1. Given the structural coordinates (X, Y, Z in Angstroms, see highlighted bold font for atom 1) from a PDB file of SPERM WHALE MYOGLOBIN (*pdb code: 102M*) below:

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ATOM      1  N   MET A   0      24.512   8.259  -9.688  1.00 33.83           N
ATOM      2  CA  MET A   0      24.523   9.740  -9.865  1.00 32.90           C
ATOM      3  C   MET A   0      25.889  10.228 -10.330  1.00 31.90           C
ATOM      4  O   MET A   0      26.886   9.516 -10.198  1.00 32.07           O
ATOM      5  CB  MET A   0      24.143  10.414  -8.560  1.00 34.34           C
ATOM      6  CG  MET A   0      24.891   9.880  -7.378  1.00 35.66           C
ATOM      7  SD  MET A   0      24.111  10.428  -5.871  1.00 38.66           S
ATOM      8  CE  MET A   0      24.454  12.221  -5.988  1.00 36.36           C
ATOM      9  N   VAL A   1      25.922  11.435 -10.891  1.00 30.10           N
ATOM     10  CA  VAL A   1      27.161  12.020 -11.393  1.00 27.92           C
ATOM     11  C   VAL A   1      27.260  13.522 -11.114  1.00 26.21           C
ATOM     12  O   VAL A   1      26.304  14.278 -11.304  1.00 26.54           O
ATOM     13  CB  VAL A   1      27.312  11.769 -12.919  1.00 27.99           C
ATOM     14  CG1 VAL A   1      28.557  12.455 -13.466  1.00 27.68           C
ATOM     15  CG2 VAL A   1      27.395  10.282 -13.189  1.00 28.05           C
ATOM     16  N   LEU A   2      28.407  13.938 -10.599  1.00 23.68           N
ATOM     17  CA  LEU A   2      28.641  15.349 -10.324  1.00 20.97           C
ATOM     18  C   LEU A   2      29.285  15.976 -11.549  1.00 19.50           C
ATOM     19  O   LEU A   2      29.976  15.300 -12.306  1.00 18.60           O
ATOM     20  CB  LEU A   2      29.602  15.516  -9.142  1.00 20.07           C
ATOM     21  CG  LEU A   2      29.003  15.462  -7.742  1.00 19.76           C
ATOM     22  CD1 LEU A   2      28.734  14.017  -7.356  1.00 18.96           C
ATOM     23  CD2 LEU A   2      29.966  16.142  -6.762  1.00 18.40           C
ATOM     24  N   SER A   3      29.056  17.260 -11.759  1.00 18.20           N
ATOM     25  CA  SER A   3      29.690  17.929 -12.882  1.00 17.70           C
ATOM     26  C   SER A   3      31.086  18.341 -12.420  1.00 17.23           C
ATOM     27  O   SER A   3      31.404  18.261 -11.230  1.00 16.47           O
ATOM     28  CB  SER A   3      28.882  19.155 -13.301  1.00 17.59           C
ATOM     29  OG  SER A   3      28.766  20.060 -12.225  1.00 17.97           O
ATOM     30  N   GLU A   4      31.935  18.742 -13.356  1.00 11.50           N
ATOM     31  CA  GLU A   4      33.283  19.175 -13.008  1.00 13.15           C
ATOM     32  C   GLU A   4      33.188  20.387 -12.086  1.00 16.93           C
ATOM     33  O   GLU A   4      33.964  20.514 -11.147  1.00 15.15           O
ATOM     34  CB  GLU A   4      34.074  19.549 -14.275  1.00 17.13           C
ATOM     35  CG  GLU A   4      35.473  20.111 -14.013  1.00 17.78           C
ATOM     36  CD  GLU A   4      36.414  19.122 -13.332  1.00 19.05           C
ATOM     37  OE1 GLU A   4      36.132  17.911 -13.343  1.00 29.34           O
ATOM     38  OE2 GLU A   4      37.452  19.559 -12.792  1.00 24.04           O
ATOM     39  N   GLY A   5      32.218  21.261 -12.358  1.00 13.76           N
ATOM     40  CA  GLY A   5      32.027  22.458 -11.553  1.00 13.72           C
ATOM     41  C   GLY A   5      31.722  22.137 -10.101  1.00 13.60           C
ATOM     42  O   GLY A   5      32.186  22.833  -9.197  1.00 13.74           O

ATOM   1207  N   GLN A 152      24.446  -4.753   3.940  1.00 34.79           N
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ATOM   1208  CA  GLN A 152      23.530  -3.665   3.569  1.00 37.20           C
ATOM   1209  C   GLN A 152      22.709  -3.098   4.737  1.00 38.24           C
ATOM   1210  O   GLN A 152      21.671  -2.466   4.532  1.00 38.67           O
ATOM   1211  CB  GLN A 152      22.597  -4.059   2.422  1.00 38.53           C
ATOM   1212  CG  GLN A 152      22.461  -2.974   1.348  1.00 47.32           C
ATOM   1213  CD  GLN A 152      22.386  -1.558   1.909  1.00 53.70           C
ATOM   1214  OE1 GLN A 152      23.408  -0.957   2.246  1.00 62.61           O
ATOM   1215  NE2 GLN A 152      21.174  -1.020   2.010  1.00 72.20           N
ATOM   1216  N   GLY A 153      23.174  -3.342   5.957  1.00 39.00           N
ATOM   1217  CA  GLY A 153      22.479  -2.839   7.122  1.00 40.00           C
ATOM   1218  C   GLY A 153      22.703  -1.350   7.301  1.00 40.37           C
ATOM   1219  O   GLY A 153      22.020  -0.745   8.154  1.00 40.86           O
ATOM   1220  OXT GLY A 153      23.555  -0.774   6.580  1.00 40.85           O
TER    1221      GLY A 153
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calculate the following:

a) End to End distance in the chain, *i.e.* residue 1 to 153
b) Distance between C-Alpha atoms of adjacent amino acids, calculate at least three to see variations
c) Dihedral angles: phi, psi and omega. Plot these in Ramachandran map to see their secondary structure.
d) Distance between hydrogen bond donor and acceptor

2. Write a mathematical equation to trace the path of helix
3. Trace the C-alpha backbone in a folded protein and an unstructured protein using the following PDB codes: 1BTA and 1B7D
4. Compare the structure of two proteins with PDB codes 1BTA and 1ADN and compute their RMSD
5. Why are non-polar amino acid residues like Ile, Leu, Val, Trp, Phe buried inside the protein interior while charged groups like Lys, Glu are exposed to solvent on the surface?
6. Explain KEY non-covalent interactions that play a role in folding a protein in ana aqueous medium
7. What is the volume occupied by 1 gram of the protein? Calculate this for multiple proteins and compare the values? What name is given to this volume parameter?
8. What are INTRINSICALLY DISORDERED proteins? How are they different from normal folded globular proteins in terms of structure and function?