
commons.wikimedia.org

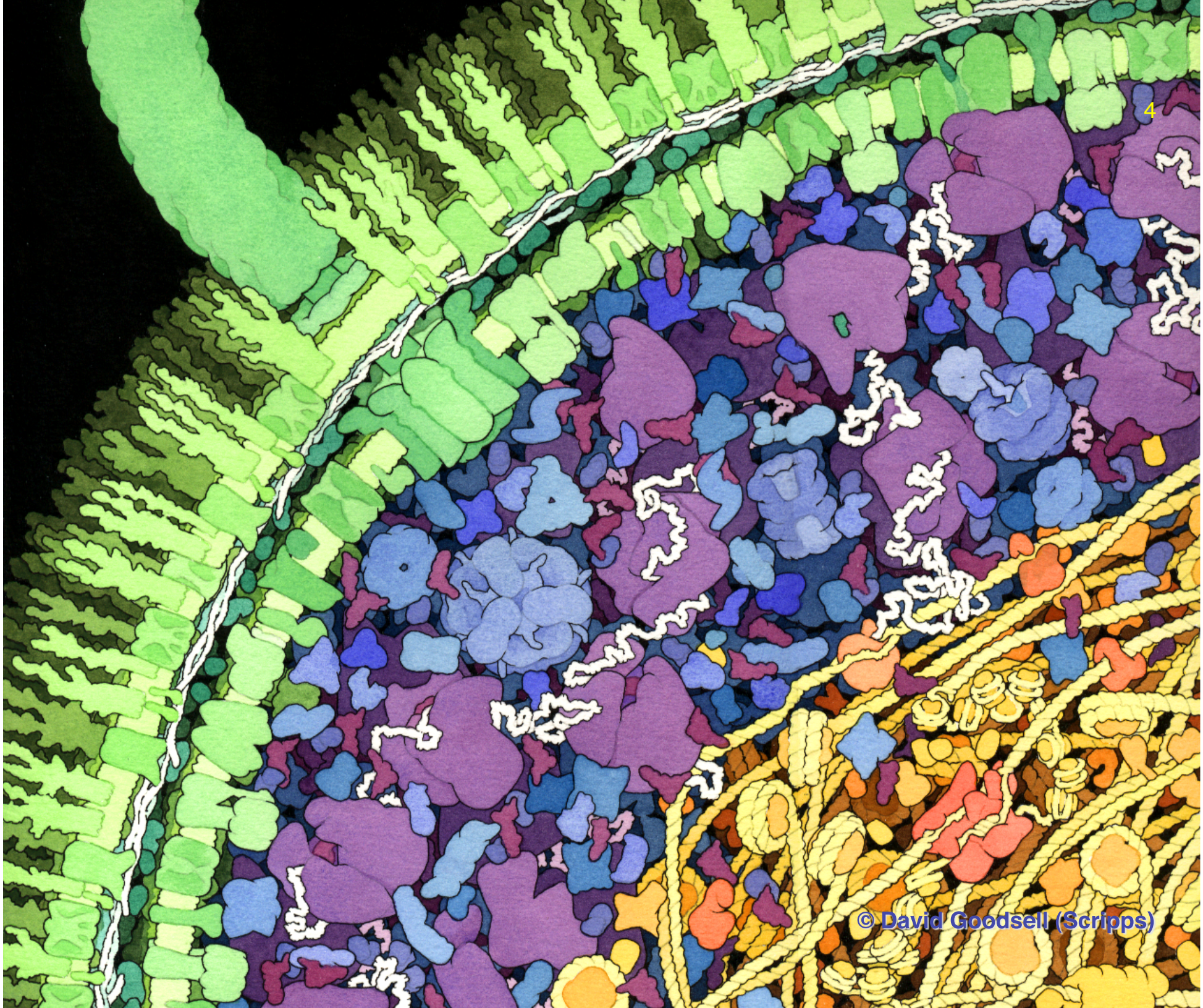
Module 2 overview

lecture	*lab*
1. Introduction to the module	1. Start-up protein eng.
2. Rational protein design	2. Site-directed mutagenesis
3. Fluorescence and sensors	3. DNA amplification
4. Protein expression	4. Prepare expression system
SPRING BREAK	
5. Review & gene analysis	5. Gene analysis & induction
6. Purification and protein analysis	6. Characterize expression
7. Binding & affinity measurements	7. Assay protein behavior
8. High throughput engineering	8. Data analysis

