosome - hybrid infertility

This suggests that when ancient humans met and mixed with Neanderthals, the two species were at the edge of biological incompatibility

2 Whole-genome sequencing data from 379 Europeans and 286 East Asians to identify Neanderthal lineages that persist in the modern DNA

Non-African humans inherit ~1 to 3% of their genomes from Neanderthal ancestors. Evidence that Neanderthal skin genes made Europeans and East Asians more evolutionarily fit

1 Sriram Sankararaman et al. The genomic landscape of Neanderthal ancestry in present-day humans. *Nature*,

2 Benjamin Vernot and Joshua M. Akey. Resurrecting Surviving Neanderthal Lineages from Modern Human Genomes. *Science*



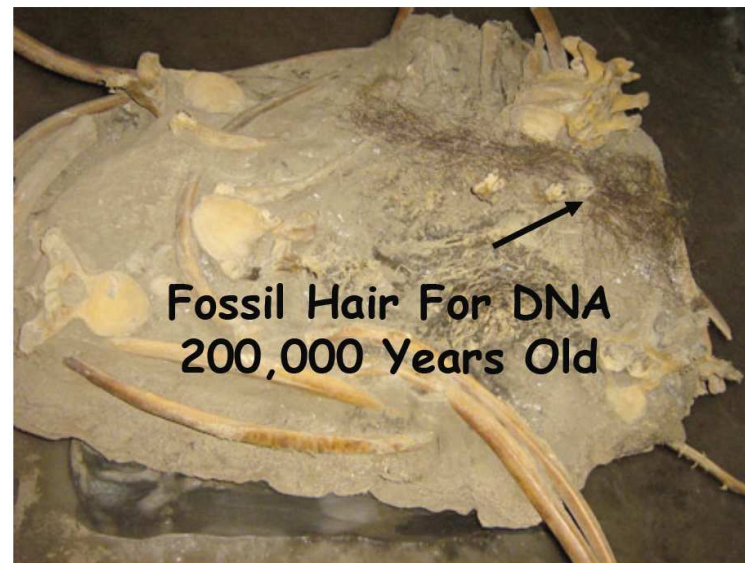
Nature, November 2008

LETTERS

# Sequencing the nuclear genome of the extinct woolly mammoth

**Think About Bringing a Woolly Mammoth Back to Life!!**

Webb Miller<sup>1</sup>, Daniela I. Drautz<sup>1</sup>, Aakrosh Ratan<sup>1</sup>, Barbara Pusey<sup>1</sup>, Ji Qi<sup>1</sup>, Arthur M. Lesk<sup>1</sup>, Lynn P. Tomsho<sup>1</sup>, Michael D. Packard<sup>1</sup>, Fangqing Zhao<sup>1</sup>, Andrei Sher<sup>2,†</sup>, Alexei Tikhonov<sup>3</sup>, Brian Raney<sup>4</sup>, Nick Patterson<sup>5</sup>, Kerstin Lindblad-Toh<sup>5</sup>, Eric S. Lander<sup>5</sup>, James R. Knight<sup>6</sup>, Gerard P. Irzyk<sup>6</sup>, Karin M. Fredrikson<sup>7</sup>, Timothy T. Harkins<sup>7</sup>, Sharon Sheridan<sup>7</sup>, Tom Pringle<sup>8</sup> & Stephan C. Schuster<sup>1</sup>



# Dna can be used to “bring back the dead”!!

PNAS

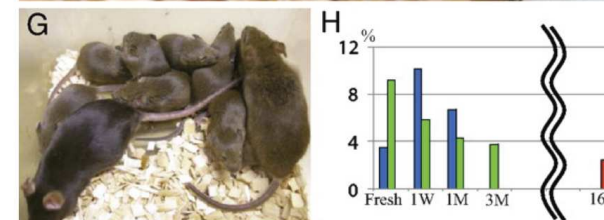
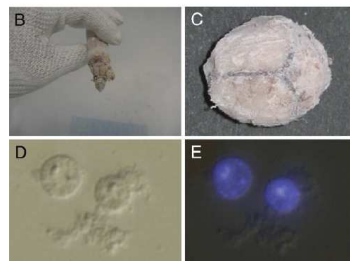
November 11, 2008

Production of healthy cloned mice from bodies frozen at  $-20^{\circ}\text{C}$  for 16 years *Think of the possibilities!*

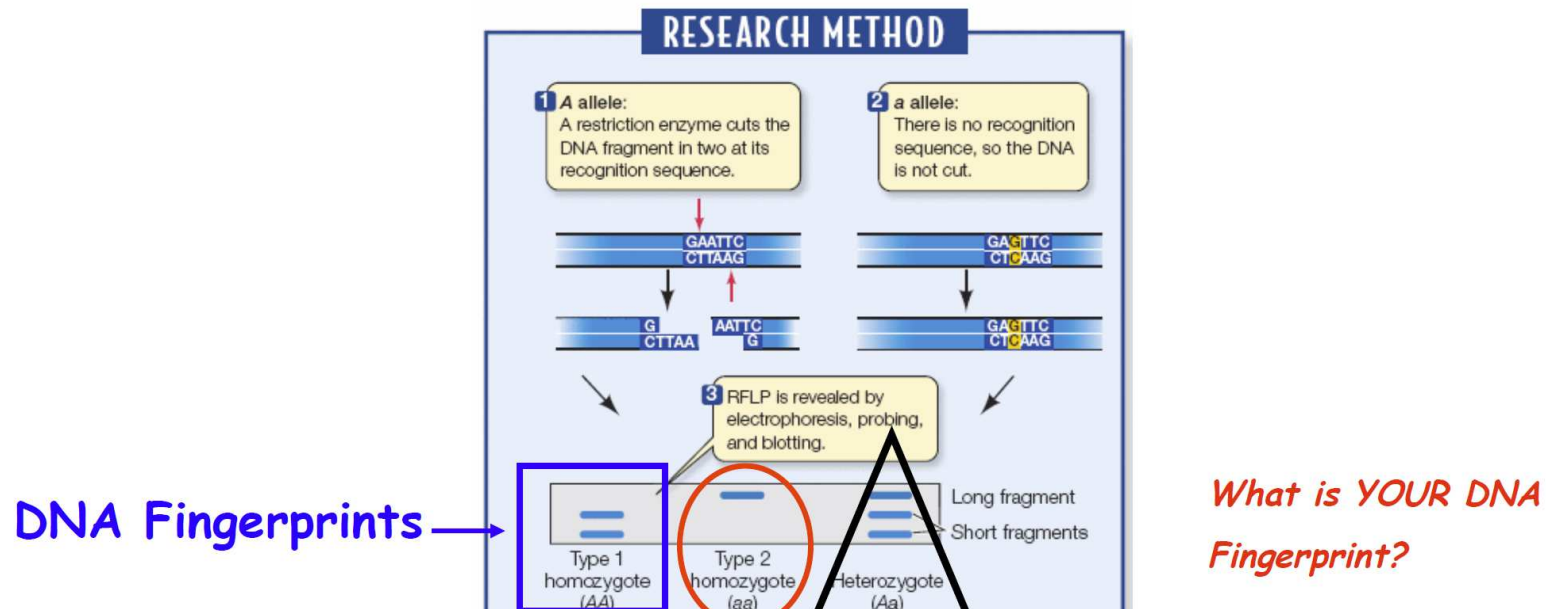
Sayaka Wakayama<sup>a</sup>, Hiroshi Ohta<sup>a</sup>, Takafusa Hikichi<sup>a</sup>, Eiji Mizutani<sup>a</sup>, Takamasa Iwaki<sup>b</sup>, Osami Kanagawa<sup>c</sup>, and Teruhiko Wakayama<sup>a,1</sup>

