



# Genetic Analysis

## Phenotype analysis: biological-biochemical analysis

Behaviour under specific environmental conditions

Behaviour of specific genetic configurations

Behaviour of progeny in crosses -

## Genotype analysis: molecular and physical analysis

DNA Fragments/Molecules

Sequence homology

Sequence



# Genetic Analysis

## Phenotype analysis: biological-biochemical analysis

### **Behaviour under specific environmental conditions**

Some examples:

Utilization of specific substrates

Loss of function (e.g. Auxotrophy)

Induction behaviour

### **Behaviour of specific genetic configurations**

Some examples:

Complementation analysis: e.g. function (auxotrophy) complementation

Cis-trans test → see regulation: *lac* operon



# Phenotype analysis: biological-biochemical analysis

Behaviour of progeny in crosses – see also introduction → Mendel

Linkage I: Basic Eukaryotic Chromosome Mapping

	Meiotic chromosomes	Meiotic products	
Meioses with no crossover between the genes			Parental
			Parental
			Parental
			Parental
Meioses with a crossover between the genes			Parental
			Recombinant
			Recombinant
			Parental

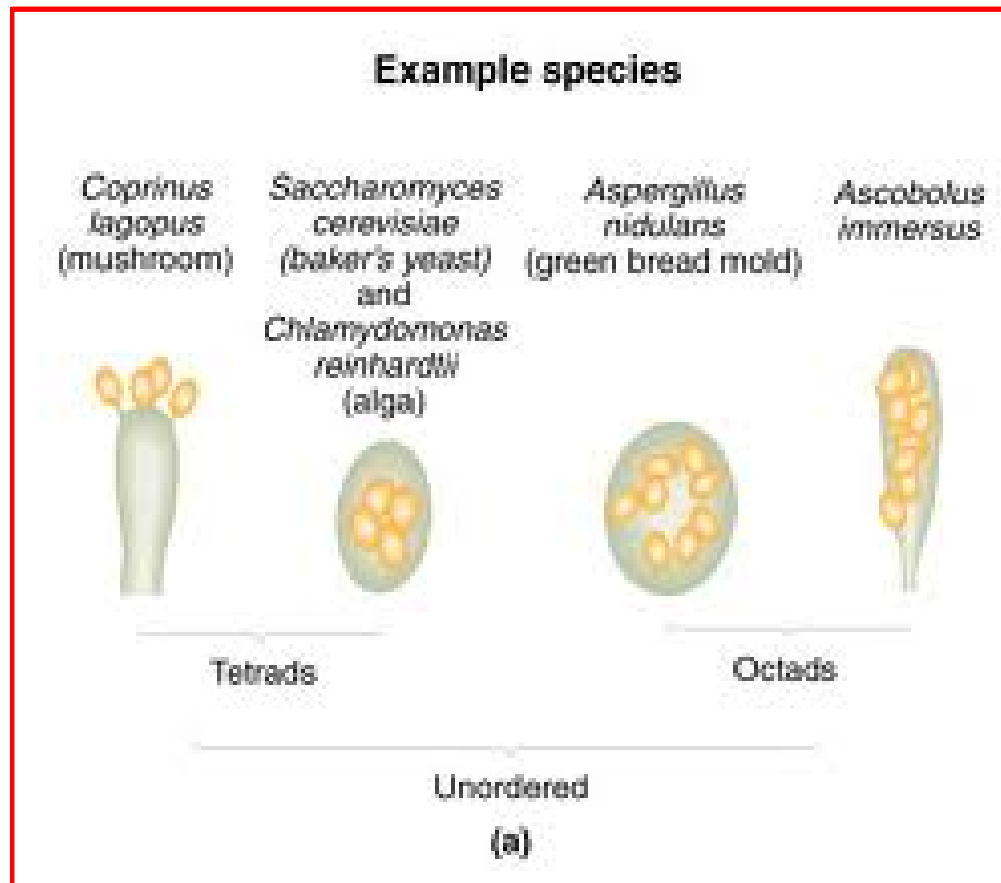
**Figure 5-7** Intrachromosomal recombinants arise from meioses in which nonsister chromatids cross over between the genes under study.



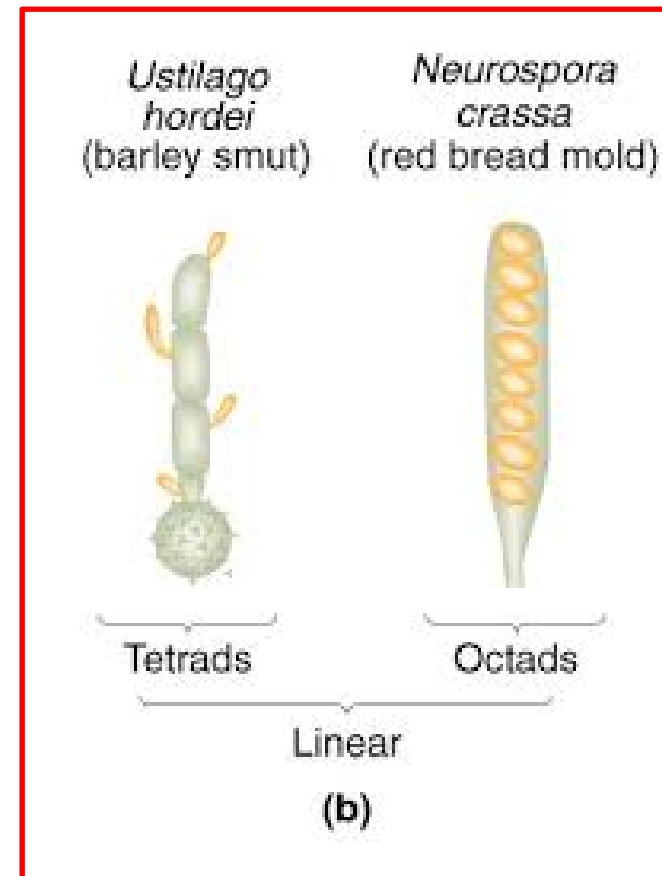
# Tetrads

Product from sexual reproduction

Specific systems is fungi



Unordered  
No connection to position in meiosis

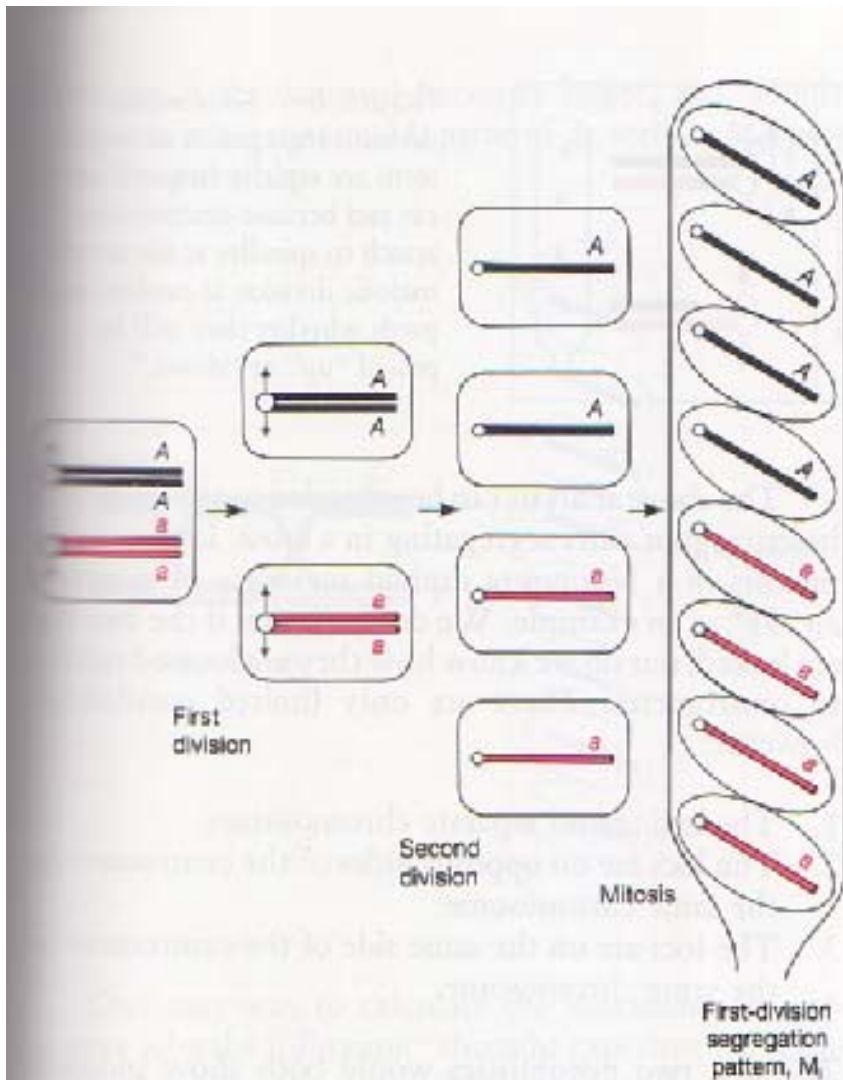


Ordered  
Position in meiosis reflected

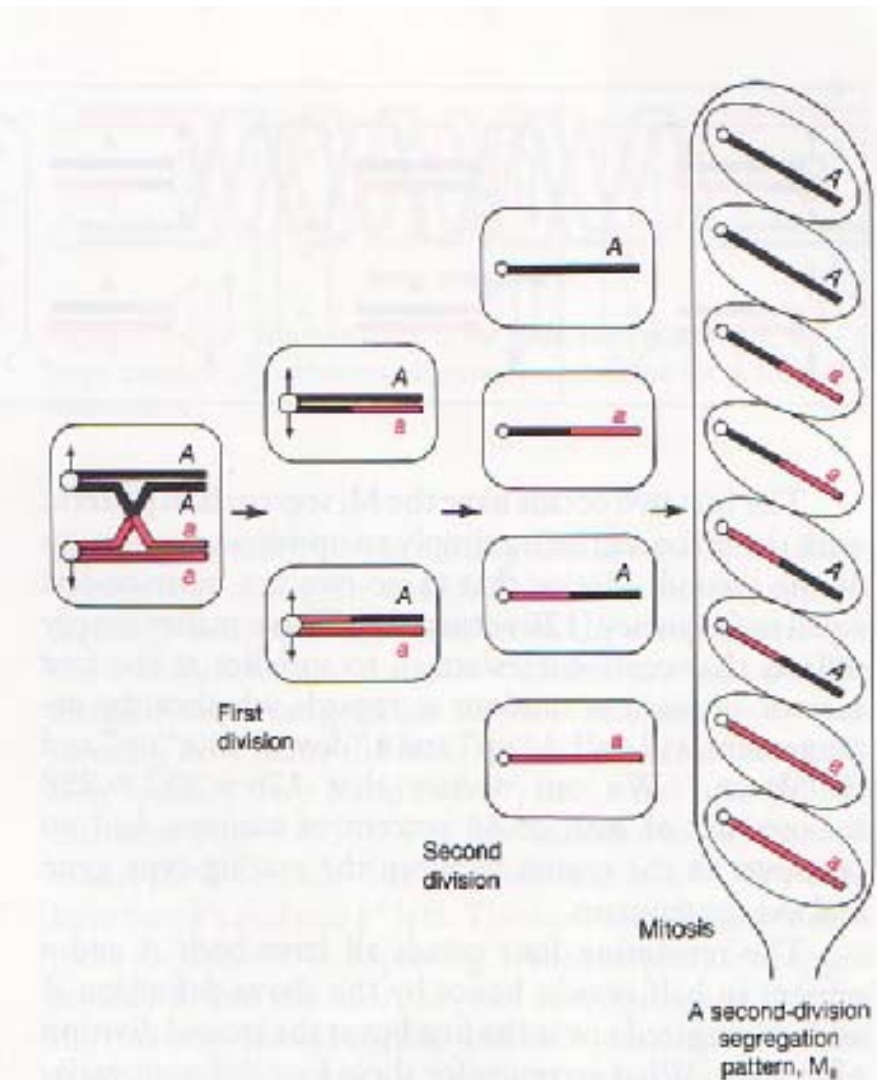


## Ordered linear tetrads in *Neurospora crassa*



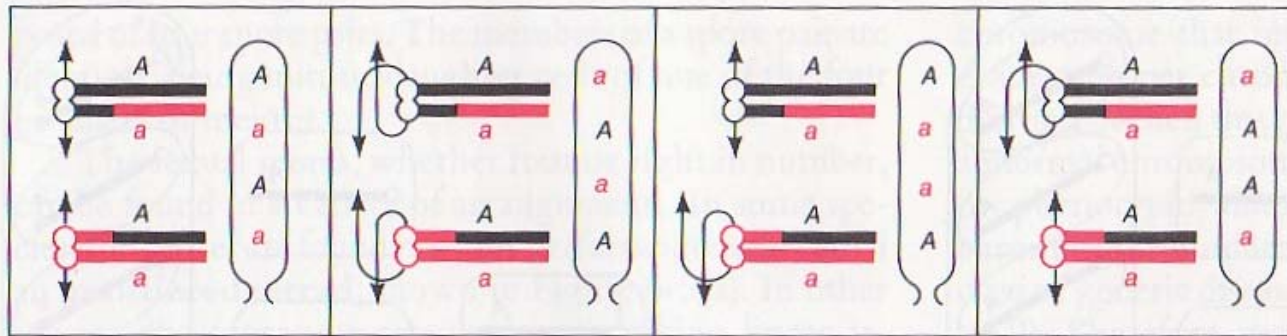
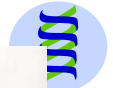


**Figure 6-7** *A* and *a* segregate into separate nuclei at the first meiotic division when there is no crossover between the centromere and the locus. The resultant allele pattern in the octad is called a first-division segregation pattern.



**Figure 6-8** *A* and *a* segregate into separate nuclei at the second meiotic division when there is a crossover between the centromere and the locus.





**Figure 6-9** Four second-division segregation ascus patterns are equally frequent in linear asci because centromeres attach to spindles at the second meiotic division at random as regards whether they will be pulled “up” or “down.”

