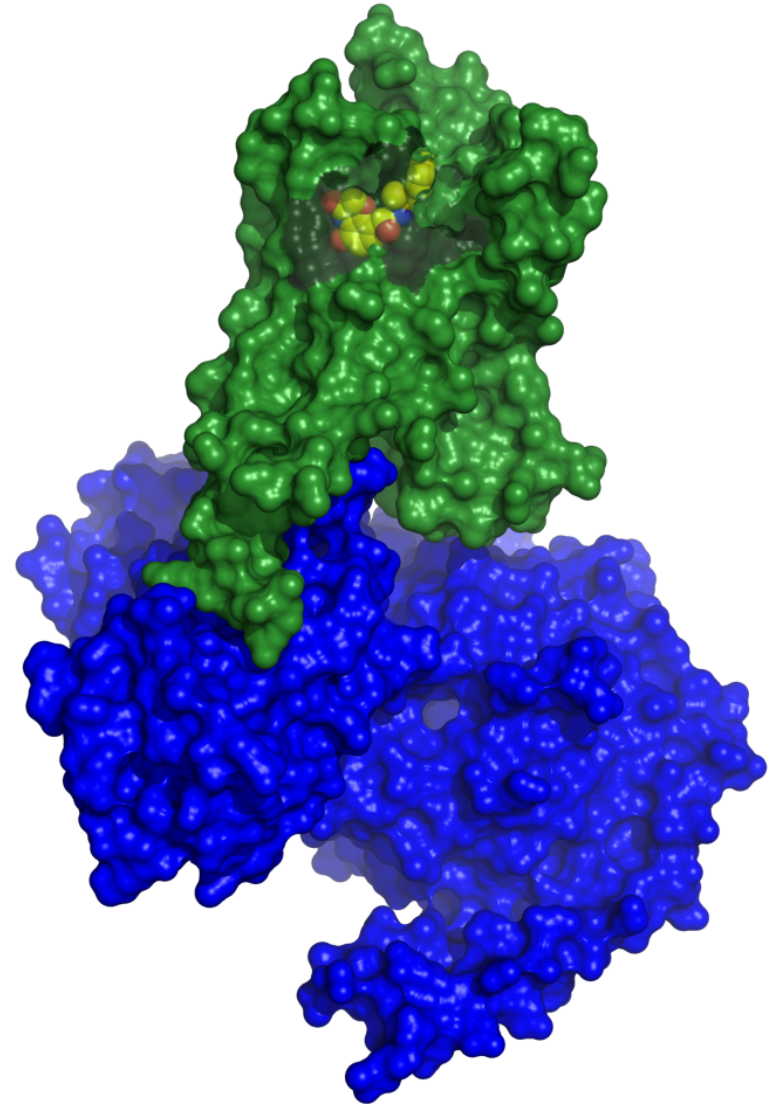# Introduction:
Protein–protein interactions

CS/CME/Biophys/BMI 371

Feb. 8, 2018

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Protein–protein interactions

- Humans have tens of thousands of proteins

- These proteins often interact with one another to form complexes of two or more proteins

  – These interactions are critical to protein function

Two challenging computational problems

- These papers address two related problems:

  - Given two (or more) proteins that interact, what is the structure of their complex?

