**Examining Molecular Structures with Chimera**

***Gibson team***

We will use 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. You should install Chimera on your own computer! It is available from <http://www.cgl.ucsf.edu/chimera/>

*Note*: The same authors have recently released ChimeraX. It has better graphics and the ability to manage larger structures, but it is still missing many features. We’ll use Chimera today, but you can explore ChimeraX for yourself at <https://www.rbvi.ucsf.edu/chimerax/>

User guide and tutorials are here: <http://www.cgl.ucsf.edu/chimera/current/docs/UsersGuide/>

The US version of the Protein Data Bank (PDB) structure database can be found at: <http://www.rcsb.org/pdb/home/home.do>

Its European counterpart, the Protein Data Bank (PDBe) structure database, is here:

<https://www.ebi.ac.uk/pdbe/>

### Starting Chimera

Locate and start Chimera, which should be installed on your computer. You can type chimera (in lower case) into the command line of a Terminal window and hit return.

### Loading structures

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

* Use the Chimera File menu to download a structure file from the internet with the Fetch by ID command. Select File → Fetch by ID and then type the PDB entry ID (e.g. 1YCR) in the ID box with PDB selected. The corresponding entry will remotely download from the PDB database.
* Use the File menu to load a file you have downloaded locally. Select File → Open and then choose the file you want to load into Chimera. (*We won’t use this today*)

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

* [1YCR.pdb](http://www.ebi.ac.uk/pdbe-srv/view/entry/1ycr/summary.html) is the MDM2-P53 peptide interaction
* [1RV1.pdb](http://www.ebi.ac.uk/pdbe-srv/view/entry/1rv1/summary.html) is the MDM2-Inhibitor complex

Here are other interesting structures that you could look at if time permits.

* [1DEV.pdb](http://www.ebi.ac.uk/pdbe-srv/view/entry/1dev) is the SMD2 MH2 domain bound to part of the SARA protein peptide
* [2AZE.pdb](http://www.ebi.ac.uk/pdbe-srv/view/entry/2aze) is a complex assembled from fragments of pRB/E2F1/DP1
* [2CCI.pdb](http://www.rcsb.org/pdb/explore/explore.do?structureId=2cci) is a complex of CDK2, Cyclin A and a fragment of the CDC6 substrate

### Visualizing structures

We want to learn about the interactions by visualizing the complexes in a few different ways, such as 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 *(center the selected molecule)*
* Atoms/Bonds
* Ribbon
* Surface
* Tools menu.: Do many manipulations. We need to use options:
* FindHbond *(show the hydrogen bonds)*
* 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