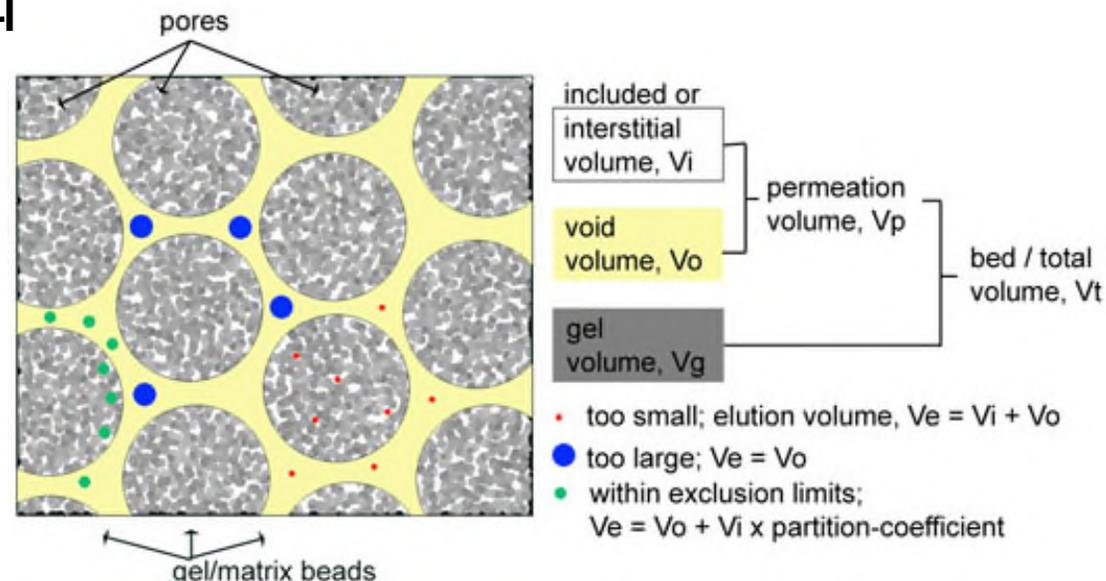


Chapter 3

단백질의 탐구 및 단백질체학

(3) 겔 거르기 (Gel filtration) chromatography: 크기에 의한 분리

- Resin: 다공성 구슬
= Sephadex, Sepharose, Biogel
= Bead size: 100 μm
- 원리: 분배 (partition) chromatograph
= 분배: 용질이 이동상 (mobile phase)과 고정상 (stationary phase)에 분배되는 정도
= 이동상: 완충용액
= 고정상: resin
= 배제한계 (Exclusion limit): 레진의 구멍의 크기에 의해 결정
- 배제한계 보다 큰 물질: Resin 사이의
공극을 통해 이동
- 배제한계 보다 작은 물질: Resin의
구멍을 통해 이동
- Void volume:
- Gel volume:
- Elution volume:



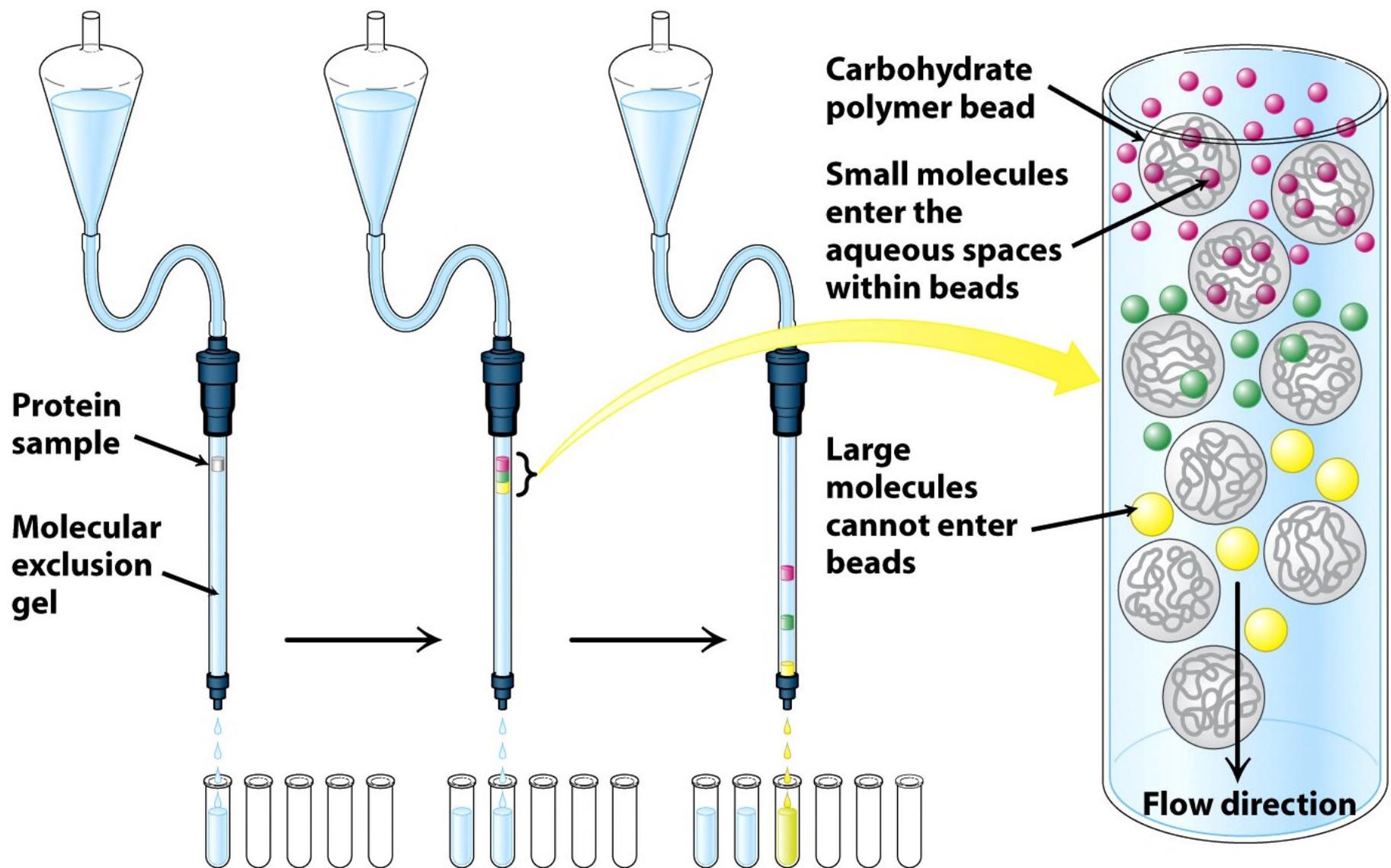
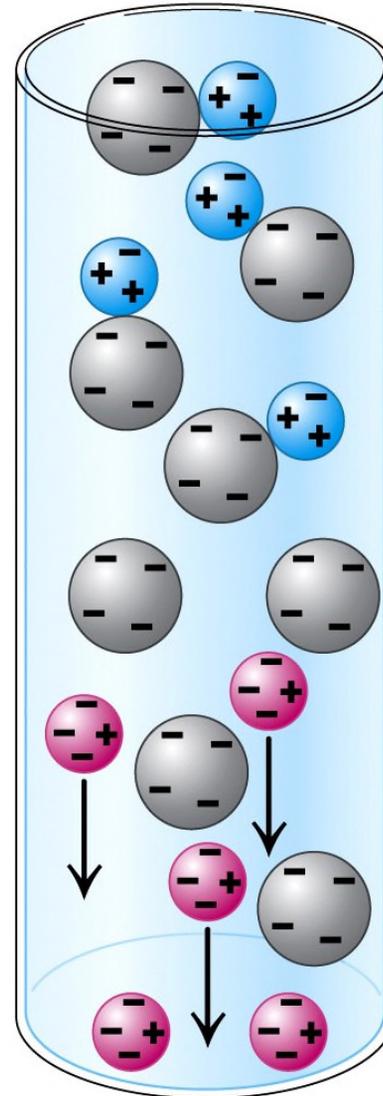


Figure 3-3
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(4) 이온 교환 (ion-exchange) chromatography: 전하의 차이를 이용

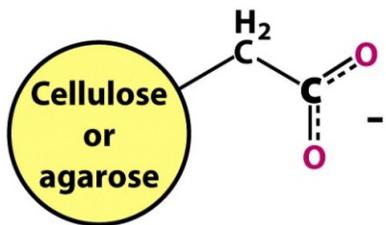
- Resin: 전하를 띤
 - = 음이온교환 (Anion): DEAE-cellulose
 - = 양이온 (Cation): CM-cellulose
- 분자의 분리는 분자의 전하에 따라 분리된다
- 용출은 buffer의 염 농도를 높인다



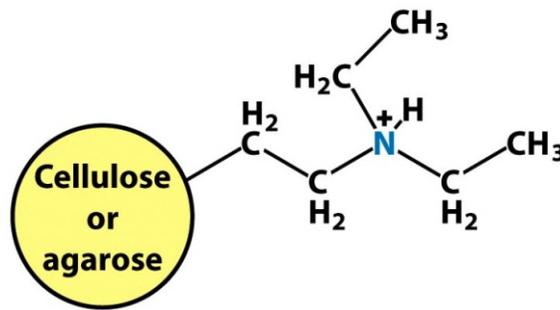
Positively charged protein binds to negatively charged bead

Negatively charged protein flows through

Figure 3-4
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Carboxymethyl (CM) group (ionized form)

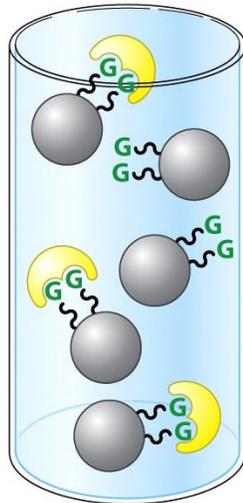


Diethylaminoethyl (DEAE) group (protonated form)

(5) 친화 (Affinity) chromatography: 단백질 결합의 특이성을 활용

- Resin: antibody-linked, Substrate-linked
- 장점: 한번에 원하는 단백질의 분리가 가능함
- 용출:
 - = Antibody: low pH (pH 3.0)
 - = Substrate-Enzyme: substrate