Lecture 6: Protein purification

I. Standard purification methods
   A. Harvesting and lysis
   B. Protein separation techniques

II. Assessing purified proteins
   A. Electrophoresis
   B. Mass spectrometry
   C. Protein sequencing and AA analysis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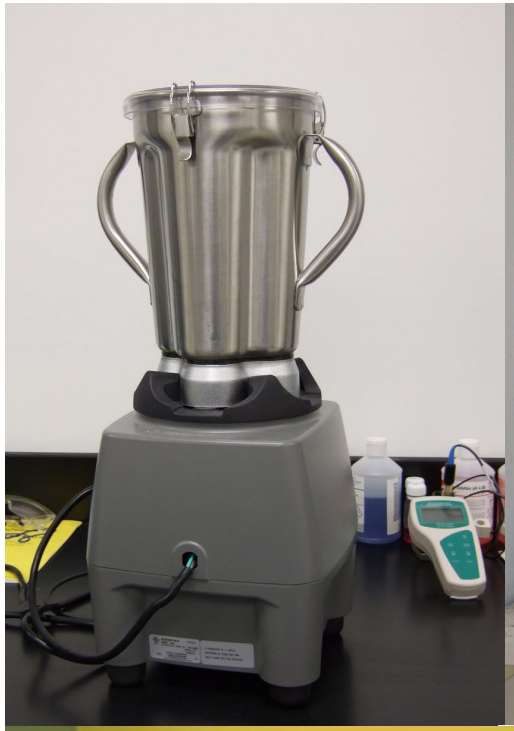
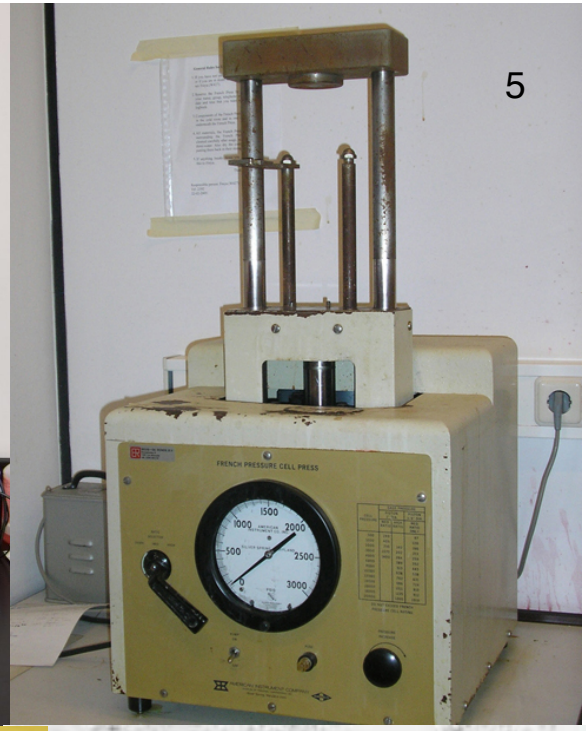
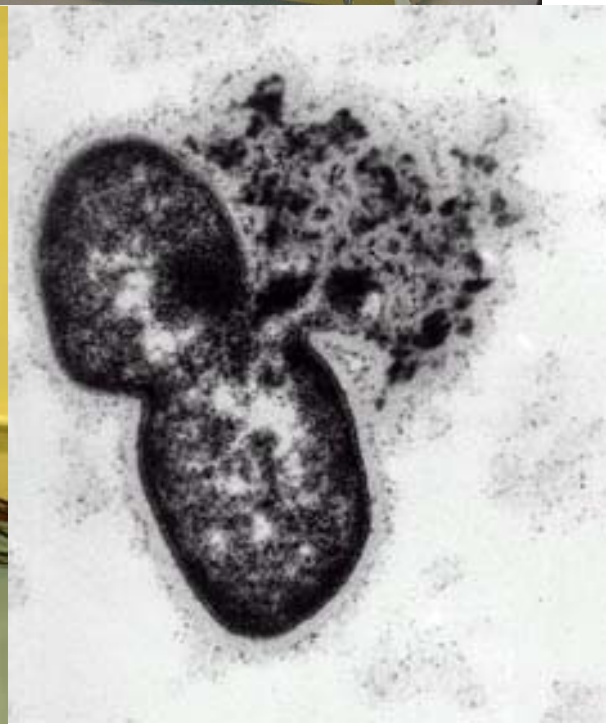
© David Goodsell (Scripps)

First problem: once we've collected the cells, how do we get our protein out?

