തന്മാത്രാ സാങ്കേതിക വിദ്യയുടെ അത്ഭുത ലോകം

പ്രപഞ്ചവും ജീവനും

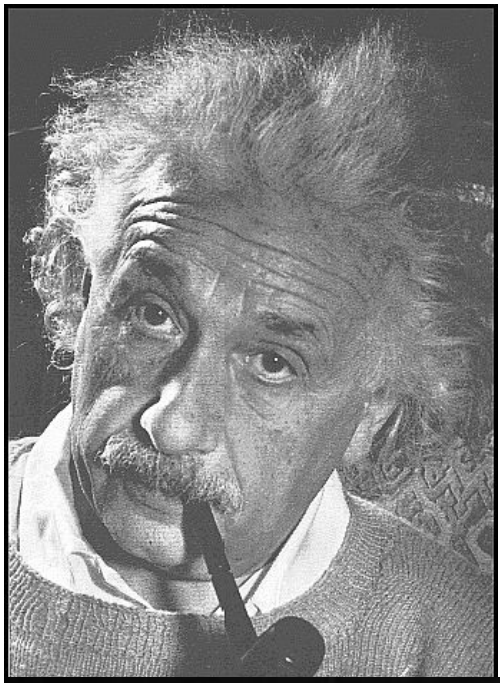
സയൻസ്ക്ലാസുകൾ

കേരള ശാസ്ത്രസാഹിത്യ പരിഷത്ത്

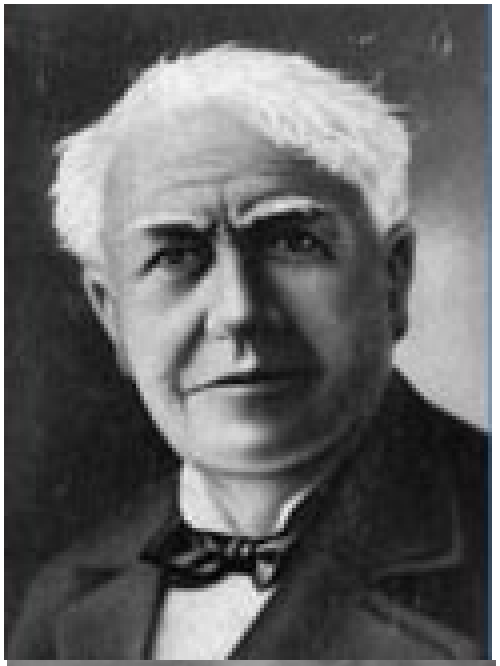
നവ ജീവശാസ്ത്രം

ശാസ്ത്രം

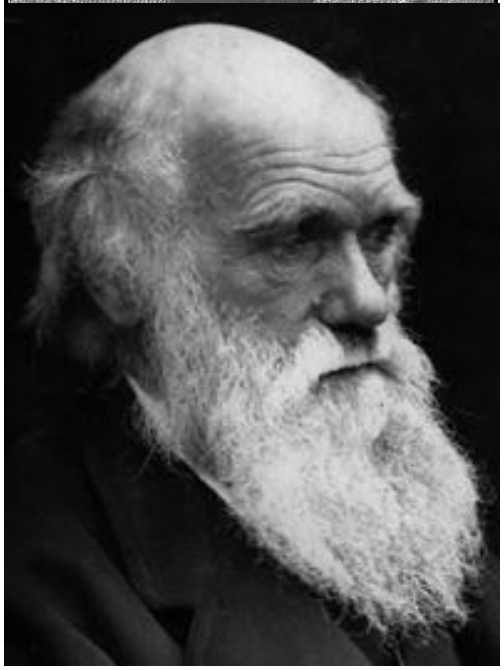
സാങ്കേതിക വിദ്യ



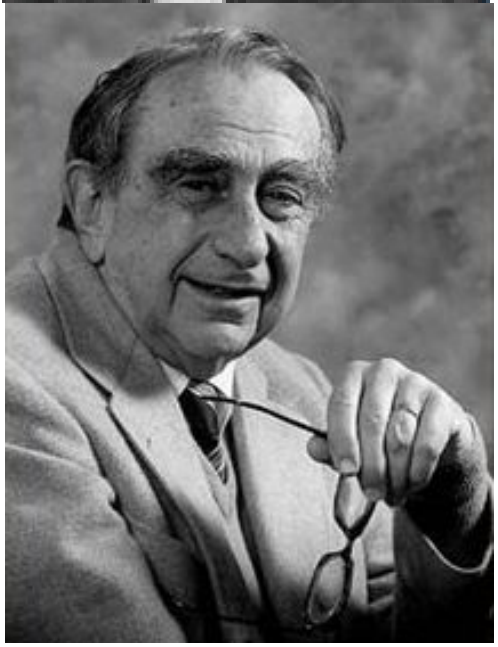
Einstein



Edison

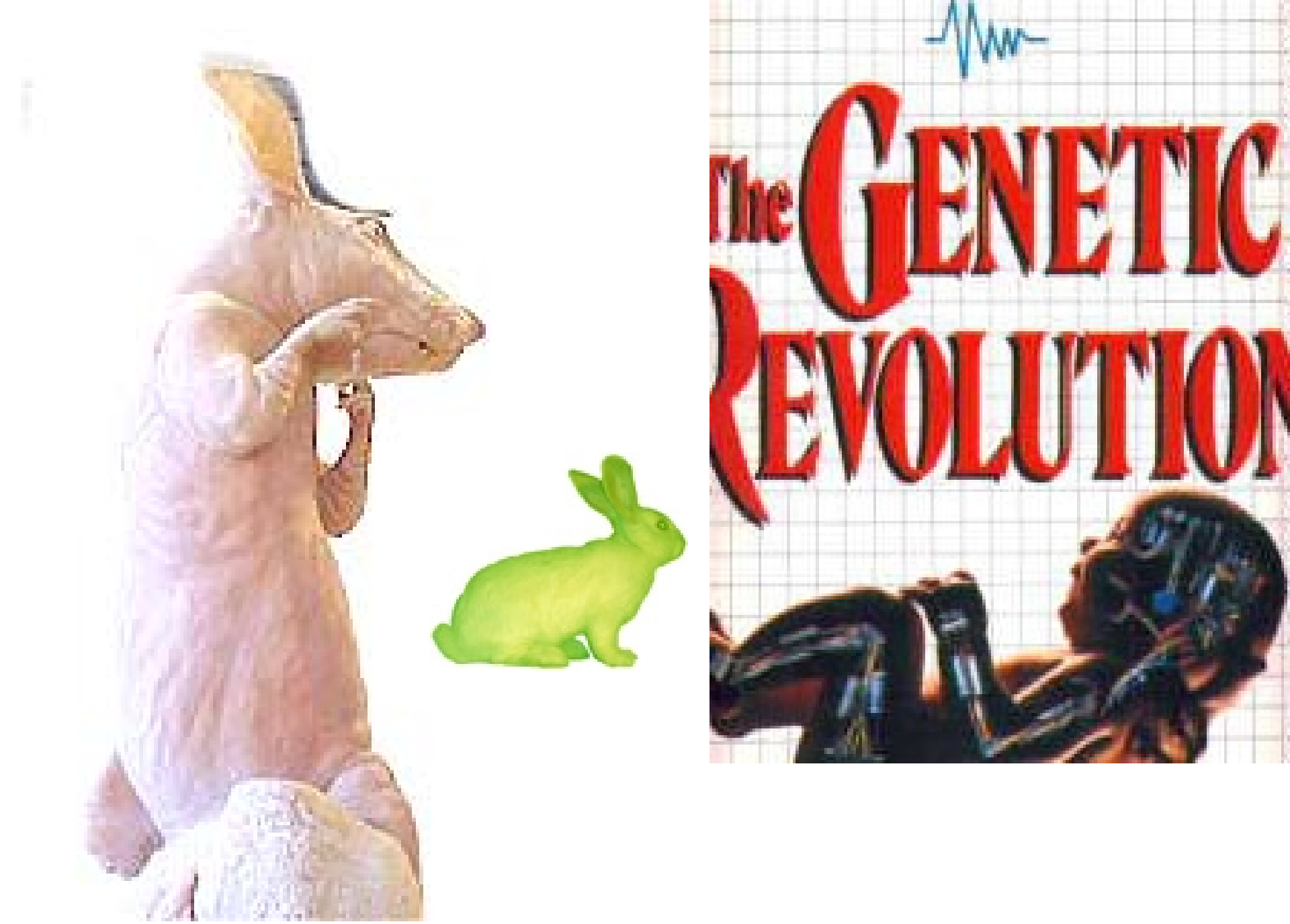


Darwin

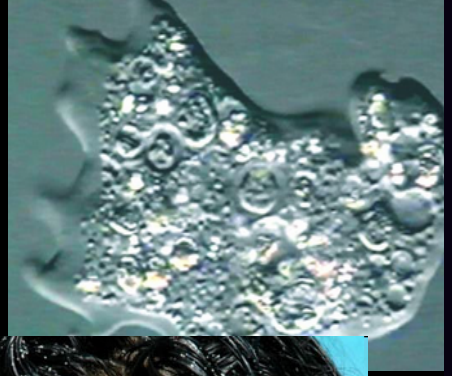


Teller

ശാസ്ത്രം ⟶ സാങ്കേതിക വിദ്യ

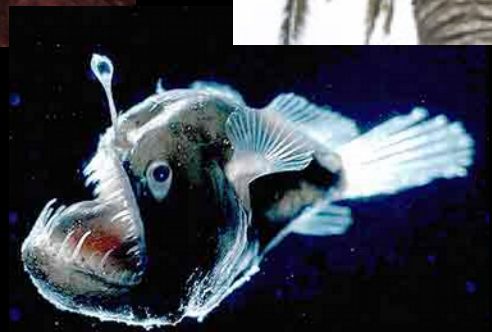

The GENETIC
REVOLUTION

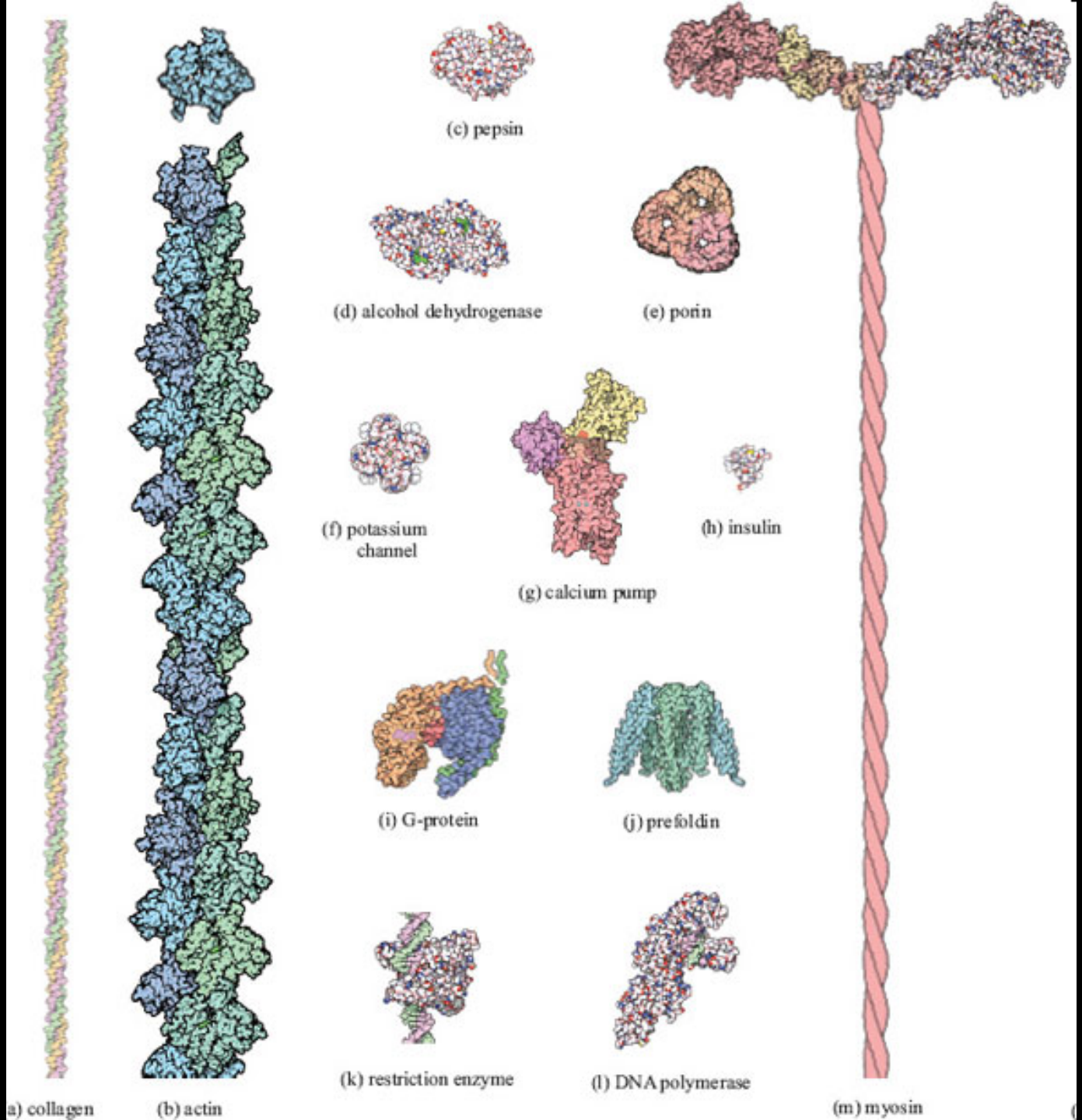
ശാസ്ത്രം  സാങ്കേതിക വിദ്യ

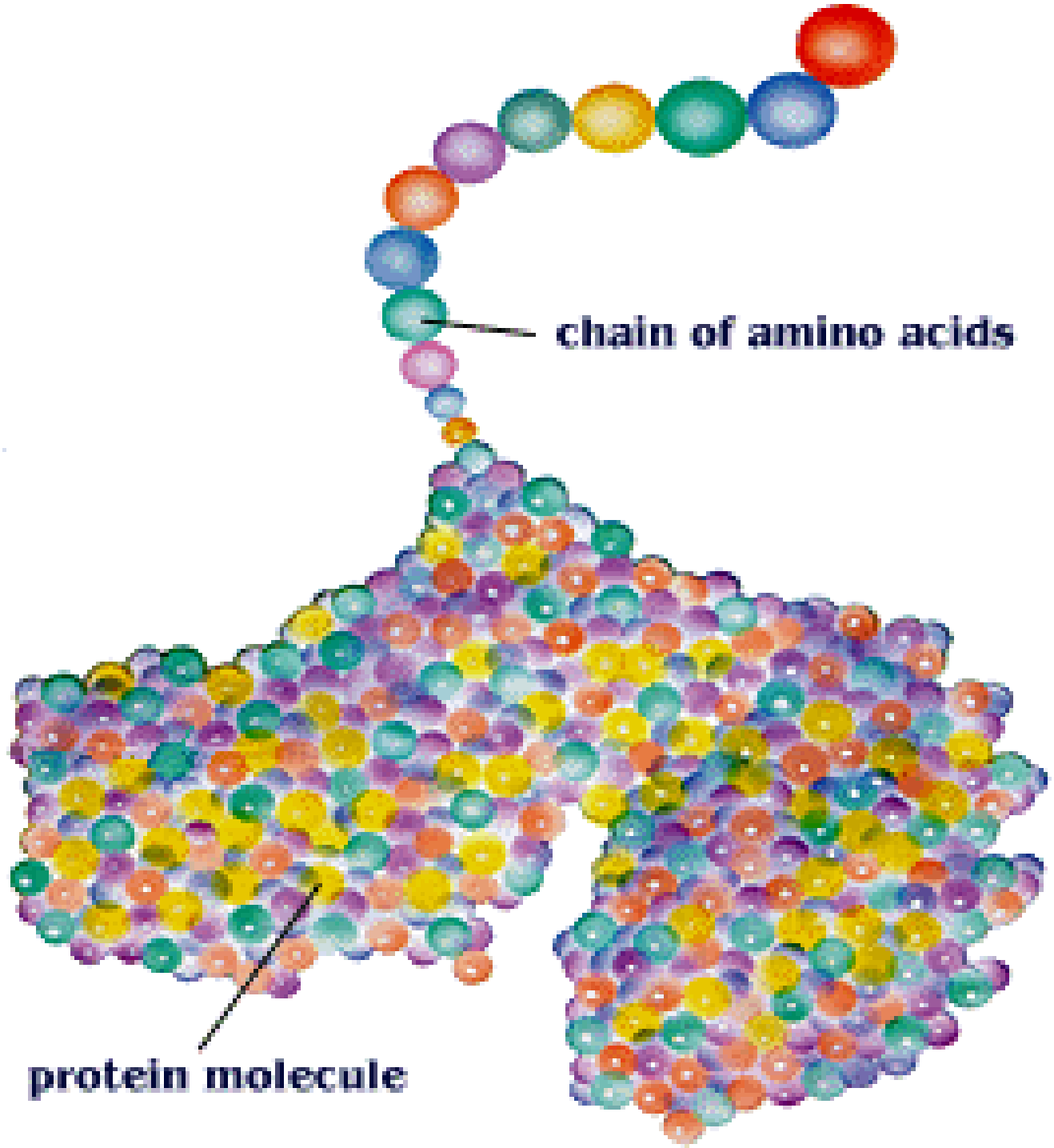





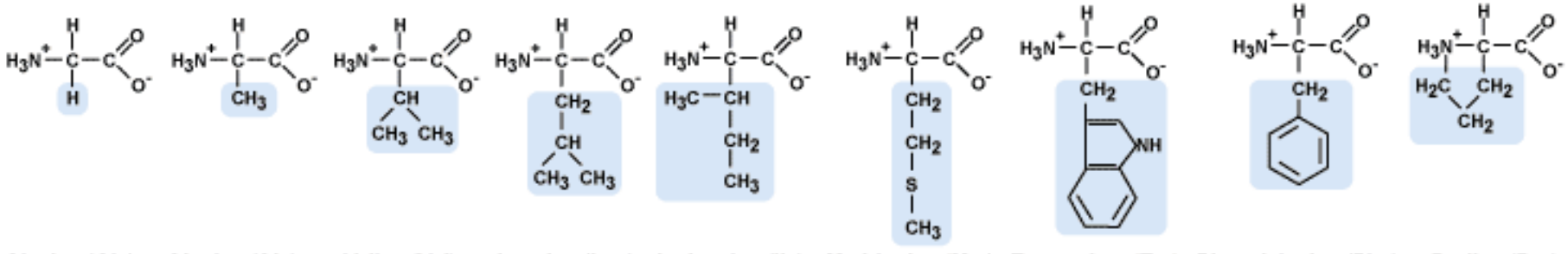



(c) pepsin
(d) alcohol dehydrogenase
(e) porin
(f) potassium channel
(g) calcium pump
(h) insulin
(i) G-protein
(j) prefoldin
(k) restriction enzyme
(l) DNA polymerase
a) collagen
(b) actin
(m) myosin

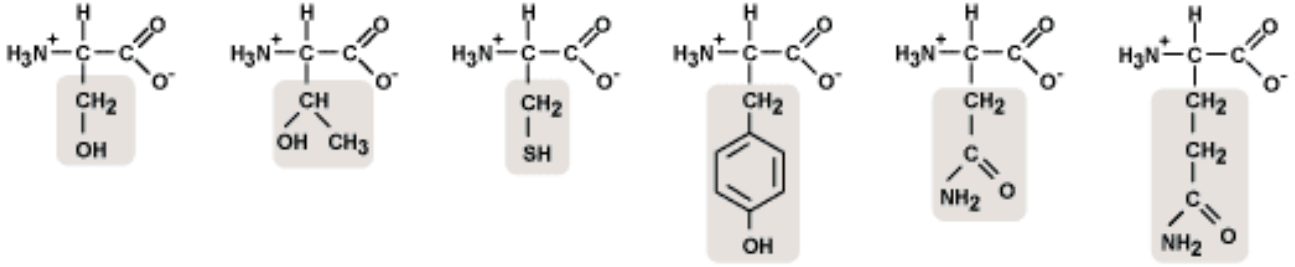

chain of amino acids
protein molecule

NONPOLAR



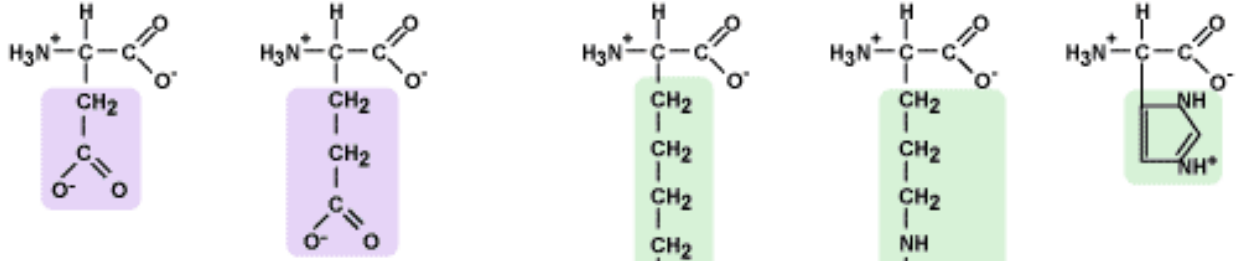
Glycine (Gly) Alanine (Ala) Valine (Val) Leucine (Leu) Isoleucine (Ile) Methionine (Met) Tryptophan (Trp) Phenylalanine (Phe) Proline (Pro)

POLAR



Serine (Ser) Threonine (Thr) Cysteine (Cys) Tyrosine (Tyr) Asparagine (Asn) Glutamine (Gln)

Electrically Charged



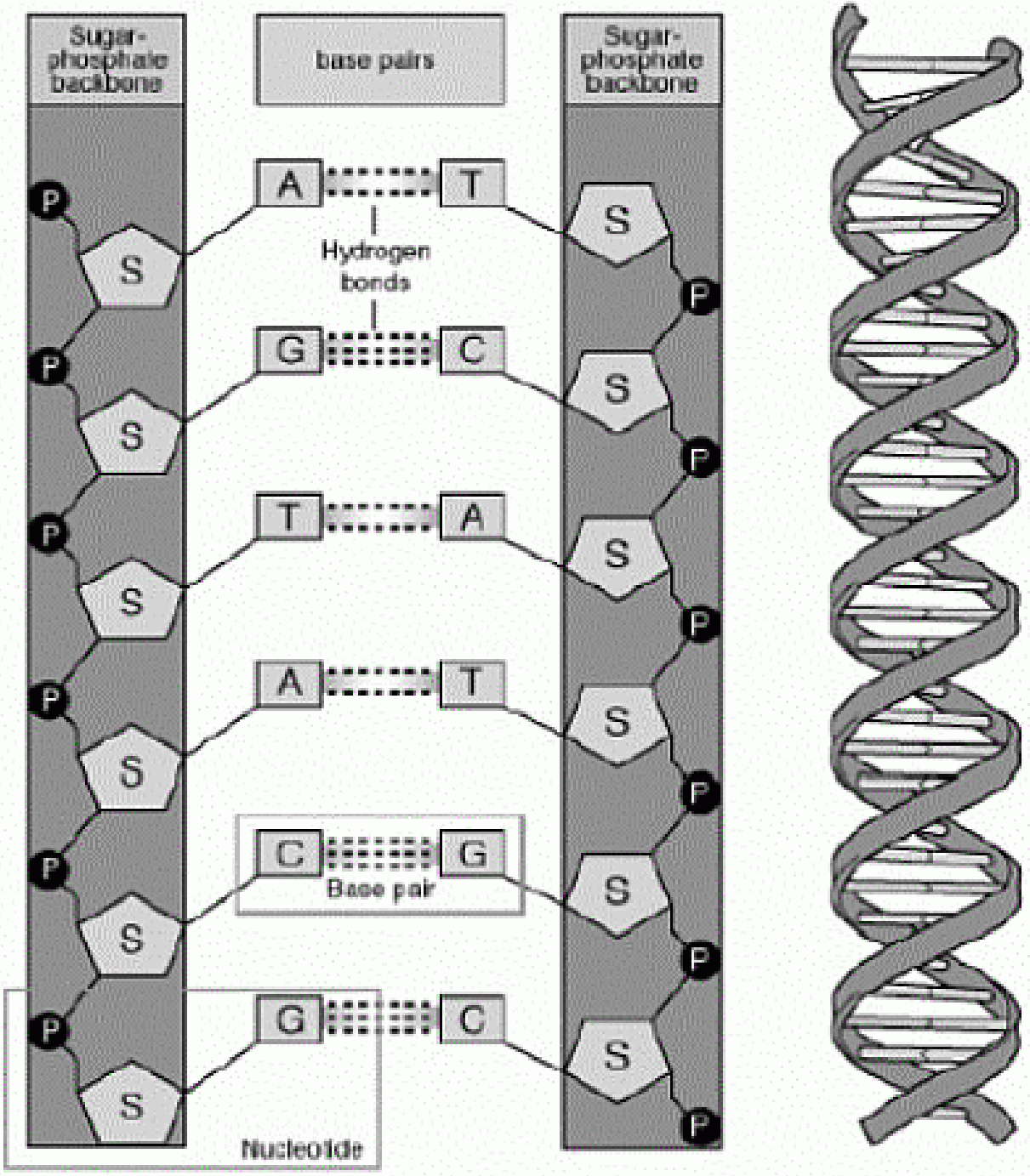
Acidic

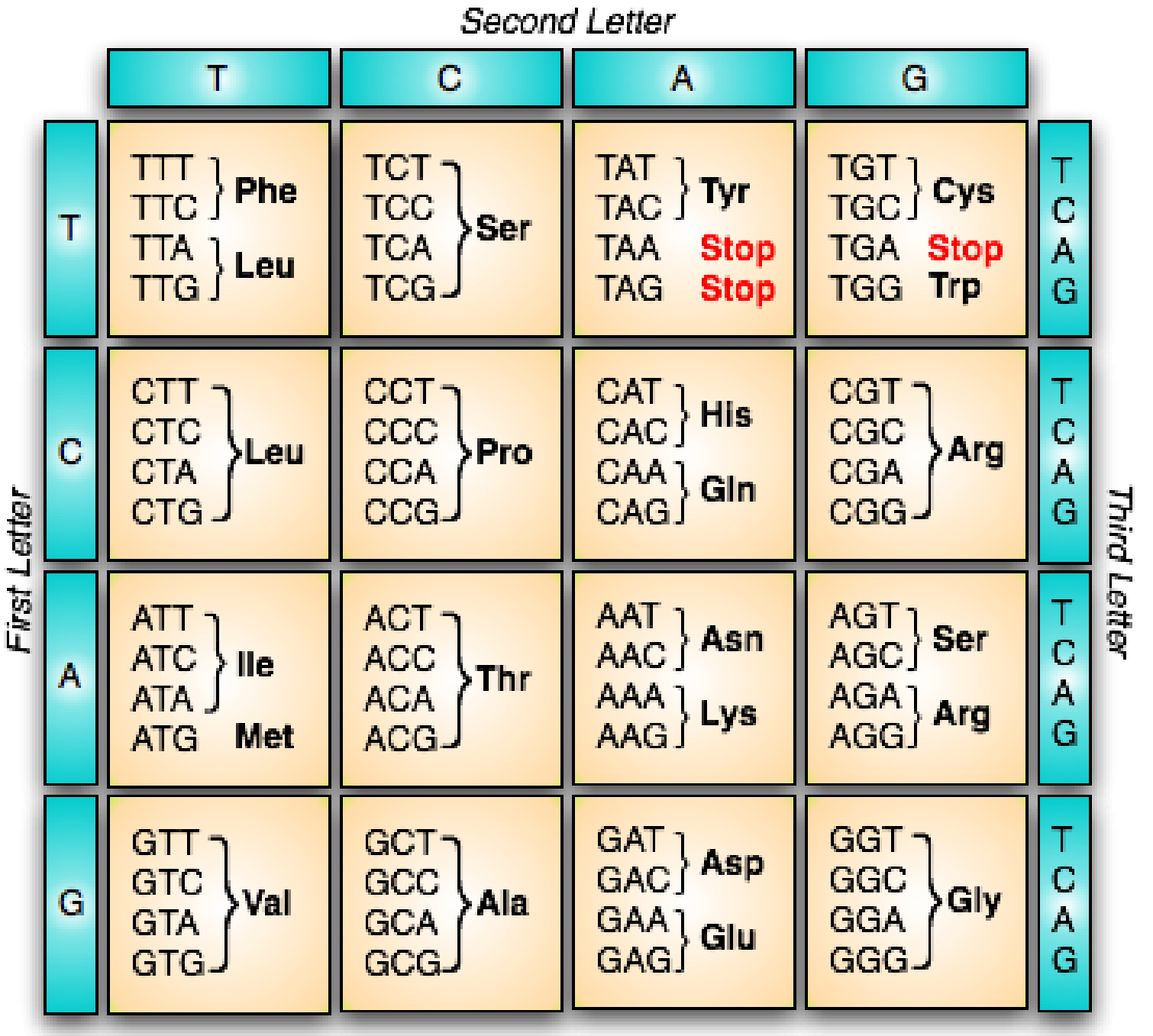
Aspartic Acid (Asp) Glutamic Acid (Glu)

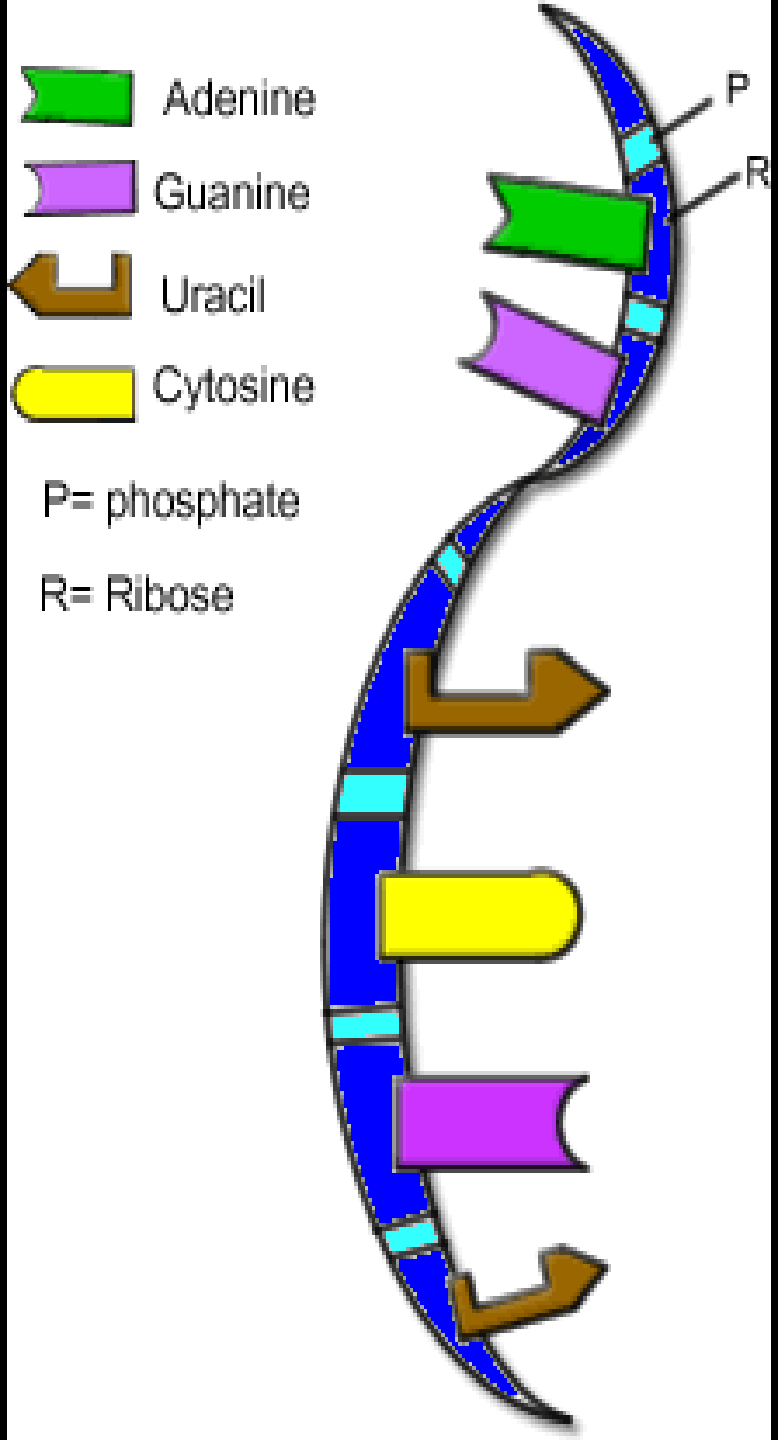
Lysine (Lys)

Basic

Arginine (Arg) Histidine (His)


Sugar-phosphate backbone
base pairs
Sugar-phosphate backbone
A
T
Hydrogen bonds
G
C
T
A
A
T
C
G
Base pair
G
C
P
S
Nucleotide


Second Letter
T
C
A
G
First Letter
Third Letter
T
C
A
G
TTT TTC Phe
TTA TTG Leu
TCT TCC TCA TCG Ser
TAT TAC Tyr
TAA Stop
TAG Stop
TGT TGC Cys
TGA Stop
TGG Trp
CTT CTC CTA CTG Leu
CCT CCC CCA CCG Pro
CAT CAC His
CAA CAG Gln
CGT CGC CGA CGG Arg
ATT ATC ATA Ile
ATG Met
ACT ACC ACA ACG Thr
AAT AAC Asn
AAA AAG Lys
AGT AGC Ser
AGA AGG Arg
GTT GTC GTA GTG Val
GCT GCC GCA GCG Ala
GAT GAC Asp
GAA GAG Glu
GGT GGC GGA GGG Gly


Adenine
Guanine
Uracil
Cytosine
P= phosphate
R= Ribose
P
R

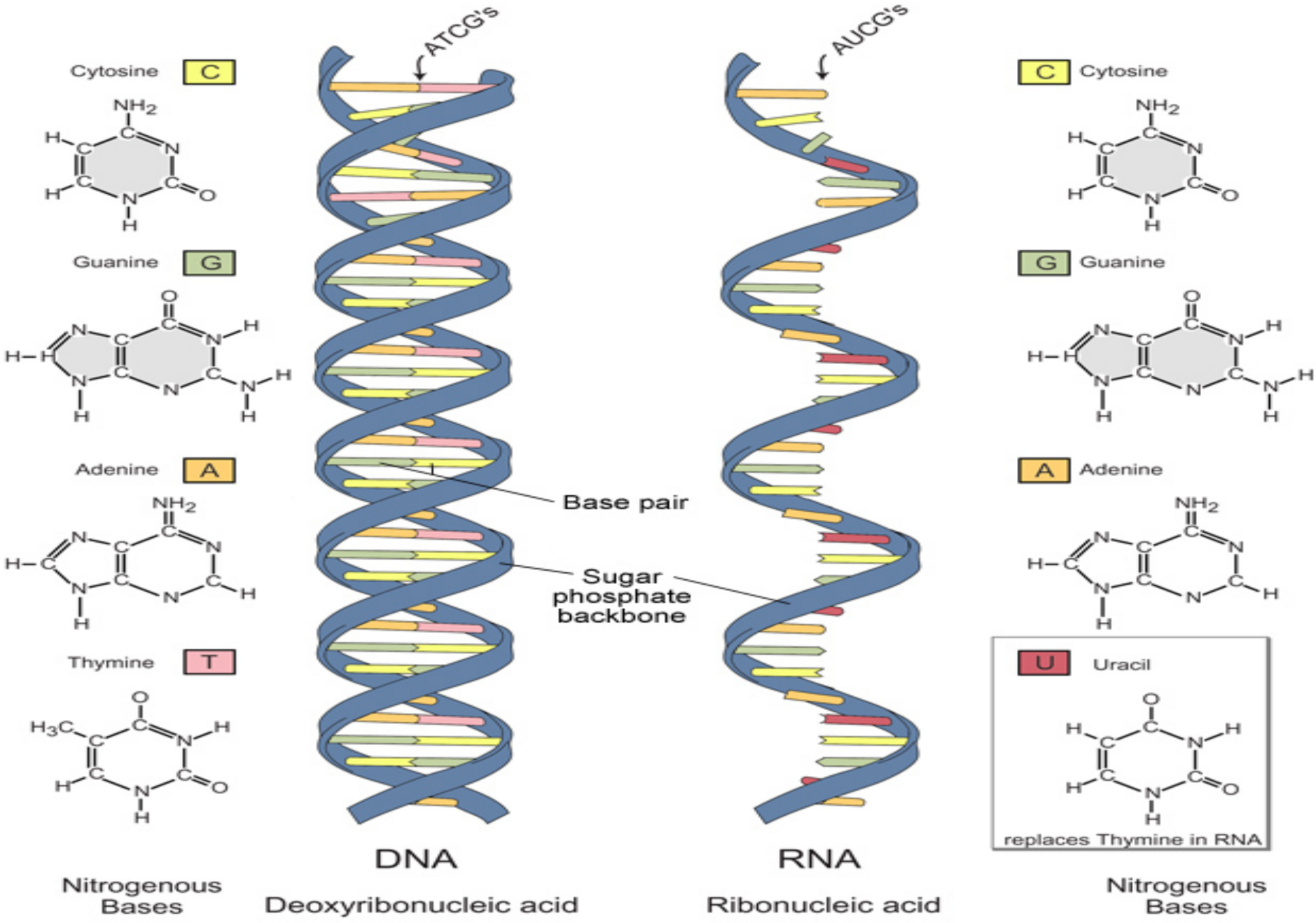
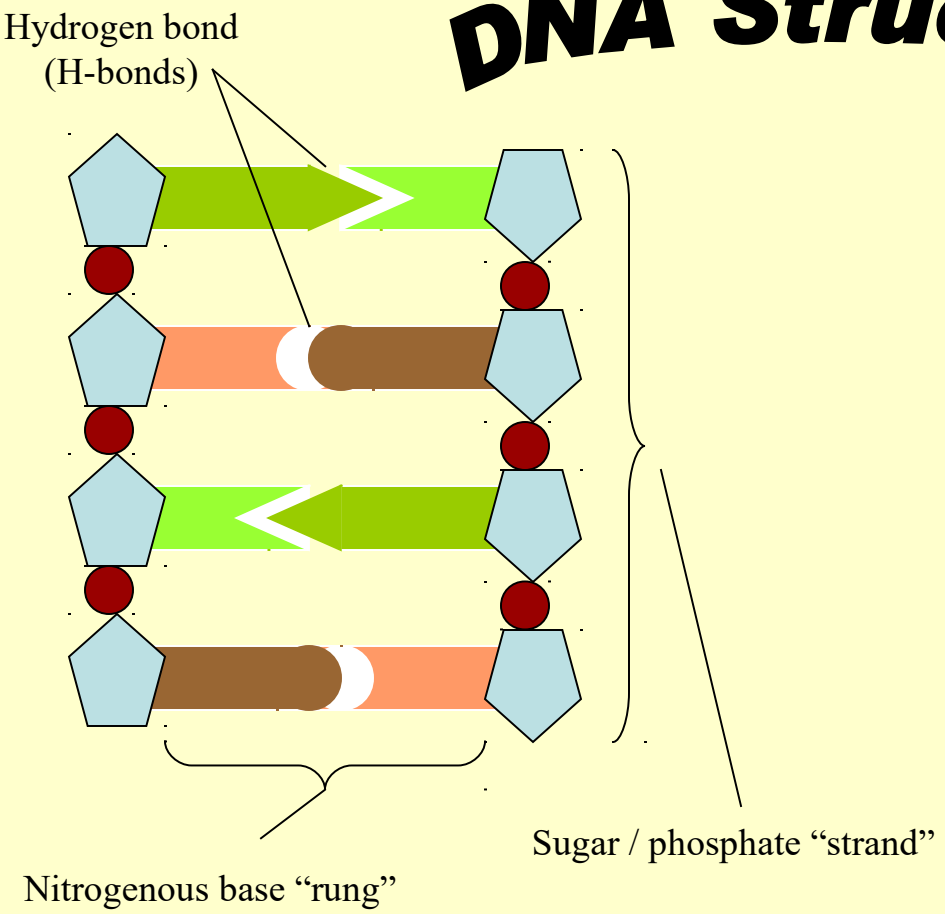
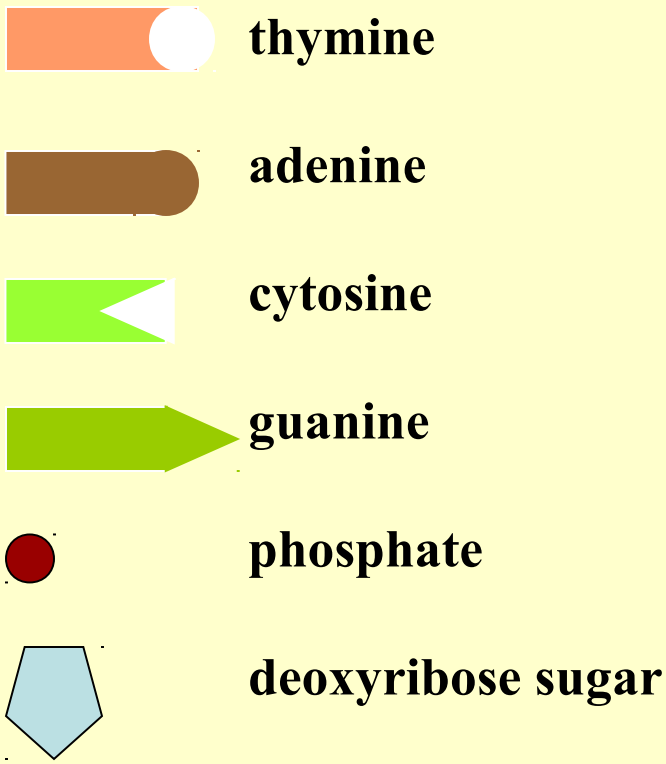


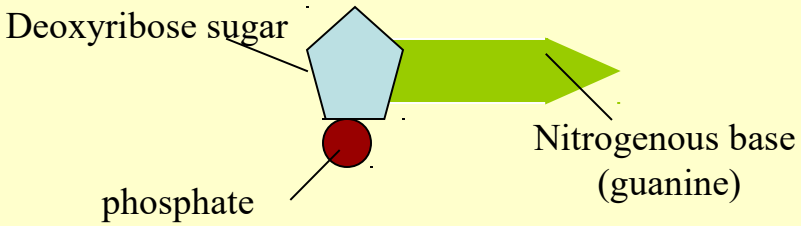
Image adapted from: National Human Genome Research Institute.