Octads					
A	a	A	a	A	a
A	a	A	a	A	a
A	a	a	A	a	A
A	a	a	A	a	A
a	A	A	a	a	A
a	A	A	a	a	A
a	A	a	A	A	a
a	A	a	A	A	a
<u>a</u>	<u>A</u>	<u>a</u>	<u>A</u>	<u>A</u>	<u>a</u>
126	132	9	11	10	12
Total = 300					

map unit (m.u.) = RF (as %)

For example: 1 map unit: RF = 0,01 = 1%

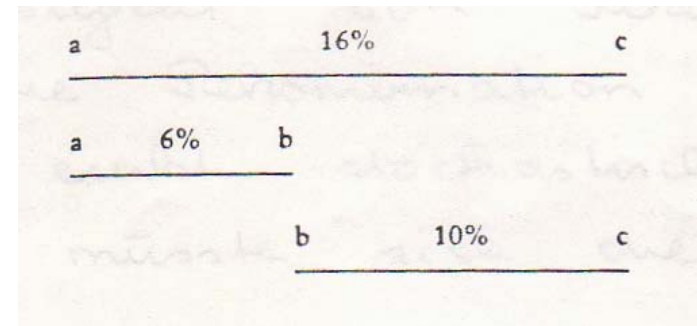
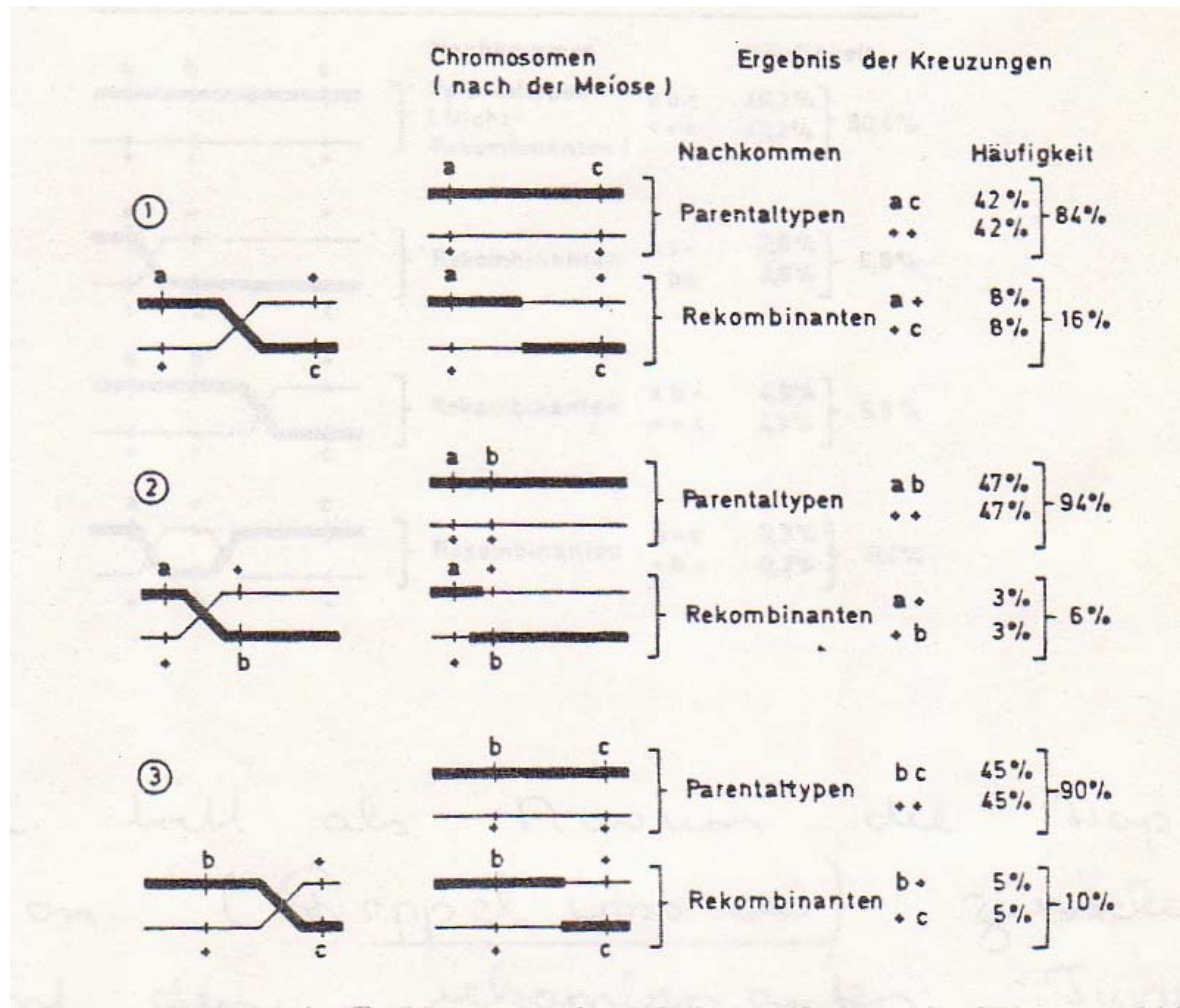
1 m.u. = 1 centi Morgan (cM)

Ordered Tetrade:  
Distance Locus – Centromer:

$$1/2 \times \frac{\text{(second division pattern tetrads)}}{\text{Total tetrads}} \times 100$$



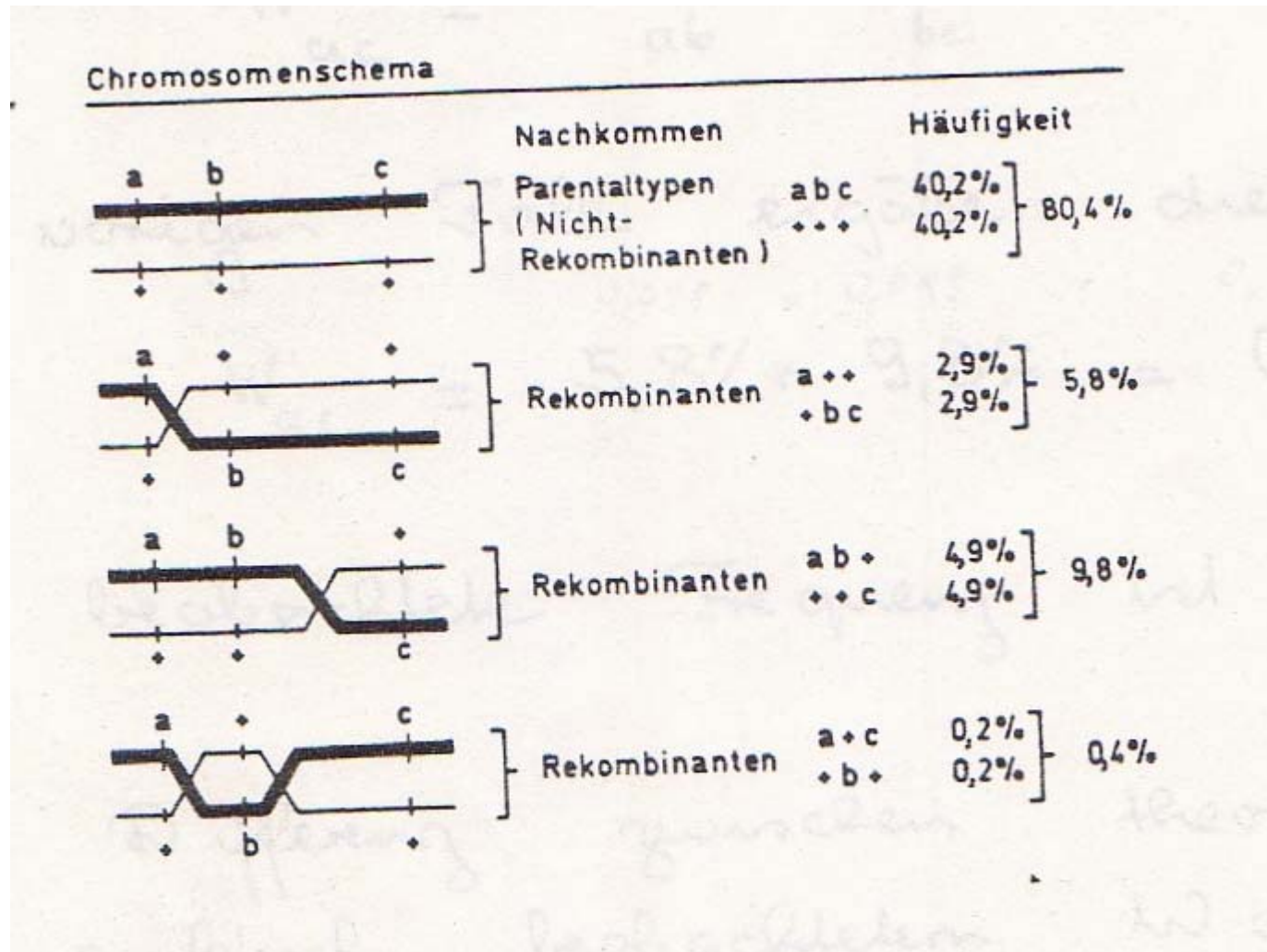
2 - factor cross analysis







### 3- factor cross analysis





13.1.15



# Genetic Analysis

## Genotype analysis: molecular and physical analysis










DNA Fragments/Molecules

Sequence homology

Sequence



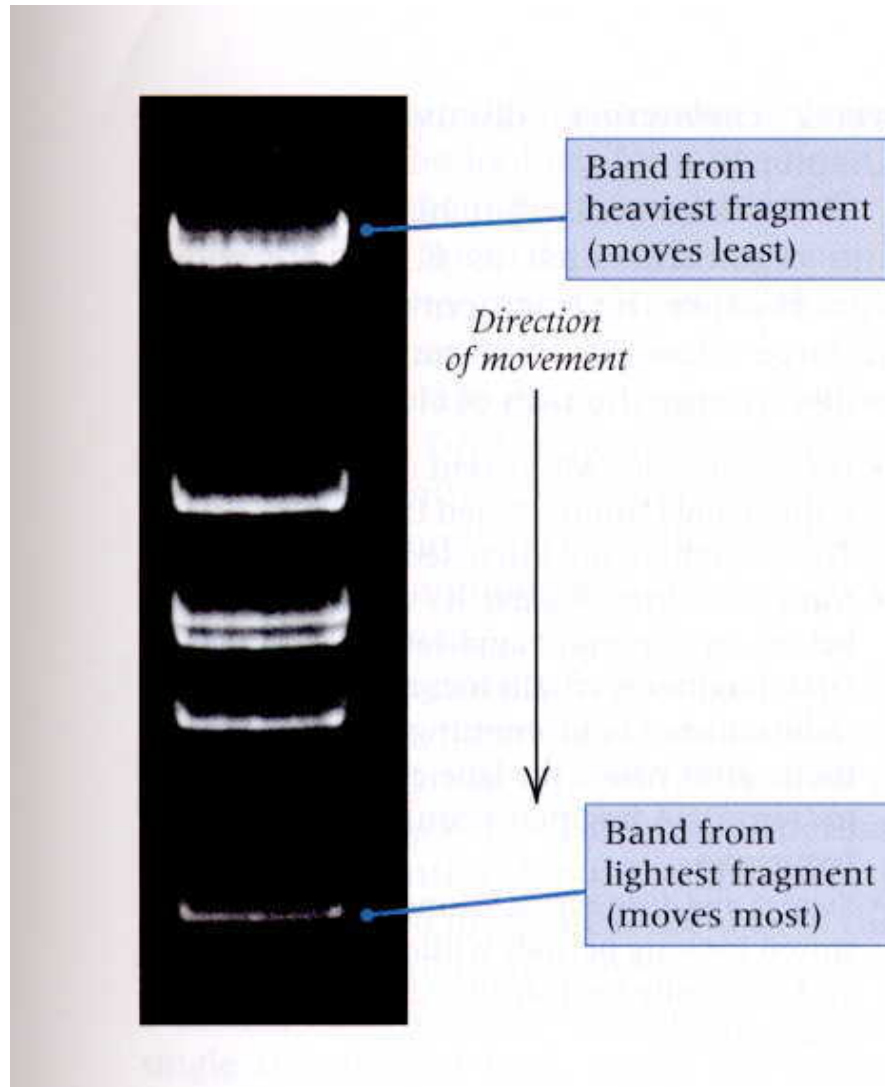
**Table 2.3** Some restriction endonucleases, their sources, and their cleavage sites

Enzyme (Microorganism)	Enzyme (Microorganism)	Enzyme (Microorganism)
<p><i>EcoRI</i> (<i>Escherichia coli</i>)</p> 	<p><i>HindIII</i> (<i>Haemophilus influenzae</i>)</p> 	<p><i>AluI</i> (<i>Arthrobacter luteus</i>)</p> 
<p><i>BamHI</i> (<i>Bacillus amyloliquefaciens</i> H)</p> 	<p><i>PstI</i> (<i>Providencia stuartii</i>)</p> 	<p><i>RsaI</i> (<i>Rhodopseudomonas sphaeroides</i>)</p> 
<p><i>HaeII</i> (<i>Haemophilus aegyptus</i>)</p> 	<p><i>TaqI</i> (<i>Thermus aquaticus</i>)</p> 	<p><i>PvuII</i> (<i>Proteus vulgaris</i>)</p> 

Target sequence and cleavage site; sticky ends

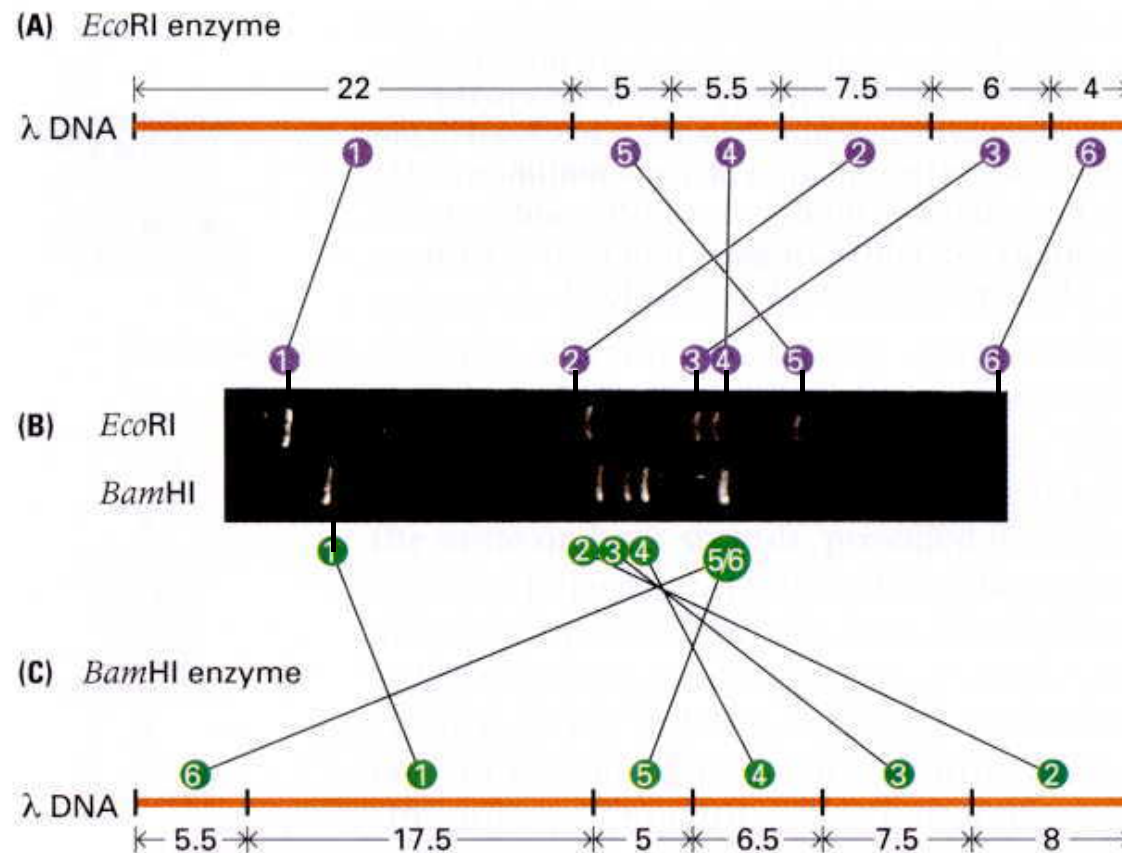
Target sequence and cleavage site; blunt ends

*Note:* The vertical dashed line indicates the axis of symmetry in each sequence. Red arrows indicate the sites of cutting. The enzyme *TaqI* yields cohesive ends consisting of two nucleotides, whereas the cohesive ends produced by the other enzymes contain four nucleotides. Pu and Py refer to any purine and pyrimidine, respectively.



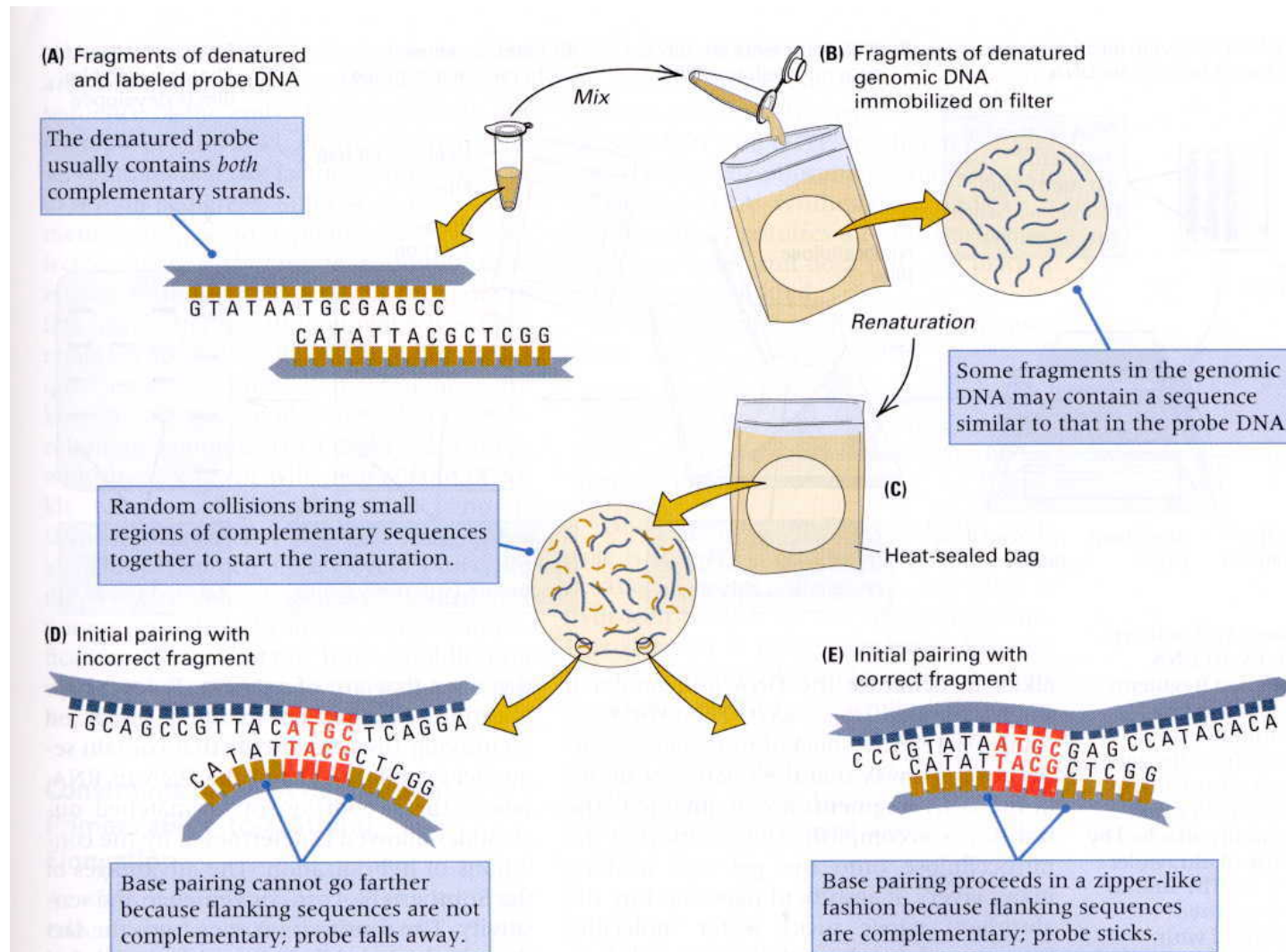
**Figure 2.12** Gel electrophoresis of DNA. Fragments of different sizes were mixed and placed in a well. Electrophoresis was in the downward direction. The DNA has been made visible by the addition of a dye (ethidium bromide) that binds only to DNA and that fluoresces when the gel is illuminated with short-wavelength ultraviolet light.





