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Übung 1: UCSF Chimera

A Molecular Graphics Program

1. Einführung

Die folgende Übung soll Sie mit der Arbeit in *UCSF Chimera* (www.cgl.ucsf.edu/chimera/) vertraut machen. *UCSF Chimera* - im Folgenden einfach *Chimera* genannt - ist ein im Bereich der strukturellen Bioinformatik sehr beliebtes Programm zur interaktiven Visualisierung von Molekülen. Allerdings ist *Chimera* nicht nur zur Darstellung von Molekülen geeignet sondern bietet dank einer umfangreichen Sammlung integrierter Werkzeuge auch vielfältige Möglichkeiten zur Analyse und Modifikation molekularer Strukturen. Für die nächsten Übungen wird vorausgesetzt, dass Sie mit der Arbeit in *Chimera* vertraut sind.

2. Starten von Chimera:

Chimera lässt sich direkt über die Konsole starten. Geben Sie hierzu den folgenden Befehl in die Eingabeaufforderung ihrer Shell ein:

/usr/local/zbh/chimera/bin/chimera &

3. Das Chimera Tutorial:

Die Aufgabenzusammenstellung dieser Übung ist eine verkürzte Version des *Chimera*-Tutorials, welches Interessierte unter folgendem Link finden können:

http://www.cgl.ucsf.edu/chimera/docs/UsersGuide/indextut.html

The Getting Started Tutorial

This is a basic tutorial in two parts: command line and menu interface on the same set of operations. It covers the procedure for selecting atoms, bonds, and residues in a PDB file, and how to display molecular structure in different ways.

Downloading PDB Files:

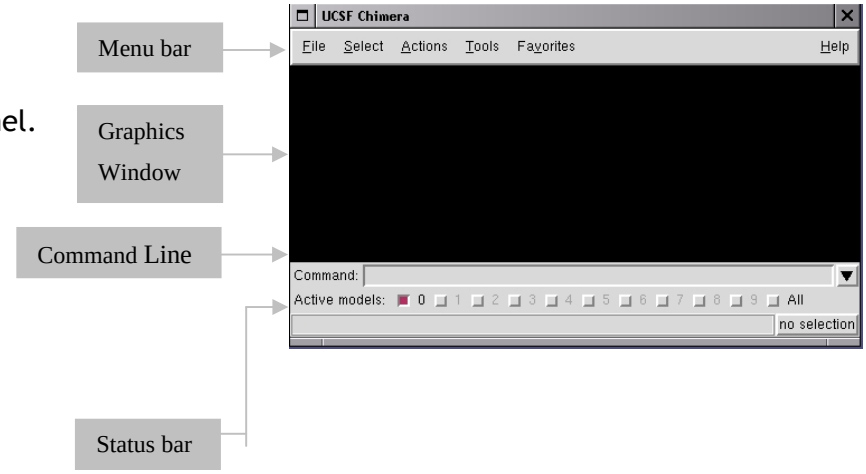
Chimera can retrieve PDB files from the Protein Data Bank via the net or from local directories.

a) Command Line Manipulation, Selection, and Chains - Part 1

Favorites»Command Line

Activates the *command line* panel.

The *chimera* window includes a
Menu bar across the top,
A graphics window,
A command line, and
A status line.



Syntax

Command: type in the command line text field for *command line* interface.

Open a structure: *Command: open 1zik*

The structure is a leucine zipper formed by two peptides.

Command Line History:

The ▼ button next to the *command line* can be used to retrieve your previous commands.

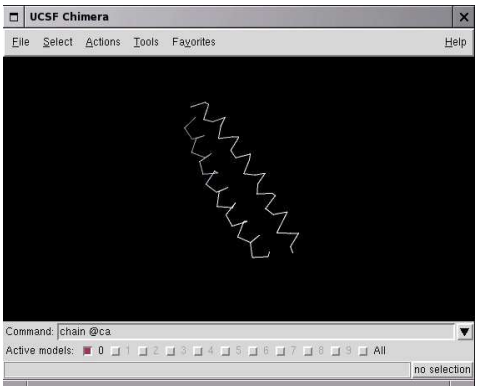
Side View: *Favorites»Side View*

Opens the *side view* window, a miniature version of the display, which shows the relationship between the eye position, the displayed item(s), and the clipping planes. By default, the miniature is shown at full resolution, with colors and representation types the same as the main display. Setting Resolution to low simplifies the miniature to only the backbone of any peptide and nucleic acid residues shown in the main display. In the low-resolution version, surfaces and objects are indicated by bounding box outlines. Using low resolution is recommended if performance seems slow.

Try moving the eye position (the small square; scales the view) and the clipping plane positions (vertical lines) with the left mouse button.

Simplify the display: *Command: chain @ca*

This command shows only the atoms named CA (alpha carbons) and connects them in the same way that the residues are connected.



Mouse:

Try manipulating the structures in the main graphics window with the mouse. Move the mouse cursor and simultaneously press

- the left mouse button to rotate
- the middle mouse button to XY-translate or
- the middle mouse button + Ctrl to Z-translate

the protein structure. Press the right mouse button while moving the mouse or use the scroll wheel to zoom in or out.

Move and scale the structures with the mouse in the *graphics windo*w and the *side view* as desired throughout the tutorial.

