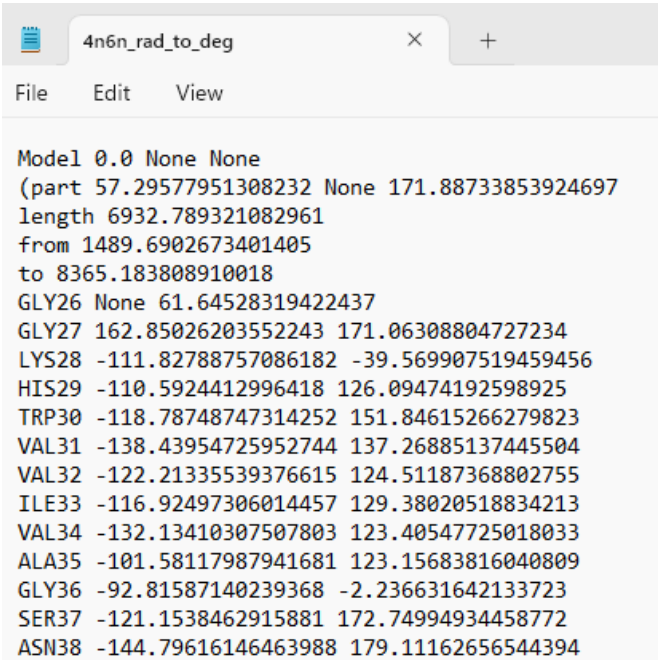
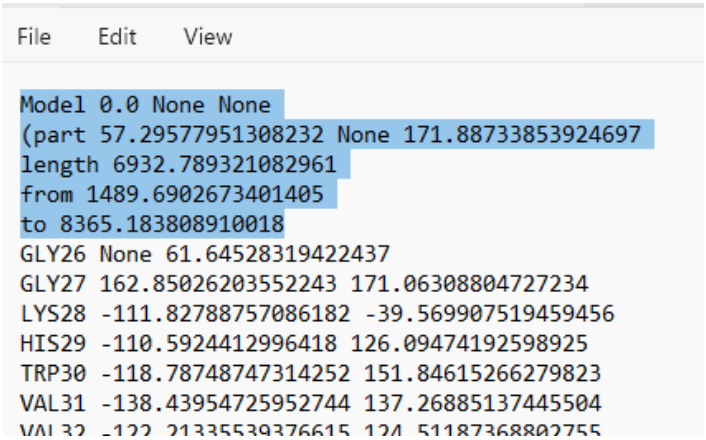
This is a continuation of the process from the “dihedral_angle_radians_to_degrees” repository, where you will find instructions on how to create a .txt file in the proper format for this secondary structure prediction module.

To find the secondary structure of your protein of interest, input a .txt file of the dihedral angles in degrees format. (You can find the modules to do this in the “dihedral_angle_radians_to_degrees” repository found here: https://github.com/sstonya/dihedral_angle_radians_to_degrees.git).

Your .txt file should look like this:



You will need to remove sections of the radian output file which do not format as ({residue}, (coordinates)). For example, the first 5 rows of the document do not follow this format (see highlighted area in the example below).



Remove the highlighted area for every part in which you see a similar formatting. Save your edited .txt file.

Copy the path to your .txt file and paste it in the “input_file_path” sections. This module will convert the degree coordinates into secondary structures (Note: you can change the angle (phi, psi) number values).

```python
#Dihedral angle to secondary structure converter

def second_struc(phi,psi):
    if phi is None or psi is None:
        return 'None'
    elif (-60 <= phi <= -40 and -70 <= psi <= -50):
        return "Right-handed Alpha-helix"
    elif (40 <= phi <= 70 and 30 <= psi <= 60):
        return "Left-handed Alpha-helix"
    elif (-150 <= phi <= 30 and 120 <= psi <= 140):
        return "Beta-sheet"
    else:
        return "Other"

def convert_degs_to_sec(input_file_path, output_file_path):
    with open(input_file_path, 'r') as input_file:
        lines = input_file.readlines()

    convert_coords = []

    for line in lines:
        parts = line.strip().split(' ')
        residue_name = parts[0]
        phi = float(parts[1]) if parts[1].upper().lower() != 'none' else None
        psi = float(parts[2]) if parts[2].upper().lower() != 'none' else None

        converted_coords = [second_struc(phi, psi)]

        converted_line = ' '.join([residue_name] + converted_coords)

        convert_coords.append(converted_line)

    with open(output_file_path, 'w') as output_file:
        output_file.write('\n'.join(convert_coords))

input_file_path = r"C:\Users\Tania\Documents\rad_2_deg.txt"
output_file_path = r"C:\Users\Tania\Documents\4n6n_sec_struc.txt"
convert_degs_to_sec(input_file_path, output_file_path)

```

You will receive an output like this:

```
GLY26 None
GLY27 Other
LYS28 Other
HIS29 Beta-sheet
TRP30 Other
VAL31 Beta-sheet
VAL32 Beta-sheet
ILE33 Beta-sheet
VAL34 Beta-sheet
ALA35 Beta-sheet
GLY36 Other
SER37 Other
ASN38 Other
GLY39 Other
TRP40 Other
TYR41 Other
ASN42 Other
TYR43 Other
ARG44 Other
HIS45 Other
GLN46 Other
ALA47 Other
ASP48 Right-handed Alpha-helix
ALA49 Other
CYS50 Other
HIS51 Other
ALA52 Other
TYR53 Other
```

This .txt file predicts the secondary structures of the PDB protein.