Structure Prediction Principles

- **Homology modeling** is most useful for closer homology. Go through http://www.bioinfo.rpi.edu/bystrc/courses/biol4550/lecture7/assets/player/KeynoteDHTMLPlayer.html#0 up to slide 11
- **Threading** is more useful for distant homologues. Watch https://www.jove.com/video/3259/a-protocol-for-computer-based-protein-structure-function up through minute 1
- Differences between approaches not completely distinct

Choosing Structure Prediction Software