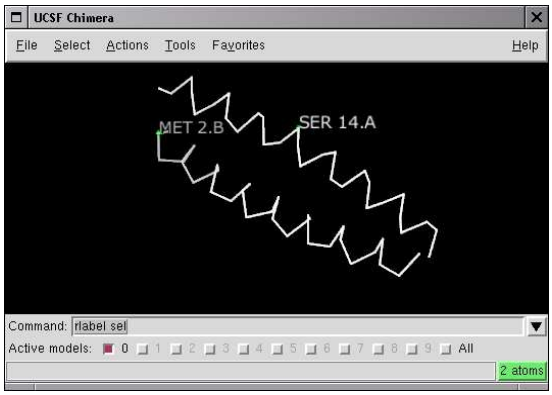
Thicken the lines: *Command: linewidth 2*

Selection:

With the Ctrl key, the mouse buttons have additional functions. By default, picking from the screen (a type of selection) is done by clicking on the atom or bond of interest with the left mouse button while holding down the Ctrl key. To add to an existing selection, also hold down the Shift key. The selection is highlighted in green, and its contents are

reported on the button near the lower right corner of the graphics window. Try picking two alpha carbons, one from each peptide (Ctrl + Shift + left mouse button).
Remember that the Shift key is needed to select both atoms; otherwise, only the most recent selection will be retained.

Labeling:
In the command line, a selection is specified by the word ***selected***, ***sel***, or ***picked***. To label the atoms you have selected:

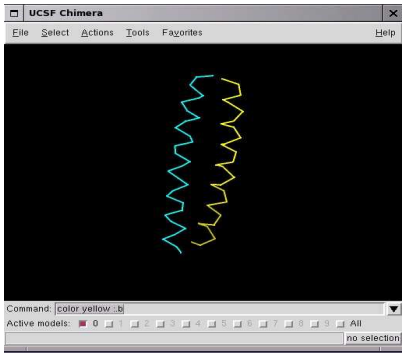


Command:rlabel sel

Each label is of the form:
atom_name (res_name res_number.chain)
It is now evident that one peptide is chain A, and the other is chain B.
To deselect the atoms, pick in a region of the graphics window away from any atoms or use the menu item
Select»Clear Selection.

To un-display the labels:
Command: ~rlabel

Specifying Chains:
One possibility is to color the two chains with different colors:



Command: color cyan :.a
Command: color yellow :.b

Chimera labels water molecules as if they were another chain:
Command: disp : HOH

It displays the water (only the oxygen are visible in the X-ray structure).
To get rid of everything except the A chain displaying all of it atoms:
Command: show :.a

To show the backbone of the A chain only (if the chain is not specified "***:.a***" then the backbones of both chains would have been displayed):

Command: chain :.a@n,ca,c

To display all the atoms:

Command: disp

To color all the atoms by the type of their elements:

Command: color byelement

The models, which are activated for motion, are shown below the command line, 0 should be in **bold** and the box next to it should be *highlighted*. Clicking the box turns off the highlighting and inactivates the model. Clicking the box again can restore it.

To close a model:

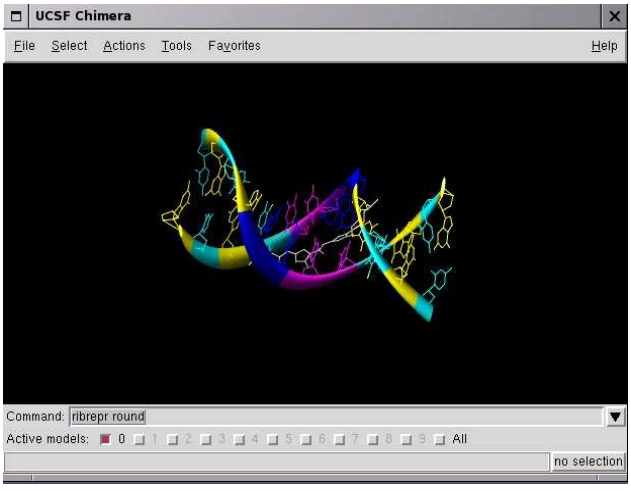
Command: close 0

b) Command Line Manipulation, Selection, and Chains - Part 2

Open another structure:

Command: open 6bna

Color the different nucleotides with different colors, and specify them by residue name:



Command: color blue :DA

Command: color magenta :DT

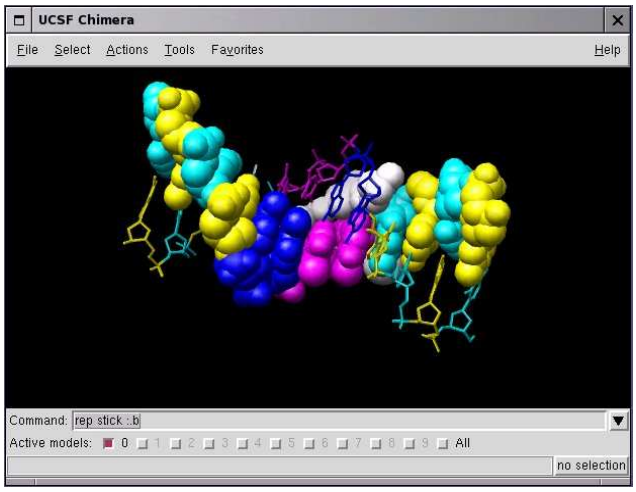
Command: color yellow :DG

Command: color cyan :DC

Un-display the water; *command: ~disp : HOH*

Command: ribbon
Command: ribrepr round

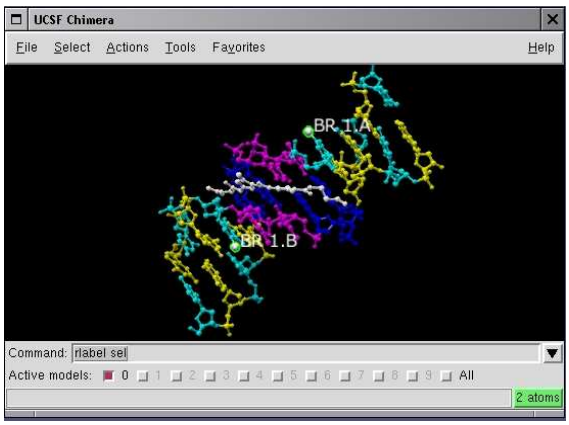
Next, try some alternate representations. Multiple representation types can be combined with each other and with surfaces (more on surfaces below).



