

# Class core values

1. Be **respectful** to yourself and others
2. Be **confident** and believe in yourself
3. Always do your **best**
4. Be **cooperative**
5. Be **creative**
6. Have **fun**
7. Be **patient** with yourself while you learn
8. Don't be shy to **ask "stupid" questions**



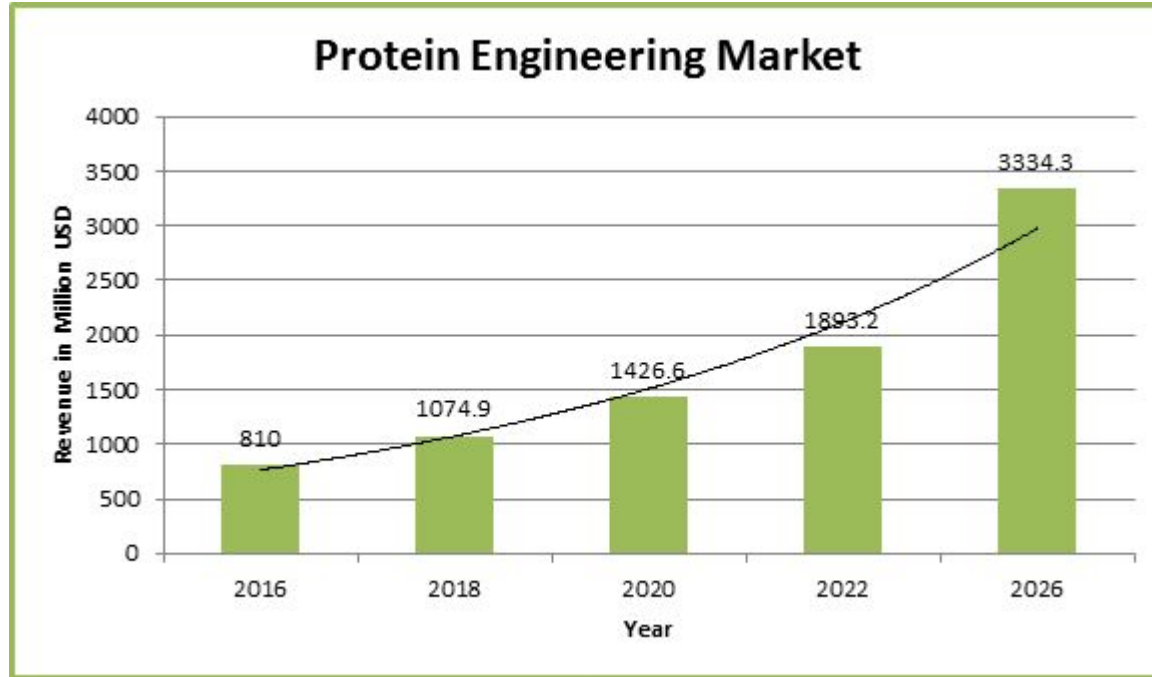
Week 2, Lecture 1

# Fantastic proteins & How to measure them

# Learning Objectives

1. Identify protein properties required to modify for different applications
2. Describe methods that can be used to measure given properties
3. Critically evaluate the limitations of methods for each property and propose alternative methods

# Protein engineering is a growing field



Protein engineering aims to improve different properties of proteins based on the application

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Engineering function

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## Engineering function

- Binding to other proteins
- Enzymatic activity
- Protein-based material

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## Engineering function

- Therapeutics: Binding to other proteins
- Enzymatic activity
- Protein-based material

## Engineering stability

- Thermal stability
- Protease stability
- Organic solvent tolerance

# To assess our success, we need to be able to measure these properties

## Engineering function

- Binding to other proteins
- Enzymatic activity
- Protein-based material

## Engineering stability

- Thermal stability
- Protease stability
- Organic solvent tolerance

Measurements can be quantitative or qualitative

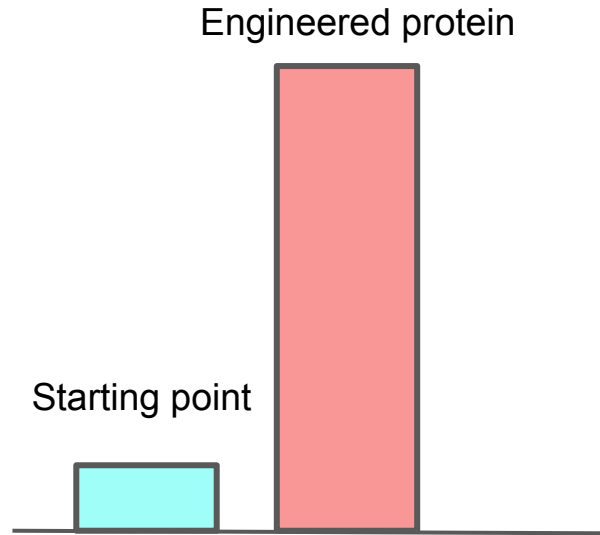
Measurements can be quantitative or **qualitative**

# Qualitative measurements are often “binary”

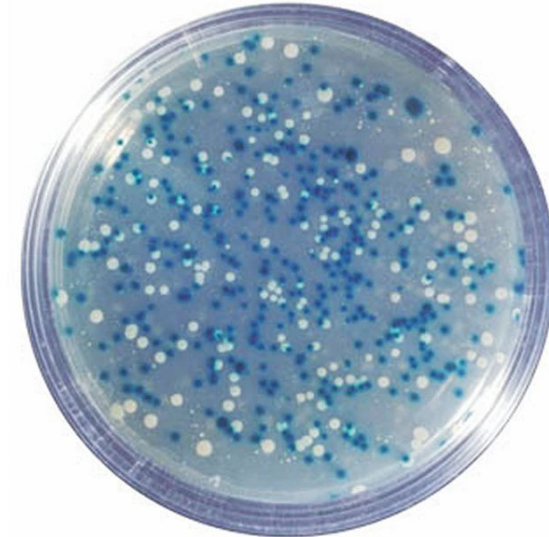
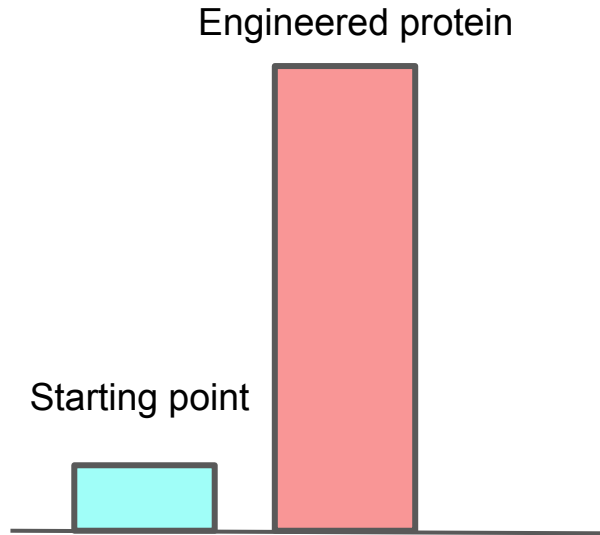
Starting point



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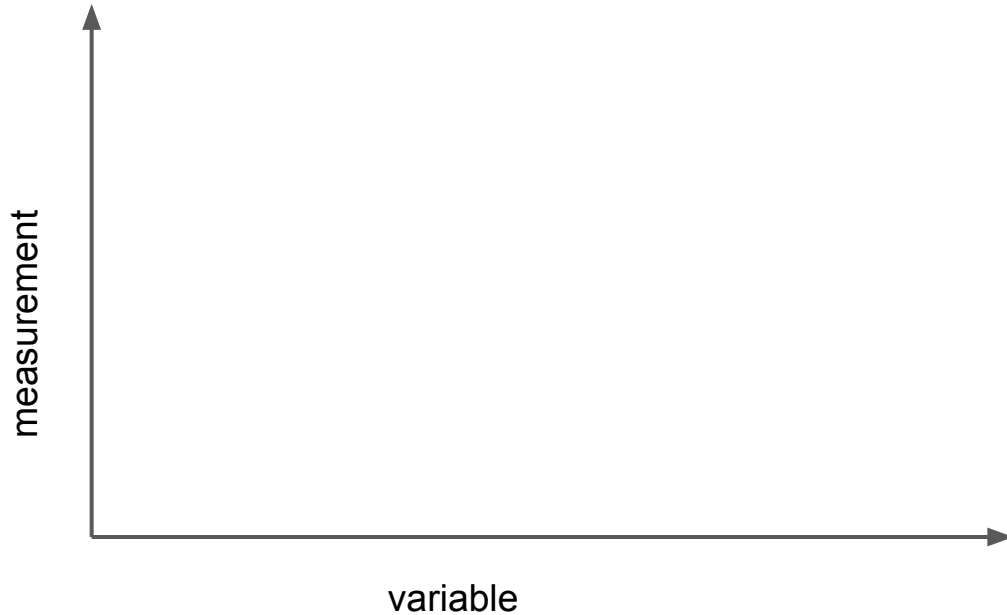


Blue-white selection

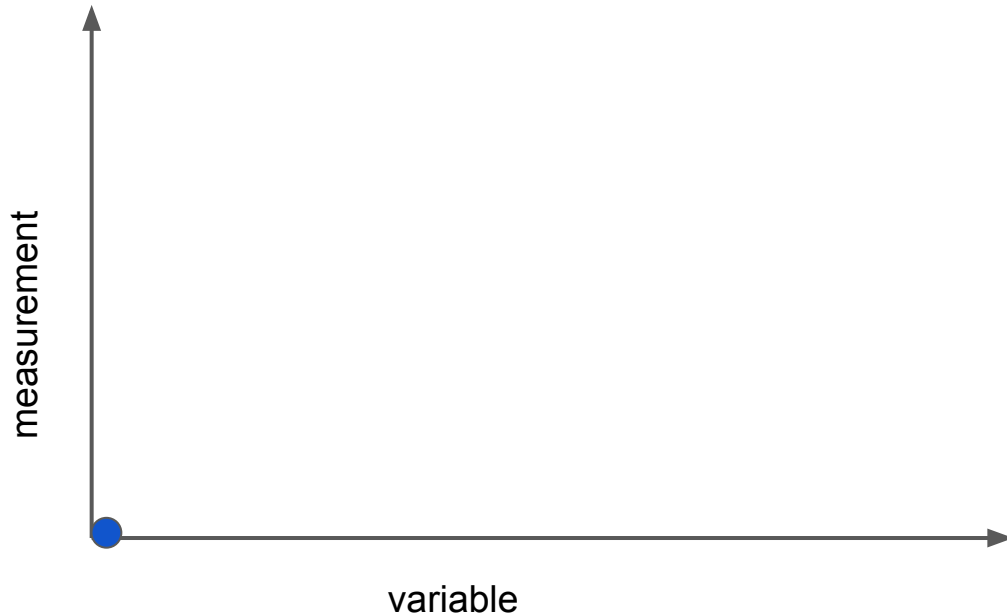
Measurements can be **quantitative** or qualitative



