Project-4

Create a PDB reader object by writing **class** to read PDB file and extract atomic coordinate of each protein and hetero (non-protein) atom. The accessible methods should be provided to find/compute:

a. Number of non-protein compounds/metals; *hetero()*
b. List of hetero residues names; *heteroNames()*
c. Details (Name, number of atoms) of a given hetero compound/metals; *heteroInfo('Name') Name of hetero residue*.
d. Atomic coordinates of a given heteroatom; *heteroCord('Name')*
e. Atomic coordinate of all protein atoms; *atomCord(i)*

Using the above object and methods to find heteroatom with the maximum number of atoms and find residues surrounding it using the following criterion given below.

- Two atoms are said to be interacting if distance between two atoms is within 5 Å.