

## TECHNIQUES OF MOLECULAR BIOLOGY: POLYMERASE CHAIN REACTION

Instruct: Dr. M. A. Srouf

Course: Molecular Biology (BIOL 333)

Textbook:

Watson J, et al. (2014). Molecular Biology of the Gene, 7<sup>th</sup> ed. [Chap 7](#)

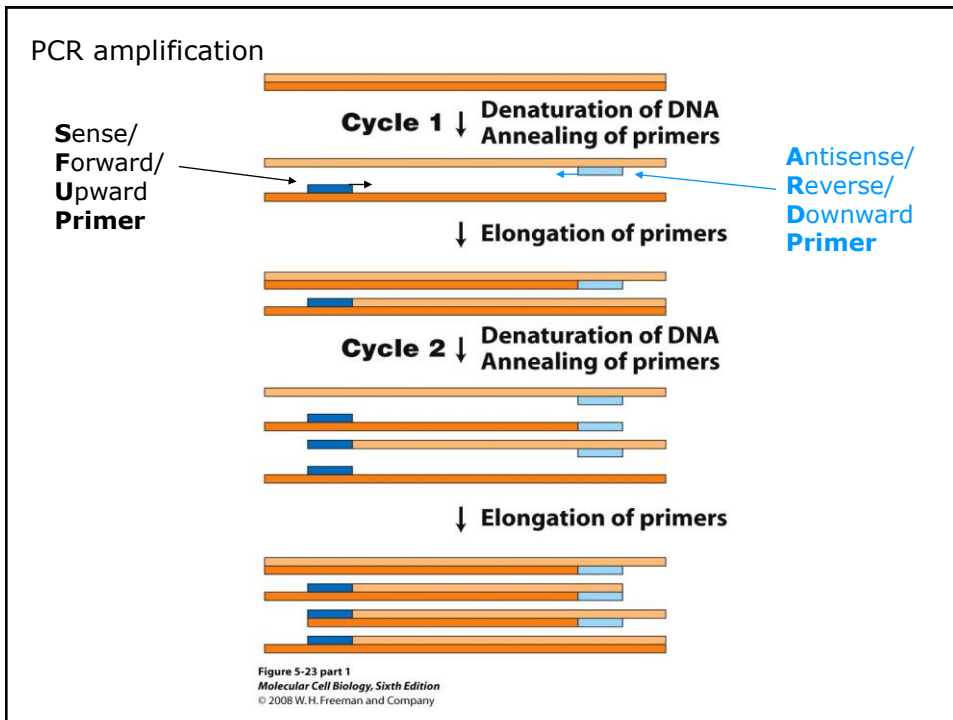
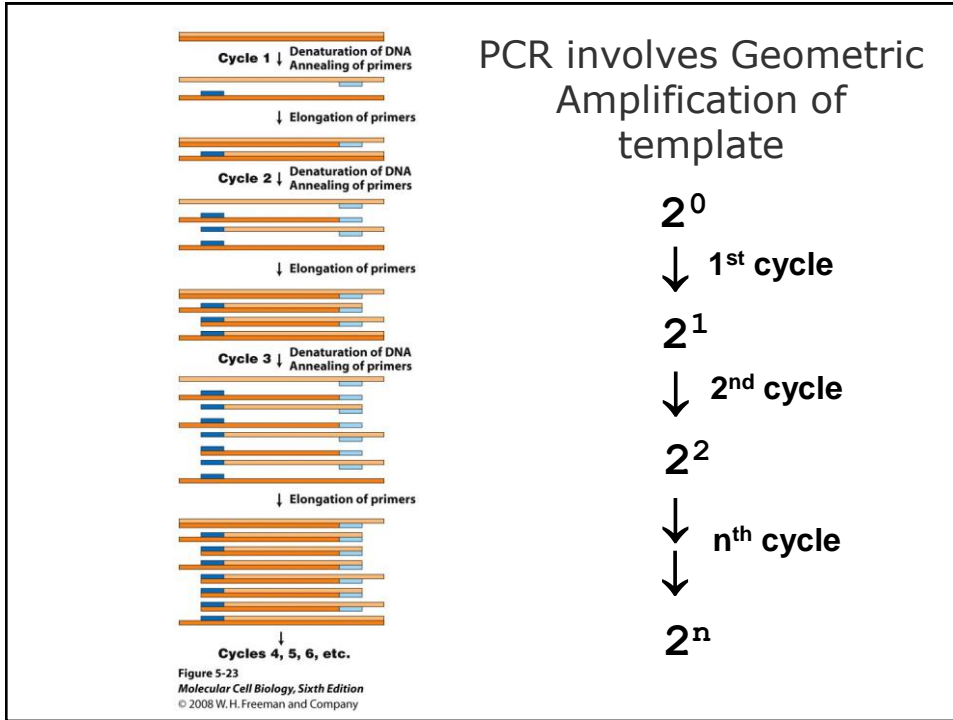
### Polymerase Chain Reaction (PCR)