Glucose-binding protein attaches to glucose residues (G) on beads



Addition of glucose (G)

Glucose-binding proteins are released on addition of glucose

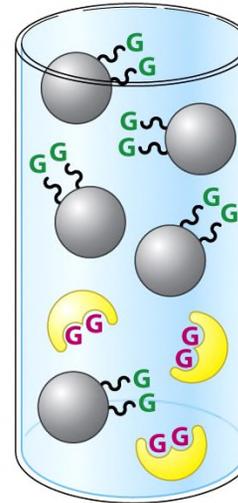
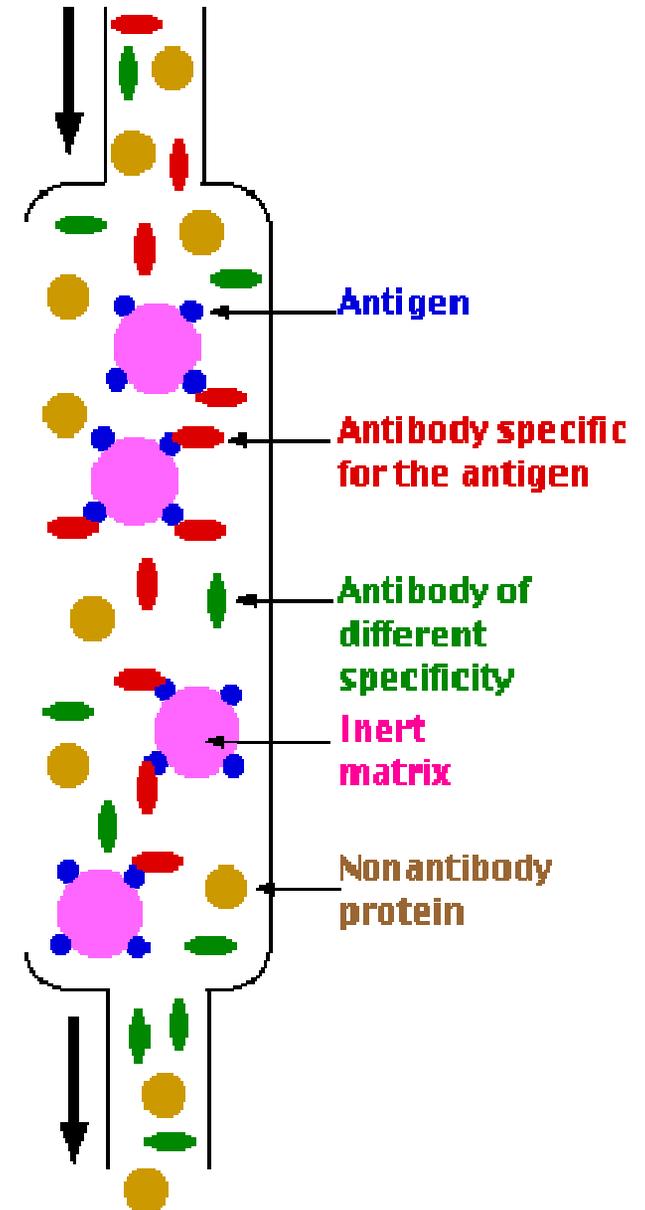


Figure 3-5
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(6) 고압액체 크로마토그래피 (High pressure liquid chromatography;HPLC)

- 용매의 압력을 높여 액체크로마토그래피의 성능을 향상시킴
- 시간을 절약할 수 있고, 분해능이 향상됨
- 일반 액체 chromatography의 단점을 보완
 - = low resolution:
 - = Time consuming:

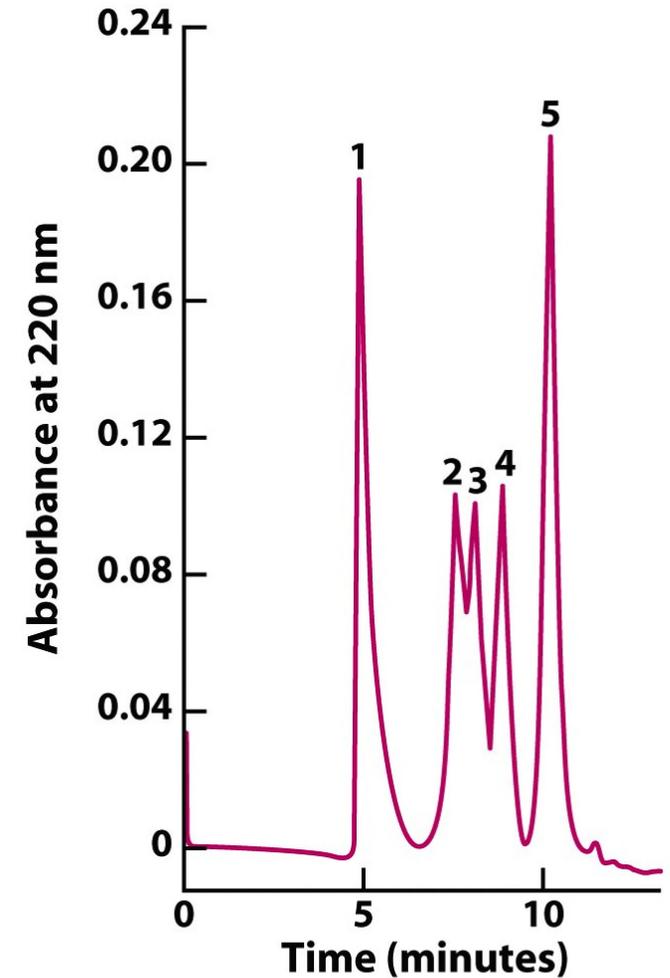


Figure 3-6
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4) 전기이동 (영동)법에 의한 단백질의 분리 및 확인

- 단백질 분리효율을 측정하는 방법

= To check increase of specific activity: assay

= To check decrease of protein contaminant: electrophoresis

(1) Gel electrophoresis

- 전기영동: 전하를 띤 물질이 전기장 안에서 움직이는 현상

$$v = Ez/f$$

v: 이동속도

E: 전기장의 세기

z: 분자의 알짜전하

f: 마찰계수

$$f = 6\pi\eta r$$

π : pi

η : 용매의 점도

r: 분자의 반지름

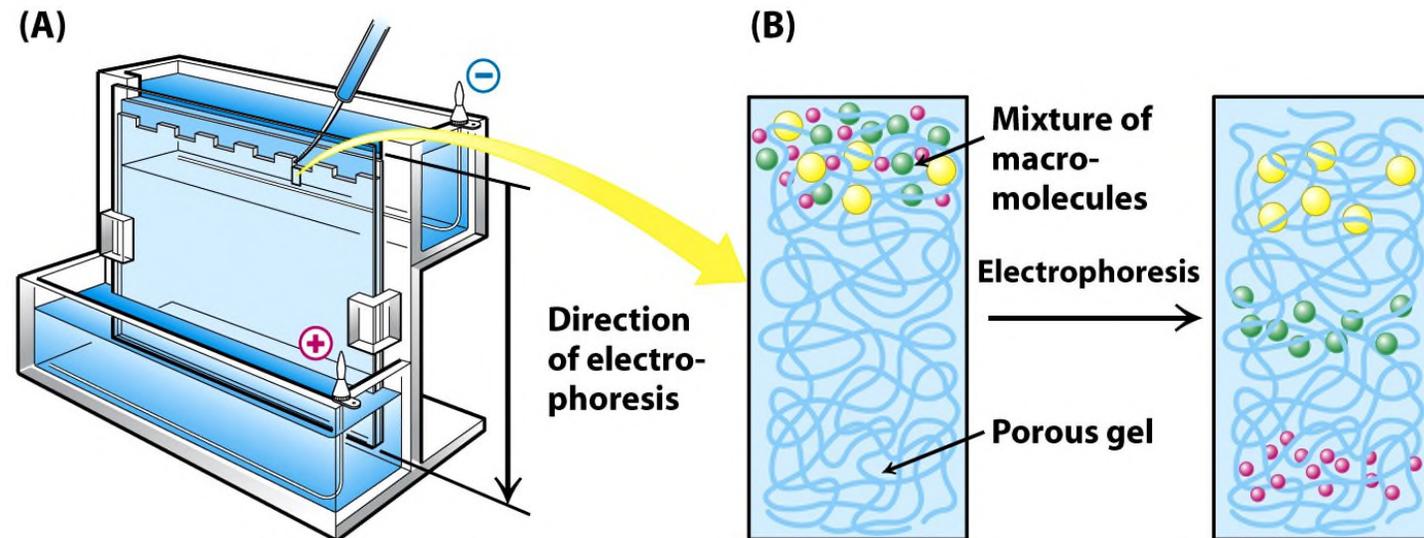


Figure 3-7
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- gel electrophoresis의 매질 (matrix)
 - = DNA/RNA: Agarose gel
 - = Protein : polyacrylamide gel

- 전기영동 시 단백질의 분리 요인:
 - = Size
 - = Charge
 - = Shape

- Polyacrylamide gel
 - = Native gel electrophoresis:
 - 단백질의 알짜전하와 모양에 의해 분리
 - = Denatured gel electrophoresis: 크기
 - Sodium dodecyl sulfate (SDS)
 - beta-mercaptoethanol

