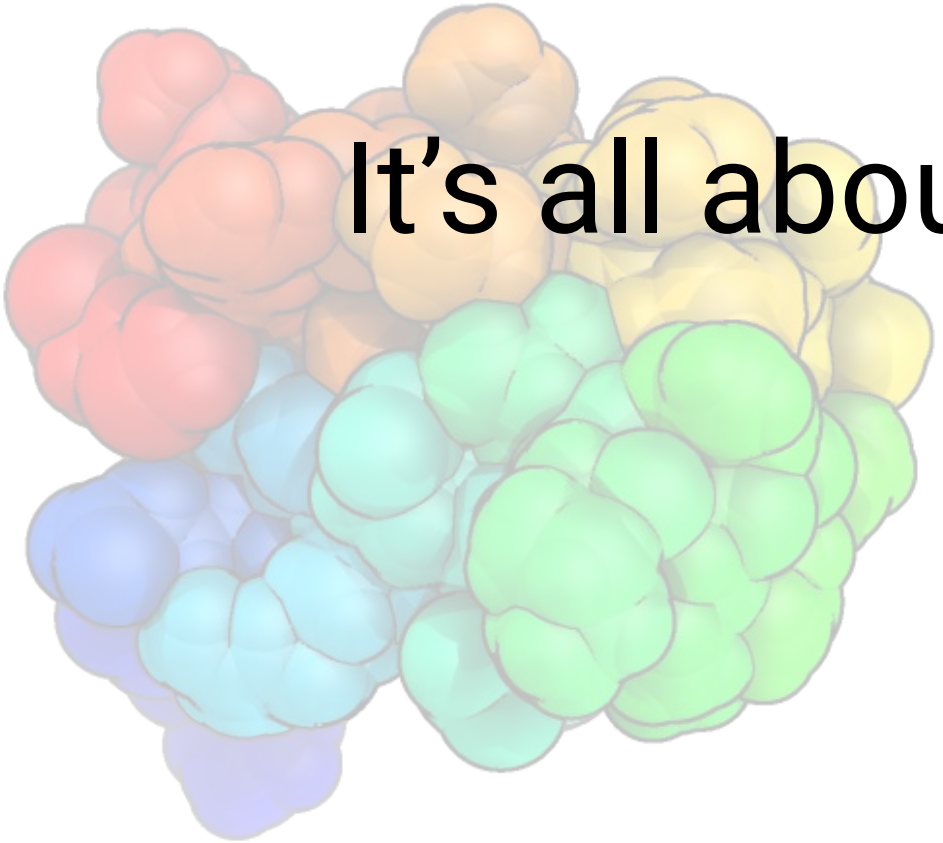
Class core values

1. Be **respect**ful 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 1, Lecture 2

It’s all about STRUCTURE!

Learning Objectives

1. Describe protein structure-function relationship
2. Explain different methods of protein structure determination
3. Evaluate the application of each method of protein structure prediction for a given test case
4. Evaluate the quality of a deposited structure
5. Use pymol for protein structure visualization

