

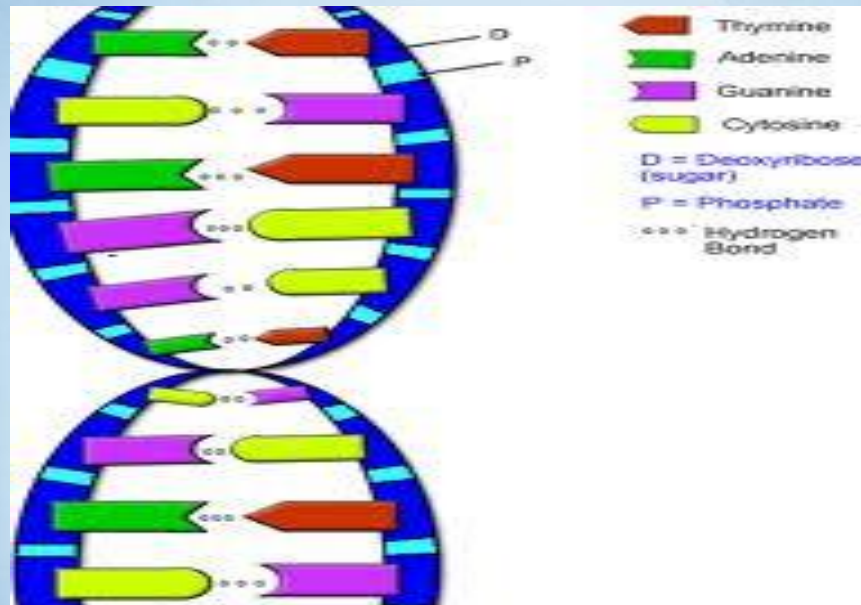
Principles of DNA Sequencing

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What is DNA Sequencing?

- DNA Sequencing is finding the order of nucleotides in a fragment of DNA



- It is involving various biochemical, biophysical and computational techniques to determine the order of the nucleotide bases- adenine, guanine, thymine & cytosine in a molecule of DNA.

Methods of DNA Sequencing



Sanger Method

DNA sequencing by
enzymatic synthesis

Nobel Prize 1958, seq. of insulin

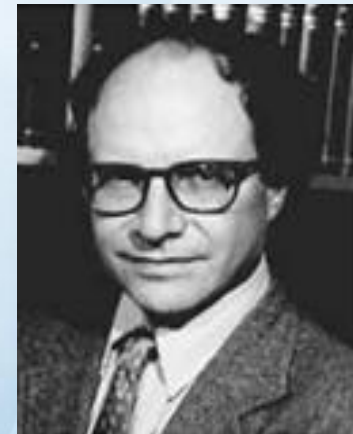
Nobel Prize 1980, DNA seq.



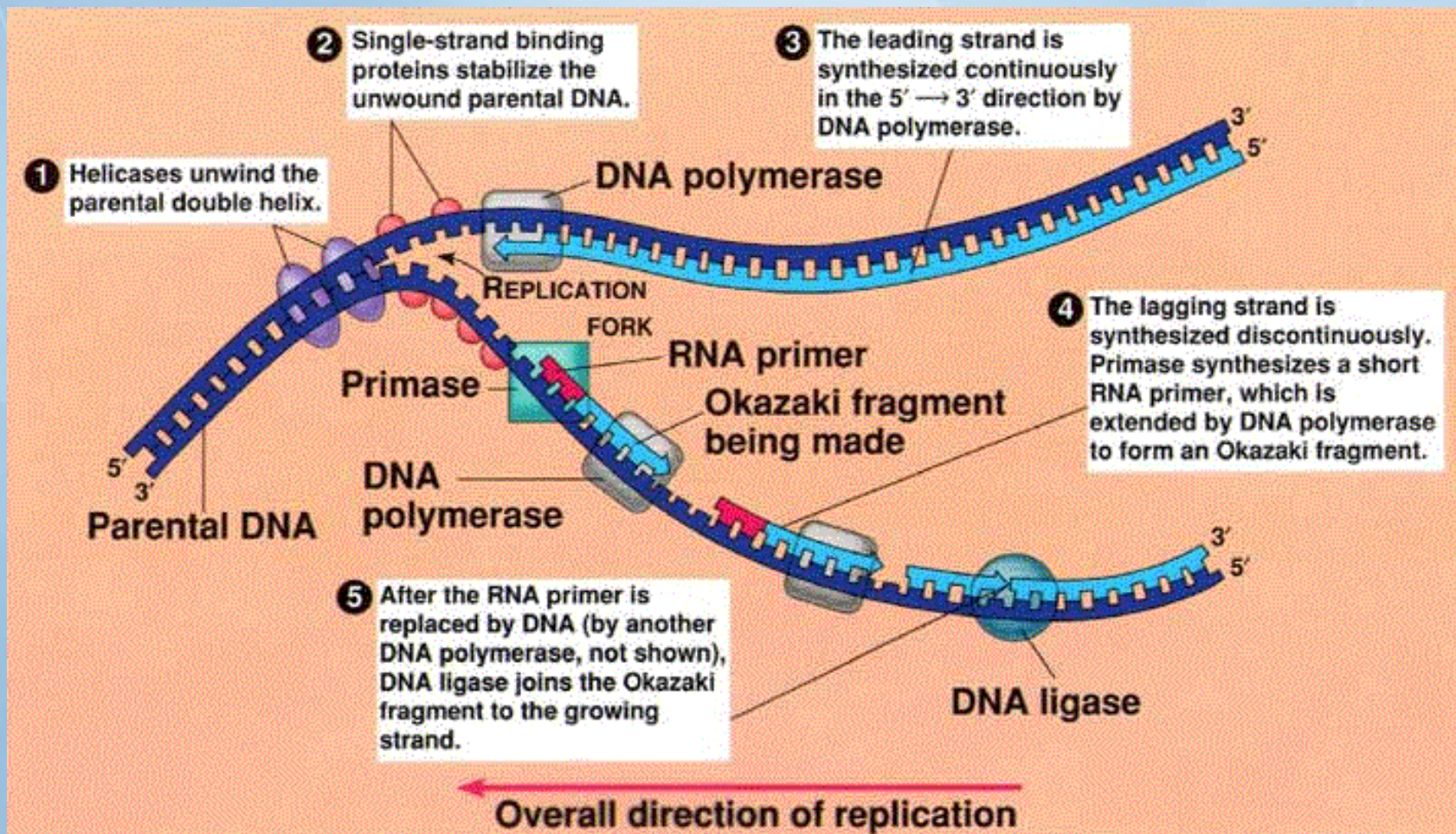
Maxam–Gilbert Method

DNA sequencing by
chemical degradation

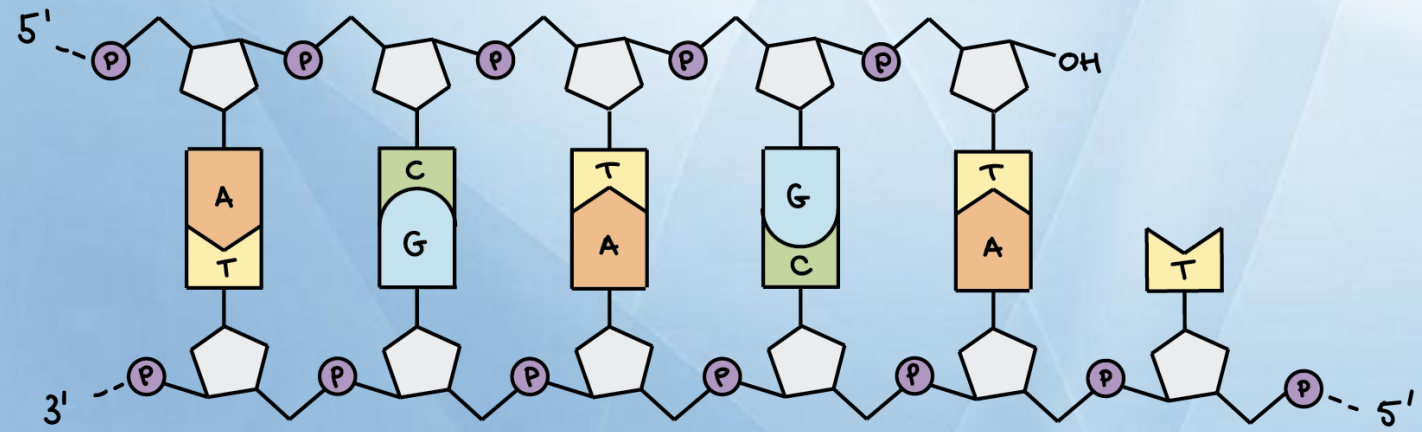
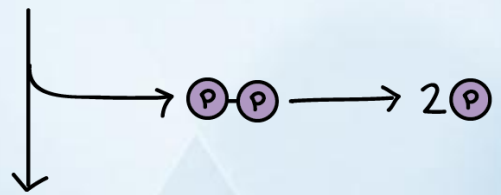
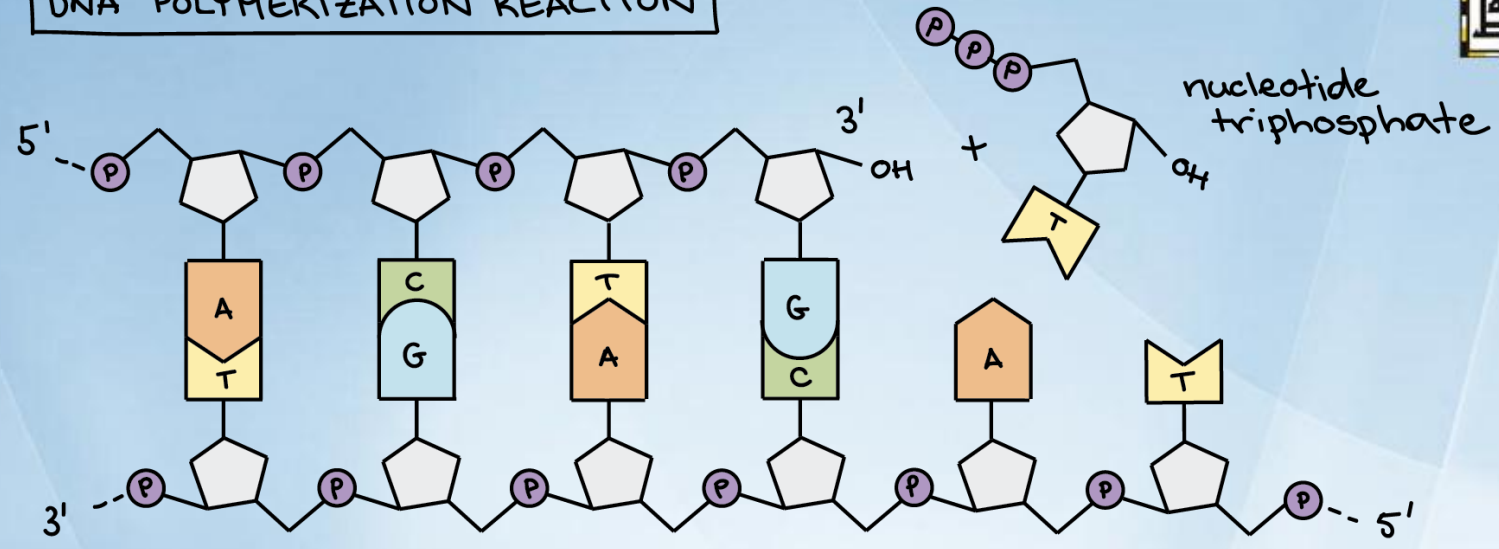
Nobel Prize 1980, DNA
sequence



