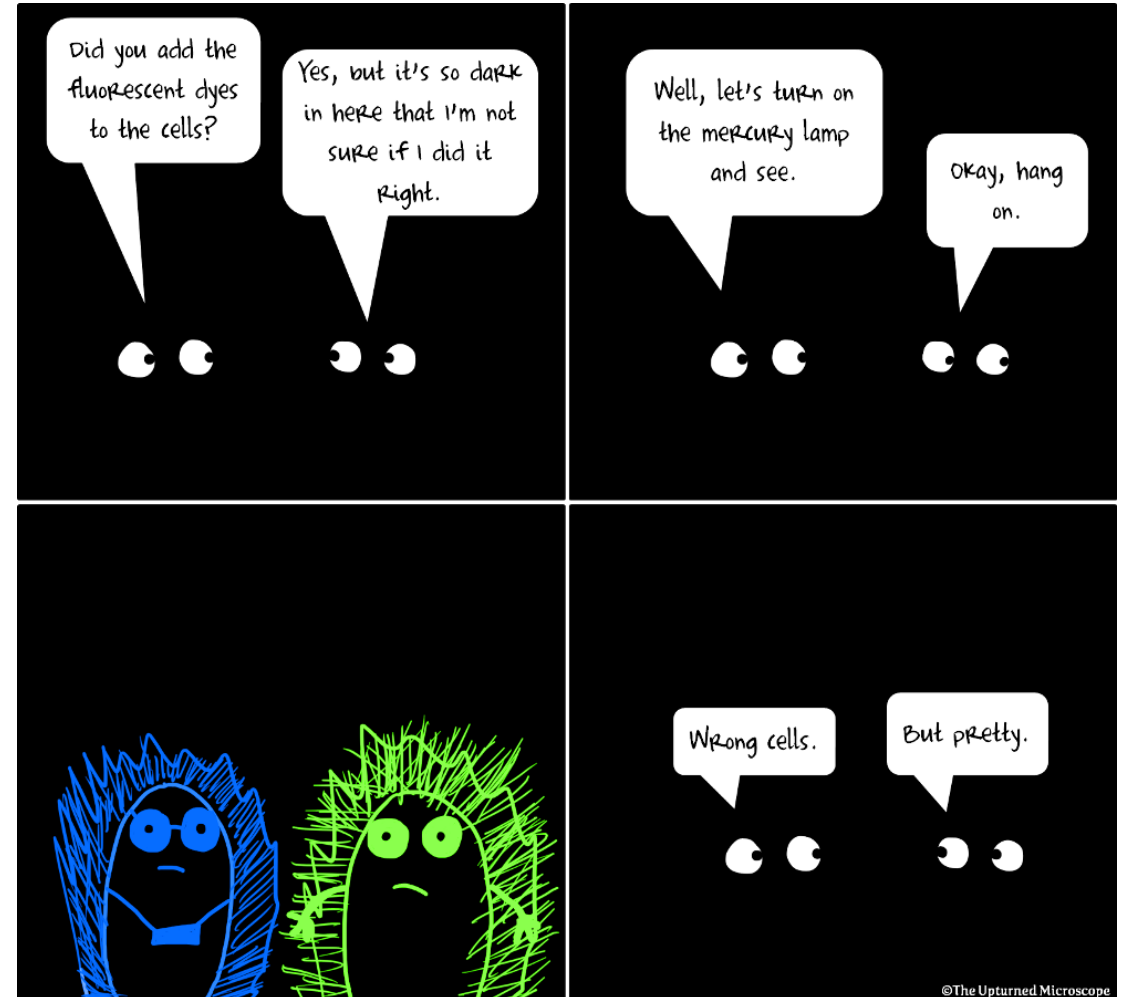


# M2D5: Immunofluorescence staining

1. Prelab
2. Fix yeast
3. Antibody staining of Fet4\_mutant



# Overview of Mod 2 experiments

## Last lab:

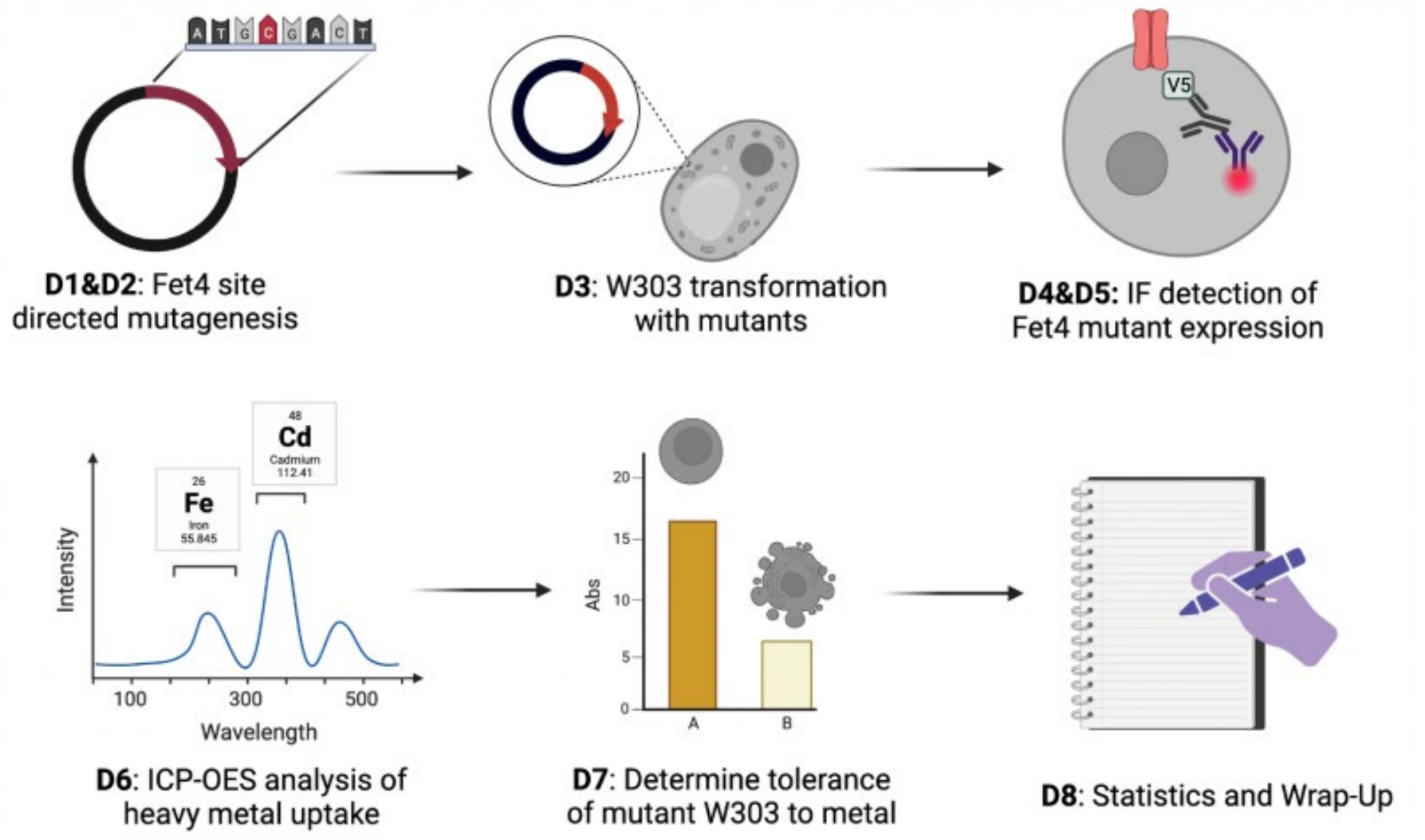
Transformed W303 yeast with mutated FET4 plasmids