Proteins take on a variety of different structures

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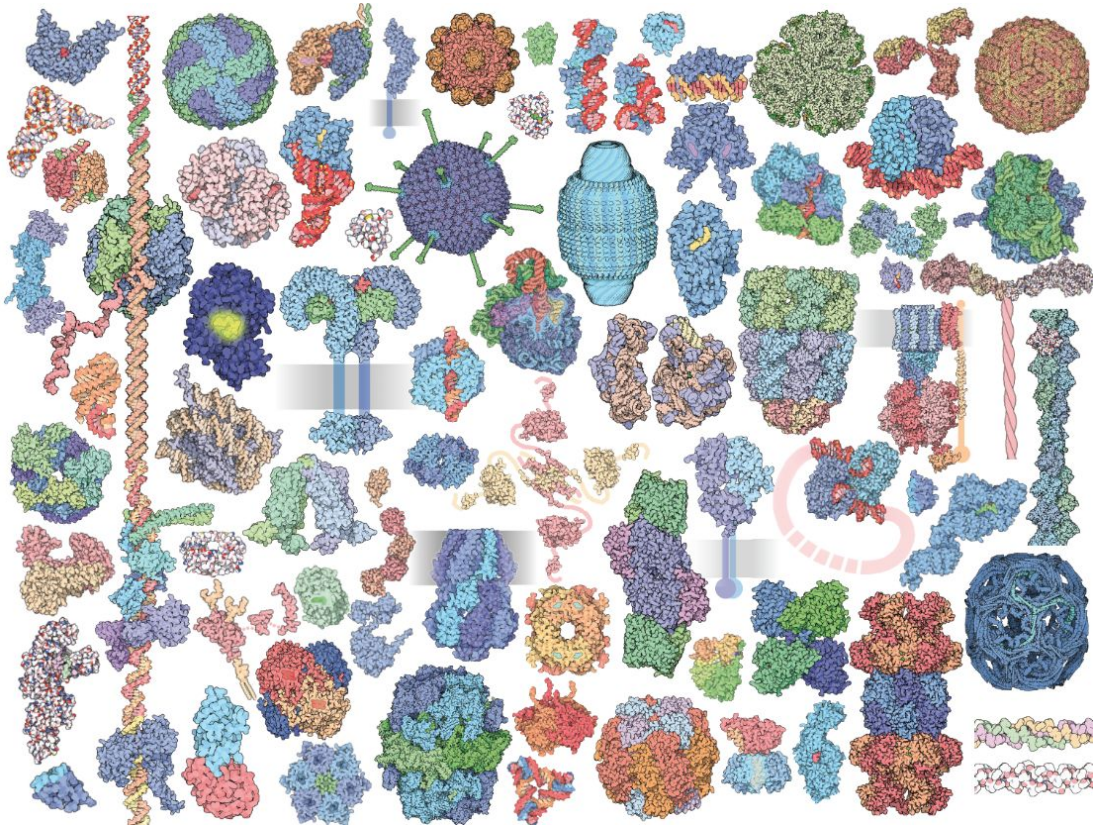
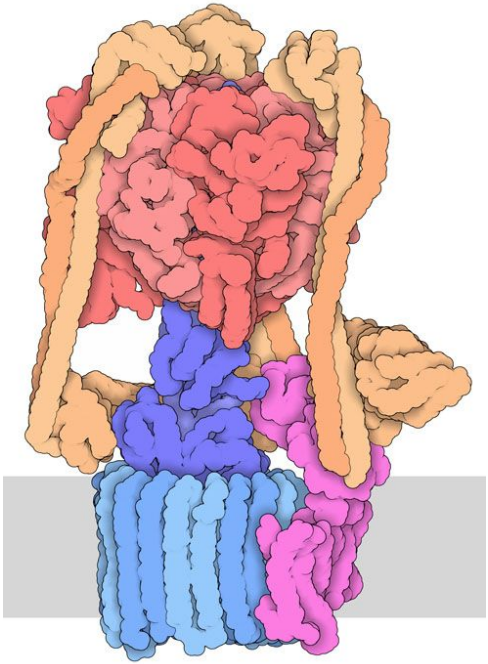


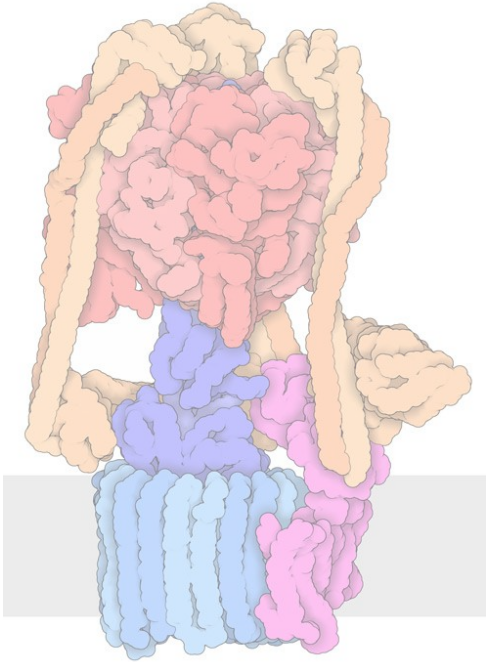
Image generated by Protein Data Bank (PDB)