<sup>a</sup>RIKEN, Center for Developmental Biology, 2-2-3 Minatojima-minamimachi, Kobe, 650-0047, Japan; <sup>b</sup>Jikei University School of medicine, Tokyo 105-8461, Japan; and <sup>c</sup>RIKEN, Research Center for Allergy and Immunology, 1-7-22, Sushiro-cho, Tsurumi-ku, Yokohama, 230-0045, Japan

*How Know a Clone or Genetically Identical Individual - DNA!*



# By Using DNA Fingerprints to Identify Individuals & Genes



Example of SNP

# The Complete Genome of Individuals Can Now Be Sequenced Very Inexpensively (\$10,000)!!

## Genome of DNA Pioneer Is Deciphered

By NICHOLAS WADE  
Published: May 31, 2007

### James Watson's Personal Genome Sequence

**README:** How do I use the James Watson Genome Browser?  
**Downloads:** Download bulk JW polymorphisms. For the complete data set, please go to the NCBI Trace Archive and search for `CENTER_NAME = 'CSHL'` and `CENTER_PROJECT = 'Project Jim'`.

**Showing 34.46 kbp from chr7, positions 75,221,807 to 75,256,264**

**Instructions**  
Search using a sequence name, gene name, locus, or other landmark. The wildcard character \* is allowed. To center on a location, click the ruler. Use the Scroll/Zoom buttons to change magnification and position.

**Examples:** HTR2A, macular degeneration, rs726455, DAOA, chr22:20230140..20330139, PARK3, SNP:rs131693, SPTB, NM\_001008496, 3q21.2, ENM010.

[Hide banner] [Bookmark this] [Link to Image] [High-res Image] [Help] [Reset]

**Search**  
Landmark or Region:

**Reports & Analysis:**

**Data Source**  
James Watson genotypes, on NCBI B36 assembly, dbSNP b126

**Scroll/Zoom:** <<<   >>> Show 34.46 kbp  Flip

**Overview**

**Region**

*The Era of Personalized Genomes is Here!*  
The goal is \$1,000 per genome

# A map of human genome variation from population-scale sequencing

The 1000 Genomes Project Consortium\*

The 1000 Genomes Project aims to provide a deep characterization of human genome sequence variation as a foundation for investigating the relationship between genotype and phenotype. Here we present results of the pilot phase of the project, designed to develop and compare different strategies for genome-wide sequencing with high-throughput platforms. We undertook three projects: low-coverage whole-genome sequencing of 179 individuals from four populations; high-coverage sequencing of two mother-father-child trios; and exon-targeted sequencing of 697 individuals from seven populations. We describe the location, allele frequency and local haplotype structure of approximately 15 million single nucleotide polymorphisms, 1 million short insertions and deletions, and 20,000 structural variants, most of which were previously undescribed. We show that, because we have catalogued the vast majority of common variation, over 95% of the currently accessible variants found in any individual are present in this data set. On average, each person is found to carry approximately 250 to 300 loss-of-function variants in annotated genes and 50 to 100 variants previously implicated in inherited disorders. We demonstrate how these results can be used to inform association and functional studies. From the two trios, we directly estimate the rate of *de novo* germline base substitution mutations to be approximately  $10^{-8}$  per base pair per generation. We explore the data with regard to signatures of natural selection, and identify a marked reduction of genetic variation in the neighbourhood of genes, due to selection at linked sites. These methods and public data will support the next phase of human genetic research.

- Sequenced Genomes of ~900 individuals
- From Seven Different Global Populations
- Found 250-300 Loss-Of-Function Mutations (KOs) Per Person
- $10^{-8}$  bp Mutations per Generation (30 per Genome)

# BGI

BGI produces 10% to 20% of the world's genetic information.



# BGI

## China's BGI to Sequence 2,200 Geniuses In Search For "Smart" Genes

(movies)



About

Software

FAQ

Volunteer

Log in

We are recruiting subjects for a Gene-Trait Association Study of intelligence. Our volunteer study of prosopagnosia has not yet begun; if you wish to learn more about this condition, please visit [faceblind.org](http://faceblind.org).

### How to qualify

We currently seek participants with high cognitive ability. You can qualify for the study if you have obtained a high SAT/ACT/GRE score, or have performed well in academic competitions such as the Math, Physics, or Informatics Olympiads, the William Lowell Putnam Mathematical Competition, TopCoder, etc. You may also qualify via exceptional academic credentials or technical accomplishments, which you will have a chance to specify in the survey.

Automatic qualifying criteria include:

- An SAT score of at least 780V/800M post-recentering or 700V/780M pre-recentering; ACT score of 35-36; GRE score of at least 700V/800Q; or revised GRE score of at least 186V/188Q.
- A PhD from a top US program in physics, math, EE, or theoretical computer science.
- Honorable mention or better in the Putnam competition.

Note that meeting one of these thresholds is sufficient for eligibility, but not necessary. For example, volunteers who fall slightly short of the math threshold but significantly exceed the verbal threshold may still be admitted.

If you qualify as a participant, we may send you DNA collection kits. After you return them, we will sequence your DNA, and the data will eventually be available to you in a format compatible with many 3rd party interpretational tools.

# SNP Single Nucleotide Polymorphism in humans

- A precise position along a chromosome where the DNA of different people may vary. Generally two alternate alleles are found at a particular SNP. At least 2,000,000 SNPs are now known and there may be over 30,000,000 in the human genome.
- The importance of SNPs comes from their ability to influence disease risk, drug efficacy and side-effects, tell you about your ancestry, and predict aspects of how you look and even act.
- Mostly not determined by sequencing -Illumina chip - movie

# Example - Rs1815739

- This SNP, in the *ACTN3* gene, encodes a premature stop codon in a muscle protein called alpha-actinin-3. The polymorphism alters position 577 of the alpha-actinin-3 protein. Normal - C, truncated - T
- (T;T) is under-represented in elite strength athletes, consistent with reports indicating that alpha-actinin-3 deficiency appears to impair muscle performance.

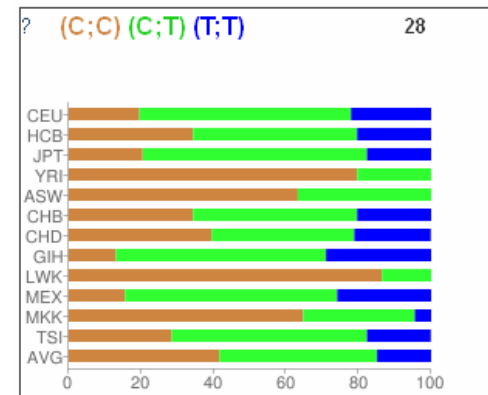
muscle performance

Orientation plus

Stabilized plus

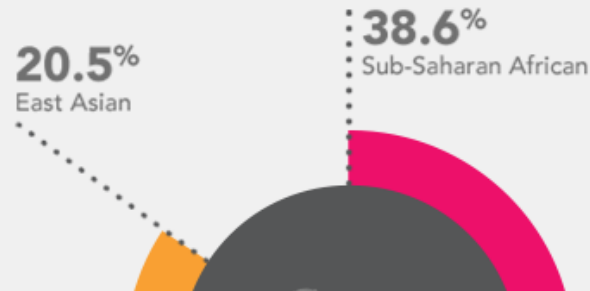
Geno  $\blacktriangleleft$  Mag  $\blacktriangleright$  Summary  $\blacktriangleleft$

(C;C)	2.2	Better performing muscles. Likely sprinter.
(C;T)	2.1	Mix of muscle types. Likely sprinter.
(T;T)	2.3	Impaired muscle performance. Likely endurance athlete.