DNA Structure

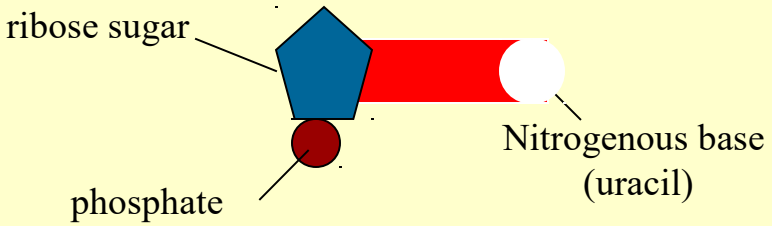




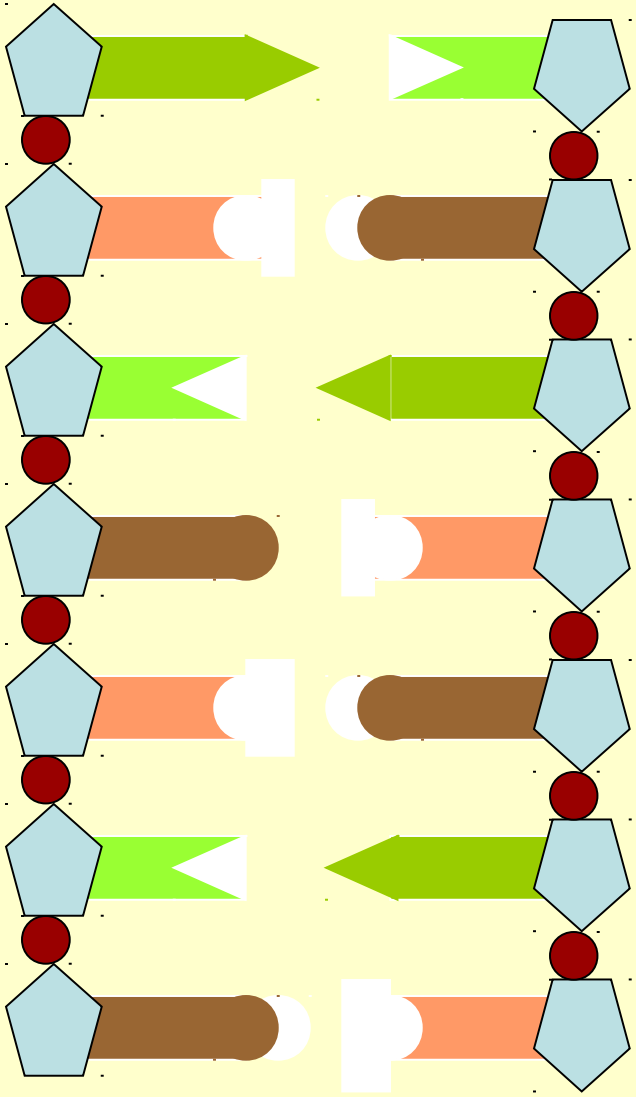
DNA nucleotide



RNA nucleotide



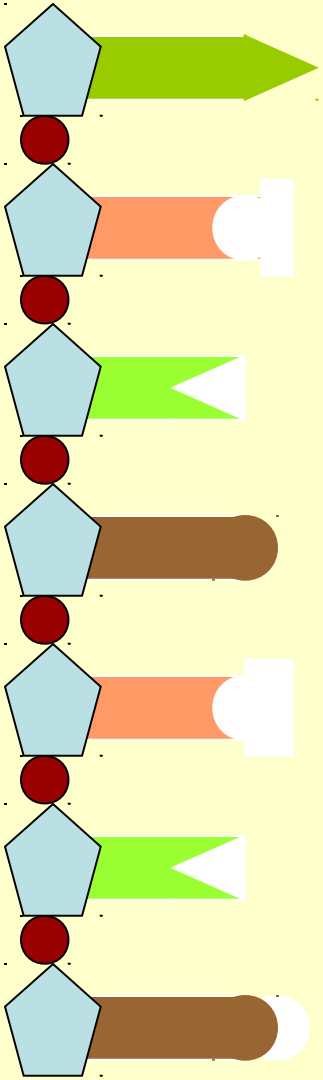
DNA Replication



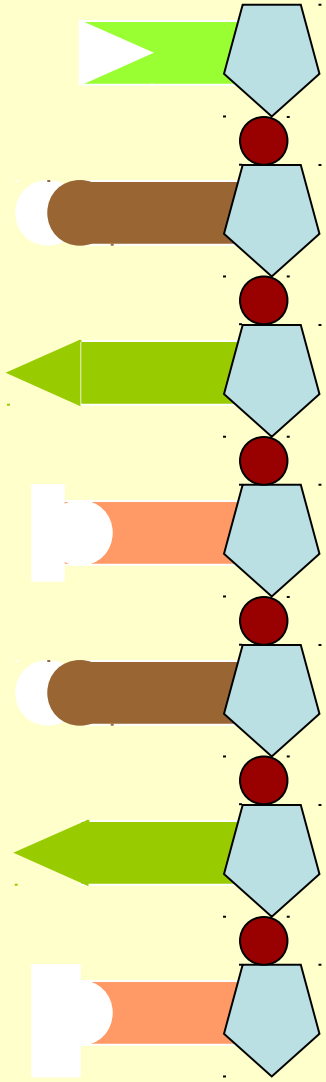
Step 1: Hydrogen bonds between complimentary bases break

DNA “unzips”

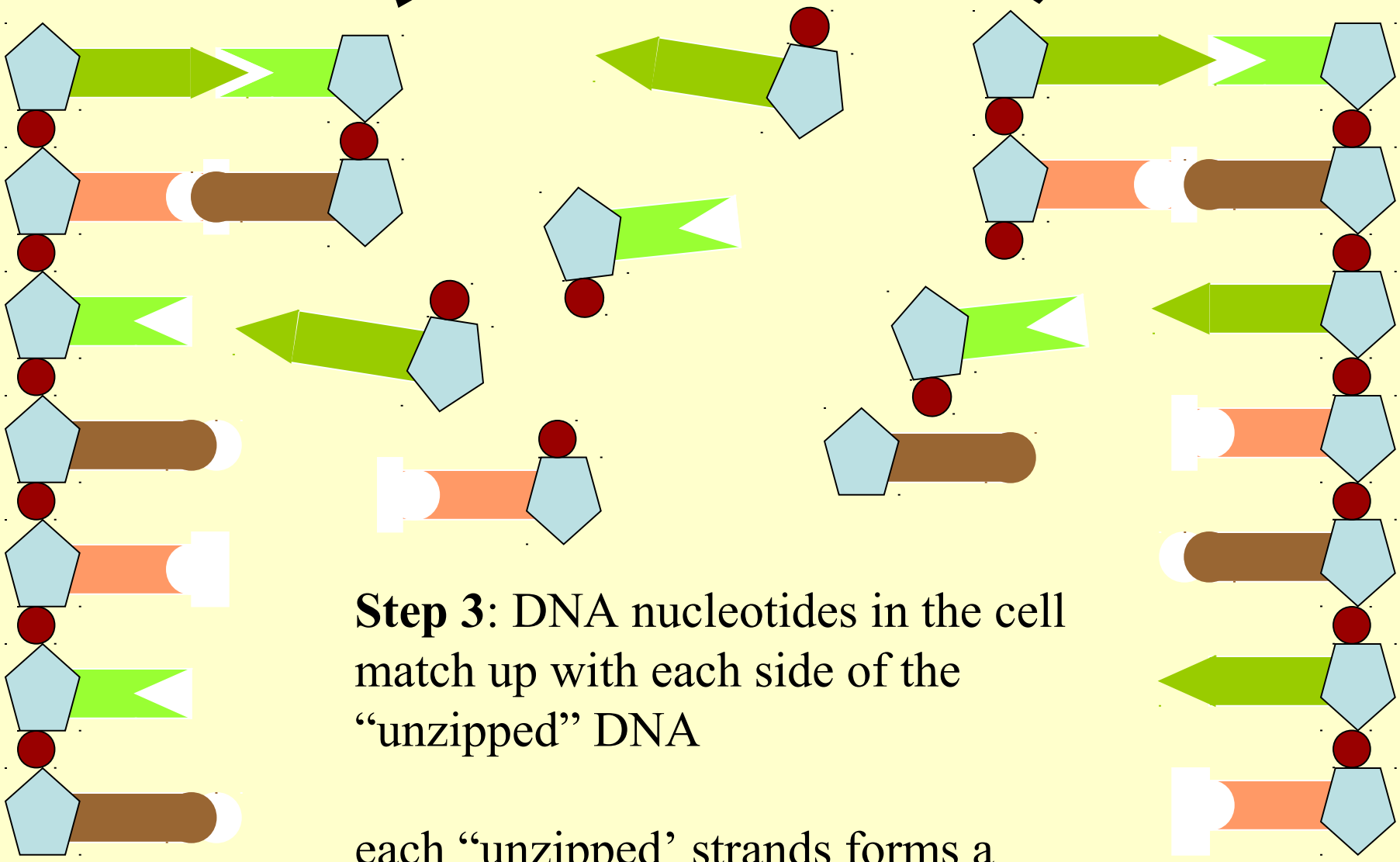
DNA Replication



Step 2: DNA strands pull apart from each other



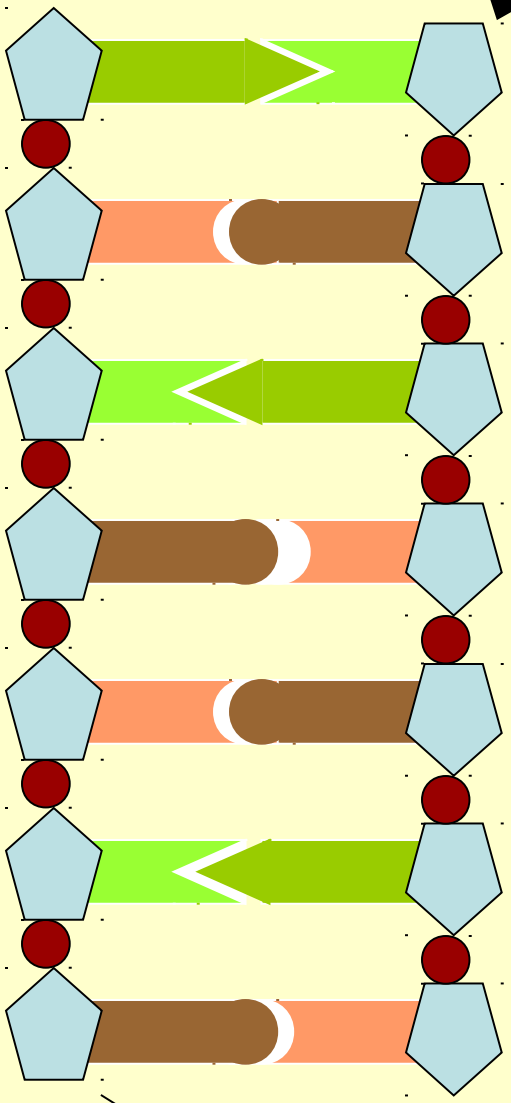
DNA Replication



Step 3: DNA nucleotides in the cell match up with each side of the "unzipped" DNA

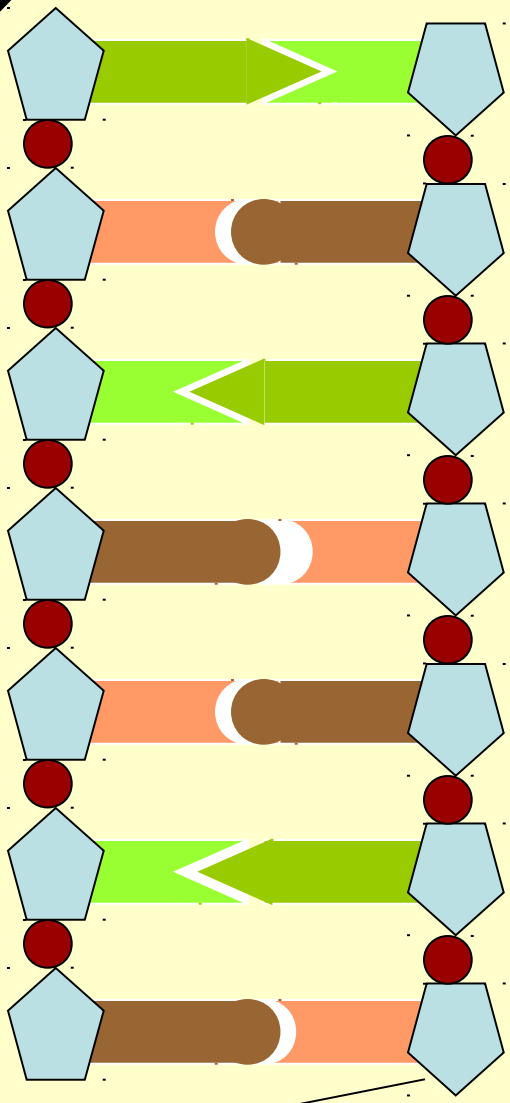
each "unzipped' strands forms a template for a new strand

DNA Replication



Step 4: Each "old' strand forms a template for a "new" strand

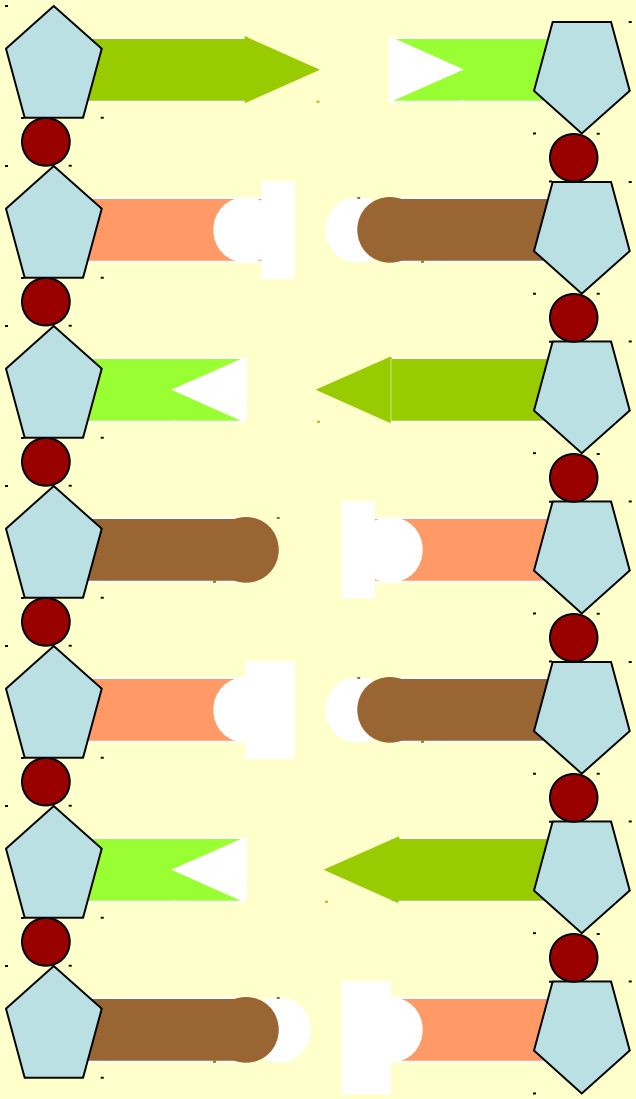
two identical DNA molecules form



"new" strand, identical sequence to the original

"old" (original) strand

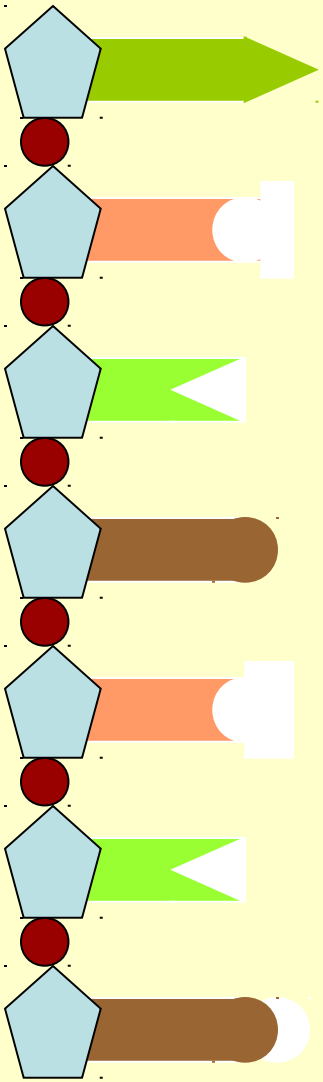
RNA Transcription



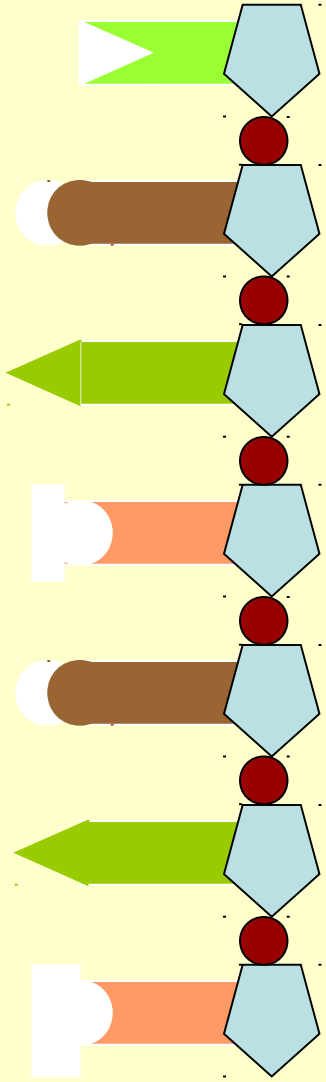
Step 1: Hydrogen bonds between complimentary bases break

DNA “unzips”

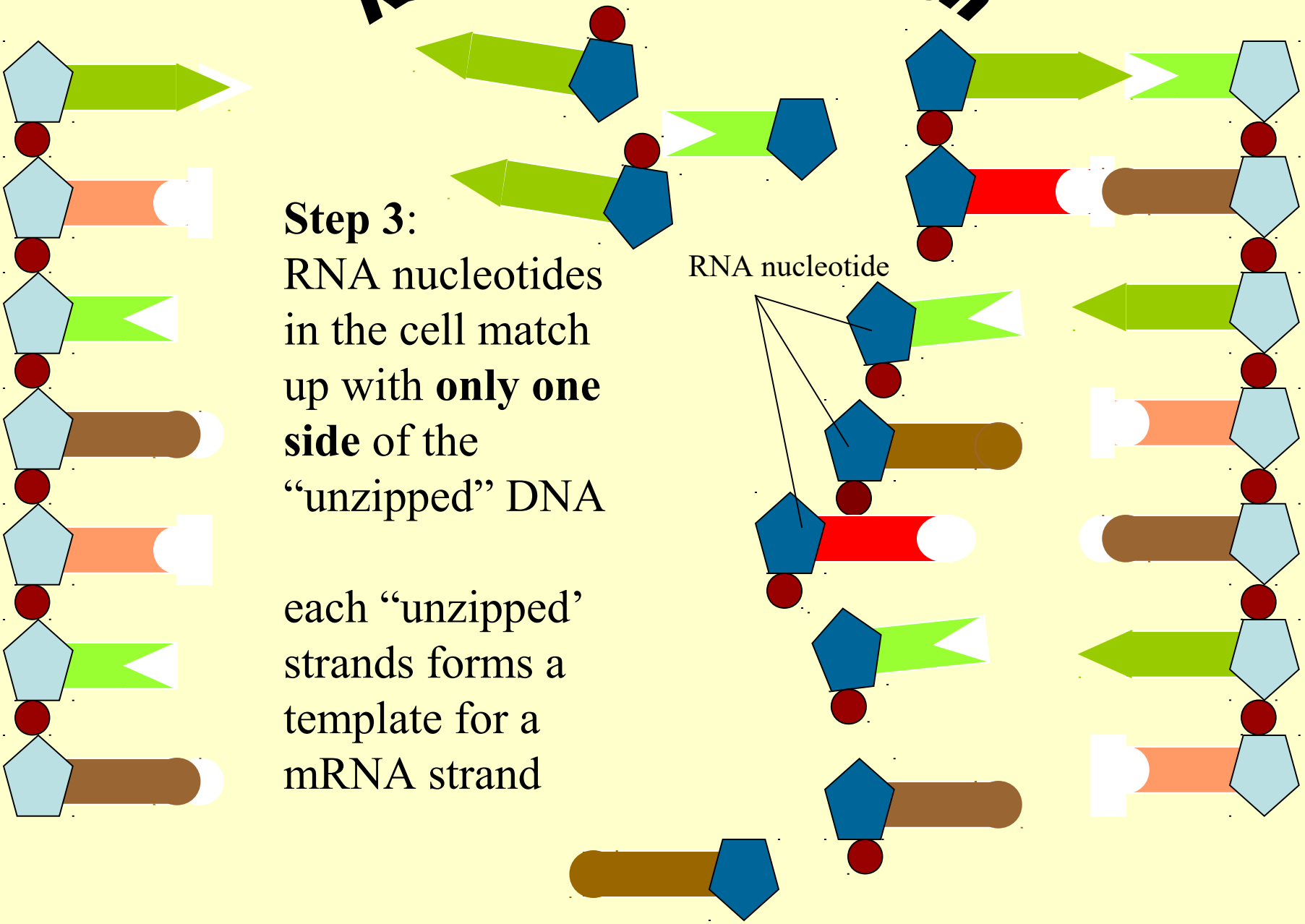
RNA Transcription



Step 2: DNA strands pull apart from each other



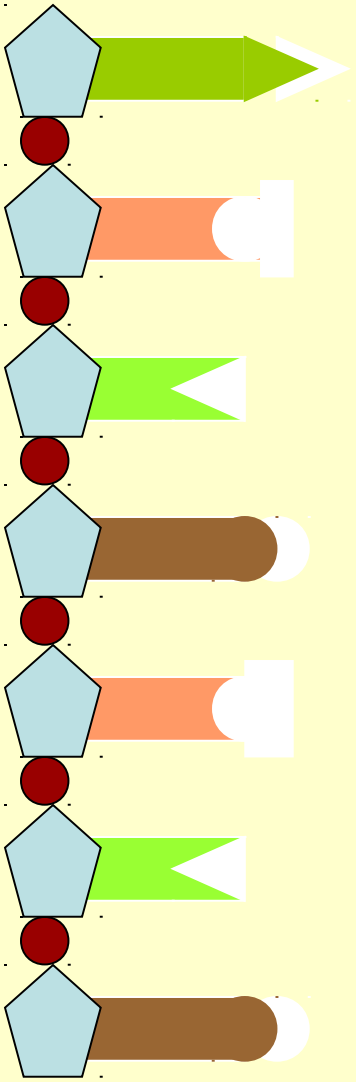
RNA Transcription



Step 3:
RNA nucleotides in the cell match up with **only one side** of the "unzipped" DNA

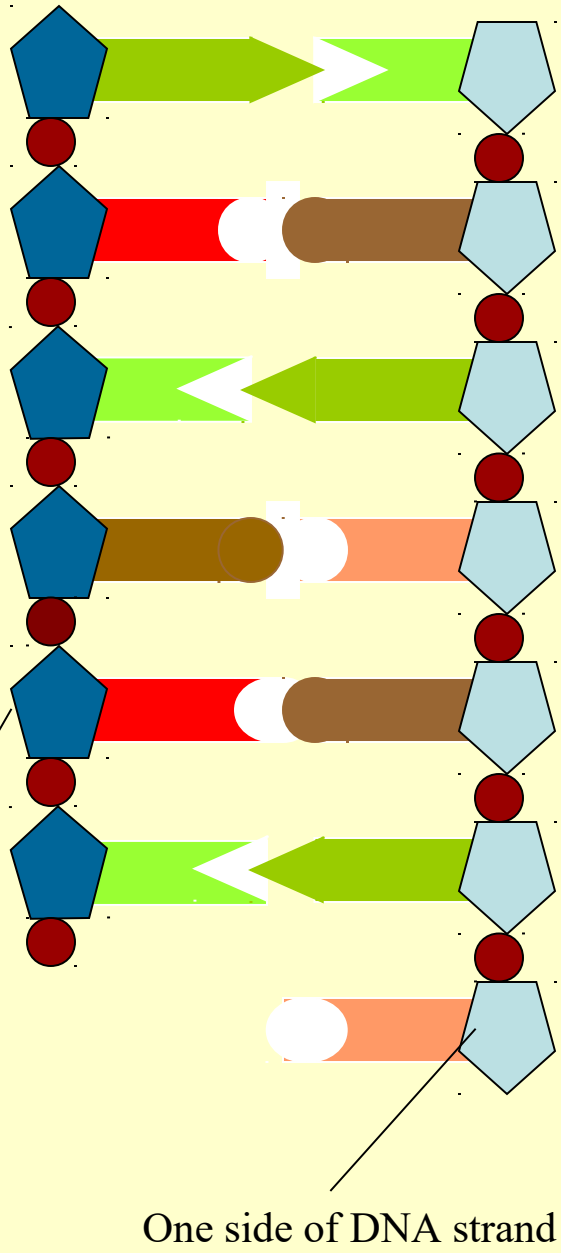
each "unzipped' strands forms a template for a mRNA strand

RNA Transcription

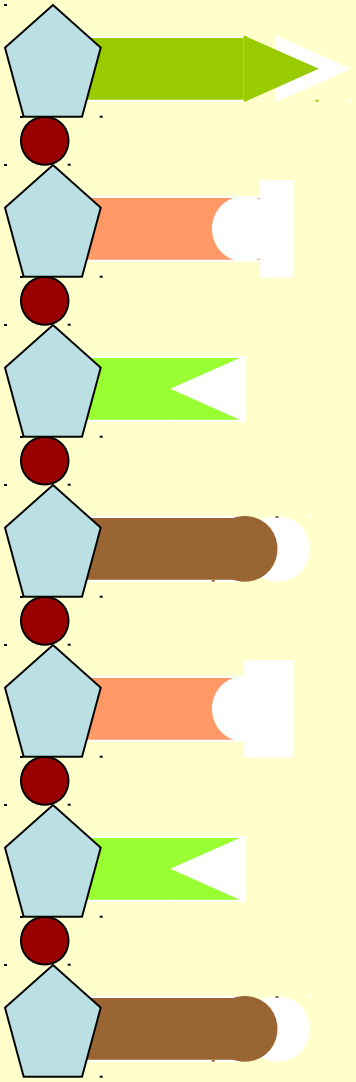


Step 4:
RNA nucleotides continue to match up with "unzipped" DNA

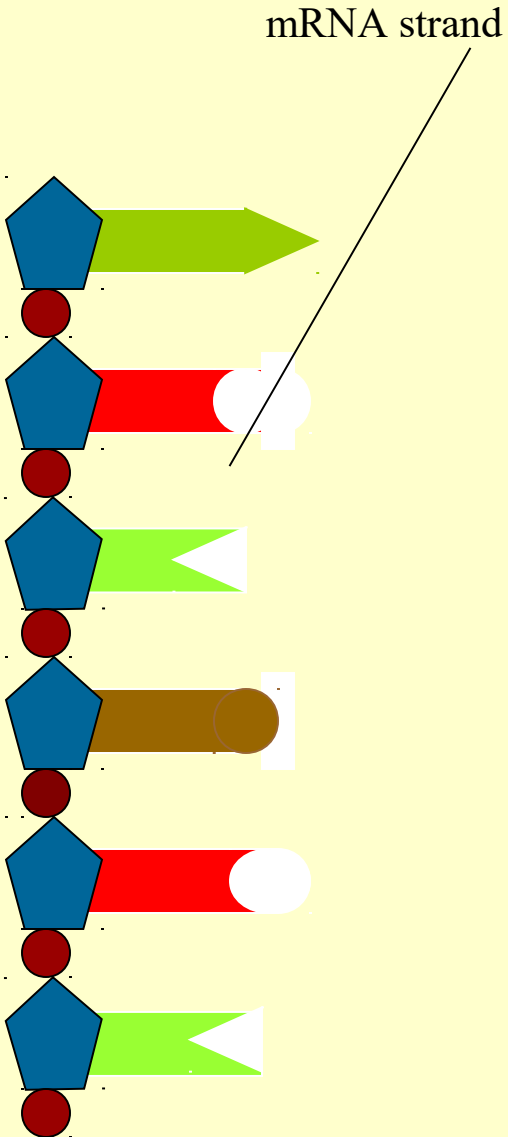
until the message is completely transcribed

