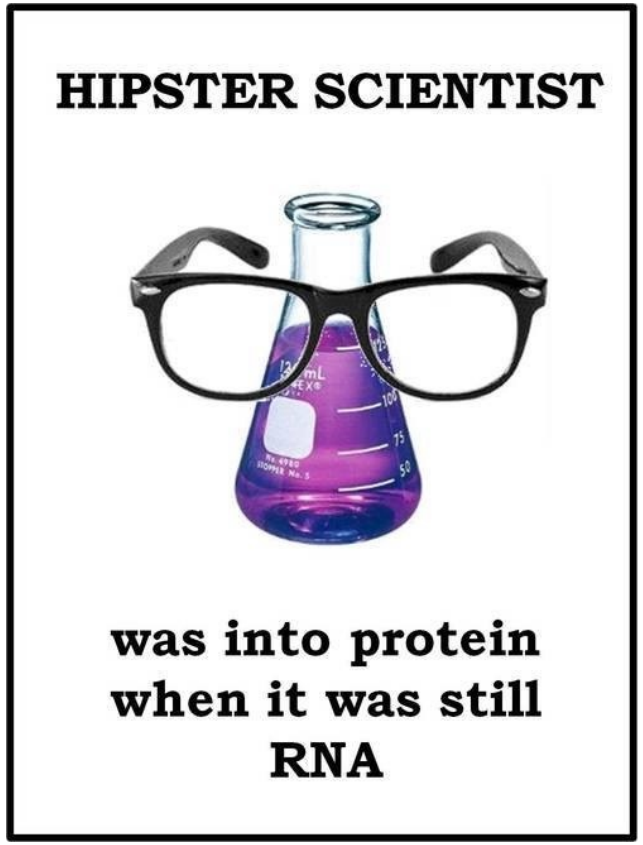
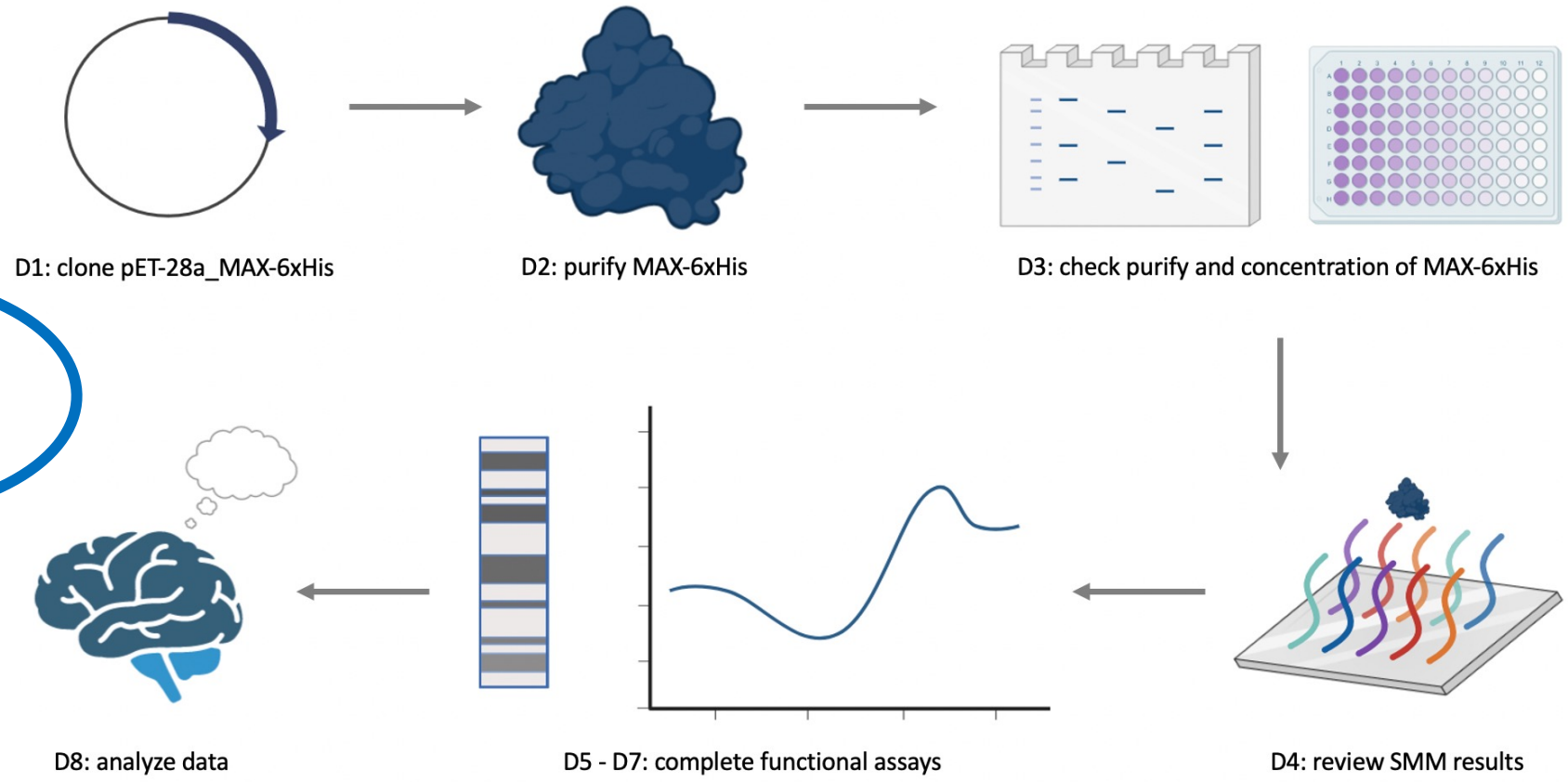
M1D3:
Assess purity and concentration of purified protein