# 23 pairs of chromosomes. One unique you.

Find out what people around the world are like in Europe and other regions such as



## Neanderthal DNA lives on in us.

Even though Neanderthals vanished about 40,000 years ago, their DNA lives on in us. Based on research, they interbred with humans around 60,000 years ago and we are able to tell you what percentage of your genome came from Neanderthals.



We estimate how much of your DNA is from Neanderthals and compare it to other users.



### Modern Human

Flatter faces  
Slender, with longer limbs  
Advanced artistic abilities and tool making

### Neanderthals

Large noses  
Wide, robust bodies  
Larger eye sockets, likely better vision

Ever wonder who's related to you? You'll likely discover dozens or even hundreds of people who share DNA and ancestors. The matches you'll get can range from close family to distant cousins.

In rare cases, participation in DNA Relatives may reveal that you are related to someone whom you didn't expect, or that you are not related to someone in the way that you expected. Consider this before you opt in to this feature.

ILT  
Absent  
Absent  
Absent  
Absent  
Absent  
status...

traits  
how you

# How About Genetically Engineered Humans?



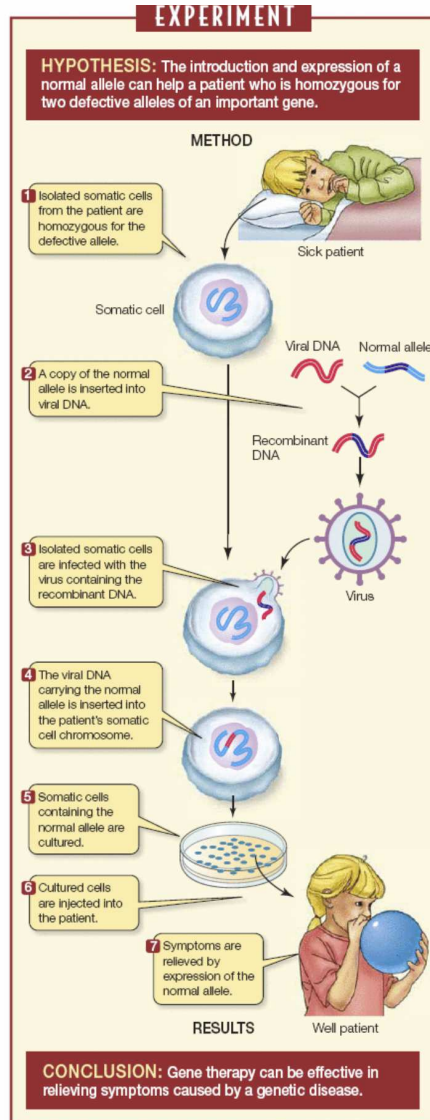
# Humans Have Been Genetically Engineered To Cure a Lethal Genetic Disease (SCID)

Severe combined immunodeficiency

Adenosine DeAminase ADA gene  
Breaking DNA metabolites  
ADA deficiency - metabolites accumulate  
-killing lymphocytes

*Several Teenagers  
Are Alive Because They  
Have Been Engineered  
With an ADA Gene That  
They Were Not Born  
With!!!*

ADA engineered T lymphocytes  
Gene Therapy



# How about Human Cloning?

**nature** International weekly journal of science  
Home | News & Comment | Research | Careers & Jobs | Current Issue | Archive | Audio & Video | For Authors

News & Comment > News > 2014 > November > Article

NATURE | NEWS

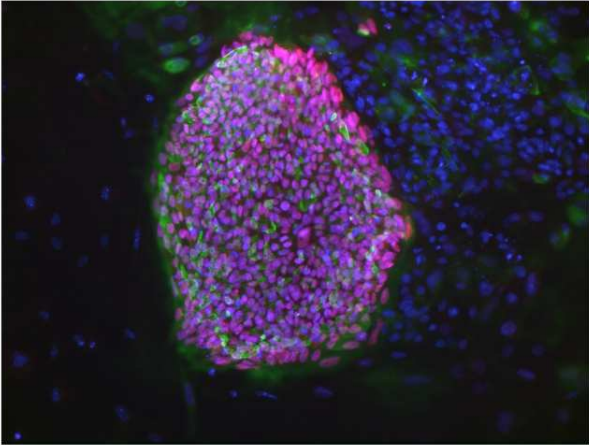
## Stem cells made by cloning adult humans

Cell lines made by two separate teams could boost the prospects of patient-specific therapies.

Monya Baker

28 April 2014

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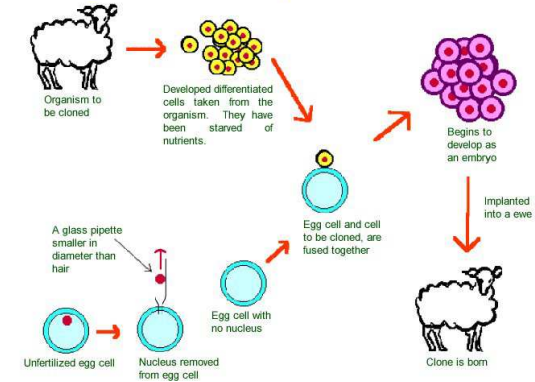


Bjarki Johannesson, NYSOF

This colony of embryonic stem cells, created from a type 1 diabetes patient, is one of the first to be cloned from an adult human.

2014

## Cloning Process of Dolly



1996

# There Are NO Genetic Limitations to What Can Be Done Using Genetic Engineering

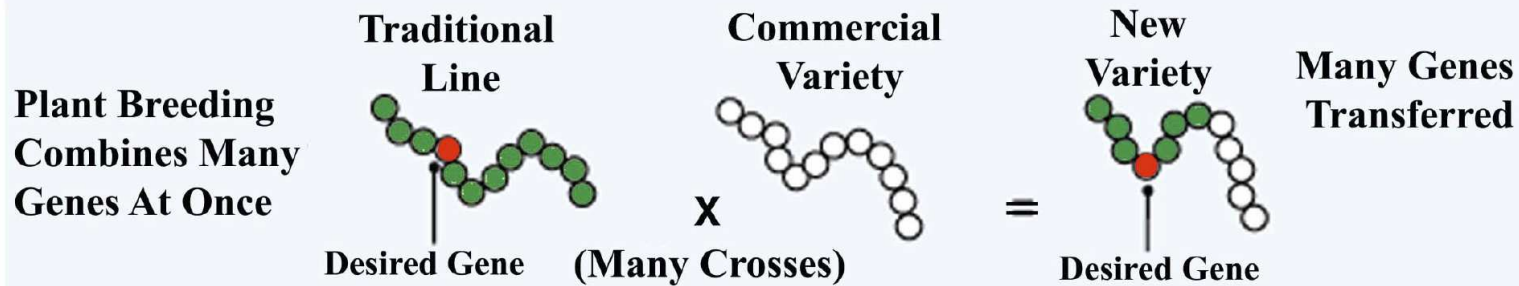
- Sequencing genomes of ancient organisms
- Chemical genome synthesis
- Animal (and human) cloning
- Reviving the dead organisms



