Code Listing:

1. dataset\_manager.py:

Converts Cryo-EM maps (.mrc files) to datasets: training sets and validation sets.

2. model.py:

Contains the convolutional neural net model and functions to train, evaluate, load and save the model.

3. helix\_prediction.py:

Splits an input protein to 32x32x32 patches, runs the model on them and returns a helix prediction for the whole protein.

4. helix\_predictor\_UI.py:

Manages the user interface of the program.

5. get\_pdb\_datasets.py:

Crawls over the all alpha and a/b classes on <https://scop.berkeley.edu/>, and downloads .pdb files of proteins.

6. get\_raw\_data.py:

Script that runs inside Chimera and synthesizes Cryo-EM map and helix mask for proteins (.pdb files)