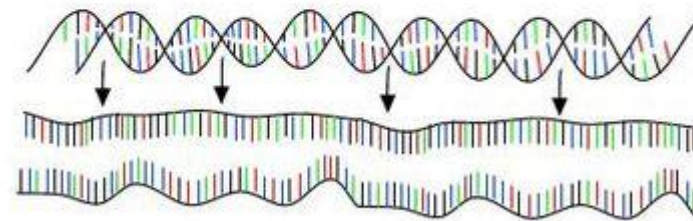
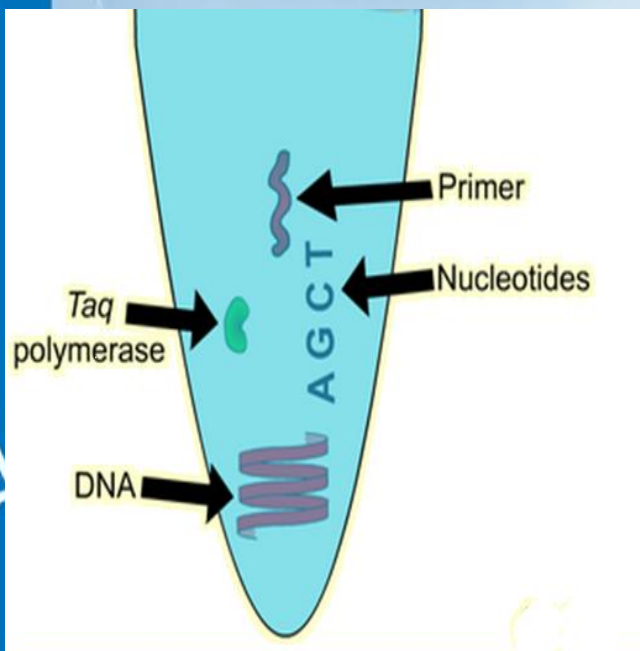
Modern sequencing equipment uses the principles of the
Sanger technique



DNA POLYMERIZATION REACTION

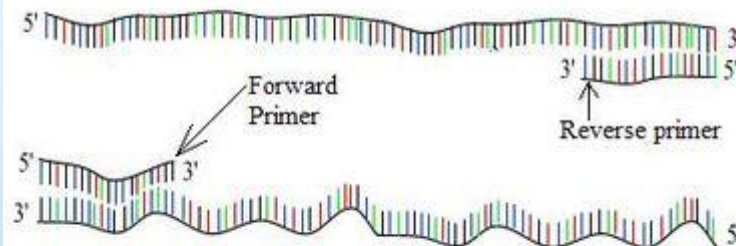


PCR : Polymerase Chain Reaction



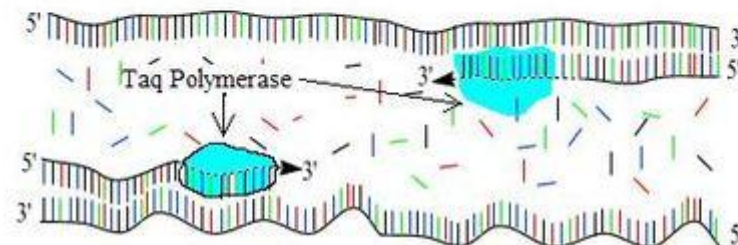
Step 1 : denaturation

94 °C



Step 2 : annealing

54 °C



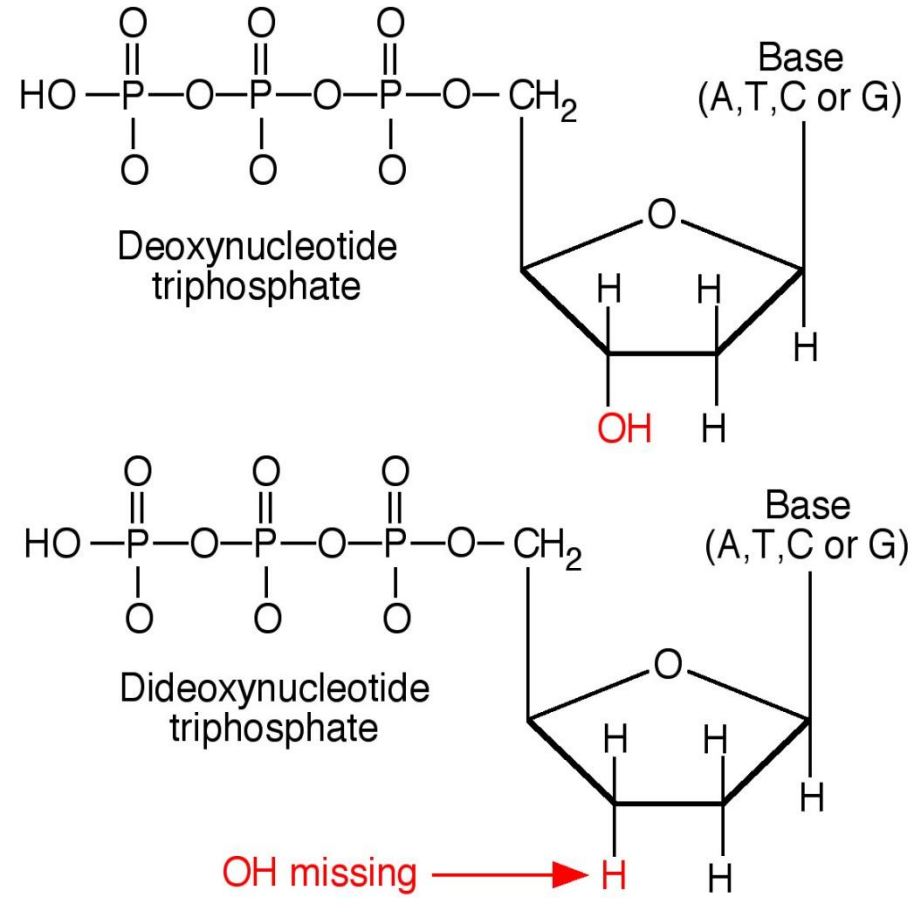
Step 3 : extension

72 °C



The Sanger method

Uses dideoxy nucleotides to terminate DNA synthesis.



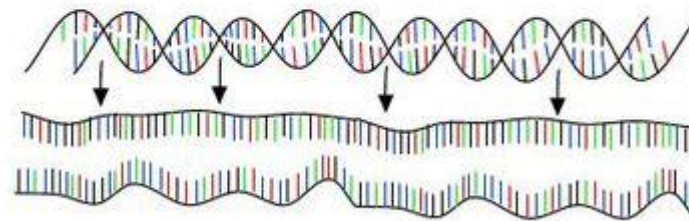
Because they lack the -OH, replication stops

What will happen if ddATP, ddGTP, ddCTP, ddTTP are added ?

PCR : Polymerase Chain Reaction

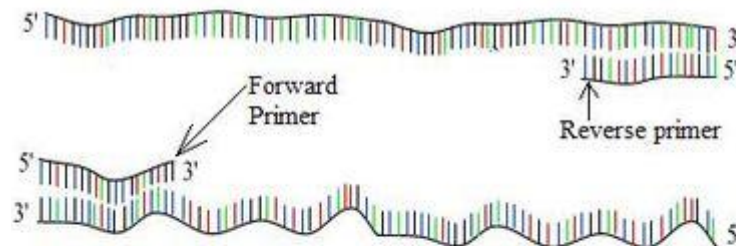
Step 1 : denaturation

94 °C



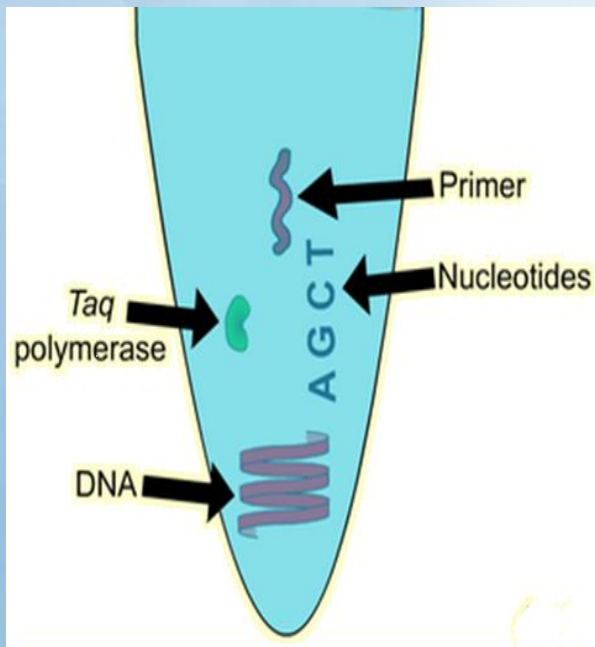
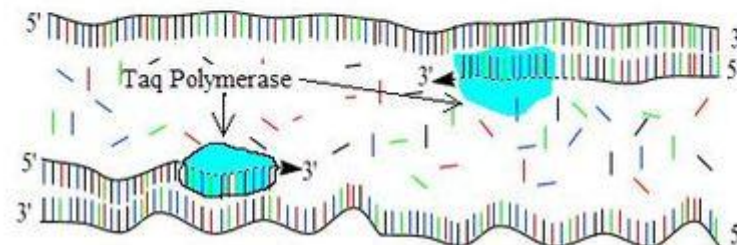
Step 2 : annealing