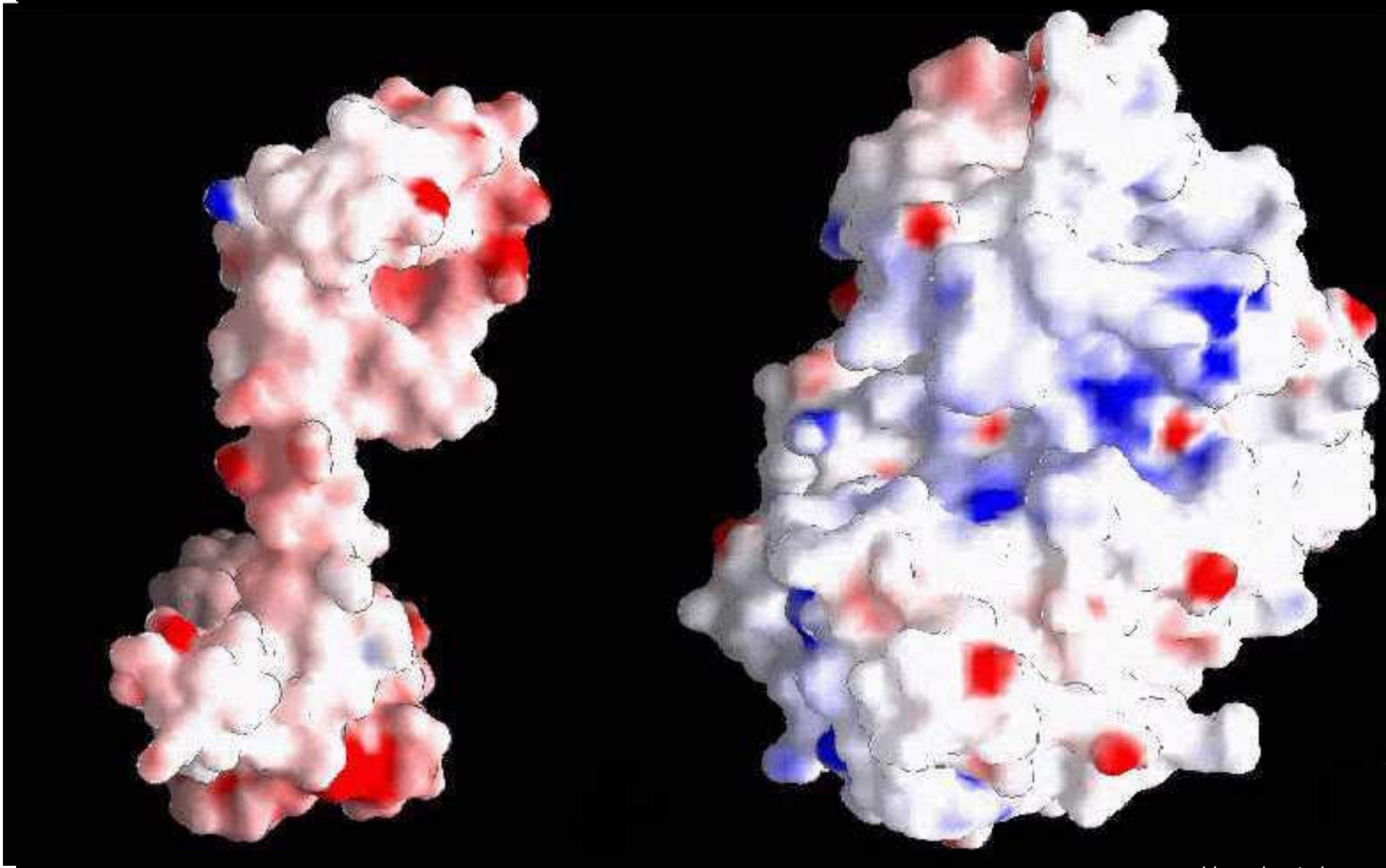






clockwise from top left:
lh6.ggpht.com
www.biomembranes.nl
bioinfo.bact.wisc.edu
matcmadison.edu

Second problem: how to separate our protein from everything else?



www.biomedcentral.com

Fish out proteins with desired properties;
if necessary fish iteratively!

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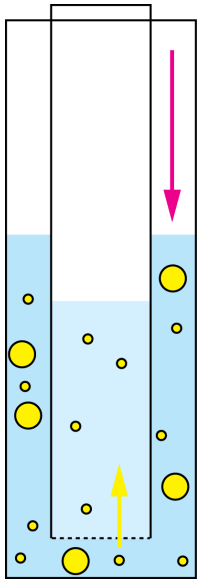
binary selection for size:
molecular weight
cut-off filters



pressure forces solution through filter

large proteins concentrated

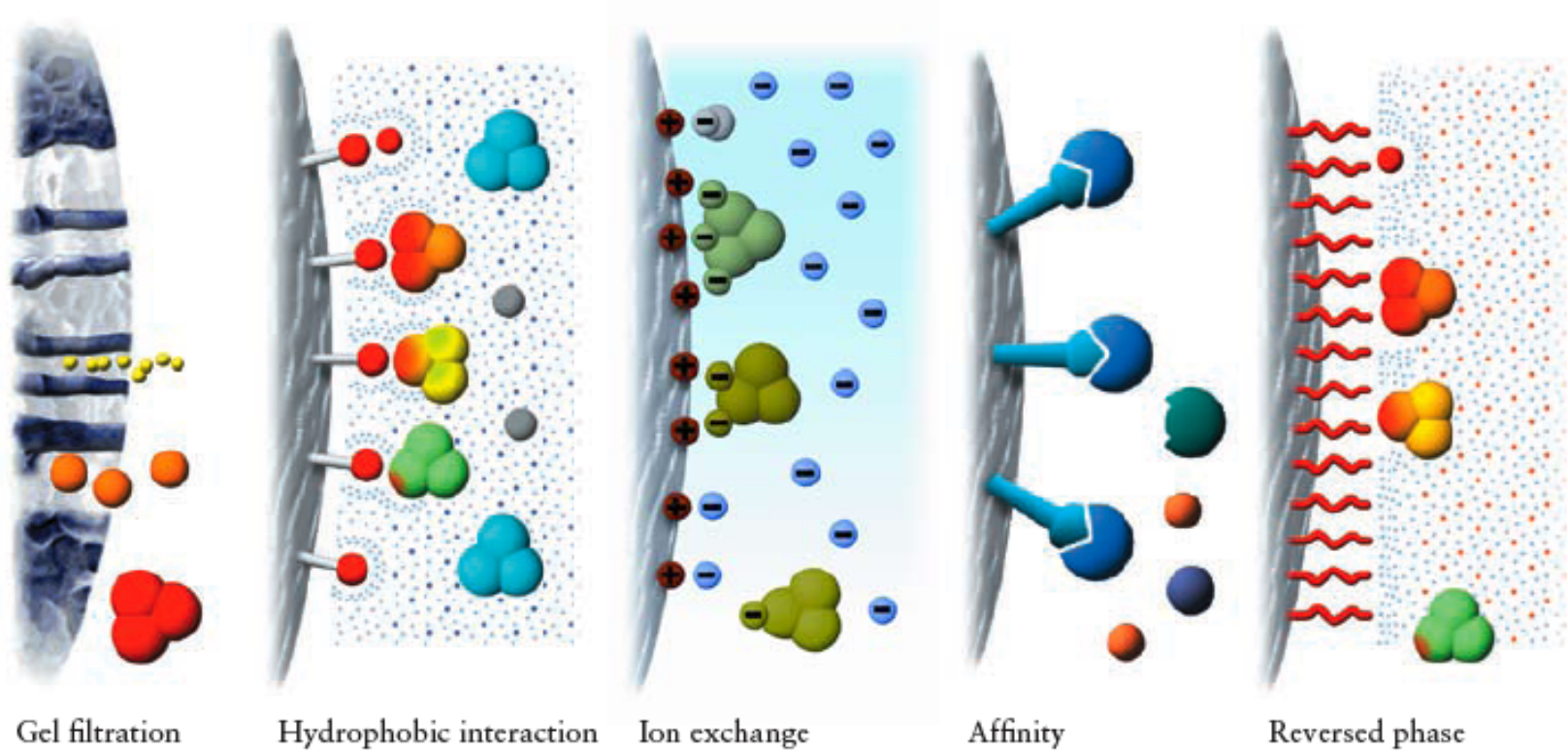
http://www.capitolscientific.com/core/media