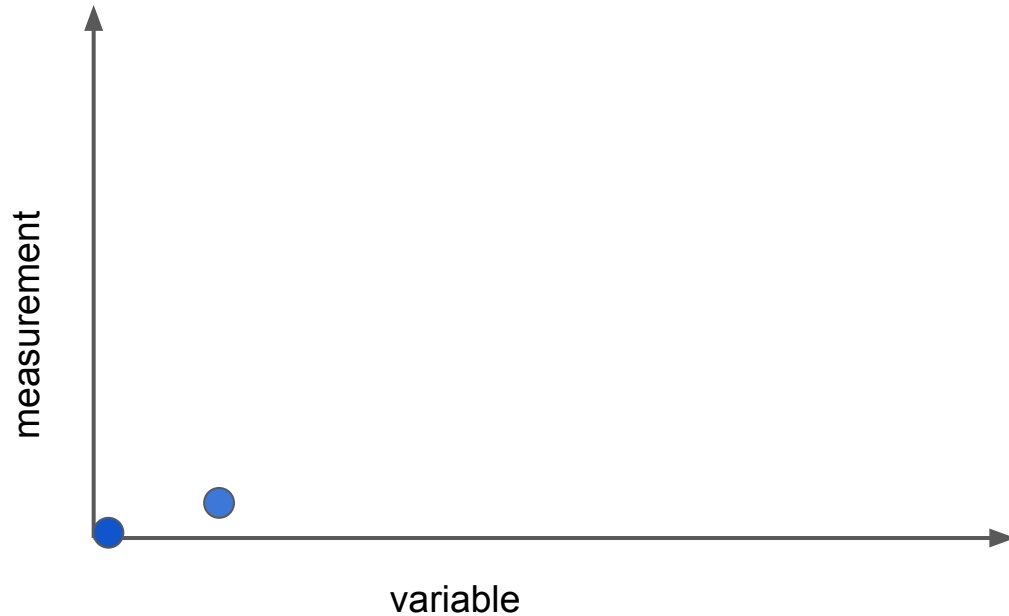
Quantitative measurements require monitoring a given property over a range



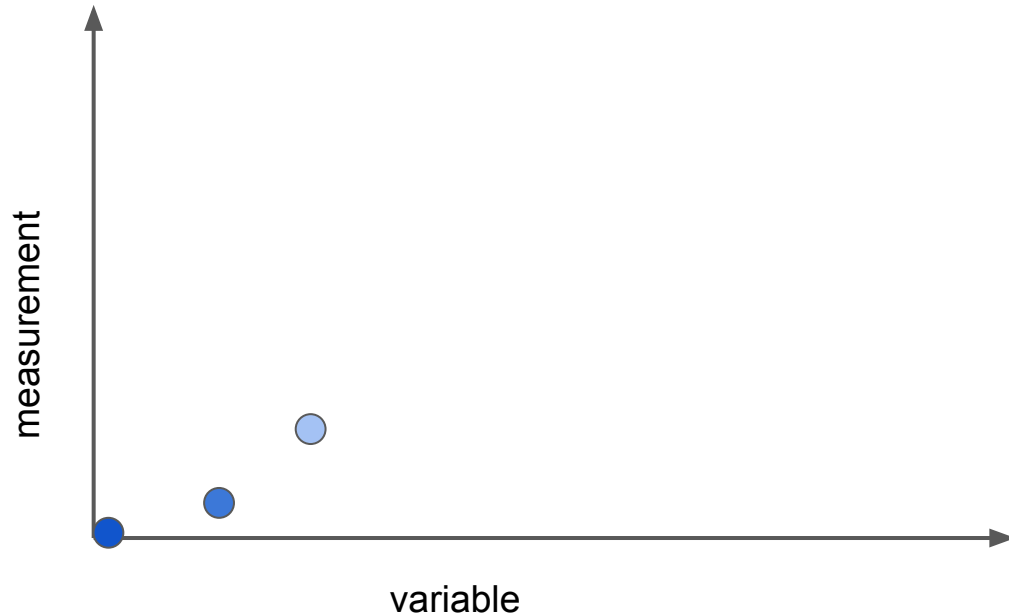
Quantitative measurements require monitoring a given property over a range



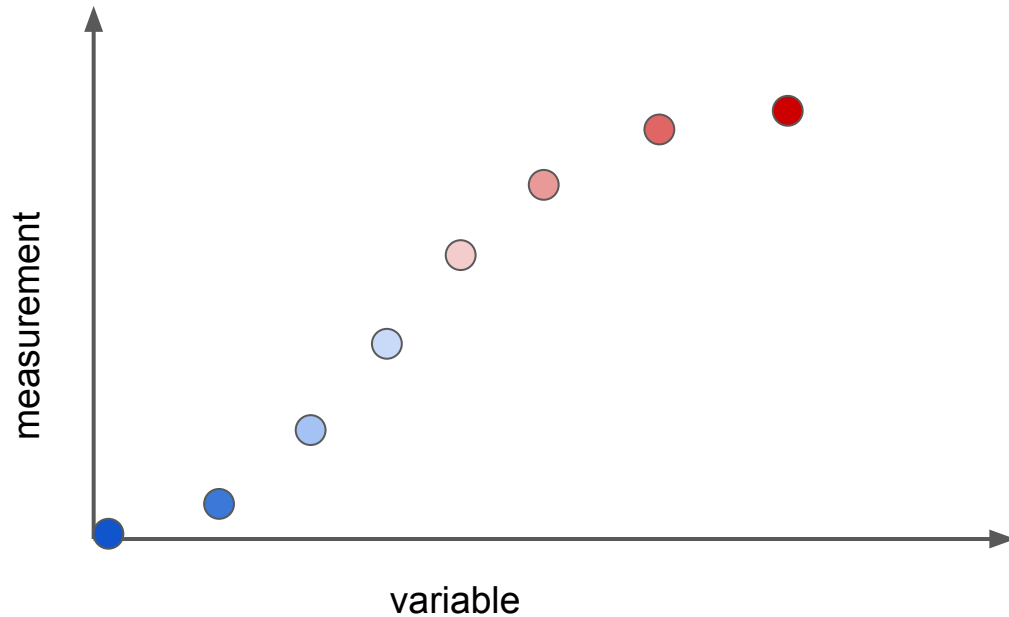
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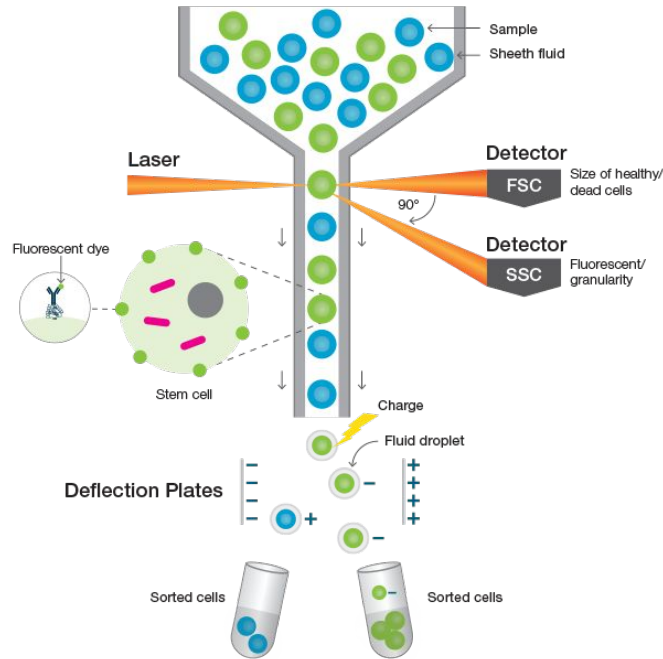


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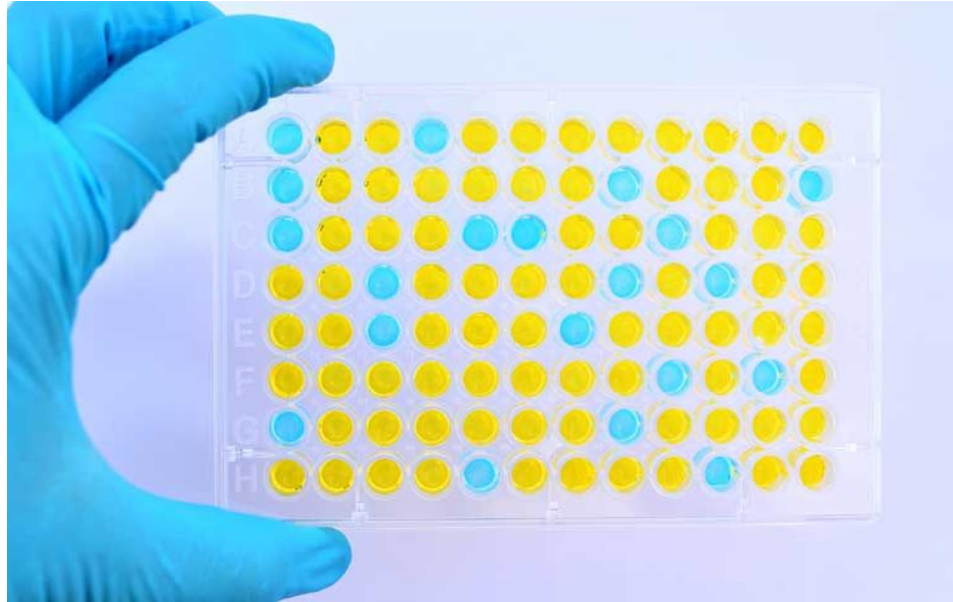


Measurements can be high, medium or low throughput

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Measurements can be high, **medium** or low throughput

