Q1)
A)py file submitted in zip
b)
Output is
-HHHHHHHHHHHSSSSSSSSSSSSSSSHHHHHHHHHHSSSSHHHHHHHHHHHHH--HHHHHHHH
HHSSSSSSSSSSSSSSSSSSSSSSSSSSSSSS----HSSSSSSSSSSSSSSSSSSSS--SSSSS
SSSSS---HHHHHH---------

Q2)

(A)server output

```
                .         .         .         .         .                  ~~~~~
1     SGFRKMAFPSGKVEGCMVQVTCGTTTLNGLWLDDTVYCPRHVICTAEDML   50          ~~~~~
      TTTT     HHHHHH EEEEEETTEEEEEEEETTEEEEGGGG  HHHHH               ~~~~~
                                                                       ~~~~~
                .         .         .         .         .            ~~~~~
51    NPNYEDLLIRKSNHSFLVQAGNVQLRVIGHSMQNCLLRLKVDTSNPKTPK  100         ~~~~~
         HHHHHHH  GGG EEEETTEEE EEEEEEETTEEEEEE   TTTT               ~~~~~
                                                                      ~~~~~
                .         .         .         .         .           ~~~~~
101   YKFVRIQPGQTFSVLACYNGSPSGVYQCAMRPNHTIKGSFLNGSCGSVGF  150         ~~~~~
            TTTEEEEEEEEETTEEEEEEEEEETTTT B    TTTTTTTEE              ~~~~~
                                                                      ~~~~~
                                                                      ~~~~~
```

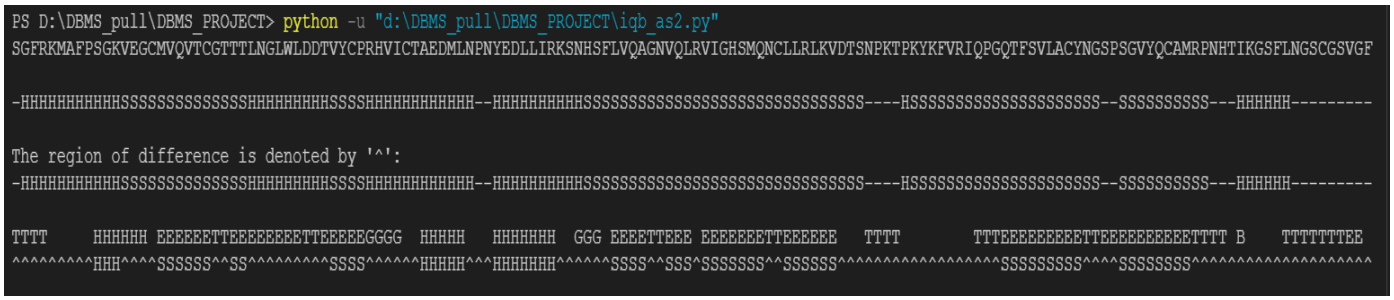
Results our:

SGFRKMAFPSGKVEGCMVQVTCGTTTLNGLWLDDTVYCPRHVICTAEDMLNPNYEDLLIRKSN
HSFLVQAGNVQLRVIGHSMQNCLLRLKVDTSNPKTPKYKFVRIQPGQTFSVLACYNGSPSGVY
QCAMRPNHTIKGSFLNGSCGSVGF

-HHHHHHHHHHHSSSSSSSSSSSSSSHHHHHHHHHSSSSHHHHHHHHHHHHH--HHHHHHHH
HHSSSSSSSSSSSSSSSSSSSSSSSSSSSSSS----HSSSSSSSSSSSSSSSSSSSS--SSSSS
SSSSS---HHHHHH---------

The region of difference is denoted by '^':
-HHHHHHHHHHHSSSSSSSSSSSSSSSHHHHHHHHHSSSSHHHHHHHHHHHHH--HHHHHHHH
HHSSSSSSSSSSSSSSSSSSSSSSSSSSSSSS----HSSSSSSSSSSSSSSSSSSSS--SSSSS
SSSSS---HHHHHH---------

TTTT HHHHHH EEEEEETTEEEEEEEETTEEEEGGGG HHHHH HHHHHHH GGG
EEEETTEEE EEEEEEETTEEEEE TTTT TTTEEEEEEEETTEEEEEEEEETTTT B
TTTTTTTEE
^^^^^^^^HHH^^^^SSSSSS^^SS^^^^^^^^SSSS^^^^^^HHHHH^^^HHHHHHH^^^^^^SSSS^^SS
S^SSSSSSS^^SSSSSS^^^^^^^^^^^^^^^^^^SSSSSSSSS^^^^SSSSSSSS^^^^^^^^^^^^^^^^^^



Our algo is working only for beta strand and alpha helix but the web server is working for all beta strand , alpha helix , turn , coil and bridge. In the web server output E refers to strand , B refers to bridge , H refers to helix , T refers to turn .

(B)

Differences in this assignment were noted because the STRIDE method uses an empirically derived H-bond energy and Psi twist angle criteria to assign secondary structure, while ChouFasman uses residue propensity, which is the percentage of residue in that percentage conformation. of all remainders in the same commit as the parameter to assign the secondary structure. In addition to hydrogen bonds, STRIDE also includes the backbone geometry in the form of dihedral angle inclinations. Their goal is to provide secondary structures that more closely match the assignment made by the experimenters who determined the structure of the protein. Also, it is assigned to the other secondary structures and the chou fasman depends entirely on the propensities of the amino acid residues that we observe the differences.Chau-Fasman method also fails to identify other parameters like protien folding and hydrophobicity between different proteins.he Chou-Fasman method is generally not able to be highly accurat