## This lab:

Perform IF on FET4 expressing yeast

## Next lab:

Prepare Metal Uptake, analyze IF data



# A rational basis for amino acid mutation in Fet4



**Me (Jamie)**

# Goals for a rational FET4 Mutation

Ultimate goal: To perform a point mutation that shifts Iron transport preference to Cadmium Transport

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- 1) Selected amino acid should bind iron
- 2) The new amino acid should bind cadmium
- 3) Mutation should NOT disrupt structure

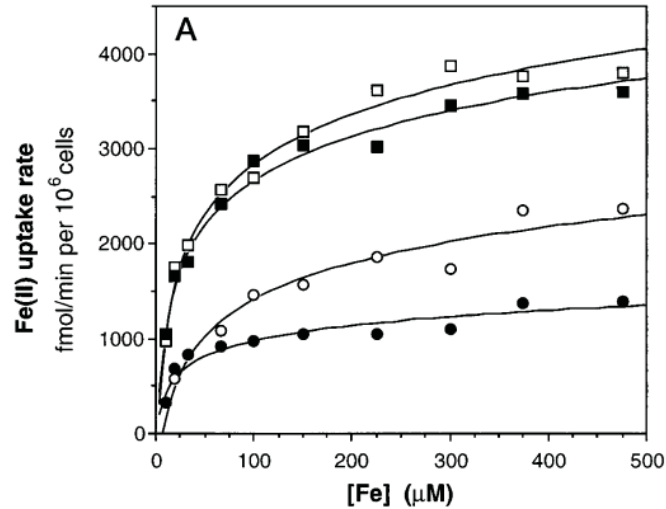
# Goals for a rational FET4 Mutation

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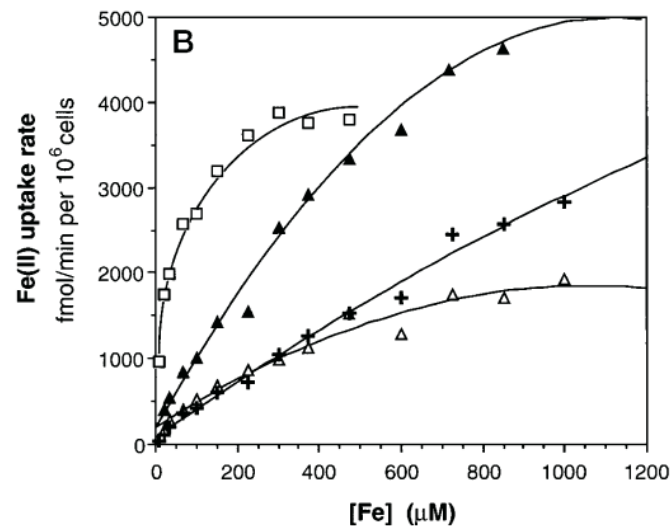
**How do we narrow down  
500+ amino acid candidates  
down to just 1-2?**

# Residues that are important for iron uptake are known by alanine screen in Dix paper



Order from Highest Fe Intake to Lowest

- 1) WT
- 2) Y222A (Dark Squares)
- 3) Y276A (Dark Triangles)
- 4) D271A (+)
- 5) Y392A (Empty Circles)
- 6) Y352A (Empty Triangles)
- 7) Y408A (Dark Circles)



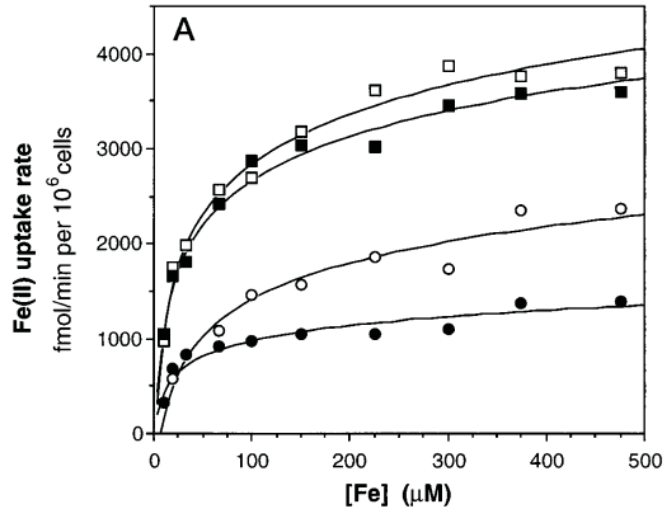
# Where are the important domains located?

Domain Locations [i](#) [?](#)



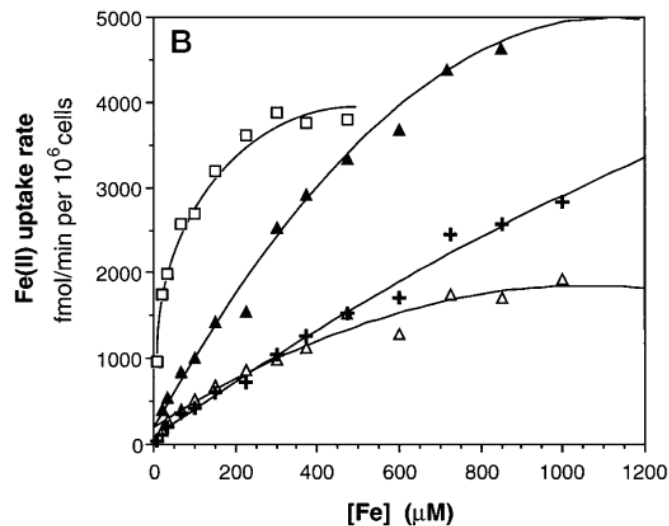


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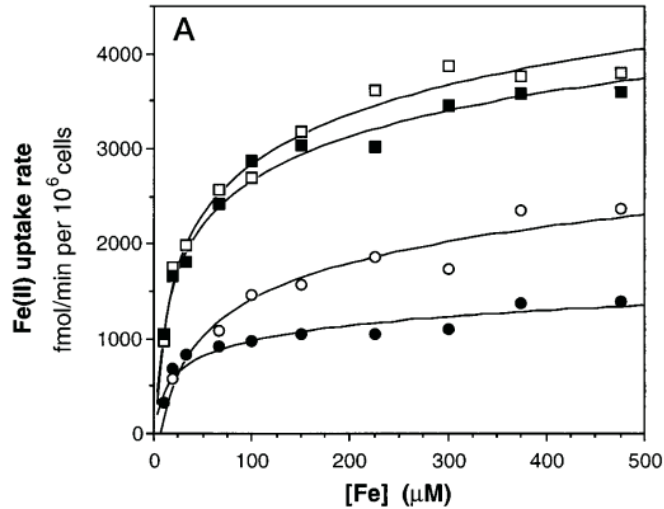


Permease Domains are: 348- 404 / 454 – 529

**Mutations are within the permease domains**

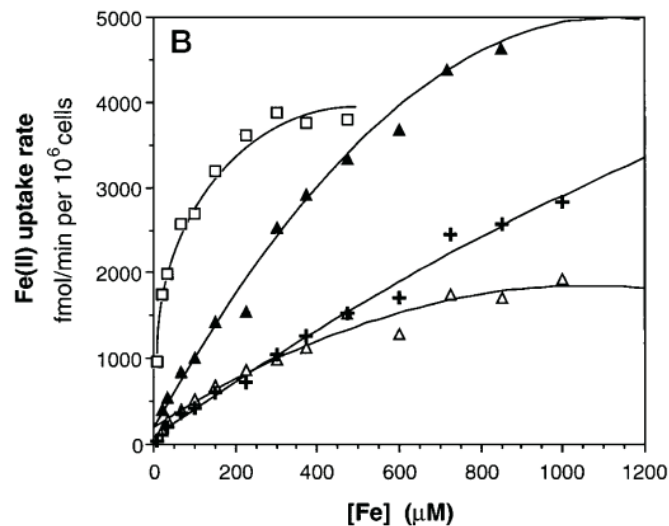
**The least impactful mutations being outside these permease domains is internally consistent.**