**Figure 2.14** Restriction maps of λ DNA for the restriction enzymes (A) *Eco*RI and (C) *Bam*HI. The vertical bars indicate the sites of cutting. The numbers within the arrows are the approximate lengths of the fragments in kilobase pairs (kb). (B) An electrophoresis gel of *Bam*HI and *Eco*RI enzyme digests of λ DNA. Numbers indicate fragments in order from largest (1) to smallest (6); the circled numbers on the maps correspond to the numbers beside the gel. The DNA has not undergone electrophoresis long enough to separate bands 5 and 6 of the *Bam*HI digest.

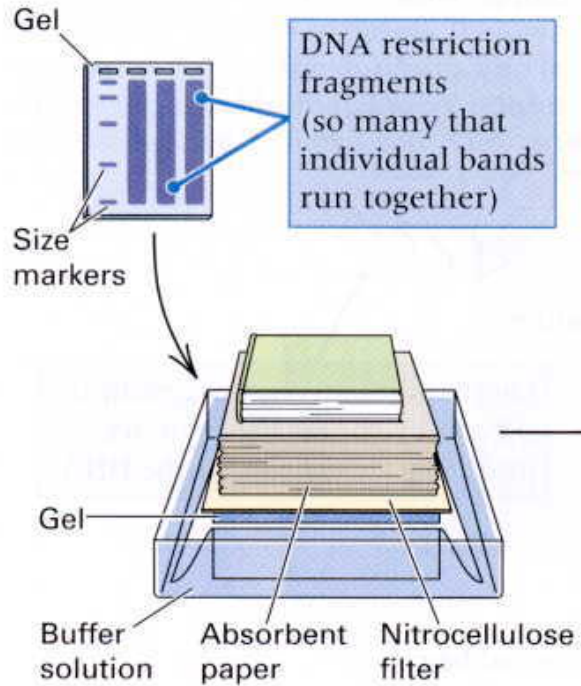
*Note:* In Problem 2 at the end of this chapter (Guide to Problem Solving), we show how to use the results of a double digest to determine the particular order of fragments for a pair of restriction enzymes.



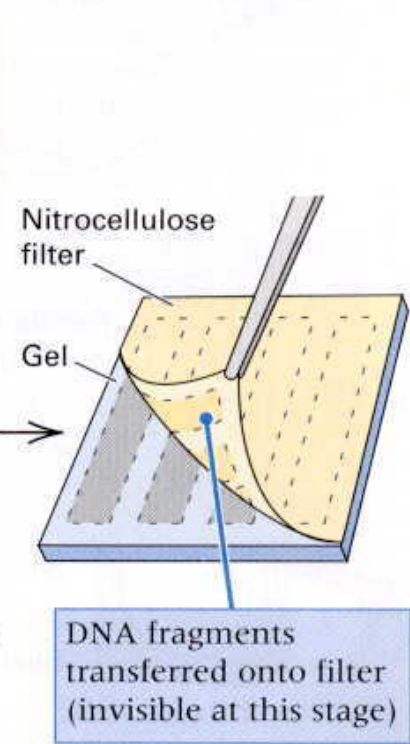
**Figure 2.16** Nucleic acid hybridization. (A) Duplex molecules of probe DNA (obtained from a clone) are denatured and (B) placed in contact with a filter to which is attached denatured strands of genomic DNA. (C) Under the proper conditions of salt concentration and temperature, short complementary stretches come together by random collision. (D) If the sequences flanking the paired region are not complementary, then the pairing is unstable and the strands come apart again. (E) If the sequences flanking the paired region are complementary, then further base pairing stabilizes the renatured duplex.



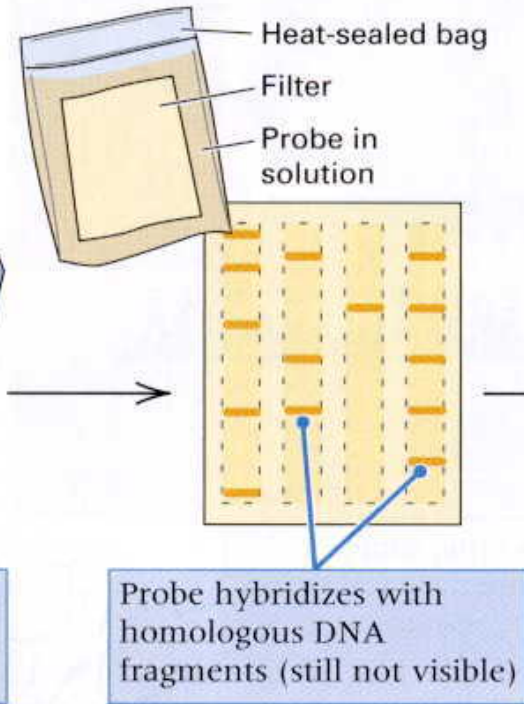
**(A)** DNA is cleaved; electrophoresis is used to separate DNA



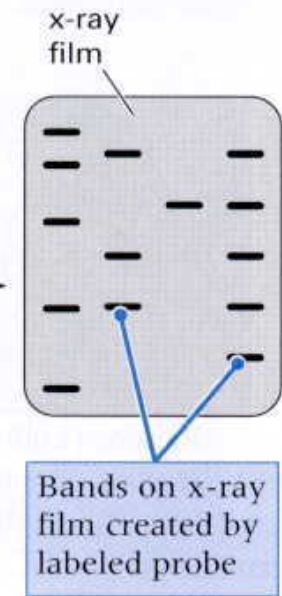
**(B)** DNA fragments are blotted onto nitrocellulose filter



**(C)** Filter is exposed to radioactive probe



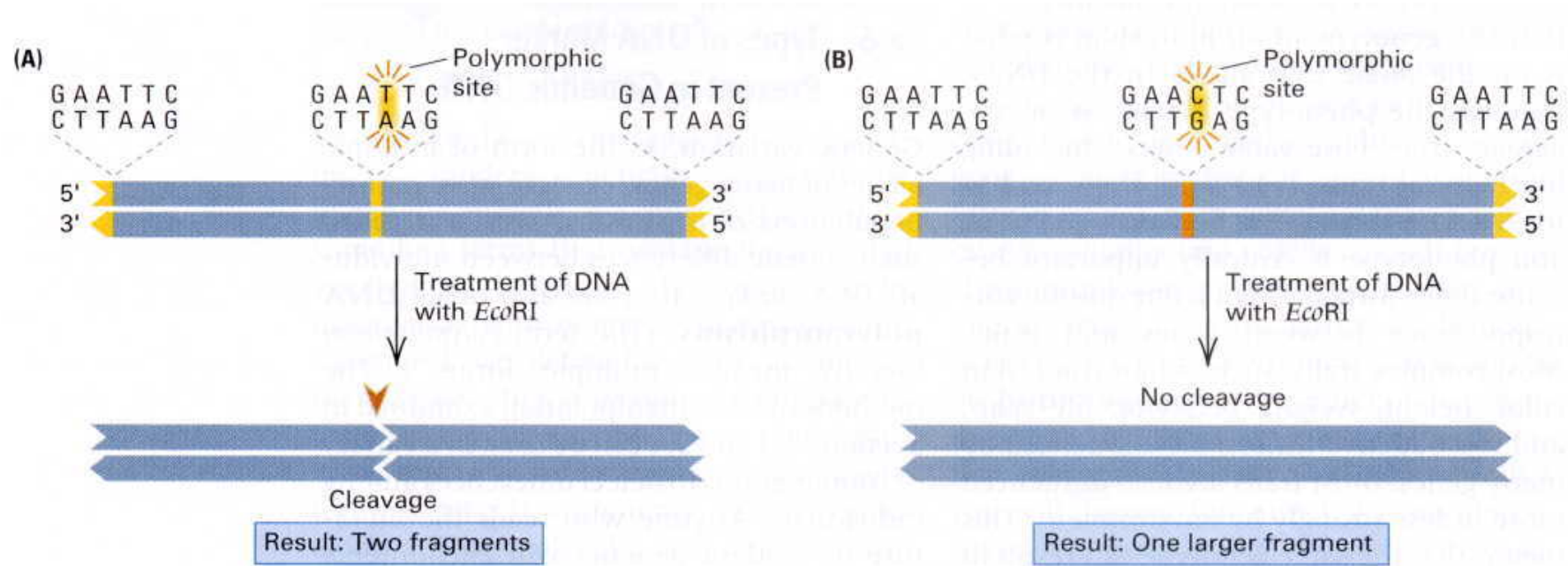
**(D)** Filter is exposed to photographic film; film is developed



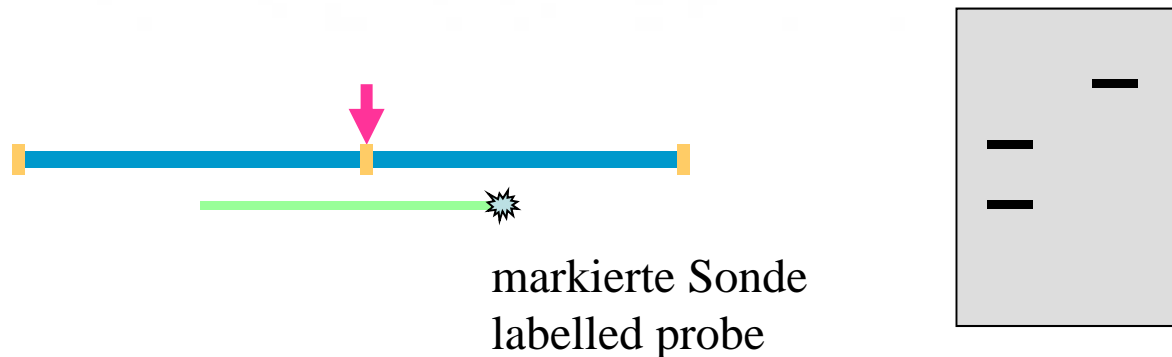




# Restriction site Polymorphism

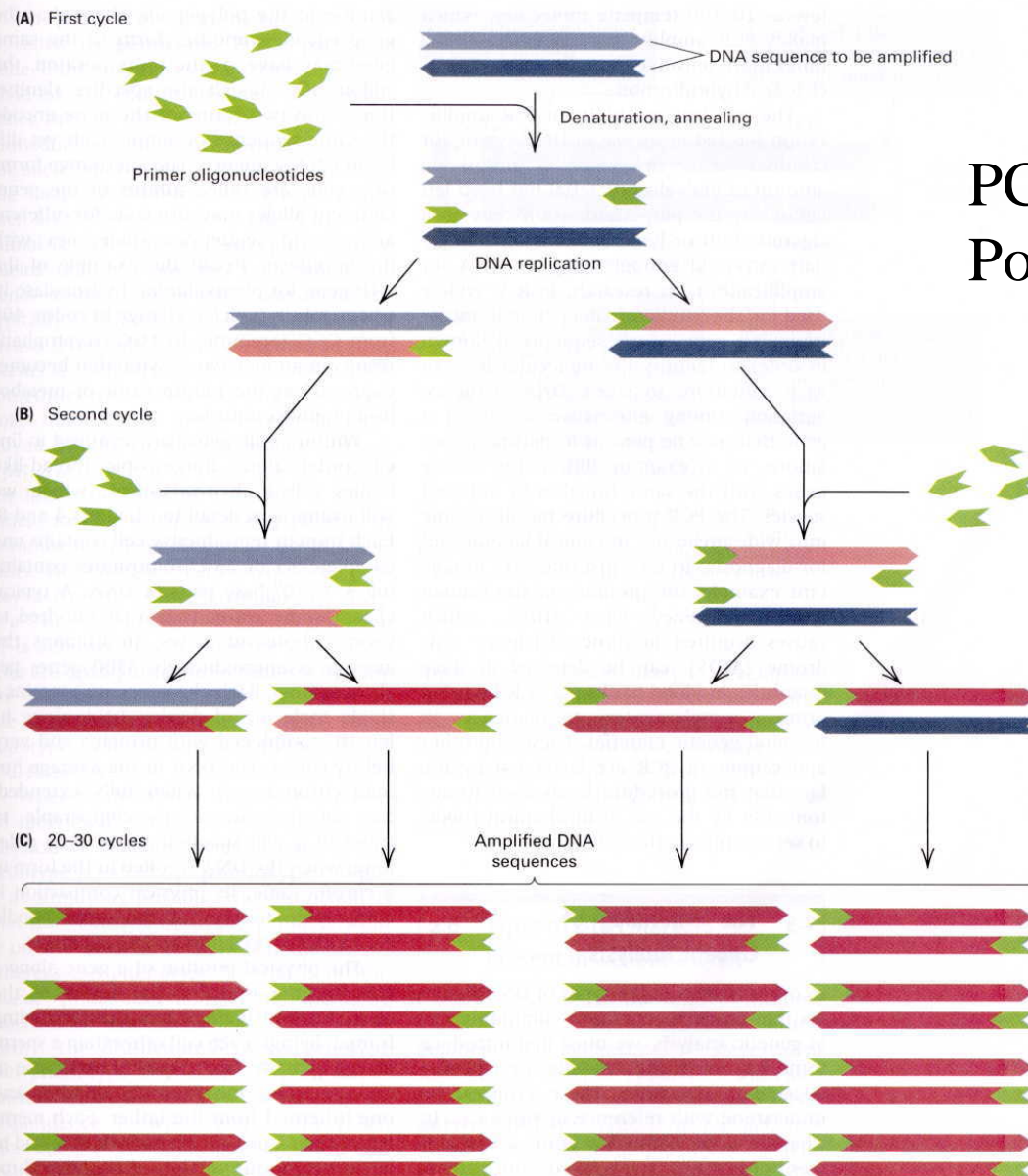


**Figure 2.23** A minor difference in the DNA sequence of two molecules can be detected if the difference eliminates a restriction site. (A) This molecule contains three restriction sites for *Eco*RI, including one at each end. It is cleaved into two fragments by the enzyme. (B) This molecule has an altered *Eco*RI site in the middle, in which 5'-GAATTC-3' becomes 5'-GAACTC-3'. The altered site cannot be cleaved by *Eco*RI, so treatment of this molecule with *Eco*RI results in one larger fragment.