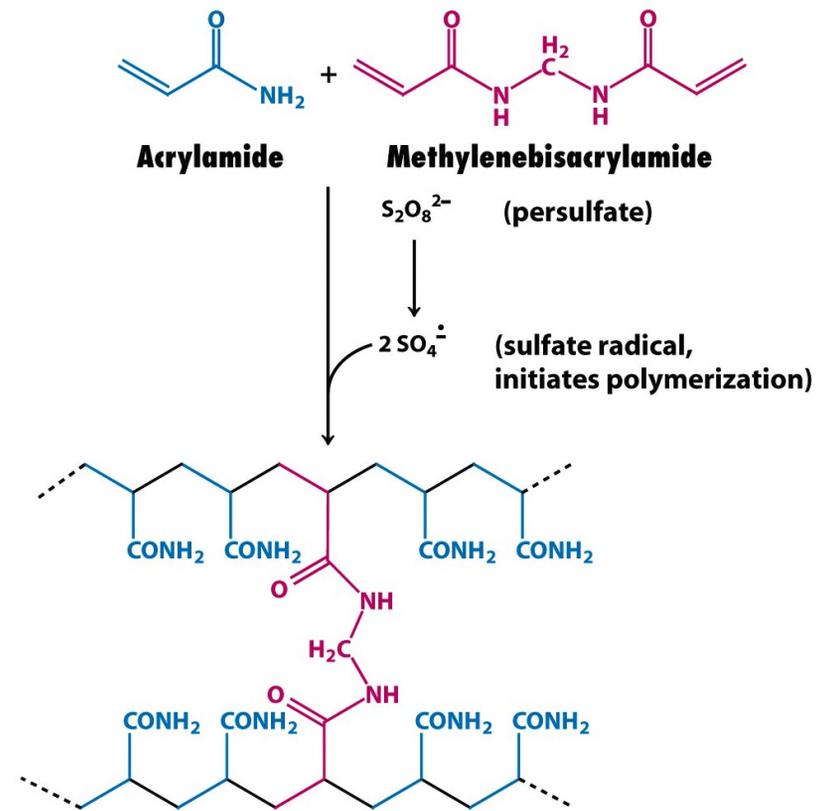
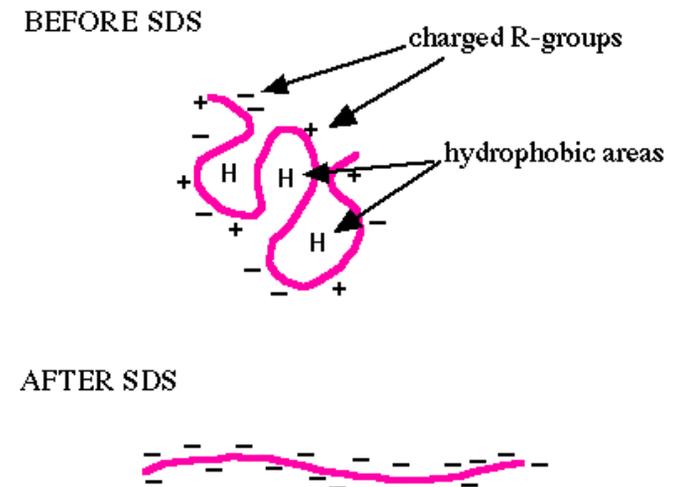
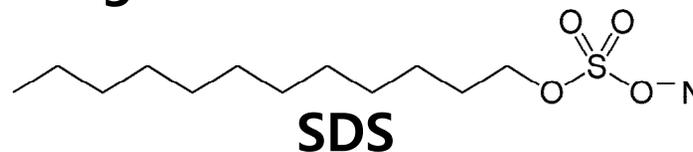


Figure 3-8
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= 단백질 검출

- Autoradiogram: Western
- Coomassie blue staining



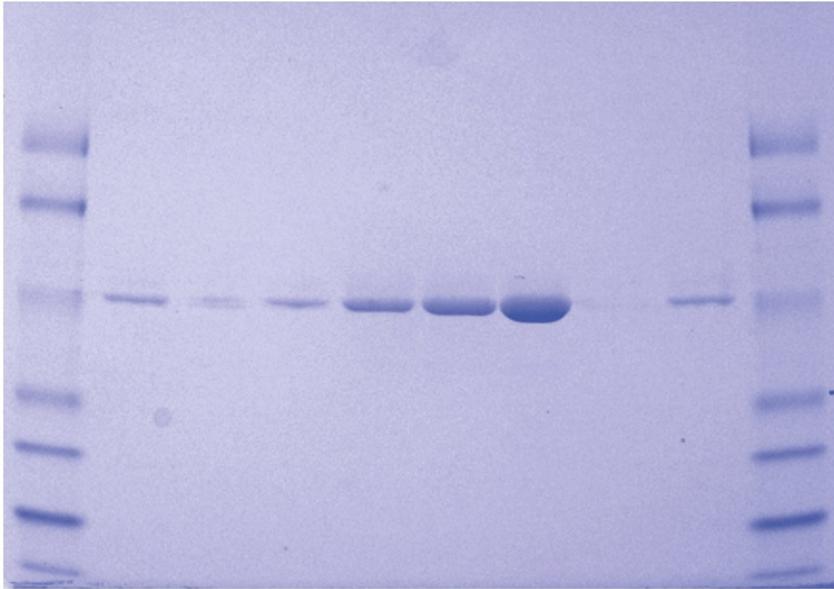


Figure 3-9
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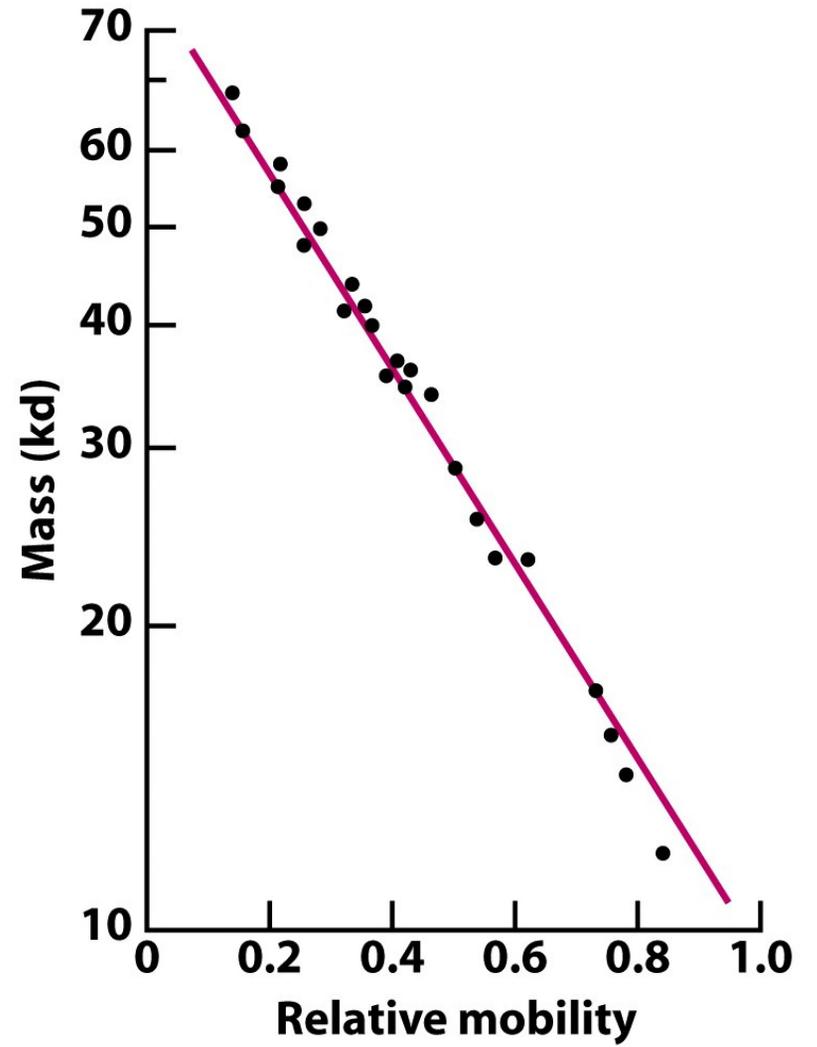
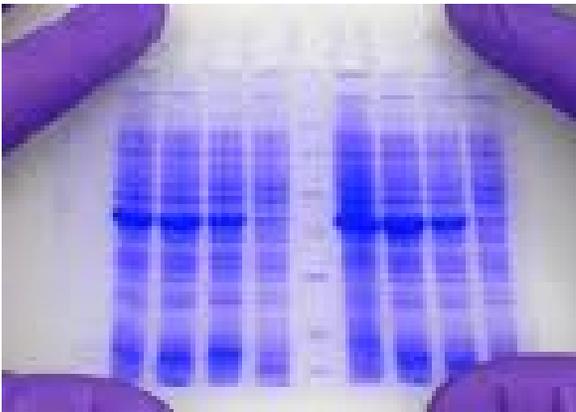


Figure 3-10
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(2) 등전점 전기영동 (Isoelectric focusing)

- 등전점 (**isoelectric point; pI**): 단백질의 알짜전하가 "0"이 되는 pH.
- 단백질의 pI는 이온성 아미노산에 의해 결정된다.
- 등전점에서 단백질은 전기장 안에서 움직이지 않는다.
- polyacrylamide gel 안에서 pH gradient를 만드는 방법.
= polyampholytes

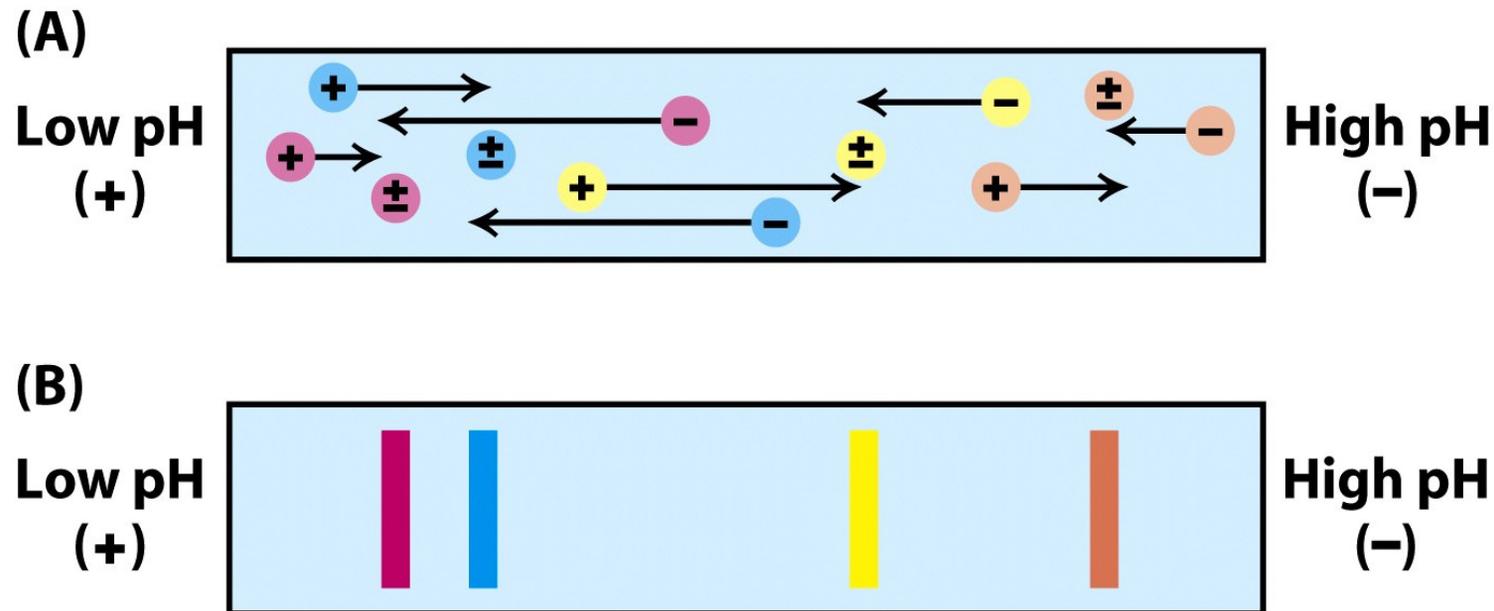


Figure 3-11
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(3) 2차원 전기영동 (Two-dimensional electrophoresis)

- 등전점 전기영동법과 SDS-전기영동법을 합쳐 단백질을 분리하는 기술
- = 1차원 전기영동: 등전점 전기영동
- = 2차원 전기영동: SDS-PAGE
- 이 기술은 단백질체 분석에 이용됨.

