

# M2D4: Purify protein

10/22/2015

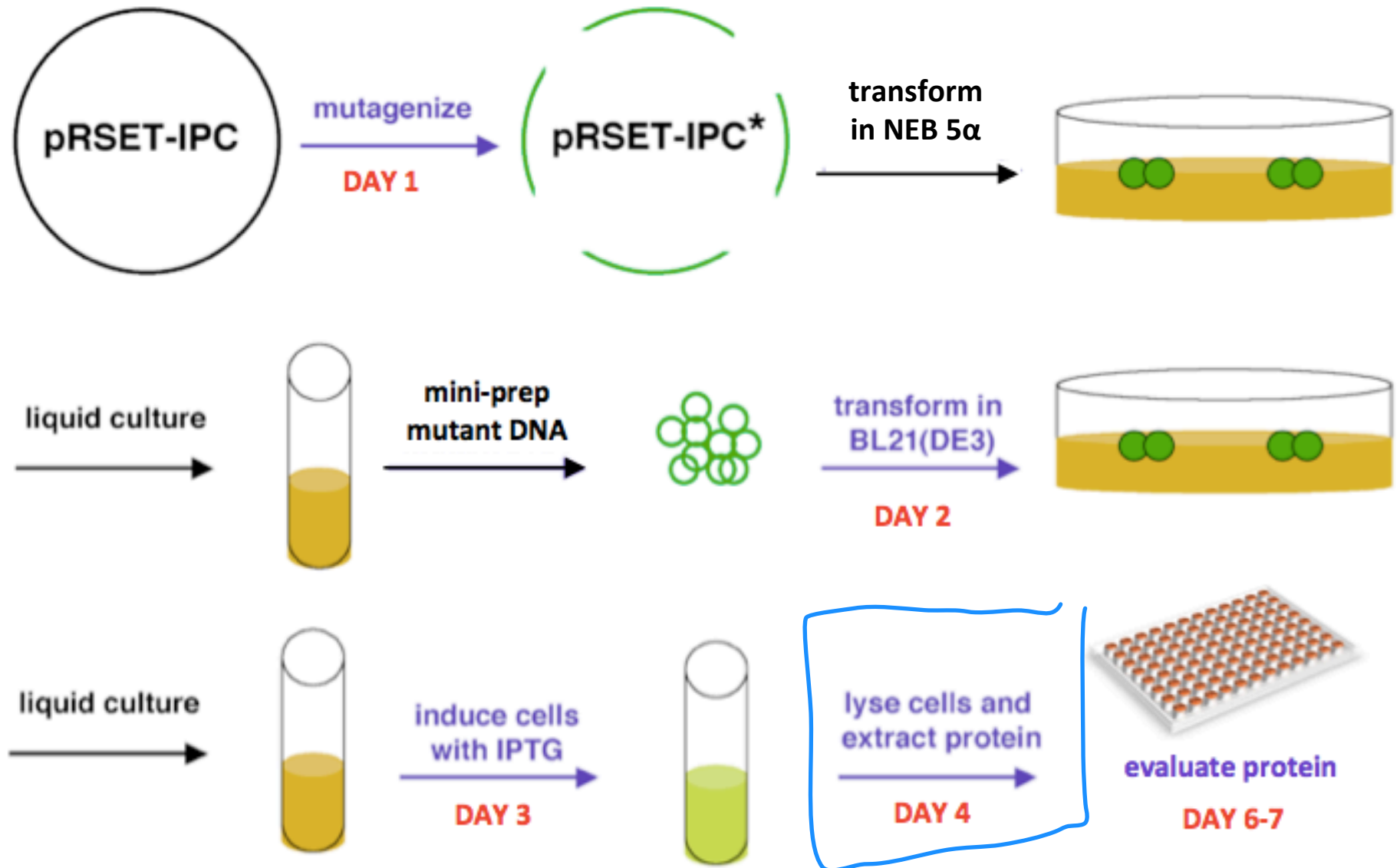
1. Prelab lecture
2. Lyse bacteria and prep SDS-PAGE samples
3. Purify protein
4. Measure purified protein