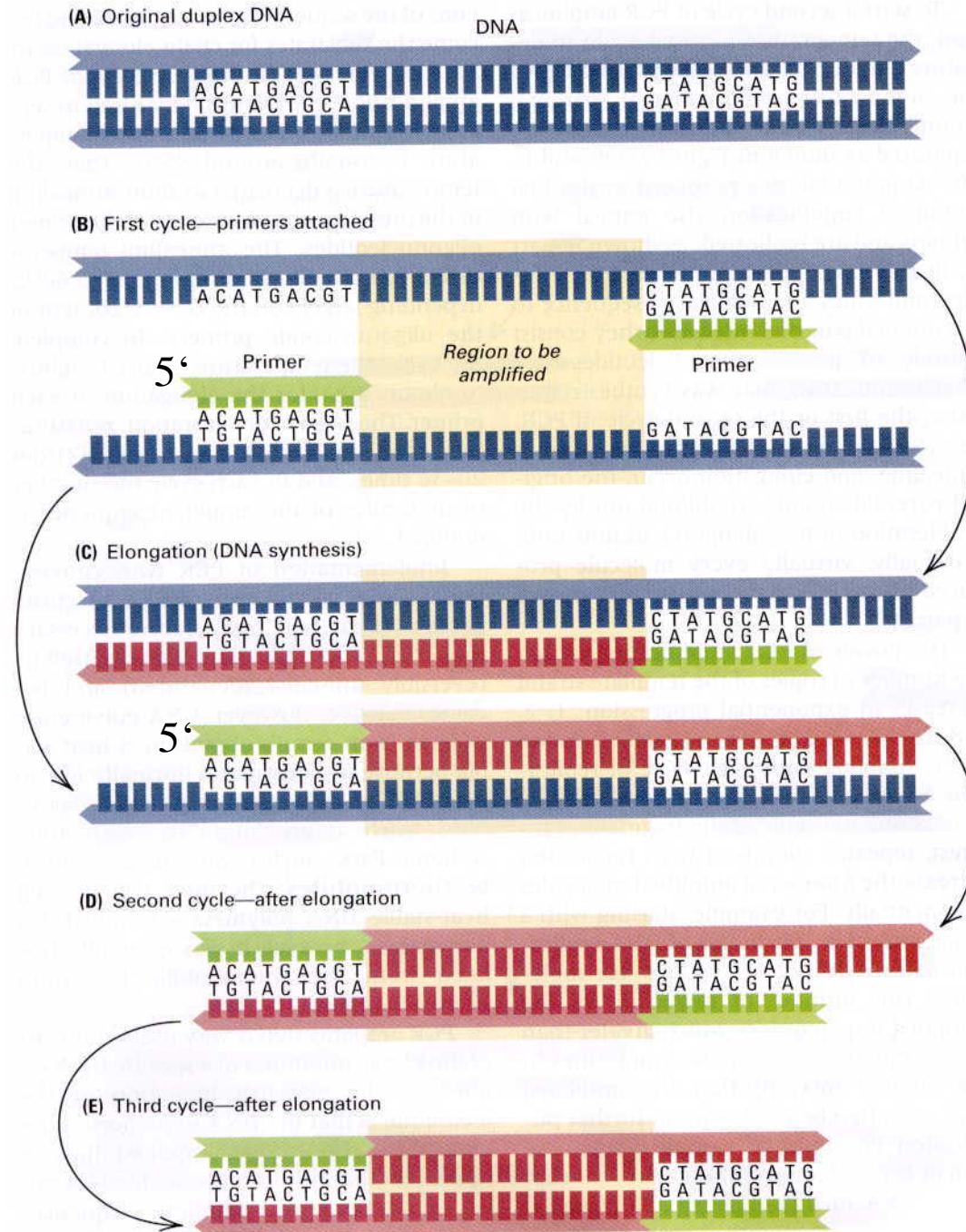


# PCR Polymerase Chain Reaction



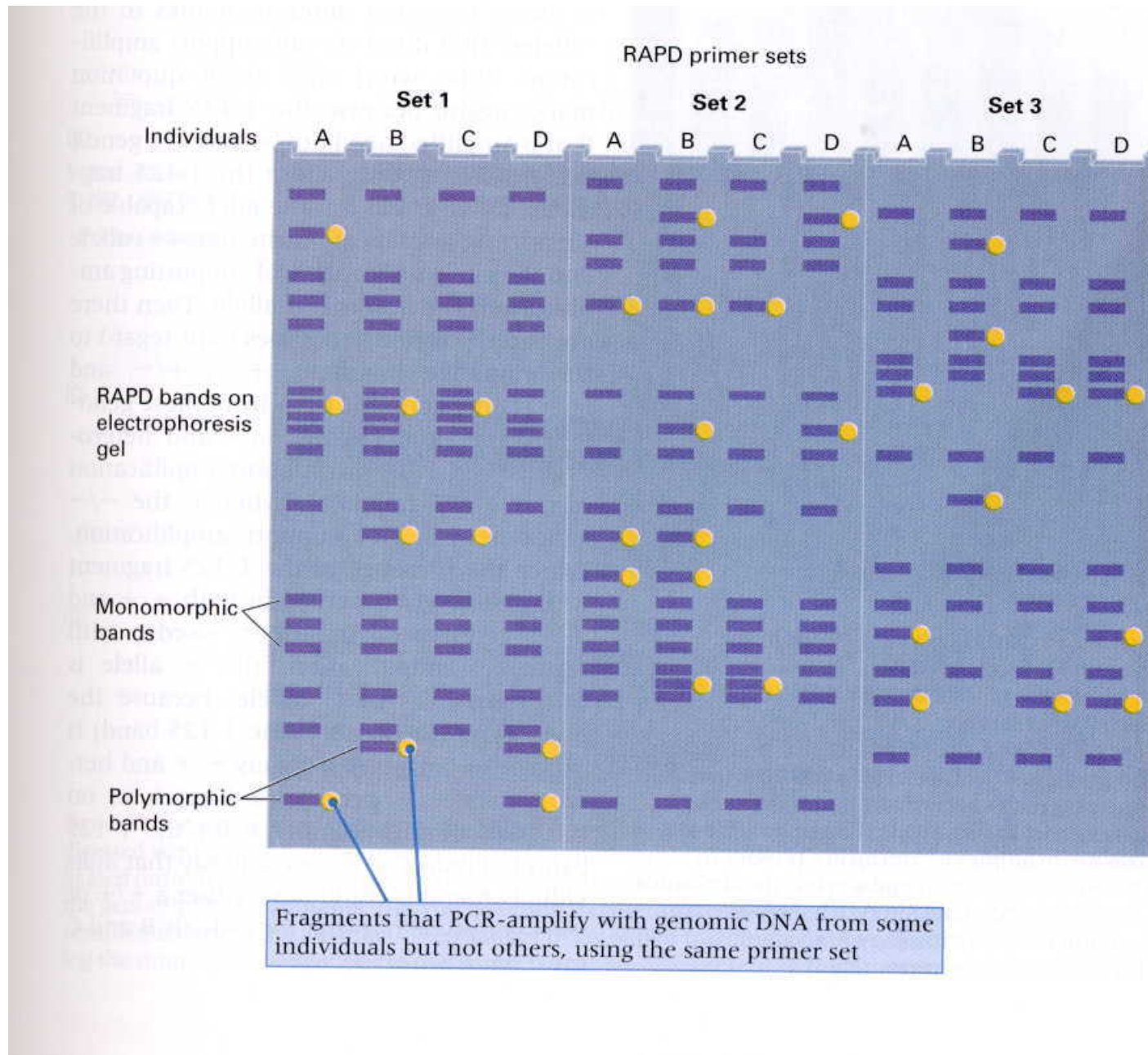
**Figure 2.21** Polymerase chain reaction (PCR) for amplification of particular DNA sequences. Only the region to be amplified is shown. Oligonucleotide primers (green) that are complementary to the ends of the target sequence (blue) are used in repeated rounds of denaturation, annealing, and DNA replication. Newly replicated DNA is shown in pink. The number of copies of the target sequence doubles in each round of replication, eventually overwhelming any other sequences that may be present.





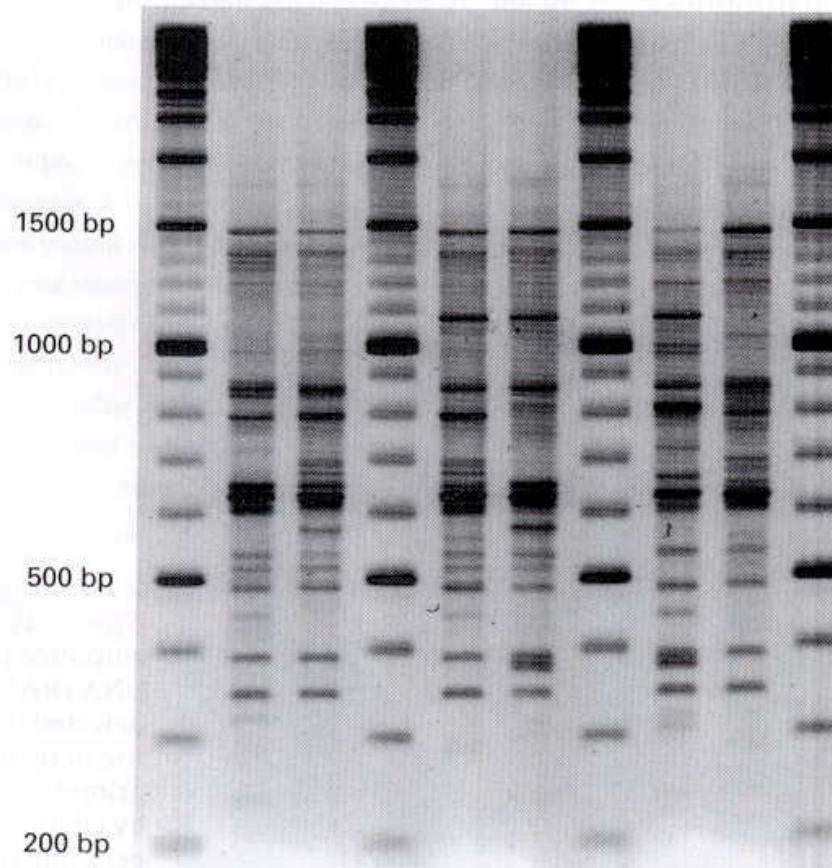
**Figure 2.20** Role of primer sequences in PCR amplification. (A) Target DNA duplex (blue), showing sequences chosen as the primer-binding sites flanking the region to be amplified. (B) Primer (green) bound to denatured strands of target DNA. (C) First round of amplification. Newly synthesized DNA is shown in pink. Note that each primer is extended *beyond* the other primer site. (D) Second round of amplification (only one strand shown); in this round, the newly synthesized strand terminates at the opposite primer site. (E) Third round of amplification (only one strand shown); in this round, both strands are truncated at the primer sites. Primer sequences are normally about twice as long as shown here.

# PCR Polymerase Chain Reaction



**Figure 2.25** Random amplified polymorphic DNA (RAPD) is detected through the use of relatively short primer sequences that, by chance, match genomic DNA at multiple sites that are close enough together to support PCR amplification. Genomic DNA from a single individual typically yields many bands, only some of which are polymorphic in the population. Different sets of primers amplify different fragments of genomic DNA.



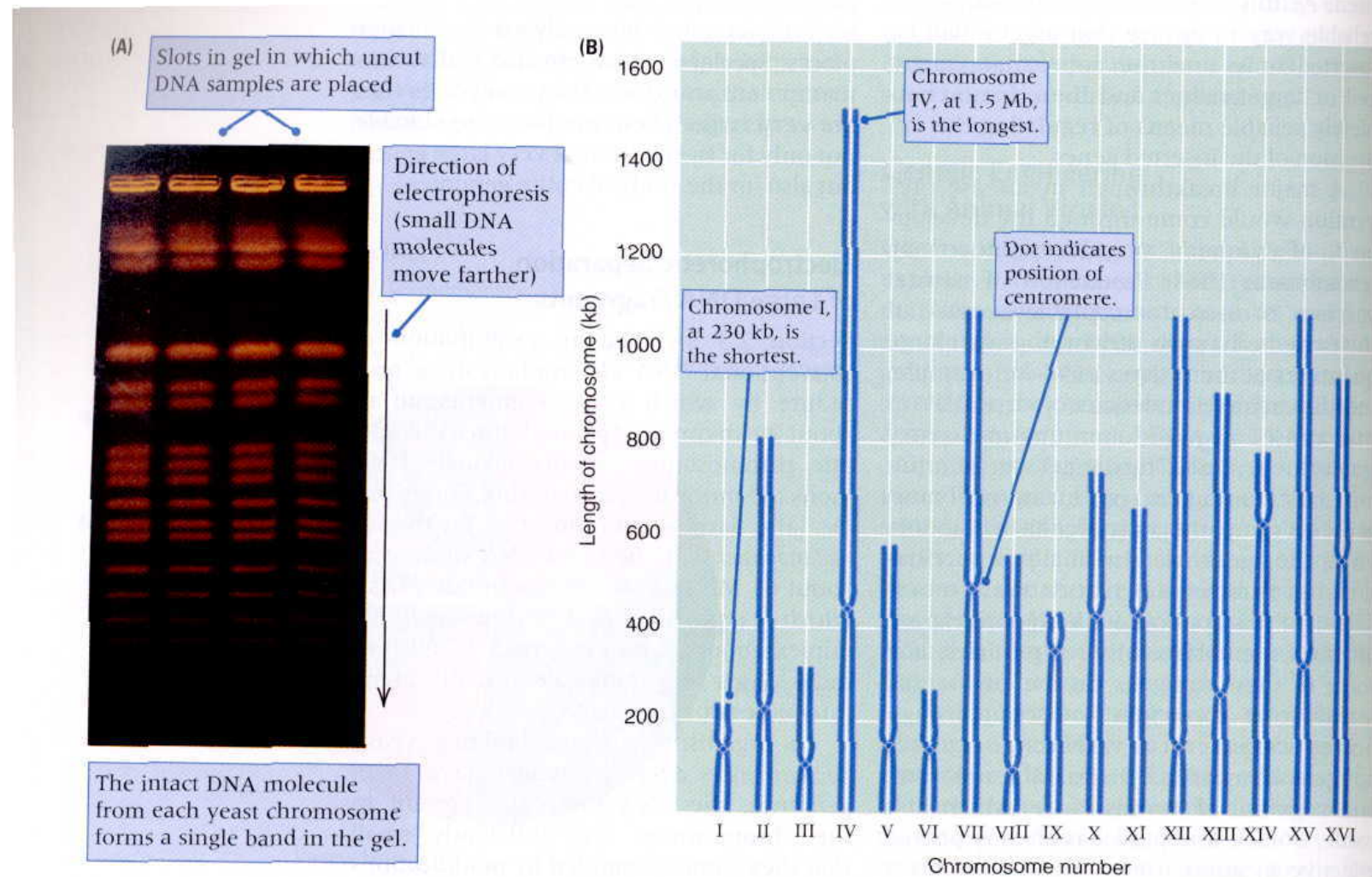


**Figure 2.26** RAPD polymorphisms in the stoneroller fish (*Camptostoma anomalum*) trapped in tributaries of the Great Miami River in Ohio. Each pair of samples is flanked by a lane containing DNA size standards; in these lanes, the smallest DNA fragment is 100 base pairs (bp), and each successively larger fragment increases in size by 100 bp. Fragments whose sizes are multiples of 500 bp are present in greater concentration and so yield darker bands. [Courtesy of Michael Simonich, Manju Garg, and Ana Braam (Pathology Associates International, Cincinnati, Ohio).]