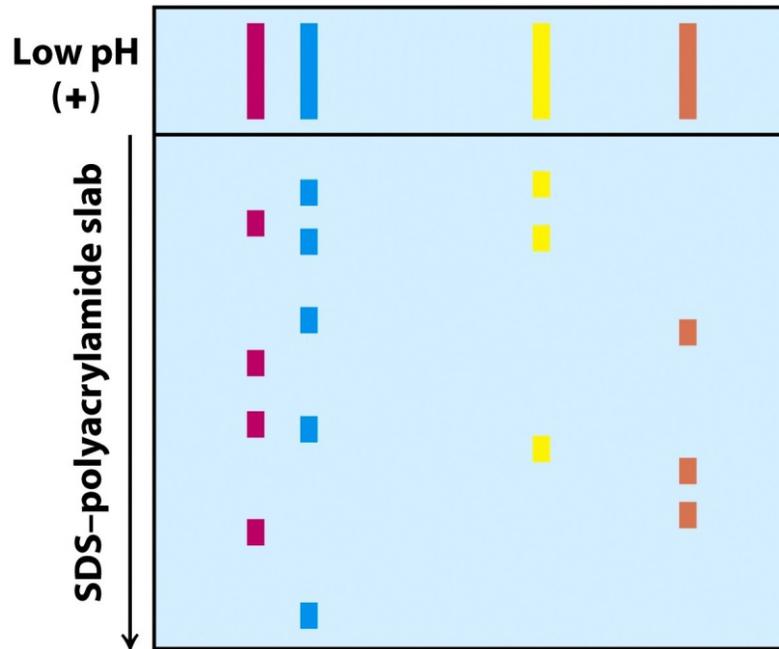


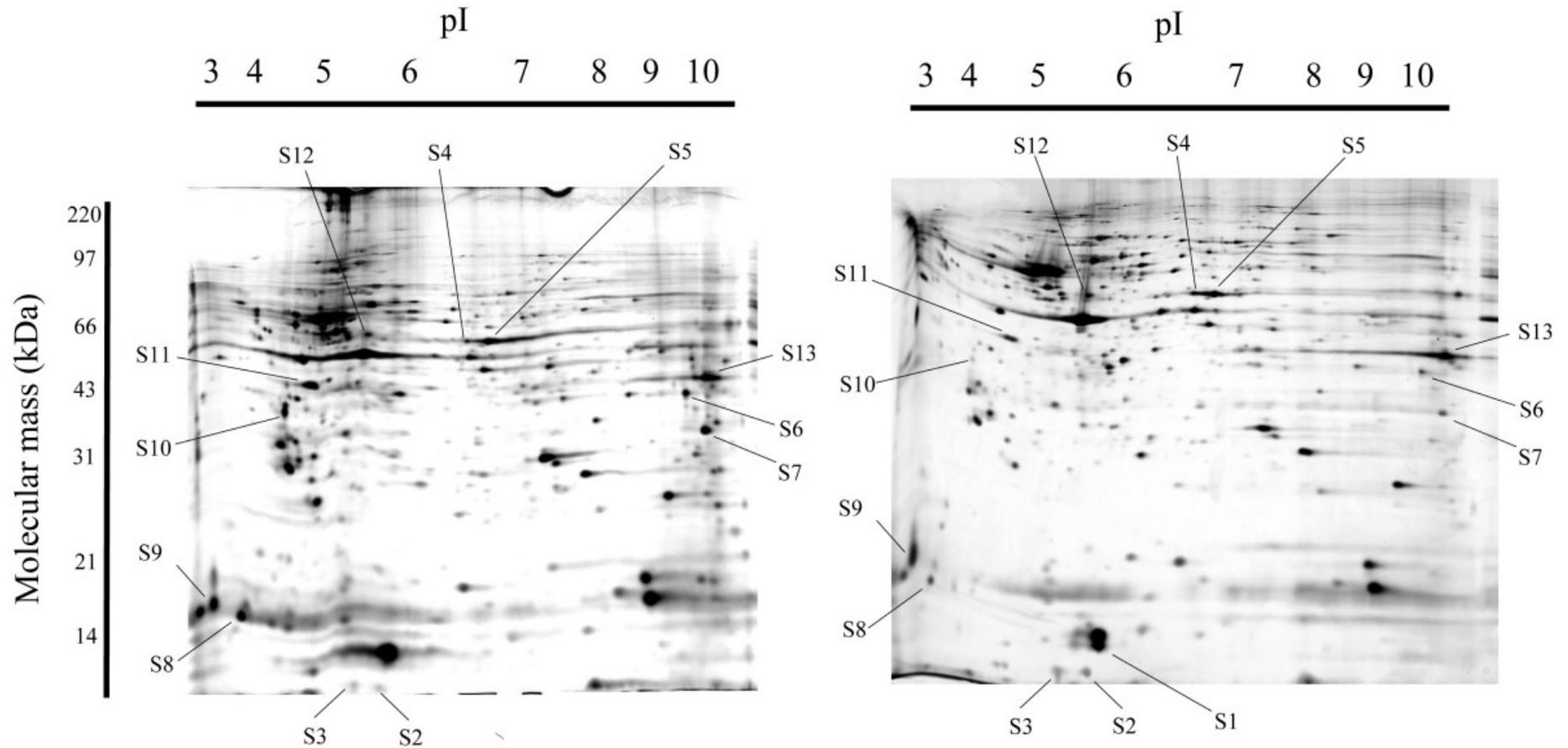
Figure 3-12a
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Isoelectric focusing



Figure 3-12b
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Application of 2D-gel electrophoresis on the proteomics analysis



5) 단백질 정제 계획을 정량적으로 검토할 수 있다.

- 각 정제 단계의 효율을 측정하는 방법

= 비활성 (specific activity)의 증가를 측정하는 방법: assay

= 단백질 순도를 측정하는 방법: electrophoresis

(1) To check increase of specific activity

TABLE 3.1 Quantification of a purification protocol for a fictitious protein

Step	Total protein (mg)	Total activity (units)	Specific activity, (units mg ⁻¹)	Yield (%)	Purification level
Homogenization	15,000	150,000	10	100	1
Salt fractionation	4,600	138,000	30	92	3
Ion-exchange chromatography	1,278	115,500	90	77	9
Gel-filtration chromatography	68.8	75,000	1,100	50	110
Affinity chromatography	1.75	52,500	30,000	35	3,000

Table 3-1
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(2) To check protein content

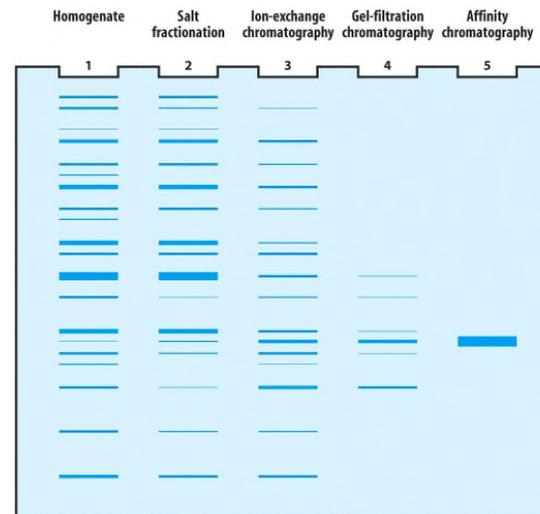


Figure 3-13
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6) 초원심분리는 생체분자를 분리하고 그 분자량을 결정할 수 있다.

- 원심분리:

= 생체물질의 침강은 질량과 밀도에 의하여 분리됨 mass and density.

= 침강계수: 원심력이 작용하는 장소에서 입자들이 움직이는 속도.

$$s = m(1 - \rho v) / f$$

m: mass

v: particle specific volume

ρ : density of medium

f: frictional coefficient

= Svedberg unit (S): ribosome small subunit (40 S), large subunit (60 S)

TABLE 3.2 S values and molecular weights of sample proteins

Protein	S value (Svedberg units)	Molecular weight
Pancreatic trypsin inhibitor	1	6,520
Cytochrome c	1.83	12,310
Ribonuclease A	1.78	13,690
Myoglobin	1.97	17,800
Trypsin	2.5	23,200
Carbonic anhydrase	3.23	28,800
Concanavalin A	3.8	51,260
Malate dehydrogenase	5.76	74,900
Lactate dehydrogenase	7.54	146,200

Source: T. Creighton, *Proteins*, 2d ed. (W. H. Freeman and Company, 1993), Table 7.1.