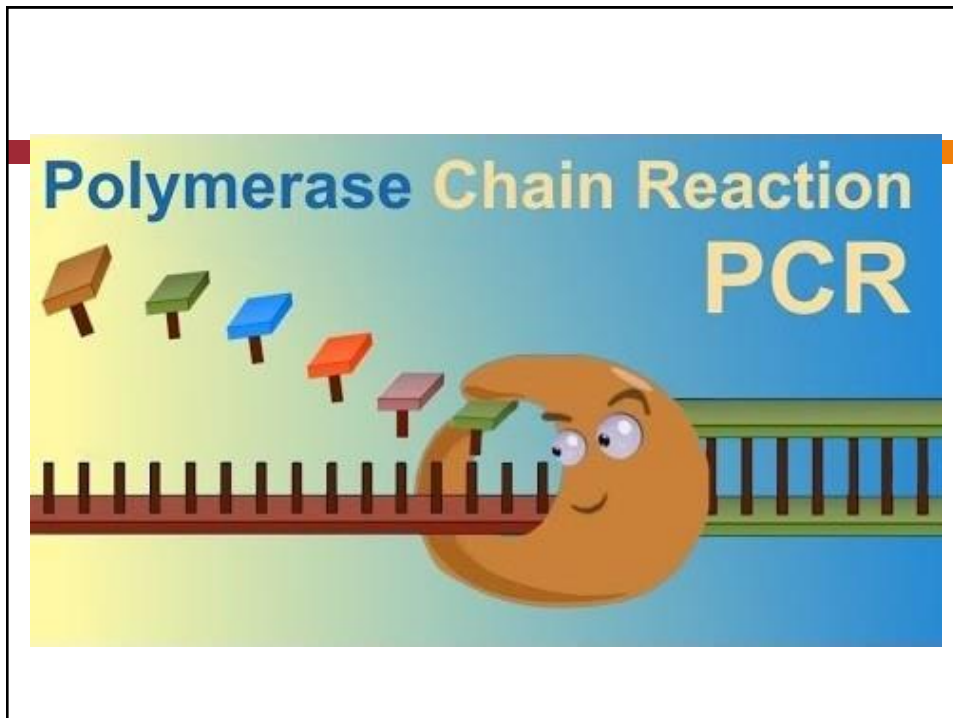
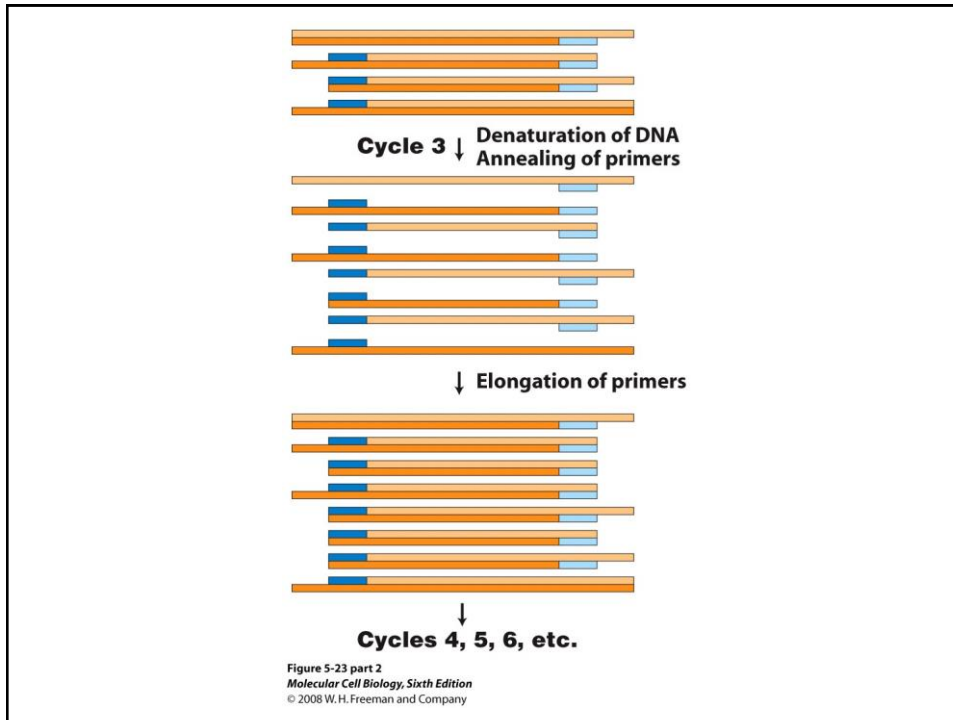
- PCR: *in vitro* amplification of a specific DNA region flanked by known sequences
- Specific DNA fragment(s) are enzymatically amplified
- 10<sup>6</sup>-fold amplification possible
- Can detect single molecule
- Tolerates impure DNA
- Assay time < day

# PCR

- PCR Requirements:
  - Heat-stable DNA polymerase
  - Deoxynucleotides (dNTPs)
  - Target DNA
  - A pair of oligonucleotides (primers)
  - Thermocycler
- Taq Polymerase
- *Thermus aquaticus* DNA polymerase
- Thermophilic organism
- Enzymes resistant to high temperatures
- 72-74°C optimum

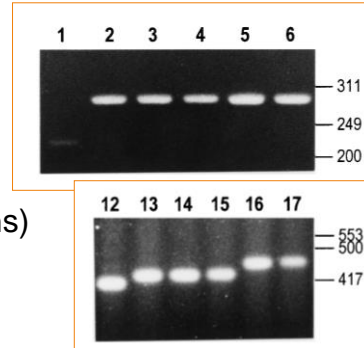
- DNA Learning center at Cold Spring Harbor Lab:  
<https://dnalc.cshl.edu/resources/animations/pcr.htm>  
↓
- Virtual labs for PCR & gel electrophoresis:  
<http://learn.genetics.utah.edu/content/labs/>





## PCR Protocol

- Mix DNA, primers, dNTPs, Taq, buffer,  $Mg^{2+}$
- Program thermocycler for times and temperatures
  - ▣ Denaturation
  - ▣ Annealing
  - ▣ Extension
- Thermal cycling: 30-35 cycles
- Analyze amplified DNA (amplicons) by agarose gel electrophoresis



## PCR: Thermal cycling

Step	Temp	Time	Notes
<b>Initial Denaturation</b>	<b>94-96°C</b>	<b>2-5 min</b>	
30-35 cycles:			
Denaturation	94-96°C	0.5-2 min	Longer: ↑ denaturation, but ↓ enzyme & template
Annealing	45-65°C	0.5-2 min	Higher/shorter: ↑ specificity, but ↓ yield
Extension	72°C	~1 min/kb	Taq processivity = 150 nt/sec
<b>Final extension</b>	<b>72°C</b>	<b>5 min</b>	

## Stringency and Melting Temperature

- Melting Temperature (T<sub>m</sub>)
  - Temperature at which strands separate
  - Can estimate T<sub>m</sub> with formulas: \*\*
- Synthetic Oligonucleotides:  

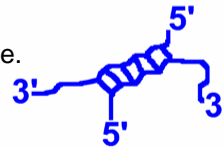
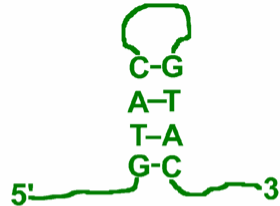
$$T_m = 2(A + T) + 4(G + C)$$
- Effective T<sub>m</sub> = 81.5 + 16.6log[Na<sup>+</sup>] + 0.41(%GC) - 0.65(600/N) - 1.4(%mismatch)\*

## Stringency and Melting Temperature

- Stringency of a hybridization reaction: refers to the tolerance (or lack thereof) for mistakes in base pairing
- High stringency: low salt conc, high formamide, high temperature > require exact base pairing
- Low stringency: high salt conc, low formamide, low temperature >> more base pair mismatches can be tolerated