Protein structure is essential for its function

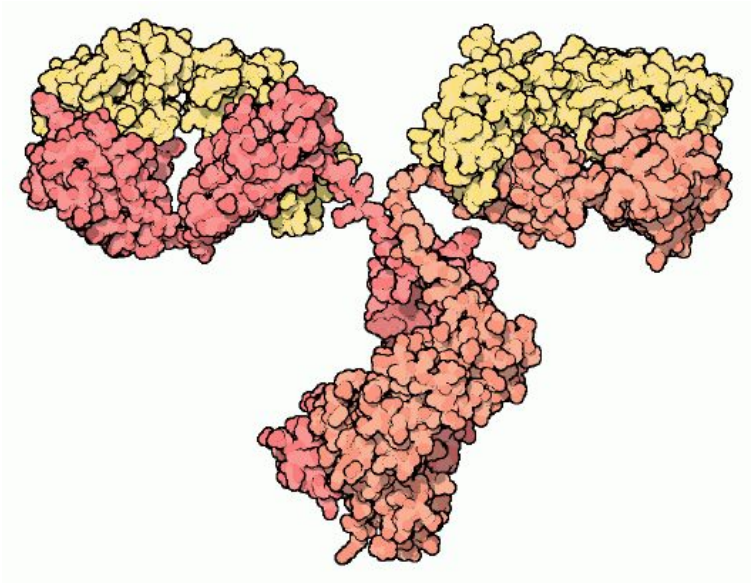


ATP synthetase

Protein structure is essential for its function

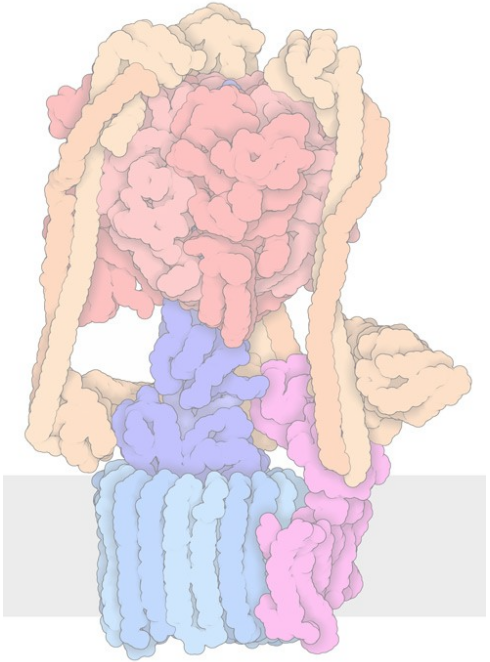


ATP synthetase



IgG antibody

Protein structure is essential for its function



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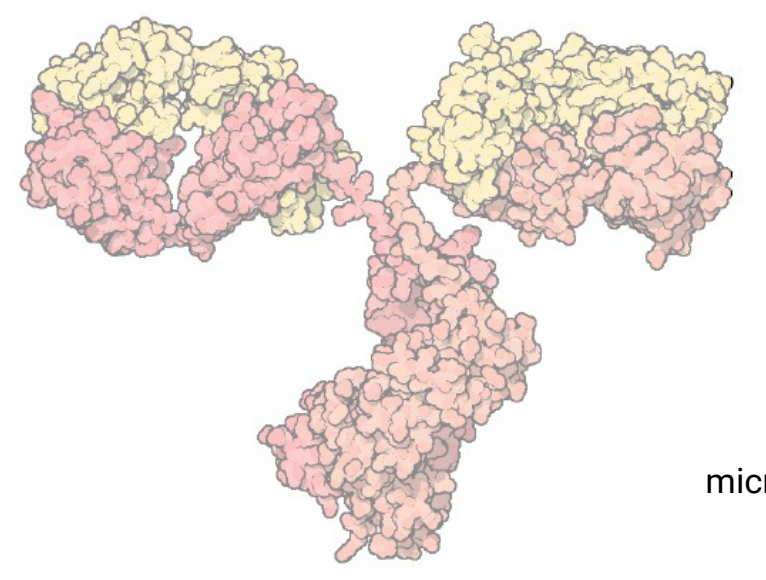