Command: ~ribbon
Command: represent stick
Command: repr sphere
Command: rep stick :.b

The latter command changes only chain B to the stick representation, with the rest remaining in the sphere representation. Note that commands (but not their keyword arguments) can be truncated to unique identifiers. For example, the command *represent* can be shortened to *repr* or *rep*.

Get ball and stick representation
Command: repr bs



In the resulting ball and stick representation, pick (*Ctrl + Left click*) one of the atoms in the white molecule; it will be outlined with green, the default highlighting color.

Command: rlabel picked

Above command will show that the labelled residue is named **NT**. The molecule is netropsin. Other than the white molecule, there are two additional white cytosine residues in the double-helical DNA. Apparently, two additional atoms are attached to these non-standard cytosines. **Pick** and then label these two atoms:

Command: rla picked

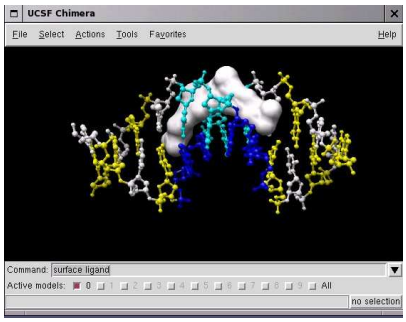
It shows that one DNA strand is chain A, the other strand is chain B, and each strand contains a brominated cytosine.

Use *Select»Clear Selection* to deselect the atoms and then un-display the labels:

Command: ~rla

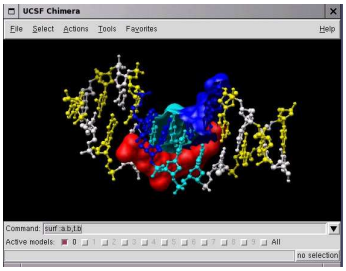
Finally, have some fun with the *surface* command. There are *built-in categories* within structures such as *ligand* (non-solvent, non-ion single residues or bonded sequences of residues no more than ¼ the size (in terms of number of atoms) of the largest bonded sequence of residues in the model) and *main* (all remaining atoms); when nothing is specified, *surface* shows the surface of *main*. Surfaces can be rotated, translated, and scaled interactively.

Command: surface
Command: ~surface
Command: surface ligand or *Command: surface :nt*



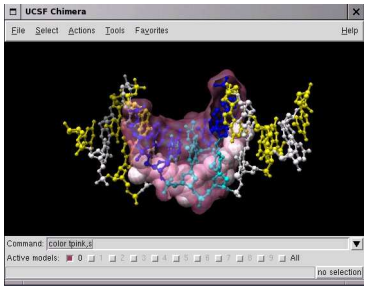
By default, a surface has the same color as the corresponding atoms; however, surface color can be specified separately.

Command: surfrepr mesh
Command: color red,s :nt
Command: surfrepr solid
Command: surf :DA.b,DT.b
Command: surf :DA,DT
Command: repr sphere :nt
Command: color green,s :DT



Sometimes it is helpful to make a solid surface transparent. One way to do this is to define a transparent color and then use the new color in a command:

Command: colordef tpink 1. .5 .7 .4 ***(Don't overlook the spaces!)***
Command: color tpink,s



The numbers in the *colordef* command refer to red, green, blue, and opacity components, respectively. To close the model: *Command: close 0*

c) Menu Molecular Manipulation, Selection, and Chains

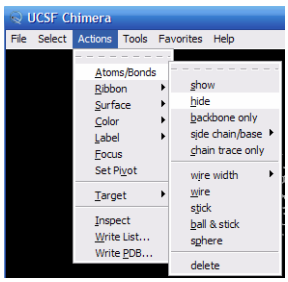
In the following section, you will apply the same operations to the molecules, except that you will use the menu instead of the command line interface.

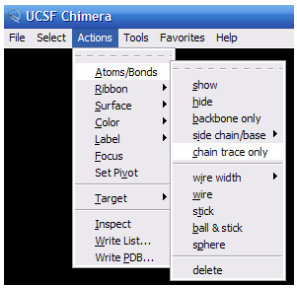
Open a structure:

File»Fetch by ID

Select *PDB* in the *Fetch Structure by ID* dialog and fetch *1zik*.

Simplify the display:





Actions»Atoms/Bonds»Hide

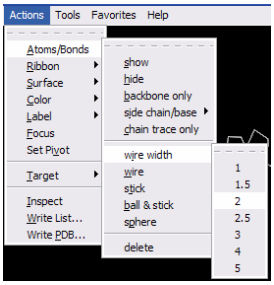
Actions»Atoms/Bonds»backbone only»chain trace

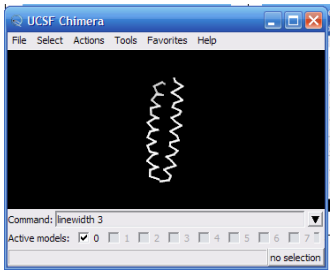
This will show only the CA atoms.

To thicken the lines:

Actions»Atoms/Bonds»wire width» 2

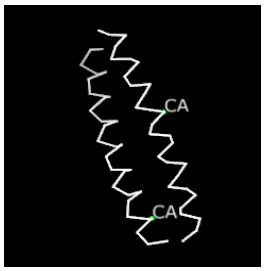
The Actions menu applies to whatever is selected. When nothing is selected, the Actions menu applies to everything

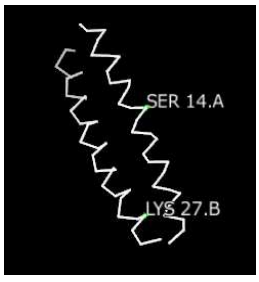




Labeling:

Pick two alpha carbons from each peptide. Label the atoms you have selected, first by atom name, and then by residue name and number:

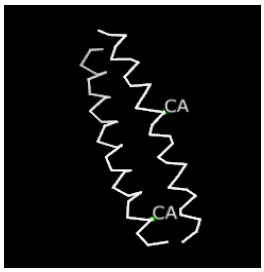


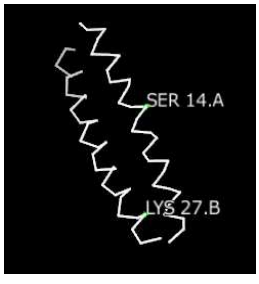


Actions»Label»name

Actions»Label»off

Actions»Label»residue»name + specifier





Same as the last part, it is now evident that one peptide is chain A, and the other is chain B. To deselect the atoms, pick in the region of the graphics window away from any atoms or use the menu item *Select»Clear Selection.*

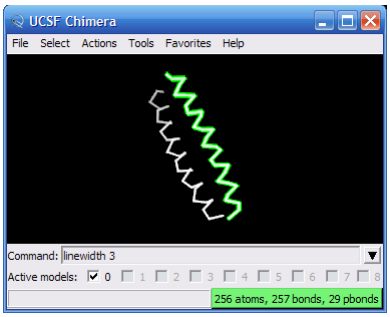
To un-display the residue labels:

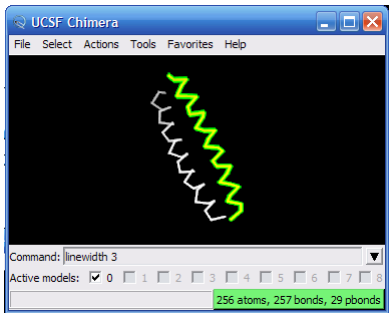
Actions»Label»residue»off

Color the two chains with different colors:

Select»Chain»A

Actions»Color»yellow





Repeat the process to color chain B cyan. Another way to select an entire chain is to pick an atom or bond in the chain and then hit the up arrow key twice, once to expand the selection to the entire residue and another time to expand it to the entire chain

Now select the water molecule as the last part:

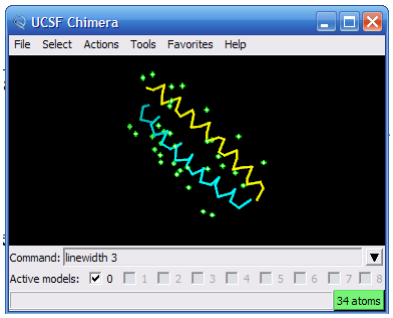
Select»Structure»solvent

Actions»Atoms/Bonds»show

Select»Clear Selection

Alternatively, the water could have been selected using

Select»Residue»name»HOH



To display all atoms of the A chain only:

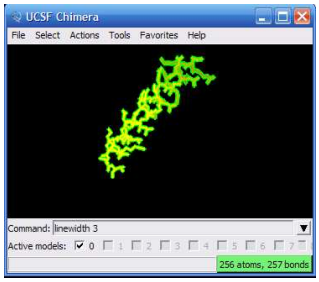
Actions»Atoms/Bonds»hide

Select»Chain»A

Actions»Atoms/Bonds»show

Then to show the backbone only,

Actions»Atoms/Bonds»Backbone only»full



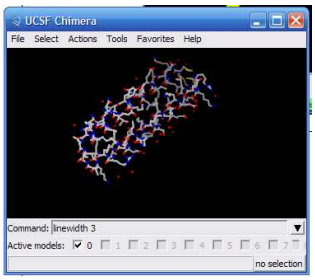
Only the A chain's backbone is displayed because chain A was selected.

To display all the atoms and to color them according to element:

Select»Clear Selection

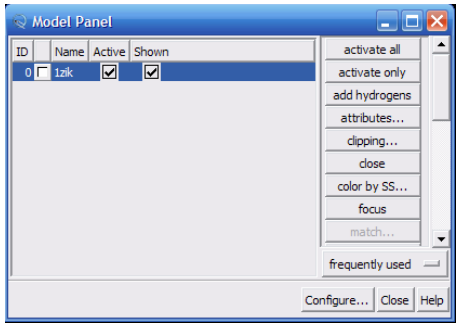
Actions»Atoms/Bonds»show

Actions»Color»by element



There is a checkbox in the Active column of the **Model Panel**

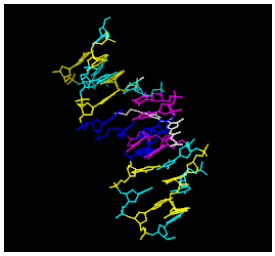
Tools»General Controls»Model Panel, or
Favorites»Model Panel



It shows that the model is activated for motion; unchecking the box inactivates the model. It can be restored by checking the box again. Close the model by highlighting **1zik** on the left side of the **Model Panel**, and then click **close** on the right.

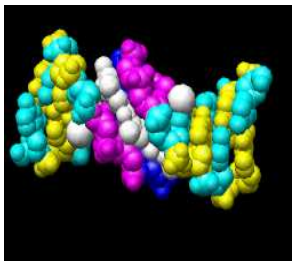
d) Menu Molecular Representations and Surfaces

Open another structure:
File»Fetch by ID. In the resulting **dialog**, select PDB and fetch *6bna*.
Try coloring the different nucleotides with different colors. For example, color the adenosine (DA) residues blue:

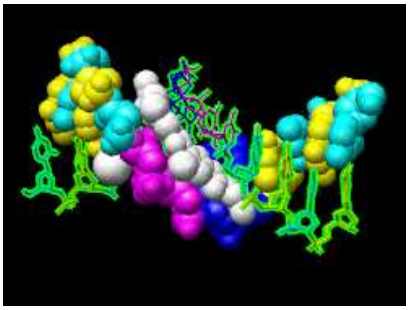


Select»Residue»DA
Actions»Color»blue

Analogously, color cytosine (**DC**) residues cyan, guanine (**DG**) residues yellow, and thymine (**DT**) residues magenta. Undisplay the water (the white dots) as you did in the last part.
Next, try some alternate representations.