## Design of Oligonucleotide Primers

- Criteria for selection of an oligo
  - Uniqueness (18-28 bases)
  - $T_m > 55^\circ$
  - 50% GC composition
  - 3'-GC 'caps'
  - No internal complementarity
  - No "primer dimers"
- How to design an oligo?
  - ▣ Manual
  - ▣ Analyze sequence with computer software.
  - ▣ Online software: NCBI/Primer BLAST; available at: [www.ncbi.nlm.nih.gov](http://www.ncbi.nlm.nih.gov)



## Types of PCR: RT-PCR

- Isolation of RNA template, requires careful handling of RNA templates
- Synthesis of cDNA using Oligo-dT, random hexamers or gene-specific primers, and reverse transcriptase at 37-42°C
- RT: Avian myeloblastosis virus (AMV) or Molony murine leukemia virus (MMLV) RT
- RNase inhibitors are usually used in cDNA synthesis rxn
- The cDNA is further amplified using a normal PCR rxn using gene-specific primers

## Types of PCR: RT-PCR

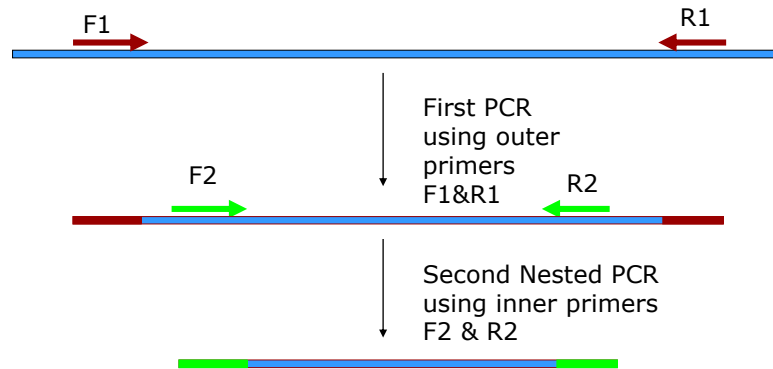
- Applications
  - Study of gene expression
  - Quantitation of mRNA and viral RNA levels
  - Detection of specific gene expression/ mRNA
  - Detection of RNA viruses

## Types of PCR: Nested PCR

- Nested: 2 outer and 2 inner primers
- Why nested PCR?
  - Increase sensitivity and specificity



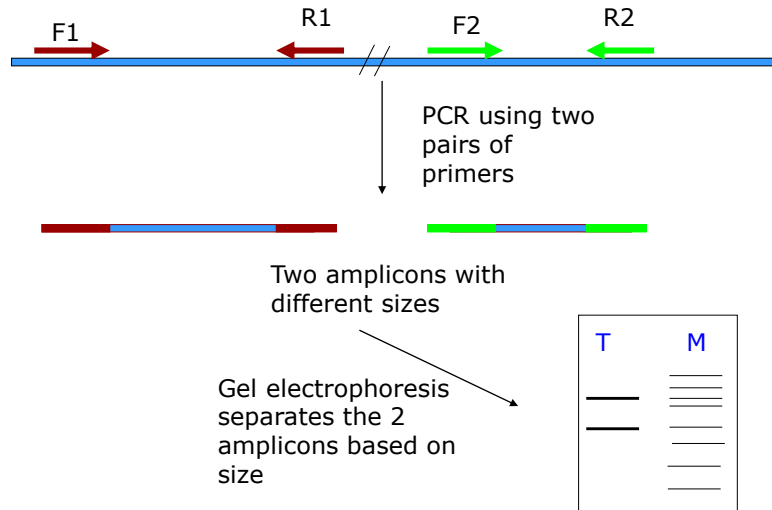
## Types of PCR: Nested PCR



## Types of PCR: Multiplex PCR

- It uses more than one pair of primers (multiplex)
- Allows co-amplification of more than one fragment/ target in one tube
- Can involve the target and internal control fragments
- Decreases the number of tubes per rxn per sample
- Requires careful optimization of rxn and design of primers

## Types of PCR: Multiplex PCR



## Types of PCR:

### Amplification Refractory Mutation System (ARMS)

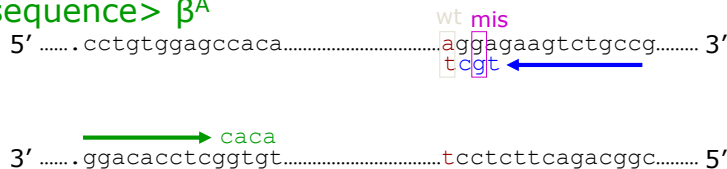
- ARMS is ideally suited for detection of point mutation and small insertion/deletions
- It involves two primers > wt allele & mutant allele >> two PCRs, one for each allele
- Multiplex ARMS
- Advantages of ARMS
  - ▣ Quick, inexpensive
  - ▣ Not suited for detection of unknown mutations

## ARMS primers

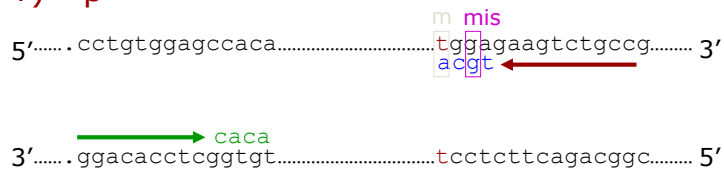
- It is useful to increase the length of primers to about 30 nts.
- Primers usually include a mismatch close to the 3' end at position -2 to -3, to improve specificity (but may decrease yield)
- A second mismatch at nt -5 is sometimes included
- The most discriminatory mismatch involves A:G/G:A

## ARMS PCR





### Wild type $\beta$ -globin gene sequence > $\beta^A$





### Mutant $\beta$ -globin gene sequence > Codon 6 (A→T) > $\beta^S$



## ARMS results: 2 rxns per sample

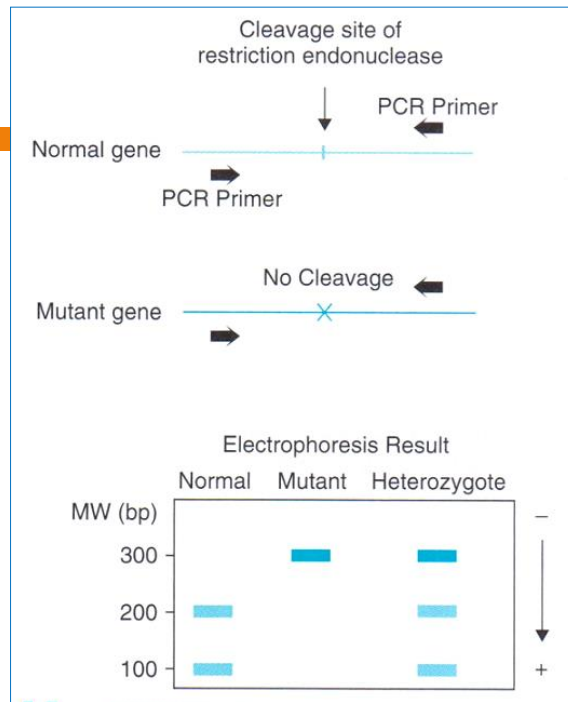
	Wt Rxn	Mut Rxn
Sample # 1: <b>Wt</b> Homozygote		
Sample # 2: <b>Wt+Mut</b> Heterozygote		
Sample # 3: <b>Mut</b> Homozygote		