1. Prelab discussion
2. Concentrate purified protein sample
3. Visualize MAX-6xHis purity
4. Measure MAX-6xHis concentration



Overview of Mod 1 experiments:

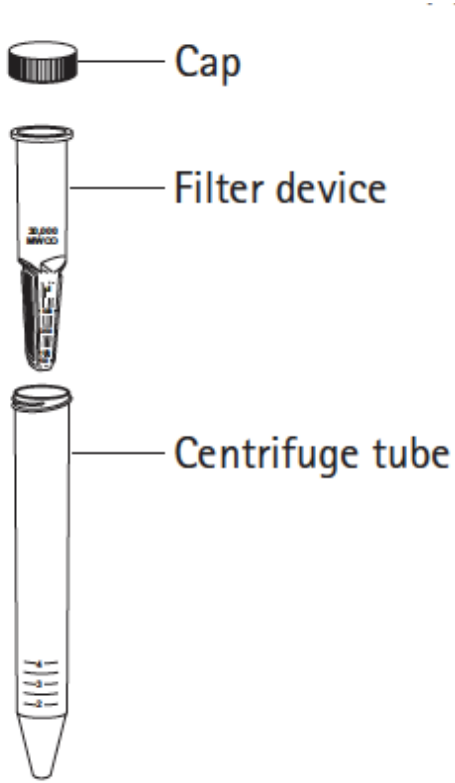


Let’s review the protein purification steps…

- Added lysonase – to what? why? Added DNaseI – to what? why?
- Centrifuged – what? why?
- Incubated with nickel resin – why?
- Washed with low concentration imidazole – why?
- Eluted with high concentration imidazole – why?

