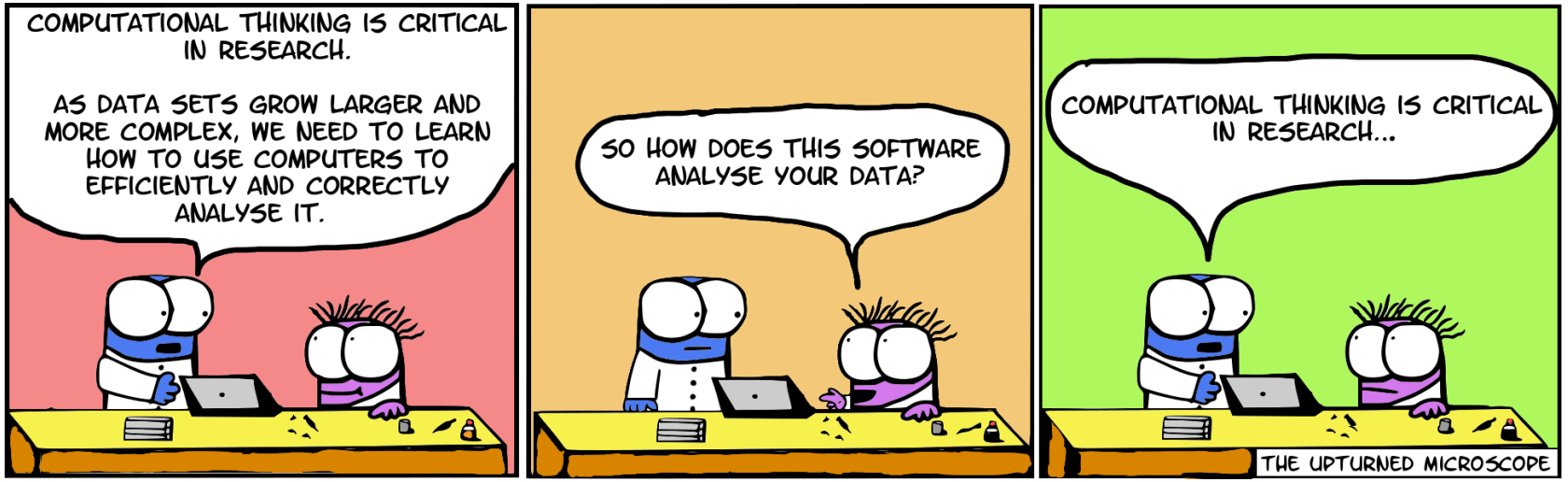
M2D1: Examine SMM data collected using TDP43 protein

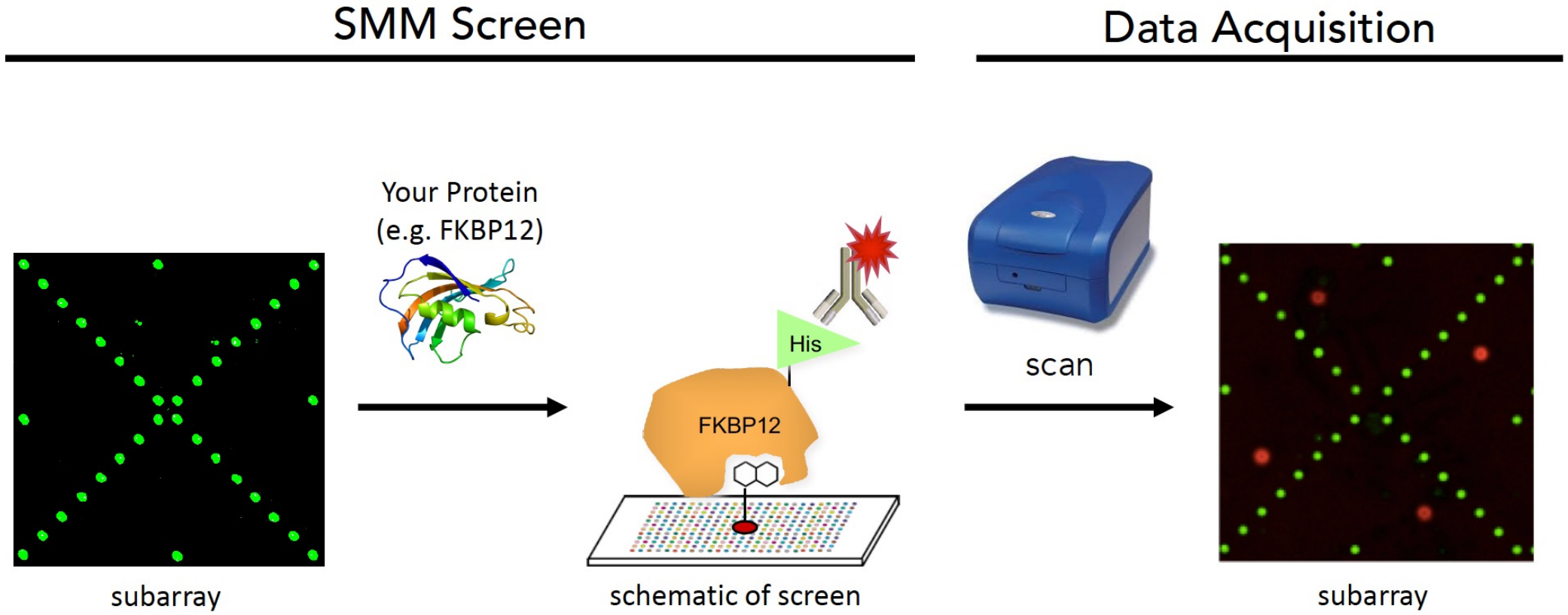
1. Prelab
2. Walk through SMM analysis
3. Examine chemical structure of hits
4. Discuss journal article