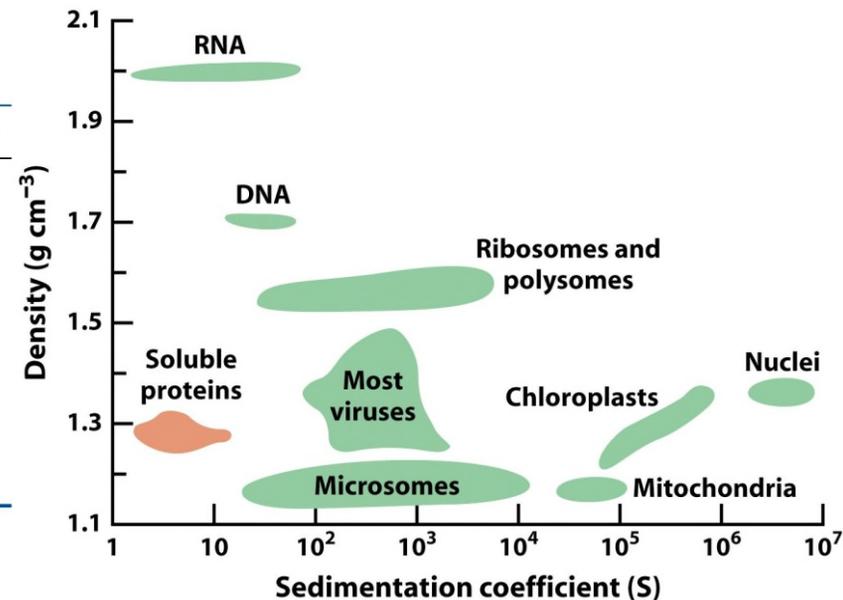


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- 농도구배 원심분리:

= 자연상태의 생체분자들의 분자량을 측정할 수 있게함.

cf) SDS-PAGE 법은 변성된 단백질의 분자량을 측정할 수 있음.

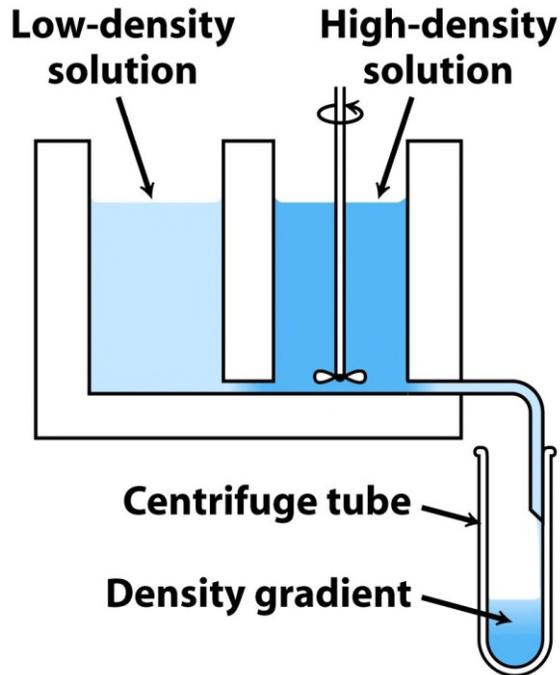


Figure 3-15a
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Layering of sample

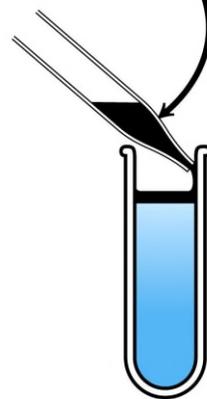


Figure 3-15b
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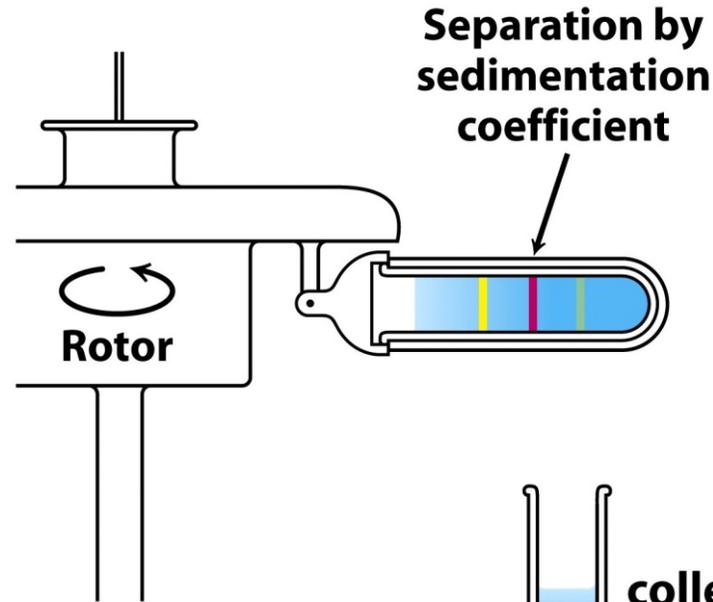


Figure 3-15c
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Fractions collected through hole in bottom of tube

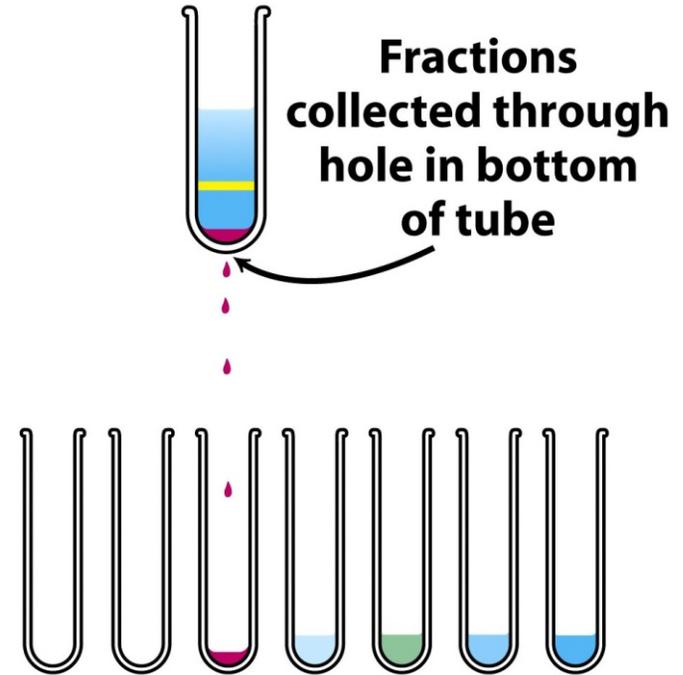


Figure 3-15d
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3.3 면역학은 단백질을 연구하는 중요한 기법들을 제공한다.

1. 특정단백질에 대한 항체를 만들 수 있다

- Antibody: Immunoglobulin G (IgG)

- Antigen:

= Epitope (antigenic determinant)

- 항체의 생산

= Immunization: inject antigen into rabbit two times (boosting)

= Antiserum:

= Polyclonal antibody:

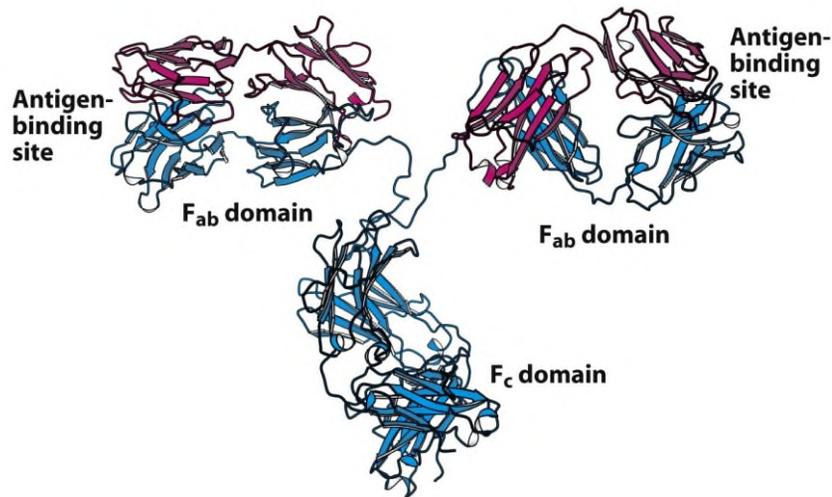


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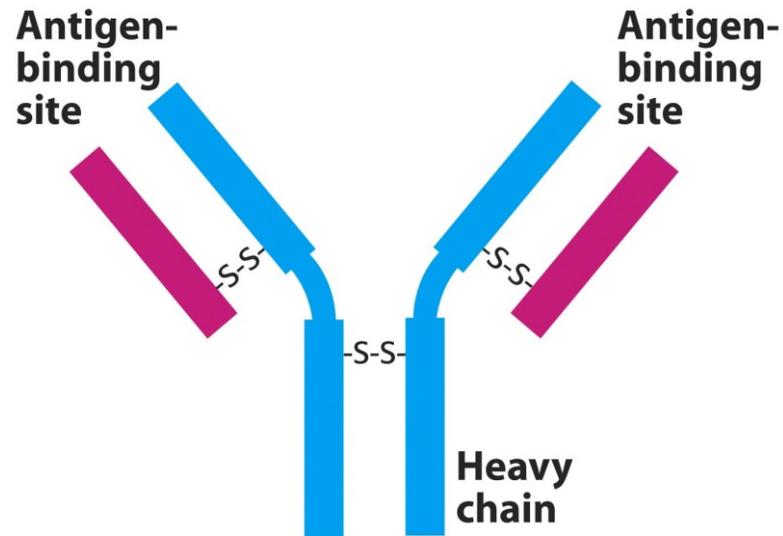