column chromatography:
separation based on everything else...

http://www.excellgen.com/images/products/chrom_i_system_explorer.jpg

chromatography resins based on:

size | hydrophobicity | charge | affinity | hydrophobicity

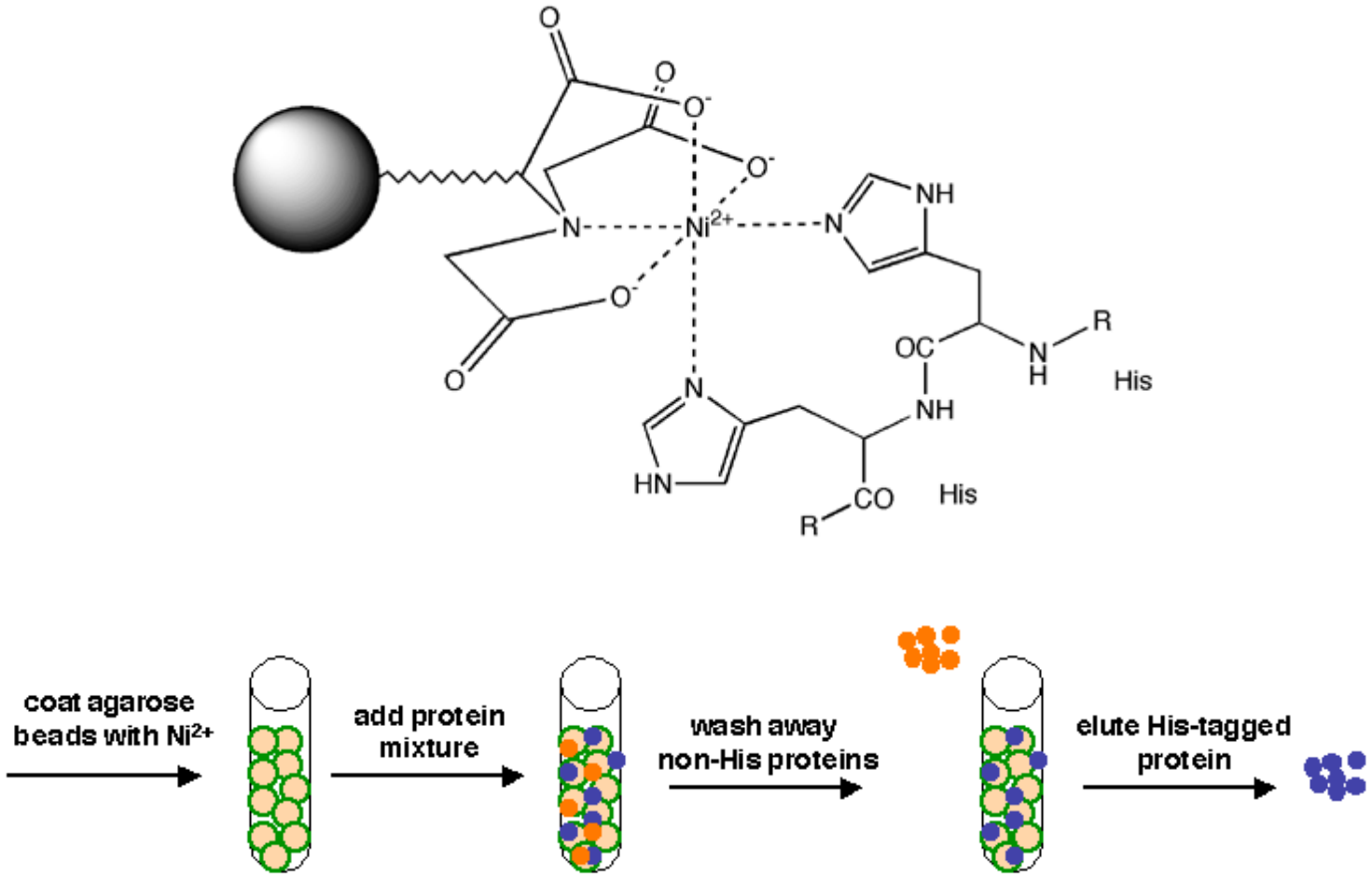


most common, in addition to affinity

e.g. Ni-NTA

GE Healthcare (2007) *Recombinant Protein Purification Handbook*

Nickel affinity purification with Ni-NTA agarose



Many other tags can be used for protein purification:

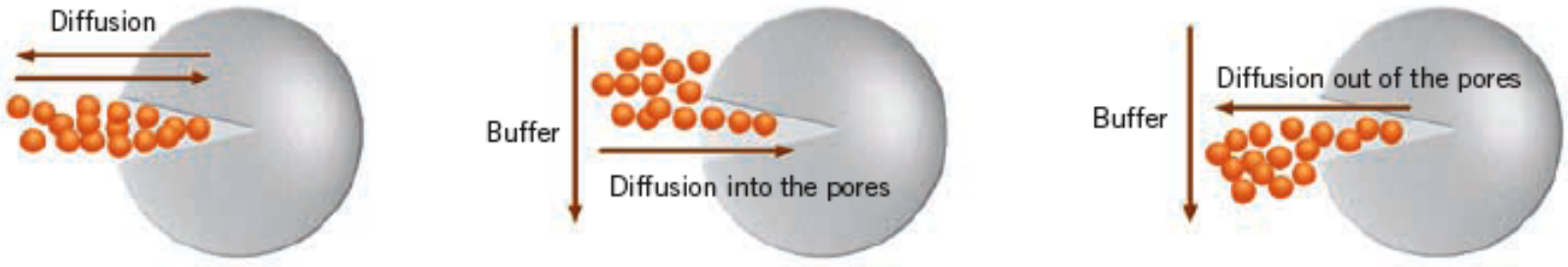
tag	*residues*	*matrix*	*elution condition*
poly-His	~6	Ni-NTA	imidazole, low pH