Office Hours:
Monday: 1-2pm @ 16-319 and Zoom Becky
3-5pm @ 16-317 and Zoom Noreen
Tuesday: 10-11am @ 1-390 Becky & Jamie
Thursday: 10-11am @ 1-390 Noreen & Jamie

*After lecture by request
*Also available by appointment



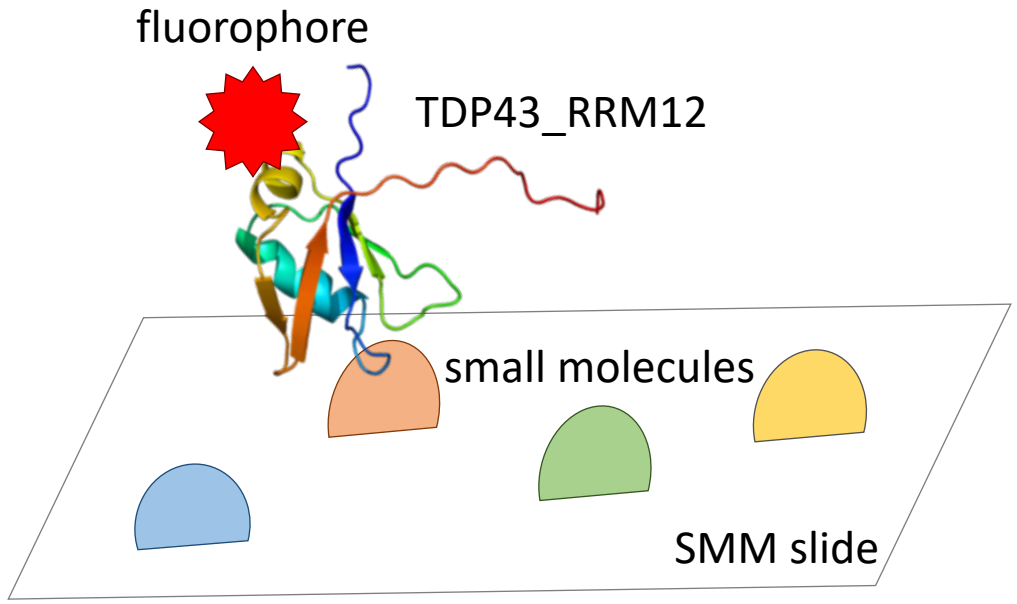
SMM workflow



B. Leifer, S. Doyle

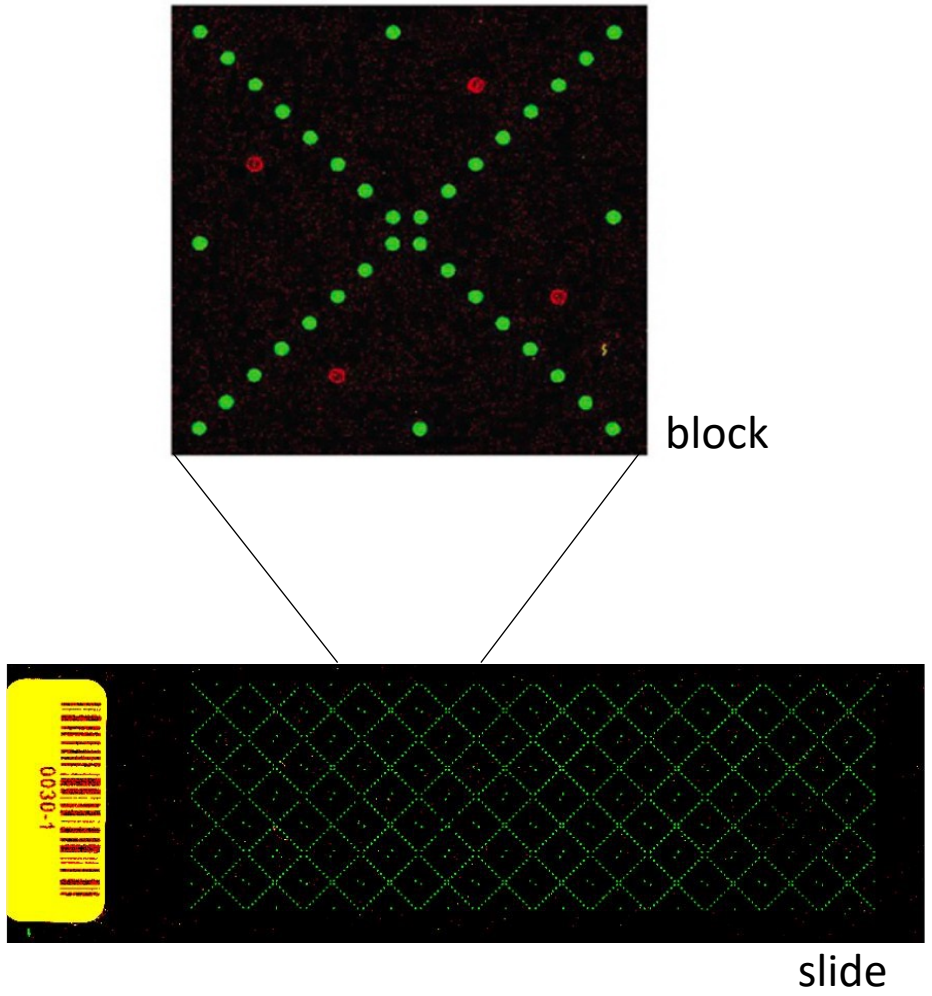
How do we use the SMM to screen for ligands that bind our protein of interest?