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Permease Domains are: 348- 404 / 454 – 529

**Mutations are within the permease domains**

**The least impactful mutations being outside these permease domains is internally consistent.**

**What characteristics are typical of good mutation candidates?**

Sun et. Al performed an alanine screen in SFM1 to design hyperaccumulators

ARTICLE

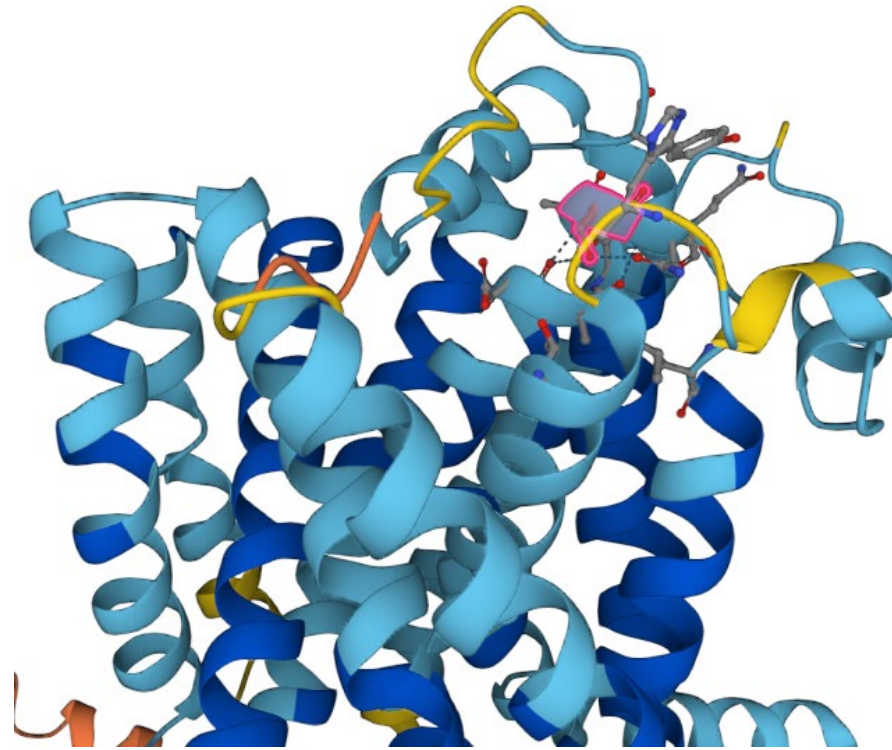
<https://doi.org/10.1038/s41467-019-13093-6>

OPEN

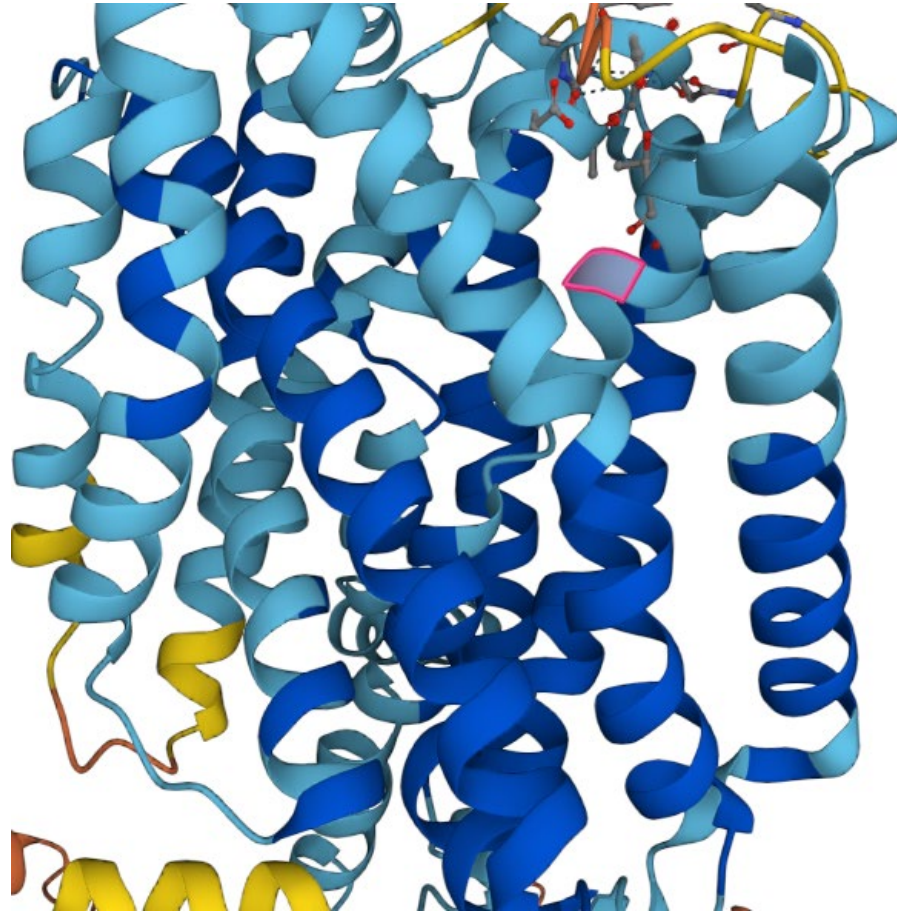
# Designing yeast as plant-like hyperaccumulators for heavy metals

George L. Sun<sup>1,2</sup>, Erin.E. Reynolds<sup>3</sup> & Angela M. Belcher <sup>1,2,4\*</sup>