	Wt
	mut

## Types of PCR: RFLP-PCR

- RFLP: Restriction Fragment Length Polymorphism
- Allows detection of mutations that generate a new or delete an existing restriction site
- Amplicons flanking the target mutation are amplified by normal PCR and then digested using an appropriate Restriction enzyme (RE)
- RFLP-PCR increase the specificity of the first PCR

## Types of PCR: RFLP-PCR



## DNA sequencing

DNA sequencing:

<https://dnalc.cshl.edu/view/15479-Sanger-method-of-DNA-sequencing-3D-animation-with-narration.html>

## DNA sequencing by Sanger method

/ Dideoxy chain termination method:

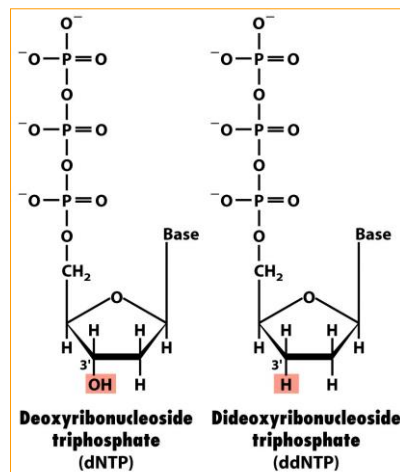
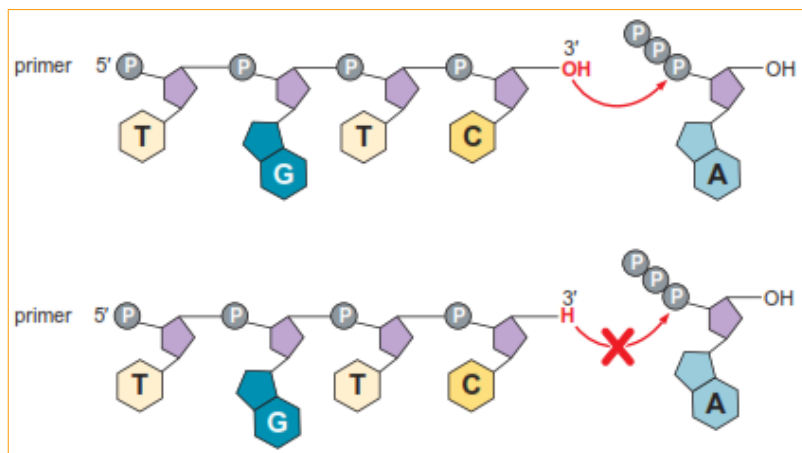


Figure 5-20  
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Structure of  
dNTP & ddNTP

## Dideoxy chain termination method in presence of ddNTPs



## DNA sequencing by Dideoxy chain termination method

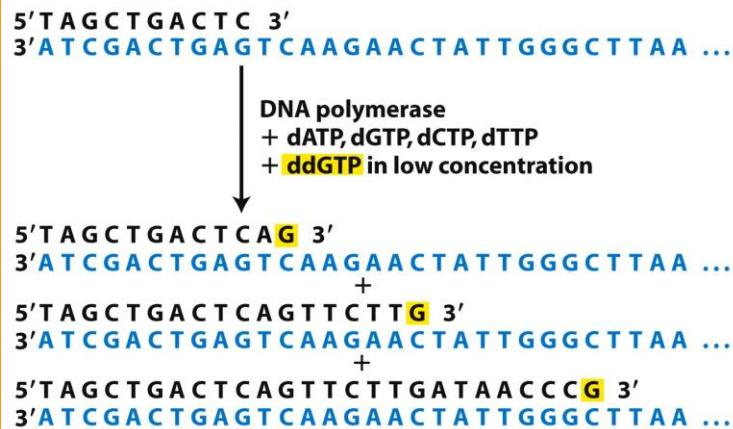


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## DNA sequencing by Dideoxy chain termination method

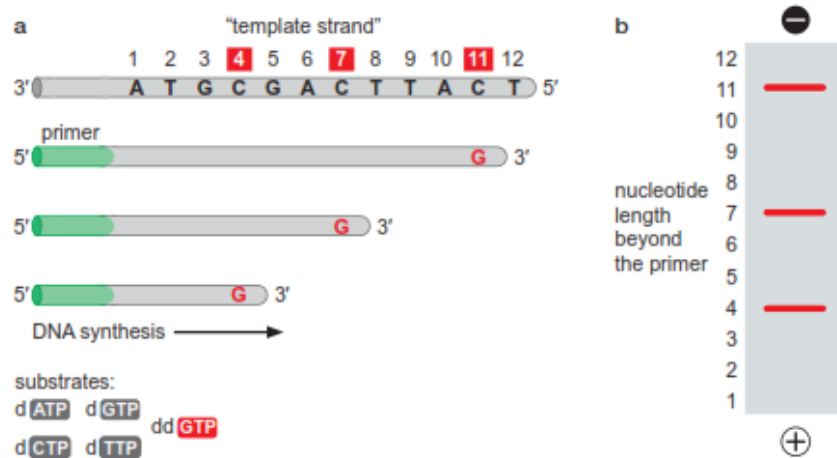


FIGURE 7-15 DNA sequencing by the chain-termination method. As described in the text, chains of different length are synthesized in the presence of dideoxynucleotides. The length of the