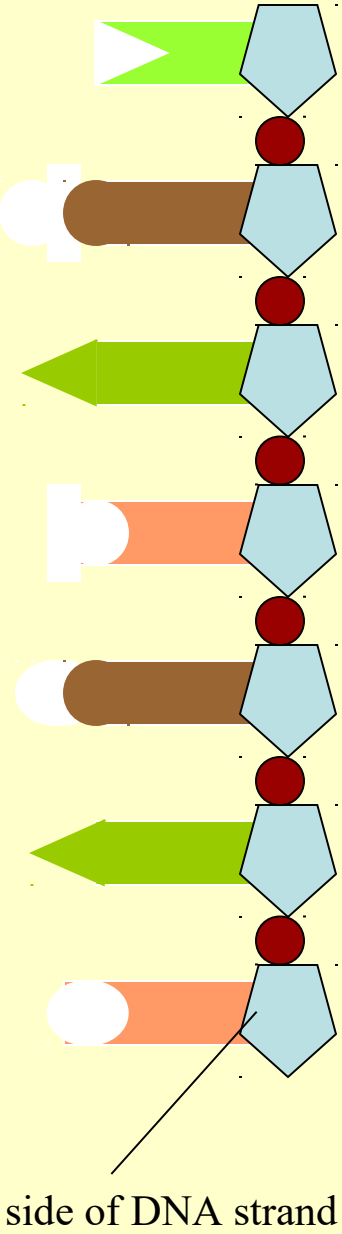


RNA Transcription

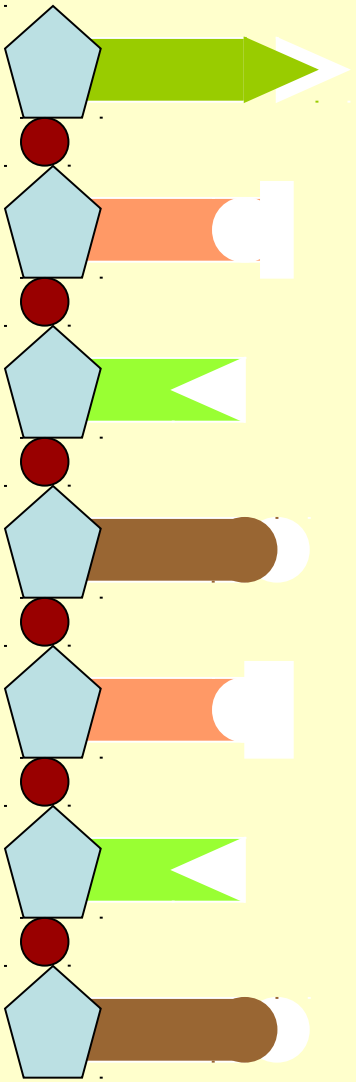


Step 4:
mRNA strand breaks off from the DNA strand

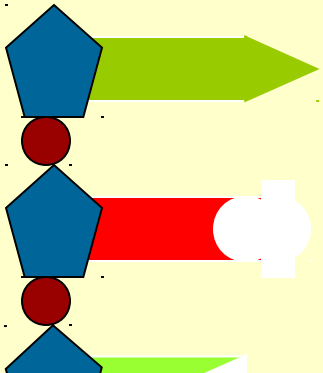


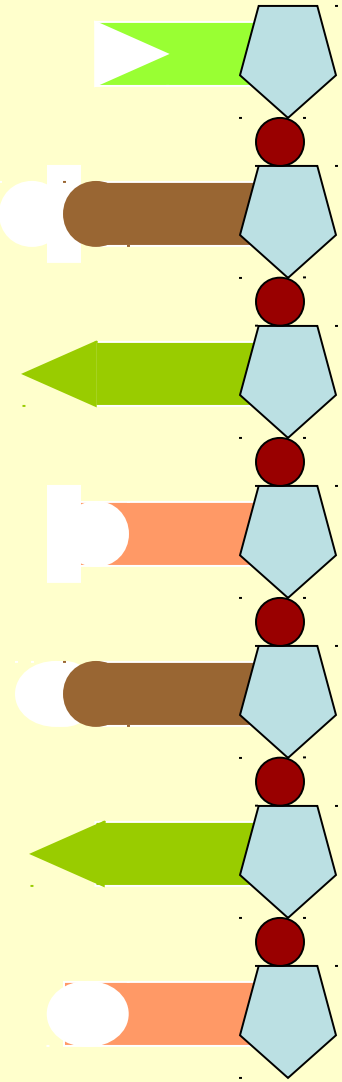


RNA Transcription

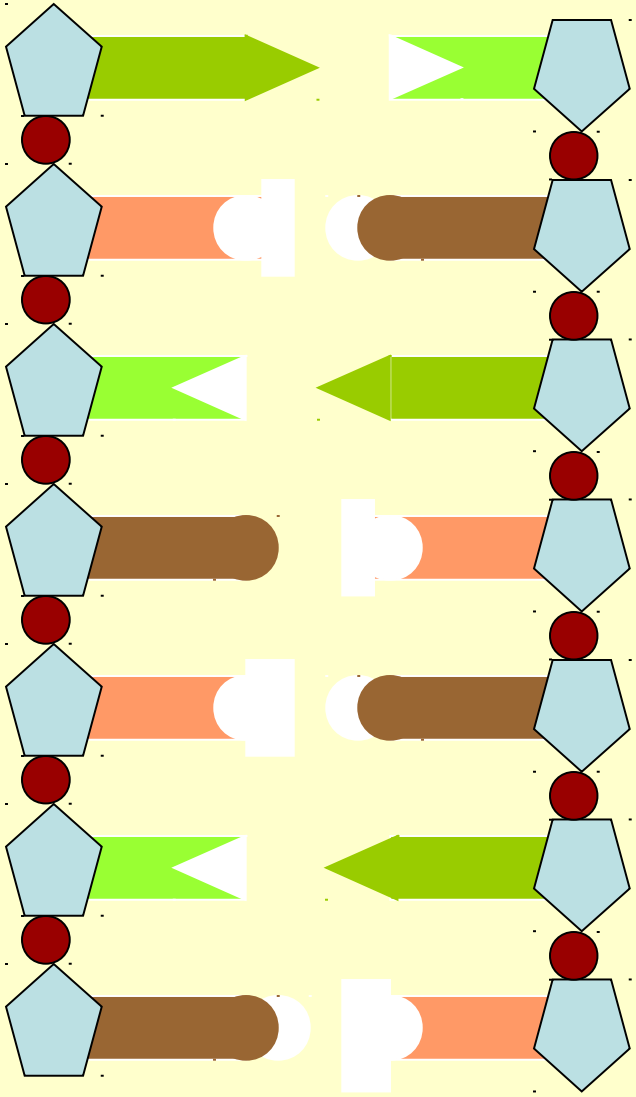


Step 5:
mRNA strand leaves the nucleus for the ribosome

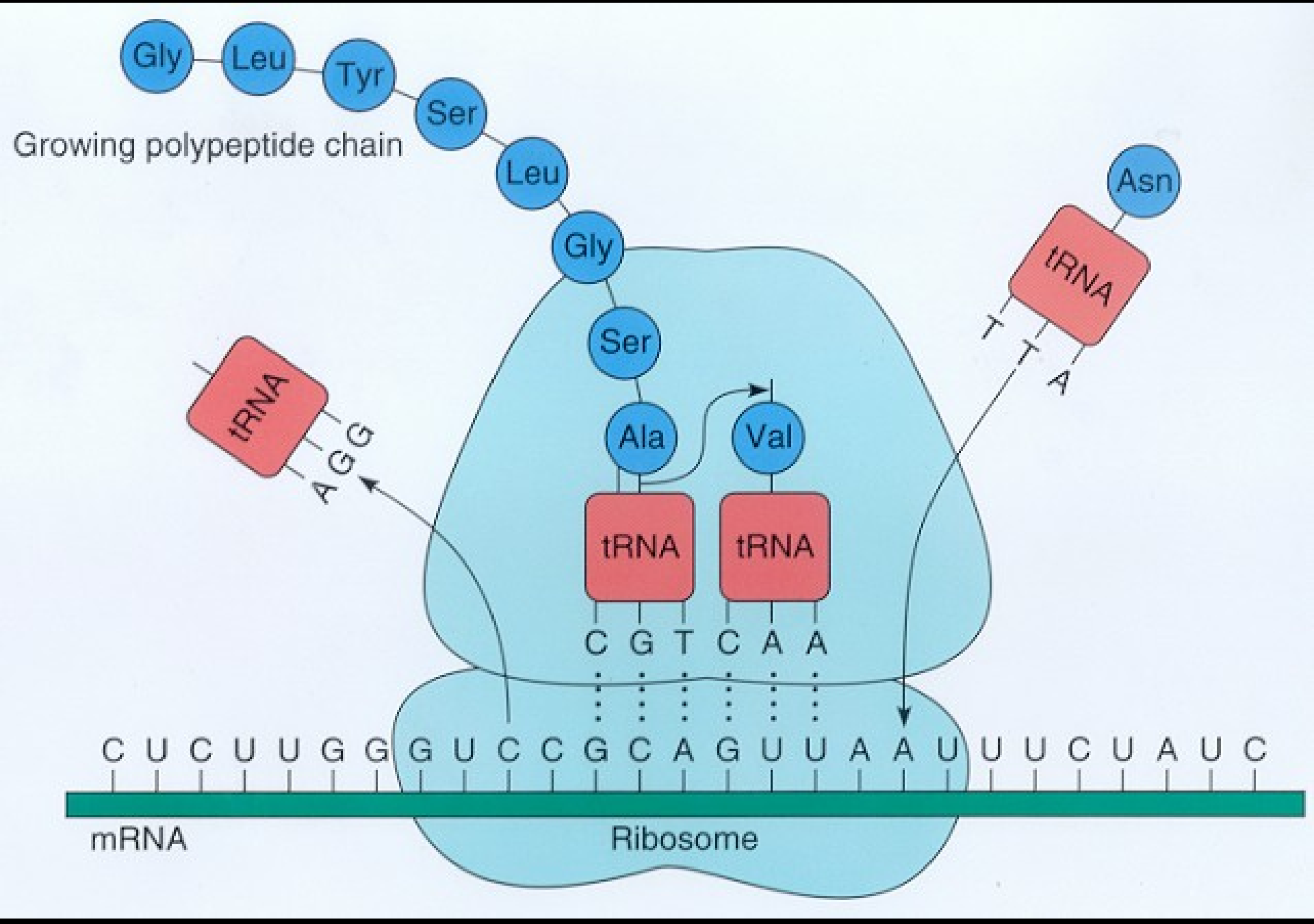




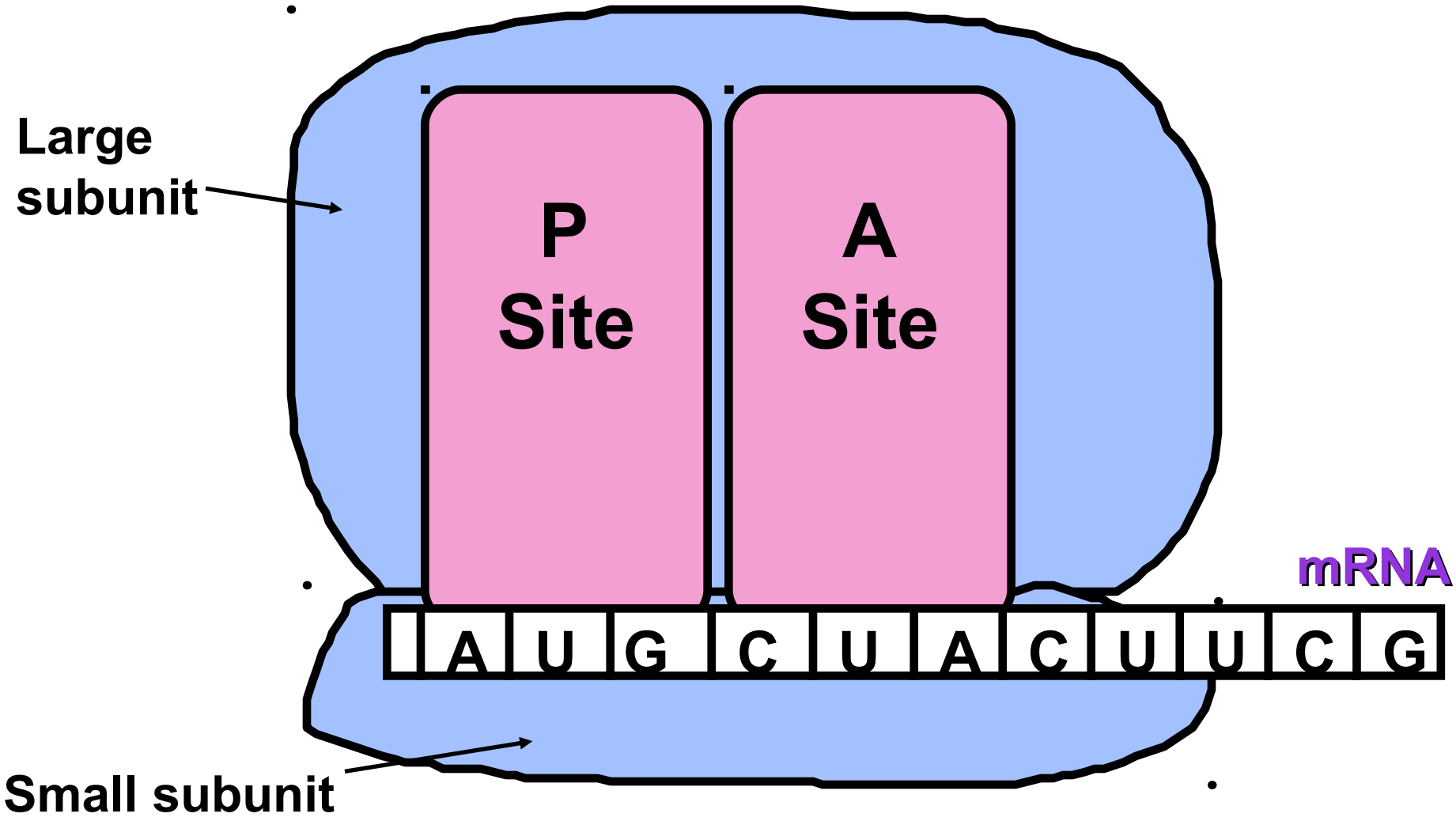
RNA Transcription



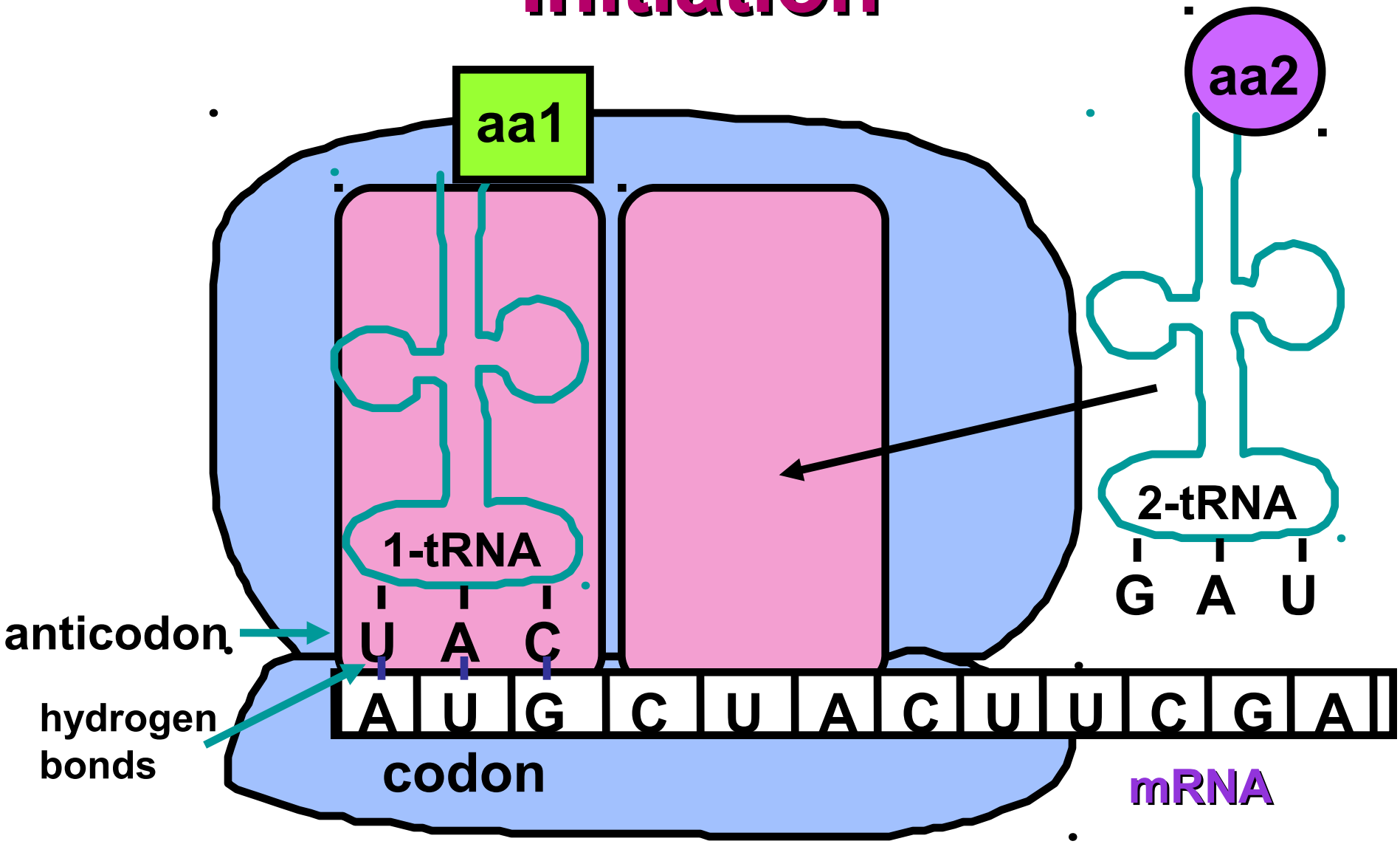
Step 6: Once the mRNA leaves, the DNA “zips” back together


Gly
Leu
Tyr
Ser
Leu
Gly
Ser
Ala
Val
Growing polypeptide chain
tRNA
A G G
tRNA
C G T C A A
tRNA
T T A
Asn
C U C U U G G G U C C G C A G U U A A U U U C U A U C
mRNA
Ribosome

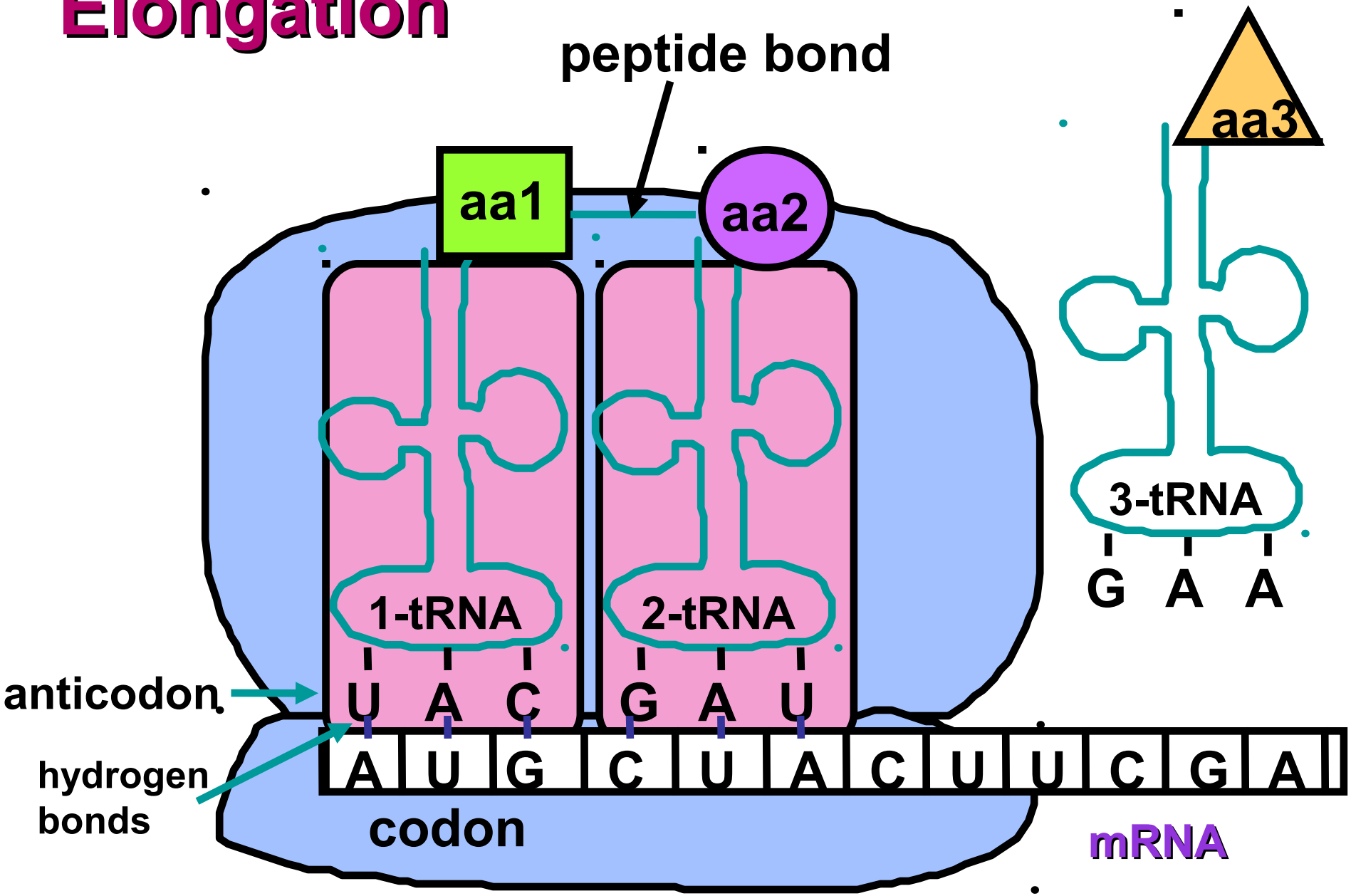
3. Translation

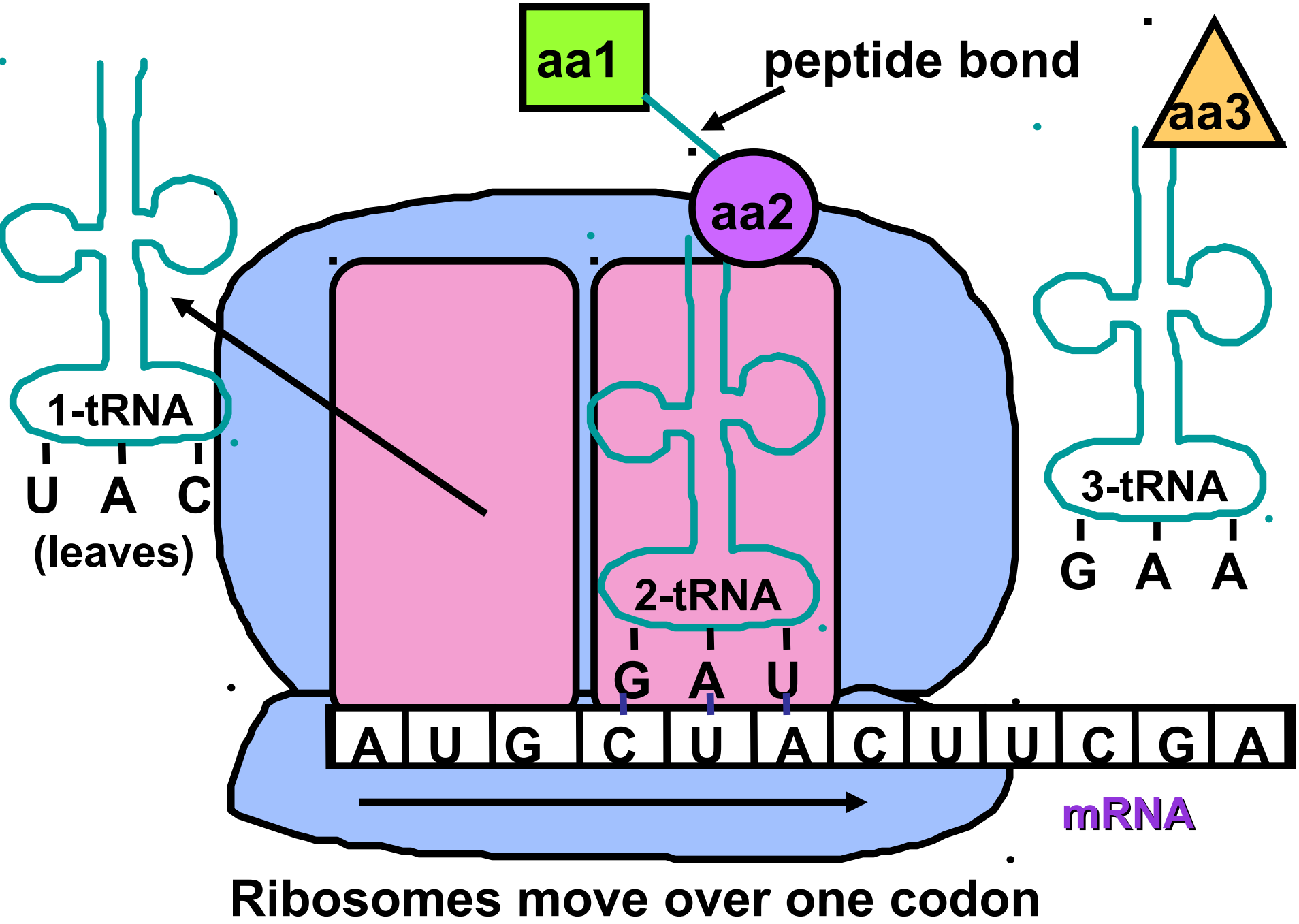


Initiation

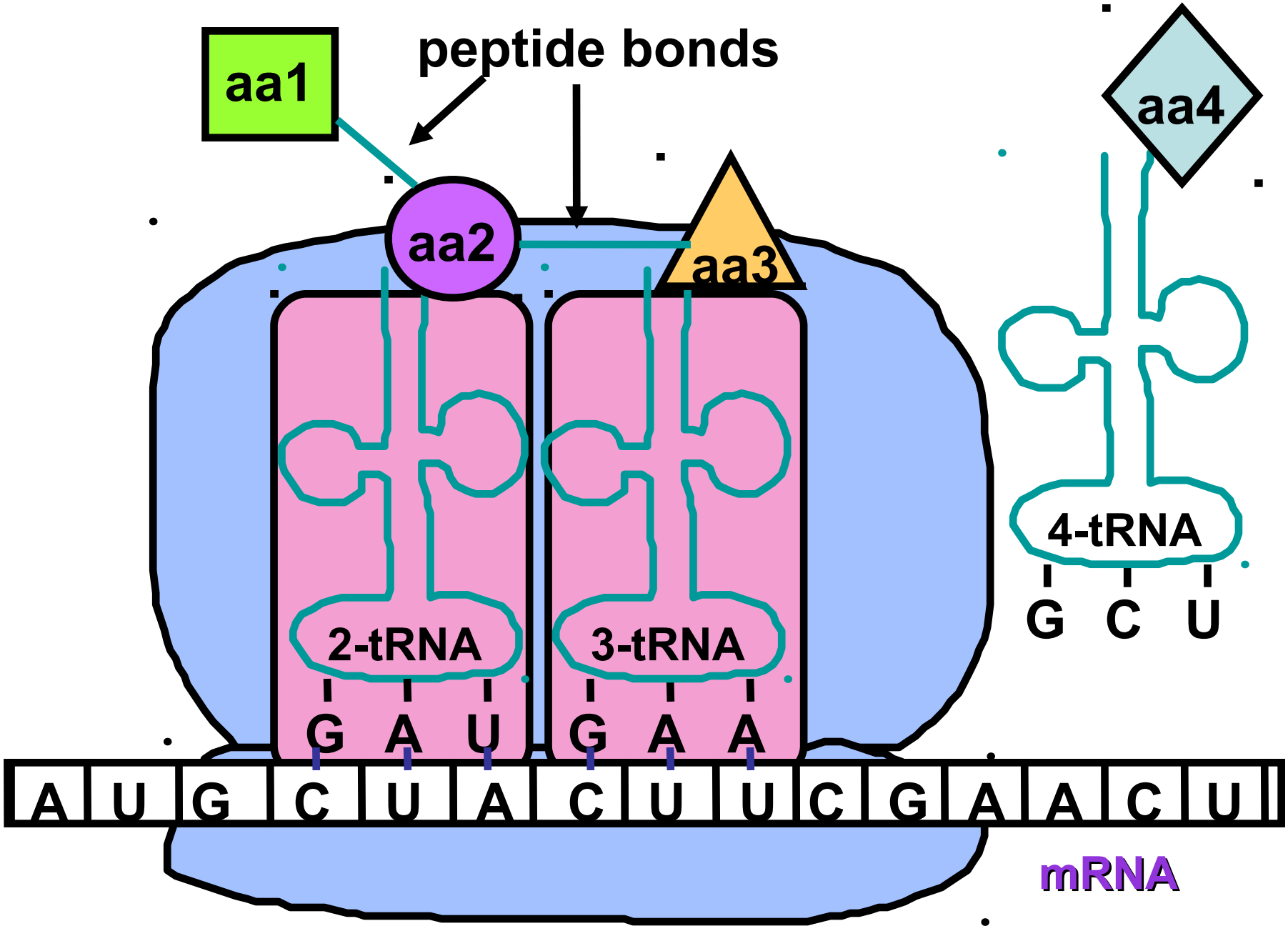

aa1
aa2
1-tRNA
2-tRNA
U A C
G A U
anticodon
hydrogen bonds
A U G C U A C U U C G A
codon
mRNA

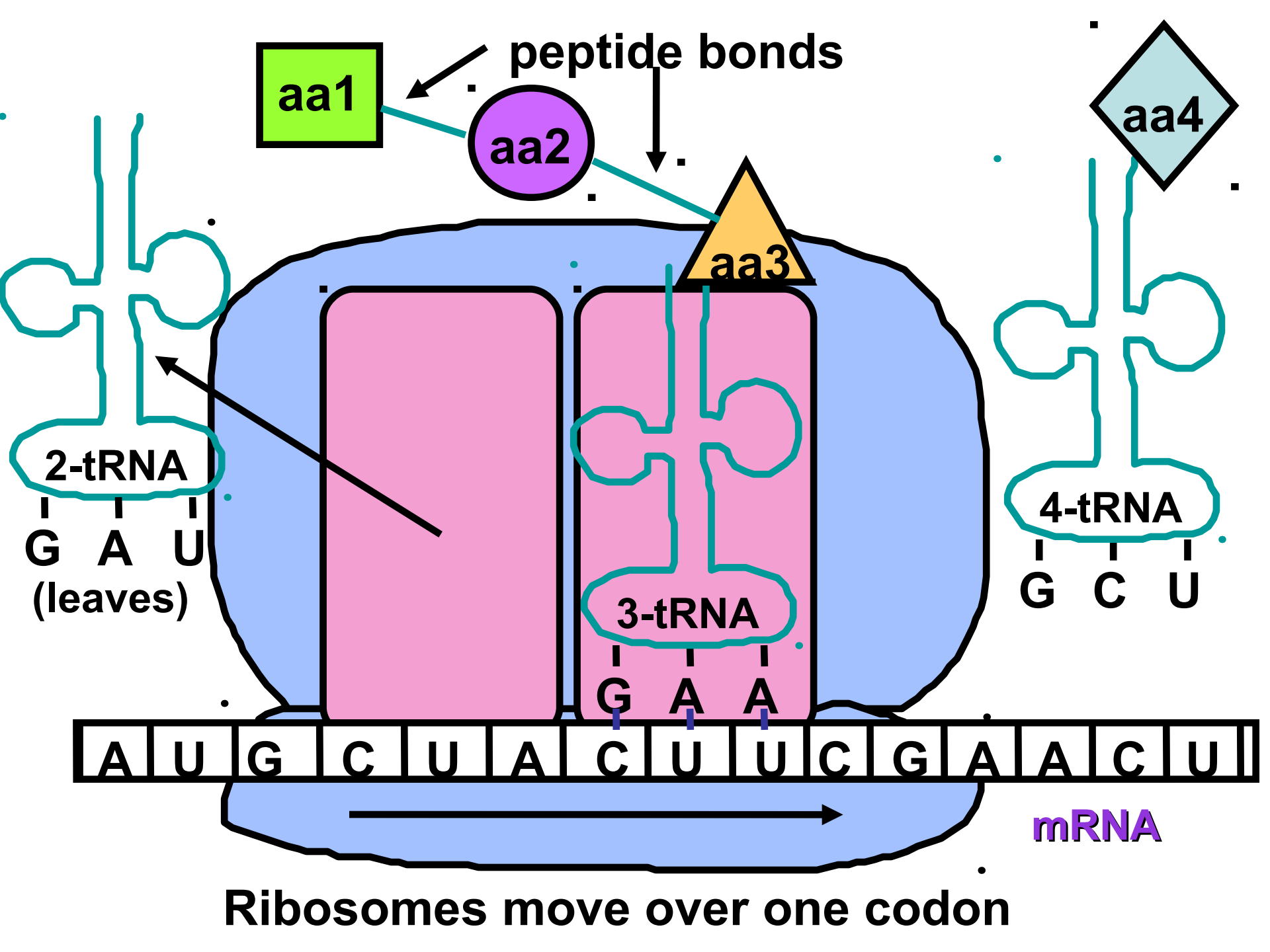
Elongation


peptide bond
aa1
aa2
aa3
1-tRNA
2-tRNA
3-tRNA
G A A
anticodon
U A C
G A U
hydrogen bonds
A U G C U A C U U C G A
codon
mRNA

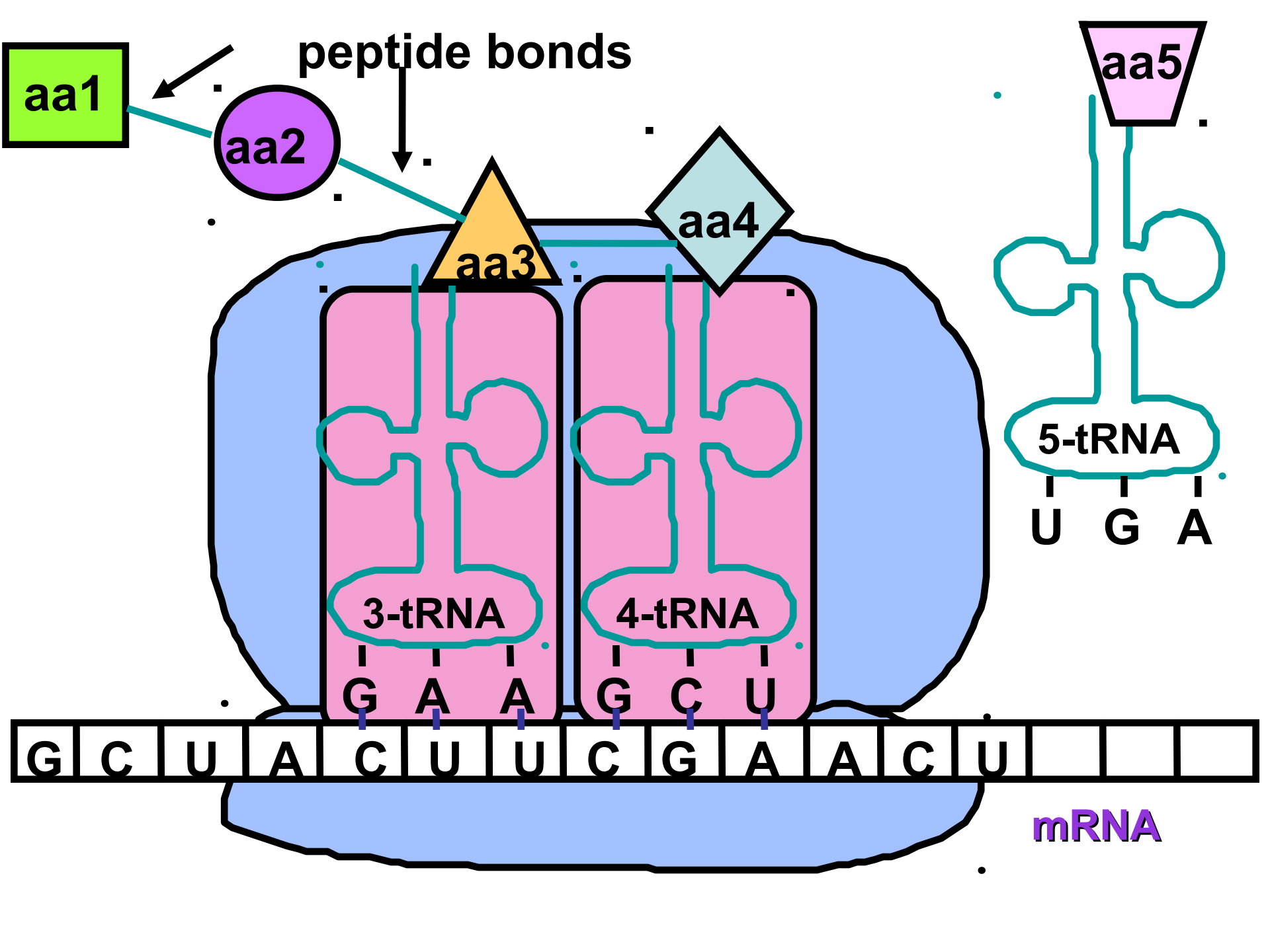


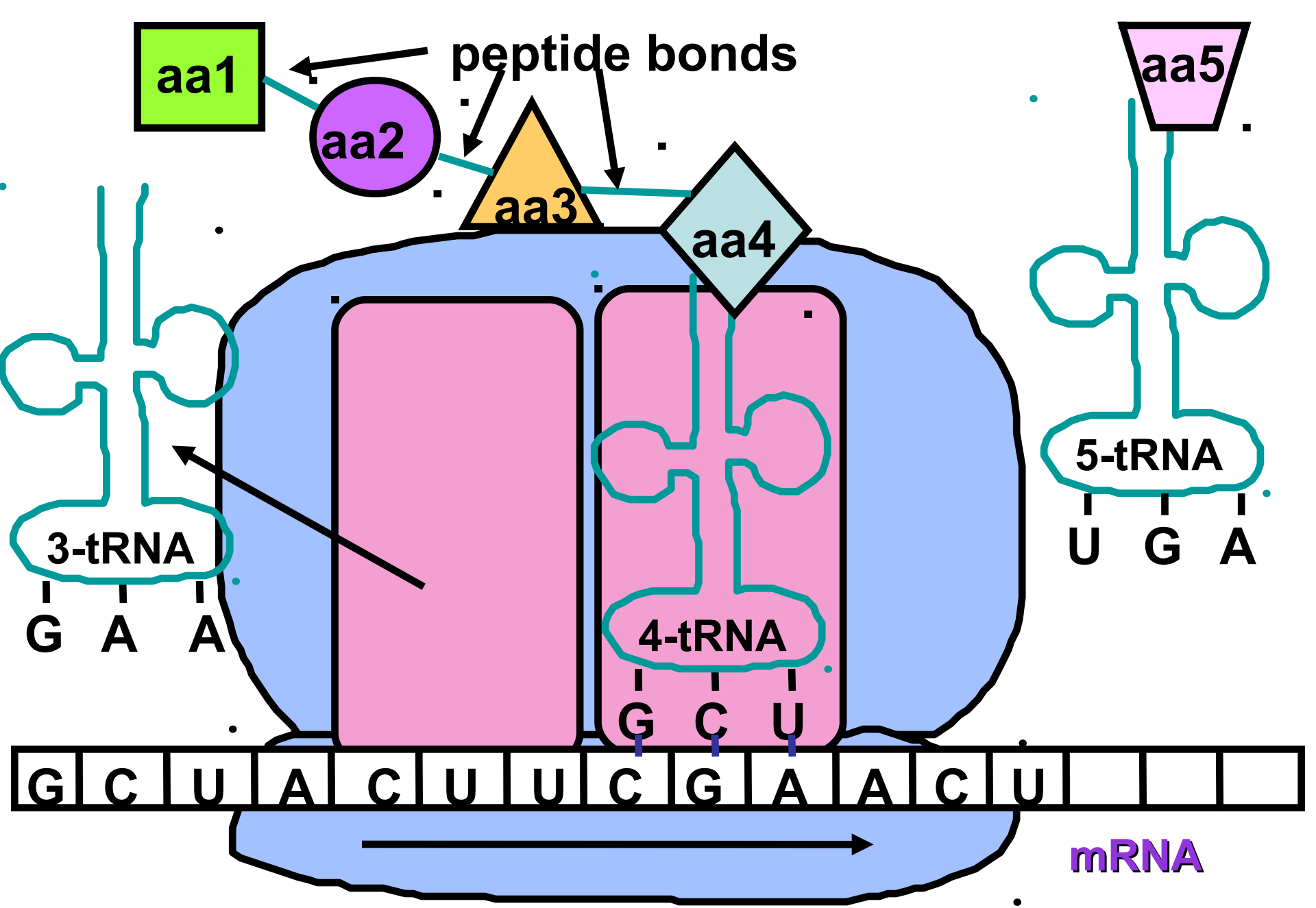
Ribosomes move over one codon


aa1
peptide bonds
aa4
aa2
aa3
4-tRNA
G C U
2-tRNA
3-tRNA
G A U
G A A
A U G C U A C U U C G A A C U
mRNA

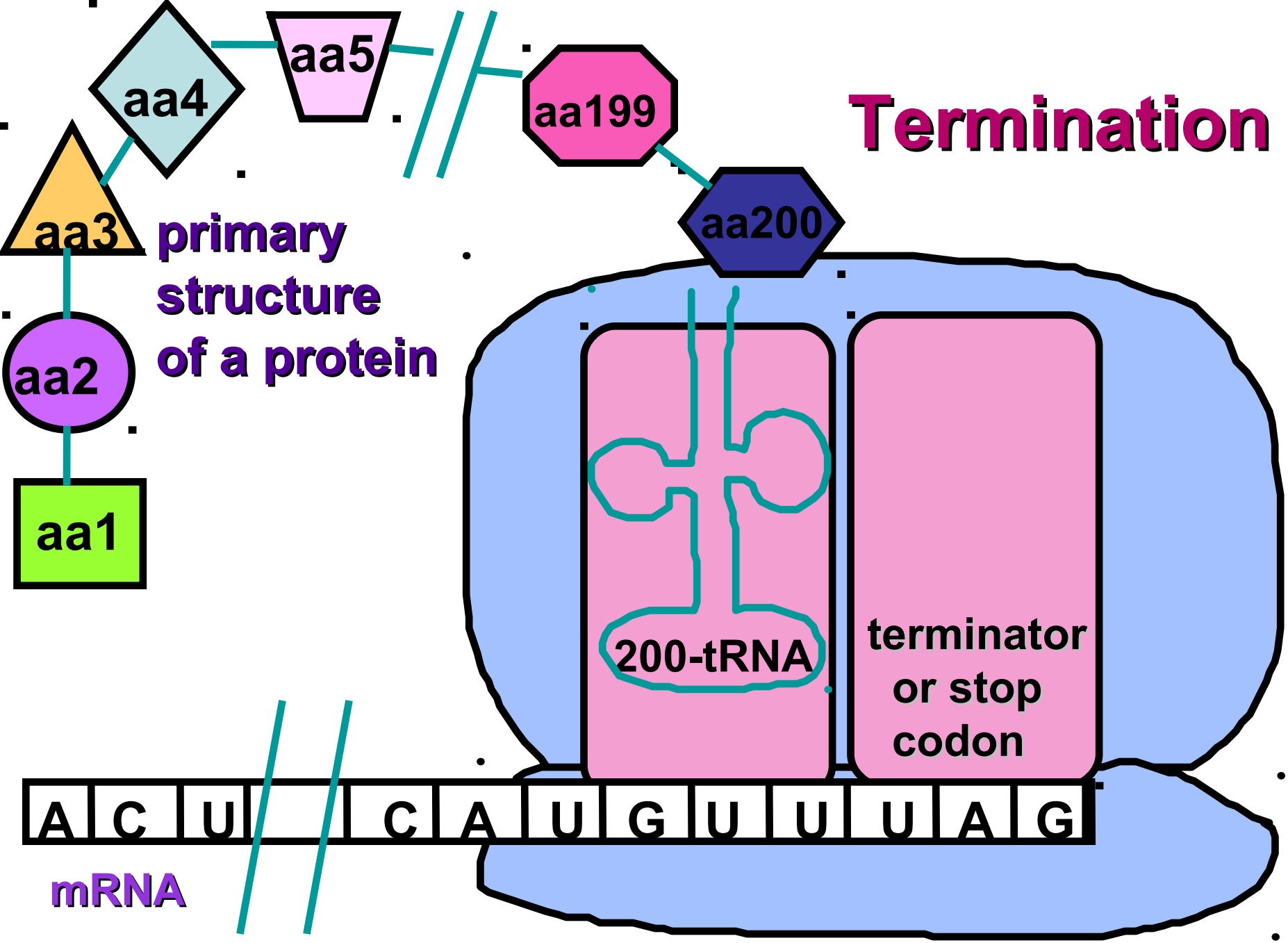


Ribosomes move over one codon

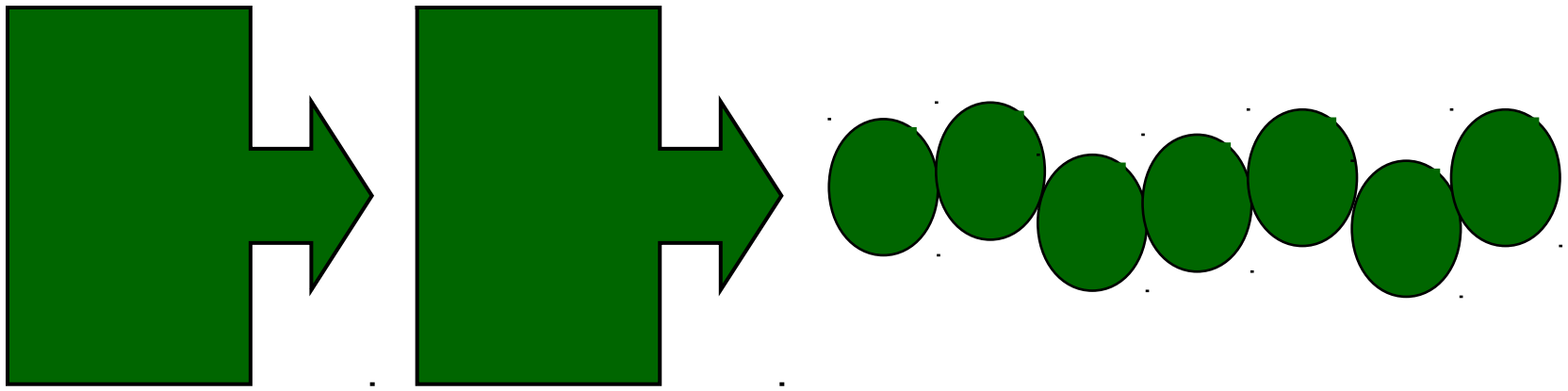

peptide bonds
aa1
aa2
aa3
aa4
aa5
3-tRNA
4-tRNA
5-tRNA
G A A
G C U
U G A
G C U A C U U C G A A C U
mRNA



Ribosomes move over one codon


aa4
aa5
aa199
aa200
aa3
aa2
aa1
primary
structure
of a protein
Termination
200-tRNA
terminator
or stop
codon
A C U C A U G U U U A G
mRNA

The Central Dogma



Central Dogma - Exceptions

- Reverse transcriptase
  - RNA >> DNA

- Retrotransposons

ഡിഎൻഎ ഇരട്ടിക്കൽ, ട്രാൻസ്ക്രിപ്ഷൻ, പരിഭാഷ

- എല്ലാ ജീവികളിലും ഒന്നു തന്നെ
- പരിണാമത്തിന്റെ ശക്തമായ തെളിവ്
- തന്മാത്രാ ജൈവ–സാങ്കേതിക വിദ്യയുടെ അടിസ്ഥാനം

ജൈവസാങ്കേതിക വിദ്യ

ജീവികളെ ഉപയോഗിച്ചു കൊണ്ടുള്ള
ഉൽപ്പാദന പ്രക്രിയകൾ

ജൈവസാങ്കേതിക വിദ്യ

- പരമ്പരാഗത ജൈവസാങ്കേതിക വിദ്യ
- ജനിതക സാങ്കേതിക വിദ്യ

ജനിതക സാങ്കേതിക വിദ്യ

- ജീവികളുടെ ജനിതക പദാർഥങ്ങൾ (**DNA**) ഉപയോഗിച്ചുള്ള ഉൽപ്പാദനം

ജനിതക സാങ്കേതിക വിദ്യ

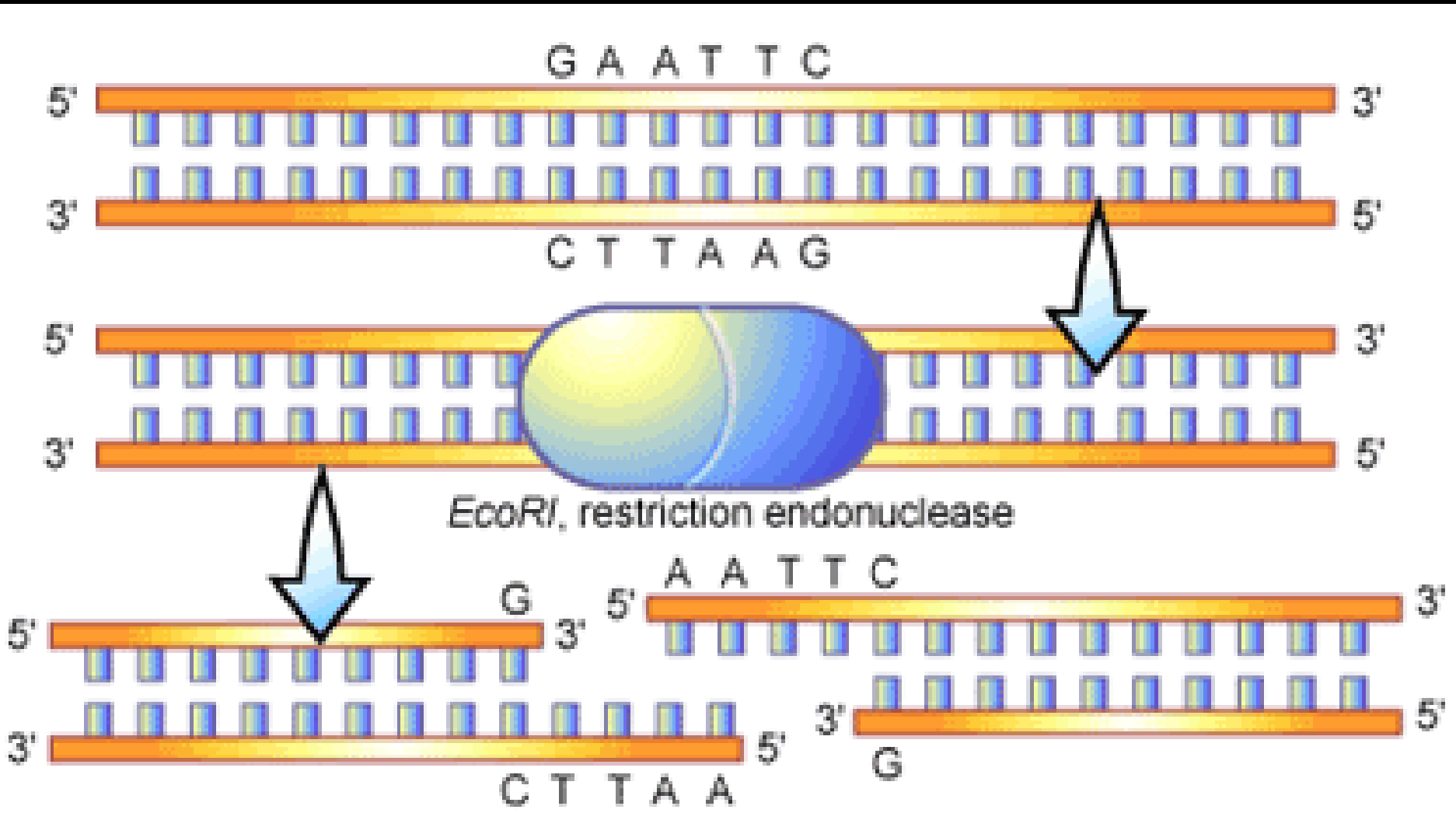
- സ്പീഷീസുകൾ തമ്മിലുള്ള പ്രതിബന്ധങ്ങൾ ഇല്ലാതാവുന്നു
- ഏതു സ്പീഷിസിൽ നിന്നും ഏതിലേക്കും ജീനുകൾ കൈമാറ്റം ചെയ്യാനുള്ള കഴിവ്
- *Genetic Engineering*

