PROTEIN STRUCTURE VISUALIZATION

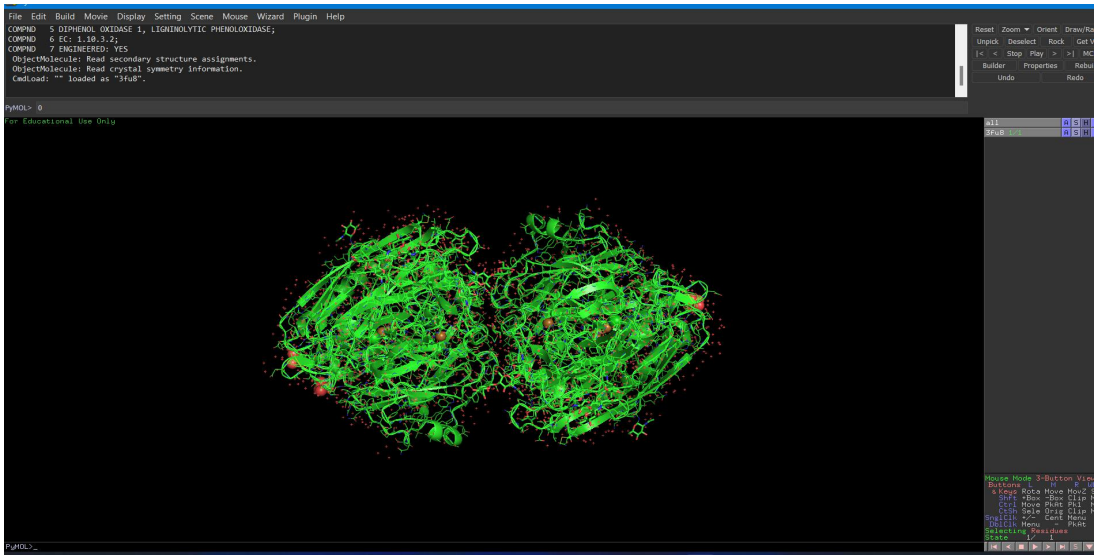
INTRODUCTION:

The main feature of computer visualization programs is interactivity, which allows users to visually manipulate the structural images through a graphical user interface. At the touch of a mouse button, a user can move, rotate, and zoom an atomic model on a computer screen in real time, or examine any portion of the structure in great detail, as well as draw it in various forms in different colours. Further manipulations can include changing the conformation of a structure by protein modelling or matching a ligand to an enzyme active site through docking exercises.
Because a Protein Data Bank (PDB) data file for a protein structure contains only x, y, and z coordinates of atoms, the most basic requirement for a visualization program is to build connectivity between atoms to make a view of a molecule.

Protein Structure:

Protein structure is the three-dimensional arrangement of atoms in an amino acid-chain molecule. Proteins are polymers – specifically polypeptides – formed from sequences of amino acids, the monomers of the polymer. A single amino acid monomer may also be called a residue indicating a repeating unit of a polymer. Most generally used visualization software's include: PYMOL, RASMOL, JMOL etc. Here we are using PYMOL software to visualize the structure of protein called:

3fu8
COMPND 5 DIPHENOL OXIDASE 1, LIGNINOLYTIC PHENOLOXIDASE;
COMPND 6 EC: 1.10.3.2;
COMPND 7 ENGINEERED: YES
ObjectMolecule: Read secondary structure assignments.
ObjectMolecule: Read crystal symmetry information.
CmdLoad: "" loaded as "3fu8". RIBBON REPRESENTATION



