

# M2D4: Purify protein

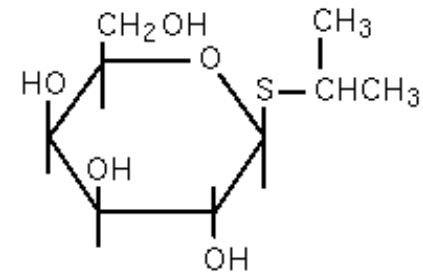
10/22/2015



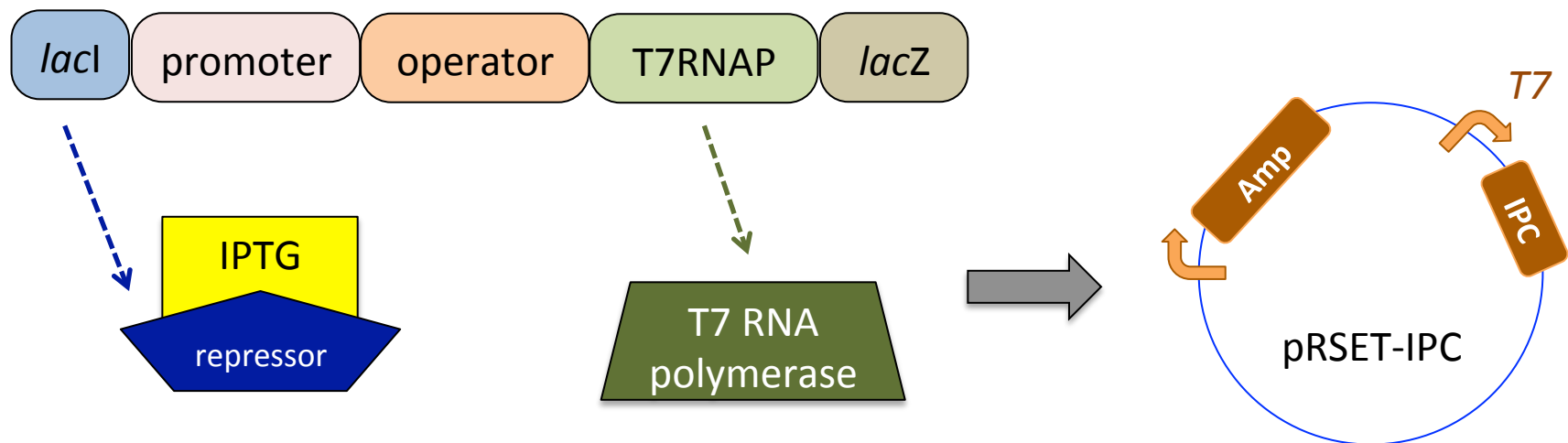
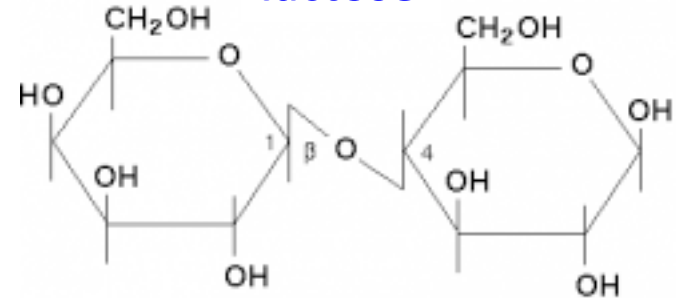
# IPTG is a lactose analogue

- isopropyl  $\beta$ -D-1-thiogalactoside
- structural mimic of lactose
- unlike lactose, **IPTG is not cleaved by  $\beta$ -galactosidase and so will not be broken down or used by the cell**  
→ [IPTG] constant

