

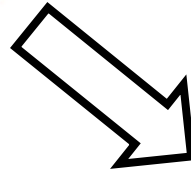
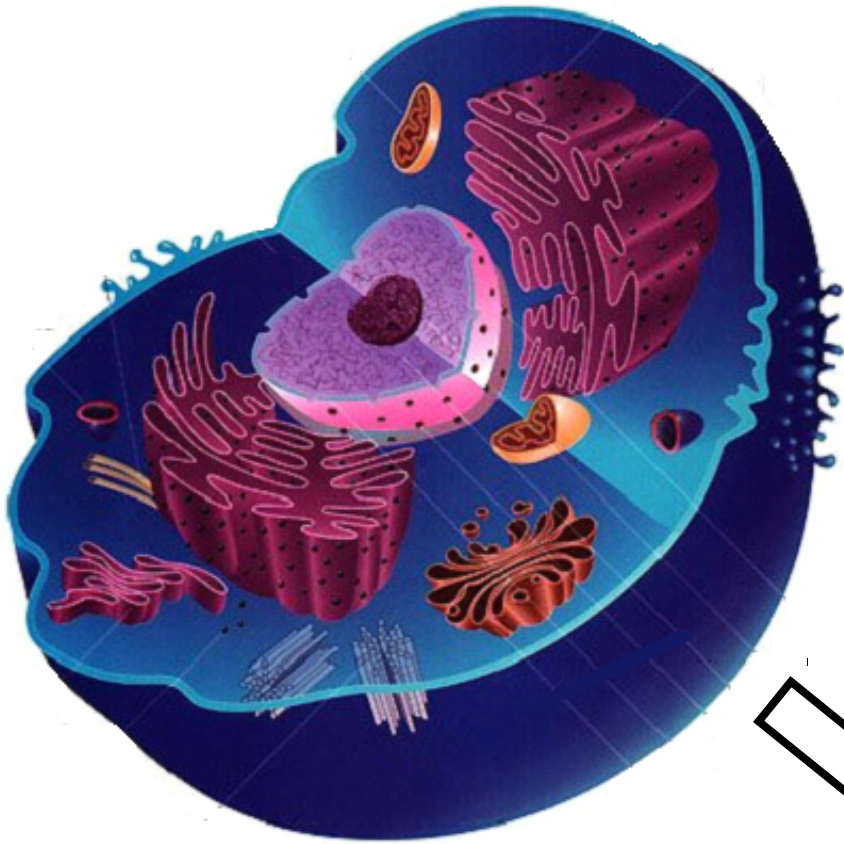
Gels and their uses

jamie.davies@ed.ac.uk

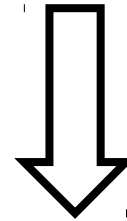


Pic: fathom.com

The problem:



100,000 proteins



We generally want to study just one or two

Separation techniques:

- Gel electrophoresis
- Filtration
- Differential precipitation
- Gel filtration
- Chromatography (generally HPLC)
- Affinity chromatography

Separation techniques:

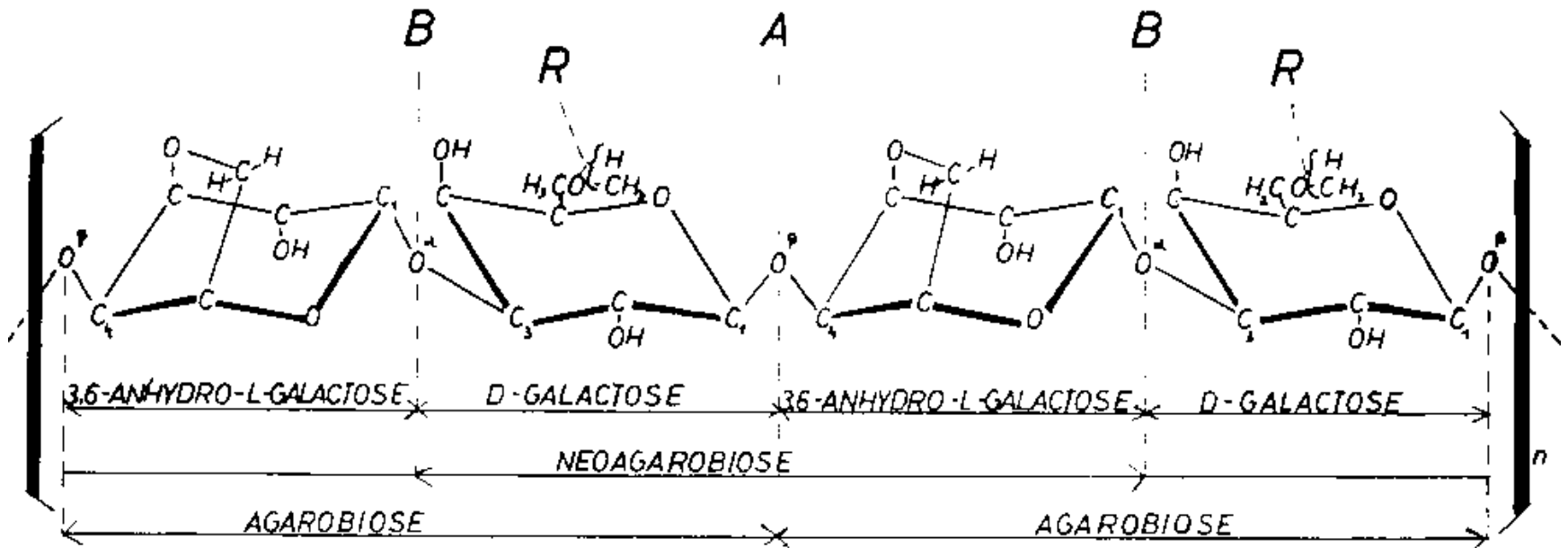
- Gel electrophoresis *****
- Filtration
- Differential precipitation
- Gel filtration
- Chromatography (generally HPLC)
- Affinity chromatography

What is a gel?

- A **gel** (from the *lat. gelu*—freezing, cold, ice or *gelatus*—frozen, immobile) is a **colloidal** system in which a porous network of interconnected nanoparticles spans the volume of a liquid medium. In general, gels are apparently solid, jelly-like materials. Both by weight and volume, gels are mostly liquid in composition and thus exhibit densities similar to liquids, however have the structural coherence of a solid. An example of a common gel is edible **gelatin**.

From Wikipedia

Agarose gels



A LINK EASILY HYDROLYSED BY ACIDS.

B LINK EASILY HYDROLYSED BY ENZYMES.

R SUBSTITUTION OF -H BY -CH₃ IS CONDITIONED BY THE SEAWEEDS USED.

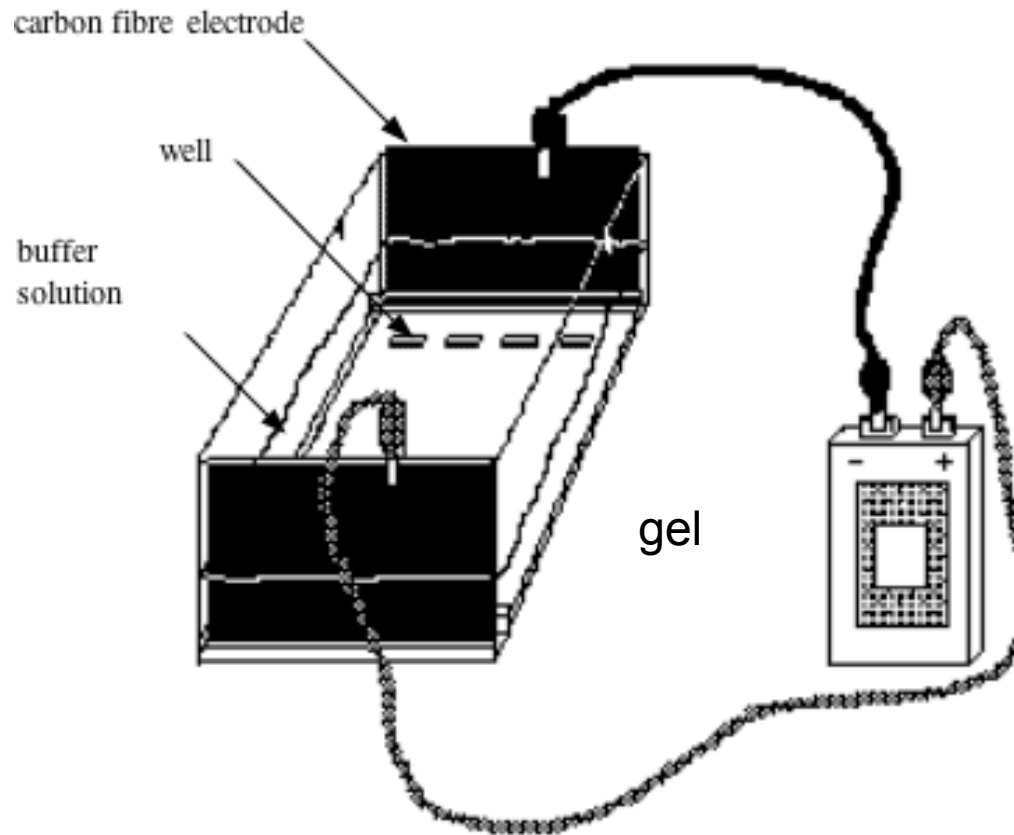
GEL POINT IS INCREASED BY A HIGHER CONTENT OF -CH₃ GROUPS.

n POLYMERIZATION GRADE IT CONDITIONS GEL STRENGTH.

Making an agarose gel:

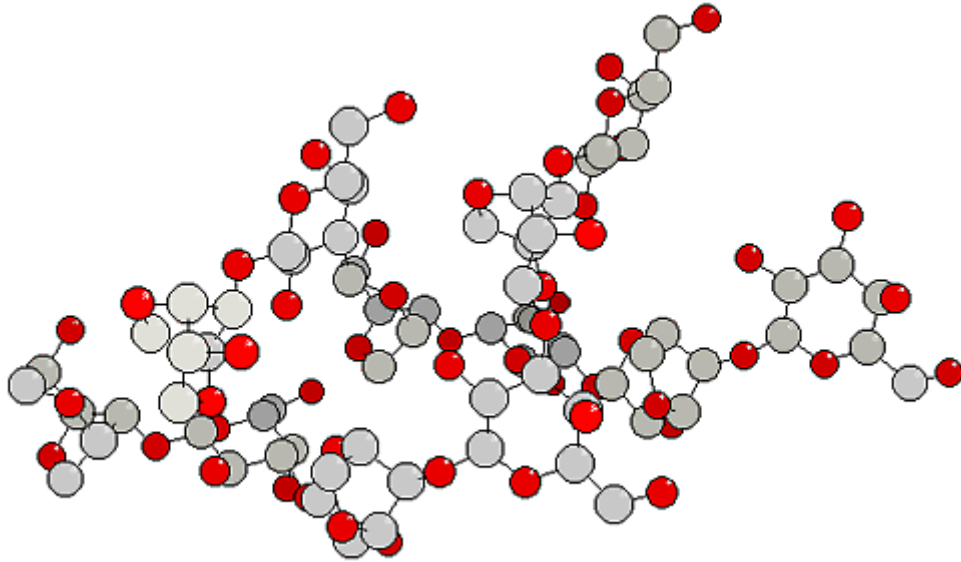
- Suspend agarose in a buffer
- Heat it (about 100 deg. C.): the agarose dissolves
- Let it cool

The basic idea of DNA agarose electrophoresis (more detail later)



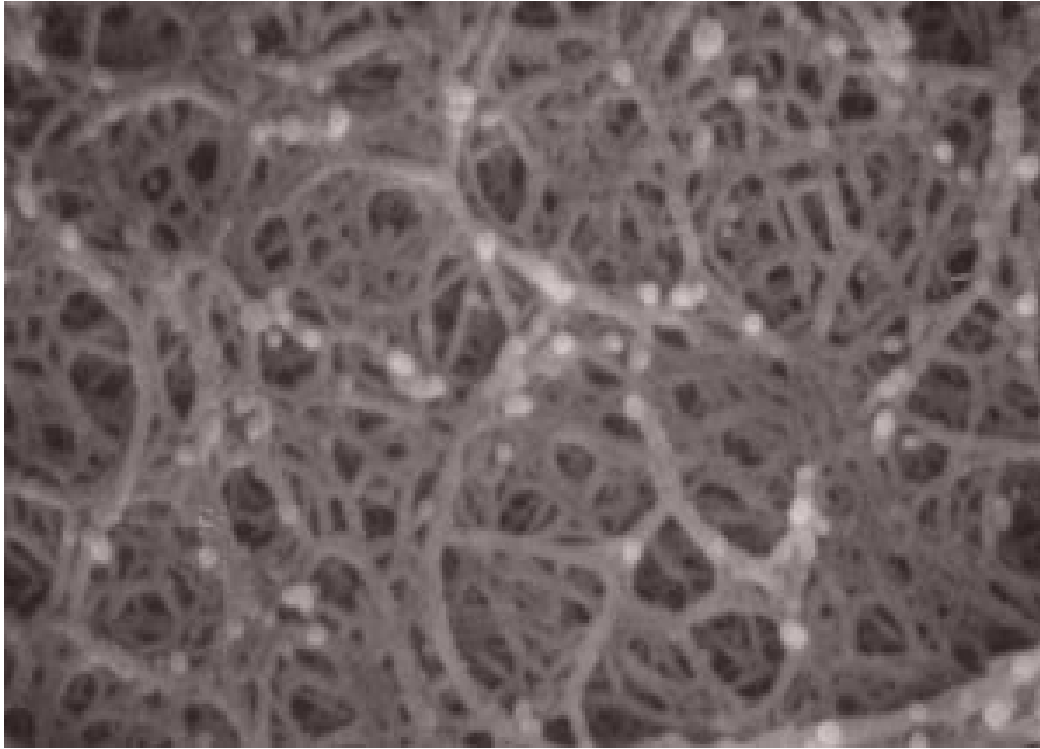
DNA is -vely charged, so seeks the anode

Properties of agarose gels

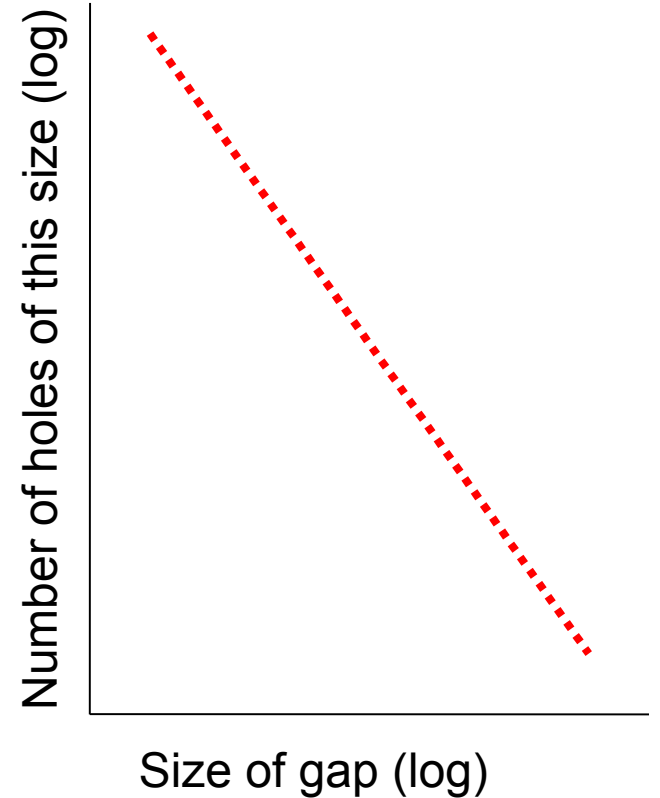


The molecules tangle to make a random network, that has some big holes and some small ones.