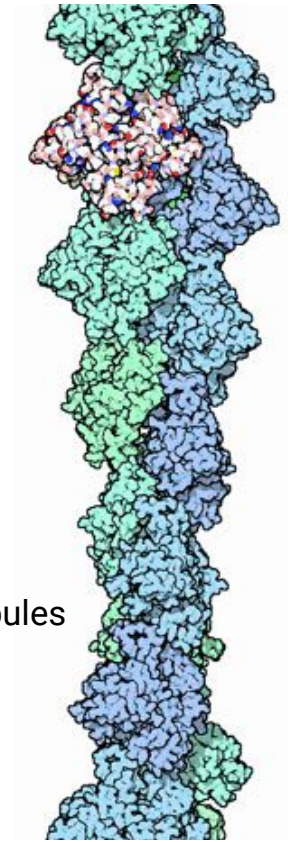
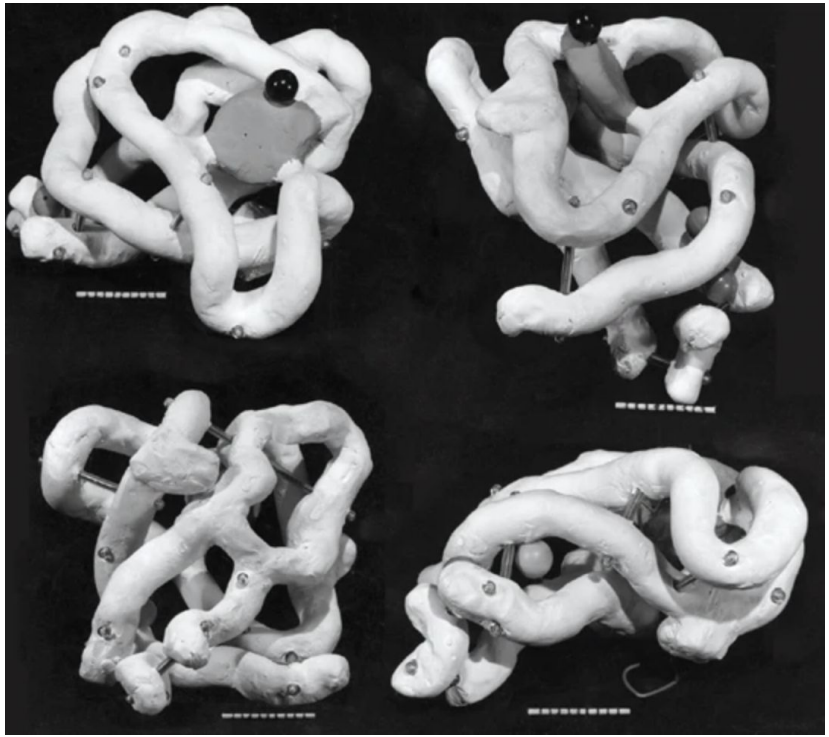


IgG antibody



microtubules

The structure-function relationship was evident from the very first protein structure



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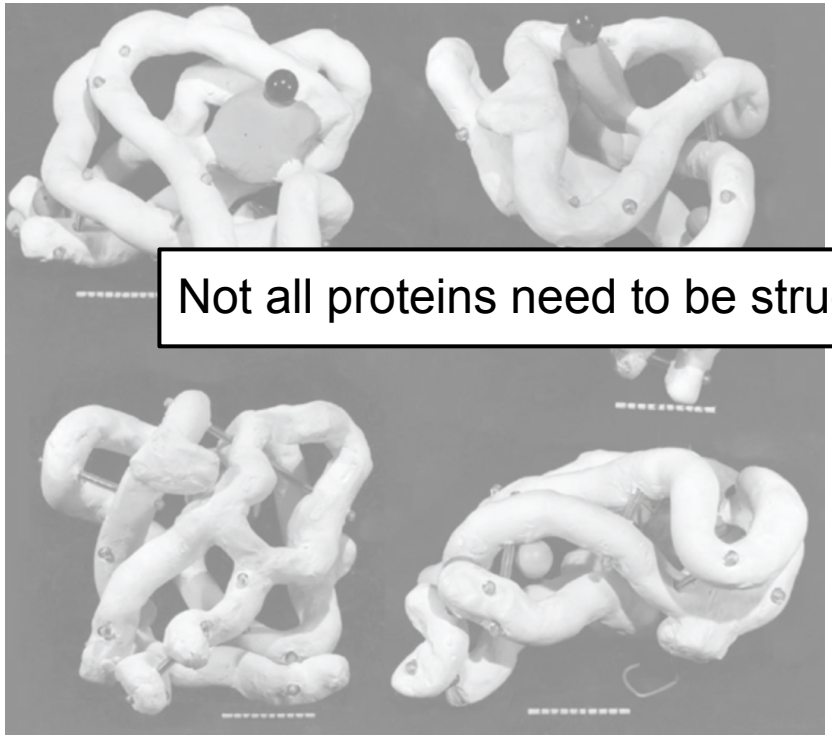