DNA sequencing by Dideoxy chain termination method

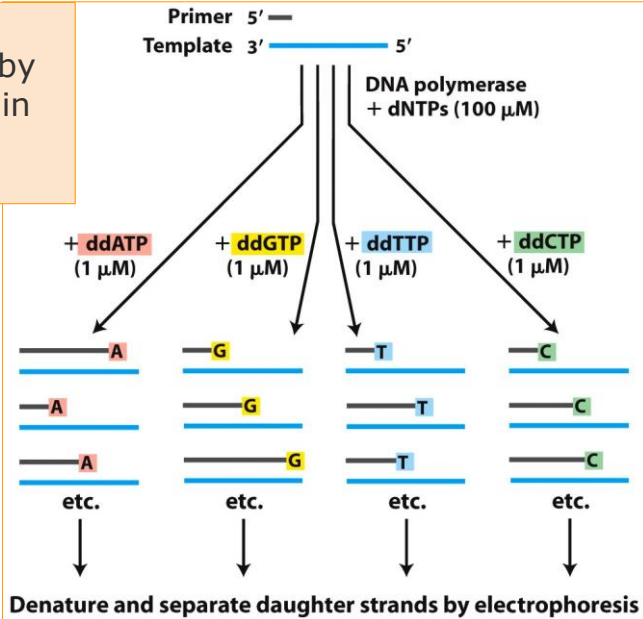
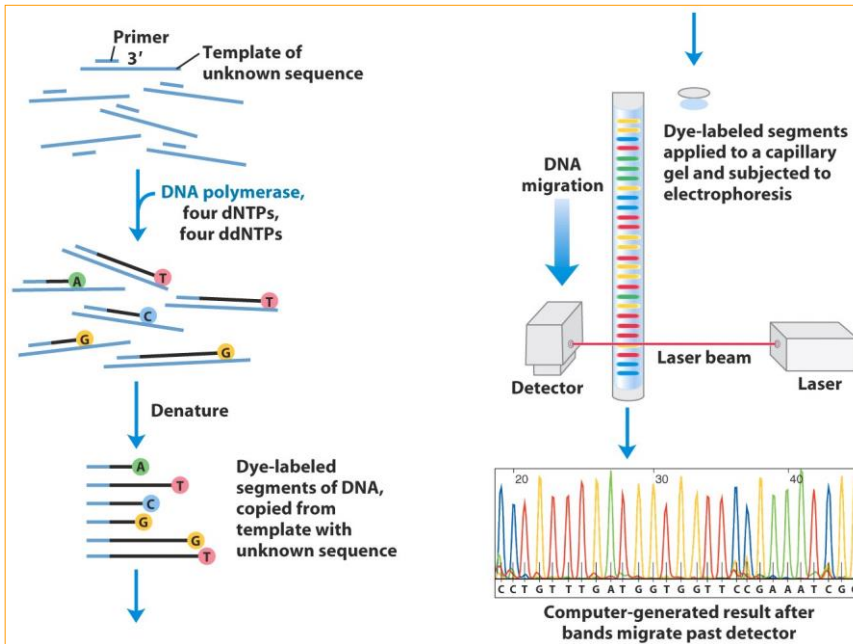
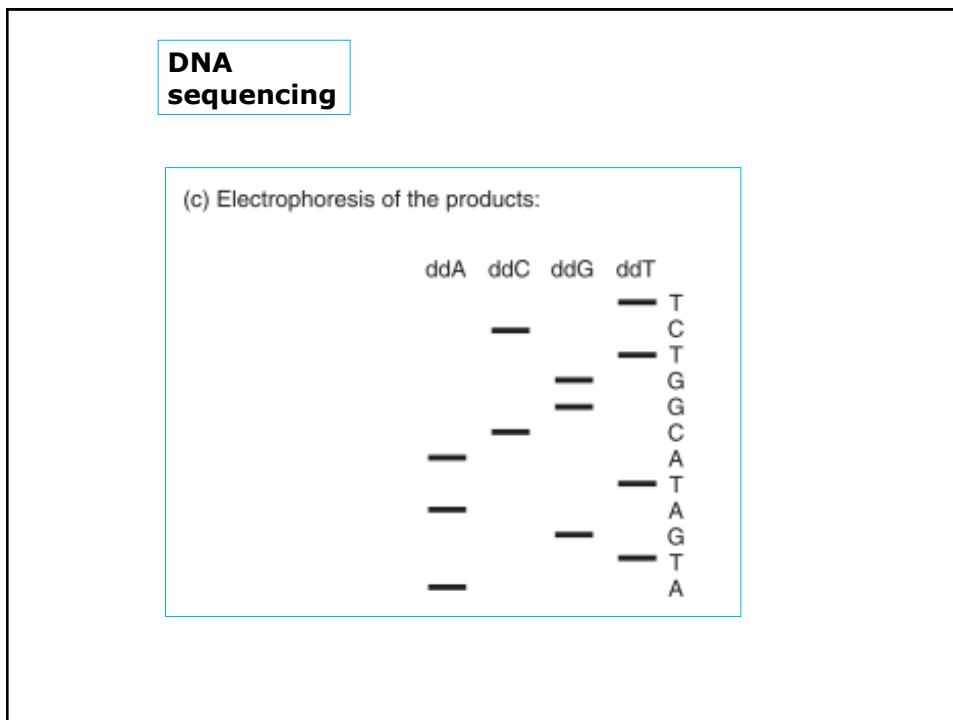
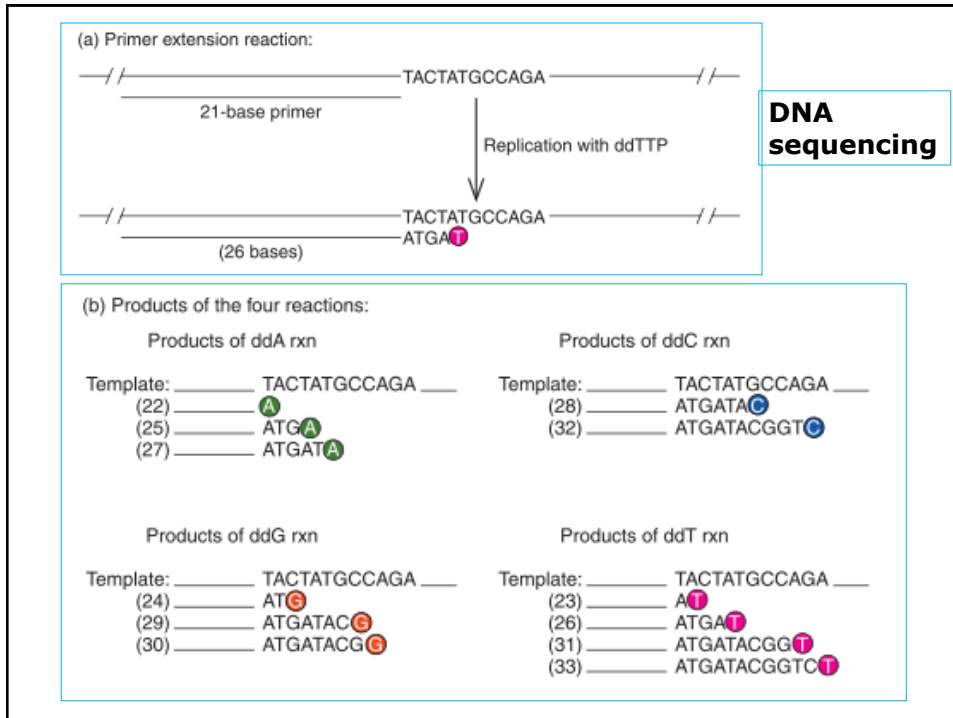