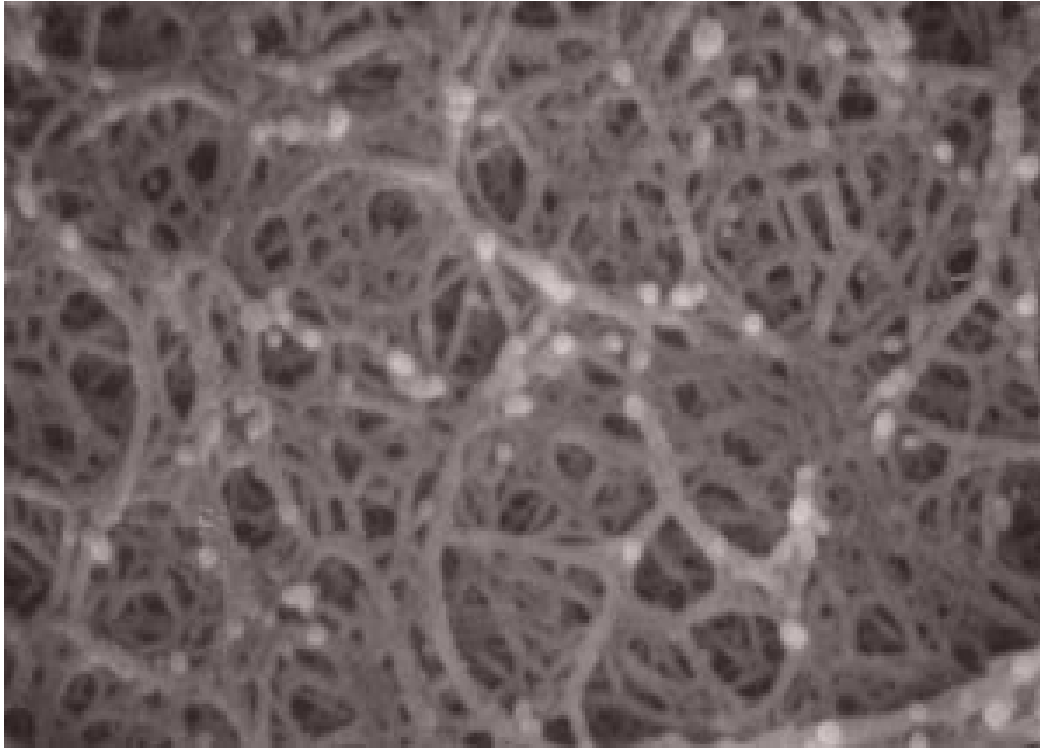
The distribution of gaps is fractal (scale free)



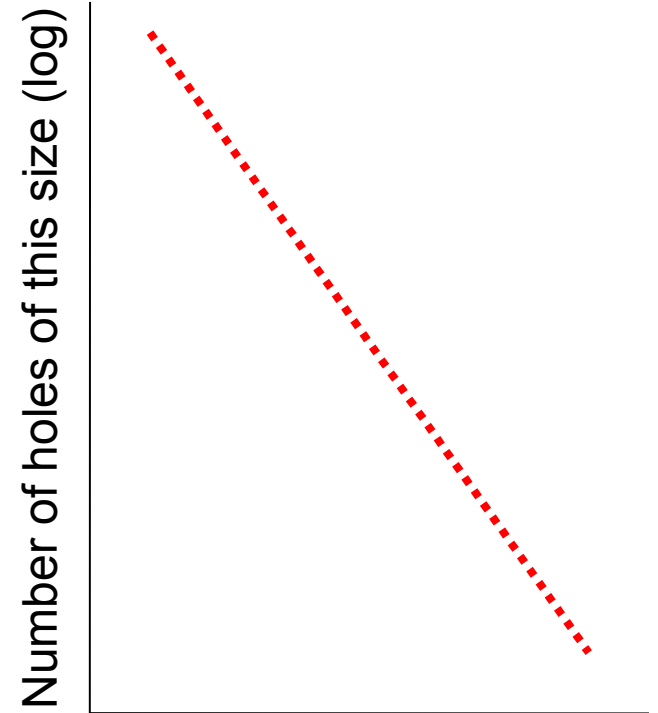
220,000x



The distribution of gaps is fractal (scale free)



220,000x



Size of gap (log)

$$P [X>x] \approx x^{-k}$$

How do large molecules get through?

- Obviously, they cannot get through passages smaller than themselves



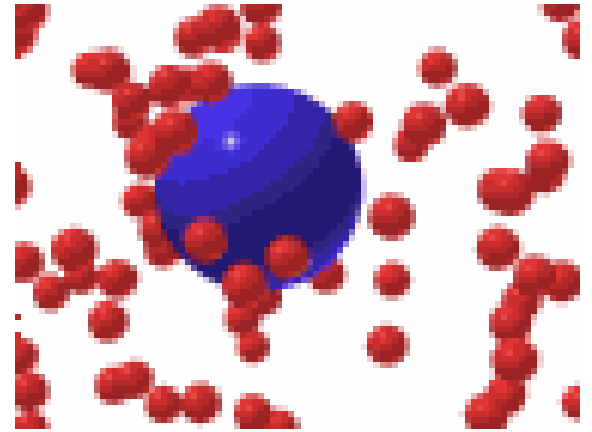
- They can get through passages larger than themselves.

Brownian Motion

$$\langle E \rangle = \frac{3kT}{2}$$

so.... (using $E=0.5mv^2$)

$$v = \sqrt{\frac{3kT}{m}}$$



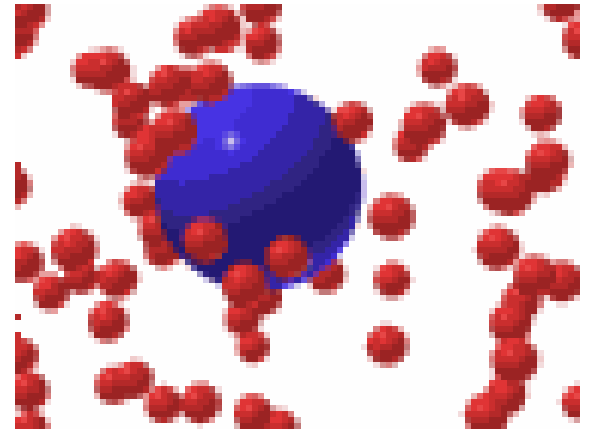
Brownian Motion

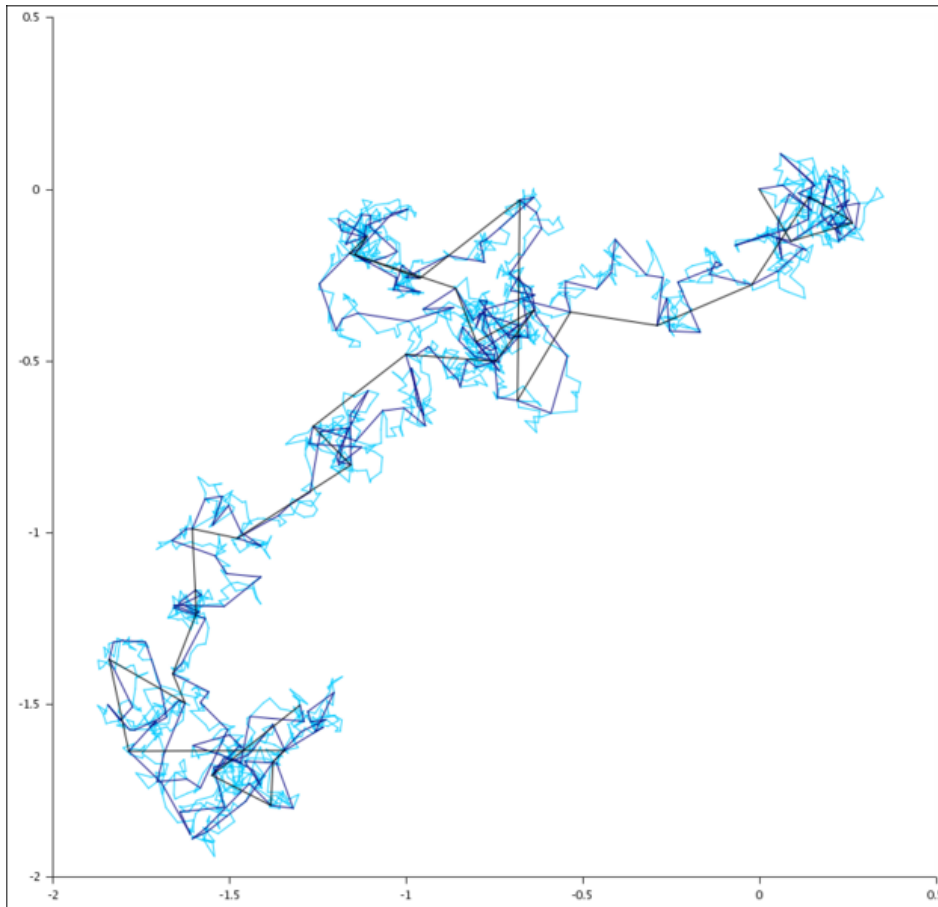
$$\langle E \rangle = \frac{3kT}{2}$$

so.....

$$v = \sqrt{\frac{3kT}{m}}$$

Large particles move more slowly





Simulated random walks

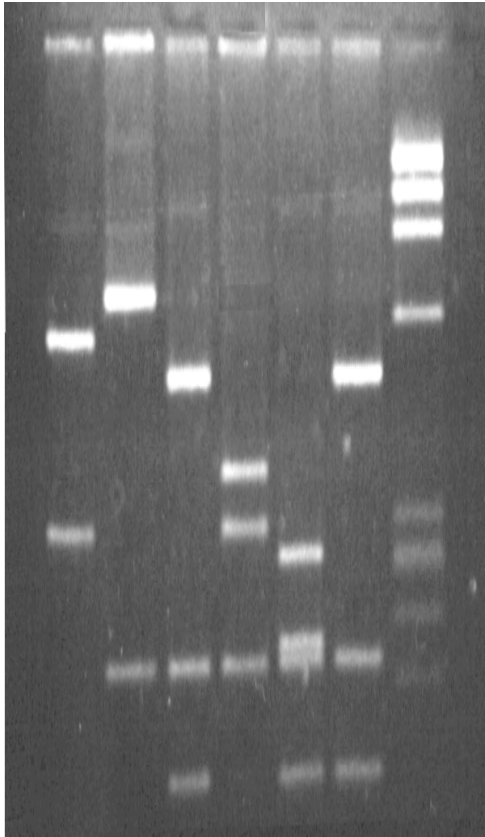
On average, the distance moved in time t ;

$$d = \sqrt{t v}$$

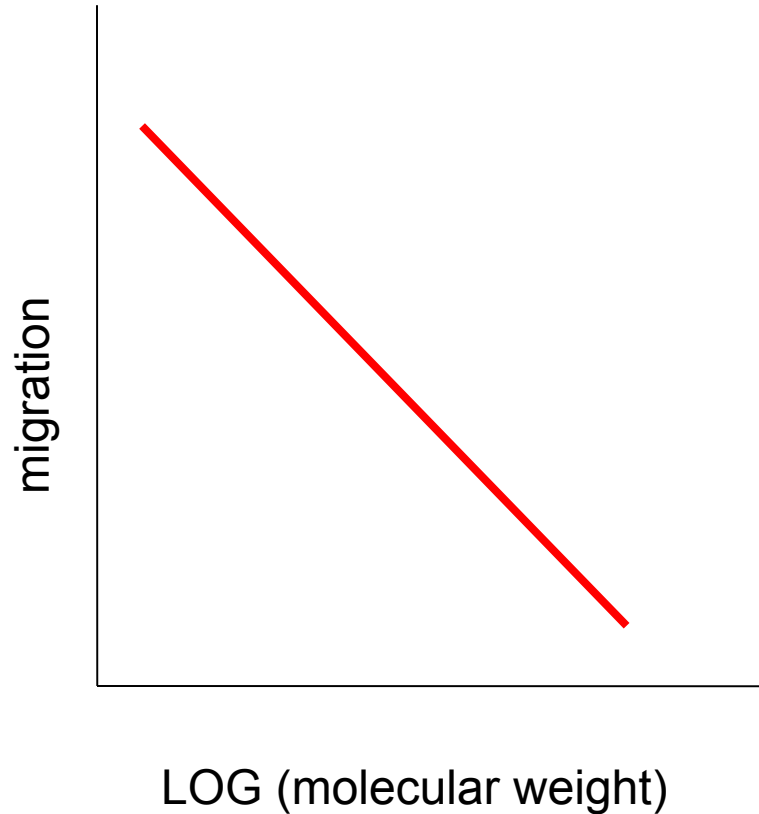
or the time to go distance d ,

$$t = d^2/v$$

On a log/lin graph:

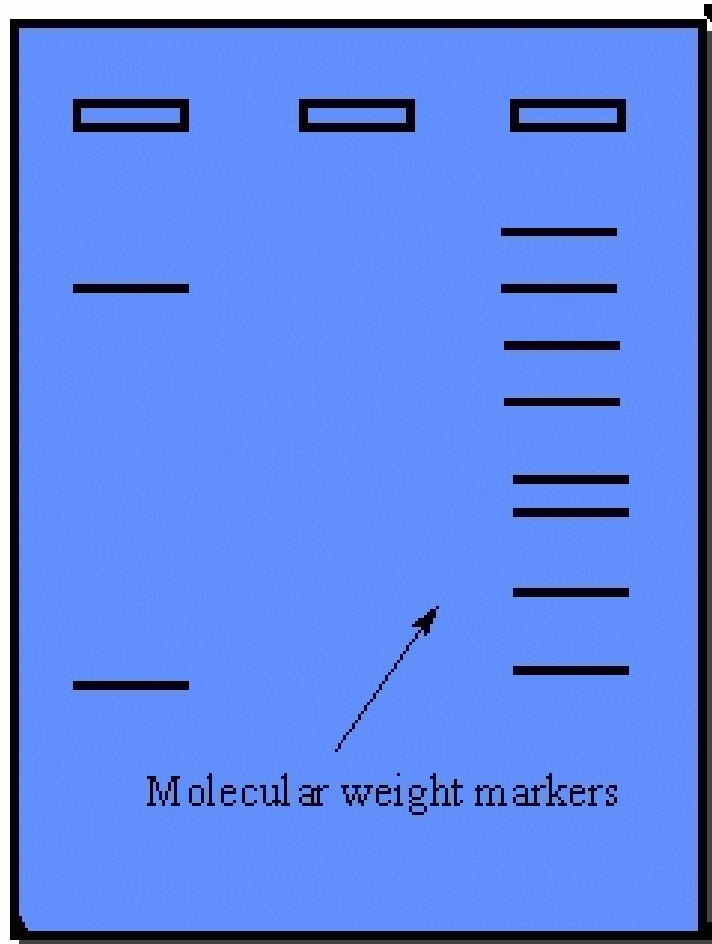


Distance
of
migration



-

+



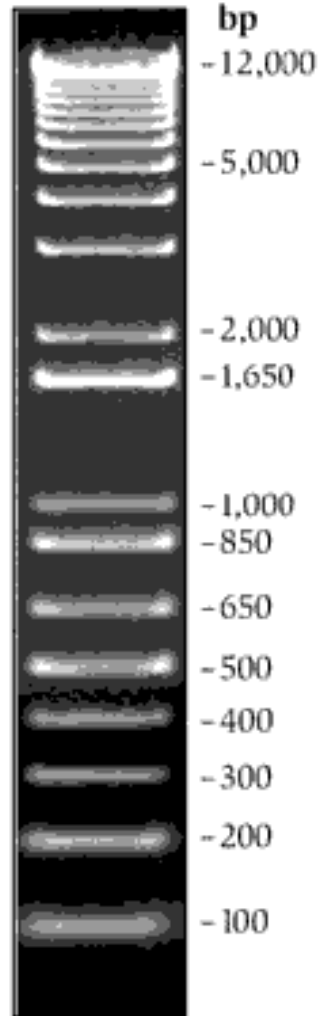
Molecular weight markers



Calibrate your graph with these

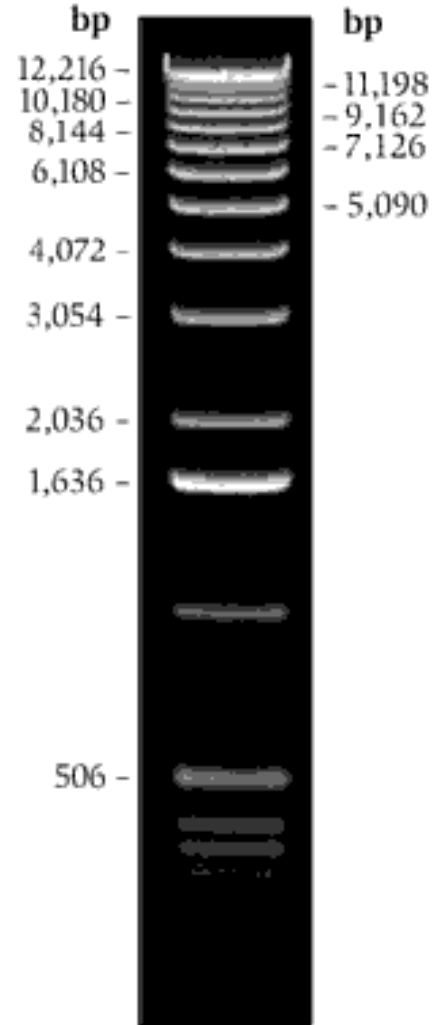
**Comparison between 1 Kb Plus DNA Ladder
and 1 Kb DNA Ladder. 0.9% agarose gel
stained with ethidium bromide**

1 Kb Plus DNA Ladder

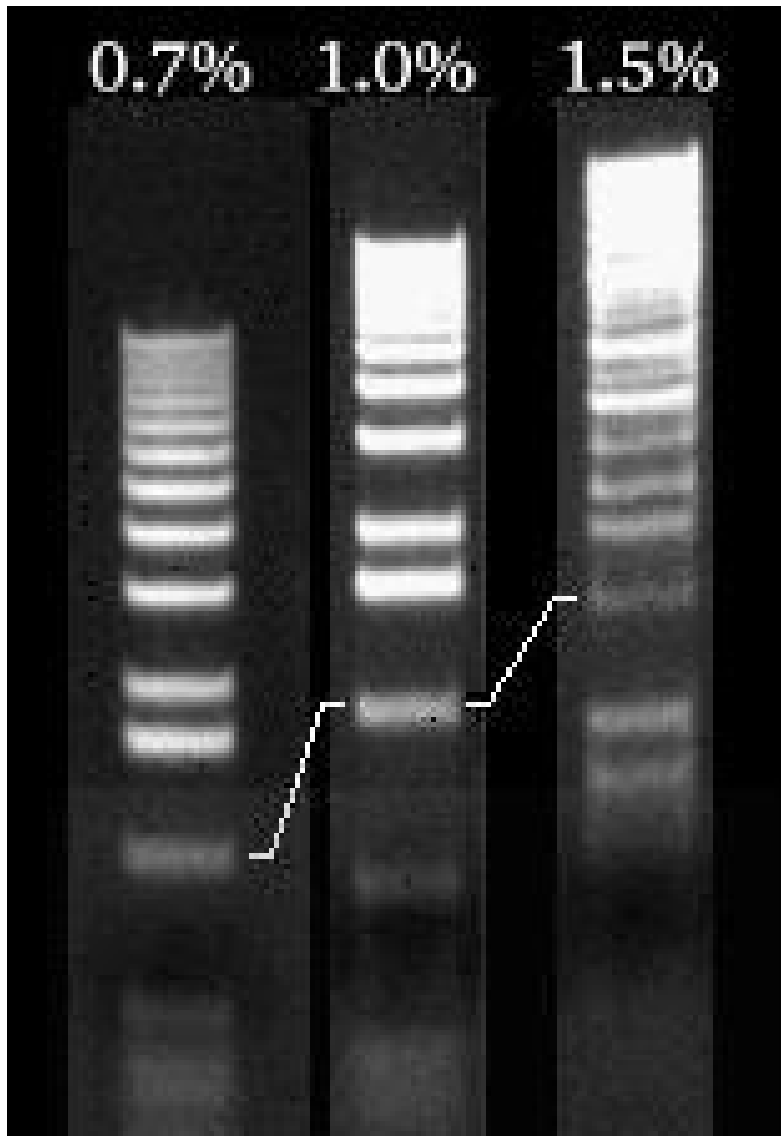


0.9 µg/lane

1 Kb DNA Ladder



0.9 µg/lane



Higher concentrations of agarose facilitate separation of small DNAs, while low agarose concentrations allow resolution of larger DNAs.

Real-world apparatus



Detecting your DNA



Stain with ethidium bromide.



View under uv light.



You can use gels to purify

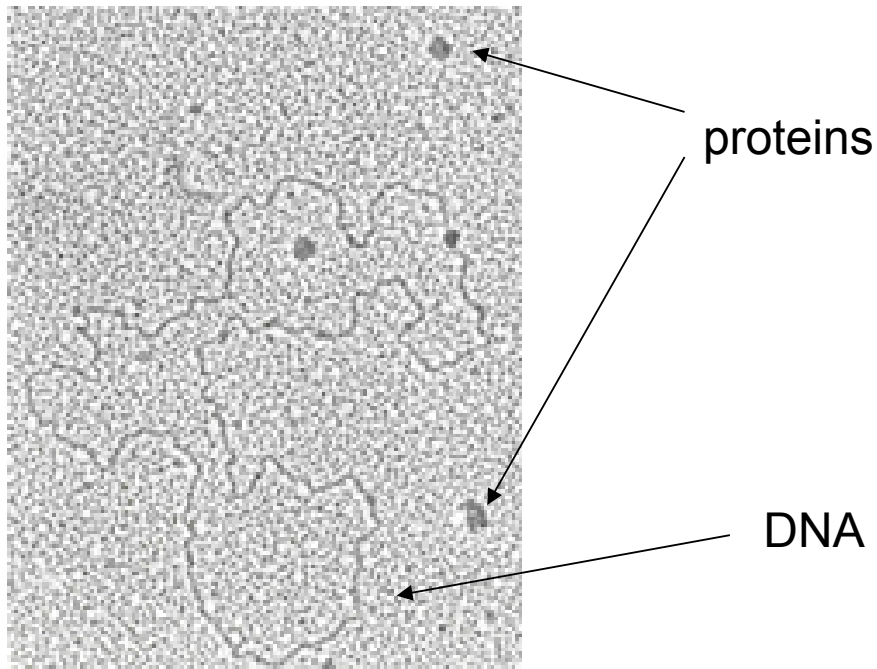


- Physically cut out the band you want (scalpel).
- Melt the agar into a recovery buffer
- Clean agarose away (spin columns).

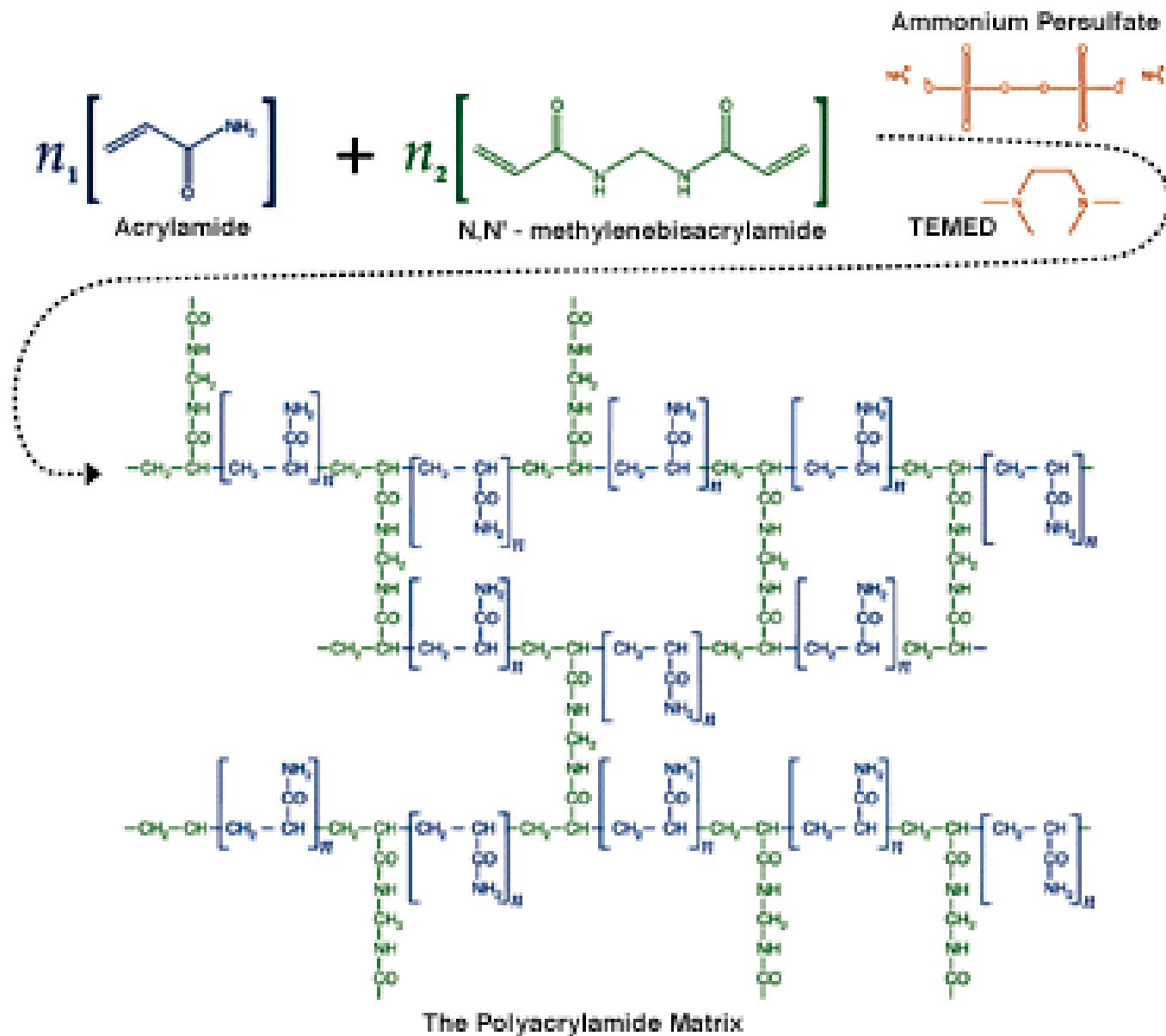
RNA can be treated the same way.

Protein electrophoresis

- Problem 1: proteins are more compact than nucleic acids. They all go through agarose gels too quickly.