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Antigen-Antibody reaction

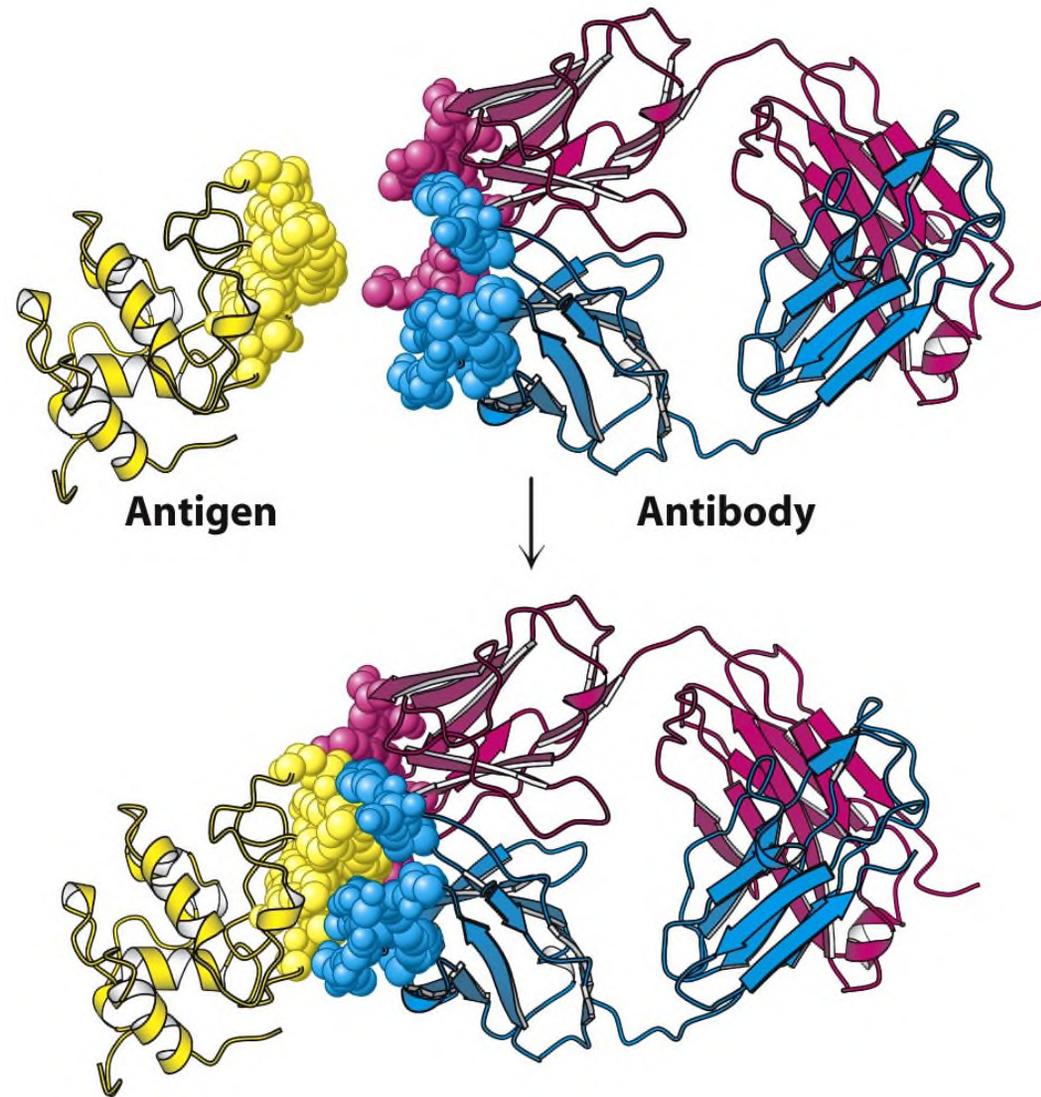


Figure 3-28
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2. 단일클론항체 (Monoclonal antibody) 생산 - Single epitope binding antibody

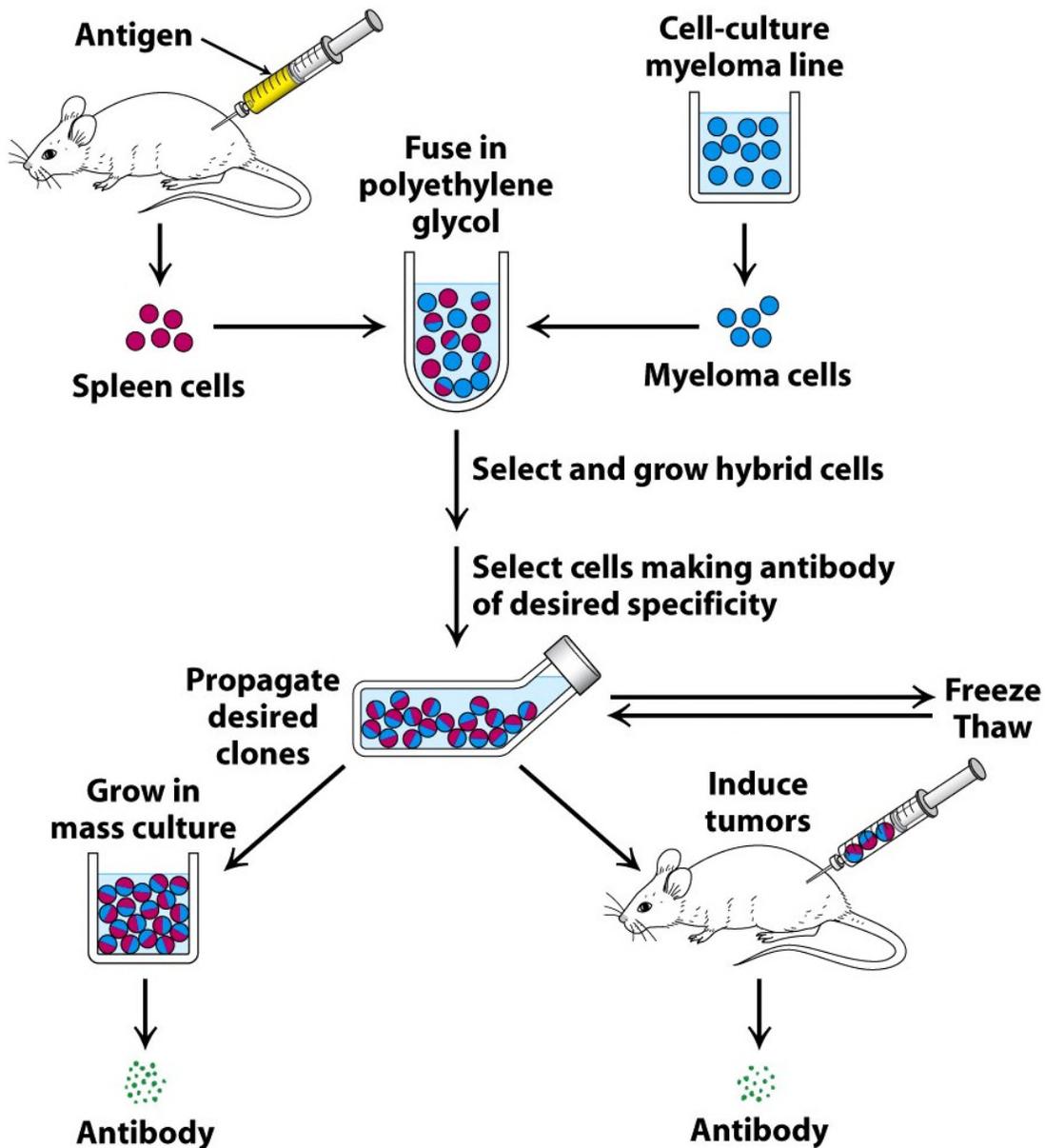


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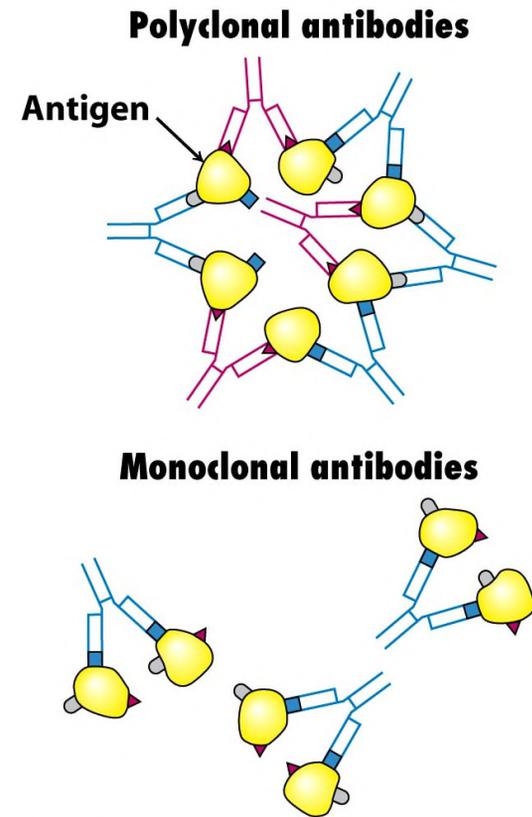


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Figure 3-31
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3. 단백질 검출은 ELISA 기술을 이용하여 가능하다.

- 샘플속에 ng 단백질을 검출할 수 있음

= AIDS virus 단백질 검출

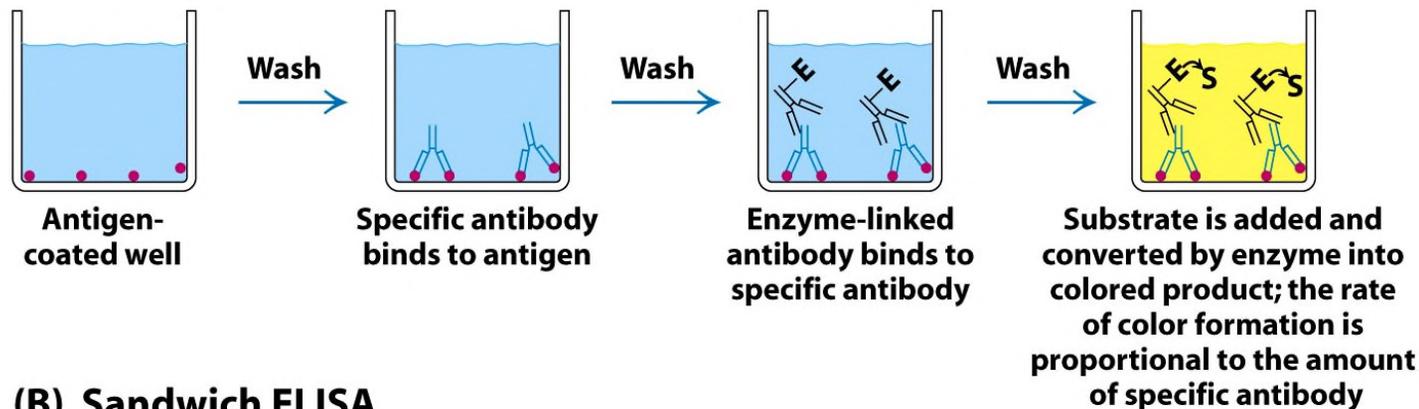
= 혈액 중 Insulin 측정

- ELISA (Enzyme Linked Immunosorbent Assay)