FLAG	8	anti-FLAG antibody	low pH, 2-5 mM EDTA
c-myc	11	anti-myc antibody	low pH
strep-tag	8	modified streptavidin	2.5 mM desthiobiotin
CBP	26	calmodulin	EGTA, EDTA
GST	211	glutathione	reduced glutathione
MBP	396	amylose	10 mM maltose

Tags may be chosen because they

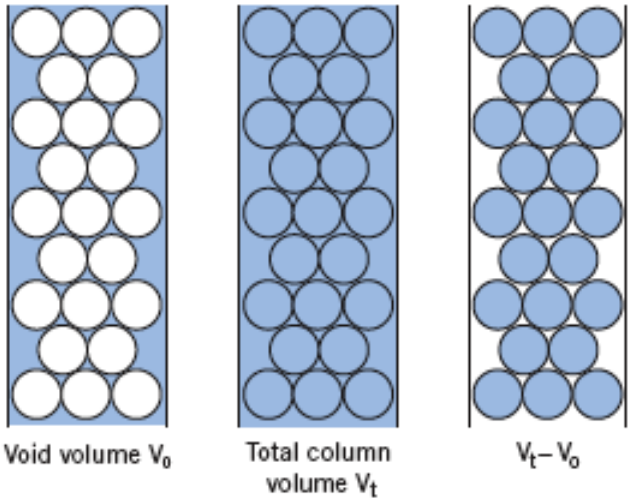
- interfere minimally with protein structure/function
- improve recombinant protein expression or solubility
- offer most convenient purification methods

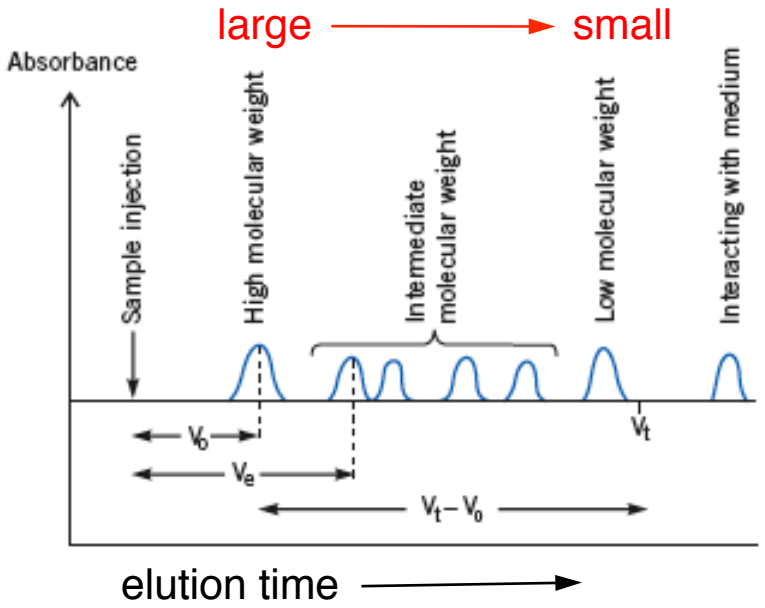
All tags may be cleaved from expressed proteins using specific proteases, if desired.