- Short Primers
- Bind to many sequences within a genome
- Set of amplified fragments depending on sequence # defined priming sites



## Pulsed Field Gel Electrophoresis

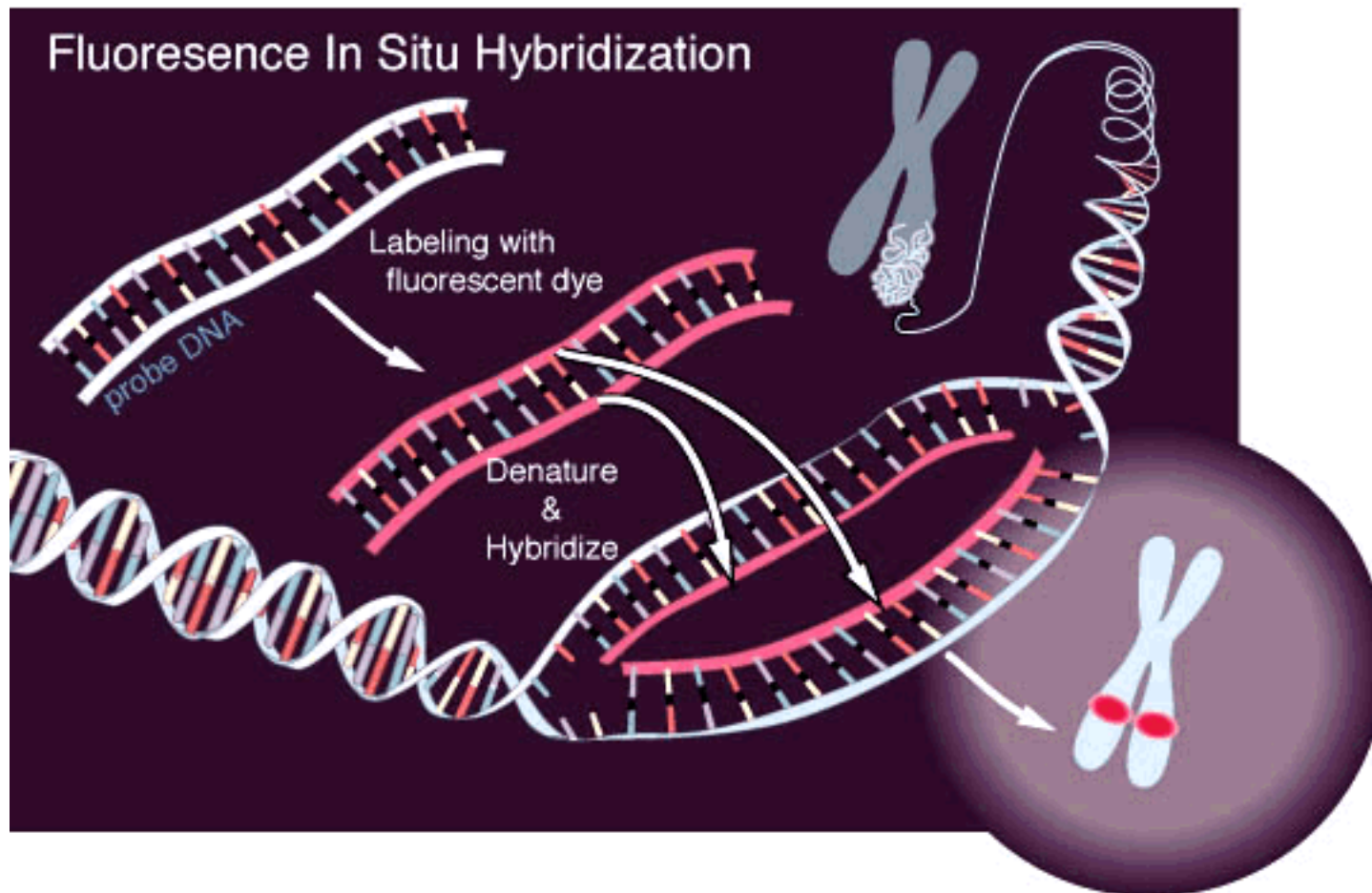


**Figure 13.23** (A) Separation of chromosomes of the yeast *Saccharomyces cerevisiae* by pulsed-field gel electrophoresis, in which there is regular change in the orientation of the electric field. (B) Histogram of sizes of the 16 yeast chromosomes. [©1988 BioRad Laboratories, Inc.; permission to use this image has been granted by Bio-Rad Laboratories Inc.]



# In situ Hybridization

## FISH - (Fluorescence In Situ Hybridization)

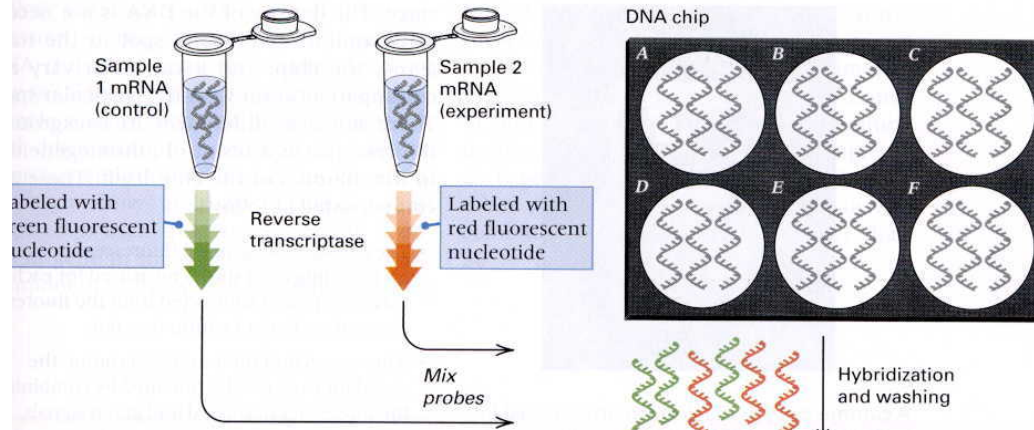






# DNA Microarrays

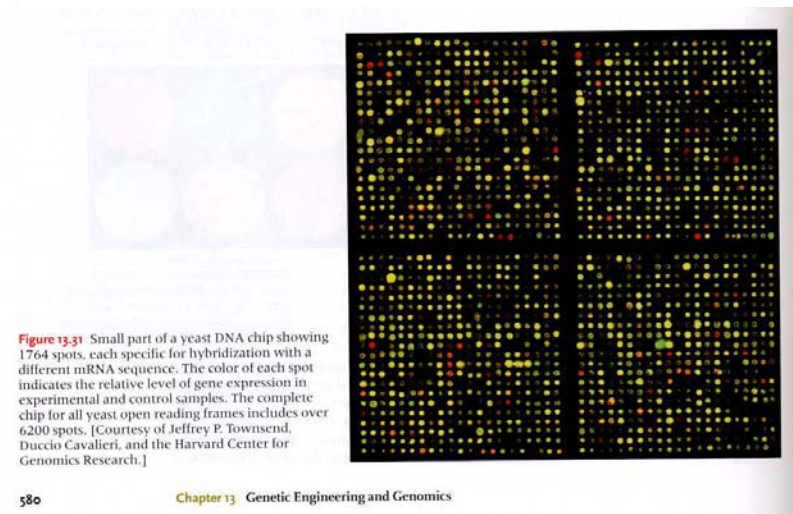
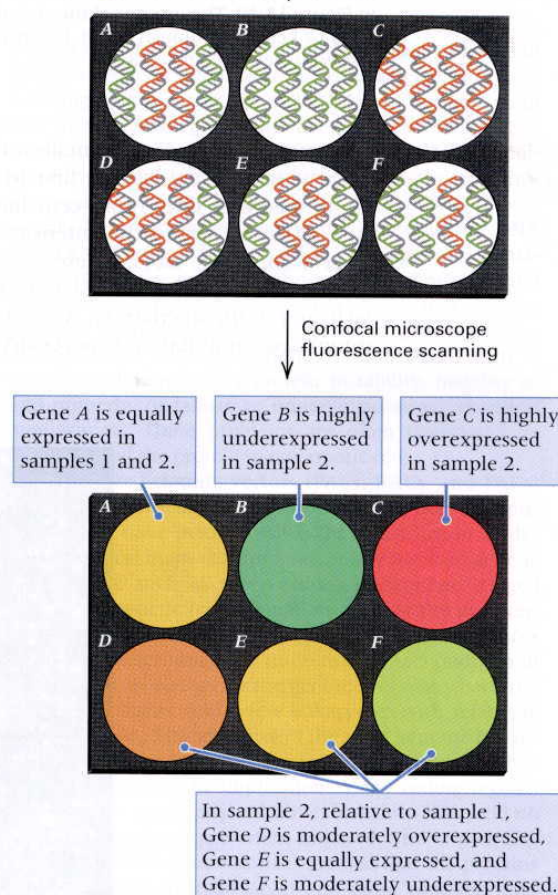
(DNA Chips)



**Figure 13.30** Principle of operation of one type DNA chip. At the top are dried microdrops, each of which contains immobilized DNA strands from a different gene (*A–F*). These are hybridized with a mixture of fluorescence-labeled DNA samples obtained by reverse transcription of cellular mRNA. Competitive hybridization of red (experimental) and green (control) label is proportional to the relative abundance of each mRNA species in the samples. The relative levels of red and green fluorescence of each spot are assayed by confocal scanning and displayed as a single color. Red or orange indicates overexpression in the experimental sample, green or yellow-green underexpression in the experimental sample, and yellow equal expression.

Gene *A* serves as a probe for a different gene, *A* through *F*. At the left is shown the experimental protocol. Messenger RNA is first extracted from both the experimental and the control samples. This material is then subjected to one or more rounds of reverse transcription, as described in Section 13.2. In the experimental material (sample 2), the primer for reverse transcription includes a red fluorescent label; and in the control material (sample 1), the primer includes a green fluorescent label. When a sufficient quantity of labeled DNA strands have accumulated, the fluorescent samples are mixed and hybridized with the DNA chip.

The result of hybridization is shown in the middle part of Figure 13.30. Because the samples are mixed, the hybridization is



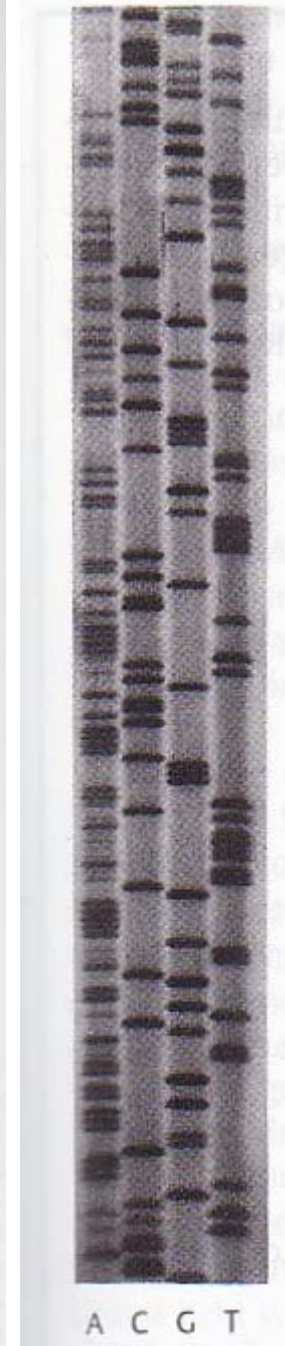
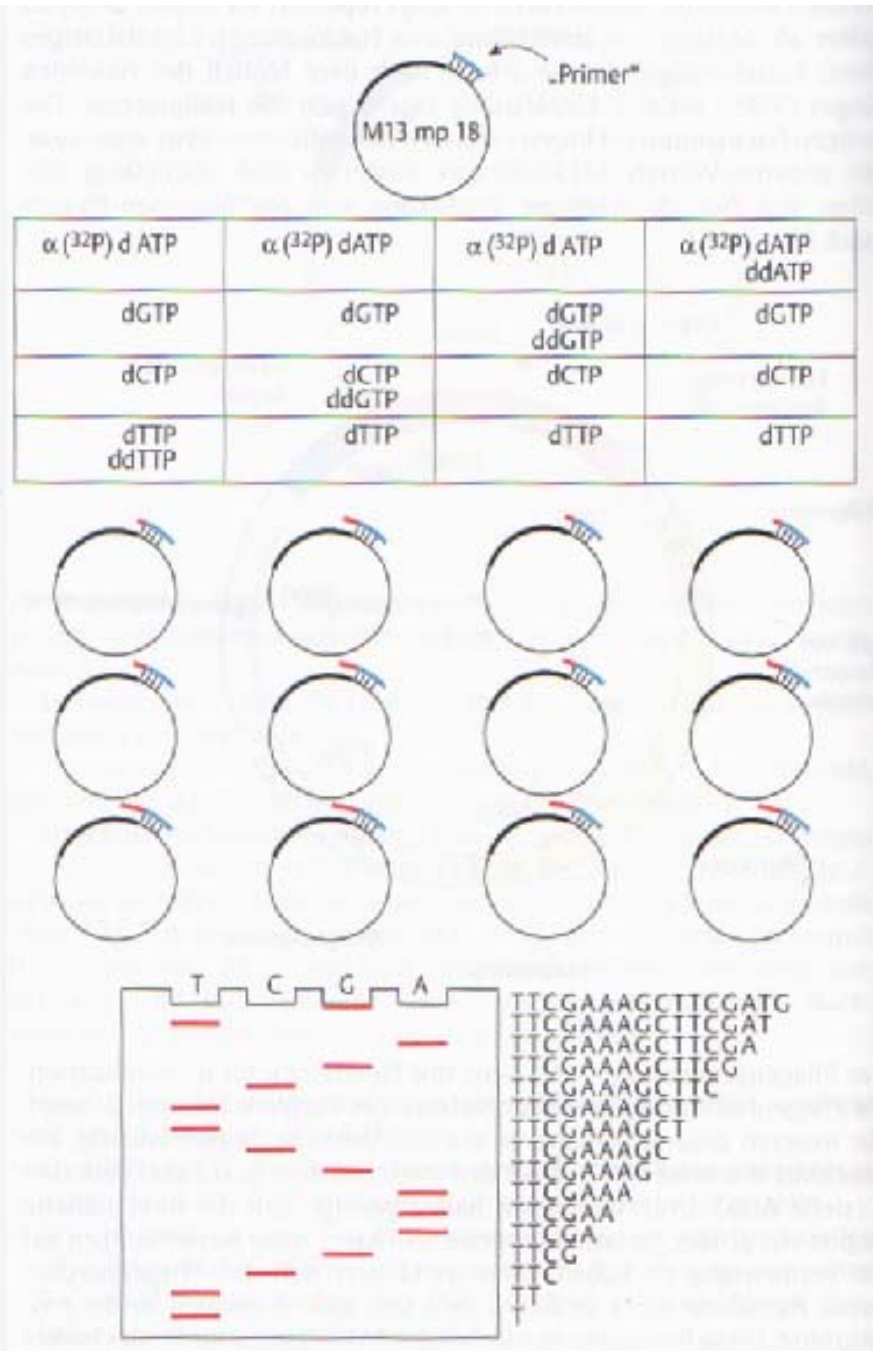




# DNA Sequencing

Abb. 9.15 Prinzip der Sequenz-Reaktion nach der Didesoxy- oder Kettenabbruch-Methode.

- Vier Ansätze werden parallel vorbereitet. Jeder Ansatz enthält ein radioaktiv oder anders markiertes Nucleotid (hier  $\alpha$ - $^{32}\text{P}$ -dATP) und die drei anderen nichtmarkierten Desoxynucleosid-Triphosphate. Jeder Ansatz enthält zudem ein Didesoxynucleotid, entweder ddTTP, ddCTP, ddGTP oder ddATP. Je nach experimenteller Situation wird ein Verhältnis von 1/50, 1/100 oder 1/200 von ddNTP zu dNTP gewählt.
- Nach Zusatz der DNA-Polymerase beginnt die Komplementärstrang-Synthese. Sie kommt zum Halt, wenn zufällig ein Didesoxynucleotid statt des normalen Desoxynucleotids in das aktive Zentrum der DNA-Polymerase gelangt. Im ersten Ansatz wird das der Fall sein, wenn die Sequenz des Matrizenstranges den Einbau eines Thymin-Nucleotids verlangt. Mit anderen Worten, im ersten Ansatz erhält man eine Kollektion von DNA-Fragmenten, deren Längen die Positionen von Adenin-Resten im Matrizen-Strang wiedergeben. Entsprechendes gilt für die Längen der Syntheseprodukte in den anderen Ansätzen.
- Der kritische methodische Vorgang ist die genaue Auftrennung der Syntheseprodukte. Dazu werden Matrize und synthetisierte Komplementärstränge durch Denaturierung voneinander gelöst und auf dünnen, besonders zubereiteten Polyacrylamid-Gelen analysiert. Die Markierung der Syntheseprodukte ermöglicht ihre Darstellung durch Autoradiographie oder geeignete Färbemethoden. Die Auswertung der Gel-Elektrophorese ist hier gezeigt. Durch das kleinste, am weitesten gewanderte Fragment wird das erste Nucleotid in der Sequenz angezeigt, durch das nächst größte Fragment das zweite usw. [nach 13].