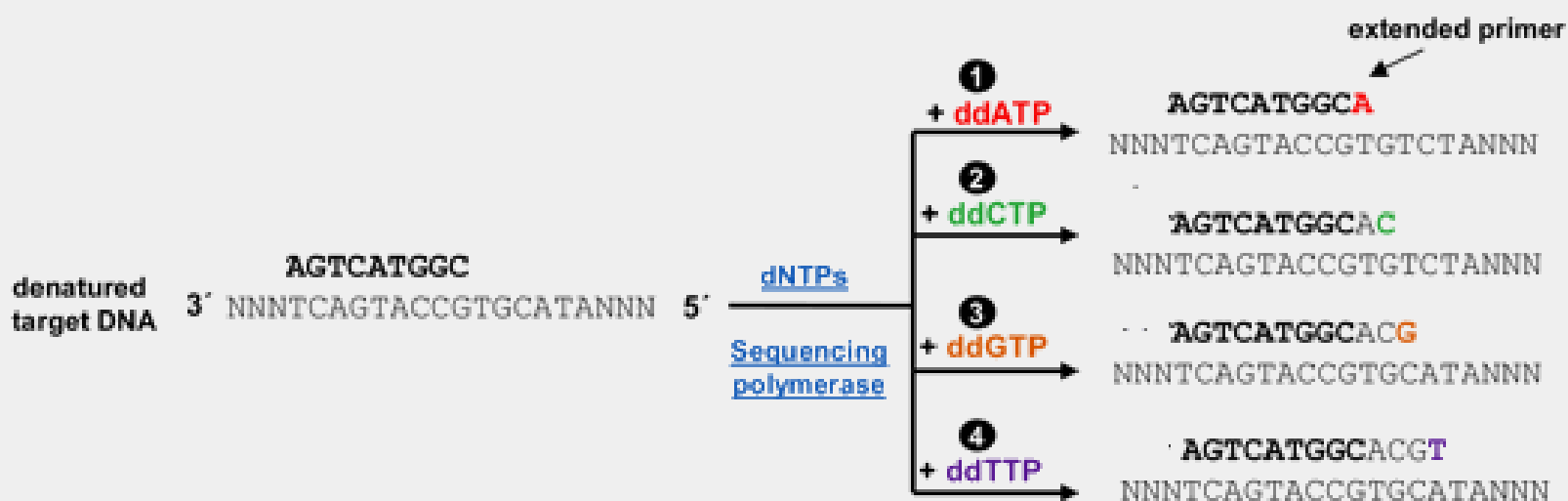
54 °C

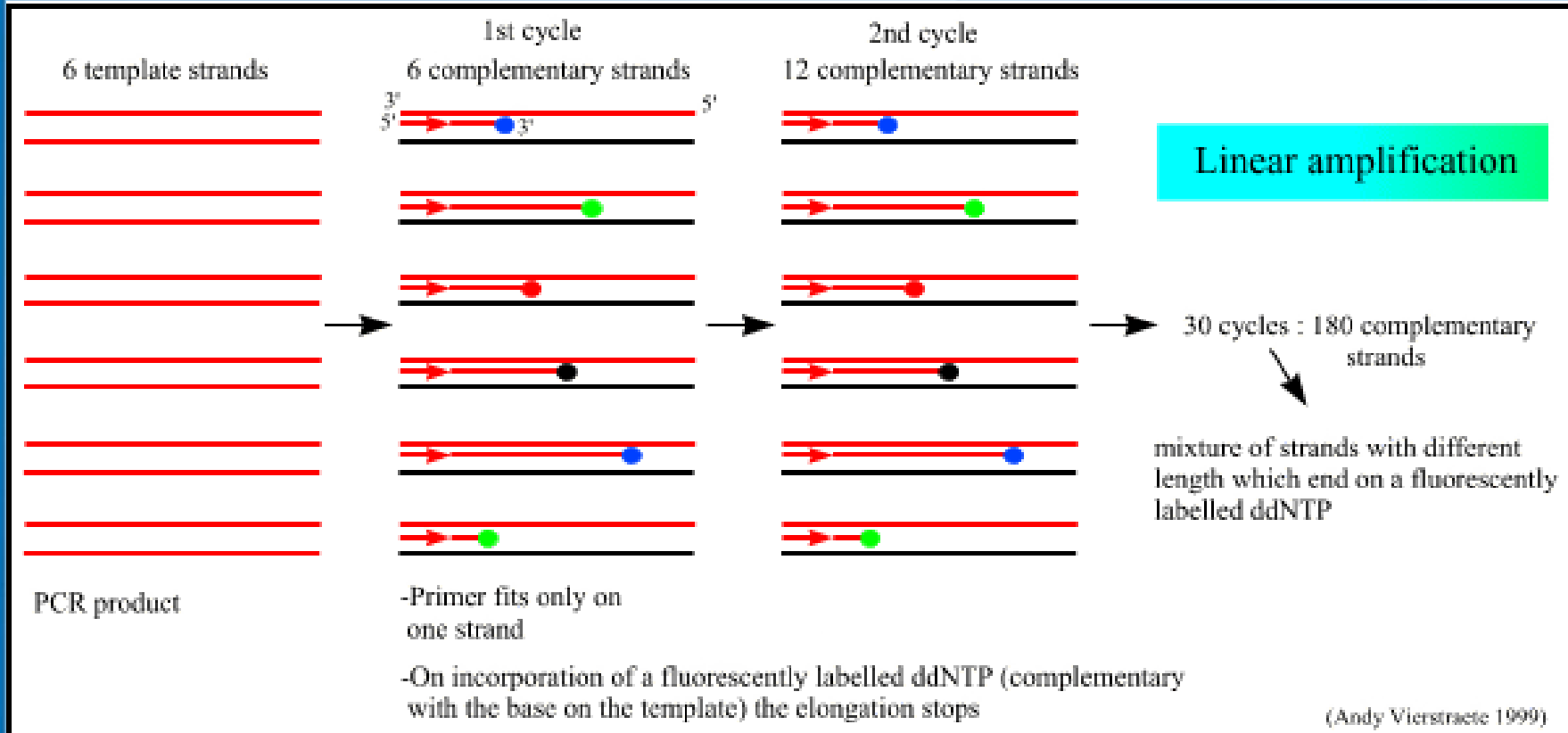


Step 3 : extension

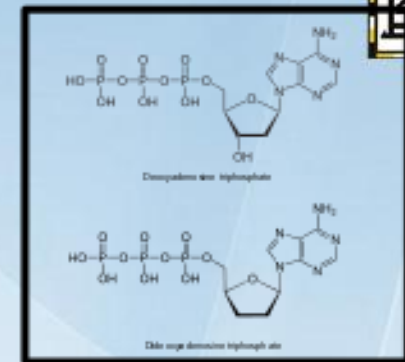
72 °C



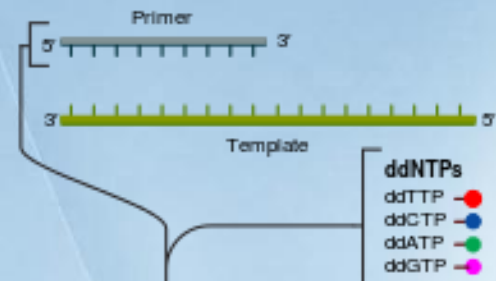




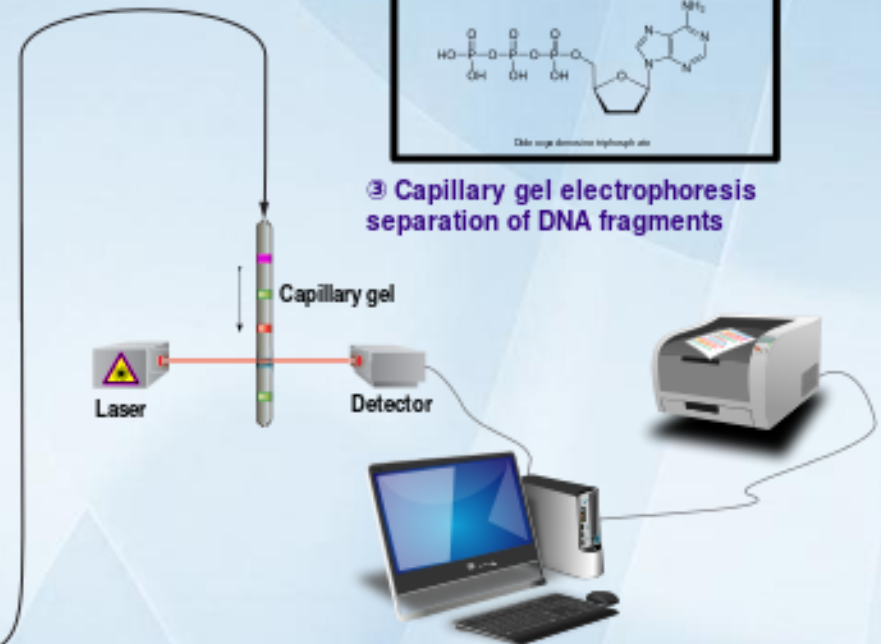
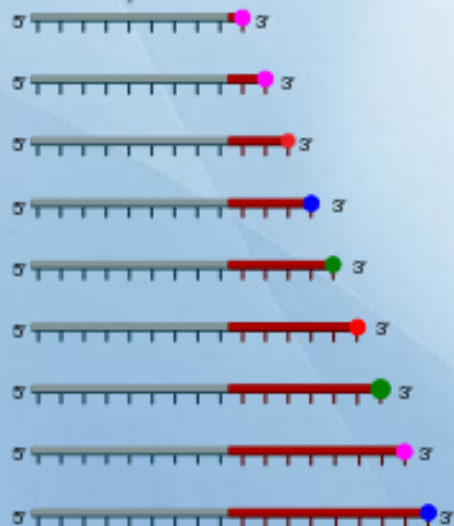
- ▶ Primer and DNA template
- ▶ DNA polymerase
- ▶ ddNTPs with flourochromes
- ▶ dNTPs (dATP, dCTP, dGTP, and dTTP)