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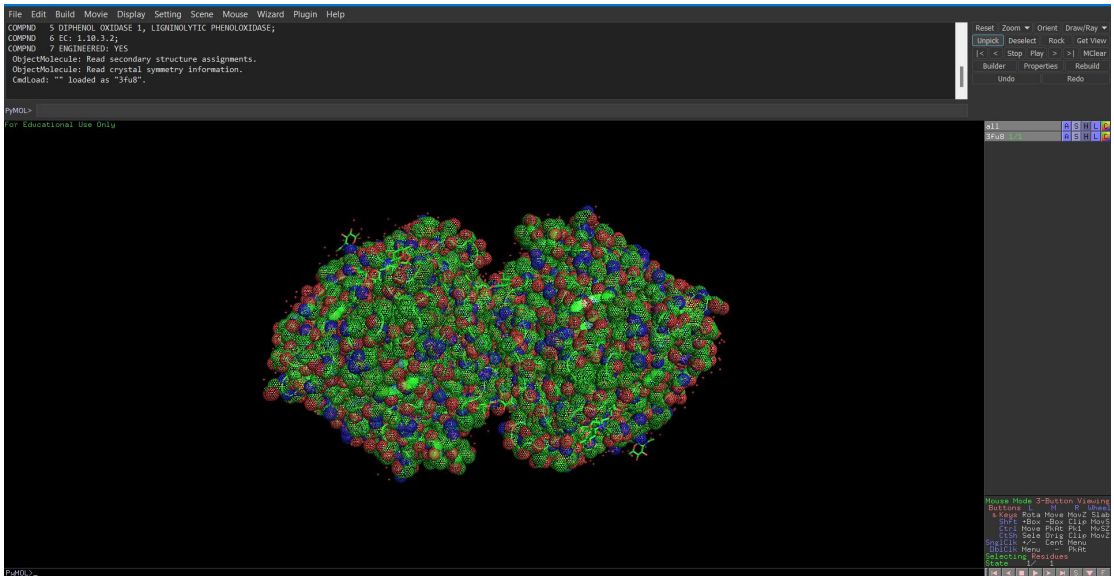
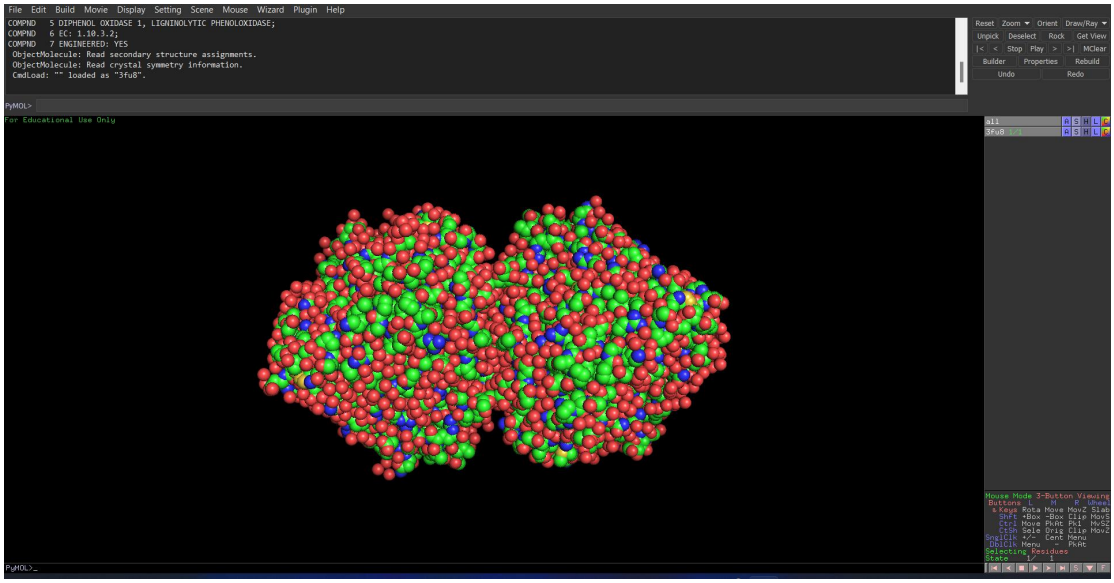
DOT REPRESENTATION