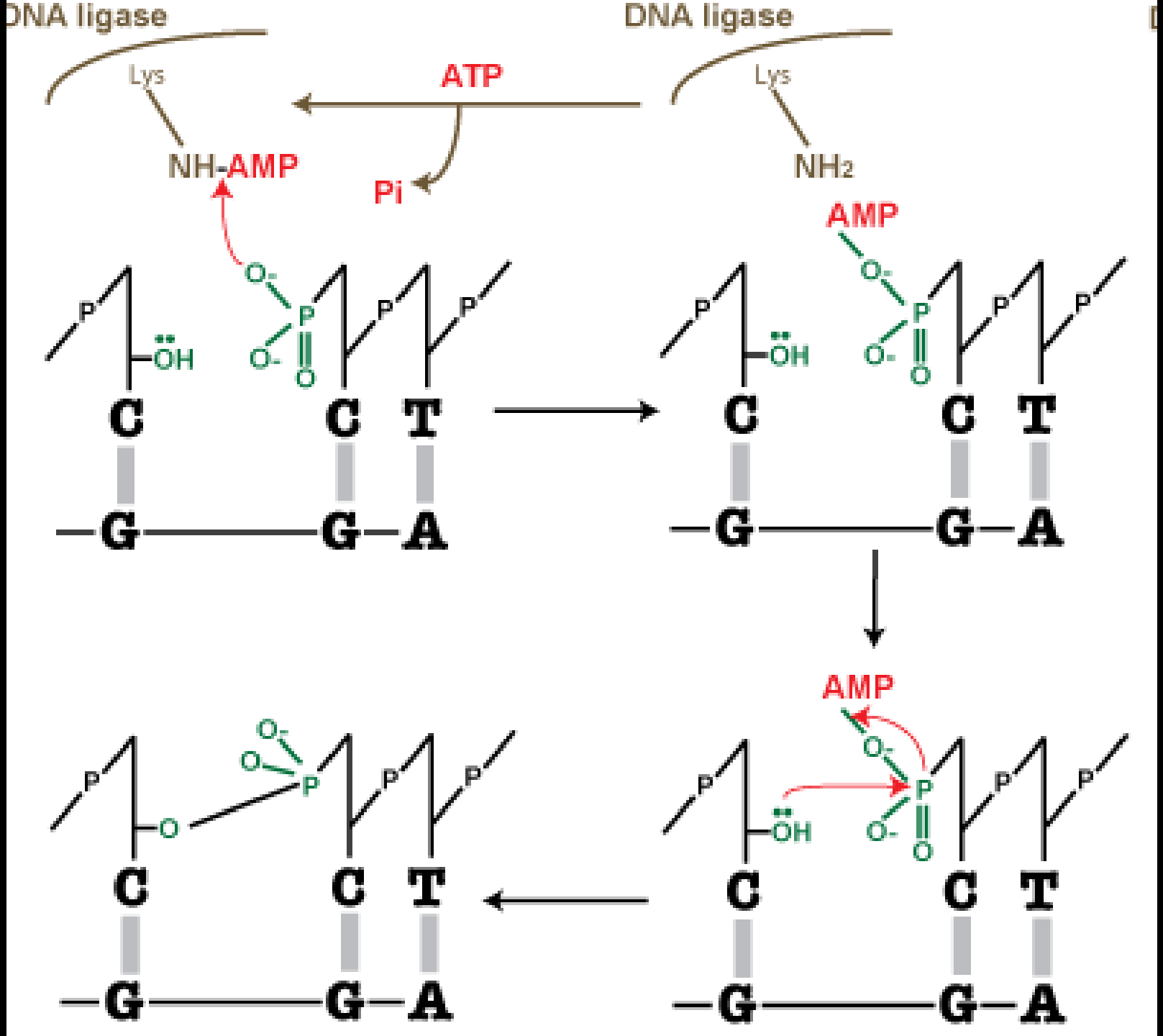
ജനിതക സാങ്കേതിക വിദ്യകൾ

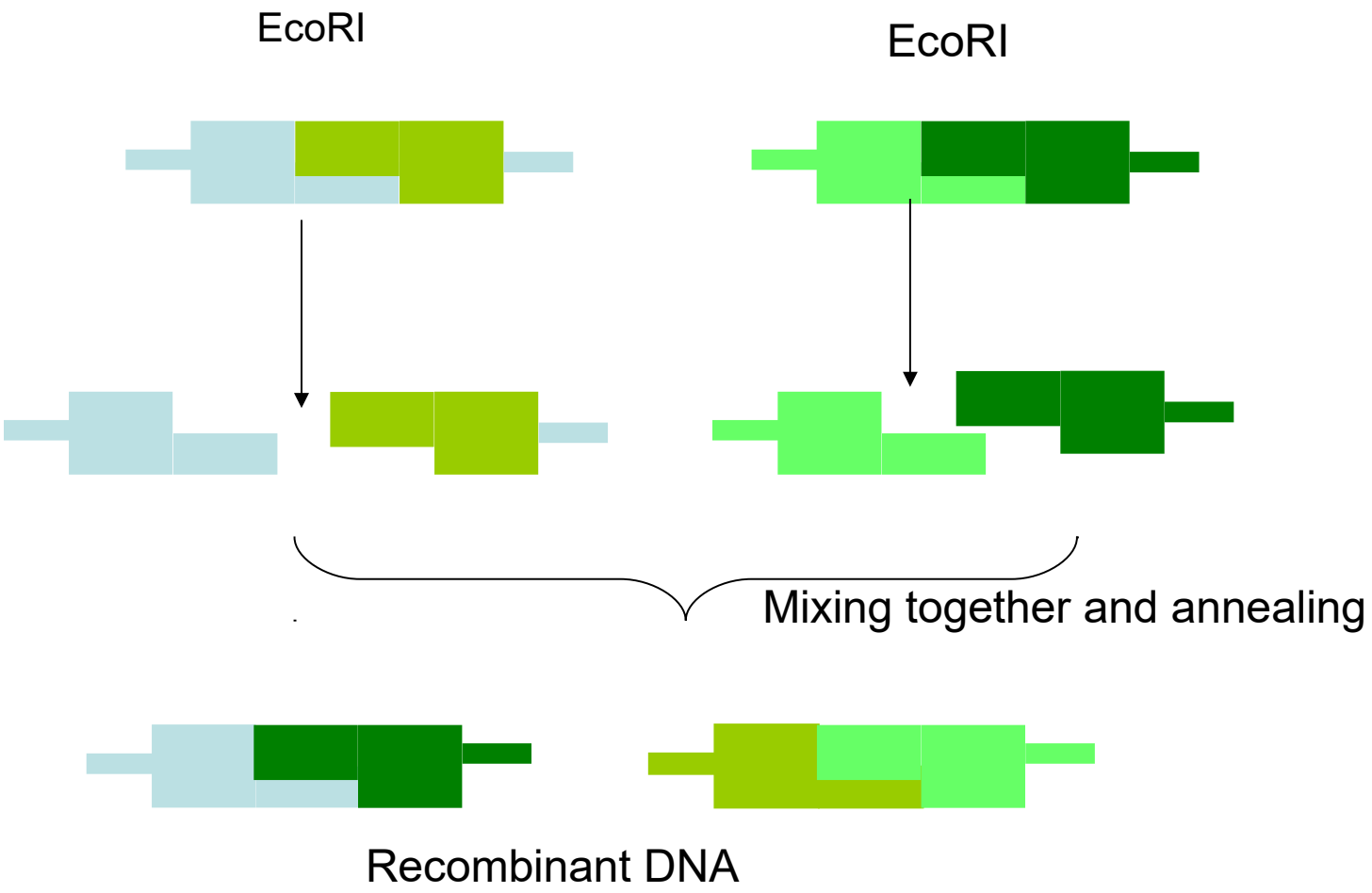
- ഡി ൻ എ പുനർസംയോജന വിദ്യ
  - *Recombinant DNA technology*
  - *(Genetic engineering)*
- മറ്റു ഡി ൻ എ സാങ്കേതിക വിദ്യകൾ
  - *Hybridization, amplification, sequencing*
- പുതിയ പ്രത്യുൽപ്പാദന സാങ്കേതിക വിദ്യകൾ
  - *New Reproductive technologies*

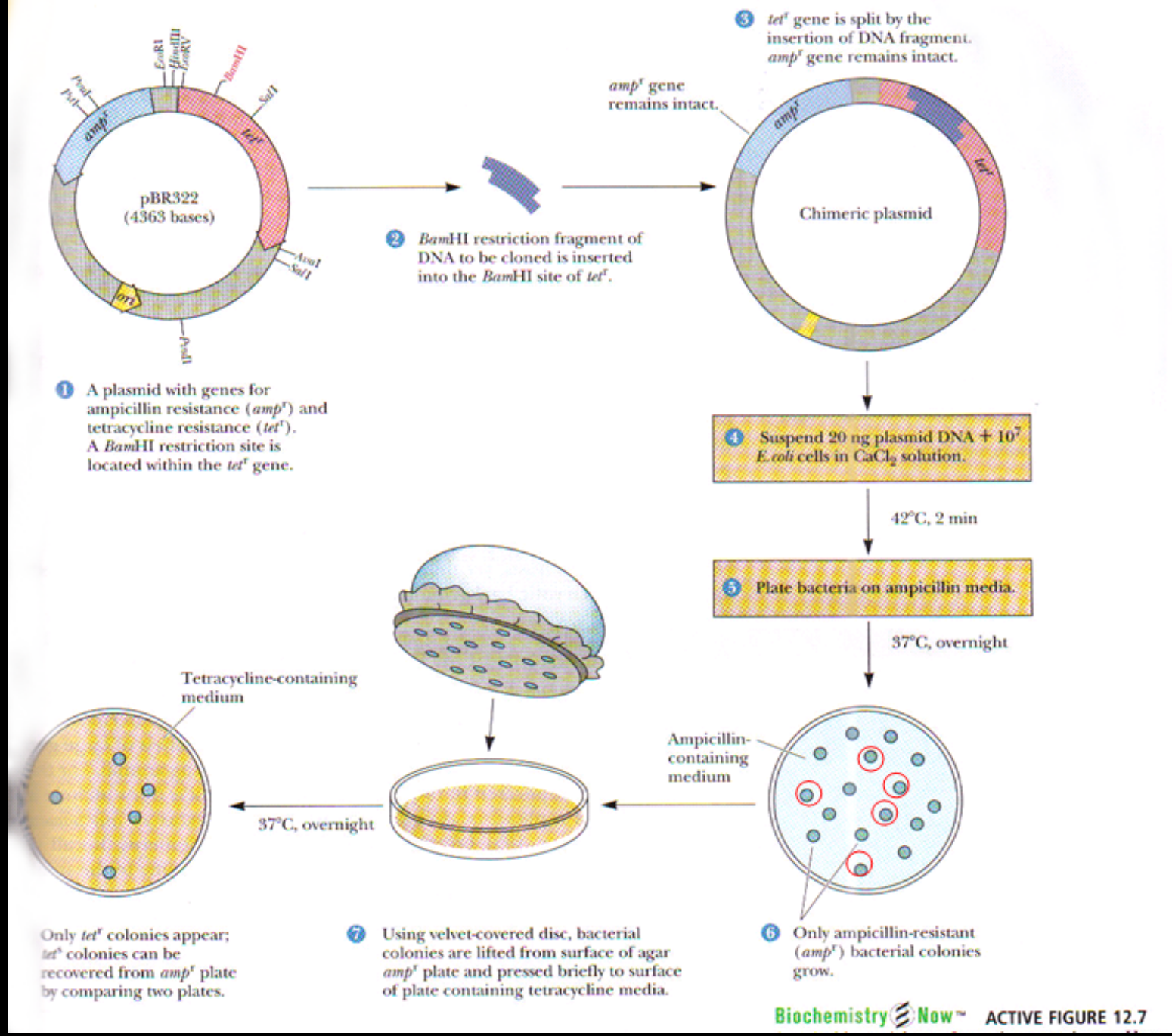
Technologies in Molecular biology

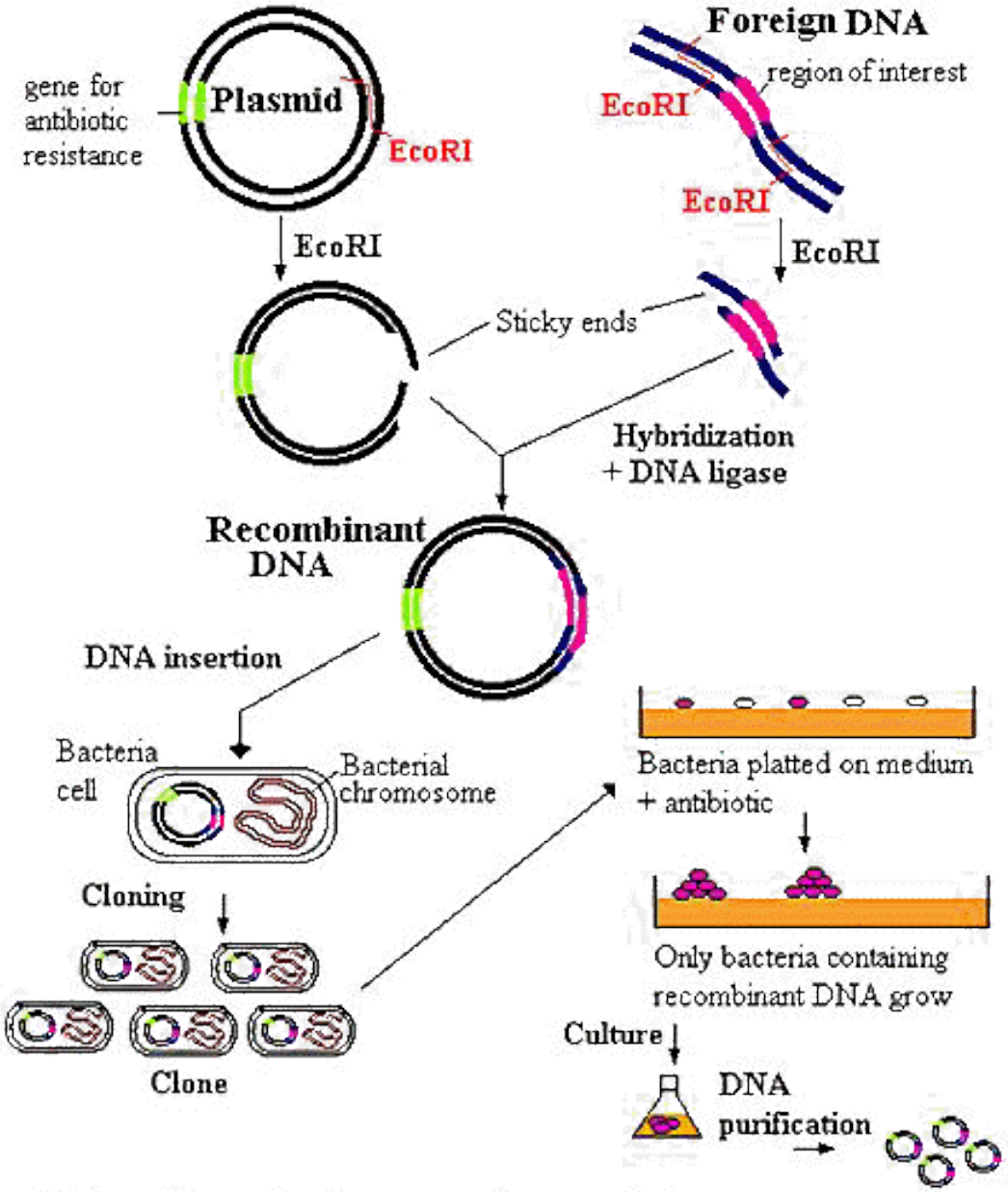
- Cutting up and joining DNA
- Cloning
- Hybridization
- Amplification
- Sequencing
- Microarrays and expression profiling


G A A T T C
5'
3'
3'
5'
C T T A A G
5'
3'
3'
5'
EcoRI, restriction endonuclease
G
5'
3'
3'
5'
C T T A A
A A T T C
5'
3'
3'
5'
G


DNA ligase
DNA ligase
Lys
ATP
Lys
NH-AMP
Pi
NH2
AMP
OH
C
C
T
G
G
A
AMP
OH
C
C
T
G
G
A
O
C
C
T
G
G
A


EcoRI
EcoRI
Mixing together and annealing
Recombinant DNA


pBR322
(4363 bases)
EcoR1
HindIII
ClaR1
BamHI
Sal1
PvuI
PvuI
ampr
tetr
AvaI
Sal1
ori
PvuII
1 A plasmid with genes for ampicillin resistance (ampr) and tetracycline resistance (tetr). A BamHI restriction site is located within the tetr gene.
2 BamHI restriction fragment of DNA to be cloned is inserted into the BamHI site of tetr.
3 tetr gene is split by the insertion of DNA fragment. ampr gene remains intact.
ampr gene remains intact.
Chimeric plasmid
4 Suspend 20 ng plasmid DNA + 10^7 E. coli cells in CaCl2 solution.
42°C, 2 min
5 Plate bacteria on ampicillin media.
37°C, overnight
Ampicillin-containing medium
6 Only ampicillin-resistant (ampr) bacterial colonies grow.
37°C, overnight
Tetracycline-containing medium
7 Using velvet-covered disc, bacterial colonies are lifted from surface of agar ampr plate and pressed briefly to surface of plate containing tetracycline media.
Only tetr colonies appear; tets colonies can be recovered from ampr plate by comparing two plates.
Biochemistry Now™ ACTIVE FIGURE 12.7

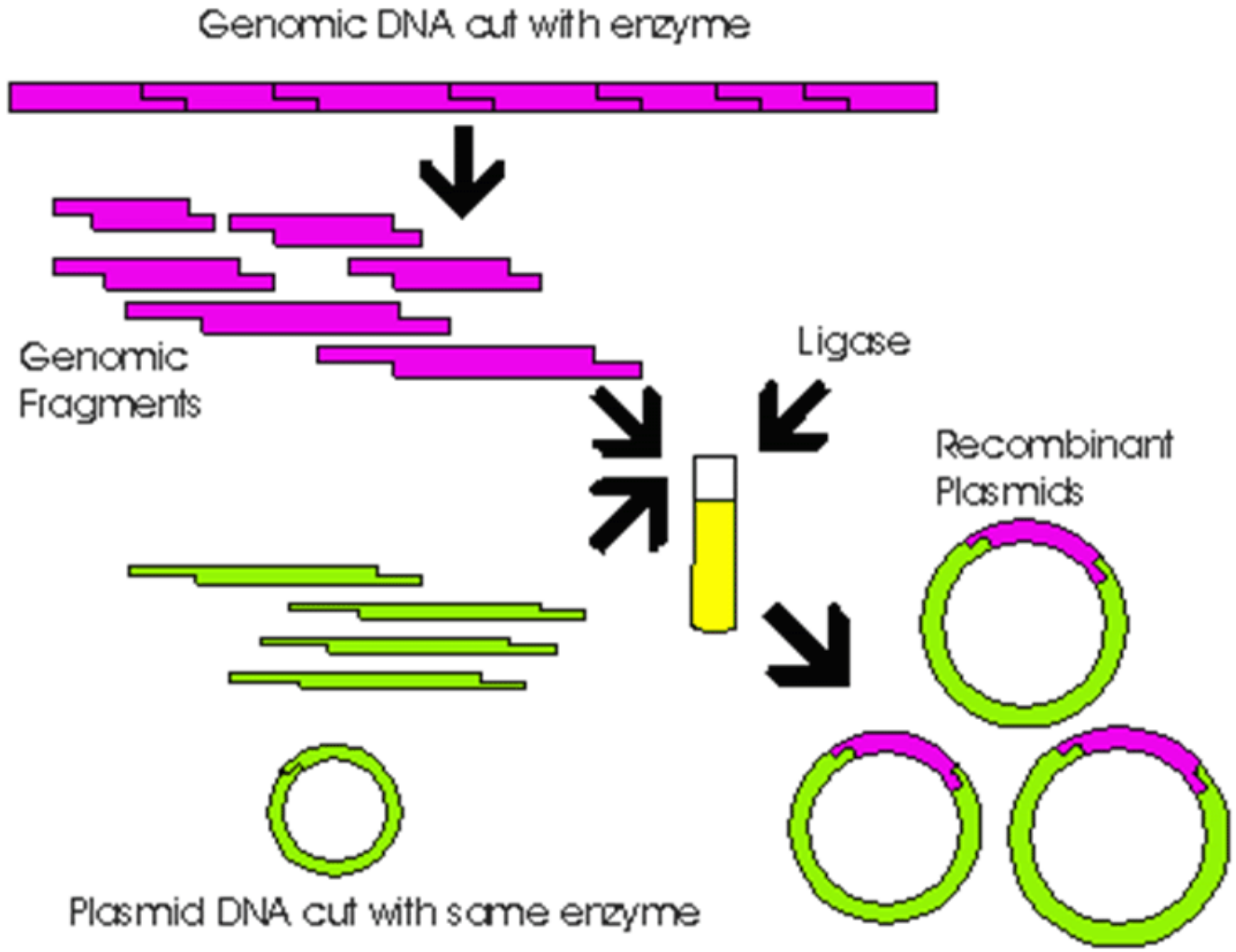


Cloning into a plasmid

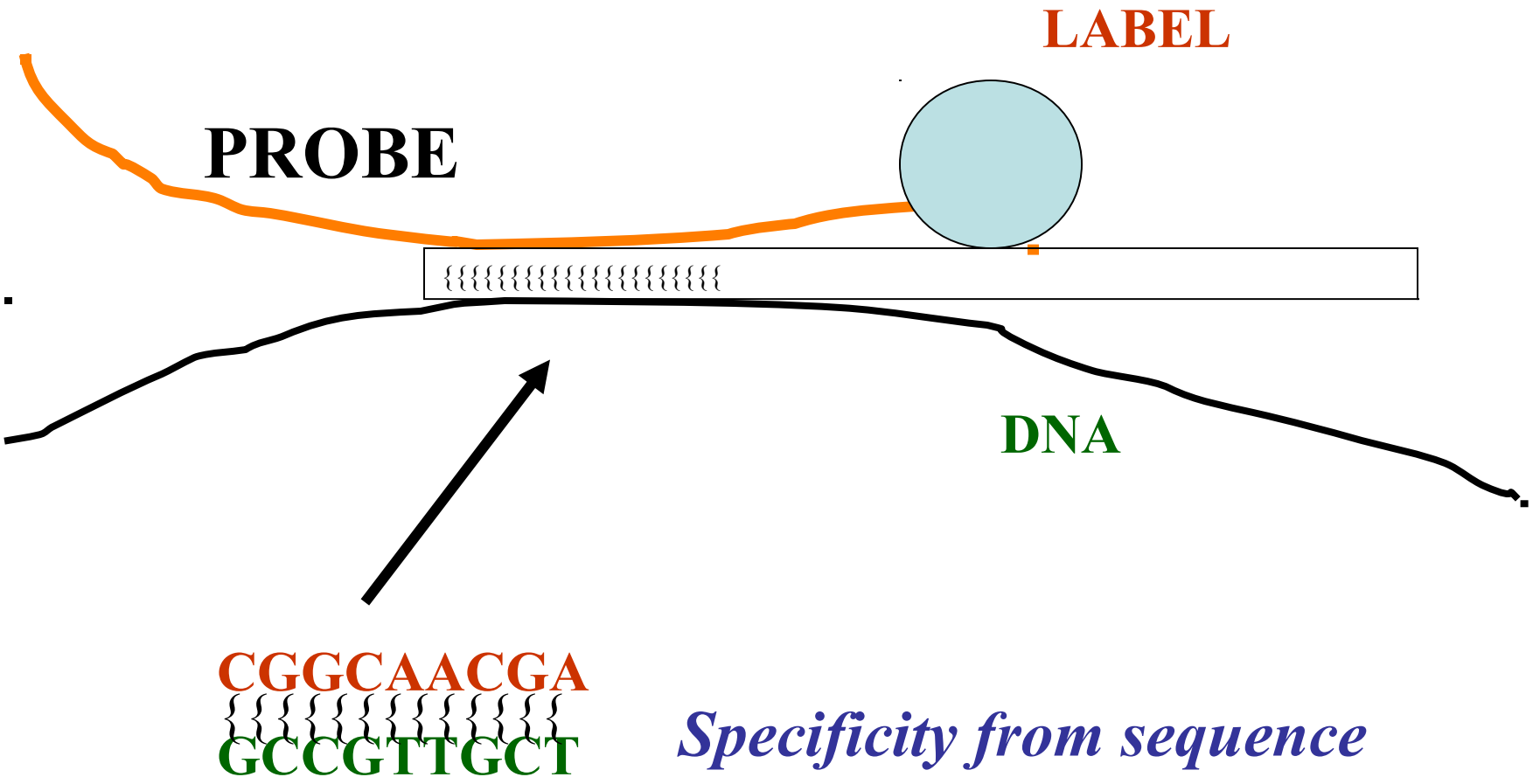
Herbert Boyer

Stanley Cohen

മനുഷ്യ ഇൻസുലിൻ ഉൽപ്പാദനം



Hybridization methods



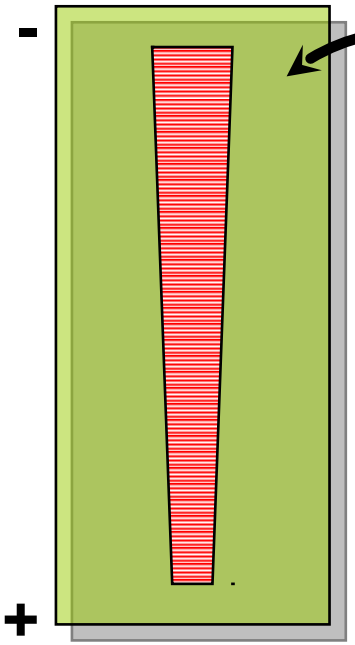
Specificity from sequence

Southern blotting procedure

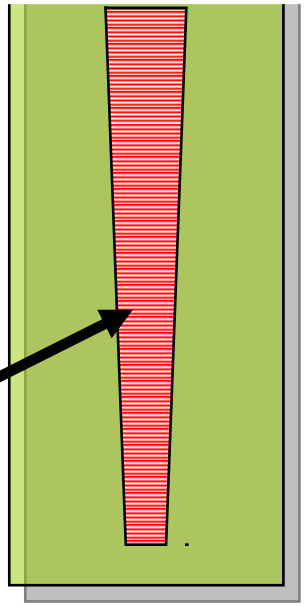
human genomic DNA (isolated from many cells)

- restriction enzyme digestion

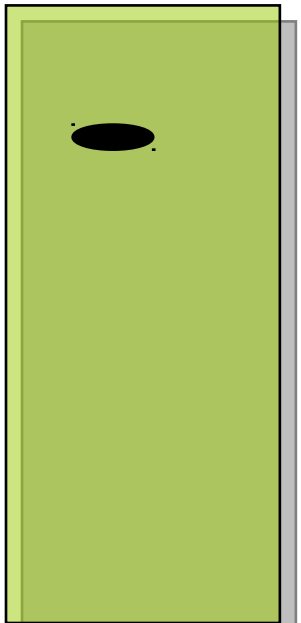
millions of DNA fragments



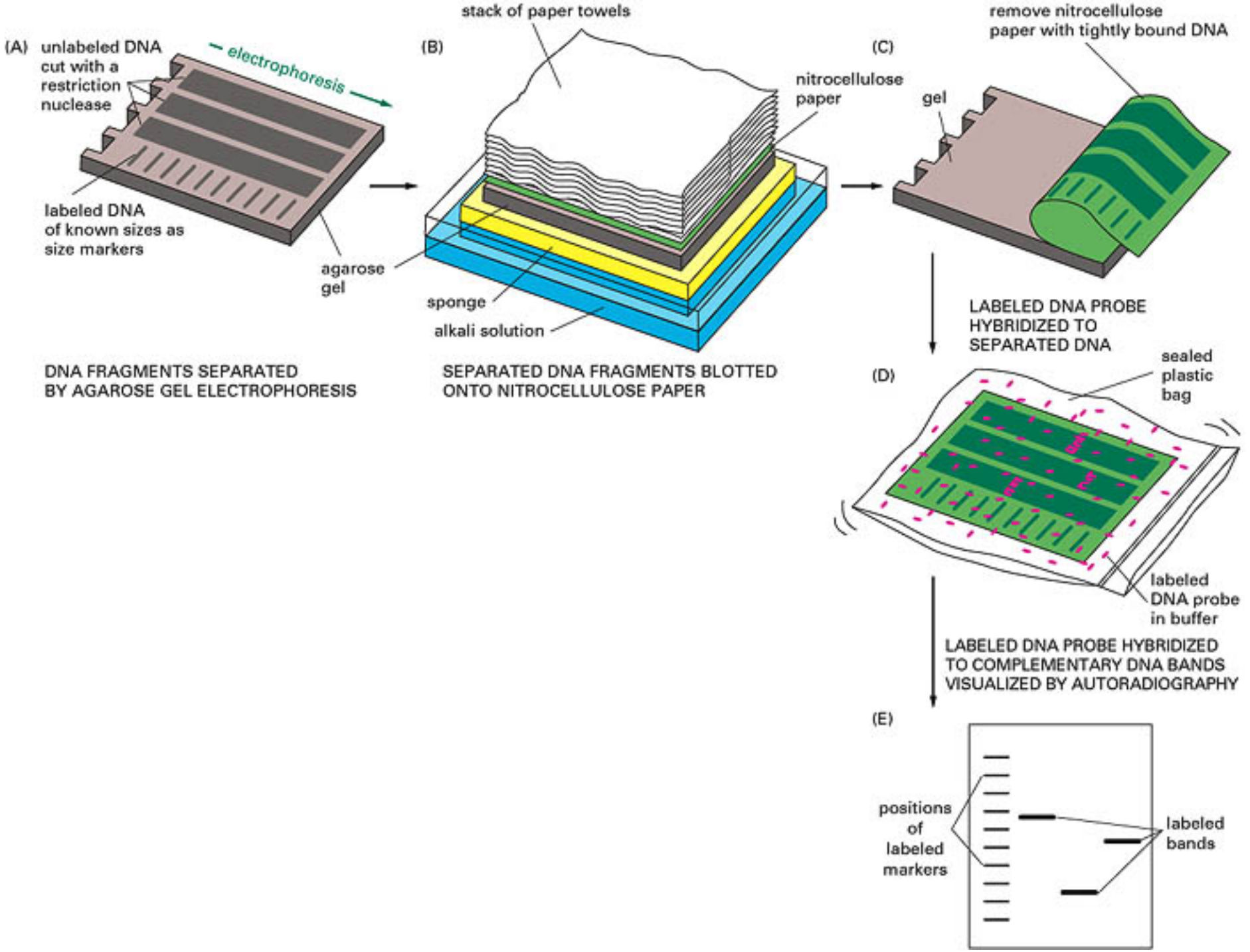
- gel electrophoresis of the DNA fragments
- gel will separate DNAs according to size

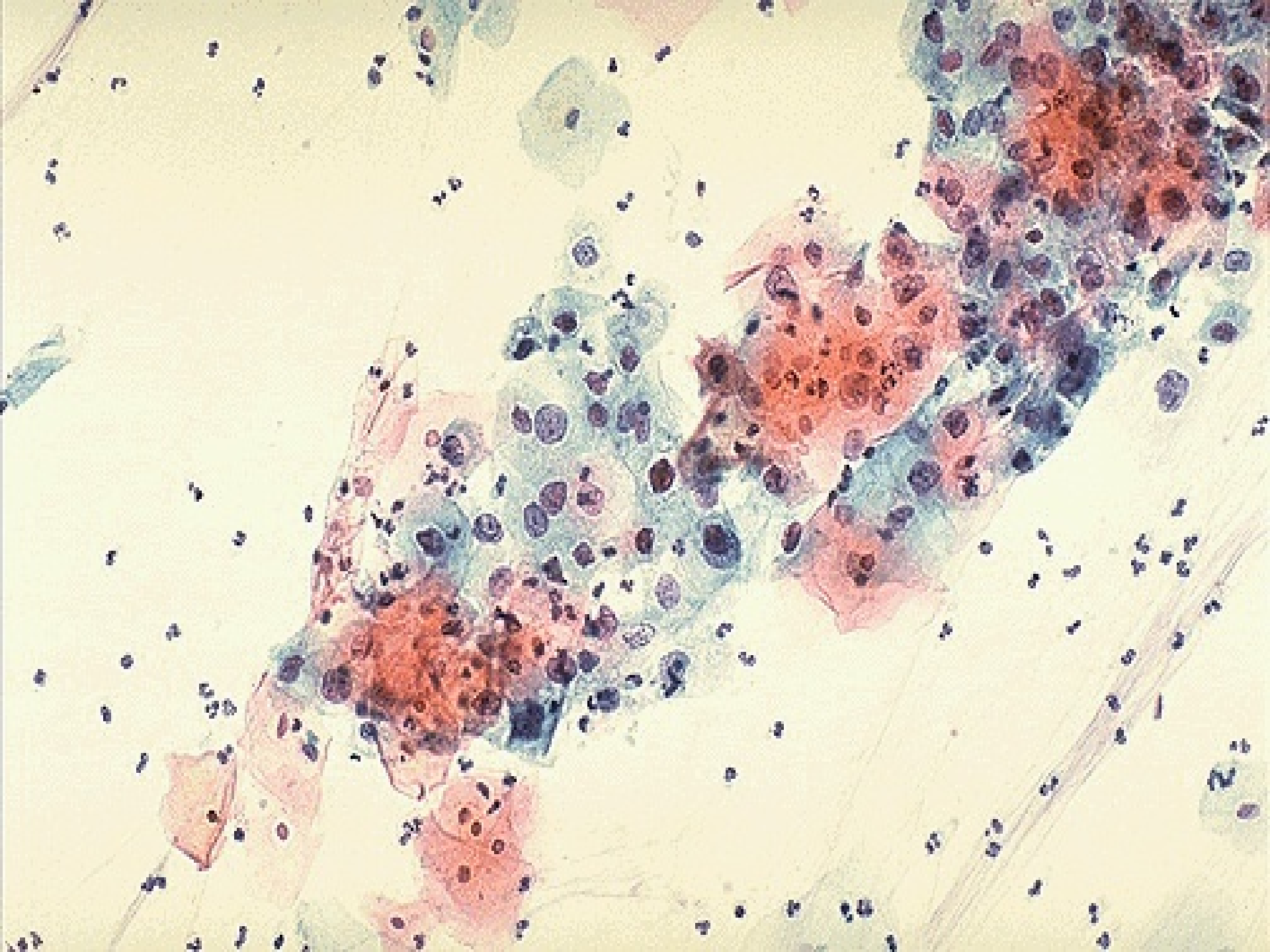


PROBE WITH RADIOACTIVE TAG



AUTORADIOGRAPHY


(A)
unlabeled DNA cut with a restriction nuclease
electrophoresis
labeled DNA of known sizes as size markers
agarose gel
DNA FRAGMENTS SEPARATED BY AGAROSE GEL ELECTROPHORESIS
(B)
stack of paper towels
nitrocellulose paper
sponge
alkali solution
SEPARATED DNA FRAGMENTS BLOTTED ONTO NITROCELLULOSE PAPER
(C)
remove nitrocellulose paper with tightly bound DNA
gel
LABELED DNA PROBE HYBRIDIZED TO SEPARATED DNA
(D)
sealed plastic bag
labeled DNA probe in buffer
LABELED DNA PROBE HYBRIDIZED TO COMPLEMENTARY DNA BANDS VISUALIZED BY AUTORADIOGRAPHY
(E)
positions of labeled markers
labeled bands