# Assignments on the horizon

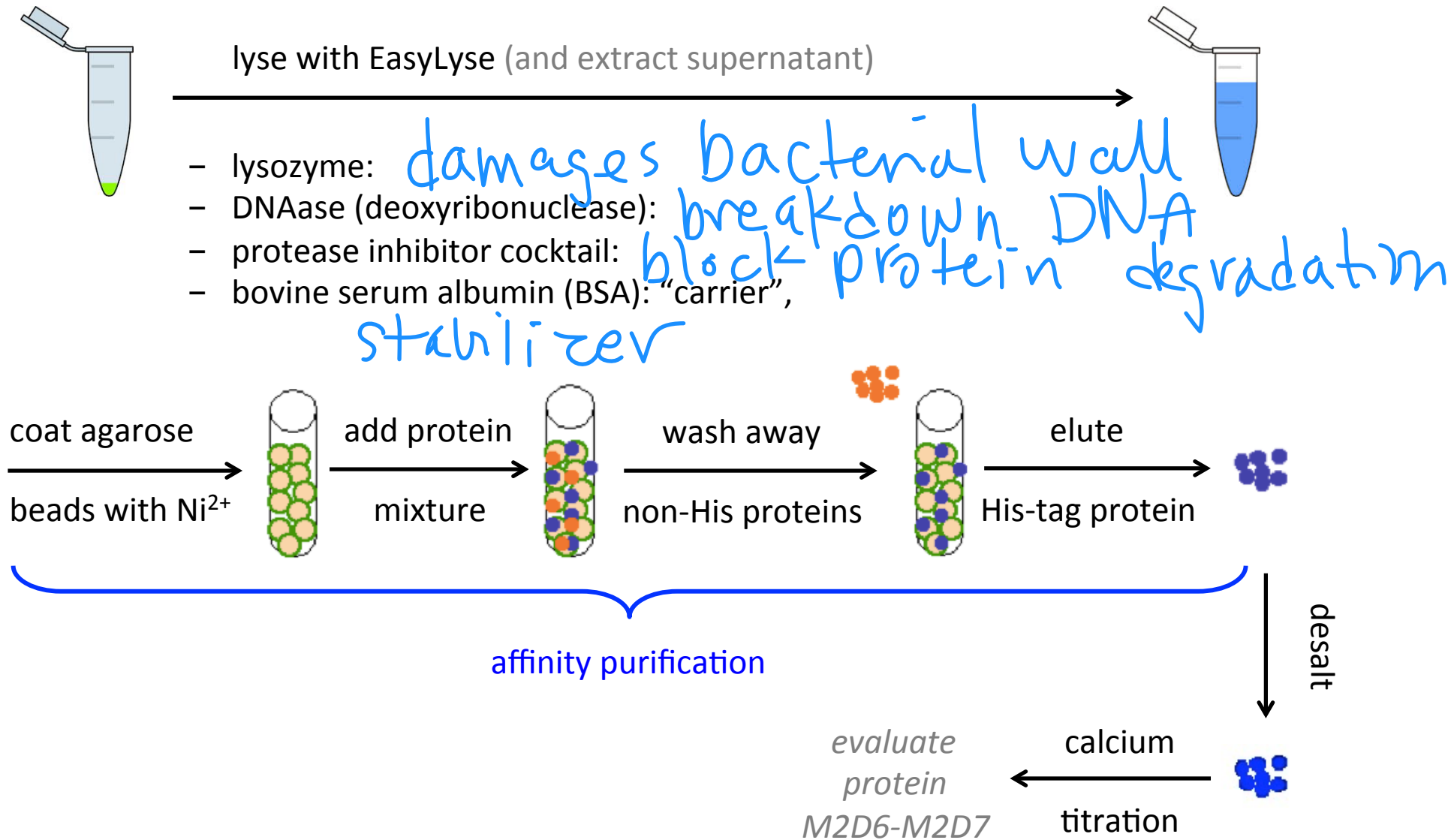


- DNA engineering summary revision
  - due by 5pm on Saturday, Oct. 24
- Blog post for M1
  - due by 5pm on Sunday, Oct. 25
- For M2D5:
  - journal club readings, meet in 16-336
- For M2D6:
  - estimate your protein concentration (from Bradford assay) in excel
  - write up Methods section