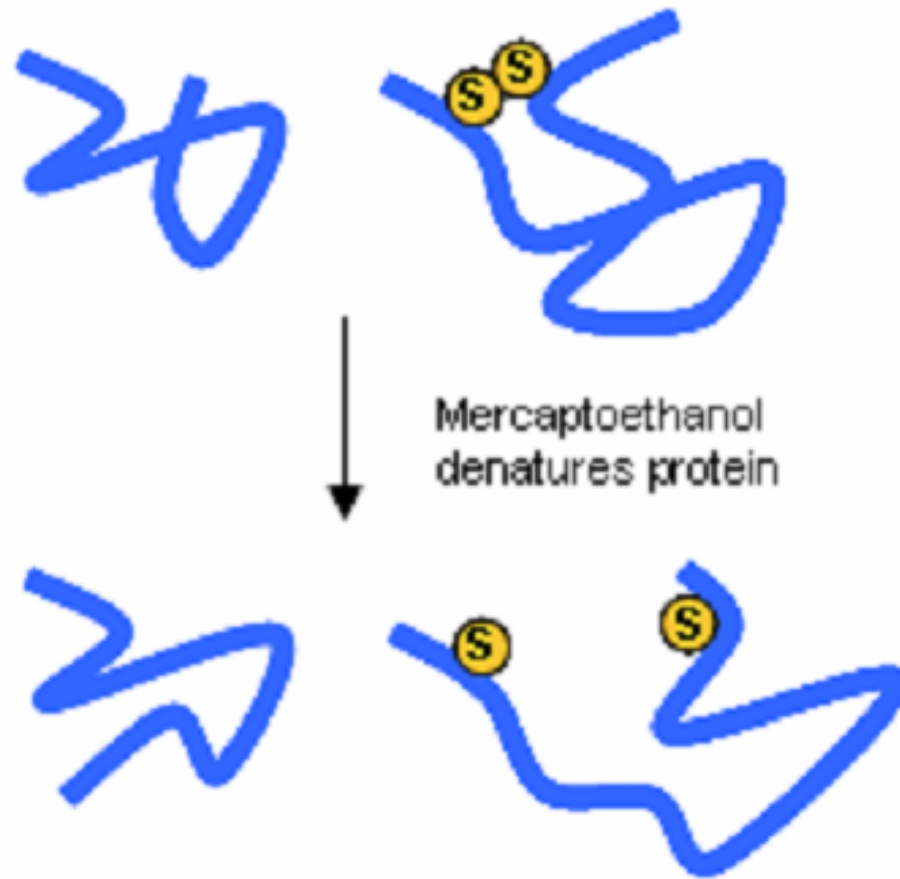


Polyacrylamide

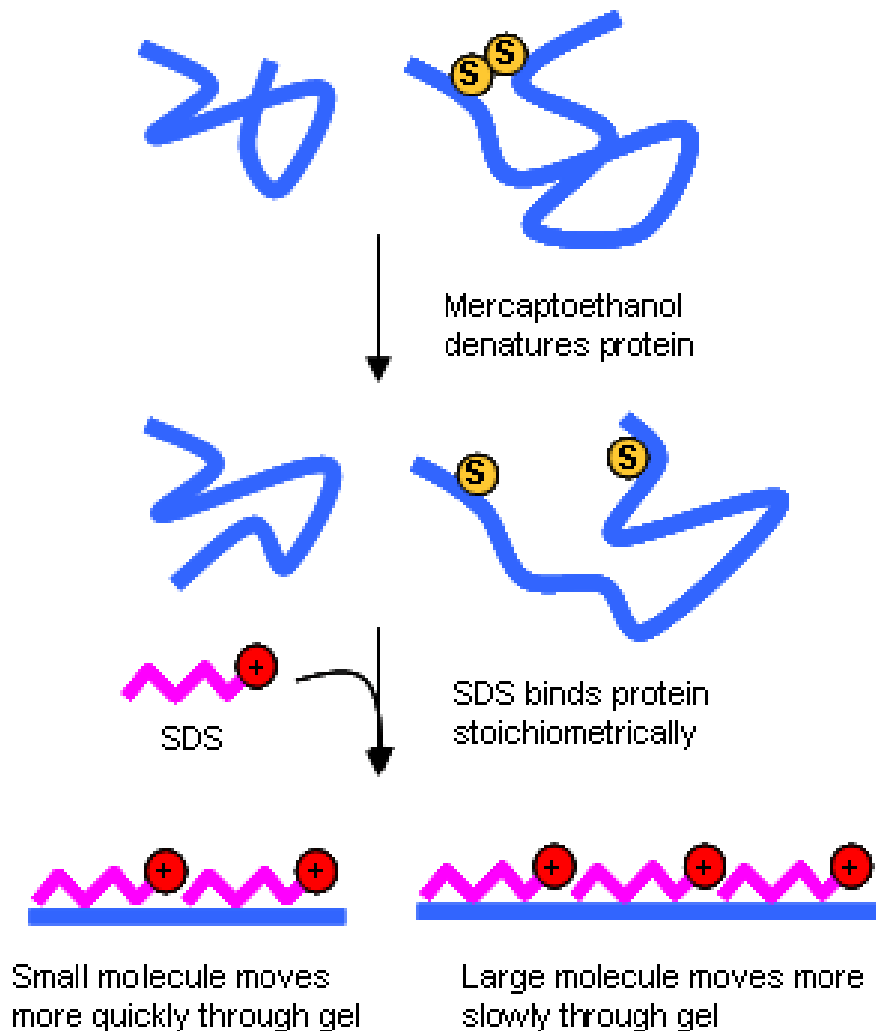


Problem 2: proteins can have S-S bonds

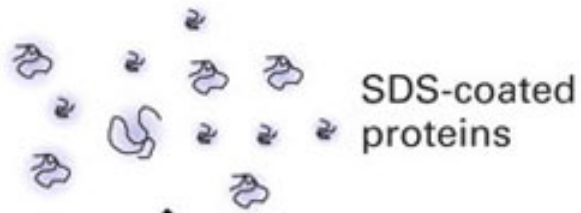
- Solution: reducing agents



- Problem 3: unlike nucleic acids, proteins do not have a constant charge/mass ratio.

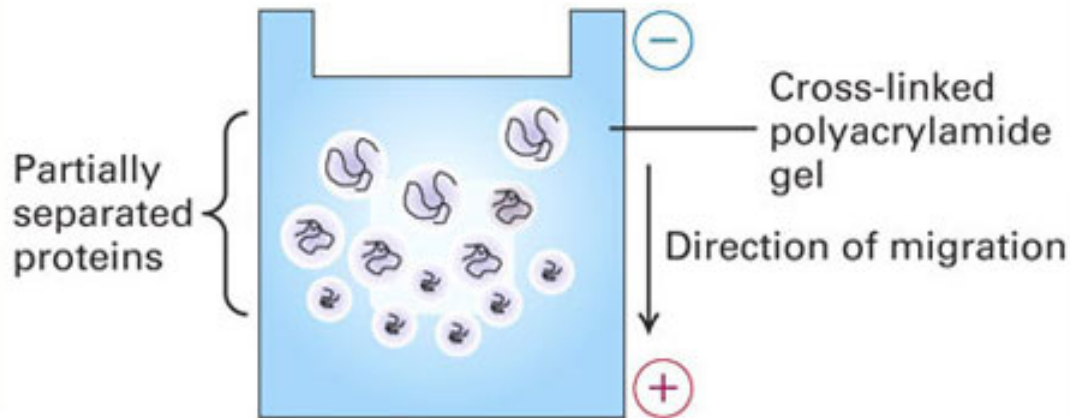


1 Denature sample with sodium dodecylsulfate



SDS-coated proteins

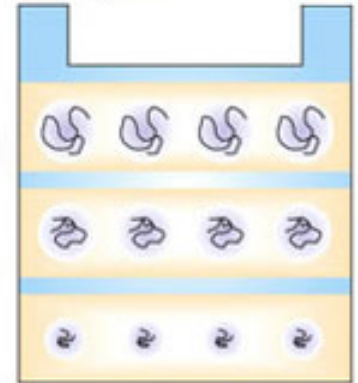
2 Place mixture of proteins on gel, apply electric field



Cross-linked polyacrylamide gel

Direction of migration

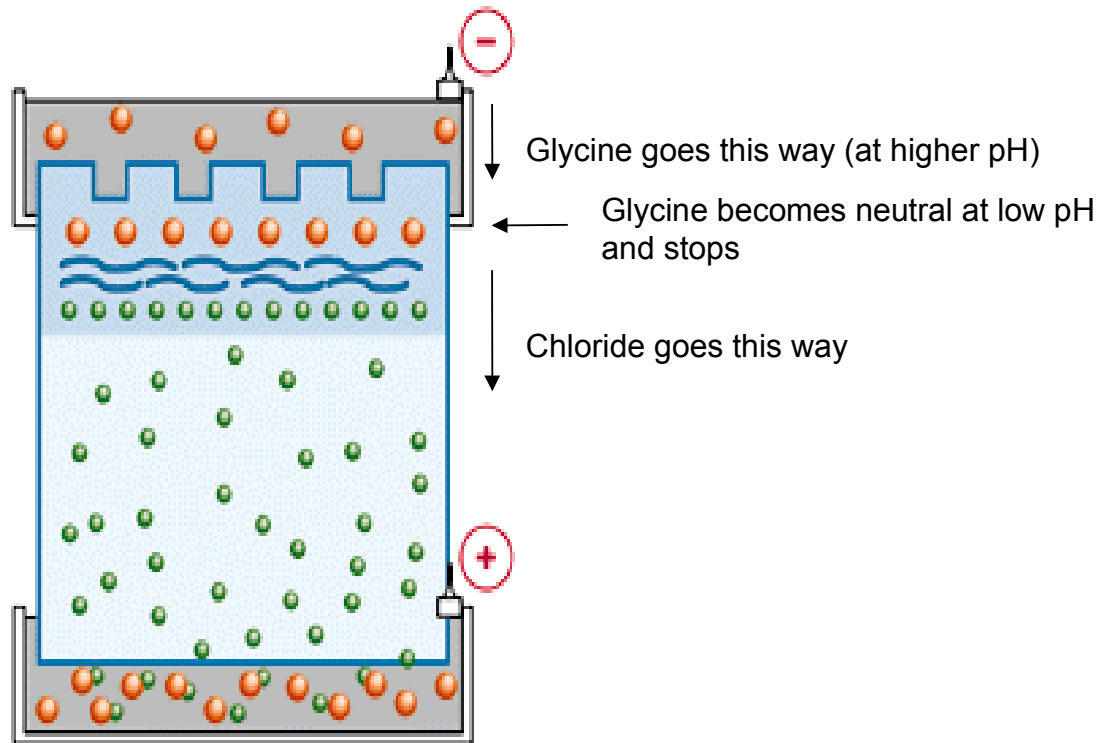
3 Stain to visualize separated bands



Decreasing size

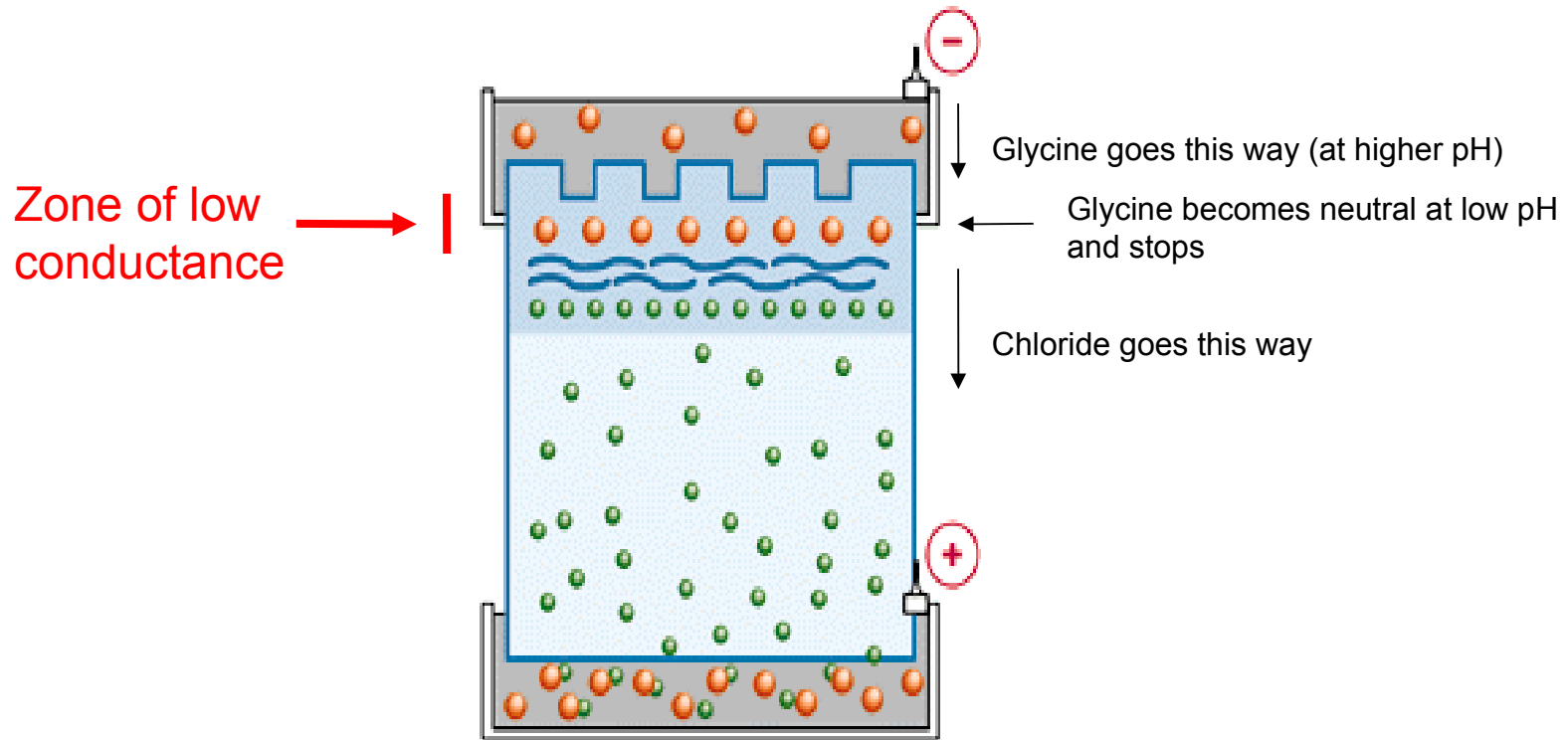
Problem 4: proteins are usually dilute, so large volumes have to be added

Solution: stacking gel (low concⁿ of acrylamide, more acid, Cl⁻ ions).