- Create a recombinant protein of the TDP43 RNA binding domains (TDP43_RM12)
  - Label this protein with a Alexa647 fluorophore
- Incubate the SMM slide with our purified and labeled TDP-43_RRM12
- Wash away unbound protein
- Store for scanning



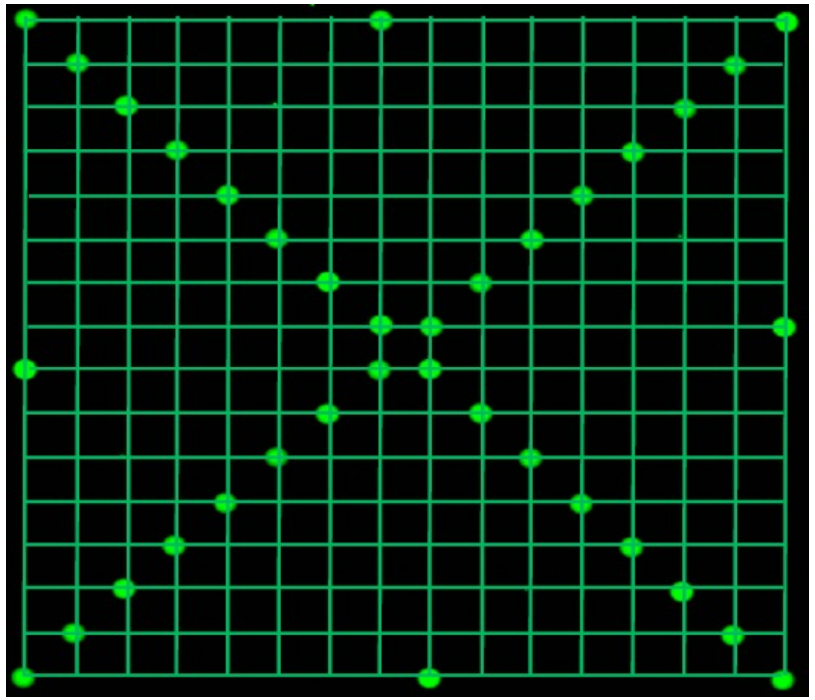
Workflow for SMM data analysis

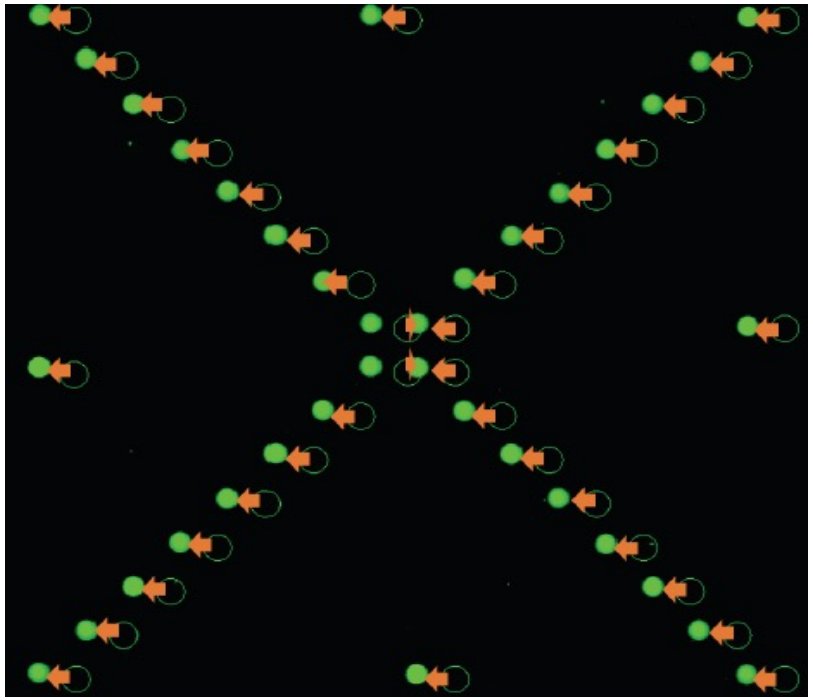
1. Align spots using fluorescence on 532 nm channel (sentinel spots)
2. Quantify fluorescence on 635 nm channel
3. Identify ‘hits’ with improbably high fluorescence
4. Complete ‘by eye’ analysis of putative hits to manually remove false positives



Align SMM using sentinel spots

- Slides are printed in block patterns (16 rows x 16 columns)
- Each ligand spot is identifiable via intersecting lines between sentinels