Southern Blot

HPV 18 Probe

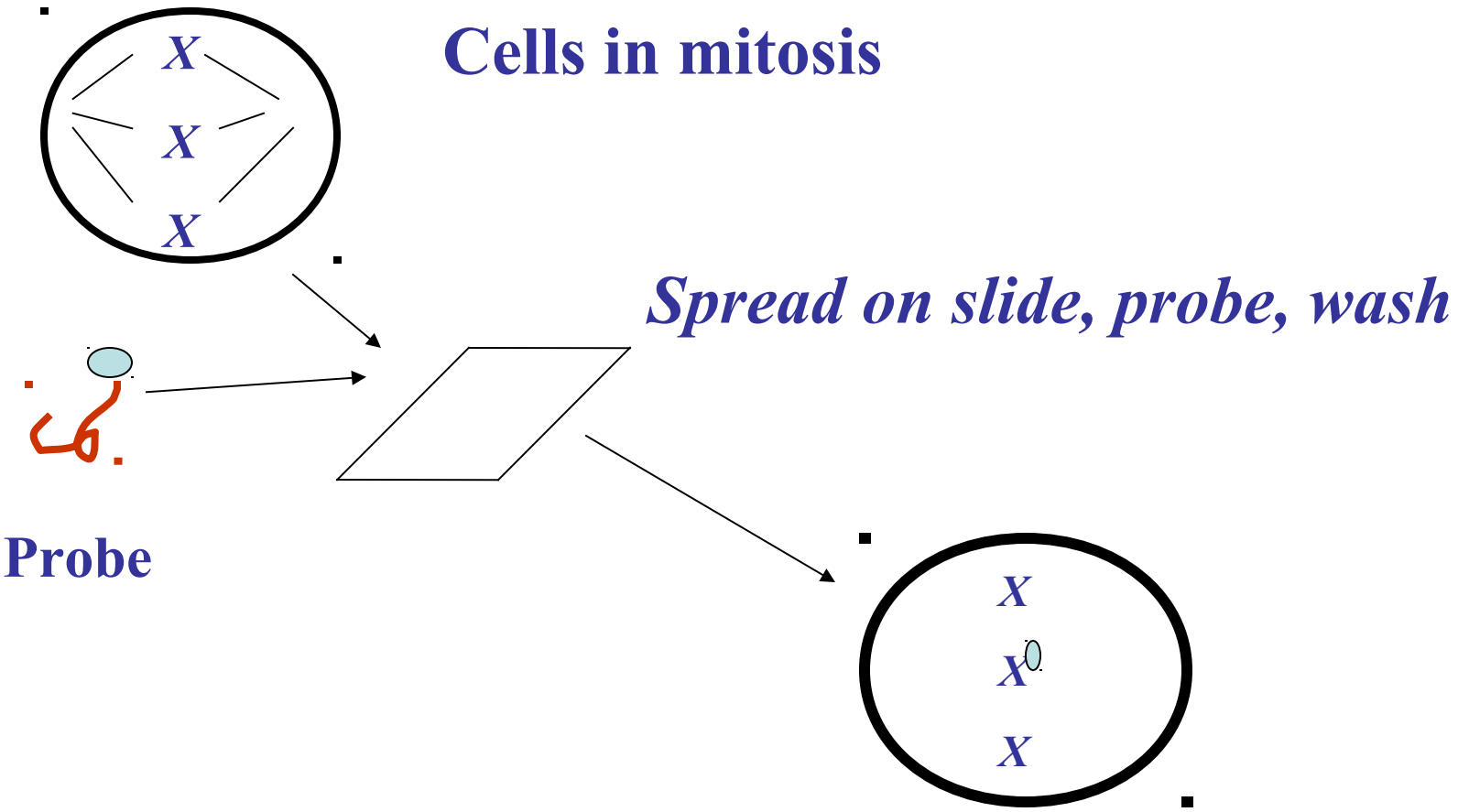
Patient 1 negative

Patient 2 positive

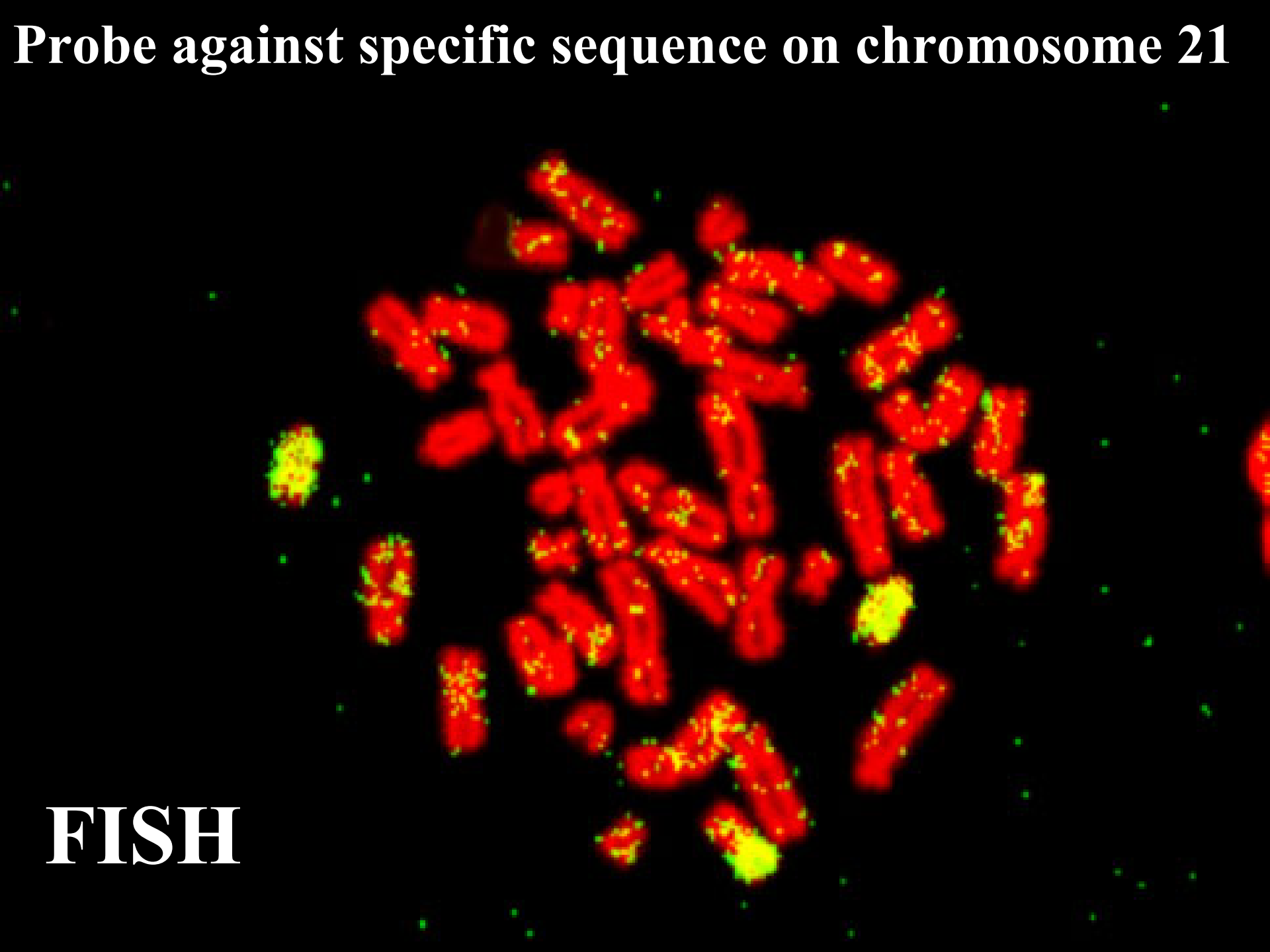
In situ hybridization

- Specific probe directed against a sequence of interest in
  - Chromososme spreads
  - Tissue sections
- The probe can be tagged with
  - Fluorescent marker (FISH)
  - Enzyme marker

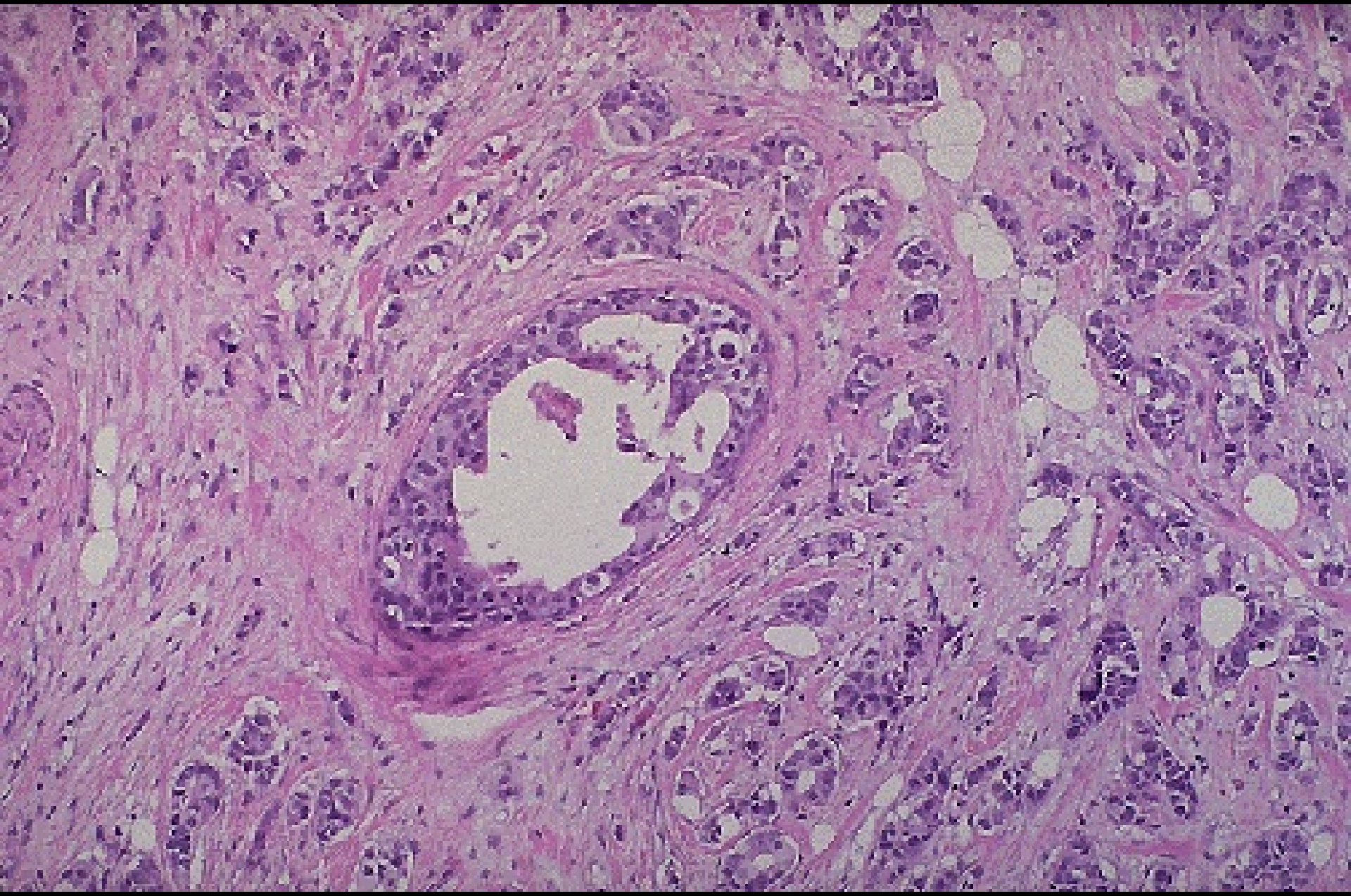
In situ hybridisation for DNA (FISH)



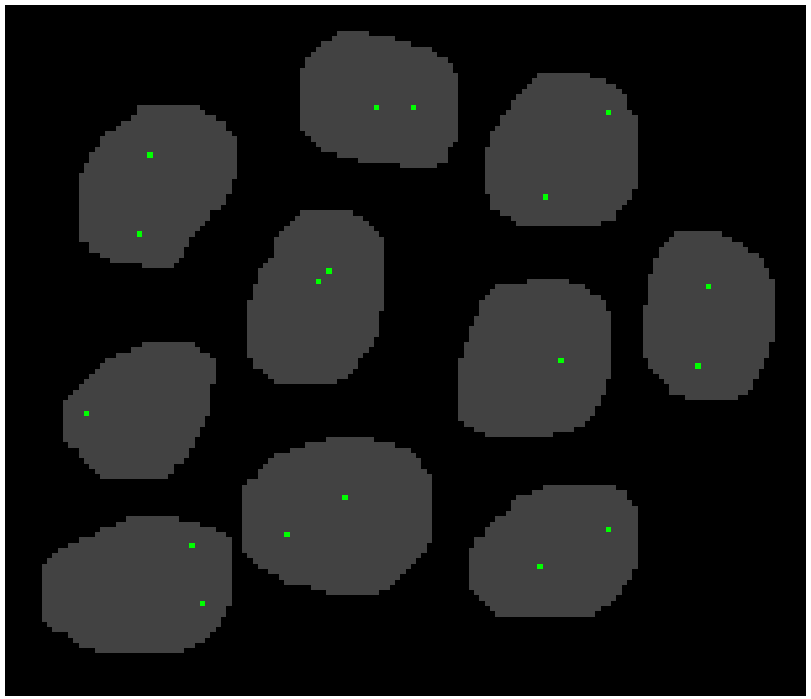
Probe against specific sequence on chromosome 21



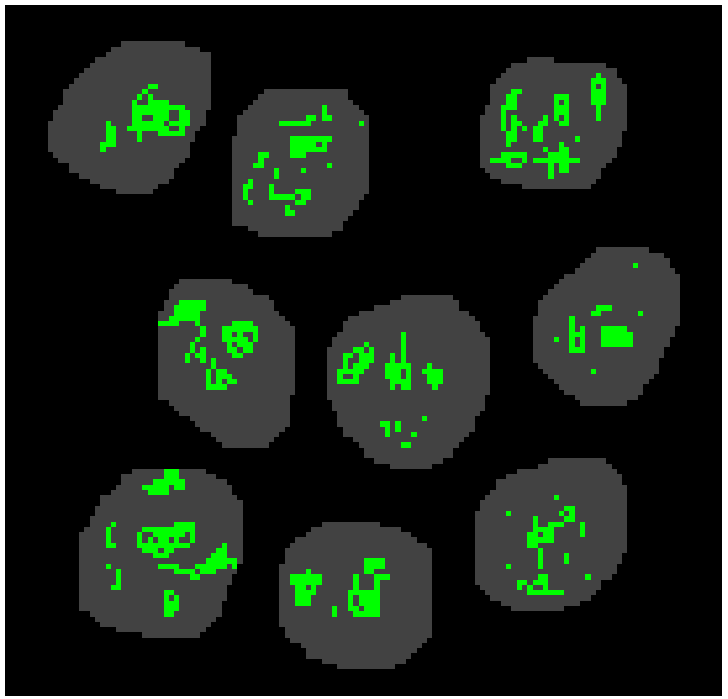
FISH



Fluorescent In-Situ Hybridization
Detecting Amplified *neu*

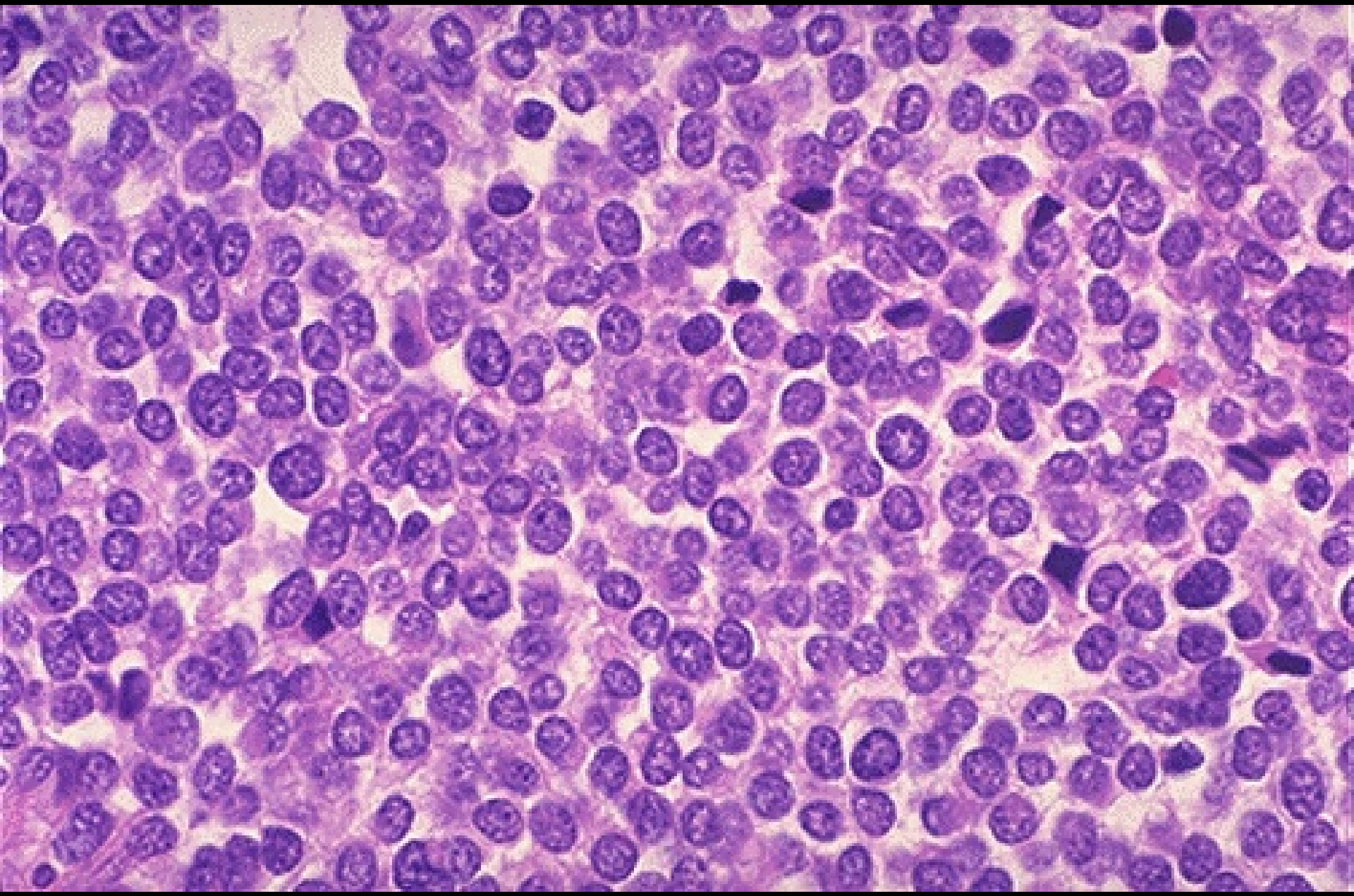


Not Amplified

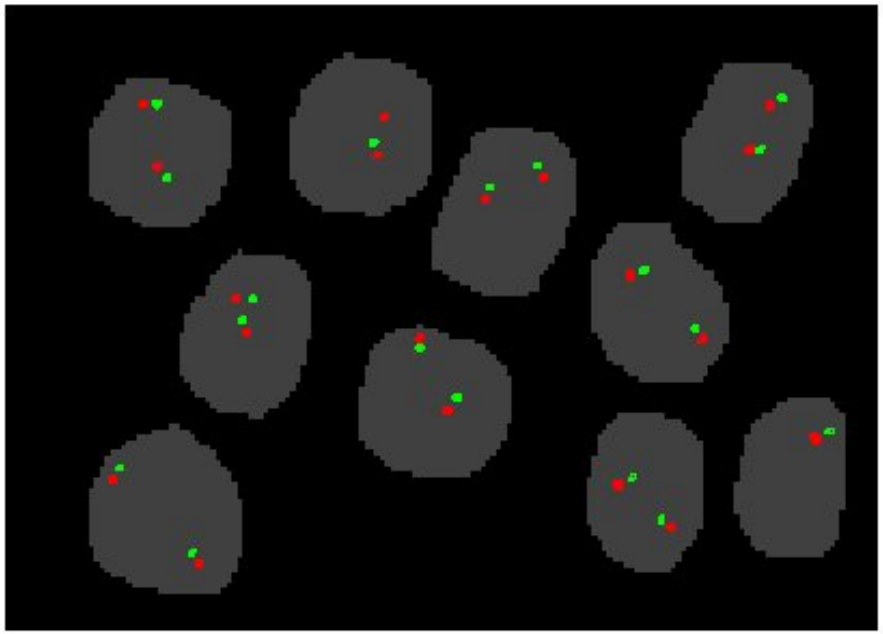


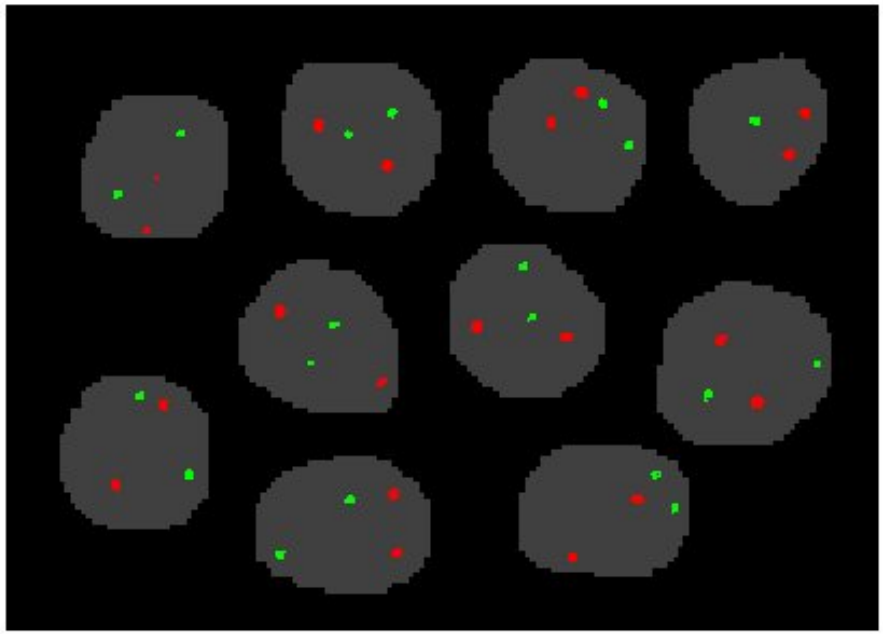
Ampified

Breast Cancer Cell Nuclei in Paraffin



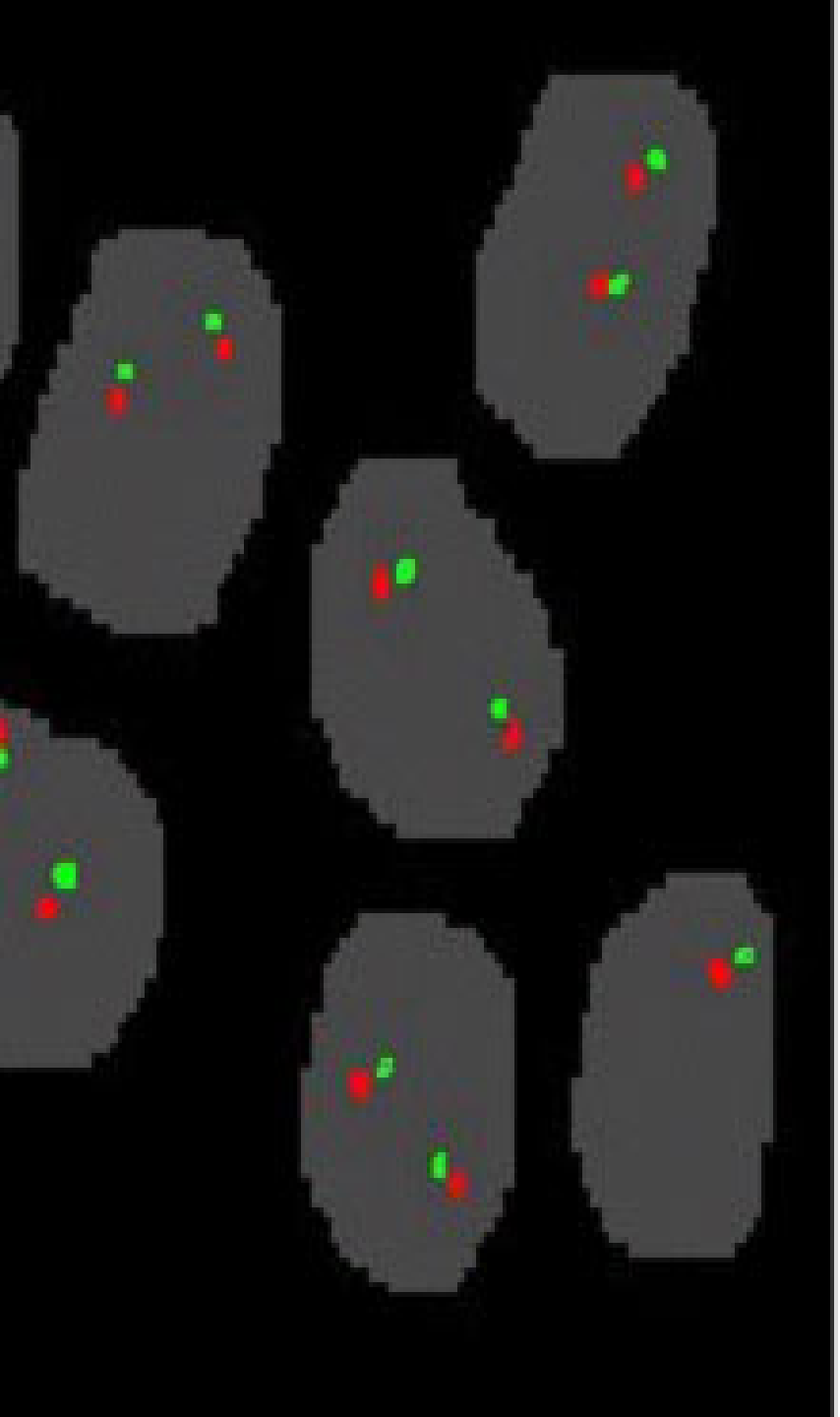
Fluorescent In-Situ Hybridization
Detecting *ews* Translocations



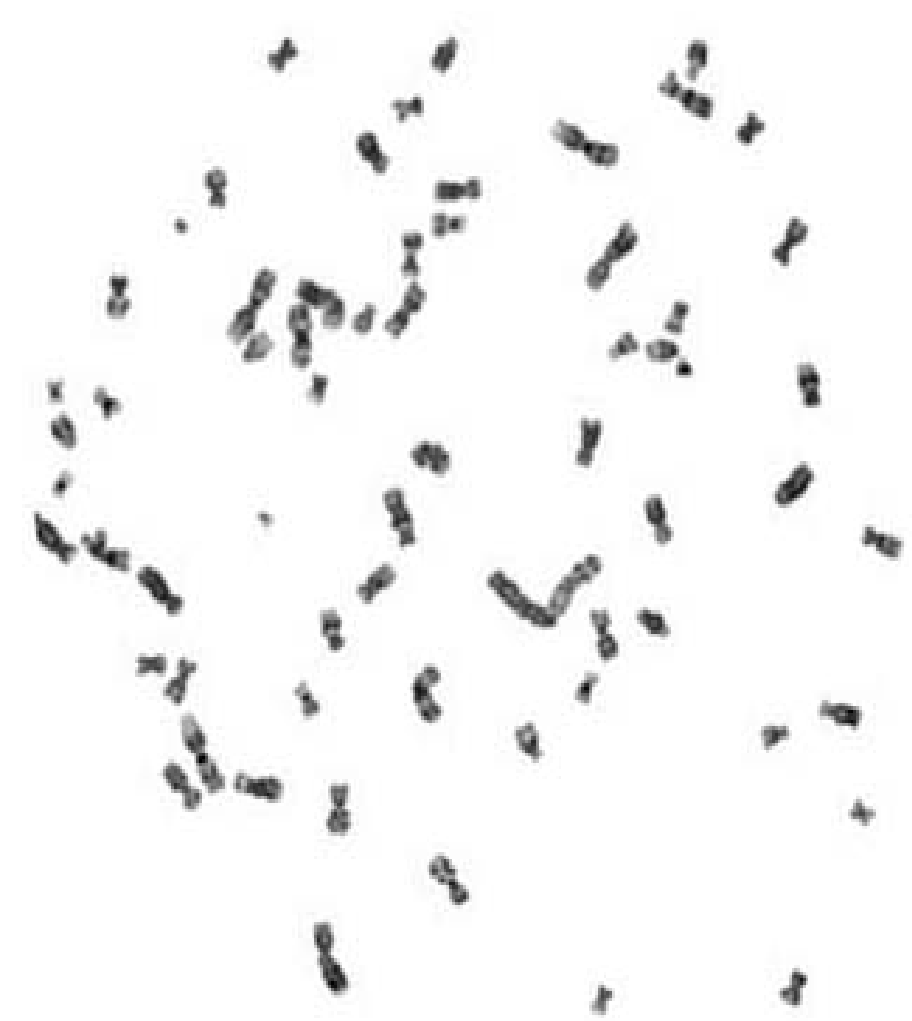


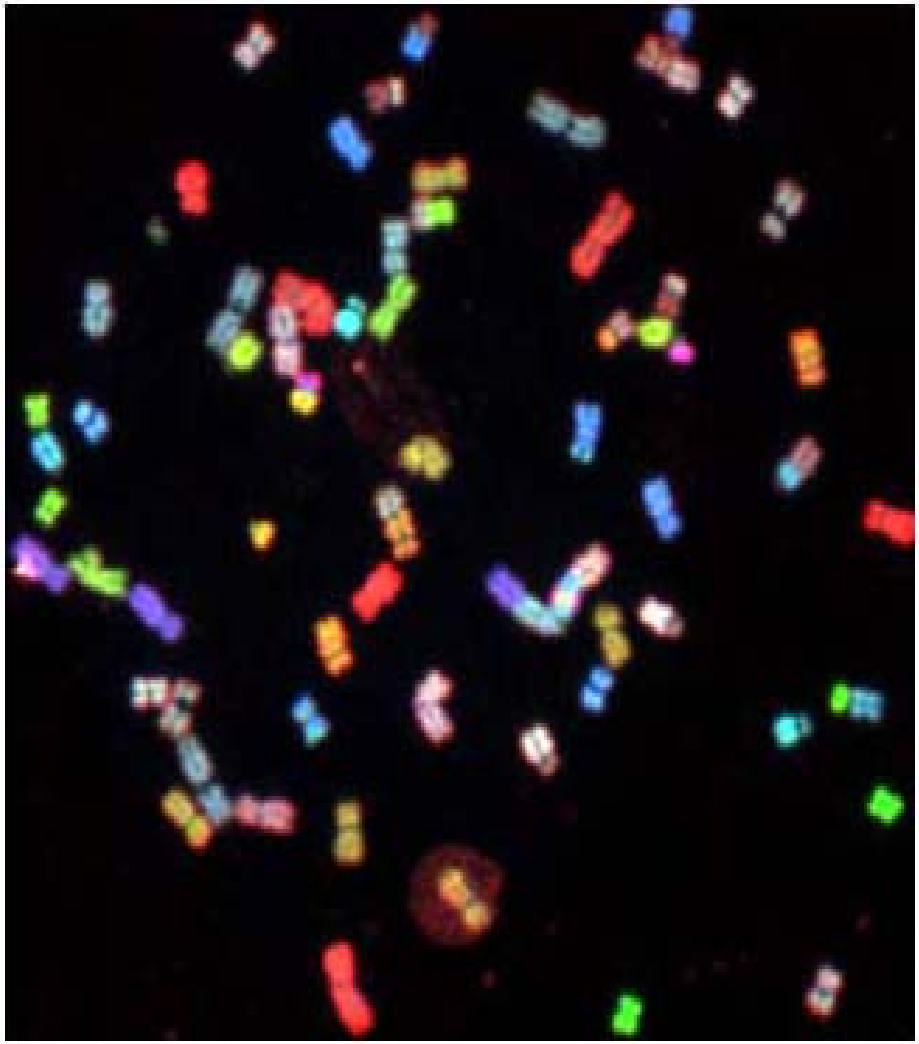
No Translocation

Translocation

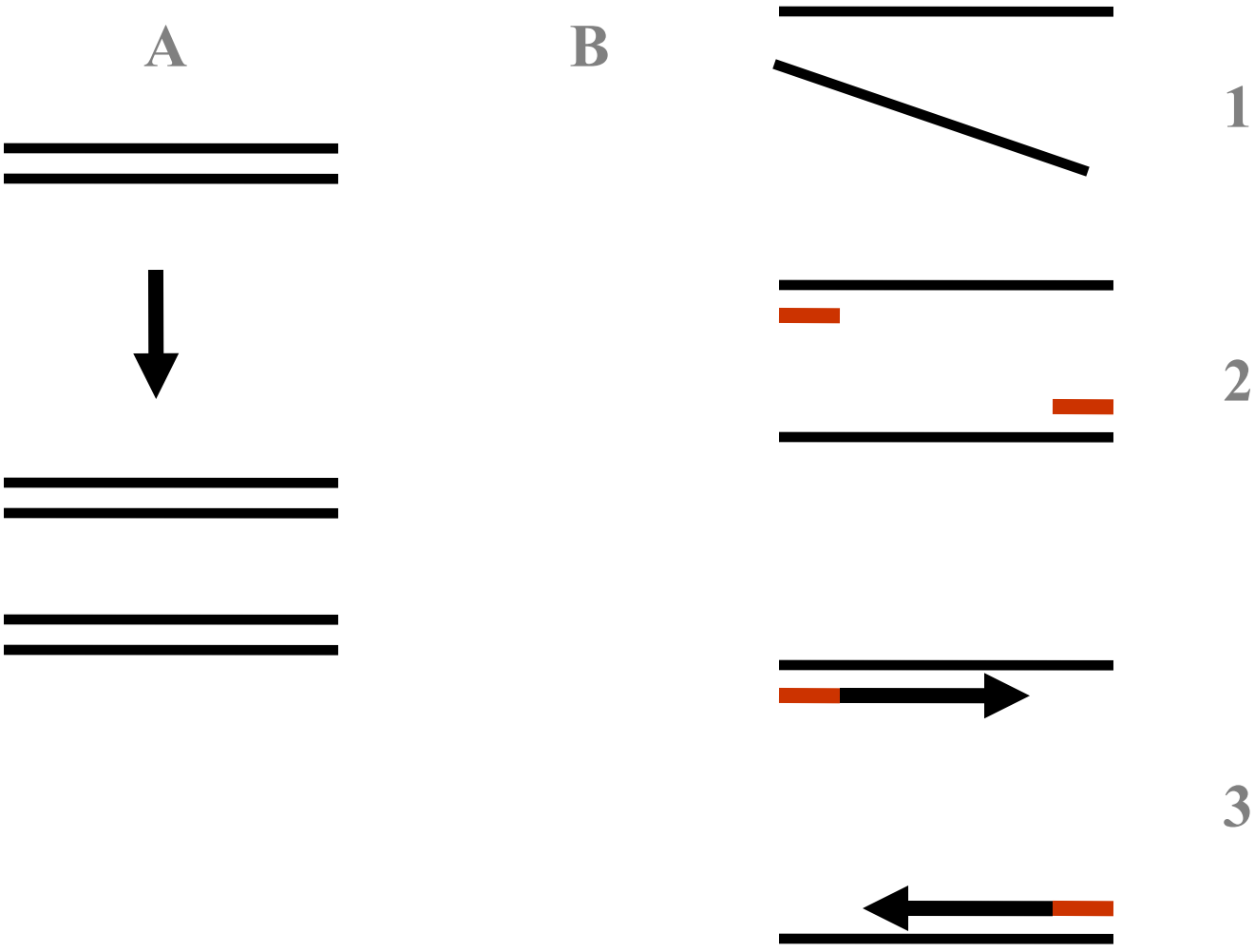


Spectral karyotyping (SKY)