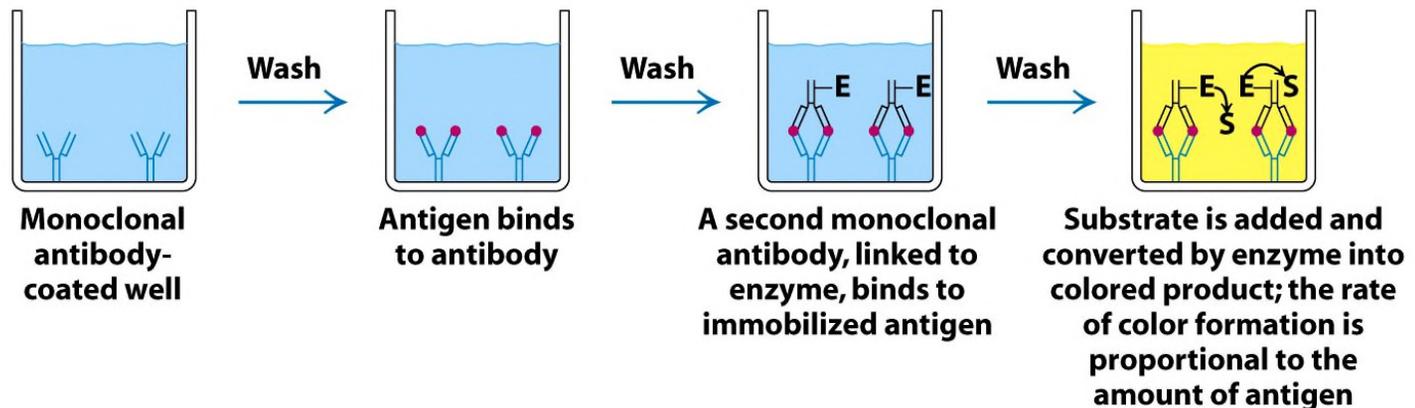
= 간접법: 특정항원에 특이적인 항체의 존재 유무를 측정함

= Sandwich ELISA: 항원을 직접 측정할 수 있음.

(A) Indirect ELISA



(B) Sandwich ELISA



4. Western blotting 기술은 gel electrophoresis에 의해 분리된 단백질을 측정할 수 있다.

- SDS-PAGE: 단백질 크기에 의한 분리
- 단백질의 검출은 특이항체 (primary Ab)에 의해 결정되고, 그 항체는 anti-IgG 항체 (2nd antibody)에 의해 검출됨

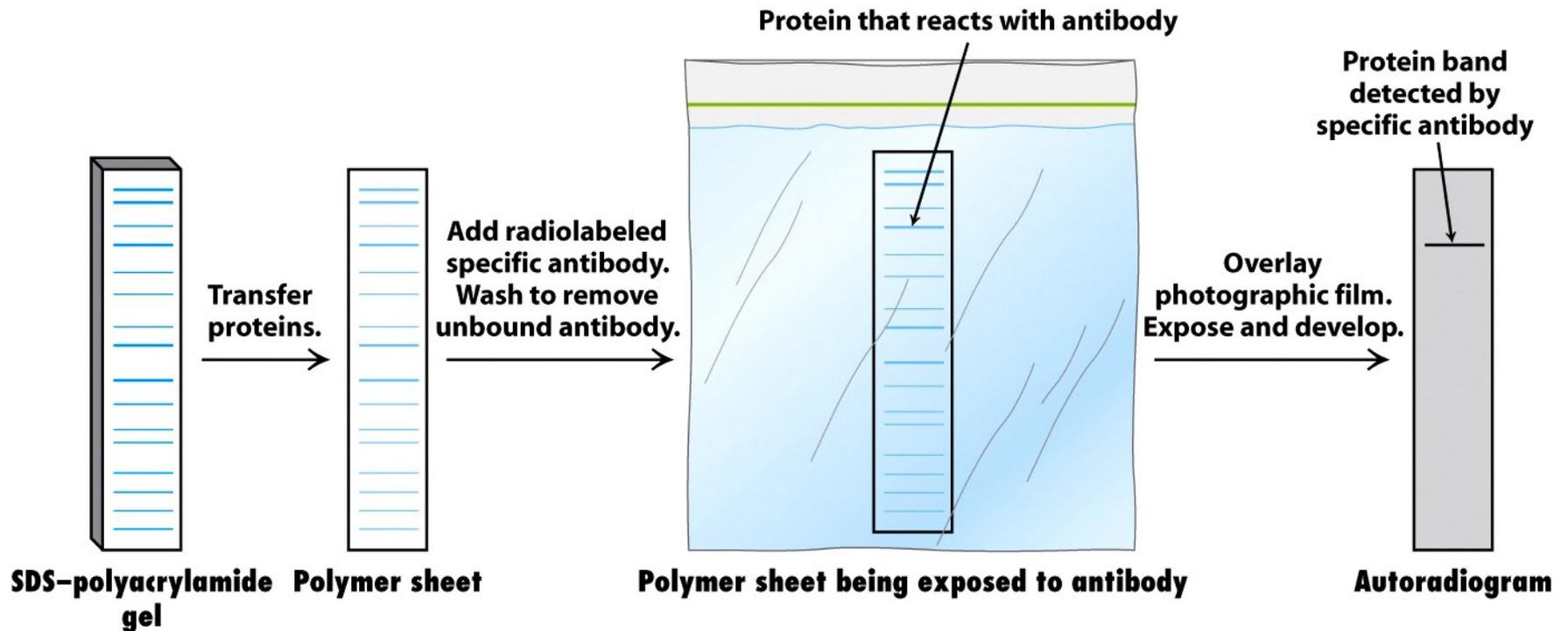


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5. 형광 표지물은 단백질을 눈으로 확인할 수 있게 해준다.

- 형광물질이 붙어 있는 항체는 세포내 단백질을 검출할 수 있음
 - = Fluorescent microscopy
 - = Immunohistochemistry
 - = Confocal microscopy (공초점 현미경)
- Green fluorescent protein (GFP): real time protein location

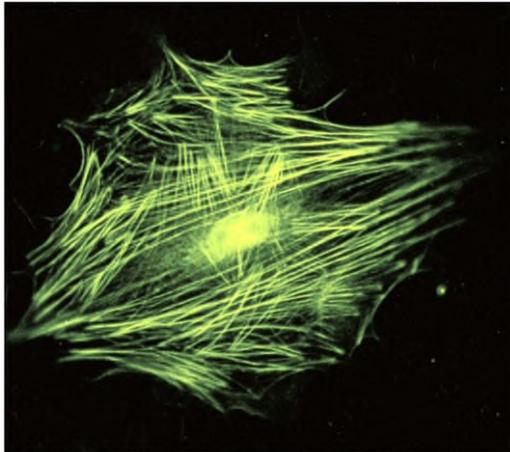


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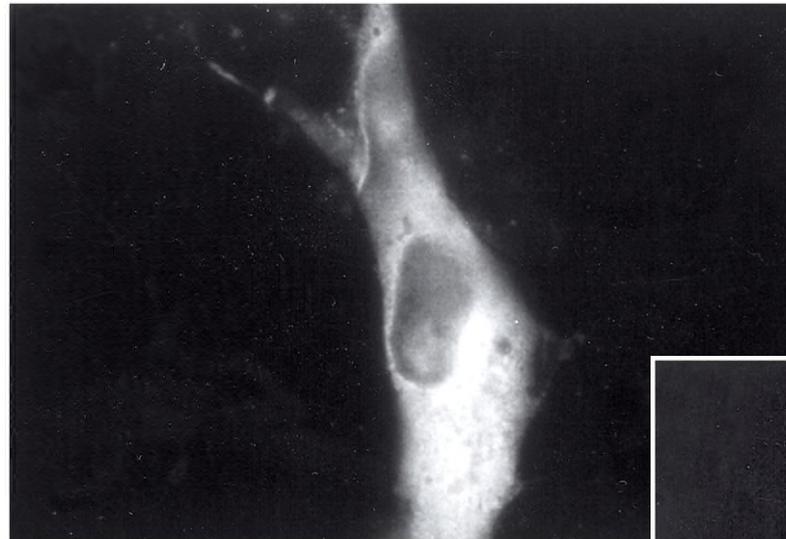


Figure 3-35a
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Figure 3-35b
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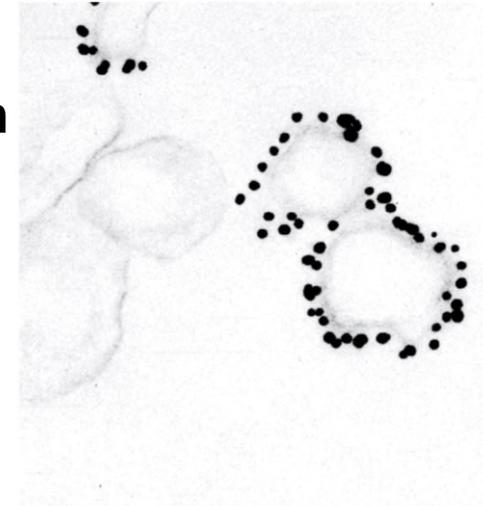


Figure 3-36
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3.5 Mass spectrometry

1. The Mass of a protein can be determined by Mass spectrometry.

- Ionization method

= Matrix-Assisted Laser Desorption-Ionization (MALDI)

= Electrospray ionization (ESI):

- Separation of mass (determine the mass of proteins or peptide):

= Time of flight (TOF)