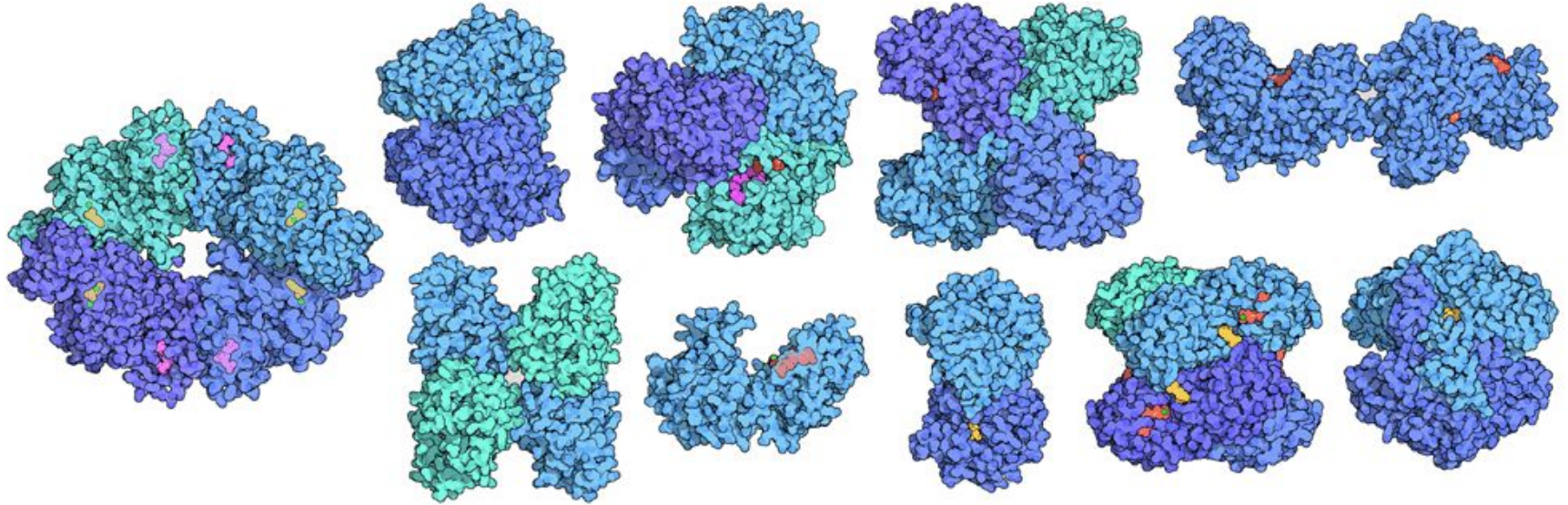




Measurements can be high, medium or **low** throughput

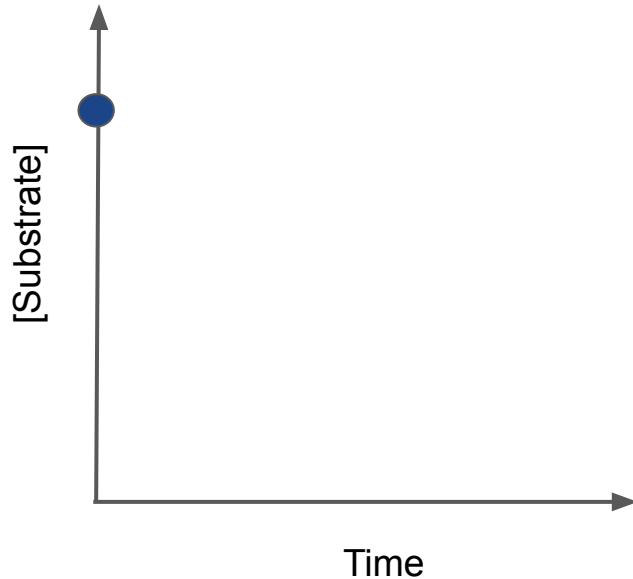


# Measuring enzyme activity

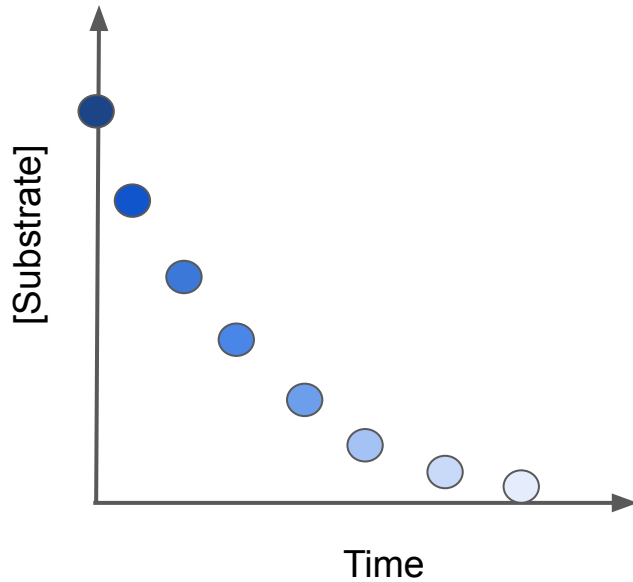


Glycolytic enzymes (from [PDB 101](#))

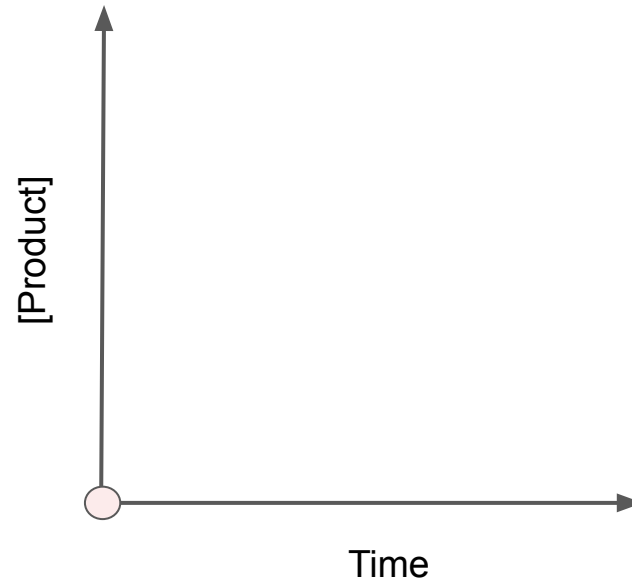
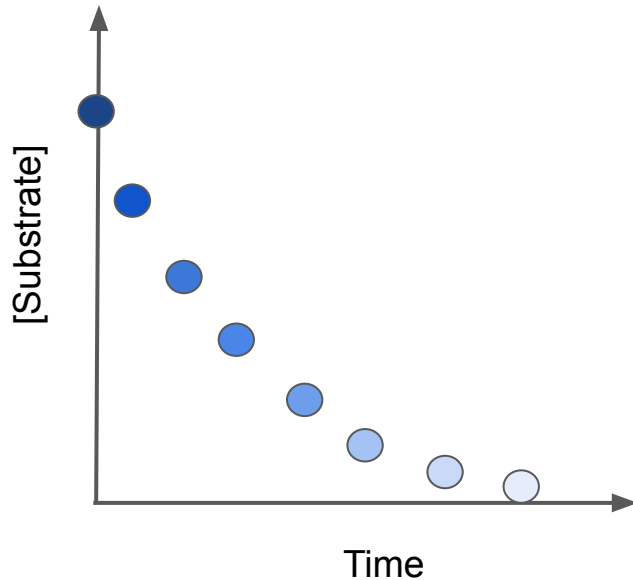
Measuring enzyme activity = measuring the substrate consumption or product generation



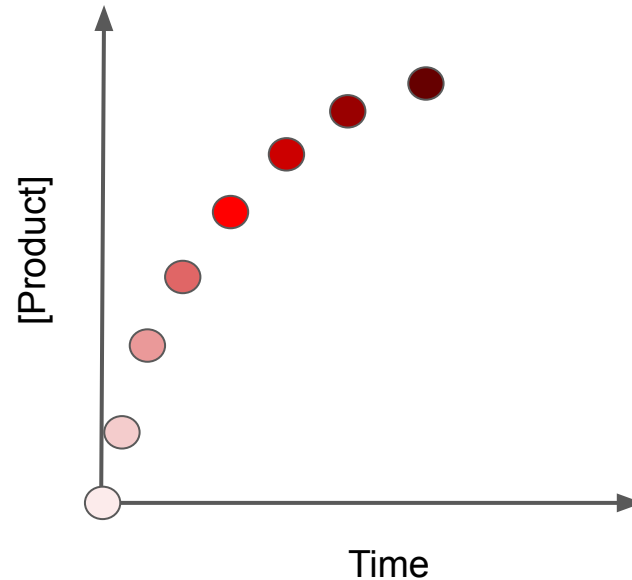
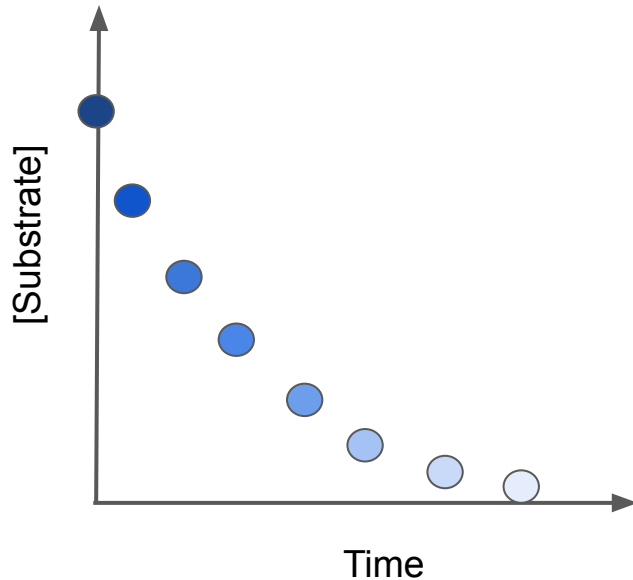
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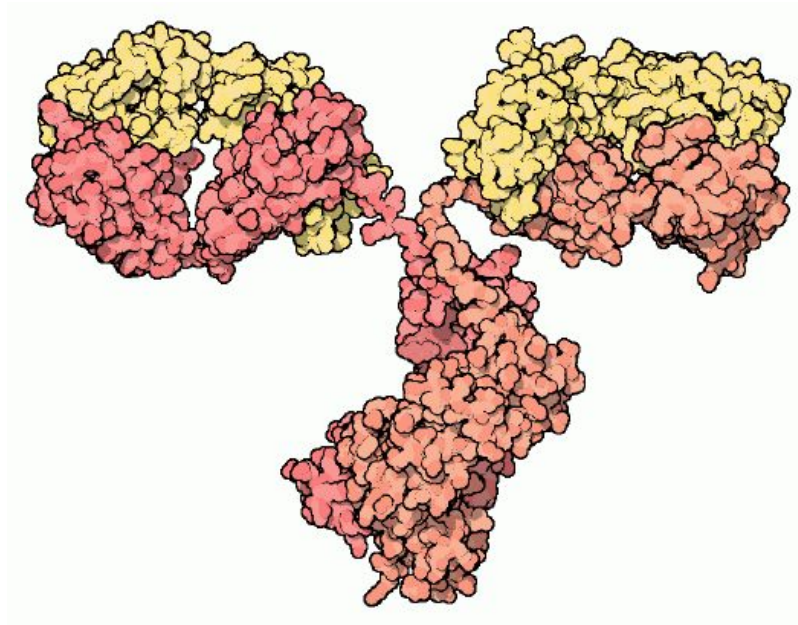
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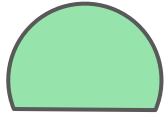