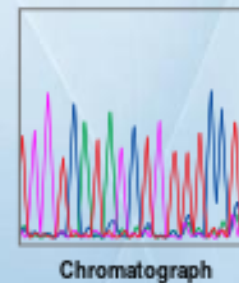
③ Capillary gel electrophoresis separation of DNA fragments

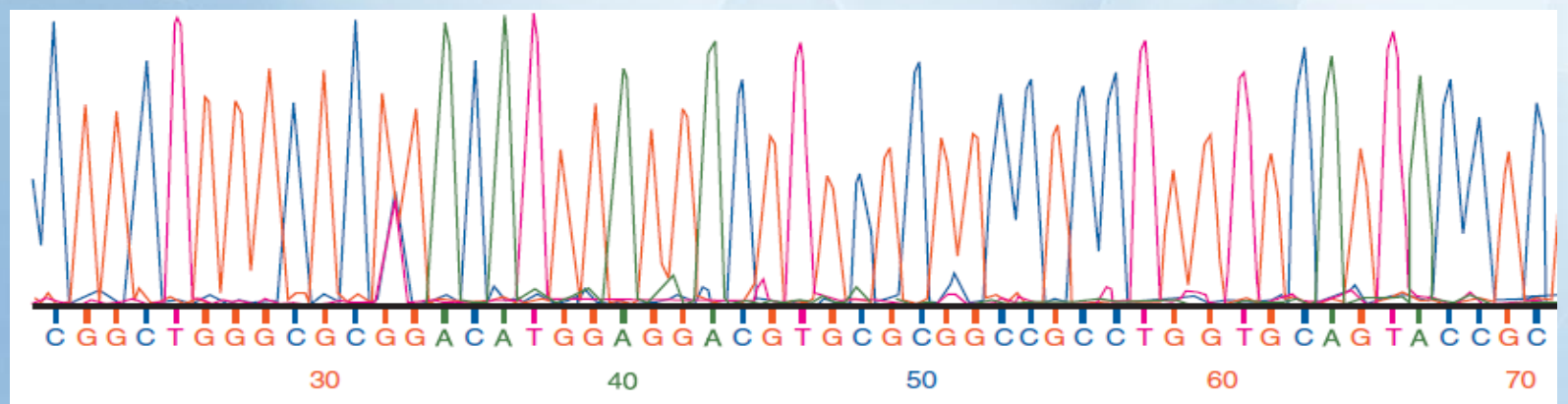
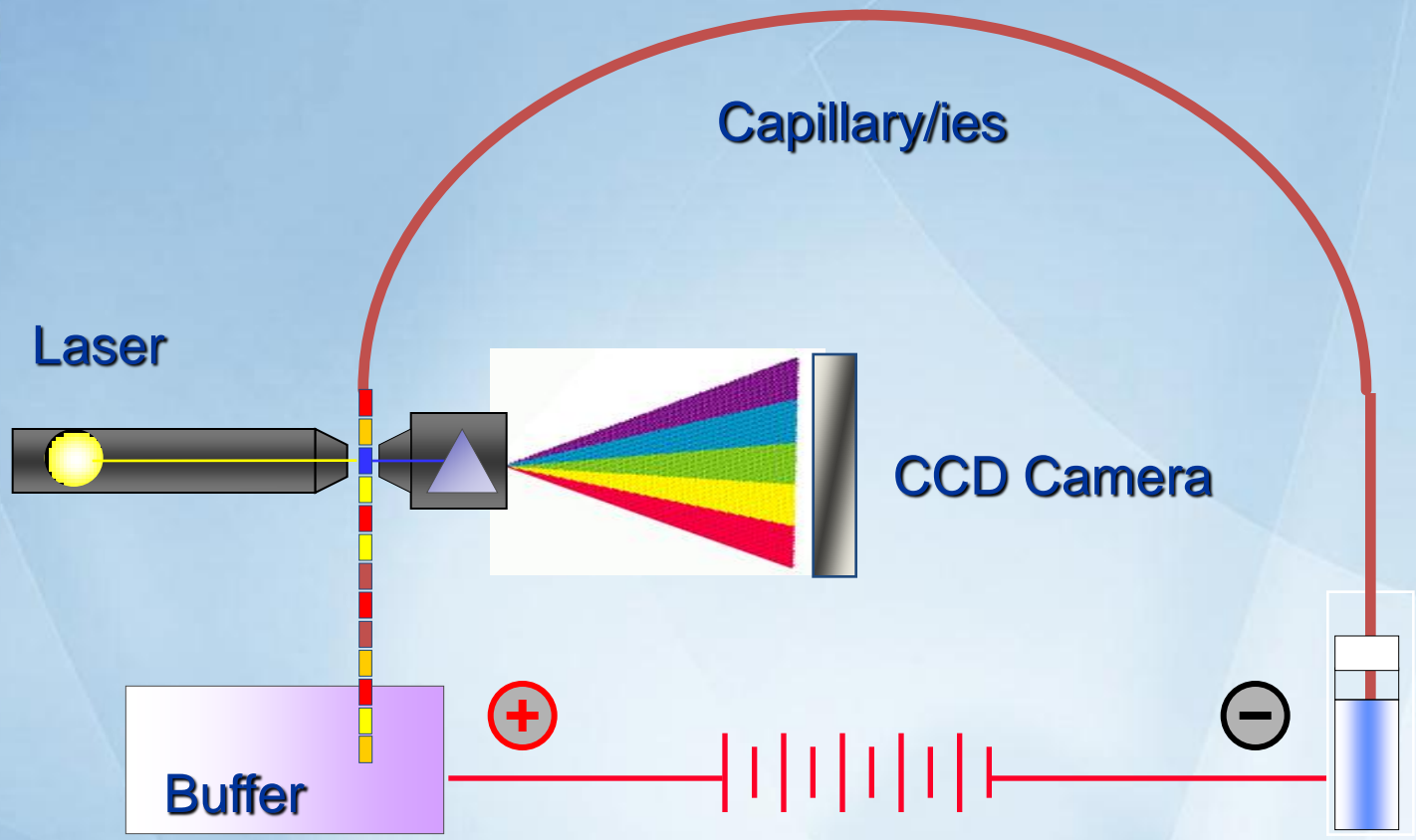


② Primer elongation and chain termination



④ Laser detection of fluorochromes and computational sequence analysis





When voltage applied,
strands separate by size
in capillary, smallest go
through first