**IPTG**



**lactose**

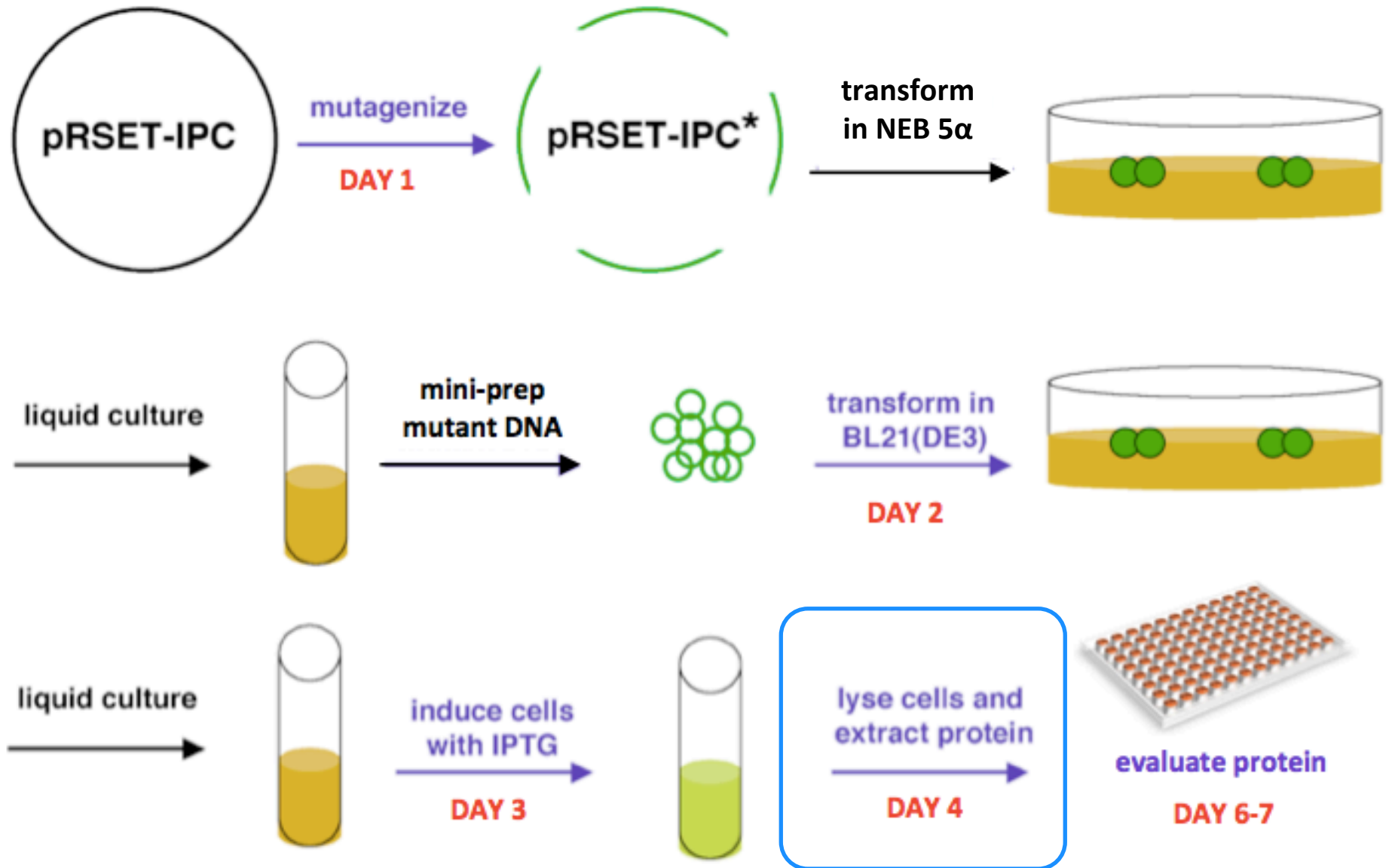


# Assignments on the horizon

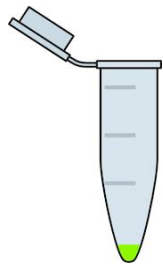


- DNA engineering summary revision
  - due by 5pm on Saturday, Oct. 24
- Blog post for M1
  - due by 5pm on Sunday, Oct. 25
- For M2D5:
  - journal club readings
- For M2D6:
  - estimate your protein concentration (from Bradford assay)
  - write up Methods section

