

# Visualization of protein structures with Chimera

Miguel Andrade

Faculty of Biology,

Institute of Organismic and Molecular Evolution

Johannes Gutenberg University

Mainz, Germany

[andrade@uni-mainz.de](mailto:andrade@uni-mainz.de)

# Chimera

# Chimera 1/3

## Start Chimera

Open Chimera from desktop (ZDV app)

**(not** ChimeraX)

(If there is an update it will take a minute or two)

## Open a 3D structure by PDB id:

Try 3PZD

This is human myosin X (chain A) in complex with a peptide (chain B)

Go to File > Fetch by ID > PDB

Type 3pzd in the window

## **Removing a structure**

At the main menu go to  
File > Close session

Then you can start again with the next structure  
(otherwise structures are added)

# Open again 3PZD

## Viewing a structure

Click mouse left button and slide to rotate.

Click right button and slide to zoom in and out (or use your mouse wheel)

Pause pointer on a residue to see number and chain  
This indicates amino acid, number and chain. (e.g.  
GLN1511.A)

Find residue 1723 in chain A.

Which type of amino acid is it?

What is the secondary structure conformation of this residue?

## **Viewing a structure**

These are fragments: the numbers correspond to the positions in the complete proteins.

Note the gaps, e.g. between positions 1963-1967 of chain A.

**What do these gaps mean?**

Note that there is a molecule represented, which is not a protein. That molecule is glycerol.

## Selecting

Ctrl and click to select a single residue

Menu Select > Chain > to select a whole chain

Select chain B. What is the most abundant secondary structure for this chain?

Select > zone > (try a distance range < 5A)

If a residue or atom is selected: arrow up selects its secondary structure element, up again selects chain, up again selects all chains. Arrow down goes back.

Left/right arrows inverts selection.

## **Selecting by residue number**

Select > Atom specifier >

This opens a little window where you can type ranges.

Examples:

:1510-1520.a

(Hint: Type Apply and not OK to keep the window open)

Selects residues 1510 to 1520 in chain A

:1425-1434.b

Selects residues 1425 to 1434 in chain B

## **Focusing**

Select a residue (Ctrl + click)

Actions > Focus

This will close the view on the selection

Get back to the original view by selecting the whole molecule (arrow up) and doing again:

Actions > Focus

Try this again with a selection of a protein fragment.  
The view will focus on the selected fragment.

## **Set pivot**

Select a residue

Actions > Set pivot

This will make the rotation center on the selection

## Try these steps on the molecule of glycerol

First, select the complete molecule of glycerol by Ctrl+click on it and hit arrow-up once.

Then, you can see which residues are close to the molecule of glycerol:

Select > zone >

Then specify in the window that appears: select all atoms at <5.0 angstroms from the selection

How many residues are at less than 5.0 angstroms from the glycerol molecule?

Is there a cysteine among those? Which residue number?

## Measuring distances

Keep the focus on the molecule of glycerol. We can measure how far from it are the atoms of the side chains of the residues around it.

Tools > Structure analysis > distances

To define a distance, select one atom in the glycerol with Ctrl+click and a second in a side chain of an amino acid in the protein with Shift+Ctrl+click. Then press the button “Create” in the small window.

What is the closest distance of an oxygen of the glycerol to the sulfur of cysteine 1706?

To get back select all (arrow up) then  
Actions > Focus

## Colouring a peptide chain

Select chain B

Select > chain > B

Actions > color > red

## Changing representation

Default is ribbon

Try other things:

Actions > Atom/Bonds > Show

Actions > Atom/Bonds > stick

You can hide the ribbon of the (selected) chain B.

Actions > Ribbon > hide

Represent the glycerol as spheres.

How can you use representation to check if the glycerol is exposed to the solvent or not? What is the result?

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## **Close session and load 3PQR**

This is rhodopsin, a transmembrane protein  
Let's find the hydrophobic part of the protein

## **Color residues by property**

First select: Select > Residue > amino acid category  
> hydrophobic

Then color:

Actions > colour > blue

## **Generate a surface**

Select > chain > A

Actions > surface > show

# Chimera 3/3

## **Close session and load 1GLU**

This is the glucocorticoid receptor dimer bound to DNA  
Let's find out if the interface of interaction with DNA  
has positively charged amino acids

### **Color residues by property**

First select: Select > Residue > Amino acid category > positive

Then color: Actions > Color > blue  
(Also color negative residues red)

# Chimera 3/3

## **Generate the surface of the protein dimer**

(This will not work well with the DNA – we remove the DNA first)

Select the DNA chains and then delete them:

Actions > Atoms/Bonds > Delete

(This cannot be undone!)

Now we do the surface:

Actions > Surface > Show

## **How to get back the DNA?**

Fetch again 1GLU without closing the session  
(the new molecule will be overlapped)