Exp 4. Protein Data Bases, Finding and Viewing

Introduction

Here are lots of protein structures information in data base.

Methods

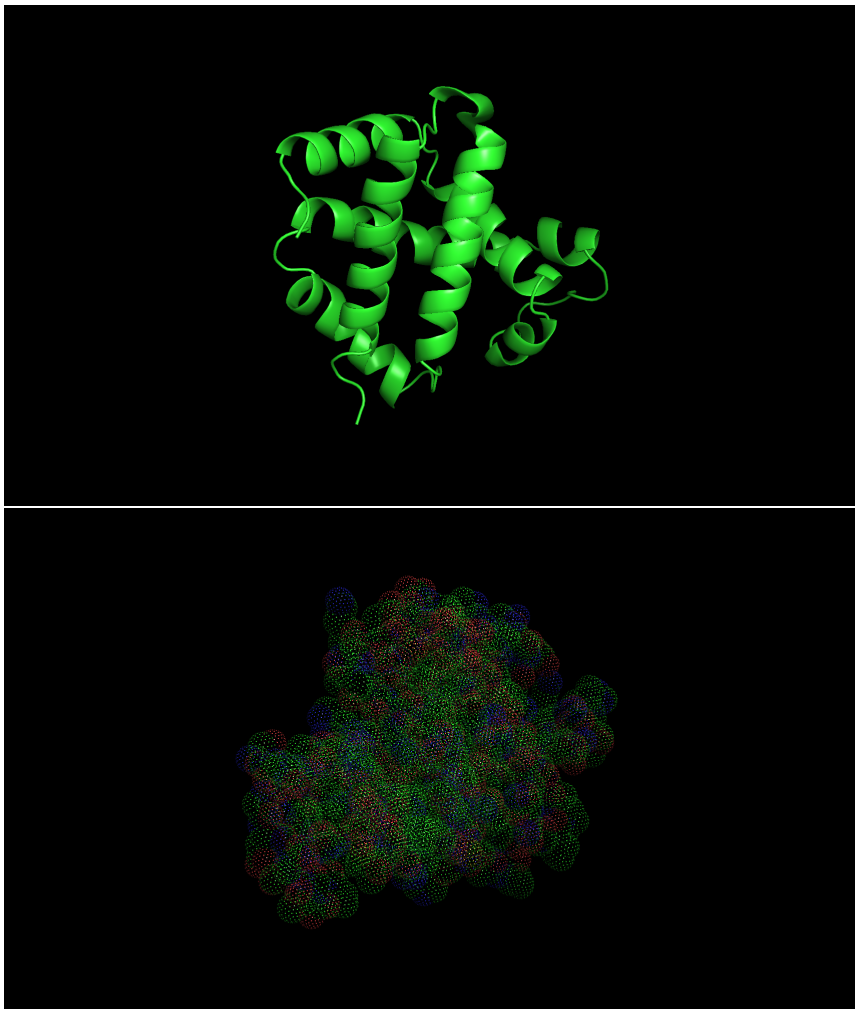
1. Find the PDB ID of human hemoglobin, whose resolution is higher than 2 A.
2. Download the PDB coordinate file and check the detailed information in the file. Find out:

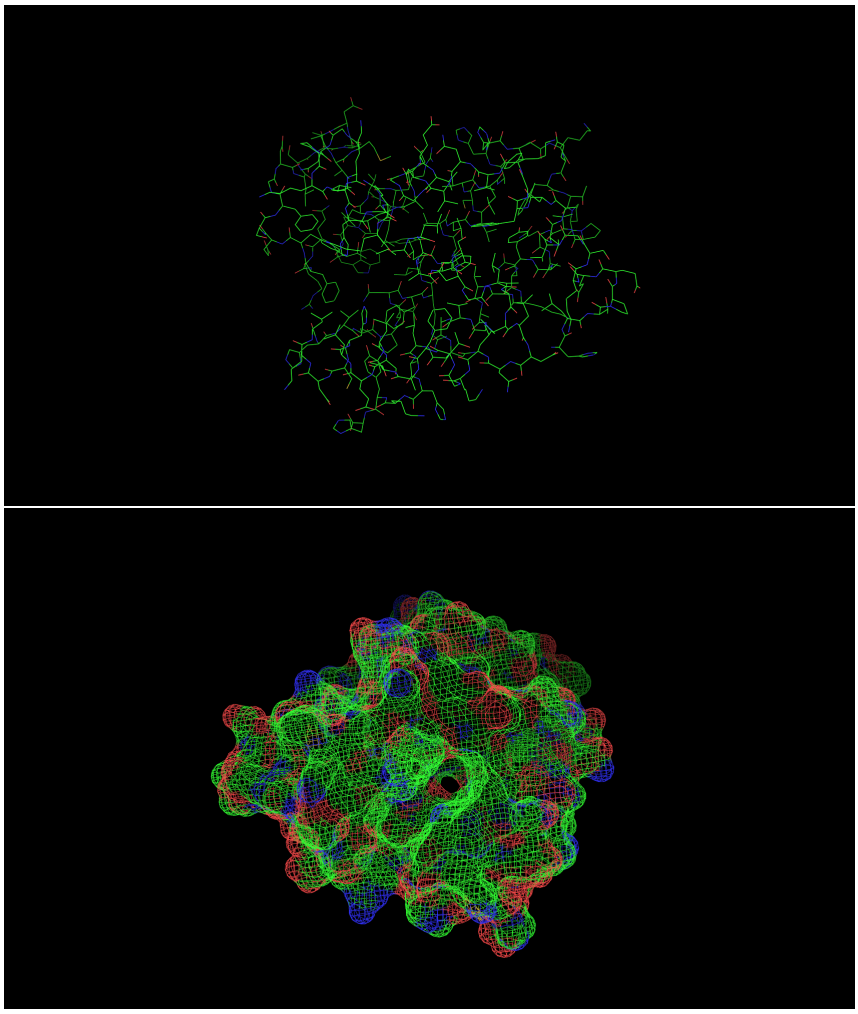
- How many protein chains? Which compounds in structures?
- Which compounds in structures?
- Which residues are missed in the coordinate?

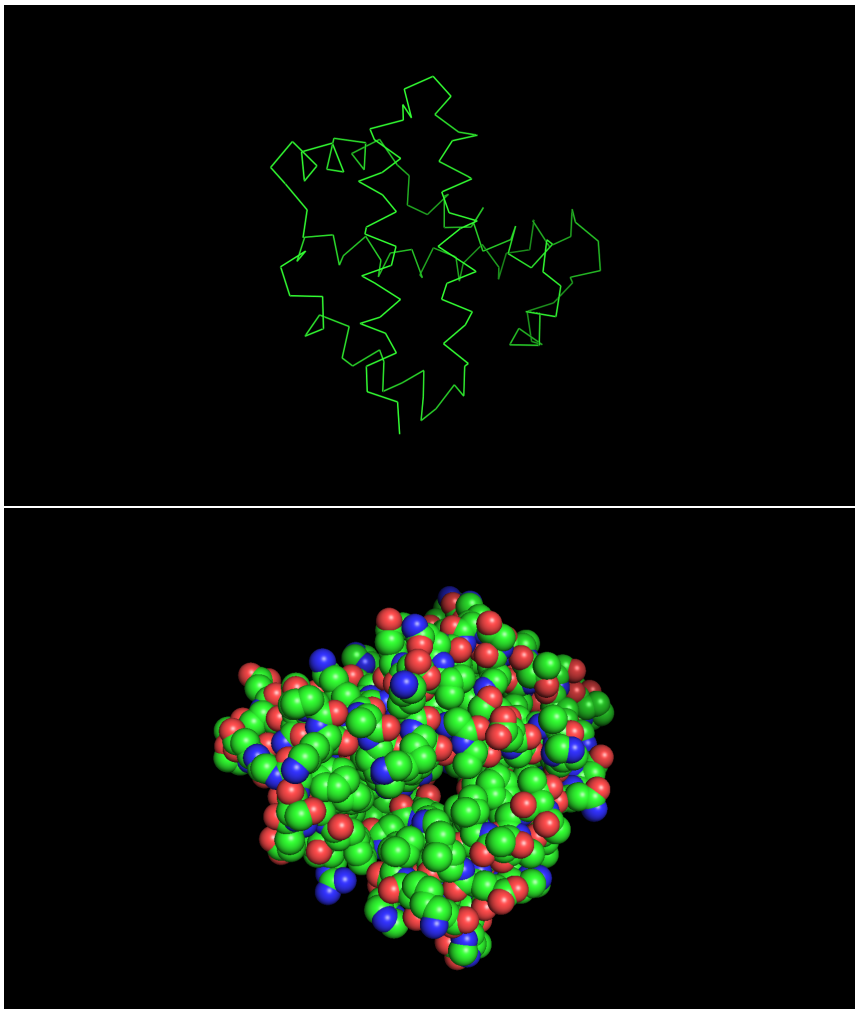
3. Edit the coordinate file to make a new coordinate file that contain only one beta subunti of hemoglobin(beta-globin). Delet the atom postion of chain A,C,D, and HETAT HOH and HEM
4. Using PyMol to visualize the beta-globin structures in different viewing. Then save the result as pictures.