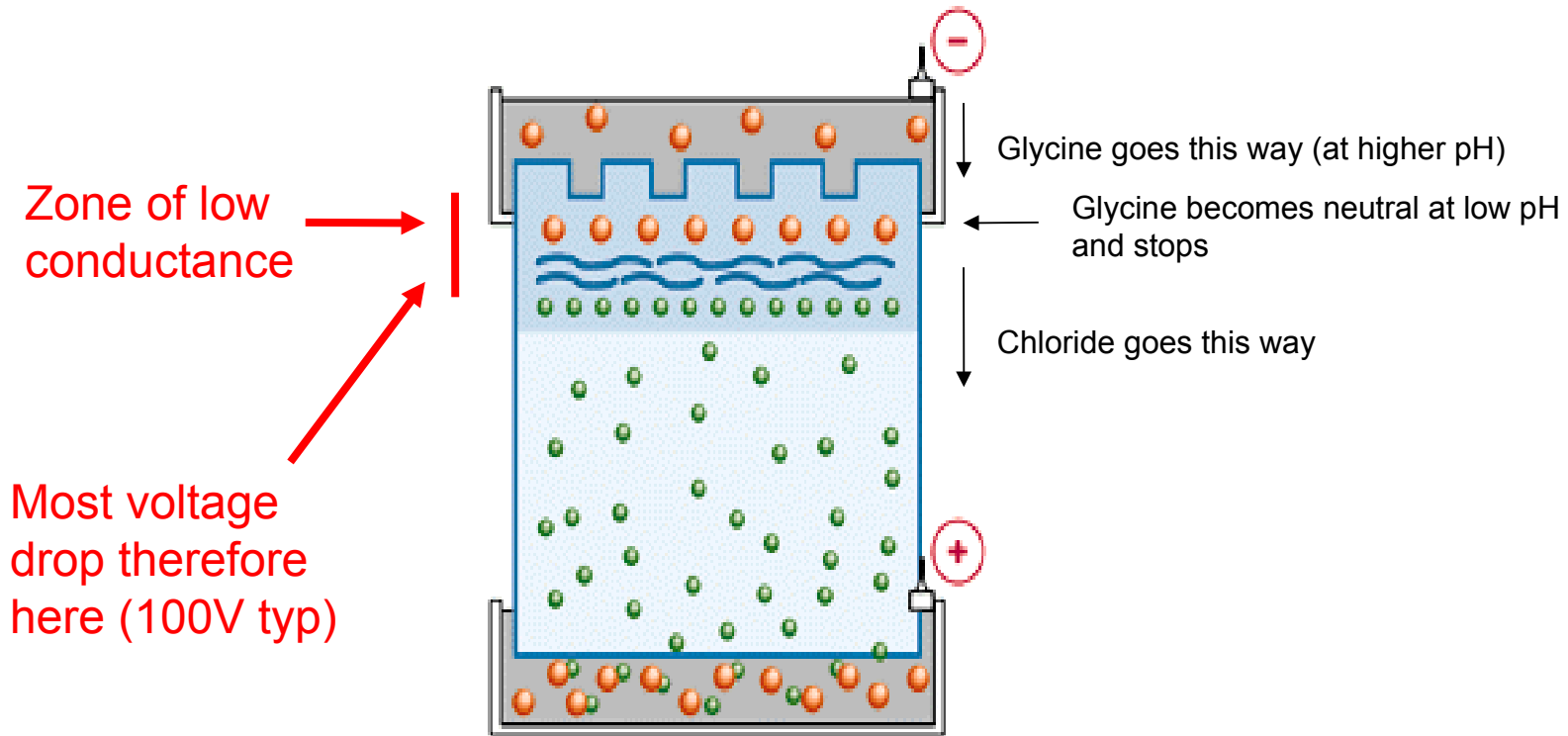
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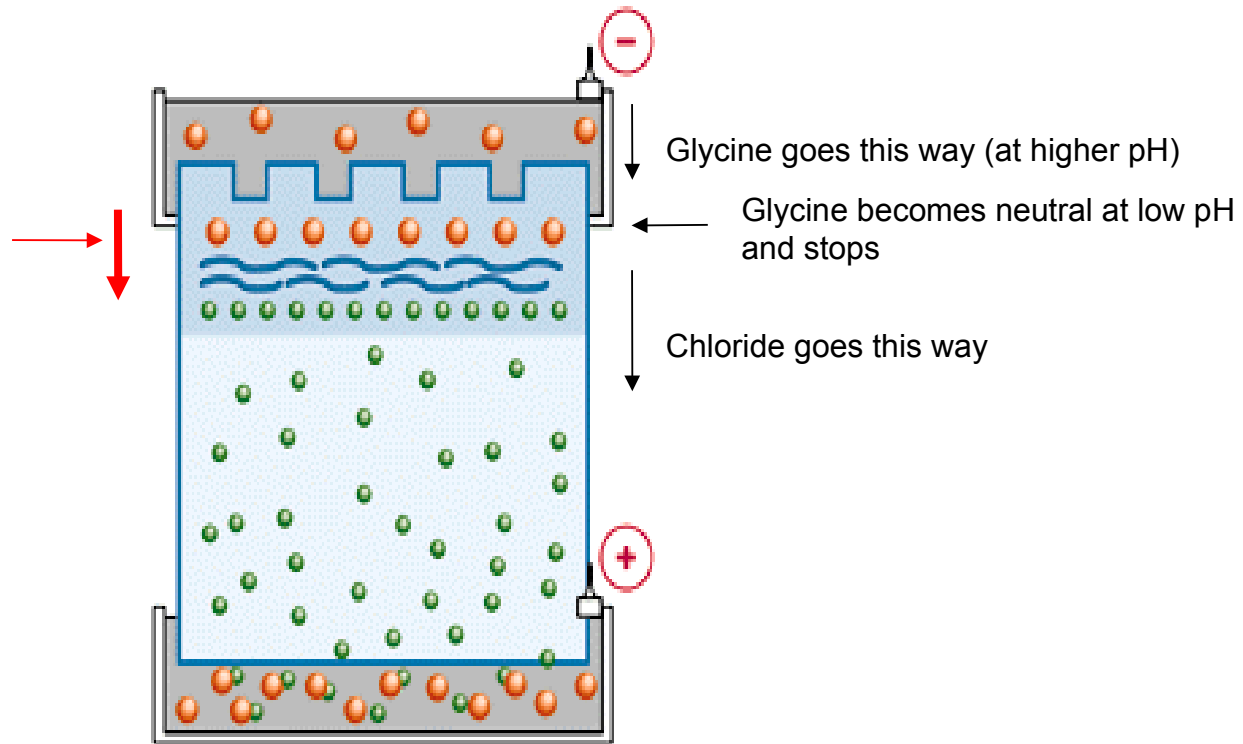
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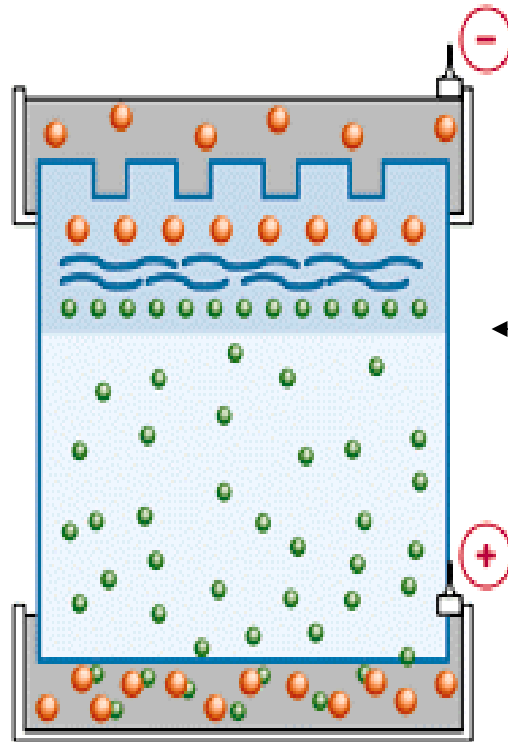
Solution: stacking gel (low concⁿ of acrylamide, more acid, Cl⁻ ions).

Proteins go fast, but have to slow a lot when they reach chloride ions (high conductance, low voltage)



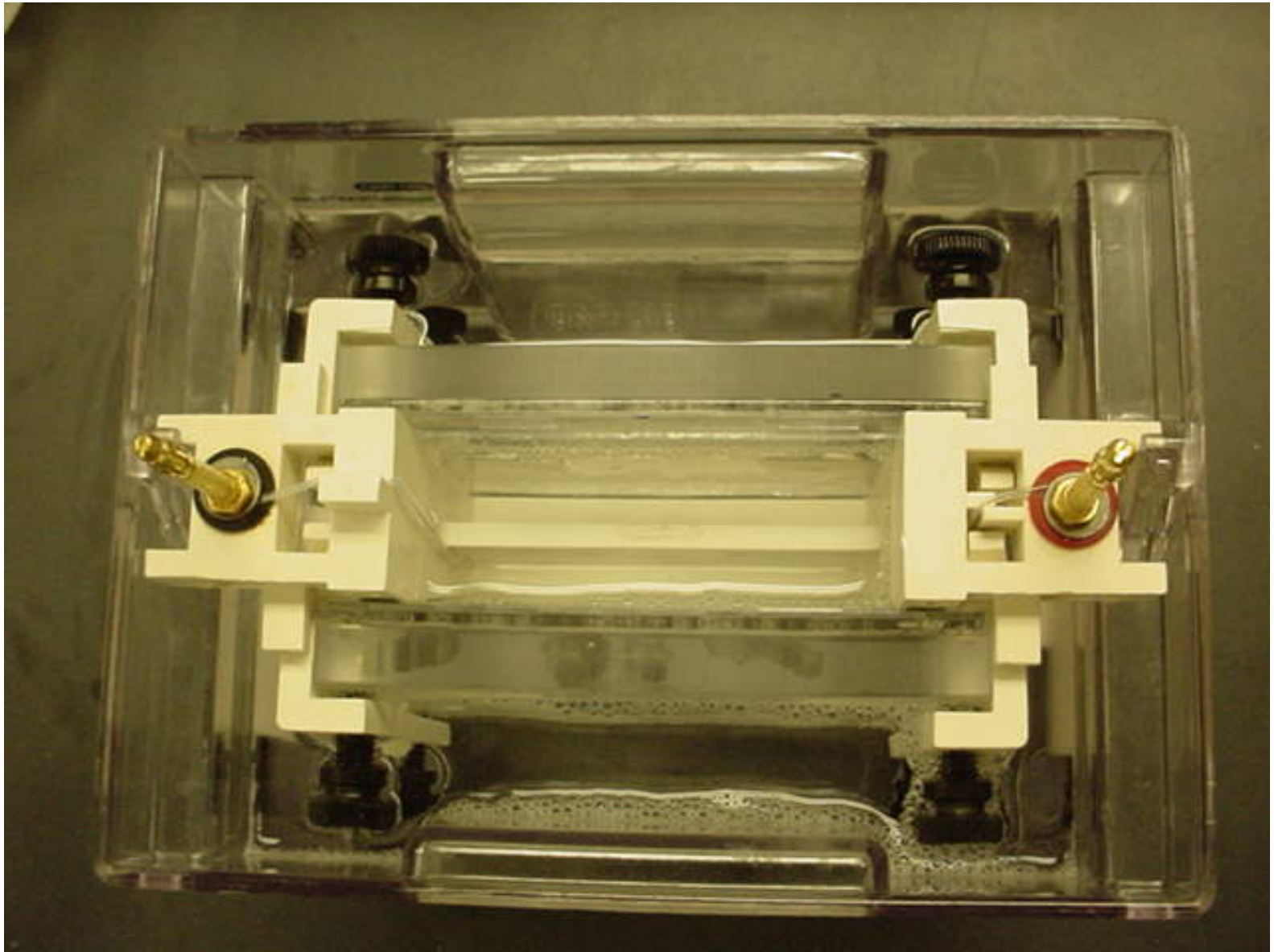
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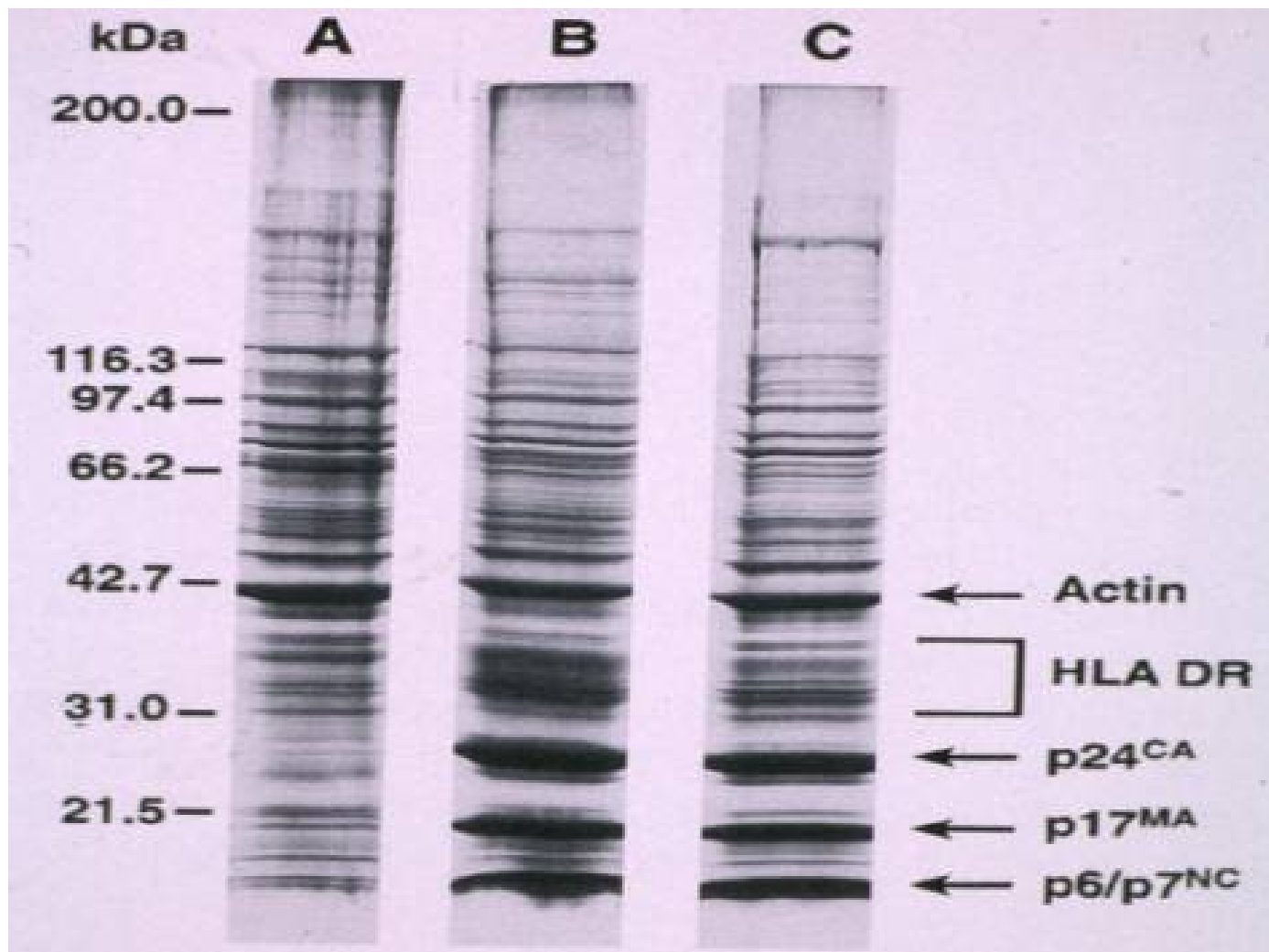
Solution: stacking gel (low concⁿ of acrylamide, more acid, Cl⁻ ions).



