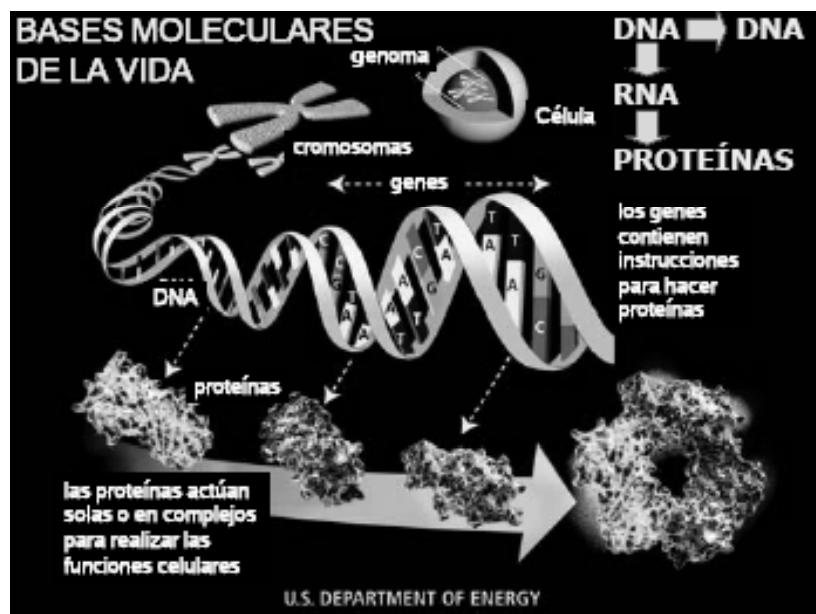
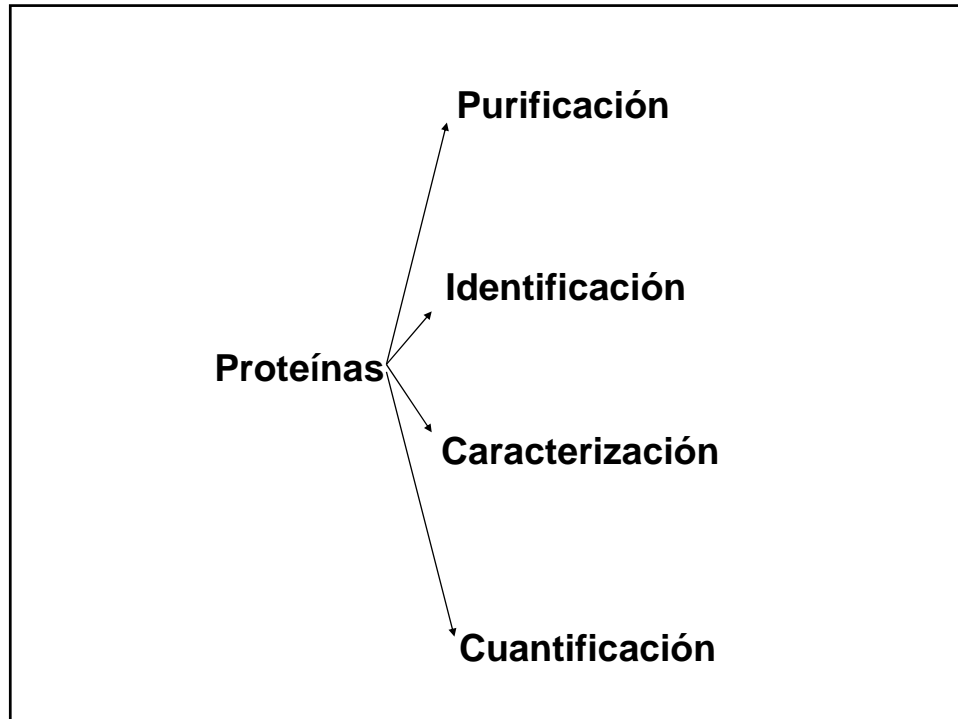


# Metodologías Básico-Clínicas





## Purificación de Proteínas

- Salting in y salting out
- Centrifugación
- Ultrafiltración y diálisis
- Cromatografía (intercambio iónico, exclusión, afinidad, HPLC)

## SEPARACIÓN DE PROTEÍNAS CENTRIFUGACIÓN DIFERENCIAL

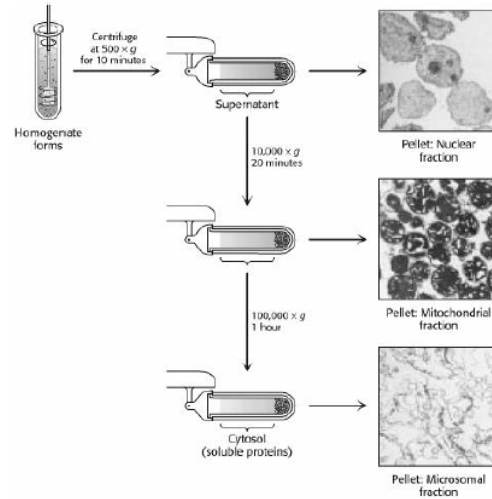


Figure 4.1. Differential Centrifugation. Cells are disrupted in a homogenizer and the resulting mixture, called the homogenate, is centrifuged in a step-by-step fashion of increasing centrifugal force. The denser material will form a pellet at lower centrifugal force than will the less-dense material. The isolated fractions can be used for further purification. [Photographs courtesy of S. Fleischer and B. Fleischer.]

## SEPARACIÓN DE PROTEÍNAS DIÁLISIS

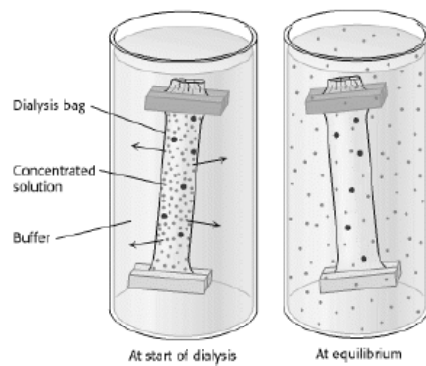


Figure 4.2. Dialysis. Protein molecules (red) are retained within the dialysis bag, whereas small molecules (blue) diffuse

## SEPARACIÓN DE PROTEÍNAS CROMATOGRFÍA DE FILTRACIÓN

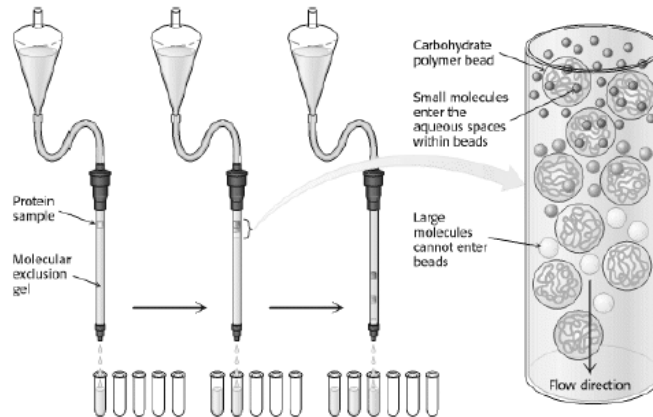


Figure 4.3. Gel Filtration Chromatography. A mixture of proteins in a small volume is applied to a column filled with porous beads. Because large proteins cannot enter the internal volume of the beads, they emerge sooner than do small ones.

## SEPARACIÓN DE PROTEÍNAS CROMATOGRFÍA CON CARGA ELÉCTRICA

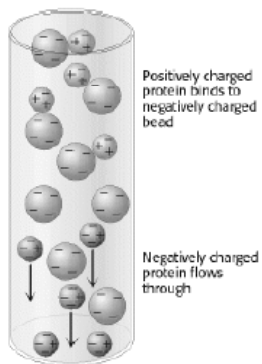


Figure 4.4. Ion-Exchange Chromatography. This technique separates proteins mainly according to their net charge.

## SEPARACIÓN DE PROTEÍNAS CROMATOGRAFÍA DE AFINIDAD

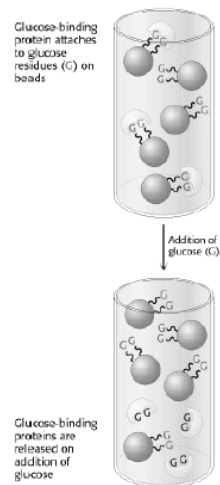


Figure 4.5. Affinity Chromatography. Affinity chromatography of concanavalin A (shown in yellow) on a solid support containing covalently attached glucose residues (G).

## SEPARACIÓN DE PROTEÍNAS CROMATOGRAFÍA LÍQUIDA DE ALTA PRESIÓN-HPLC

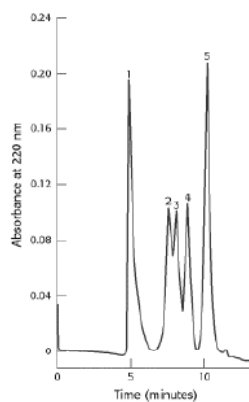
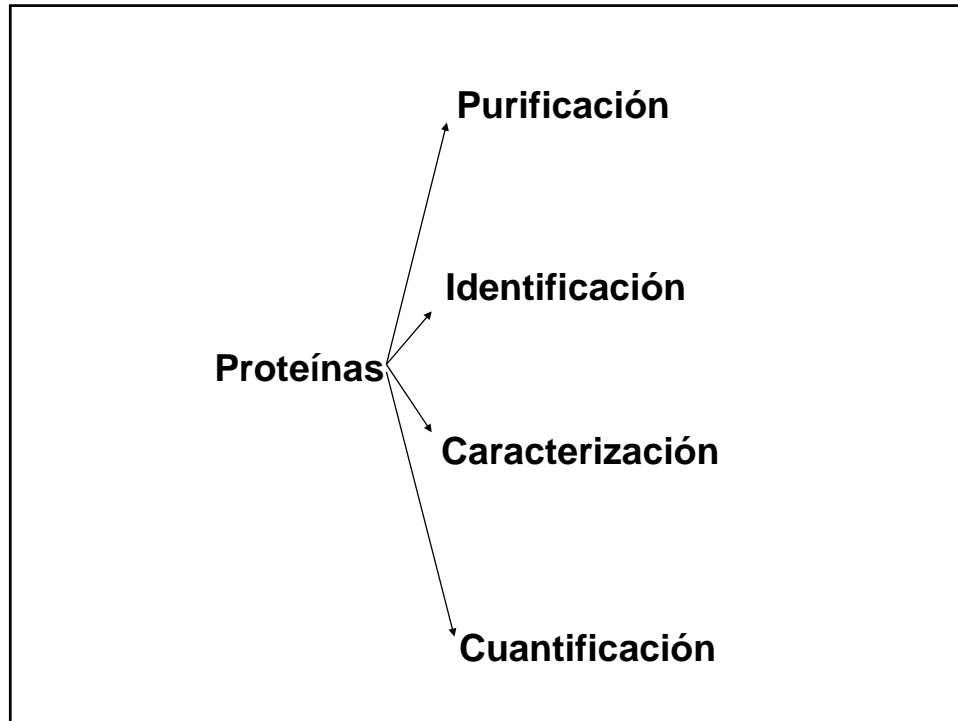