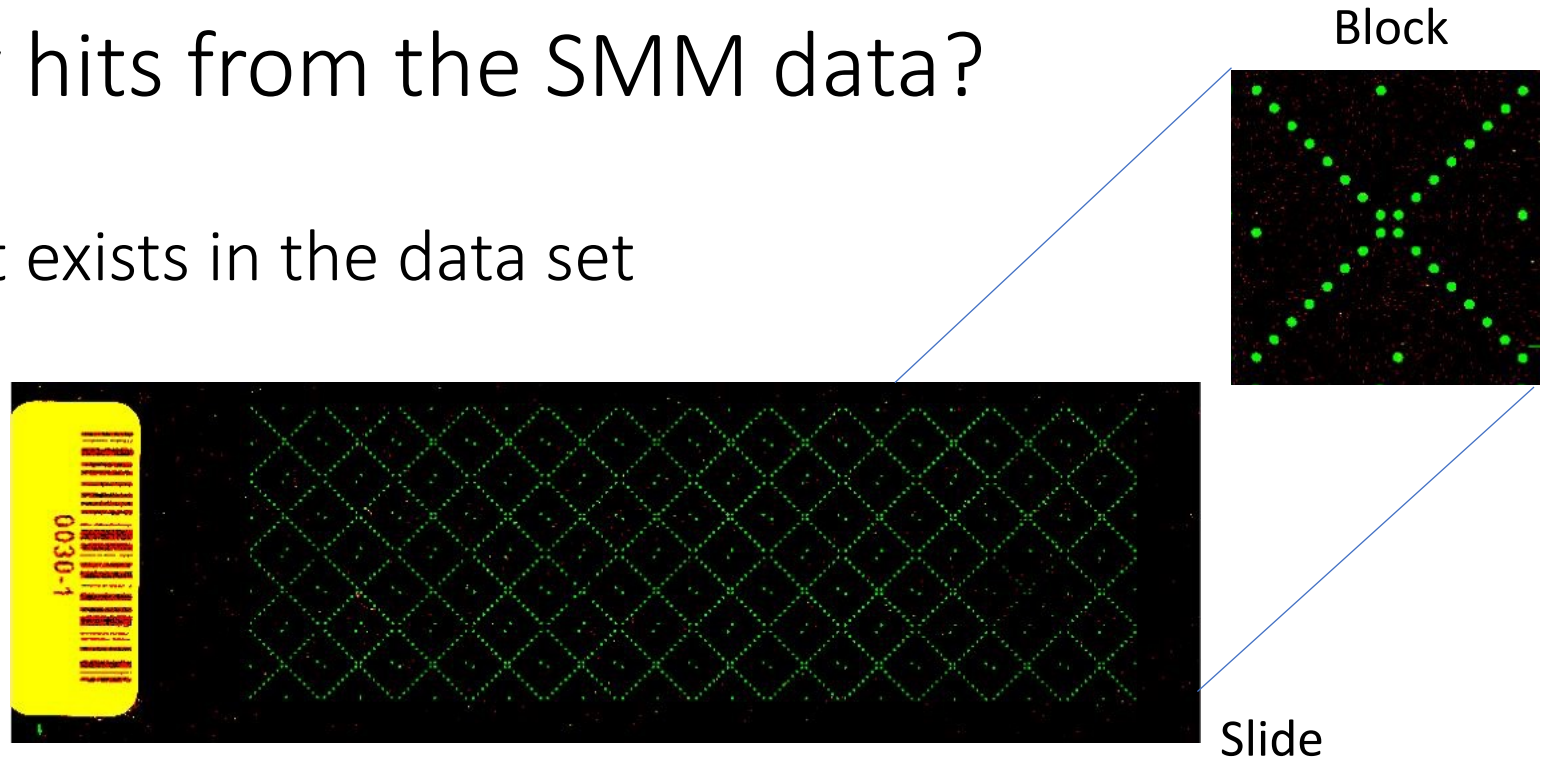




How do you identify hits from the SMM data?

