# Using ChimeraX to visualise structures

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*AlphaFold & beyond 2025, IFB*

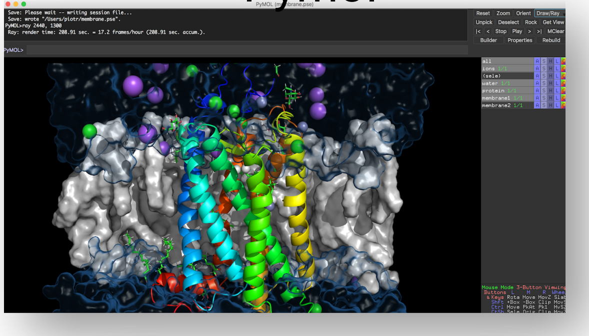
# Protein viewers

## Free Protein viewers

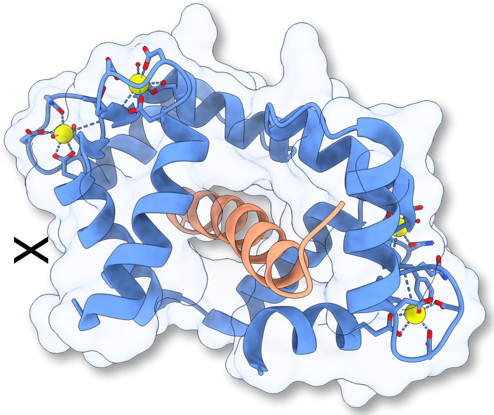
Standalone softwares

- ○ Pymol (educational version free, or open source version)
- ○ VMD
- ○ UnityMol
- ○ **ChimeraX**

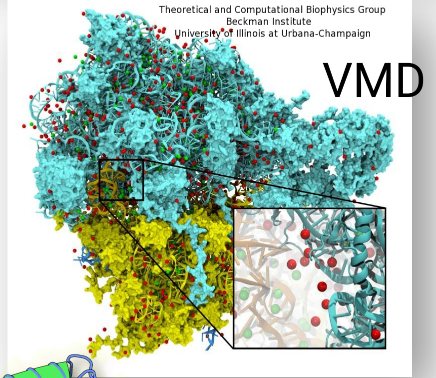
- Web based
  - ○ 3DProteinImaging
  - ○ Molstar
  - ○ NGLViewer



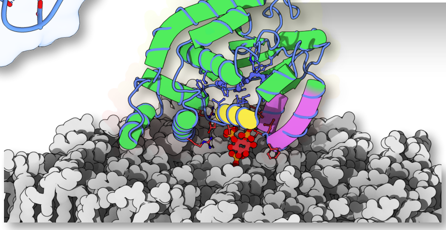
Pymol



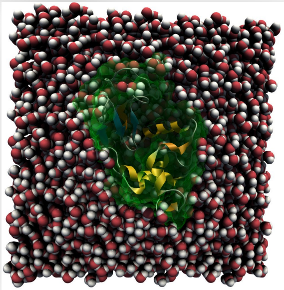
Chimera X



VMD



https://3dproteinimaging.com/



Unitymol

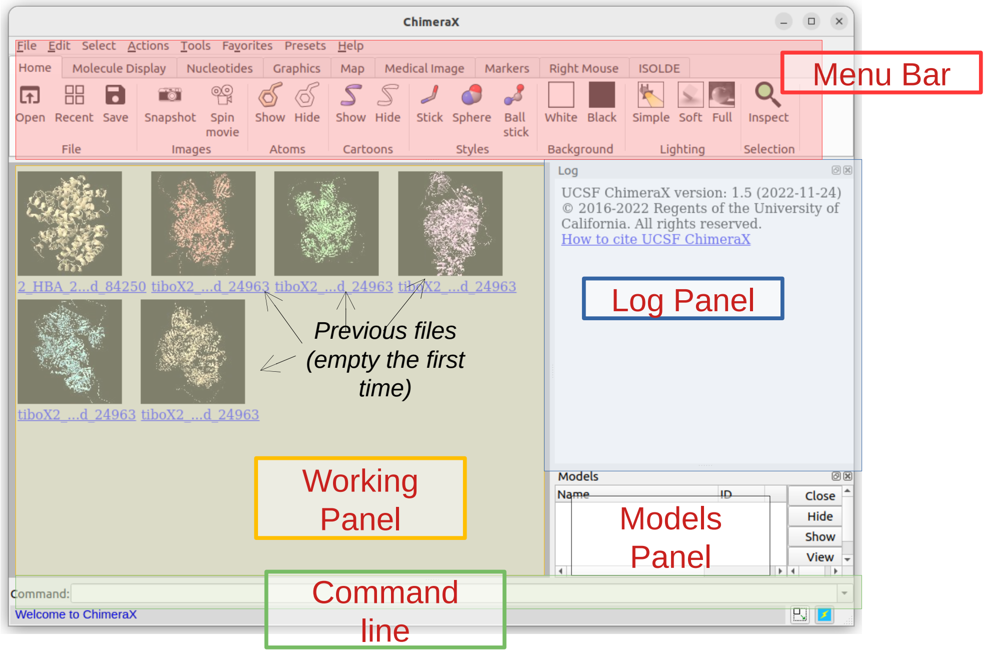
# Why ChimeraX?

ChimeraX is the new version of USCFChimera and is **free** (for academics) and available on every platform.

- Optimized for CryoEM data and large systems as well.
- No ray tracing engine, but can generate smooth images.
- **Interactive viewing of AlphaFold outputs**

# A (very) quick overview

Window



UCSF ChimeraX version: 1.5 (2022-11-24)
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How to cite UCSF ChimeraX

Welcome to ChimeraX

Menu Bar

Log Panel

*Previous files (empty the first time)*

Working Panel

Models Panel

Command line

ChimeraX interface is very modular : several detachable panels

**Today's practical :**

- load a structure
- learn how to change texture
- learn how to move & rotate
- learn how to explore AF outputs

**Practice makes perfect!**