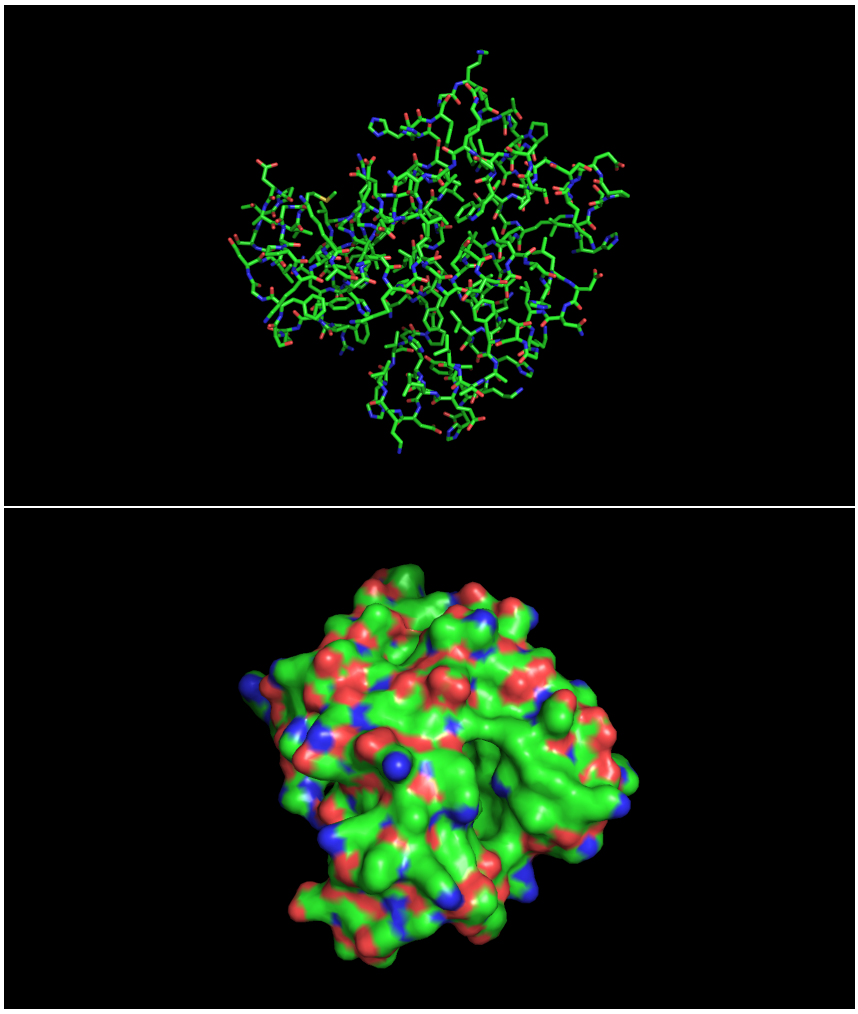
Results

1. The Human Hemoglobin PDB ID is 1A3N. 1A3N's resolution is 1.80 ANGSTROMS, has 574 residues, related in 4/29/1998.
2. 1A3N has 4 chains, 2 alpha chains and 2 beta chains. Each chain contains one HEM cofactor HEM PROTOPORPHYRIN IX CONTAINING FE. and 450 Water molecure. And the first amino acid VAL in chain D is missed.
3. The file name is 1A3N_beta.pdb

4. 







Conclusion PyMOL is a big and interactive draft paper for studying structure biology.