Homework(18.01.24/Tutorial - 1):

Write a program to compare a FASTA and a PDB to check whether they represent the same bio-molecule or not. The name of the FASTA and PDB will be given input as command line arguments. The output of your program should be as described below.

Make your program robust enough to handle the following five sample test cases. Necessary PDBs and FASTAs can be downloaded from: RCSB(https://www.rcsb.org/). Your program will be tested against 10 hidden test cases.

Sample test cases:

1. Input: python3 your_program.py 12as.fasta 12as.pdb
   Output: Same
2. python3 your_program.py 1a05.pdb 1a05.fasta
   Output: Same
3. python3 your_program.py 1a05.fasta 1a05.fasta
   Output: You have entered two FASTA files
4. python3 your_program.py 1a05.pdb 12as.pdb
   Output: You have entered two PDB files
5. python3 your_program.py 12as.fasta 1a05.pdb
   Output: Not Same

Sample code to traverse a PDB:

```
#Read the PBD
filename = "12as.pdb"
with open(filename) as f:
    lines = f.readlines()

#Only traverse the ATOM lines
atoms = [line for line in lines if line[0:4] == "ATOM"]

#Get the list of Residues
list_of_residues = [atom[17:20].strip() for atom in atoms]
print(f'List of residues: {list_of_residues}')

#Get the chains
chains = list(set([atom[21:22] for atom in atoms]))
print(f'Chains present in the PDB: {chains}')
```