  - Which pairs (or larger sets) of proteins interact to form complexes

Calderwood et al., PNAS 104:7606-11, 2007

http://bmm.crick.ac.uk/~bmmadmin/Affinity/

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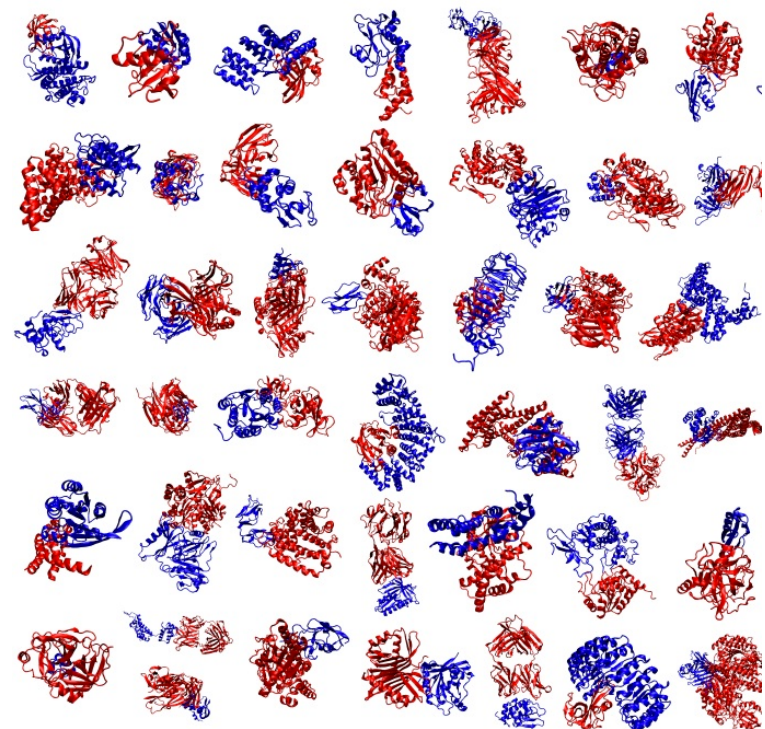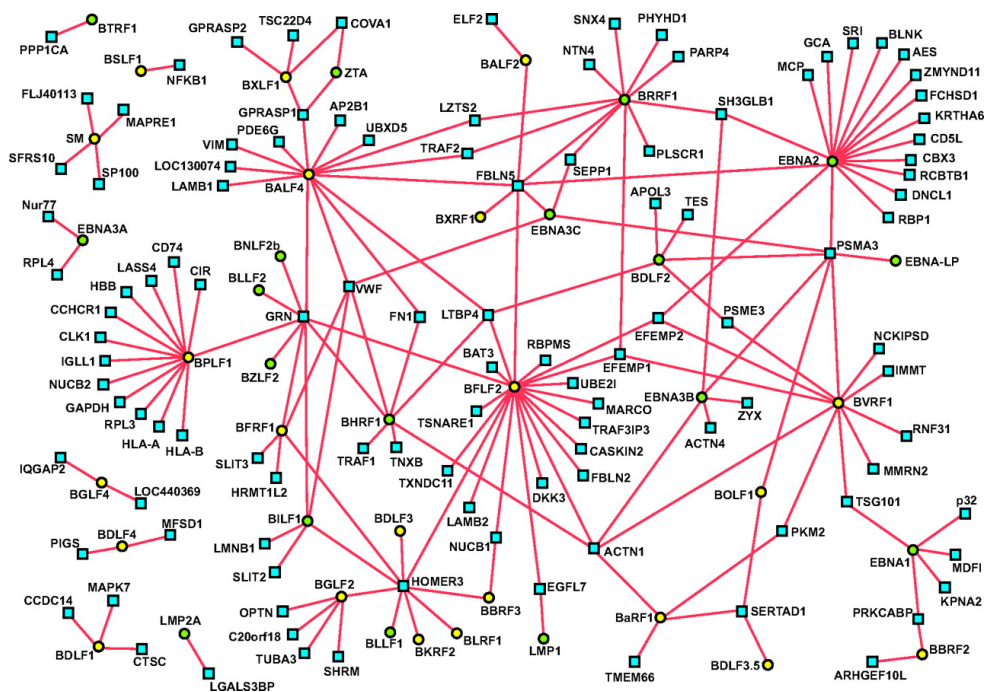
Why is this challenging?

- Answers are often not available experimentally
  - This is particularly true for structures of protein–protein complexes. There are far more protein–protein complexes than individual proteins, and far fewer solved experimental structures in the Protein Data Bank
- A straight physics-based solution to these problems is difficult
  - Like protein–ligand binding, but worse
- Heuristic protein–protein docking strategies are available, but not particularly reliable

Next Tuesday's papers

- One reports a method that predicts whether or not a pair of proteins interact, taking into account the structures of those proteins and all available structures of protein complexes
- The other analyzes a dataset of thousands of immune proteins that bind to the same few foreign proteins, and identifies similarities and differences between the interactions

Background information

- Homology modeling = template-based modeling (predicting protein structures "by analogy")

    – For more detail on homology modeling, see http://web.stanford.edu/class/cs279/lectures/lecture5.pdf

CURIS (summer reserach)

- For undergrads:
  - Consider applying to the CS department's summer research program https://curis.stanford.edu/