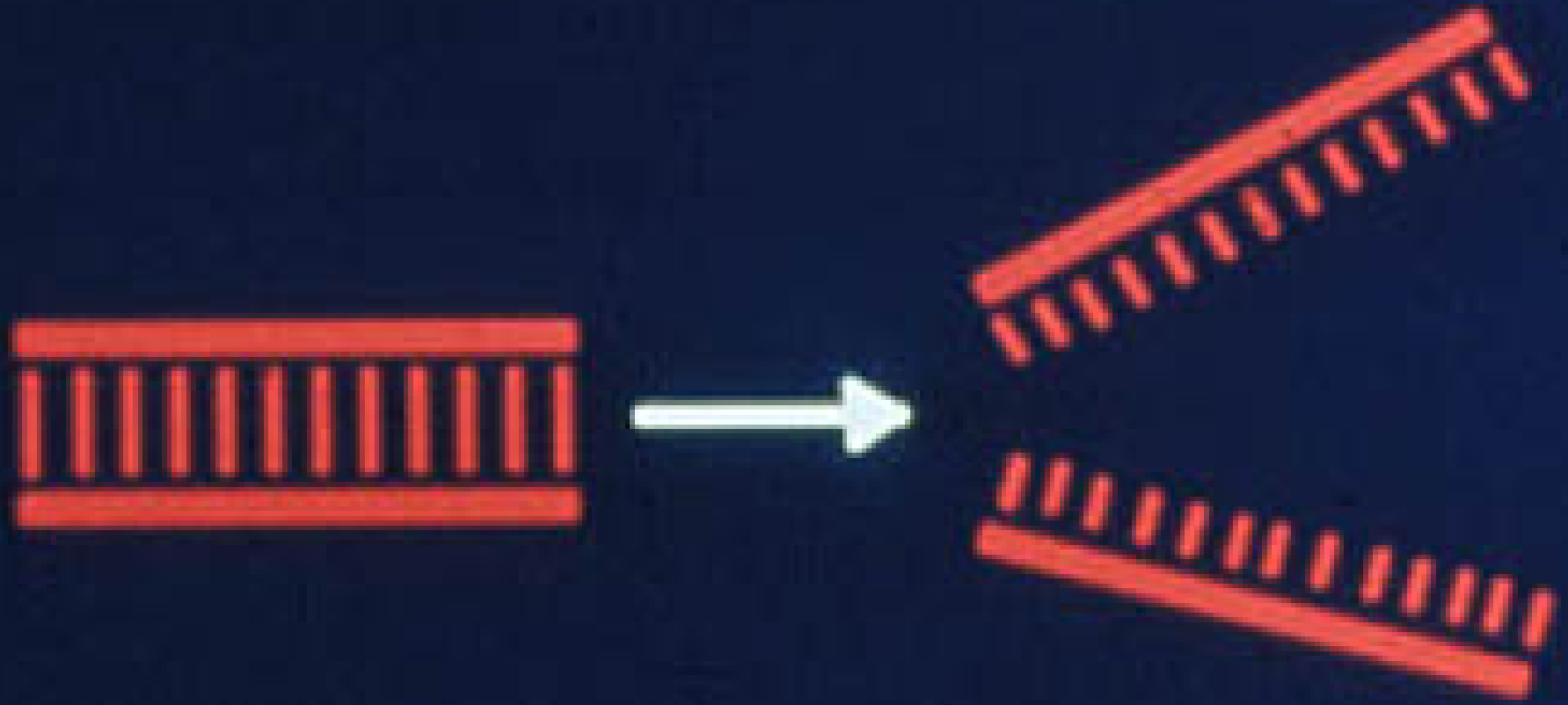


PCR

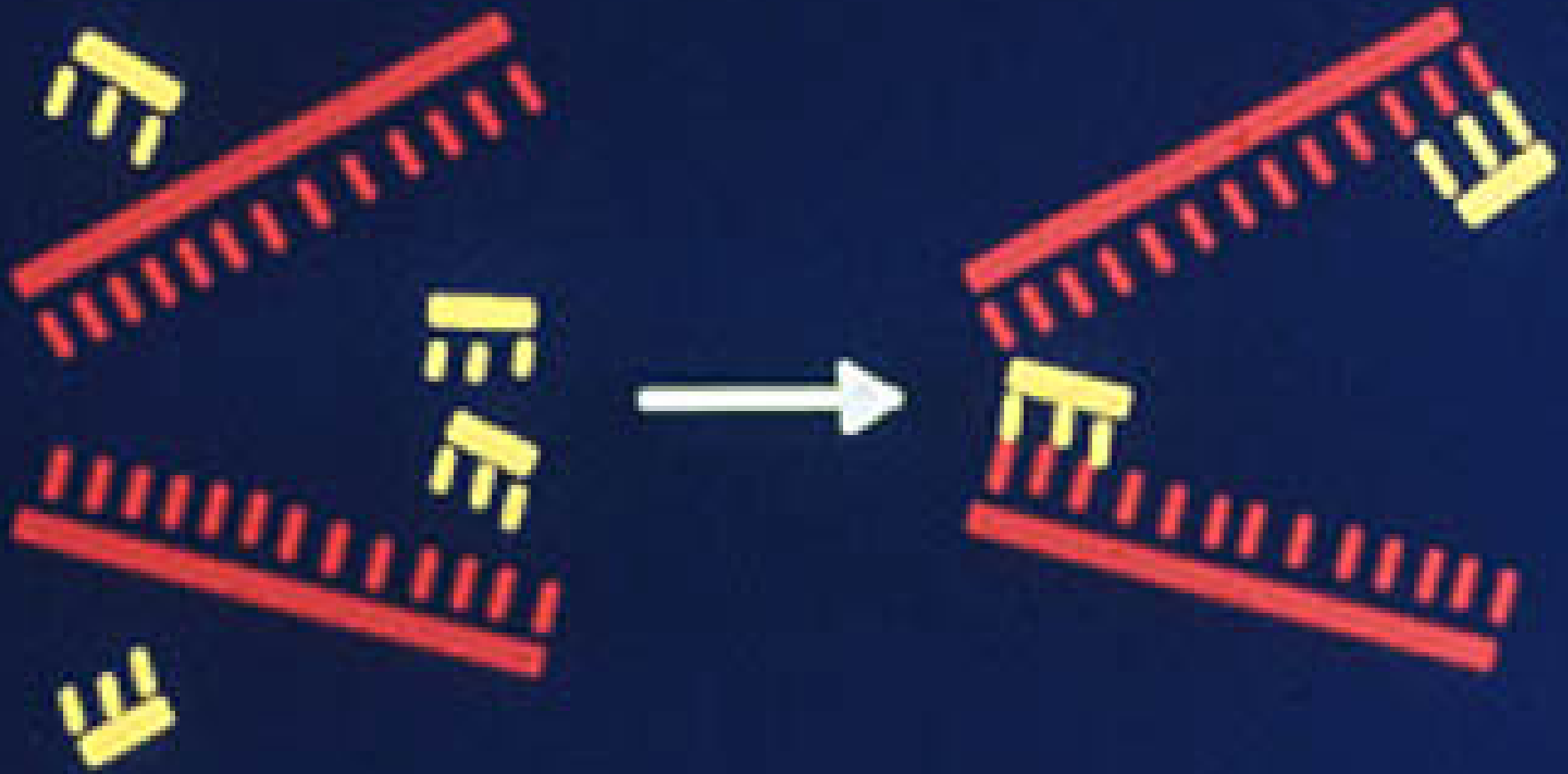



HR-2
eppendorf
Centrifuge 5415 D

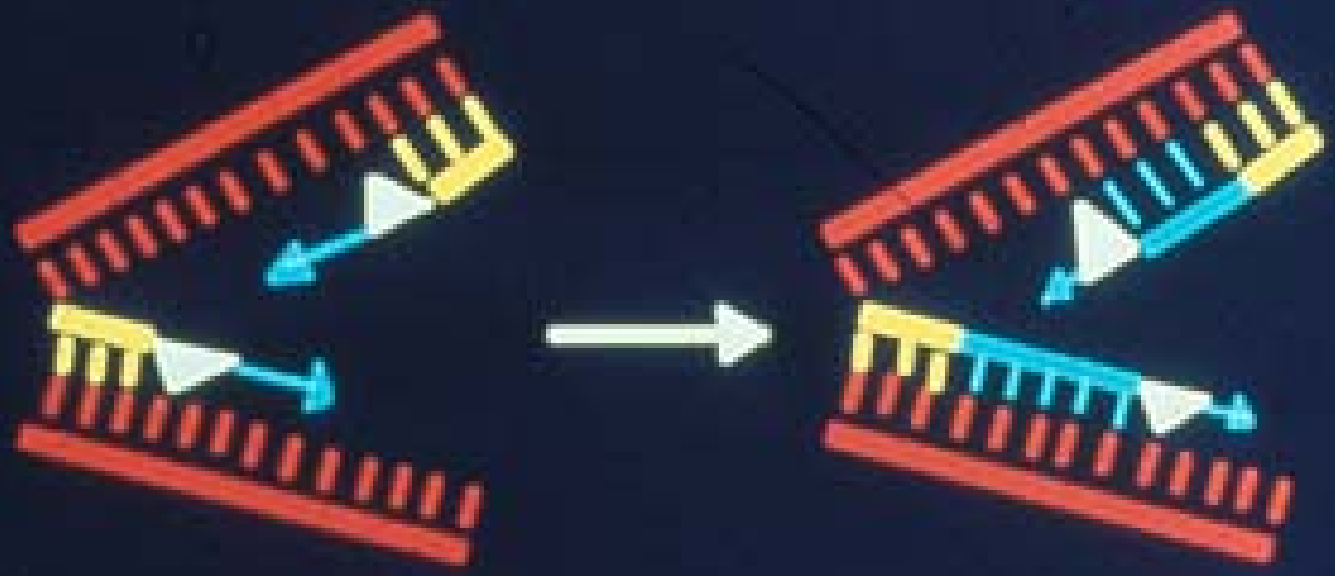
Denature DNA



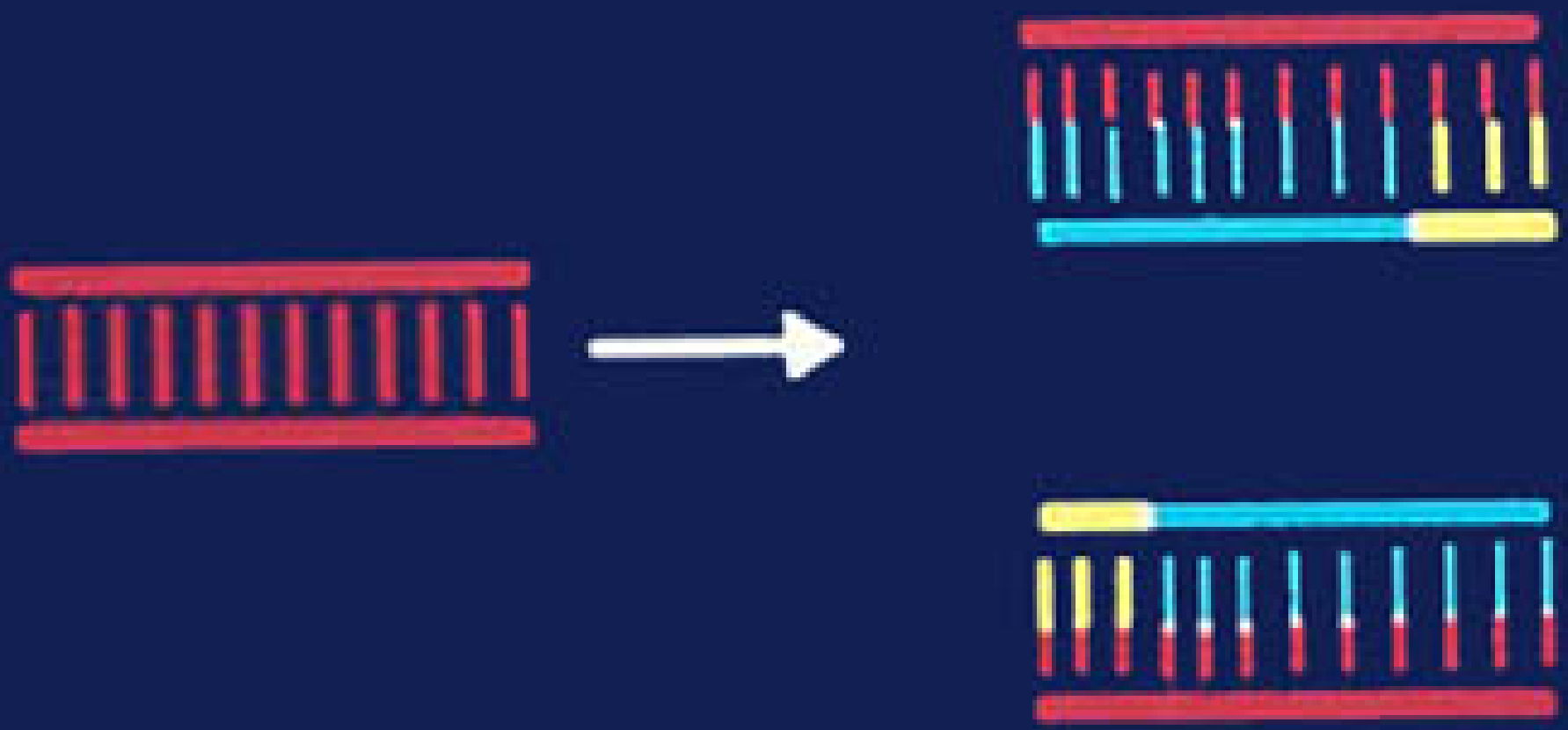
Anneal primers



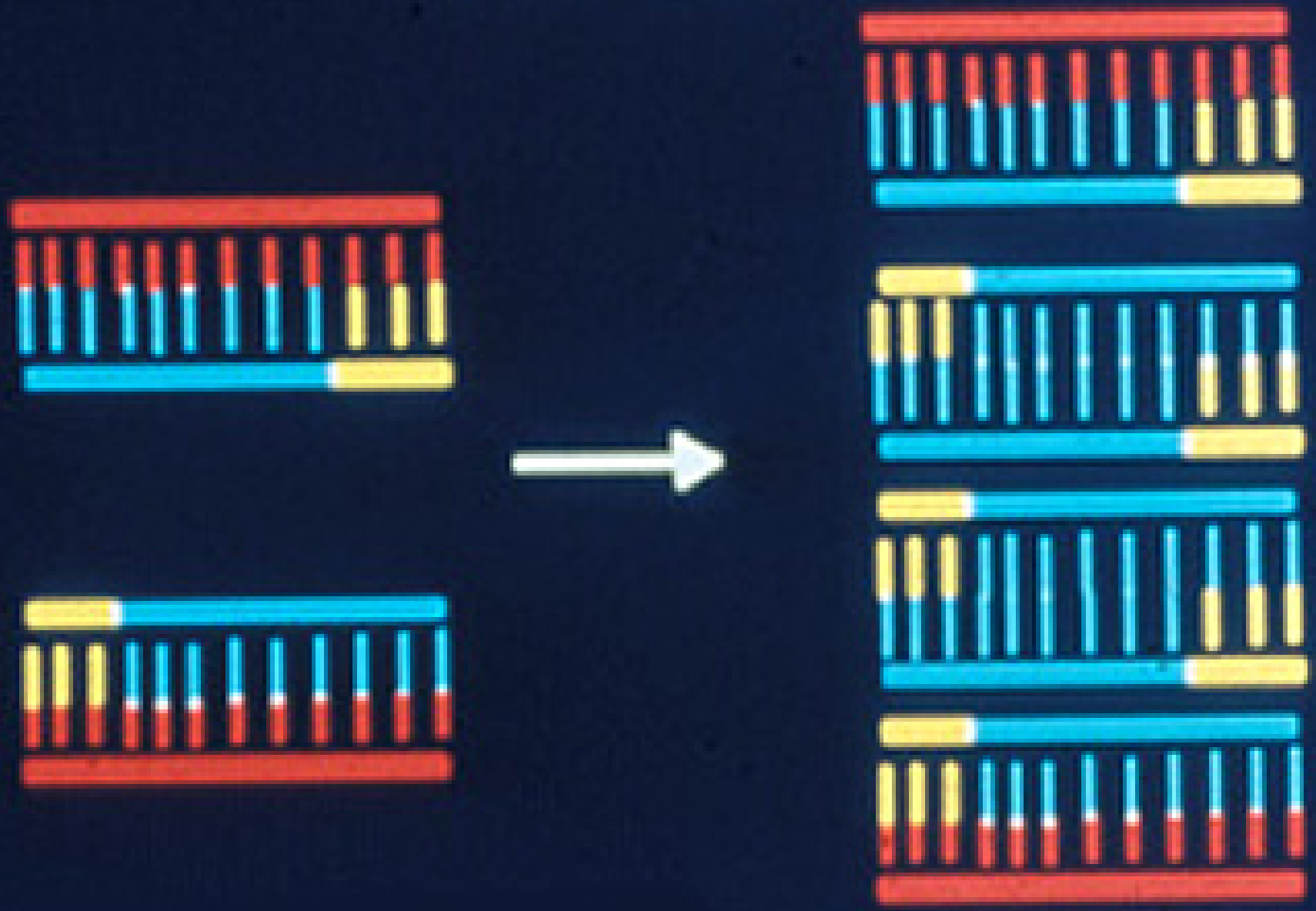
Extend with polymerase (▼)



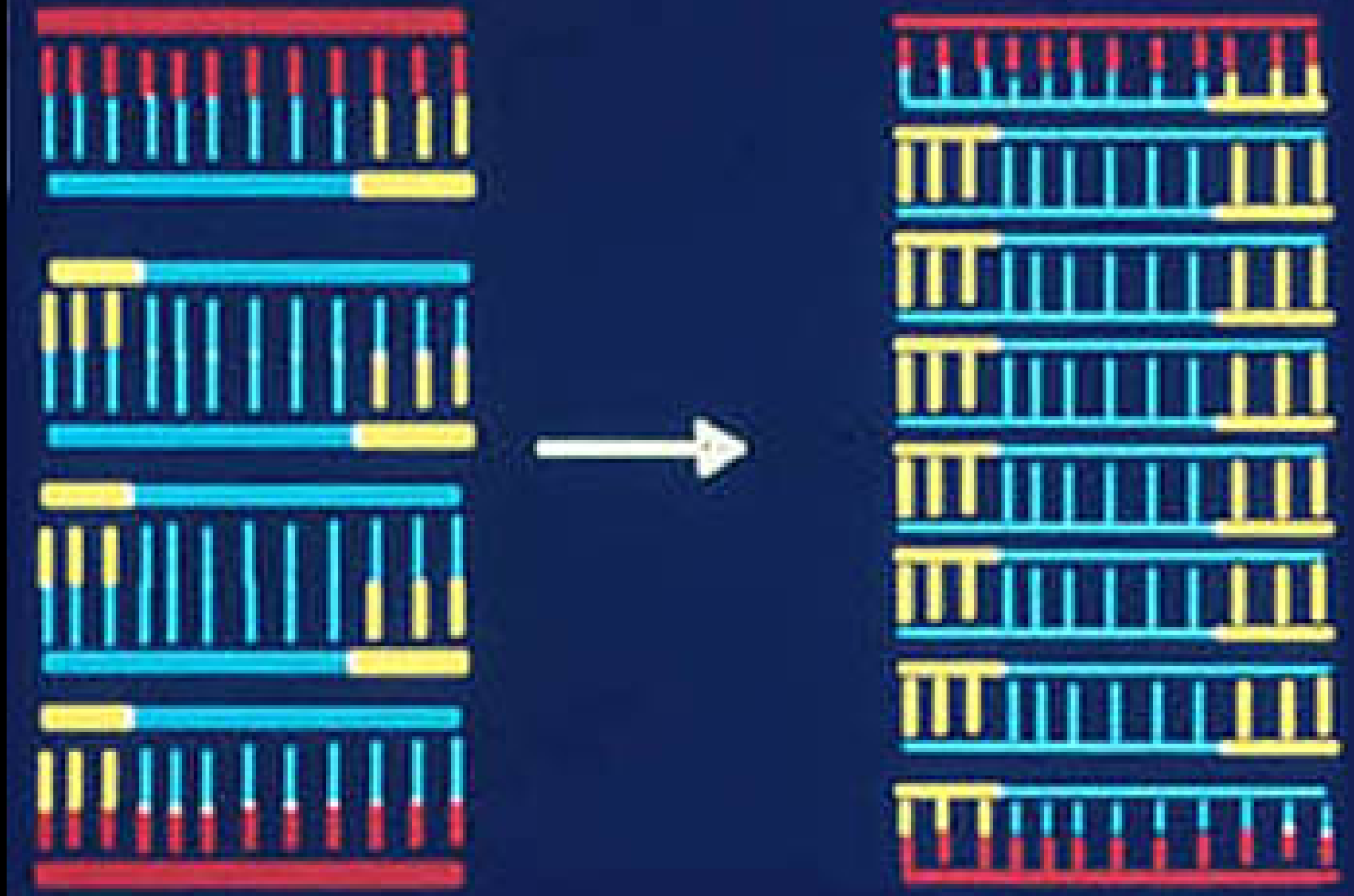
One Cycle



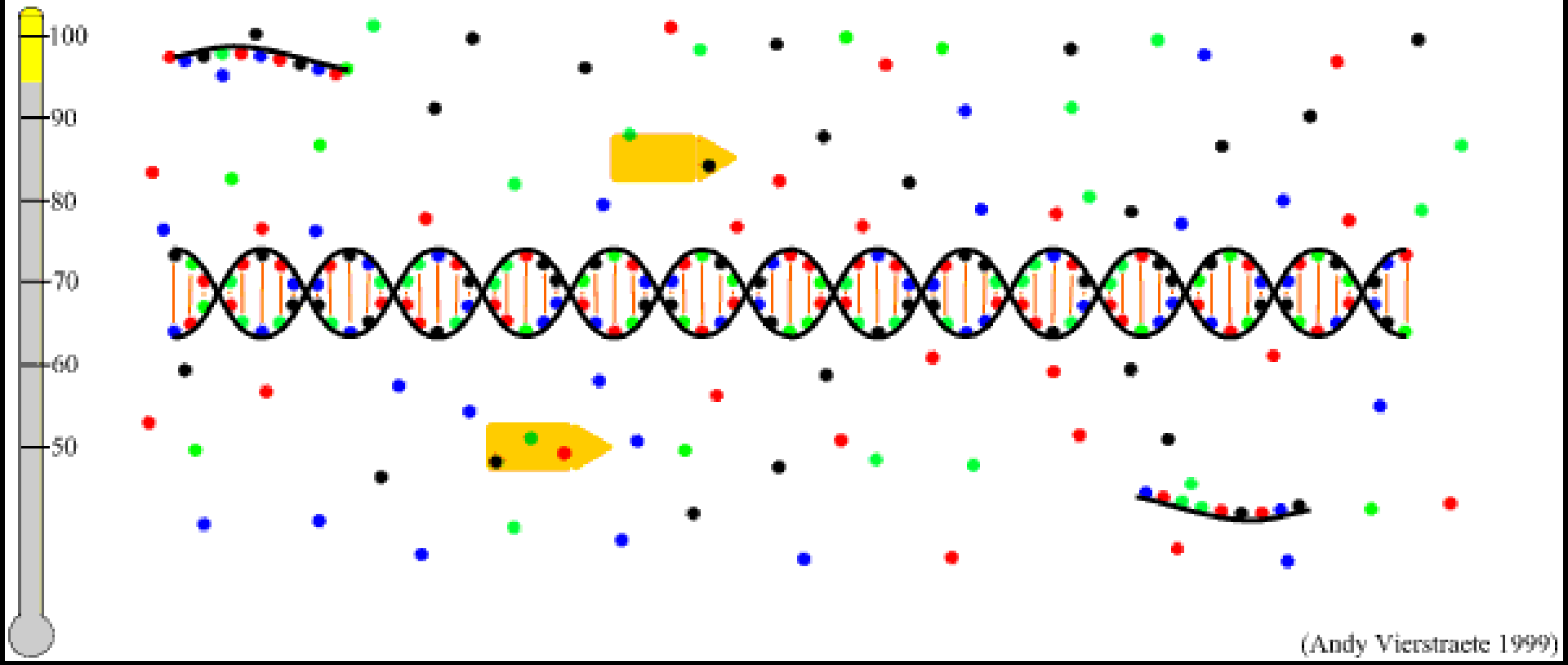
Two Cycles



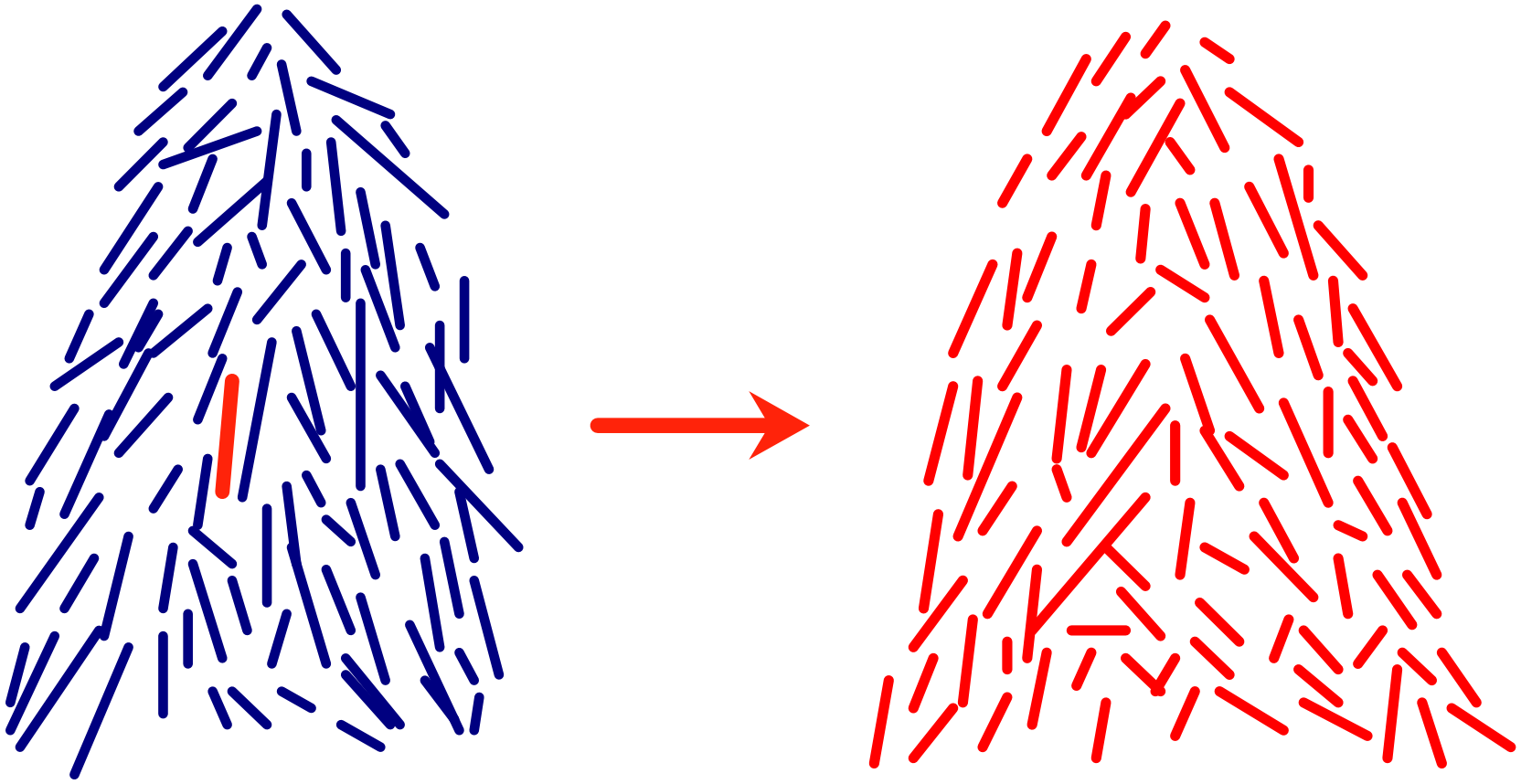
Three Cycles



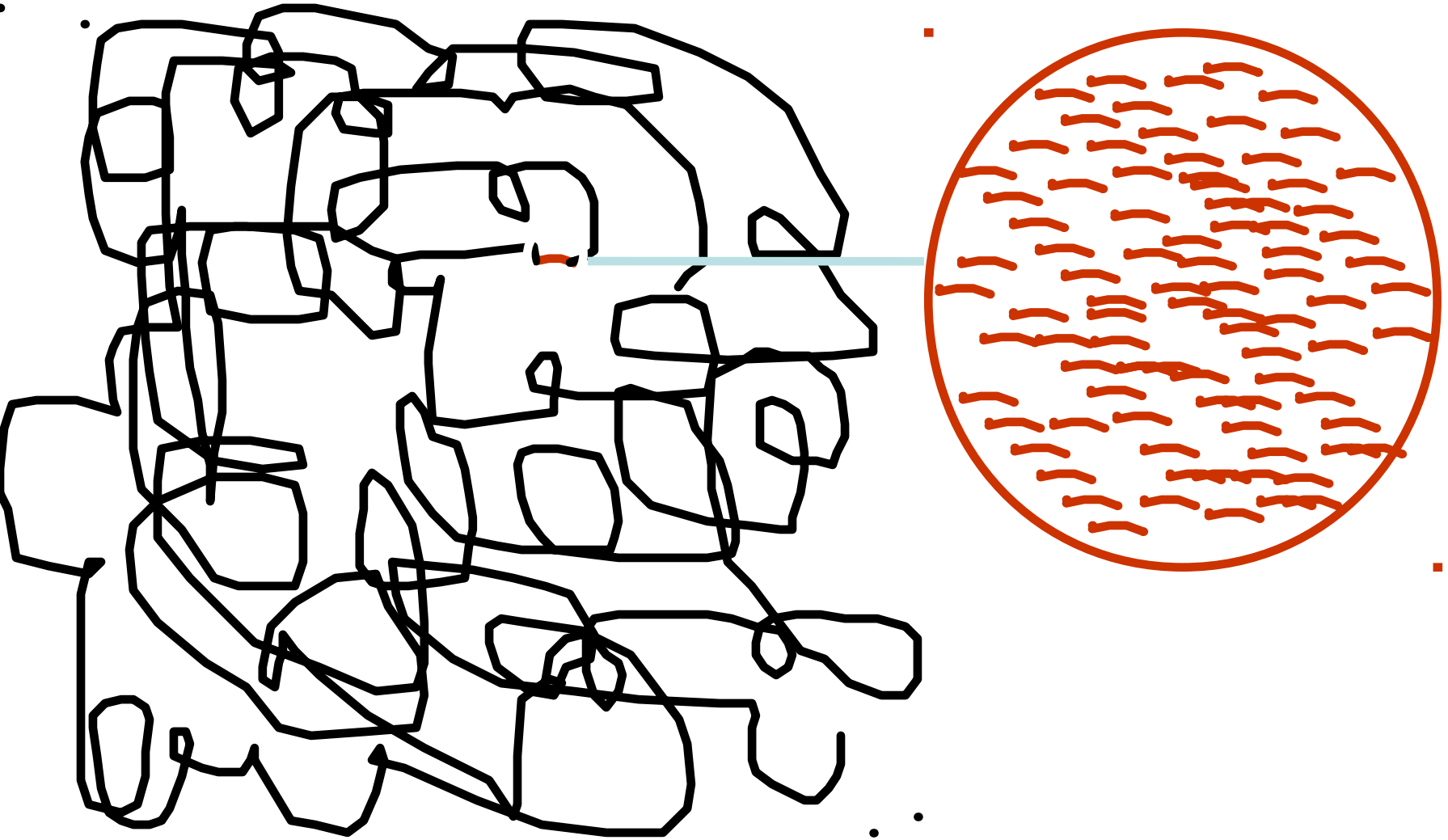
PCR : Denaturation 94°C



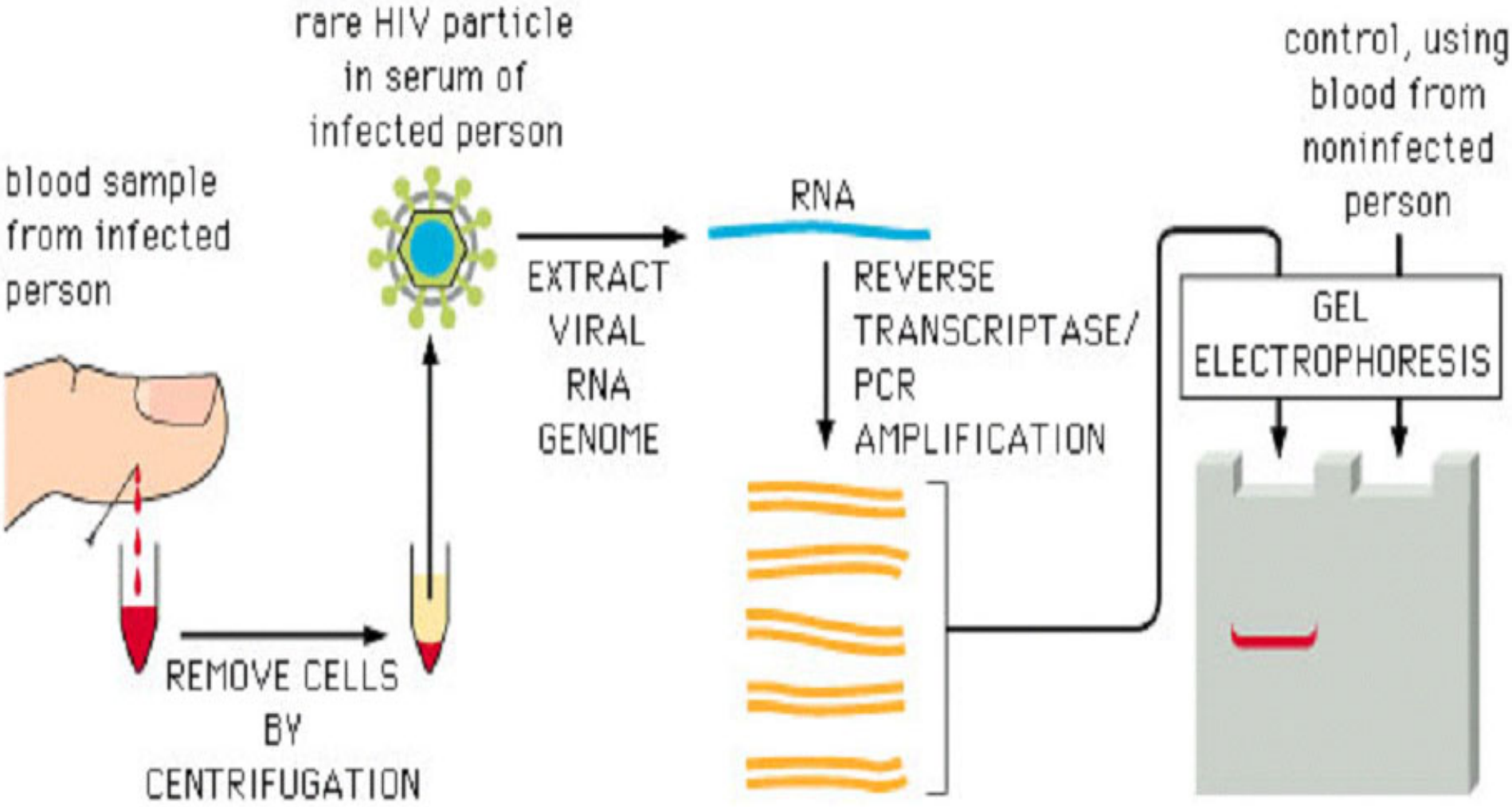
PCR

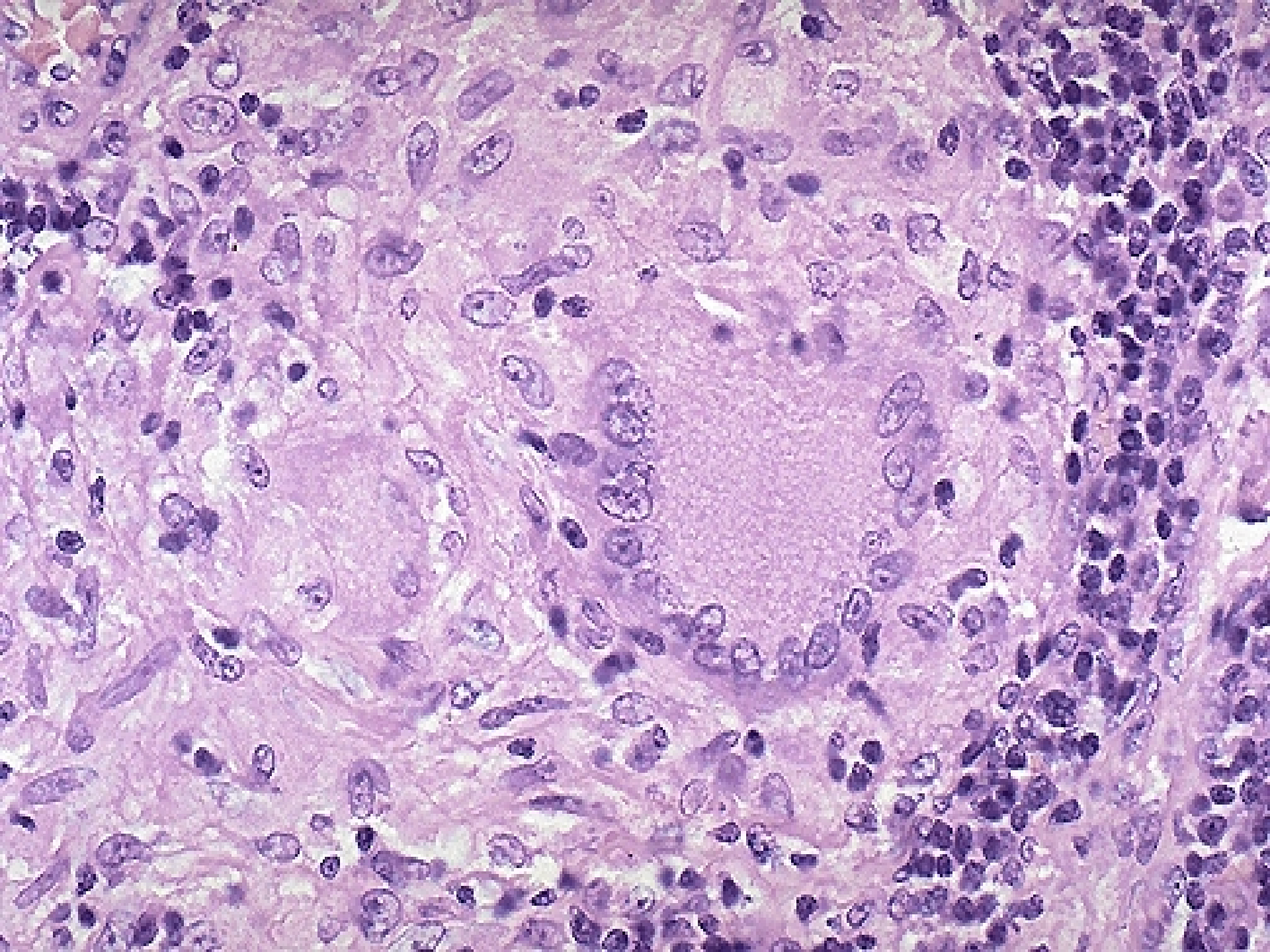


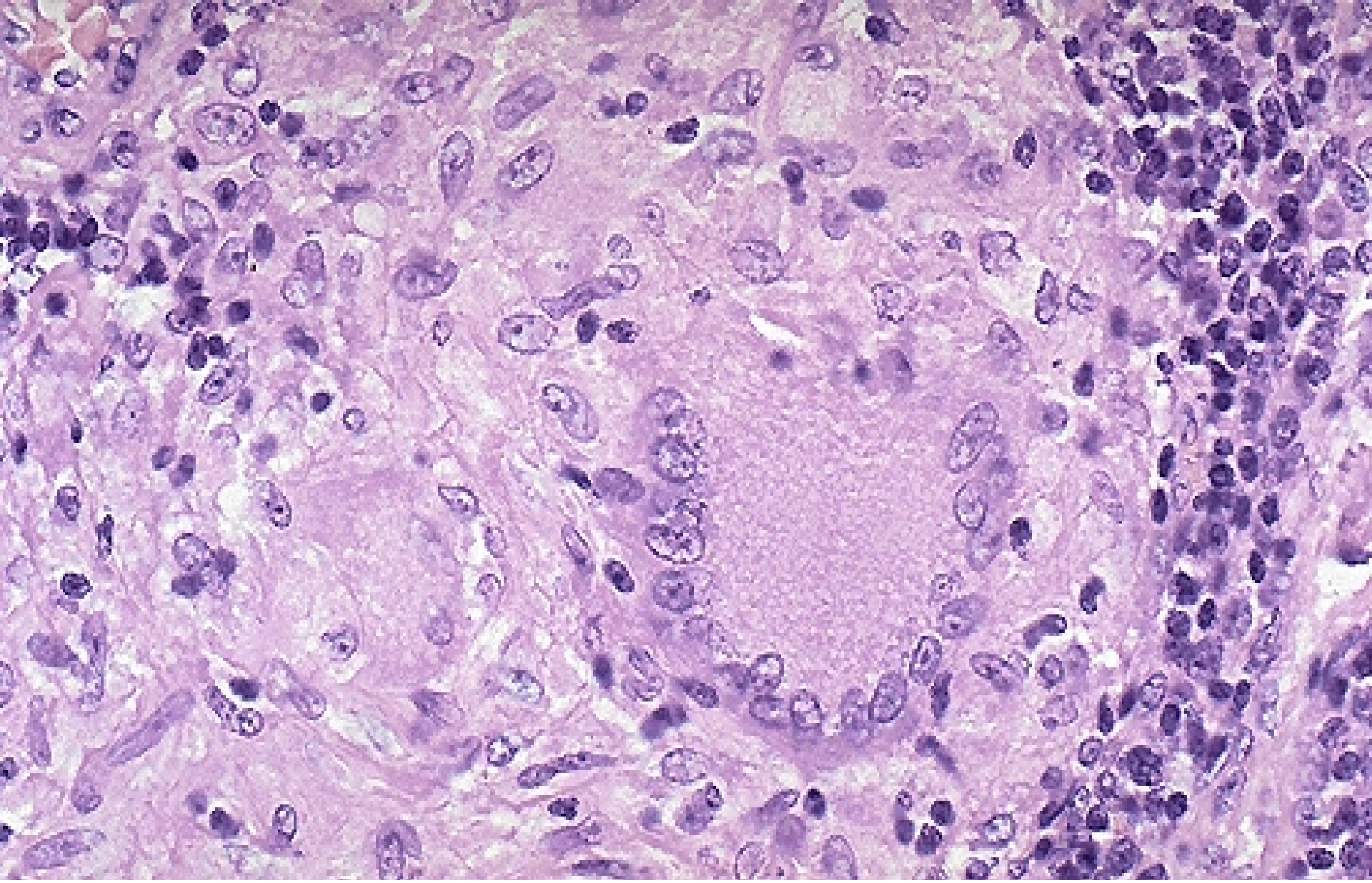
SPECIFIC PRIMERS TARGET ANY GENE



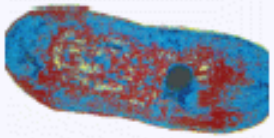
PCR for Medical Diagnostics







Tuberculosis or Crohn disease?