# Measuring binding

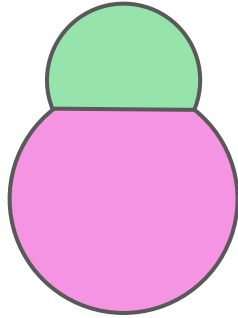


Glycolytic enzymes (from [PDB 101](#))

# Binding measurements follow changes in the properties of single protein vs complex



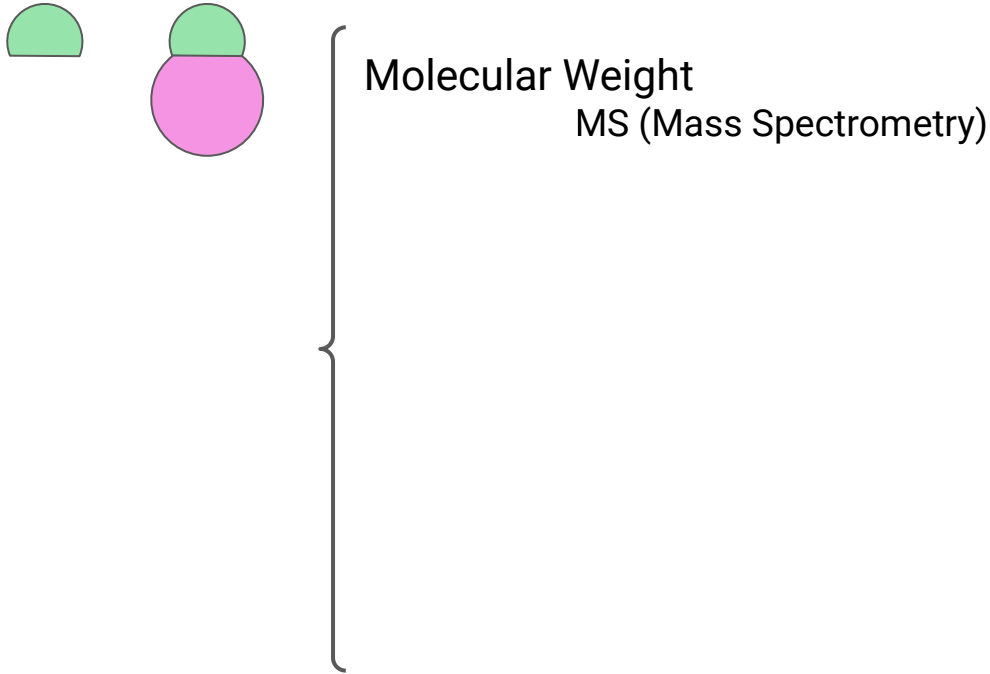
Free



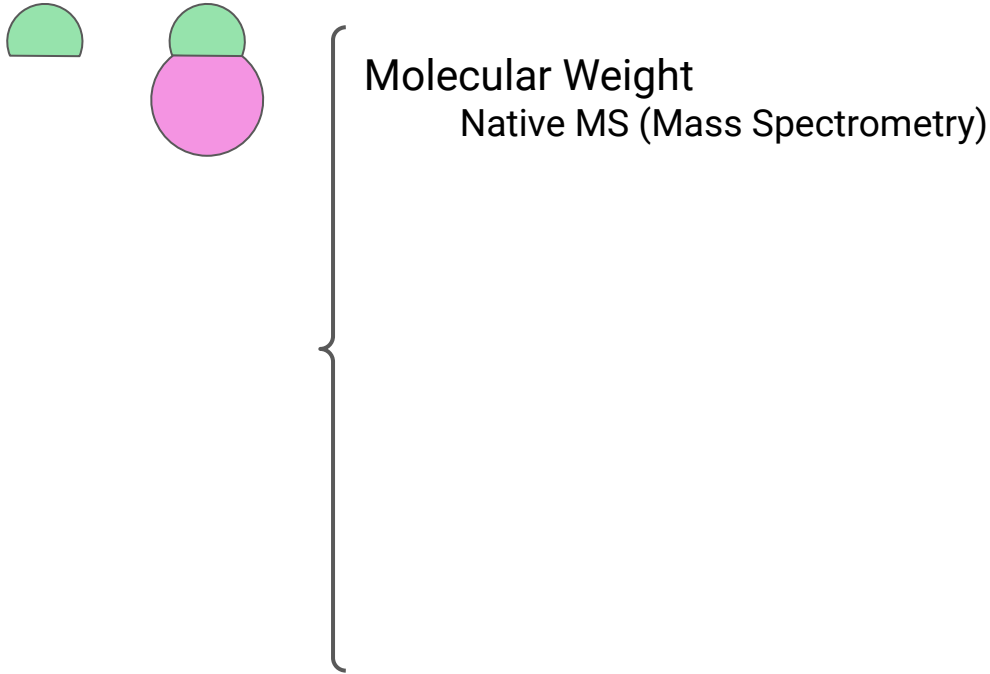
Complex



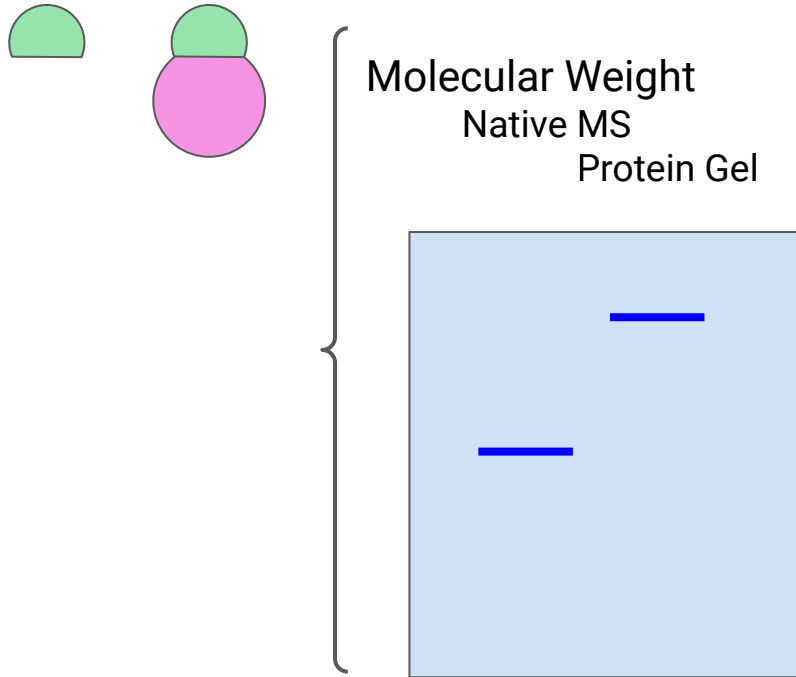
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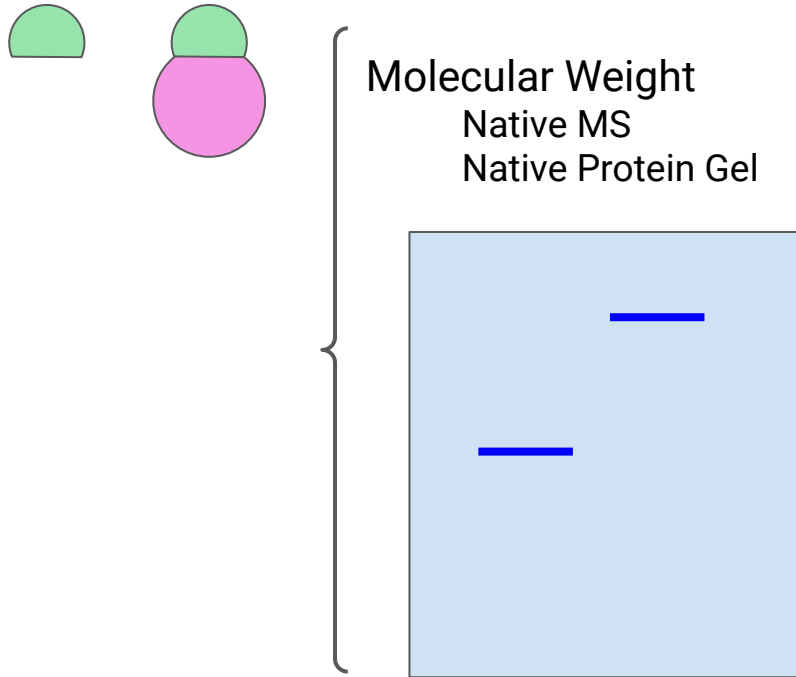
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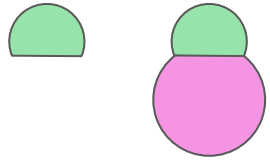
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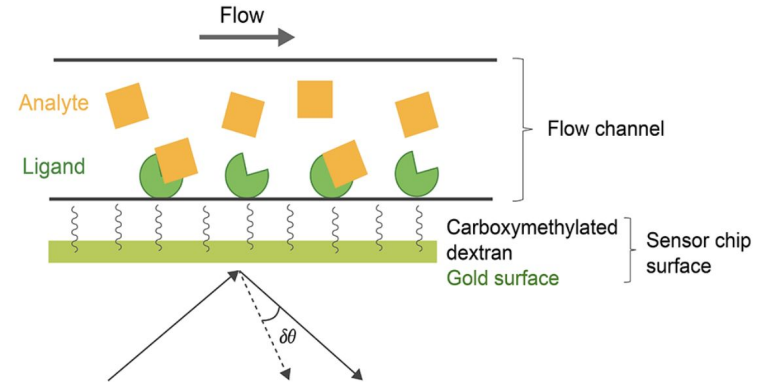


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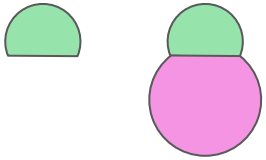