First, consider bias that exists in the data set

- Across all slides
- Within each block
- Within each slide

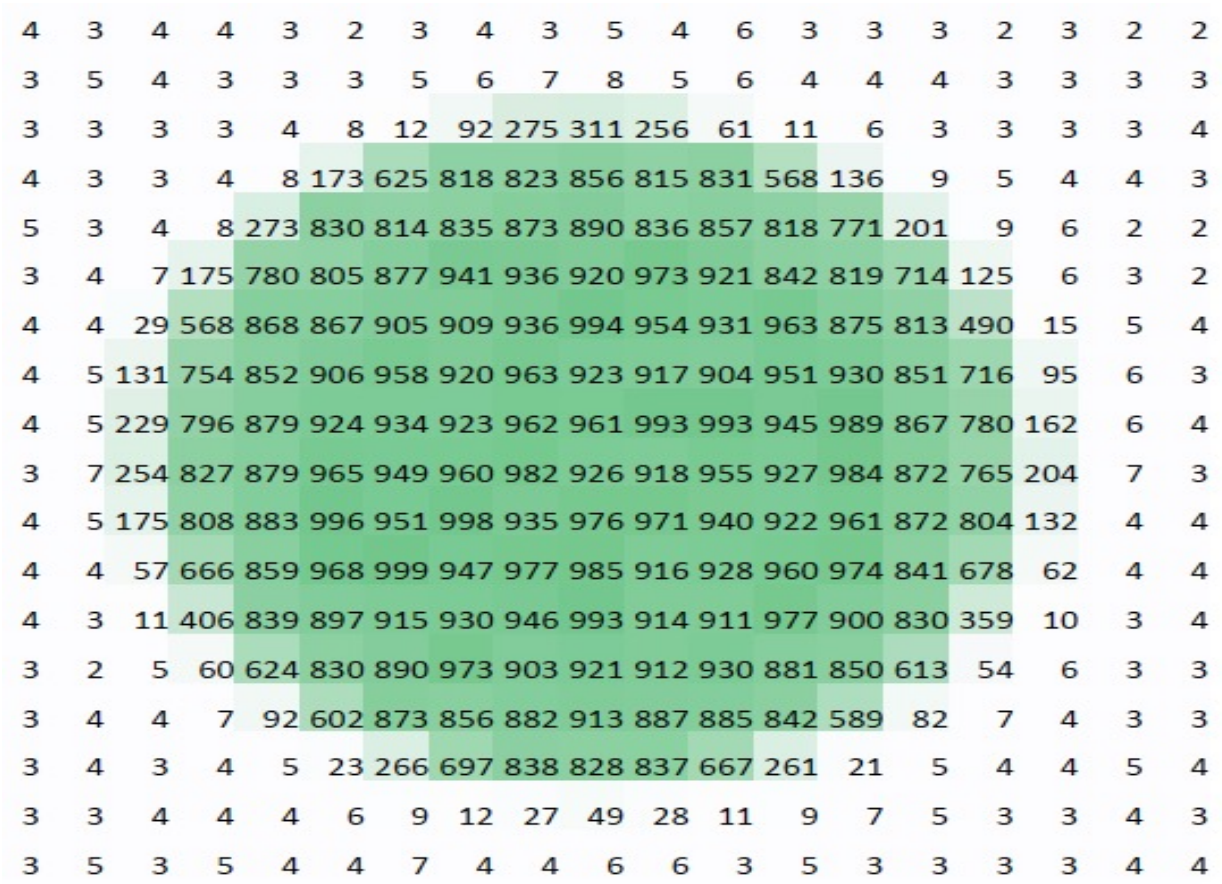


Then, identify hits with significantly higher fluorescence over background

Lastly, manually confirm hits to eliminate false positives

Spots are represented by an array of numerical values

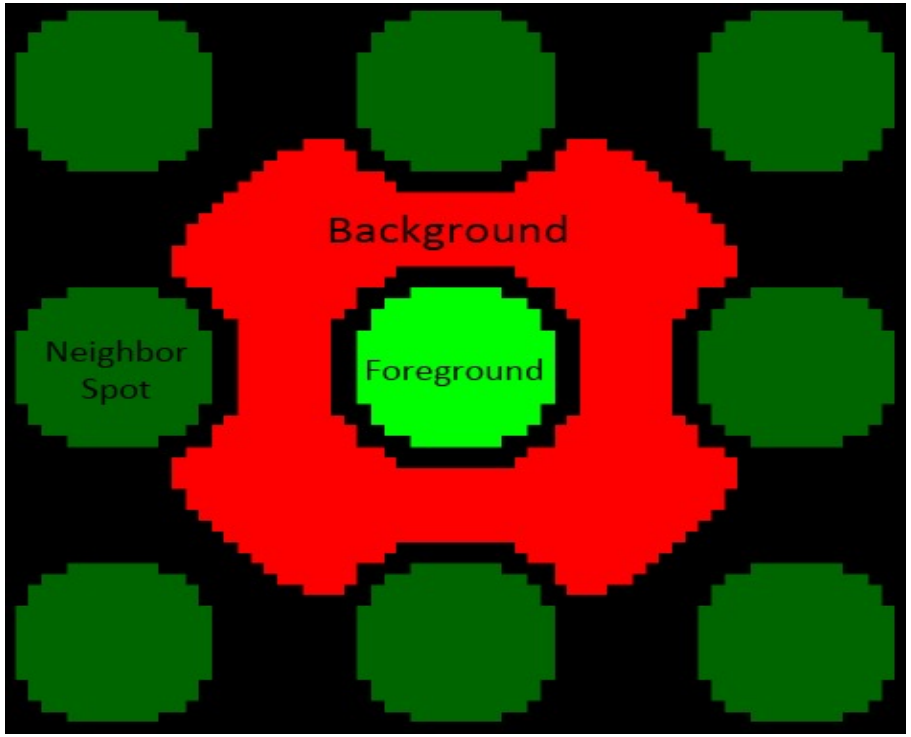
- Each pixel is represented by a number that indicates intensity of the signal
- Computational analysis used to define ‘hits’



Fluorescence is quantified to identify hits

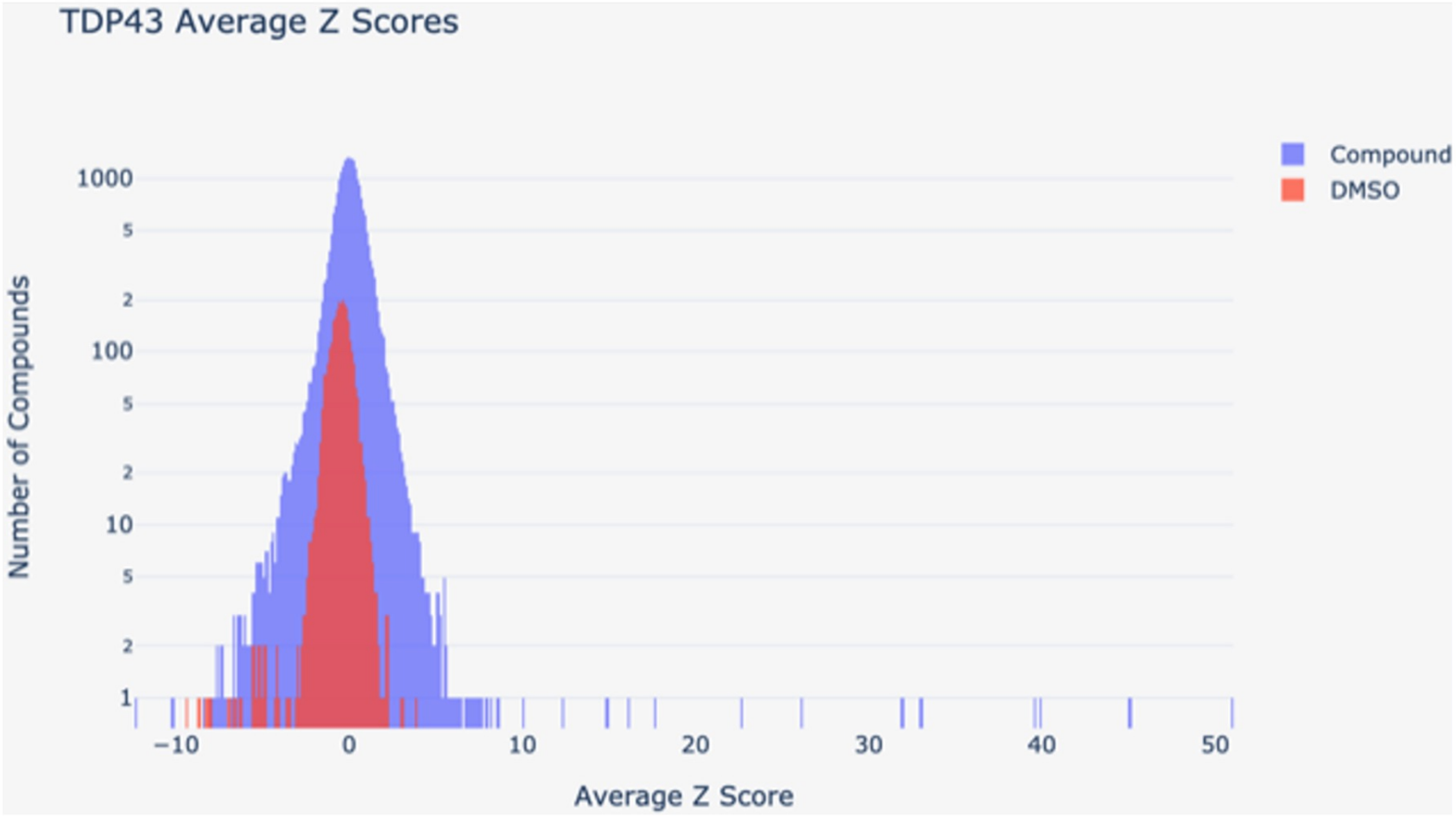
- Foreground:

- Background:



$$\text{Signal-to-noise ratio (SNR)} = \frac{\mu_{foreground} - \mu_{background}}{\sigma_{background}}$$

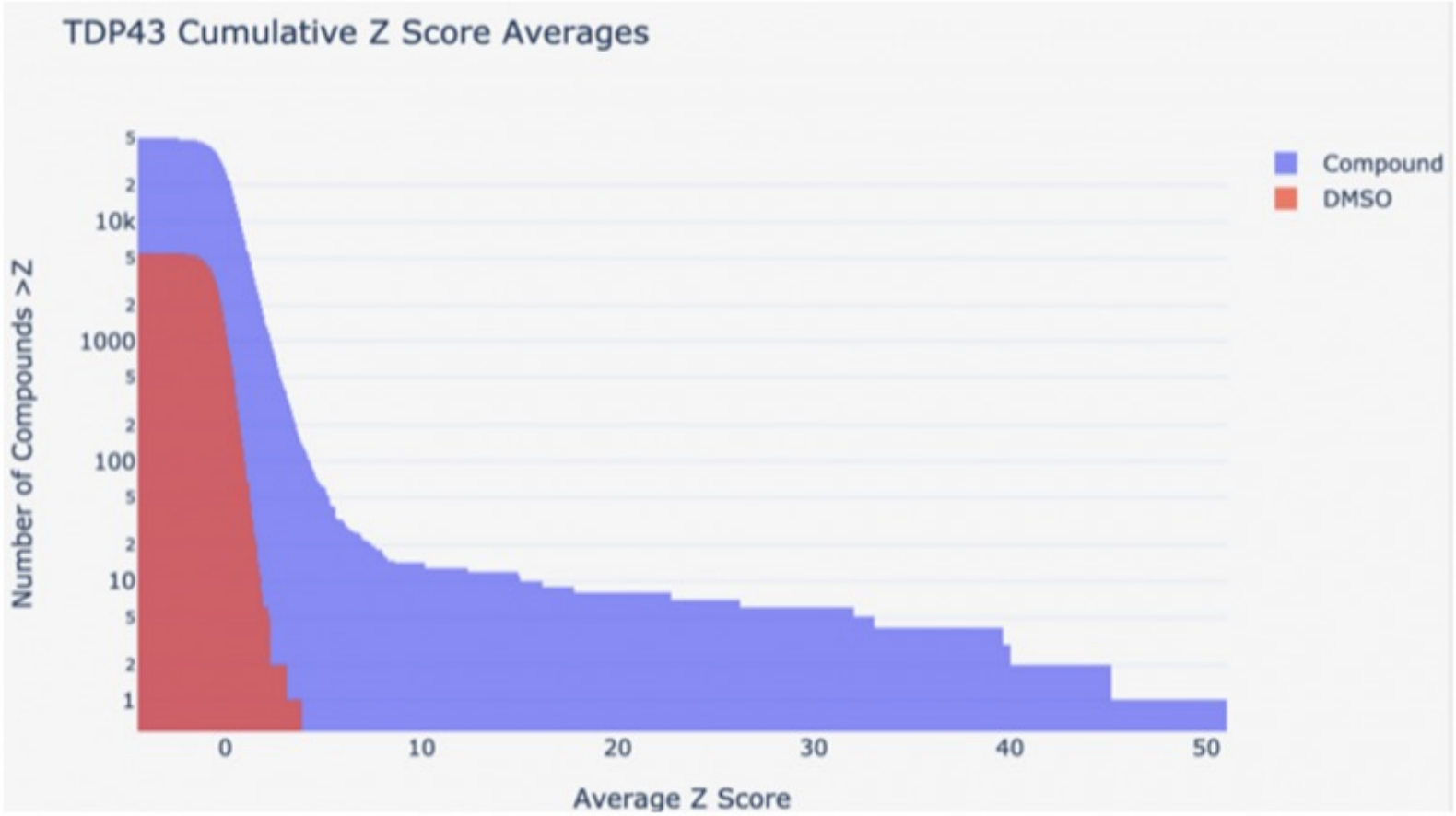
Average Z-score calculated for all compounds



Replicate spots averaged

Each count = unique compound

How many compounds have a particular z score?