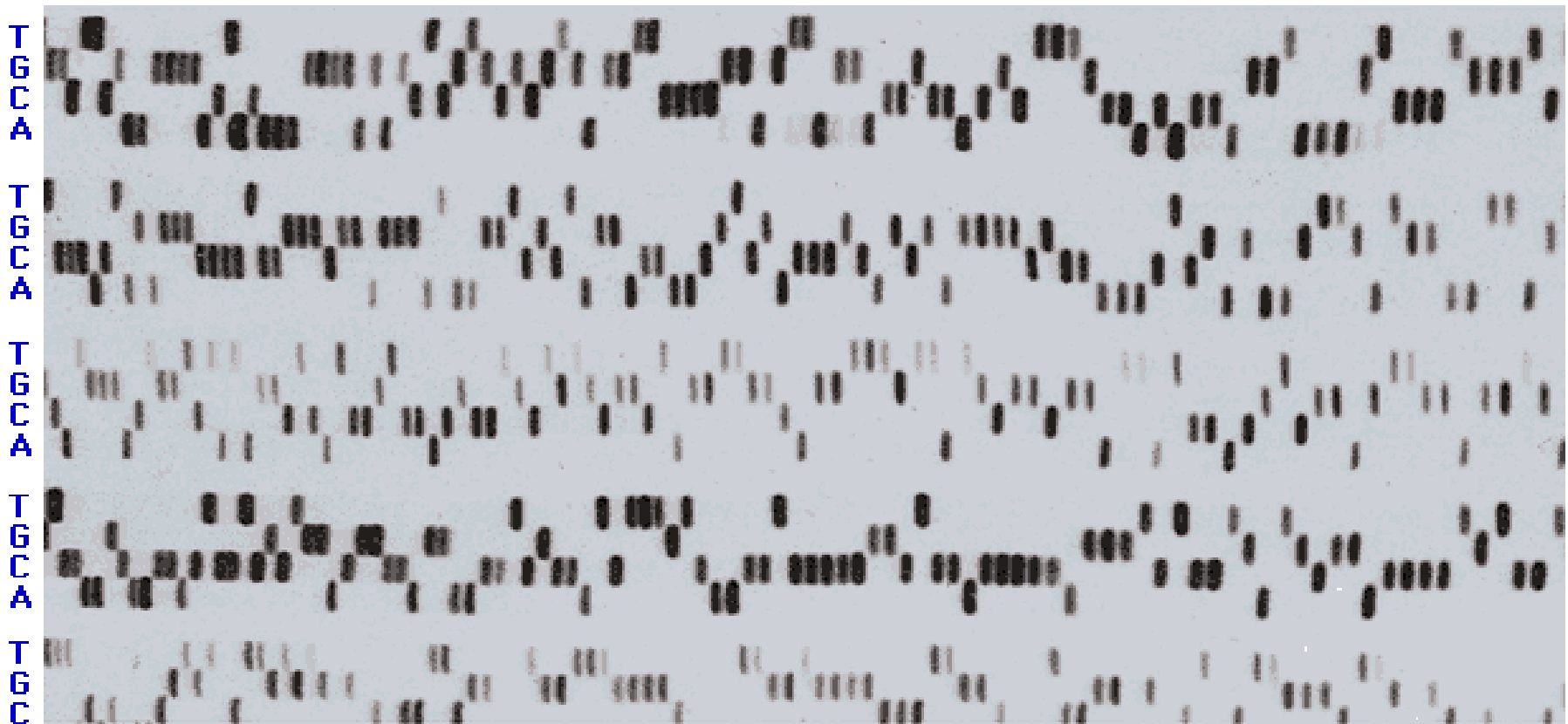
Here, pH rises, glycine becomes charged, and conductivity rises: proteins are sieved by gel.







PAGE can also be used for short pieces of DNA

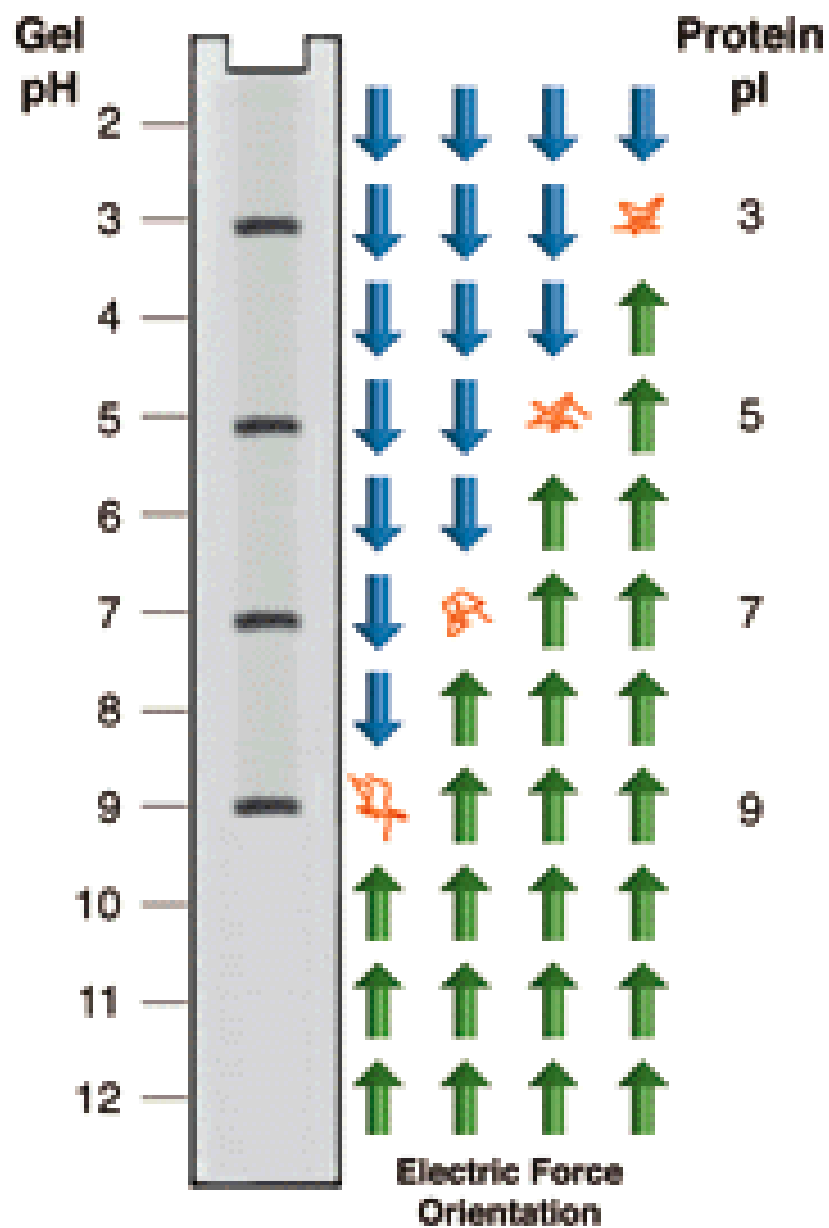


Isoelectric Focusing

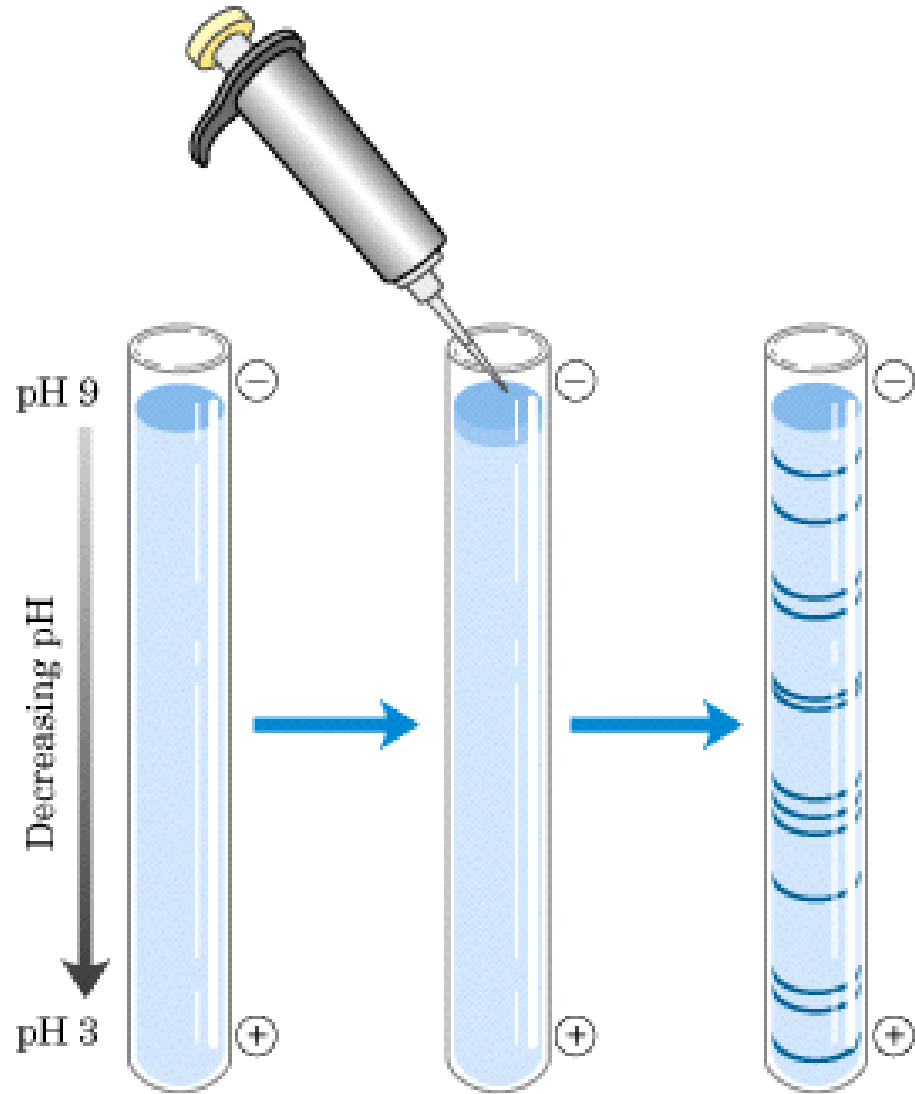
- The pI of a protein is the pH at which it carries no net charge.
- (more acid than the pI, and the basic groups become NH_3^+ and the protein becomes positive: less acid than the pI, and the COOH groups become COO^- and the protein becomes negative).

How to use this:

- Make a gel with a gradient of pH
- Apply an electric field, positive to alkaline end.
- Proteins negatively charged will be pulled towards the positive electrode until they meet the part of the gel where $\text{pH}=\text{pI}$.
- Proteins positively charged will be pulled towards the negative electrode until they meet the part of the gel where $\text{pH}=\text{pI}$



An ampholyte solution is incorporated into a gel.



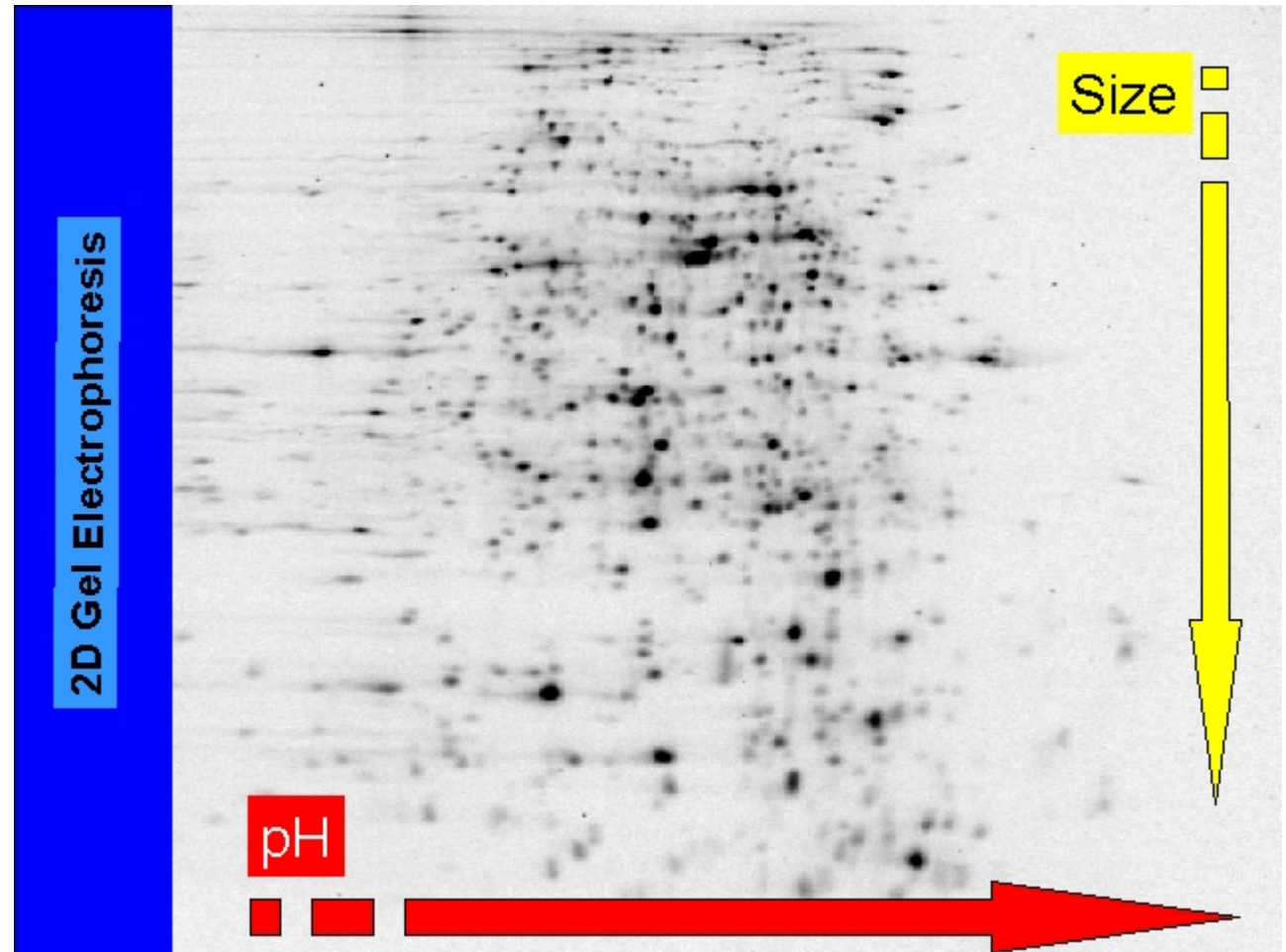
A stable pH gradient is established in the gel after application of an electric field.