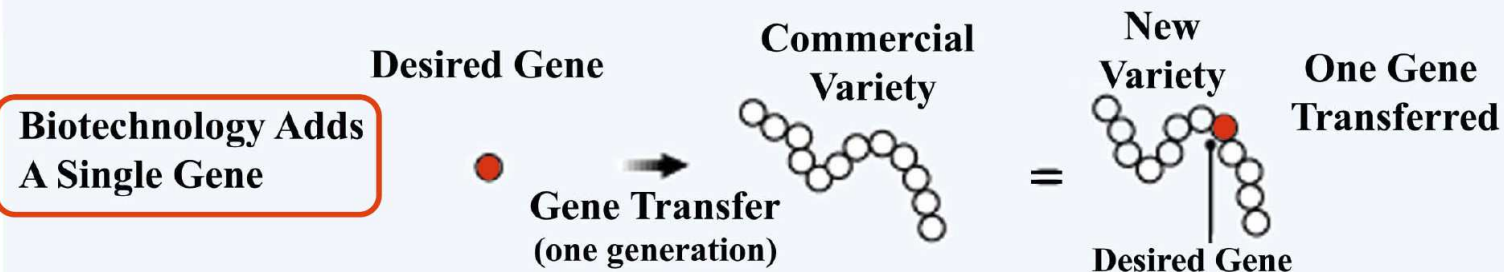
# Is genetic engineering a new technology?

## Classical vs. Molecular Genetic Engineering

### TRADITIONAL PLANT BREEDING



### PLANT BIOTECHNOLOGY



There is principally nothing new about genetic engineering

**How Was Genetic  
Engineering Invented?**

**&**

**How Did It Lead To All of  
These Remarkable Advances  
With DNA?**

Genetic engineering started in  
a Hawaii delicatessen in 1972

With An Unexpected "Eureka" Moment  
Dealing With Two Unrelated Areas of  
Study:

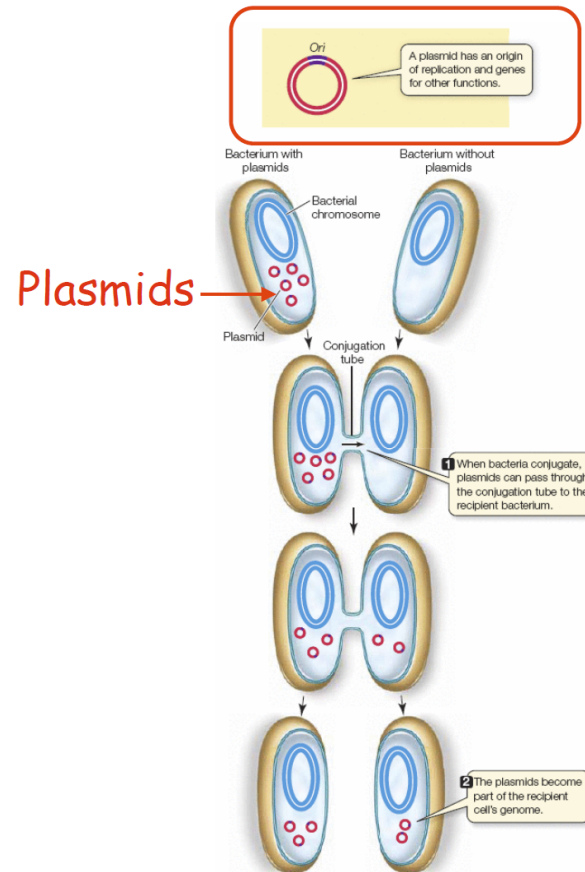
1. The Mechanism of Bacterial  
Antibiotic Resistance