In SMF1 S105 is points into the pore

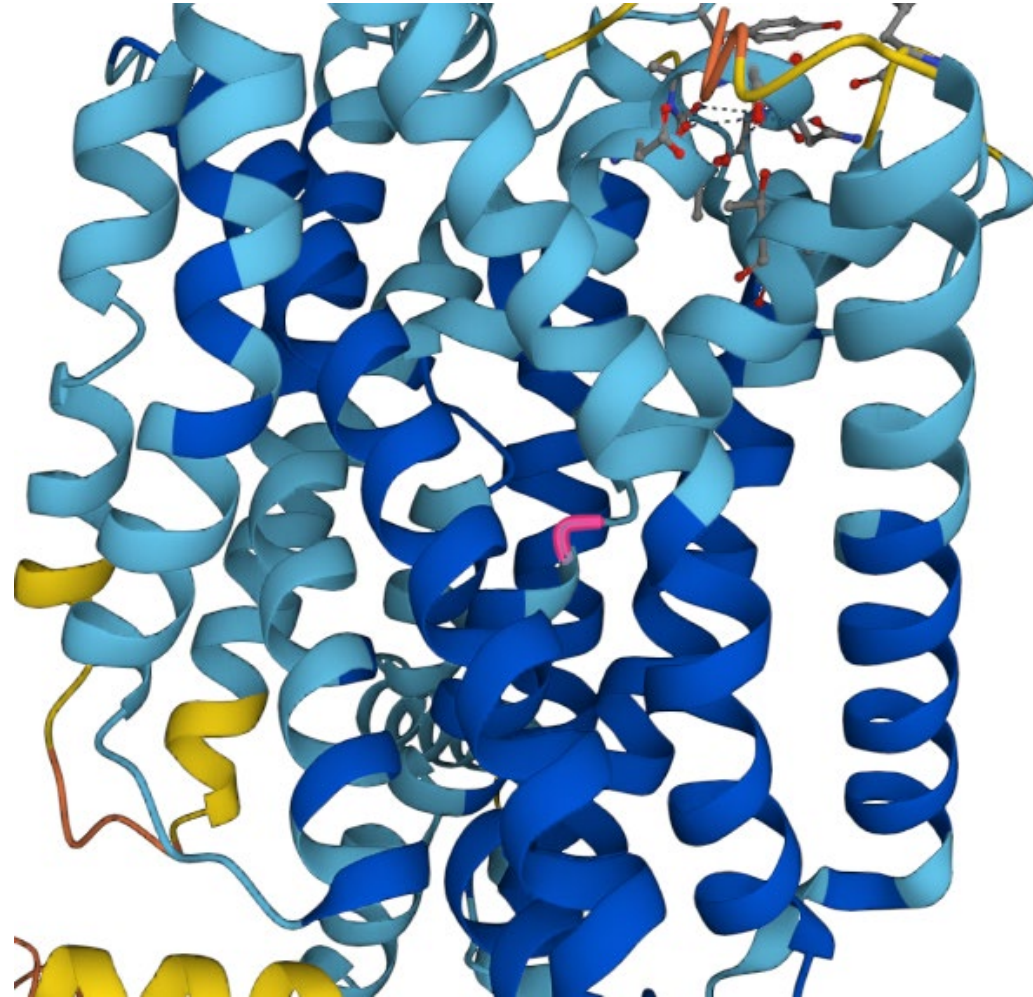


In SMF1 S269 is in the pore





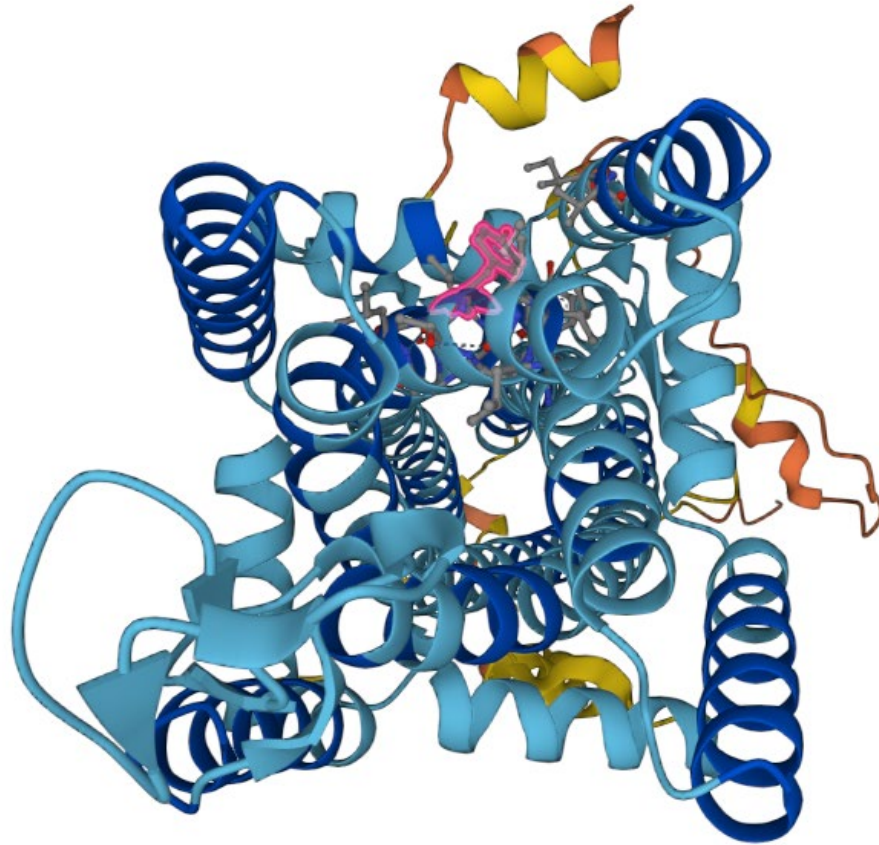
M276 is straight up in the pore (rationally chosen due to conservation) in SMF1



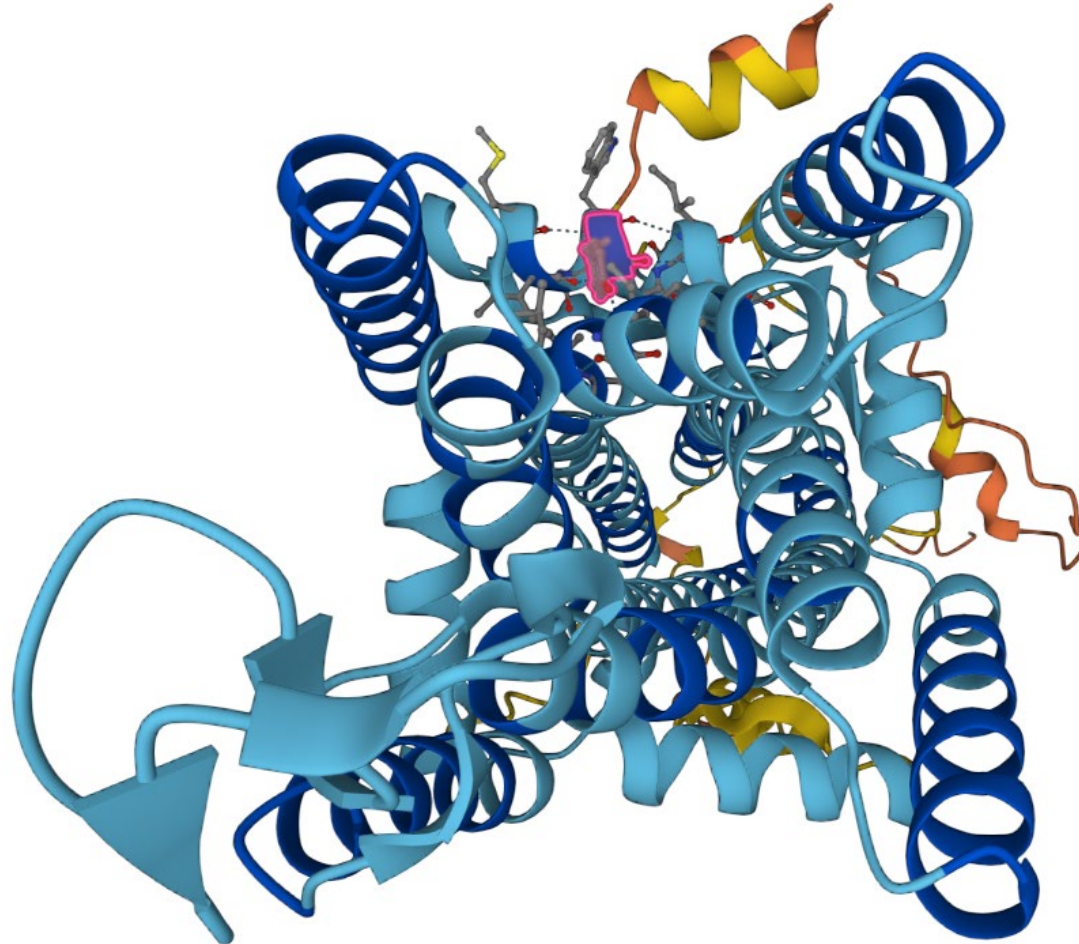
**The best residues to mutate in SMF1 were all in the pore**