# Module 2 experimental overview

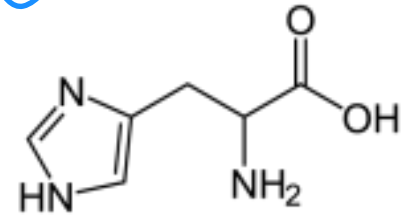


# Protein purification: protocol overview

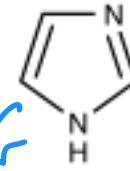


(2) 1 wt IPC 1 mut IPC

# Protein purification: a few notes

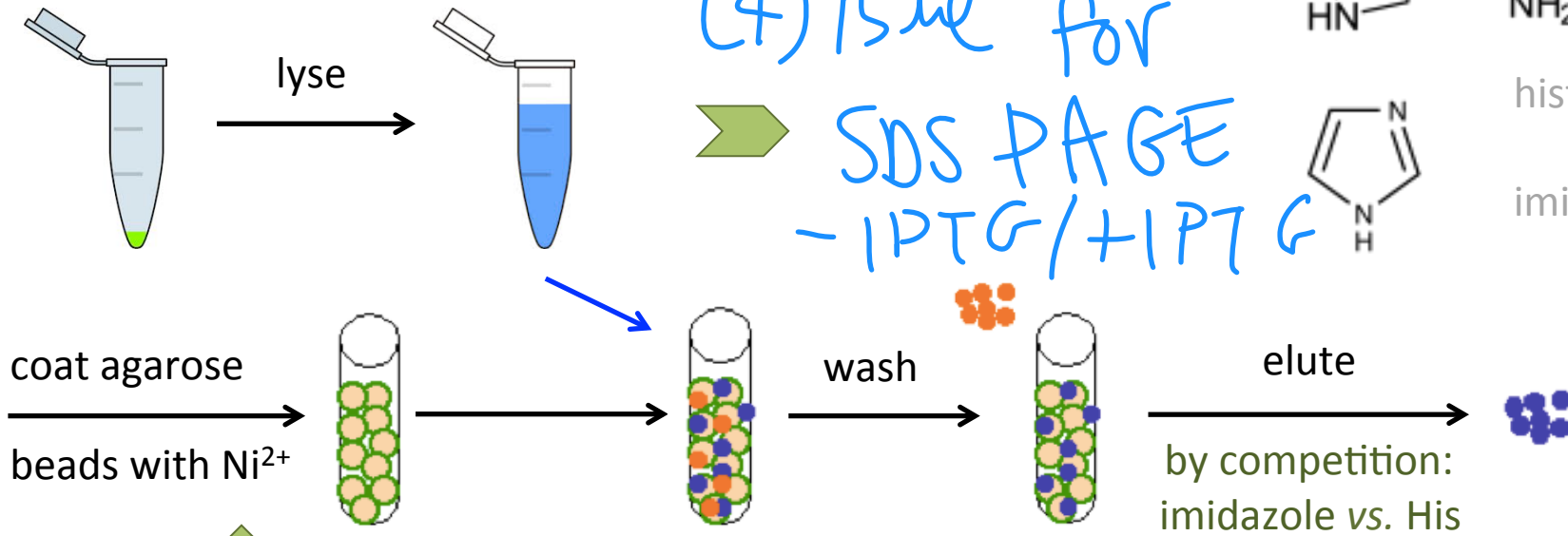


histidine

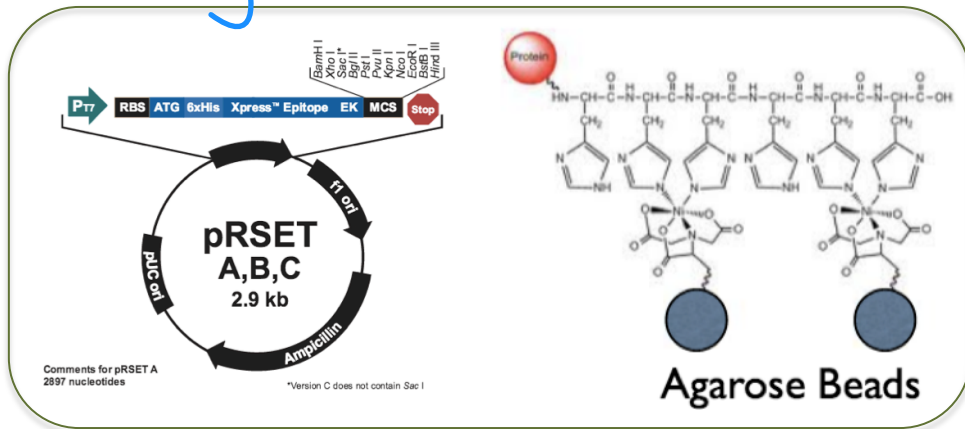


imidazole

(4) 15µl for  
 SDS PAGE  
 -IPTG / +IPTG



HIS tag binds to metals

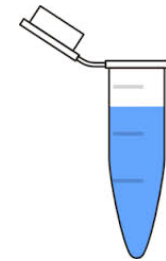


remove salts + imidazole  
 IPC - Ca<sup>2+</sup> interferes

evaluate protein  
 M2D6-M2D7

desalt

# Prepare samples for SDS-PAGE



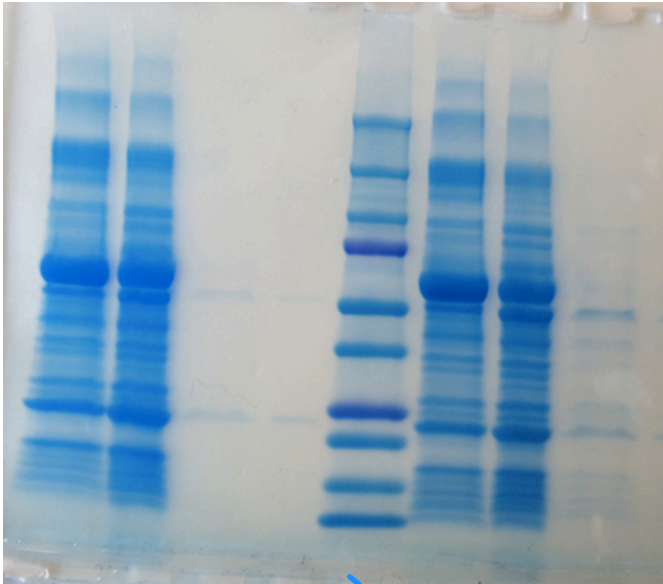
- Set aside whole cell extracts
  - equal number of cells based on OD<sub>600</sub> (from M2D3)

1      2      3      4

sample	example		wt IPC		selected X#Z	
	- IPTG	+ IPTG	- IPTG	+ IPTG	- IPTG	+ IPTG
OD600	lowest: 0.5	0.75				
sample volume (μL)	15	15*0.5/0.75 → 10				
water volume(μL)	0	5				
total volume (μL)	15	15	15	15	15	15
add 6x buffer (μL)	3	3	3	3	3	3

- SDS-PAGE: sodium dodecyl sulfate polyacrylamide gel
  - separation by size? shape? charge?

# SDS-PAGE separates proteins by size



coomassie

- Laemmli sample buffer:

- + SDS: surfactant / detergent

- denatures proteins, coats them with negative charge

- +  $\beta$ -mercaptoethanol