Herbert Boyer

2. How Novel Enzymes That Protect  
Bacteria From Destruction By  
Viruses "Cut" DNA Into Pieces

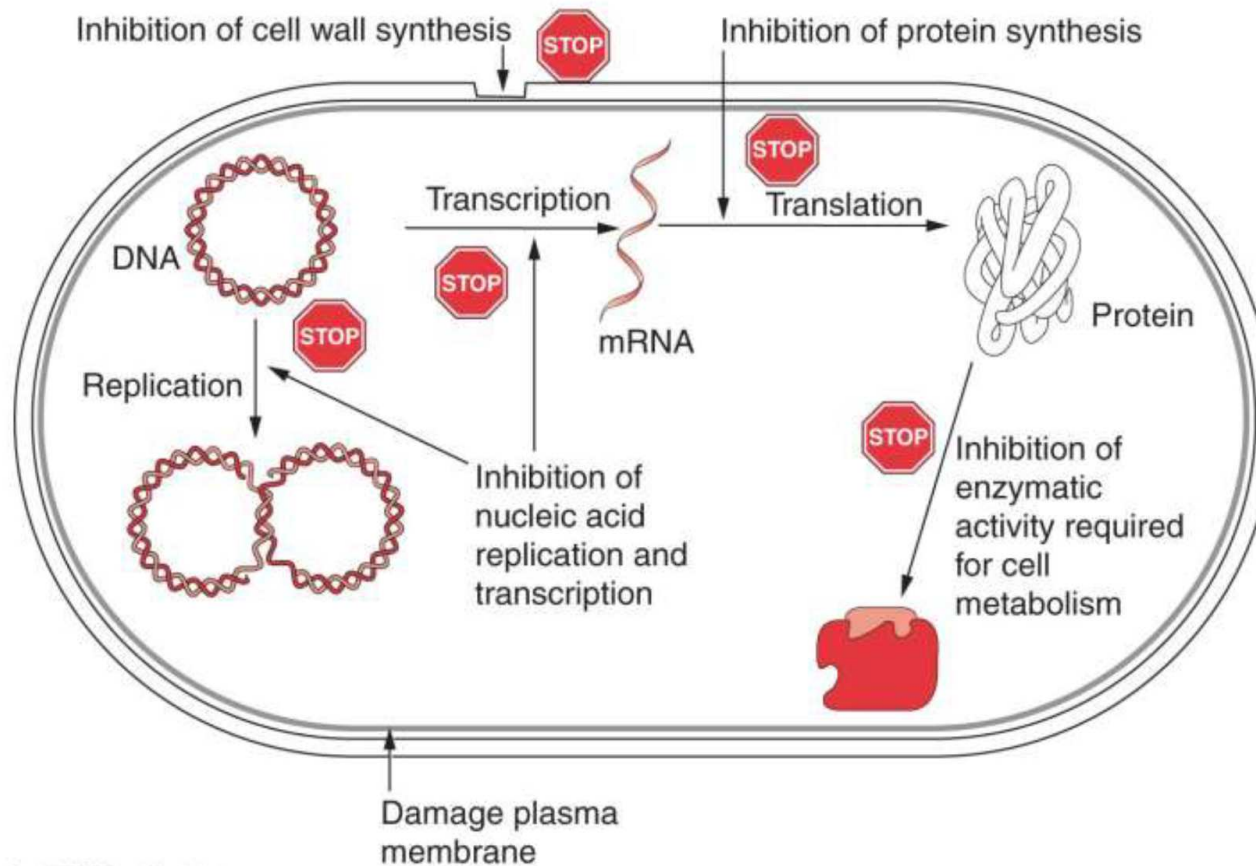
Stanley Cohen

# Plasmids Are Circular Self-Relicating DNA Molecules in Bacterial Cells That Carry Antibiotic Resistance Genes



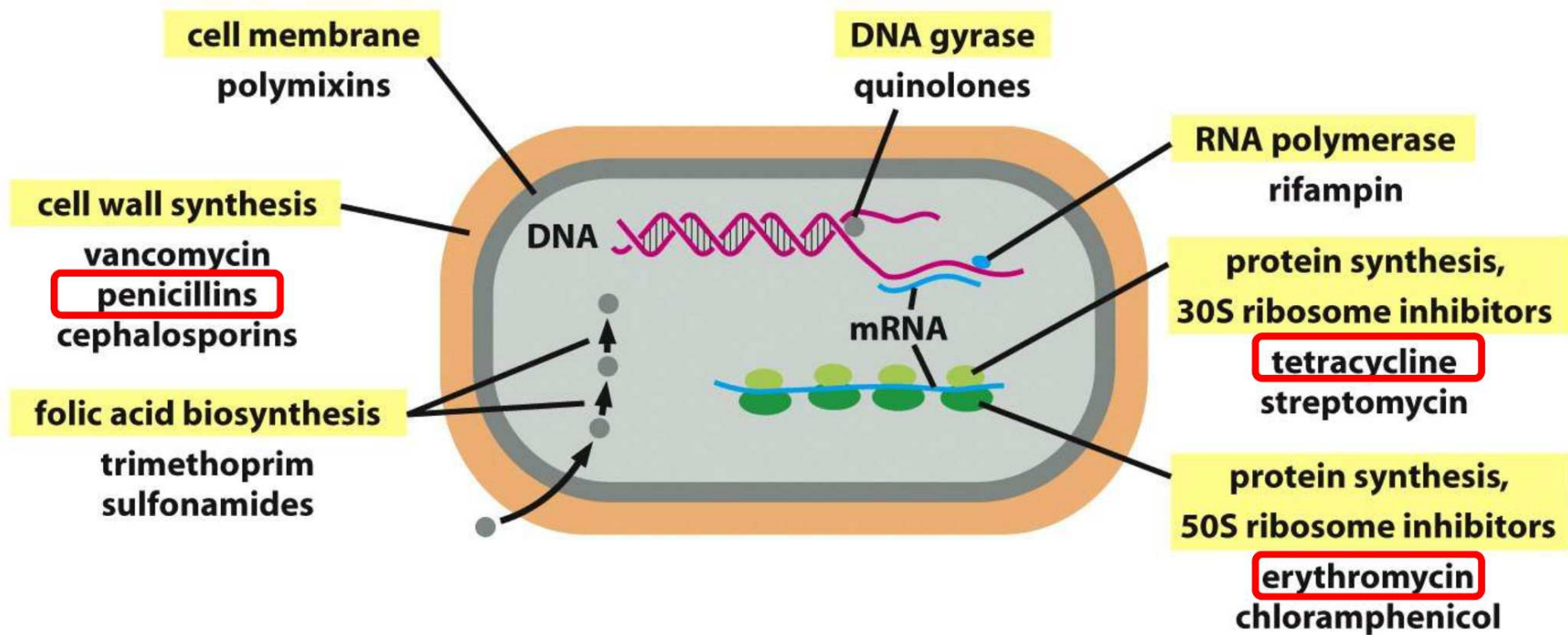
**Plasmids Defend Bacteria Against Antibiotics!**

