Instruction on how to submit a PDB pool

1- The PDB pool file should be saved as a ".txt" and the user needs to have access to the URL of the PDB pool (i.e. http://www.stat.tamu.edu/~madoliat/LagSVD/pdb-p.txt).
2- The line starts with `#` is considered as a remark line and it will not be interpreted by the LagSVD web-tool.
3- The colon symbol `:` is used for separation of the different fields.
4- Each row contains the information of an amino acid as follows:
    a. Protein name: is a consistent name used to indicate the protein name of the amino acids.
    b. Model: is set to be 1 in LagSVD v0.10.
    c. Chain: is set to be A in LagSVD v0.10.
    d. Number: indicates the position of the amino acid in the sequence (It should be right adjusted in a four characters word).
    e. Ins: can be filled by indicating the secondary structure.
        i. 0: α-helix 1:β-sheet 2: coil
    f. Type: three letters words for the amino acid.
    g. η (θ, ϕ, …): the first element of the pair of the dihedral/planar angles.
    h. ζ (τ, ψ, …): the second element of the pair of the dihedral/planar angles.