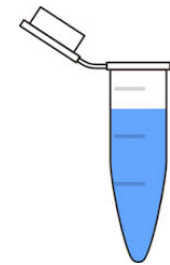
# Module 2 experimental overview



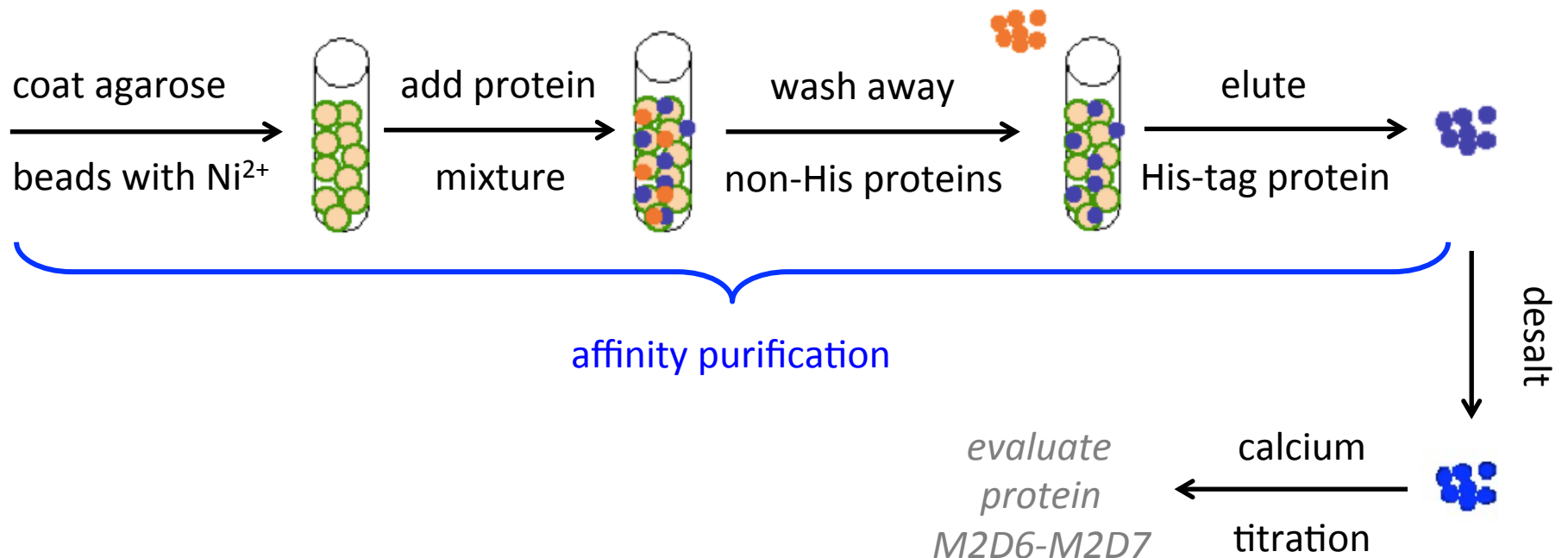
# Protein purification: protocol overview