Figure 4.6. High-Pressure Liquid Chromatography (HPLC). Gel filtration by HPLC clearly defines the individual proteins because of its greater resolving power: (1) thyroglobulin (669 kd), (2) catalase (232 kd), (3) bovine serum albumin (67 kd), (4) ovalbumin (45 kd), and (5) ribonuclease (13.4 kd). [After K. J. Wilson and T. D. Schlabach. In *Current Protocols in Molecular Biology*, vol. 2, suppl. 41, F. M. Ausbel, R. Brent, R. E. Kingston, D. D. Moore, J. G. Seidman, J. A. Smith, and K. Struhl, Eds. (Wiley, 1998), p. 10.14.1.]



## Identificación y Caracterización de Proteínas

- Electroforesis
- Electroenfoque
- Western blot
- Inmunodetección
- Técnicas espectroscópicas (NMR, difracción óptica rotatoria, EPR, espectrometría de masa, difracción de rayos X)

## SEPARACIÓN DE PROTEÍNAS ELECTROFORESIS

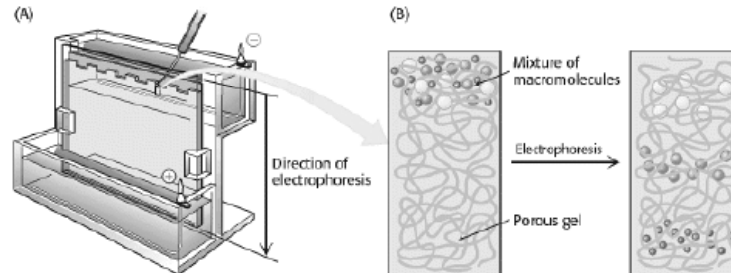


Figure 4.7. Polyacrylamide Gel Electrophoresis. (A) Gel electrophoresis apparatus. Typically, several samples undergo electrophoresis on one flat polyacrylamide gel. A microliter pipette is used to place solutions of proteins in the wells of the slab. A cover is then placed over the gel chamber and voltage is applied. The negatively charged SDS (sodium dodecyl sulfate)-protein complexes migrate in the direction of the anode, at the bottom of the gel. (B) The sieving action of a porous polyacrylamide gel separates proteins according to size, with the smallest moving most rapidly.

## SEPARACIÓN DE PROTEÍNAS ELECTROENFOQUE

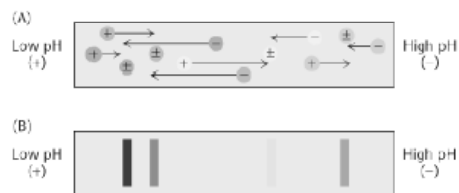


Figure 4.11. The Principle of Isoelectric Focusing. A pH gradient is established in a gel before loading the sample. (A) The sample is loaded and voltage is applied. The proteins will migrate to their isoelectric pH, the location at which they have no net charge. (B) The proteins form bands that can be excised and used for further experimentation.

## SEPARACIÓN DE PROTEÍNAS

## ELECTROFORESIS BIDIMENSIONAL

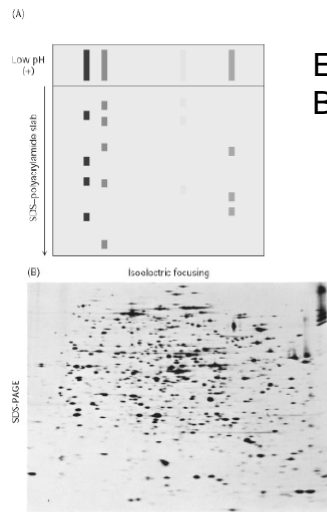


Figure 4.12. Two-Dimensional Gel Electrophoresis. (A) A protein sample is initially fractionated in one dimension by isoelectric focusing as described in Figure 4.11. The isoelectric focusing gel is then attached to an SDS-polyacrylamide gel, and electrophoresis is performed in the second dimension, perpendicular to the original separation. Proteins with the same pI are now separated on the basis of mass. (B) Proteins from *E. coli* were separated by two-dimensional gel electrophoresis, resolving more than a thousand different proteins. The proteins were first separated according to their isoelectric pH in the horizontal direction and then by their apparent mass in the vertical direction. [(B) Courtesy of Dr. Patrick H. O'Farrell.]

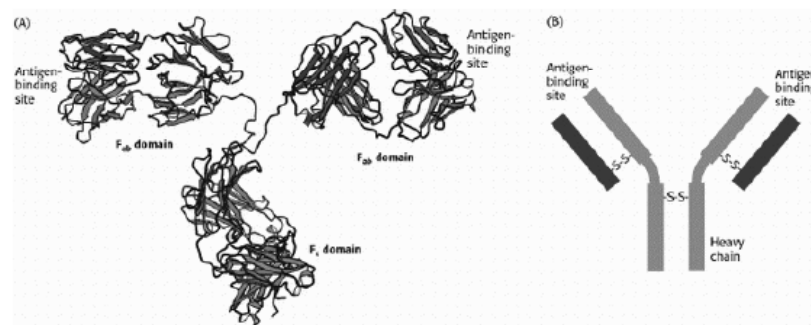
DETECCIÓN DE PROTEÍNAS  
USO DE ANTICUERPOS

Figure 4.30. Antibody Structure. (A) IgG antibodies consist of four chains, two heavy chains (blue) and two light chains (red), linked by disulfide bonds. The heavy and light chains come together to form Fab domains, which have the antigen-binding sites at the ends. The two heavy chains form the Fc domain. The Fab domains are linked to the Fc domain by flexible linkers. (B) A more schematic representation of an IgG molecule.

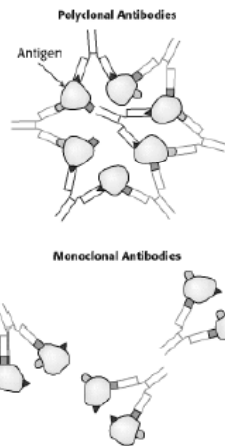


## DETECCIÓN DE PROTEÍNAS INTERACCIONES ANTÍGENO-ANTICUERPO



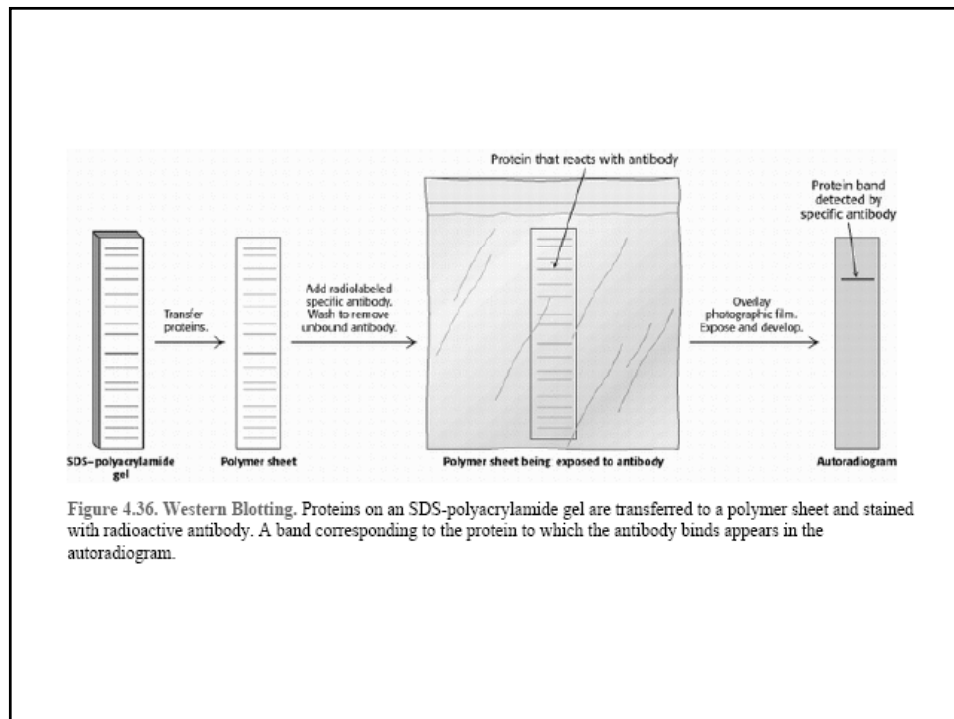
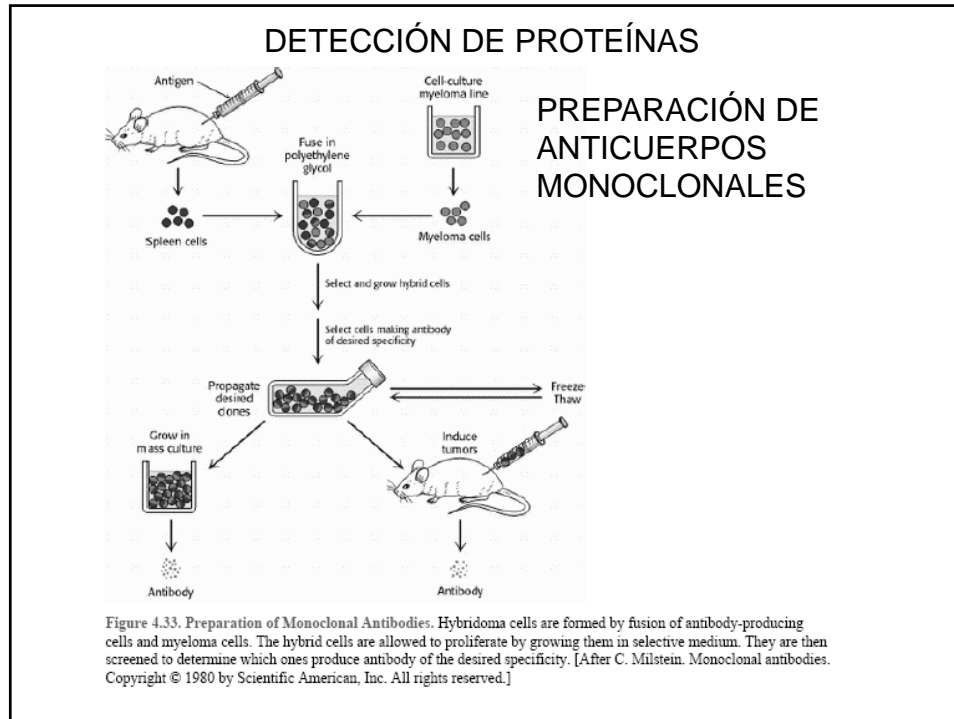
Figure 4.31. Antigen-Antibody Interactions. A protein antigen, in this case lysozyme, binds to the end of an Fab domain from an antibody. The end of the antibody and the antigen have complementary shapes, allowing a large amount of surface to be buried on binding.