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## DNA sequence readout: by Dideoxy chain termination method

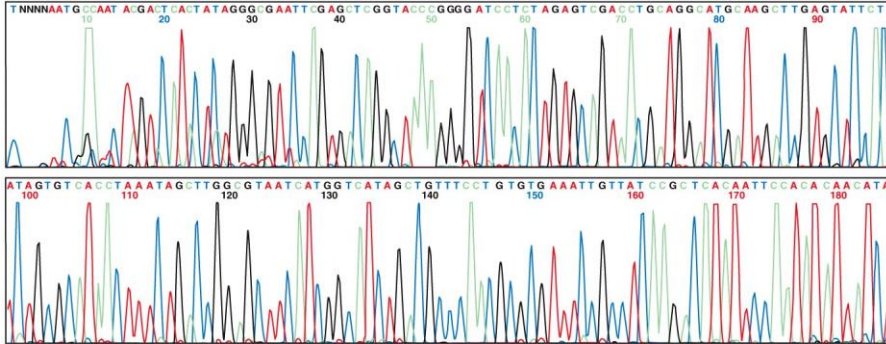
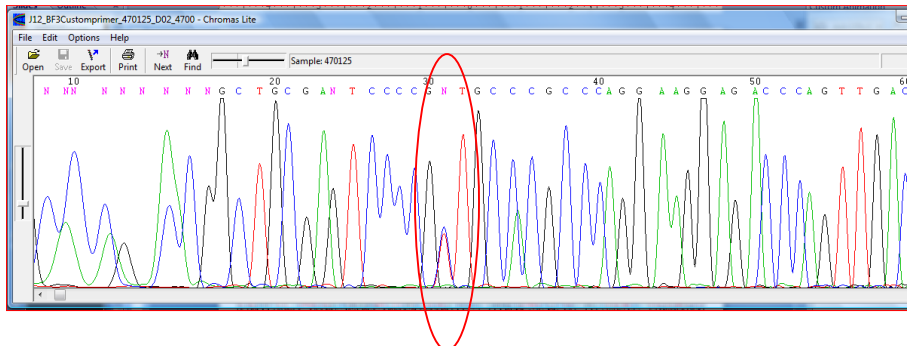


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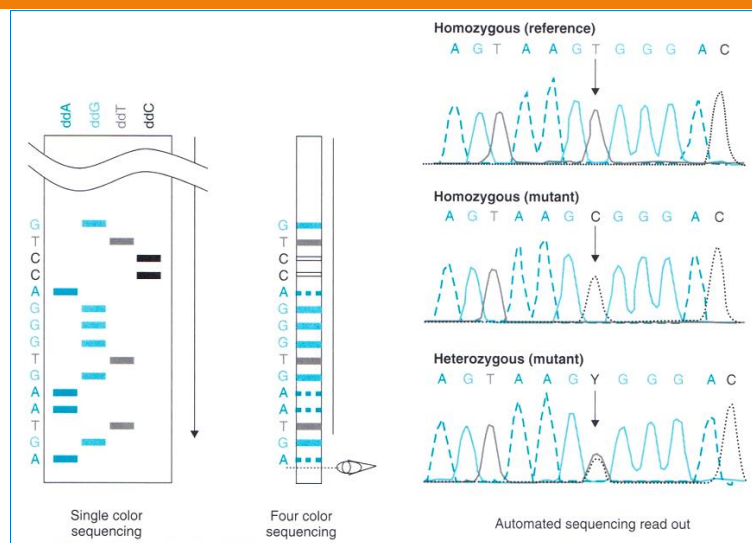
## DNA sequence readout: chromatogram



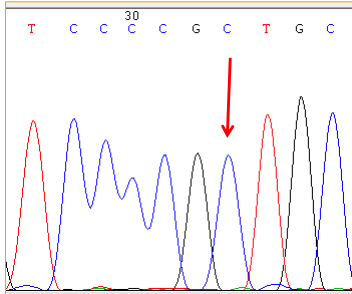
## Applications of DNA sequencing

- Study gene sequence & structure
- Allows genome sequencing, e.g. Human genome project completed sequencing human genome in 2003
- Detection of mutations (known & unknown)
  
- Sequencing is now being done using “DNA sequencing machines” or “Sequencers”

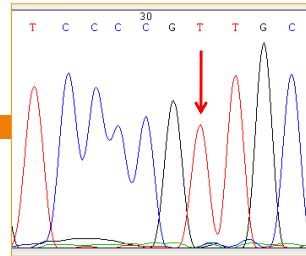
## Detection of point mutations using DNA sequencing



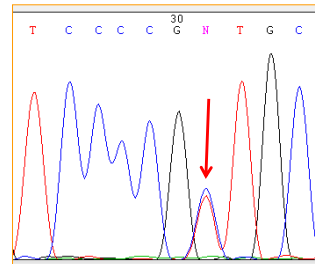
## Detection of point mutations using DNA sequencing



Homozygous  
(Reference, Normal)  
5'-TCCCCG **C** T G C-3'