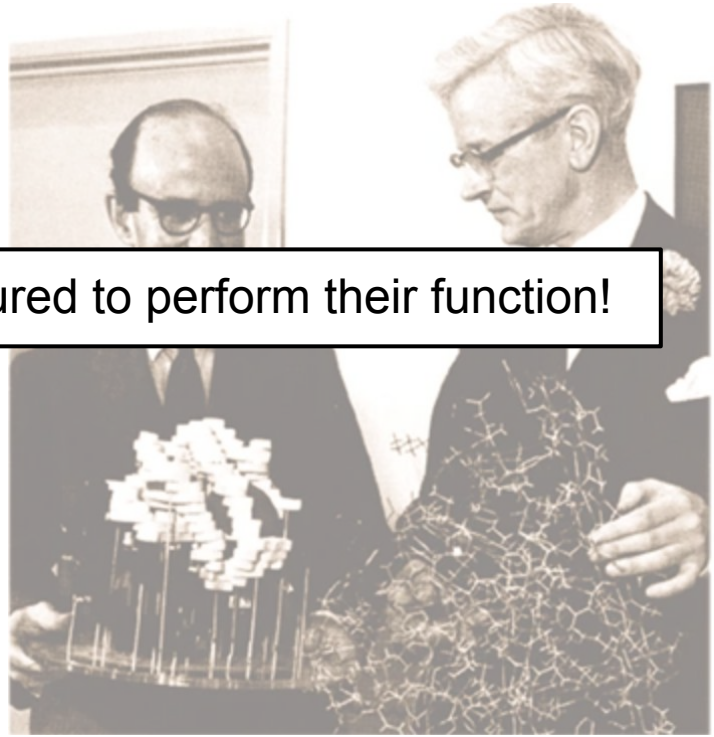

Not all proteins need to be structured to perform their function!

Obtaining experimental structures of proteins and learning from it is essential for engineering

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Methods for obtaining these structures:

- X-ray crystallography
- NMR
- Cryo-EM

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Methods for predicting these structures:

- AlphaFold2
- RoseTTaFold through Robetta

Obtaining experimental structures of proteins and learning from it is essential for engineering

Visualizing protein structure

- Pymol
- UCSF Chimera
- VMD

X-ray crystallography is one of the most commonly used methods for protein structure determination

Dr. Richard Cooley

Research Assistant Professor
Oregon State University

NMR has been widely used to determine structure of proteins and observe dynamics of proteins in solution

