Chimera: Visualization and Analysis

For all aspects discussed in this document, we will focus on GUI elements for ease of use. Please not that command line options for the respective elements exist but we will not discuss these any further.

# Opening and saving files

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Door AI gegenereerde inhoud is mogelijk onjuist.There are two ways to open PDB files:

1. **File > Open…**  
   This requires to have an actual file saved locally on your desktop
2. **Afbeelding met tekst, schermopname, nummer, scherm

   Door AI gegenereerde inhoud is mogelijk onjuist.File > Fetch by ID…**  
   This is a very convenient way to open PDB files. In the following window you can select specific structures from various databases by their respective identifier. For PDB structures, this refers to 4 character code available on the PDB website.

If you have performed your operations with your PDB, you can save a version of the structure in your current workspace through ‘**File > Save PDB…**’ . This will only save the coordinates of the structure. If you want to save your entire analysis you are better of saving your current workspace through ‘**File > Save Session As…**’. This will save the structures but also performed analysis (e.g. measured bond lengths or angles) in a .py file which can be read by Chimera to start again where you left of.

Let us continue by focusing on PDB 5Q0J:

* **File > Fetch by ID…**
* Make sure ‘PDB’ is selected and **enter 5Q0J**
* Click ‘**Fetch**’ or simply **press Enter**

# Viewing and analyzing molecular structures

After opening PDB 5Q0J, you will notice two distinct protein assemblies:

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On the PDB website you can find more information about the Asymmetric unit and Biological assembly. Only for X-ray diffraction structures can the biological assembly and asymmetric unit differ. In this particular case, Chimera loads the asymmetric unit which consists of 2 biological assemblies.

General navigation in the molecular viewer is performed with the mouse:

1. **Clicking and holding left mouse button** allows to rotate the molecule around a specified pivot point.
2. **Clicking and holding center mouse button** (scroll wheel) allows to move the molecule.
3. **Clicking and holding the right mouse button** allows to zoom in or out. This can also be done with the scroll wheel.

## Afbeelding met tekst, schermopname, Lettertype, nummer Door AI gegenereerde inhoud is mogelijk onjuist.The “Model Panel”

The “Model Panel” is a very useful tool, especially if you loaded multiple structures. You can acces the model panel via **Favorites > Model Panel** or **Tools > General > Model Panel**.

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Door AI gegenereerde inhoud is mogelijk onjuist.The “**Active**” property allows you to activate or deactivate specific models. If you deactivate a model, all motions performed in the viewer will not apply to the deactivated model(s). This allows different models to move relative to each other.

The “**Shown**” property indicates whether or not a model is currently visible in the viewer.

On the right hand side is a column with specific actions that can be performed for each model or a selection of models

## Afbeelding met tekst, elektronica, schermopname, software Door AI gegenereerde inhoud is mogelijk onjuist.“Select” menu

The “Select" menu is a very versatile and useful menu. This allows you to carefully select individual residues or multiple. The ‘**Residue’** subsection is very convenient: this allows you to select specific residues based on the residue name in the PDB. Selecting e.g. ‘ALA’ residues will select all alanine residues in the PDB.

If you have selected ‘ALA’ and you click ‘**Invert (all models)**’ you will select everything except the previously selected alanine residues. (‘Invert (selected model) has the same functionality but limits the possible selection to the models that are selected if you have loaded multiple structures in the current workspace.)

‘**Clear Selection**’ removes any current selection.

You can also select in the viewer:

1. Individual atoms (or bonds) can be selected by **pressing and holding Ctrl** and clicking on the specified object with your **left mouse button**. The selection can be expanded if you additionally **press and** **hold Shift**.
2. If you **press and hold Ctrl**, you can also **click and drag with your left mouse button** to select a specific zone. The zone can also be expanded by additionally **pressing and holding Shift** and selecting another zone.

## Afbeelding met tekst, schermopname, nummer, Lettertype Door AI gegenereerde inhoud is mogelijk onjuist.“Action” menu

The “Action” menu is your “bread and butter” when it comes to manipulating the representation of your loaded structure.

**Atoms/Bonds** allows to change the representation of atoms and bonds. Additionally, you can hide and/or delete selected atoms and bonds.

**Ribbon** allows to modify the aspects of the “cartoon” representation.

**Surface** allows to generate and modify generated molecular surfaces.

**Focus** is very useful because it does a few things simultaneously: 1) zooms in on the current selection, 2) sets the pivot point according to current selection and 3) applies depth cueing to clearly show the selected structure.

**Set Pivot** changes the current pivot point to match the current selection. This will change how to molecule is rotated in the viewer. This can also be done manually in the viewer by pressing and holding Ctrl and clicking with the right mouse button where you want to set the pivot point.