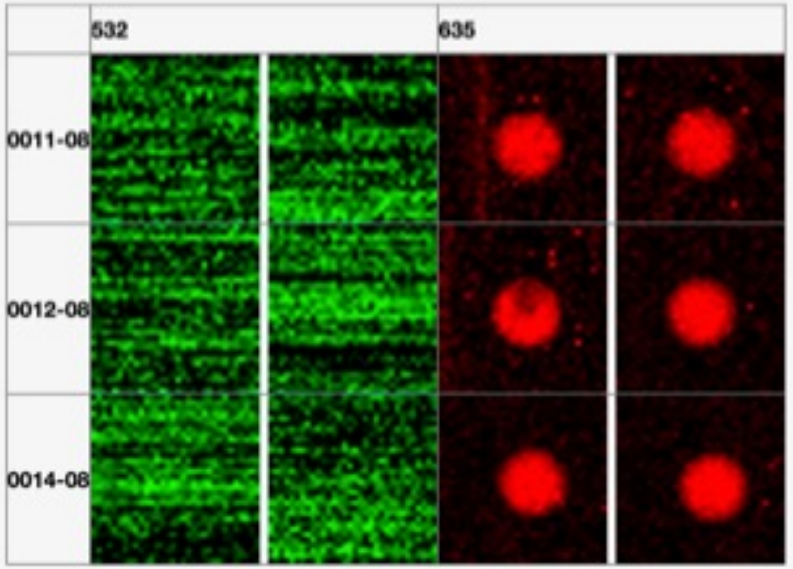


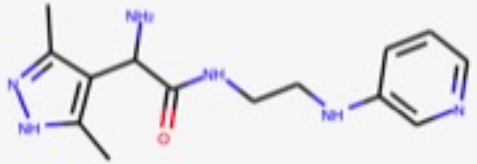
Height at x (average z score) = number of compounds (y) with that z-score or higher

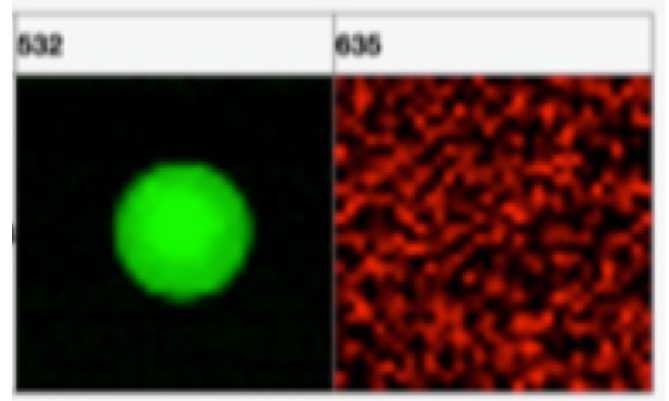
- Useful for setting a threshold to exclude likely non-binders

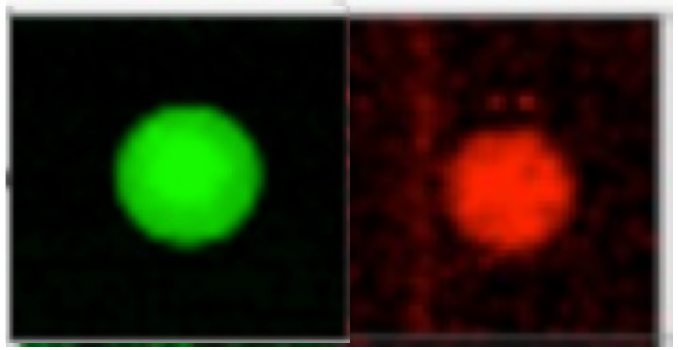
How do you validate hits manually?

	ID	Robust Z	SMILES	Validated
49592	13:KI0001...	51.03151	C[C@H](C...	-1
42089	11:KI0001...	45.09263	CC1=C(C(...	example
6782	02:KI0001...	39.91118	CCNC(=O...	-1
29108	08:KI0001...	39.59436	C1C(C2=...	-1
44736	12:KI0001...	33.03555	C1CN(C2...	-1
29660	08:KI0001...	31.94118	CC1=NC2...	-1
11360	03:KI0001...	26.13059	C1CN(CC...	-1