Movie

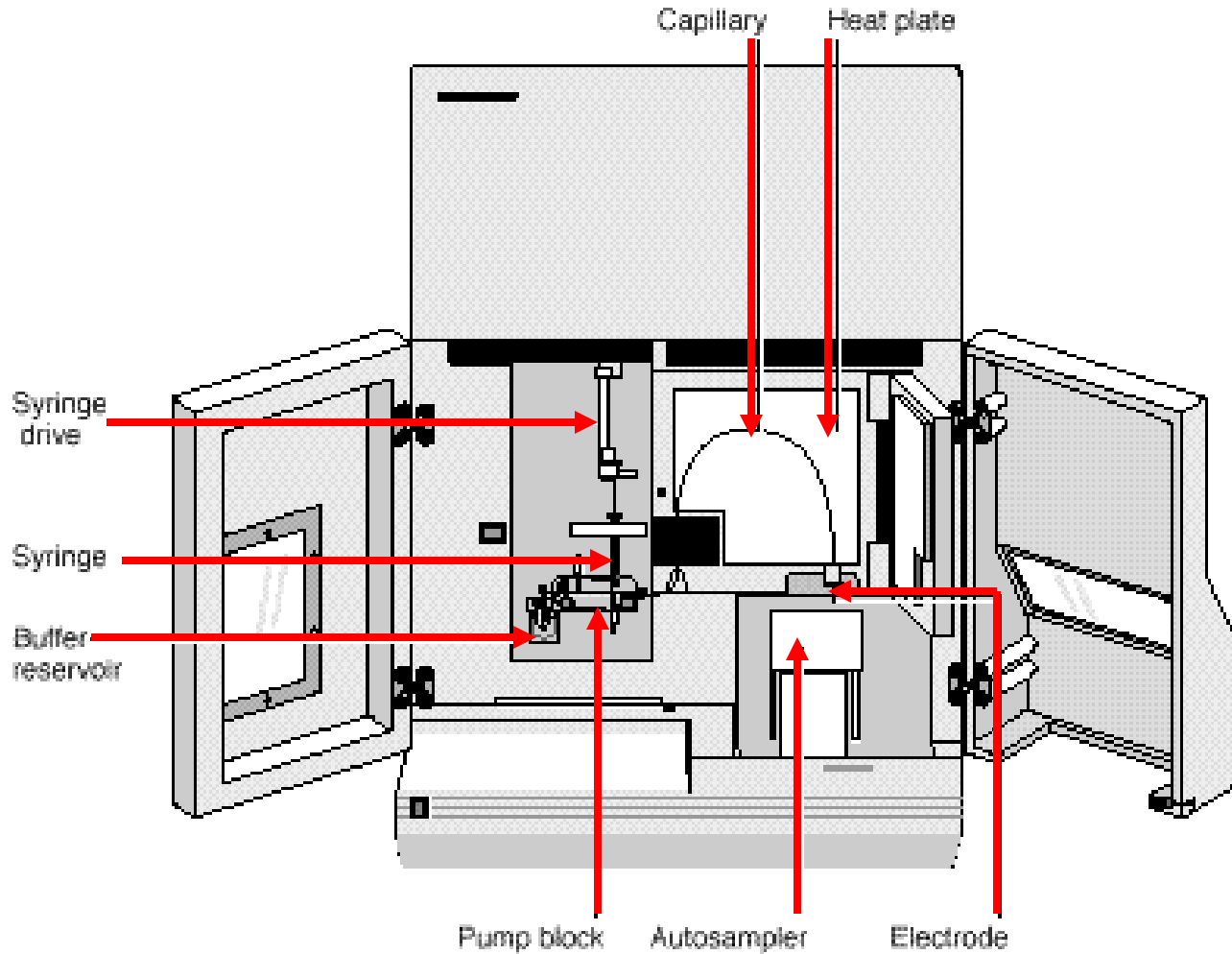
ABI prism 310

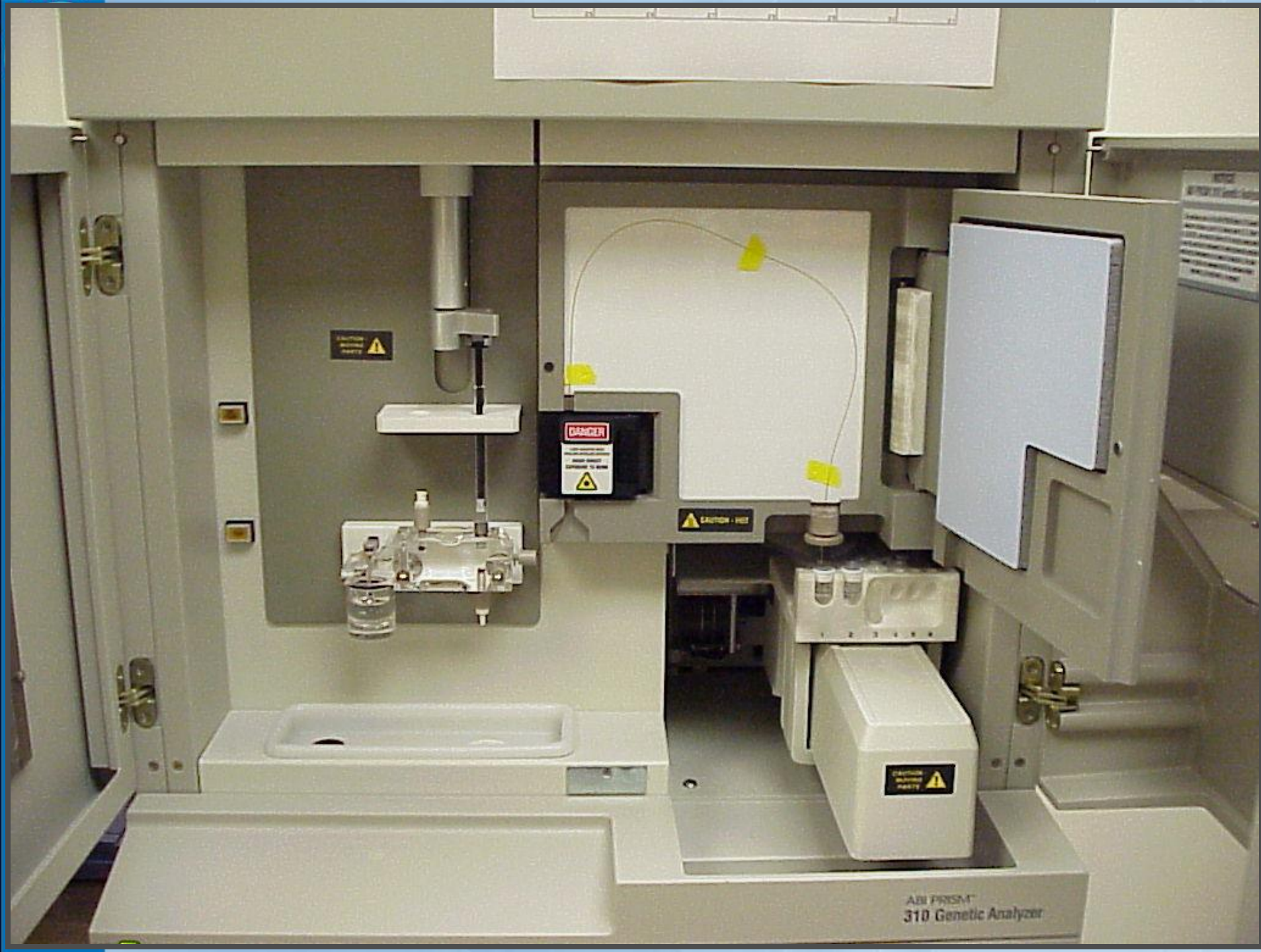
Capillary electrophoresis



ABI prism 310

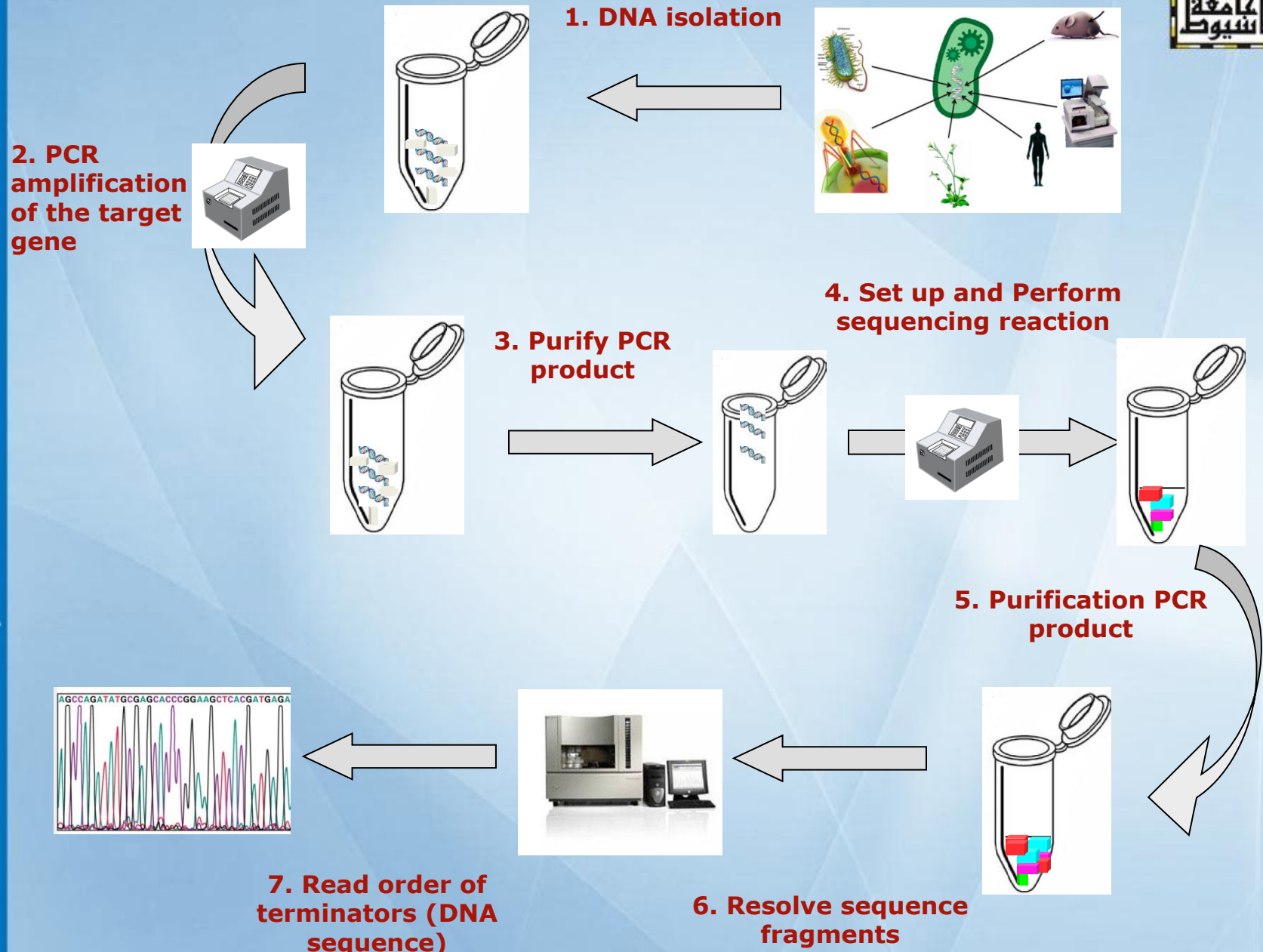
Capillary electrophoresis





Setting up sequencing reaction

Sequencing workflow

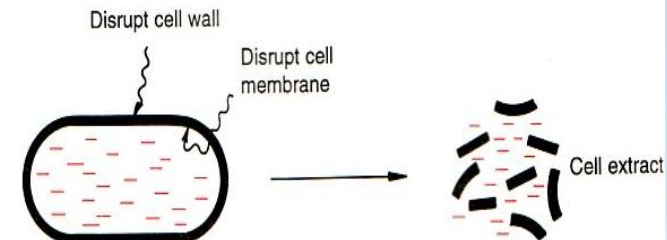


1.DNA isolation

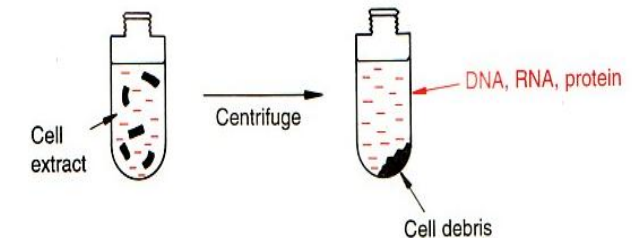
Most DNA extraction protocols consist of 3 parts

1. Cell lysis
2. Removing contaminating proteins, RNA, or macromolecules
3. Recovery of the DNA

(a) Cell lysis



(b) Centrifugation to remove cell debris

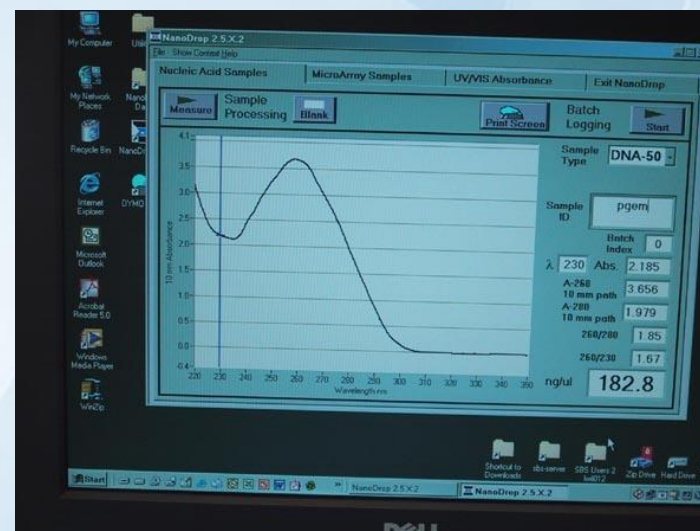


NanoDrop spectrophotometer

Check samples on a Nanodrop first to measure:

1. Purity
2. Concentration

Can accurately measure tiny volumes of sample as low as 1 μL .



dsDNA	50 – 100 fmol
ssDNA	25 – 50 fmol
Purified PCR product	10 – 50 fmol

2. Amplify the target Gene Using (PCR)

PCR Ingredients

1. DNA “template”
2. *Taq* Polymerase
3. Deoxynucleotides (dNTPs)
4. Primers (Fw + Rv)
5. Buffer and water

PCR Program

Step 1: 5 min at 95°C

Step 2: 40 cycles of:

30 sec at 95°C

30 sec at 50-60°C

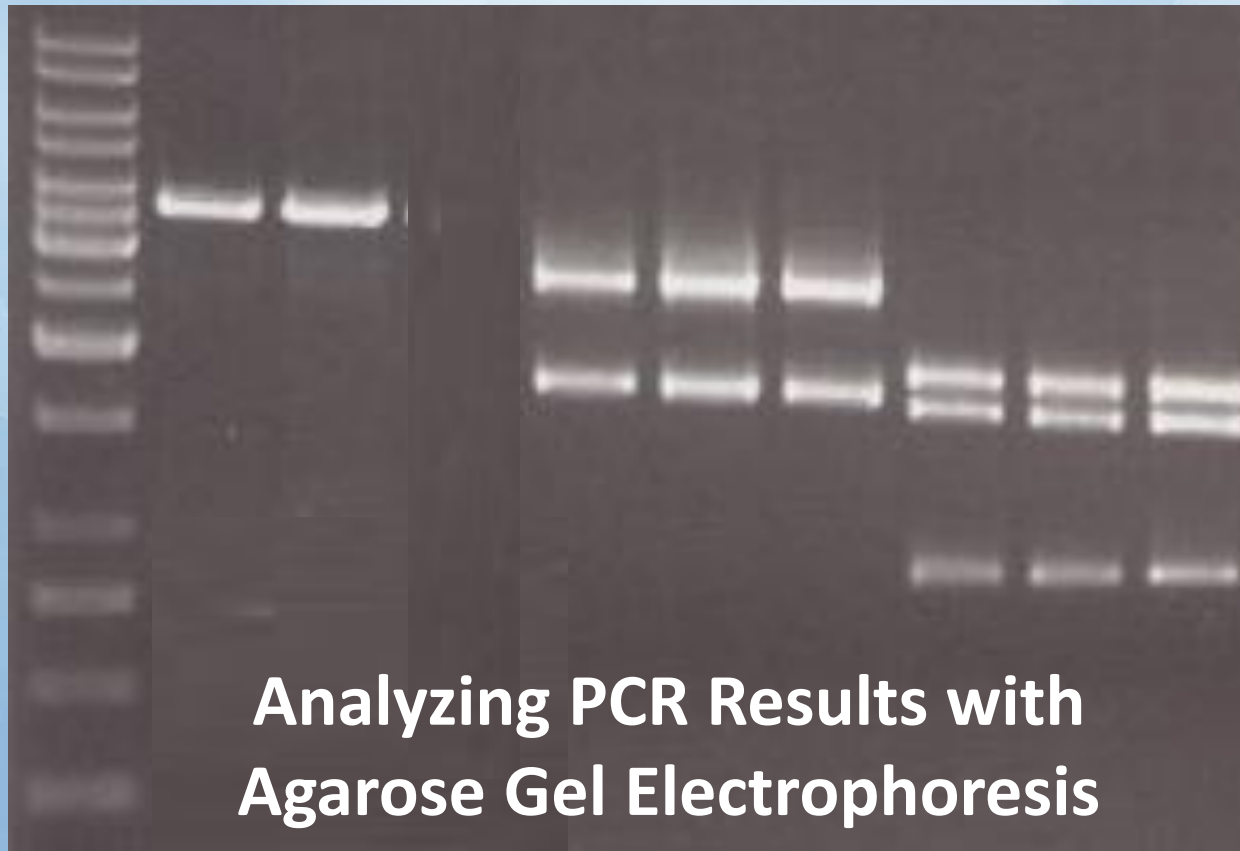
1 min at 72°C

Step 3: 7 min at 72°C

Step 4: hold at 4°C



DID YOUR PCR WORK?



**Analyzing PCR Results with
Agarose Gel Electrophoresis**

Factors Influencing PCR Success

- Contamination
- DNA
- Cycle parameters
- Primers

Avoiding Contamination

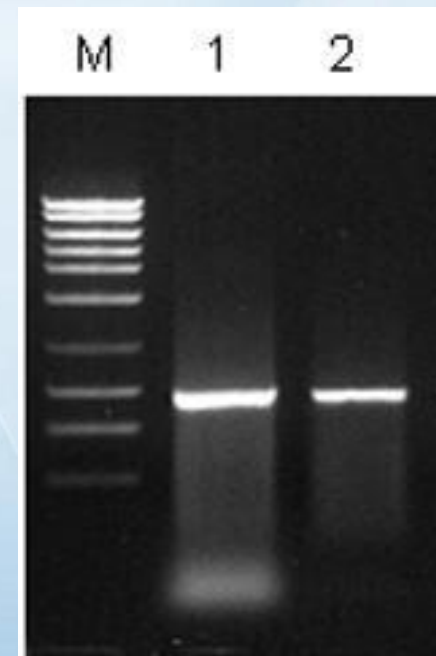
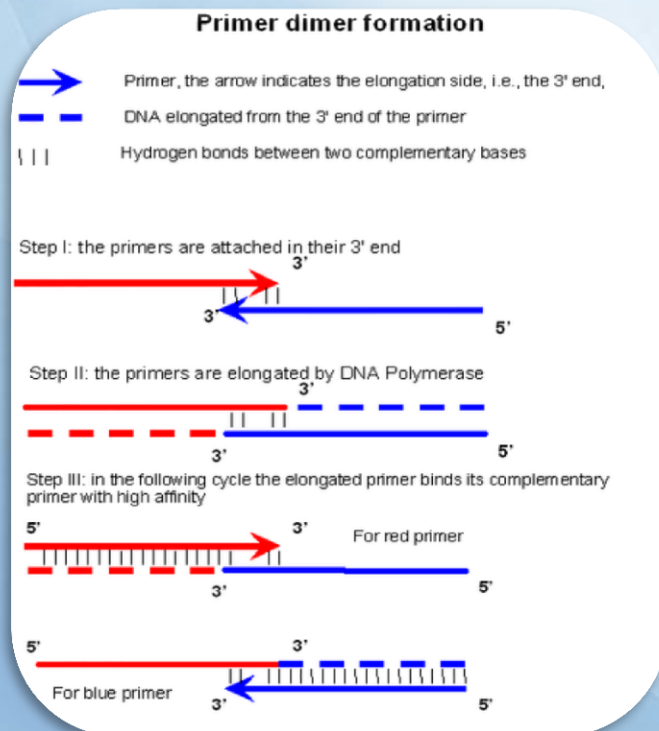
- Sample preparation, reaction mixture assemblage should be performed in separate areas.
- A Laminar Flow Cabinet with a UV lamp is recommended for preparing the reaction mixture.
- New gloves should be used for DNA/RNA purification.
- The use of tips with filters for both sample and reaction mixture preparation
- Autoclaving of all buffers is recommended.

DNA Influencing PCR Success

- Tissue type used for DNA extraction
- Quantity of the Sample
- Length of the DNA fragment to be amplified
- PCR Inhibitors
 - Detergent
 - Phenol
 - Heparin
 - Heme
 - Dyes (bromphenol blue)
 - Urine
 - High concentration of DNA

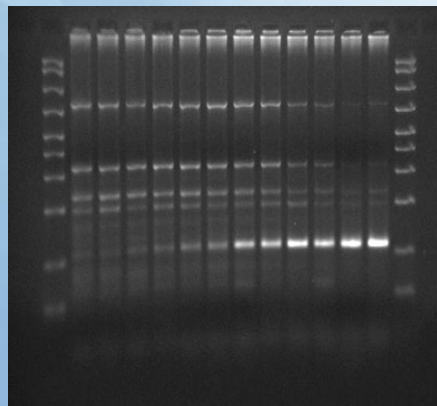
Primers

- The primer should not be self-complementary or complementary to any other primer in the reaction mixture, to prevent primer-dimers.
- Primer-dimers interferes with Sequencing

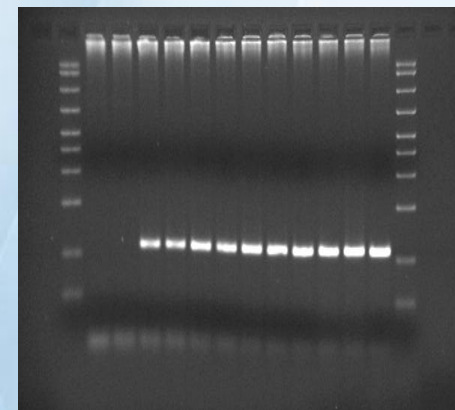


Cycle parameters

- **Annealing temperature**
 - starting approximately 5°C below calculated T_m
- **Extension time**
 - every 1kb of amplicon: 1 minute (Is it always true?)
- **Number of cycles**
 - 25-40 cycles