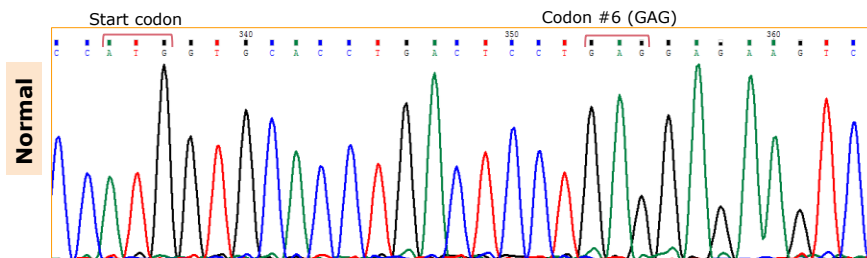
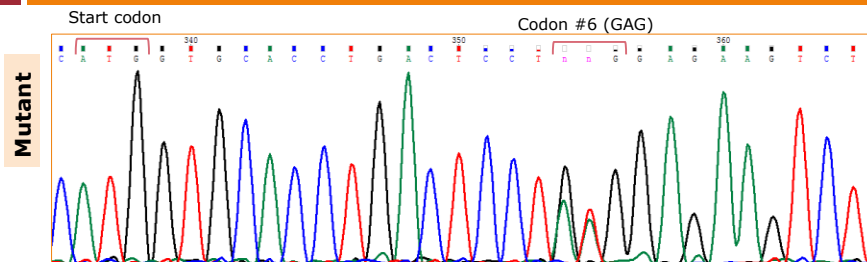
Homozygous (Mutant)  
5'-TCCCCG **T** T G C-3'



Heterozygous (Mutant)  
5'-TCCCCG (**C/T**) T G C-3'

## Heterozygous for HbS & HbC

**HbS:** GAG>GTG, Glu>Val; **HbC:** GAG>AAG, Glu>Lys



## Chemical synthesis of DNA

### Chemical synthesis of DNA oligos

- It allows the chemical synthesis of short, custom designed segments of single-stranded DNA (ssDNA), known as oligonucleotides
- Synthesis is performed on solid supports using automated machines.
- Precursors used for nucleotide addition are chemically protected molecules called phosphoramidites

## Chemical synthesis of DNA oligos (cont'd)

- In chemical synthesis, the DNA chain grows by addition to the 5' end of the molecule ( $3' \rightarrow 5'$ ), while in vivo polymerization is  $5' \rightarrow 3'$ .
- Synthesis of ssDNA molecules 10-100 bases long is efficient and accurate
- Molecules  $>100$  nucleotides long are difficult to synthesize in the quantity and with the accuracy desirable for most molecular analysis.

## Chemical synthesis of DNA oligos

- Method:
- The first nt is attached to silica support via its 3'-OH & is protected at 5'-OH by an acid-labile Dimethoxytrityl (DMT) group
- The DMT is removed by washing with acid
- The next nt is activated with a Diisopropylamino group (MeO), which is oxidized with iodine to form phosphotriester linkage ( $5'-3'$ )
- The synthesis continues to the desired length
- The protecting groups are removed from P
- The oligo is separated from solid support & purified