Select»Clear Selection
Actions»Ribbon»show
Actions»Ribbon»hide
Actions»Atoms/Bonds»stick
Actions»Atoms/Bonds»sphere

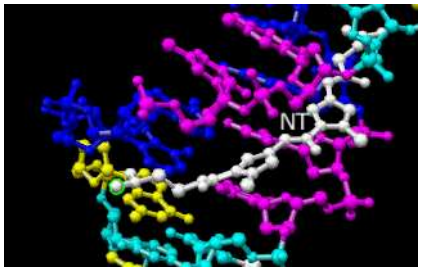


Change the representation of only one of the DNA strands, chain B:

Select»Chain»B
Actions»Atoms/Bonds»stick
Next, change everything to a ball-and-stick representation:
Select»Clear Selection Actions»Atoms/Bonds»ball & stick

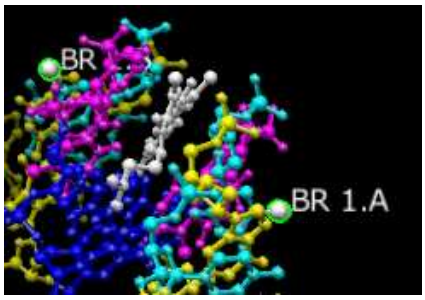
In this representation, pick one of the atoms in the white netropsin molecule. Label the residue by residue name:

Actions»Label»residue»name



Since it is a residue label, the label may be closer to other parts of the residue than to the selected atom. Remove the label:

Actions»Label»residue»off



The first submenu under Label controls individual atom labels, while the second controls residue labels. *Actions»Label»name* would have shown the name of the atom instead of the name of the residue. Other than the white molecule, there are two additional white cytosine residues in the double-helical DNA. Apparently, two additional atoms are attached to these non-standard cytosines. **Pick** and then label these two atoms:

Actions»Label»residue»name + specifier

It shows that one DNA strand is chain A, the other strand is chain B, and each strand contains a brominated cytosine. Use *Select»Clear Selection* to deselect the atoms and then un-display the labels.

Actions»Label»residue»off

Actions»Label»off

Finally, have some fun with surfaces:

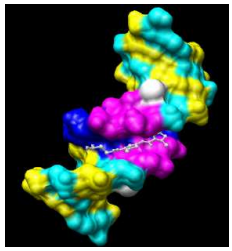
Actions»Surface»show

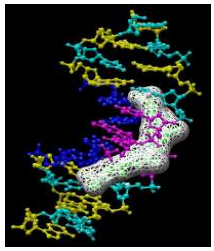
Actions»Surface»hide

Select»Structure»ligand

Actions»Surface»show

Actions»Surface»mesh





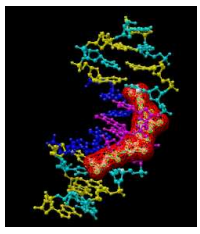
By default, a surface has the same color as the corresponding atoms; however, surface color can be specified separately.

To change the surface color of only netropsin (which is still selected)

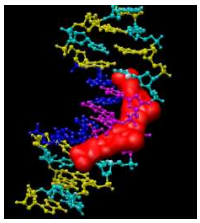
Actions»Color»surfaces to change the coloring target

Actions»Color»red

Actions»Color»all of the above to restore the default coloring target.

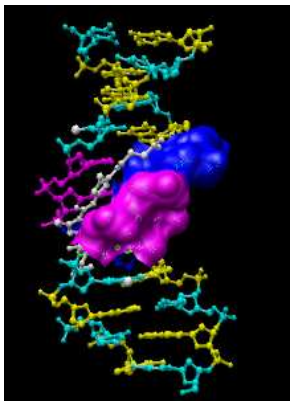


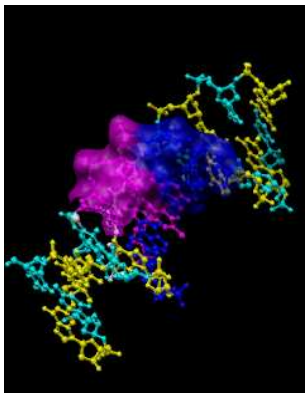
Clear the selection, change back to solid surface, and then un-display the surface:



Select»Clear Selection
Actions»Surface»solid
Actions»Surface»hide

As an example of a more complicated selection process, show the surface of the adenine and thymine in chain B only:





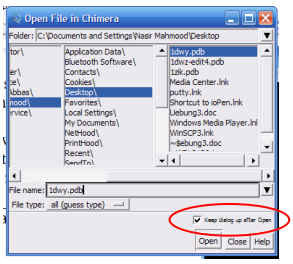
Select»Selection Mode»append (to change selection mode)
*Select»Residue»name»**DA***
*Select»Residue»name»**DT***
Select»Selection Mode»intersect (to change selection mode)
Select»Chain»B
Action»Surface»show
To prepare for any future commands, restore the selection mode and clear the selection:
Select»Selection Mode»replace
Select»Clear Selection
Sometimes, it is helpful to make a solid surface transparent:
Actions»Surface»transparency»50%
This is the end of this section. You can close the model. At this point, you can decide, which is easier to operate ? The menus or command-line ?

The Model Panel Tutorial

This tutorial introduces one of the most useful windows in *chimera*, and gives a little more information on how the *chimera* data-model works. The aim is to analyze a PDB file containing an ensemble of models that have been generated from NMR data.
From NMR data, one does not usually have a single structure. Instead, one often has a group (ensemble) of possible structures. This tutorial focuses on using the **Model Panel** and handling ensembles of structures (such as those determined by NMR). Note that the **Model Panel** is generally useful whether or not ensembles are being viewed.

You will work on two PDB files, which contain NMR-determined structures of a bovine prion protein fragment. *1dwz* contains an ensemble of 20 structures, whereas *1dwy* is a single representative minimized structure.