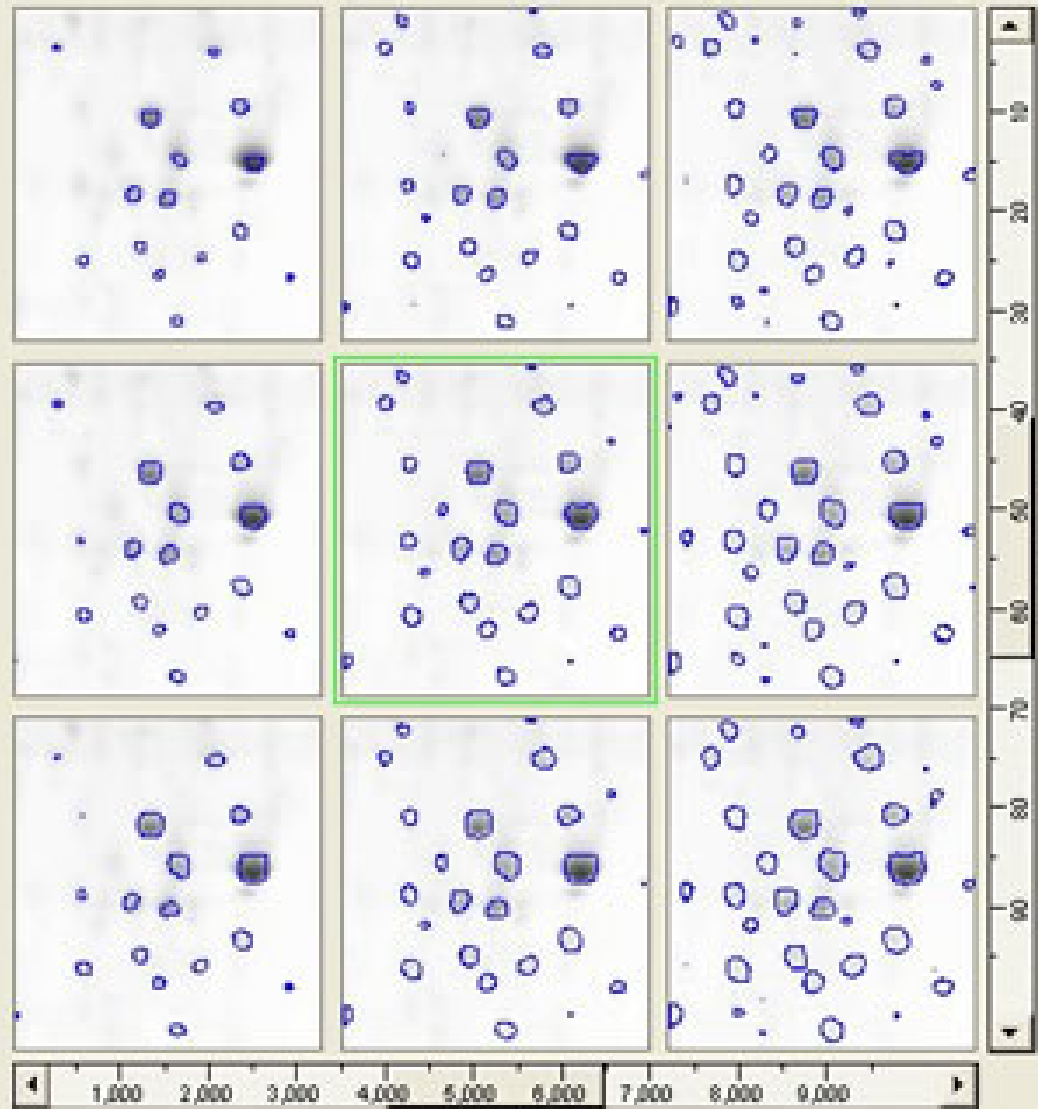
Protein solution is added and electric field is reapplied.

After staining, proteins are shown to be distributed along pH gradient according to their pI values.

2D electrophoresis

- Make a rod gel and conduct isoelectric focussing.
- Lay the rod on top of a 2D SDS gel
- Run the gel.





You have made 3 selections. Stop iterating when you are happy with the centre pane and all the other panes are reasonably acceptable.

Alternatively you can use the scrollbars to alter the range displayed.