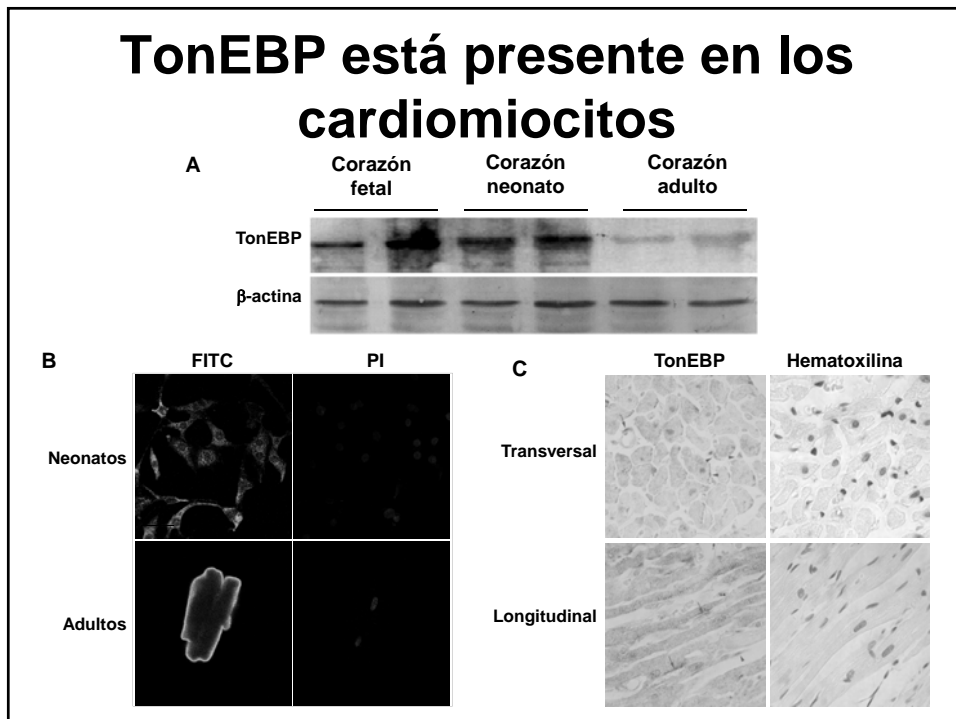
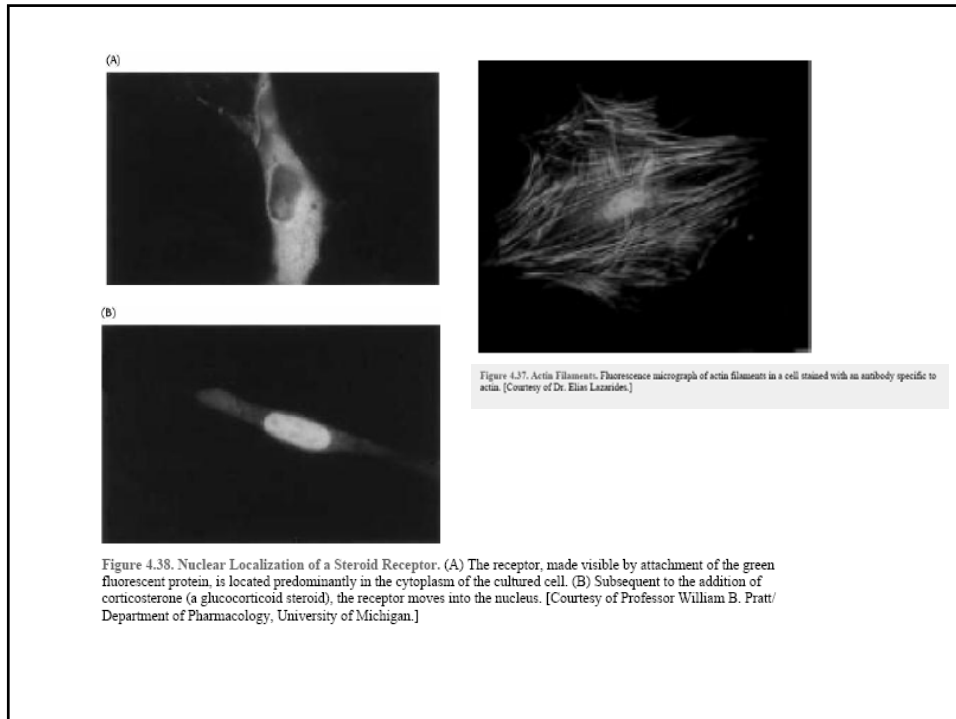
## DETECCIÓN DE PROTEÍNAS



## ANTICUERPOS POLICLONALES Y MONOCLONALES

Figure 4.32. Polyclonal and Monoclonal Antibodies. Most antigens have several epitopes. Polyclonal antibodies are heterogeneous mixtures of antibodies, each specific for one of the various epitopes on an antigen. Monoclonal antibodies are all identical, produced by clones of a single antibody-producing cell. They recognize one specific epitope. [After R. A. Goldsby, T. J. Kindt, B. A. Osborne, *Kuby Immunology*, 4th ed. (W. H. Freeman and Company, 2000), p. 154.]