SPHERE REPRESENTATION



MESH REPRESENTATION

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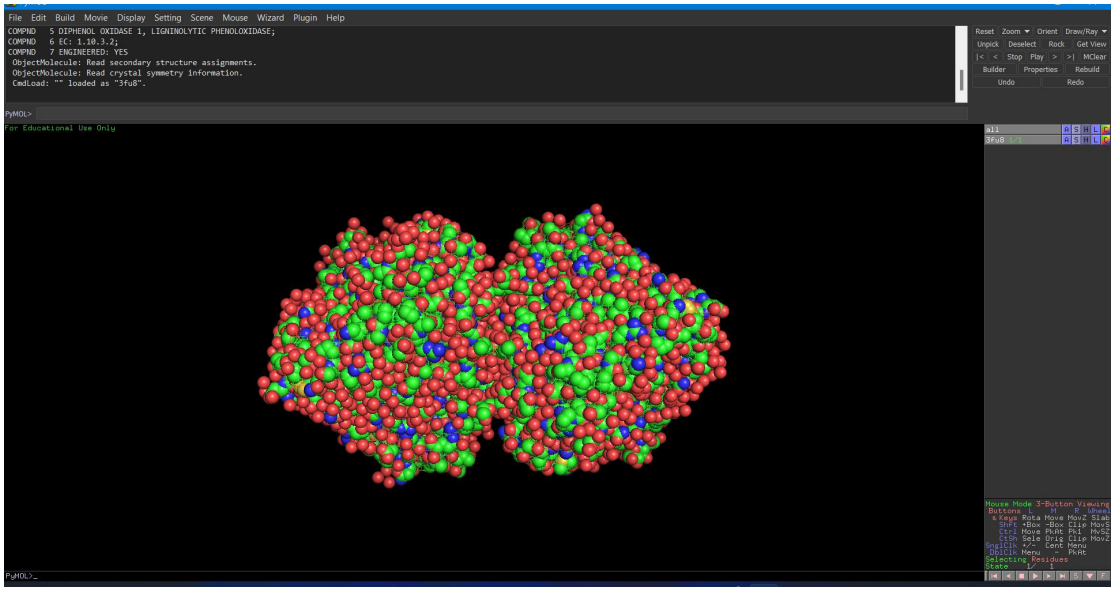
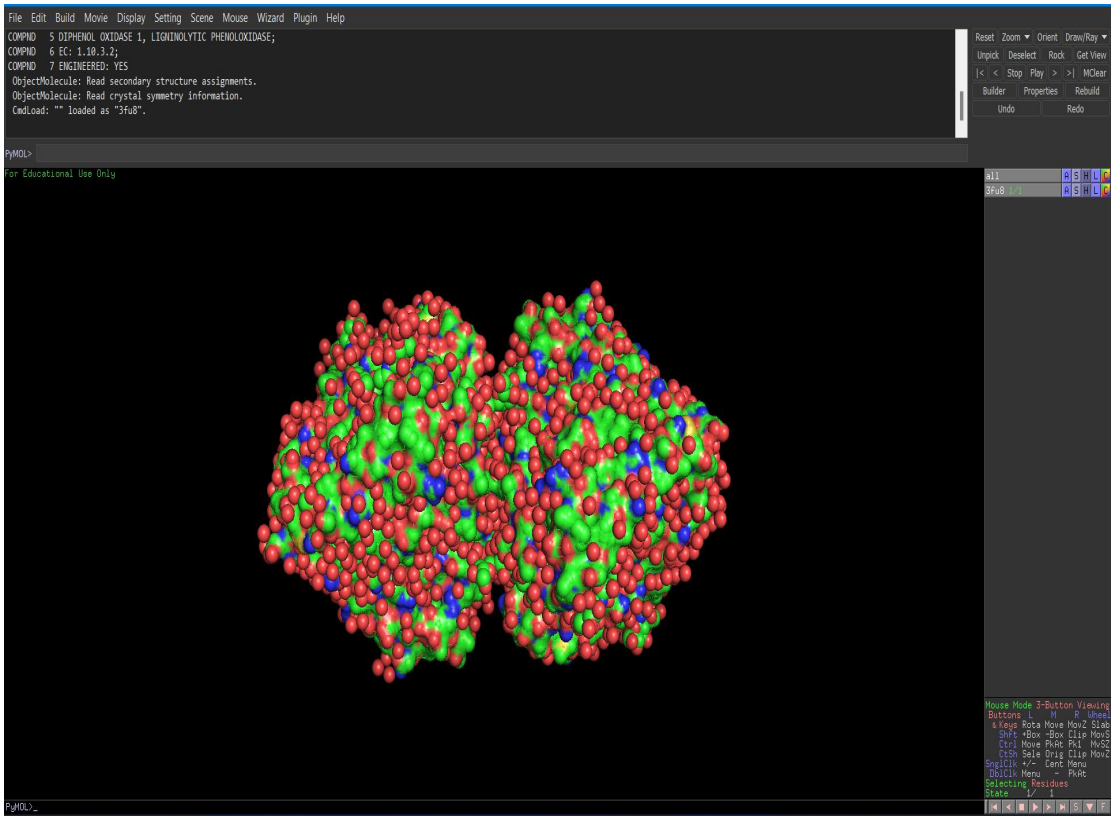
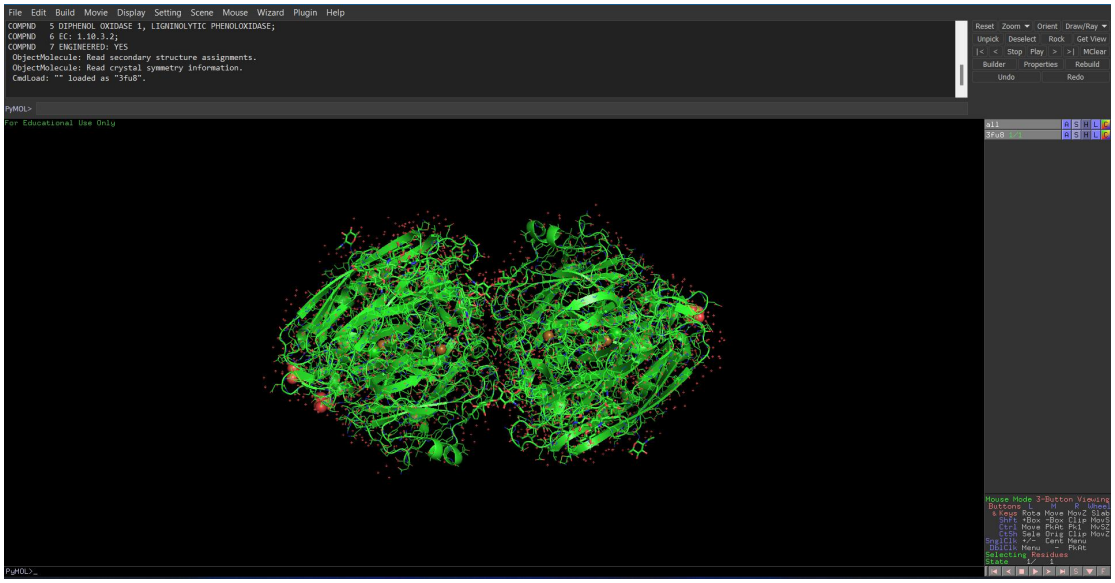


SURFACE REPRESNTATION



WIRE REPRESENTATION



CONCLUSION:
The crystal structure of 3fu8
visualized using PYMOL software. we have observed ribbon,dot , sphere ,mesh,surface, wire representation of protein