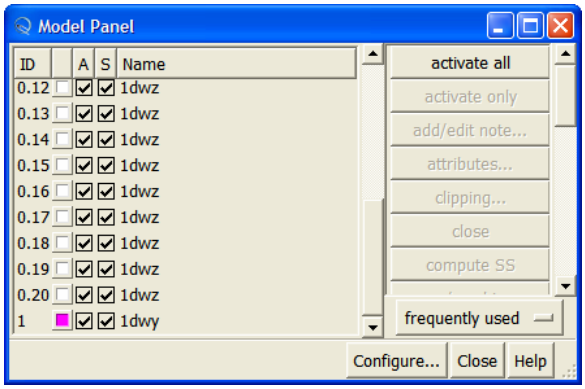
Make the window a convenient size, then choose the menu item *File»Fetch by ID*.



In the resulting *dialog*, select *PDB,* check the box '*Keep dialog up after Fetch* so that the dialog does not disappear and then fetch *1dwz* and *1dwy*. Click *Close* to also dismiss the *dialog*.

Thicken the lines: *Actions»Atoms/Bonds»wire width»3*. The structure includes all atoms, even the hydrogens. Simplify the display using *Actions»Atoms/Bonds»backbone only»full*. Now, only the N, CA, and C atoms are shown.

Open the Model Panel (*Favorites»Model Panel*). Each file of coordinates opened in *chimera* becomes a model with an associated model ID number and model-level color. Some PDB files are further subdivided into multiple structures designated with MODEL and ENDMDL records; when the input file contains more than one set of such records, sub-model numbers are assigned sequentially starting with 1. In this case, the 20 ensemble members in *1dwz* are sub-models 1-20 of model 0. Each sub-model (0.3, for example) can be treated as a separate model. Thus, "models" will be used to indicate sub-models and/or models that are not subdivided into sub-models. By default, the Model Panel shows the model-level colors behind the names.



Once one or more models have been chosen within the left side, any of several functions represented by buttons on the right side may be executed. At first, most buttons are grayed out since no model has been chosen in the left side of the panel. Individual models or blocks of models may be chosen (highlighted) using the left mouse button. Ctrl-Click adds to an existing choice rather than replacing it. To highlight a block of models without having to hold down the mouse button, click on the first (or last) and then Shift-Click on the last (or first) in the desired block. Click on *1dwy* in the left side of the Model Panel and then try various functions on the right side:

show only hide the other models

trace chains display the chain trace, which includes only CA atoms

show all atoms display all atoms

select select the entire model for further operations

Complete the follow steps in the menu:

Actions»Color»by element

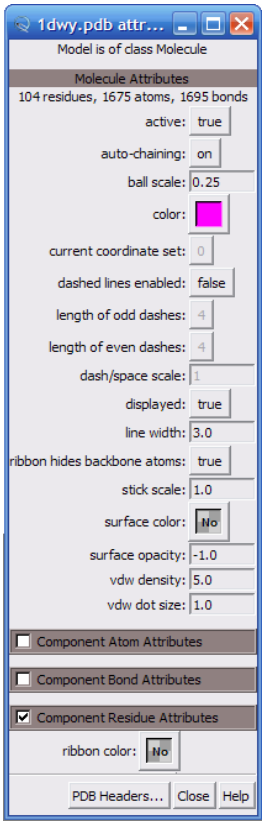
Select»Chemistry»element»H

Actions»Atoms/Bonds»hide

Select»Clear Selection (important, or else the invisible hydrogens will still be selected)

Back to the **Model Panel**:

sequence opens a **sequence panel** for the model; Click-Select one or a string of residues in the sequence and see how the corresponding residues of the structure become selected. Next, **Close** the panel and perform some action in the menu upon the new selection, such as:



Actions»Atoms/Bonds»sphere

Select»Clear Selection

Back to the **Model Panel**:

attributes opens a **molecule model attributes panel**; Click on the **Component Residue Attributes**:

set **ribbon display** to **on**

set **ribbon cross section** to **round**

set **ribbon display** back to **off**

click **Close** to dismiss the panel

uncheck the **Shown** checkbox for *1dwy*

check the **Shown** checkbox for *1dwy*

Note that using the **Shown** checkbox is not the same as using the command **display**, which works on individual atoms and bonds; instead, it enables/disables the whole model's display. Checking **Shown** enables the display, but the display settings of individual atoms and bonds are not changed; in this example, the hydrogens are still un-displayed, as they were before the model was hidden. Toggling checkmarks in the **Shown** column is the same as using the **hide** and **show** buttons; toggling checkmarks in the **Active** column is the same as using **activate** and **deactivate** buttons. By default, these buttons are not included on the right side of the **Model Panel** because they are classified as **infrequently used**.

uncheck the **Active** checkbox for *1dwy* deactivate the model for motion (so it cannot be moved with the mouse) *check* the **Shown** checkbox for all of the models. Move the four sub-models of 0 so that they do not overlap with model 1

(which is deactivated and will not move). Scaling the view down with the mouse or **Side View** may be helpful.

check the **Active** checkbox for *1dwy*

Choose sub-model #0.1 in the **Model Panel**, **select** it, and use the **Actions** menu to color it. Repeat the process with the three other sub-models (choosing different colors), then clear the selection (*Select»Clear Selection*) and **Close** the **Model Panel**.

4. Summary

The first two introductory tutorials for *chimera* introduce you to:

- Menu and mouse driven selection and the *comman*d *lin*e equivalents for specifying the rendering style of an atom or molecule.
- Another way of rendering molecules, by *molecular surfaces*.
- The concept of atom specification.
- The different states that a particular model or set of models may have (active, inactive, hidden, displayed).
- Handling of ensembles of structures (such as those determined by NMR).ensembles of structures (such as those determined by NMR).

