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

Output

get alpha helix as follows		

_ННННННННННННННННН	НННННННННН	НННННННННННН_	НННННННН
НННННННННННННННН	ІНННННННННН	_НННННННННН_ННЬ	ІНННННН
get beta sheet is as follows			
SSSSSSSSSSSSS	SSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSS	SSSSSSSSSSSS	SSSS_SSSS

#### final struture as follows

### 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
- Attitudes 100 Garia i
- 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 131 - S and T
At index 132 - S and T
At index 133 - and T
At index 134 - _ and T
At index 135 - _ and
At index 136 - H and B
At index 137 - H and
At index 138 - H and
At index 139 - H and
At index 140 - H and
At index 141 - H and T
At index 142 - _ and T
At index 143 - _ and T
At index 144 - _ and T
At index 145 - and T
At index 146 - _ and T
At index 147 - _ and T
At index 148 - _ and E
At index 149 - _ and E
At index 150 - and
```

## Part b) Comments on the difference observed with proper reasoning

#### Regions differing

From above we are able to see that infrequently any alpha area is being anticipated correctly, however we also can see that each one the areas that have been anticipated beta nearly fits with the prediction of the server.

We aren't evaluating the turns, as we've got assigned turns anyplace the set of rules isn't predicting both alpha or beta.

We can see that our **version** does **awful in particular at the beginning** of the sequence At index 54-60 our **set of rules** is **not able** to **are expecting** the helix.

From index 86-ninety one our set of rules predicts helix in preference to S
We can see that withinside the conflicting area of 65-seventy five it's far running great

We are not predicting the small length of the sequence. we can see that the server predicts even a single nucliotide, 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 nucliotide behaviour at starting or end part of the sequence.

The algorithm is very basic and it is 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 beacause 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.