- Mass spectrometry: MALDI-TOF

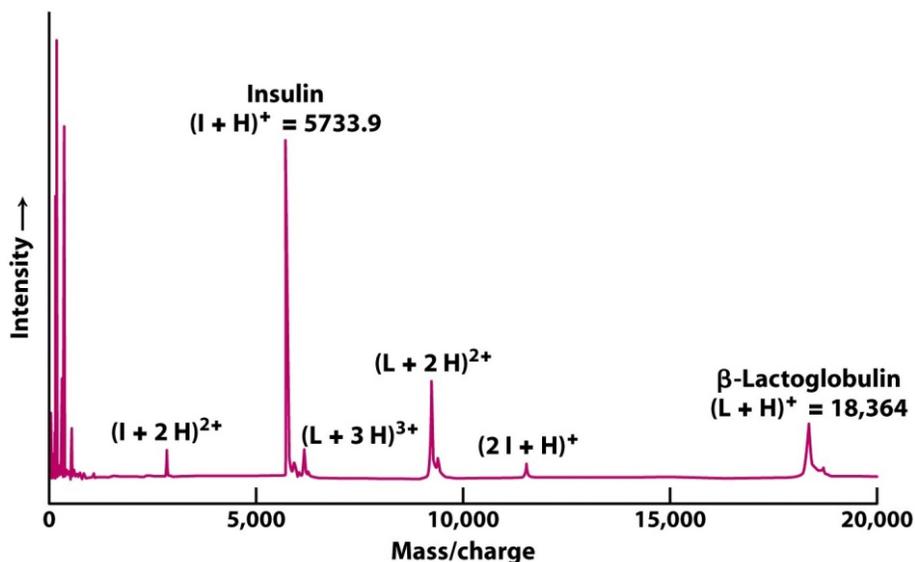


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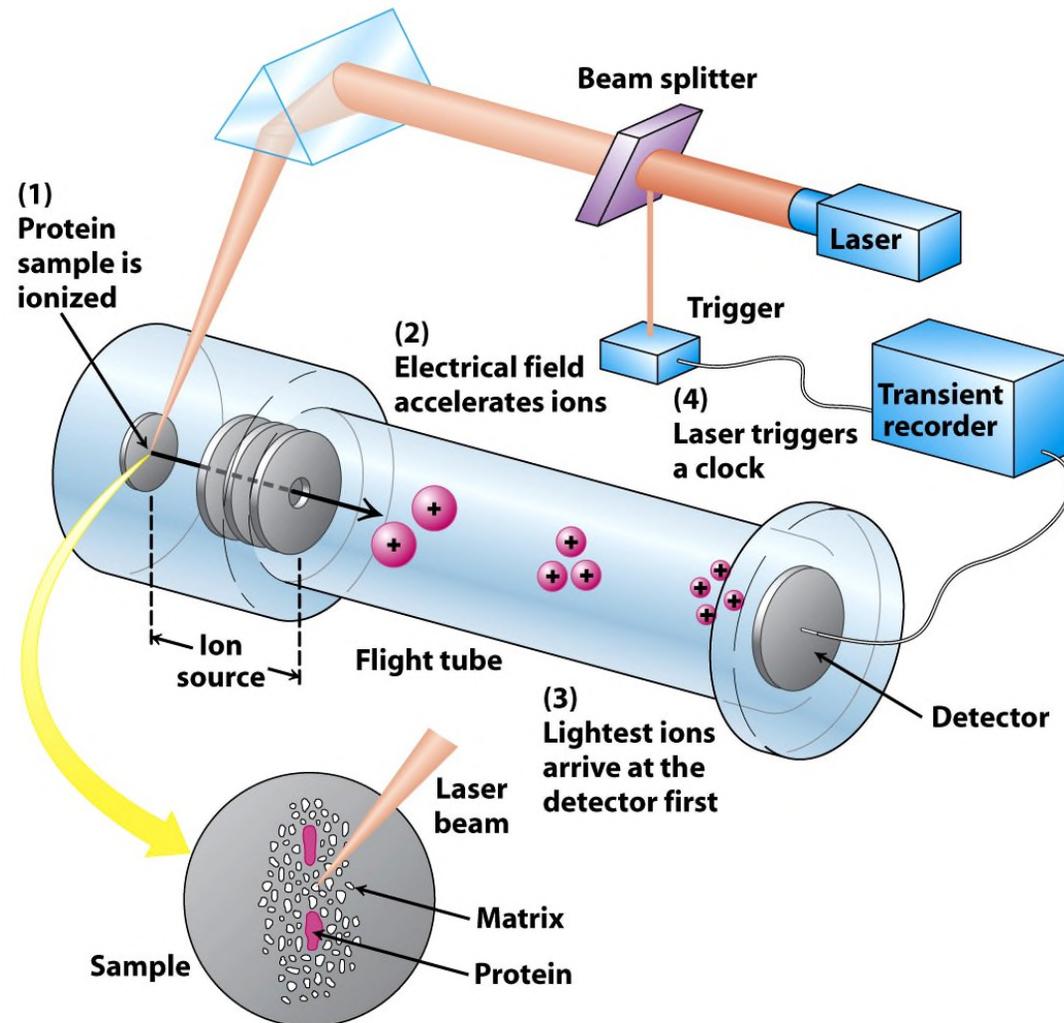


Figure 3-40
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3.6 3차원 단백질의 구조는 X-ray 결정학과 NMR 분광법으로 결정될 수 있다.

1. X-ray 결정학은 단백질의 3차 구조를 밝힐 수 있음.

- Protein crystal: depends on the proteins
- Source of X-ray: x-ray generator or synchrotron radiation
- Detector: Detect the scattered beam.
- Electron density determination

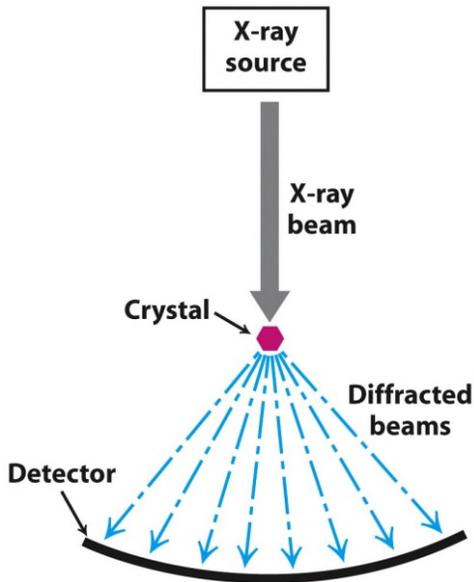


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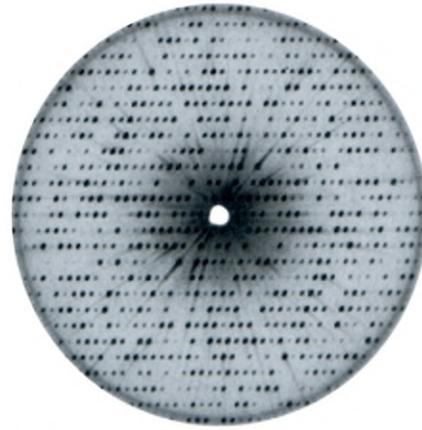


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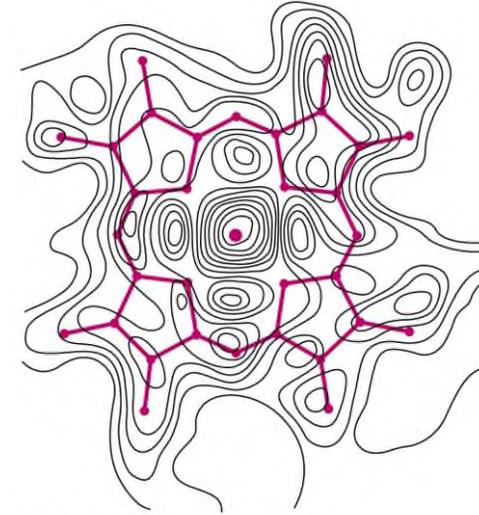
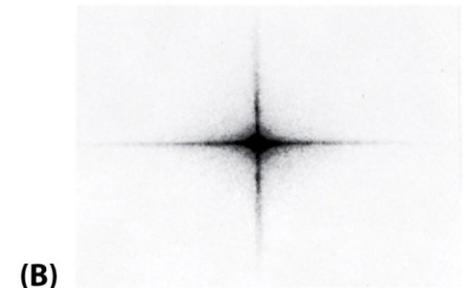


Figure 3-45
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Resolution is depended on wave length



Figure 3-47
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(D)

2. NMR 분광법은 용액속에 존재하는 단백질을 검출할 수 있음.
- Calculate the hydrogen atom distribution in molecules.

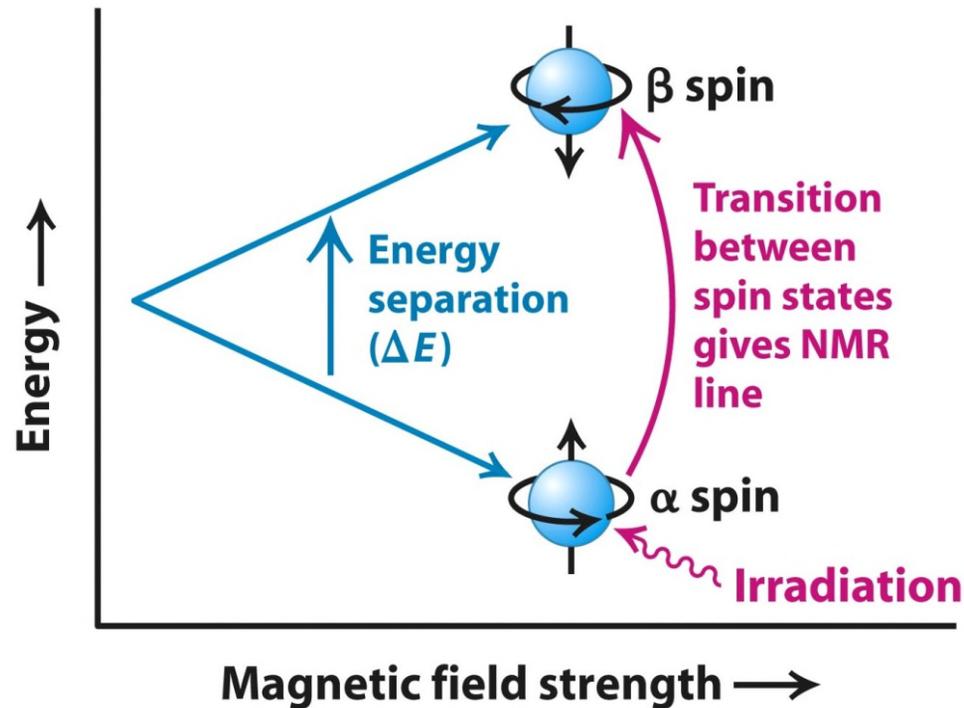


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