**Examining Molecular Structures with Chimera**

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We will use UCSF Chimera to look at and contrast globular and non-globular protein modules. We will do it together with the trainer projecting on the screen.

**Question**: Who has used Chimera already?

**Useful links**

Chimera is free software for working with macromolecular structures. It has developed into the most advanced freely available software for this purpose. Note that a major revision, Chimera X, a major upgrade with a revised interface and gorgeous graphics will be released. You should install Chimera on your own computer! Available from [http://www.cgl.ucsf.edu/chimera/](https://www.google.com/url?q=http://www.cgl.ucsf.edu/chimera/&sa=D&ust=1511399501199000&usg=AFQjCNHpbdkVICaHhEn0l_eAw0lPf6mcaw)

User guide and tutorials are here. [http://www.cgl.ucsf.edu/chimera/current/docs/UsersGuide/](https://www.google.com/url?q=http://www.cgl.ucsf.edu/chimera/current/docs/UsersGuide/&sa=D&ust=1511399501200000&usg=AFQjCNFhFcLncimbMp9LqgeG3bYo64sptg)

The Protein Data Bank (PDB) structure database is here. [http://www.rcsb.org/pdb/home/home.do](https://www.google.com/url?q=http://www.rcsb.org/pdb/home/home.do&sa=D&ust=1511399501201000&usg=AFQjCNHrt7sSnnqgNZASGvYZxG64b52mqw)

The European version of the Protein Data Bank (PDBe) structure database is here.

[https://www.ebi.ac.uk/pdbe/](https://www.google.com/url?q=https://www.ebi.ac.uk/pdbe/&sa=D&ust=1511399501201000&usg=AFQjCNEzgpHsUxOz7bPKVxtCRT4NGfMr-Q)

**Molecular Structure Files**

**PDB format:** Venerable file structure used for decades. Has a fixed number of lines which can no longer handle very large macromolecular complexes, virus particles etc.

**MMCIF format:** The new file structure developed to handle very large macromolecular complexes. This format is not supported by older structural software.

**Key aims of the structure visualization exercises**

Learn to visualize interaction interfaces

Role of hydrogen bonds

Role of charged interactions

Role of hydrophobic interactions

Learn to superpose related structures

**Starting Chimera**

Locate and start Chimera which is installed on your computer with an icon on the desktop.

**Loading structures into Chimera**

There are several different ways of loading structures into Chimera. Two of these are:

.                Using the Chimera “File” menu to download a structure file from the internet with the Fetch by ID command. Do File-> Fetch by ID and then type 1DEV in the ID box with PDB selected. 1DEV will remotely download from the PDB database.

.                 Using the “File” menu to load a file you have downloaded locally: File->Open and then selecting the file you want to load into Chimera. (We won’t use this today.)

In this exercise we will work with several different PDB files:

[**1DEV.pdb**](https://www.google.com/url?q=http://www.ebi.ac.uk/pdbe-srv/view/entry/1dev&sa=D&ust=1511399501203000&usg=AFQjCNGce1NEAC6SX_p1m01dfhc7MVNfPw) is the SMD2 MH2 domain bound to a part of the SARA protein peptide interaction

**5ELQ.pdb** sorting nexin SNX27 PDZ domain bound to peptide

**5EM9.pdb** sorting nexin SNX27 PDZdomain bound to phosphopeptide

**[2AZE.pdb](https://www.google.com/url?q=http://www.ebi.ac.uk/pdbe-srv/view/entry/2aze&sa=D&ust=1511399501203000&usg=AFQjCNFRz5yK1L2Zl-nelKuSl229Tic-1A)** is a complex assembled from fragments of pRB/E2F1/DP1

[**2CCI.pdb**](https://www.google.com/url?q=http://www.rcsb.org/pdb/explore/explore.do?structureId%3D2cci&sa=D&ust=1511399501204000&usg=AFQjCNFRVNW04pEWzuvLvqZ7-Q7JKWCsmw) is a complex of CDK2, Cyclin A and a fragment of the CDC6 substrate

We want to learn about the interactions by visualizing the complexes in a few different ways, using ribbons, atoms, H-bonds, surfaces and transparency. We will do this together as it would be too complicated in the time available to follow written instructions.

Chimera has a huge menu system which is initially rather bewildering. We will only use a few commands, mainly listed here:

**Select Menu**: Select and deselect sections of structures. We need to use options

             - chain

             - clear selection

**Actions Menu**: Do things to the molecules. We need to use options

             - Focus: Centre the selected molecule

             - Atoms/Bonds

             - Ribbon

             - Surface

**Tools Menu**: Do many manipulations. We need to use options

* Structure Analysis > FindHbond: Show the Hydrogen bonds
* Structure Comparison > MatchMaker: superpose structures

**Model Panel**: Collection of commands for manipulating the molecules. We may need to use options

             - select

             - copy/combine

**Presets Menu**: useful views of the molecular system.

**Command line**: Used by advanced users for manipulating the structures.  We need to use one option

             - split