Molecular Weight  
Native MS  
Native Protein Gel

Light diffraction properties  
SPR (Surface Plasmon Resonance)

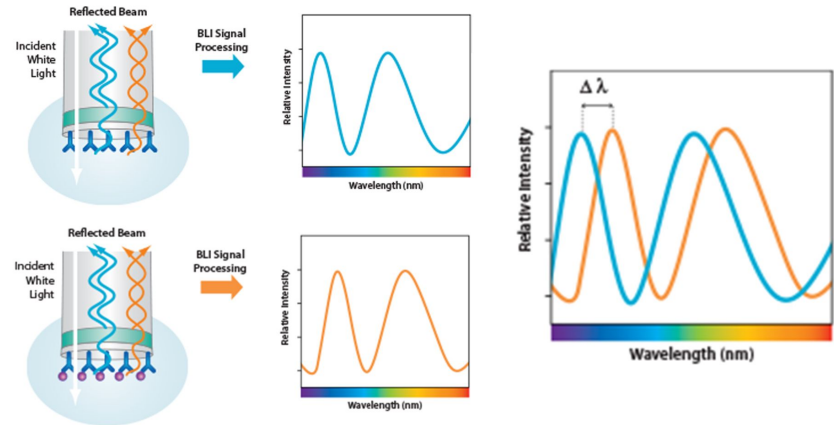


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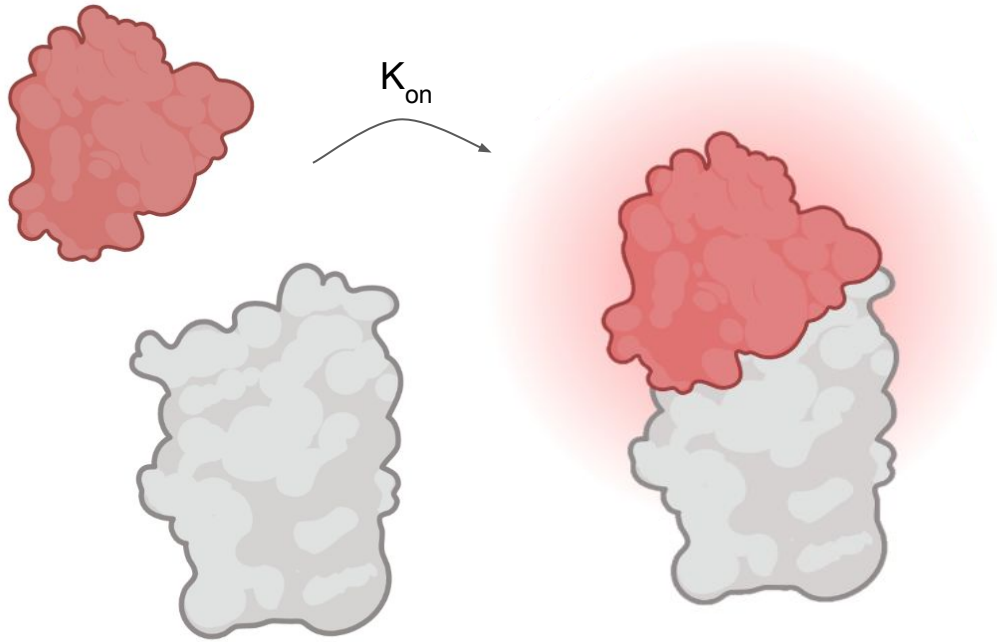


Molecular Weight  
Native MS  
Native Protein Gel

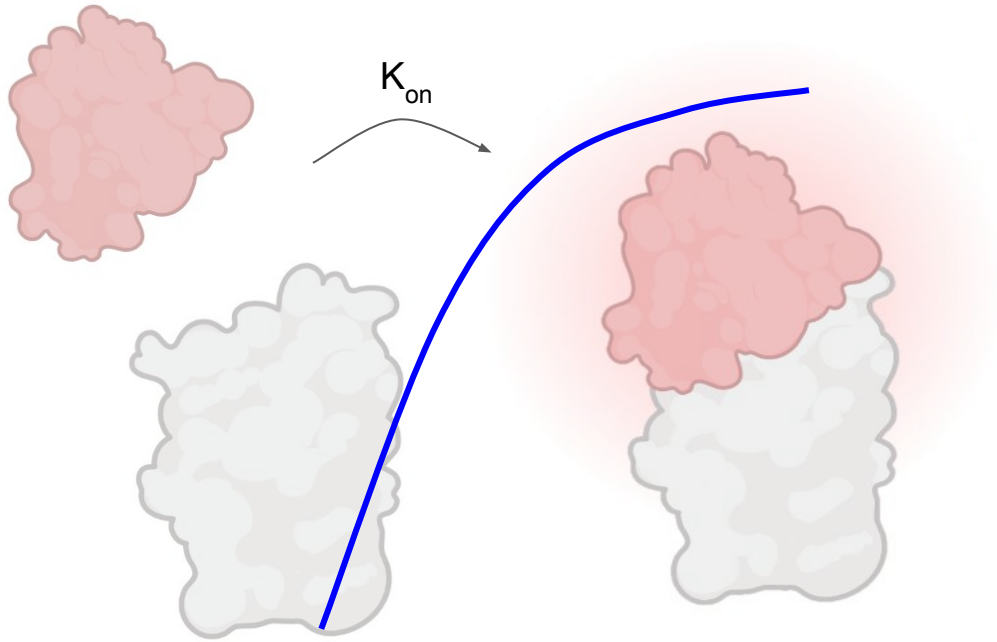
Light diffraction properties  
SPR  
BLI (Biolayer Interferometry)