# Chemical synthesis of oligos

## Blocking >

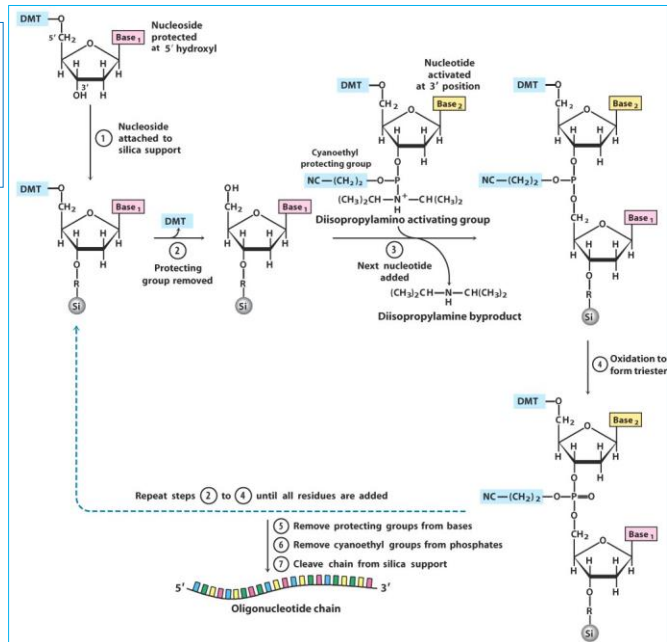
DMT: 4',4'-dimethoxytrityl

## Activation >

MeO:  
diisopropylamino group

## Protection >

NIP3: Cyanoethyl group



## Blocking >

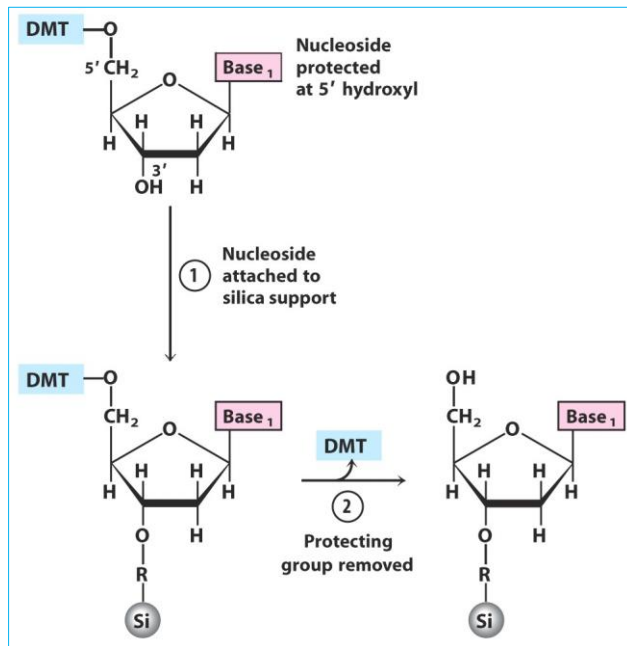
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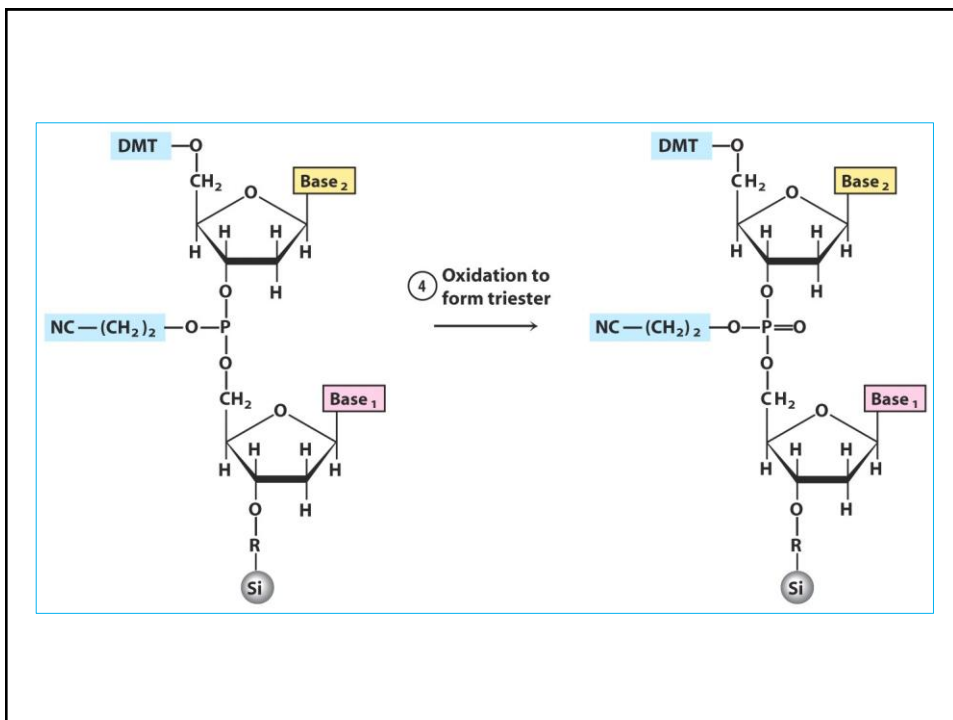
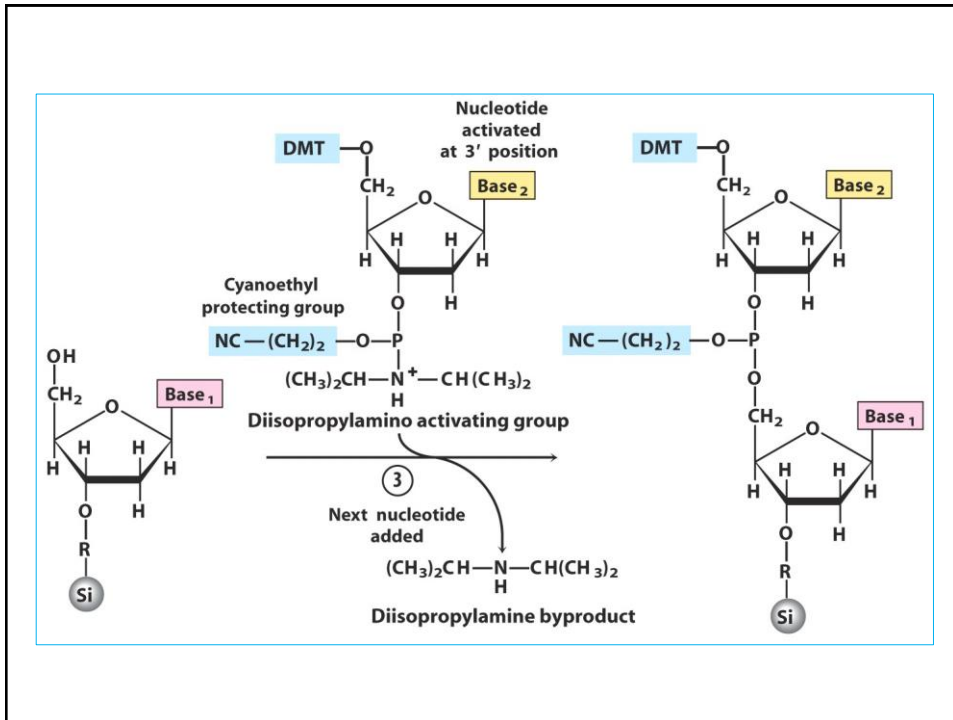
## Activation >

MeO:  
diisopropylamino group

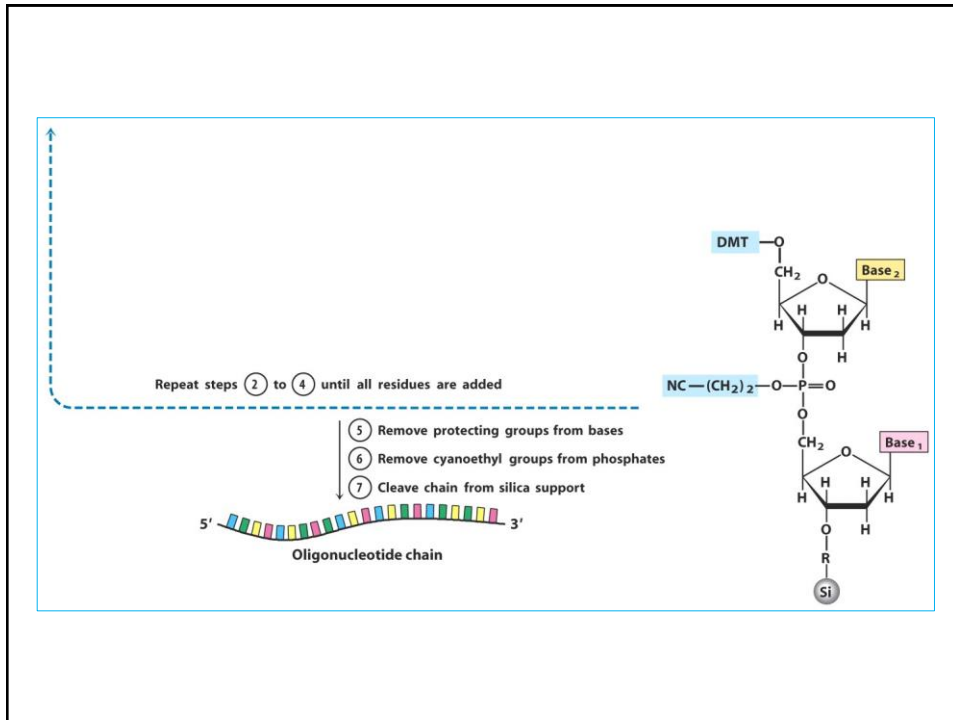
## Protection >

NIP3: Cyanoethyl group









## Applications of chemically synthesized ssDNA molecules

- Custom designed oligonucleotides (oligos) or PCR primers: used for amplification of a specific DNA fragment using the PCR
- Custom designed oligos harboring a mismatch for a cloned DNA fragment >> a method called site-directed mutagenesis
- Custom designed oligos: used to introduce a restriction site in a DNA fragment to facilitate cloning or to create various recombinant DNAs
- Probes