## Next Generation Sequencing – Deep Sequencing

Sequencing platform	ABI3730xl Genome Analyzer	Roche (454) FLX	Illumina Genome Analyzer	ABI SOLiD
Sequencing chemistry	Automated Sanger sequencing	Pyrosequencing on solid support	Sequencing-by-synthesis with reversible terminators	Sequencing by ligation
Template amplification method	In vivo amplification via cloning	Emulsion PCR	Bridge PCR	Emulsion PCR
Read length	700–900 bp	200–300 bp	32–40 bp	35 bp
Sequencing throughput	0.03–0.07 Mb/h	13 Mb/h	25 Mb/h	21–28 Mb/h

### Applications:

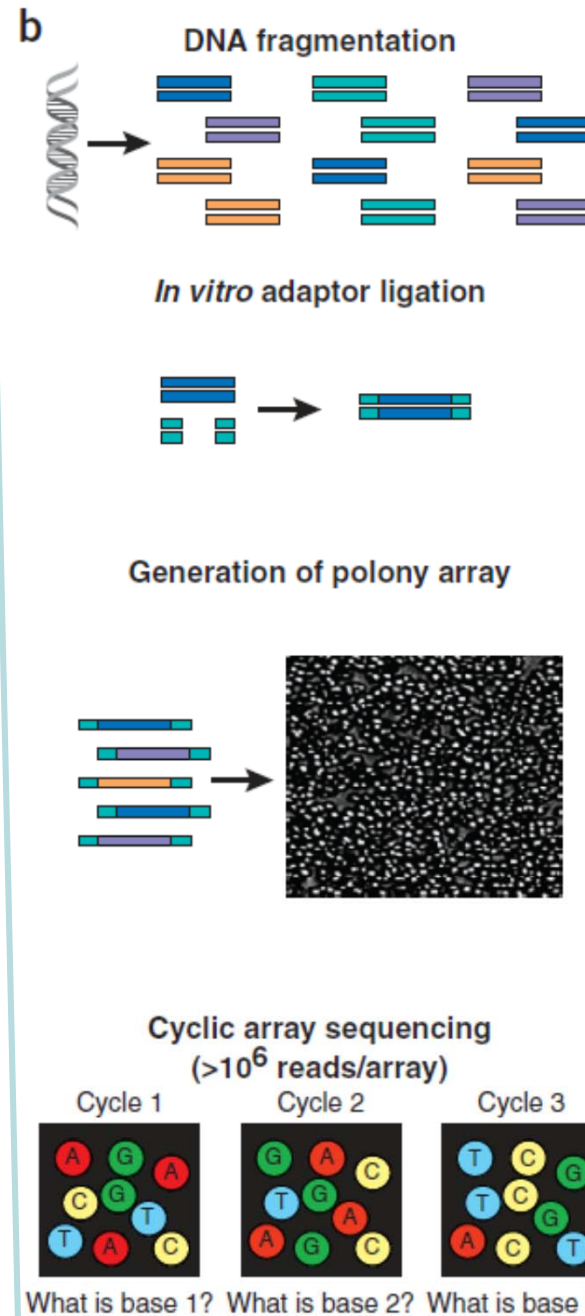
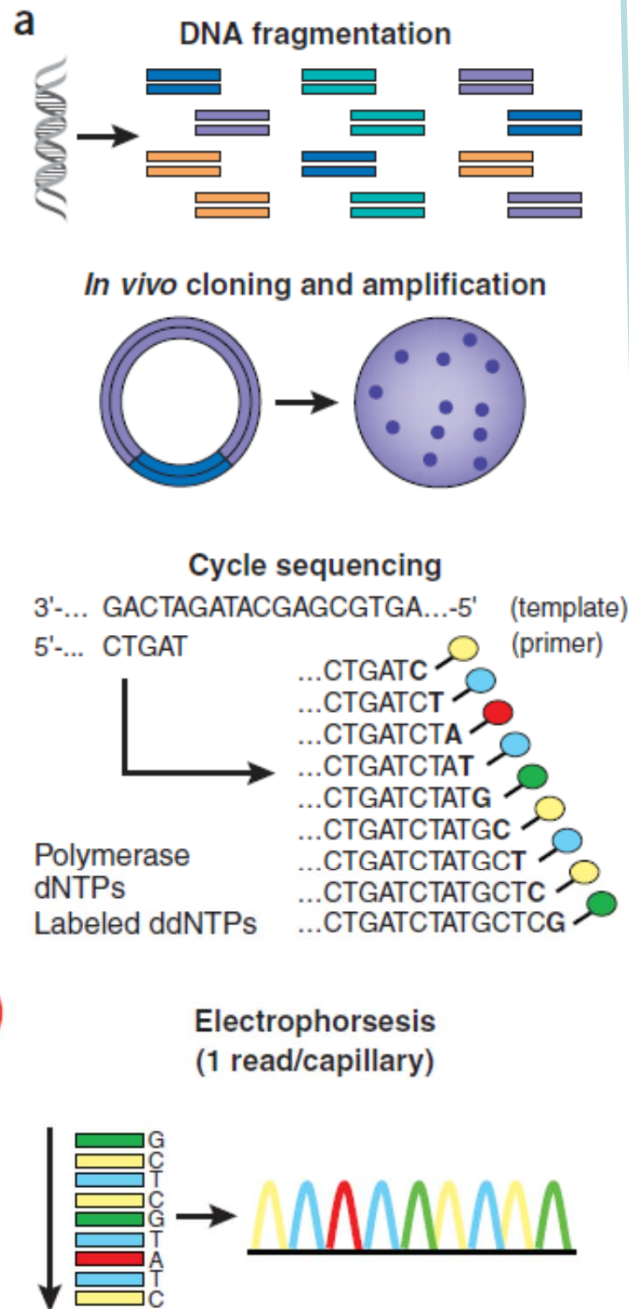
Genome sequencing, Metagenome Sequencing,  
 Transcriptome Sequencing (incl. Non-coding RNA)  
 Gene Expression profiling

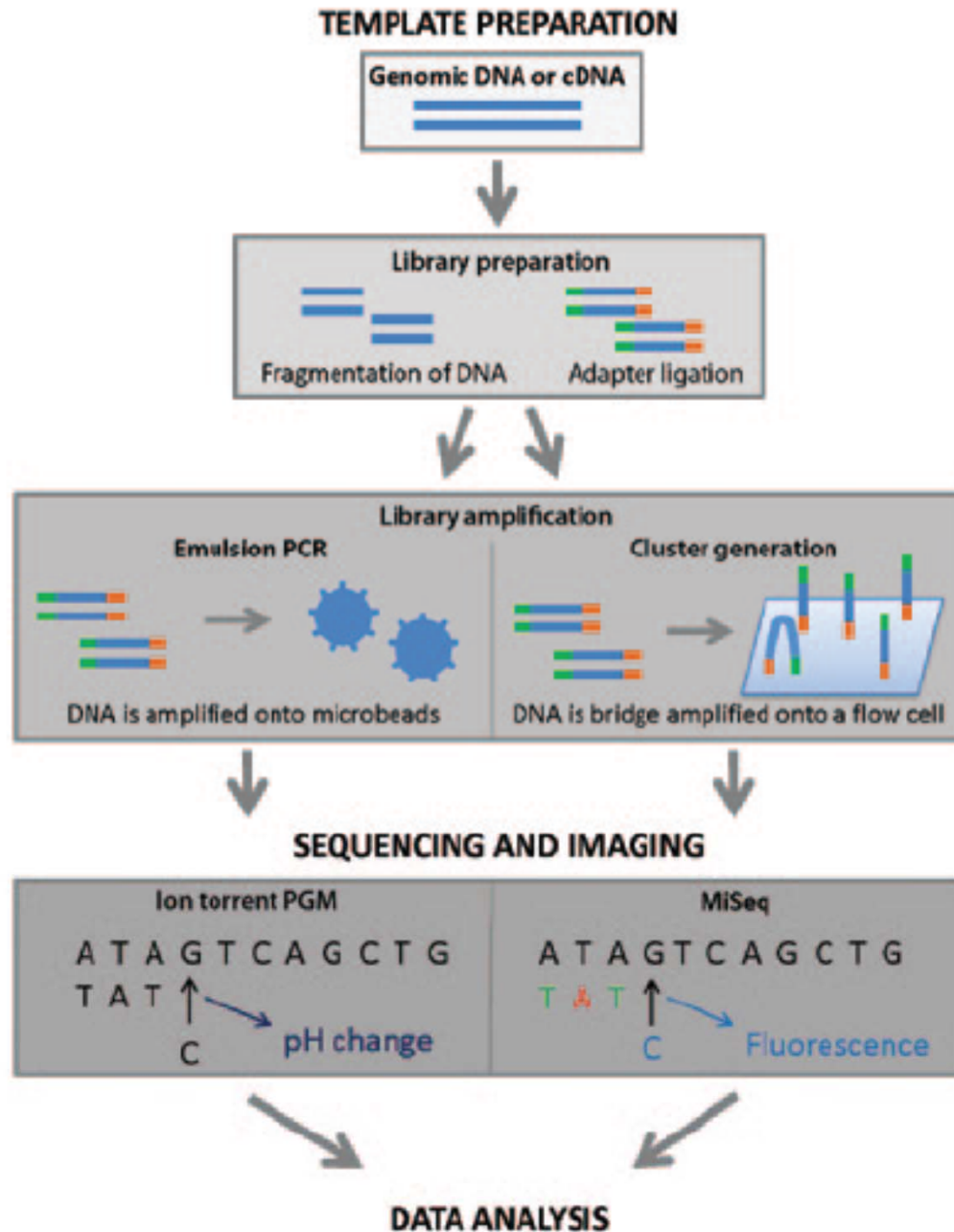


	APPLICATION	HISEQ 2500	MISEQ	PACBIO RS II	GS FLX++	GS JUNIOR+	ION PROTON
GENOME SEQ	De novo sequencing of bacterial & fungal genomes	✓✓	✓✓✓	✓✓	✓✓✓		
	De novo sequencing of higher eukaryotic genomes	✓✓✓		✓	✓		
	Resequencing of genomes	✓✓✓	✓✓✓				
TRANSCRIP- TOME SEQ	De novo transcriptome sequencing	✓✓	✓✓✓		✓✓✓		✓
	Expression profiling	✓✓✓	✓				
EXOME & AMPLICONS	Ultra deep amplicon sequencing	✓	✓✓✓		✓✓✓	✓✓✓	✓✓
	Exome sequencing	✓✓✓	✓✓				✓✓

Our ratings are based on factors such as data output, read length, turnaround time, data quality and cost efficiency.

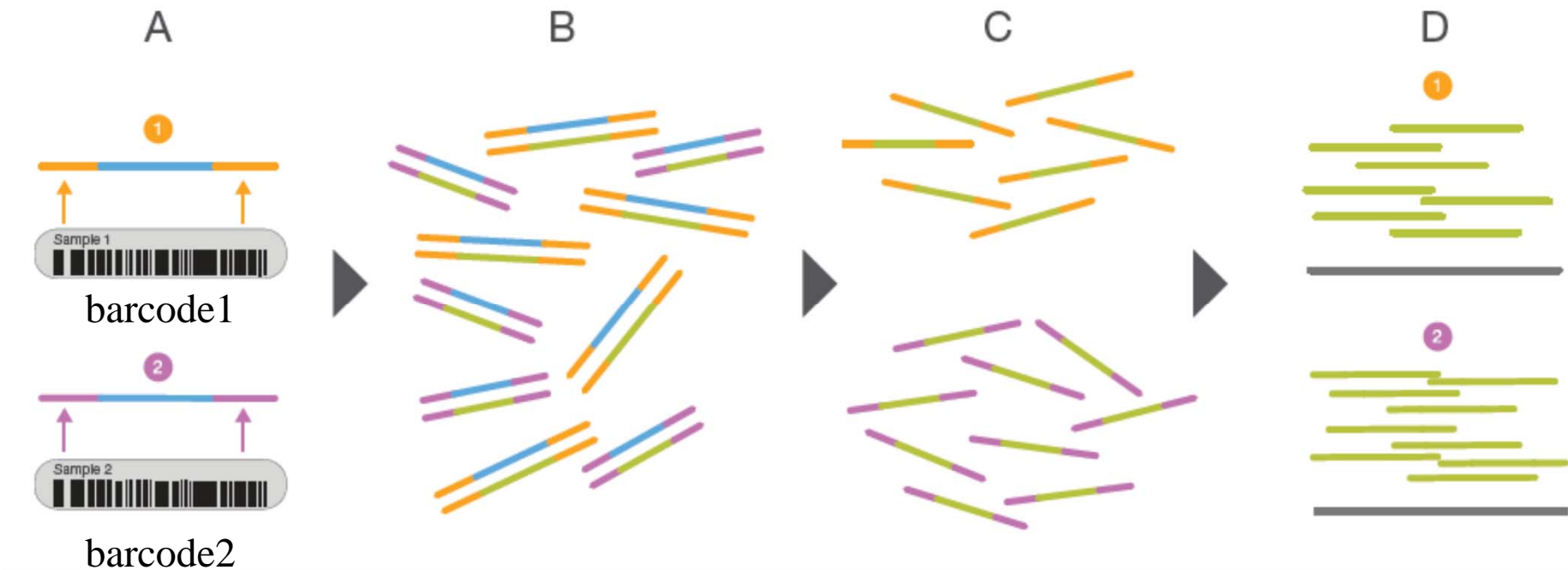
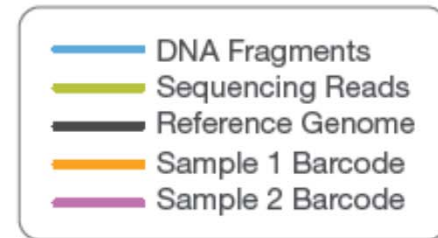