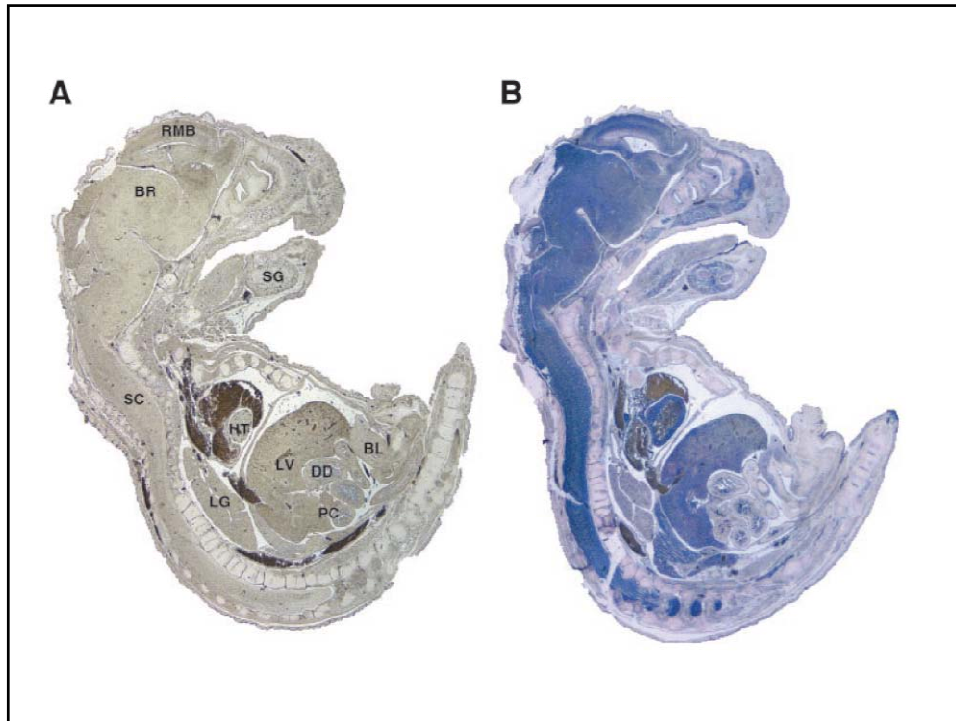
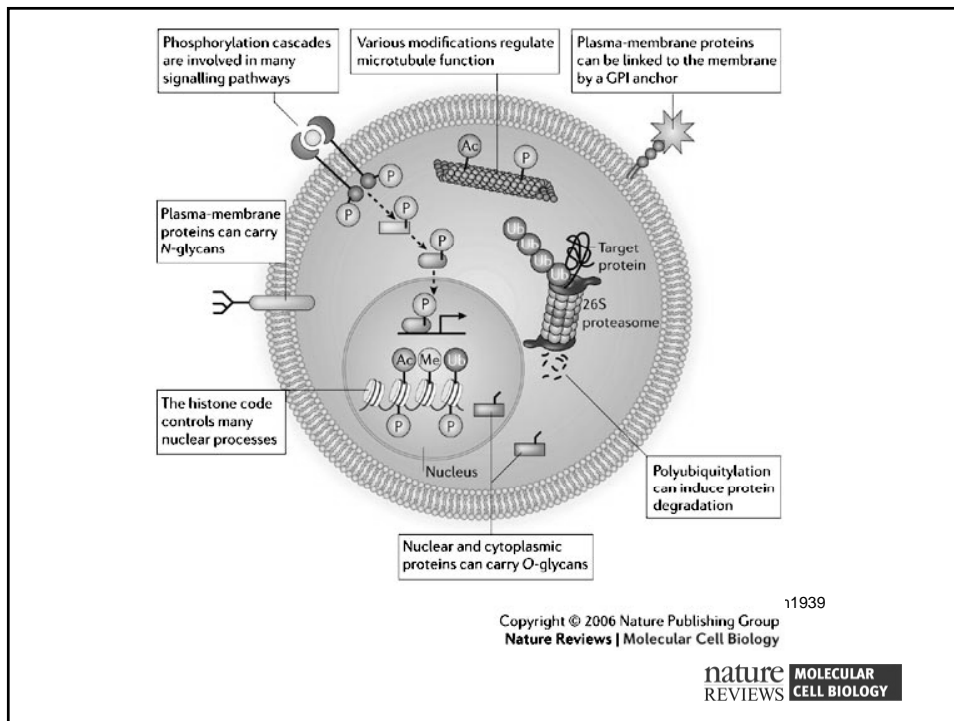
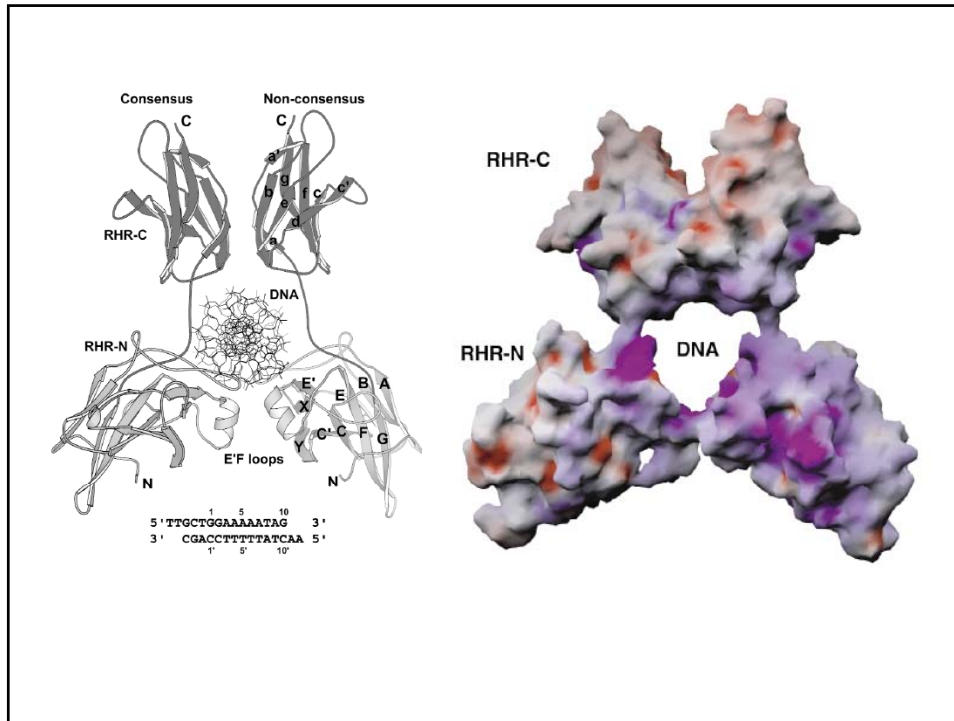
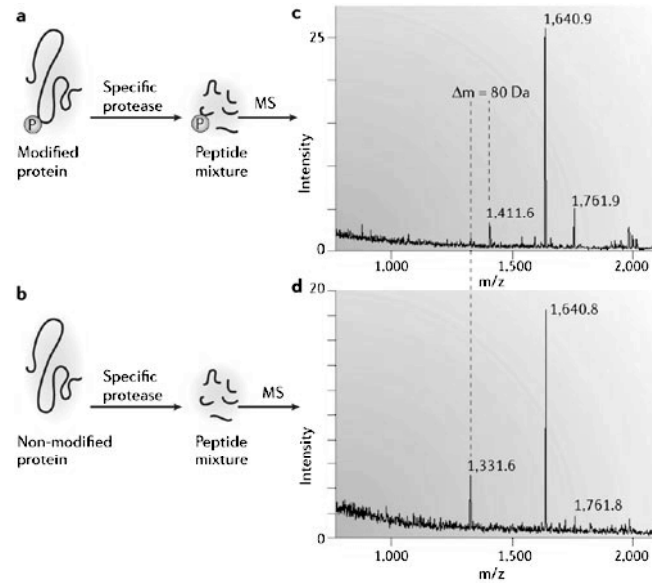
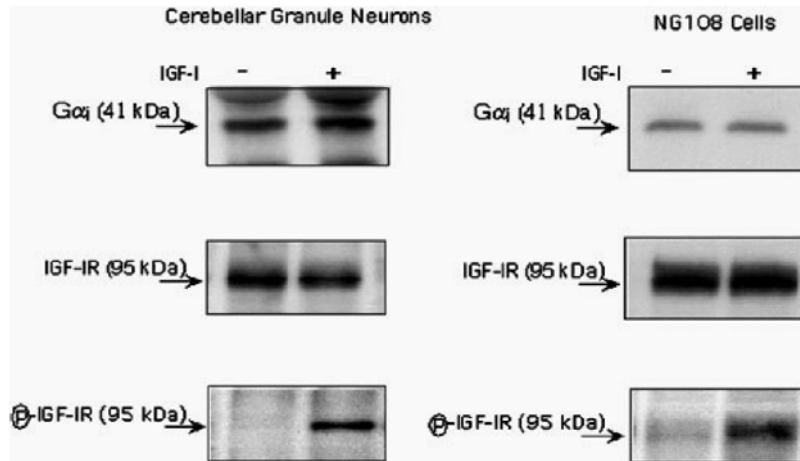


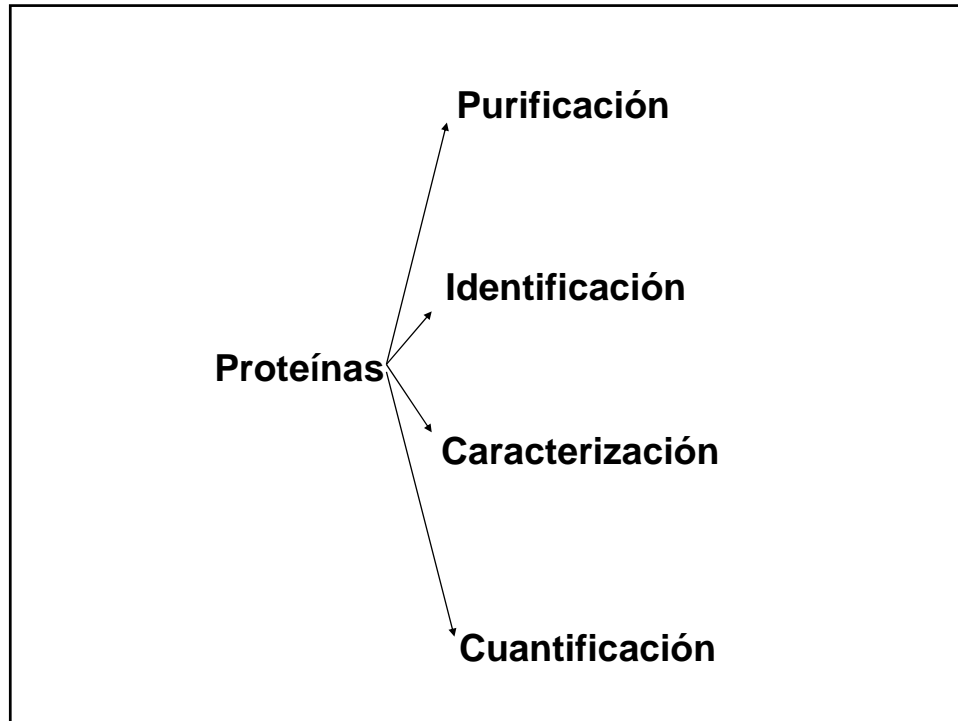
Figure 4.52. Section of the Electron-Density Map of Myoglobin. This section of the electron-density map shows the heme group. The peak of the center of this section corresponds to the position of the iron atom. [From J. C. Kendrew. The three-dimensional structure of a protein molecule. Copyright © 1961 by Scientific American, Inc. All rights reserved.]



## Fosforilación de proteínas



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## **Cuantificación de Proteínas**

- Western blot
- ELISA

## SEPARACIÓN DE PROTEÍNAS

## ELECTROFORESIS-WESTERN BLOT

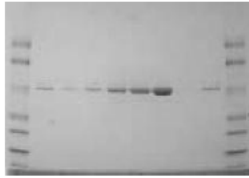


Figure 4.9. Staining of Proteins After Electrophoresis. Proteins subjected to electrophoresis on an SDS-polyacrylamide gel can be visualized by staining with Coomassie blue. [Courtesy of Kodak Scientific Imaging Systems.]

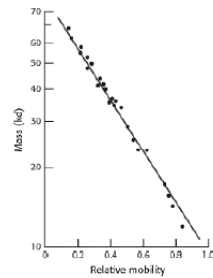
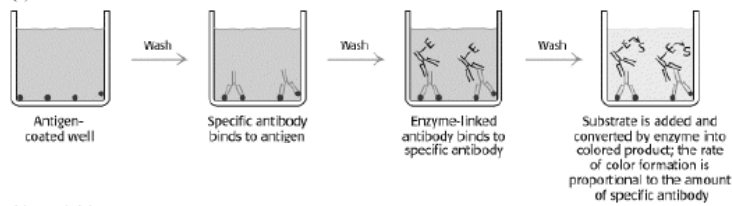


Figure 4.10. Electrophoresis Can Determine Mass. The electrophoretic mobility of many proteins in SDS-polyacrylamide gels is inversely proportional to the logarithm of their mass. [After K. Weber and M. Osborn, *The Proteins*, vol. 1, 3d ed. (Academic Press, 1975), p. 179.]

