Homology

* Comparison of unknown proteins with existing protein structures to figure out their structures.
* Protein DataBank contains numerous protein structures, verified experimentally or with AlphaFold

### File Formats We'll Deal With (list is not exhaustive):

* .cif
  + Crystallographics Information Framework
* .pir
  + Alignment Files for comparative modelling
* .pdb
  + Textual File Format describing three-dimensional structures of molecules held in the Protein Data Bank
* .ali
  + ~something

### Modelling Apps:

1. AlphaFold
   1. AI-based, pretty good
2. SwissModel
   1. Has shortcomings
3. Modeller
   1. Can be imported into Python as a package
   2. Manual, but gives higher accuracy for protein structures
   3. We'll be using this mostly, to tweak and optimize our structures

### Visualization:

PDB files can be visualized using:

* ProteinDataBase's 3D View
* RasMol
* PyMol

### Important Websites

* [RCSB PDB: Homepage](https://www.rcsb.org/)
  + ProteinDataBase
  + Also need to get famililar with the website and its interface
* [Tutorial (salilab.org)](https://salilab.org/modeller/tutorial/basic.html)
  + It has all required blocks of code along with explanations for relevant pieces.
* <https://github.com/iGEMIISc/scFv-Modelling>
  + IISc iGEM Github page with a compilation of resources and documentation

### Pointers:

* We might need to go through the protocols based on which the given applications run, lest those get doubted. Basically need to go through official documentation and check out any relevant references they might've mentioned.
* Need to understand Z-Score and other metrics for seeing best matches and further optimizing our modelling
* Just go through tutorials on the websites of relevant applications

### A few studies comparing Protein Modelling Apps:

1. [All are not equal: A benchmark of different homology modeling programs - PMC (nih.gov)](https://www.ncbi.nlm.nih.gov/pmc/articles/PMC2253266/)
2. [Comparative studies of AlphaFold, RoseTTAFold and Modeller: a case study involving the use of G-protein-coupled receptors | Briefings in Bioinformatics | Oxford Academic](https://academic.oup.com/bib/article/23/5/bbac308/6658852)

General Overview: [Homology Modeling - an overview | ScienceDirect Topics](https://www.sciencedirect.com/topics/biochemistry-genetics-and-molecular-biology/homology-modeling)