# Binding is an equilibrium process

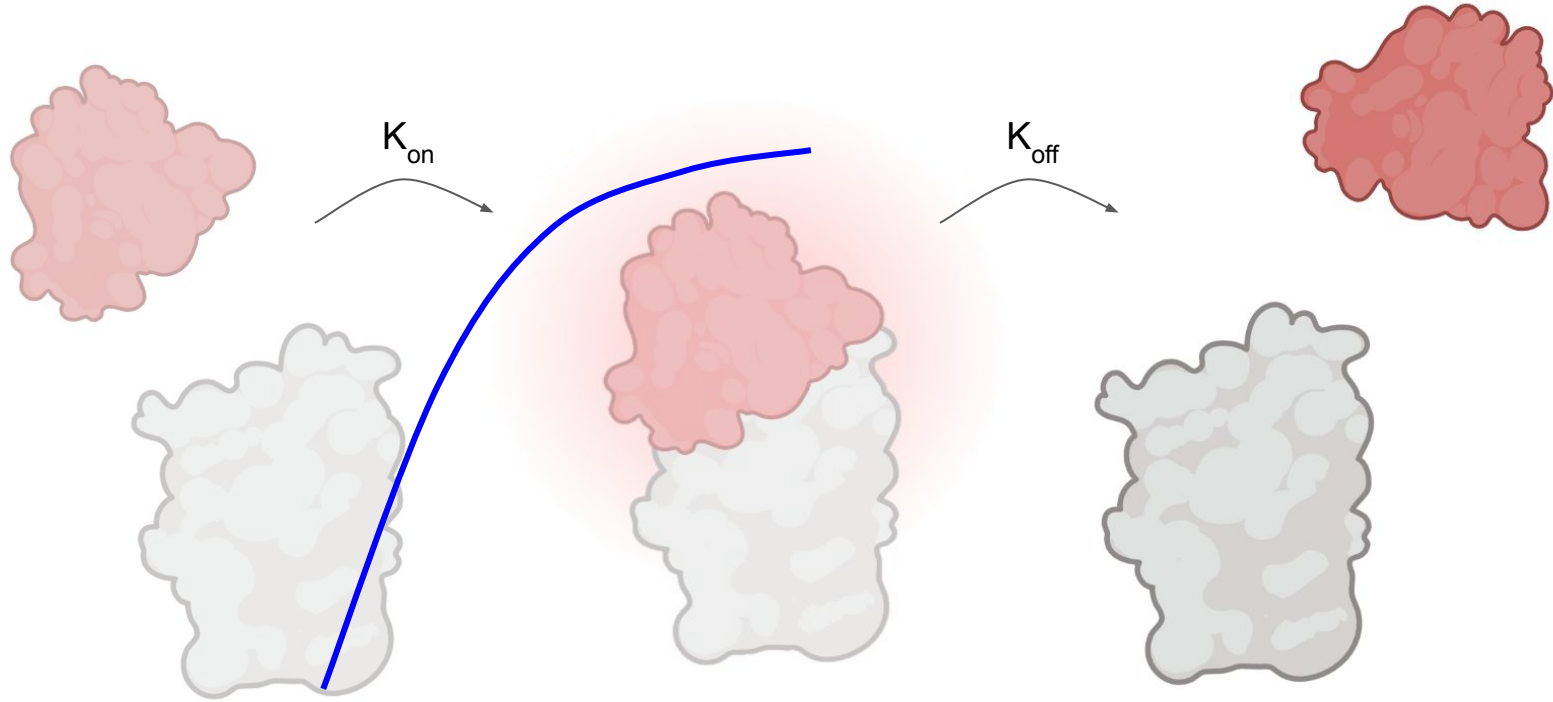


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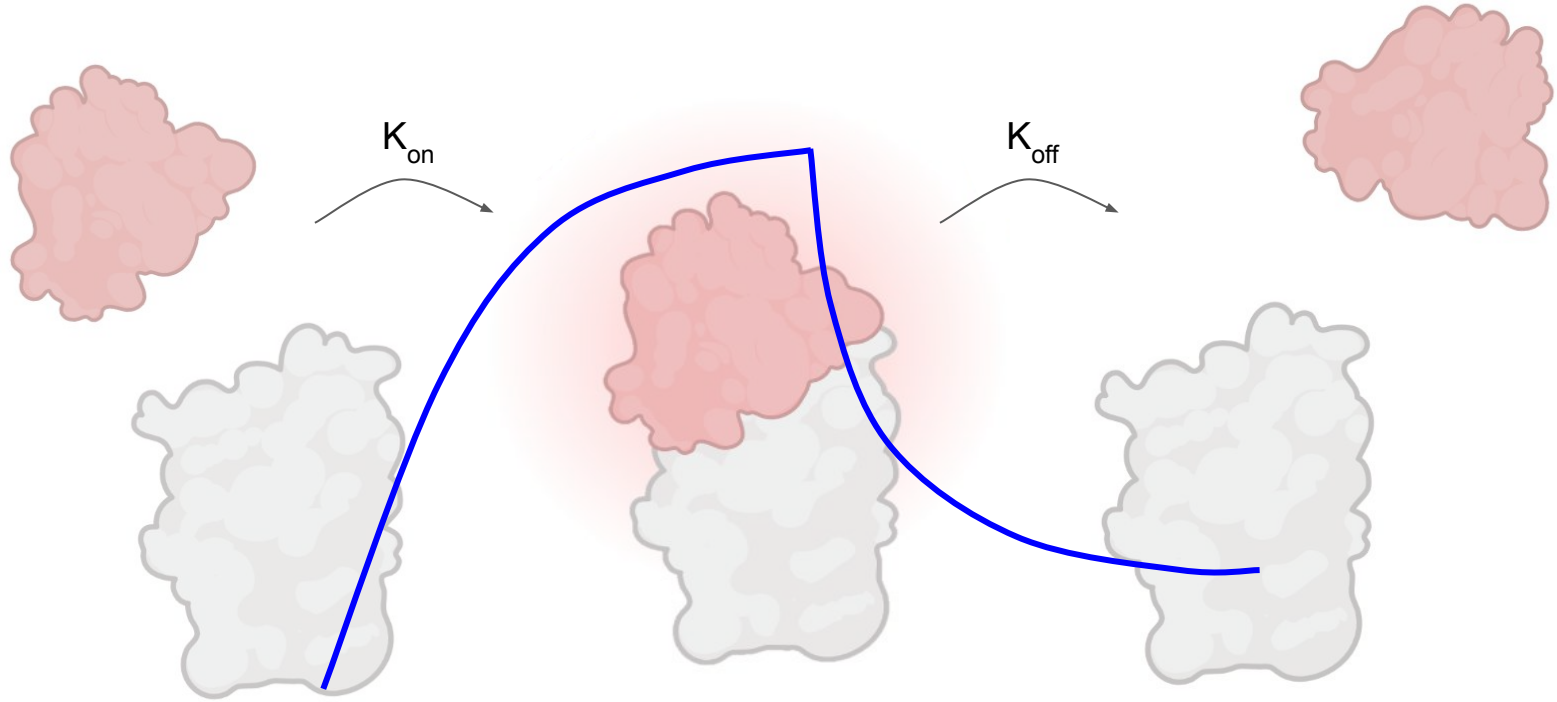




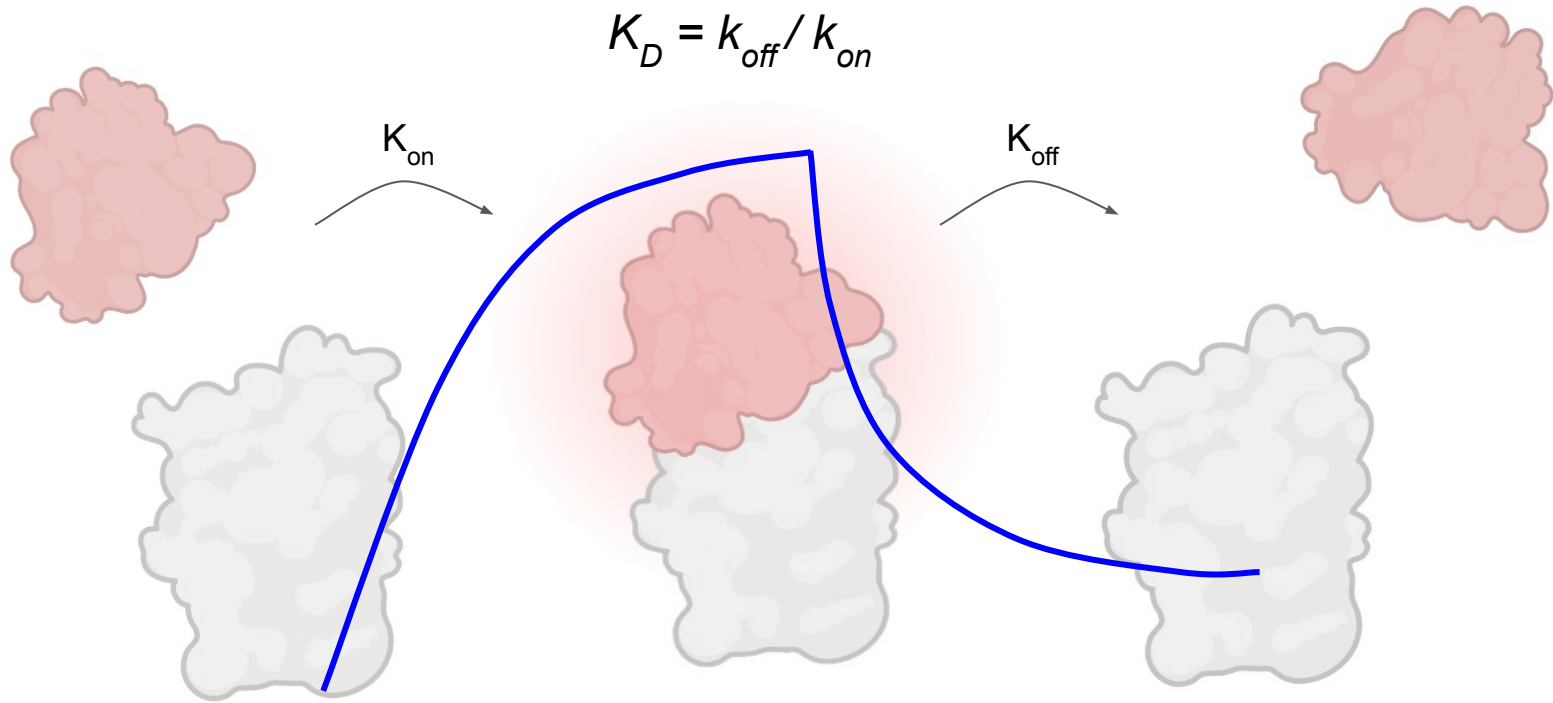
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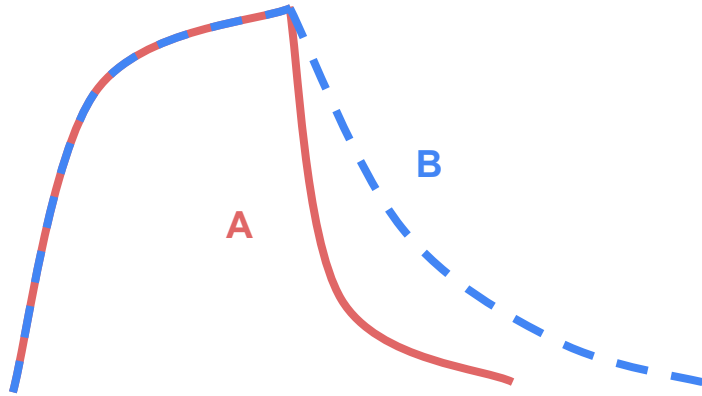


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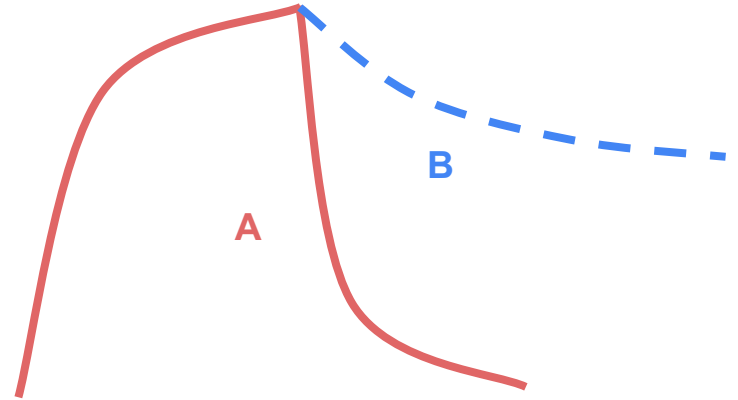


# In-class activity

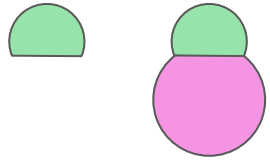
Which one has lower  $K_D$  (ie higher affinity)?



Which one is a covalent binder?



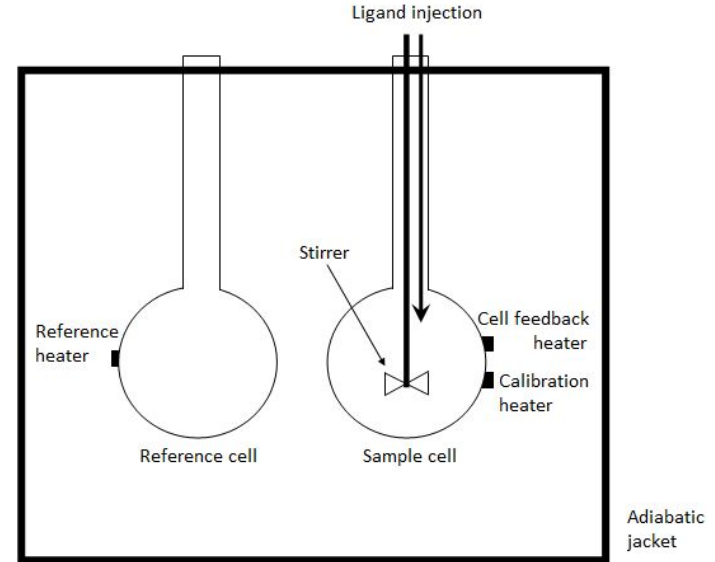
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Molecular Weight  
Native MS  
Native Protein Gel

Light diffraction properties  
SPR  
BLI

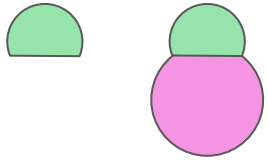
Changes in free energy  
ITC (Isothermal Titration  
Calorimetry)



$$\Delta G = -RT \ln K_a = \Delta H - T\Delta S$$

$$c = n * K_a * M$$

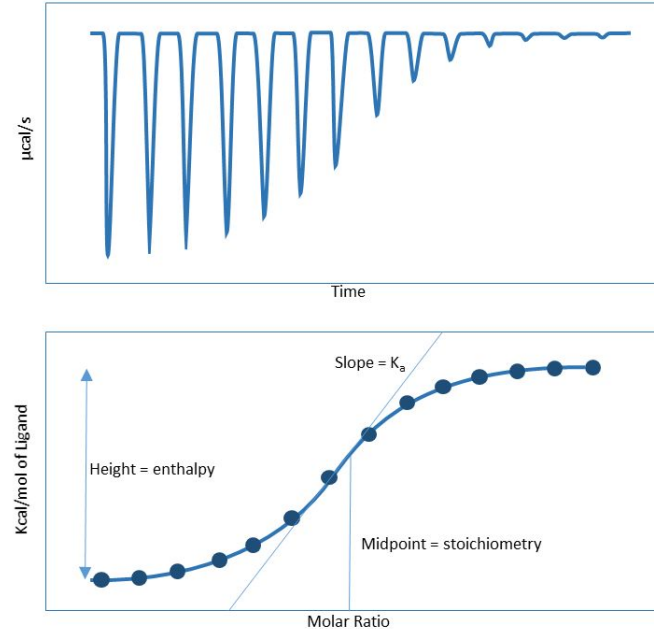
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Molecular Weight  
Native MS  
Native Protein Gel