## (A) Indirect ELISA



## (B) Sandwich ELISA

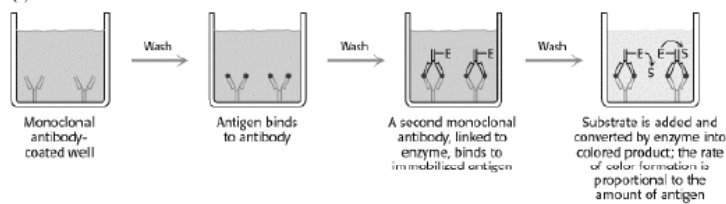
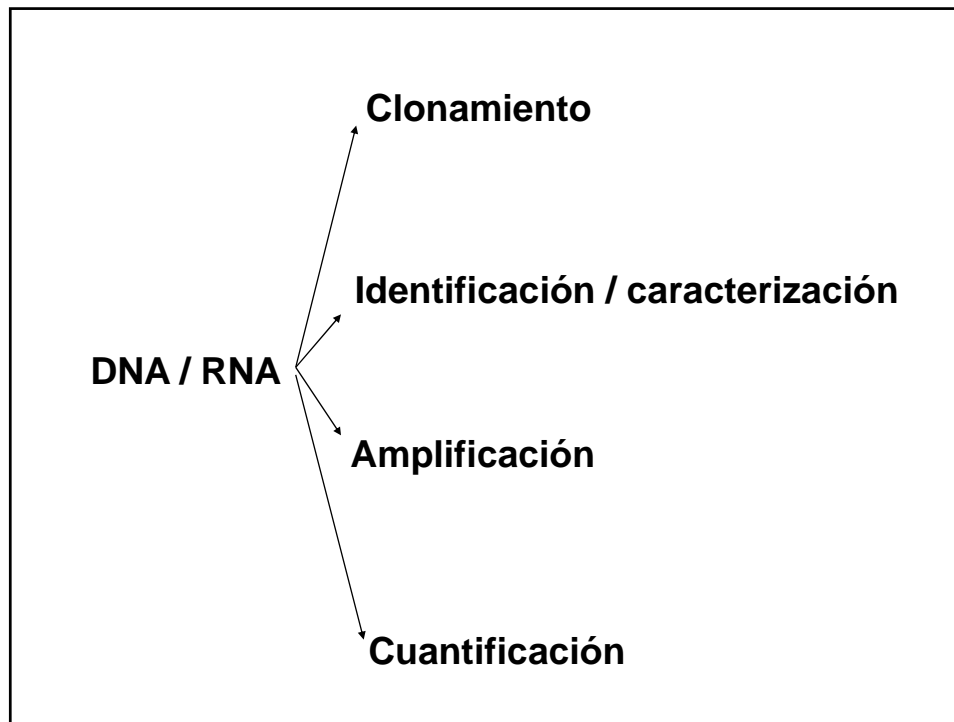


Figure 4.35. Indirect ELISA and Sandwich ELISA (A) In indirect ELISA, the production of color indicates the amount of an antibody to a specific antigen. (B) In sandwich ELISA, the production of color indicates the quantity of antigen. [After R. A. Goldsby, T. J. Kindt, B. A. Osborne, *Kuby Immunology*, 4th ed. (W. H. Freeman and Company, 2000), p. 162.]





## **Clonamiento de DNA**

- Enzimas de restricción
- Vectores de clonamiento
- DNA ligasa

## Análisis de DNA

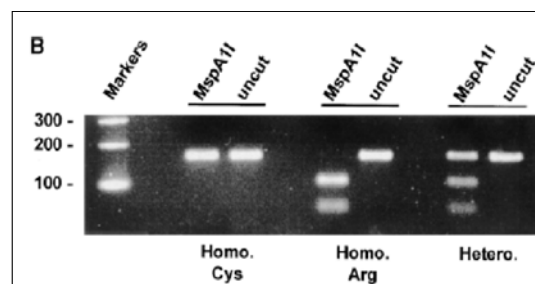
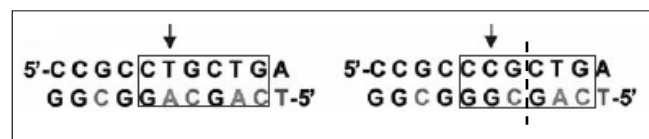
### ENZIMAS DE RESTRICIÓN

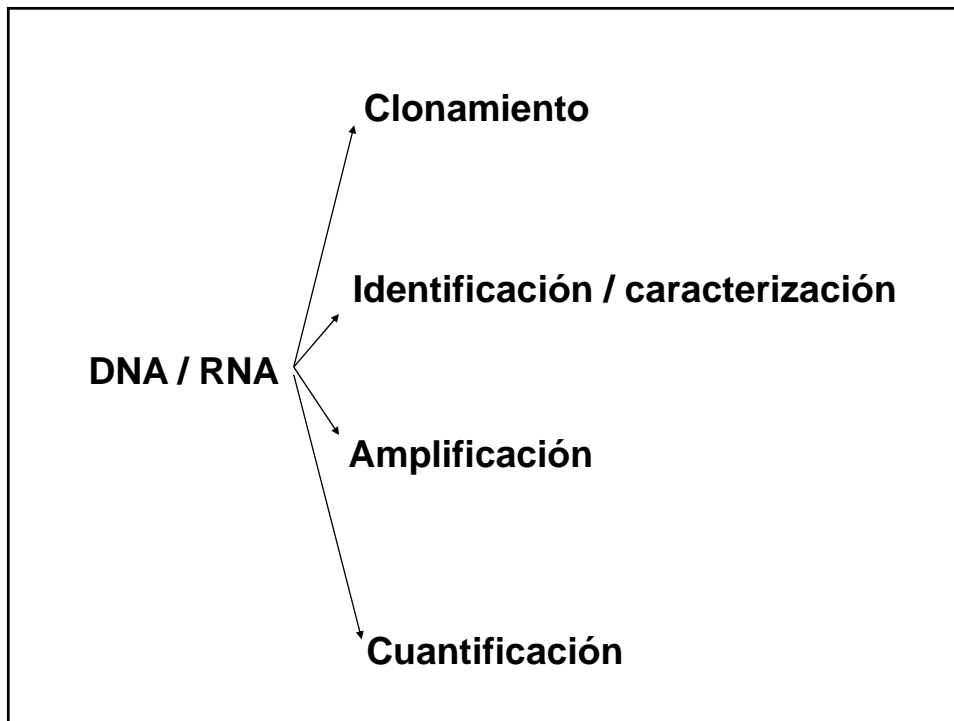
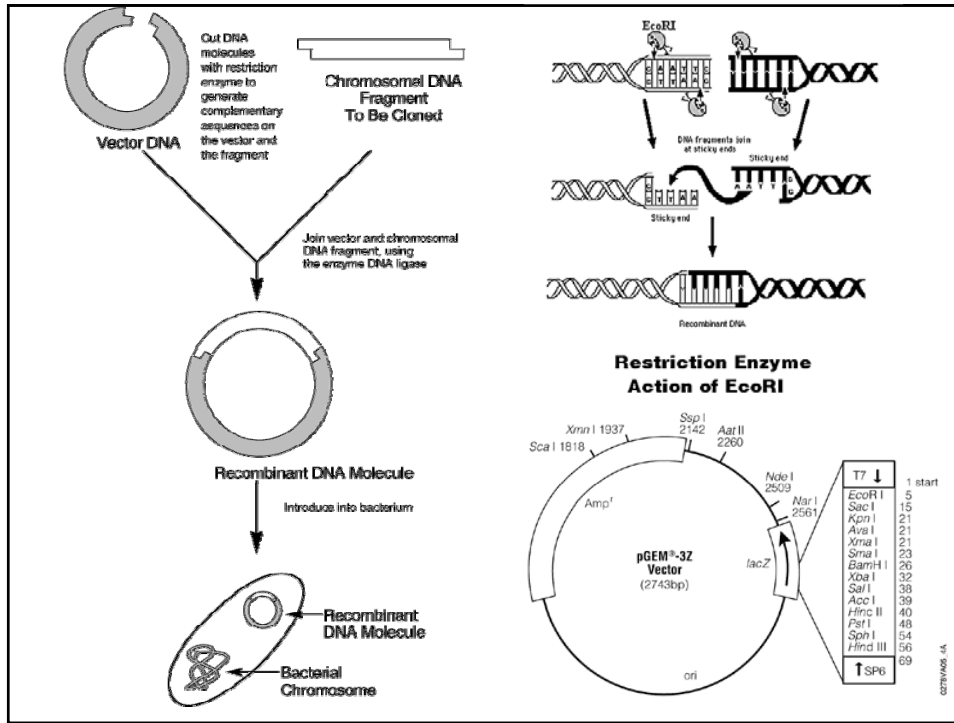
A restriction enzyme (or restriction endonuclease) is an enzyme that cuts double-stranded DNA. The enzyme makes two incisions, one through each of the sugar-phosphate backbones (i.e., each strand) of the double helix without damaging the nitrogenous bases. The term restriction comes from the fact that these enzymes were discovered in *E. coli* strains that appeared to be restricting the infection by certain bacteriophages. Restriction enzymes therefore are believed to be a mechanism evolved by bacteria to resist viral attack and to help in the removal of viral sequences. They are part of what is called the restriction modification system.



The 1978 Nobel Prize in Medicine was awarded to Daniel Nathans, Werner Arber and Hamilton Smith for the discovery of restriction endonucleases, leading to the development of recombinant DNA technology. The first practical use of their work was the manipulation of *E. coli* bacteria to produce human insulin for diabetics.