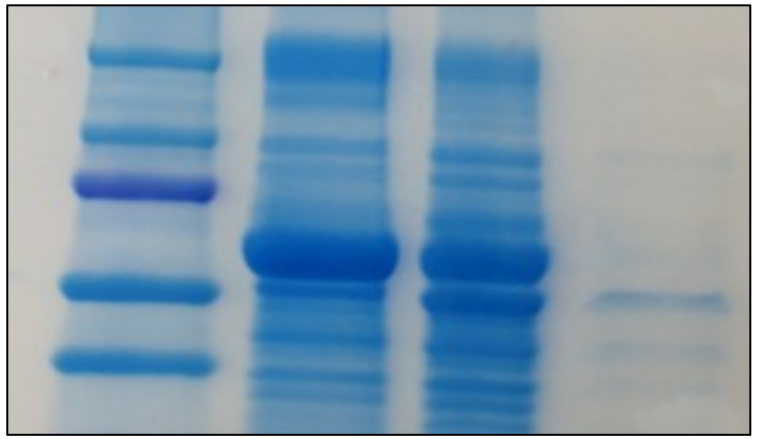
First, you will concentrate your purified protein

- Filter device sits within centrifuge tube…add protein to filter device for centrifugation
- Filter device has MW cutoff of 10 kDa …protein is retained in the filter device during centrifugation
- How does this concentrate the protein?

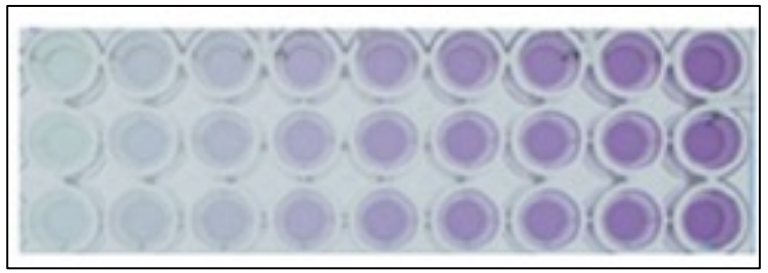


How will you assess the quality of your protein?

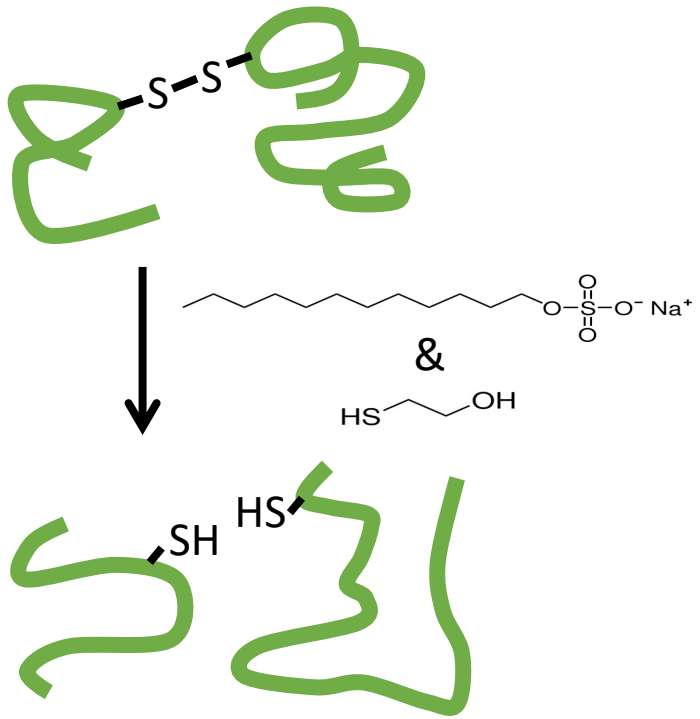
- Check purity using SDS-PAGE
  - Visual detection of all proteins in sample
  - Used to assess purity / quality



- Measure concentration using BCA assay
  - Quantitative measure of all proteins in the sample
  - Used to calculate concentration



Purity: Sodium dodecyl sulfate polyacrylamide gel electrophoresis (SDS-PAGE)