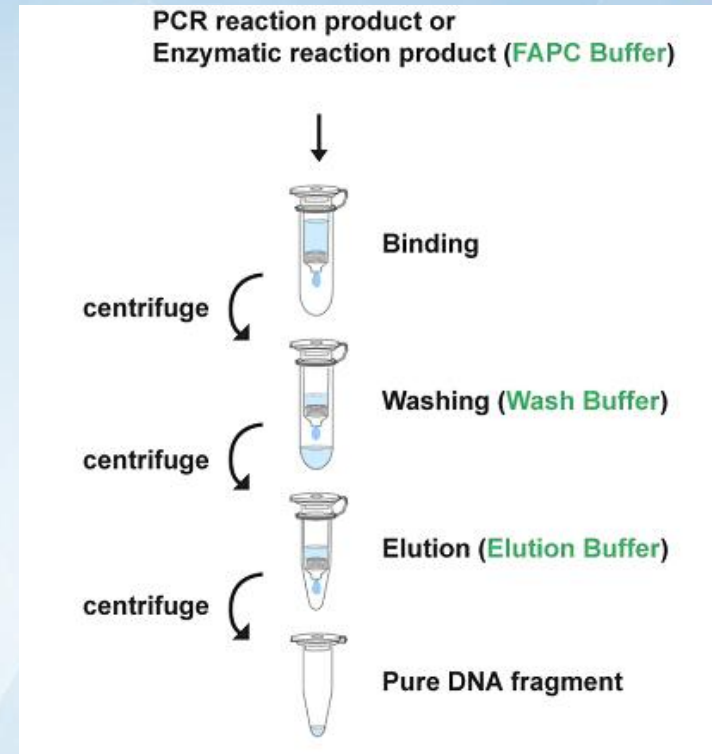
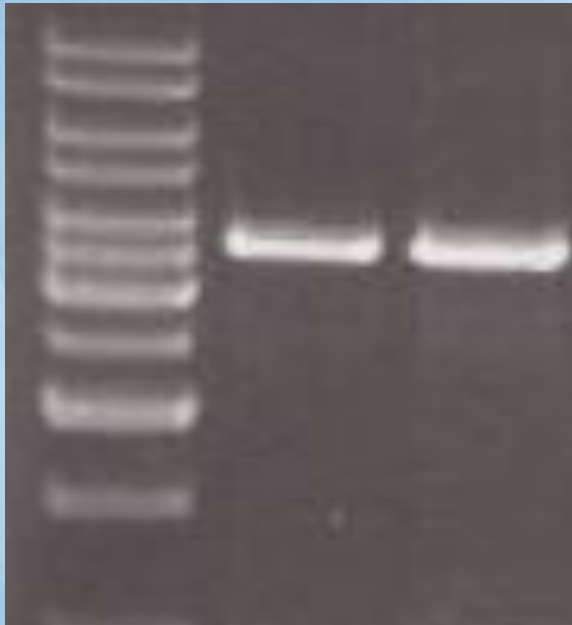


Not optimized



Well optimized

PCR purification



Prepare templates properly:

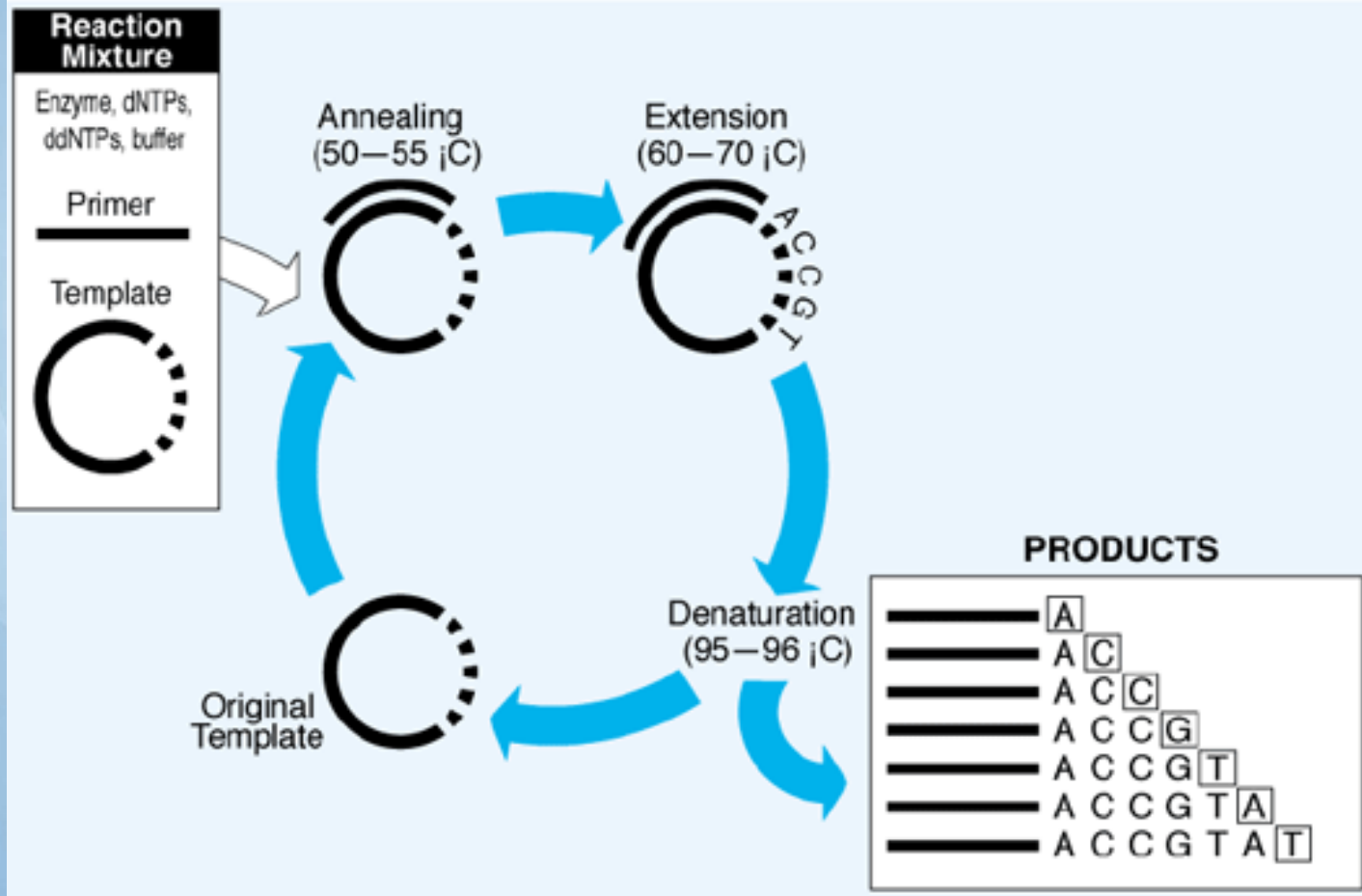
Resuspend in water.

Do not resuspend in TE or EDTA reagents.

Best to use a commercial kit for purification!

*****REMEMBER: HIGH QUALITY TEMPLATE WILL LEAD TO HIGH QUALITY DATA!!!!**

Preparation of Sequencing Reaction



- Cycle sequencing is **linear** amplification
- Only **one** primer per reaction

Sequencing Reaction

PCR Ingredients

1. DNA "PCR prouduct"
2. Primers (Fw OR Rv)
3. Bigdye terminator
4. Seqeuncing buffer

PCR Program

Step 1: 1 min at 96°C

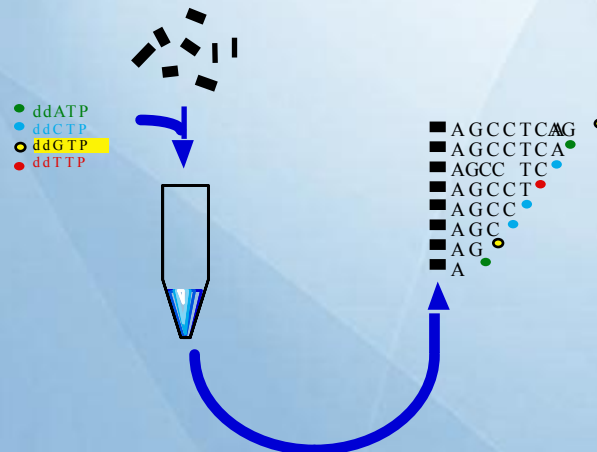
Step 2: 25 cycles of:

10 sec at 96°C

5 sec at 50°C

4 min at 60°C

Step 3: hold at 4°C

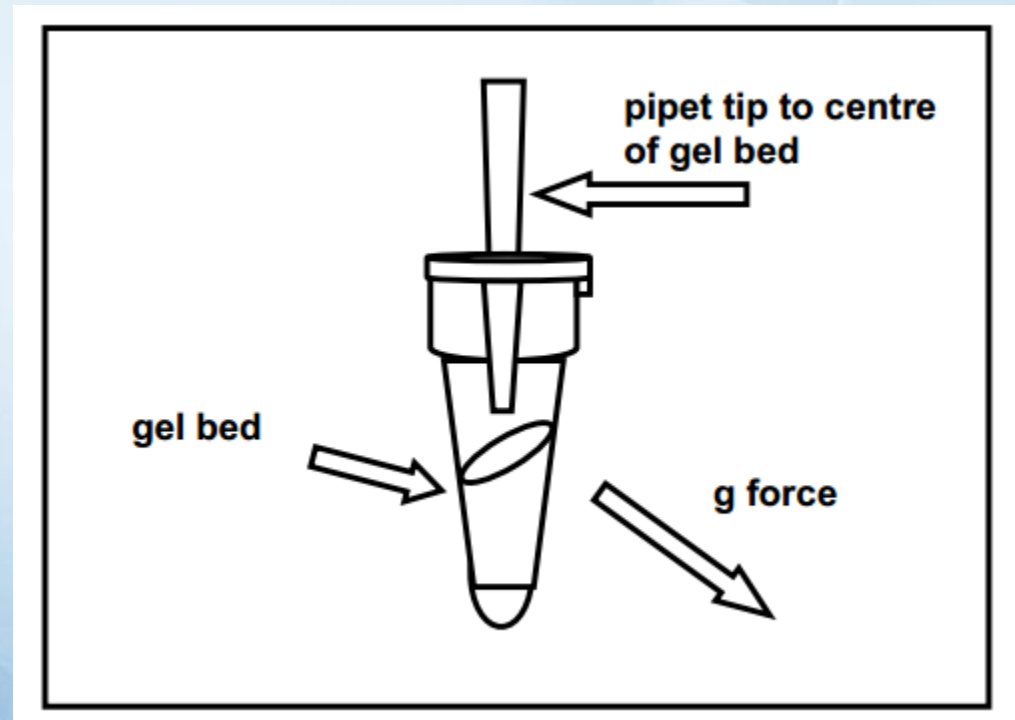


Sequencing Reaction Purification



Centri - Sep Protocol

These are useful for removing excess, nucleotides, small primers, radioactive and fluorescent precursors salts and buffers