**Are there Iron-binding residues in the pore of the FET4?**

Y392 is a tyrosine that points to the outer edge of the protein

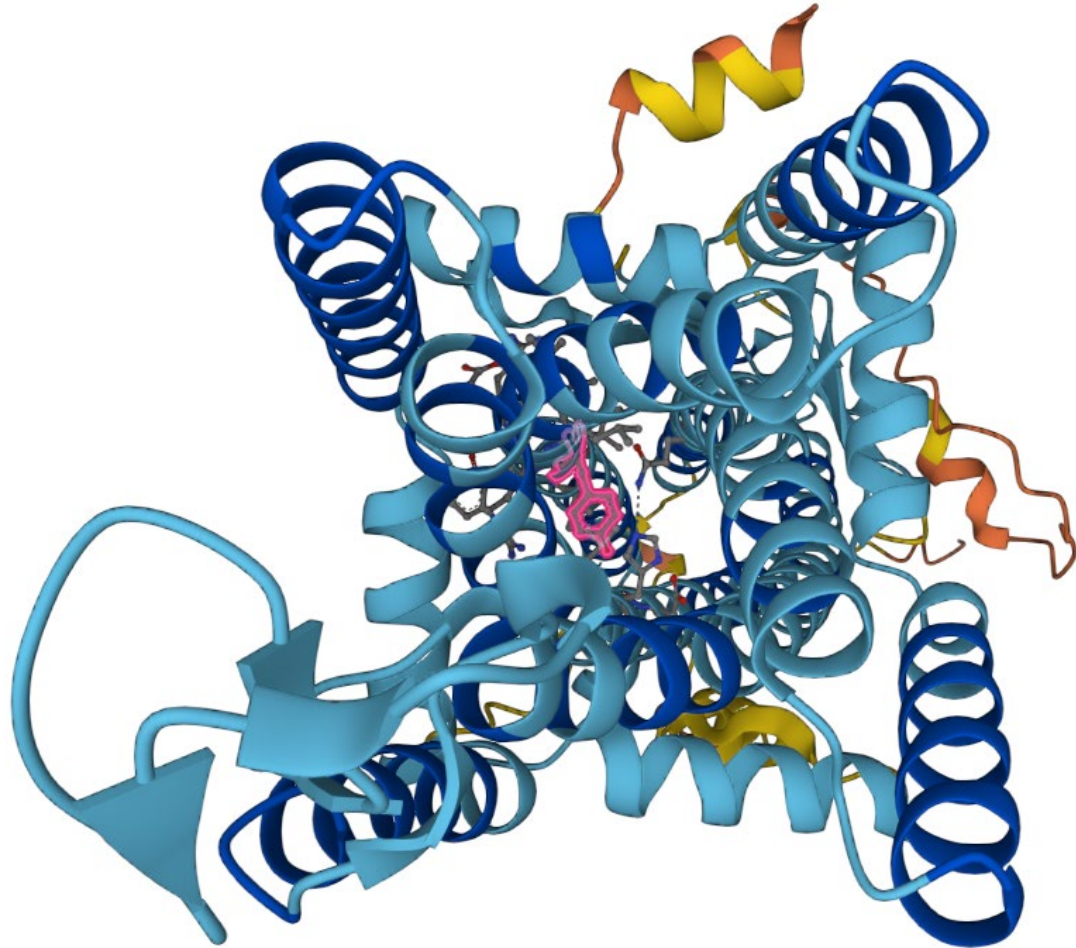


Y352 is a tyrosine pointing inward, potentially interacting with the helix that makes up the pore(?)





Y408 has a tyrosine jutting out into the pore



# What to mutate the amino acid to?

Sun et. Al screened mutations in a different protein for HM binders

## Cadmium

105 S-> C (Polar, Uncharged -> Terminal Sulfur)

276 M-> C (Hydrophobic -> Terminal Sulfur, also,

This one was rationally designed)

269 S->T (Polar -> Polar)

## Strontium

G->R (Kink -> Positive)

T->S (Polar -> Polar)

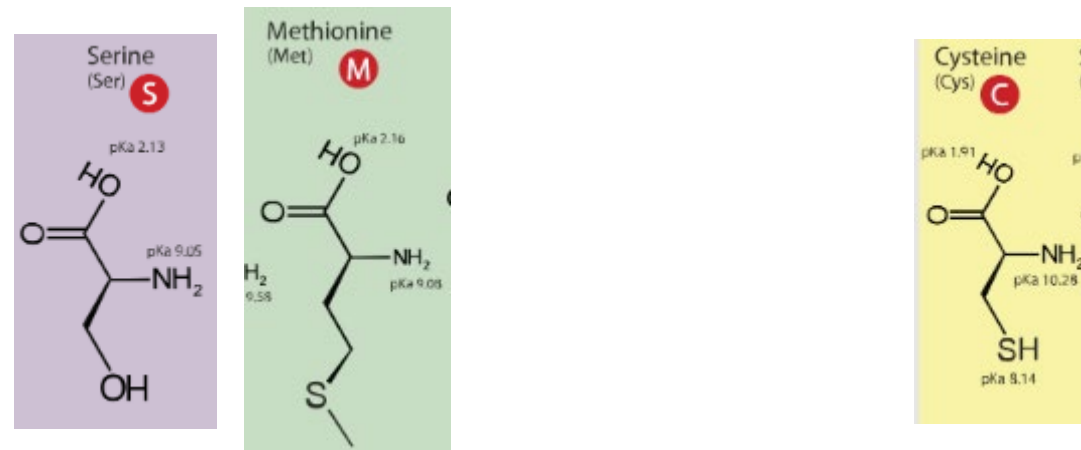
M->C (Hydrophobic -> Terminal Sulfur)

G->Q (Kink -> Polar Uncharged)

Importantly, no amino acid conferring affinity for cadmium or strontium are hydrophobic residues.

None are negatively charged

**More than half of them are -> cysteine mutations if you don't count the glycine kink mutations**



Cysteine has a very high stability constant w/  
cadmium

---

**Amino acids with a sulfur-containing side chain**

S-Methyl-cysteine	3.79	7.04
Methionine	3.65	6.76
Cysteine <sup>a,b</sup>	12.82	21.71