# How Do Antibiotics Kill Bacterial Cells?

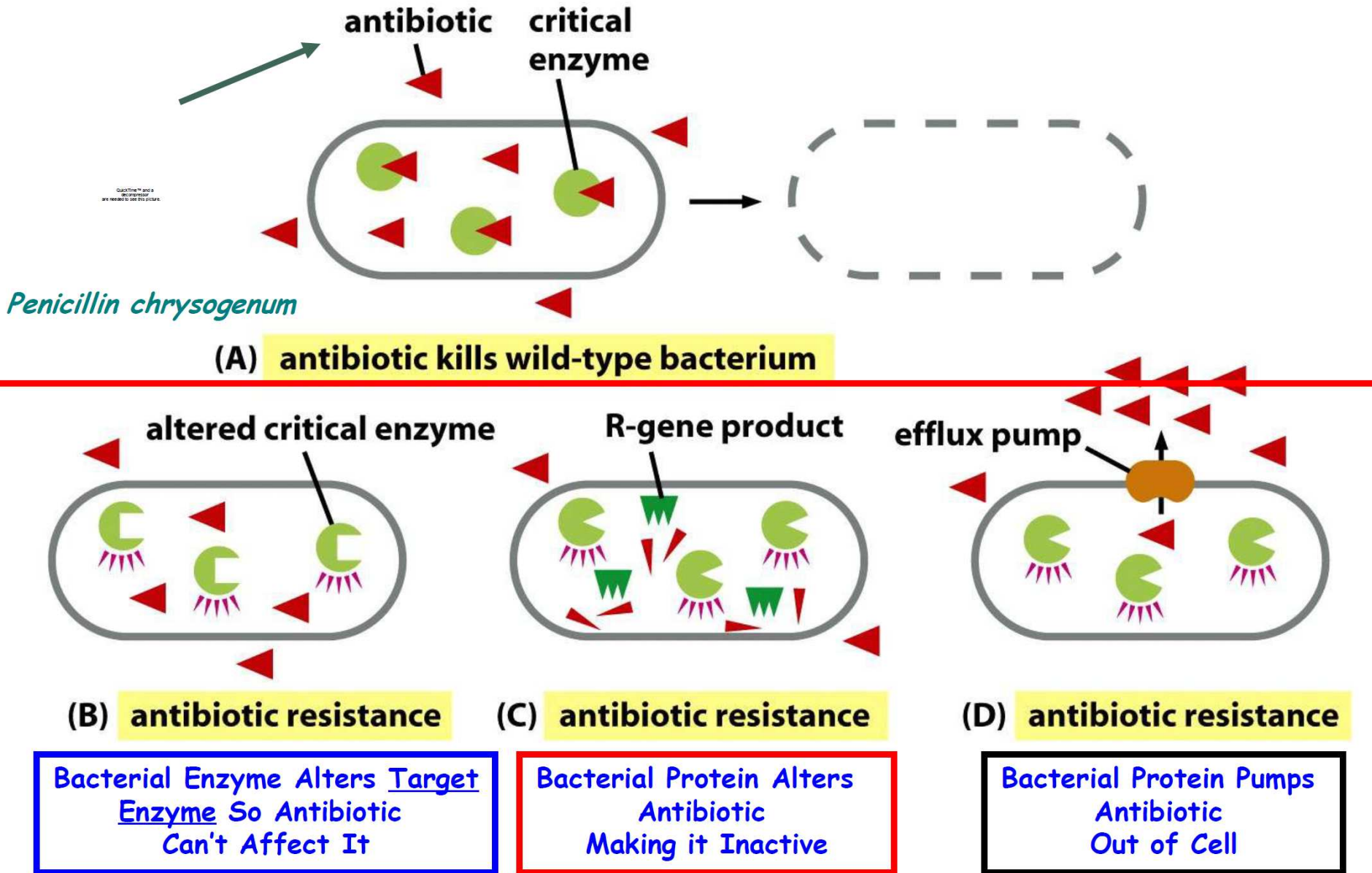


**Inhibiting Basic Microbial Cell Processes**

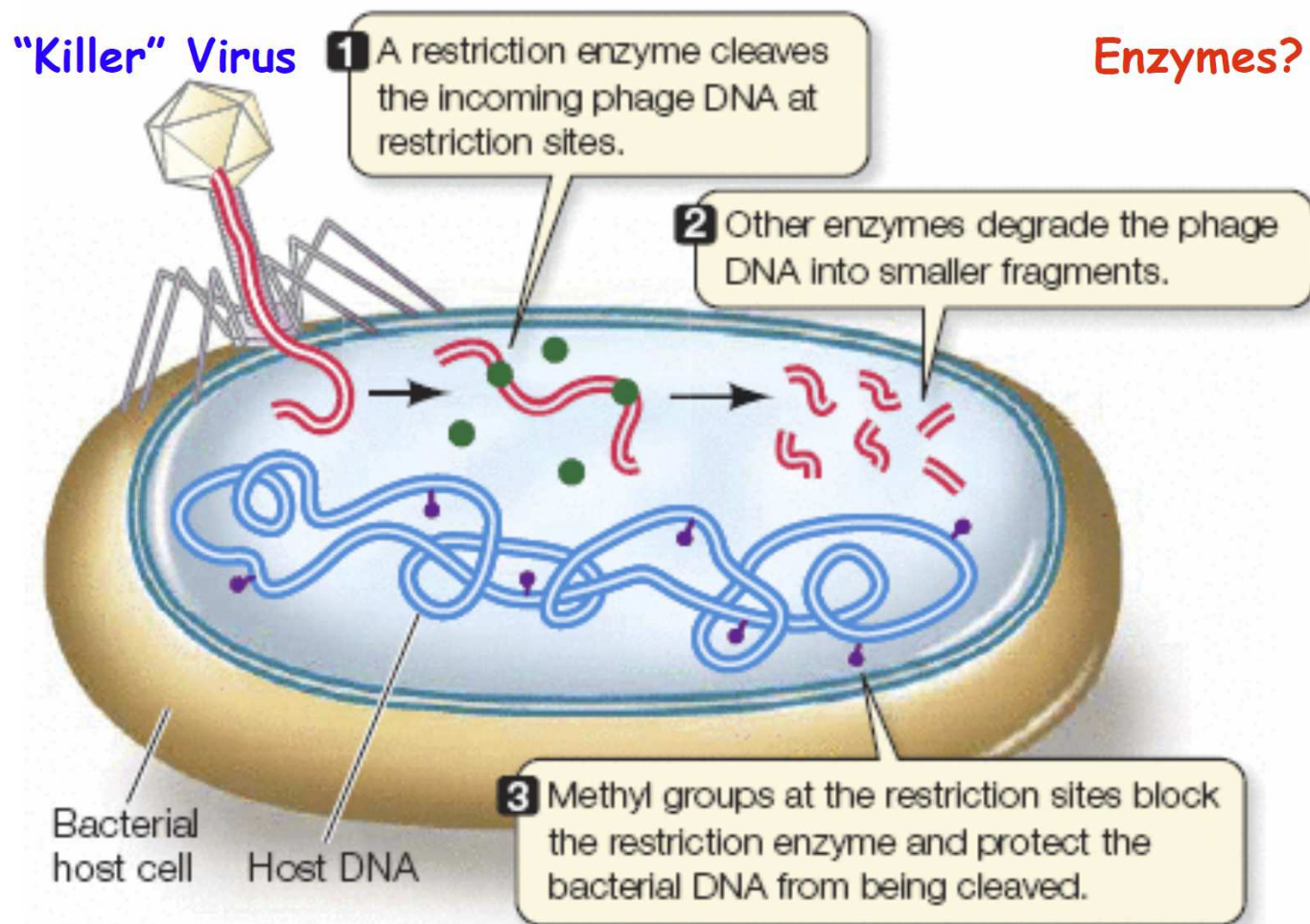
# Selected Antibiotics and Their Cell Targets