## “Tools” menu

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Door AI gegenereerde inhoud is mogelijk onjuist.The “**Tools**” menu contains a very large number of options to analyze your structure or actions to perform with your structure. Here we will focus on two things: analysis of structural parameters (bond lengths, bond angles and dihedrals) and alignment of structures (see further).

**Tools > Structure Analysis > Distances** will open the window to analyze bonded parameters. Angles and torsions (also known as dihedral angles) are available in a different tab. Hence, **Tools >** **Structure Analysis > Angles/Torsions** will open the same window, but in the respective tab.

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You can analyze specific bonds by selecting two atoms and clicking “Create” in the Distances tab. Similarly, you can analyze angles and dihedral angles after selecting respectively three and four atoms and clicking “Create” in the Angles/Torsions tab.

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# Visualization of biomolecules

## The “Sequence” viewer

Accessible through the “Tools” menu via **Tools > Sequence > Sequence**, the Sequence viewer is very useful for biological molecules, e.g nucleic acids or proteins.

It is very useful to quickly identify and/or select particular residues. Additionally, you secondary structural elements are also indicated for respective residues if applicable.

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## Alignment of proteins

Alignment of proteins is also performed via the “Tools” menu. Let us **open PDB 5Q13**.

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You will immediately notice the similarity between 5Q0J and 5Q13. They are structures of the same protein, but with different ligands. However, we need to properly overlay these structures if we want so study these differences more closely. This is done by ‘aligning’ the structures. Chimera has built-in algorithms that find identical stretches of residues and aligns the structures based on these identical residues. To access this tool, we go to **Tools > Structure Comparison > MatchMaker**.

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Door AI gegenereerde inhoud is mogelijk onjuist.In the MatchMaker window, you first need to define a reference structure and structures to match that reference. Typically, the default settings for all other settings should suffice, but if required you could finetune the matching to provide better results.

After aligning both models, you will notice that only one the biological units will be aligned. This is caused by differences in the asymmetric unit, i.e. a rotation of the second biological unit. You can try to align both monomers simultaneously by changing the reference chain of chain to match but you will notice that this is not possible. The algorithms in MatchMaker will only work for biological molecules, i.e. proteins and nucleic acids. For small molecules, you need to use the command line but this is beyond the scope of these instructions.

### RMSD

After each alignment, you will notice a message appearing in the bottom left corner of the Chimera window:



This message can also be found in the “**Reply Log**” (**Favorites > Reply Log** or **Tools > Utilities > Reply Log**)

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The abbreviation RMSD stands for “Root Mean Squared Deviation” and is a measure of spatial similarity between the matched atom pairs. Technically, the RMSD between atoms is calculated by the following formula:

Where *N* is the number of matched atoms and *δ* is the distance between the matched atoms in each model. In Cartesian coordinates, *δ* for a given atom pair can be simply calculated through their respective coordinates:

# Modifying molecular structures

## Modifying molecules

Via **Tools > Structure Editing > Adjust Torsion** you can open up a window that allows to modify structures. Opening the window this way, you end up in the “Adjust Torsions” tab where you can change dihedral angle values. You simply have to select a rotatable bond and click “Activate”. This will allow you to change the value of the dihedral angle over the selected bond, both numerically or through a little rotatable wheel.

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Door AI gegenereerde inhoud is mogelijk onjuist.This window, however, allows you to change more than just dihedral angles.

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“**Start Structure**” allows to build new molecules (see further).

“**Modify Structure**” allows to change selected atoms to different atoms, but also to different geometries. Be careful that the atom you are modifying does not have a number of bonds larger than suitable for the geometry you select.

Similarly to “Adjust Torsions”, “**Adjust Bonds**” and “**Adjust Bond Angles**” allows to modify bond lengths and bond angles respectively. This only works for bonded parameters. (As opposed to the analysis measurements which can also be applied to non-bonded atoms.)

“**Join Models**” is particularly useful when building more complicated molecules as it allows to covalently link specific fragments.

## Building molecules

Building molecules can be performed from the same window in the “Start Structure” tab, or it can be opened directly via **Tools > Structure Editing > Build Structure**.

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Door AI gegenereerde inhoud is mogelijk onjuist.You have a lot of options to start from. The most easiest ones are to either start from “atom” or “fragment”. For the latter, Chimera contains a small library of cyclic fragments which you can use as a starting point. You can build multiple fragments, modify them and finally link them covalently through the “Join Models” tab.

Additionally, structures can be incorporated from biomolecule sequence or online database of small molecules PubChem.