## Strategy #1: Mutate the Tyrosine

Take Y408 and turn it into C

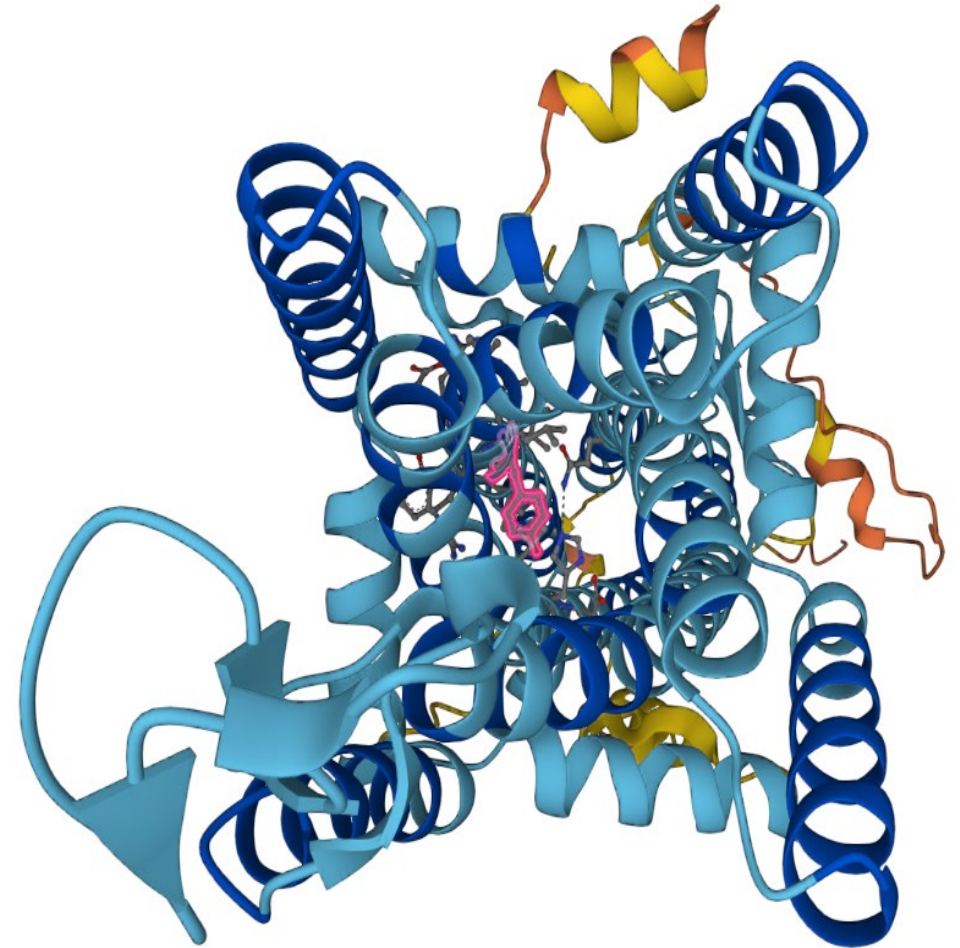
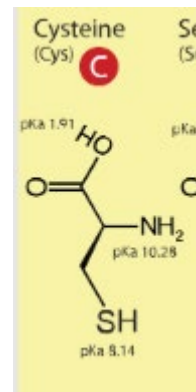
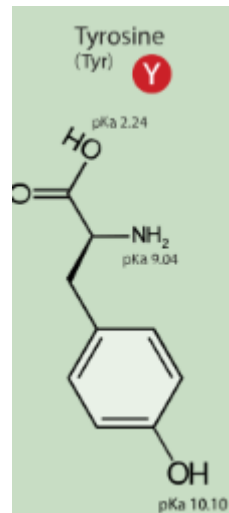
- 1) Removes the most important Fe complexing tyrosine (with regards to uptake rate)
- 2) Changes it into a good binder

For cadmium

3) -> C mutations consistent with SFM1 work

4) Potential

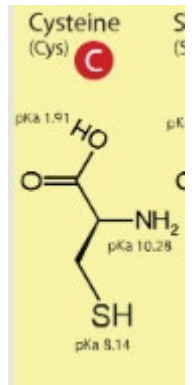
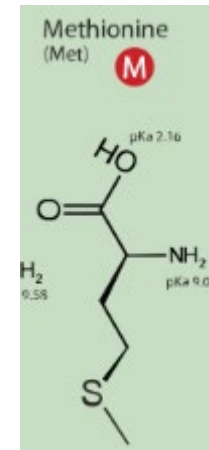
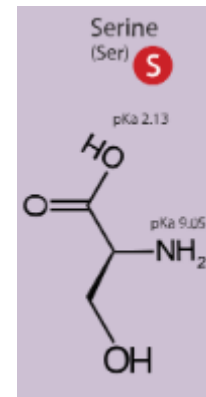
Structure issues



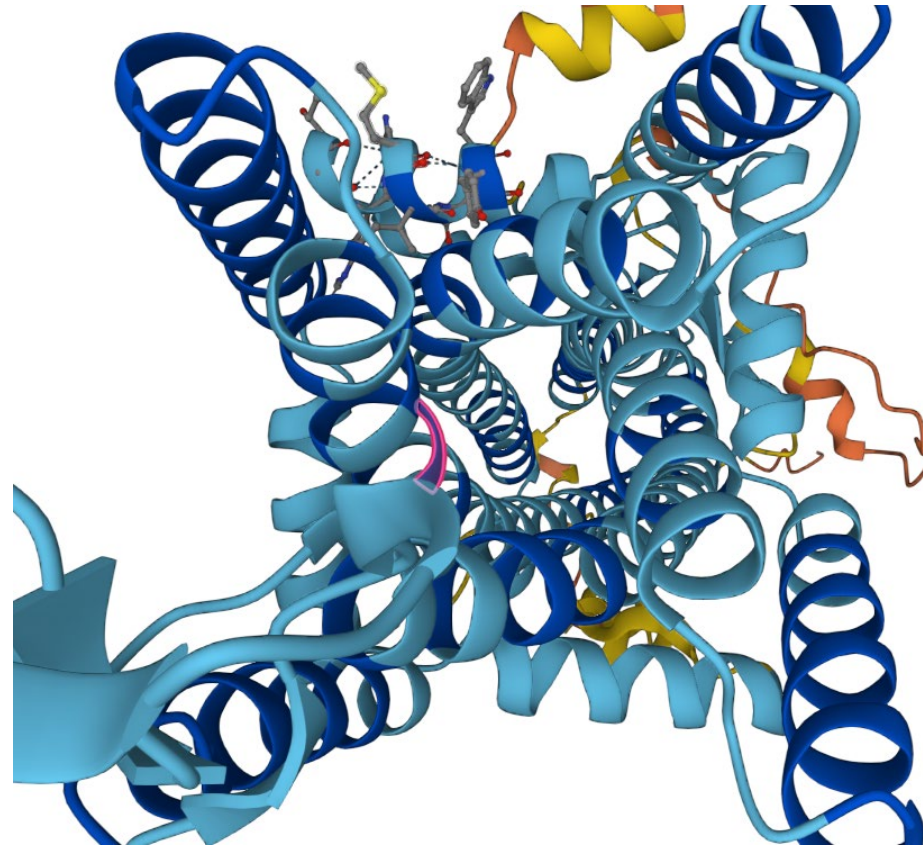
Strategy #2: Turn a nearby S or M into a C

Pro: Looks like the SMF1 work

Con: Iron affinity might still be too strong



M501 is within the permease domain and sticks out into the pore.

