Steps for alpha fold prediction

1. Create a folder in your home directory for alphafold prediction.
2. In it save the fasta file that contains the sequence of the protein you want to predict.
3. Save one of the attached alphafold slurm scripts in the same folder you saved the fasta file.
4. Make the following necessary changes to the script based on your input
   1. Line 5 #SBATCH --mail-user=YOUR-EMAIL-ADDRESS
   2. Line 12 #SBATCH --time=0-00:00:00
      1. Format is DD-HH:MM:SS typical time I uses is 23 hours. The prediction is normall done is 1-2 hours
   3. Line 13 #SBATCH --account=YOUR-ASSOCIATED-ACCOUNT
   4. Line 21 change --fasta\_paths=/the/path/to/your/fasta/file
   5. Line 21 change --output\_dir=/point/to/the/directory/where/fasta/file/stored
5. Run slurm script with the following command sbatch alpha\_fold.sh

Additional directions for homodimer and other complicated runs and the descriptions of alphafold output can be found here.

https://github.com/deepmind/alphafold