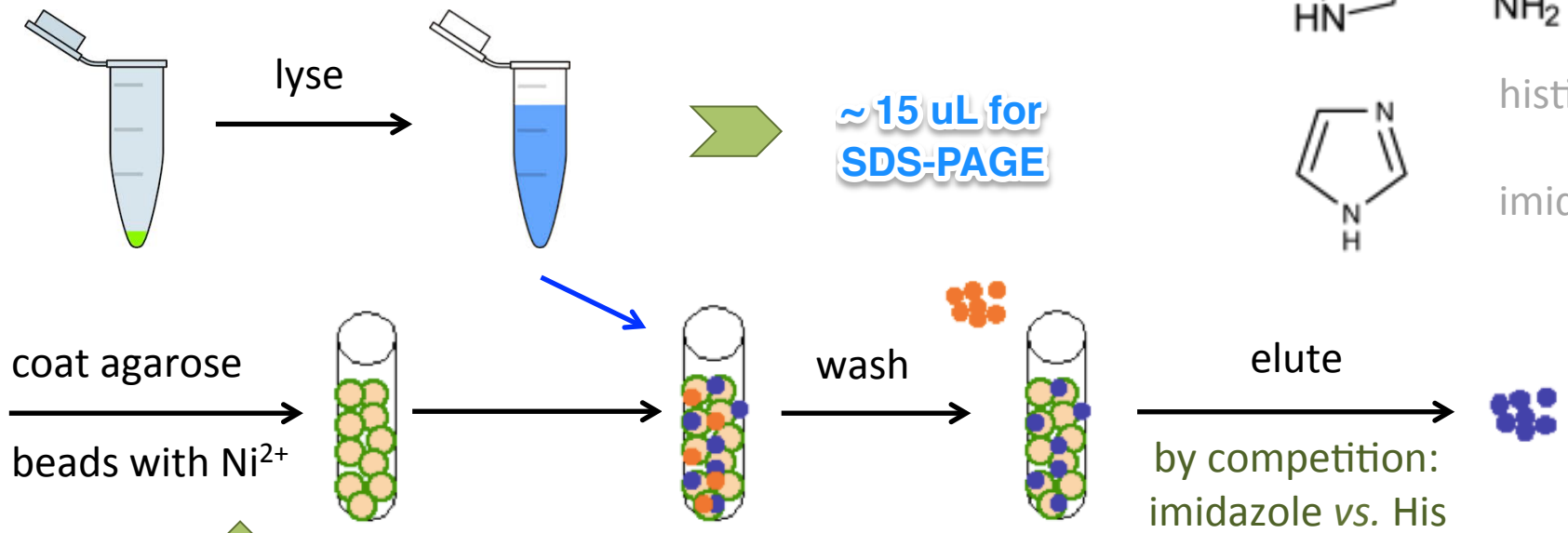
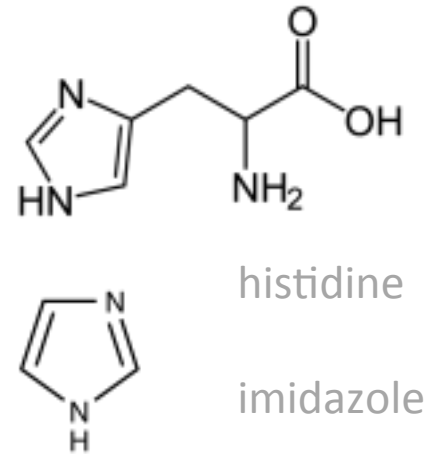
lyse with EasyLyse (and extract supernatant)



- lysozyme: **damages bacterial walls, opens up E. coli BL21**
- DNAase (deoxyribonuclease): **chews up DNA**
- protease inhibitor cocktail: **against protein degradation**
- bovine serum albumin (BSA): "carrier", **stabilizer**



# Protein purification: a few notes



**His-tag** binds to metals

**get rid of imidazole because it interferes with IPC-calcium binding**

desalt

evaluate protein  
M2D6-M2D7

**pRSET A,B,C**  
2.9 kb

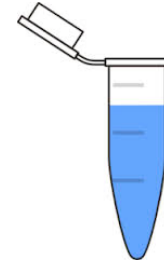
Comments for pRSET A  
2897 nucleotides

\*Version C does not contain Sac I

Agarose Beads

Protein

# Prepare samples for SDS-PAGE



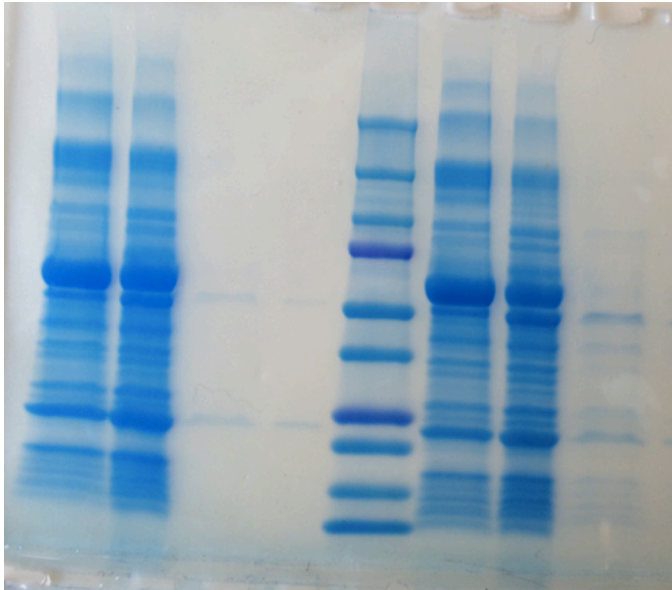
- Set aside whole cell extracts
  - equal number of cells based on  $OD_{600}$  (from M2D3)