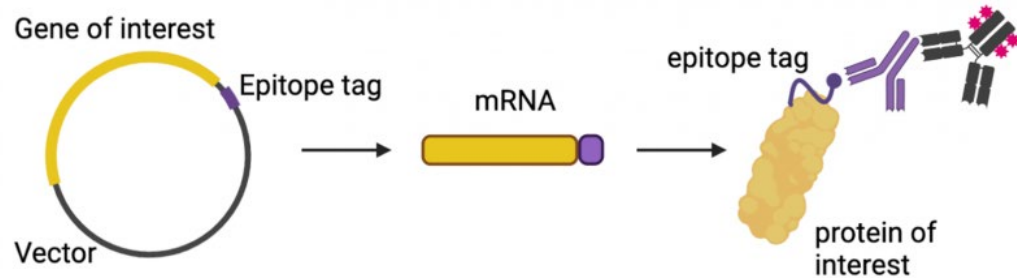




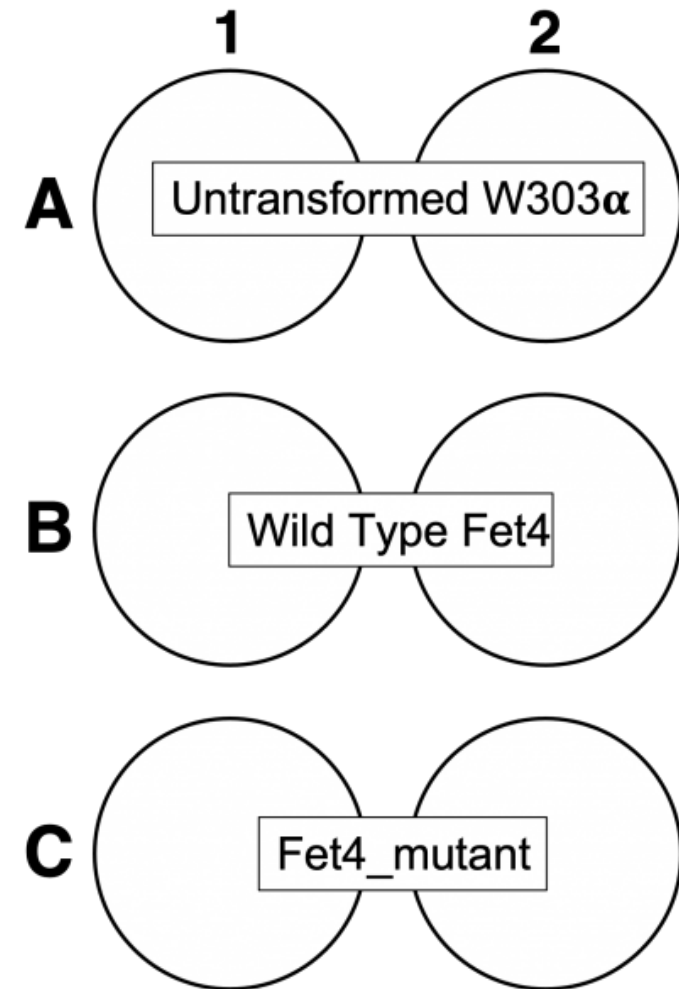


# Using immunofluorescence: Expression of Fet4\_mutant in yeast

- Yeast cells transformed to express Fet4\_mutant protein

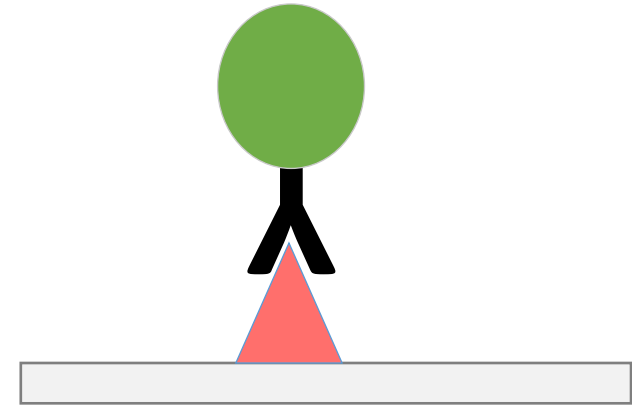
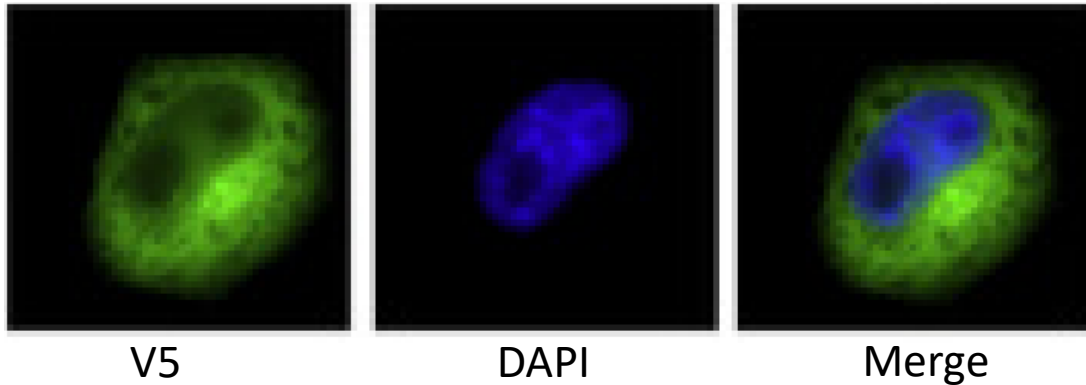





- Why do immuno at all?
- Why untransformed cells?
- Why wild-type Fet4?





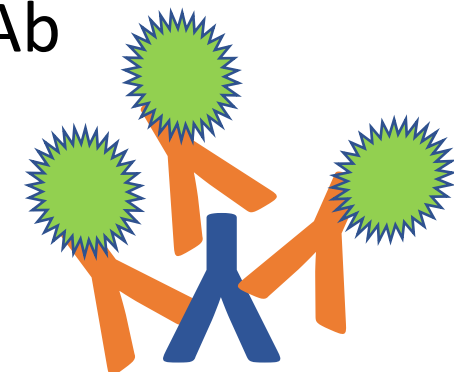
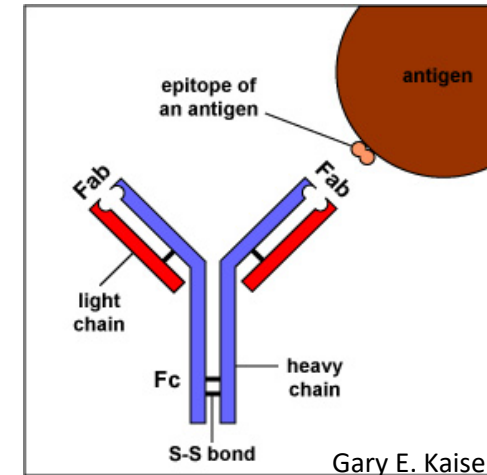
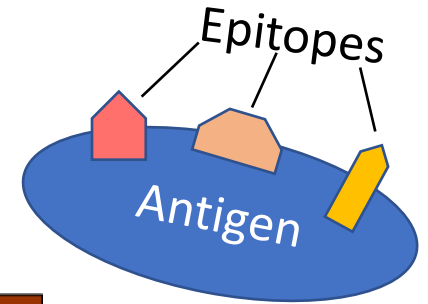
# Using immunofluorescence: Identification of Fet4\_mutant expression



protein of interest	 V5
primary antibody	 mouse anti-V5
secondary antibody	none
Fluorophore (conjugated to secondary antibody) exc./ em. wavelengths	 488/525 nm

# Considerations for using antibodies in the lab

- Antibodies bind to specific epitopes on antigens
  - Antigens may have multiple epitopes
- Primary antibody recognizes the antigen
  - Specific protein sequence
  - Specific conformation of protein
  - Specific state of protein (i.e. phosphorylation)
- Secondary Ab recognizes the species of the primary Ab
  - Often conjugated to tag for visualization
    - Enzyme or fluorophore
  - Amplifies signal through multiple bindings
  - Consider sample species when choosing antibodies!