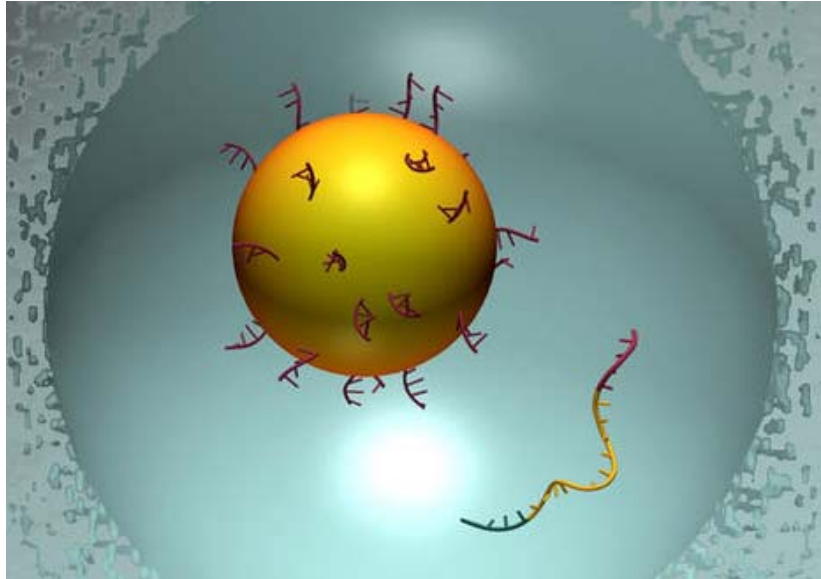


# Sample multiplexing

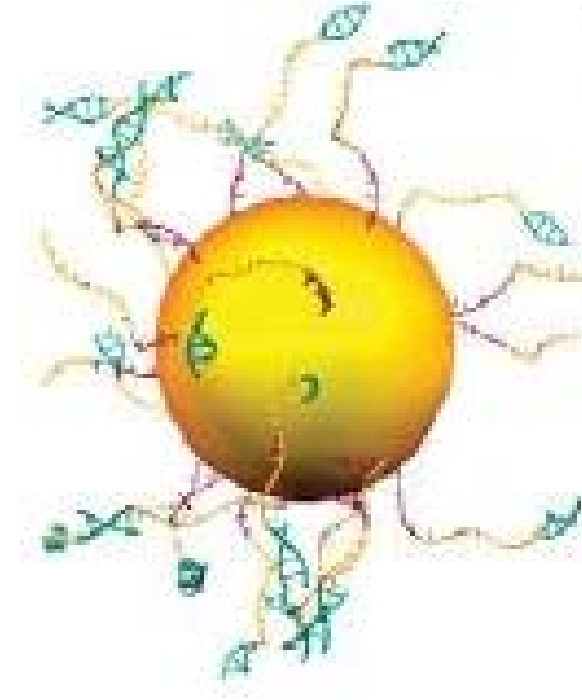


Codes defined by sequence of adaptor

# The Roche 454/GS FLX Sequencing Technology

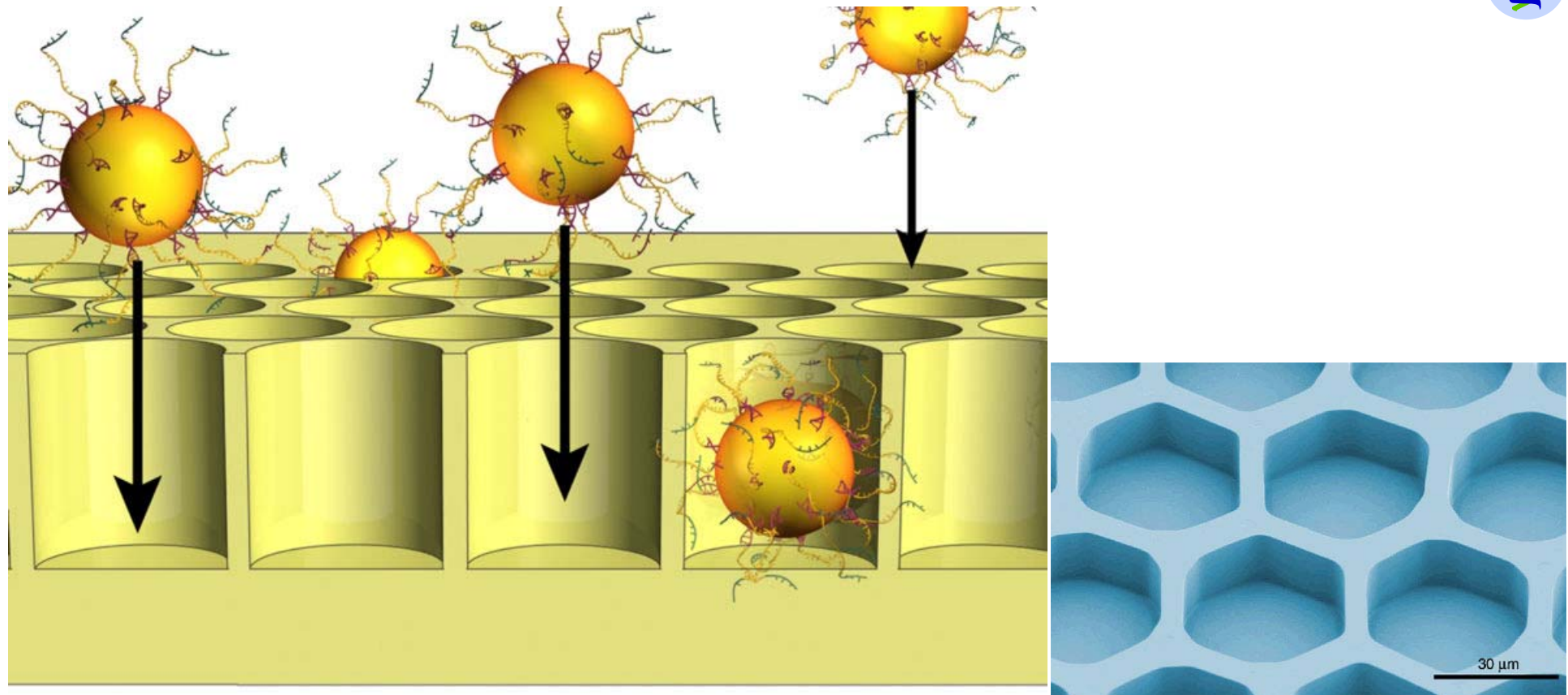


Aided by the adaptors individual fragments are captured on their own unique beads. A bead and the bound fragment together with a water-in-oil emulsion form a microreactor so that each fragment can be amplified without contamination via the so called emulsion PCR (emPCR). The entire fragment collection is amplified in parallel.



The emPCR amplifies each fragment several million times. After amplification the emulsion shell is broken and the clonally amplified beads are ready for loading onto the fibre-optic PicoTiterDevice for sequencing

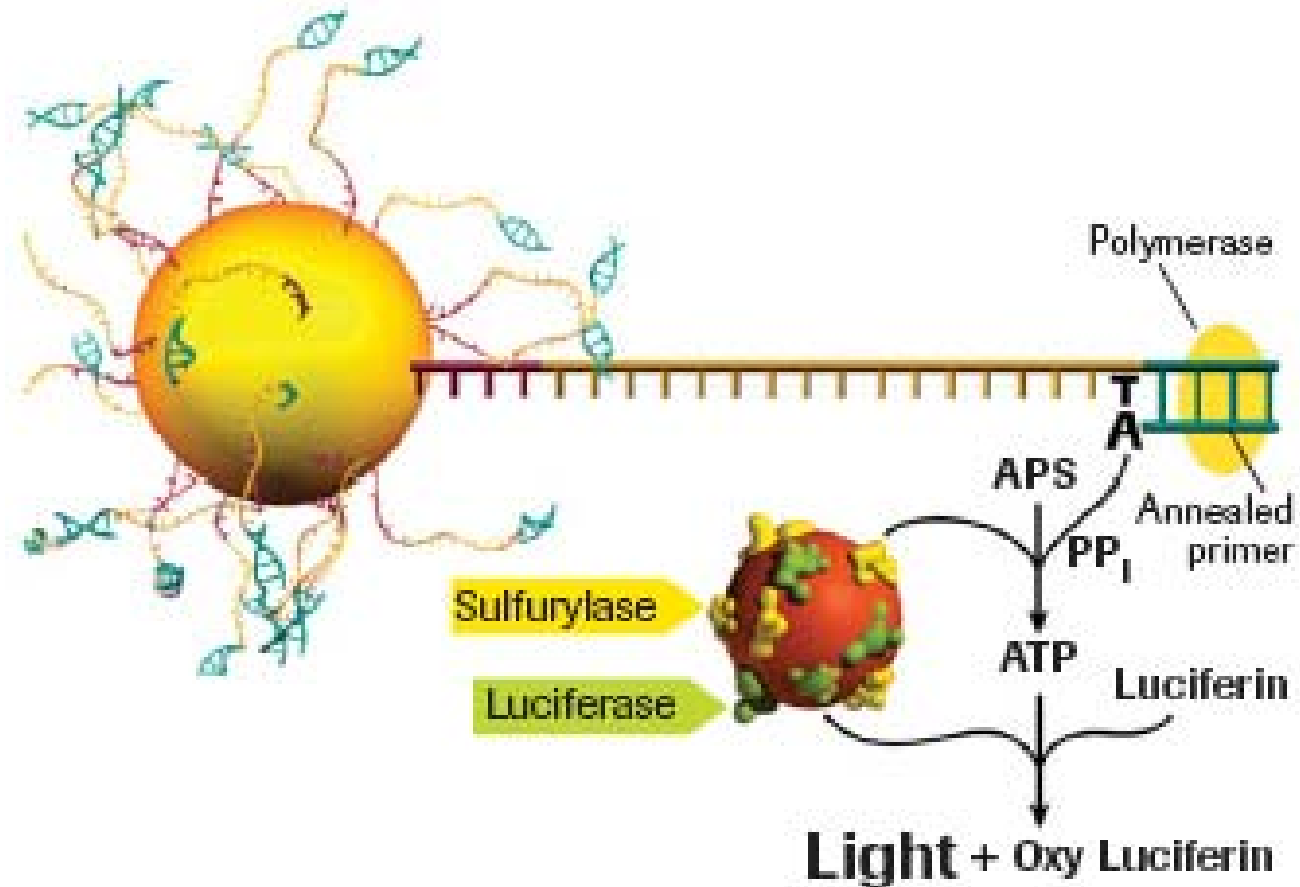




**Figure 1. Scanning electron micrograph of etched well in 454 PicoTiter sequencing plate.**

454's technology is based on performing hundreds of thousands of simultaneous sequencing reactions in 75 picoliter ( $44 \mu\text{m}$ ) wells. All molecular biology reactions—DNA amplification, sequencing by synthesis, and signal light generation—occur in a single well.

# The Roche 454/GS FLX Sequencing Technology



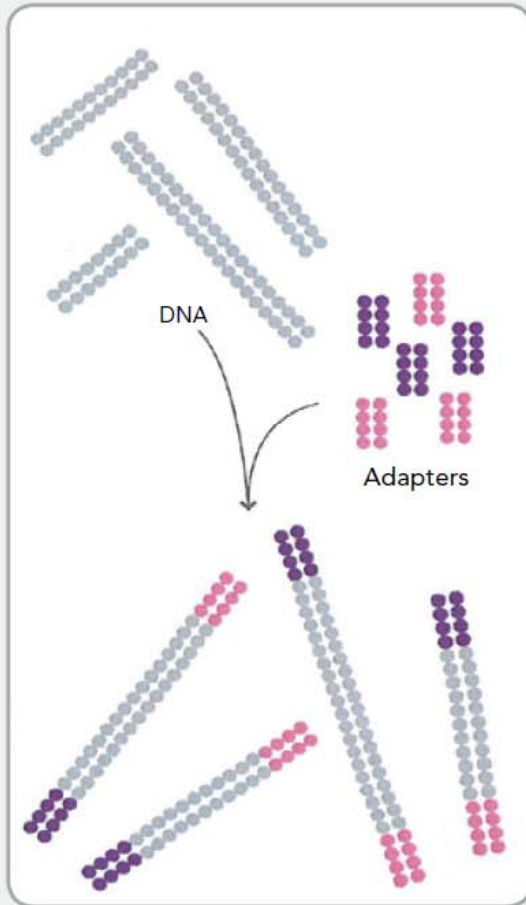
Sequencing is accomplished by synthesizing the complementary strands of the bead attached templates. In a number of cycles the four bases (ATGC) are sequentially washed over the PicoTiterPlate. The incorporation of a new base is associated with the release of inorganic pyrophosphate starting a chemical cascade. This results in the generation of a light signal which is captured by a CCD camera.

# DNA Sequencing with Illumina (Solexa®) Technology



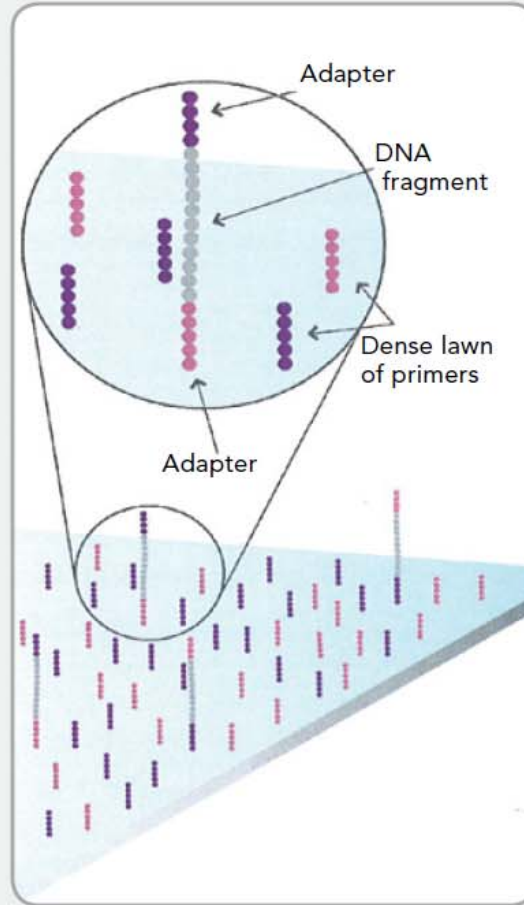
FIGURE 2: SEQUENCING TECHNOLOGY OVERVIEW

### 1. PREPARE GENOMIC DNA SAMPLE



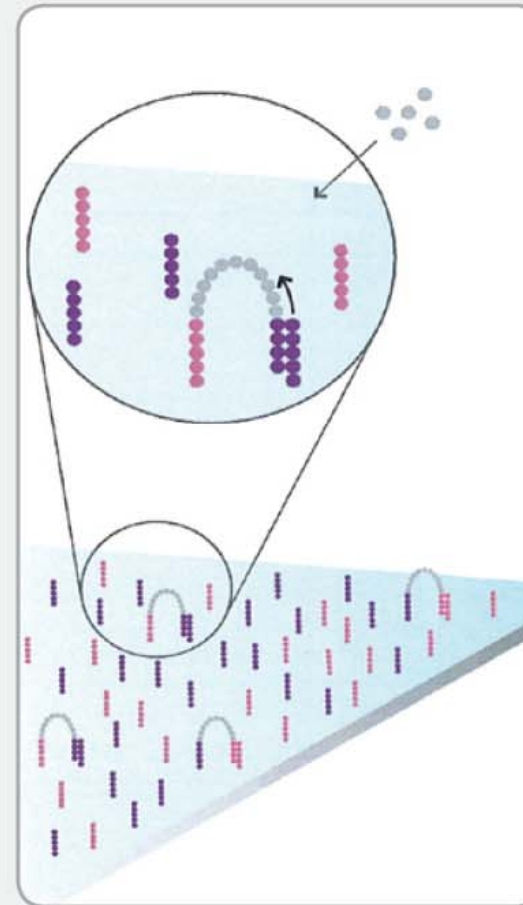
Randomly fragment genomic DNA and ligate adapters to both ends of the fragments.

### 2. ATTACH DNA TO SURFACE

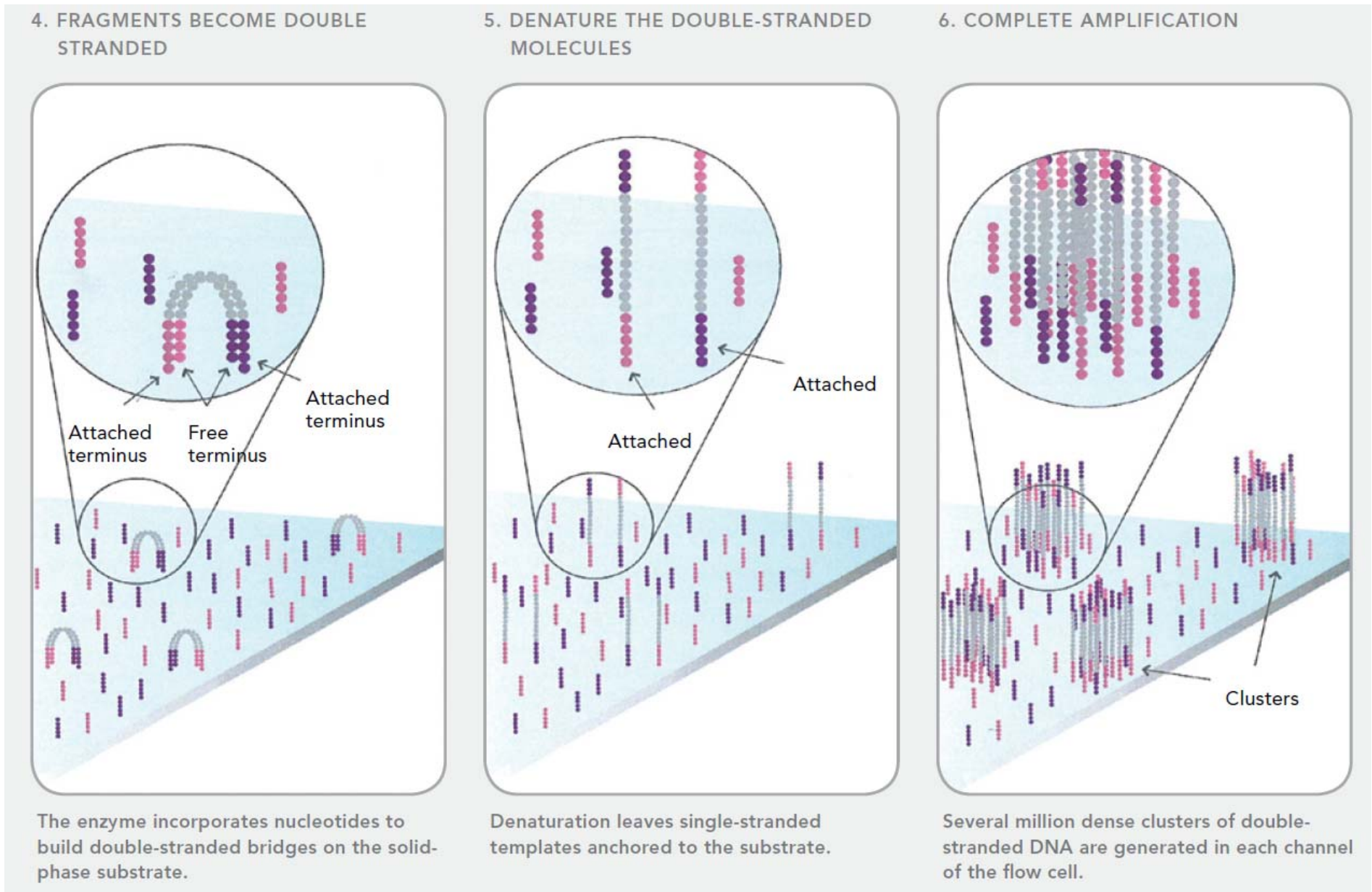


Bind single-stranded fragments randomly to the inside surface of the flow cell channels.