5. Assignment

Please answer the following questions in a brief written report and bring it with you on ***November 6, 2012***. The students to present the answers will be selected randomly.

a) Which part of the double stranded DNA does Netropsin bind? (6P)
b) What is the difference between *label* and *rlabel* commands? (6P)
c) What does #0:1-50.a@C mean? (6P)
d) If you use the program *Chimera*, what representation would you pick in order to see the secondary structure? (6P)
e) Name and describe the different surface styles used in *Chimera* to represent the surface of a structure. (6P)

UCSF Chimera Quick Reference Guide

January 2011

Commands (*reverse function ~**command** available)

2dlabels	create labels with text, symbols, and arrows in 2D
ac	enable accelerators (keyboard shortcuts)
addaa	add an amino acid to a peptide C-terminus
addcharge	assign partial charges to atoms
addh	add hydrogens
*alias**	create an alias or list the existing aliases
align	align two atoms or sets of atoms along the line of sight
angle	measure a bond angle or torsion angle
*aniso**	show thermal ellipsoids
*aromatic**	show ring aromaticity
*bond**	add/delete bonds
*bondcolor**	color bonds independently from atoms
*bondzone**	make zoning tools use points along bonds
cd	change the working directory
center	center the view on specified atoms
chain	chain specified atoms, undisplay the others
chirality	report the R/S configuration of a chiral center
*clip**	move clipping planes
close	close a model
*cofr**	report or change the center of rotation
*color**	color atoms/bonds, ribbons, labels, molecular surfaces
colordef	define a new color
combine	combine molecule models into a single model
conic	create a shadowed space-filling image
coordset	play through frames of a trajectory
copy	save an image (Chimera graphics or POV-Ray)
coulombic	color molecular surfaces by Coulombic electrostatics
crystalcontacts	identify clashes between PDB symmetry copies
defattr	assign attribute values to atoms, residues, or models
*define**	calculate axes, planes for sets of atoms
delete	delete atoms and bonds
*display**	display specified atoms
*distance**	measure the distance between two atoms
echo	send text to the status line and Reply Log
export	save the scene (x3d, vrml, pov-ray, renderman, obj)
*fillring**	show rings as filled
*findclash**	identify clashes and/or contacts
*findhbond**	(*hbonds*) identify possible hydrogen bonds
fly	smoothly traverse a series of saved positions
*focus**	adjust the view and center of rotation
freeze	stop all motion
getcrd	report untransformed coordinates
help	display the manual page for a command
hkcage	create icosahedron as hexagon/pentagon mesh
intersurf	generate and display interface surfaces
ksdssp	determine secondary structure from protein coordinates
*label**	display atom labels
labelopt	control the information in atom labels
lighting	adjust lighting and shininess
linewidth	control the width of wire bonds
*longbond**	show/hide pseudobonds representing missing segments
mask	extract volume data bounded by surfaces
match	superimpose two models using specified atoms
matchmaker	(*mmaker*) align models in sequence, then in 3D
matrixcopy	apply the transformation matrix of one model to another
matrixget	write the current transformation matrices to a file
matrixset	read and apply transformation matrices from a file
*mclip**	control per-model clipping
mcopy	copy settings from one molecule model to another
measure	perform calculations on structures, surfaces, maps
meshmol	create a "molecule" to show surface mesh as sticks
minimize	energy-minimize structures
modelcolor	set color at the model level
*modeldisplay**	set display at the model level
molmap	create a density map from atomic coordinates
morph	create a morph trajectory from two or more structures
move	translate along the X, Y, or Z axis
movie	capture image frames and assemble them into a movie
*msc**	color multiscale surfaces to match atoms
namesel	name and save the current selection
neon	create a shadowed stick/tube image (not on Windows)
*nucleotides**	create special nucleotide representations
*objdisplay**	display graphical objects
*open**	read local files or fetch by ID
pause	pause script execution until the user presses a key
pdbrun	send an annotated PDB file to the system shell
*perframe**	specify an alias to be executed at each display frame
preset	apply a predefined combination of display settings
rainbow	color residues, chains, or models over a range
rangecolor	color over a range according to attribute values
read	execute a command file, updating display at the end
represent	control atom/bond style (wire, stick, bs, sphere)
reset	restore default or saved orientations
*ribbackbone**	allow display of both ribbon and backbone atoms
*ribbon**	display ribbon
*ribinsidecolor**	set a separate color for inside protein helix ribbons
ribrepr	control ribbon style (flat, edged, rounded)
ribscale	control ribbon scaling (Chimera default, licorice)
*rlabel**	display residue labels
rmsd	evaluate the RMSD between specified sets of atoms
rock	rock about the X, Y or Z axis
roll	roll about the X, Y, or Z axis
*rotation**	make a bond rotatable
runscript	run Python script with command-line arguments
save	save the current Chimera session
*savepos**	save the current orientations
*scale**	scale the view
scolor	color surfaces by volume data or geometry
section	move the clipping planes in parallel
segment	act on segmentation models
*select**	activate models for motion or select atoms
*set**	set background color, visual effects, individual rotation
*setattr**	set an attribute to a specified value
shape	create a surface of a specified geometric shape
*show**	display specified atoms, undisplay the others
sleep	pause script execution for a specified time
solvate	add solvent using AmberTools
sop	edit a surface model
split	make chains of a molecule model separate submodels
start	start Chimera tools by name
*stereo**	switch amongst stereo options and mono viewing
stop	exit from Chimera
*surface**	calculate and display molecular surfaces
surfcat	(*msms cat*) group atoms for surface calculations
surfrepr	(*msms repr*) control surface style (solid, mesh, dot)
*surftransparency**	adjust surface transparency
swapaa	mutate amino acids or swap rotamers
swapna	mutate nucleic acid residues
*sym**	generate symmetry-related copies of a structure
system	send a command to the system shell
thickness	move the clipping planes in opposite directions
*tile**	arrange models in a plane
topography	plot values in a volume data plane as surface heights
turn	rotate about the X, Y, or Z axis
*vdw**	display van der Waals (VDW) dot surface
*vdwdefine**	set VDW radii
vdwdensity	set VDW surface dot density
version	show copyright information and Chimera version
viewdock	start ViewDock and load docking results
volume	visualize volume data such as electron density
vop	edit volume data to create a new volume data set
wait	suspend command processing until motion has stopped
window	adjust the view to contain the specified atoms
windoworigin	set graphics window location
*windowsize**	adjust the dimensions of the graphics window
write	save atomic coordinates (pdb, mol2)
writesel	write a list of the currently selected (or unselected) items
zonesel	select atoms/surfs within cutoff of specified atoms/surfs