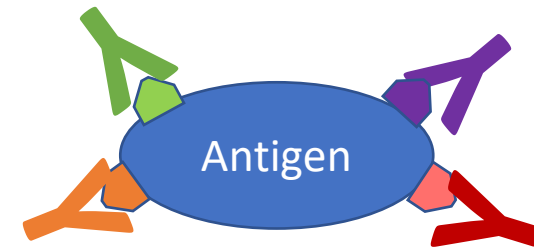
Secondary antibody conjugated to a fluorophore

Primary antibody

# Polyclonal vs. monoclonal antibodies

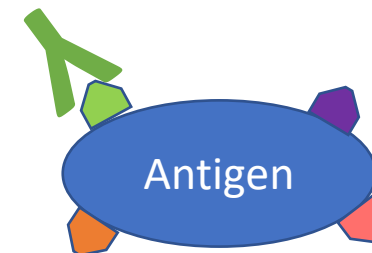
## Polyclonal

- **How it's made:** animal (often rabbit) immunized with antigen of interest then antibodies collected from blood sera and affinity purified
- **Advantages:**
  - Less expensive and faster to produce than monoclonal
  - Multiple antibodies in one polyclonal mixture can increase antigen recognition by binding multiple epitopes
    - Especially useful for proteins with low expression
- **Disadvantages:**
  - Variability from lot to lot

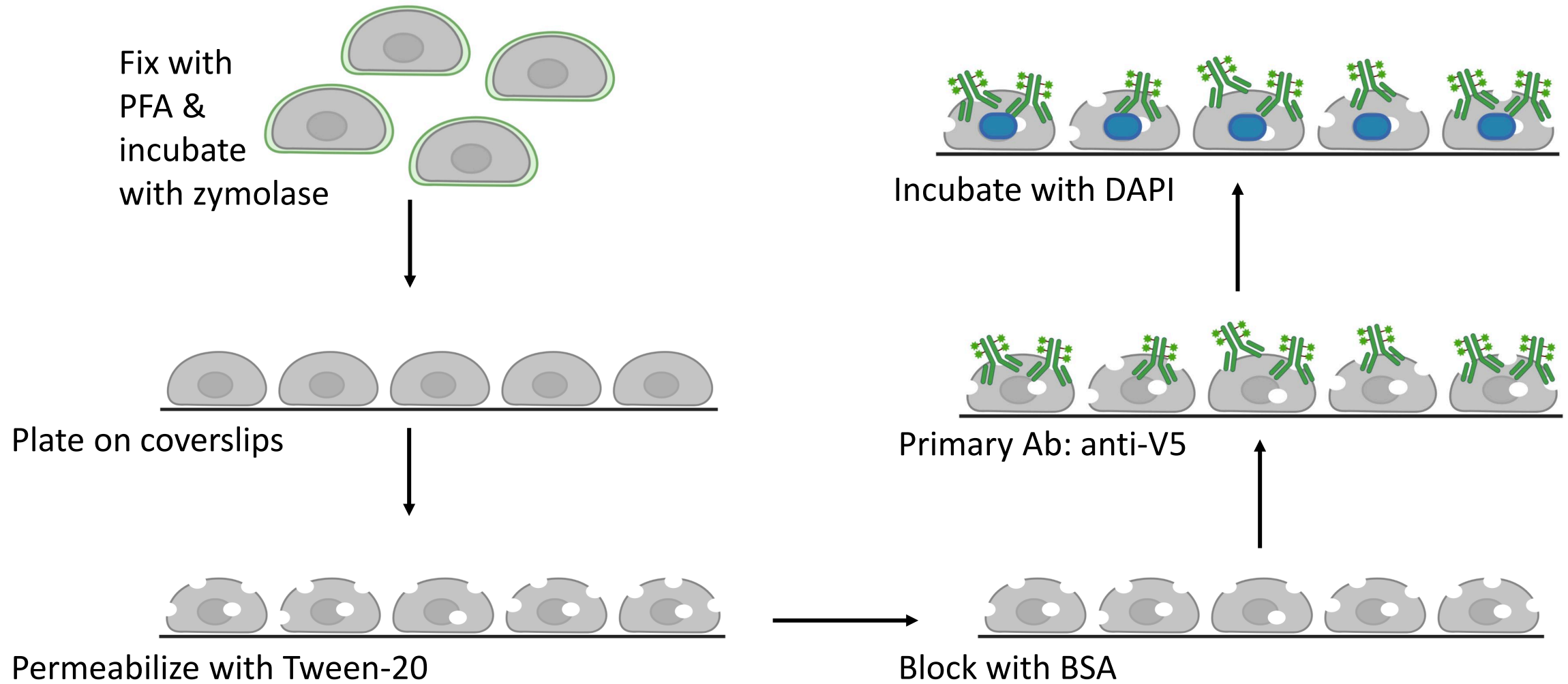


## Monoclonal

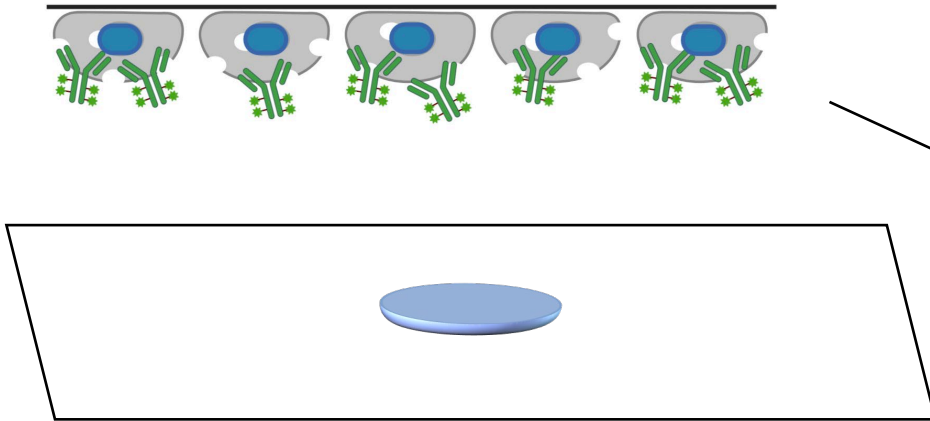
- **How it's made:** animal (usually mouse) immunized with antigen of interest then B cells from spleen are harvested and fused with myeloma cells to create hybridoma cell line that will continually produce single antibody clone
- **Advantages:**
  - Very consistent
  - Binds single epitope (can also be disadvantage)
- **Disadvantages:**
  - More expensive and requires animal sacrifice



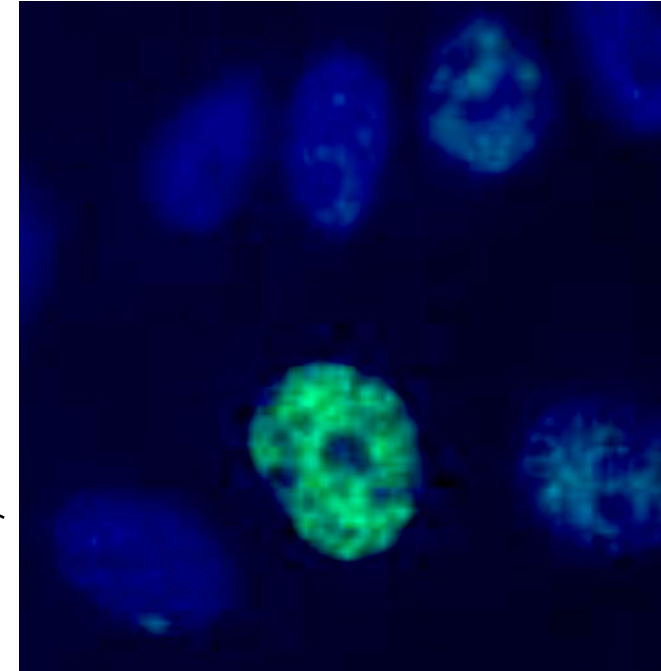
# Using immunofluorescence (IF) in yeast: steps in protocol



# Finish IF by mounting coverslips on slides



Mount coverslip on glass slide  
with mounting media



Blue= DAPI  
Green= antibody staining

# For today:

1. Fix yeast samples
2. Perform IF
  1. Downtime: Look at new alignments on Dropbox that show the mutations
3. Mount coverslips on slides for imaging

## For M2D6

1. Write methods for M2D2-M2D5
- \*\*\* Individual Assignment \*\*\*