Gel filtration (size exclusion chromatography) principle



smaller species permeate pores better, interact preferentially





GE Healthcare (2007) *Gel Filtration Principles & Methods*

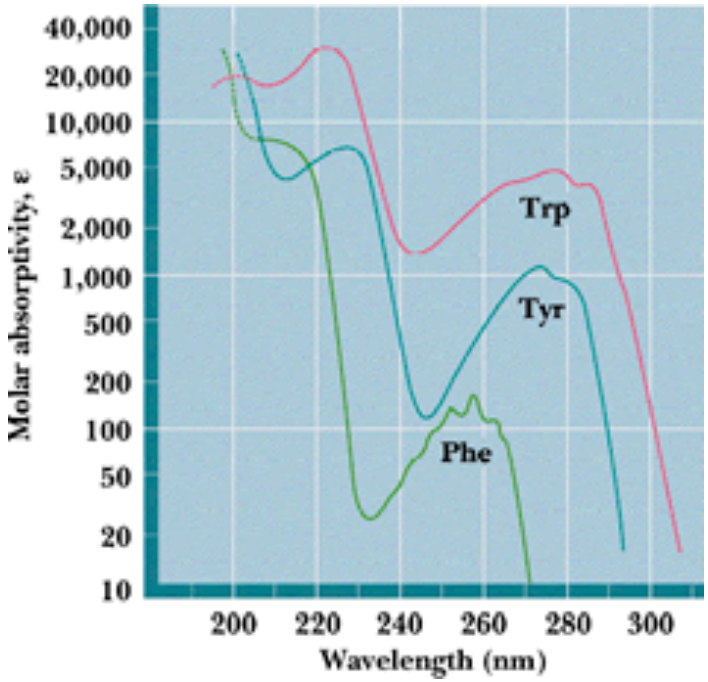
Quantification of purified proteins

use Beer-Lambert law:

$$A_{280} = \varepsilon_{280} c l$$

ε_{280} is the extinction coefficient; it can be determined rigorously, or estimated:

$$\varepsilon_{280} \sim n_W \times 5500 + n_Y \times 1490 + n_C \times 125$$

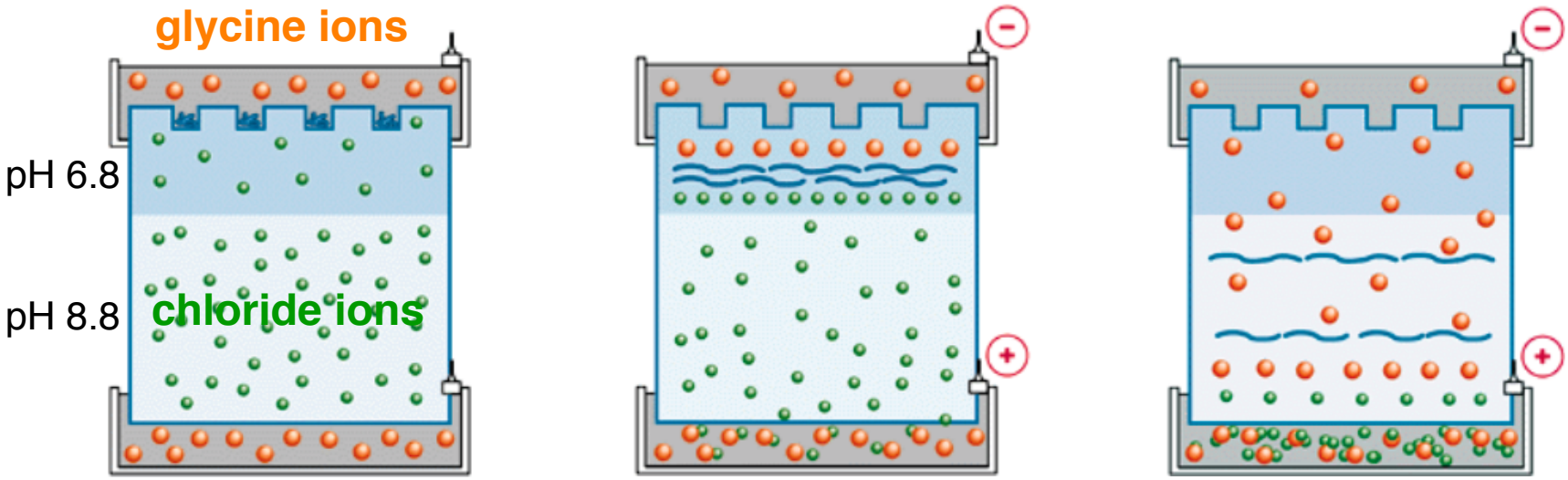


http://www.imb-jena.de/~rake/Bioinformatics_WEB/proteins_quantitation.html

Assessing proteins for identity and purity

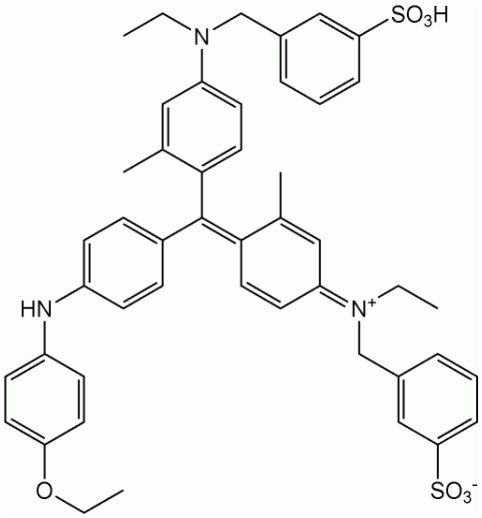
Most standard technique is sodium dodecylsulfate polyacrylamide gel electrophoresis (SDS-PAGE):

- basis is the tendency of proteins to unfold in SDS and bind a fixed amount SDS per protein (1.4 g/g)
- negative charge of SDS overwhelms protein charges
- proteins have same charge to mass ratio, but are differentially retarded by the separation gel
- stacking layer "focuses" proteins before separation layer

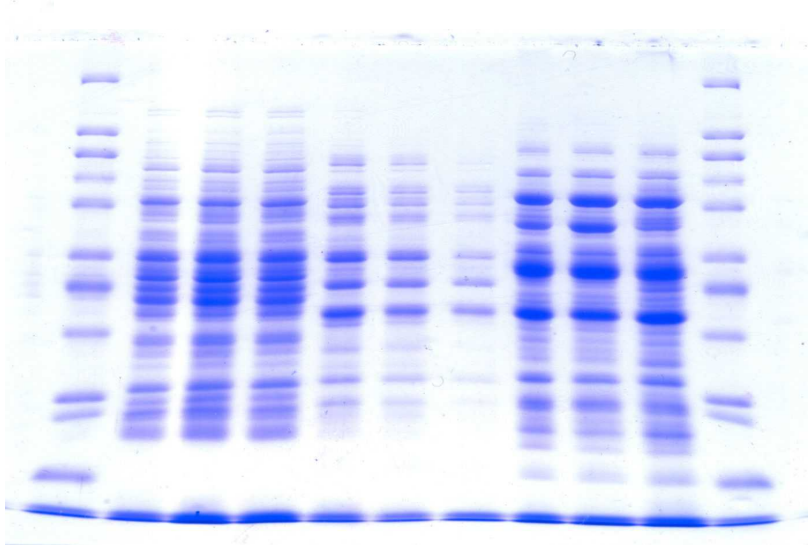


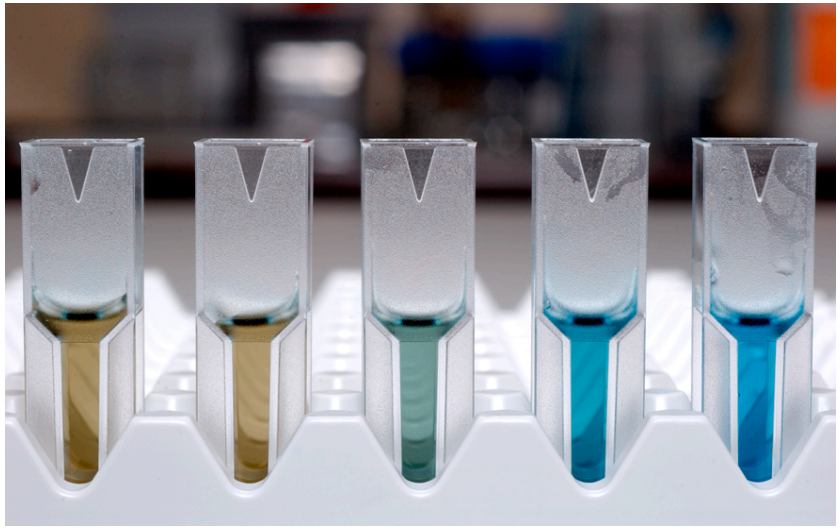
http://nationaldiagnostics.com/article_info.php/articles_id/10

Coomassie brilliant blue staining



- binds proteins primarily via aromatic residues and arginine
- undergoes absorbance shift from 465 nm (brownish) to 595 nm (blue)
- basis for Bradford Assay; can be used to quantify proteins over ~3 kD