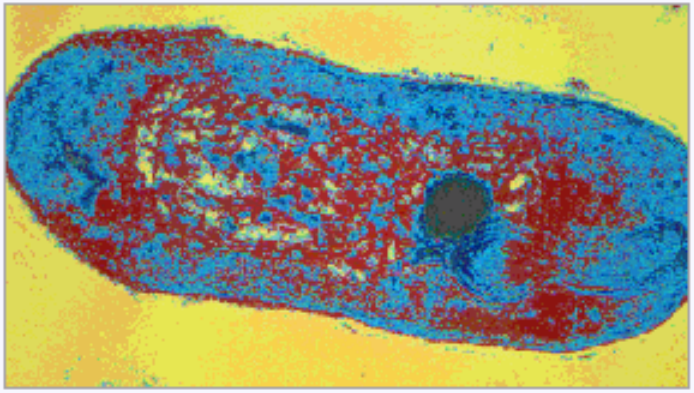
Projects Home

M.tuberculosis
Blast Search
Sequence FTP
Artemis

Related Projects
M.bovis
M.leprae

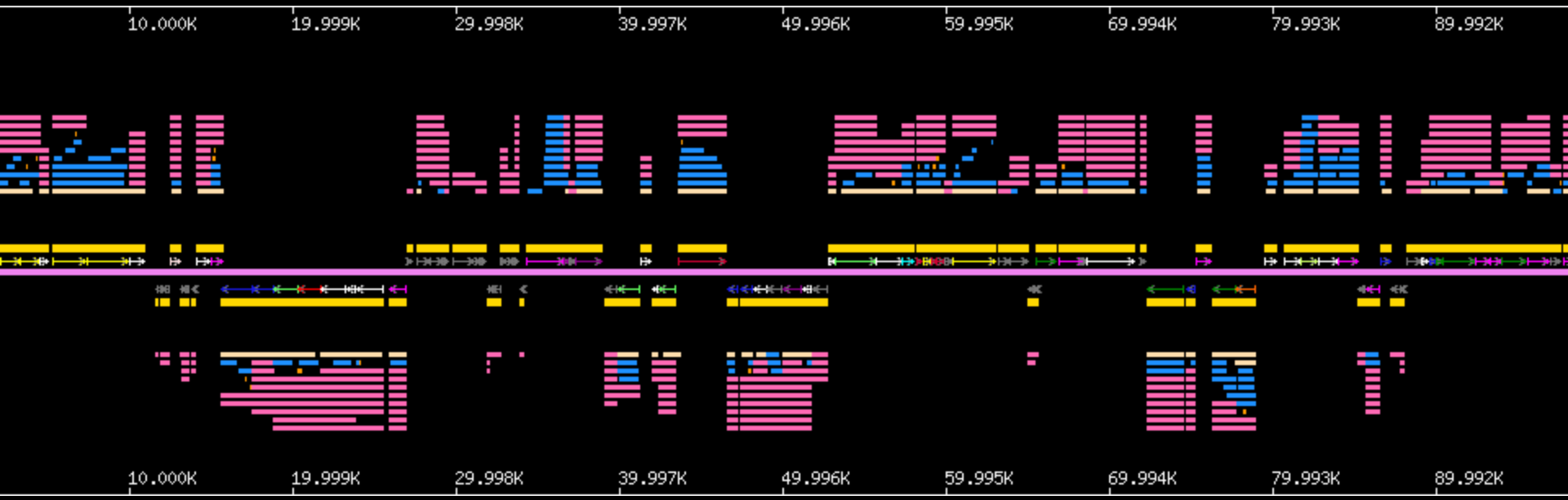
Mycobacterium tuberculosis

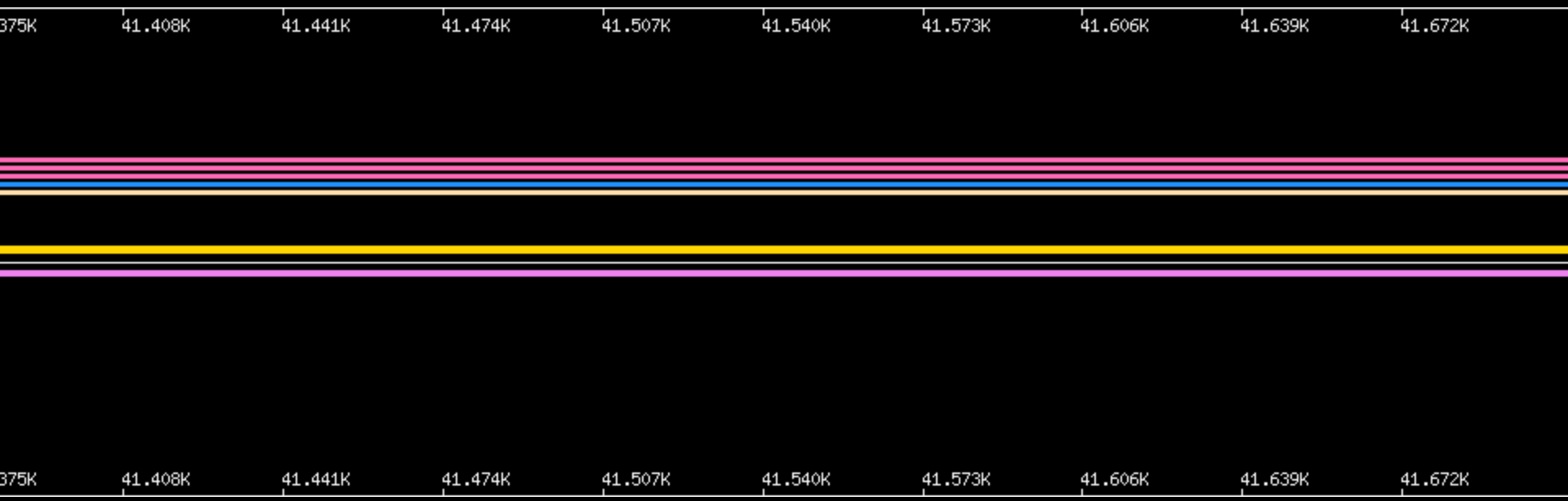
Mycobacterium tuberculosis



Electron micrograph of *M. tuberculosis* courtesy of the Institut Pasteur image library

The recently re-annotated genome of Mycobacterium tuberculosis has been published in Microbiology:


10.000K
19.999K
29.998K
39.997K
49.996K
59.995K
69.994K
79.993K
89.992K
10.000K
19.999K
29.998K
39.997K
49.996K
59.995K
69.994K
79.993K
89.992K



375K
41.408K
41.441K
41.474K
41.507K
41.540K
41.573K
41.606K
41.639K
41.672K

DNA Sequence

>
GTGGTGGCGCCGCACGAAGACCCCGAGGACCATGTCGCACCCGCCGCACAACGGGTGCGA
GCGGGCACCTTATTGTTGGCCAACACCGATCTCCTTGAACCGACATTTCGCCGCAGTGTG
ATCTACATCGTGGAGCACAACGACGGCGGCACCCTCGGTGTGGTCCTCAATCGGCCCAGC
GAAACCGCGGTCTACAACGTGTTGCCGCAGTGGGCCAAACTCGCGGCCAAGCCAAAGACA
ATGTTCATCGGTGGGCCGGTGAAGCGCGACGCGGCGCTGTGTCTGGCGGTATTGCGGGTT
GGCGCTGACCCGGAAGGCGTGCCGGGCCTAAGGCATGTCGCGGGCAGGCTGGTGATGGTC
GATCTGGATGCCGACCCCGAGGTGCTCGCAGCGGCGGTGGAAGGGGTGCGCATCTACGCC
GGGTACTCCGGCTGGACCATCGGTCAGCTCGAAGGTGAAATCGAGCGCGACGACTGGATT
GTGTTGTCGGCGTTGCCATCTGACGTTTTGGTGGGGCCGAGAGCCGACCTGTGGGGGCAG
GTGCTGCGACGGCAGCCGCTGCCGCTGTCGCTGCTGGCCACCCACCCGATCGATCTGAGC
CGGAAC

Protein Sequence

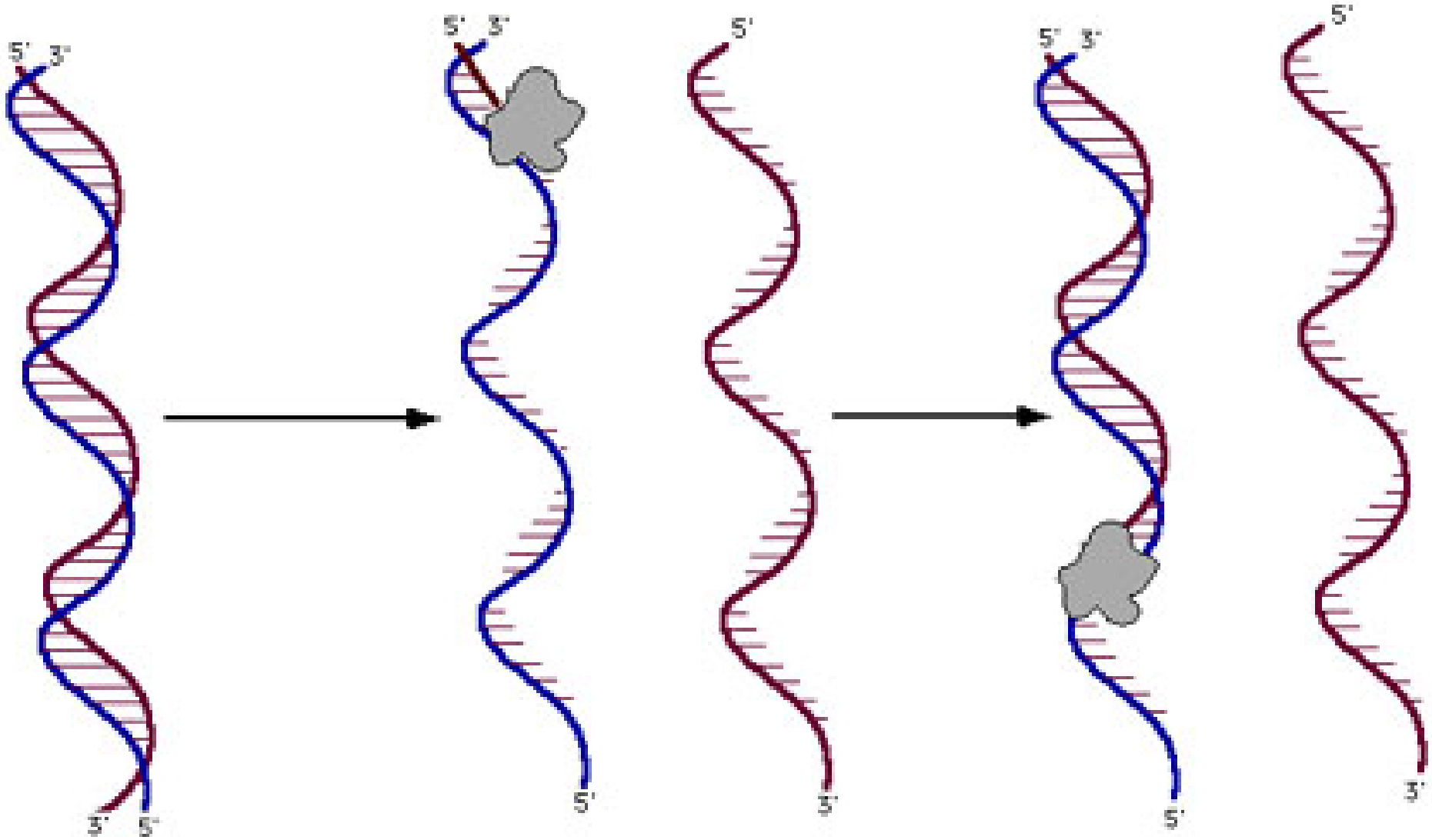
>
MVAPHEDPEDHVAPAAQRVRAGTLLLANTDLLEPTFRRSVIYIVEHNDGGTLGVVLNRPS
ETAVYNVLPQWAKLAAKPKTMFIGGPVKRDAALCLAVLRVGADPEGVPGLRHVAGRLVMV
DLDADPEVLAAAVEGVRIYAGYSGWTIGQLEGEIERDDWIVLSALPSDVLVGPRADLWGQ
VLRRQPLPLSLLATHPIDLSRN

1 Sample

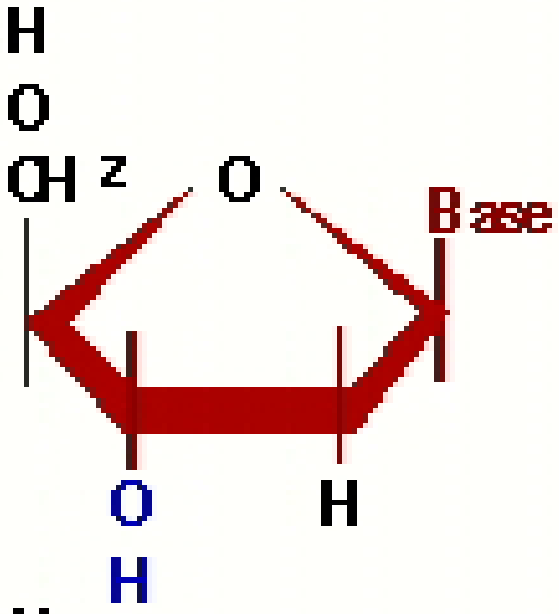
2 Positive control

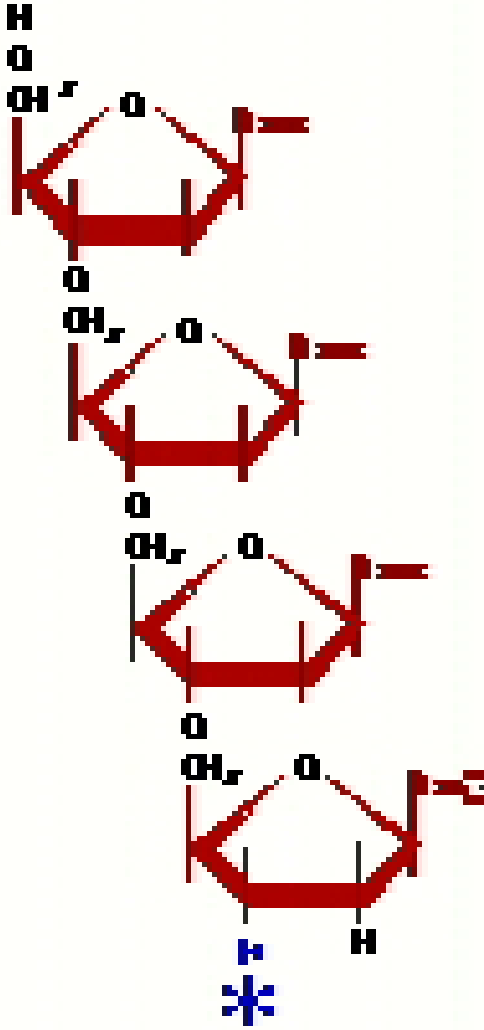
3 Negative control

DNA Sequencing

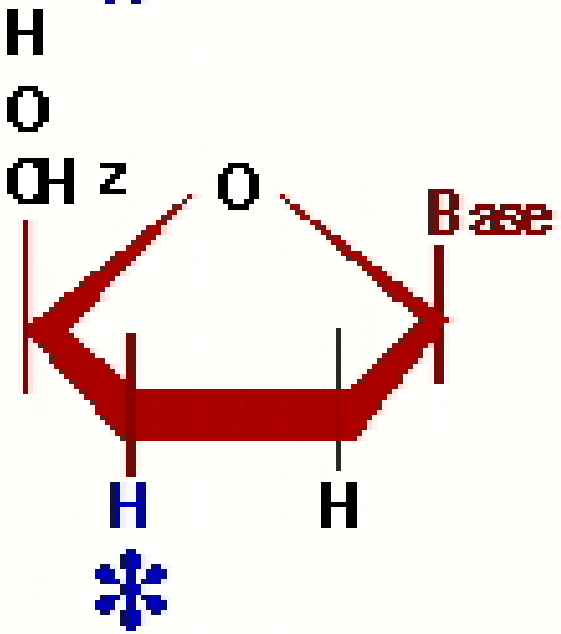


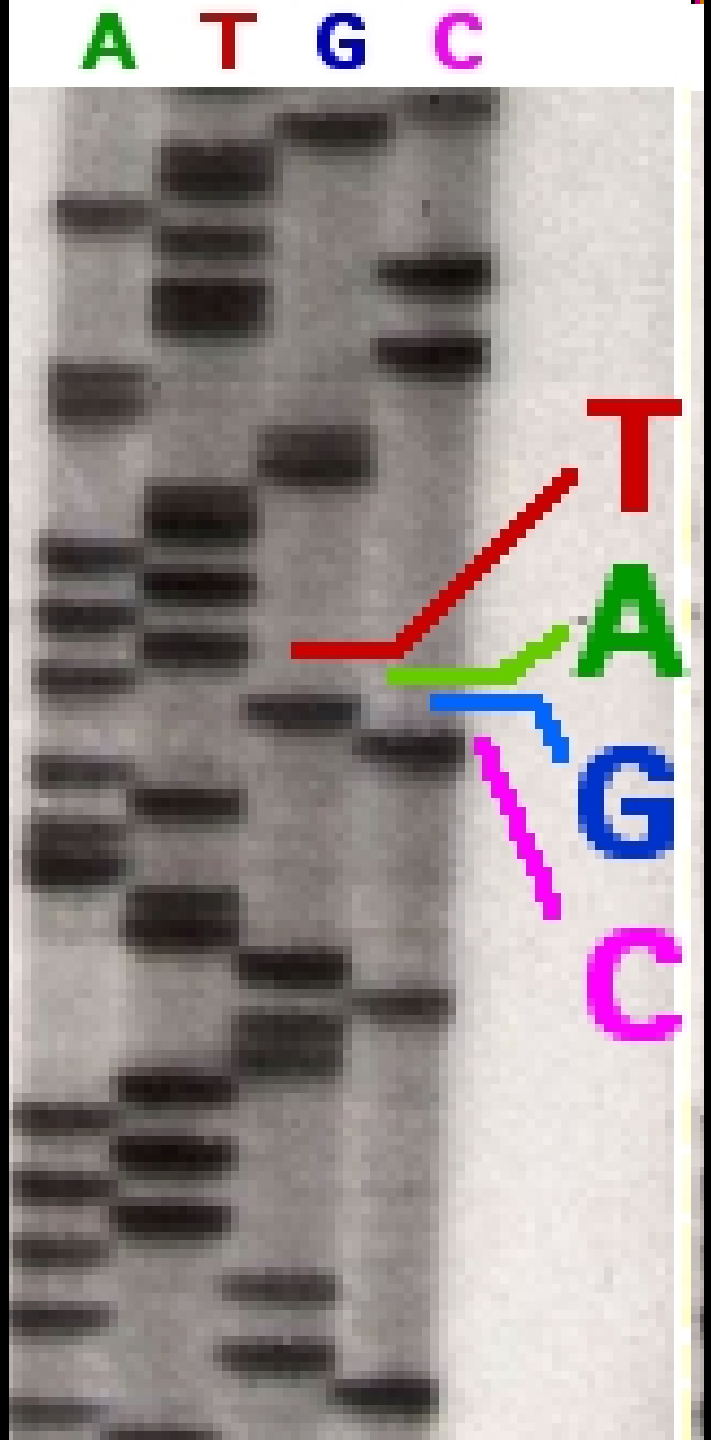
Normal nucleotides:

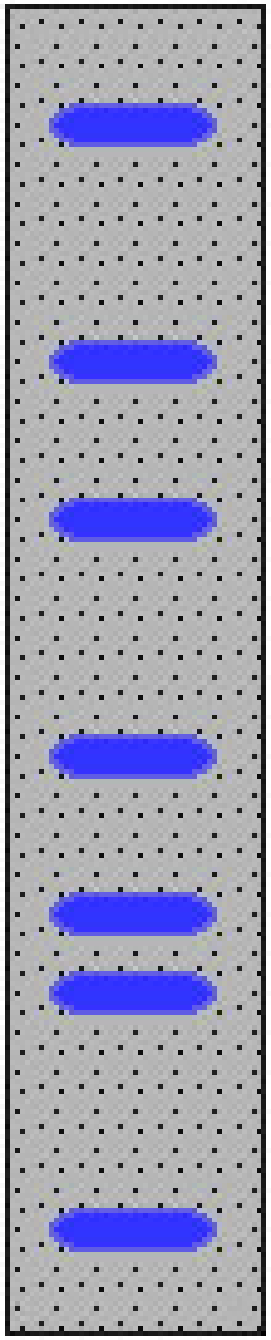




Dideoxy Chain Terminators:




A T G C
T
A
G
C



GCGAATGCGTCCACAACGCTAC

GCGAATGCGTCCACAACGC

GCGAATGCGTCCACAAC

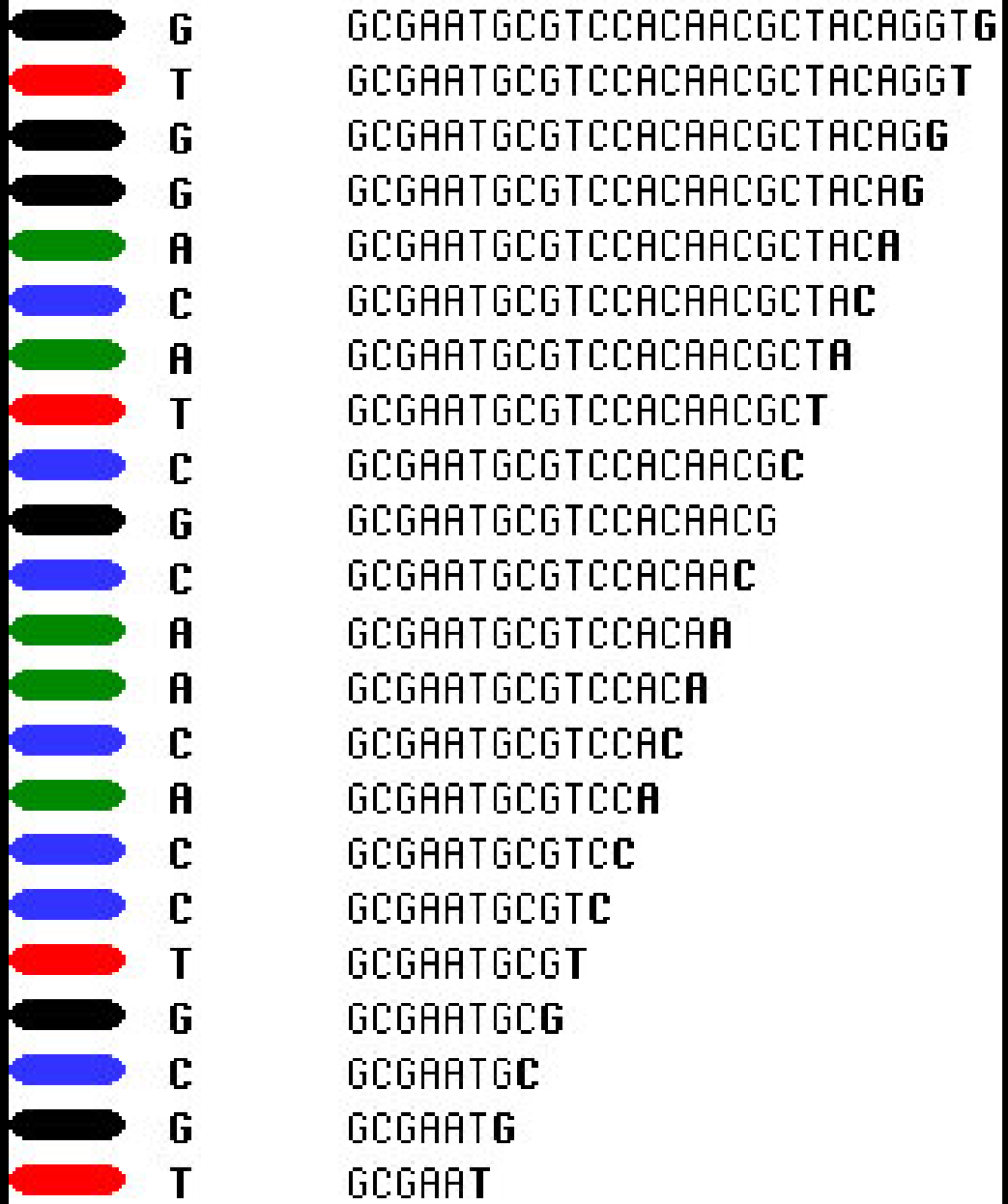
GCGAATGCGTCCAC

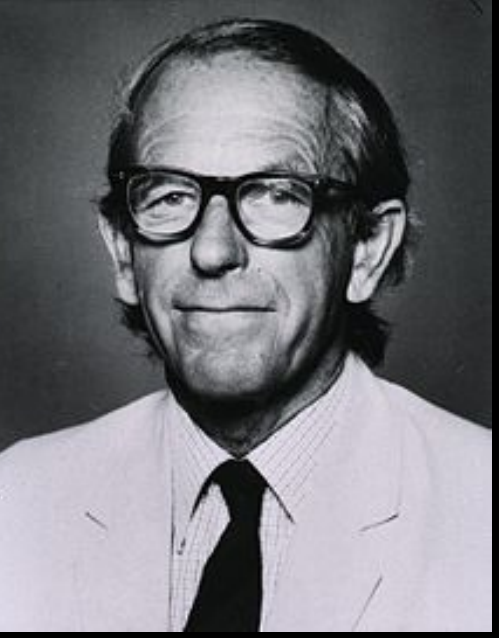
GCGAATGCGTCC

GCGAATGCGTC

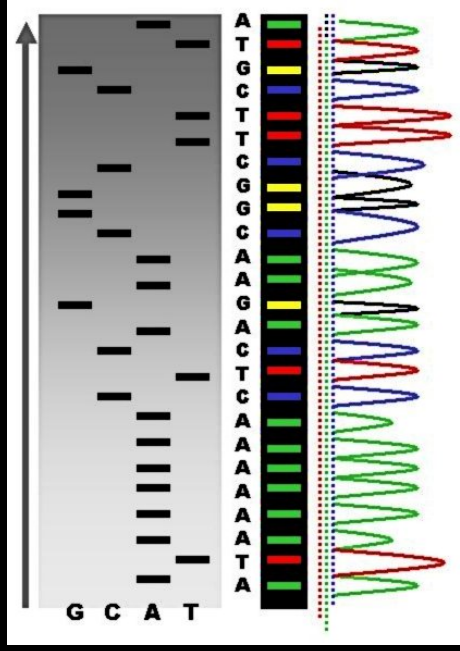
GCGAATG

Gel:

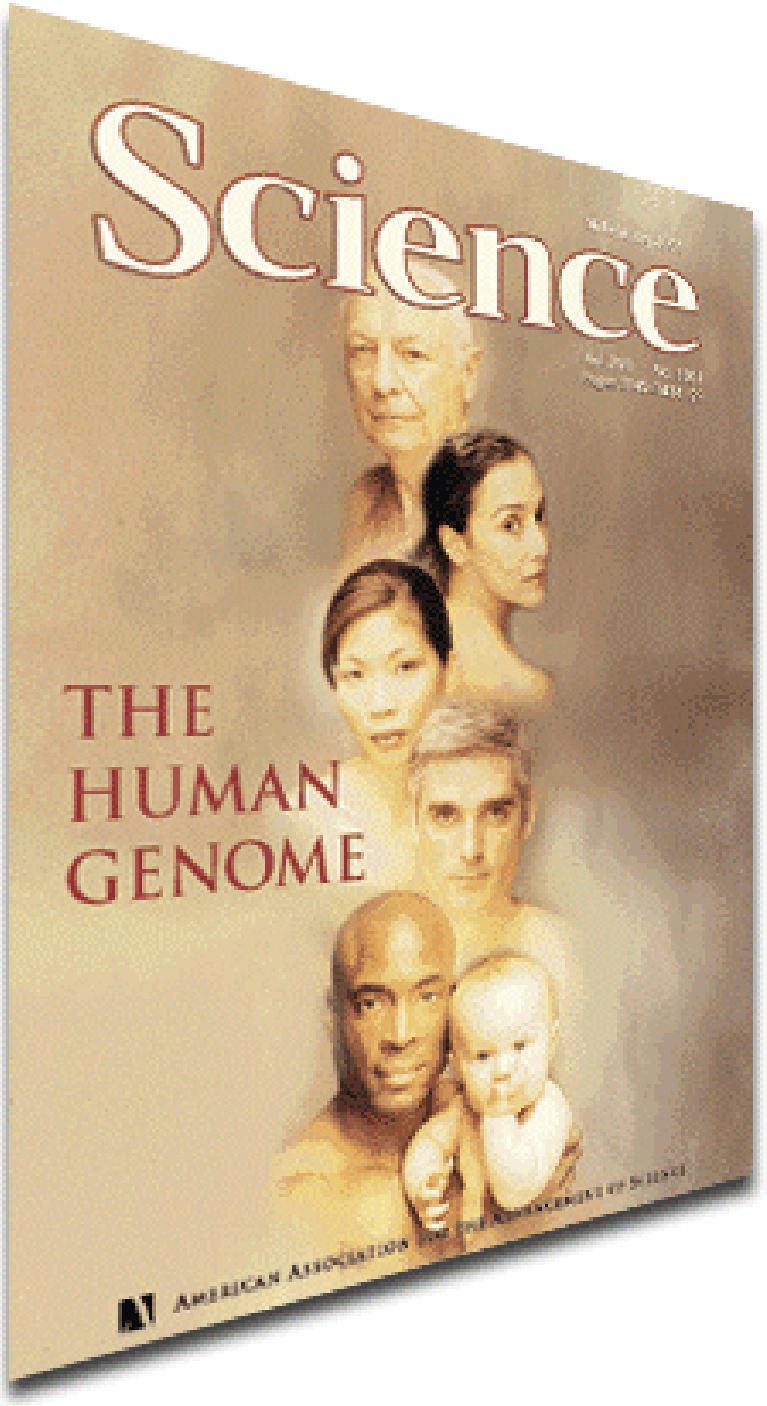

G GCGAATGCGTCCACAACGCTACAGGTG
T GCGAATGCGTCCACAACGCTACAGGT
G GCGAATGCGTCCACAACGCTACAGG
G GCGAATGCGTCCACAACGCTACA
A GCGAATGCGTCCACAACGCTAC
C GCGAATGCGTCCACAACGCTA
A GCGAATGCGTCCACAACGCT
T GCGAATGCGTCCACAACGC
C GCGAATGCGTCCACAACG
G GCGAATGCGTCCACAACG
C GCGAATGCGTCCACAAC
A GCGAATGCGTCCACA
A GCGAATGCGTCCAC
C GCGAATGCGTCCA
A GCGAATGCGTCC
C GCGAATGCGTC
C GCGAATGCGT
T GCGAATGCG
G GCGAATGC
C GCGAATG
G GCGAAT
T GCGAAT

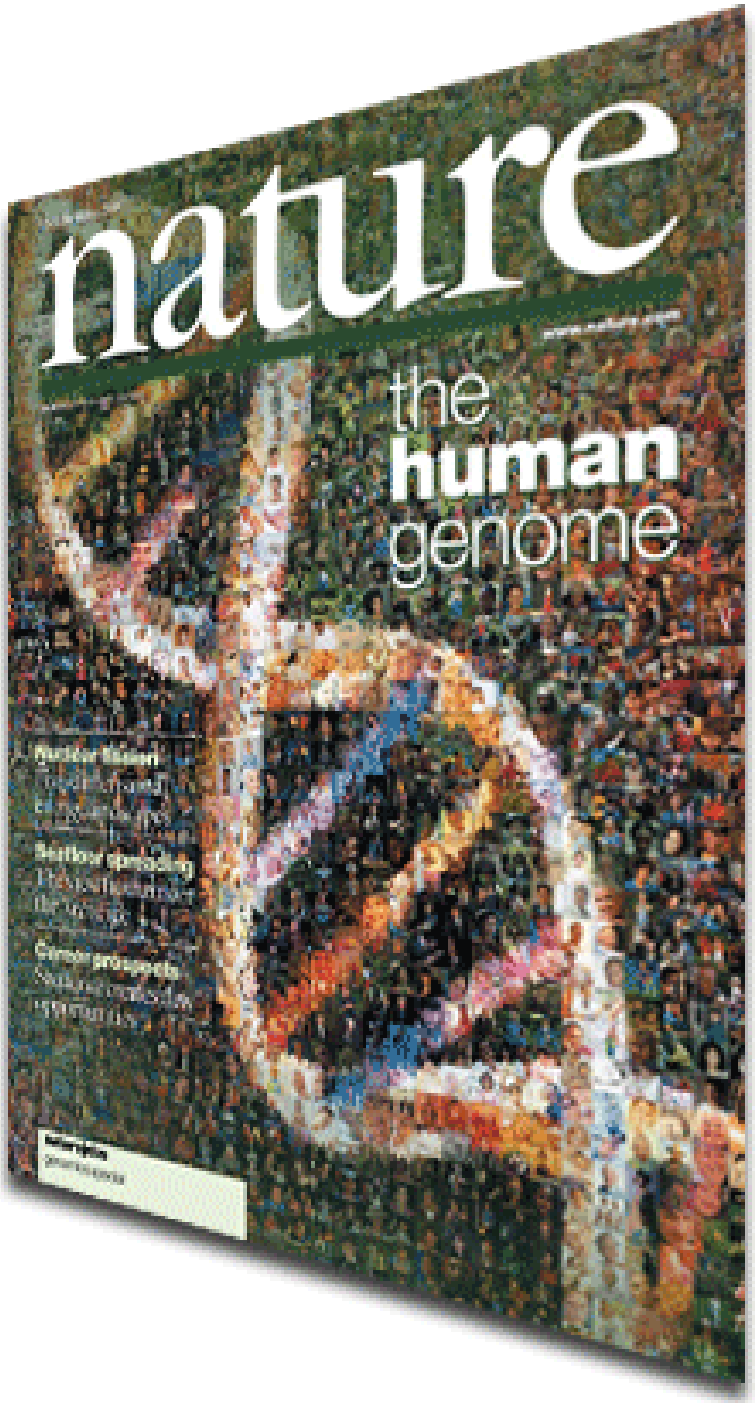


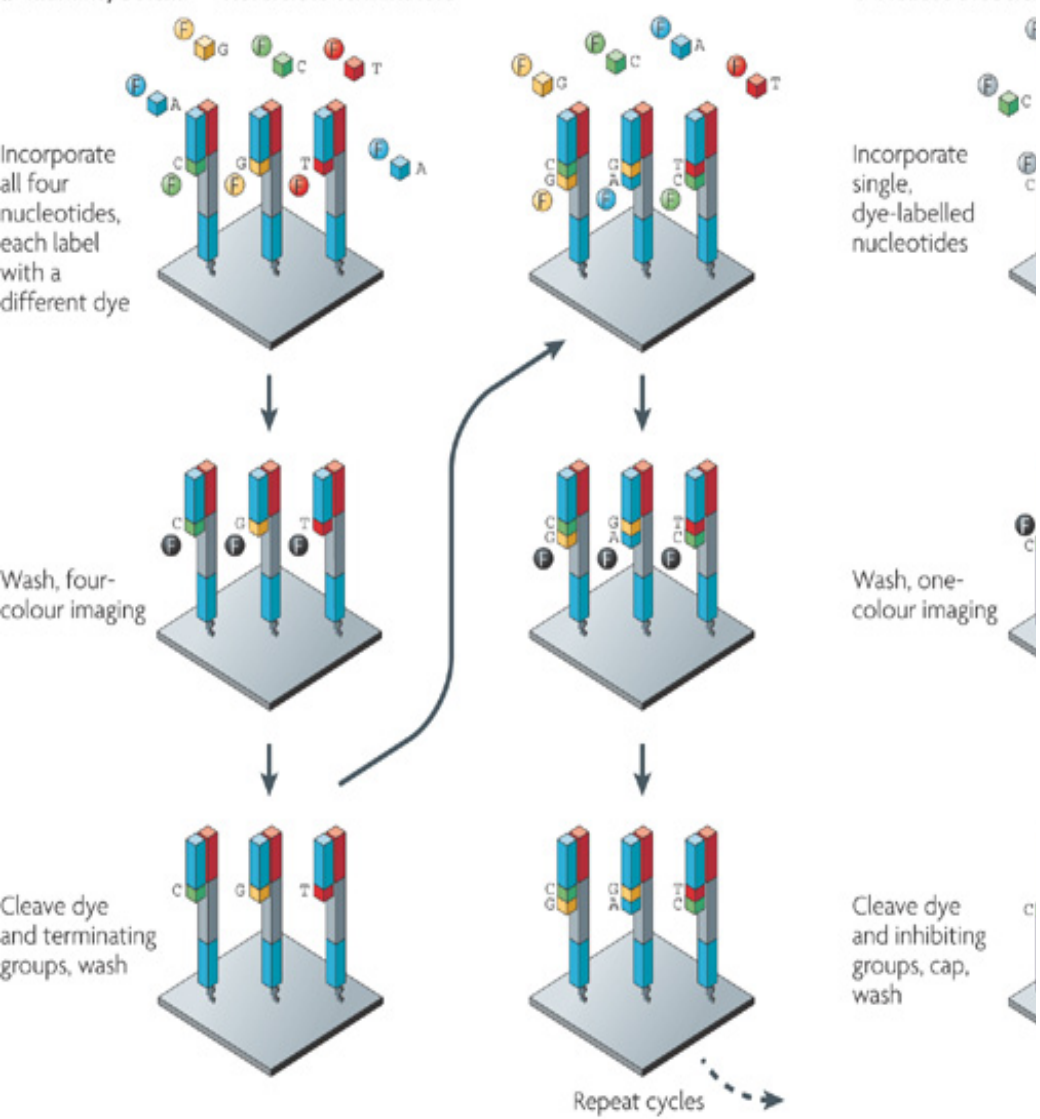
Frederick Sanger



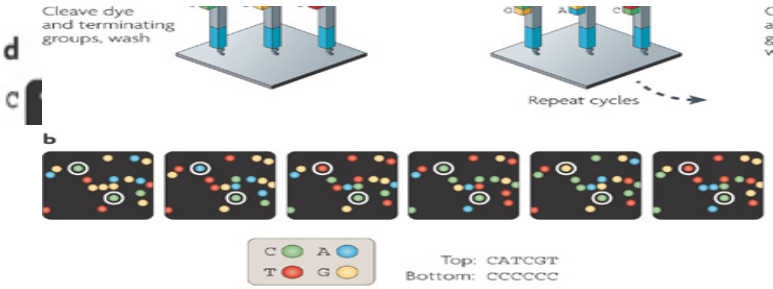
"just a chap who messed about in a lab"


Science
THE HUMAN GENOME

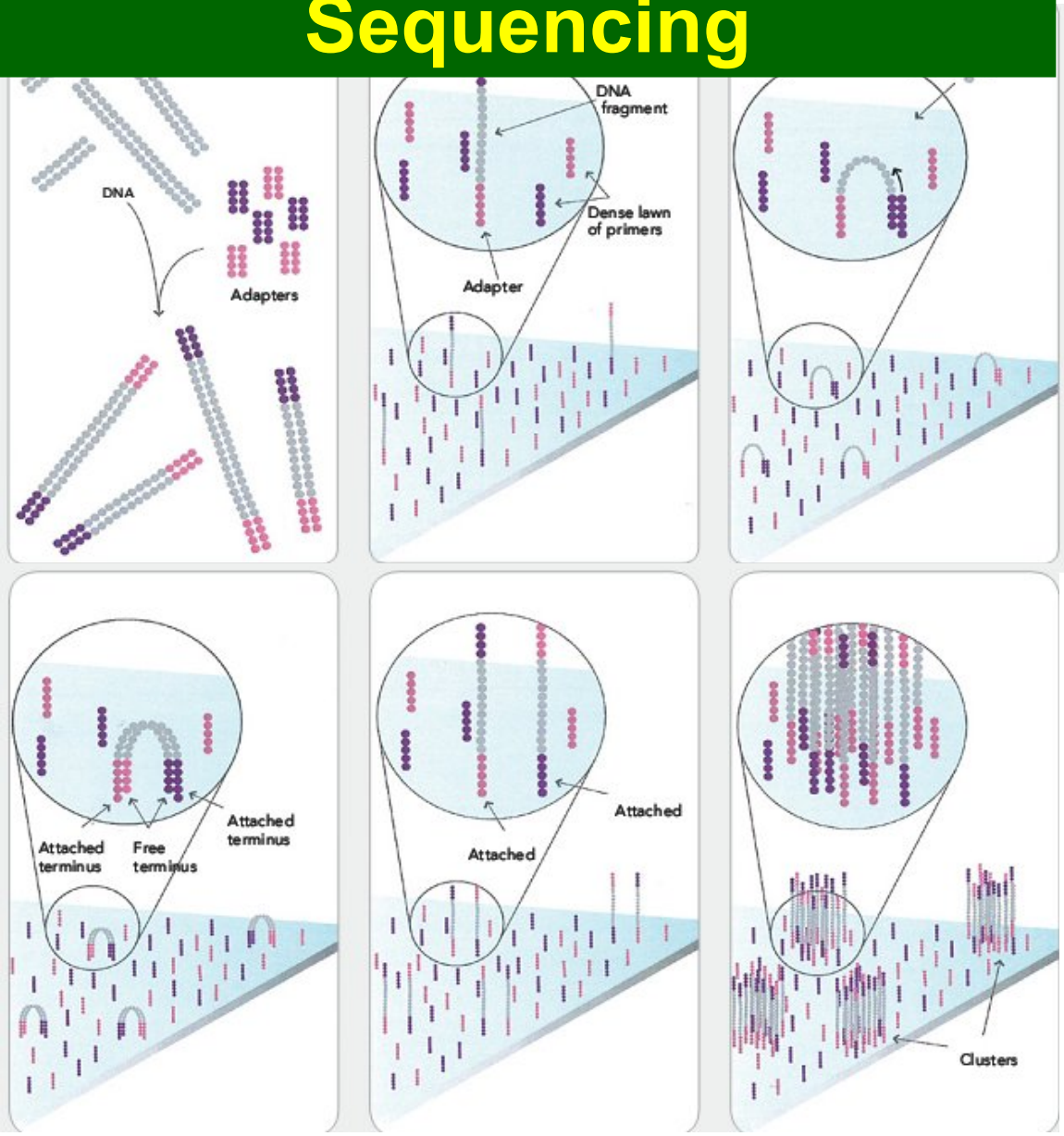

nature
the human genome

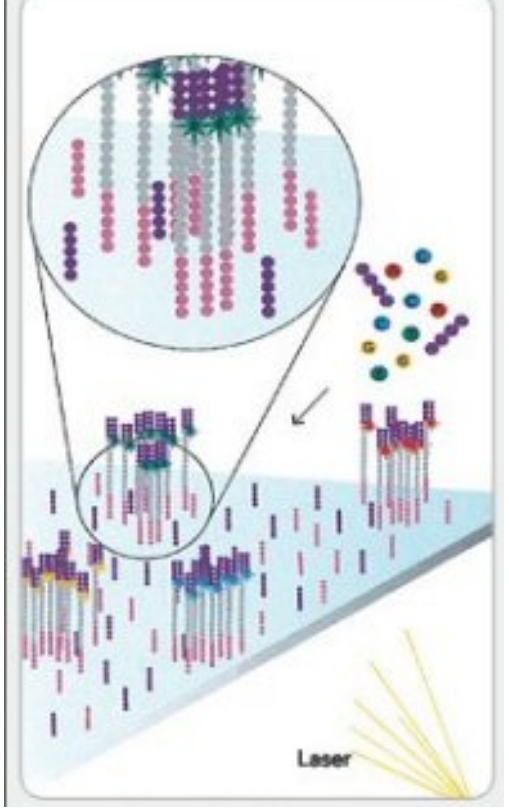

Incorporate all four nucleotides, each label with a different dye
Wash, four-colour imaging
Cleave dye and terminating groups, wash
Repeat cycles
Incorporate single, dye-labelled nucleotides
Wash, one-colour imaging
Cleave dye and inhibiting groups, cap, wash

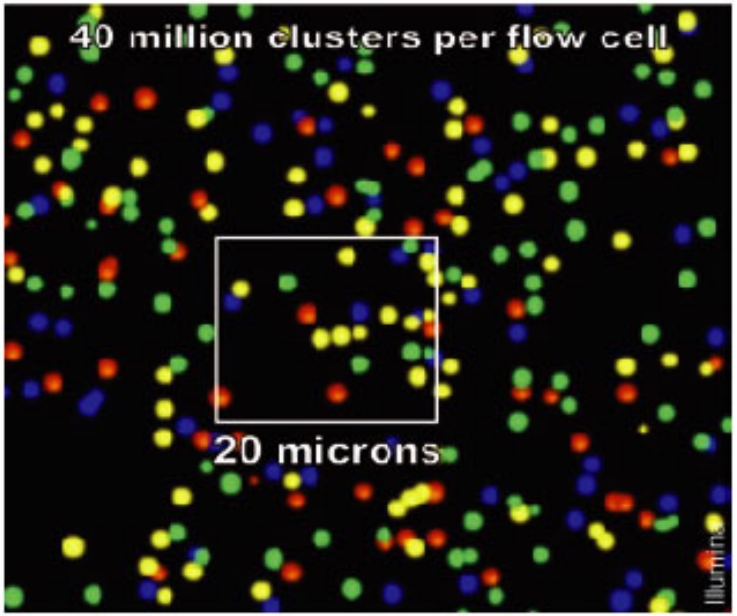

b


d
Cleave dye and terminating groups, wash
Repeat cycles
Cleave dye and inhibiting groups, cap, wash
b
C A
T G
Top: CATCGT
Bottom: CCCCCC