Miscellaneous Operations (Default Settings)

selection from screen	Ctrl-left mouse button
add/toggle selection	Shift-Ctrl-left mouse button
rotation	left mouse button
XY-translation	middle mouse button
scaling	right mouse button or Side View
preferences	Favorites... Preferences...
searching help	Help... Search Documentation...
reporting a problem	Help... Report a Bug...
mailing list	chimera-users@cgl.ucsf.edu

Specification Symbols

Symbol	Function	Usage
#	model number	# *model* (integer)
#.	submodel number	#. *submodel* (integer)
:	residue	: *residue* (name or number)
::	residue name	:: *residue*
:.	chain ID	:. *chain*
@	atom name	@*atom*
@.	alternate location ID	@. *alt_loc*
–	range	specifies a range of models, submodels, or residues
,	name separator	separates models or residues, ranges of models or residues, or names of atoms
*	whole wildcard	matches whole atom or residue names, *e.g.*,**:*@CA** specifies the alpha carbons of all residues
=	partial wildcard	matches partial atom or residue names, *e.g.*, **@C=** specifies all atoms with names beginning with C
?	single-char wildcard	used for atom and residue names only, *e.g.*, **:G??** selects all residues with three-letter names beginning with G
;	command separator	separates multiple commands on a single line
z<	zone specifier	**z<***zone* or **zr<***zone* specifies all residues within *zone* angstroms, **za<***zone* specifies all atoms (rather than entire residues) within that distance. Using > instead of < gives the complement.
&	intersection	intersection of specified sets
|	union	union of specified sets
~	negation	negation of specified set (when space-delimited)

Selected Atom Attributes

Usage	Description
@/altLoc=*altloc*	alternate location ID
@/areaSAS=*sasa*	solvent-accessible surface area
@/areaSES=*sesa*	solvent-excluded surface area
@/bfactor=*bfactor*	B-factor
@/color=*color*	atom-level color assignment
@/defaultRadius=*rad*	default VDW radius
@/display	whether atom display bit is "on"
@/drawMode=*mode*	*mode* can be 0 (dot, as in wireframe), 1 (sphere, as in CPK), 2 (endcap, as in stick), or 3 (ball, as in ball-and-stick)
@/element=*atno*	atomic number
@/idatmType=*type*	Chimera atom type
@/label	whether the atom is labeled
@/label=*label*	text of the atom label
@/labelColor=*labcolor*	color of the atom label
@/name=*name*	atom name
@/occupancy=*occupancy*	crystallographic occupancy
@/radius=*radius*	current VDW radius
@/serialNumber=*n*	serial number in the input file
@/surfaceCategory=*category*	surface calculation category (main, ligand, *etc.*)
@/surfaceDisplay	per-atom surface display bit (can be true for buried atoms with no surface)

Selected Residue Attributes

Usage	Description
:/areaSAS=*sasa*	solvent-accessible surface area
:/areaSES=*sesa*	solvent-excluded surface area
:/isHet	residues in PDB HETATM records (or the mmCIF equivalent)
:/isHelix	amino acid residues in helices
:/isStrand *or* **:/isSheet**	amino acid residues in beta-strands
:/kdHydrophobicity=*value*	Kyte-Doolittle amino acid hydrophobicity
:/phi=*angle*	protein/peptide backbone phi angle
:/psi=*angle*	protein/peptide backbone psi angle
:/ribbonColor=*ribcolor*	color of the residue's ribbon segment
:/ribbonDisplay	per-residue ribbon display bit (can be true for residues such as water that cannot be shown with ribbon)

Selected Molecule Model Attributes

Usage	Description
#/ballScale=*factor*	ball radius relative to VDW radius
#/color=*color*	model-level color assignment
#/display	model display bit
#/lineWidth=*width*	linewidth of wire representation
#/stickScale=*factor*	stick radius relative to bond radius

Specification Examples

#
- all models

#0
- model 0

#3:45-83,90-98
- residues 45-83 and 90-98 in model 3

:lys,arg
- lysine and arginine residues

:12,14@ca
- alpha carbons in residues 12 and 14

:12:14@ca
- all atoms in residue 12 and the alpha carbon in residue 14

:.A@ca,c,n,o
- peptide backbone atoms in chain A

:50.B,.D
- residue 50 in chain B and all residues in chain D

:12-15,26-28.a,45.b
- residues 12-15 in all chains (except het/water), 26-28 in chain A, and 45 in chain B

#0.1-3,5
- submodels 1-3 of model 0 and all of model 5

#0.1-3,.5
- submodels 1-3 of model 0 and submodel 5 of all models

ligand
- any/all residues automatically classified as ligand

element.S
- all sulfur atoms

@ca/!label and color!=green and color!=red
- atoms named CA which are not labeled, and are not green or red

@/color=yellow or color=blue and label
- atoms that are yellow and atoms that are both blue and labeled

:asn/isHelix
- asparagine residues in alpha helices

#1:asp,glu & #0 z<10
- aspartate and glutamate residues in model 1 within 10 angstroms of model 0

solvent & Ng+ z<3 | solvent & N3+ z<3
- solvent residues within 3 angstroms of guanidinium nitrogens or *sp*3-hybridized, formally positive nitrogens

@/bfactor>50 & ~ solvent & ~ ions
- atoms with B-factor values over 50, excluding solvent and ions