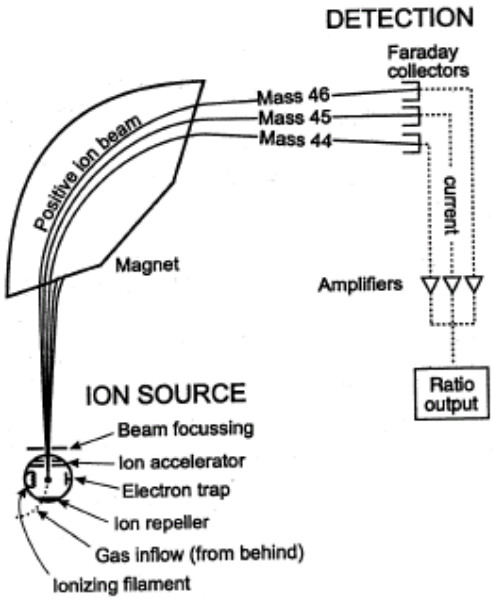


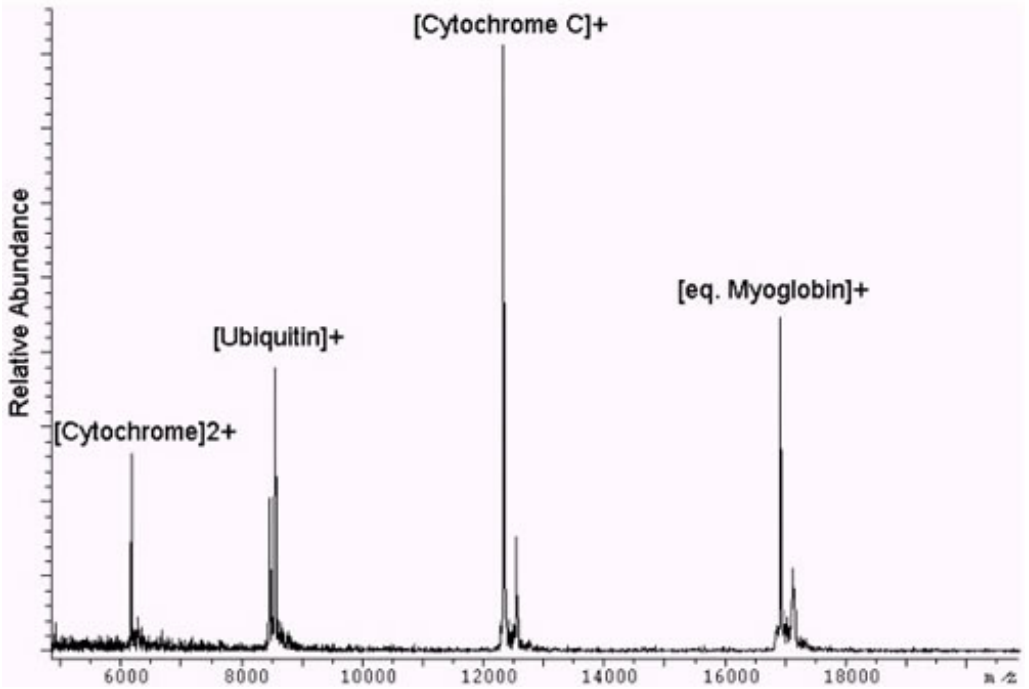


www.eiroforum.org/press/media_embl.html

SDS-PAGE gives an approximate MW and purity estimate, but how can we be sure the protein we've purified is the correct one?

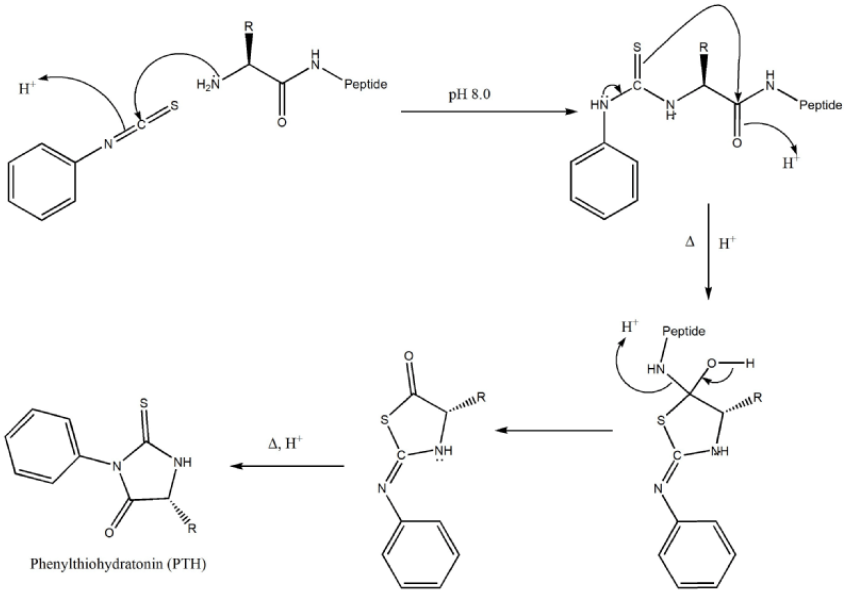
- activity assay if one is available
- knowledge of exact mass: mass spectrometry
- N-term. sequencing and AA analysis, if necessary





en.wikipedia.org/wiki/Mass_spectrometry
www.kcl.ac.uk/ms-facility/images/maldispec2.jpg

N-terminal sequencing (Edman degradation)



- products identified by chromatography or electrophoresis
- typically ~5 cycles practical for routine N-term. sequencing

en.wikipedia.org/wiki/Edman_degradation

Amino acid analysis

- HCl digestion to digest peptide bonds
- HPLC to quantify AA components