- reduces disulfide bonds

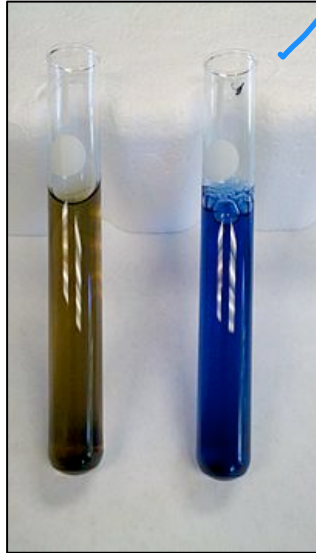
- + bromophenol blue

- + glycerol

→ visualize smallest + migration

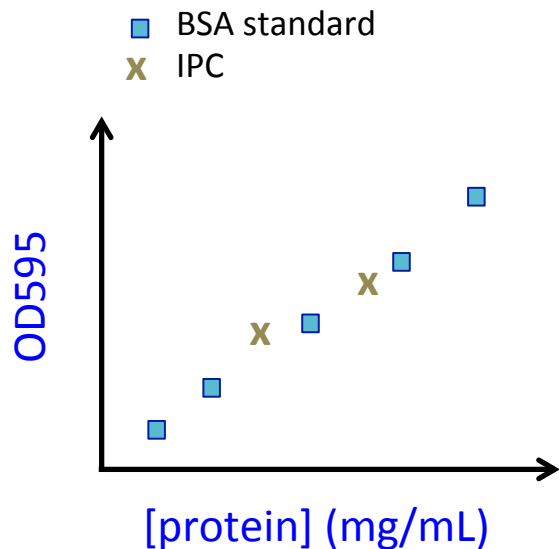
- boiling denatures higher-order structures

blue, absorbs orange ~595nm



## The Bradford colorimetric assay measures protein concentration

- Coomassie brilliant blue G-250 dye
  - red if unbound (cationic form)
  - blue if bound to protein (anionic)
  - Van der Waals & hydrophobic interactions
  - arginine residues in particular
  - monitor OD<sub>595</sub> absorption



- calibration with BSA
  - 0.1 – 1.0 mg/mL **BSA**
  - relative (not absolute) estimate of [IPC]:  
 $[Arg]_{BSA} \neq [Arg]_{IPC}$
- work fast! (5-20min ideal)



# Today in lab

- Lyse 4 cell pellets (wt IPC -/+ IPTG and “good” mutant -/+ IPTG)
- Set aside aliquots for SDS-PAGE (M2D6)  $\sim 15\mu\text{l}$ 
  - add 6X sample buffer (Laemmli buffer) to each
- Purify protein (1 wt IPC + 1 mutant)  $\text{+IPTG}$   $\text{+IPTG}$ 
  - long!
  - 2 steps: affinity purification + desalting
- Immediately aliquot 10  $\mu\text{L}$  for Bradford assay and 15 $\mu\text{L}$  for SDS-PAGE
- Stabilize rest of purified protein with BSA
  - $\sim 1$  mL protein + 10  $\mu\text{L}$  of 10% BSA
  - to be titrated against  $\text{Ca}^{2+}$  on M2D6