# How Do Bacterial Plasmid Antibiotic Resistance Genes Work?

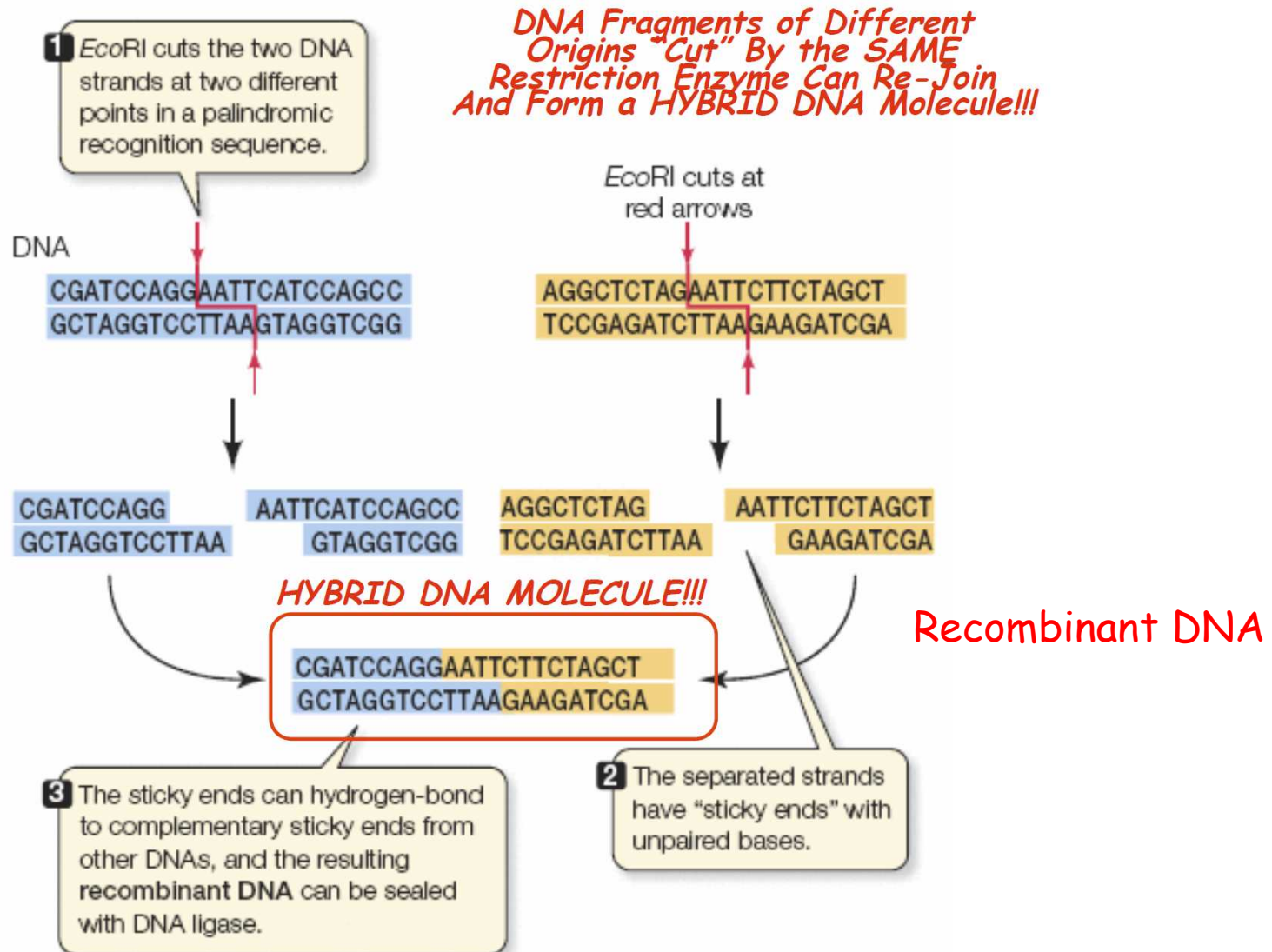


# Restriction Enzymes Are Proteins That "Cut" DNA Into Pieces



**Restriction Enzymes Protect Bacteria From "Killer" Viruses!**

# Restriction Enzymes Are Proteins That "Cut" DNA Into Pieces At Specific Sequences

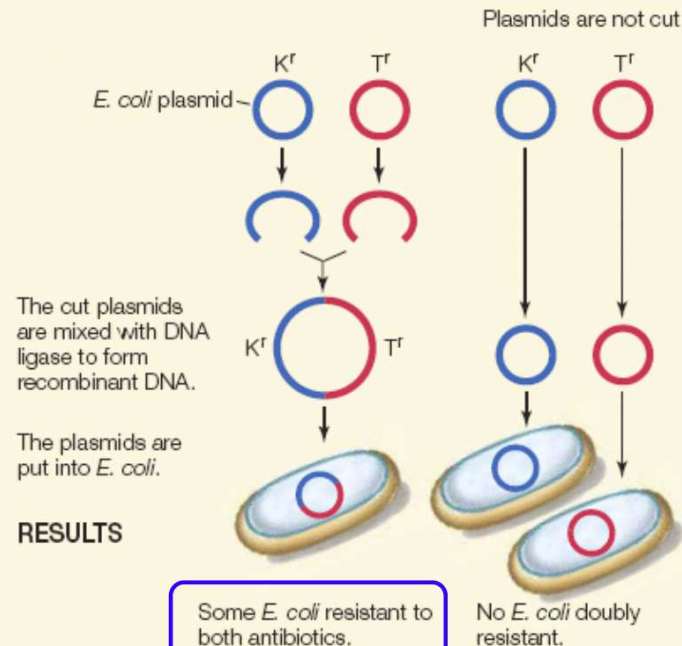


# Genetic Engineering Technology Can Combine DNA (Genes) From Different Sources Leading to New Gene Combinations!!

## EXPERIMENT

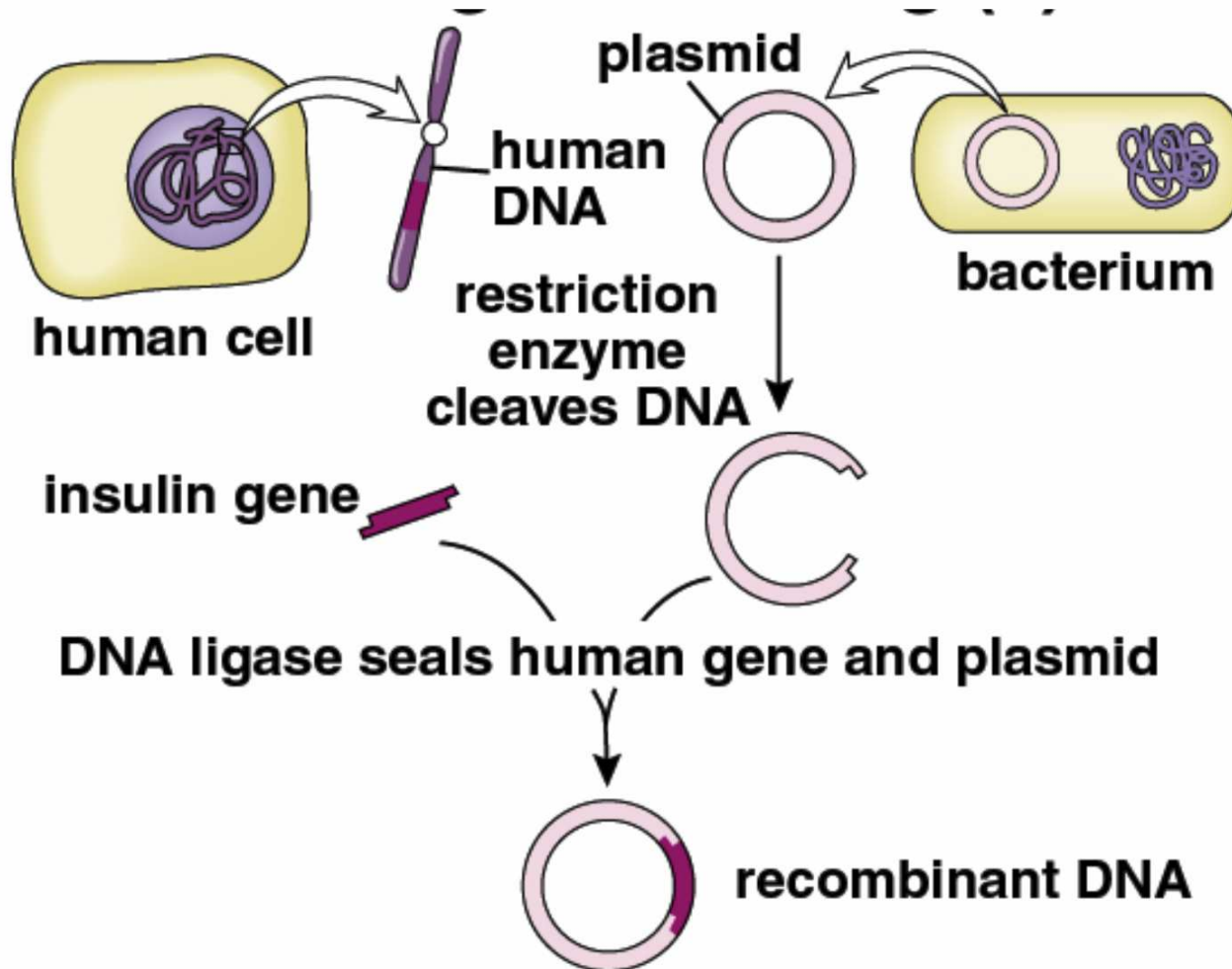
**HYPOTHESIS:** Biologically functional recombinant chromosomes can be made in the laboratory.

**METHOD** *E. coli* plasmids carrying a gene for resistance to either the antibiotic kanamycin or tetracycline are cut with a restriction enzyme.



**CONCLUSION:** Two DNA fragments with different genes can be joined to make a recombinant DNA molecule, and the resulting DNA is functional.

# The Human Insulin Gene Can Be Separated From Other Human Genes and Cloned in Bacteria Using Recombinant DNA Methods!



Leading to a **REVOLUTION** in  
Technology and Making it Possible  
For the First Time to Isolate,  
Manipulate, and Study Genes

The Genes of Any Organism Can  
Be Isolated, Combined With  
Those of Another Organism, and  
Made to Function Normally in  
New Cellular Environments!

For Example: Human Genes in  
Bacteria, Bacterial Genes in  
Plants, Jellyfish Genes in  
Monkeys, etc., etc., etc., etc.