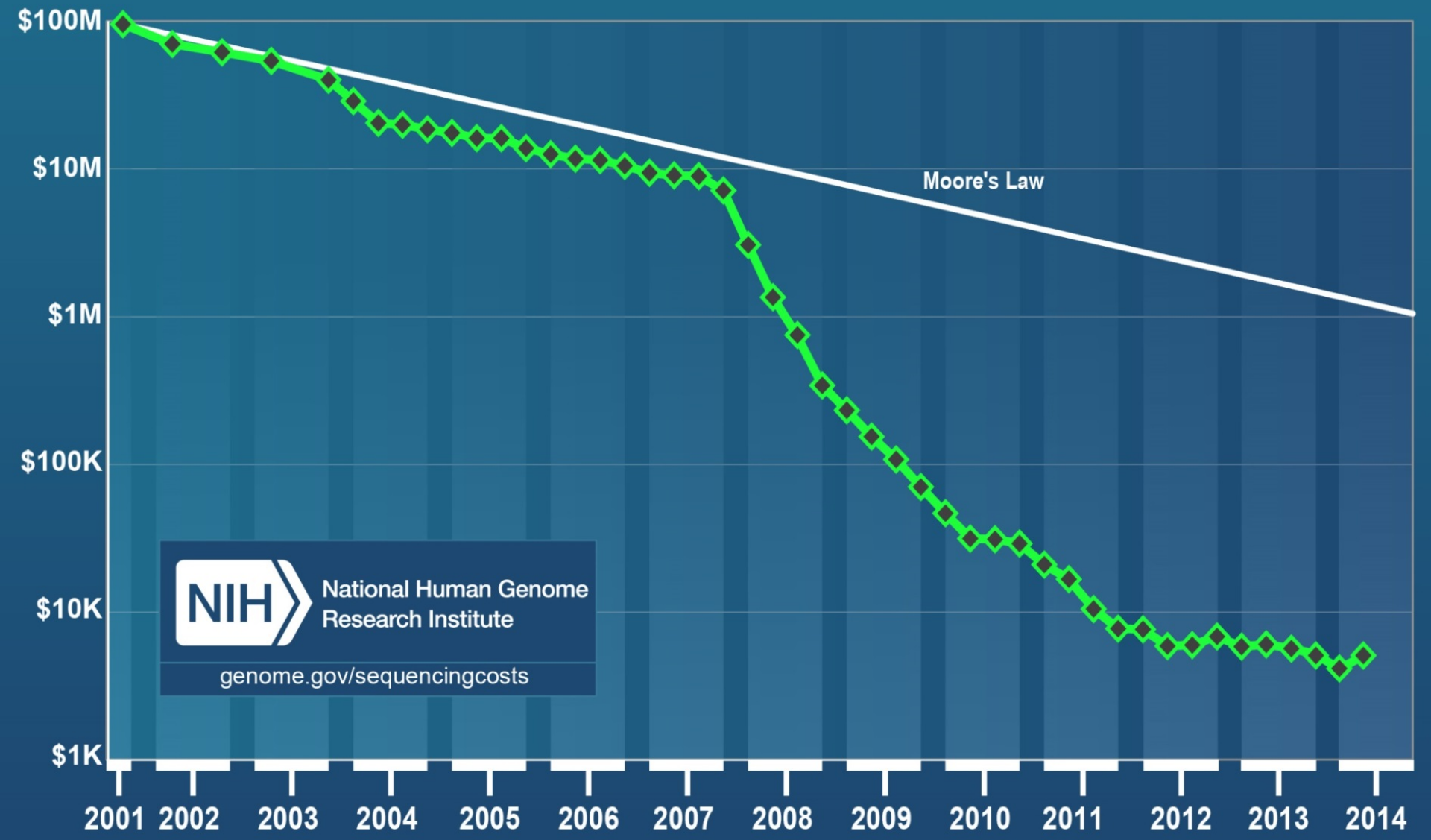
Next Generation Sequencing



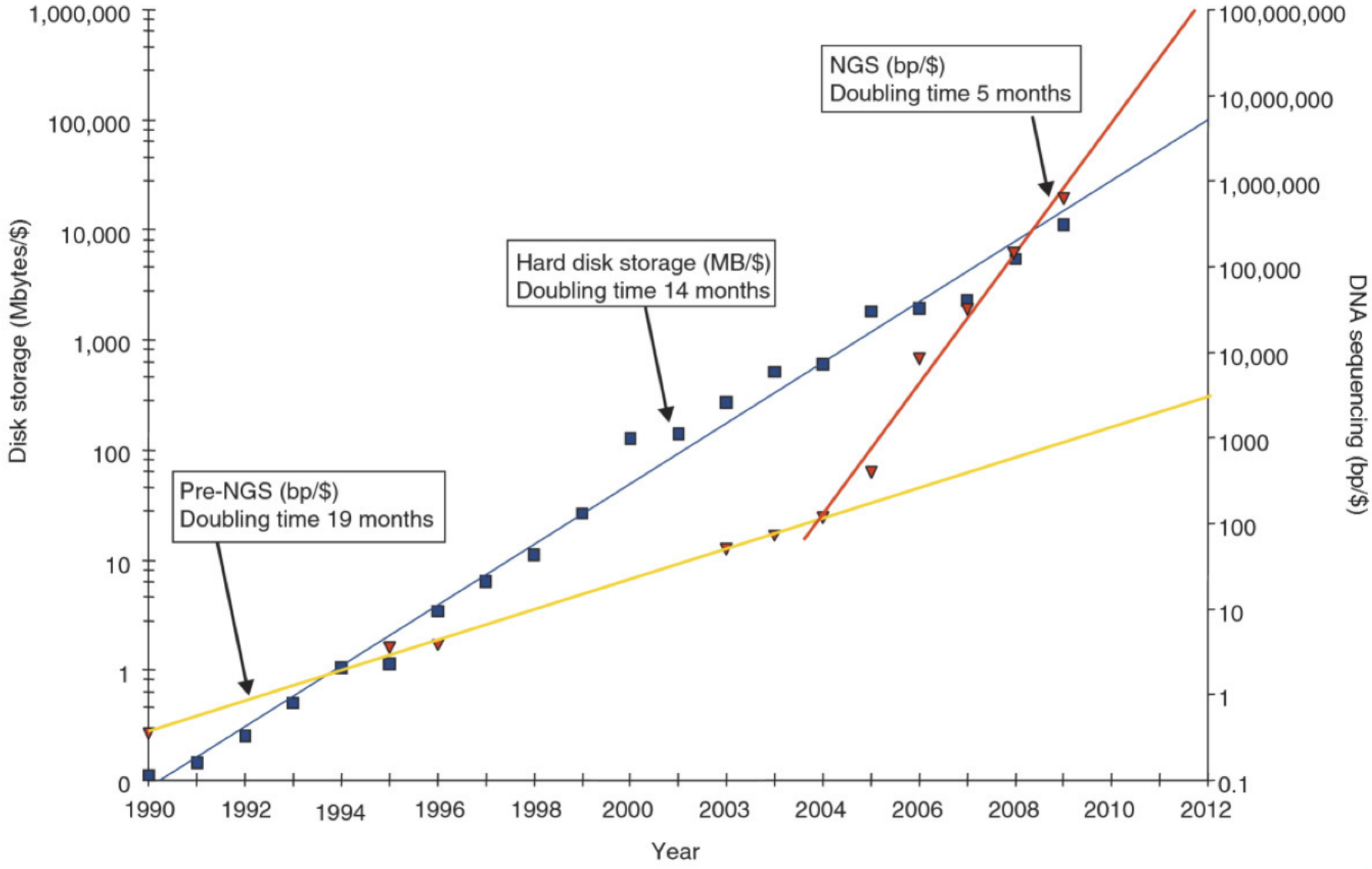




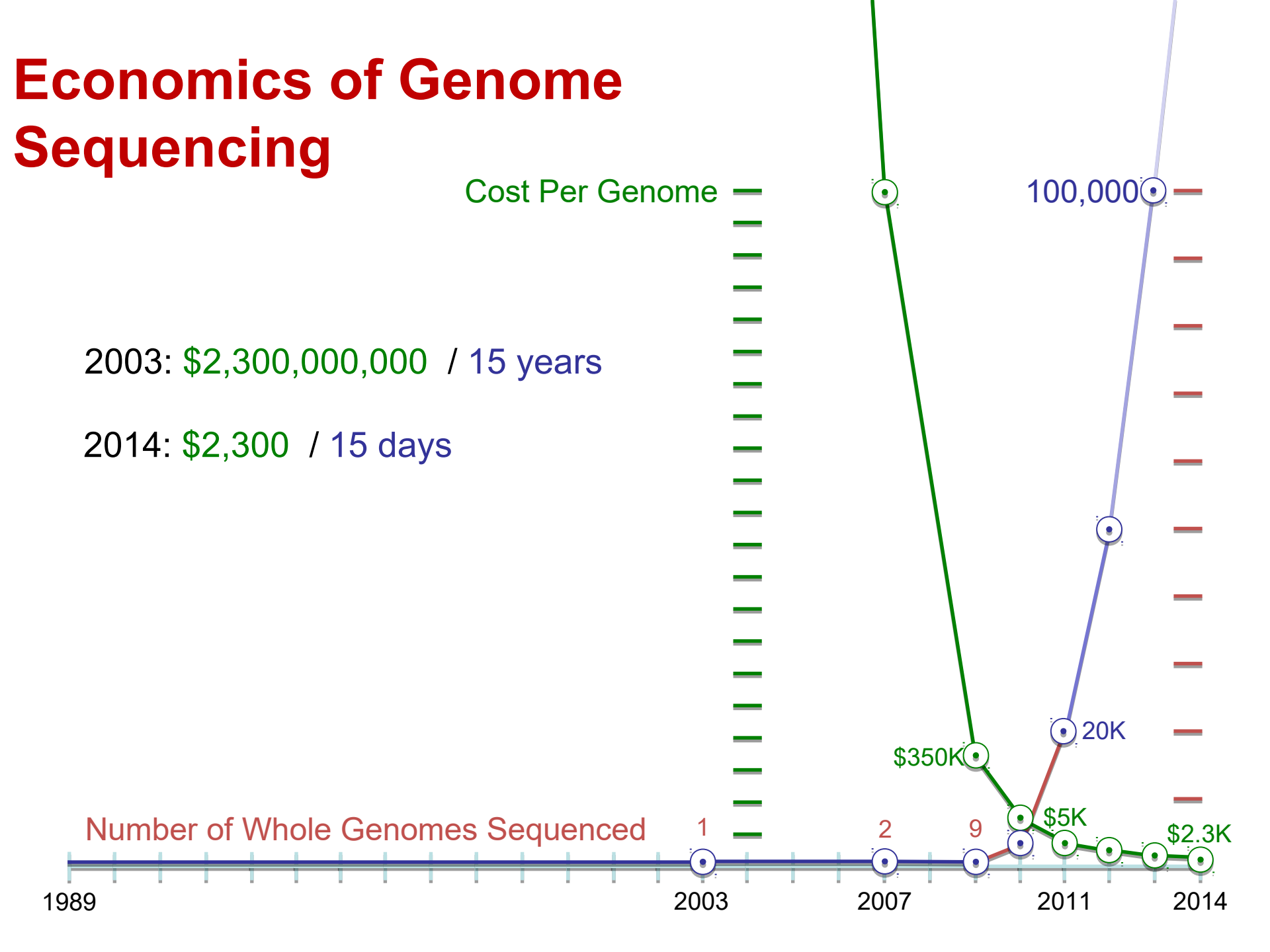
Cost per Genome



NextGen Sequencing a Game-Changer



Economics of Genome Sequencing



2003: $2,300,000,000 / 15 years

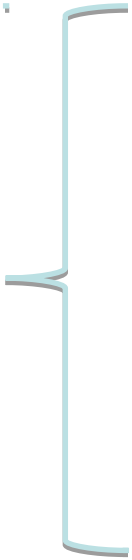
2014: $2,300 / 15 days

Next Generation Sequencing

Next Generation = Massively Parallel

“Read Depth”

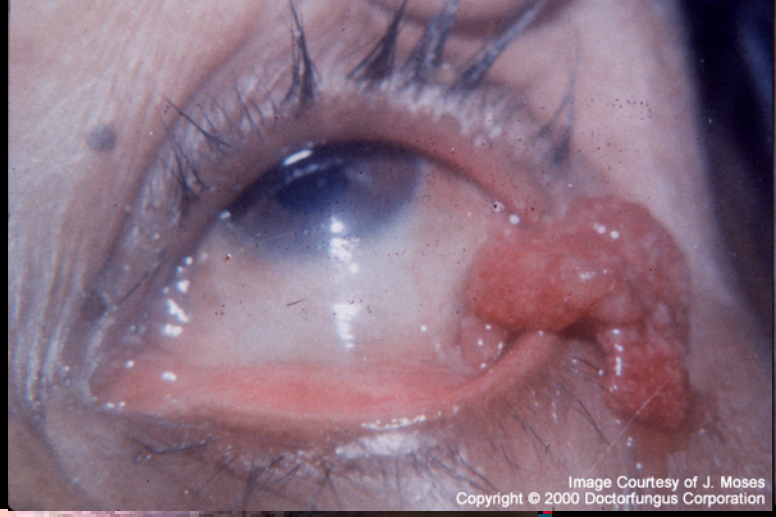
“Depth of Coverage”

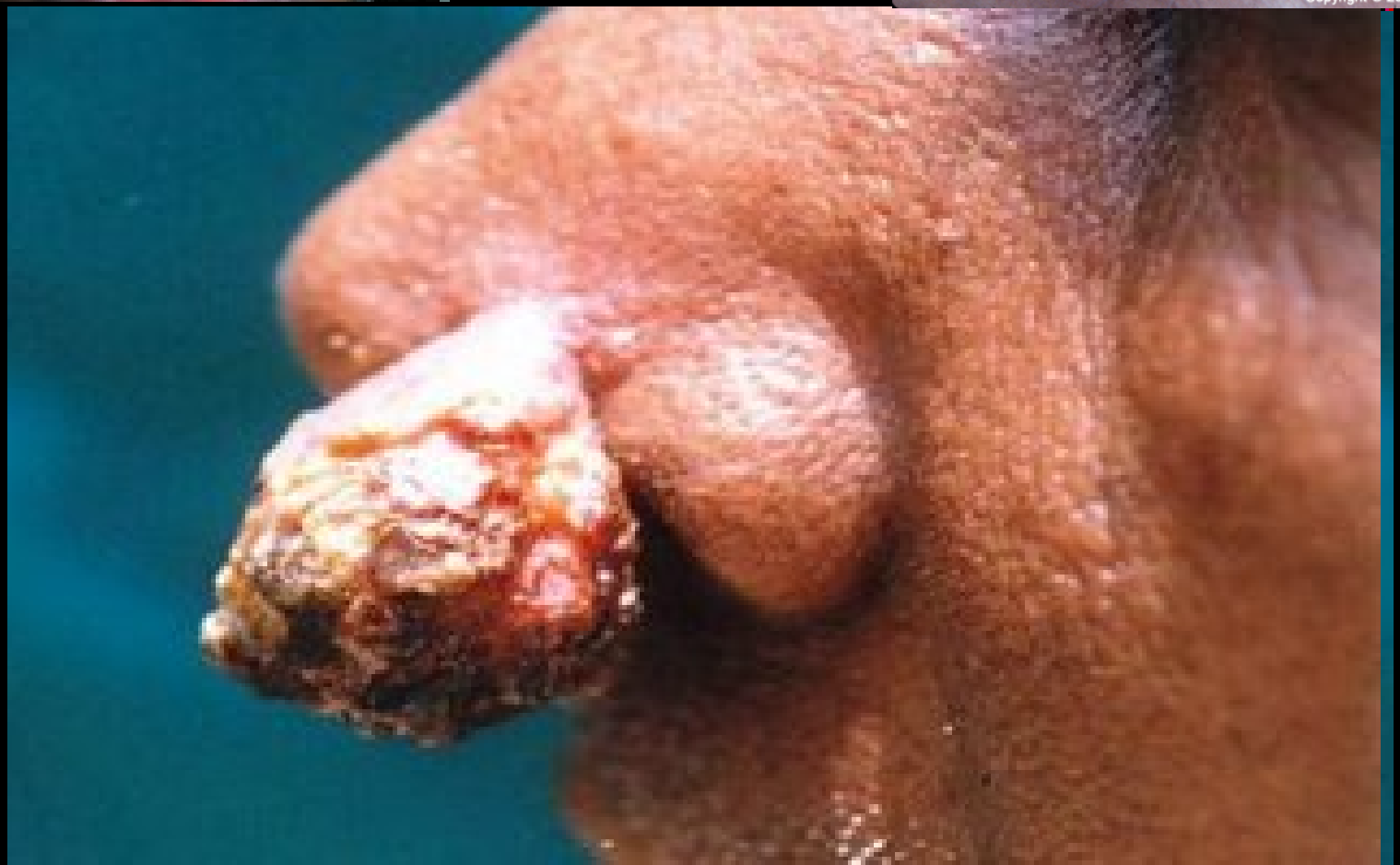


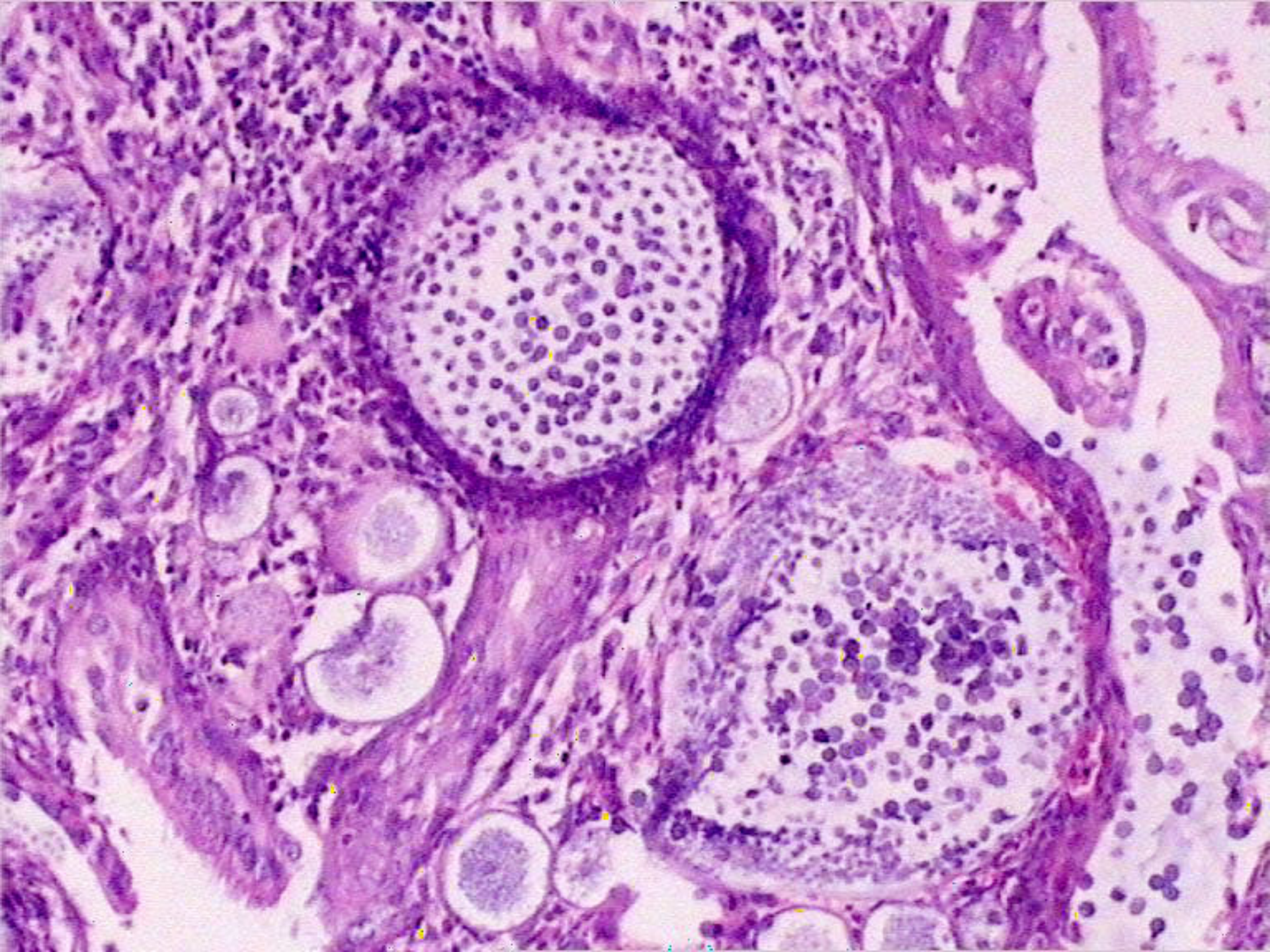
```
                CGATGAACTAGTCTC
                                CTCGGACCCGTAATG
          TTTCGATGAACTAGT                GACCCGTAATGGTCT
         ATTTCGATGAACTAG
                              CTAGTCTCGGACCCG
    GTGCCATTTCGATGA
                          ACTAGTCTCGGACCC
               TCGATGAACTAGTCT
                  GATGAACTAGTCTCG
          CCATTTCGATGAACT
```

REFERENCE 5’-

AGTGCCATTTCGATGAACATGTCTCGGACCCGTAATGGTCTCTTGGGTCTGAA - 3’

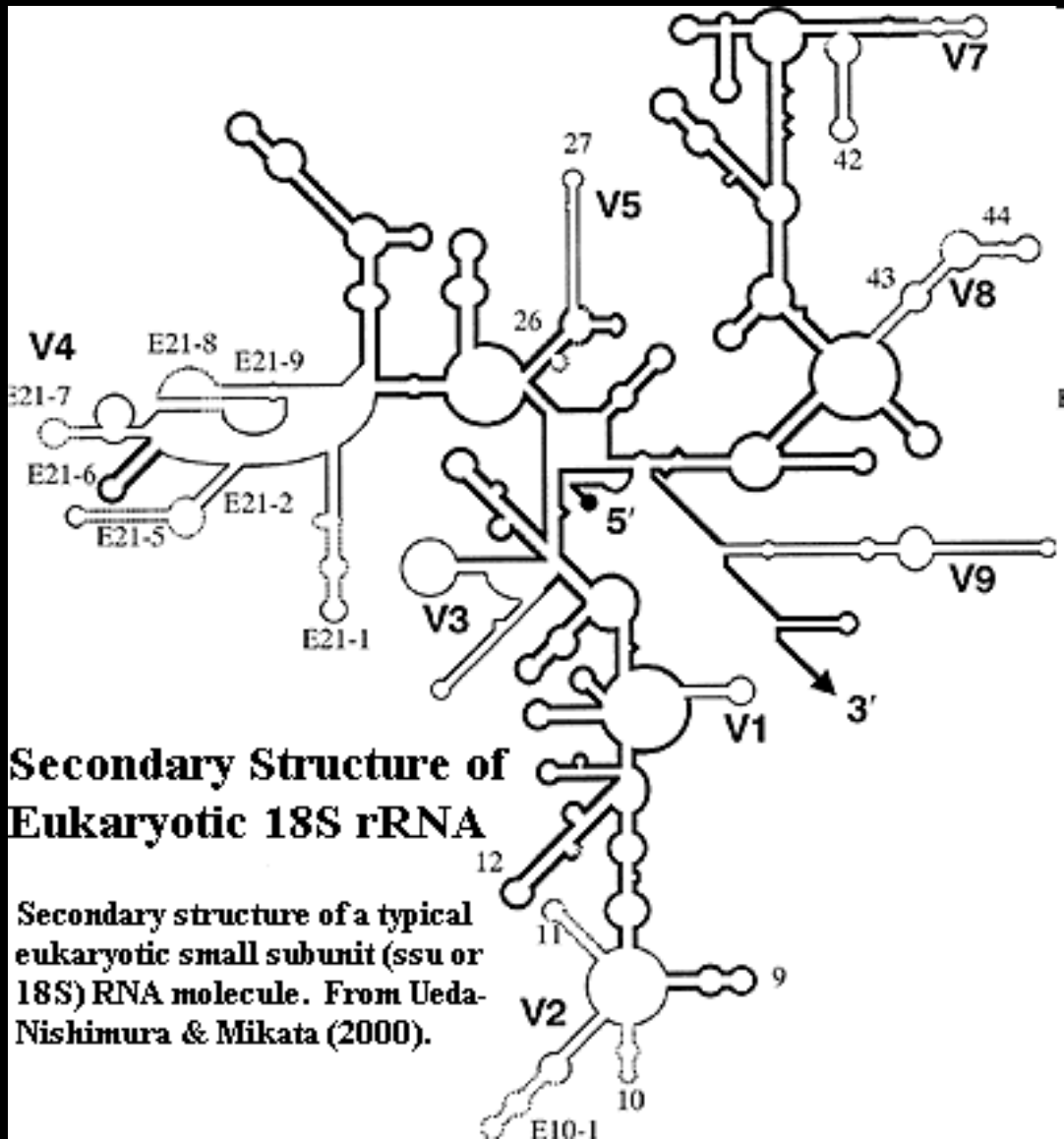






റൈനോസ്പൊറിഡിയോസിസ്

- ഫൻഗസ് എന്ന് കരുതിയിരുന്നു
- തെളിവൊന്നുമില്ല
- ലബോറട്ടറിയിൽ വളർത്താനായിട്ടില്ല



Secondary Structure of Eukaryotic 18S rRNA

Secondary structure of a typical eukaryotic small subunit (ssu or 18S) RNA molecule. From Ueda-Nishimura & Mikata (2000).

JOURNAL OF CLINICAL MICROBIOLOGY, Sept. 1999, p. 2750–2754 Vol. 37, No. 9
0095-1137/99/$04.00+0

Phylogenetic Analysis of *Rhinosporidium seeberi*'s 18S Small-Subunit Ribosomal DNA Groups This Pathogen among Members of the Protoctistan Mesomycetozoa Clade

ROGER A. HERR,[1] LIBERO AJELLO,[2] JOHN W. TAYLOR,[3] SARATH N. ARSECULERATNE,[4] AND LEONEL MENDOZA[1]*

Medical Technology Program, Department of Microbiology, Michigan State University, East Lansing, Michigan 48824-1031[1]; Department of Ophthalmology, Emory University School of Medicine, Atlanta, Georgia 30322[2]; Department of Plant and Microbial Biology, University of California, Berkeley, California 94720-3102[3]; and Department of Microbiology, Faculty of Medicine, University of Peradeniya, Peradeniya 20400, Sri Lanka[4]

Received 26 February 1999/Returned for modification 4 May 1999/Accepted 25 May 1999

For the past 100 years the phylogenetic affinities of *Rhinosporidium seeberi* have been controversial. Based on its morphological features, it has been classified as a protozoan or as a member of the kingdom Fungi. We have amplified and sequenced nearly a full-length 18S small-subunit (SSU) ribosomal DNA (rDNA) sequence from *R. seeberi*. Using phylogenetic analysis, by parsimony and distance methods, of *R. seeberi*'s 18S SSU rDNA and that of other eukaryotes, we found that this enigmatic pathogen of humans and animals clusters with a novel group of fish parasites referred to as the DRIP clade (*Dermocystidium*, rossete agent, *Ichthyophonus*, and *Psorospermium*), near the animal-fungal divergence. Our phylogenetic analyses also indicate that *R. seeberi* is the sister taxon of the two *Dermocystidium* species used in this study. This molecular affinity is remarkable since

Rhinosporidium seeberi: A Human Pathogen from a Novel Group of Aquatic Protistan Parasites

David N. Fredricks,*† Jennifer A. Jolley,* Paul W. Lepp,*
Jon C. Kosek,† and David A. Relman*†
*Stanford University, Stanford, California, USA; and †Veterans Affairs, Palo Alto Health Care System, Palo Alto, California, USA

Rhinosporidium seeberi, a microorganism that can infect the mucosal surfaces of humans and animals, has been classified as a fungus on the basis of morphologic and histochemical characteristics. Using consensus polymerase chain reaction (PCR), we amplified a portion of the *R. seeberi* 18S rRNA gene directly from infected tissue. Analysis of the aligned sequence and inference of phylogenetic relationships showed that *R. seeberi* is a protist from a novel clade of parasites that infect fish and amphibians. Fluorescence in situ hybridization and *R. seeberi*-specific PCR showed that this unique 18S rRNA sequence is also present in other tissues infected with *R. seeberi*. Our data support the *R. seeberi* phylogeny recently suggested by another group. *R. seeberi* is not a classic fungus, but rather the first known human pathogen from the DRIPs clade, a novel clade of aquatic protistan parasites (Ichthyosporea).

Rhinosporidiosis manifests as slow-growing, tumorlike masses, usually of the nasal mucosa or ocular conjunctivae of humans and animals, that has been difficult to classify. Recently, *R. seeberi* has been considered a fungus, but it was originally thought to be a protozoan parasite (2).

1. POLYMERASE CHAIN REACTION

F1-fwb CAAGTCTGGTGCCAGCAGCC 554-573

F2-revc GATTTCTCGTAAGGTGCCGA 1068-1087

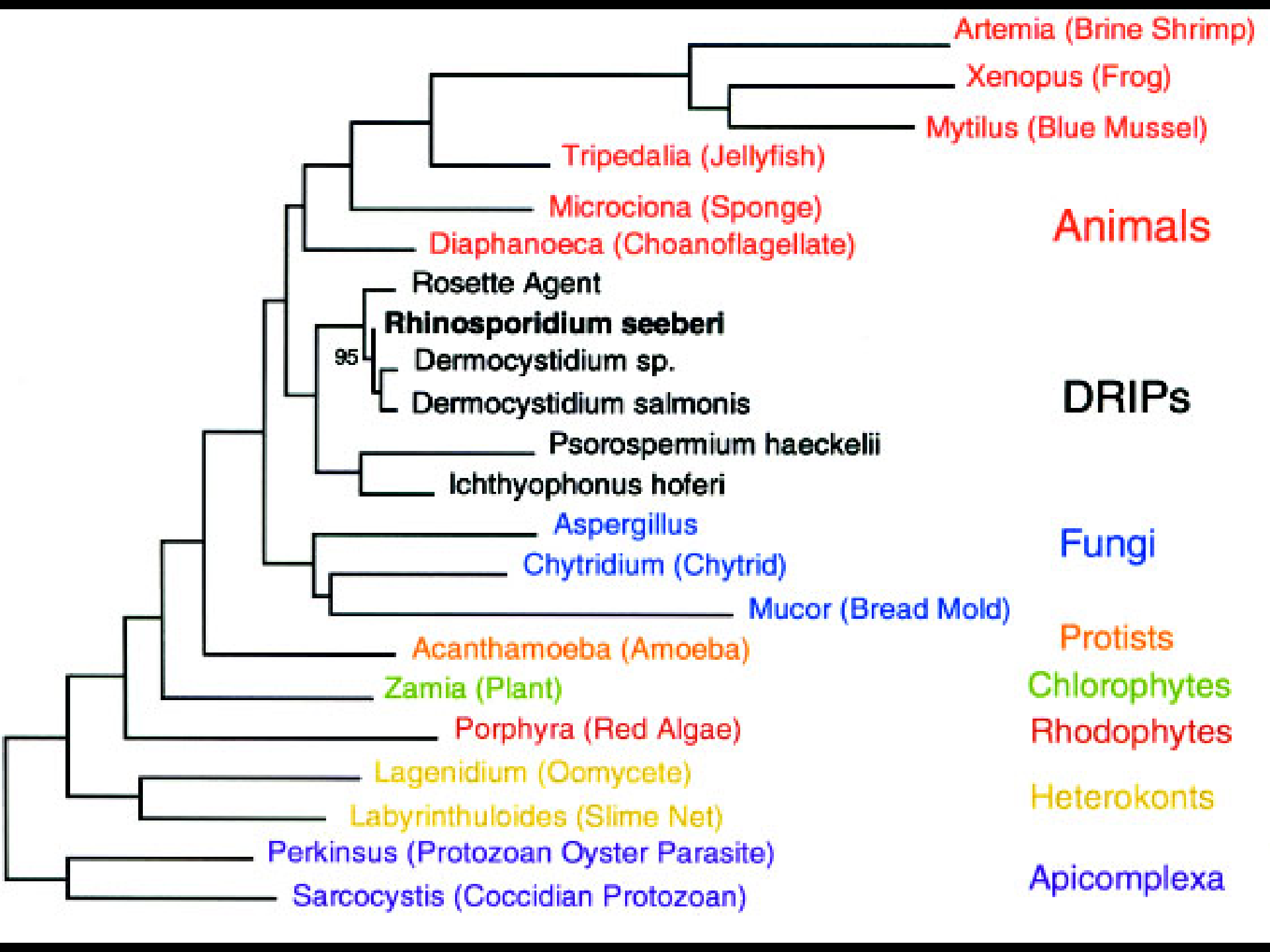
2. CLONING

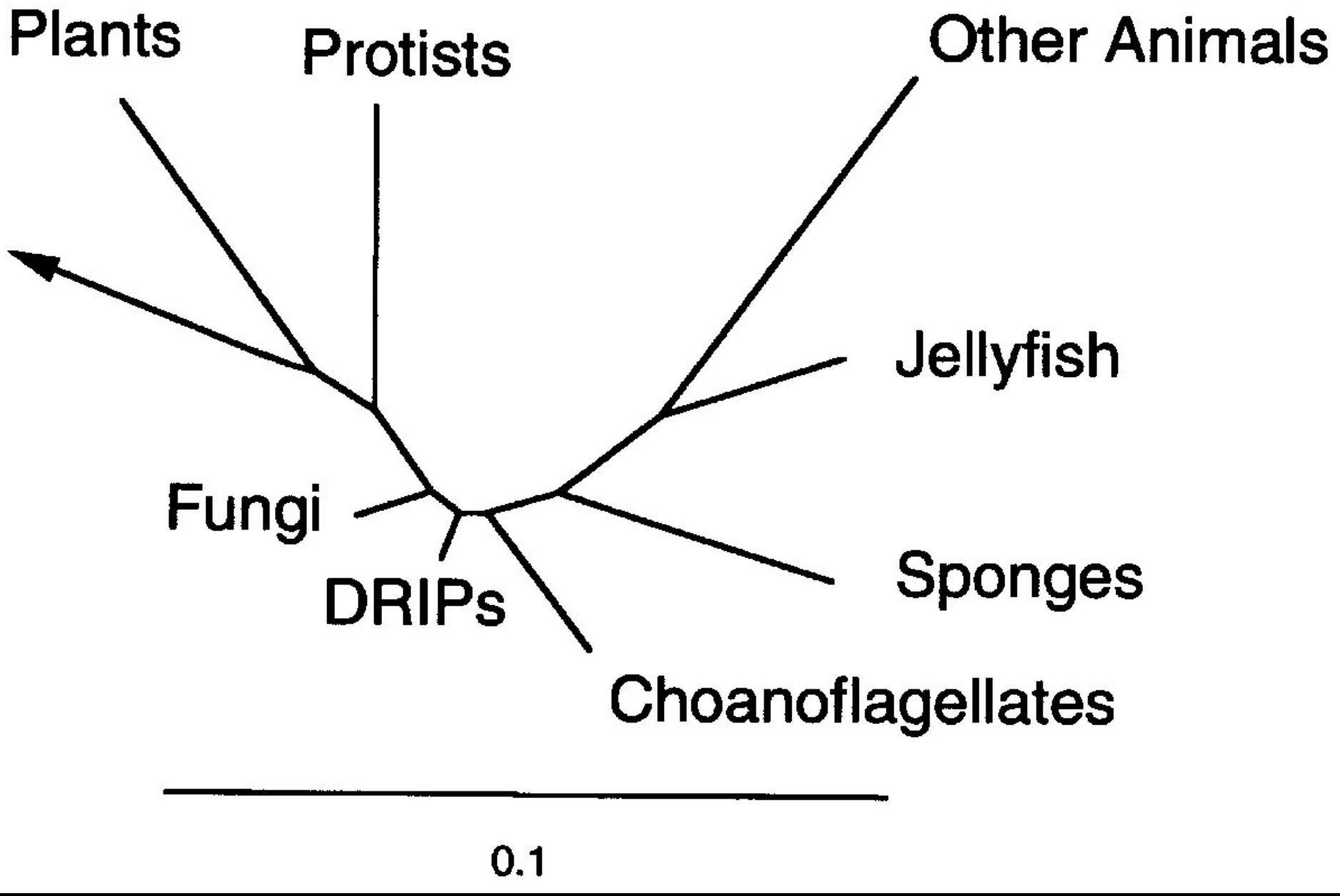
3. SEQUENCING

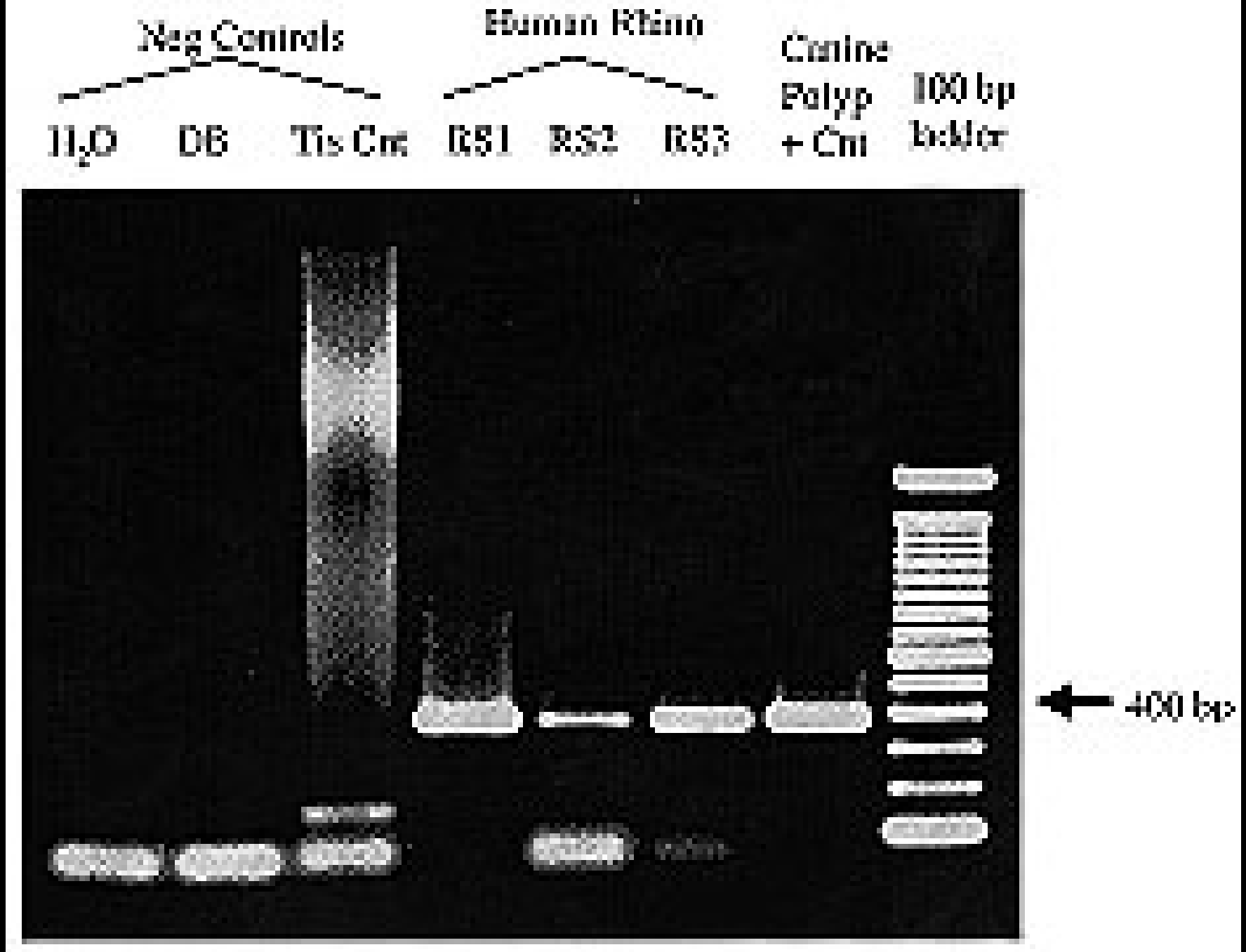
4. RHINOSPORIDIUM PROBES

Rhino FISH probe BTGCTGATAGAGTCATTGAATTAACATCTACB

Control FISH probe BACGACTATCTCAGTAACTTAATTGTAGATGB


Artemia (Brine Shrimp)
Xenopus (Frog)
Mytilus (Blue Mussel)
Tripedalia (Jellyfish)
Microciona (Sponge)
Diaphanoeca (Choanoflagellate)
Animals
Rosette Agent
Rhinosporidium seeberi
95
Dermocystidium sp.
Dermocystidium salmonis
DRIPs
Psorospermium haeckelii
Ichthyophonus hoferi
Aspergillus
Chytridium (Chytrid)
Fungi
Mucor (Bread Mold)
Acanthamoeba (Amoeba)
Protists
Zamia (Plant)
Chlorophytes
Porphyra (Red Algae)
Rhodophytes
Lagenidium (Oomycete)
Labyrinthuloides (Slime Net)
Heterokonts
Perkinsus (Protozoan Oyster Parasite)
Sarcocystis (Coccidian Protozoan)
Apicomplexa


Plants
Protists
Other Animals
Jellyfish
Fungi
DRIPs
Sponges
Choanoflagellates
0.1


Neg Controls
Human Rhino
Canine Polyp + Cnl
100 bp ladder
H2O
DB
Tis Cnt
RS1
RS2
RS3
400 bp