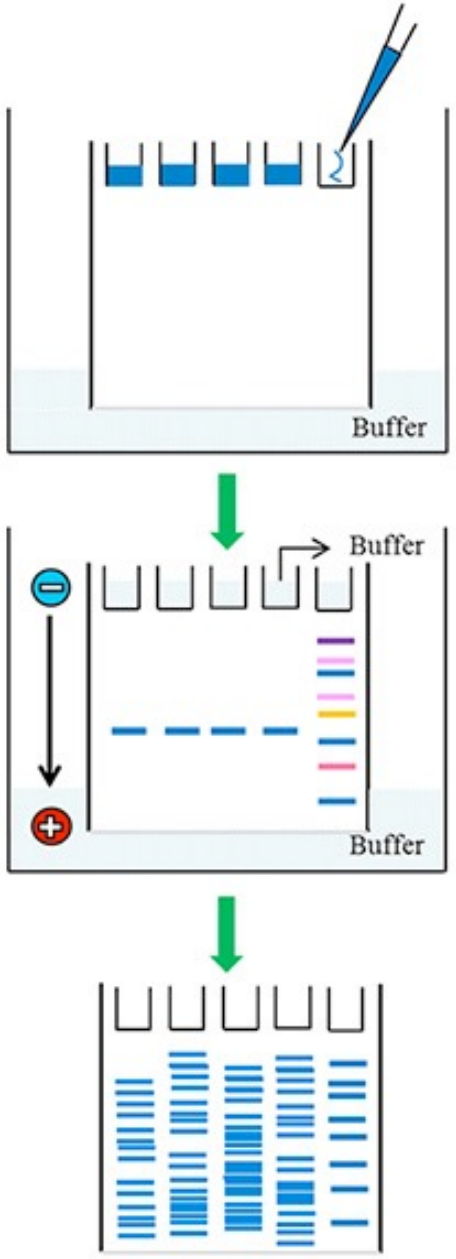


- Laemmli sample buffer (loading dye):
  - sodium dodecyl sulfate (SDS)
  - β-mercaptoethanol (BME)
  - bromophenol blue
  - glycerol
- Boiling:

How are proteins separated?

- Electrophoresis completed in TGS buffer
  - Tris-HCl
  - SDS
  - Glycine

- How does adding Laemmli buffer and boiling change protein structure?
- What determines how far a protein migrates in the gel?



Be mindful when loading protein samples!

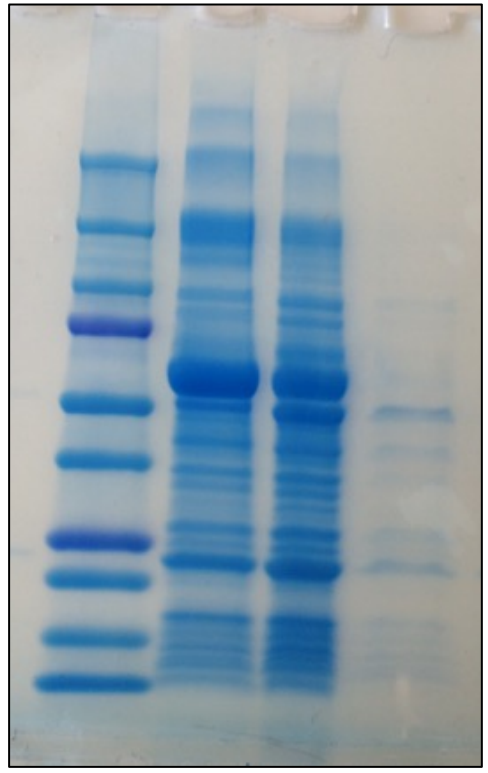
- Consider the order of your samples:
  - Pellet
  - Lysate
  - Flowthrough
  - Wash
  - Concentrated MAX-6xHis
  - Slurry
  - Ladder

- Figure for these results will be used for your due M1D4 homework and included in your Data summary!