## The Era Of DNA Manipulation Means.....

1. Specific DNA/Genes Can Be Isolated From Any Organism
2. DNA Segments of Any Kind From Any Organism Can Be Combined
3. Isolated Genes Can Be Re-Inserted Into the Chromosomes of Any Organism and Made to Work
4. Genes and Genomes Can Be Synthesized and Made To Work in Any Organism

*There Are No Genetic Limits. All Biological Organisms Use the Same Genetic Rules. The Implications Are Enormous!!*

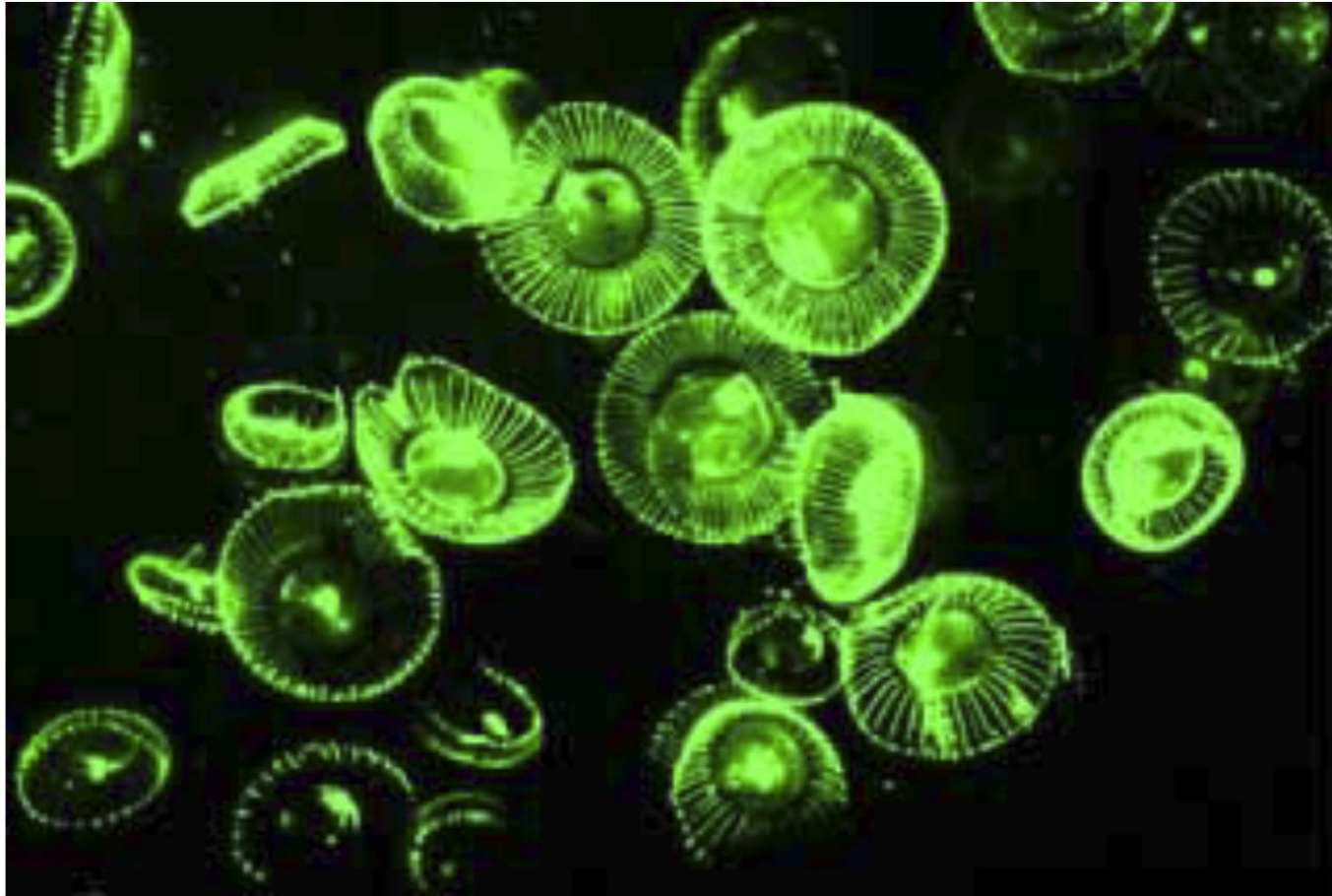
# "Why" Clone Genes From An Organism's Genome?

1. PURIFY Individual Genes From the Genome ( e.g., one of 25,000 human genes)
2. AMPLIFY The Gene to Obtain Enough DNA For Study
3. Use the Cloned Gene To:
  - a) Study Gene Structure & Function ( THE Major Use!)
  - b) Use to Convert Cells Into Factories To Make Drugs and Pharmaceuticals
  - c) Use to Diagnose Genetic Diseases
  - d) Use to Identify Individuals (e.g., paternity, forensics)
  - e) Use to Correct Genetic Disease
  - f) Use to Engineer New Crops and Farm Animals
  - g) Synthesize New Genomes and Many Other Uses

*Genetic Engineering Has Lead to New Knowledge About How Cells and Genes Function and Has Lead to Applications That Have Improved Our Lives!!*

What can be done?

*Using a Jellyfish Gene to Make Animals and Plants Glow!!!!*



*Green Fluorescence Protein*

*A "GloFish!!!!!"*



# GloFish Fluorescing With Different Colors!!



## *How About a GloFly!*



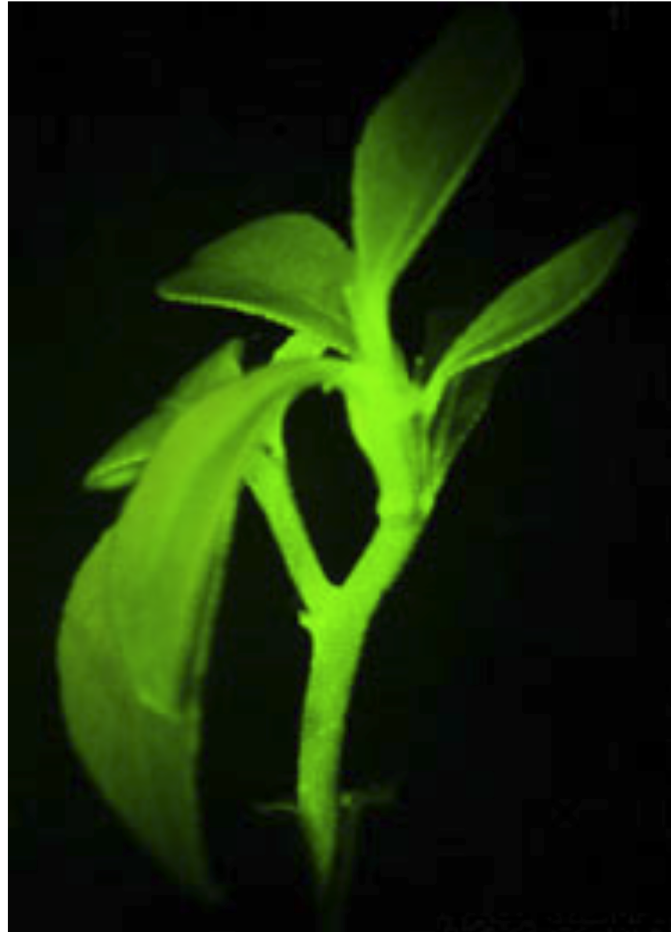
## *What About "GloMice!!!"*



# What About Glo Monkeys, Cats and Pigs!!



And a GloPlant With the Same Jellyfish Gene!!!



Genetic code is universal, gene from one organism can be expressed in another - some limitations