### 3. BRIDGE AMPLIFICATION



Add unlabeled nucleotides and enzyme to initiate solid-phase bridge amplification.

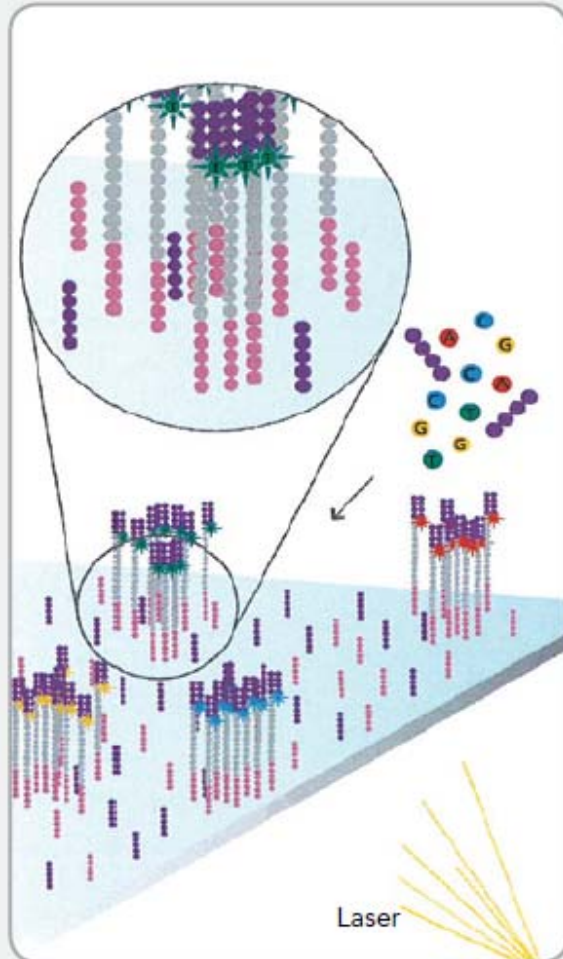




# DNA Sequencing with Illumina (Solexa®) Technology

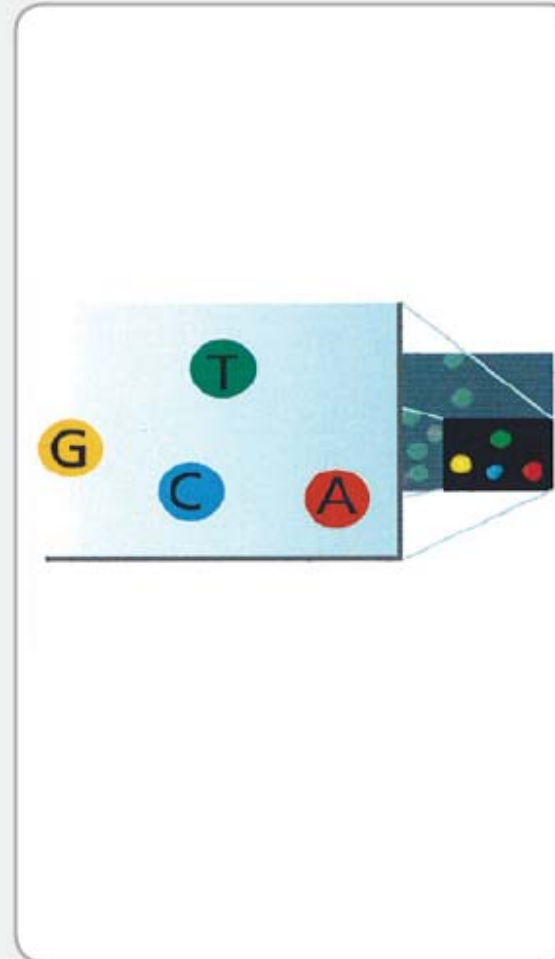


## 7. DETERMINE FIRST BASE



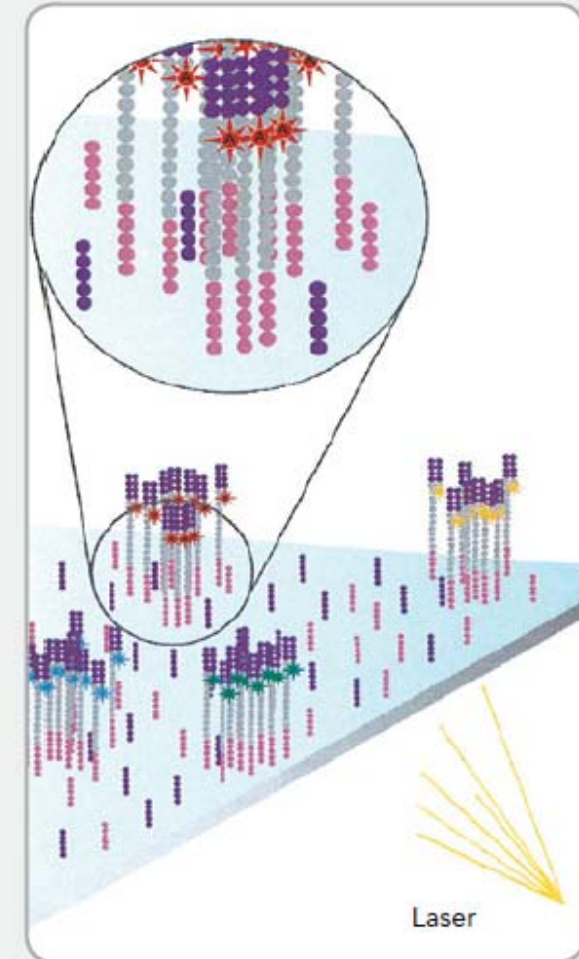
First chemistry cycle: to initiate the first sequencing cycle, add all four labeled reversible terminators, primers and DNA polymerase enzyme to the flow cell.

## 8. IMAGE FIRST BASE



After laser excitation, capture the image of emitted fluorescence from each cluster on the flow cell. Record the identity of the first base for each cluster.

## 9. DETERMINE SECOND BASE

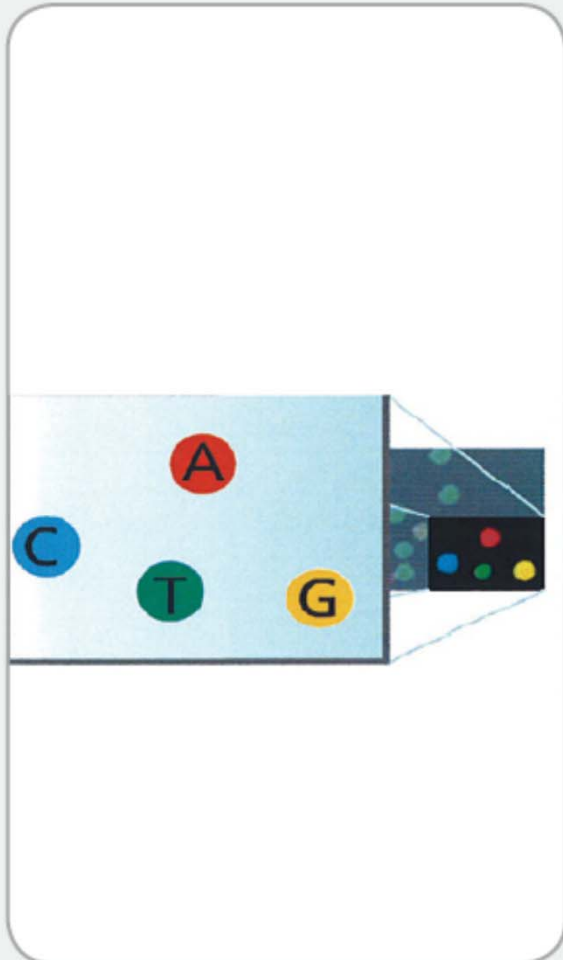


Second chemistry cycle: to initiate the next sequencing cycle, add all four labeled reversible terminators and enzyme to the flow cell.

# DNA Sequencing with Illumina (Solexa®) Technology

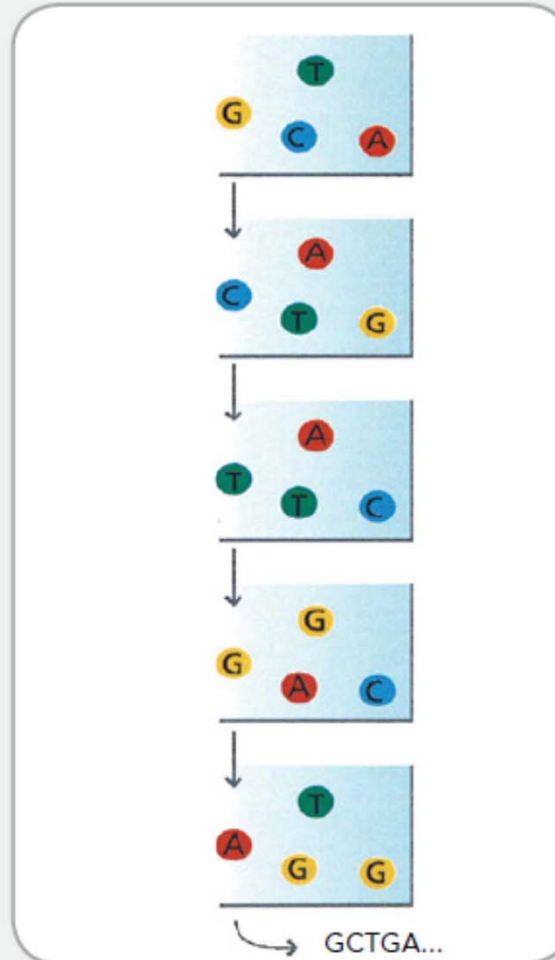


## 10. IMAGE SECOND CHEMISTRY CYCLE



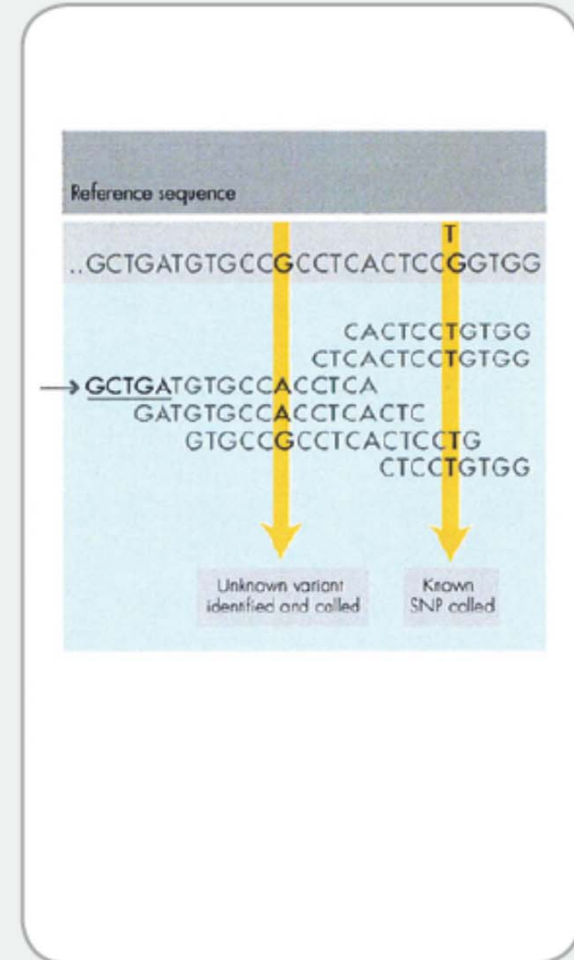
After laser excitation, collect the image data as before. Record the identity of the second base for each cluster.

## 11. SEQUENCE READS OVER MULTIPLE CHEMISTRY CYCLES

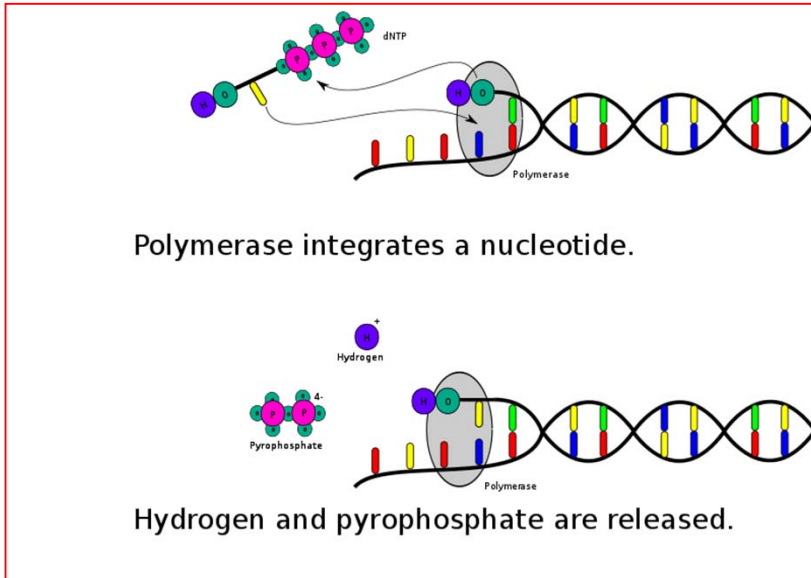


Repeat cycles of sequencing to determine the sequence of bases in a given fragment a single base at time.

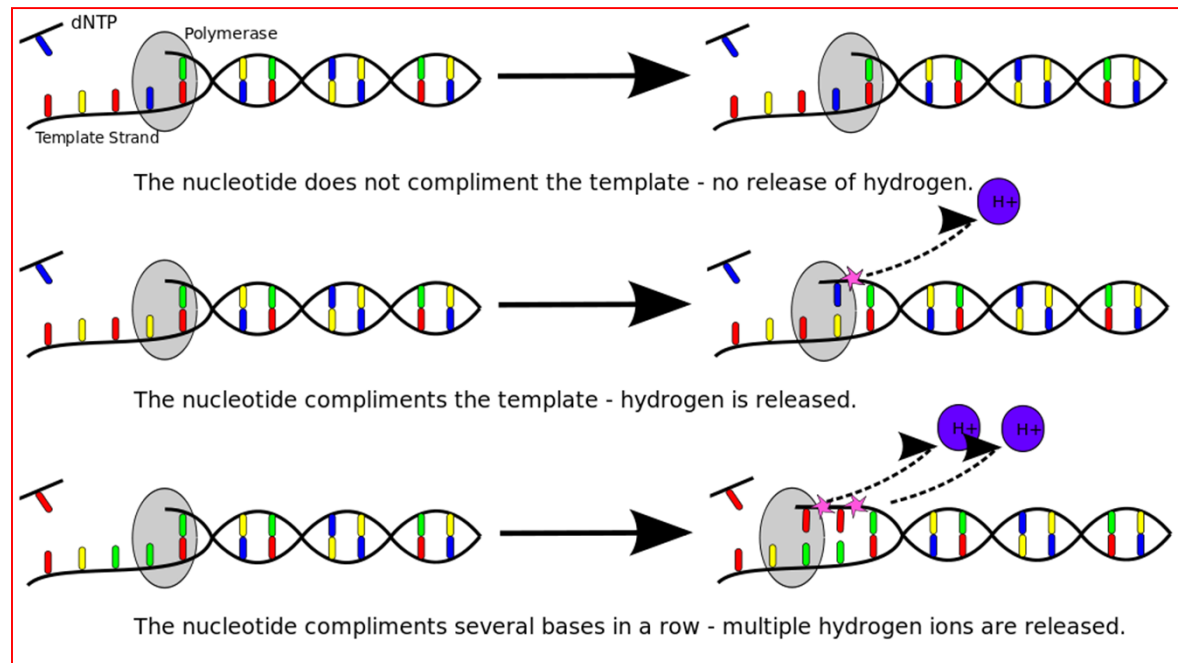
## 12. ALIGN DATA



Align data, compare to a reference, and identify sequence differences.



## Ion Torrent Sequencing



[http://en.wikipedia.org/wiki/Ion\\_semi-conductor\\_sequencing](http://en.wikipedia.org/wiki/Ion_semi-conductor_sequencing)