sample	example		wt IPC		selected X#Z	
	- IPTG	+ IPTG	- IPTG	+ IPTG	- IPTG	+ IPTG
OD600	lowest: 0.5	0.75				
sample volume ( $\mu\text{L}$ )	15	$15 \cdot 0.5 / 0.75$				
water volume ( $\mu\text{L}$ )	0	5				
total volume ( $\mu\text{L}$ )	15	15	15	15	15	15
add 6x buffer ( $\mu\text{L}$ )	3	3	3	3	3	3

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

  
toxic

# SDS-PAGE separates proteins by **size**



- Laemmli sample buffer:

- + SDS: surfactant / detergent  
denatures proteins, coats them with  
negative charge

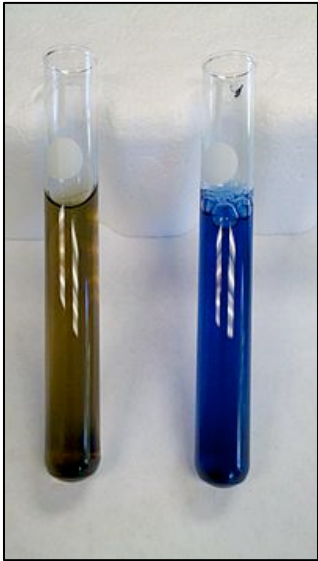
- +  $\beta$ -mercaptoethanol  
reduces disulfide bonds

- + bromophenol blue

- + **glycerol**

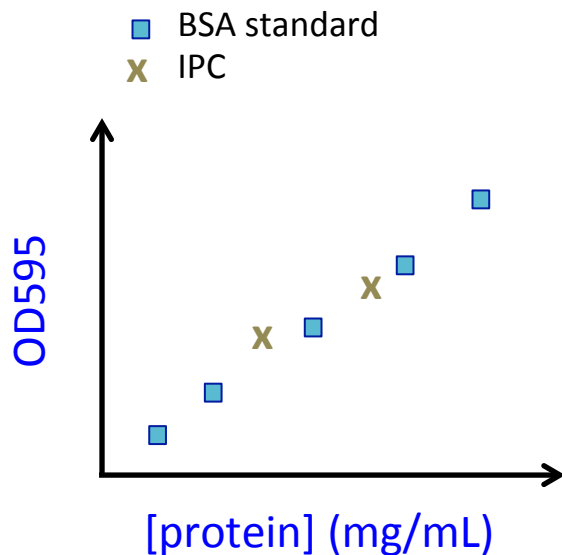
- boiling denatures higher-order  
structures





# 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
  - relative (not absolute) estimate of [IPC]:  
 $[Arg]_{BSA} \neq [Arg]_{IPC}$
- work fast!

# Today in lab

- Lyse 4 cell pellets (wt IPC -/+ IPTG and “good” mutant -/+ IPTG)
- Set aside aliquots for SDS-PAGE (M2D6)
  - add Laemmli buffer to each
- Purify protein (1 wt IPC + 1 mutant)
  - long!
  - 2 steps: affinity purification + desalting
- Immediately aliquot 10  $\mu$ L for Bradford assay
  - + 15  $\mu$ L for SDS-PAGE
- Stabilize rest of purified protein with BSA
  - $\sim$  1 mL protein + 10  $\mu$ L of 10% BSA (0.1% BSA total in samples)
  - to be titrated against  $\text{Ca}^{2+}$  on M2D6