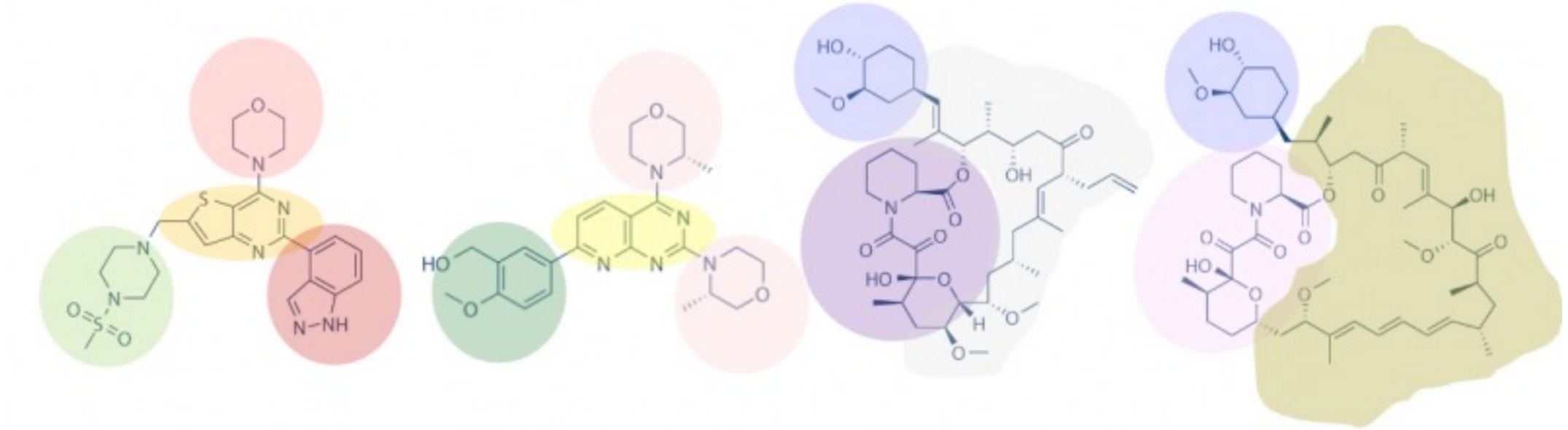






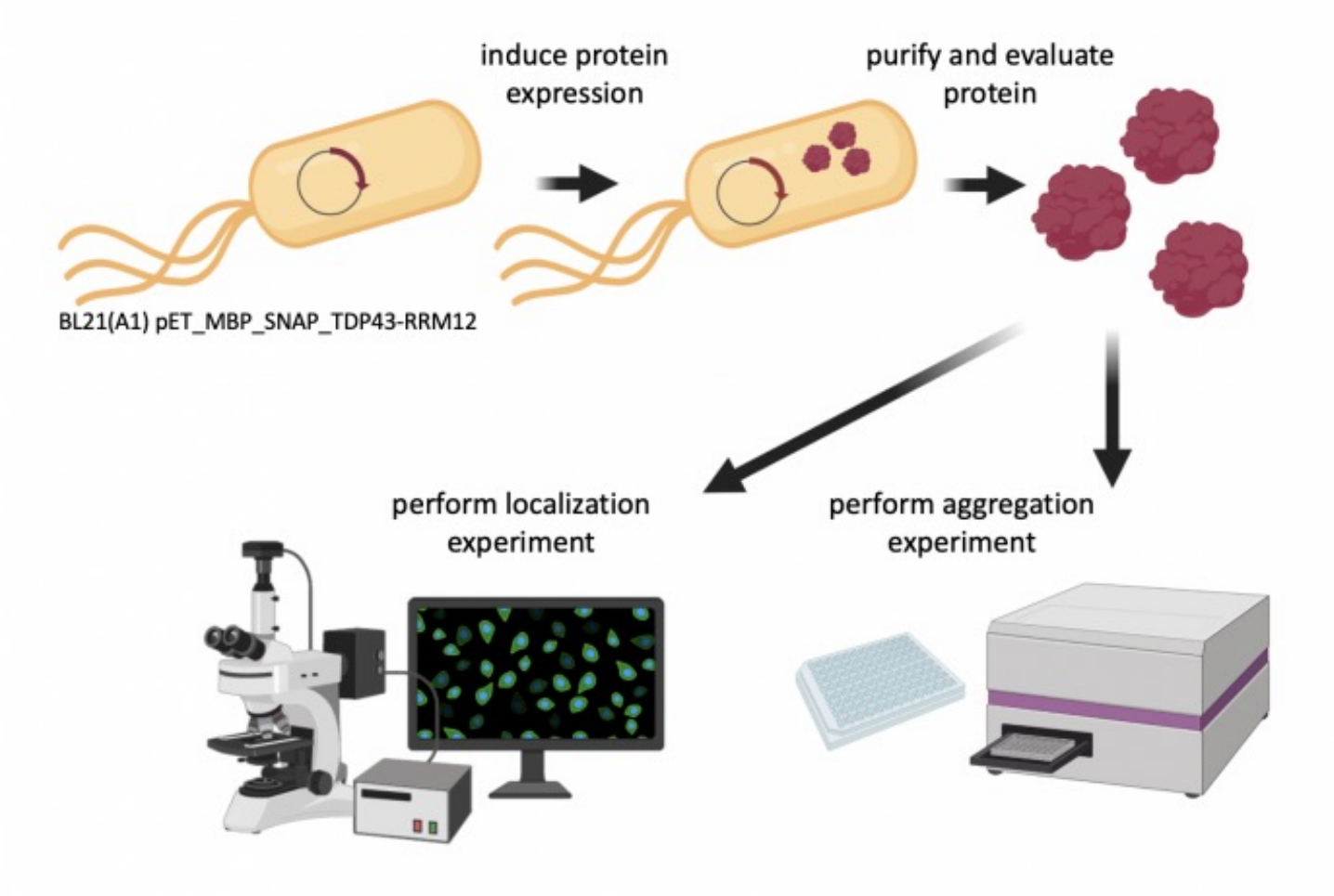


How will you identify common structures?



Overview of Mod1 experiments

Research goal: Use functional assays to characterize ligands identified as binders to TDP43 from SMM technology



For Today

- Work through SMM analysis procedure
- Evaluate chemical structures of identified hits
- Discuss reading of scientific papers with Noreen
  - Group 1: Teal, White, Gray, Purple, Pink
  - Group 2: Blue, Green, Yellow, Orange, Red

For M1D3

- Begin thinking about Background and Motivation for Data Summary
  - Submit document answering questions on the Homework section of wiki
  - Due Thursday, Feb. 10 at 1:05pm on Stellar

- Visit Comm Lab by M1D5
  - Can visit to discuss an assignment from any class, a personal statement for an internship application, etc…