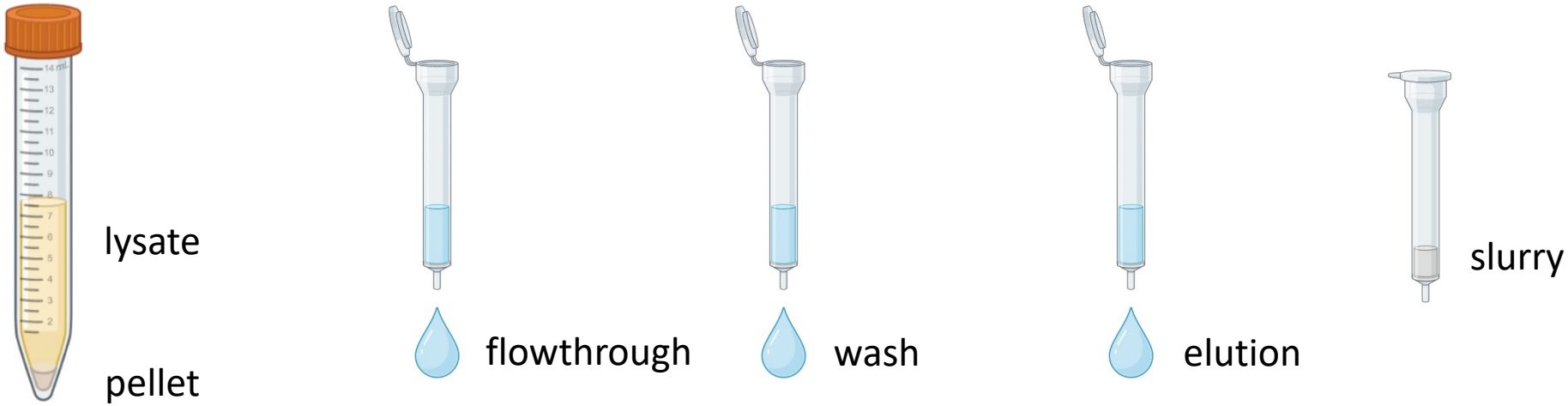
How are proteins visualized?

- Coomassie dye used to stain protein bands
  - Hydrophobic and electrostatic interactions with basic residues
  - Arg (also His, Lys, Phe, Trp)

- How will you know which band corresponds to MAX-6xHis?
- How does SDS-PAGE provide information regarding the purity of your protein sample?



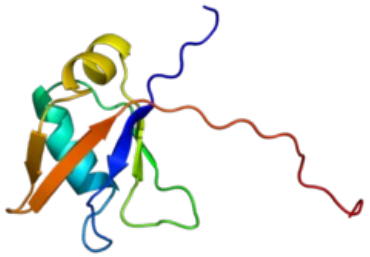
What are the expected results?



- Where do you / do you not expect to see MAX-6xHis? Why / why not?
- Where do you expect to see other cellular proteins?
- How will the elution sample differ from the concentrated protein sample?

Concentration: Bicinchoninic acid (BCA) protein assay

Step 1: Biuret reaction; chelation of copper with protein, reduction of copper



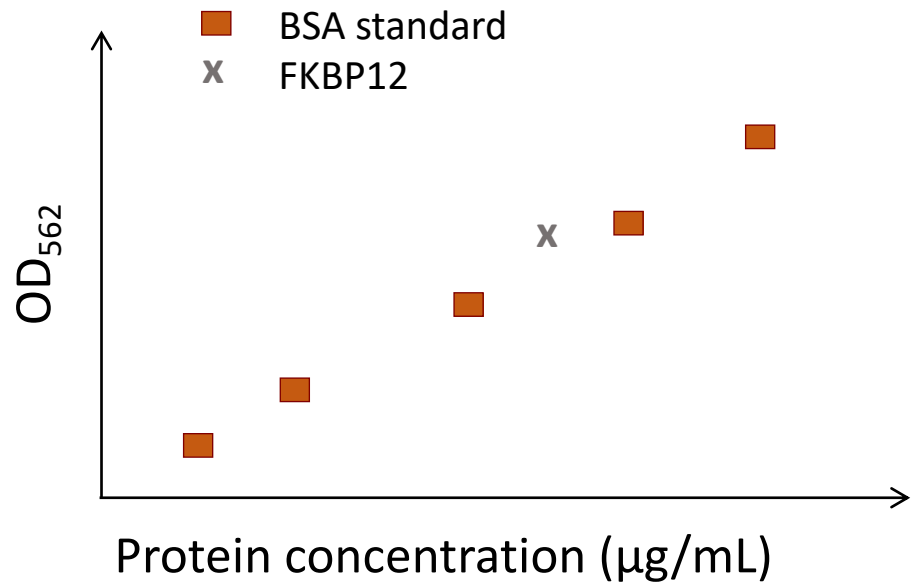
+ Cu^{2+} $\xrightarrow[\text{Temperature-dependent}]{OH^-}$ Cu^{1+}