Light diffraction properties  
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Changes in free energy  
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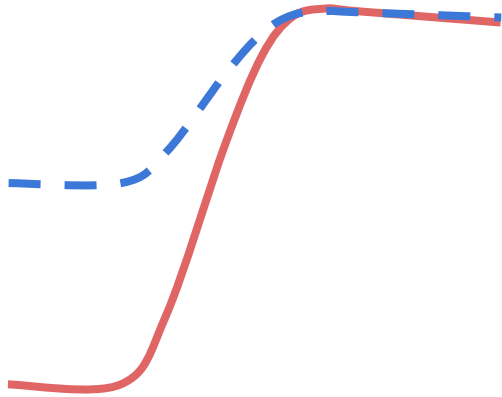
# In-class activity

Enthalpy vs Entropy driven

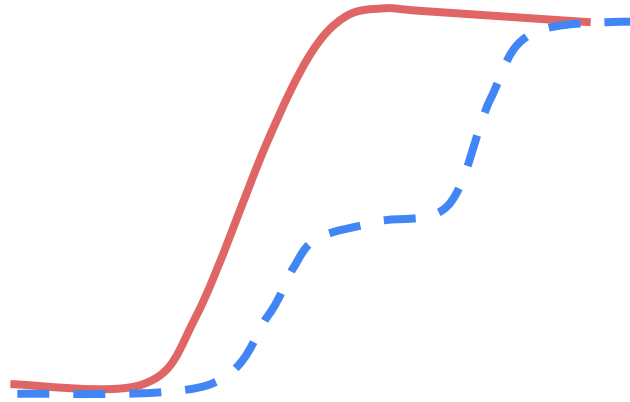
One vs two binding sites

# In-class activity

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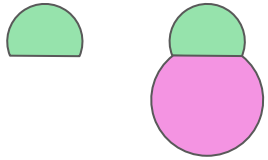


One vs two binding sites





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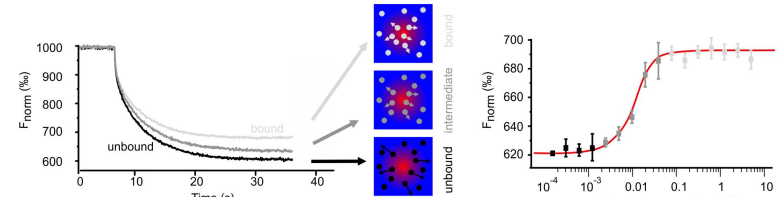
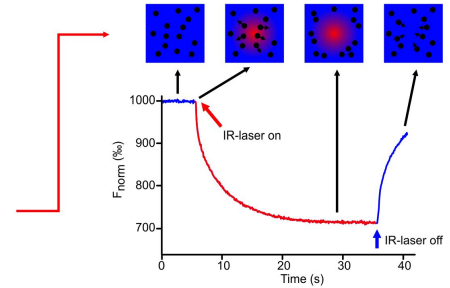
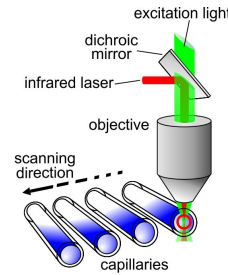


Molecular Weight  
Native MS  
Native Protein Gel

Light diffraction properties  
SPR  
BLI

Changes in free energy  
ITC

Movement  
MST (Micro Scale  
Thermophoresis)



# Summary of binding methods

	<b>SPR</b>	<b>ITC</b>	<b>BLI</b>	<b>MST</b>
Label/Immobiliz.	N/Y	N/N	N/Y	Y/N
Throughput	Medium	Low	Medium	Medium/High
Accuracy	High	Thermodynamics	Low	High (but sens.)
Range	Wide	Limited	Wide	Wide (complex)
Sample quantity	Small	Large	Medium	Small
Cost/expertise	High	Medium	Medium	Medium
Maintenance	High	Medium	Low	Medium

# High throughput binding measurements

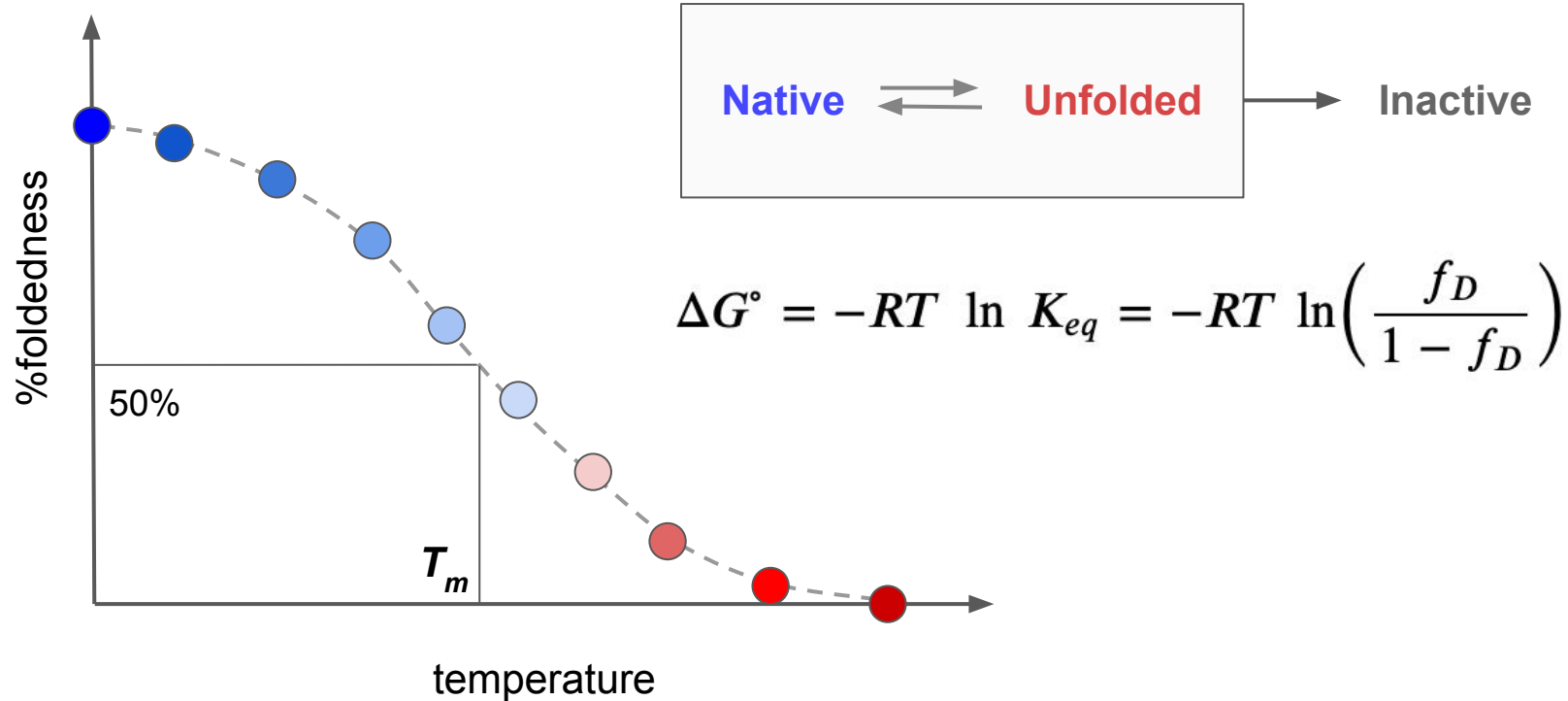
High throughput binding measurements can be achieved by linking binding to fluorescence, or life/death



# Measuring Stability



# Thermal stability is often correlated to proper folding of the protein

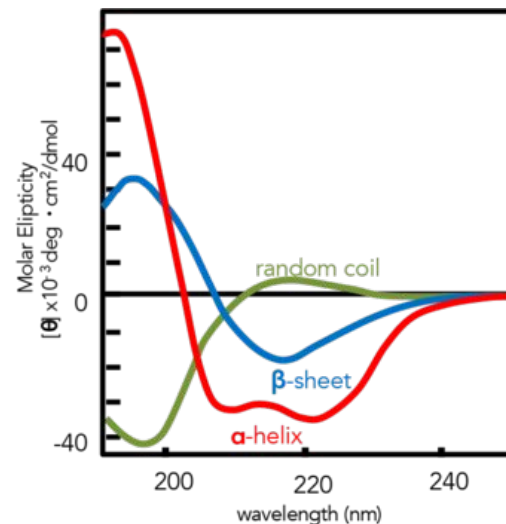
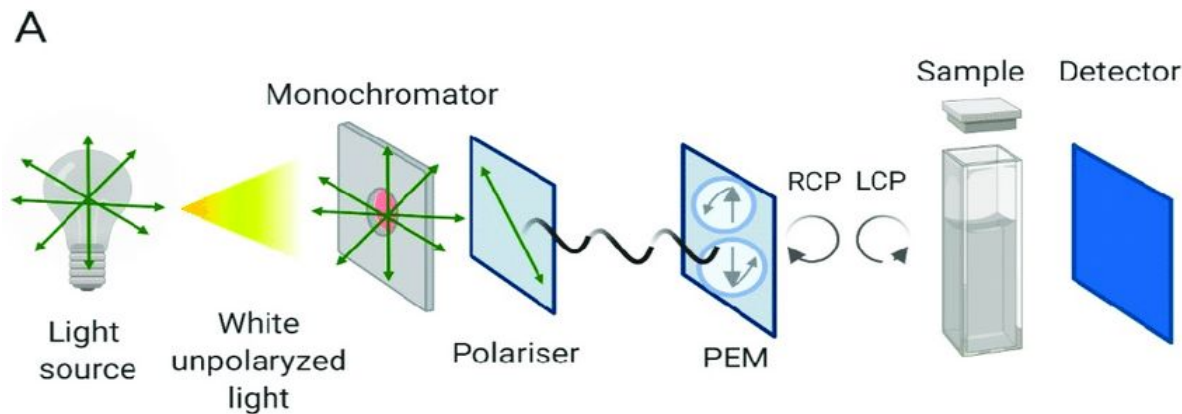


Protein fold can be assessed by measuring ...