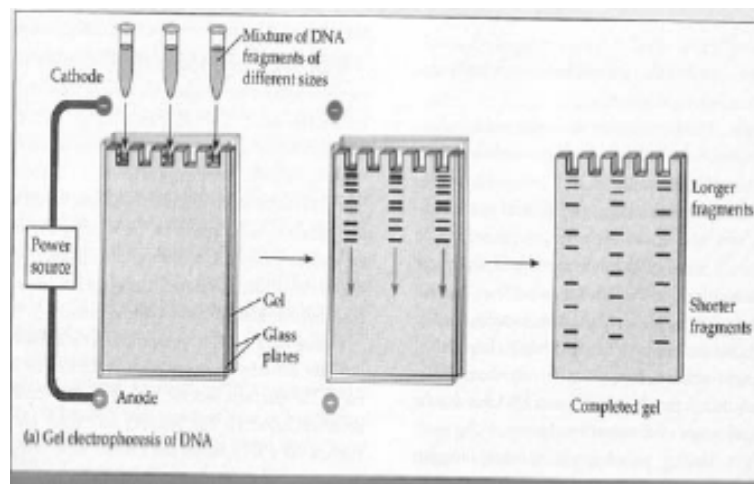
### Sitio de restricción MspA11

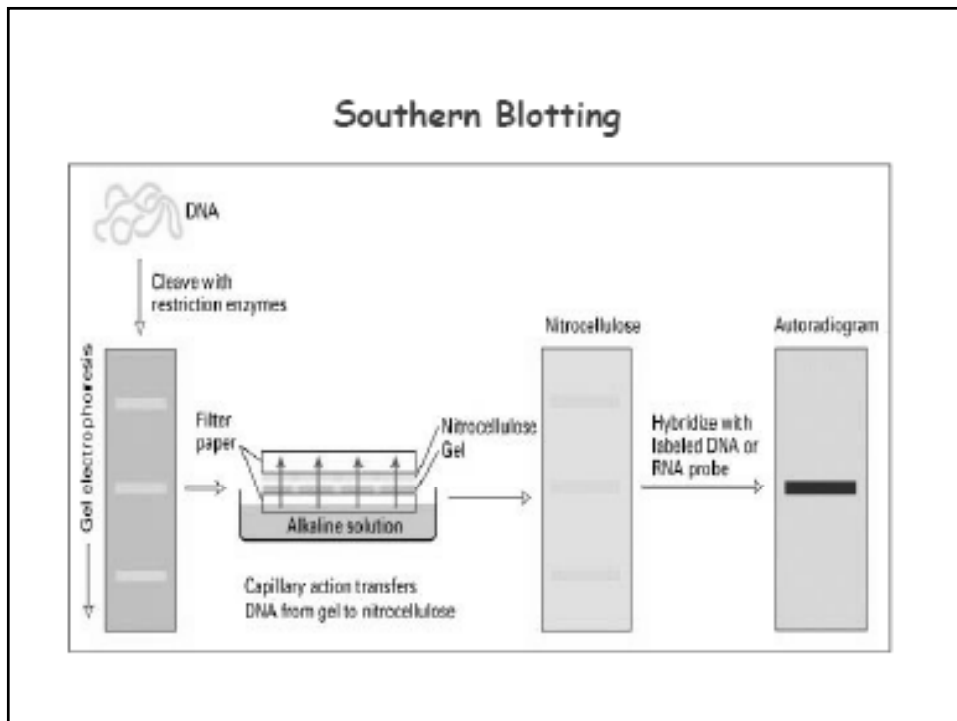
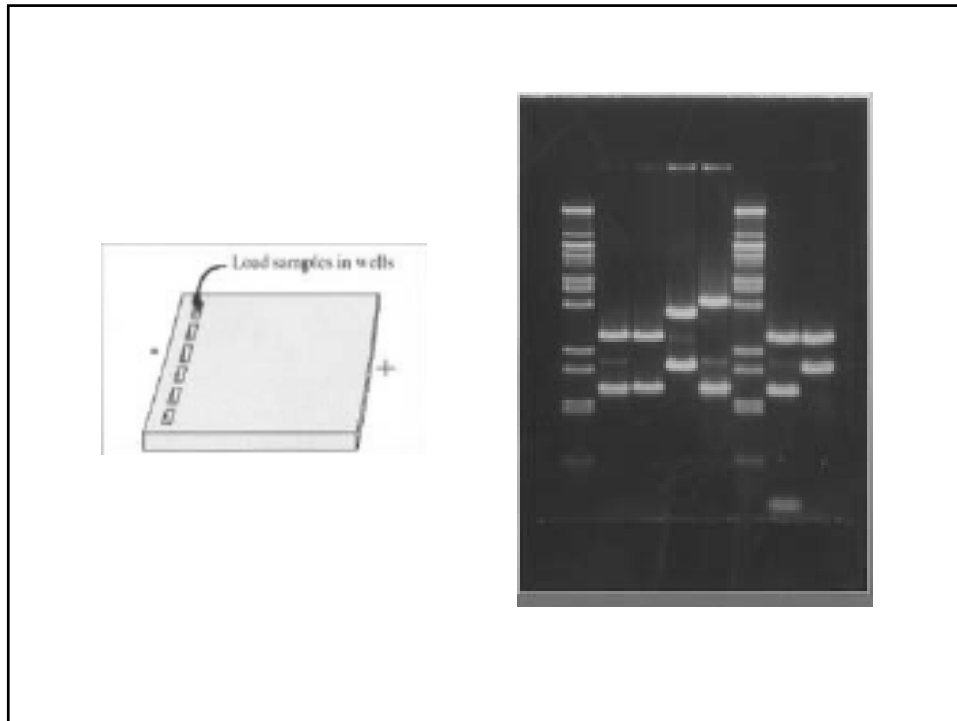


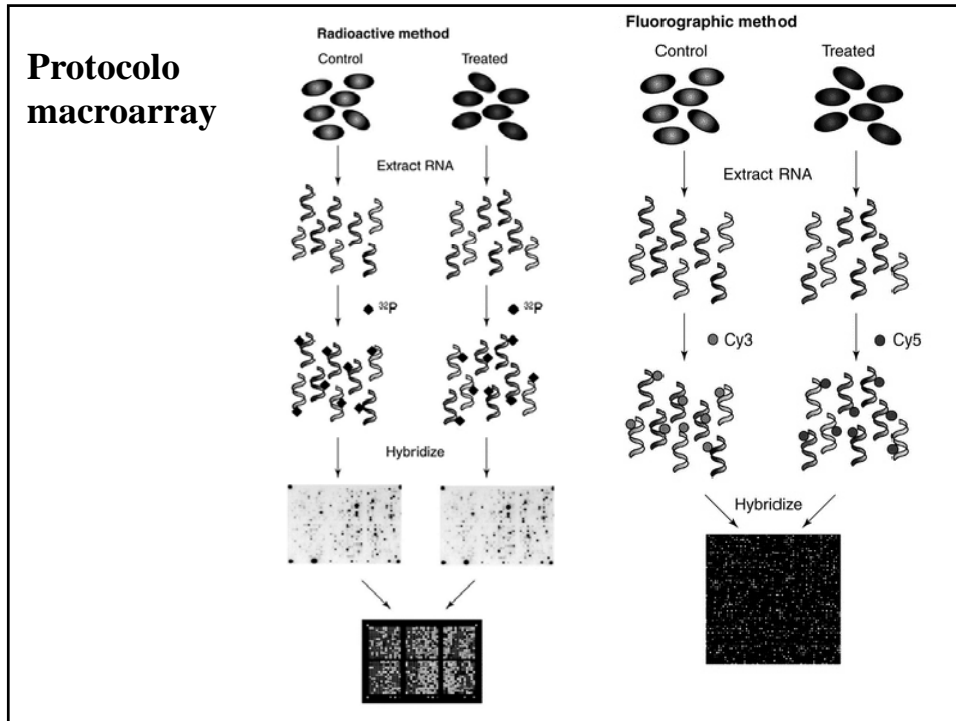


## Identificación y caracterización de DNA / RNA

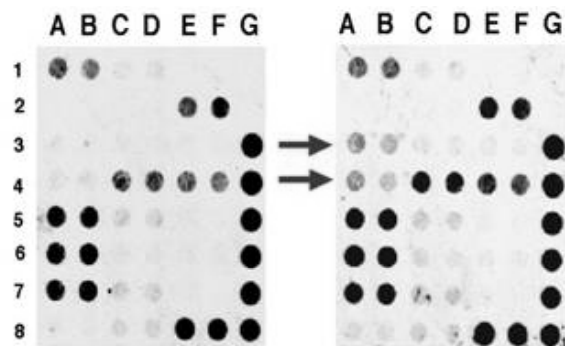
- Electroforesis en agarosa
- Southern blot
- Northern blot
- Microarray
- Secuenciación



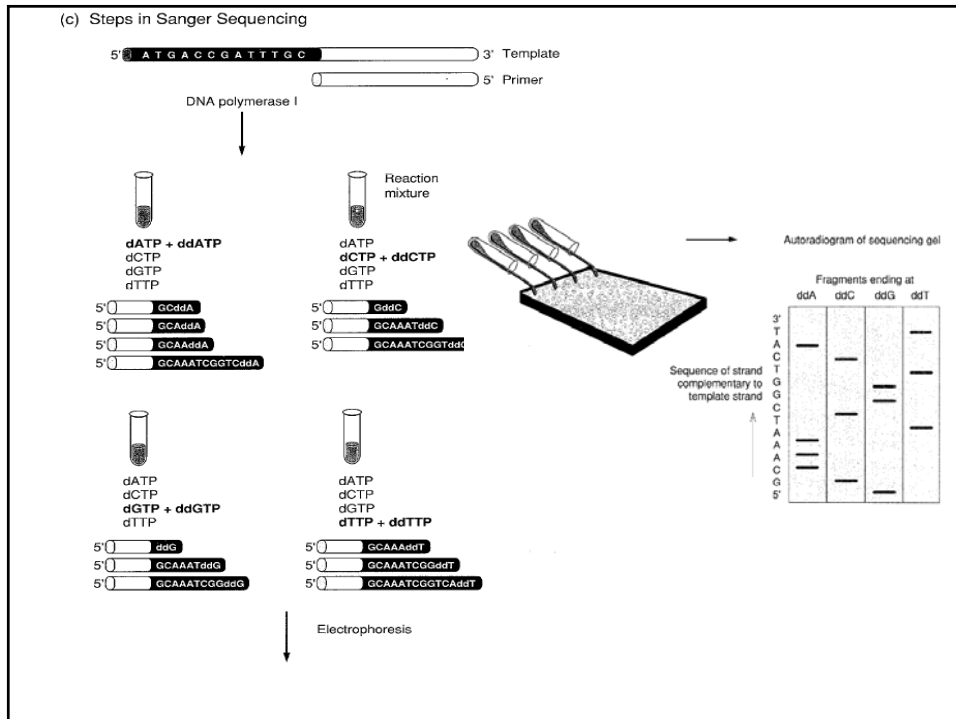
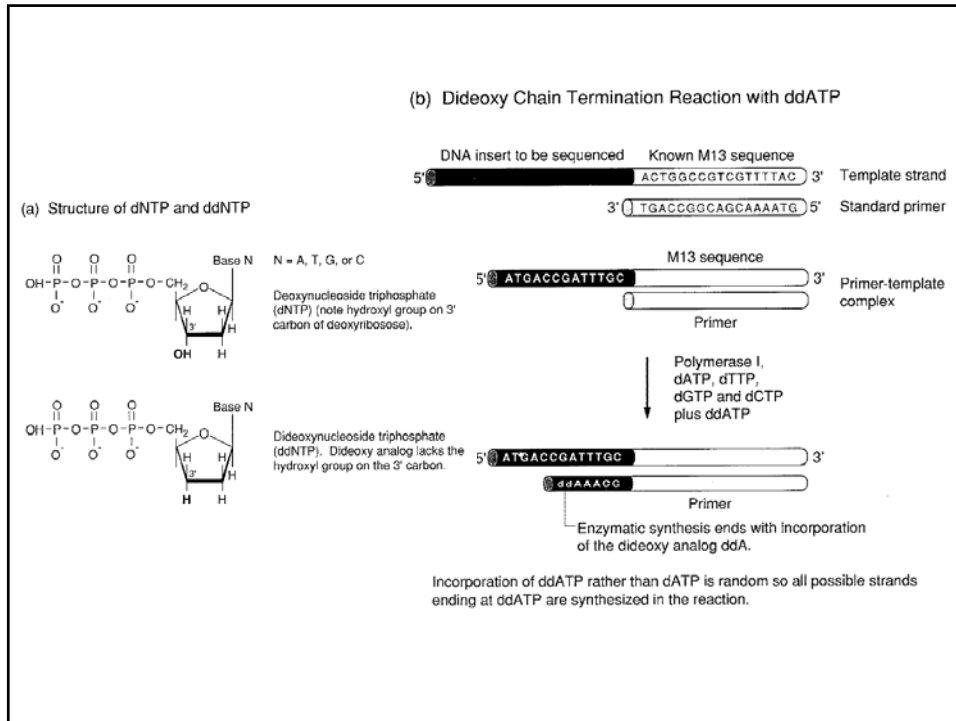