Step 2: BCA complexes with cuprous cation

Cu^{1+} + 2 BCA $\longrightarrow$ BCA-Cu^{1+} complex (A = 562 nm, violet)

BCA/Cu^{1+} absorbance proportional to protein concentration

- Standard curve generated using serial dilutions of bovine serum albumin (BSA)
  - Use fresh tips between tubes
  - Mix well between dilutions
  - Be sure to add correct volumes



- Is the calculated concentration an accurate measure of the amount of MAX-6xHis in your sample?

For today…

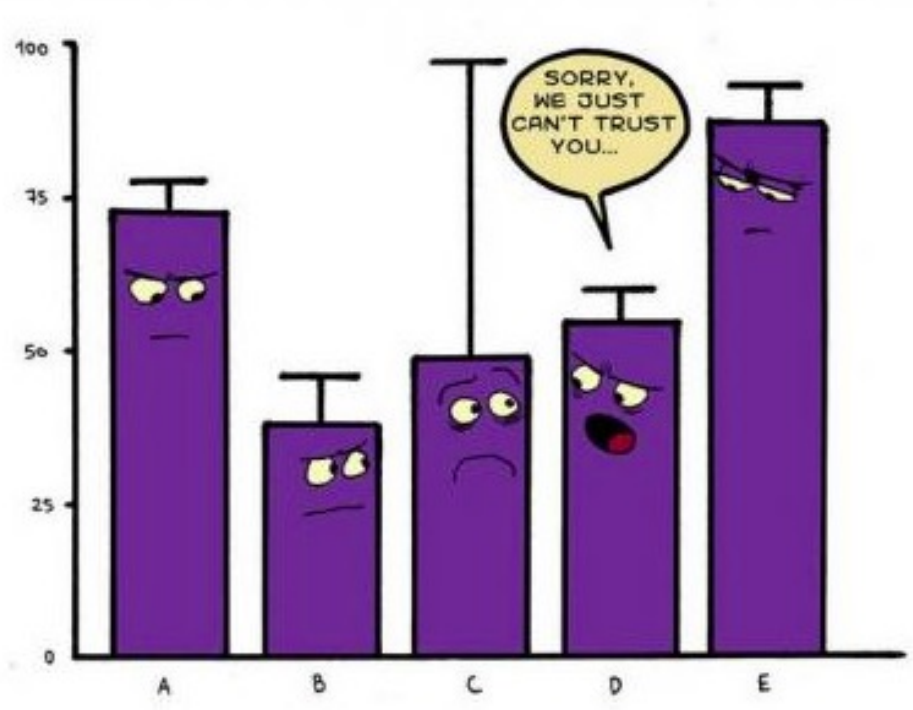
- Divide experiments between partners to ensure work is completed during class time
  - Be sure to share data / results!

For M1D4…

- Craft data figure for SDS-PAGE and BCA results
- *Draft outline of Background & Motivation for bonus feedback* ☺

Notes on figure making…

- Be sure image is appropriately sized
  - Only needs to be large enough to be legible
  - Should not be entire page
- Eliminate visual noise and clutter
  - Unnecessary labeling and graphics distract from the data
- Use clear labels / legends
  - Be sure labels / legends do not obstruct the data



How can you improve this example?