Protein fold can be assessed by measuring its activity

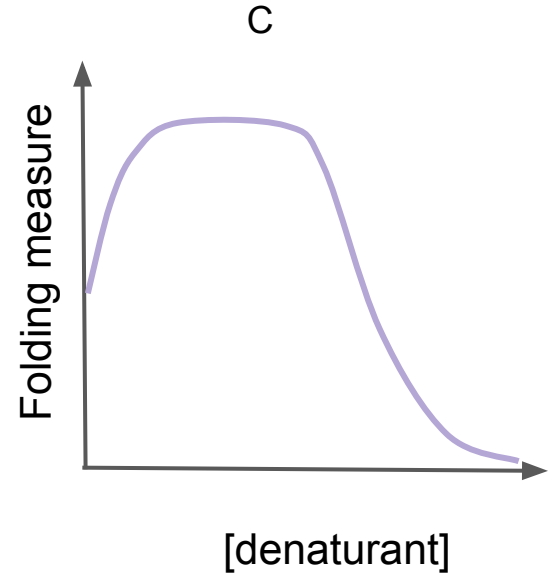
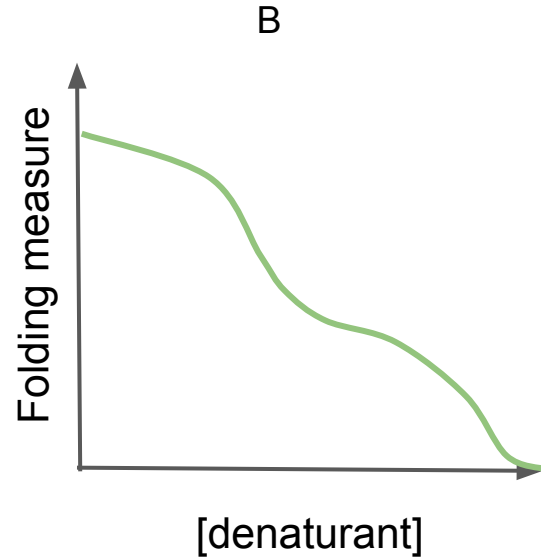
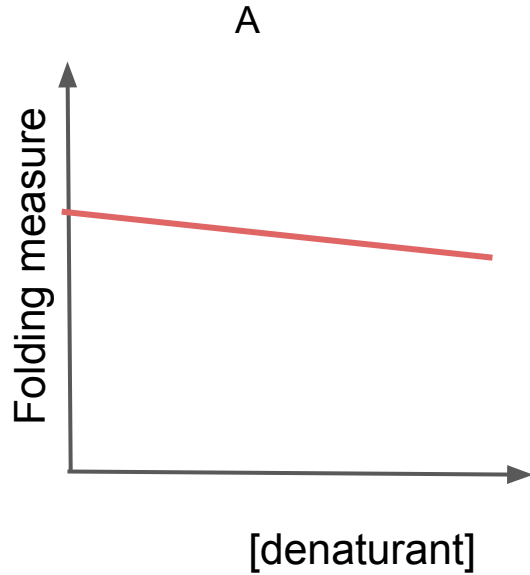


# Protein fold can be assessed by measuring its activity or its secondary structure content

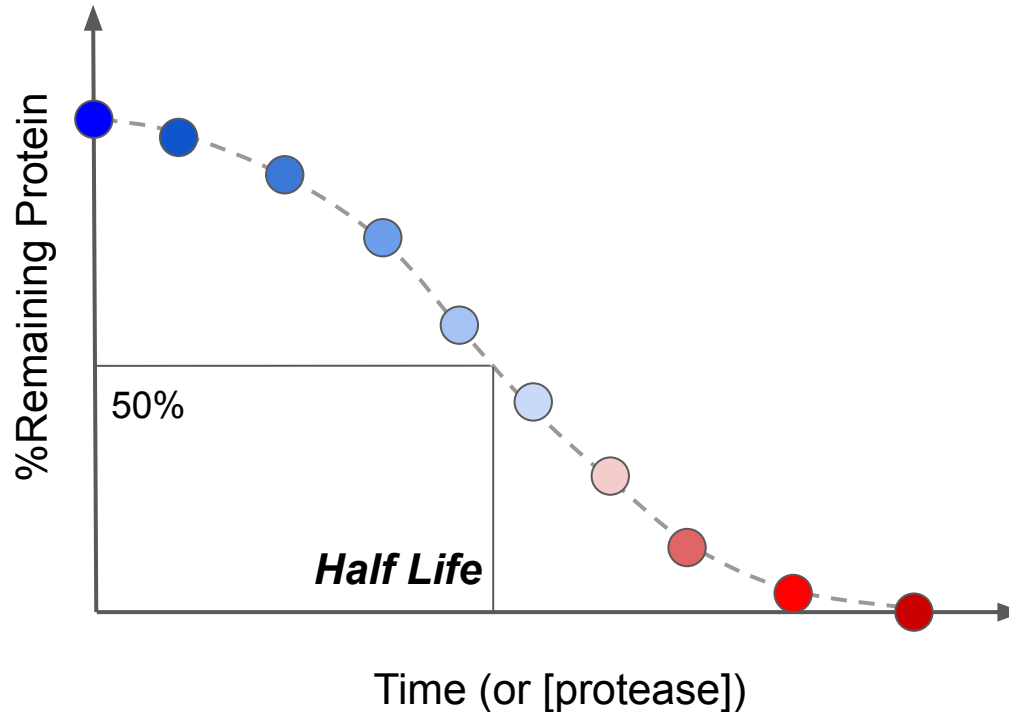


(Adapted from N. Greenfield, 1969)

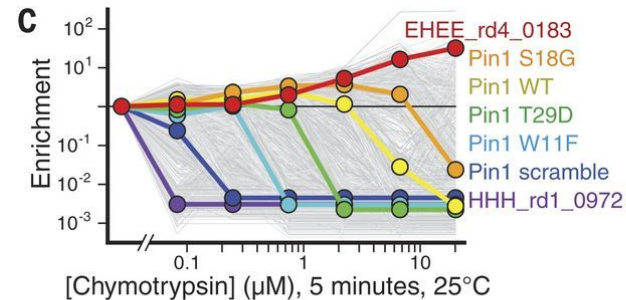
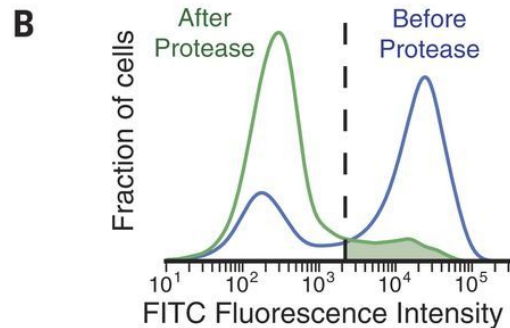
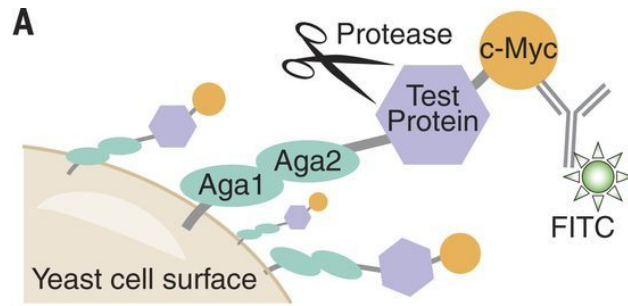
# In-class activity



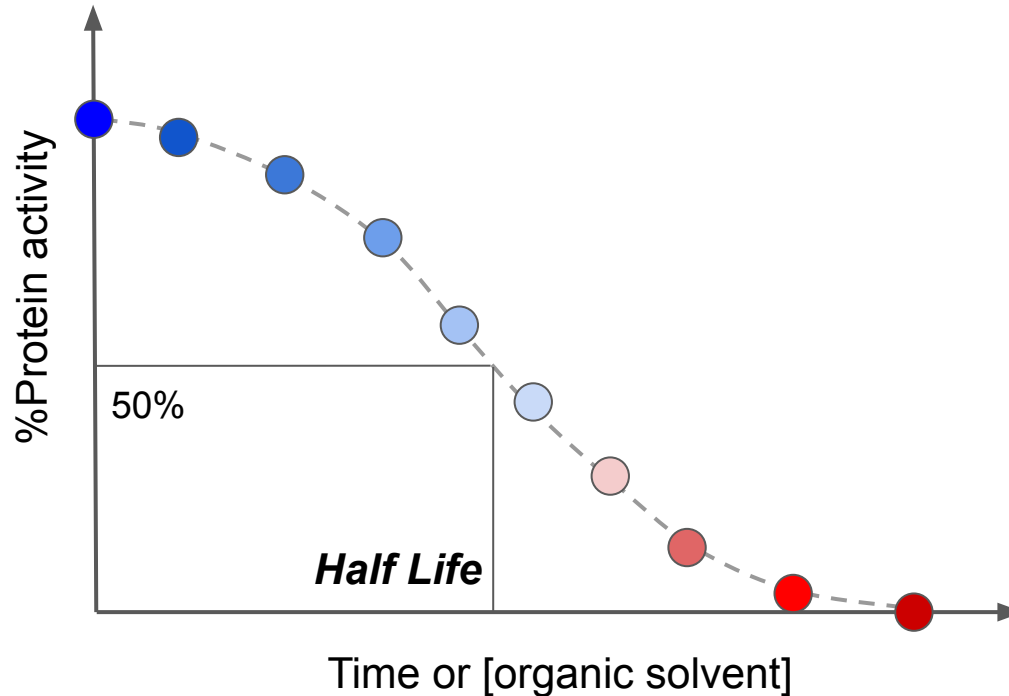
# Protease stability monitors protein degradation over time



# Protease stability monitors protein degradation over time and can be made high throughput



To measure stability against harsh conditions, we often measure activity



# For the next lecture:

1. Pre-class assessment for the next lecture  
Needs to be done before the start of class, will be available after this class
2. Post-class assignment  
The one from W1L2 due next lecture  
This lecture assignment: Proposal write-up  
Read journal for the next lecture
3. Make sure foldx is installed!

Next lecture:

*Rational design of proteins guided by structure*