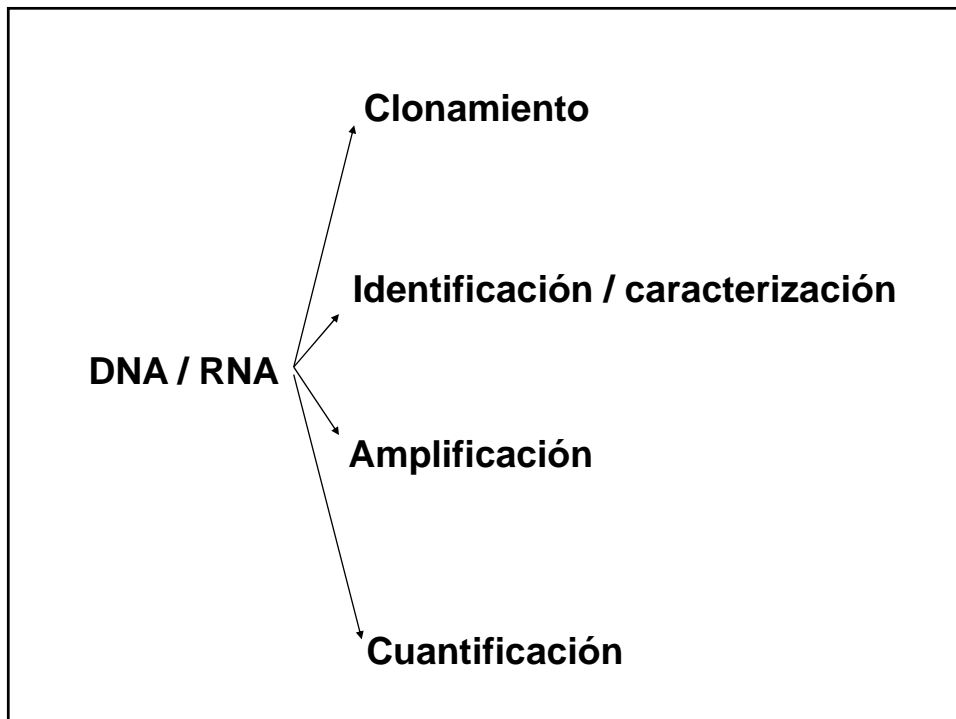
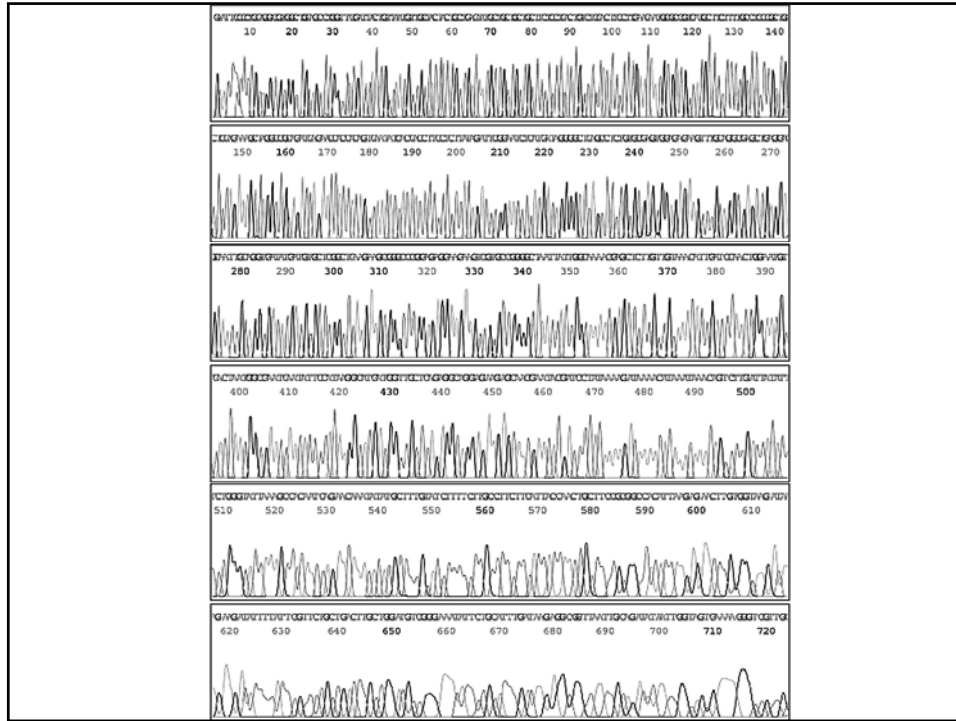


## Protocolo de macroarray



**Cell Cycle Genes**



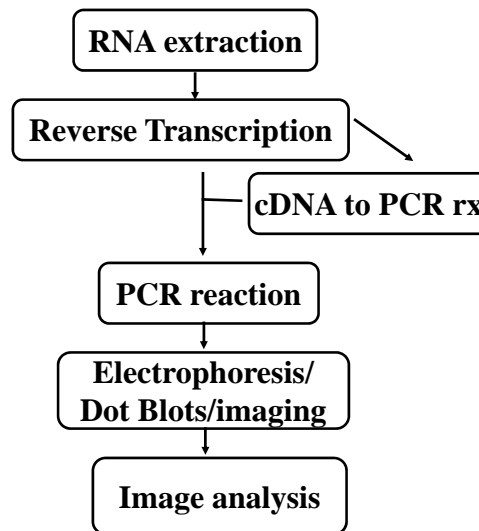




## Amplificación de DNA

- Reacción de polimerización en cadena (PCR)

### Transcriptasa Reversa y Reacción en Cadena de la Polimerasa (RT-PCR)



## Reacción en Cadena de la Polimerasa (PCR)

---

PCR es básicamente una técnica *in vitro* para amplificar una secuencia específica de DNA.

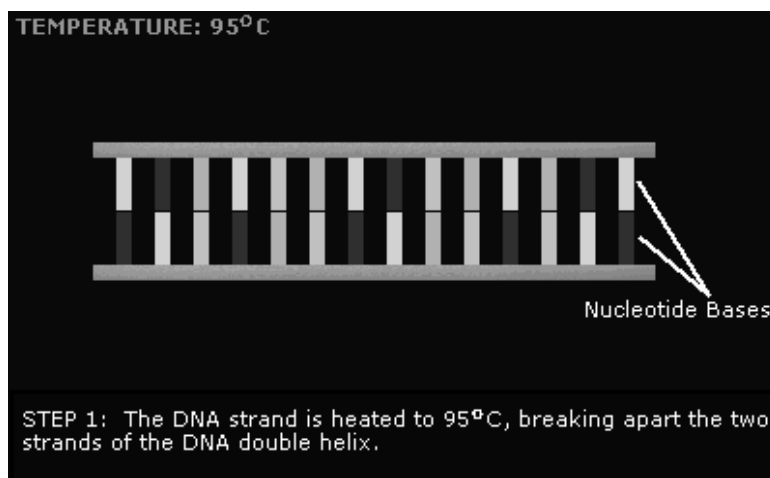
Método consiste en tres etapas básicas:

1. Desnaturación (~95°C)
2. Alineamiento (~55- 60°C, varía)
3. Extensión (~72°C)

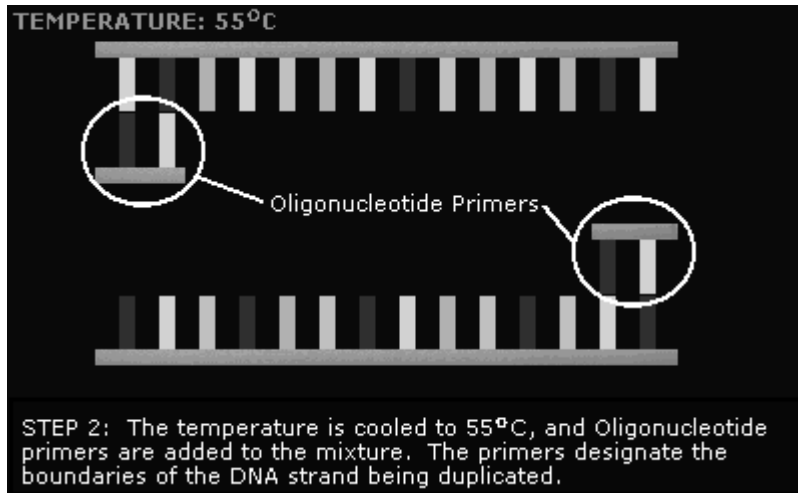
Las tres etapas se repiten Cíclicamente

### Desnaturación: altas temperaturas separan las dos hebras

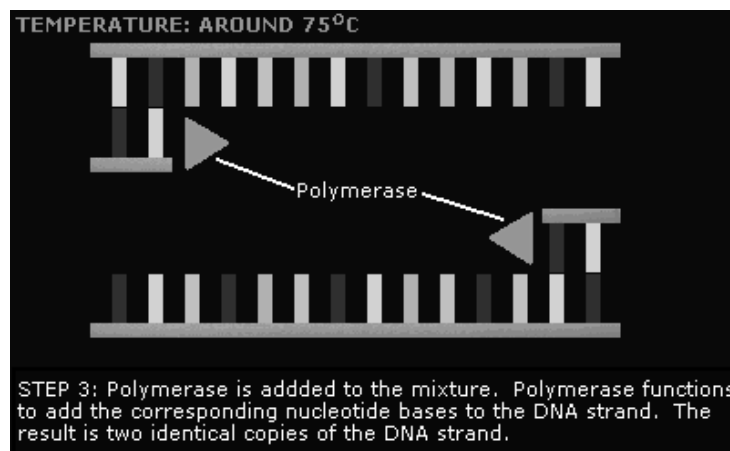
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**Alineamiento: Partidor comúnmente son usados ~20 nucleótidos.**

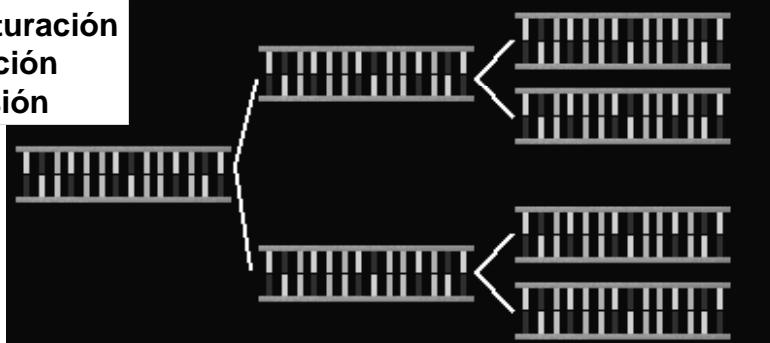


**Extensión: La polimerasa agrega dNTPs uno a la vez**



## Repetición de ciclos

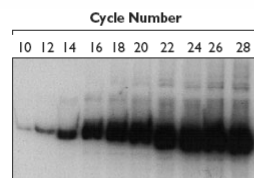
Desnaturación  
Alineación  
Extensión



This process is repeated, each time doubling the number of copies of the DNA strand in the mixture. After 30 repetitions, over 1 million copies of the DNA strand can be made.

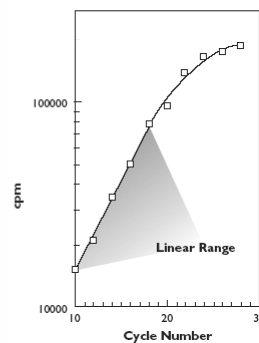
Número promedio de ciclos = 30

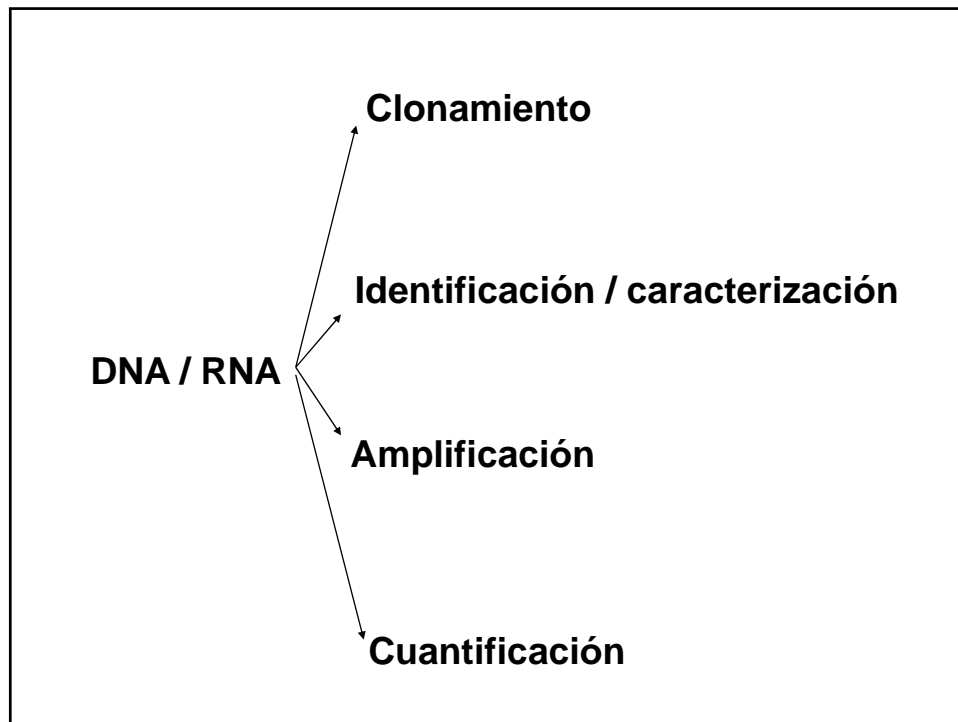
$$2^{30} = 1.07 \times 10^9 \text{ copias}$$



**Figure 4. Determining Linear Range**

A PCR master mix was prepared including 10  $\mu\text{l}$  [ $\alpha$ - $^{32}\text{P}$ ]dCTP in addition to the normal reaction components. The master mix was split into 10 aliquots which were then subjected to PCR. Aliquots were removed from the thermocycler at the indicated cycle numbers and resolved by electrophoresis on a 5% polyacrylamide/urea gel. The products were quantitated with a Bio-Rad Molecular Imager. Cycle number is plotted against the log of the signal and a straight line is obtained for samples in linear range of amplification.



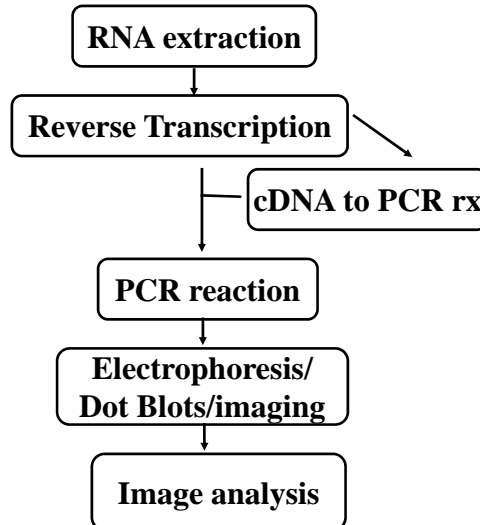


## **Cuantificación de DNA / RNA**

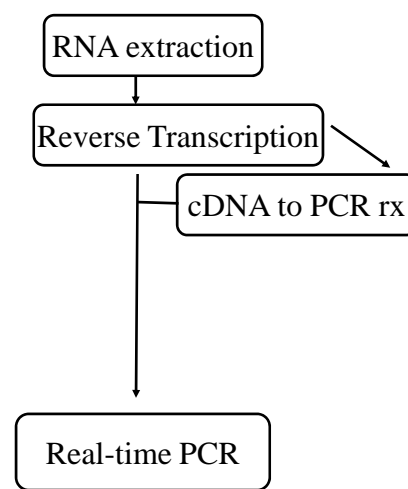
- Southern y Northern Blot
- Microarray
- RT-PCR en tiempo real

## Transcriptasa Reversa y Reacción en Cadena de Polimerasa (RT-PCR)

### Convencional



### Real-time



hardware real-time real-time real-time real-time PCR



**iCycler**  
BioRad

- Intuitive programming
- Fast and accurate performance
- Flexibility for multiple users
- Small footprint

The optical module fits on the iCycler base unit, offering you Real Time Quantitative PCR capability.



**5700**  
Applied Biosystems



**7700**  
Applied Biosystems



**FluorTracker**  
Stratagene



**FluorImager**  
Molecular Dynamics



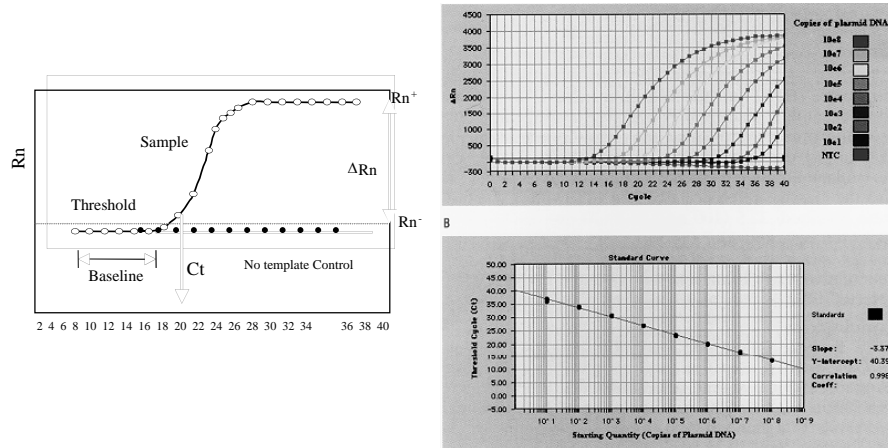
**LightCycler**  
Roche



**Opticon 1**  
MJ research

PCR en tiempo real

## Perfil de Amplificación de cDNA



## PCR en tiempo real

Los productos de amplificación se observan a medida que transcurren los ciclos del PCR

Esta basado en:

- ✓ La detección y cuantificación de un *reportero* fluorescente, cuya señal aumenta en proporción directa a la cantidad de producto de PCR en la reacción.
- ✓ El empleo de un termociclador que tiene acoplado un sistema de detección que es capaz de adquirir y cuantificar la señal emitida por el *reportero* al final de cada ciclo para cada muestra.