Operator Size

Background Factor: 1



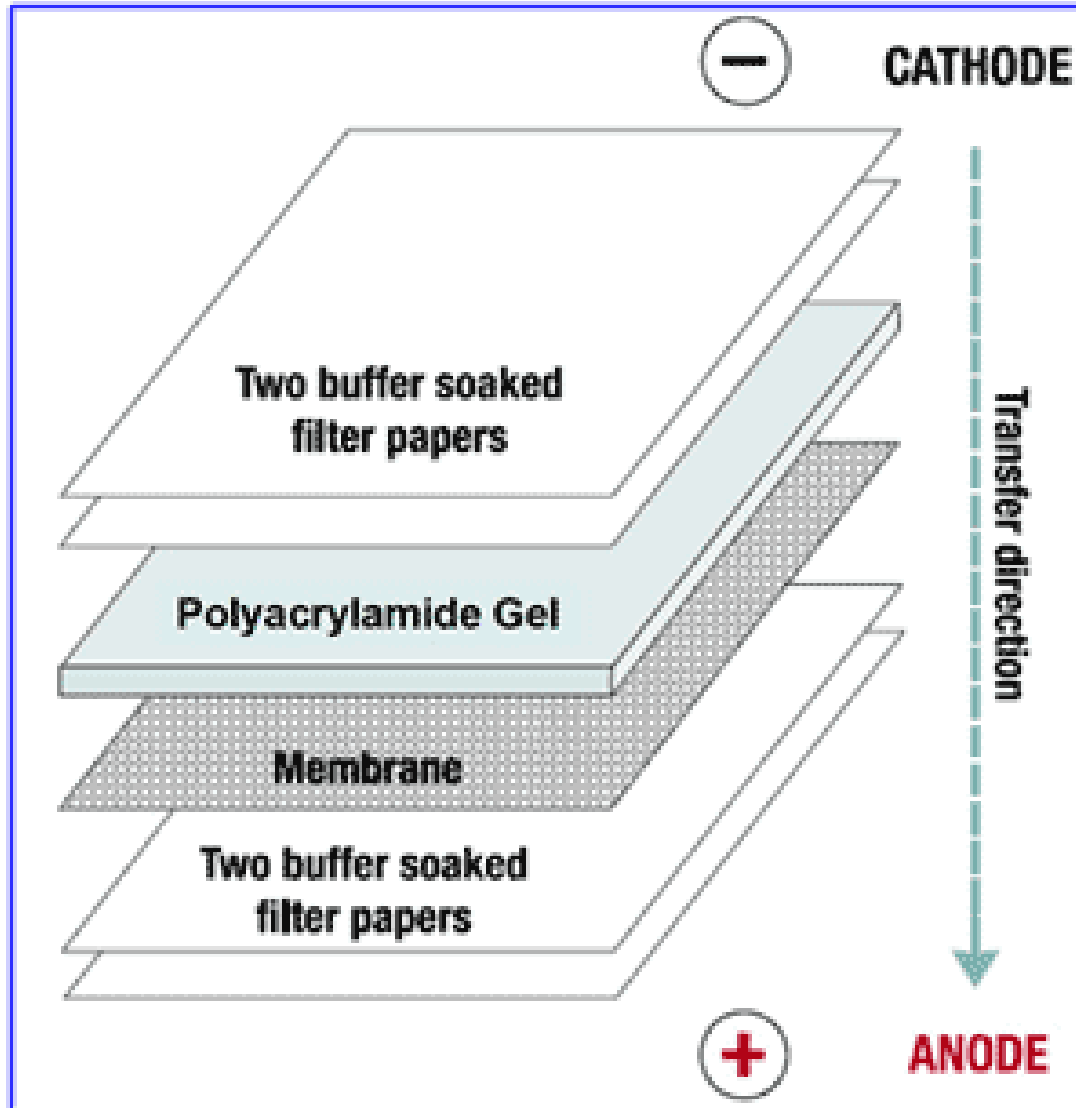
Undo

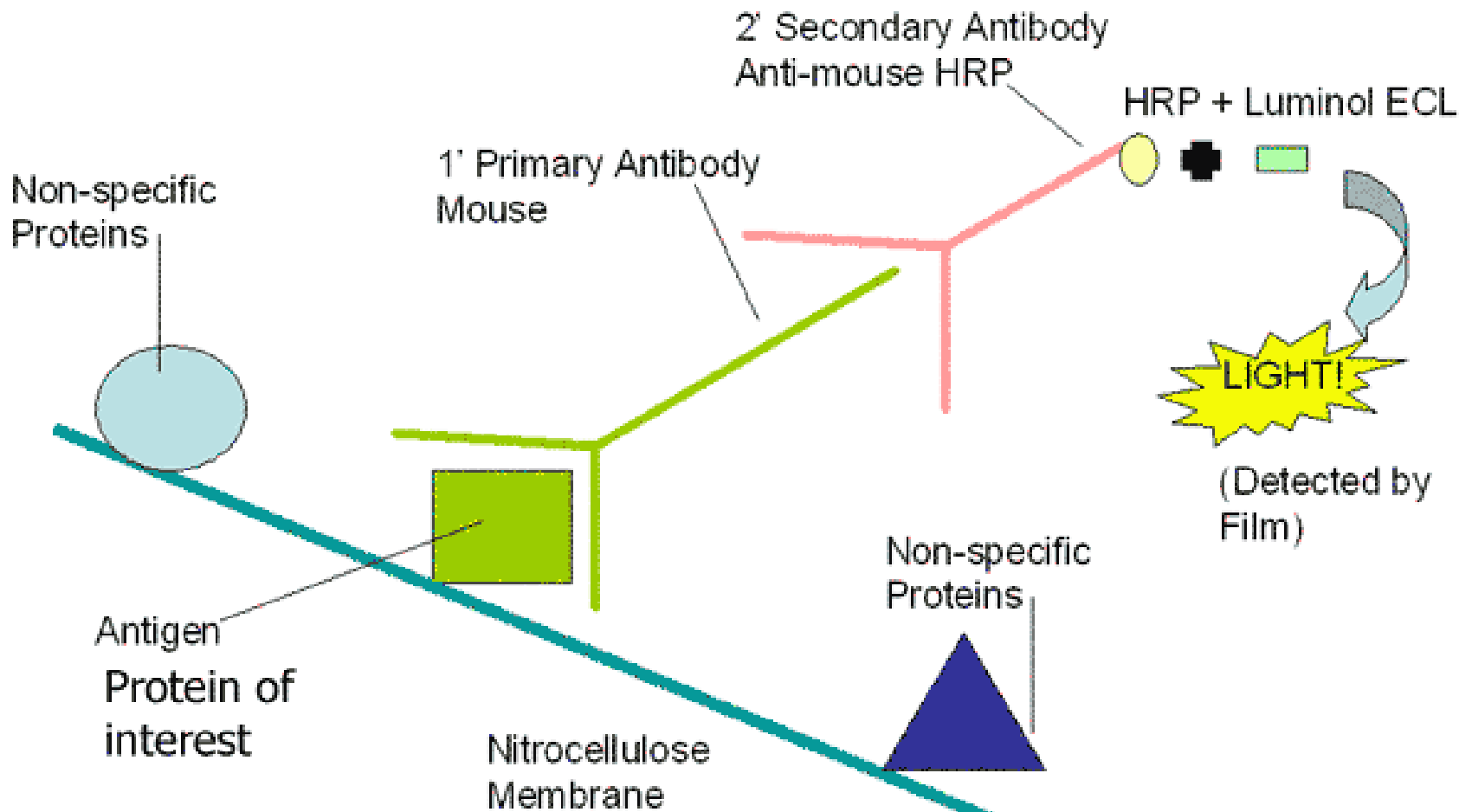
< Back

Next >

Cancel

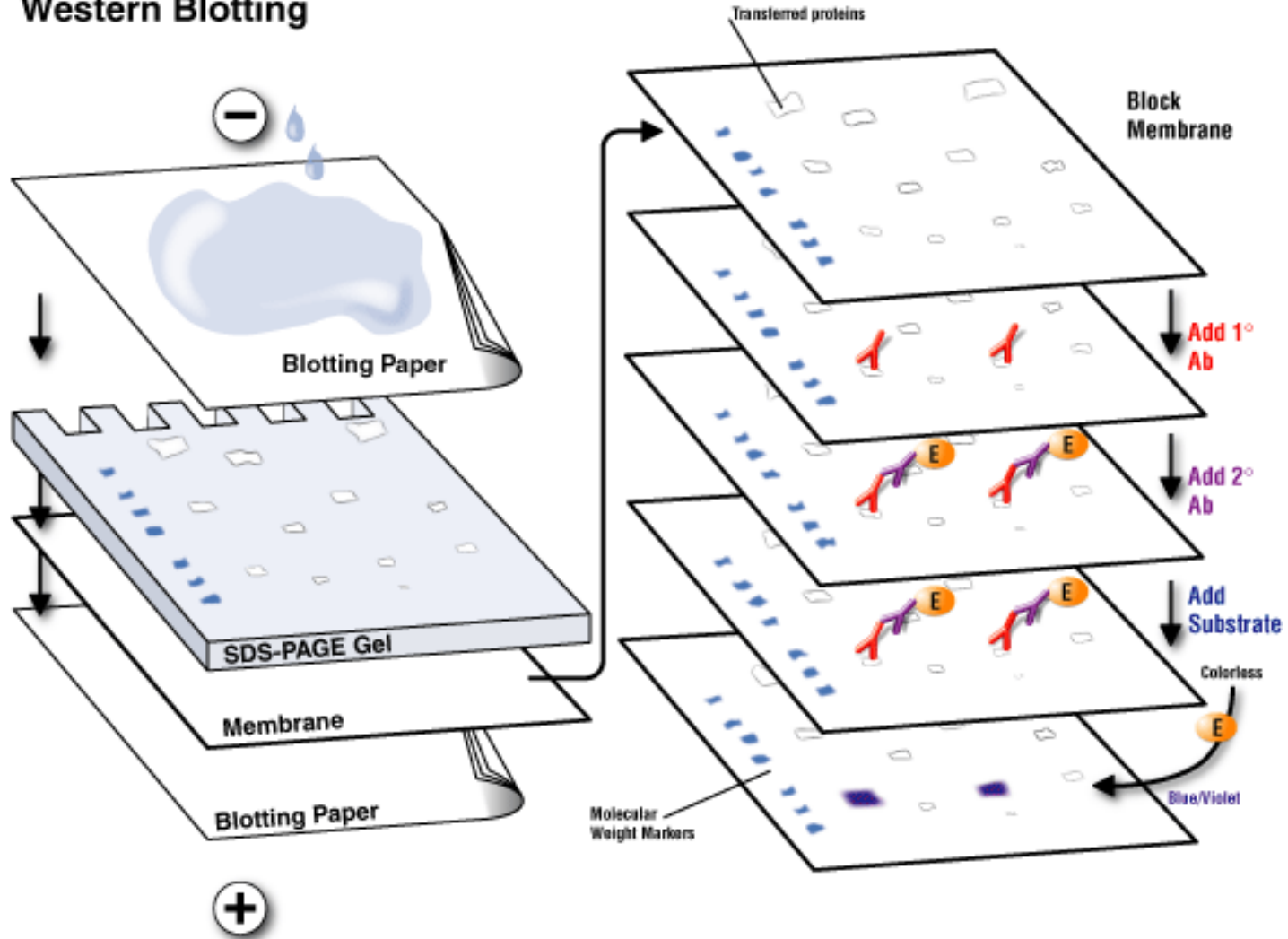
Western Blotting





Blotting

Western Blotting

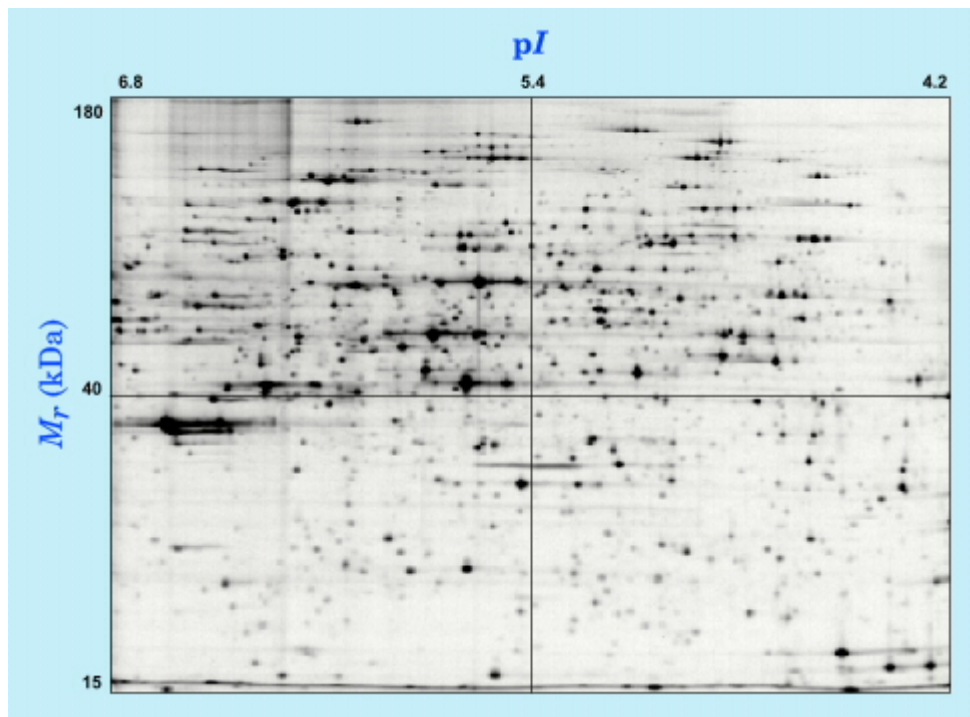


There are databases:

Yeast 2D Map

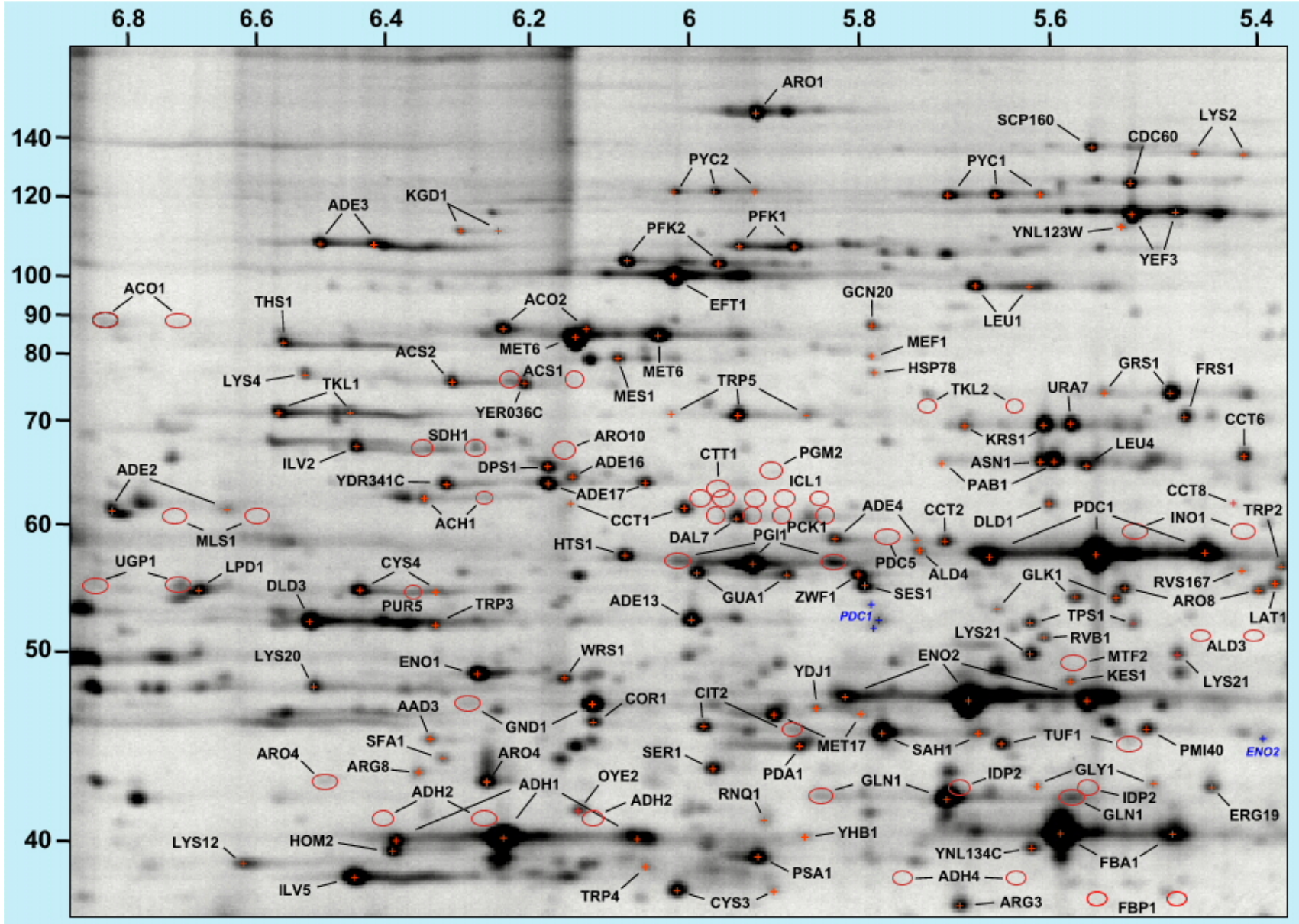
The pattern shown corresponds to the soluble proteins synthesized by strain S288C exponentially growing on glucose. First dimension was carried out using ampholytes. Second dimension was run on 11% slab gel.

Click on one of the four parts of this map, and you will obtain a zoom of it:



<http://www.ibgc.u-bordeaux2.fr/YPM/carte.htm>

Click on a spot to get information about it (blue crosses correspond to protein fragments)

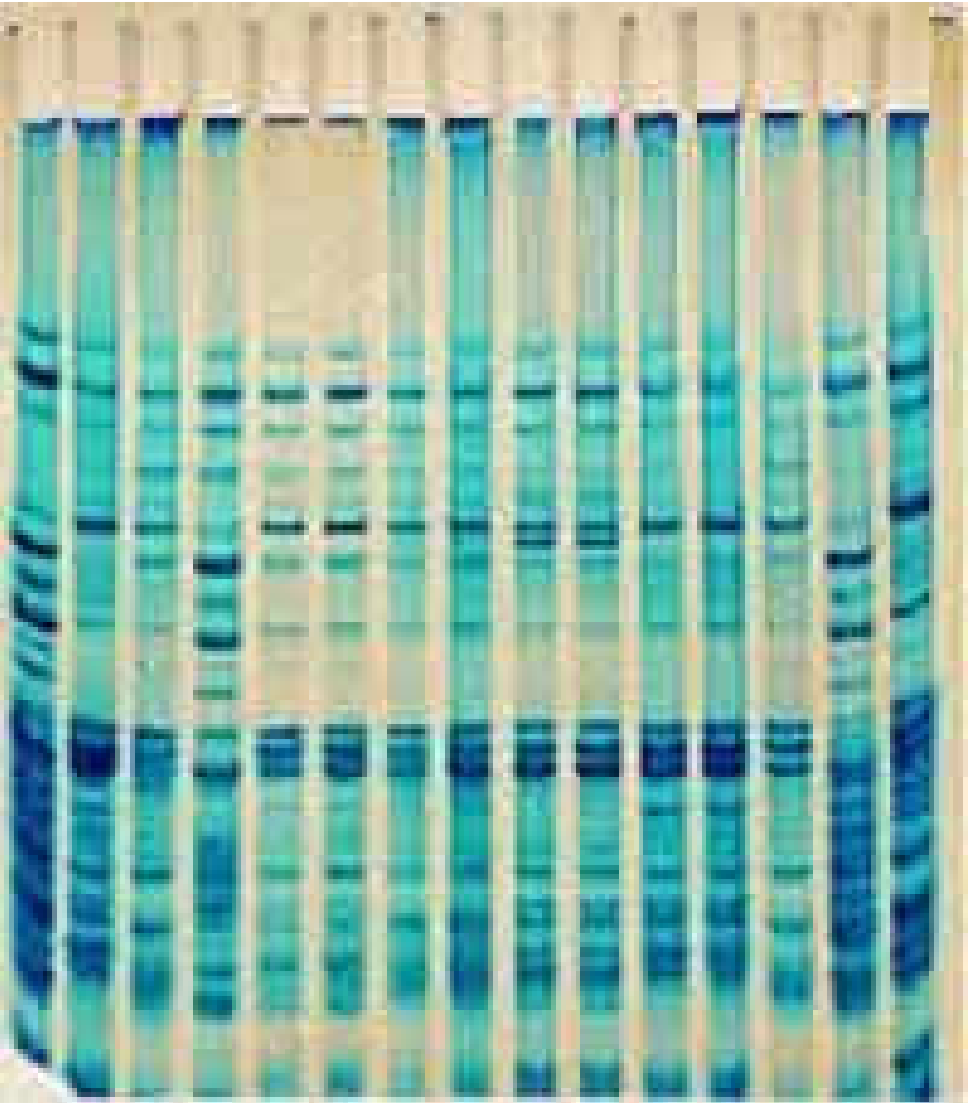


Spot report

Spot number :	B48C95
Gene :	MET6
CBI / CAI :	0.77 / 0.66
Protein :	homocysteine methyltransferase
SWISSPROT :	P05694
SGD :	S000000893
Acetylation :	non acetylated
NH2 aa removed :	1
Apparent pI :	6.15
Calculated pI :	6.01
Apparent Mr :	84100
Calculated Mr :	85727
Localisation :	cyt
Identification method :	sequencing, aa ratio, MS
Physiol. behaviour :	

Problems:

- **Anomalous MW:** (eg tubulin – usually caused by high endogenous charge or non-stoichiometric binding of SDS)
- **Poor focus of bands:** (usually because you messed up the stacking gel or buffer in some way, or tried to re-use a gel)
- **Smiles:** either you managed to compress the middle of the gel (thinner, lower conductance so higher voltage) or you got it hot.
- **Precipitation as the sample goes in:** You have KCl in your sample (it makes SDS precipitate)



Problems: PAGE

- **Anomalous MW:** (eg tubulin – usually caused by high endogenous charge or non-stoichiometric binding of SDS)
- **Poor focus of bands:** (usually because you messed up the stacking gel or buffer in some way, or tried to re-use a gel)
- **Smiles:** either you managed to compress the middle of the gel (thinner, lower conductance so higher voltage) or you got it hot.
- **Precipitation as the sample goes in:** You have KCl in your sample (it makes SDS precipitate)
- **Bands all clustered together:** wrong concentration of acrylamide

Problems: Western Blots

- **No protein on blot:** wrong polarity, buffer or time. Try staining the gel afterwards to see if you didn't move them, or if they went right through.
- **High background on probed blot:** insufficient blocking, or too much antibody. First do a titration of secondary only, having run the primary in the gel and blotted it. Then titrate the primary on the real samples in the gel.

Electrophoresis sniglets

- **Multiple agarasms:** the need to pour a gel many times, because it keeps leaking (usually into the draw below the bench) before it has set.
- **Retrophoresis:** running a gel backwards due to mis-connection of the electrodes or a mis-set polarity switch on the power lack.
- **Broadbanding:** failure of focus (usually a problem with the stacking gel)
- **Aeroblot:** a blot that has failed due to bubbles being trapped between layers

Good luck !!!