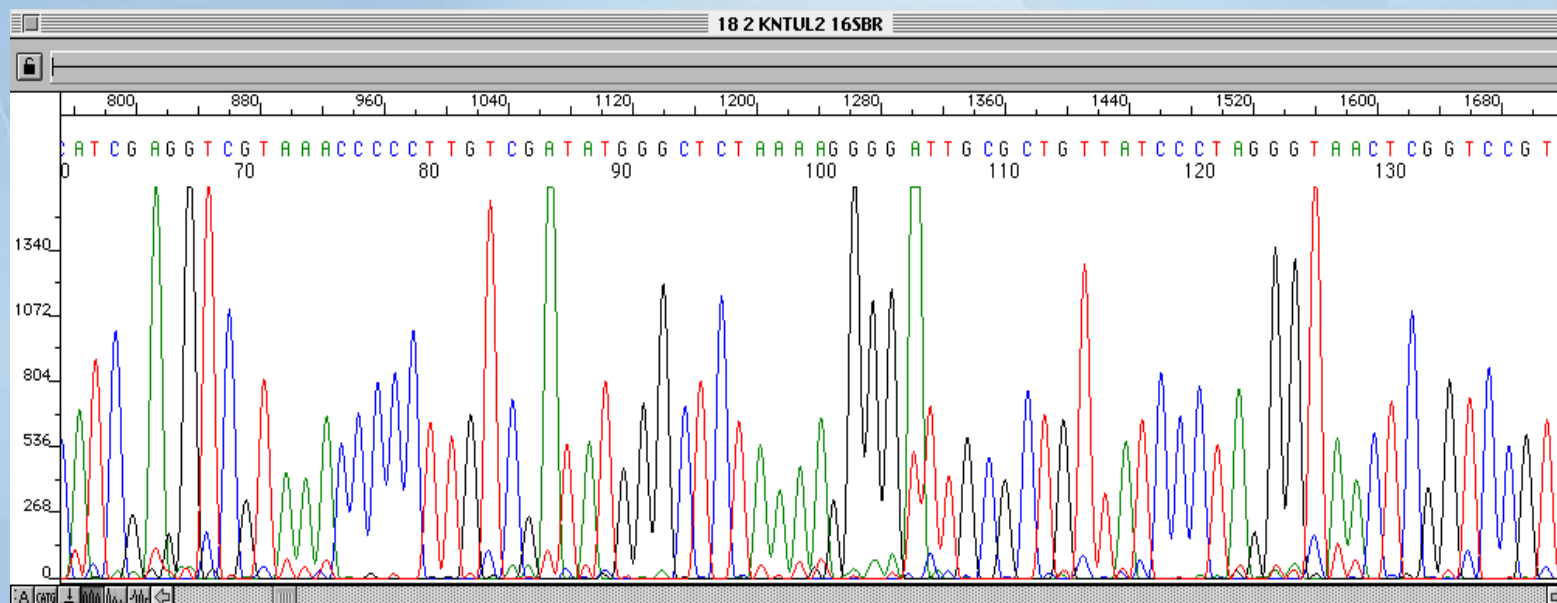
Loading the Reaction on the 310 ABI sequencer



Accuracy is approx 99%

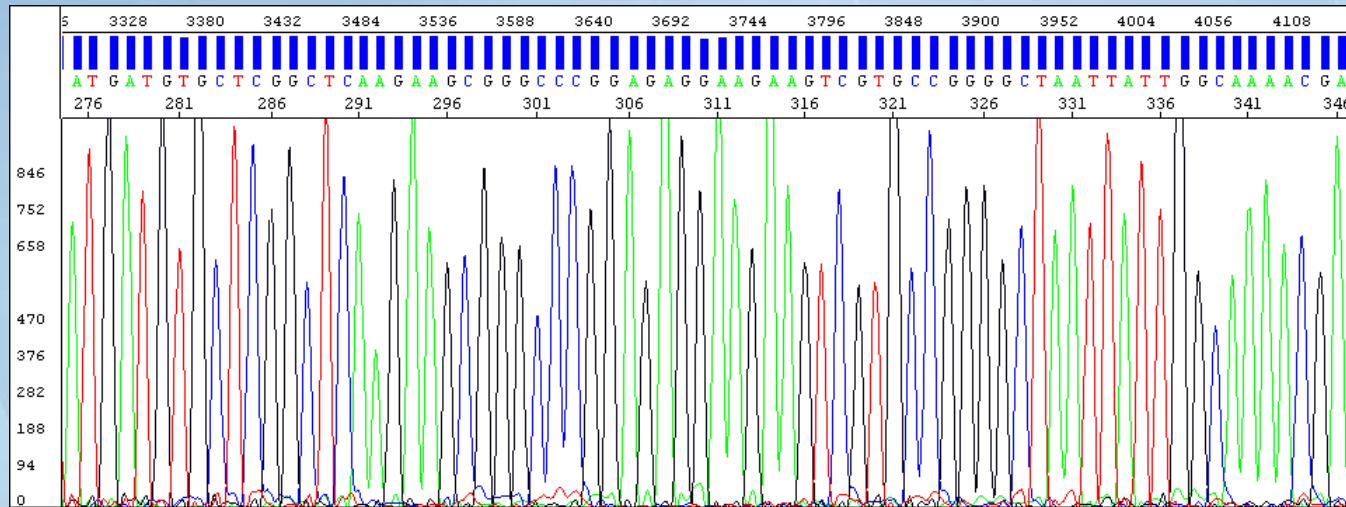
Data output

Data in electropherogram format shows peaks [.abi file](#)
Free software [sequence scanner v1.0](#) (Life Tech).



Data in sequence file format shows text [.seq file](#)

Recommendations for successful sequencing



Good quality sequence data, with sharp peaks, no N's and high quality value scores

- * Check **sample** using a Nanodrop. Check for contaminants.
- * Check the **primer** melting temperature..
- * Submit samples at the correct concentrations. Use **water** not EDTA or TRIS.
- * For **Ethanol** precipitation always use fresh stocks and ensure it is completely removed.

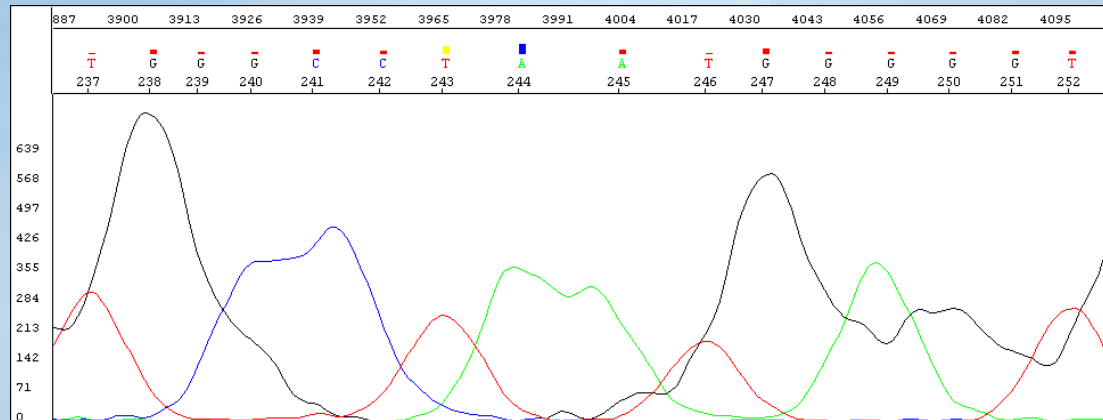
Troubleshooting



Contaminants such as excess salt, RNA or protein in your sample:

These cause the bands to be distorted and wide and the quality scores are low.

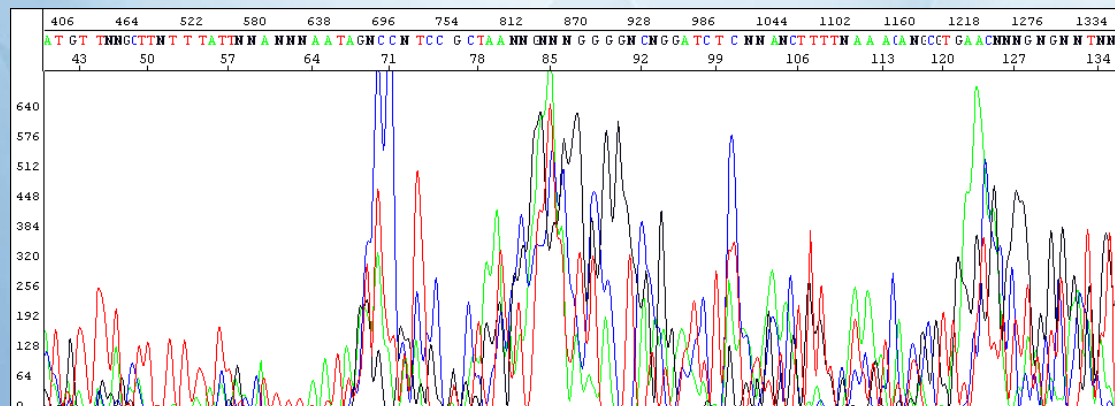
The software has problems calling the right bases.



A failed reaction:

There are many Ns called as the reaction has failed due to template and/or primer problems with high background noise observed.

The software cannot call the correct bases.



Submitting your template

Sample Requirements

Please supply your templates as detailed below:

Template type	Plasmid	M13	PCR product
Template concentration	200 ng/ μ L	100 ng/ μ L	5-20 ng/ μ L
Template volume	5 μ L	5 μ L	5 μ L
Primer concentration	5 pmol/ μ L	1 pmol/ μ L	5 pmol/ μ L
Primer volume	5 μ L	5 μ L	5 μ L

Sequencing workflow