Dr. Afua Nyarko

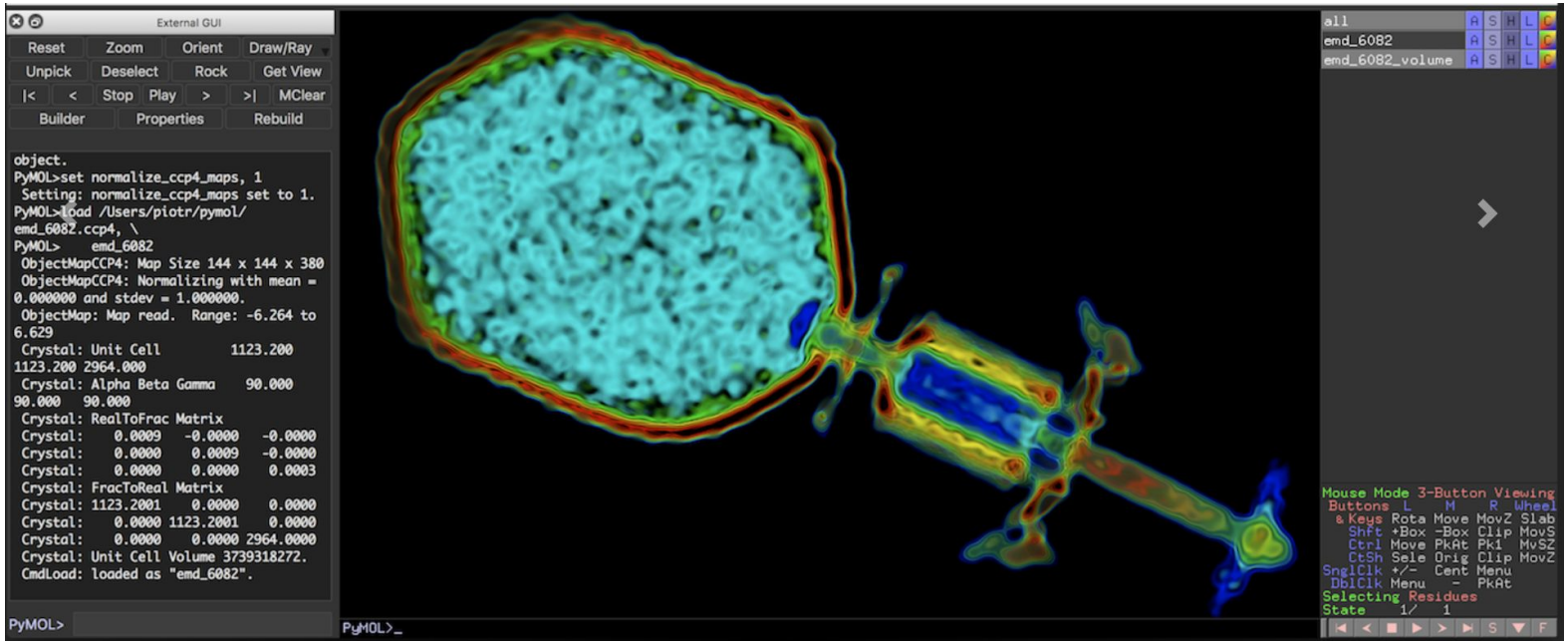
Assistant Professor
Oregon State University

Cryo-EM is the method of choice for structure of large complexes in biologically relevant conditions

Dr. Liz Kellogg

Assistant Professor
Cornell University

A lot can be learnt from looking at protein structures and analyzing them



From Schrödinger's website

For the next lecture:

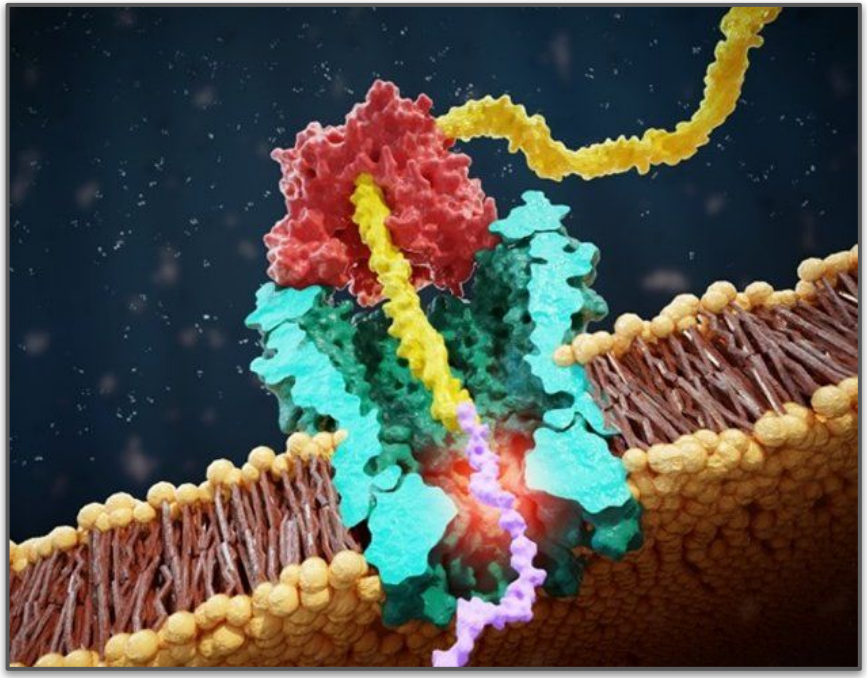
1. Pre-class assessment for the next lecture
   Needs to be done before the start of class, will be available after this class

2. Post-class assignment
   The one from W1L1 due next lecture
   This lecture assignment due next week
   Watch Cryo-EM video

3. Start installing FoldX

Next lecture:

Fantastic Proteins & How to measure them



Picture of a protein sequencer, from TU Delft