

Q1

**Part a)** for code choufastman.py file has been attached

### Part b)

## Output

get alpha helix as follows

```
_HHHHHHHHHHHHHHHHHHHHHHH____HHHHHHHHH_____HHHHHHHHHHHHHH_HHHHHHHH  
HHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHH____HHHHHHHHHH_HHHHHHHHH___  
_HHHHHHHHH__HHHHHH_____
```

get beta sheet is as follows

\_\_\_\_\_SS\_\_\_\_SSSSSSSS\_SSSS  
SS\_\_\_\_SS  
S\_\_\_\_\_

final struture as follows

```
-HHHHHHHHHHSSSSSSSSSSSSSHHHHHHHHSSSSHHHHHHHHHHH--HHHHHHHH  
HHSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSS---HSSSSSSSSSSSSSSSSSSSSSS--SSSS  
SSSS---HHHHHH-----
```

```
get alpha helix as follows
```

```

_XXXXXXXXXXXXXXXXXXXXX_XXXXXXXXXX_XXXXXXXXXXXX_XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX_____XXXXXXXXXX_X
XXXXXXXX   XXXXXXXX   XXXXXX

```

get beta sheet is as follows

```

_____SSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSS_____SSSSSSSS_SSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSS_____SSSSSSSSSSSS
SSSSSSSSSS  SSSSSSSSSSS_____

```

final struture as follows

[illegible]

**Q2)**

**Differences in 2 approach has been as follows**

At index 1 - \_ and T  
At index 2 - H and T  
At index 3 - H and T  
At index 4 - H and T  
At index 5 - H and  
At index 6 - H and  
At index 7 - H and  
At index 8 - H and  
At index 9 - H and  
At index 10 - H and H  
At index 11 - H and H  
At index 12 - H and H  
At index 13 - S and H  
At index 14 - S and H  
At index 15 - S and H  
At index 16 - S and  
At index 17 - S and E  
At index 18 - S and E  
At index 19 - S and E  
At index 20 - S and E  
At index 21 - S and E  
At index 22 - S and E  
At index 23 - S and T  
At index 24 - S and T  
At index 25 - S and E  
At index 26 - S and E  
At index 27 - H and E  
At index 28 - H and E  
At index 29 - H and E  
At index 30 - H and E  
At index 31 - H and E  
At index 32 - H and E  
At index 33 - H and T  
At index 34 - H and T  
At index 35 - H and E  
At index 36 - S and E  
At index 37 - S and E  
At index 38 - S and E  
At index 39 - S and E  
At index 40 - H and G  
At index 41 - H and G  
At index 42 - H and G

At index 43 - H and G  
At index 44 - H and  
At index 45 - H and  
At index 46 - H and H  
At index 47 - H and H  
At index 48 - H and H  
At index 49 - H and H  
At index 50 - H and H  
At index 51 - H and  
At index 52 - \_ and  
At index 53 - \_ and  
At index 54 - H and H  
At index 55 - H and H  
At index 56 - H and H  
At index 57 - H and H  
At index 58 - H and H  
At index 59 - H and H  
At index 60 - H and H  
At index 61 - H and  
At index 62 - H and  
At index 63 - H and G  
At index 64 - S and G  
At index 65 - S and G  
At index 66 - S and  
At index 67 - S and E  
At index 68 - S and E  
At index 69 - S and E  
At index 70 - S and E  
At index 71 - S and T  
At index 72 - S and T  
At index 73 - S and E  
At index 74 - S and E  
At index 75 - S and E  
At index 76 - S and  
At index 77 - S and E  
At index 78 - S and E  
At index 79 - S and E  
At index 80 - S and E  
At index 81 - S and E  
At index 82 - S and E  
At index 83 - S and E  
At index 84 - S and T  
At index 85 - S and T  
At index 86 - S and E

At index 87 - S and E  
At index 88 - S and E  
At index 89 - S and E  
At index 90 - S and E  
At index 91 - S and E  
At index 92 - S and  
At index 93 - S and  
At index 94 - S and  
At index 95 - \_ and T  
At index 96 - \_ and T  
At index 97 - \_ and T  
At index 98 - \_ and T  
At index 99 - H and  
At index 100 - S and  
At index 101 - S and  
At index 102 - S and  
At index 103 - S and  
At index 104 - S and  
At index 105 - S and  
At index 106 - S and  
At index 107 - S and T  
At index 108 - S and T  
At index 109 - S and T  
At index 110 - S and E  
At index 111 - S and E  
At index 112 - S and E  
At index 113 - S and E  
At index 114 - S and E  
At index 115 - S and E  
At index 116 - S and E  
At index 117 - S and E  
At index 118 - S and E  
At index 119 - S and T  
At index 120 - S and T  
At index 121 - \_ and E  
At index 122 - \_ and E  
At index 123 - S and E  
At index 124 - S and E  
At index 125 - S and E  
At index 126 - S and E  
At index 127 - S and E  
At index 128 - S and E  
At index 129 - S and E  
At index 130 - S and E

At index 150 - and

We are not predicting the small length of the sequence. we can see that the server predicts even a single nuclotide, we on the other hand is predicting for minimum of 5 lenght. This makes our algorithm bypass small sequences, which can be of importance. This can explain why our model is predicting with less accuracy

Our algorithm does really bad at the starting of the sequence, which can be reasoned as we are not considering the nucleotide behaviour at starting or end part of the sequence.

The algorithm is very basic and it misses on the details. Therefore it predicts wrong inbetween

In the conflicting region we can see that it is predicting right, this means that the basic way of resolving conflict(give the position the sequence which give the maximum score) works.

**Moreover The output secondary shape of protein expected through this application isn't like the secondary shape given through the STRIDE webserver because STRIDE makes use of a extraordinary set of rules for prediction of secondary protein shape. In addition to hydrogen bond standards utilized by DSSP set of rules, STRIDE additionally makes use of dihedral perspective potentials. This application makes use of Chou-Fasman algorithm for secondary shape prediction it is why we take a look at many variations withinside the output sequence.**